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	Up-regulation
Differentially expressed with *q*<5%	*M*<0	Down-regulation
Non-differentially expressed, *q* of 5% or higher		Insignificant

Orthogonal contrasts examined:		*up*	*down*	*non-diff*
(5 dpi and 15 dpi Syncytium) vs Root	**... Table S1**	page 2	page 189	page 355

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Rank	Description	Sync	Root	M	t	adj.q	B
18	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	11.0	3.3	7.7	33.0	1.2E-6	13.0
23	AT5G64870.1 | expressed protein | chr5:25946764-25948610 REVERSE | Aliases: MXK3.10, MXK3_10	10.4	2.9	7.5	30.0	1.9E-6	12.4
26	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	11.5	4.1	7.4	29.8	1.9E-6	13.1
36	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	10.9	2.1	8.8	27.6	2.6E-6	10.8
37	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	9.2	3.2	6.1	27.4	2.6E-6	14.9
38	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	9.9	2.7	7.3	27.3	2.6E-6	12.3
40	AT3G63140.1 | mRNA-binding protein, putative, similar to mRNA binding protein precursor (GI:26453355) (Lycopersicon esculentum) | chr3:23337347-23339684 REVERSE | Aliases: T20O10.240	8.9	2.5	6.4	27.1	2.6E-6	13.4
47	AT1G64110.2 | AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family | chr1:23800382-23805388 REVERSE | Aliases: F22C12.12, F22C12_12	11.0	3.3	7.7	26.6	2.7E-6	13.9
51	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	9.9	3.8	6.2	25.6	3.3E-6	12.5
66	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	11.5	4.7	6.9	24.0	4.4E-6	11.4
68	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	12.0	5.6	6.4	23.5	5.0E-6	11.5
76	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	11.5	7.0	4.4	22.4	6.6E-6	13.4
77	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	8.5	2.3	6.1	22.3	6.6E-6	13.1
78	AT1G68470.1 | exostosin family protein, contains Pfam profile: PF03016	9.6	3.5	6.2	22.2	6.8E-6	13.3
84	AT1G28400.1 | expressed protein, similar to E6 (GI:1000090) (Gossypium barbadense) | chr1:9972370-9973779 REVERSE | Aliases: F3M18.16, F3M18_16	12.9	10.0	3.0	21.5	8.1E-6	14.5
85	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	9.7	3.7	6.1	21.5	8.1E-6	13.1
90	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 ENDOTRANSGLUCOSYLASE/HYDROLASE 9	10.0	4.1	5.9	21.2	8.5E-6	12.4
93	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	12.7	5.5	7.2	21.1	8.5E-6	11.0
96	AT4G24040.1 | Symbol: ATTRE1 |	9.9	3.8	6.0	21.1	8.5E-6	12.3

Rank	Description	Sync	Root	M	t	adj.q	B
99	AT5G01300.1 | phosphatidylethanolamine-binding family protein, similar to cold-regulated protein (Hordeum vulgare subsp. vulgare) GI:10799810; contains Pfam profile PF01161: Phosphatidylethanolamine-binding protein	9.1	2.5	6.6	20.9	9.0E-6	10.9
104	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	10.4	2.9	7.4	20.4	1.0E-5	11.5
106	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	10.9	5.5	5.4	20.4	1.0E-5	11.5
120	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	9.8	5.9	3.9	19.7	1.2E-5	13.0
124	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	7.8	2.6	5.3	19.4	1.3E-5	11.2
134	AT2G42570.1 | expressed protein | chr2:17724453-17727158 REVERSE | Aliases: F14N22.16, F14N22_16	9.1	5.2	3.9	18.6	1.6E-5	12.5
135	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 GI: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	8.6	3.5	5.1	18.6	1.6E-5	11.6
137	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	10.5	3.8	6.7	18.6	1.6E-5	10.9
140	AT3G52180.2 | similar to protein phosphatase-related [Arabidopsis thaliana] (TAIR:At3g10940.1); similar to unknown protein [Oryza sativa (japonica 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)	9.1	4.2	4.9	18.5	1.6E-5	11.7
146	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	11.9	5.5	6.4	18.3	1.7E-5	12.4
149	AT5G54270.1 | Symbol: LHCB3 | chlorophyll A-B binding protein / LHCII 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	4.5	6.8	18.0	2.0E-5	11.6
151	AT4G15910.1 | Symbol: ATDI21 |	11.4	7.6	3.8	18.0	2.0E-5	12.2
154	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	11.1	4.1	7.0	17.9	2.0E-5	11.2
155	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	3.6	3.8	17.8	2.0E-5	11.7
158	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	4.2	4.7	17.7	2.1E-5	11.4
162	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	8.9	3.3	5.6	17.4	2.4E-5	10.2
164	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	10.4	6.7	3.7	17.4	2.4E-5	12.3
166	AT4G38370.1 | phosphoglycerate/bisphosphoglycerate mutase family protein, contains Pfam profile PF00300: phosphoglycerate mutase family | chr4:17969521-17971289 REVERSE | Aliases: F22I13.140, F22I13_140	8.6	3.5	5.2	17.3	2.4E-5	10.7
168	AT3G23325.1 | splicing factor, putative, similar to Splicing factor 3B subunit 10 (SF3b10) (Pre-mRNA splicing factor SF3b 10 kDa subunit) (Swiss-Prot:Q9BWJ5) (Homo sapiens) | chr3:8345778-8347056 FORWARD | Aliases: None	9.8	4.4	5.3	17.2	2.5E-5	10.3

Rank	Description	Sync	Root	M	t	adj.q	B
169	AT4G17600.1 | Symbol: LIL3:1 |	9.8	3.2	6.7	17.2	2.5E-5	9.0
175	AT1G68585.1 | expressed protein | chr1:25760521-25761532 FORWARD | Aliases: None	7.4	3.4	4.1	17.1	2.5E-5	11.4
176	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	8.8	3.6	5.2	17.0	2.6E-5	10.4
187	AT3G23940.1 | dehydratase family, contains Pfam profile: PF00920 dehydratase family | chr3:8648712-8652564 FORWARD | Aliases: F14O13.18	11.1	7.2	4.0	16.8	2.8E-5	11.9
189	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	7.6	4.1	3.5	16.7	2.8E-5	11.8
190	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	3.7	5.5	16.7	2.8E-5	10.0
193	AT1G73177.1 | expressed protein | chr1:27520248-27521515 REVERSE | Aliases: None	8.0	4.7	3.4	16.7	2.8E-5	12.2
194	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	9.8	4.5	5.3	16.7	2.8E-5	10.6
195	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	9.2	1.7	16.7	2.8E-5	13.3
199	AT5G62610.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	9.2	5.0	4.2	16.6	2.8E-5	11.7
200	AT1G32900.1 | starch synthase, putative, similar to starch synthase SP:Q42857 from (Ipomoea batatas) | chr1:11920371-11923746 REVERSE | Aliases: F9L11.8, F9L11_8	8.3	3.1	5.2	16.6	2.8E-5	11.1
201	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	8.2	2.6	5.6	16.6	2.8E-5	10.1
202	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	9.0	3.9	5.2	16.6	2.8E-5	9.8
203	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	9.2	4.1	5.1	16.6	2.8E-5	11.0
205	AT5G16060.1 | expressed protein | chr5:5246125-5247434 FORWARD | Aliases: F1N13.200, F1N13_200	11.5	7.9	3.6	16.5	2.8E-5	12.2
206	AT5G02240.1 | expressed protein | chr5:451421-453155 FORWARD | Aliases: T1E22.5	12.3	8.6	3.7	16.5	2.9E-5	12.1
208	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	8.5	3.1	5.4	16.4	2.9E-5	10.0
209	AT4G30950.1 | Symbol: FAD6 | omega-6 fatty acid desaturase, chloroplast (FAD6) (FADC), identical to GI:493068	10.2	4.5	5.7	16.4	3.0E-5	11.6
212	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	12.2	8.5	3.6	16.2	3.2E-5	11.8

Rank	Description	Sync	Root	M	t	adj.q	B
213	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	2.2	5.4	16.2	3.2E-5	9.4
222	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	11.5	3.8	7.8	15.9	3.6E-5	10.5
223	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	8.4	2.4	6.0	15.8	3.7E-5	9.7
227	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) (RPB7.0) (RPB10alpha) {Homo sapiens}; contains Pfam profile PF03604: DNA directed RNA polymerase, 7 kDa subunit | chr5:16441278-16442180 FORWARD | Aliases: MEE6.8, MEE6_8	10.6	8.6	2.0	15.8	3.7E-5	12.7
228	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	10.3	5.5	4.7	15.7	3.8E-5	11.3
229	AT1G55490.2 | Symbol: CPN60B |	11.1	5.9	5.3	15.7	3.9E-5	10.1
233	AT5G48220.1 | indole-3-glycerol phosphate synthase, putative, similar to SP:P49572 | chr5:19567071-19569460 FORWARD | Aliases: MIF21.11, MIF21_11	8.1	4.4	3.7	15.6	3.9E-5	11.1
240	AT5G17170.1 | rubredoxin family protein, contains Pfam profile PF00301: Rubredoxin | chr5:5649205-5651160 FORWARD | Aliases: MKP11.2, MKP11_2	8.4	3.6	4.8	15.5	4.1E-5	9.6
241	AT1G28110.2 | Symbol: SCPL45 |	9.7	5.2	4.5	15.5	4.1E-5	11.2
242	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	7.6	3.3	4.2	15.5	4.1E-5	10.6
243	AT2G43780.1 | expressed protein | chr2:18143521-18143724 REVERSE | Aliases: F18O19.11	10.9	8.6	2.2	15.5	4.1E-5	12.5
244	AT5G05710.1 | pleckstrin homology (PH) domain-containing protein, similar to AtPH1 (Arabidopsis thaliana) GI:5926716; contains Pfam profile PF00169: PH domain	10.2	5.9	4.3	15.4	4.1E-5	10.9
250	AT1G27435.1 | expressed protein | chr1:9527561-9528865 REVERSE | Aliases: None	11.0	8.3	2.7	15.3	4.3E-5	11.6
252	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	8.2	3.5	4.8	15.3	4.3E-5	9.5
253	AT5G06210.1 | RNA-binding protein, putative, contains similarity to RNA-binding protein from (Nicotiana tabacum) GI:15822703, (Nicotiana sylvestris) 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	9.7	6.1	3.5	15.2	4.3E-5	11.3
255	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	9.5	2.2	7.3	15.2	4.3E-5	9.3
259	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	7.0	2.5	4.5	15.1	4.5E-5	10.3
267	AT4G39235.1 | expressed protein | chr4:18268043-18269320 FORWARD | Aliases: None	7.1	3.0	4.1	15.0	4.7E-5	10.8
269	AT4G30800.1 | 40S ribosomal protein S11 (RPS11B), ribosomal protein S11, Arabidopsis thaliana,PIR2:C35542 | chr4:15001173-15002677 FORWARD | Aliases: T10C21.1	8.1	3.9	4.2	15.0	4.7E-5	10.2
277	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	9.5	5.0	4.5	14.8	5.0E-5	10.5

Rank	Description	Sync	Root	M	t	adj.q	B
280	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	9.0	4.5	4.5	14.8	5.1E-5	10.0
281	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	9.5	3.1	6.4	14.7	5.2E-5	9.4
282	AT1G76450.1 | oxygen-evolving complex-related, SP:Q9S720; contains a PsbP domain | chr1:28689465-28691614 FORWARD | Aliases: F15M4.5	7.0	1.8	5.3	14.7	5.2E-5	10.2
284	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	8.6	3.6	5.0	14.7	5.2E-5	9.1
289	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	10.3	3.6	6.7	14.5	5.6E-5	10.9
293	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	9.8	6.1	3.7	14.4	5.9E-5	10.4
295	AT1G73940.1 | expressed protein | chr1:27801974-27803248 REVERSE | Aliases: F2P9.19, F2P9_19	10.1	5.5	4.7	14.4	5.9E-5	11.4
296	AT3G48930.1 | Symbol: EMB1080 | 40S ribosomal protein S11 (RPS11A) | chr3:18151756-18153251 REVERSE | Aliases: EMB1080, EMBRYO DEFECTIVE 1080, T2I13.230	11.6	9.1	2.5	14.4	5.9E-5	12.0
297	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 protile PF00155 aminotransferase, classes I and II	8.4	3.6	4.8	14.4	5.9E-5	9.4
298	AT1G08430.1 | expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	7.2	3.2	4.1	14.3	6.0E-5	9.9
300	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	8.6	4.7	3.9	14.3	6.2E-5	10.0
301	AT3G51820.1 | chlorophyll synthetase, putative, identical to gi:972938 putative chlorophyll synthetase from Arabidopsis thaliana | chr3:19226980-19230027 REVERSE | Aliases: ATEM1.7, ATG4	10.2	5.6	4.6	14.3	6.2E-5	9.8
304	AT2G43710.2 | Symbol: SSI2 | acyl-(acyl-carrier-protein) desaturase / stearoyl-ACP desaturase (SSI2), identical to gi:15149310; contains Pfam profile PF03405: Fatty acid desaturase; identical to cDNA stearoyl ACP desaturase (SSI2), SSI2-FAB2 allele, GI:15149309 | chr2:18127039-18129966 FORWARD | Aliases: F18O19.18, FAB2	9.3	5.2	4.1	14.2	6.3E-5	10.9
305	AT4G21610.1 | Symbol: LOL2 | zinc finger protein, putative, similar to zinc-finger protein Lsd1 (Arabidopsis thaliana) gi:1872521:gb:AAC49660	8.6	4.3	4.3	14.2	6.3E-5	10.1
306	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	13.4	10.9	2.5	14.2	6.3E-5	11.8
309	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) GI: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	8.8	4.5	4.3	14.2	6.4E-5	9.8
310	AT1G79260.1 | expressed protein | chr1:29818154-29819202 FORWARD | Aliases: YUP8H12R.14, YUP8H12R_14	7.8	2.3	5.5	14.2	6.4E-5	10.2
313	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	6.8	3.6	3.3	14.1	6.7E-5	10.5
315	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	9.1	5.4	3.6	14.0	6.7E-5	10.6
323	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	9.2	5.6	3.7	14.0	6.7E-5	10.6

Rank	Description	Sync	Root	M	t	adj.q	B
326	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	9.1	5.2	3.9	13.9	6.9E-5	9.9
330	AT5G40370.1 | glutaredoxin, putative, similar to glutaredoxin (Ricinus communis) SWISS-PROT:P55143 | chr5:16164833-16166382 REVERSE | Aliases: MPO12.80, MPO12_80	13.1	10.5	2.5	13.8	7.2E-5	11.5
331	AT1G15820.1 | Symbol: LHCB6 | chlorophyll A-B binding protein, chloroplast (LHCB6), nearly identical to Lhcb6 protein (Arabidopsis thaliana) GI:4741960; contains Pfam profile PF00504: Chlorophyll A-B binding protein | chr1:5446123-5447776 REVERSE | Aliases: CP24, F7H2.16, F7H2_16, LHCB6	9.7	4.0	5.7	13.8	7.2E-5	9.2
336	AT3G55170.2 | 60S ribosomal protein L35 (RPL35C), various ribosomal L35 proteins | chr3:20463946-20465316 REVERSE | Aliases: T26I12.50	9.3	6.1	3.2	13.8	7.3E-5	10.3
338	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	11.1	8.2	2.8	13.7	7.5E-5	11.4
339	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	8.1	2.8	5.3	13.7	7.5E-5	9.9
341	AT1G28395.3 | expressed protein | chr1:9969428-9971504 REVERSE | Aliases: None	8.1	3.6	4.5	13.7	7.6E-5	10.5
342	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	8.8	4.6	4.2	13.7	7.6E-5	10.7
343	AT2G16890.2 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:7323971-7326263 FORWARD | Aliases: F12A24.7, F12A24_7	9.8	4.1	5.7	13.7	7.6E-5	10.1
351	AT1G11430.1 | plastid developmental protein DAG, putative, similar to DAG protein, chloroplast precursor (Garden snapdragon) SWISS-PROT:Q38732	9.8	6.5	3.3	13.5	8.3E-5	10.3
354	AT1G53460.1 | expressed protein | chr1:19958158-19960300 REVERSE | Aliases: T3F20.22, T3F20_22	10.1	7.1	3.0	13.5	8.3E-5	10.8
355	AT3G50610.1 | expressed protein | chr3:18790704-18791393 REVERSE | Aliases: T20E23.210	8.2	2.1	6.1	13.4	8.5E-5	8.8
356	AT4G24780.1 | pectate lyase family protein, similar to pectate lyase GP:14289169 from (Salix gilgiana)	11.3	4.5	6.8	13.4	8.5E-5	10.0
359	AT3G09500.1 | 60S ribosomal protein L35 (RPL35A), similar to 60S ribosomal protein L35 GB:AAC27830 | chr3:2916986-2918036 FORWARD | Aliases: F11F8.7	11.6	9.3	2.3	13.4	8.6E-5	11.4
365	AT5G47680.1 | expressed protein, contains Pfam profile PF04243: Protein of unknown function (DUF425) | chr5:19332309-19334748 REVERSE | Aliases: MNJ7.27, MNJ7_27	9.4	5.6	3.8	13.3	8.9E-5	9.9
366	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	8.7	5.7	3.0	13.3	8.9E-5	10.3
368	AT2G36620.1 | 60S ribosomal protein L24 (RPL24A) | chr2:15357486-15358944 REVERSE | Aliases: F13K3.2, F13K3_2	10.6	8.0	2.6	13.3	9.0E-5	11.0
369	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	7.8	3.1	4.8	13.2	9.2E-5	9.0
373	AT5G53880.1 | expressed protein | chr5:21890020-21890529 REVERSE | Aliases: K19P17.4, K19P17_4	9.5	4.1	5.4	13.2	9.4E-5	10.9
375	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	9.4	4.4	4.9	13.2	9.4E-5	9.8
376	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	11.7	7.6	4.1	13.1	9.5E-5	9.6
377	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	9.6	6.1	3.6	13.1	9.6E-5	10.1
379	AT4G35980.1 | expressed protein | chr4:17030575-17031695 REVERSE | Aliases: T19K4.110	8.3	5.0	3.3	13.1	9.6E-5	10.6

Rank	Description	Sync	Root	M	t	adj.q	B
380	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	11.1	7.0	4.1	13.1	9.6E-5	9.6
381	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	8.5	3.7	4.7	13.0	9.9E-5	8.6
383	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	10.6	7.8	2.7	13.0	1.0E-4	11.0
386	AT2G32220.1 | 60S ribosomal protein L27 (RPL27A) | chr2:13685996-13686600 FORWARD | Aliases: F22D22.3, F22D22_3	7.2	2.9	4.3	13.0	1.0E-4	9.8
387	AT3G26070.1 | plastid-lipid associated protein PAP / fibrillin family protein, contains Pfam profile PF04755: PAP_fibrillin | chr3:9527985-9529820 FORWARD | Aliases: MPE11.24	8.3	1.2	7.2	13.0	1.0E-4	6.4
388	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	8.3	1.2	7.2	13.0	1.0E-4	6.4
389	AT4G27380.1 | expressed protein | chr4:13701262-13703156 FORWARD | Aliases: F27G19.4	8.7	4.1	4.5	13.0	1.0E-4	9.7
390	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	7.3	3.3	4.1	13.0	1.0E-4	9.9
391	AT3G24310.1 | Symbol: MYB305 |	8.2	3.8	4.3	13.0	1.0E-4	9.3
393	AT3G62870.1 | 60S ribosomal protein L7A (RPL7aB), 60S RIBOSOMAL PROTEIN L7A - Oryza sativa, SWISSPROT:RL7A_ORYSA | chr3:23253640-23255328 REVERSE | Aliases: F26K9.300	11.9	9.9	2.0	12.9	1.0E-4	11.1
396	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	10.0	6.5	3.5	12.9	1.0E-4	9.7
398	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	6.9	2.8	4.1	12.9	1.0E-4	10.0
405	AT1G74730.1 | expressed protein | chr1:28082592-28084009 FORWARD | Aliases: F25A4.30, F25A4_30	8.0	4.1	3.9	12.8	1.1E-4	9.5
406	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	9.9	5.7	4.2	12.8	1.1E-4	10.0
407	AT5G04310.1 | pectate lyase family protein, similar to pectate lyase GP:14531296 from (Fragaria x ananassa) | chr5:1203204-1207353 REVERSE | Aliases: T19N18.40, T19N18_40	8.0	5.2	2.8	12.8	1.1E-4	10.6
408	AT5G48790.1 | expressed protein | chr5:19797086-19799266 REVERSE | Aliases: K24G6.12, K24G6_12	7.5	3.8	3.7	12.8	1.1E-4	9.5
410	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	10.2	4.7	5.5	12.7	1.1E-4	9.5
411	AT2G38465.1 | expressed protein | chr2:16113341-16113978 REVERSE | Aliases: None	6.6	3.7	2.8	12.7	1.1E-4	10.2
413	AT1G15250.1 | 60S ribosomal protein L37 (RPL37A), almost identical to GB:Q43292 | chr1:5248660-5249457 REVERSE | Aliases: F9L1.46, F9L1_46	9.1	4.9	4.1	12.7	1.1E-4	9.6
415	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	7.7	3.3	4.4	12.7	1.1E-4	9.7
417	AT3G50550.2 | expressed protein, isoform contains a non-consensus AT donor site at intron 1 | chr3:18770444-18771420 FORWARD | Aliases: T20E23.150	9.3	5.6	3.7	12.7	1.1E-4	10.3
422	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	9.1	2.0	12.6	1.1E-4	11.2

Rank	Description	Sync	Root	M	t	adj.q	B
423	AT3G55800.1 | Symbol: SBPASE |	8.0	3.5	4.6	12.6	1.1E-4	8.9
426	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	8.8	2.4	12.6	1.2E-4	10.8
428	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	8.3	4.8	3.6	12.6	1.2E-4	9.9
429	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	12.3	10.0	2.3	12.6	1.2E-4	11.0
433	AT3G01740.1 | expressed protein | chr3:267836-268845 FORWARD | Aliases: F4P13.29	10.7	7.7	3.0	12.5	1.2E-4	10.9
434	AT5G06720.1 | peroxidase, putative, identical to peroxidase (Arabidopsis thaliana) gi:1491617:emb:CAA68212 | chr5:2077430-2079006 REVERSE | Aliases: MPH15.8, MPH15_8	7.4	2.8	4.6	12.5	1.2E-4	9.3
435	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	6.5	3.7	12.5	1.2E-4	10.4
436	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	10.2	5.5	4.6	12.5	1.2E-4	10.1
438	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	12.2	10.3	2.0	12.5	1.2E-4	11.0
439	AT2G37660.1 | expressed protein | chr2:15802392-15804137 REVERSE | Aliases: F13M22.16, F13M22_16	9.5	5.7	3.8	12.5	1.2E-4	9.6
440	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	8.9	4.9	3.9	12.5	1.2E-4	9.9
441	AT2G18400.1 | ribosomal protein L6 family protein | chr2:7996561-7997668 REVERSE | Aliases: T30D6.9, T30D6_9	9.7	6.5	3.1	12.5	1.2E-4	10.0
444	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	5.8	3.3	12.5	1.2E-4	10.2
445	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	8.9	2.7	6.2	12.4	1.2E-4	9.5
446	AT2G30000.1 | expressed protein, contains Pfam domain PF03660: Uncharacterised protein family (UPF0123) | chr2:12810932-12812054 REVERSE | Aliases: F23F1.8, F23F1_8	10.9	8.8	2.1	12.4	1.2E-4	11.0
447	AT5G23460.1 | expressed protein | chr5:7912772-7913498 FORWARD | Aliases: K19M13.9, K19M13_9	9.0	6.0	2.9	12.4	1.2E-4	9.9
449	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	11.2	8.2	3.0	12.4	1.2E-4	10.8
452	AT5G23740.1 | Symbol: RPS11 BETA | 40S ribosomal protein S11 (RPS11C)	11.5	8.8	2.7	12.4	1.2E-4	10.6
454	AT4G01897.1 | expressed protein | chr4:819957-821484 REVERSE | Aliases: None	8.0	4.9	3.2	12.4	1.3E-4	10.2
455	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	8.6	5.4	3.2	12.3	1.3E-4	9.7
457	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	5.8	3.2	2.7	12.3	1.3E-4	10.3
459	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	6.4	3.0	12.3	1.3E-4	10.7

Rank	Description	Sync	Root	M	t	adj.q	B
462	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	8.8	2.8	5.9	12.2	1.3E-4	10.3
463	AT5G64650.1 | ribosomal protein L17 family protein, contains Pfam profile: PF01196 ribosomal protein L17 | chr5:25856586-25858035 REVERSE | Aliases: MUB3.17, MUB3_17	7.5	3.6	4.0	12.2	1.3E-4	9.6
466	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)	9.2	7.3	1.9	12.2	1.4E-4	10.8
468	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	9.6	4.9	4.7	12.2	1.4E-4	8.3
469	AT3G15900.1 | expressed protein | chr3:5376257-5377089 REVERSE | Aliases: MVC8.2	7.1	3.9	3.2	12.2	1.4E-4	9.7
472	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	11.2	8.6	2.6	12.2	1.4E-4	10.6
473	AT1G14620.1 | Symbol: DECOY | expressed protein | chr1:5014749-5016599 REVERSE | Aliases: DECOY, EXGT A2, T5E21.12, T5E21_12, XTR2	8.2	3.6	4.6	12.2	1.4E-4	10.0
475	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	7.3	3.2	4.1	12.1	1.4E-4	8.8
479	AT3G58700.1 | 60S ribosomal protein L11 (RPL11B), ribosomal protein L11, cytosolic, Arabidopsis thaliana, PIR:S49033 | chr3:21722540-21723930 FORWARD | Aliases: T20N10.50	10.1	7.7	2.4	12.1	1.4E-4	10.2
480	AT3G47070.1 | expressed protein | chr3:17348050-17348718 REVERSE | Aliases: F13I12.120	7.9	3.1	4.8	12.1	1.4E-4	8.6
484	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	7.6	4.3	3.4	12.1	1.4E-4	9.9
485	AT3G61100.1 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537 | chr3:22621427-22622296 REVERSE | Aliases: T27I15.190	7.6	2.5	5.1	12.1	1.4E-4	8.0
489	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	9.1	3.4	5.7	12.1	1.4E-4	10.1
493	AT1G80560.1 | 3-isopropylmalate dehydrogenase, chloroplast, putative, strong similarity to 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR GB:P29102 SP:P29102 from (Brassica napus)	10.4	5.4	5.0	12.0	1.4E-4	9.4
495	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	10.5	6.3	4.2	12.0	1.5E-4	9.2
496	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	7.8	5.1	2.7	12.0	1.5E-4	10.1
497	AT3G09970.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 Calcineurin-like phosphoesterase	10.6	8.4	2.2	12.0	1.5E-4	10.4
504	AT4G33560.1 | expressed protein | chr4:16135403-16135917 FORWARD | Aliases: T16L1.50, T16L1_50	6.7	3.2	3.6	11.9	1.5E-4	9.5
505	AT3G05560.2 | 60S ribosomal protein L22-2 (RPL22B), identical to 60S ribosomal protein L22-2 SP:Q9M9W1 from (Arabidopsis thaliana) | chr3:1614221-1615449 FORWARD | Aliases: F18C1.17, F18C1_17	12.4	10.0	2.4	11.9	1.5E-4	10.8
506	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	10.0	4.9	5.1	11.9	1.5E-4	9.0

Rank	Description	Sync	Root	M	t	adj.q	B
508	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	10.6	8.4	2.2	11.9	0.02%	10.4
510	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	9.8	5.8	4.0	11.9	0.02%	9.3
511	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	7.9	3.1	4.8	11.9	0.02%	8.2
512	AT3G44590.2 | 60S acidic ribosomal protein P2 (RPP2D), acidic ribosomal protein P2, maize, PIR:S54179	10.2	7.7	2.5	11.9	0.02%	10.3
514	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	9.8	4.6	5.2	11.9	0.02%	9.4
524	AT3G05810.1 | expressed protein | chr3:1730982-1732390 REVERSE | Aliases: F10A16.10, F10A16_10	7.7	3.4	4.3	11.8	0.02%	8.7
527	AT4G29390.1 | 40S ribosomal protein S30 (RPS30B), RIBOSOMAL PROTEIN S30 - Arabidopsis thaliana,PID:e1358183 | chr4:14464993-14465989 REVERSE | Aliases: F17A13.210, F17A13_210	12.0	10.1	1.9	11.8	0.02%	10.6
528	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	7.2	2.4	11.8	0.02%	10.3
530	AT3G02720.1 | DJ-1 family protein / protease-related, similar to Intracellular Protease (Pyrococcus horikoshii) GI:11513902; contains Pfam profile: PF01965 ThiJ/PfpI family | chr3:586270-588270 FORWARD | Aliases: F16B3.36	7.9	5.7	2.2	11.8	0.02%	10.4
531	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	11.0	5.0	6.0	11.7	0.02%	8.5
534	AT5G06590.1 | expressed protein | chr5:2016646-2018836 FORWARD | Aliases: F15M7.12, F15M7_12	9.1	4.7	4.4	11.7	0.02%	9.2
535	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	7.5	3.2	11.7	0.02%	9.1
536	AT4G19710.2 | bifunctional aspartate kinase/homoserine dehydrogenase, putative / AK-HSDH, putative, similar to gb:X71364 (PIR:S46497) aspartate kinase / homoserine dehydrogenase from Arabidopsis thaliana | chr4:10724865-10729681 FORWARD | Aliases: T16H5.70, T16H5_70	8.9	4.3	4.5	11.7	0.02%	9.1
537	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	10.1	8.2	1.9	11.7	0.02%	10.4
538	AT2G42740.1 | Symbol: RPL16A |	8.5	5.6	2.9	11.7	0.02%	9.8
542	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	8.0	4.9	3.1	11.7	0.02%	9.2
543	AT1G50450.1 | expressed protein | chr1:18691453-18694039 REVERSE | Aliases: F11F12.19, F11F12_19	8.7	4.2	4.5	11.7	0.02%	8.6
544	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	8.1	5.5	2.6	11.7	0.02%	9.9
545	AT1G33810.1 | expressed protein | chr1:12265050-12266827 FORWARD | Aliases: F14M2.27	9.2	4.4	4.8	11.7	0.02%	9.4
550	AT5G18040.1 | expressed protein | chr5:5972421-5974158 FORWARD | Aliases: MCM23.14, MCM23_14	9.7	7.4	2.3	11.6	0.02%	9.9
551	AT3G51030.1 | Symbol: ATTRX1 |	10.8	5.2	5.6	11.6	0.02%	8.8
553	AT4G14385.3 | expressed protein | chr4:8287892-8288669 REVERSE | Aliases: None	8.3	5.8	2.5	11.6	0.02%	9.7
554	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	9.1	5.0	4.1	11.6	0.02%	9.6

Rank	Description	Sync	Root	M	t	adj.q	B
555	AT5G64130.2 | expressed protein | chr5:25681625-25683425 REVERSE | Aliases: MHJ24.11, MHJ24_11	11.9	10.4	1.5	11.6	0.02%	10.5
560	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	9.1	5.2	3.8	11.5	0.02%	9.3
561	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	5.7	2.2	3.5	11.5	0.02%	8.9
562	AT2G27240.1 | expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	7.8	3.5	4.3	11.5	0.02%	8.1
563	AT3G62050.1 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537 | chr3:22989221-22989994 FORWARD | Aliases: T17J13.10	5.3	2.5	2.8	11.5	0.02%	9.6
567	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 SUBUNI, TATA BINDING PROTEIN ASSOCIATED FACTOR 21KDA SUBUNIT	7.5	4.2	3.3	11.5	0.02%	9.3
571	AT3G52580.1 | 40S ribosomal protein S14 (RPS14C), ribosomal protein S14 -Zea mays,PIR2:A30097 | chr3:19514203-19515902 FORWARD | Aliases: F3C22.6	10.6	6.5	4.1	11.5	0.02%	9.8
572	AT1G22270.1 | expressed protein, contains Pfam domain PF03966: Protein of unknown function (DUF343) | chr1:7865482-7866128 FORWARD | Aliases: T16E15.11, T16E15_11	8.6	4.4	4.2	11.5	0.02%	9.4
575	AT1G57540.2 | expressed protein, contains similarity to T-box domain GI:5931592 from (Cynops pyrrhogaster) | chr1:21313995-21315077 REVERSE | Aliases: F25P12.4	9.7	6.3	3.3	11.4	0.02%	9.8
579	AT3G53020.1 | 60S ribosomal protein L24 (RPL24B), 60S ribosomal protein L24, Arabidopsis thaliana, EMBL:AC006282 | chr3:19671545-19673003 REVERSE | Aliases: F8J2.190	12.0	10.3	1.6	11.4	0.02%	10.4
584	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	4.2	3.5	11.4	0.02%	9.9
589	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	6.7	3.1	3.6	11.4	0.02%	8.7
594	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	8.0	3.0	5.1	11.4	0.02%	8.7
599	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	10.2	6.8	3.5	11.3	0.02%	9.8
602	AT1G17380.1 | expressed protein | chr1:5955481-5957205 REVERSE | Aliases: F28G4.16	6.8	2.7	4.1	11.3	0.02%	8.8
603	AT2G40880.1 | Symbol: FL3 27 |	8.1	5.1	3.0	11.3	0.02%	9.5
604	AT3G21110.2 | Symbol: PUR7 | similar to SAICAR synthetase [Nicotiana tabacum] (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, SAIRCAR SYNTHETASE	9.0	5.9	3.1	11.3	0.02%	9.4
606	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	9.1	2.5	11.3	0.02%	9.9
607	AT2G29670.1 | expressed protein | chr2:12689221-12692164 REVERSE | Aliases: T27A16.23, T27A16_23	8.7	4.9	3.8	11.3	0.02%	8.2
608	AT3G18940.1 | clast3-related, contains Prosite PS00626: Regulator of chromosome condensation (RCC1) signature 2; similar to Clast3 protein (GI:9857631) (Mus musculus)	6.3	3.7	2.7	11.2	0.02%	9.4
610	AT5G04850.1 | SNF7 family protein, contains Pfam domain, PF03357: SNF7 family | chr5:1408063-1409893 REVERSE | Aliases: MUK11.17, MUK11_17	10.9	7.8	3.1	11.2	0.02%	9.9

Rank	Description	Sync	Root	M	t	adj.q	B
611	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	7.5	4.0	3.5	11.2	0.02%	9.1
612	AT2G37240.1 | expressed protein, weak similarity to fmHP (GI:22902096) (Takifugu rubripes) | chr2:15647018-15648842 REVERSE | Aliases: F3G5.3, F3G5_3	7.8	4.2	3.6	11.2	0.02%	8.6
614	AT4G37090.2 | expressed protein, similar to hypothetical protein DDB0205993 [Dictyostelium discoideum] (GB:EAL67624.1)	7.3	4.1	3.3	11.2	0.02%	9.3
616	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	10.8	7.0	3.8	11.2	0.02%	9.7
618	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	7.1	2.4	4.8	11.2	0.02%	8.1
621	AT1G29250.1 | expressed protein, contains TIGRFAM TIGR00285: conserved hypothetical protein TIGR00285 | chr1:10223252-10224713 REVERSE | Aliases: F28N24.7, F28N24_7	9.7	6.6	3.1	11.1	0.02%	9.5
622	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	10.1	7.1	3.0	11.1	0.02%	9.4
623	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	7.7	3.8	3.8	11.1	0.02%	8.5
624	AT2G45710.1 | 40S ribosomal protein S27 (RPS27A) | chr2:18838235-18839281 FORWARD | Aliases: F4I18.31	9.2	5.7	3.5	11.1	0.02%	9.4
625	AT3G46970.1 | Encodes a cytosolic alpha-glucan phosphorylase. | chr3:17312379-17317431 REVERSE | Aliases: F13I12.20	8.2	5.1	3.1	11.1	0.02%	9.4
629	AT2G05620.1 | Symbol: PGR5 | expressed protein | chr2:2081050-2081837 REVERSE | Aliases: T20G20.3, T20G20_3	8.8	4.5	4.3	11.1	0.02%	9.5
630	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	10.7	1.5	11.1	0.02%	10.1
631	AT5G15750.1 | RNA-binding S4 domain-containing protein, 40S RIBOSOMAL PROTEINs - different species | chr5:5141194-5142861 FORWARD | Aliases: F14F8.130, F14F8_130	8.5	6.4	2.1	11.1	0.02%	9.7
632	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	9.1	3.5	5.5	11.1	0.02%	8.9
633	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	8.0	4.7	3.3	11.1	0.02%	9.6
640	AT5G44560.1 | SNF7 family protein, contains Pfam domain, PF03357: SNF7 family | chr5:17963206-17965627 FORWARD | Aliases: MFC16.25, MFC16_25	8.2	4.2	4.0	11.0	0.02%	8.5
641	AT1G52590.1 | expressed protein | chr1:19592678-19593942 REVERSE | Aliases: F6D8.19, F6D8_19	7.0	4.3	2.7	11.0	0.02%	9.3
642	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	10.3	7.9	2.4	11.0	0.02%	10.0
643	AT1G08380.1 | expressed protein | chr1:2640858-2641825 REVERSE | Aliases: T27G7.25, T27G7_25	7.6	3.5	4.1	11.0	0.02%	8.4
644	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	7.9	3.2	4.7	11.0	0.02%	7.1

Rank	Description	Sync	Root	M	t	adj.q	B
647	AT3G03910.1 | glutamate dehydrogenase, putative, similar to glutamate dehydrogenase 1 (GDH 1) (Arabidopsis thaliana) SWISS-PROT:Q43314	7.7	3.5	4.2	11.0	0.02%	7.5
651	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	12.3	10.3	2.0	11.0	0.02%	10.1
655	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	10.9	6.8	4.0	11.0	0.02%	9.0
658	AT1G05205.1 | expressed protein | chr1:1509212-1510280 REVERSE | Aliases: None	10.3	8.1	2.1	10.9	0.02%	10.0
661	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	9.3	4.5	4.8	10.9	0.02%	8.6
662	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	3.4	5.0	10.9	0.02%	7.6
663	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	7.3	3.0	4.2	10.9	0.02%	8.7
664	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	10.2	7.0	3.3	10.9	0.02%	9.3
666	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	11.9	1.4	10.9	0.02%	10.0
667	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	11.9	1.4	10.9	0.02%	10.0
669	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	9.4	6.2	3.2	10.9	0.02%	9.4
671	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	9.2	6.5	2.7	10.9	0.02%	9.4
674	AT2G22540.1 | Symbol: SVP | short vegetative phase protein (SVP), identical to cDNA short vegetative phase protein (SVP) GI:10944319;	7.9	5.9	2.0	10.9	0.02%	9.7
676	AT1G64700.1 | expressed protein | chr1:24043473-24044258 REVERSE | Aliases: F13O11.2, F13O11_2	7.0	4.6	2.4	10.9	0.02%	9.7
678	AT5G45750.1 | Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303744 from (Pisum sativum)	9.1	5.3	3.8	10.8	0.02%	9.7
679	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	3.8	2.6	10.8	0.02%	9.4
682	AT4G33985.1 | expressed protein | chr4:16288117-16288918 REVERSE | Aliases: None	7.3	3.8	3.5	10.8	0.02%	8.6
683	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	6.1	3.3	2.8	10.8	0.02%	9.4
684	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	10.4	2.1	10.8	0.02%	10.0
685	AT1G04480.1 | 60S ribosomal protein L23 (RPL23A), identical to GB:AAB80655 | chr1:1216094-1217457 FORWARD | Aliases: F19P19.5, F19P19_5	11.1	9.5	1.6	10.8	0.02%	10.0
686	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	7.6	4.9	2.7	10.8	0.02%	9.5
688	AT3G54260.1 | expressed protein, various predicted proteins, Arabidopsis thaliana | chr3:20095988-20097741 REVERSE | Aliases: F24B22.220	10.2	7.7	2.5	10.8	0.02%	9.5

Rank	Description	Sync	Root	M	t	adj.q	B
690	AT3G53890.1 | 40S ribosomal protein S21 (RPS21B), ribosomal protein S21, cytosolic - Oryza sativa, PIR:S38357 | chr3:19966322-19967327 REVERSE | Aliases: F5K20.190	11.2	8.1	3.0	10.8	0.02%	9.7
692	AT4G10270.1 | wound-responsive family protein, similar to wound induced protein (GI:19320) (Lycopersicon esculentum) | chr4:6374730-6375206 FORWARD | Aliases: T9A4.6	8.7	4.2	4.6	10.8	0.02%	8.3
695	AT3G12320.1 | expressed protein | chr3:3923742-3925442 FORWARD | Aliases: T2E22.34	7.0	3.3	3.7	10.8	0.02%	8.2
696	AT2G44860.1 | 60S ribosomal protein L24, putative | chr2:18507444-18509617 REVERSE | Aliases: T13E15.13	10.1	6.7	3.4	10.7	0.02%	9.7
702	AT4G02790.1 | GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function | chr4:1247399-1249588 FORWARD | Aliases: T5J8.11, T5J8_11	6.7	3.7	3.1	10.7	0.02%	8.7
703	AT2G25720.1 | expressed protein | chr2:10962597-10963130 REVERSE | Aliases: F3N11.17, F3N11_17	9.8	6.9	2.9	10.7	0.02%	9.1
704	AT2G42220.1 | rhodanese-like domain-containing protein, contains rhodanese-like domain PF:00581 | chr2:17599167-17600783 FORWARD | Aliases: T24P15.13, T24P15_13	8.3	3.5	4.7	10.7	0.02%	7.8
705	AT2G36160.1 | 40S ribosomal protein S14 (RPS14A) | chr2:15176897-15178428 FORWARD | Aliases: F9C22.9, F9C22_9	11.0	9.4	1.6	10.7	0.02%	9.9
708	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	8.1	3.8	4.3	10.7	0.03%	8.3
709	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	7.4	4.6	2.8	10.7	0.03%	8.8
711	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	9.0	6.9	2.1	10.7	0.03%	9.6
716	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	7.4	2.5	10.7	0.03%	9.3
718	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	11.2	9.1	2.1	10.7	0.03%	9.7
720	AT5G43150.1 | expressed protein | chr5:17342246-17343126 FORWARD | Aliases: MMG4.18, MMG4_18	11.2	10.1	1.1	10.7	0.03%	9.9
724	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	8.1	5.0	3.0	10.6	0.03%	8.9
725	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	11.9	6.3	5.6	10.6	0.03%	9.5
728	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	7.4	3.9	3.5	10.6	0.03%	8.5
729	AT5G08565.1 | expressed protein | chr5:2775899-2777400 FORWARD | Aliases: None	6.2	2.9	3.3	10.6	0.03%	8.8
731	AT2G21820.1 | expressed protein | chr2:9309965-9310327 REVERSE | Aliases: F7D8.14, F7D8_14	9.2	6.2	3.0	10.6	0.03%	9.2
732	AT3G03490.1 | peroxisomal protein PEX19 family protein, contains Pfam profile: PF04614 Pex19 protein family | chr3:830172-831853 REVERSE | Aliases: T21P5.9, T21P5_9	9.2	7.0	2.2	10.6	0.03%	9.7
734	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	9.6	4.6	5.1	10.6	0.03%	8.0
735	AT4G21620.1 | glycine-rich protein | chr4:11491495-11492179 FORWARD | Aliases: F17L22.80, F17L22_80	10.2	6.4	3.8	10.6	0.03%	7.9

Rank	Description	Sync	Root	M	t	adj.q	B
736	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	11.1	9.0	2.1	10.6	0.03%	9.7
737	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	9.0	5.7	3.4	10.6	0.03%	9.2
739	AT1G16000.1 | expressed protein | chr1:5494530-5495317 FORWARD | Aliases: T24D18.10, T24D18_10	9.8	6.4	3.5	10.6	0.03%	8.8
742	AT5G45170.1 | CbbY protein-related, low similarity to SP:P40119 CbbY protein, chromosomal {Alcaligenes eutrophus} | chr5:18287571-18290396 REVERSE | Aliases: K18C1.5, K18C1_5	8.4	6.3	2.1	10.5	0.03%	9.6
744	AT1G50575.1 | lysine decarboxylase family protein, contains Pfam profile PF03641: lysine decarboxylase family | chr1:18732387-18734055 REVERSE | Aliases: None	7.2	4.1	3.1	10.5	0.03%	8.8
745	AT1G53120.1 | RNA-binding S4 domain-containing protein	6.6	4.2	2.5	10.5	0.03%	9.1
746	AT2G29460.1 | Symbol: ATGSTU4 | glutathione S-transferase, putative | chr2:12633624-12634755 REVERSE | Aliases: F16P2.16, F16P2_16, GLUTATHIONE S TRANSFERASE 22, GST22	7.7	2.9	4.8	10.5	0.03%	8.6
748	AT4G30270.1 | Symbol: MERI5B |	7.4	3.5	3.9	10.5	0.03%	8.2
749	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	7.2	4.1	3.1	10.5	0.03%	8.6
750	AT1G13270.2 | Symbol: MAP1C | metallopeptidase M24 family protein, similar to SP:Q01662 Methionine aminopeptidase 1 precursor (EC 3.4.11.18) {Saccharomyces cerevisiae}; contains Pfam profile PF00557: metallopeptidase family M24 | chr1:4544953-4547295 FORWARD | Aliases: MAP1B, METHIONINE AMINOPEPTIDASE 1B	8.4	4.7	3.7	10.5	0.03%	8.1
752	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	8.1	5.4	2.7	10.5	0.03%	9.5
754	AT1G63420.1 | expressed protein | chr1:23519539-23522575 FORWARD | Aliases: F2K11.20, F2K11_20	8.0	5.9	2.1	10.5	0.03%	9.3
756	AT5G02120.1 | Symbol: OHP | thylakoid membrane one helix protein (OHP), identical to one helix protein GI:3283057 from (Arabidopsis thaliana)	7.6	2.2	5.4	10.5	0.03%	7.7
758	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	8.8	3.5	5.3	10.5	0.03%	7.6
760	AT5G16570.1 | Symbol: GLN1;4 |	9.6	7.3	2.3	10.5	0.03%	9.4
761	AT4G09550.1 | expressed protein | chr4:6039132-6040171 FORWARD | Aliases: T15G18.30, T15G18_30	9.7	6.2	3.6	10.5	0.03%	9.6
762	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	7.7	3.6	4.2	10.5	0.03%	8.8
763	AT1G78630.1 | Symbol: EMB1473 | ribosomal protein L13 family protein, similar to ribosomal protein L13 GI:170132 from (Spinacia oleracea) | chr1:29580849-29582551 FORWARD | Aliases: EMB1473, EMBRYO DEFECTIVE 1473, T30F21.4, T30F21_4	8.9	4.1	4.7	10.5	0.03%	8.4
764	AT5G27560.1 | expressed protein, hypothetical protein slr1702 - Synechocystis sp., PIR:S75312 | chr5:9731731-9733921 FORWARD | Aliases: F15A18.20, F15A18_20	8.2	5.4	2.7	10.5	0.03%	9.1
767	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	10.0	7.2	2.8	10.4	0.03%	9.3
772	AT4G10300.1 | expressed protein | chr4:6384458-6386185 FORWARD | Aliases: T9A4.16	8.7	5.5	3.2	10.4	0.03%	8.6
774	AT2G23530.1 | expressed protein, ; expression supported by MPSS | chr2:10027732-10029875 REVERSE | Aliases: F26B6.18, F26B6_18	7.1	3.7	3.3	10.4	0.03%	8.5

Rank	Description	Sync	Root	M	t	adj.q	B
775	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	12.1	10.3	1.8	10.4	0.03%	9.7
777	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	8.9	2.0	10.4	0.03%	9.7
778	AT5G14105.1 | expressed protein | chr5:4551991-4553053 REVERSE | Aliases: None	9.0	6.2	2.8	10.4	0.03%	9.2
781	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	3.1	4.2	10.4	0.03%	8.5
785	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	7.0	3.3	3.8	10.3	0.03%	8.3
786	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	8.0	2.0	10.3	0.03%	9.5
787	AT1G35420.1 | dienelactone hydrolase family protein, low similarity to dienelactone hydrolase (Rhodococcus opacus) GI:23094407; contains Pfam profile PF01738: Dienelactone hydrolase family | chr1:13026292-13027645 FORWARD | Aliases: F12A4.4, F12A4_4	7.3	3.6	3.7	10.3	0.03%	7.6
788	AT1G77710.1 | expressed protein, similar to hypothetical protein GB:P34661 (Caenorhabditis elegans) | chr1:29211577-29212943 FORWARD | Aliases: T32E8.4, T32E8_4	11.5	8.8	2.7	10.3	0.03%	9.5
789	AT3G12110.1 | Symbol: ACT11 | actin 11 (ACT11), identical to SP:P53496 Actin 11 {Arabidopsis thaliana} | chr3:3857860-3859804 FORWARD | Aliases: ACTIN 11, T21B14.7	7.8	4.0	3.8	10.3	0.03%	8.7
790	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	8.2	5.3	3.0	10.3	0.03%	8.7
791	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	6.8	3.3	3.6	10.3	0.03%	8.3
794	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	8.4	4.8	3.6	10.3	0.03%	8.7
795	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	8.6	4.7	3.9	10.3	0.03%	8.6
797	AT3G23700.1 | S1 RNA-binding domain-containing protein, contains Pfam domain, PF00575: S1 RNA binding domain | chr3:8531436-8533774 REVERSE | Aliases: MYM9.4	7.5	3.5	4.0	10.3	0.03%	8.8
798	AT3G08690.1 | ubiquitin-conjugating enzyme 11 (UBC11), E2; identical to gi:12643427, SP:P35134	10.4	6.9	3.4	10.3	0.03%	8.8
799	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	9.0	5.7	3.3	10.3	0.03%	8.8
801	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	11.3	7.2	4.1	10.3	0.03%	8.4
804	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	11.3	8.8	2.4	10.2	0.03%	9.3
805	AT2G30140.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:12879211-12880897 FORWARD | Aliases: T27E13.12, T27E13_12	9.8	7.1	2.8	10.2	0.03%	9.4

Rank	Description	Sync	Root	M	t	adj.q	B
806	AT5G64816.2 | expressed protein | chr5:25930226-25931229 FORWARD | Aliases: None	8.9	6.3	2.6	10.2	0.03%	9.1
807	AT5G35700.1 | fimbrin-like protein, putative, similar to fimbrin-like protein (ATFIM1) (Arabidopsis thaliana) GI:2905893, fimbrin (Schizosaccharomyces pombe) GI:3057144; contains Pfam profile PF00307: Calponin homology (CH) domain	9.1	5.4	3.7	10.2	0.03%	9.3
809	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	9.8	7.4	2.3	10.2	0.03%	9.4
811	AT1G08580.1 | expressed protein | chr1:2715086-2716387 REVERSE | Aliases: F22O13.6, F22O13_6	8.8	5.9	3.0	10.2	0.03%	8.8
812	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	7.7	4.5	3.2	10.2	0.03%	8.6
814	AT5G14780.1 | Symbol: FDH | formate dehydrogenase (FDH), identical to GI:7677266 | chr5:4776987-4779497 FORWARD | Aliases: FORMATE DEHYDROGENASE, T9L3.80, T9L3_80	9.5	4.9	4.5	10.2	0.03%	8.8
815	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	10.0	6.6	3.4	10.2	0.03%	9.4
816	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 (GI:984052) (Arabidopsis thaliana) | chr3:881031-884163 FORWARD | Aliases: BETA GLUCOSIDASE, T12J13.8, T12J13_8	11.0	6.7	4.3	10.2	0.03%	8.6
817	AT4G19390.1 | expressed protein | chr4:10574779-10576439 REVERSE | Aliases: T5K18.170, T5K18_170	9.0	6.4	2.6	10.2	0.03%	8.9
818	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	9.3	6.6	2.7	10.2	0.03%	8.8
820	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	8.5	5.0	3.4	10.2	0.03%	7.9
821	AT1G07830.1 | ribosomal protein L29 family protein, similar to GB:CAA83057 from (Saccharomyces cerevisiae) | chr1:2422295-2423650 FORWARD | Aliases: F24B9.7, F24B9_7	7.8	5.0	2.8	10.2	0.03%	9.0
823	AT3G44450.1 | expressed protein | chr3:16085084-16085607 REVERSE | Aliases: F14L2.1	5.5	2.2	3.3	10.2	0.03%	8.2
824	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	8.1	4.5	3.6	10.2	0.03%	8.5
825	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	7.9	4.4	3.5	10.2	0.03%	8.8
827	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	10.0	5.1	4.9	10.2	0.03%	7.7
830	AT4G17540.1 | expressed protein | chr4:9775868-9777827 FORWARD | Aliases: DL4805W, FCAALL.37	6.7	3.9	2.8	10.1	0.03%	9.1
831	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	7.7	2.3	10.1	0.03%	9.4
832	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	8.8	4.8	4.0	10.1	0.03%	8.6
834	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	6.0	2.3	10.1	0.03%	8.9

Rank	Description	Sync	Root	M	t	adj.q	B
835	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	12.9	10.4	2.5	10.1	0.03%	9.4
836	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	4.6	3.6	10.1	0.03%	8.0
839	AT3G52420.1 | outer envelope membrane protein, putative, similar to outer envelope membrane protein gi:703236:gb:AAA63414 | chr3:19440753-19440947 FORWARD | Aliases: F22O6.200	8.8	6.6	2.2	10.1	0.03%	9.2
843	AT2G28000.1 | Symbol: CPN60A |	10.1	7.3	2.9	10.1	0.03%	9.1
844	AT5G11480.1 | expressed protein | chr5:3669198-3671575 REVERSE | Aliases: F15N18.70, F15N18_70	8.4	5.5	2.9	10.1	0.03%	8.8
848	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, PPIase (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	9.4	5.6	3.8	10.1	0.03%	8.4
853	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	9.5	3.3	6.2	10.1	0.03%	8.3
854	AT3G56680.1 | expressed protein | chr3:21002259-21004646 FORWARD | Aliases: T8M16.10	9.4	6.7	2.6	10.1	0.03%	9.0
855	AT2G19750.1 | 40S ribosomal protein S30 (RPS30A) | chr2:8522119-8522888 FORWARD | Aliases: F6F22.22, F6F22_22	7.9	4.5	3.4	10.1	0.03%	8.8
856	AT4G33640.1 | expressed protein | chr4:16159551-16160306 REVERSE | Aliases: T16L1.130, T16L1_130	10.9	9.8	1.1	10.1	0.03%	9.4
857	AT1G16520.1 | expressed protein | chr1:5648763-5651160 FORWARD | Aliases: F3O9.32	6.9	3.5	3.4	10.1	0.03%	8.8
858	AT4G16060.1 | expressed protein | chr4:9094437-9096293 FORWARD | Aliases: DL4070W, FCAALL.269	8.1	5.7	2.4	10.1	0.03%	9.0
859	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	10.1	6.9	3.2	10.1	0.03%	8.9
860	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	7.5	3.7	3.8	10.1	0.03%	7.7
862	AT5G52650.1 | 40S ribosomal protein S10 (RPS10C), contains similarity to 40S ribosomal protein S10 | chr5:21372841-21374301 REVERSE | Aliases: F6N7.14, F6N7_14	11.2	9.4	1.7	10.0	0.03%	9.3
864	AT3G57320.1 | expressed protein | chr3:21221008-21221827 FORWARD | Aliases: F28O9.170	7.8	4.0	3.8	10.0	0.03%	8.5
866	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	7.7	2.5	5.2	10.0	0.03%	6.9
867	AT3G17300.1 | expressed protein | chr3:5907240-5908898 FORWARD | Aliases: MGD8.14	9.6	6.9	2.7	10.0	0.03%	9.0
870	AT3G10610.1 | 40S ribosomal protein S17 (RPS17C), similar to 40S ribosomal protein S17 GB:AAD50774 (Lycopersicon esculentum) | chr3:3319041-3320154 FORWARD | Aliases: F13M14.10	8.5	5.8	2.6	10.0	0.03%	9.0
871	AT4G26230.1 | 60S ribosomal protein L31 (RPL31B), ribosomal protein L31, Nicotiana glutinosa, U23784 | chr4:13285837-13286800 FORWARD | Aliases: T25K17.40, T25K17_40	11.8	10.1	1.7	10.0	0.03%	9.4
873	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	9.7	6.1	3.5	10.0	0.03%	8.3
876	AT1G73470.2 | expressed protein | chr1:27628983-27631359 FORWARD | Aliases: T9L24.34, T9L24_34	8.0	5.8	2.2	10.0	0.03%	8.8

Rank	Description	Sync	Root	M	t	adj.q	B
878	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	6.2	3.2	3.0	10.0	0.03%	8.3
879	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	9.2	5.2	4.0	10.0	0.03%	9.0
880	AT3G55010.2 | phosphoribosylformylglycinamidine cyclo-ligase, chloroplast / phosphoribosyl-aminoimidazole synthetase / AIR synthase (PUR5), identical to phosphoribosylformylglycinamidine 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	8.2	4.4	3.8	10.0	0.03%	8.8
883	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	9.7	8.1	1.7	9.9	0.04%	9.2
885	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	9.6	6.4	3.2	9.9	0.04%	8.5
889	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	11.5	10.0	1.5	9.9	0.04%	9.3
891	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	6.6	4.1	2.5	9.9	0.04%	8.8
892	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	14.0	12.2	1.8	9.9	0.04%	9.2
893	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	9.1	4.3	4.9	9.9	0.04%	8.4
894	AT3G08030.2 | expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642 | chr3:2564159-2566008 FORWARD | Aliases: F17A17.37	8.2	3.4	4.8	9.9	0.04%	8.2
895	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	8.0	3.9	4.1	9.9	0.04%	8.9
896	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	7.5	2.1	5.4	9.9	0.04%	7.7
897	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	7.7	3.7	4.0	9.9	0.04%	7.8
901	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) {Arabidopsis thaliana}, immunophilin (FKBP15-1) GB:U52046 (Arabidopsis thaliana) (Proc. Natl. Acad. Sci. U.S.A. 93 (14), 6964-6969 (1996)) | chr3:9183855-9185849 FORWARD | Aliases: MJL12.19	9.9	8.3	1.7	9.9	0.04%	9.3
902	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	5.7	3.4	2.3	9.9	0.04%	8.7
904	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	12.2	10.7	1.6	9.9	0.04%	9.3
905	AT2G41650.1 | expressed protein | chr2:17370985-17371512 FORWARD | Aliases: T32G6.17, T32G6_17	10.2	8.1	2.1	9.9	0.04%	9.1
907	AT1G71260.1 | expressed protein | chr1:26865327-26867080 REVERSE | Aliases: F3I17.9, F3I17_9	7.8	3.5	4.3	9.9	0.04%	8.6
908	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	7.6	5.2	2.4	9.8	0.04%	8.9
909	AT3G15780.1 | expressed protein | chr3:5341433-5342564 FORWARD | Aliases: MSJ11.18	7.7	4.6	3.2	9.8	0.04%	8.7

Rank	Description	Sync	Root	M	t	adj.q	B
910	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	8.8	5.1	3.7	9.8	0.04%	7.9
911	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	7.5	4.0	3.5	9.8	0.04%	7.9
914	AT1G22840.1 | cytochrome c, putative, similar to cytochrome c (Pumpkin, Winter squash) SWISS-PROT:P00051 | chr1:8079279-8080563 FORWARD | Aliases: F19G10.20, F19G10_20	12.1	10.3	1.9	9.8	0.04%	9.3
919	AT2G37790.1 | aldo/keto reductase family protein, similar to chalcone reductase (Sesbania rostrata)(GI:2792155), and aldose reductase ALDRXV4 (Xerophyta viscosa)(GI:4539944),	8.6	5.5	3.1	9.8	0.04%	8.7
920	AT2G25210.1 | 60S ribosomal protein L39 (RPL39A) | chr2:10746934-10747631 FORWARD | Aliases: T22F11.20, T22F11_20	10.7	7.4	3.3	9.8	0.04%	8.5
922	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	12.4	10.0	2.4	9.8	0.04%	9.1
923	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	7.7	2.4	5.3	9.8	0.04%	6.3
927	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	7.9	4.6	3.2	9.8	0.04%	8.2
928	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	6.9	3.3	3.6	9.8	0.04%	8.5
929	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	5.8	3.4	2.4	9.8	0.04%	8.9
930	AT4G14320.1 | 60S ribosomal protein L36a/L44 (RPL36aB)	9.9	7.8	2.1	9.8	0.04%	9.1
931	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	8.0	3.8	4.2	9.8	0.04%	8.1
935	AT5G61170.1 | 40S ribosomal protein S19 (RPS19C), 40S ribsomal protein S19, Oryza sativa, SWISSPROT:RS19_ORYSA	10.8	8.1	2.7	9.7	0.04%	9.0
938	AT4G36910.1 | CBS domain-containing protein, contains Pfam profile PF00571: CBS domain	9.1	4.6	4.5	9.7	0.04%	7.2
940	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	6.3	3.8	2.4	9.7	0.04%	8.5
941	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	8.3	1.9	9.7	0.04%	9.1
942	AT3G15840.3 | expressed protein | chr3:5356657-5358506 REVERSE | Aliases: MSJ11.24, MSJ11_24	4.3	2.3	2.0	9.7	0.04%	9.1
944	AT5G10850.1 | expressed protein | chr5:3428160-3428825 FORWARD | Aliases: T30N20.120, T30N20_120	8.0	4.5	3.5	9.7	0.04%	7.7
945	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	10.9	8.2	2.7	9.7	0.04%	8.4
946	AT1G30070.1 | SGS domain-containing protein, similar to calcyclin binding protein (Mus musculus) GI:3142331; contains Pfam profile PF05002: SGS domain	8.3	3.6	4.6	9.7	0.04%	8.2
948	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	10.8	9.2	1.7	9.7	0.04%	9.1

Rank	Description	Sync	Root	M	t	adj.q	B
950	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	10.8	8.5	2.3	9.7	0.04%	9.1
951	AT4G39860.2 | expressed protein | chr4:18499878-18501636 FORWARD | Aliases: T5J17.30, T5J17_30	7.7	4.1	3.5	9.7	0.04%	8.6
953	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	6.9	3.3	9.7	0.04%	9.1
955	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	9.2	5.8	3.4	9.7	0.04%	8.4
956	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	10.3	3.9	6.3	9.7	0.04%	8.5
957	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	7.2	3.8	3.4	9.7	0.04%	8.0
958	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	6.8	1.8	9.7	0.04%	9.1
960	AT2G20585.2 | expressed protein | chr2:8872180-8873848 FORWARD | Aliases: None	6.6	3.0	3.6	9.7	0.04%	8.4
962	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	8.2	5.7	2.5	9.6	0.04%	8.5
963	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	7.1	4.2	2.9	9.6	0.04%	8.2
964	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	7.6	4.5	3.1	9.6	0.04%	8.6
967	AT3G06020.1 | expressed protein, ; expression supported by MPSS | chr3:1813273-1814175 FORWARD | Aliases: F2O10.2, F2O10_2	6.1	3.9	2.2	9.6	0.04%	8.8
970	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	7.1	3.7	3.4	9.6	0.04%	7.8
971	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	4.5	3.9	9.6	0.04%	8.0
973	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	10.2	7.0	3.2	9.6	0.04%	9.1
975	AT3G18760.1 | ribosomal protein S6 family protein, contains TIGRFAM profile TIGR00166: ribosomal protein S6 | chr3:6457696-6459633 REVERSE | Aliases: MVE11.12	7.7	4.8	2.8	9.6	0.04%	8.6
976	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	10.2	7.7	2.5	9.6	0.04%	9.1
978	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	11.5	10.0	1.5	9.6	0.04%	8.9
980	AT2G32060.3 | 40S ribosomal protein S12 (RPS12C) | chr2:13646122-13647257 REVERSE | Aliases: F22D22.19, F22D22_19	11.1	8.5	2.6	9.6	0.04%	8.9
983	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	12.9	9.5	3.4	9.6	0.04%	9.0

Rank	Description	Sync	Root	M	t	adj.q	B
985	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	8.7	6.9	1.8	9.6	0.04%	9.0
987	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	8.2	5.0	3.2	9.6	0.04%	8.3
989	AT5G54770.1 | Symbol: THI1 | thiazole biosynthetic enzyme, chloroplast (ARA6) (THI1) (THI4), identical to SP:Q38814 Thiazole biosynthetic enzyme, chloroplast precursor (ARA6) {Arabidopsis thaliana}	12.1	6.6	5.5	9.6	0.04%	7.9
990	AT4G13950.1 | Symbol: RALFL31 | rapid alkalinization 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	3.8	2.8	9.6	0.04%	8.2
994	AT2G26340.1 | expressed protein | chr2:11222353-11223701 FORWARD | Aliases: T1D16.2, T1D16_2	7.2	4.9	2.3	9.6	0.04%	8.5
995	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	7.6	5.0	2.6	9.6	0.04%	8.5
996	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	12.1	7.9	4.2	9.6	0.04%	8.6
999	AT2G44190.1 | expressed protein, contains Pfam profile: PF04484 family of unknown function (DUF566) | chr2:18279267-18281573 FORWARD | Aliases: F6E13.32	7.2	3.8	3.4	9.5	0.04%	8.4
1002	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	7.3	4.0	3.3	9.5	0.04%	8.1
1003	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	9.9	6.7	3.2	9.5	0.04%	8.8
1004	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	8.3	4.3	4.0	9.5	0.04%	8.4
1005	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	6.3	3.3	2.9	9.5	0.04%	8.1
1006	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	8.5	4.4	4.1	9.5	0.04%	8.3
1008	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	9.1	6.6	2.5	9.5	0.04%	8.7
1012	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	6.1	2.7	3.5	9.5	0.04%	7.4
1013	AT4G38490.1 | expressed protein | chr4:18006282-18007366 FORWARD | Aliases: F20M13.50, F20M13_50	8.7	6.9	1.9	9.5	0.04%	8.9
1015	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	9.6	6.4	3.2	9.5	0.04%	8.4
1018	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	12.7	6.5	6.3	9.5	0.04%	8.7
1020	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	8.7	4.8	3.9	9.5	0.04%	8.4
1021	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	7.2	4.8	2.4	9.5	0.04%	8.6

Rank	Description	Sync	Root	M	t	adj.q	B
1024	AT5G02220.1 | expressed protein | chr5:441705-442144 REVERSE | Aliases: T7H20.270, T7H20_270	6.0	2.7	3.3	9.5	0.04%	8.3
1025	AT2G33530.1 | Symbol: SCPL46 |	7.1	4.7	2.4	9.5	0.04%	8.3
1028	AT3G02180.2 | Symbol: SP1L | expressed protein | chr3:404891-405656 FORWARD | Aliases: F1C9.3, SPIRAL 1 LIKE	10.1	8.1	2.0	9.5	0.04%	8.9
1030	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	8.0	4.3	3.7	9.5	0.04%	8.2
1033	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	6.7	4.6	2.2	9.4	0.04%	8.8
1034	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	7.8	4.9	2.9	9.4	0.04%	8.1
1035	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	10.3	6.5	3.9	9.4	0.04%	8.0
1036	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	8.6	3.2	5.4	9.4	0.04%	8.4
1037	AT3G52040.1 | expressed protein | chr3:19315151-19315839 REVERSE | Aliases: F4F15.150	8.1	4.9	3.2	9.4	0.04%	8.2
1039	AT1G29070.1 | ribosomal protein L34 family protein, similar to plastid ribosomal protein L34 precursor GB:AAF64157 GI:7578860 from (Spinacia oleracea)	7.0	3.6	3.4	9.4	0.04%	8.0
1041	AT4G14615.1 | expressed protein | chr4:8383765-8385074 FORWARD | Aliases: None	10.6	8.7	1.9	9.4	0.04%	9.0
1042	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	8.9	6.9	2.0	9.4	0.04%	8.6
1044	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	3.5	2.0	1.5	9.4	0.05%	8.9
1047	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	10.1	6.2	3.9	9.4	0.05%	8.3
1048	AT1G60970.1 | clathrin adaptor complex small chain family protein, contains Pfam profile: PF01217 clathrin adaptor complex small chain	7.0	3.0	4.0	9.4	0.05%	7.3
1049	AT3G59840.1 | expressed protein | chr3:22116499-22117175 REVERSE | Aliases: F24G16.110	8.1	3.6	4.5	9.4	0.05%	8.1
1050	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	9.0	7.2	1.8	9.4	0.05%	8.7
1052	AT3G24430.1 | Symbol: HCF101 |	7.2	3.7	3.5	9.4	0.05%	8.0
1053	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	6.1	2.2	9.4	0.05%	8.6
1054	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	7.3	4.0	3.3	9.4	0.05%	8.2
1055	AT4G13170.1 | 60S ribosomal protein L13A (RPL13aC), ribosomal protein L13a -Lupinus luteus,PID:e1237871 | chr4:7654940-7656561 REVERSE | Aliases: F17N18.60, F17N18_60	10.3	6.9	3.3	9.4	0.05%	8.6

Rank	Description	Sync	Root	M	t	adj.q	B
1060	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)	8.5	5.6	2.9	9.4	0.05%	8.1
1063	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	10.5	8.2	2.3	9.3	0.05%	8.8
1064	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	7.9	4.5	3.4	9.3	0.05%	7.4
1065	AT5G23120.1 | Symbol: HCF136 |	8.6	5.8	2.8	9.3	0.05%	8.4
1066	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	8.6	4.2	4.4	9.3	0.05%	7.9
1068	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	11.9	8.0	3.9	9.3	0.05%	8.3
1069	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	8.2	3.0	5.3	9.3	0.05%	6.5
1072	AT3G60480.1 | expressed protein | chr3:22358426-22359213 REVERSE | Aliases: T8B10.140	8.9	7.2	1.8	9.3	0.05%	8.8
1073	AT2G06520.1 | membrane protein, putative, contains 2 transmembrane domains; | chr2:2587781-2588355 REVERSE | Aliases: T12H3.7, T12H3_7	9.5	4.7	4.8	9.3	0.05%	8.1
1074	AT3G15353.1 | Symbol: MT3 | metallothionein protein, putative	12.1	8.0	4.1	9.3	0.05%	8.7
1076	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	8.0	4.0	4.0	9.3	0.05%	6.7
1077	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	9.4	7.3	2.1	9.3	0.05%	8.7
1079	AT4G02510.1 | Symbol: TOC159 |	10.0	8.2	1.8	9.3	0.05%	8.8
1081	AT5G27770.1 | 60S ribosomal protein L22 (RPL22C), ribosomal protein L22 (cytosolic), Rattus norvegicus, PIR:S52084 | chr5:9835890-9837332 FORWARD | Aliases: T1G16.100, T1G16_100	10.3	8.0	2.3	9.3	0.05%	8.5
1082	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	10.7	6.7	4.0	9.3	0.05%	8.7
1087	AT5G64140.1 | Symbol: RPS28 | 40S ribosomal protein S28 (RPS28C) | chr5:25684550-25685518 REVERSE | Aliases: MHJ24.12, MHJ24_12, RIBOSOMAL PROTEIN S28	11.1	9.0	2.1	9.3	0.05%	8.8
1088	AT1G32220.1 | expressed protein | chr1:11607881-11609713 FORWARD | Aliases: F3C3.2, F3C3_2	8.3	3.7	4.6	9.3	0.05%	8.0
1089	AT3G12510.1 | expressed protein | chr3:3967134-3967804 FORWARD | Aliases: T2E22.17	6.5	3.9	2.6	9.3	0.05%	8.0
1091	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	7.1	3.3	3.8	9.3	0.05%	7.6

Rank	Description	Sync	Root	M	t	adj.q	B
1095	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	11.3	9.6	1.8	9.3	0.05%	8.8
1096	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	4.7	4.6	9.3	0.05%	7.9
1102	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	10.9	8.8	2.2	9.2	0.05%	8.8
1103	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	9.1	6.3	2.9	9.2	0.05%	8.5
1106	AT2G46540.1 | expressed protein | chr2:19117544-19118841 REVERSE | Aliases: F13A10.7, F13A10_7	12.3	11.5	0.8	9.2	0.05%	8.5
1107	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: methlytransferase, UbiE/COQ5 family | chr3:23426190-23428093 REVERSE | Aliases: ALBINO OR PALE GREEN MUTANT 1, MAA21.40, VITAMIN E DEFECTIVE, VTE3	10.4	5.7	4.7	9.2	0.05%	7.9
1108	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	11.3	10.2	1.1	9.2	0.05%	8.8
1109	AT2G39390.1 | 60S ribosomal protein L35 (RPL35B) | chr2:16457738-16458956 REVERSE | Aliases: F12L6.5, F12L6_5	10.8	8.9	1.9	9.2	0.05%	8.8
1111	AT1G55480.1 | expressed protein | chr1:20717350-20719200 FORWARD | Aliases: T5A14.12, T5A14_12	8.4	5.3	3.1	9.2	0.05%	7.6
1112	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	11.0	7.7	3.3	9.2	0.05%	8.5
1113	AT1G26470.1 | expressed protein | chr1:9155080-9156233 FORWARD | Aliases: T1K7.16, T1K7_16	7.2	3.9	3.3	9.2	0.05%	8.0
1114	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	13.9	12.3	1.6	9.2	0.05%	8.8
1117	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	11.1	2.0	9.2	0.05%	8.7
1118	AT5G26220.1 | ChaC-like family protein, contains Pfam profile: PF04752 ChaC-like protein | chr5:9162972-9164680 REVERSE | Aliases: T19G15.70, T19G15_70	7.8	3.6	4.2	9.2	0.05%	7.5
1120	AT4G02530.1 | chloroplast thylakoid lumen protein, SP:022773 ;TL16_ARATH | chr4:1112146-1114026 REVERSE | Aliases: T10P11.17, T10P11_17	6.9	4.0	3.0	9.2	0.05%	7.8
1121	AT4G34090.2 | expressed protein | chr4:16326861-16330183 REVERSE | Aliases: F28A23.150, F28A23_150	7.5	4.3	3.2	9.2	0.05%	8.1
1122	AT3G19790.1 | expressed protein, ; expression supported by MPSS | chr3:6874943-6875446 REVERSE | Aliases: MMB12.25	8.3	5.7	2.6	9.2	0.05%	8.4
1124	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	6.7	3.4	3.3	9.2	0.05%	7.5
1125	AT3G47836.1 | expressed protein | chr3:17661246-17662750 REVERSE | Aliases: None	11.5	9.5	1.9	9.2	0.05%	8.7
1127	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	9.9	7.2	2.7	9.2	0.05%	8.1
1128	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 {Arabidopsis thaliana} SP:P53665, {Neurospora crassa} SP:P11943; contains Pfam profile PF00550: Phosphopantetheine attachment site | chr5:19323373-19324629 FORWARD | Aliases: MNJ7.22, MNJ7_22	6.7	3.0	3.7	9.2	0.05%	7.0

Rank	Description	Sync	Root	M	t	adj.q	B
1129	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	6.7	3.1	3.5	9.2	0.05%	7.9
1130	AT3G60770.1 | 40S ribosomal protein S13 (RPS13A), AtRPS13A mRNA for cytoplasmic ribosomal protein S13, Arabidopsis thaliana,AB031739 | chr3:22471265-22472718 REVERSE | Aliases: T4C21.180	11.8	9.2	2.5	9.2	0.05%	8.7
1131	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	7.7	4.0	3.7	9.2	0.05%	8.2
1132	AT5G66410.1 | expressed protein | chr5:26537032-26538922 FORWARD | Aliases: K1F13.6, K1F13_6	9.0	7.0	2.1	9.2	0.05%	8.5
1133	AT5G55640.1 | expressed protein | chr5:22550385-22551304 REVERSE | Aliases: MDF20.8, MDF20_8	9.1	7.1	2.0	9.1	0.05%	8.6
1134	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	12.0	11.1	1.0	9.1	0.05%	8.6
1135	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	12.0	11.1	1.0	9.1	0.05%	8.6
1137	AT2G34570.1 | expressed protein, contains Pfam profile: PF04900 protein of unknown function, DUF652 | chr2:14569980-14571861 REVERSE | Aliases: T31E10.9, T31E10_9	6.3	4.3	1.9	9.1	0.05%	8.5
1138	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	8.7	5.4	3.3	9.1	0.05%	8.1
1141	AT5G67490.1 | expressed protein | chr5:26951379-26952178 REVERSE | Aliases: K9I9.5, K9I9_5	10.3	7.7	2.6	9.1	0.05%	8.3
1143	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	11.0	7.1	3.9	9.1	0.05%	8.2
1145	AT3G44735.1 | phytosulfokines-related, contains similarities to phytosulfokines from (Arabidopsis thaliana) | chr3:16302187-16303137 REVERSE | Aliases: None	5.9	3.3	2.6	9.1	0.05%	8.1
1152	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	7.5	4.1	3.4	9.1	0.05%	7.6
1154	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	8.3	4.6	3.7	9.1	0.05%	7.6
1156	AT3G18610.1 | nucleolin, putative, contains Pfam profile: PF00076 RNA recognition motif | chr3:6404276-6407828 REVERSE | Aliases: K24M9.10	6.8	4.0	2.8	9.1	0.05%	8.1
1158	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	6.6	4.1	2.5	9.1	0.05%	8.3
1159	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	7.5	2.6	4.9	9.1	0.05%	6.6
1160	AT3G55280.1 | 60S ribosomal protein L23A (RPL23aB), various ribosomal L23a proteins | chr3:20511312-20512686 FORWARD | Aliases: T26I12.160	9.4	5.9	3.5	9.1	0.05%	8.1
1164	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	11.8	9.6	2.2	9.1	0.05%	8.7
1168	AT4G24830.1 | arginosuccinate synthase family, contains Pfam profile: PF00764 arginosuccinate synthase	12.1	7.2	4.9	9.1	0.05%	8.1
1169	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	7.6	4.5	3.1	9.1	0.05%	8.1
1170	AT4G10040.1 | cytochrome c, putative, similar to cytochrome c (Pumpkin, Winter squash) SWISS-PROT:P00051 | chr4:6276995-6278501 FORWARD | Aliases: F28M11.5	10.3	7.5	2.8	9.0	0.05%	8.5

Rank	Description	Sync	Root	M	t	adj.q	B
1173	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	9.3	6.0	3.4	9.0	0.05%	8.1
1174	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	7.2	4.6	2.6	9.0	0.05%	8.0
1176	AT2G21385.1 | expressed protein | chr2:9156723-9158934 FORWARD | Aliases: None	8.0	5.0	3.0	9.0	0.05%	8.2
1177	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)	9.2	5.5	3.7	9.0	0.05%	7.9
1178	AT3G27690.1 | Symbol: LHCB2:4 | chlorophyll A-B binding protein (LHCB2:4), nearly identical to Lhcb2 protein (Arabidopsis thaliana) GI: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	7.0	3.3	3.7	9.0	0.05%	7.4
1179	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	7.9	6.0	1.9	9.0	0.06%	8.4
1181	AT2G28600.1 | expressed protein | chr2:12258862-12261900 FORWARD | Aliases: T8O18.11, T8O18_11	6.1	3.3	2.8	9.0	0.06%	8.0
1182	AT2G34200.1 | zinc finger (C3HC4-type RING finger) family protein | chr2:14447727-14449084 FORWARD | Aliases: F13P17.4, F13P17_4	5.9	3.4	2.5	9.0	0.06%	8.1
1183	AT4G00585.1 | expressed protein | chr4:250955-252532 REVERSE | Aliases: None	11.3	9.2	2.1	9.0	0.06%	8.6
1184	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	8.4	5.0	3.4	9.0	0.06%	8.3
1186	AT5G58250.1 | expressed protein | chr5:23576703-23577739 FORWARD | Aliases: MCK7.12, MCK7_12	6.6	3.4	3.3	9.0	0.06%	7.8
1187	AT2G40765.1 | expressed protein | chr2:17019276-17020403 FORWARD | Aliases: None	10.8	9.1	1.7	9.0	0.06%	8.5
1191	AT1G30500.2 | CCAAT-binding transcription factor (CBF-B/NF-YA) family protein, contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA)	7.7	5.3	2.4	9.0	0.06%	7.9
1195	AT2G20450.1 | 60S ribosomal protein L14 (RPL14A) | chr2:8820947-8822332 FORWARD | Aliases: T13C7.4, T13C7_4	9.4	6.9	2.6	9.0	0.06%	8.4
1197	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	6.6	3.0	3.6	9.0	0.06%	7.1
1198	AT2G31490.1 | expressed protein | chr2:13419060-13420323 FORWARD | Aliases: T28P16.2, T28P16_2	12.0	10.4	1.5	9.0	0.06%	8.6
1202	AT5G09770.1 | ribosomal protein L17 family protein, contains Pfam profile: PF01196 ribosomal protein L17 | chr5:3035047-3036543 REVERSE | Aliases: F17I14.40, F17I14_40	8.9	6.1	2.8	9.0	0.06%	8.3
1204	AT1G09340.1 | expressed protein | chr1:3015388-3018236 FORWARD | Aliases: None	7.6	4.2	3.4	9.0	0.06%	7.2
1206	AT1G12400.1 | expressed protein | chr1:4221861-4222835 FORWARD | Aliases: F5O11.12, F5O11_12	8.1	5.0	3.1	9.0	0.06%	8.1
1208	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	9.6	6.5	3.1	9.0	0.06%	8.2
1209	AT2G44670.1 | senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana); | chr2:18432255-18433135 FORWARD | Aliases: F16B22.16	9.3	5.7	3.7	9.0	0.06%	8.2

Rank	Description	Sync	Root	M	t	adj.q	B
1212	AT4G35570.1 | Symbol: HMGB5 | high mobility group protein delta (HMGdelta) / HMG protein delta, identical to HMG protein (HMGdelta) (Arabidopsis thaliana) GI:2832363	7.8	5.7	2.1	9.0	0.06%	8.4
1214	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	6.9	4.6	2.3	8.9	0.06%	8.0
1216	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	6.8	3.1	3.8	8.9	0.06%	6.8
1217	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	5.3	2.8	8.9	0.06%	8.1
1218	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	10.2	6.7	3.5	8.9	0.06%	8.0
1219	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, T1J8_17	6.0	3.8	2.2	8.9	0.06%	8.2
1220	AT3G09210.1 | KOW domain-containing transcription factor family protein, ; est match | chr3:2825290-2826886 REVERSE | Aliases: F3L24.8	8.4	5.7	2.7	8.9	0.06%	7.8
1221	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	7.2	3.3	3.9	8.9	0.06%	6.9
1222	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	6.0	3.9	2.2	8.9	0.06%	8.1
1229	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	9.6	6.8	2.8	8.9	0.06%	8.3
1230	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	8.9	5.4	3.5	8.9	0.06%	7.8
1231	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	3.3	2.9	8.9	0.06%	7.6
1233	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	8.0	5.2	2.7	8.9	0.06%	7.9
1235	AT5G39340.1 | Symbol: AHP3 | two-component phosphorelay mediator 2 (HP2), nearly identical to ATHP2 (Arabidopsis thaliana) GI:4156243	9.0	7.6	1.4	8.9	0.06%	8.5
1236	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	6.7	2.8	4.0	8.9	0.06%	7.4
1238	AT3G49010.3 | Symbol: ATBBC1 |	12.9	10.8	2.1	8.9	0.06%	8.5
1239	AT5G47110.1 | lil3 protein, putative, similar to Lil3 protein (Arabidopsis thaliana) gi:4741966:gb:AAD28780 | chr5:19151215-19152544 REVERSE | Aliases: K14A3.6, K14A3_6	8.7	5.9	2.8	8.9	0.06%	8.1
1243	AT3G57160.1 | expressed protein | chr3:21168589-21169795 REVERSE | Aliases: None	7.2	4.8	2.4	8.9	0.06%	8.0
1246	AT1G20430.1 | expressed protein | chr1:7083186-7083825 REVERSE | Aliases: F5M15.30, F5M15_30	6.3	3.5	2.8	8.8	0.06%	7.8
1247	AT1G19130.1 | expressed protein | chr1:6609360-6610593 REVERSE | Aliases: F14D16.29, F14D16_29	9.1	6.8	2.3	8.8	0.06%	8.2
1248	AT3G06790.2 | plastid developmental protein DAG, putative, similar to DAG protein, chloroplast precursor (Garden snapdragon) SWISS-PROT:Q38732	8.8	5.5	3.3	8.8	0.06%	8.1

Rank	Description	Sync	Root	M	t	adj.q	B
1249	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	11.6	9.9	1.6	8.8	0.06%	8.5
1250	AT5G42150.1 | expressed protein | chr5:16863378-16865507 FORWARD | Aliases: MJC20.26, MJC20_26	9.5	6.7	2.8	8.8	0.06%	8.2
1252	AT3G17930.1 | expressed protein | chr3:6141834-6143316 REVERSE | Aliases: MEB5.15	8.6	5.8	2.8	8.8	0.06%	7.9
1253	AT2G20270.1 | glutaredoxin family protein, contains glutaredoxin domain, Pfam:PF00462 | chr2:8744786-8746741 REVERSE | Aliases: F11A3.18, F11A3_18	7.7	3.0	4.6	8.8	0.06%	7.9
1254	AT1G15980.1 | expressed protein | chr1:5489292-5491303 FORWARD | Aliases: T24D18.8, T24D18_8	7.1	3.7	3.4	8.8	0.06%	7.2
1255	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	8.5	5.3	3.1	8.8	0.06%	8.3
1256	AT4G26860.1 | alanine racemase family protein, contains Pfam domain, PF01168: Alanine racemase, N-terminal domain | chr4:13503092-13504756 REVERSE | Aliases: F10M23.200, F10M23_200	6.4	4.7	1.7	8.8	0.06%	8.4
1258	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	10.4	6.0	4.4	8.8	0.06%	7.7
1260	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	7.5	4.1	3.4	8.8	0.06%	7.7
1261	AT3G26980.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr3:9947403-9949277 REVERSE | Aliases: MOJ10.7	8.6	5.4	3.2	8.8	0.06%	8.4
1262	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-utilising enzyme, mobile region (InterPro:IPR008279) | chr4:8864826-8870905 REVERSE | Aliases: DL3805C, FCAALL.325	5.3	2.7	2.6	8.8	0.06%	7.7
1263	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	2.7	2.8	8.8	0.06%	7.7
1264	AT1G17350.1 | auxin-induced-related / indole-3-acetic acid induced-related, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesnerian)	7.9	4.5	3.3	8.8	0.06%	8.2
1265	AT4G38225.3 | expressed protein | chr4:17927216-17928888 FORWARD | Aliases: None	6.6	3.8	2.8	8.8	0.06%	7.7
1266	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	7.1	4.2	2.9	8.8	0.06%	7.9
1267	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	8.0	4.2	3.8	8.8	0.06%	7.9
1269	AT3G49720.1 | expressed protein | chr3:18450988-18453182 REVERSE | Aliases: T16K5.70	9.7	7.0	2.7	8.8	0.06%	8.4
1271	AT3G16100.1 | Ras-related GTP-binding family protein, contains Pfam profile: PF00071 Ras family | chr3:5459178-5460783 FORWARD | Aliases: MSL1.14	9.2	6.4	2.8	8.8	0.06%	7.8
1273	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	8.0	3.8	4.2	8.8	0.06%	7.5
1274	AT3G55500.1 | Symbol: ATEXPA16 | expansin, putative (EXP16), similar to expansin GI:2828241 from (Brassica napus); alpha-expansin gene family, PMID:11641069 | chr3:20586052-20587125 REVERSE | Aliases: ARABIDOPSIS THALIANA EXPANSIN A16, ATEXP16, ATHEXP ALPHA 1.7, EXP16, T22E16.160	7.3	3.4	3.8	8.8	0.06%	6.6
1275	AT2G17280.1 | phosphoglycerate/bisphosphoglycerate mutase family protein, contains Pfam profile PF00300: phosphoglycerate mutase family | chr2:7520293-7522122 FORWARD | Aliases: F5J6.4, F5J6_4	9.3	4.1	5.1	8.8	0.06%	7.0
1276	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	8.3	5.1	3.2	8.8	0.06%	8.1

Rank	Description	Sync	Root	M	t	adj.q	B
1278	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	6.6	2.6	3.9	8.8	0.06%	7.7
1281	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	8.0	4.6	3.3	8.8	0.06%	7.2
1282	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	9.0	2.0	8.8	0.06%	8.3
1285	AT1G70560.1 | alliinase C-terminal domain-containing protein, contains Pfam profiles: PF04864 allinase C-terminal domain, PF04863 alliinase EGF-like domain | chr1:26608518-26611166 FORWARD | Aliases: F24J13.13, F24J13_13	6.5	3.0	3.5	8.8	0.06%	6.7
1290	AT3G29185.2 | expressed protein | chr3:11156166-11158444 REVERSE | Aliases: MXO21.1	6.7	4.7	1.9	8.7	0.06%	8.2
1291	AT4G36710.1 | scarecrow transcription factor family protein | chr4:17305762-17307647 FORWARD | Aliases: AP22.56, AP22_56	7.4	4.3	3.1	8.7	0.06%	7.6
1292	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	6.7	4.3	2.4	8.7	0.06%	8.1
1294	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	11.5	9.5	1.9	8.7	0.06%	8.4
1295	AT3G56910.1 | expressed protein | chr3:21080395-21081312 REVERSE | Aliases: T8M16.240	9.5	7.6	1.9	8.7	0.06%	8.3
1306	AT1G08390.1 | expressed protein | chr1:2642211-2643282 FORWARD | Aliases: T27G7.27	6.2	3.7	2.5	8.7	0.06%	7.7
1310	AT3G07410.1 | Ras-related GTP-binding family protein, contains Pfam profile: PF00071 Ras family | chr3:2372323-2373562 REVERSE | Aliases: F21O3.12	9.3	5.2	4.1	8.7	0.07%	7.8
1311	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	7.3	4.3	3.0	8.7	0.07%	7.8
1312	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	3.7	3.2	8.7	0.07%	7.7
1316	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	3.0	3.5	8.7	0.07%	6.8
1324	AT3G05070.1 | expressed protein | chr3:1416165-1417743 FORWARD | Aliases: T12H1.3, T12H1_3	8.5	4.8	3.7	8.6	0.07%	7.8
1325	AT1G54780.1 | thylakoid lumen 18.3 kDa protein, SP:Q9ZVL6 | chr1:20443101-20444826 FORWARD | Aliases: T22H22.19, T22H22_19	8.5	6.4	2.2	8.6	0.07%	8.0
1326	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	8.2	4.3	3.9	8.6	0.07%	7.0
1327	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	4.5	2.6	8.6	0.07%	7.7
1331	AT3G57490.1 | 40S ribosomal protein S2 (RPS2D), 40S ribosomal protein S2 - Arabidopsis thaliana, SWISSPROT:RS2_ARATH | chr3:21290643-21291925 REVERSE | Aliases: T8H10.90	8.0	5.0	3.0	8.6	0.07%	7.7
1335	AT1G56150.1 | auxin-responsive family protein, similar to SP:P33082 Auxin-induced protein X15. (Soybean) {Glycine max}	5.0	1.9	3.1	8.6	0.07%	7.1
1336	AT2G24040.1 | 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 | chr2:10231057-10231686 FORWARD | Aliases: T29E15.24, T29E15_24	7.4	5.8	1.6	8.6	0.07%	8.3
1337	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	12.2	7.3	5.0	8.6	0.07%	8.0

Rank	Description	Sync	Root	M	t	adj.q	B
1338	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	7.5	4.6	2.9	8.6	0.07%	7.7
1339	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	8.3	5.3	3.0	8.6	0.07%	7.5
1340	AT5G64670.1 | ribosomal protein L15 family protein | chr5:25869493-25871215 REVERSE | Aliases: MUB3.19, MUB3_19	8.2	6.5	1.7	8.6	0.07%	8.1
1342	AT4G27090.1 | 60S ribosomal protein L14 (RPL14B), ribosomal protein L14 - Human,PIR3:JC5954 | chr4:13593911-13595257 REVERSE | Aliases: T24A18.40, T24A18_40	12.8	11.4	1.4	8.6	0.07%	8.3
1344	AT1G72170.1 | expressed protein, contains Pfam PF04418: Domain of unknown function (DUF543) | chr1:27159997-27161338 FORWARD | Aliases: T9N14.2	9.6	7.1	2.5	8.6	0.07%	8.1
1347	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	11.5	9.2	2.3	8.6	0.07%	8.3
1348	AT4G38400.1 | Symbol: ATEXLA2 | expansin family protein (EXPL2), contains Pfam profile: PF01357 pollen allergen; expansin-like gene, PMID:11641069, www.bio.psu.edu/expansins	6.4	3.2	3.2	8.6	0.07%	6.8
1349	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	7.9	6.0	2.0	8.6	0.07%	8.0
1351	AT2G47260.1 | Symbol: WRKY23 |	6.3	4.4	1.9	8.6	0.07%	8.1
1353	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)	9.7	6.6	3.1	8.6	0.07%	7.6
1354	AT2G15000.2 | expressed protein | chr2:6488440-6489469 REVERSE | Aliases: T15J14.4, T15J14_4	6.6	3.9	2.8	8.6	0.07%	7.9
1355	AT3G15190.1 | chloroplast 30S ribosomal protein S20, putative, contains Pfam profile: PF01649 ribosomal protein S20 | chr3:5116154-5117622 FORWARD | Aliases: F4B12.10	7.2	5.4	1.8	8.6	0.07%	8.0
1359	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	8.6	5.7	2.8	8.6	0.07%	7.9
1360	AT2G16070.2 | expressed protein | chr2:6990974-6992544 REVERSE | Aliases: F7H1.9, F7H1_9	8.2	5.8	2.4	8.6	0.07%	8.0
1367	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	10.0	6.2	3.7	8.5	0.07%	7.7
1368	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	5.6	4.0	1.7	8.5	0.07%	8.2
1370	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	5.0	2.8	8.5	0.07%	7.5
1373	AT3G56340.1 | 40S ribosomal protein S26 (RPS26C), several 40S ribosomal protein S26 | chr3:20903116-20904395 REVERSE | Aliases: T5P19.4	11.5	8.6	2.9	8.5	0.07%	8.2
1376	AT5G56670.1 | 40S ribosomal protein S30 (RPS30C) | chr5:22952639-22953207 REVERSE | Aliases: MIK19.12	11.5	9.4	2.1	8.5	0.07%	8.2
1377	AT5G57930.2 | Symbol: APO2 | expressed protein | chr5:23471843-23473719 FORWARD | Aliases: ACCUMULATION OF PHOTOSYSTEM ONE 2, EMB1629, EMBRYO DEFECTIVE 1629, MTI20.19, MTI20_19	7.0	5.2	1.7	8.5	0.07%	8.1
1379	AT3G54960.1 | Symbol: ATPDIL1 3 | Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	8.4	5.3	3.0	8.5	0.07%	7.6

Rank	Description	Sync	Root	M	t	adj.q	B
1384	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	8.3	3.2	8.5	0.07%	8.1
1385	AT5G07020.1 | proline-rich family protein | chr5:2180503-2182387 REVERSE | Aliases: MOJ9.19, MOJ9_19	6.9	3.9	2.9	8.5	0.07%	7.4
1386	AT5G42310.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:16933011-16936156 FORWARD | Aliases: K5J14.11, K5J14_11	5.8	2.9	2.9	8.5	0.07%	7.6
1389	AT5G47700.1 | 60S acidic ribosomal protein P1 (RPP1C) | chr5:19345029-19346209 REVERSE | Aliases: MCA23.2, MCA23_2	10.3	8.2	2.0	8.5	0.07%	7.9
1390	AT3G60245.1 | 60S ribosomal protein L37a (RPL37aC) | chr3:22279721-22280981 FORWARD | Aliases: None	13.7	12.6	1.2	8.5	0.07%	8.1
1393	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) (Hevea brasiliensis); similar to Stress-related protein (Swiss-Prot:Q9SW70) (Vitis riparia) | chr2:19577132-19578494 FORWARD | Aliases: F17A22.17	6.7	3.0	3.7	8.5	0.07%	6.6
1394	AT4G09800.1 | Symbol: RPS18C |	11.2	10.0	1.1	8.5	0.07%	8.0
1398	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	9.8	6.4	3.4	8.5	0.07%	7.2
1402	AT1G27120.1 | galactosyltransferase family protein, contains Pfam profile:PF01762 galactosyltransferase | chr1:9421164-9424054 FORWARD | Aliases: T7N9.18, T7N9_18	6.1	2.9	3.2	8.5	0.08%	7.3
1403	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	10.7	7.4	3.3	8.5	0.08%	7.8
1405	AT5G02590.1 | chloroplast lumen common family protein, various predicted proteins, Arabidopsis thaliana | chr5:583084-584177 FORWARD | Aliases: T22P11.180, T22P11_180	5.0	2.5	2.5	8.5	0.08%	7.7
1406	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	7.9	4.6	3.2	8.4	0.08%	7.7
1407	AT5G47320.1 | Symbol: RPS19 | 30S ribosomal protein S19, mitochondrial (RPS19) | chr5:19220379-19222499 FORWARD | Aliases: MQL5.18, MQL5_18	8.6	5.7	2.9	8.4	0.08%	7.9
1411	AT5G23850.1 | expressed protein | chr5:8038129-8040934 FORWARD | Aliases: MRO11.11, MRO11_11	6.9	4.6	2.3	8.4	0.08%	7.6
1412	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	9.3	5.2	4.1	8.4	0.08%	7.8
1413	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	8.1	5.4	2.8	8.4	0.08%	7.9
1416	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	7.2	3.7	3.5	8.4	0.08%	7.0
1418	AT4G22890.3 | expressed protein | chr4:12006997-12009529 FORWARD | Aliases: F7H19.70, F7H19_70	9.5	6.6	2.9	8.4	0.08%	8.0
1420	AT5G56910.1 | expressed protein | chr5:23040148-23041428 FORWARD | Aliases: MHM17.2, MHM17_2	8.5	4.9	3.6	8.4	0.08%	7.6
1421	AT2G34260.2 | transducin family protein / WD-40 repeat family protein, similar to Vegetatible incompatibility protein HET-E-1 (SP:Q00808) {Podospora anserina}	7.3	5.0	2.3	8.4	0.08%	7.9
1423	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	10.3	8.8	1.4	8.4	0.08%	8.1
1424	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	5.9	2.7	3.3	8.4	0.08%	7.0

Rank	Description	Sync	Root	M	t	adj.q	B
1425	AT4G16720.1 | 60S ribosomal protein L15 (RPL15A) | chr4:9399987-9401404 REVERSE | Aliases: DL4385C, FCAALL.416	11.9	10.6	1.3	8.4	0.08%	8.1
1426	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	7.9	5.3	2.6	8.4	0.08%	7.9
1427	AT5G20040.2 | Symbol: ATIPT9 |	8.4	5.1	3.3	8.4	0.08%	7.4
1429	AT3G50360.1 | Symbol: ATCEN2 |	8.8	6.3	2.5	8.4	0.08%	8.0
1430	AT4G18400.1 | expressed protein | chr4:10169877-10171268 REVERSE | Aliases: F28J12.60, F28J12_60	7.8	6.0	1.8	8.4	0.08%	8.1
1431	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	7.5	2.9	4.6	8.4	0.08%	6.9
1438	AT5G44710.1 | expressed protein, similar to unknown protein (ref:NP_011731.1) | chr5:18058153-18059787 FORWARD | Aliases: K23L20.5, K23L20_5	8.8	5.5	3.4	8.4	0.08%	7.7
1439	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	6.5	1.8	8.4	0.08%	7.9
1442	AT3G29280.1 | expressed protein, ; expression supported by MPSS | chr3:11237942-11239184 REVERSE | Aliases: MMF24.3	6.3	4.0	2.3	8.4	0.08%	7.7
1443	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	11.1	7.5	3.5	8.4	0.08%	7.7
1445	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	12.1	10.6	1.5	8.3	0.08%	8.1
1447	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	6.0	4.2	8.3	0.08%	8.0
1448	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	7.6	4.4	3.2	8.3	0.08%	7.6
1449	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 GI:21241 from (Spinacia oleracea) | chr1:5402564-5403813 REVERSE | Aliases: F7H2.4, F7H2_4	6.7	4.3	2.5	8.3	0.08%	7.8
1453	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	7.0	5.0	1.9	8.3	0.08%	8.0
1454	AT5G56940.1 | ribosomal protein S16 family protein, contains Pfam profile PF00886: ribosomal protein S16 | chr5:23048027-23049637 FORWARD | Aliases: MHM17.5, MHM17_5	9.6	7.4	2.2	8.3	0.08%	7.9
1455	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	5.0	2.2	2.8	8.3	0.08%	7.3
1456	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	10.3	2.2	8.3	0.08%	8.0
1458	AT2G33450.1 | 50S ribosomal protein L28, chloroplast (CL28) | chr2:14180655-14181609 FORWARD | Aliases: F4P9.22, F4P9_22	6.1	2.8	3.3	8.3	0.08%	7.1
1460	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	5.6	2.6	3.0	8.3	0.08%	7.0

Rank	Description	Sync	Root	M	t	adj.q	B
1461	AT1G06010.1 | expressed protein | chr1:1822617-1823996 FORWARD | Aliases: T21E18.6, T21E18_6	6.4	3.5	2.9	8.3	0.08%	7.7
1462	AT4G22160.2 | expressed protein | chr4:11733135-11734039 FORWARD | Aliases: T10I14.8	6.0	3.6	2.3	8.3	0.08%	7.7
1463	AT1G67430.1 | 60S ribosomal protein L17 (RPL17B), similar to ribosomal protein GI:19101 from (Hordeum vulgare)	12.1	10.0	2.1	8.3	0.08%	8.0
1466	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	7.1	4.0	3.0	8.3	0.08%	6.8
1467	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	8.4	5.7	2.7	8.3	0.08%	7.6
1470	AT2G37470.1 | histone H2B, putative, strong similarity to histone H2B from Lycopersicon esculentum GI:3021483, GI:3021485, Capsicum annuum SP:O49118; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4	8.9	5.4	3.5	8.3	0.08%	7.2
1471	AT4G01150.1 | expressed protein | chr4:493548-494795 FORWARD | Aliases: F2N1.18, F2N1_18	10.1	6.7	3.4	8.3	0.08%	7.7
1472	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	8.8	3.6	8.3	0.08%	8.0
1473	AT3G50440.1 | similar to esterase, putative [Arabidopsis thaliana] (TAIR:At2g23620.1); similar to methyl jasmonate esterase [Solanum tuberosum] (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	7.5	3.7	3.8	8.3	0.08%	6.3
1474	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	6.2	3.1	3.1	8.3	0.08%	6.8
1476	AT5G57280.1 | expressed protein | chr5:23221696-23223877 FORWARD | Aliases: MJB24.9, MJB24_9	8.5	6.0	2.5	8.3	0.08%	7.7
1478	AT2G21280.1 | Symbol: GC1 | expressed protein, similar to YfhF (GI:2804536) (Bacillus subtilis) | chr2:9117394-9119776 REVERSE | Aliases: GIANT CHLOROPLAST 1	7.0	3.4	3.5	8.3	0.08%	7.2
1479	AT5G24010.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:8113798-8116618 FORWARD | Aliases: MZF18.11, MZF18_11	6.3	3.9	2.4	8.3	0.08%	7.9
1480	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	10.3	7.2	3.1	8.3	0.08%	7.7
1481	AT2G03430.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr2:1036029-1037613 REVERSE | Aliases: T4M8.14, T4M8_14	7.6	5.9	1.7	8.3	0.08%	8.0
1482	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	11.9	10.8	1.1	8.3	0.08%	7.8
1485	AT2G35635.1 | Symbol: UBQ7 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr2:14988073-14989195 FORWARD | Aliases: None	10.5	6.6	3.9	8.3	0.08%	7.7
1486	AT4G29660.1 | Symbol: EMB2752 | expressed protein, predicted proteins, Arabidopsis thaliana | chr4:14534269-14535298 REVERSE | Aliases: EMB2752, EMBRYO DEFECTIVE 2752, T16L4.170, T16L4_170	8.3	6.3	2.0	8.3	0.08%	7.9
1487	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	6.7	4.1	2.7	8.3	0.08%	7.4
1488	AT3G04550.1 | expressed protein | chr3:1225928-1227442 FORWARD | Aliases: F7O18.2, F7O18_2	9.6	7.5	2.1	8.3	0.08%	8.0
1489	AT4G27660.1 | expressed protein, ; expression supported by MPSS | chr4:13816890-13818033 REVERSE | Aliases: T29A15.150, T29A15_150	6.4	3.3	3.1	8.3	0.08%	7.0
1490	AT5G03050.1 | expressed protein | chr5:715028-716320 REVERSE | Aliases: F15A17.80, F15A17_80	6.4	2.8	3.6	8.3	0.08%	7.6
1491	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	6.2	2.7	3.4	8.3	0.08%	7.2

Rank	Description	Sync	Root	M	t	adj.q	B
1495	AT5G54580.1 | RNA recognition motif (RRM)-containing protein, low similarity to RNA-binding protein RGP-3 (Nicotiana sylvestris) GI:1009363; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	8.4	6.4	2.0	8.3	0.08%	7.9
1497	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	8.3	4.7	3.6	8.2	0.09%	7.7
1500	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	4.7	2.9	8.2	0.09%	7.7
1503	AT2G43460.1 | 60S ribosomal protein L38 (RPL38A) | chr2:18053081-18054478 REVERSE | Aliases: T1O24.20	10.6	8.5	2.1	8.2	0.09%	8.0
1505	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	8.0	4.3	3.7	8.2	0.09%	7.3
1508	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	7.1	4.9	2.1	8.2	0.09%	7.7
1511	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	7.7	4.2	3.5	8.2	0.09%	7.8
1512	AT2G19385.1 | expressed protein, weak similarity to Cell growth regulating nucleolar protein (Swiss-Prot:Q08288) (Mus musculus) | chr2:8394117-8395794 FORWARD | Aliases: None	5.7	3.4	2.3	8.2	0.09%	7.6
1514	AT1G63970.2 | Symbol: ISPF | 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, putative, similar to 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase GI:7621712 from (Catharanthus roseus) | chr1:23742354-23743999 REVERSE | Aliases: 2C METHYL D ERYTHRITOL 2,4 CYCLODIPHOSPHATE SYNTHASE, T12P18.1, T12P18_1	7.3	4.2	3.2	8.2	0.09%	7.5
1518	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	6.5	3.8	2.8	8.2	0.09%	7.3
1519	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	7.4	4.2	3.3	8.2	0.09%	6.8
1521	AT3G60810.2 | expressed protein | chr3:22481494-22483079 FORWARD | Aliases: T4C21.220	6.9	5.3	1.7	8.2	0.09%	7.8
1522	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	8.4	6.5	1.8	8.2	0.09%	7.9
1523	AT3G55250.1 | expressed protein, predicted pectate-lyase, Arabidopsis thaliana, PIR:T06728 | chr3:20490266-20491611 FORWARD | Aliases: T26I12.130	8.4	4.9	3.5	8.2	0.09%	7.5
1531	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	7.0	3.4	3.6	8.2	0.09%	7.3
1532	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	4.6	2.4	8.2	0.09%	7.7
1533	AT3G63420.2 | Symbol: AGG1 | heterotrimeric G protein gamma-subunit (AGG1) | chr3:23428292-23429673 FORWARD | Aliases: HETEROTRIMERIC G PROTEIN GAMMA SUBUNIT, MAA21.50	8.3	6.3	2.0	8.2	0.09%	7.9
1536	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	7.3	4.7	2.6	8.2	0.09%	7.5
1539	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	9.4	6.7	2.7	8.1	0.09%	7.8
1543	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	6.3	3.2	3.2	8.1	0.09%	7.6

Rank	Description	Sync	Root	M	t	adj.q	B
1545	AT2G20390.1 | expressed protein | chr2:8803364-8805299 REVERSE | Aliases: F11A3.6, F11A3_6	7.9	5.8	2.1	8.1	0.09%	7.6
1546	AT2G18050.2 | Symbol: HIS1 3 |	4.9	2.8	2.1	8.1	0.09%	7.7
1548	AT3G45160.1 | expressed protein | chr3:16544436-16545063 REVERSE | Aliases: T14D3.100	9.3	5.5	3.8	8.1	0.09%	7.8
1550	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	10.8	9.5	1.2	8.1	0.09%	7.8
1551	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	6.9	3.5	3.4	8.1	0.09%	7.0
1552	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	7.5	2.5	8.1	0.09%	7.6
1553	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	7.5	2.5	8.1	0.09%	7.6
1556	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	9.1	6.2	2.9	8.1	0.09%	7.6
1557	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	5.8	2.9	2.9	8.1	0.09%	7.0
1558	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	5.6	2.8	2.8	8.1	0.09%	7.2
1559	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	9.5	5.6	4.0	8.1	0.09%	6.5
1560	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	6.8	4.1	2.8	8.1	0.09%	7.6
1562	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	8.6	7.2	1.4	8.1	0.09%	7.8
1563	AT1G51400.1 | photosystem II 5 kD protein, 100% identical to GI:4836947 (F5D21.10) | chr1:19055730-19056250 REVERSE | Aliases: F5D21.10, F5D21_10	8.7	5.3	3.4	8.1	0.09%	7.5
1564	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	7.1	4.2	2.9	8.1	0.09%	7.4
1565	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	9.2	6.9	2.3	8.1	0.09%	7.7
1566	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	10.1	8.0	2.1	8.1	0.09%	7.8
1567	AT2G17972.1 | expressed protein | chr2:7828667-7829403 FORWARD | Aliases: None	6.1	3.2	2.9	8.1	0.09%	6.8
1568	AT3G04620.1 | expressed protein | chr3:1255532-1256857 REVERSE | Aliases: F7O18.10, F7O18_10	5.8	3.0	2.8	8.1	0.09%	6.9
1570	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	9.3	6.3	2.9	8.1	0.09%	7.5

Rank	Description	Sync	Root	M	t	adj.q	B
1571	AT3G08740.1 | elongation factor P (EF-P) family protein, similar to SP:P33398 Elongation factor P (EF-P) {Escherichia coli O157:H7}; contains Pfam profile PF01132: Elongation factor P (EF-P)	8.3	5.2	3.2	8.1	0.09%	7.0
1572	AT5G50410.1 | expressed protein | chr5:20545425-20547053 REVERSE | Aliases: MXI22.13, MXI22_13	6.7	4.0	2.6	8.1	0.09%	7.1
1573	AT3G02900.1 | expressed protein | chr3:645828-647622 FORWARD | Aliases: F13E7.15, F13E7_15	7.1	4.8	2.2	8.1	0.09%	7.4
1574	AT3G19800.1 | expressed protein | chr3:6876120-6878156 FORWARD | Aliases: MPN9.4	5.8	3.1	2.6	8.1	0.09%	7.2
1575	AT2G29630.2 | thiamine biosynthesis family protein / thiC family protein, contains Pfam profile: PF01964 ThiC family | chr2:12674111-12677388 FORWARD | Aliases: T27A16.27, T27A16_27	7.0	3.8	3.2	8.1	0.09%	6.7
1577	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	7.9	5.9	2.0	8.1	0.09%	7.6
1580	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	6.7	3.4	3.3	8.1	0.09%	6.7
1581	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	6.7	3.5	3.2	8.1	0.09%	6.8
1582	AT1G07430.1 | protein phosphatase 2C, putative / PP2C, putative, similar to GB:CAB90633 from (Fagus sylvatica)	8.8	4.2	4.6	8.1	0.09%	7.5
1583	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	10.0	7.9	2.1	8.1	0.09%	7.7
1584	AT3G61870.2 | expressed protein, hypothetical protein - Synechocystis sp. (strain PCC 6803), PIR:S75899 | chr3:22913627-22915034 FORWARD | Aliases: F21F14.40	6.5	3.8	2.7	8.1	0.09%	7.1
1589	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	7.3	1.7	8.1	0.10%	7.8
1595	AT2G38450.1 | expressed protein | chr2:16109115-16109993 FORWARD | Aliases: T19C21.6, T19C21_6	7.7	5.8	1.9	8.0	0.10%	7.7
1596	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)	8.5	5.2	3.2	8.0	0.10%	7.0
1601	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	11.4	7.1	4.4	8.0	0.10%	7.7
1602	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	6.5	4.1	2.4	8.0	0.10%	7.7
1603	AT3G14190.1 | expressed protein | chr3:4710490-4711976 FORWARD | Aliases: MAG2.18	8.3	6.1	2.3	8.0	0.10%	7.5
1604	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	9.3	5.8	3.4	8.0	0.10%	7.6
1612	AT4G08390.2 | L-ascorbate peroxidase, stromal (sAPX), identical to stromal ascorbate peroxidase (Arabidopsis thaliana) gi:1419388:emb:CAA67425	9.1	5.8	3.2	8.0	0.10%	7.5
1613	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	8.1	5.4	2.7	8.0	0.10%	7.2
1614	AT1G74390.1 | exonuclease family protein, contains exonuclease domain, Pfam:PF00929 | chr1:27965198-27967508 REVERSE | Aliases: F1M20.7, F1M20_7	5.1	3.3	1.9	8.0	0.10%	7.6

Rank	Description	Sync	Root	M	t	adj.q	B
1616	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	3.8	4.0	8.0	0.10%	7.3
1617	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	8.0	5.8	2.2	8.0	0.10%	7.7
1618	AT4G30660.1 | 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 | chr4:14955453-14956069 FORWARD | Aliases: T10C21.10, T10C21_10	9.1	7.1	1.9	8.0	0.10%	7.7
1619	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	10.2	7.6	2.6	8.0	0.10%	7.4
1620	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	6.4	3.5	3.0	8.0	0.10%	7.5
1621	AT5G06110.1 | 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 | chr5:1840831-1843001 REVERSE | Aliases: K16F4.7, K16F4_7	8.2	6.7	1.5	8.0	0.10%	7.7
1622	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	10.3	7.2	3.1	8.0	0.10%	7.7
1623	AT5G55190.1 | Symbol: RAN3 | Ras-related GTP-binding protein (RAN3), identical to atran3 (Arabidopsis thaliana) GI:2058280 | chr5:22409402-22411392 FORWARD | Aliases: MCO15.14, MCO15_14	11.1	9.8	1.3	8.0	0.10%	7.8
1624	AT2G21640.1 | expressed protein | chr2:9261539-9262705 FORWARD | Aliases: F2G1.9, F2G1_9	4.1	2.4	1.7	8.0	0.10%	7.6
1625	AT2G39795.1 | mitochondrial glycoprotein family protein / MAM33 family protein, low similarity to SUAPRGA1 (Emericella nidulans) GI:6562379; contains Pfam profile PF02330: Mitochondrial glycoprotein	6.6	4.8	1.9	8.0	0.10%	7.6
1627	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	7.7	4.2	3.5	8.0	0.10%	7.4
1629	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	5.9	2.9	8.0	0.10%	7.4
1630	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	7.9	5.6	2.4	8.0	0.10%	7.3
1632	AT2G21320.1 | zinc finger (B-box type) family protein | chr2:9133344-9134924 FORWARD | Aliases: F3K23.8, F3K23_8	6.8	4.0	2.7	8.0	0.10%	7.1
1633	AT1G32310.1 | expressed protein | chr1:11653544-11654771 FORWARD | Aliases: F27G20.14	7.9	4.5	3.3	8.0	0.10%	7.3
1638	AT5G27760.1 | hypoxia-responsive family protein, contains Pfam profile: PF04588 hypoxia induced protein conserved region | chr5:9830368-9831787 FORWARD | Aliases: T1G16.90, T1G16_90	10.8	8.0	2.7	8.0	0.10%	7.7
1640	AT5G01600.1 | Symbol: ATFER1 |	11.1	8.5	2.6	8.0	0.10%	7.6
1643	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	6.7	3.9	2.8	8.0	0.10%	7.2
1644	AT1G22140.2 | expressed protein | chr1:7814830-7815620 REVERSE | Aliases: F2E2.21, F2E2_21	9.1	6.8	2.2	8.0	0.10%	7.6
1647	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	8.4	6.3	2.1	8.0	0.10%	7.7
1648	AT1G17510.1 | expressed protein | chr1:6023497-6024302 REVERSE | Aliases: F1L3.22, F1L3_22	10.4	7.6	2.8	8.0	0.10%	7.7

Rank	Description	Sync	Root	M	t	adj.q	B
1649	AT4G37200.1 | Symbol: HCF164 |	7.2	5.6	1.6	8.0	0.10%	7.7
1653	AT2G39140.1 | pseudouridine synthase family protein | chr2:16337261-16340438 FORWARD | Aliases: AT2G39150, T16B24.22, T16B24_22	5.9	4.0	1.8	7.9	0.10%	7.5
1654	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	7.4	5.4	2.0	7.9	0.10%	7.6
1655	AT3G51800.2 | Symbol: ATG2 | metallopeptidase M24 family protein, similar to SP:P50580 Proliferation-associated protein 2G4 {Mus musculus}; contains Pfam profile PF00557: metallopeptidase family M24 | chr3:19222004-19224646 REVERSE | Aliases: ATEM1.5	11.1	9.2	1.8	7.9	0.10%	7.7
1657	AT5G63670.1 | transcription initiation protein-related, contains weak similarity to Transcription initiation protein SPT4 homolog 1 (Swiss-Prot:Q16550) (Mus musculus)	9.1	6.6	2.5	7.9	0.10%	7.6
1662	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	5.6	4.3	1.3	7.9	0.10%	7.7
1664	AT1G55805.1 | BolA-like family protein, contains Pfam profile: PF01722 BolA-like protein | chr1:20862397-20863105 REVERSE | Aliases: None	8.8	5.6	3.2	7.9	0.10%	7.3
1665	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	7.5	5.1	2.3	7.9	0.10%	7.3
1666	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	8.1	5.5	2.5	7.9	0.10%	7.3
1669	AT3G57360.1 | expressed protein | chr3:21236549-21237662 FORWARD | Aliases: F28O9.210	7.4	4.9	2.5	7.9	0.10%	7.3
1670	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	7.9	4.2	3.7	7.9	0.10%	6.7
1671	AT2G35900.1 | expressed protein | chr2:15077076-15078732 REVERSE | Aliases: F11F19.19, F11F19_19	7.3	4.1	3.3	7.9	0.10%	7.2
1673	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	6.3	3.1	3.2	7.9	0.10%	6.9
1674	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) (Homo sapiens) | chr1:817983-819563 REVERSE | Aliases: F15K9.7, F15K9_7	10.7	8.8	1.9	7.9	0.10%	7.6
1675	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	5.4	2.1	7.9	0.10%	7.6
1676	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	7.5	5.5	2.1	7.9	0.10%	7.6
1678	AT3G18740.1 | 60S ribosomal protein L30 (RPL30C), similar to 60S RIBOSOMAL PROTEIN L30 GB:O49884 from (Lupinus luteus)	11.2	9.9	1.2	7.9	0.10%	7.7
1679	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	5.3	3.1	2.2	7.9	0.10%	7.4
1680	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	7.3	4.7	2.6	7.9	0.10%	7.4
1681	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	3.4	2.2	7.9	0.10%	7.3

Rank	Description	Sync	Root	M	t	adj.q	B
1685	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	7.5	5.2	2.4	7.9	0.10%	7.6
1686	AT1G02475.1 | expressed protein | chr1:513916-515343 REVERSE | Aliases: None	6.3	3.8	2.5	7.9	0.10%	7.2
1687	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	7.6	3.4	4.2	7.9	0.10%	6.3
1690	AT5G39960.1 | GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function | chr5:16011423-16014048 FORWARD | Aliases: MYH19.120, MYH19_120	5.2	3.7	1.5	7.9	0.11%	7.6
1691	AT5G42980.1 | Symbol: ATTRX3 |	13.3	12.2	1.1	7.9	0.11%	7.5
1693	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	7.9	4.2	3.7	7.9	0.11%	7.0
1694	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	10.8	9.0	1.8	7.9	0.11%	7.6
1695	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	6.8	4.2	2.5	7.9	0.11%	7.1
1696	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)	10.3	8.4	1.9	7.9	0.11%	7.6
1698	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	8.7	5.3	3.4	7.9	0.11%	6.8
1699	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	5.3	3.6	1.7	7.9	0.11%	7.5
1701	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	5.9	3.0	2.9	7.9	0.11%	7.2
1702	AT4G32350.1 | expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292	5.1	3.4	1.7	7.9	0.11%	7.5
1703	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	9.6	8.3	1.3	7.9	0.11%	7.6
1704	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	8.8	6.5	2.3	7.9	0.11%	7.2
1706	AT1G66820.1 | glycine-rich protein | chr1:24933703-24934214 FORWARD | Aliases: F4N21.5, F4N21_5	7.0	5.1	2.0	7.9	0.11%	7.3
1708	AT5G09510.1 | 40S ribosomal protein S15 (RPS15D), ribosomal protein S15 - Arabidopsis thaliana, EMBL:Z23161 | chr5:2955114-2956674 REVERSE | Aliases: T5E8.310, T5E8_310	8.2	5.5	2.7	7.9	0.11%	7.6
1709	AT2G41950.1 | expressed protein | chr2:17520157-17521921 FORWARD | Aliases: T6D20.26, T6D20_26	6.8	4.4	2.3	7.9	0.11%	7.4
1710	AT5G02050.1 | mitochondrial glycoprotein family protein / MAM33 family protein, low similarity to SUAPRGA1 (Emericella nidulans) GI:6562379; contains Pfam profile PF02330: Mitochondrial glycoprotein	7.9	4.6	3.3	7.9	0.11%	6.8
1712	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	6.3	3.6	2.8	7.8	0.11%	6.8
1715	AT5G57230.1 | expressed protein | chr5:23207798-23208711 FORWARD | Aliases: MJB24.4, MJB24_4	6.6	4.6	2.0	7.8	0.11%	7.5
1716	AT1G28150.1 | expressed protein | chr1:9834930-9835886 REVERSE | Aliases: F13K9.24	7.5	5.7	1.8	7.8	0.11%	7.6

Rank	Description	Sync	Root	M	t	adj.q	B
1718	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	7.9	4.0	3.9	7.8	0.11%	7.5
1721	AT1G13380.1 | expressed protein | chr1:4589068-4590408 REVERSE | Aliases: T6J4.13, T6J4_13	8.2	6.0	2.2	7.8	0.11%	7.6
1724	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	10.6	8.2	2.4	7.8	0.11%	7.3
1725	AT1G17490.1 | expressed protein | chr1:6008582-6009409 FORWARD | Aliases: F28G4.23	8.7	7.5	1.2	7.8	0.11%	7.6
1728	AT2G45860.1 | expressed protein | chr2:18881834-18882649 REVERSE | Aliases: F4I18.16	6.9	5.0	1.9	7.8	0.11%	7.4
1729	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	8.2	1.8	7.8	0.11%	7.5
1731	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	3.3	2.9	7.8	0.11%	7.3
1734	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	9.2	7.2	2.0	7.8	0.11%	7.5
1738	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	5.9	2.4	7.8	0.11%	7.4
1741	AT3G61080.1 | fructosamine kinase family protein, contains Pfam PF03881: Fructosamine kinase | chr3:22618105-22620074 FORWARD | Aliases: T27I15.170	6.0	3.3	2.7	7.8	0.11%	6.7
1742	AT5G03650.1 | Symbol: SBE2.2 |	8.6	4.9	3.7	7.8	0.11%	7.3
1744	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	7.5	4.3	3.2	7.8	0.11%	7.0
1746	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	10.4	7.5	2.9	7.8	0.11%	7.4
1747	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	7.7	5.7	2.0	7.8	0.11%	7.5
1748	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	11.4	8.9	2.5	7.8	0.11%	7.6
1749	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	5.8	2.1	3.7	7.8	0.11%	7.5
1751	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	7.0	4.7	2.3	7.8	0.11%	7.2
1752	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	7.2	4.9	2.3	7.8	0.11%	7.3
1753	AT3G09735.1 | DNA-binding S1FA family protein, contains Pfam profile: PF04689 DNA binding protein S1FA	9.7	8.2	1.5	7.8	0.11%	7.6
1754	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	6.5	3.2	3.4	7.8	0.11%	6.9
1756	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	6.8	3.7	3.1	7.8	0.11%	6.7

Rank	Description	Sync	Root	M	t	adj.q	B
1757	AT3G62940.2 | OTU-like cysteine protease family protein, contains Pfam profile PF02338: OTU-like cysteine protease | chr3:23273925-23275646 REVERSE | Aliases: T20O10.40	8.6	6.9	1.7	7.8	0.11%	7.5
1758	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	2.5	2.0	7.8	0.11%	7.2
1759	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	9.8	7.6	2.3	7.8	0.11%	7.4
1762	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	10.2	6.6	3.5	7.8	0.11%	7.3
1763	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	8.2	5.3	2.9	7.8	0.11%	7.3
1769	AT3G63390.1 | expressed protein | chr3:23422141-23422943 REVERSE | Aliases: MAA21.20	8.9	7.1	1.8	7.8	0.11%	7.5
1771	AT2G37120.1 | DNA-binding S1FA family protein, contains Pfam profile: PF04689 DNA binding protein S1FA	9.5	7.7	1.8	7.8	0.11%	7.5
1772	AT5G53400.1 | nuclear movement family protein, contains Pfam profile: PF03593 nuclear movement protein	10.0	6.7	3.3	7.8	0.11%	7.3
1773	AT2G14890.2 | Symbol: AGP9 | arabinogalactan-protein (AGP9), identical to gi:10880495:gb:AAG24277 | chr2:6406703-6408064 FORWARD | Aliases: ARABINOGALACTAN PROTEIN 9, T26I20.5, T26I20_5	9.3	7.0	2.3	7.7	0.11%	7.3
1774	AT1G19240.1 | expressed protein | chr1:6649089-6650411 REVERSE | Aliases: T29M8.11, T29M8_11	8.3	6.3	2.0	7.7	0.11%	7.3
1775	AT5G23060.1 | expressed protein | chr5:7736593-7738518 REVERSE | Aliases: MYJ24.5, MYJ24_5	6.2	3.2	2.9	7.7	0.11%	6.7
1777	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	4.9	2.4	7.7	0.11%	7.3
1783	AT5G62575.2 | expressed protein | chr5:25134749-25136118 FORWARD | Aliases: None	7.5	5.5	1.9	7.7	0.12%	7.3
1784	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	6.3	4.3	2.0	7.7	0.12%	7.3
1785	AT5G39600.1 | expressed protein | chr5:15871157-15872420 REVERSE | Aliases: MIJ24.9, MIJ24_9	6.6	3.8	2.9	7.7	0.12%	7.0
1787	AT2G46450.1 | Symbol: ATCNGC12 | cyclic nucleotide-regulated ion channel, putative (CNGC12), similar to cyclic nucleotide and calmodulin-regulated ion channel (cngc3) GI:4581201 from (Arabidopsis thaliana)	6.6	3.9	2.8	7.7	0.12%	7.1
1789	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	9.6	6.2	3.4	7.7	0.12%	7.4
1792	AT4G34555.1 | 40S ribosomal protein S25, putative | chr4:16504235-16505477 REVERSE | Aliases: None	8.1	5.1	3.0	7.7	0.12%	7.1
1794	AT4G37380.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:17572034-17573932 REVERSE | Aliases: F6G17.30, F6G17_30	6.2	4.3	1.9	7.7	0.12%	7.3
1795	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	6.2	3.4	2.8	7.7	0.12%	6.5
1797	AT1G33030.1 | O-methyltransferase family 2 protein, similar to caffeic acid 3-O-methyltransferase (SP:Q00763) (Populus tremuloides), catechol O-methyltransferase (GI:4808524)(Thalictrum tuberosum) | chr1:11964756-11966256 REVERSE | Aliases: F9L11.18, F9L11_18	5.7	2.7	3.0	7.7	0.12%	7.0
1798	AT3G09890.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr3:3032564-3034448 FORWARD | Aliases: F8A24.6	4.8	2.8	1.9	7.7	0.12%	7.4
1800	AT2G33570.1 | expressed protein | chr2:14224299-14226324 FORWARD | Aliases: F4P9.34, F4P9_34	6.4	3.0	3.4	7.7	0.12%	7.1

Rank	Description	Sync	Root	M	t	adj.q	B
1802	AT3G53580.1 | diaminopimelate epimerase family protein, contains Pfam profile PF01678: Diaminopimelate epimerase | chr3:19875742-19878112 FORWARD | Aliases: F4P12.280	10.9	9.5	1.3	7.7	0.12%	7.5
1803	AT5G65220.1 | ribosomal protein L29 family protein, contains Pfam profile PF00831: ribosomal protein L29 | chr5:26078455-26079888 FORWARD | Aliases: MQN23.16, MQN23_16	6.6	4.7	1.9	7.7	0.12%	7.3
1804	AT3G60210.1 | chloroplast chaperonin 10, putative, similar to chloroplast chaperonin 10 GI:14041813 from (Arabidopsis thaliana) | chr3:22262219-22263800 REVERSE | Aliases: F27H5.5	9.6	6.3	3.3	7.7	0.12%	7.3
1806	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	6.2	3.1	3.2	7.7	0.12%	6.5
1807	AT2G21960.1 | expressed protein | chr2:9361999-9364499 FORWARD | Aliases: F7D8.28, F7D8_28	7.8	5.4	2.4	7.7	0.12%	7.2
1808	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	5.1	3.0	2.1	7.7	0.12%	7.1
1809	AT5G25630.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:8947392-8949602 FORWARD | Aliases: T14C9.170, T14C9_170	8.1	5.7	2.3	7.7	0.12%	7.3
1813	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	3.1	3.1	7.7	0.12%	6.5
1814	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	4.2	2.6	1.6	7.7	0.12%	7.4
1815	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	8.9	4.3	4.6	7.7	0.12%	7.1
1816	AT4G28830.1 | expressed protein | chr4:14232452-14234005 FORWARD | Aliases: F16A16.60, F16A16_60	8.8	6.5	2.4	7.7	0.12%	7.1
1818	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	6.3	4.5	1.8	7.7	0.12%	7.4
1820	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	12.4	11.0	1.4	7.7	0.12%	7.3
1821	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	5.9	3.9	2.0	7.7	0.12%	7.2
1823	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	7.4	5.0	2.4	7.7	0.12%	7.1
1825	AT5G53420.2 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g27900.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g27900.2); similar to zinc finger CONSTANS-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD73395.1) | chr5:21691615-21692959 FORWARD | Aliases: MYN8.3, MYN8_3	8.7	6.6	2.0	7.7	0.12%	7.3
1826	AT1G20340.1 | Symbol: DRT112 |	9.2	4.9	4.3	7.7	0.12%	6.8
1827	AT4G16146.1 | expressed protein | chr4:9142445-9144588 REVERSE | Aliases: None	5.7	3.3	2.4	7.7	0.12%	7.1
1831	AT5G62840.1 | phosphoglycerate/bisphosphoglycerate mutase family protein, contains Pfam profile PF00300: phosphoglycerate mutase family | chr5:25245451-25246909 REVERSE | Aliases: MQB2.16, MQB2_16	5.5	2.9	2.6	7.6	0.12%	6.5
1834	AT3G53370.1 | DNA-binding S1FA family protein, contains Pfam profile: PF04689 DNA binding protein S1FA	7.1	3.9	3.2	7.6	0.12%	6.5
1835	AT5G06730.1 | peroxidase, putative, similar to peroxidase (Arabidopsis thaliana) gi:1491617:emb:CAA68212 | chr5:2079956-2081685 REVERSE | Aliases: MPH15.9, MPH15_9	7.0	2.3	4.6	7.6	0.12%	6.7
1837	AT1G06460.1 | Symbol: ACD32.1 | 31.2 kDa small heat shock family protein / hsp20 family protein, contains Pfam profile: PF00011 Hsp20/alpha crystallin family	5.5	2.9	2.6	7.6	0.12%	7.2

Rank	Description	Sync	Root	M	t	adj.q	B
1840	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	6.9	4.5	2.4	7.6	0.12%	7.0
1842	AT3G14600.1 | 60S ribosomal protein L18A (RPL18aC), similar to GB:CAA08791 from (Podocoryne carnea) | chr3:4910704-4912180 FORWARD | Aliases: MIE1.10	10.3	7.7	2.6	7.6	0.12%	7.3
1845	AT2G37500.1 | arginine biosynthesis protein ArgJ family, contains Pfam profile: PF01960 ArgJ family | chr2:15746418-15749836 REVERSE | Aliases: F3G5.29, F3G5_29	8.1	5.5	2.6	7.6	0.12%	7.2
1847	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	8.3	5.2	3.2	7.6	0.12%	7.0
1848	AT4G09640.1 | expressed protein, several hypothetical proteins - Arabidopsis thaliana | chr4:6088214-6090885 REVERSE | Aliases: T25P22.80, T25P22_80	5.8	3.8	2.0	7.6	0.12%	7.1
1849	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	4.2	2.6	7.6	0.12%	7.3
1850	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	9.3	5.9	3.3	7.6	0.12%	7.2
1851	AT3G49320.1 | expressed protein, contains Pfam profile PF03690: Uncharacterised protein family (UPF0160) | chr3:18299232-18301643 REVERSE | Aliases: F2K15.180	6.6	4.6	2.0	7.6	0.12%	7.2
1855	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	6.0	3.2	2.8	7.6	0.12%	6.8
1859	AT4G20150.1 | expressed protein | chr4:10888309-10889606 REVERSE | Aliases: F1C12.70, F1C12_70	12.9	11.6	1.2	7.6	0.12%	7.3
1861	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	9.3	7.8	1.5	7.6	0.12%	7.4
1865	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	8.5	4.5	4.0	7.6	0.12%	6.9
1867	AT2G19680.1 | mitochondrial ATP synthase g subunit family protein, contains Pfam profile: PF04718 mitochondrial ATP synthase g subunit	10.5	7.0	3.5	7.6	0.12%	7.3
1869	AT5G47930.1 | 40S ribosomal protein S27 (RPS27D) | chr5:19423403-19424624 REVERSE | Aliases: K16F13.2, K16F13_2	12.1	10.2	1.9	7.6	0.13%	7.3
1872	AT3G18510.1 | expressed protein | chr3:6355670-6356159 FORWARD | Aliases: MYF24.41	6.2	3.4	2.7	7.6	0.13%	6.9
1873	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	4.6	2.9	7.6	0.13%	7.2
1874	AT1G74240.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr1:27921057-27923800 FORWARD | Aliases: F1O17.9, F1O17_9	8.5	6.3	2.1	7.6	0.13%	7.3
1875	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	9.5	7.7	1.8	7.6	0.13%	7.4
1876	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	10.2	6.6	3.7	7.6	0.13%	7.2
1879	AT4G21110.1 | G10 family protein, contains Pfam profile: PF01125 G10 protein | chr4:11267196-11268968 FORWARD | Aliases: F7J7.50, F7J7_50	10.5	8.9	1.5	7.6	0.13%	7.4

Rank	Description	Sync	Root	M	t	adj.q	B
1881	AT1G50840.1 | polI-like DNA polymerase, putative, similar to PolI-like DNA polymerase (Oryza sativa) GI:19912795 contains Pfam profiles PF01612: 3'-5' exonuclease, PF00476: DNA polymerase I family A	7.6	5.2	2.4	7.6	0.13%	6.8
1882	AT3G28700.1 | expressed protein, contains Pfam PF02636: Uncharacterized ACR, COG1565 | chr3:10760802-10763351 FORWARD | Aliases: MZN14.19	7.3	5.2	2.1	7.6	0.13%	7.2
1885	AT3G54120.1 | reticulon family protein (RTNLB12), contains Pfam profile PF02453: Reticulon | chr3:20051974-20053318 REVERSE | Aliases: F24B22.80	6.7	3.7	3.0	7.6	0.13%	6.9
1886	AT5G58420.1 | 40S ribosomal protein S4 (RPS4D), ribosomal protein S4, Arabidopsis thaliana, PIR:T48480	10.4	8.5	1.9	7.6	0.13%	7.3
1890	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	9.6	7.8	1.8	7.6	0.13%	7.3
1891	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	7.2	4.4	2.8	7.6	0.13%	6.5
1892	AT2G23670.1 | expressed protein | chr2:10070235-10070943 REVERSE | Aliases: F26B6.28	5.6	3.6	2.0	7.6	0.13%	7.0
1894	AT5G02570.1 | histone H2B, putative, similar to histone H2B-2 Lycopersicon esculentum GI:3021483, Gossypium hirsutum SP:O22582, Asparagus officinalis GI:563329; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 | chr5:576740-577138 REVERSE | Aliases: T22P11.160, T22P11_160	7.5	3.5	4.0	7.6	0.13%	6.6
1895	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	11.3	9.3	2.1	7.6	0.13%	7.3
1897	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	9.2	7.6	1.7	7.6	0.13%	7.3
1899	AT5G43970.1 | Symbol: TOM22 V | expressed protein | chr5:17710034-17710630 FORWARD | Aliases: ATTOM22 V, MRH10.8, MRH10_8, TOM22, TOM9 2	8.2	6.0	2.2	7.6	0.13%	7.3
1900	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	6.0	3.5	2.5	7.6	0.13%	6.9
1901	AT1G77670.1 | aminotransferase class I and II family protein, similar to kynurenine aminotransferase /glutamine transaminase K GI:1030066 (Rattus norvegicus) | chr1:29193795-29195869 REVERSE | Aliases: T5M16.26, T5M16_26	8.5	4.7	3.8	7.6	0.13%	6.7
1902	AT3G50910.1 | expressed protein | chr3:18930494-18933219 FORWARD | Aliases: F18B3.190	9.6	7.9	1.7	7.6	0.13%	7.3
1903	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	7.4	3.4	4.0	7.6	0.13%	5.8
1905	AT3G03150.1 | expressed protein | chr3:727561-729467 REVERSE | Aliases: T17B22.16, T17B22_16	9.6	7.0	2.5	7.5	0.13%	7.1
1907	AT5G54380.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:22094318-22097106 REVERSE | Aliases: GA469.3, GA469_3	5.8	4.1	1.8	7.5	0.13%	7.2
1908	AT5G24840.1 | expressed protein, contains Pfam profile PF02390: Putative methyltransferase | chr5:8533790-8535046 REVERSE | Aliases: F6A4.50, F6A4_50	7.9	6.0	1.9	7.5	0.13%	7.1
1912	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	6.7	3.7	3.1	7.5	0.13%	6.6
1916	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	6.4	3.5	2.9	7.5	0.13%	6.3

Rank	Description	Sync	Root	M	t	adj.q	B
1920	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	8.9	6.8	2.1	7.5	0.13%	7.2
1921	AT1G66890.1 | expressed protein | chr1:24961221-24961777 FORWARD | Aliases: T4O24.4, T4O24_4	7.2	5.7	1.5	7.5	0.13%	7.3
1922	AT5G52220.1 | expressed protein, ; expression supported by MPSS | chr5:21224456-21224904 REVERSE | Aliases: F17P19.12, F17P19_12	6.1	2.8	3.3	7.5	0.13%	6.7
1925	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	9.6	6.3	3.2	7.5	0.13%	7.2
1926	AT1G74970.1 | Symbol: RPS9 | ribosomal protein S9 (RPS9), identical to ribosomal protein S9 (Arabidopsis thaliana) GI:5456946	5.9	2.8	3.0	7.5	0.13%	6.6
1927	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	9.8	7.1	2.7	7.5	0.13%	7.3
1929	AT1G32160.1 | expressed protein | chr1:11568647-11570367 FORWARD | Aliases: F3C3.6, F3C3_6	7.2	5.3	1.8	7.5	0.13%	7.3
1930	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	5.7	2.1	7.5	0.13%	7.2
1931	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	10.9	9.1	1.8	7.5	0.13%	7.3
1934	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	5.8	3.9	2.0	7.5	0.13%	7.3
1936	AT2G36130.1 | peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type	8.2	5.6	2.6	7.5	0.13%	7.1
1937	AT5G06460.1 | Symbol: ATUBA2 |	8.2	6.5	1.7	7.5	0.13%	7.3
1938	AT3G59140.1 | Symbol: ATMRP14 | ABC transporter family protein, putative multi resistance protein mrp - Arabidopsis thaliana, EMBL:ATMRPPROT | chr3:21874496-21879678 REVERSE | Aliases: F17J16.190	6.4	3.8	2.6	7.5	0.13%	6.4
1940	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	6.3	3.4	2.8	7.5	0.13%	6.3
1944	AT4G29770.1 | expressed protein | chr4:14575846-14577645 FORWARD | Aliases: F27B13.10, F27B13_10	6.6	3.1	3.5	7.5	0.13%	5.8
1948	AT5G10360.1 | Symbol: EMB3010 | 40S ribosomal protein S6 (RPS6B) | chr5:3258475-3260228 REVERSE | Aliases: EMB3010, EMBRYO DEFECTIVE 3010, F12B17.290, F12B17_290	10.7	9.2	1.5	7.5	0.13%	7.2
1949	AT5G24970.1 | ABC1 family protein, contains Pfam domain, PF03109: ABC1 family | chr5:8604339-8608820 REVERSE | Aliases: F6A4.180, F6A4_180	6.9	4.6	2.2	7.5	0.13%	7.1
1951	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	4.7	1.9	7.5	0.13%	7.0
1953	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	8.0	5.1	2.9	7.5	0.13%	7.2
1954	AT1G06190.1 | expressed protein | chr1:1892272-1894137 REVERSE | Aliases: F9P14.5, F9P14_5	5.0	3.5	1.5	7.5	0.13%	7.2
1956	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	7.5	4.4	3.1	7.5	0.13%	7.0

Rank	Description	Sync	Root	M	t	adj.q	B
1958	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	6.7	3.9	2.9	7.5	0.13%	7.2
1960	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	9.0	7.0	1.9	7.5	0.13%	7.3
1961	AT5G13510.1 | ribosomal protein L10 family protein, ribosomal protein L10- Nicotiana tabacum, EMBL:AB010879 | chr5:4341267-4342098 FORWARD | Aliases: T6I14.40, T6I14_40	8.1	4.8	3.3	7.5	0.13%	7.0
1962	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	11.1	5.8	5.2	7.5	0.13%	7.1
1964	AT5G55560.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:22523603-22525075 REVERSE | Aliases: MWC10.1, MWC10_1	6.3	4.1	2.2	7.5	0.13%	7.1
1965	AT1G77540.1 | expressed protein, similar to GB:AAD41433 | chr1:29142570-29143103 REVERSE | Aliases: T5M16.13, T5M16_13	8.9	6.1	2.8	7.5	0.13%	6.9
1966	AT3G28900.1 | 60S ribosomal protein L34 (RPL34C), similar to 60S ribosomal protein L34 GB:P41098 (Nicotiana tabacum) | chr3:10903924-10905686 REVERSE | Aliases: MLD15.7	8.2	4.8	3.5	7.5	0.13%	7.0
1967	AT1G31970.1 | DEAD/DEAH box helicase, putative, similar to p68 RNA helicase (Schizosaccharomyces pombe) GI:173419 | chr1:11479846-11482870 FORWARD | Aliases: F5M6.3	9.5	7.7	1.8	7.5	0.13%	7.3
1968	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	10.8	7.9	2.9	7.5	0.13%	7.3
1971	AT5G36170.3 | Symbol: HCF109 |	7.3	5.7	1.6	7.5	0.14%	7.2
1972	AT1G75210.1 | 5' nucleotidase family protein, contains Pfam profile: PF05761 5' nucleotidase family | chr1:28227530-28232636 FORWARD | Aliases: F22H5.7, F22H5_7	7.7	5.7	2.0	7.5	0.14%	7.0
1974	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	7.9	5.1	2.8	7.4	0.14%	6.9
1975	AT4G34265.2 | expressed protein | chr4:16402284-16403827 FORWARD | Aliases: None	7.6	4.4	3.2	7.4	0.14%	7.0
1976	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	12.6	11.0	1.6	7.4	0.14%	7.2
1977	AT1G01170.2 | similar to stress-related ozone-induced protein (OZI1) / 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	8.4	6.1	2.4	7.4	0.14%	7.2
1981	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	11.3	9.8	1.5	7.4	0.14%	7.2
1983	AT3G24030.1 | hydroxyethylthiazole kinase family protein, contains Pfam profile: PF02110 hydroxyethylthiazole kinase family | chr3:8679196-8680819 REVERSE | Aliases: F14O13.24	7.8	5.7	2.1	7.4	0.14%	7.0
1984	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	8.2	5.1	3.1	7.4	0.14%	7.0
1986	AT3G05910.1 | pectinacetylesterase, putative, similar to pectinacetylesterase precursor GI:1431629 from (Vigna radiata) | chr3:1764301-1767581 REVERSE | Aliases: F2O10.13	8.1	5.7	2.4	7.4	0.14%	7.2

Rank	Description	Sync	Root	M	t	adj.q	B
1987	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	6.8	3.9	2.9	7.4	0.14%	6.8
1989	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	10.2	7.7	2.5	7.4	0.14%	7.2
1996	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	9.7	7.6	2.1	7.4	0.14%	7.1
1998	AT2G47950.1 | expressed protein | chr2:19631293-19631879 FORWARD | Aliases: T9J23.9, T9J23_9	6.1	3.4	2.7	7.4	0.14%	6.9
1999	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	9.0	7.4	1.5	7.4	0.14%	7.1
2001	AT1G06680.1 | Symbol: PSBP | photosystem II oxygen-evolving complex 23 (OEC23), JBC 14:211-238 (2002); identical to 23 kDa polypeptide of oxygen-evolving comlex (OEC) GB:CAA66785 GI:1769905 (Arabidopsis thaliana) | chr1:2047878-2049417 FORWARD | Aliases: F12K11.3, F12K11_3, OE23, OEE2, OXYGEN EVOLVING ENHANCER PROTEIN 2	10.5	6.7	3.8	7.4	0.14%	7.0
2002	AT5G08320.1 | expressed protein, predicted proteins, Homo sapiens and Caenorhabditis elegans | chr5:2677053-2678679 FORWARD | Aliases: F8L15.50, F8L15_50	6.8	4.4	2.4	7.4	0.14%	7.1
2003	AT5G50930.1 | expressed protein, similar to unknown protein (emb:CAB61034.1) | chr5:20739295-20741543 FORWARD | Aliases: K3K7.8, K3K7_8	6.7	3.5	3.2	7.4	0.14%	5.8
2004	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	7.9	5.0	2.9	7.4	0.14%	6.8
2005	AT3G14290.1 | Symbol: PAE2 | 20S proteasome alpha subunit E2 (PAE2), identical to 20S proteasome subunit PAE2 GB:AAC32061 from (Arabidopsis thaliana)	10.2	8.9	1.4	7.4	0.14%	7.2
2007	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	6.6	4.5	2.1	7.4	0.14%	6.9
2008	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	7.4	5.4	2.0	7.4	0.14%	7.0
2012	AT2G27690.1 | Symbol: CYP94C1 | cytochrome P450, putative, similar to Cytochrome P450 94A1 (P450-dependent fatty acid omega-hydroxylase) (SP:O81117) {Vicia sativa}; contains Pfam profile: PF00067 cytochrome P450; supported by cDNA: gi_13877668 | chr2:11816383-11818292 FORWARD | Aliases: F15K20.21, F15K20_21	5.6	3.6	2.0	7.4	0.15%	6.8
2013	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	7.2	5.0	2.2	7.4	0.15%	7.1
2014	NA	11.0	9.8	1.2	7.4	0.15%	7.1
2015	AT2G31725.1 | expressed protein | chr2:13493394-13494522 REVERSE | Aliases: T9H9.25, T9H9_25	5.2	3.9	1.3	7.4	0.15%	7.2
2016	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	8.1	6.2	1.9	7.4	0.15%	7.0
2017	AT4G01430.2 | nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula) | chr4:585609-588027 FORWARD | Aliases: F3D13.4, F3D13_4	8.2	3.9	4.4	7.4	0.15%	7.0
2018	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	9.3	5.6	3.6	7.4	0.15%	6.5
2019	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	6.6	2.9	3.7	7.4	0.15%	6.5

Rank	Description	Sync	Root	M	t	adj.q	B
2020	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	6.6	4.3	2.2	7.4	0.15%	6.7
2024	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 doamins PF00069: Protein kinase domain and PF00560: Leucine Rich Repeat | chr1:25390004-25394736 FORWARD | Aliases: F12A21.30	6.5	4.7	1.8	7.3	0.15%	7.1
2026	AT1G59640.2 | Symbol: ZCW32 | basic helix-loop-helix (bHLH) family protein | chr1:21913300-21914837 REVERSE | Aliases: T30E16.21, T30E16_21, ZCW32	7.2	4.7	2.5	7.3	0.15%	6.8
2028	AT1G18500.1 | 2-isopropylmalate synthase, putative, strong similarity to 2-isopropylmalate synthase (IMS1) (Arabidopsis thaliana) GI:12330687; contains Pfam profile PF00682: HMGL-like | chr1:6369340-6373018 FORWARD | Aliases: F15H18.3, F15H18_3	10.3	7.5	2.8	7.3	0.15%	7.1
2030	AT2G30920.1 | Symbol: ATCOQ3 |	6.4	4.4	2.0	7.3	0.15%	7.0
2032	AT4G31360.1 | expressed protein | chr4:15221892-15223633 FORWARD | Aliases: F8F16.180, F8F16_180	6.4	4.1	2.3	7.3	0.15%	6.6
2036	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	7.4	4.6	2.8	7.3	0.15%	7.0
2037	AT1G32550.1 | ferredoxin family protein, similar to ferredoxin from Synechocystis 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	4.5	1.8	7.3	0.15%	6.9
2042	AT1G74720.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr1:28078834-28082417 FORWARD | Aliases: F25A4.35, F25A4_35	7.1	4.6	2.5	7.3	0.15%	6.7
2043	AT1G76100.1 | plastocyanin, identical to plastocyanin GI:1865683 from (Arabidopsis thaliana) | chr1:28558881-28559651 REVERSE | Aliases: T23E18.3, T23E18_3	5.1	2.4	2.6	7.3	0.15%	6.5
2046	AT1G48170.1 | expressed protein | chr1:17792455-17793762 FORWARD | Aliases: F21D18.10	6.2	3.9	2.3	7.3	0.15%	7.1
2048	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	6.3	3.9	2.4	7.3	0.15%	6.6
2050	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	9.2	6.8	2.4	7.3	0.15%	7.0
2054	AT1G46264.1 | Symbol: AT HSFB4 | heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain | chr1:17227282-17228720 FORWARD | Aliases: F2G19.8, F2G19_8, HSFB4	4.7	2.9	1.8	7.3	0.15%	7.0
2055	AT1G53520.1 | chalcone-flavanone isomerase-related, low similarity to GI:499036 (Vitis vinifera) | chr1:19980083-19981623 REVERSE | Aliases: F22G10.11	6.1	3.6	2.5	7.3	0.15%	6.9
2061	AT5G42060.1 | expressed protein | chr5:16835616-16836183 REVERSE | Aliases: MJC20.17, MJC20_17	6.3	4.2	2.1	7.3	0.15%	6.9
2062	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	10.4	6.9	3.5	7.3	0.15%	6.9
2063	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	10.4	7.9	2.5	7.3	0.15%	7.0
2064	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	12.4	10.1	2.3	7.3	0.15%	7.1
2065	AT2G24945.1 | expressed protein | chr2:10616492-10619311 FORWARD | Aliases: None	12.4	10.1	2.3	7.3	0.15%	7.1
2067	AT2G40750.1 | Symbol: WRKY54 |	5.8	4.5	1.3	7.3	0.15%	7.1
2068	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	7.8	5.9	1.9	7.3	0.15%	7.1

Rank	Description	Sync	Root	M	t	adj.q	B
2069	AT3G51510.1 | expressed protein | chr3:19120041-19121030 FORWARD | Aliases: F26O13.150	6.8	3.9	2.9	7.3	0.15%	6.3
2073	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	8.4	6.5	2.0	7.3	0.16%	7.1
2074	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	7.3	6.2	1.1	7.3	0.16%	7.1
2078	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	6.5	4.5	2.0	7.3	0.16%	6.8
2081	AT5G58110.1 | expressed protein, predicted proteins, Homo sapiens and Drosophila melanogaster | chr5:23532412-23533860 FORWARD | Aliases: K21L19.11, K21L19_11	10.2	8.7	1.5	7.3	0.16%	7.1
2083	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	6.5	3.9	2.6	7.3	0.16%	7.0
2084	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	3.6	3.0	7.3	0.16%	6.5
2087	AT5G11160.1 | adenine phosphoribosyltransferase, putative, strong similarity to SP:Q42563 Adenine phosphoribosyltransferase 2 (EC 2.4.2.7) (APRT) {Arabidopsis thaliana}; contains Pfam profile PF00156: Phosphoribosyl transferase domain | chr5:3550551-3552145 FORWARD | Aliases: F2I11.50, F2I11_50	5.9	4.2	1.7	7.2	0.16%	6.9
2088	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	8.8	5.7	3.0	7.2	0.16%	6.9
2089	AT2G24020.1 | expressed protein, contains Pfam domain PF02575: Uncharacterized BCR, YbaB family COG0718 | chr2:10224781-10226361 REVERSE | Aliases: T29E15.22, T29E15_22	7.8	5.7	2.1	7.2	0.16%	6.8
2092	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	7.6	4.9	2.8	7.2	0.16%	6.9
2093	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	4.6	1.4	7.2	0.16%	7.1
2096	AT1G69380.1 | expressed protein, predicated by genscan+ | chr1:26085004-26087269 REVERSE | Aliases: F23O10.4, F23O10_4	6.2	4.1	2.1	7.2	0.16%	6.9
2098	AT2G35605.1 | SWIB complex BAF60b domain-containing protein, contains Pfam profile PF02201: BAF60b domain of the SWIB complex | chr2:14953143-14954355 FORWARD | Aliases: None	7.8	4.2	3.6	7.2	0.16%	6.6
2099	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	4.9	2.5	7.2	0.16%	6.8
2101	AT4G20170.1 | expressed protein | chr4:10896689-10899151 FORWARD | Aliases: F1C12.90, F1C12_90	7.4	5.8	1.5	7.2	0.16%	7.0
2103	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	5.1	3.1	2.0	7.2	0.16%	7.0
2104	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	7.2	4.9	2.3	7.2	0.16%	6.8
2105	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	5.1	2.3	7.2	0.16%	6.9
2106	AT2G44310.1 | calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain | chr2:18316288-18316902 FORWARD | Aliases: F4I1.12	9.9	7.5	2.3	7.2	0.16%	6.9

Rank	Description	Sync	Root	M	t	adj.q	B
2108	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	8.4	5.6	2.8	7.2	0.16%	7.0
2111	AT5G40970.1 | expressed protein | chr5:16431266-16431732 FORWARD | Aliases: MEE6.4, MEE6_4	6.0	2.4	3.6	7.2	0.16%	6.9
2114	AT3G10620.1 | 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 | chr3:3320268-3322022 FORWARD | Aliases: F13M14.9	7.6	5.0	2.6	7.2	0.16%	6.5
2115	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	6.3	3.4	2.9	7.2	0.16%	6.4
2116	AT2G23150.1 | Symbol: NRAMP3 |	6.9	3.7	3.2	7.2	0.16%	6.3
2117	AT1G33040.1 | 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 | chr1:11966479-11967823 FORWARD | Aliases: F9L11.19, F9L11_19	10.6	7.1	3.5	7.2	0.16%	7.0
2119	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	9.1	5.4	3.7	7.2	0.16%	7.0
2120	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	6.8	1.4	7.2	0.16%	7.0
2121	AT1G02150.1 | pentatricopeptide (PPR) repeat-containing protein, low similiarity to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile: PF01535 PPR repeat | chr1:408622-410611 FORWARD | Aliases: T6A9.13	6.5	5.5	1.0	7.2	0.16%	7.0
2122	AT5G47810.1 | phosphofructokinase family protein, similar to phosphofructokinase (Amycolatopsis methanolica) GI:17432243; contains Pfam profile PF00365: Phosphofructokinase | chr5:19373582-19375351 REVERSE | Aliases: MCA23.13, MCA23_13	9.8	8.0	1.8	7.2	0.16%	7.0
2126	AT4G15790.1 | expressed protein | chr4:8982253-8984216 FORWARD | Aliases: DL3935W, FCAALL.69	5.7	3.7	2.0	7.2	0.16%	7.0
2127	AT1G47960.1 | Symbol: C/VIF1 |	9.8	7.4	2.4	7.2	0.16%	7.0
2135	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	5.7	2.9	2.8	7.2	0.16%	6.5
2136	AT4G35905.1 | expressed protein, contains Pfam domain PF03966: Protein of unknown function (DUF343) | chr4:17007031-17008157 REVERSE | Aliases: None	6.0	4.6	1.4	7.2	0.16%	7.0
2137	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	6.7	4.4	2.3	7.2	0.16%	6.8
2138	AT5G49510.2 | similar to unnamed protein product [Mus musculus] (GB:BAC37066.1); similar to PREDICTED: similar to von Hippel-Lindau binding protein 1 [Canis familiaris] (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 [Homo sapiens] (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	8.8	7.0	1.8	7.2	0.16%	6.9
2147	AT4G19400.1 | expressed protein | chr4:10580838-10582000 REVERSE | Aliases: T5K18.180, T5K18_180	7.7	6.1	1.6	7.2	0.16%	7.0
2149	AT1G76520.2 | auxin efflux carrier family protein, contains auxin efflux carrier domain, Pfam:PF03547 | chr1:28720049-28722308 FORWARD | Aliases: F14G6.12, F14G6_12	8.6	4.5	4.1	7.2	0.16%	6.7

Rank	Description	Sync	Root	M	t	adj.q	B
2153	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	11.3	8.2	3.1	7.2	0.16%	7.0
2155	AT3G15080.1 | exonuclease family protein, contains exonuclease domain, Pfam:PF00929 | chr3:5074272-5076528 FORWARD | Aliases: K15M2.23	6.6	4.4	2.2	7.2	0.16%	7.0
2156	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	6.1	3.6	2.5	7.2	0.16%	6.5
2157	AT1G71750.1 | phosphoribosyltransferase family protein, similar to SP:Q02522 Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT) (HGPRTase) {Lactococcus lactis}; contains Pfam profile PF00156: Phosphoribosyl transferase domain | chr1:26991465-26992822 REVERSE | Aliases: F14O23.13, F14O23_13	5.6	3.7	1.9	7.2	0.16%	7.0
2160	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	6.6	2.5	7.2	0.16%	6.9
2161	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	9.5	6.7	2.8	7.2	0.16%	6.9
2162	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	8.0	5.6	2.5	7.2	0.16%	6.6
2163	AT5G08270.1 | expressed protein | chr5:2661748-2663483 FORWARD | Aliases: F8L15.1, F8L15_1	4.5	3.6	1.0	7.2	0.16%	7.0
2164	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	8.6	5.9	2.7	7.2	0.16%	6.8
2165	AT1G14450.1 | expressed protein, contains similarity to cytochrome c oxidase subunit I GI:5678701 from (Loligo pealei)	9.2	7.6	1.7	7.2	0.17%	7.0
2166	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	7.0	4.6	2.4	7.2	0.17%	6.7
2167	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	9.1	6.5	2.6	7.2	0.17%	6.8
2171	AT5G01920.1 | Symbol: STN8 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr5:359127-362901 FORWARD | Aliases: T20L15.190, T20L15_190	7.8	6.3	1.5	7.2	0.17%	7.0
2180	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	9.5	6.2	3.3	7.1	0.17%	6.6
2183	AT2G34460.1 | flavin reductase-related, low similarity to SP:P30043 Flavin reductase {Homo sapiens} | chr2:14536687-14538037 FORWARD | Aliases: F13P17.33	7.5	4.2	3.3	7.1	0.17%	6.5
2185	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	4.2	2.1	7.1	0.17%	6.6
2186	AT3G02650.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:566278-570110 FORWARD | Aliases: F16B3.28, F16B3_28	7.1	4.6	2.5	7.1	0.17%	6.9

<table>
<tr><th>Rank</th><th>Description</th><th>Sync</th><th>Root</th><th>M</th><th>t</th><th>adj.q</th><th>B</th></tr>
<tr><td>2187</td><td>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</td><td>10.6</td><td>8.4</td><td>2.2</td><td>7.1</td><td>0.17%</td><td>7.0</td></tr>
<tr><td>2190</td><td>AT3G50410.1 | Symbol: OBP1 | Dof-type zinc finger domain-containing protein | chr3:18720729-18721724 FORWARD | Aliases: F11C1.250, OBF BINDING PROTEIN</td><td>6.3</td><td>3.1</td><td>3.2</td><td>7.1</td><td>0.17%</td><td>5.9</td></tr>
<tr><td>2191</td><td>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</td><td>10.5</td><td>6.3</td><td>4.3</td><td>7.1</td><td>0.17%</td><td>6.7</td></tr>
<tr><td>2193</td><td>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</td><td>8.2</td><td>7.0</td><td>1.2</td><td>7.1</td><td>0.17%</td><td>6.9</td></tr>
<tr><td>2195</td><td>AT1G13810.1 | expressed protein, ; expression supported by MPSS | chr1:4734085-4735161 FORWARD | Aliases: F16A14.30, F16A14_30</td><td>5.9</td><td>3.9</td><td>2.0</td><td>7.1</td><td>0.17%</td><td>6.7</td></tr>
<tr><td>2198</td><td>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</td><td>5.1</td><td>3.2</td><td>2.0</td><td>7.1</td><td>0.17%</td><td>6.6</td></tr>
<tr><td>2199</td><td>AT3G17890.1 | expressed protein | chr3:6127047-6127880 FORWARD | Aliases: MEB5.11</td><td>5.4</td><td>3.1</td><td>2.4</td><td>7.1</td><td>0.17%</td><td>6.5</td></tr>
<tr><td>2200</td><td>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</td><td>7.1</td><td>5.1</td><td>2.0</td><td>7.1</td><td>0.17%</td><td>6.9</td></tr>
<tr><td>2201</td><td>AT5G01210.1 | transferase family protein, contains Pfam profile PF02458 transferase family | chr5:84473-86274 FORWARD | Aliases: F7J8.190, F7J8_190</td><td>11.1</td><td>9.0</td><td>2.1</td><td>7.1</td><td>0.17%</td><td>6.9</td></tr>
<tr><td>2203</td><td>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</td><td>7.0</td><td>5.2</td><td>1.8</td><td>7.1</td><td>0.17%</td><td>6.9</td></tr>
<tr><td>2207</td><td>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</td><td>8.8</td><td>6.6</td><td>2.2</td><td>7.1</td><td>0.17%</td><td>6.8</td></tr>
<tr><td>2209</td><td>AT3G61450.1 | Symbol: SYP73 | syntaxin 73 (SYP73), identical to syntaxin 73 (AtSYP73) (Swiss-Prot:Q94KK5) (Arabidopsis thaliana) | chr3:22749369-22750959 FORWARD | Aliases: ATSYP73, F2A19.50, SYNTAXIN OF PLANTS 73</td><td>5.3</td><td>3.2</td><td>2.1</td><td>7.1</td><td>0.17%</td><td>6.6</td></tr>
<tr><td>2210</td><td>AT2G40760.1 | rhodanese-like domain-containing protein, contains rhodanese-like domain PF00581</td><td>7.8</td><td>6.2</td><td>1.6</td><td>7.1</td><td>0.17%</td><td>6.9</td></tr>
<tr><td>2211</td><td>AT3G56630.1 | Symbol: CYP94D2 | cytochrome P450, putative, cytochrome P450 CYP94A1 - Vicia sativa, PIR:T08014</td><td>6.6</td><td>3.9</td><td>2.6</td><td>7.1</td><td>0.17%</td><td>6.1</td></tr>
<tr><td>2212</td><td>AT3G07910.1 | expressed protein | chr3:2523163-2524171 REVERSE | Aliases: F17A17.25</td><td>10.1</td><td>8.5</td><td>1.6</td><td>7.1</td><td>0.17%</td><td>6.9</td></tr>
<tr><td>2213</td><td>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</td><td>6.5</td><td>4.0</td><td>2.4</td><td>7.1</td><td>0.17%</td><td>6.7</td></tr>
<tr><td>2214</td><td>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</td><td>6.2</td><td>4.4</td><td>1.8</td><td>7.1</td><td>0.17%</td><td>6.8</td></tr>
<tr><td>2218</td><td>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</td><td>5.7</td><td>3.7</td><td>2.0</td><td>7.1</td><td>0.17%</td><td>6.7</td></tr>
<tr><td>2220</td><td>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</td><td>5.3</td><td>3.0</td><td>2.2</td><td>7.1</td><td>0.18%</td><td>6.7</td></tr>
<tr><td>2227</td><td>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</td><td>6.7</td><td>3.9</td><td>2.7</td><td>7.1</td><td>0.18%</td><td>6.3</td></tr>
<tr><td>2228</td><td>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</td><td>10.3</td><td>6.7</td><td>3.6</td><td>7.1</td><td>0.18%</td><td>6.8</td></tr>
<tr><td>2229</td><td>AT5G06670.1 | kinesin motor protein-related | chr5:2048244-2055020 REVERSE | Aliases: F15M7.20, F15M7_20</td><td>6.1</td><td>4.8</td><td>1.3</td><td>7.1</td><td>0.18%</td><td>6.9</td></tr>
</table>

Rank	Description	Sync	Root	M	t	adj.q	B
2231	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	8.1	5.7	2.4	7.1	0.18%	6.8
2232	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	5.3	3.9	1.4	7.1	0.18%	6.9
2233	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	7.1	3.5	3.7	7.1	0.18%	6.3
2236	AT3G53560.1 | chloroplast lumen common family protein | chr3:19870605-19872009 REVERSE | Aliases: F4P12.260	6.7	4.6	2.1	7.0	0.18%	6.8
2237	AT1G44920.1 | expressed protein | chr1:16985344-16986849 REVERSE | Aliases: T12C22.21, T12C22_21	6.7	4.2	2.5	7.0	0.18%	6.2
2238	AT3G06730.1 | thioredoxin family protein, contains Pfam profile: PF00085 Thioredoxin | chr3:2124240-2126148 FORWARD | Aliases: F3E22.13	5.0	2.7	2.3	7.0	0.18%	6.4
2239	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	8.6	5.9	2.7	7.0	0.18%	6.5
2241	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	9.7	7.2	2.5	7.0	0.18%	6.8
2242	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	8.1	4.8	3.3	7.0	0.18%	6.6
2243	AT3G16520.3 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:5619134-5620879 REVERSE | Aliases: MDC8.15	9.0	5.4	3.6	7.0	0.18%	5.8
2244	AT5G14600.1 | expressed protein | chr5:4706948-4709146 FORWARD | Aliases: T15N1.90, T15N1_90	5.7	3.7	2.0	7.0	0.18%	6.6
2245	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	6.6	4.1	2.6	7.0	0.18%	6.6
2247	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	9.0	7.3	1.7	7.0	0.18%	6.8
2250	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	5.3	3.7	1.6	7.0	0.18%	6.7
2251	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	4.6	3.4	1.2	7.0	0.18%	6.9
2252	AT1G70350.1 | expressed protein | chr1:26510777-26511932 REVERSE | Aliases: F17O7.11, F17O7_11	6.0	3.1	2.8	7.0	0.18%	6.6
2253	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	6.6	4.0	2.5	7.0	0.18%	6.7
2254	AT3G29375.1 | XH domain-containing protein, contains Pfam profile: PF03469: XH domain | chr3:11281388-11283196 FORWARD | Aliases: None	5.3	3.1	2.2	7.0	0.18%	6.4
2257	AT2G19720.1 | Symbol: RPS15AB | 40S ribosomal protein S15A (RPS15aB) | chr2:8516562-8518399 REVERSE | Aliases: F6F22.25, F6F22_25, RPS15AB	6.8	3.8	3.0	7.0	0.18%	6.4
2259	AT5G16290.2 | acetolactate synthase small subunit, putative, similar to gi:5931761 from Nicotiana plumbaginifolia | chr5:5333830-5337747 FORWARD | Aliases: MQK4.1, MQK4_1	7.5	4.9	2.6	7.0	0.18%	6.6
2261	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	7.2	2.1	7.0	0.18%	6.8
2268	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	8.3	5.8	2.5	7.0	0.18%	6.7

Rank	Description	Sync	Root	M	t	adj.q	B
2269	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	6.2	2.7	3.5	7.0	0.18%	6.3
2270	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	7.4	4.5	3.0	7.0	0.18%	6.7
2272	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	5.1	2.9	7.0	0.19%	5.9
2273	AT3G56090.1 | Symbol: ATFER3 |	7.5	3.5	4.0	7.0	0.19%	5.9
2274	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	6.9	4.6	2.3	7.0	0.19%	6.3
2276	AT1G15790.2 | expressed protein | chr1:5438252-5440082 REVERSE | Aliases: F7H2.13, F7H2_13	4.2	3.2	1.0	7.0	0.19%	6.8
2277	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	7.6	5.8	1.7	7.0	0.19%	6.8
2282	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	7.0	4.5	2.6	7.0	0.19%	6.6
2283	AT1G36320.1 | expressed protein, similar to hypothetical protein GB:CAB37532 from (Arabidopsis thaliana), | chr1:13673029-13675310 FORWARD | Aliases: F7F23.4, F7F23_4	7.7	6.0	1.8	7.0	0.19%	6.8
2286	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	4.7	2.8	2.0	7.0	0.19%	6.5
2289	AT2G26440.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr2:11254461-11256562 FORWARD | Aliases: T9J22.11, T9J22_11	5.7	3.7	2.0	7.0	0.19%	6.5
2290	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	10.0	6.4	3.6	7.0	0.19%	6.5
2293	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	5.1	3.2	1.9	7.0	0.19%	6.6
2294	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	6.7	4.7	2.0	7.0	0.19%	6.5
2296	AT5G06000.1 | Symbol: EIF3G2 |	6.3	4.2	2.1	7.0	0.19%	6.4
2298	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	9.1	7.4	1.7	7.0	0.19%	6.8
2299	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	7.5	5.8	1.7	7.0	0.19%	6.7
2301	AT1G32990.1 | Symbol: PRPL11 |	6.7	3.6	3.2	7.0	0.19%	5.6
2302	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	6.0	3.6	2.4	7.0	0.19%	6.2
2304	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	9.0	5.4	3.7	7.0	0.19%	6.6
2305	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	8.4	5.7	2.6	7.0	0.19%	6.6

Rank	Description	Sync	Root	M	t	adj.q	B
2306	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	7.2	5.3	1.9	7.0	0.19%	6.5
2307	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	11.6	7.3	4.3	7.0	0.19%	6.8
2309	AT1G52300.1 | 60S ribosomal protein L37 (RPL37B), similar to SP:Q43292 from (Arabidopsis thaliana) | chr1:19478716-19479887 REVERSE | Aliases: F19K6.12, F19K6_12	13.0	11.8	1.2	7.0	0.19%	6.3
2311	AT2G27530.2 | 60S ribosomal protein L10A (RPL10aB) | chr2:11770332-11771821 REVERSE | Aliases: F10A12.22	10.7	8.3	2.4	7.0	0.19%	6.7
2312	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	7.2	5.3	2.0	7.0	0.19%	6.5
2313	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-glucoronosyl and UDP-glucosyl transferase	6.0	4.4	1.5	7.0	0.19%	6.7
2314	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	8.7	6.2	2.4	6.9	0.19%	6.8
2315	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	7.3	5.5	1.7	6.9	0.19%	6.7
2316	AT5G44520.1 | ribose 5-phosphate isomerase-related, low similarity to SP:P47968 Ribose 5-phosphate isomerase (EC 5.3.1.6) (Phosphoriboisomerase) {Mus musculus} | chr5:17951514-17953751 REVERSE | Aliases: MFC16.20, MFC16_20	5.8	4.3	1.5	6.9	0.19%	6.7
2319	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	10.5	6.9	3.6	6.9	0.19%	6.7
2320	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	7.8	5.2	2.7	6.9	0.19%	6.2
2323	AT3G13226.1 | regulatory protein RecX family protein, contains Pfam PF02631: regulatory protein RecX | chr3:4264311-4266369 REVERSE | Aliases: None	7.5	5.9	1.6	6.9	0.19%	6.7
2324	AT3G52910.1 | Symbol: AtGRF4 |	7.6	4.8	2.8	6.9	0.19%	6.0
2325	AT5G16200.1 | 50S ribosomal protein-related, contains weak similarity to Cyanelle 50S ribosomal protein L35. (Swiss-Prot:P14810) (Cyanophora paradoxa)	5.5	3.8	1.7	6.9	0.19%	6.7
2328	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	8.2	6.2	2.0	6.9	0.19%	6.5
2332	AT1G64185.1 | lactoylglutathione lyase family protein / glyoxalase I family protein, contains Pfam domain PF00903: glyoxalase family protein | chr1:23828177-23829447 FORWARD | Aliases: None	5.1	3.5	1.6	6.9	0.20%	6.7
2335	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	7.6	4.5	3.0	6.9	0.20%	6.3
2337	AT4G13200.1 | expressed protein, hypothetical protein sll1769 - Synechocystis sp,PID:d1018406 | chr4:7668146-7669197 REVERSE | Aliases: F17N18.90, F17N18_90	6.3	5.2	1.1	6.9	0.20%	6.7
2340	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	6.0	3.8	2.2	6.9	0.20%	6.4
2341	AT4G31930.1 | mitochondrial glycoprotein family protein / MAM33 family protein, similar to SUAPRGA1 (Emericella nidulans) GI:6562379; contains Pfam profile PF02330: Mitochondrial glycoprotein | chr4:15449667-15450842 REVERSE | Aliases: F11C18.4	5.8	3.4	2.4	6.9	0.20%	6.2

Rank	Description	Sync	Root	M	t	adj.q	B
2343	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	8.0	5.9	2.2	6.9	0.20%	6.7
2344	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	4.4	2.3	6.9	0.20%	6.3
2345	AT3G20930.1 | RNA recognition motif (RRM)-containing protein, contains Pfam profile: PF00076 RNA recognition motif | chr3:7331731-7334034 FORWARD | Aliases: MFD22.4	6.6	4.0	2.5	6.9	0.20%	6.4
2346	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 | chr4:222348-225457 FORWARD | Aliases: F6N23.1, F6N23_1	7.3	3.7	3.6	6.9	0.20%	6.3
2347	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	7.1	3.6	3.5	6.9	0.20%	6.1
2348	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	9.8	7.0	2.8	6.9	0.20%	6.6
2349	AT1G18640.2 | Symbol: PSP | 3-phosphoserine phosphatase (PSP), nearly identical to 3-phosphoserine phosphatase GI:3759177 from (Arabidopsis thaliana)	9.7	7.7	2.0	6.9	0.20%	6.7
2351	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	5.2	2.7	2.5	6.9	0.20%	6.4
2354	AT5G56710.1 | 60S ribosomal protein L31 (RPL31C) | chr5:22961062-22962196 REVERSE | Aliases: MIK19.16, MIK19_16	12.0	10.2	1.8	6.9	0.20%	6.7
2355	AT1G63960.1 | hypothetical protein | chr1:23741864-23742169 FORWARD | Aliases: T12P18.2, T12P18_2	3.7	2.5	1.2	6.9	0.20%	6.7
2359	AT2G36145.1 | expressed protein | chr2:15175620-15176585 FORWARD | Aliases: None	5.3	2.8	2.5	6.9	0.20%	6.0
2360	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	4.7	3.2	1.5	6.9	0.20%	6.6
2361	AT2G27330.1 | RNA recognition motif (RRM)-containing protein | chr2:11702112-11703693 REVERSE | Aliases: F12K2.9	6.3	4.8	1.5	6.9	0.20%	6.7
2363	AT4G32930.1 | expressed protein, predicted protein, Caenorhabditis elegans, gb:Z70780 | chr4:15898840-15900824 FORWARD | Aliases: F26P21.50, F26P21_50	8.4	6.6	1.8	6.9	0.20%	6.7
2364	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	4.0	1.8	6.9	0.20%	6.6
2365	AT1G20830.1 | expressed protein | chr1:7242909-7244893 FORWARD | Aliases: F2D10.35, F2D10_35	5.9	4.1	1.7	6.9	0.20%	6.7
2366	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	6.7	3.2	3.5	6.9	0.20%	6.4
2369	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	6.9	4.2	2.8	6.9	0.20%	6.4
2374	AT5G50890.1 | expressed protein | chr5:20719910-20721461 FORWARD | Aliases: K3K7.3, K3K7_3	7.5	4.9	2.6	6.9	0.20%	6.4
2376	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	5.5	3.3	2.2	6.9	0.21%	6.6
2377	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	6.5	3.6	2.9	6.9	0.21%	6.6
2379	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	6.6	5.6	1.0	6.8	0.21%	6.7

Rank	Description	Sync	Root	M	t	adj.q	B
2380	AT5G07240.1 | calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif | chr5:2271920-2274288 FORWARD | Aliases: T28J14.180, T28J14_180	3.7	2.3	1.4	6.8	0.21%	6.6
2383	AT1G32580.1 | plastid developmental protein DAG, putative, similar to DAG protein, chloroplast precursor (Garden snapdragon) SWISS-PROT:Q38732	6.2	3.9	2.3	6.8	0.21%	6.5
2384	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	6.9	3.1	3.8	6.8	0.21%	6.3
2385	AT4G27652.1 | expressed protein | chr4:13809839-13810362 FORWARD | Aliases: None	7.7	4.7	3.0	6.8	0.21%	6.5
2387	AT4G37710.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr4:17718122-17718736 FORWARD | Aliases: T28I19.3	4.4	1.8	2.6	6.8	0.21%	6.6
2389	AT4G37280.1 | MRG family protein, contains Pfam domain PF05712: MRG | chr4:17546578-17549409 REVERSE | Aliases: AP22.79, AP22_79	7.6	5.8	1.8	6.8	0.21%	6.6
2391	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	6.1	3.7	2.3	6.8	0.21%	6.5
2393	AT2G42770.1 | peroxisomal membrane 22 kDa family protein, contains Mpv17 / PMP22 family domain, Pfam:PF04117 | chr2:17805363-17807083 REVERSE | Aliases: F7D19.23, F7D19_23	7.3	4.9	2.5	6.8	0.21%	6.0
2395	AT5G42680.1 | expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617 | chr5:17131824-17132640 FORWARD | Aliases: MJB21.5, MJB21_5	6.4	4.1	2.2	6.8	0.21%	6.4
2399	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	6.7	5.2	1.4	6.8	0.21%	6.7
2403	AT3G49670.1 | leucine-rich repeat transmembrane protein kinase, putative, CLAVATA1 receptor kinase, Arabidopsis thaliana, EMBL:ATU96879 | chr3:18428553-18432091 FORWARD | Aliases: T16K5.20	5.8	3.3	2.4	6.8	0.21%	6.0
2404	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	5.2	3.8	1.4	6.8	0.21%	6.6
2406	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	6.2	3.7	2.5	6.8	0.21%	6.2
2407	AT5G02830.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:643609-648451 REVERSE | Aliases: F9G14.140, F9G14_140	7.4	5.2	2.2	6.8	0.21%	6.3
2409	AT3G57810.2 | OTU-like cysteine protease family protein, contains Pfam profile PF02338: OTU-like cysteine protease | chr3:21426805-21428925 FORWARD | Aliases: T10K17.20	6.9	5.1	1.8	6.8	0.21%	6.5
2411	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	11.3	9.3	2.0	6.8	0.21%	6.6
2412	AT3G24590.1 | signal peptidase I family protein, contains Pfam profile: PF00461 signal peptidase I | chr3:8970679-8972175 FORWARD | Aliases: MOB24.17	8.5	7.4	1.1	6.8	0.21%	6.6
2414	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	5.3	3.9	1.4	6.8	0.21%	6.6
2416	AT3G57010.1 | strictosidine synthase family protein, similar to strictosidine synthase (Rauvolfia serpentina)(SP:P15324) | chr3:21106633-21108430 REVERSE | Aliases: F24I3.90	9.5	6.6	2.9	6.8	0.21%	6.5
2417	AT3G23570.1 | dienelactone 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 dienelactone hydrolase family | chr3:8457785-8459698 REVERSE | Aliases: MDB19.5	10.3	6.6	3.7	6.8	0.21%	6.2
2419	AT1G41880.1 | 60S ribosomal protein L35a (RPL35aB), identical to GB:CAB81600 from (Arabidopsis thaliana) | chr1:15653564-15654932 REVERSE | Aliases: F5A13.4, F5A13_4	11.5	9.5	2.0	6.8	0.21%	6.4
2420	AT3G55750.1 | 60S ribosomal protein L35a (RPL35aD), ribosomal protein L35a.e.c15, Saccharomyces cerevisiae, PIR:S44069	11.5	9.5	2.0	6.8	0.21%	6.4

Rank	Description	Sync	Root	M	t	adj.q	B
2421	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	7.1	5.4	1.7	6.8	0.21%	6.6
2426	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	5.9	3.2	2.7	6.8	0.22%	6.1
2431	AT5G54180.1 | mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF | chr5:22005732-22007454 FORWARD | Aliases: K18G13.5, K18G13_5	5.4	3.9	1.4	6.8	0.22%	6.6
2432	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	7.4	4.7	2.8	6.8	0.22%	6.1
2436	AT2G25270.1 | expressed protein | chr2:10766828-10769797 FORWARD | Aliases: T22F11.14, T22F11_14	7.1	4.6	2.5	6.8	0.22%	6.2
2437	AT3G62300.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr3:23065079-23068163 FORWARD | Aliases: T17J13.260	6.6	4.9	1.7	6.8	0.22%	6.5
2442	AT2G01290.1 | expressed protein | chr2:148918-150381 REVERSE | Aliases: F10A8.17, F10A8_17	6.2	3.8	2.4	6.8	0.22%	6.0
2443	AT2G41780.1 | expressed protein | chr2:17435176-17435890 FORWARD | Aliases: T11A7.12, T11A7_12	8.3	7.3	1.1	6.8	0.22%	6.6
2445	AT2G20940.1 | expressed protein | chr2:9009113-9009782 REVERSE | Aliases: F26H11.30, F26H11_30	6.5	3.5	3.1	6.8	0.22%	6.1
2446	AT1G79200.1 | expressed protein | chr1:29799281-29800933 FORWARD | Aliases: YUP8H12R.41, YUP8H12R_41	4.9	3.4	1.6	6.8	0.22%	6.5
2448	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	7.3	3.3	4.0	6.8	0.22%	6.2
2449	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	11.2	10.0	1.2	6.8	0.22%	6.4
2450	AT2G01250.1 | 60S ribosomal protein L7 (RPL7B)	11.7	10.2	1.5	6.8	0.22%	6.4
2451	AT1G60870.1 | expressed protein | chr1:22413137-22414159 FORWARD | Aliases: T7P1.2, T7P1_2	7.5	4.4	3.0	6.8	0.22%	5.7
2452	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	7.0	4.2	2.8	6.8	0.22%	6.5
2453	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	7.4	4.6	2.8	6.8	0.22%	6.4
2454	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	8.2	6.7	1.5	6.8	0.22%	6.6
2455	AT3G58540.1 | expressed protein | chr3:21659570-21660364 FORWARD | Aliases: F14P22.130	4.8	3.0	1.7	6.8	0.22%	6.6
2458	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	9.8	7.6	2.2	6.7	0.22%	6.6
2460	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	6.8	4.7	2.1	6.7	0.22%	6.5
2463	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	8.5	6.7	1.8	6.7	0.22%	6.5
2464	AT5G52960.1 | expressed protein, similar to unknown protein (pir :S77140) | chr5:21494372-21495662 FORWARD | Aliases: MNB8.2, MNB8_2	4.8	2.6	2.2	6.7	0.22%	6.3
2465	AT1G74530.3 | expressed protein | chr1:28013294-28015823 REVERSE | Aliases: F1M20.21, F1M20_21	5.8	3.7	2.0	6.7	0.22%	6.5
2466	AT5G59740.1 | UDP-galactose/UDP-glucose transporter-related, weak similarity to UDP-galactose/UDP-glucose transporter (Arabidopsis thaliana) GI:22651763 | chr5:24087277-24090243 REVERSE | Aliases: MTH12.11, MTH12_11	6.2	4.8	1.4	6.7	0.22%	6.5

Rank	Description	Sync	Root	M	t	adj.q	B
2467	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	7.1	4.8	2.3	6.7	0.22%	6.3
2469	AT5G06120.1 | Ran-binding protein, putative, similar to SP:Q9UIA9 Ran-binding protein 16 {Homo sapiens}; contains Pfam profile PF03810: Importin-beta N-terminal domain | chr5:1844079-1852602 FORWARD | Aliases: K16F4.8, K16F4_8	7.7	5.5	2.2	6.7	0.22%	6.5
2471	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	6.4	5.3	1.1	6.7	0.22%	6.5
2472	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)	5.8	3.8	2.0	6.7	0.22%	6.4
2474	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	10.9	7.6	3.2	6.7	0.22%	6.5
2476	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), Arabidopsis thaliana | chr5:5579146-5580783 REVERSE | Aliases: F2K13.130, F2K13_130	6.0	3.9	2.1	6.7	0.22%	6.1
2477	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	6.3	4.7	1.6	6.7	0.22%	6.5
2478	AT3G55600.1 | expressed protein, predicted proteins, Arabidopsis thaliana | chr3:20631661-20633449 FORWARD | Aliases: F1I16.10	5.5	4.1	1.4	6.7	0.23%	6.6
2479	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)	12.7	10.6	2.1	6.7	0.23%	6.5
2480	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	10.3	8.1	2.2	6.7	0.23%	6.5
2484	AT2G44120.2 | 60S ribosomal protein L7 (RPL7C)	8.5	6.5	2.0	6.7	0.23%	6.5
2488	AT5G05180.2 | expressed protein | chr5:1536227-1538493 FORWARD | Aliases: K2A11.5, K2A11_5	6.4	4.3	2.1	6.7	0.23%	6.3
2489	AT5G49280.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr5:19993820-19994675 REVERSE | Aliases: K21P3.16, K21P3_16	5.4	3.5	1.9	6.7	0.23%	6.4
2490	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	7.3	4.2	3.1	6.7	0.23%	6.2
2491	AT2G29440.1 | Symbol: ATGSTU6 | glutathione S-transferase, putative | chr2:12627161-12628224 REVERSE | Aliases: F16P2.18, F16P2_18, GLUTATHIONE S TRANSFERASE 24, GST24	5.9	4.2	1.7	6.7	0.23%	6.5
2493	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: T5I7.12, T5I7_12	5.3	3.3	2.1	6.7	0.23%	6.1
2494	AT3G09860.1 | expressed protein | chr3:3026125-3027213 FORWARD | Aliases: F8A24.9	10.5	7.5	3.0	6.7	0.23%	6.3
2495	AT5G32450.1 | RNA recognition motif (RRM)-containing protein, various predicted proteins, Arabidopsis thaliana and others | chr5:12096848-12098803 FORWARD | Aliases: F18O9.60, F18O9_60	9.3	8.5	0.9	6.7	0.23%	6.4
2499	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	8.3	4.7	3.6	6.7	0.23%	6.5
2500	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	4.9	3.2	1.7	6.7	0.23%	6.4

Rank	Description	Sync	Root	M	t	adj.q	B
2501	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	10.0	1.5	6.7	0.23%	6.4
2503	AT5G26710.1 | glutamate-tRNA ligase, putative / glutamyl-tRNA synthetase, putatuve / GluRS, putative, identical to gi:3435196 | chr5:9305600-9308774 FORWARD | Aliases: None	10.7	8.8	1.9	6.7	0.23%	6.5
2506	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	11.9	9.5	2.4	6.7	0.23%	6.4
2509	AT2G32480.2 | membrane-associated zinc metalloprotease, putative, similar to Hypothetical zinc metalloprotease All3971 (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	7.6	1.5	6.7	0.23%	6.5
2510	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	7.3	4.3	3.0	6.7	0.23%	6.2
2511	AT5G27750.1 | F-box family protein, contains F-box domain Pfam:PF00646	5.8	4.0	1.8	6.7	0.23%	6.4
2512	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	6.3	4.5	1.8	6.7	0.23%	6.4
2514	AT1G52930.1 | brix domain-containing protein, contains Pfam domain, PF04427: Brix domain | chr1:19714905-19716898 FORWARD | Aliases: F14G24.20, F14G24_20	7.8	4.9	2.9	6.7	0.23%	6.4
2518	AT1G67250.1 | proteasome maturation factor UMP1 family protein, contains Pfam profile PF05348: Proteasome maturation factor UMP1 | chr1:25167305-25168715 REVERSE | Aliases: F1N21.7	10.9	8.8	2.1	6.7	0.24%	6.5
2524	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	4.9	3.4	1.5	6.7	0.24%	6.4
2526	AT5G19570.1 | expressed protein | chr5:6606702-6607205 FORWARD | Aliases: T20D1.90, T20D1_90	7.6	5.8	1.8	6.7	0.24%	6.5
2527	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	8.4	5.7	2.7	6.7	0.24%	6.4
2528	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	6.5	4.9	1.6	6.7	0.24%	6.4
2530	AT5G62440.1 | expressed protein | chr5:25089709-25091215 REVERSE | Aliases: AT5G62450, K19B1.5, K19B1_5	7.4	6.2	1.2	6.7	0.24%	6.4
2532	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;	10.7	8.5	2.2	6.6	0.24%	6.5
2533	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	7.6	4.3	3.3	6.6	0.24%	6.4
2534	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	12.2	10.5	1.6	6.6	0.24%	6.2
2536	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	9.0	8.2	0.8	6.6	0.24%	6.4
2538	AT1G75270.1 | dehydroascorbate reductase, putative, similar to GI:6939839 from (Oryza sativa) | chr1:28253736-28255010 REVERSE | Aliases: F22H5.1, F22H5_1	9.9	7.7	2.2	6.6	0.24%	6.5
2539	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	4.5	3.4	1.2	6.6	0.24%	6.5
2541	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	7.7	1.6	6.6	0.24%	6.5

Rank	Description	Sync	Root	M	t	adj.q	B
2543	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)	7.0	5.4	1.7	6.6	0.24%	6.4
2548	AT2G03420.1 | expressed protein | chr2:1034995-1035966 REVERSE | Aliases: T4M8.15, T4M8_15	4.7	2.7	2.0	6.6	0.24%	6.2
2549	AT5G14710.1 | expressed protein | chr5:4746365-4747936 FORWARD | Aliases: T9L3.10, T9L3_10	6.8	4.5	2.3	6.6	0.24%	6.4
2550	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	8.4	4.7	3.7	6.6	0.24%	6.4
2553	AT2G28430.1 | expressed protein | chr2:12166639-12167528 REVERSE | Aliases: T1B3.5, T1B3_5	8.5	6.0	2.5	6.6	0.24%	6.3
2557	AT5G63650.1 | serine/threonine protein kinase, putative, similar to serine/threonine-protein kinase ASK2(Arabidopsis thaliana), SWISS-PROT:P43292; contains protein kinase domain, Pfam:PF00069 | chr5:25498743-25500945 REVERSE | Aliases: MBK5.13, MBK5_13	5.4	3.4	2.0	6.6	0.24%	6.4
2558	AT1G69935.1 | expressed protein | chr1:26345464-26346789 REVERSE | Aliases: None	6.1	4.3	1.8	6.6	0.24%	6.2
2560	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	9.8	8.3	1.4	6.6	0.24%	6.4
2561	AT5G47070.1 | protein kinase, putative, similar to protein kinase (Lophopyrum elongatum) gi:13022177:gb:AAK11674 | chr5:19135770-19138136 REVERSE | Aliases: K14A3.2, K14A3_2	6.1	3.7	2.4	6.6	0.24%	6.4
2562	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	6.5	4.9	1.6	6.6	0.24%	6.4
2563	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	6.5	4.1	2.5	6.6	0.24%	6.3
2564	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	5.6	1.8	6.6	0.24%	6.4
2568	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	7.0	5.6	1.4	6.6	0.25%	6.4
2570	AT5G61330.1 | rRNA processing protein-related, contains weak similarity to rRNA processing protein EBP2 (EBNA1-binding protein homolog) (Swiss-Prot:P36049) (Saccharomyces cerevisiae)	7.7	6.5	1.2	6.6	0.25%	6.4
2572	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	5.1	3.2	1.9	6.6	0.25%	6.2
2573	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	10.4	8.2	2.2	6.6	0.25%	6.4
2576	AT3G25400.1 | expressed protein | chr3:9214469-9215516 FORWARD | Aliases: MWL2.8	8.5	6.8	1.7	6.6	0.25%	6.4
2577	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	6.0	3.7	2.3	6.6	0.25%	6.3
2578	AT3G53400.1 | expressed protein | chr3:19809129-19811114 FORWARD | Aliases: F4P12.100	7.2	5.2	2.0	6.6	0.25%	6.2
2579	AT5G44650.1 | expressed protein | chr5:18030376-18032630 FORWARD | Aliases: K15C23.10, K15C23_10	7.5	5.9	1.6	6.6	0.25%	6.4
2582	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	4.8	1.7	6.6	0.25%	6.4
2583	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	3.8	2.1	6.6	0.25%	6.3

Rank	Description	Sync	Root	M	t	adj.q	B
2584	AT5G50170.1 | C2 domain-containing protein / GRAM domain-containing protein, low similarity to SP:P40748 Synaptotagmin III (SytIII) {Rattus norvegicus}; contains Pfam profiles PF00168: C2 domain, PF02893: GRAM domain | chr5:20438299-20442812 FORWARD | Aliases: K6A12.3, K6A12_3	5.5	3.6	2.0	6.6	0.25%	6.3
2589	AT5G10160.1 | beta-hydroxyacyl-ACP dehydratase, putative, similar to beta-hydroxyacyl-ACP dehydratase from Toxoplasma gondii (GI:3850997); contains Pfam profile PF01377 Thioester dehydratase	7.6	4.1	3.4	6.6	0.25%	6.1
2590	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	5.8	4.7	1.2	6.6	0.25%	6.4
2591	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	7.2	4.5	2.7	6.6	0.25%	6.0
2593	AT3G05190.1 | aminotransferase class IV family protein, contains Pfam profile: PF01063 aminotransferase class IV | chr3:1471403-1475790 FORWARD | Aliases: T12H1.16, T12H1_16	5.8	3.7	2.2	6.6	0.25%	6.0
2595	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	8.3	1.9	6.6	0.25%	6.4
2596	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	7.0	4.4	2.6	6.6	0.25%	6.3
2599	AT5G66570.1 | Symbol: PSBO 1 |	7.7	3.3	4.4	6.6	0.25%	6.2
2600	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	5.8	4.8	1.0	6.6	0.25%	6.4
2601	AT2G34160.1 | expressed protein | chr2:14433282-14434462 FORWARD | Aliases: T14G11.28, T14G11_28	6.7	4.5	2.1	6.6	0.25%	6.4
2608	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	13.1	12.0	1.1	6.6	0.25%	5.9
2609	AT3G22210.1 | expressed protein | chr3:7838791-7839474 REVERSE | Aliases: MKA23.19	4.8	2.5	2.3	6.6	0.25%	6.3
2610	AT4G37110.1 | expressed protein | chr4:17484119-17486265 REVERSE | Aliases: AP22.72, AP22_72	4.5	2.8	1.7	6.6	0.25%	6.4
2611	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	6.8	3.9	2.9	6.6	0.25%	6.3
2612	AT4G21680.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr4:11517043-11519777 REVERSE | Aliases: F17L22.140, F17L22_140	6.6	4.1	2.5	6.6	0.25%	5.9
2613	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	5.5	3.0	2.5	6.6	0.25%	5.9
2614	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	11.0	8.4	2.7	6.6	0.25%	6.4
2615	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	3.6	2.4	1.1	6.6	0.25%	6.4
2616	AT2G39500.1 | expressed protein | chr2:16496151-16496666 FORWARD | Aliases: F12L6.16, F12L6_16	6.8	4.8	2.0	6.6	0.26%	6.3
2617	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	12.8	11.6	1.1	6.6	0.26%	6.3
2619	AT2G43030.1 | ribosomal protein L3 family protein, contains Pfam profile PF00297: ribosomal protein L3	8.3	5.5	2.8	6.6	0.26%	6.2
2620	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	7.0	5.4	1.6	6.6	0.26%	6.4

Rank	Description	Sync	Root	M	t	adj.q	B
2621	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	4.8	3.6	1.2	6.6	0.26%	6.4
2622	AT5G27390.1 | expressed protein, CG6949 - Drosophila melanogaster, EMBL:AE003739 | chr5:9671848-9676121 REVERSE | Aliases: F21A20.100, F21A20_100	6.5	4.9	1.7	6.6	0.26%	6.2
2624	AT5G57290.1 | 60S acidic ribosomal protein P3 (RPP3B) | chr5:23224055-23225121 REVERSE | Aliases: MJB24.10, MJB24_10	9.4	6.9	2.5	6.6	0.26%	6.1
2625	AT2G19740.1 | 60S ribosomal protein L31 (RPL31A) | chr2:8520599-8521601 FORWARD | Aliases: F6F22.23, F6F22_23	8.9	6.1	2.8	6.6	0.26%	6.2
2629	AT4G22740.2 | glycine-rich protein | chr4:11942812-11945967 REVERSE | Aliases: T12H17.1	10.3	8.0	2.3	6.5	0.26%	6.4
2635	AT4G12700.1 | expressed protein | chr4:7482463-7484402 REVERSE | Aliases: T20K18.50, T20K18_50	5.1	3.9	1.2	6.5	0.26%	6.4
2636	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	6.7	4.0	2.7	6.5	0.26%	6.0
2637	AT3G23760.1 | expressed protein | chr3:8562836-8564677 REVERSE | Aliases: MYM9.10	5.0	2.6	2.4	6.5	0.26%	5.8
2638	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	9.6	8.3	1.3	6.5	0.26%	6.4
2640	AT1G70070.1 | Symbol: PDE317 |	5.6	4.0	1.6	6.5	0.26%	6.2
2641	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	5.4	3.9	1.6	6.5	0.26%	6.3
2642	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	8.3	5.9	2.4	6.5	0.26%	6.3
2643	AT5G02790.1 | In2-1 protein, putative, similar to In2-1, Zea mays, EMBL:X58573	10.1	6.3	3.8	6.5	0.26%	6.2
2644	AT4G29480.1 | mitochondrial ATP synthase g subunit family protein, contains Pfam profile: PF04718 mitochondrial ATP synthase g subunit	12.1	10.4	1.7	6.5	0.26%	6.3
2645	AT5G38510.1 | rhomboid family protein, contains Pfam profile PF01694: Rhomboid family | chr5:15435069-15437232 REVERSE | Aliases: MBB18.4, MBB18_4	5.3	3.7	1.6	6.5	0.26%	6.3
2648	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	11.0	8.6	2.4	6.5	0.26%	6.4
2649	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	7.1	5.9	1.2	6.5	0.26%	6.3
2651	AT1G71350.1 | eukaryotic translation initiation factor SUI1 family protein, weak similarity to SP:P41214 Ligatin (Hepatocellular carcinoma-associated antigen 56) {Homo sapiens}; contains Pfam profile PF01253: Translation initiation factor SUI1 | chr1:26892070-26894893 REVERSE | Aliases: F3I17.23, F3I17_23	8.5	6.5	2.0	6.5	0.26%	6.3
2654	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	6.8	5.2	1.7	6.5	0.26%	6.3
2655	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	10.8	8.3	2.6	6.5	0.26%	6.2
2656	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	6.9	5.4	1.5	6.5	0.26%	6.3
2658	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	6.2	4.7	1.5	6.5	0.26%	6.3

Rank	Description	Sync	Root	M	t	adj.q	B
2659	AT1G64750.2 | DSS1/SEM1 family protein, contains Pfam profile PF05160: DSS1/SEM1 family | chr1:24056244-24057568 REVERSE | Aliases: F13O11.6, F13O11_6	8.8	6.6	2.1	6.5	0.26%	6.2
2662	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	6.1	4.1	2.0	6.5	0.26%	6.1
2664	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	8.0	5.4	2.6	6.5	0.26%	6.2
2665	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	9.3	7.2	2.1	6.5	0.26%	6.3
2667	AT4G24090.1 | expressed protein | chr4:12512746-12514591 FORWARD | Aliases: T19F6.80, T19F6_80	5.3	3.8	1.5	6.5	0.26%	6.3
2668	AT4G09020.1 | Symbol: ATISA3/ISA3 | isoamylase, putative / starch debranching enzyme, putative, similar to isoamylase isoform 3 (Solanum tuberosum) GI:27728149, isoamylase (Oryza sativa) GI: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	5.4	1.9	6.5	0.26%	6.3
2669	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	7.2	5.7	1.5	6.5	0.26%	6.3
2670	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	8.1	5.5	2.6	6.5	0.27%	6.1
2674	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	6.2	4.1	2.1	6.5	0.27%	6.1
2676	AT5G15200.1 | 40S ribosomal protein S9 (RPS9B), 40S ribosomal protein S9, Chlamydomonas sp., EMBL:AU066528 | chr5:4934886-4936384 REVERSE | Aliases: F8M21.90, F8M21_90	11.6	10.1	1.5	6.5	0.27%	6.3
2680	AT4G31730.1 | Symbol: GDU1 | expressed protein | chr4:15361097-15361801 FORWARD | Aliases: F28M20.80, F28M20_80, GLUTAMINE DUMPER 1	6.9	5.2	1.7	6.5	0.27%	6.3
2681	AT5G14910.1 | heavy-metal-associated domain-containing protein, Pfam profile PF00403: Heavy-metal-associated domain | chr5:4823717-4825373 FORWARD | Aliases: F2G14.30, F2G14_30	6.5	4.1	2.5	6.5	0.27%	6.1
2682	AT5G27700.1 | 40S ribosomal protein S21 (RPS21C), ribosomal protein S21, Zea mays, PIR:T03945 | chr5:9807323-9808480 REVERSE | Aliases: T1G16.30, T1G16_30	11.2	8.9	2.3	6.5	0.27%	6.3
2683	AT2G32520.1 | dienelactone hydrolase family protein, low similarity to dienelactone hydrolase (Pseudomonas resinovorans) GI:13094163; contains Pfam profile PF01738: Dienelactone hydrolase family | chr2:13812596-13814613 REVERSE | Aliases: T26B15.8, T26B15_8	11.3	9.4	1.9	6.5	0.27%	6.2
2684	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	4.3	2.0	6.5	0.27%	6.2
2685	AT3G24506.1 | expressed protein | chr3:8928177-8929336 REVERSE | Aliases: None	6.3	4.6	1.7	6.5	0.27%	6.3
2687	AT1G08980.1 | Symbol: ATAMI1 |	6.8	5.2	1.7	6.5	0.27%	6.2
2693	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	3.6	2.5	1.0	6.5	0.27%	6.3
2694	AT5G25475.2 | expressed protein | chr5:8867843-8869824 REVERSE | Aliases: None	6.3	4.1	2.1	6.5	0.27%	6.2
2696	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	6.4	5.1	1.3	6.5	0.27%	6.3

Rank	Description	Sync	Root	M	t	adj.q	B
2697	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	10.0	7.1	2.9	6.5	0.27%	6.1
2699	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	9.0	2.0	6.5	0.27%	6.3
2700	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	10.1	5.5	4.6	6.5	0.27%	6.1
2701	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	7.9	2.2	5.7	6.5	0.27%	5.8
2702	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	6.6	4.9	1.7	6.5	0.27%	6.2
2704	AT2G46390.1 | expressed protein | chr2:19049374-19050133 REVERSE | Aliases: F11C10.8	11.6	10.4	1.2	6.5	0.27%	6.2
2705	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	5.8	3.0	2.8	6.5	0.27%	5.7
2707	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	6.2	4.0	2.2	6.5	0.27%	6.2
2708	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	8.0	6.3	1.7	6.5	0.27%	6.3
2709	AT3G13190.2 | myosin heavy chain-related, contains weak similarity to Myosin II heavy chain, non muscle (Swiss-Prot:P05659) (Acanthamoeba castellanii)	5.9	4.0	2.0	6.5	0.27%	6.2
2710	AT5G22875.2 | expressed protein, similar to hypothetical protein [Ipomoea trifida] (GB:AAS79573.1) | chr5:7650585-7651779 FORWARD | Aliases: None	4.7	3.1	1.6	6.5	0.27%	6.3
2711	AT3G20560.1 | Symbol: ATPDIL5 3 | Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	6.7	4.8	1.9	6.5	0.27%	6.2
2712	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	9.6	7.8	1.8	6.5	0.27%	6.3
2713	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	3.6	3.1	6.5	0.27%	5.2
2716	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	5.8	3.3	2.5	6.5	0.28%	6.2
2718	AT2G20810.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8 | chr2:8964874-8966861 FORWARD | Aliases: F5H14.44	6.6	5.3	1.3	6.5	0.28%	6.3
2719	AT3G43980.1 | 40S ribosomal protein S29 (RPS29A), ribosomal protein S29, rat, PIR:S30298 | chr3:15789389-15790298 REVERSE | Aliases: T15B3.120, T15B3_120	13.0	11.8	1.2	6.4	0.28%	5.5
2720	AT3G44010.1 | 40S ribosomal protein S29 (RPS29B), ribosomal protein S29, rat, PIR:S30298 | chr3:15810918-15812187 REVERSE | Aliases: T15B3.150	13.0	11.8	1.2	6.4	0.28%	5.5
2721	AT4G39040.2 | expressed protein, contains PF01985: Uncharacterised protein family | chr4:18189006-18190550 REVERSE | Aliases: F19H22.140, F19H22_140	8.4	6.6	1.8	6.4	0.28%	6.2
2723	AT2G40960.1 | expressed protein | chr2:17102600-17104527 FORWARD | Aliases: T20B5.16, T20B5_16	3.7	2.6	1.2	6.4	0.28%	6.3
2725	AT1G56450.1 | Symbol: PBG1 | 20S proteasome beta subunit G1 (PBG1) (PRCH), identical to 20S proteasome beta subunit (PBG1) GI:3421123 (Arabidopsis thaliana); identical to cDNA proteasome subunit prch GI:2511597 | chr1:21145558-21148065 FORWARD | Aliases: F13N6.3, F13N6_3, PROTEASOME BETA SUBUNIT PBG1	10.8	8.0	2.8	6.4	0.28%	6.2

Rank	Description	Sync	Root	M	t	adj.q	B
2726	AT4G19460.1 | glycosyl transferase family 1 protein, contains Pfam profile: PF00534 Glycosyl transferases group 1 | chr4:10610320-10612016 REVERSE | Aliases: F24J7.20, F24J7_20	6.4	5.0	1.4	6.4	0.28%	6.3
2728	AT2G21530.1 | forkhead-associated domain-containing protein / FHA domain-containing protein | chr2:9226404-9227666 FORWARD | Aliases: F3K23.29, F3K23_29	5.0	2.6	2.4	6.4	0.28%	5.6
2729	AT4G27480.1 | glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/I-Branching enzyme | chr4:13736841-13738921 REVERSE | Aliases: F27G19.80, F27G19_80	5.7	4.0	1.8	6.4	0.28%	6.1
2730	AT4G39200.1 | 40S ribosomal protein S25 (RPS25E), ribosomal protein S25, Lycopersicon esculentum, PIR2:S40089 | chr4:18257330-18258670 FORWARD | Aliases: T22F8.100, T22F8_100	11.3	9.6	1.7	6.4	0.28%	6.2
2731	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	6.8	4.1	2.7	6.4	0.28%	6.2
2732	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	6.7	4.9	1.8	6.4	0.28%	6.1
2733	AT3G15110.1 | expressed protein | chr3:5084295-5085836 REVERSE | Aliases: F4B12.2	4.1	2.8	1.3	6.4	0.28%	6.2
2735	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	11.2	8.3	2.9	6.4	0.28%	6.2
2736	AT1G26740.1 | expressed protein, similar to 50S ribosomal protein L32 (SP:P80339) {Thermus thermophilus} | chr1:9244974-9246588 REVERSE | Aliases: T24P13.27	7.3	4.4	2.9	6.4	0.28%	6.0
2738	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	7.3	1.6	6.4	0.28%	6.2
2739	AT5G03880.1 | expressed protein | chr5:1038507-1041479 REVERSE | Aliases: MED24.18, MED24_18	8.3	6.3	2.0	6.4	0.28%	6.2
2741	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	11.4	9.5	1.9	6.4	0.28%	6.2
2743	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	8.9	5.6	3.3	6.4	0.28%	6.0
2744	AT5G65880.1 | expressed protein | chr5:26370262-26370900 FORWARD | Aliases: K14B20.5, K14B20_5	8.0	6.0	2.0	6.4	0.28%	6.2
2745	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	7.9	5.6	2.2	6.4	0.28%	6.0
2746	AT3G48510.1 | expressed protein | chr3:17978341-17979523 REVERSE | Aliases: T8P19.20	6.7	4.2	2.5	6.4	0.28%	5.9
2749	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	5.2	3.6	1.6	6.4	0.28%	6.2
2750	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	6.3	3.3	2.9	6.4	0.28%	5.8
2751	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	7.0	5.3	1.7	6.4	0.28%	6.1
2755	AT5G39570.1 | expressed protein | chr5:15861187-15863406 FORWARD | Aliases: MIJ24.6, MIJ24_6	13.4	12.6	0.8	6.4	0.28%	6.1
2756	AT1G18730.1 | expressed protein | chr1:6460590-6462212 FORWARD | Aliases: F6A14.16, F6A14_16	6.0	3.9	2.1	6.4	0.28%	6.1
2758	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	7.4	3.7	3.7	6.4	0.28%	5.8

Rank	Description	Sync	Root	M	t	adj.q	B
2759	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	9.0	5.6	3.4	6.4	0.29%	6.2
2760	AT1G09660.2 | KH domain-containing quaking protein, putative, similar to GB:AAC67357 | chr1:3127783-3131049 REVERSE | Aliases: F21M12.5, F21M12_5	5.7	4.4	1.3	6.4	0.29%	6.2
2761	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	7.5	4.7	2.8	6.4	0.29%	5.6
2762	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	8.2	6.2	2.0	6.4	0.29%	6.2
2763	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	10.6	9.3	1.3	6.4	0.29%	6.2
2765	AT4G32330.2 | expressed protein | chr4:15608918-15612291 FORWARD | Aliases: F8B4.30	7.4	5.7	1.6	6.4	0.29%	6.2
2770	AT4G31820.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr4:15390656-15394436 REVERSE | Aliases: F11C18.20, F11C18_20	6.5	4.3	2.2	6.4	0.29%	6.0
2771	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	8.6	6.3	2.3	6.4	0.29%	6.1
2773	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	11.7	9.9	1.8	6.4	0.29%	6.0
2776	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	13.3	12.7	0.6	6.4	0.29%	5.5
2778	AT1G06510.1 | expressed protein | chr1:1992384-1993839 FORWARD | Aliases: F12K11.16, F12K11_16	4.5	3.2	1.3	6.4	0.29%	6.2
2779	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	7.1	5.1	2.0	6.4	0.29%	6.1
2785	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	4.1	1.7	6.4	0.29%	6.0
2787	AT3G16780.1 | 60S ribosomal protein L19 (RPL19B), similar to ribosomal protein L19 GB:CAA45090 from (Homo sapiens) | chr3:5708931-5710415 FORWARD | Aliases: MGL6.7	9.3	7.3	1.9	6.4	0.29%	6.2
2791	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	6.8	1.3	6.4	0.29%	6.2
2794	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	8.1	6.0	2.1	6.4	0.29%	5.8
2795	AT1G09300.1 | metallopeptidase 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: metallopeptidase family M24, PF05195: Aminopeptidase P, N-terminal domain | chr1:3003928-3008215 FORWARD | Aliases: T31J12.2, T31J12_2	6.0	4.8	1.2	6.4	0.29%	6.2
2797	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	10.4	8.4	2.1	6.4	0.29%	6.1
2798	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	10.8	8.7	2.1	6.4	0.29%	6.2
2799	AT1G73790.1 | expressed protein | chr1:27748333-27749038 FORWARD | Aliases: F25P22.21, F25P22_21	7.3	5.9	1.5	6.4	0.30%	6.2

Rank	Description	Sync	Root	M	t	adj.q	B
2800	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	6.7	4.9	1.8	6.4	0.30%	6.2
2801	AT1G69930.1 | Symbol: ATGSTU11 | glutathione S-transferase, putative, similar to glutathione transferase GB:CAA09188 (Alopecurus myosuroides)	6.4	3.5	2.9	6.4	0.30%	5.2
2804	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	6.1	4.6	1.5	6.4	0.30%	6.1
2805	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	12.2	10.3	1.9	6.4	0.30%	6.1
2807	AT3G21400.1 | expressed protein | chr3:7534639-7536515 REVERSE | Aliases: MHC9.8	6.3	4.7	1.6	6.4	0.30%	6.2
2808	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	4.5	1.6	6.4	0.30%	6.2
2809	AT2G40060.1 | expressed protein | chr2:16733562-16735263 FORWARD | Aliases: T28M21.22, T28M21_22	9.6	8.6	1.0	6.4	0.30%	6.1
2811	AT1G07010.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	6.2	4.3	1.9	6.3	0.30%	6.0
2812	AT3G19270.1 | Symbol: CYP707A4 | cytochrome P450 family protein, similar to Cytochrome P450 85 (SP:Q43147) {Lycopersicon esculentum};	6.9	3.7	3.2	6.3	0.30%	5.9
2813	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	8.8	5.9	3.0	6.3	0.30%	6.1
2814	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	8.6	7.1	1.5	6.3	0.30%	6.1
2816	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	7.2	5.3	1.9	6.3	0.30%	6.1
2817	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)	4.7	3.1	1.6	6.3	0.30%	6.1
2819	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	7.3	4.7	2.5	6.3	0.30%	5.9
2820	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	7.5	6.2	1.3	6.3	0.30%	6.2
2822	AT2G31240.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain | chr2:13324492-13326637 REVERSE | Aliases: F16D14.8, F16D14_8	6.1	4.1	2.0	6.3	0.30%	6.1
2825	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	6.6	5.0	1.6	6.3	0.30%	6.1
2827	AT2G29590.1 | thioesterase family protein, contains Pfam profile PF03061: thioesterase family protein | chr2:12661533-12662525 REVERSE | Aliases: F16P2.3, F16P2_3	7.4	6.1	1.2	6.3	0.30%	6.1
2830	AT3G54090.1 | pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase | chr3:20039102-20040964 FORWARD | Aliases: F24B22.50	5.8	3.4	2.4	6.3	0.30%	5.9
2831	AT4G12580.1 | expressed protein, predicted protein | chr4:7449371-7449676 REVERSE | Aliases: T1P17.170, T1P17_170	5.2	3.4	1.8	6.3	0.30%	6.1
2833	AT2G21090.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:9052597-9054657 REVERSE | Aliases: F26H11.15, F26H11_15	4.5	3.4	1.1	6.3	0.31%	6.1
2834	AT1G51380.1 | eukaryotic translation initiation factor 4A, putative / eIF-4A, putative	4.8	3.6	1.2	6.3	0.31%	6.1

Rank	Description	Sync	Root	M	t	adj.q	B
2835	AT5G52050.1 | MATE efflux protein-related, contains Pfam profile PF01554: Uncharacterized membrane protein family | chr5:21156088-21157869 FORWARD | Aliases: MSG15.13, MSG15_13	6.7	3.3	3.3	6.3	0.31%	5.3
2836	AT4G20430.1 | subtilase family protein, contains Pfam profile: PF00082 subtilase family | chr4:11017667-11021116 REVERSE | Aliases: F9F13.80, F9F13_80	4.7	3.5	1.3	6.3	0.31%	6.1
2839	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	5.3	3.2	2.1	6.3	0.31%	5.7
2841	AT1G67700.2 | expressed protein | chr1:25377897-25379693 FORWARD | Aliases: F12A21.32	7.3	4.2	3.1	6.3	0.31%	6.0
2842	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	6.5	4.5	2.0	6.3	0.31%	6.1
2852	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	7.1	4.0	3.1	6.3	0.31%	5.8
2856	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	4.0	1.4	6.3	0.31%	6.1
2857	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	8.3	5.5	2.8	6.3	0.31%	5.9
2858	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	8.8	7.2	1.6	6.3	0.31%	6.1
2859	AT3G26570.2 | Symbol: PHT2;1 |	7.5	4.4	3.1	6.3	0.31%	5.4
2860	AT3G13580.3 | 60S ribosomal protein L7 (RPL7D), similar to 60S ribosomal protein L7 GB:AAD14525 GI:4262232 from (Arabidopsis thaliana)	10.3	8.7	1.5	6.3	0.31%	6.1
2861	AT1G02870.1 | expressed protein | chr1:637214-638677 REVERSE | Aliases: F22D16.13, F22D16_13	6.4	3.1	3.3	6.3	0.31%	6.0
2862	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	11.5	9.0	2.4	6.3	0.31%	6.1
2863	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	9.3	6.0	3.3	6.3	0.31%	5.9
2867	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	6.5	4.8	1.7	6.3	0.32%	6.0
2871	AT3G05570.1 | expressed protein | chr3:1616271-1616642 REVERSE | Aliases: F18C1.16, F18C1_16	7.7	6.3	1.5	6.3	0.32%	6.0
2873	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	8.2	4.8	3.4	6.3	0.32%	6.0
2874	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	6.2	3.7	2.5	6.3	0.32%	5.3
2876	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	5.1	3.6	1.5	6.3	0.32%	6.1
2878	AT3G16500.1 | Symbol: PAP1 | auxin-responsive AUX/IAA family protein, similar to SP:O24408:AXII_ARATH Auxin-responsive protein IAA18 (Indoleacetic acid-induced protein 18) {Arabidopsis thaliana}; contains Pfam profile: PF02309: AUX/IAA family | chr3:5612506-5614416 REVERSE | Aliases: IAA26, MDC8.13, PAP1, PHYTOCHROME ASSOCIATED PROTEIN 1	7.0	5.2	1.8	6.3	0.32%	6.0

Rank	Description	Sync	Root	M	t	adj.q	B
2881	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	5.5	3.2	2.3	6.3	0.32%	5.8
2883	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	7.4	6.0	1.5	6.3	0.32%	6.1
2886	AT5G16950.1 | expressed protein | chr5:5572579-5573073 FORWARD | Aliases: F2K13.100, F2K13_100	7.6	6.2	1.4	6.3	0.32%	6.1
2887	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	4.4	4.3	6.3	0.32%	5.6
2888	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	9.8	7.5	2.3	6.3	0.32%	6.1
2890	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	9.1	6.3	2.7	6.3	0.32%	5.9
2891	AT5G09960.1 | expressed protein, similar to unknown protein (emb:CAB61744.1) | chr5:3106321-3107830 FORWARD | Aliases: MYH9.17, MYH9_17	8.2	5.2	3.0	6.3	0.32%	6.0
2892	AT3G61670.1 | expressed protein, weak similarity to extra-large G-protein (Arabidopsis thaliana) GI:3201682 | chr3:22829564-22832985 FORWARD | Aliases: F15G16.60	5.9	4.6	1.3	6.3	0.32%	6.1
2902	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	6.0	3.8	2.2	6.2	0.32%	5.7
2906	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	6.3	4.8	1.5	6.2	0.33%	6.0
2907	AT1G49245.1 | expressed protein | chr1:18222418-18222922 FORWARD | Aliases: None	4.3	3.1	1.2	6.2	0.33%	6.0
2908	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	5.9	4.5	1.4	6.2	0.33%	6.0
2909	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	9.0	6.0	3.0	6.2	0.33%	6.0
2910	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	7.7	6.3	1.4	6.2	0.33%	6.0
2913	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	11.9	10.3	1.5	6.2	0.33%	6.0
2914	AT4G28210.1 | Symbol: EMB1923 | expressed protein | chr4:13990626-13992084 FORWARD | Aliases: EMB1923, EMBRYO DEFECTIVE 1923, F26K10.90, F26K10_90	7.0	4.2	2.7	6.2	0.33%	5.5
2916	AT4G18100.1 | 60S ribosomal protein L32 (RPL32A), ribosomal protein L32, human, PIR1:R5HU32 | chr4:10035497-10036552 REVERSE | Aliases: F15J5.70, F15J5_70	9.5	6.2	3.2	6.2	0.33%	5.9
2917	AT5G46430.2 | 60S ribosomal protein L32 (RPL32B) | chr5:18850494-18851791 FORWARD | Aliases: K11I1.2, K11I1_2	9.5	6.2	3.2	6.2	0.33%	5.9
2918	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	5.3	3.5	1.9	6.2	0.33%	5.9
2919	AT3G46430.1 | expressed protein | chr3:17098672-17099482 FORWARD | Aliases: F18L15.150, F18L15_150	10.4	8.6	1.8	6.2	0.33%	6.0
2920	AT3G03900.1 | adenylylsulfate kinase, putative, similar to adenylylsulfate kinase 1, chloroplast precursor (APS kinase, Adenosine-5'phosphosulfate kinase, ATP adenosine-5'- phosphosulfate 3'-phosphotransferase) (Arabidopsis thaliana) SWISS-PROT:Q43295 | chr3:1002982-1004278 REVERSE | Aliases: F20H23.5, F20H23_5	6.5	4.6	1.9	6.2	0.33%	6.0

Rank	Description	Sync	Root	M	t	adj.q	B
2921	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	6.4	3.7	2.7	6.2	0.33%	5.9
2922	AT2G27710.3 | 60S acidic ribosomal protein P2 (RPP2B) | chr2:11823868-11824944 FORWARD | Aliases: F15K20.19, F15K20_19	10.1	7.6	2.5	6.2	0.33%	6.0
2923	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	7.7	3.6	4.1	6.2	0.33%	6.0
2924	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	2.8	1.3	6.2	0.33%	6.0
2926	AT3G54210.1 | ribosomal protein L17 family protein, contains Pfam profile: PF01196 ribosomal protein L17 | chr3:20078525-20079413 REVERSE | Aliases: F24B22.170	8.7	6.2	2.4	6.2	0.33%	6.0
2928	AT5G10700.1 | expressed protein | chr5:3378054-3378868 REVERSE | Aliases: MAJ23.60, MAJ23_60	5.2	3.6	1.6	6.2	0.33%	5.9
2929	AT1G63020.1 | Symbol: NRPD1a |	6.0	3.7	2.3	6.2	0.33%	5.7
2930	AT3G55605.1 | mitochondrial glycoprotein family protein / MAM33 family protein, low similarity to SUAPRGA1 (Emericella nidulans) GI:6562379; contains Pfam profile PF02330: Mitochondrial glycoprotein	7.1	5.5	1.6	6.2	0.33%	5.9
2932	AT5G14970.1 | expressed protein | chr5:4847281-4848868 FORWARD | Aliases: F2G14.90, F2G14_90	8.3	6.9	1.4	6.2	0.33%	6.0
2934	AT2G30170.1 | expressed protein | chr2:12886757-12888575 REVERSE | Aliases: T27E13.9, T27E13_9	6.5	4.8	1.7	6.2	0.33%	6.0
2935	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	8.9	6.8	2.0	6.2	0.33%	6.0
2939	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	8.9	5.2	3.6	6.2	0.34%	5.7
2940	AT3G13560.3 | glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase GI:15150341 from (Camellia sinensis)	6.3	4.6	1.8	6.2	0.34%	5.9
2941	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	4.3	3.0	1.3	6.2	0.34%	6.0
2942	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	9.3	6.4	2.9	6.2	0.34%	5.8
2943	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	4.5	3.4	1.1	6.2	0.34%	6.0
2944	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	10.5	7.6	2.9	6.2	0.34%	6.0
2945	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	8.0	6.2	1.8	6.2	0.34%	5.9
2946	AT4G37040.1 | Symbol: MAP1D | metallopeptidase M24 family protein, similar to SP:O33343 Methionine aminopeptidase (EC 3.4.11.18) (Peptidase M) {Mycobacterium tuberculosis}; contains Pfam profile PF00557: metallopeptidase family M24 | chr4:17455133-17457351 FORWARD | Aliases: METHIONINE AMINOPEPTIDASE 1D	6.7	4.4	2.2	6.2	0.34%	6.0
2947	AT2G22420.1 | peroxidase 17 (PER17) (P17), identical to SP:Q9SJZ2 Peroxidase 17 precursor (EC 1.11.1.7) (Atperox P17) (ATP25a) {Arabidopsis thaliana} | chr2:9520299-9521615 FORWARD | Aliases: F14M13.18, F14M13_18	7.1	5.5	1.5	6.2	0.34%	6.0
2948	AT2G34640.1 | expressed protein | chr2:14588969-14591736 REVERSE | Aliases: T31E10.2, T31E10_2	5.9	3.8	2.0	6.2	0.34%	6.0
2952	AT5G23070.1 | thymidine kinase, putative, similar to thymidine kinase (Oryza sativa) SWISS-PROT:O81263	6.6	5.3	1.3	6.2	0.34%	6.0

Rank	Description	Sync	Root	M	t	adj.q	B
2955	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	5.2	3.4	1.8	6.2	0.34%	5.9
2956	AT1G67750.1 | pectate lyase family protein, similar to pectate lyase GI:14289169 from (Salix gilgiana)	6.1	3.3	2.7	6.2	0.34%	5.2
2958	AT3G07510.1 | expressed protein | chr3:2393697-2394681 REVERSE | Aliases: F21O3.22	5.6	4.7	0.9	6.2	0.34%	5.9
2961	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	7.3	5.6	1.8	6.2	0.34%	6.0
2962	AT2G25570.1 | expressed protein | chr2:10892776-10894999 REVERSE | Aliases: F3N11.2, F3N11_2	7.5	5.4	2.1	6.2	0.34%	5.9
2964	AT5G44785.2 | expressed protein, contains Pfam PF05329: Protein of unknown function (DUF731) | chr5:18087918-18090356 REVERSE | Aliases: None	6.4	4.7	1.7	6.2	0.34%	6.0
2966	AT5G62620.1 | galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase | chr5:25153977-25157148 FORWARD | Aliases: MRG21.3, MRG21_3	6.0	4.5	1.5	6.2	0.34%	5.9
2967	AT5G02450.1 | 60S ribosomal protein L36 (RPL36C), 60S ribosomal protein L36, Arabidopsis thaliana, EMBL:AC004684 | chr5:533119-534635 FORWARD | Aliases: T22P11.40, T22P11_40	11.2	9.9	1.3	6.2	0.34%	5.8
2968	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	7.0	4.2	2.9	6.2	0.34%	5.7
2969	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	4.9	3.2	1.7	6.2	0.34%	5.9
2971	AT1G12830.1 | expressed protein | chr1:4374248-4375168 REVERSE | Aliases: F13K23.8, F13K23_8	7.5	4.7	2.8	6.2	0.35%	5.9
2974	AT5G08650.1 | GTP-binding protein LepA, putative | chr5:2806324-2813227 REVERSE | Aliases: T2K12.1	5.5	3.8	1.7	6.2	0.35%	6.0
2975	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	4.1	3.0	1.2	6.2	0.35%	6.0
2979	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	5.7	3.8	1.9	6.2	0.35%	5.9
2980	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	6.4	3.8	2.7	6.2	0.35%	5.7
2981	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	5.8	3.7	2.1	6.2	0.35%	5.7
2982	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	4.4	2.3	6.2	0.35%	5.4
2987	AT2G27720.1 | 60S acidic ribosomal protein P2 (RPP2A) | chr2:11825568-11826655 FORWARD | Aliases: F15K20.18, F15K20_18	11.7	10.4	1.3	6.1	0.35%	5.8
2991	AT1G74640.1 | expressed protein, contains Pfam profile: PF00561 alpha/beta hydrolase fold | chr1:28036424-28038434 FORWARD | Aliases: F1M20.32, F1M20_32	8.1	5.8	2.3	6.1	0.35%	5.9
2992	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	10.5	8.6	2.0	6.1	0.35%	5.9
2993	AT3G11510.1 | 40S ribosomal protein S14 (RPS14B), similar to 40S ribosomal protein S14 GB:P19950 (Zea mays) | chr3:3623463-3624945 REVERSE | Aliases: F24K9.19	9.6	6.3	3.2	6.1	0.35%	5.9

Rank	Description	Sync	Root	M	t	adj.q	B
2994	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	5.7	3.9	1.8	6.1	0.35%	5.9
2995	AT4G30810.1 | Symbol: SCPL29 |	9.1	7.1	1.9	6.1	0.35%	5.9
2996	AT3G23690.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	8.7	7.7	1.1	6.1	0.35%	5.9
2997	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	5.8	2.2	6.1	0.35%	5.9
2998	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	6.1	4.6	1.5	6.1	0.35%	5.9
2999	AT3G03160.1 | expressed protein | chr3:729775-730474 FORWARD | Aliases: T17B22.15, T17B22_15	9.8	8.8	1.1	6.1	0.35%	5.7
3000	AT1G78790.1 | expressed protein | chr1:29628422-29629935 REVERSE | Aliases: F9K20.17, F9K20_17	6.9	5.0	1.9	6.1	0.35%	5.7
3001	AT1G05070.1 | expressed protein | chr1:1457067-1458742 REVERSE | Aliases: T7A14.6, T7A14_6	8.2	5.6	2.6	6.1	0.35%	5.9
3002	AT2G25100.1 | ribonuclease HII family protein, contains Pfam profile: PF01351 ribonuclease HII	5.3	3.8	1.5	6.1	0.35%	5.9
3003	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	4.7	2.4	6.1	0.35%	5.7
3004	AT3G27340.2 | similar to B1065G12.33 [Oryza sativa (japonica cultivar-group)] (GB:NP_915228.1)	7.9	6.5	1.5	6.1	0.35%	5.9
3010	AT5G06980.2 | expressed protein | chr5:2167624-2169392 FORWARD | Aliases: MOJ9.15, MOJ9_15	6.0	3.9	2.2	6.1	0.35%	5.7
3011	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	9.2	7.9	1.3	6.1	0.35%	5.9
3012	AT2G42130.5 | expressed protein, contains weak hit to Pfam PF04755: PAP_fibrillin | chr2:17573301-17575182 FORWARD | Aliases: T24P15.4, T24P15_4	5.3	3.4	1.9	6.1	0.35%	5.9
3014	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	5.0	3.5	1.6	6.1	0.35%	5.9
3015	AT5G67510.1 | 60S ribosomal protein L26 (RPL26B) | chr5:26955039-26955677 REVERSE | Aliases: K9I9.7, K9I9_7	8.5	6.7	1.8	6.1	0.35%	5.9
3016	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	5.0	3.8	1.2	6.1	0.35%	5.9
3019	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	10.6	9.2	1.4	6.1	0.36%	5.9
3020	AT3G47470.1 | Symbol: CAB4 | chlorophyll A-B binding protein 4, chloroplast / LHCI type III CAB-4 (CAB4), identical to SP:P27521 Chlorophyll A-B binding protein 4, chloroplast precursor (LHCI type III CAB-4) (LHCP) {Arabidopsis thaliana}	10.1	6.5	3.6	6.1	0.36%	5.7
3021	AT3G13640.1 | Symbol: ATRLI1 |	4.1	2.8	1.3	6.1	0.36%	5.9
3022	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	11.1	9.9	1.2	6.1	0.36%	5.7
3023	AT3G61640.1 | Symbol: AGP20 | arabinogalactan-protein (AGP20)	6.3	4.2	2.1	6.1	0.36%	5.9
3025	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	3.5	3.2	6.1	0.36%	5.8

Rank	Description	Sync	Root	M	t	adj.q	B
3026	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	5.2	3.6	1.7	6.1	0.36%	5.9
3027	AT3G47833.1 | expressed protein | chr3:17659618-17661125 FORWARD | Aliases: None	9.6	8.5	1.2	6.1	0.36%	5.8
3032	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	10.3	8.7	1.6	6.1	0.36%	5.9
3033	AT5G45010.1 | DSS1/SEM1 family protein, contains Pfam profile PF05160: DSS1/SEM1 family | chr5:18184471-18185601 REVERSE | Aliases: K21C13.20, K21C13_20	10.6	8.9	1.7	6.1	0.36%	5.9
3035	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	4.5	1.5	6.1	0.36%	5.9
3036	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	8.2	5.4	2.8	6.1	0.36%	5.9
3037	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	5.1	3.6	1.5	6.1	0.36%	5.9
3040	AT1G49410.1 | Symbol: TOM6 | expressed protein | chr1:18289409-18290570 REVERSE | Aliases: F13F21.16, F13F21_16, TOM6	6.8	4.0	2.8	6.1	0.37%	5.9
3041	AT2G40460.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr2:16903985-16908358 FORWARD | Aliases: T2P4.19, T2P4_19	5.7	4.0	1.7	6.1	0.37%	5.8
3042	AT5G24280.1 | expressed protein, ; expression supported by MPSS | chr5:8251381-8261431 REVERSE | Aliases: MOP9.10, MOP9_10	4.8	3.6	1.3	6.1	0.37%	5.9
3043	AT5G13720.1 | expressed protein | chr5:4427844-4429136 FORWARD | Aliases: MSH12.19, MSH12_19	5.6	4.3	1.3	6.1	0.37%	5.9
3044	AT1G59840.2 | expressed protein | chr1:22030172-22033044 FORWARD | Aliases: F23H11.16, F23H11_16	5.8	3.0	2.8	6.1	0.37%	5.3
3051	AT2G22600.1 | KH domain-containing protein | chr2:9603697-9606130 FORWARD | Aliases: T9I22.4, T9I22_4	5.0	3.6	1.4	6.1	0.37%	5.8
3054	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	5.5	4.2	1.3	6.1	0.37%	5.9
3055	AT3G46110.2 | expressed protein | chr3:16943097-16944627 FORWARD | Aliases: F12M12.80	4.8	3.2	1.6	6.1	0.37%	5.8
3057	AT3G17040.1 | Symbol: HCF107 |	5.2	3.9	1.3	6.1	0.37%	5.8
3058	AT5G01340.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr5:143054-144719 REVERSE | Aliases: T10O8.50, T10O8_50	9.7	6.9	2.8	6.1	0.37%	5.7
3060	ATCG00470.1 | Symbol: ATPE | ATPase epsilon subunit | chrC:52265-52663 REVERSE | Aliases: ATPE	13.4	12.4	1.0	6.1	0.37%	5.6
3061	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	5.6	4.2	1.4	6.1	0.37%	5.8
3062	AT5G35530.1 | 40S ribosomal protein S3 (RPS3C)	11.8	10.6	1.1	6.1	0.37%	5.7
3063	AT3G14700.1 | expressed protein | chr3:4940325-4941405 FORWARD | Aliases: MIE1.20	5.7	3.5	2.1	6.1	0.37%	5.6
3064	AT2G24970.1 | expressed protein | chr2:10627198-10628386 REVERSE | Aliases: F27C12.11, F27C12_11	5.5	2.4	3.0	6.1	0.38%	5.7
3066	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	6.2	4.4	1.9	6.1	0.38%	5.9
3068	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	7.1	3.6	3.6	6.1	0.38%	5.5

Rank	Description	Sync	Root	M	t	adj.q	B
3070	AT4G29590.1 | expressed protein | chr4:14512555-14514449 REVERSE | Aliases: T16L4.100, T16L4_100	7.7	5.0	2.8	6.1	0.38%	5.8
3072	AT4G30840.1 | WD-40 repeat protein family | chr4:15017625-15019741 REVERSE | Aliases: F6I18.250, F6I18_250	5.2	3.2	2.0	6.1	0.38%	5.6
3073	AT2G04795.1 | expressed protein | chr2:1682950-1683472 FORWARD | Aliases: None	8.0	6.5	1.5	6.1	0.38%	5.8
3077	AT2G04845.1 | GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profile PF00583: acetyltransferase, GNAT family | chr2:1702220-1704000 REVERSE | Aliases: None	5.6	3.5	2.0	6.0	0.38%	5.6
3078	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	5.0	1.4	6.0	0.38%	5.8
3080	AT1G48560.1 | expressed protein | chr1:17956533-17958973 FORWARD | Aliases: T1N15.18, T1N15_18	4.6	3.3	1.3	6.0	0.38%	5.8
3081	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	6.8	5.0	1.8	6.0	0.38%	5.8
3082	AT1G31150.1 | expressed protein, EST gb:Z33866 comes from this gene | chr1:11120078-11122568 FORWARD | Aliases: F28K20.8, F28K20_8	4.7	3.3	1.4	6.0	0.38%	5.8
3084	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	5.3	3.2	2.1	6.0	0.39%	5.7
3085	AT4G26210.2 | mitochondrial ATP synthase g subunit family protein, contains Pfam profile: PF04718 mitochondrial ATP synthase g subunit	8.0	5.9	2.1	6.0	0.39%	5.8
3090	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	6.8	3.8	3.0	6.0	0.39%	5.6
3091	AT1G63780.1 | Symbol: IMP4 | brix domain-containing protein, contains Pfam domain, PF04427: Brix domain | chr1:23668536-23671015 REVERSE | Aliases: F24D7.3	6.6	5.4	1.2	6.0	0.39%	5.8
3092	AT4G02400.1 | U3 ribonucleoprotein (Utp) family protein, contains Pfam profile: PF04615 Utp14 protein | chr4:1054243-1058236 FORWARD | Aliases: T14P8.20, T14P8_20	6.6	3.8	2.8	6.0	0.39%	5.7
3094	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	3.1	1.7	6.0	0.39%	5.7
3095	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	5.2	3.2	2.0	6.0	0.39%	5.5
3097	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	9.1	6.5	2.6	6.0	0.39%	5.8
3099	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	3.8	1.5	6.0	0.39%	5.8
3100	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	3.4	2.9	6.0	0.39%	5.7
3101	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	5.0	3.7	1.3	6.0	0.40%	5.8
3103	AT1G68260.1 | thioesterase family protein, contains Pfam profile: PF03061: thioesterase family protein	5.5	3.3	2.2	6.0	0.40%	5.7
3104	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	12.2	10.5	1.7	6.0	0.40%	5.5
3107	AT3G03320.1 | expressed protein, similar to hypothetical protein GB:BAA29429 (Pyrococcus horikoshii) | chr3:781722-783471 FORWARD | Aliases: T21P5.26, T21P5_26	5.6	3.7	1.8	6.0	0.40%	5.7
3108	AT3G53960.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr3:19989100-19991912 REVERSE | Aliases: F5K20.260	5.4	3.7	1.7	6.0	0.40%	5.6

Rank	Description	Sync	Root	M	t	adj.q	B
3109	AT5G64350.1 | Symbol: FKBP12 |	13.2	12.2	1.0	6.0	0.40%	5.6
3114	AT3G18420.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile: PF00515 tetratricopeptide repeat domain (TPR domain) | chr3:6324639-6325799 REVERSE | Aliases: MYF24.14	7.4	4.9	2.5	6.0	0.40%	5.7
3115	AT5G24800.1 | Symbol: BZO2H2 |	10.3	8.7	1.7	6.0	0.40%	5.7
3116	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	3.2	2.1	6.0	0.40%	5.7
3117	AT3G50685.1 | expressed protein | chr3:18845200-18845815 REVERSE | Aliases: None	9.7	8.5	1.2	6.0	0.40%	5.8
3118	AT2G35820.1 | expressed protein | chr2:15057991-15059318 FORWARD | Aliases: F11F19.27, F11F19_27	4.5	1.9	2.6	6.0	0.40%	5.4
3119	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	7.5	1.8	6.0	0.40%	5.8
3121	AT2G01320.4 | ABC transporter family protein | chr2:154427-158181 REVERSE | Aliases: F10A8.20, F10A8_20	5.1	3.5	1.6	6.0	0.40%	5.7
3122	AT3G53470.2 | expressed protein, ribosomal protein S25, cytosolic, Arabidopsis thaliana, PIR:T08568 | chr3:19833728-19834384 FORWARD | Aliases: F4P12.170	5.8	3.9	1.9	6.0	0.40%	5.6
3124	AT1G22520.1 | expressed protein, contains Pfam PF04418: Domain of unknown function (DUF543) | chr1:7953011-7954391 REVERSE | Aliases: F12K8.27, F12K8_27	7.6	5.7	1.9	6.0	0.40%	5.8
3127	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	3.9	1.5	6.0	0.40%	5.8
3130	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	8.0	6.3	1.7	6.0	0.40%	5.8
3132	AT5G08540.1 | expressed protein, similar to unknown protein (pir::T27191) | chr5:2763824-2766156 FORWARD | Aliases: MAH20.10, MAH20_10	7.3	4.8	2.5	6.0	0.40%	5.8
3133	AT5G17520.1 | Symbol: RCP1 | root cap 1 (RCP1), identical to GI:6137138 | chr5:5772586-5775347 REVERSE | Aliases: K3M16.90, K3M16_90, MALTOSE EXCESS 1, MEX1, ROOT CAP 1	7.1	4.4	2.7	6.0	0.40%	5.4
3135	AT4G15640.1 | expressed protein | chr4:8918983-8921928 REVERSE | Aliases: DL3860C, FCAALL.350	6.5	3.7	2.8	6.0	0.41%	5.6
3136	AT4G17670.1 | senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana); | chr4:9833681-9834740 REVERSE | Aliases: DL4870C, FCAALL.414	6.5	4.4	2.0	6.0	0.41%	5.7
3141	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	8.6	6.7	1.9	6.0	0.41%	5.7
3144	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	7.7	5.9	1.8	6.0	0.41%	5.8
3146	AT3G51870.1 | mitochondrial substrate carrier family protein, peroxisomal Ca-dependent solute carrier - Oryctolagus cuniculus, EMBL:AF004161 | chr3:19254931-19257913 FORWARD | Aliases: ATEM1.12	4.9	3.2	1.7	6.0	0.41%	5.7
3148	AT3G45740.1 | hydrolase family protein / HAD-superfamily protein, contains TIGRfam domians TIGR01460: HAD-superfamily hydrolase, subfamily IIA and TIGR01456: HAD-superfamily subfamily IIA hydrolase, TIGR01456, CECR5 | chr3:16801746-16804519 FORWARD | Aliases: T6D9.70	6.0	4.4	1.6	6.0	0.41%	5.7
3150	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	3.9	3.1	0.7	6.0	0.41%	5.5
3153	AT4G27340.1 | Met-10+ like family protein, ; contains Pfam profile PF02475: Met-10+ like-protein | chr4:13687202-13690376 REVERSE | Aliases: F27G19.9	5.2	4.0	1.3	6.0	0.41%	5.7

Rank	Description	Sync	Root	M	t	adj.q	B
3155	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	6.5	5.1	1.4	6.0	0.41%	5.7
3156	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	5.7	2.6	3.1	6.0	0.41%	5.5
3159	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	9.4	5.5	3.9	5.9	0.42%	5.6
3161	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	7.1	6.1	1.0	5.9	0.42%	5.7
3163	AT2G18040.1 | Symbol: PIN1AT |	9.8	7.6	2.3	5.9	0.42%	5.7
3164	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	4.9	3.4	1.5	5.9	0.42%	5.7
3165	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	10.6	0.8	5.9	0.42%	5.5
3167	AT5G20580.2 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:6958619-6962768 REVERSE | Aliases: F7C8.170, F7C8_170	5.6	3.9	1.7	5.9	0.42%	5.7
3168	AT5G64900.1 | expressed protein | chr5:25954396-25955302 FORWARD | Aliases: MXK3.13, MXK3_13	5.6	4.1	1.4	5.9	0.42%	5.7
3170	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	5.9	4.1	1.7	5.9	0.42%	5.5
3171	AT2G40300.1 | Symbol: ATFER4 |	5.8	3.3	2.5	5.9	0.42%	5.4
3172	AT2G17240.1 | expressed protein | chr2:7505214-7506288 FORWARD | Aliases: T23A1.10, T23A1_10	6.8	3.5	3.3	5.9	0.42%	5.6
3173	AT3G51100.2 | expressed protein | chr3:18991762-18993241 REVERSE | Aliases: F24M12.140	9.1	7.5	1.6	5.9	0.42%	5.7
3174	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	5.9	4.9	1.0	5.9	0.42%	5.7
3175	AT4G19985.1 | GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profile PF00583: acetyltransferase, GNAT family | chr4:10830318-10832104 REVERSE | Aliases: None	5.0	3.3	1.7	5.9	0.42%	5.7
3179	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	11.9	10.8	1.0	5.9	0.42%	5.5
3181	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	9.2	7.3	1.9	5.9	0.42%	5.7
3184	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	8.0	6.3	1.7	5.9	0.42%	5.6
3185	AT4G23820.1 | glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, weak similarity to polygalacturonase PG1 (Glycine max) GI:5669846; contains PF00295: Glycosyl hydrolases family 28	5.6	3.9	1.7	5.9	0.42%	5.6
3186	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	5.8	3.4	2.4	5.9	0.42%	5.4
3189	AT2G19310.1 | expressed protein | chr2:8376876-8377488 REVERSE | Aliases: F27F23.11, F27F23_11	6.0	4.1	1.9	5.9	0.42%	5.7
3192	AT3G29230.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:11190040-11191842 FORWARD | Aliases: MXO21.8	6.8	5.0	1.8	5.9	0.43%	5.6

Rank	Description	Sync	Root	M	t	adj.q	B
3193	AT2G46420.1 | expressed protein | chr2:19060759-19064163 FORWARD | Aliases: F11C10.11	5.8	2.4	3.4	5.9	0.43%	5.4
3194	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	5.8	3.7	2.2	5.9	0.43%	5.6
3195	AT5G08050.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:2578370-2579164 FORWARD | Aliases: T22D6.3	7.1	5.0	2.1	5.9	0.43%	5.5
3196	AT2G01640.1 | expressed protein | chr2:283003-284124 FORWARD | Aliases: T8O11.19, T8O11_19	5.3	3.8	1.5	5.9	0.43%	5.7
3197	AT1G26665.2 | expressed protein | chr1:9214164-9215538 FORWARD | Aliases: None	8.6	6.9	1.6	5.9	0.43%	5.7
3200	AT5G24660.1 | expressed protein | chr5:8443282-8443837 REVERSE | Aliases: MXC17.2, MXC17_2	11.9	8.8	3.1	5.9	0.43%	5.7
3201	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	8.2	5.5	2.6	5.9	0.43%	5.7
3202	AT5G57120.1 | expressed protein, weak similarity to SP:Q14978 Nucleolar phosphoprotein p130 {Homo sapiens} | chr5:23139766-23141739 REVERSE | Aliases: MUL3.6, MUL3_6	9.7	8.2	1.5	5.9	0.43%	5.6
3204	AT3G08010.1 | expressed protein | chr3:2555988-2557511 FORWARD | Aliases: F17A17.35	8.0	6.2	1.8	5.9	0.43%	5.6
3207	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	8.2	6.8	1.4	5.9	0.43%	5.7
3210	AT3G24315.1 | sec20 family protein, contains Pfam PF03908: Sec20 | chr3:8820464-8822810 REVERSE | Aliases: None	9.3	7.9	1.4	5.9	0.43%	5.7
3212	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	4.7	2.3	2.3	5.9	0.43%	5.4
3213	AT5G40500.1 | expressed protein | chr5:16245062-16245839 FORWARD | Aliases: MNF13.2, MNF13_2	4.4	3.0	1.4	5.9	0.43%	5.7
3215	AT5G10040.1 | expressed protein | chr5:3143724-3144158 FORWARD | Aliases: T31P16.30, T31P16_30	6.3	4.1	2.2	5.9	0.43%	5.6
3216	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	10.8	9.6	1.2	5.9	0.43%	5.2
3217	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	4.9	3.3	1.6	5.9	0.43%	5.7
3219	AT4G13220.1 | expressed protein | chr4:7674295-7675303 REVERSE | Aliases: F17N18.110, F17N18_110	5.3	3.7	1.6	5.9	0.43%	5.6
3220	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	6.1	4.3	1.8	5.9	0.43%	5.5
3221	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	4.6	3.1	1.5	5.9	0.43%	5.7
3222	AT2G39725.2 | complex 1 family protein / LVR family protein, contains Pfam PF05347: Complex 1 protein (LYR family) | chr2:16576508-16577595 FORWARD | Aliases: None	7.1	4.6	2.5	5.9	0.43%	5.6
3224	AT2G05520.5 | Symbol: GRP 3 | similar to glycine-rich protein (GRP3S) [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	6.0	1.4	5.9	0.44%	5.7
3225	AT2G37190.1 | 60S ribosomal protein L12 (RPL12A) | chr2:15626486-15627198 REVERSE | Aliases: T2N18.5, T2N18_5	9.1	6.9	2.2	5.9	0.44%	5.6
3227	AT3G20390.1 | endoribonuclease L-PSP family protein, contains Pfam domain PF01042: Endoribonuclease L-PSP | chr3:7109955-7111830 REVERSE | Aliases: MQC12.17	11.6	9.8	1.8	5.9	0.44%	5.6
3228	AT4G30410.2 | expressed protein, similar to cDNA bHLH transcription factor (bHLH eta gene) gi:32563007	5.5	3.6	1.9	5.9	0.44%	5.5

Rank	Description	Sync	Root	M	t	adj.q	B
3229	AT4G19150.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr4:10471346-10472753 REVERSE | Aliases: T18B16.120, T18B16_120	7.7	5.9	1.8	5.9	0.44%	5.7
3230	AT3G04260.1 | SAP domain-containing protein, contains Pfam domain PF02037: SAP domain | chr3:1123030-1127522 REVERSE | Aliases: T6K12.12, T6K12_12	5.2	3.5	1.6	5.9	0.44%	5.6
3232	AT5G03850.1 | 40S ribosomal protein S28 (RPS28B), ribosomal protein S28, Arabidopsis thaliana, EMBL:ATRP28A | chr5:1028339-1029120 REVERSE | Aliases: MED24.14	12.1	11.0	1.1	5.9	0.44%	5.2
3233	AT3G47490.2 | HNH endonuclease domain-containing protein, contains Pfam domain PF01844: HNH endonuclease | chr3:17509322-17510286 FORWARD | Aliases: F1P2.40	6.3	4.9	1.4	5.9	0.44%	5.6
3234	AT2G01080.1 | expressed protein | chr2:77888-79333 FORWARD | Aliases: F23H14.5, F23H14_5	5.6	4.7	0.9	5.9	0.44%	5.6
3235	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}	9.0	6.5	2.4	5.9	0.44%	5.6
3236	AT1G16080.1 | expressed protein | chr1:5514311-5516012 FORWARD | Aliases: T24D18.18, T24D18_18	6.0	4.3	1.7	5.9	0.44%	5.6
3238	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)	7.0	3.2	3.8	5.9	0.44%	5.4
3239	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	4.6	2.8	1.8	5.9	0.44%	5.6
3241	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	4.0	1.4	5.9	0.44%	5.6
3243	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	7.6	1.3	5.9	0.44%	5.6
3244	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	3.6	2.1	5.9	0.44%	5.6
3245	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	6.9	4.5	2.4	5.9	0.44%	5.5
3247	AT3G52155.1 | expressed protein | chr3:19354673-19355827 FORWARD | Aliases: None	3.2	2.3	0.9	5.9	0.45%	5.5
3248	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	8.8	1.5	5.9	0.45%	5.6
3249	AT2G40010.1 | 60S acidic ribosomal protein P0 (RPP0A) | chr2:16715457-16717526 REVERSE | Aliases: T28M21.17, T28M21_17	6.6	2.6	4.0	5.9	0.45%	5.5
3251	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	3.4	2.6	5.9	0.45%	5.5
3253	AT2G38730.1 | peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, similar to cyclophilin (Homo sapiens) gi:3647230:gb:AAC60793	7.2	3.6	3.6	5.9	0.45%	5.4
3259	AT3G59780.1 | expressed protein | chr3:22097904-22101421 FORWARD | Aliases: F24G16.50	8.0	6.0	2.1	5.9	0.45%	5.4
3260	AT5G13770.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:4445426-4447839 FORWARD | Aliases: MXE10.6, MXE10_6	7.9	4.6	3.4	5.8	0.45%	5.6
3261	AT1G25275.3 | expressed protein | chr1:8860659-8861349 FORWARD | Aliases: None	11.3	10.4	0.9	5.8	0.45%	5.3

Rank	Description	Sync	Root	M	t	adj.q	B
3263	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	9.5	8.7	0.8	5.8	0.45%	5.4
3264	AT5G19150.2 | carbohydrate kinase family, contains Pfam profile PF01256: Carbohydrate kinase | chr5:6423307-6428456 REVERSE | Aliases: T24G5.50, T24G5_50	8.1	7.2	1.0	5.8	0.45%	5.6
3265	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	6.3	5.2	1.0	5.8	0.45%	5.6
3266	AT1G07040.1 | expressed protein | chr1:2160944-2163302 REVERSE | Aliases: F10K1.25, F10K1_25	9.4	6.9	2.5	5.8	0.45%	5.6
3267	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	7.6	6.6	1.0	5.8	0.45%	5.6
3268	AT5G23900.1 | 60S ribosomal protein L13 (RPL13D) | chr5:8064016-8065520 REVERSE | Aliases: MRO11.6, MRO11_6	9.9	8.0	1.9	5.8	0.45%	5.6
3269	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	9.8	7.8	2.0	5.8	0.45%	5.6
3270	AT1G15420.1 | expressed protein | chr1:5301608-5303372 REVERSE | Aliases: None	6.0	4.3	1.7	5.8	0.46%	5.6
3274	AT3G12210.2 | expressed protein | chr3:3894800-3896073 FORWARD | Aliases: F28J15.5	6.9	4.9	2.0	5.8	0.46%	5.5
3275	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	7.7	5.0	2.6	5.8	0.46%	5.5
3276	AT4G34670.1 | 40S ribosomal protein S3A (RPS3aB) | chr4:16548651-16550453 FORWARD | Aliases: T4L20.250, T4L20_250	11.4	9.9	1.5	5.8	0.46%	5.4
3277	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	7.9	6.5	1.4	5.8	0.46%	5.6
3279	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	4.1	2.7	1.4	5.8	0.46%	5.6
3280	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	6.1	4.5	1.5	5.8	0.46%	5.6
3283	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	5.4	2.9	5.8	0.46%	5.6
3285	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	7.4	5.6	1.7	5.8	0.46%	5.6
3288	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	12.1	11.5	0.6	5.8	0.46%	5.2
3291	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	9.8	7.7	2.1	5.8	0.46%	5.6
3292	AT3G19810.1 | expressed protein, contains Pfam PF02620: Uncharacterized ACR, COG1399 | chr3:6877581-6879405 REVERSE | Aliases: MPN9.5	5.5	4.2	1.3	5.8	0.46%	5.6

Rank	Description	Sync	Root	M	t	adj.q	B
3293	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	5.2	3.3	1.9	5.8	0.46%	5.5
3294	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	7.2	4.7	2.6	5.8	0.46%	5.5
3295	AT5G37010.1 | expressed protein | chr5:14637962-14640171 REVERSE | Aliases: K15O15.3, K15O15_3	7.4	6.2	1.2	5.8	0.46%	5.6
3296	AT5G42765.1 | expressed protein | chr5:17166762-17168907 REVERSE | Aliases: None	5.3	4.1	1.1	5.8	0.46%	5.6
3298	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	6.7	1.3	5.8	0.46%	5.5
3300	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	8.7	6.6	2.1	5.8	0.46%	5.5
3301	AT4G21800.2 | ATP-binding family protein, contains Pfam domain, PF03029: Conserved hypothetical ATP binding protein | chr4:11572877-11575504 FORWARD | Aliases: F17L22.260, F17L22_260	6.5	5.2	1.3	5.8	0.46%	5.6
3303	AT3G43540.2 | expressed protein, hypothetical protein slr1699 - Synechocystis sp. (strain PCC 6803), PIR:S75306 | chr3:15441747-15444175 FORWARD | Aliases: T18D12.110	6.4	3.6	2.8	5.8	0.47%	5.5
3305	AT3G42660.1 | transducin family protein / WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); AND-1 protein - Homo sapiens, EMBL:AJ006266	7.2	4.4	2.7	5.8	0.47%	5.5
3306	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	6.3	4.1	2.1	5.8	0.47%	5.5
3307	AT5G52390.1 | photoassimilate-responsive protein, putative, similar to PIR:S62698 photoassimilate-responsive protein precursor (clone PAR-1a) - common tobacco	6.5	2.2	4.3	5.8	0.47%	4.7
3308	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	2.4	1.6	5.8	0.47%	5.6
3309	AT1G70280.2 | NHL repeat-containing protein, contains Pfam profile PF01436: NHL repeat	5.0	3.1	1.9	5.8	0.47%	5.6
3310	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	4.8	1.3	5.8	0.47%	5.6
3314	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	11.1	9.0	2.2	5.8	0.47%	5.5
3315	AT5G51010.1 | rubredoxin family protein, similar to SP:P04170 Rubredoxin (Rd) {Desulfovibrio desulfuricans}; contains Pfam profile PF00301: Rubredoxin	6.8	5.0	1.8	5.8	0.47%	5.5
3317	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	5.4	3.0	2.4	5.8	0.47%	5.5
3318	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	8.0	6.4	1.7	5.8	0.47%	5.6
3319	AT1G76405.2 | expressed protein | chr1:28666817-28668683 FORWARD | Aliases: None	6.3	4.1	2.3	5.8	0.47%	5.5
3322	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	7.5	6.0	1.5	5.8	0.47%	5.5
3323	AT1G53645.1 | hydroxyproline-rich glycoprotein family protein | chr1:20029841-20032303 REVERSE | Aliases: None	7.2	5.5	1.8	5.8	0.47%	5.6

Rank	Description	Sync	Root	M	t	adj.q	B
3326	AT4G36430.1 | peroxidase, putative, identical to peroxidase (Arabidopsis thaliana) gi:6822093:emb:CAB71009; identical to cDNA class III peroxidase ATP31, GI:17530561	6.9	2.7	4.1	5.8	0.47%	5.2
3328	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	11.8	10.8	1.0	5.8	0.47%	5.3
3334	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	7.1	6.1	1.1	5.8	0.47%	5.5
3335	AT3G01660.1 | expressed protein, similar to putative protein GB:CAB45319 (Arabidopsis thaliana) | chr3:245485-246439 FORWARD | Aliases: F4P13.20, F4P13_20	4.5	2.8	1.7	5.8	0.47%	5.4
3336	AT2G16200.1 | expressed protein | chr2:7031806-7032186 FORWARD | Aliases: F7H1.22, F7H1_22	3.3	2.3	1.0	5.8	0.47%	5.5
3339	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	5.2	3.4	1.8	5.8	0.48%	5.3
3341	AT3G47590.1 | esterase/lipase/thioesterase family protein, low similarity to cinnamoyl ester hydrolase CinI (Butyrivibrio fibrisolvens) GI:1622732; contains Interpro entry IPR000379 | chr3:17546605-17548508 REVERSE | Aliases: F1P2.140	8.2	6.8	1.4	5.8	0.48%	5.5
3343	AT4G11120.1 | translation elongation factor Ts (EF-Ts), putative, similar to ethylene-responsive elongation factor EF-Ts precursor (Lycopersicon esculentum) GI:5669636; contains Pfam profile PF00889: Elongation factor TS | chr4:6777800-6780162 FORWARD | Aliases: T22B4.100, T22B4_100	6.6	5.1	1.5	5.8	0.48%	5.5
3344	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	9.6	1.8	5.8	0.48%	5.5
3345	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	8.2	4.7	3.5	5.8	0.48%	5.5
3346	AT5G58970.2 | Symbol: ATUCP2 |	8.1	5.7	2.4	5.8	0.48%	5.5
3347	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	4.1	2.9	1.3	5.8	0.48%	5.5
3350	AT1G28140.1 | expressed protein, contains similarity to cytochrome oxidase I GI:1289267 from (Xantholinus sp.)	6.3	4.8	1.6	5.8	0.48%	5.5
3352	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	7.5	4.6	2.9	5.8	0.48%	5.5
3354	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	7.0	5.4	1.6	5.8	0.49%	5.5
3357	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	7.3	5.6	1.7	5.8	0.49%	5.5
3358	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	5.0	3.4	1.6	5.8	0.49%	5.5
3361	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	5.6	4.0	1.5	5.8	0.49%	5.5
3362	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	5.0	3.5	1.5	5.8	0.49%	5.5
3363	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	8.8	1.4	5.8	0.49%	5.5

Rank	Description	Sync	Root	M	t	adj.q	B
3365	AT2G26680.1 | expressed protein, similar to NLPE1 (GI:13022100) (Rhizobium etli); | chr2:11350879-11352480 REVERSE | Aliases: F18A8.5, F18A8_5	5.2	4.0	1.2	5.7	0.49%	5.5
3366	AT5G66000.1 | expressed protein | chr5:26413171-26414726 REVERSE | Aliases: K2A18.6, K2A18_6	4.9	3.5	1.3	5.7	0.49%	5.5
3368	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	6.2	4.5	1.7	5.7	0.49%	5.5
3369	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	5.0	3.7	1.2	5.7	0.49%	5.5
3370	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	3.2	1.4	5.7	0.49%	5.5
3372	AT1G48580.1 | expressed protein | chr1:17961931-17964278 REVERSE | Aliases: T1N15.20, T1N15_20	4.0	2.8	1.2	5.7	0.49%	5.5
3373	AT5G52470.1 | Symbol: FIB1 | fibrillarin 1 (FBR1) (FIB1) (SKIP7), identical to fibrillarin 1 GI:9965653 from (Arabidopsis thaliana); C-terminus identical to SKP1 interacting partner 7 GI:10716959 from (Arabidopsis thaliana); contains Pfam domain PF01269: Fibrillarin | chr5:21311454-21313902 FORWARD | Aliases: ATFBR1, ATFIB1, FBR1, FIBRILLARIN 1, K24M7.22, K24M7_22, SKIP7, SKP1 INTERACTING PARTNER 7	11.2	10.4	0.8	5.7	0.49%	5.2
3374	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	5.6	2.7	2.8	5.7	0.50%	4.9
3376	AT4G02230.1 | 60S ribosomal protein L19 (RPL19C), similar to L19 from several species | chr4:979229-980667 REVERSE | Aliases: T2H3.3, T2H3_3	10.6	8.3	2.3	5.7	0.50%	5.5
3379	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	6.1	4.5	1.6	5.7	0.50%	5.5
3380	AT5G57330.1 | aldose 1-epimerase family protein, contains Pfam profile PF01263 Aldose 1-epimerase | chr5:23235440-23238315 FORWARD | Aliases: MJB24.14, MJB24_14	9.0	6.7	2.4	5.7	0.50%	5.5
3383	AT5G28060.1 | 40S ribosomal protein S24 (RPS24B), 40S ribosomal protein S19, Cyanophora paradoxa, EMBL:CPA245654 | chr5:10069553-10070897 REVERSE | Aliases: F15F15.130, F15F15_130	9.2	6.9	2.3	5.7	0.50%	5.5
3384	AT2G37600.1 | 60S ribosomal protein L36 (RPL36A) | chr2:15781323-15782420 REVERSE | Aliases: F13M22.10, F13M22_10	6.2	3.7	2.5	5.7	0.50%	5.5
3386	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	5.4	1.5	5.7	0.50%	5.5
3392	AT5G51280.1 | DEAD-box protein abstrakt, putative | chr5:20858474-20861032 FORWARD | Aliases: MWD22.23, MWD22_23	8.7	7.1	1.6	5.7	0.50%	5.5
3399	AT5G53070.1 | ribosomal protein L9 family protein, contains similarity to ribosomal protein L9	4.6	2.9	1.6	5.7	0.50%	5.4
3402	AT4G24175.1 | expressed protein | chr4:12546979-12548968 FORWARD | Aliases: None	4.9	3.4	1.5	5.7	0.50%	5.5
3404	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	5.5	3.0	2.5	5.7	0.50%	4.8
3405	AT5G16840.1 | RNA recognition motif (RRM)-containing protein, predicted proteins - Arabidopsis thaliana | chr5:5535923-5538253 FORWARD | Aliases: F5E19.180, F5E19_180	9.5	7.2	2.2	5.7	0.50%	5.5
3406	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	3.3	2.4	0.9	5.7	0.50%	5.3
3407	AT1G09210.1 | calreticulin 2 (CRT2), identical to SP:Q38858 Calreticulin 2 precursor {Arabidopsis thaliana} | chr1:2972844-2976731 REVERSE | Aliases: T12M4.8, T12M4_8	8.5	6.6	1.9	5.7	0.50%	5.5
3408	AT5G17560.1 | BolA-like family protein, contains Pfam profile: PF01722 BolA-like protein | chr5:5788456-5789925 FORWARD | Aliases: K10A8.40, K10A8_40	6.7	5.2	1.5	5.7	0.50%	5.5

Rank	Description	Sync	Root	M	t	adj.q	B
3410	AT5G01230.2 | FtsJ-like methyltransferase family protein, contains Pfam profile: PF01728 FtsJ-like methyltransferase | chr5:92600-95685 REVERSE | Aliases: F7J8.210, F7J8_210	6.0	4.9	1.2	5.7	0.50%	5.4
3414	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	5.1	3.3	1.9	5.7	0.51%	5.4
3415	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	10.7	9.6	1.2	5.7	0.51%	5.4
3416	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	8.6	6.3	2.4	5.7	0.51%	5.5
3417	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	4.9	3.1	1.9	5.7	0.51%	5.4
3418	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	7.4	1.8	5.7	0.51%	5.5
3424	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	8.4	5.9	2.6	5.7	0.51%	5.5
3425	AT3G04950.1 | expressed protein, contains InterPro domain SEC-C motif (InterPro:IPR004027) | chr3:1371711-1373483 FORWARD | Aliases: T9J14.10, T9J14_10	3.4	2.2	1.3	5.7	0.51%	5.5
3428	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	6.8	3.2	5.7	0.51%	5.4
3429	AT4G18730.1 | Symbol: RPL16B |	10.1	8.0	2.1	5.7	0.51%	5.5
3430	AT5G45775.2 | 60S ribosomal protein L11 (RPL11D) | chr5:18582292-18583785 REVERSE | Aliases: None	10.1	8.0	2.1	5.7	0.51%	5.5
3431	AT5G62630.1 | expressed protein | chr5:25160821-25163685 REVERSE | Aliases: MRG21.5, MRG21_5	8.9	7.1	1.8	5.7	0.51%	5.5
3432	AT3G07440.1 | expressed protein | chr3:2381376-2383146 FORWARD | Aliases: F21O3.15	5.2	3.5	1.7	5.7	0.51%	5.3
3433	AT5G38900.1 | DSBA oxidoreductase family protein, contains Pfam profile: PF01323 DSBA-like thioredoxin domain | chr5:15590735-15592848 REVERSE | Aliases: K15E6.80, K15E6_80	6.1	4.1	2.0	5.7	0.51%	5.3
3435	NA	9.7	4.3	5.3	5.7	0.51%	5.2
3436	AT4G11100.1 | expressed protein | chr4:6768611-6770180 FORWARD | Aliases: T22B4.80, T22B4_80	3.4	2.5	0.8	5.7	0.51%	5.4
3437	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	7.0	5.3	1.6	5.7	0.51%	5.5
3438	AT5G03455.1 | Symbol: CDC25 | rhodanese-like domain-containing protein, contains Rhodanese-like domain PF:00581 | chr5:862558-864107 FORWARD | Aliases: ARATH;CDC25	10.2	9.0	1.2	5.7	0.51%	5.2
3440	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	6.7	1.7	5.7	0.51%	5.4
3441	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	5.6	3.3	2.3	5.7	0.51%	4.9
3443	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	6.1	1.5	5.7	0.51%	5.5
3444	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	5.9	2.9	3.0	5.7	0.51%	5.4

Rank	Description	Sync	Root	M	t	adj.q	B
3445	AT3G01130.1 | expressed protein | chr3:44491-45597 REVERSE | Aliases: T4P13.18, T4P13_18	12.3	11.2	1.1	5.7	0.51%	4.6
3448	AT5G17670.1 | expressed protein | chr5:5821062-5822738 FORWARD | Aliases: MVA3.2, MVA3_2	7.4	4.9	2.5	5.7	0.51%	5.3
3453	AT5G26670.2 | pectinacetylesterase, putative, similar to pectinacetylesterase precursor GI:1431629 from (Vigna radiata) | chr5:9318283-9320990 FORWARD | Aliases: None	5.9	4.6	1.3	5.7	0.52%	5.4
3454	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	7.4	3.1	5.7	0.52%	5.4
3460	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	6.9	4.4	2.5	5.7	0.52%	5.4
3462	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	6.4	4.4	2.1	5.7	0.52%	5.4
3463	AT1G11720.1 | starch synthase, putative, strong similarity to soluble-starch-synthase (Solanum tuberosum) GI:1911166 | chr1:3952511-3957044 FORWARD | Aliases: F25C20.13, F25C20_13	5.1	3.6	1.5	5.7	0.52%	5.4
3464	AT5G46030.1 | expressed protein, contains Pfam profile PF05129: Putative zinc binding domain (DUF701) | chr5:18687356-18688566 FORWARD | Aliases: MCL19.8, MCL19_8	9.6	8.4	1.2	5.7	0.52%	5.4
3465	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	8.2	6.2	2.0	5.7	0.52%	5.4
3467	AT4G23885.1 | expressed protein | chr4:12419404-12420477 FORWARD | Aliases: None	9.4	8.2	1.2	5.7	0.52%	5.4
3468	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	5.5	1.5	5.7	0.52%	5.4
3470	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	10.5	7.1	3.3	5.7	0.52%	5.4
3472	AT4G37430.1 | Symbol: CYP91A2 | cytochrome P450 81F1 (CYP81F1) (CYP91A2), identical to cytochrome P450 81F1 (91A2) (SP:O65790) (Arabidopsis thaliana)	5.2	4.2	1.1	5.7	0.52%	5.4
3476	AT3G07568.1 | expressed protein | chr3:2416249-2417796 REVERSE | Aliases: None	10.5	8.4	2.1	5.7	0.52%	5.4
3479	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	11.7	9.1	2.5	5.7	0.52%	5.4
3480	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)	8.7	6.6	2.1	5.7	0.52%	5.4
3481	AT2G34050.1 | expressed protein, contains Pfam PS00030: Eukaryotic putative RNA-binding region RNP-1 signature	6.2	3.8	2.4	5.7	0.52%	5.0
3483	AT5G22440.1 | 60S ribosomal protein L10A (RPL10aC) | chr5:7435128-7436642 REVERSE | Aliases: MWD9.24, MWD9_24	7.7	5.3	2.4	5.7	0.52%	5.4
3484	AT5G41960.1 | expressed protein | chr5:16806942-16808270 FORWARD | Aliases: MJC20.6, MJC20_6	7.6	6.4	1.2	5.7	0.52%	5.4
3485	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	5.1	3.8	1.3	5.7	0.53%	5.4
3490	AT5G42300.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr5:16929561-16931158 REVERSE | Aliases: K5J14.10, K5J14_10	13.3	12.7	0.6	5.7	0.53%	4.9
3491	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	4.5	3.3	1.2	5.7	0.53%	5.4

Rank	Description	Sync	Root	M	t	adj.q	B
3492	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	7.5	4.8	2.7	5.7	0.53%	5.3
3495	AT2G01870.1 | expressed protein | chr2:389469-390376 REVERSE | Aliases: T23K3.6, T23K3_6	3.6	2.5	1.1	5.6	0.53%	5.3
3496	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	6.1	1.4	5.6	0.53%	5.4
3499	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	7.3	5.3	2.0	5.6	0.53%	5.2
3500	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	6.0	4.7	1.3	5.6	0.53%	5.4
3502	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	4.0	2.0	5.6	0.53%	5.4
3503	AT1G18680.1 | HNH endonuclease domain-containing protein, contains Pfam domain PF01844: HNH endonuclease | chr1:6431930-6433437 REVERSE | Aliases: F6A14.21, F6A14_21	6.0	4.9	1.1	5.6	0.53%	5.4
3505	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	5.2	3.6	1.5	5.6	0.53%	5.4
3506	AT3G01060.3 | expressed protein | chr3:16650-18847 REVERSE | Aliases: T4P13.26, T4P13_26	4.8	3.8	1.0	5.6	0.53%	5.4
3507	AT5G13310.1 | expressed protein | chr5:4263496-4265340 FORWARD | Aliases: T22N19.1	5.2	4.2	1.0	5.6	0.53%	5.3
3509	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	9.3	7.0	2.2	5.6	0.54%	5.3
3510	AT3G13230.1 | expressed protein | chr3:4269985-4271211 FORWARD | Aliases: MDC11.5	6.3	4.4	1.9	5.6	0.54%	5.4
3511	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	7.1	4.7	2.3	5.6	0.54%	5.3
3512	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	7.0	2.0	5.6	0.54%	5.4
3514	AT3G09250.1 | expressed protein | chr3:2839007-2840871 FORWARD | Aliases: F3L24.12	5.8	4.7	1.1	5.6	0.54%	5.4
3516	AT5G02820.1 | Symbol: RHL2 | DNA topoisomerase VIA (SPO11), identical to topoisomerase 6 subunit A (spo11) (Arabidopsis thaliana) GI:12331186	7.4	5.6	1.8	5.6	0.54%	5.3
3518	AT2G31410.1 | expressed protein | chr2:13399099-13399928 REVERSE | Aliases: T28P16.10, T28P16_10	5.1	3.5	1.6	5.6	0.55%	5.4
3519	AT3G59540.1 | 60S ribosomal protein L38 (RPL38B), 60S RIBOSOMAL PROTEIN L38 - Lycopersicon esculentum, EMBL:X69979 | chr3:22006655-22007783 REVERSE | Aliases: T16L24.90	10.3	7.7	2.6	5.6	0.55%	5.4
3522	AT2G15690.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:6838077-6840859 REVERSE | Aliases: F9O13.34	6.2	4.3	1.9	5.6	0.55%	5.2
3523	AT2G33250.1 | expressed protein | chr2:14104509-14105788 FORWARD | Aliases: F25I18.1, F25I18_1	9.2	7.8	1.3	5.6	0.55%	5.3
3524	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	5.4	4.3	1.2	5.6	0.55%	5.3
3525	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	6.1	4.2	1.8	5.6	0.55%	5.3

Rank	Description	Sync	Root	M	t	adj.q	B
3527	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	6.5	3.9	2.6	5.6	0.55%	5.3
3534	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	7.2	6.0	1.1	5.6	0.56%	5.3
3537	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	5.8	2.7	3.0	5.6	0.56%	4.4
3538	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	6.0	3.8	2.2	5.6	0.56%	5.3
3539	AT3G20330.1 | aspartate carabmoyltransferase, chloroplast / aspartate transcarbamylase / ATCase (PYRB), identical to SP:P49077 Aspartate carbamoyltransferase, chloroplast precursor (EC 2.1.3.2) (Aspartate transcarbamylase) (ATCase) {Arabidopsis thaliana}	8.5	5.6	2.8	5.6	0.56%	5.3
3543	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	7.8	4.8	3.0	5.6	0.56%	5.3
3545	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	6.6	5.3	1.3	5.6	0.56%	5.3
3546	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	7.0	5.1	1.9	5.6	0.56%	5.3
3547	AT5G24310.2 | expressed protein, strong similarity to unknown protein (emb:CAB66408.1)	8.4	6.6	1.7	5.6	0.56%	5.3
3548	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	6.5	5.4	1.2	5.6	0.56%	5.3
3550	AT5G58590.1 | Symbol: RANBP1 |	11.3	8.9	2.4	5.6	0.56%	5.3
3553	AT1G54500.1 | rubredoxin family protein, similar to SP:P00270 Rubredoxin (Rd) {Desulfovibrio gigas}; contains Pfam profile PF00301: Rubredoxin	7.3	5.8	1.5	5.6	0.56%	5.3
3556	AT5G18440.1 | expressed protein | chr5:6113250-6115750 FORWARD | Aliases: F20L16.160, F20L16_160	5.5	4.7	0.8	5.6	0.56%	5.2
3558	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	4.6	1.4	5.6	0.56%	5.3
3560	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	6.6	4.5	2.1	5.6	0.57%	5.2
3563	AT4G40045.1 | expressed protein | chr4:18559778-18560651 REVERSE | Aliases: None	6.7	5.3	1.4	5.6	0.57%	5.3
3564	AT2G33370.1 | 60S ribosomal protein L23 (RPL23B) | chr2:14150646-14151797 REVERSE | Aliases: F4P9.14	8.5	6.7	1.8	5.6	0.57%	5.3
3565	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	7.1	5.5	1.6	5.6	0.57%	5.3
3566	AT5G10730.1 | expressed protein | chr5:3390615-3393107 REVERSE | Aliases: MAJ23.90, MAJ23_90	8.6	6.6	2.1	5.6	0.57%	5.3
3570	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	11.7	10.2	1.5	5.6	0.57%	5.0
3574	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	5.7	3.8	1.9	5.6	0.57%	5.3
3579	AT5G42900.3 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g33980.1) | chr5:17215358-17217007 REVERSE | Aliases: MBD2.9, MBD2_9	5.7	4.1	1.6	5.6	0.57%	5.3

Rank	Description	Sync	Root	M	t	adj.q	B
3580	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	11.3	9.1	2.2	5.6	0.57%	5.3
3583	AT1G26750.1 | expressed protein | chr1:9246774-9248261 FORWARD | Aliases: T24P13.13, T24P13_13	7.5	5.4	2.0	5.6	0.57%	5.2
3585	AT3G21250.1 | Symbol: ATMRP6 |	6.7	5.3	1.5	5.6	0.57%	5.3
3587	AT5G39850.1 | 40S ribosomal protein S9 (RPS9C), 40S ribosomal protein S9 - Chlamydomonas sp.,EMBL:AU066528 | chr5:15967250-15968653 FORWARD | Aliases: MYH19.10, MYH19_10	8.2	6.1	2.1	5.6	0.57%	5.2
3589	AT2G34480.1 | 60S ribosomal protein L18A (RPL18aB) | chr2:14539787-14541280 REVERSE | Aliases: F13P17.34	11.2	9.4	1.7	5.6	0.57%	5.1
3590	AT4G17720.1 | RNA recognition motif (RRM)-containing protein | chr4:9862459-9864676 REVERSE | Aliases: DL4895C, FCAALL.73	7.0	4.8	2.2	5.6	0.57%	5.3
3591	AT5G58600.2 | expressed protein, various predicted proteins, Arabidopsis thaliana and Oryza sativa | chr5:23701017-23702941 REVERSE | Aliases: MZN1.6, MZN1_6	5.4	3.7	1.7	5.6	0.58%	5.2
3592	AT3G13160.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:4229978-4231293 REVERSE | Aliases: MJG19.11	6.3	4.3	2.0	5.6	0.58%	5.3
3593	AT5G64780.1 | expressed protein, similar to unknown protein (pir::T04031) | chr5:25917785-25919351 REVERSE | Aliases: MVP7.11, MVP7_11	3.9	2.8	1.1	5.6	0.58%	5.3
3595	AT5G12410.1 | THUMP domain-containing protein, contains Pfam profile PF02926: THUMP domain | chr5:4021816-4023989 REVERSE | Aliases: None	7.2	5.4	1.8	5.6	0.58%	5.3
3596	AT5G10320.3 | expressed protein | chr5:3244006-3246721 REVERSE | Aliases: F18D22.90, F18D22_90	4.8	4.0	0.8	5.6	0.58%	5.2
3599	AT4G12340.1 | expressed protein | chr4:7321276-7322448 REVERSE | Aliases: T4C9.180, T4C9_180	9.8	8.1	1.7	5.6	0.58%	5.3
3602	AT3G57220.1 | UDP-GlcNAc:dolichol phosphate N-acetylglucosamine-1-phosphate transferase, putative, strong similarity to GI:5804772 | chr3:21185438-21188080 FORWARD | Aliases: F28O9.70, F28O9_70	6.6	4.6	2.0	5.6	0.58%	5.2
3603	AT2G02880.1 | mucin-related, similar to putative mucin GI:18071389 (Oryza sativa) | chr2:841260-843359 FORWARD | Aliases: T17M13.5, T17M13_5	6.2	4.6	1.7	5.6	0.58%	5.3
3605	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	6.0	4.2	1.8	5.6	0.58%	5.2
3608	AT5G48570.1 | peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative, similar to rof1 (Arabidopsis thaliana) GI:1373396 | chr5:19707768-19711071 REVERSE | Aliases: K15N18.12, K15N18_12	10.2	8.2	2.0	5.6	0.58%	5.3
3610	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	5.9	1.6	5.5	0.58%	5.2
3611	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	4.4	3.0	5.5	0.58%	5.3
3614	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	7.0	4.4	2.6	5.5	0.58%	5.2
3616	AT1G34350.1 | expressed protein | chr1:12534432-12536073 FORWARD | Aliases: F7P12.4, F7P12_4	7.0	4.9	2.1	5.5	0.58%	5.2
3617	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	4.5	2.7	1.9	5.5	0.58%	5.3
3618	AT4G18170.1 | Symbol: WRKY28 |	5.9	4.4	1.5	5.5	0.58%	5.3
3619	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	5.7	4.2	1.5	5.5	0.58%	5.3

Rank	Description	Sync	Root	M	t	adj.q	B
3620	AT3G53450.1 | hypothetical protein, contains Pfam profile PF03641: decarboxylase family protein | chr3:19823955-19826408 REVERSE | Aliases: F4P12.150	4.9	3.8	1.1	5.5	0.58%	5.3
3621	AT4G26370.2 | antitermination NusB domain-containing protein, contains Pfam profile: PF01029 NusB family | chr4:13333733-13336184 REVERSE | Aliases: T25K17.4	3.8	2.6	1.2	5.5	0.58%	5.3
3622	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	9.2	7.7	1.6	5.5	0.58%	5.3
3623	AT5G66470.1 | expressed protein | chr5:26558965-26561585 REVERSE | Aliases: K1F13.13, K1F13_13	5.1	3.6	1.5	5.5	0.58%	5.2
3624	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	6.7	5.4	1.3	5.5	0.58%	5.3
3625	AT1G76820.1 | expressed protein | chr1:28842467-28843745 FORWARD | Aliases: F28O16.19, F28O16_19	7.9	5.0	2.9	5.5	0.58%	5.2
3628	AT4G19410.1 | pectinacetylesterase, putative, similar to pectinacetylesterase precursor GI:1431629 from (Vigna radiata) | chr4:10582032-10585769 REVERSE | Aliases: T5K18.190, T5K18_190	11.5	9.7	1.8	5.5	0.59%	5.2
3631	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	2.5	2.6	5.5	0.59%	4.9
3633	AT4G16370.1 | Symbol: ATOPT3 |	9.4	6.4	2.9	5.5	0.59%	5.3
3635	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	8.2	6.5	1.7	5.5	0.59%	5.2
3636	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 [Zoysia 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	11.7	8.6	3.1	5.5	0.59%	5.3
3638	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	5.8	3.1	2.6	5.5	0.59%	5.0
3639	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	6.5	5.6	0.9	5.5	0.59%	5.2
3641	AT1G55890.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:20905011-20906465 FORWARD | Aliases: F14J16.14, F14J16_14	8.1	5.7	2.4	5.5	0.59%	5.3
3643	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	6.1	4.4	1.7	5.5	0.59%	5.2
3644	AT4G21140.1 | expressed protein, ; expression supported by MPSS | chr4:11277546-11278232 REVERSE | Aliases: F7J7.80, F7J7_80	6.2	4.8	1.4	5.5	0.59%	5.3
3646	AT3G44380.1 | expressed protein, predicted proteins, Arabidopsis thaliana | chr3:16047170-16047867 REVERSE | Aliases: T22K7.60	4.5	3.2	1.3	5.5	0.59%	5.3
3649	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	6.6	4.7	1.9	5.5	0.59%	5.3
3650	AT1G32500.1 | Symbol: ATNAP6 |	7.7	5.7	2.0	5.5	0.59%	5.3
3652	AT1G66580.1 | 60S ribosomal protein L10 (RPL10C), contains Pfam profile: PF00826: Ribosomal L10 | chr1:24842828-24844275 FORWARD | Aliases: T12I7.3, T12I7_3	11.9	10.7	1.2	5.5	0.59%	5.2

Rank	Description	Sync	Root	M	t	adj.q	B
3657	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	11.7	8.5	3.2	5.5	0.59%	5.1
3659	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	10.1	8.1	2.0	5.5	0.59%	5.3
3660	AT5G01350.1 | expressed protein | chr5:145635-147199 REVERSE | Aliases: T10O8.60, T10O8_60	11.1	9.9	1.1	5.5	0.59%	4.9
3661	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	5.0	3.7	1.3	5.5	0.59%	5.2
3663	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: PCRF domain | chr2:19326755-19329461 REVERSE | Aliases: F14M4.15	3.4	2.7	0.7	5.5	0.60%	5.1
3665	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	7.6	6.0	1.6	5.5	0.60%	5.2
3666	AT3G62060.1 | pectinacetylesterase family protein, similar to pectinacetylesterase precursor GI:1431629 from (Vigna radiata); contains Pfam profile: PF03283 pectinacetylesterase | chr3:22991031-22993919 FORWARD | Aliases: T17J13.20	5.0	3.3	1.7	5.5	0.60%	5.3
3668	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	3.1	2.4	0.6	5.5	0.60%	5.0
3672	AT5G42370.1 | expressed protein | chr5:16956367-16958953 REVERSE | Aliases: MDH9.6, MDH9_6	6.0	4.0	2.0	5.5	0.60%	5.1
3674	AT5G58930.1 | expressed protein, contains Pfam PF05340: Protein of unknown function (DUF740) | chr5:23811541-23813687 REVERSE | Aliases: K19M22.12, K19M22_12	9.8	9.2	0.7	5.5	0.60%	5.1
3675	AT5G41270.1 | expressed protein | chr5:16524937-16526107 FORWARD | Aliases: K1O13.7, K1O13_7	4.3	3.4	0.9	5.5	0.60%	5.2
3676	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	12.1	10.7	1.4	5.5	0.60%	5.0
3678	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	10.2	8.9	1.3	5.5	0.60%	5.2
3680	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	3.1	2.4	0.7	5.5	0.60%	5.0
3681	AT1G18060.1 | expressed protein | chr1:6211867-6213358 REVERSE | Aliases: T10F20.7	6.9	5.8	1.2	5.5	0.60%	5.2
3688	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	6.1	4.3	1.8	5.5	0.61%	5.2
3689	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	5.9	4.5	1.4	5.5	0.61%	5.2
3692	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	6.6	3.4	3.1	5.5	0.61%	5.0
3695	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	5.2	3.4	1.8	5.5	0.61%	5.2
3700	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	5.7	5.0	0.6	5.5	0.61%	5.0

Rank	Description	Sync	Root	M	t	adj.q	B
3706	AT1G50710.1 | expressed protein | chr1:18788177-18791470 REVERSE | Aliases: F17J6.23, F17J6_23	6.0	4.6	1.4	5.5	0.62%	5.2
3707	AT1G48440.1 | expressed protein | chr1:17910669-17912191 FORWARD | Aliases: T1N15.5, T1N15_5	11.0	9.8	1.2	5.5	0.62%	4.9
3708	AT1G55500.1 | expressed protein, contains Pfam profile PF04146: YT521-B-like family | chr1:20723241-20726399 FORWARD | Aliases: T5A14.10, T5A14_10	5.5	4.5	1.1	5.5	0.62%	5.2
3709	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	8.5	6.0	2.6	5.5	0.62%	5.2
3710	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) {Arabidopsis thaliana} | chr4:16560067-16562936 REVERSE | Aliases: ARGININE DECARBOXYLASE, ARGININE DECARBOXYLASE 2, SPE2, T4L20.290, T4L20_290	9.4	7.7	1.7	5.5	0.62%	5.2
3711	NA	12.0	10.7	1.3	5.5	0.62%	4.7
3712	AT5G27400.1 | expressed protein, hypothetical proteins - different species | chr5:9676351-9678506 FORWARD | Aliases: F21A20.110, F21A20_110	7.4	5.8	1.7	5.5	0.62%	5.2
3713	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	3.9	1.0	5.5	0.62%	5.2
3714	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	4.1	1.1	5.5	0.62%	5.2
3718	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	6.8	5.0	1.7	5.5	0.62%	5.2
3721	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	9.2	1.0	5.5	0.62%	5.1
3722	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	5.1	0.9	5.5	0.62%	5.1
3723	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	8.4	6.5	1.9	5.5	0.62%	5.2
3724	ATCG00380.1 | Symbol: RPS4 | Chloroplast encoded ribosomal protein S4	11.7	9.2	2.6	5.5	0.62%	5.1
3726	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	5.2	2.9	2.3	5.5	0.62%	4.8
3727	AT5G51110.1 | expressed protein | chr5:20795360-20796660 REVERSE | Aliases: MWD22.5, MWD22_5	5.9	4.4	1.4	5.5	0.62%	5.2
3728	AT4G15000.1 | 60S ribosomal protein L27 (RPL27C) | chr4:8571829-8572485 FORWARD | Aliases: DL3545W, FCAALL.99	10.4	8.0	2.4	5.5	0.62%	5.2
3729	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	4.8	3.3	1.5	5.5	0.62%	5.2
3730	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	6.5	2.5	5.5	0.62%	5.2
3731	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	11.4	9.5	1.9	5.5	0.62%	5.0
3733	AT5G08040.1 | expressed protein | chr5:2577203-2578120 REVERSE | Aliases: T22D6.2	10.2	8.3	1.9	5.5	0.63%	5.2
3737	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	6.3	2.4	5.5	0.63%	5.2

Rank	Description	Sync	Root	M	t	adj.q	B
3738	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	6.4	4.7	1.7	5.5	0.63%	5.0
3740	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	6.6	4.5	2.2	5.5	0.63%	5.1
3743	AT1G16310.1 | cation efflux family protein, contains cation efflux family protein domain, Pfam:PF01545	10.1	7.0	3.1	5.5	0.63%	5.2
3745	AT3G23330.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:8347207-8349354 FORWARD | Aliases: MLM24.6	4.9	3.3	1.6	5.4	0.63%	5.2
3747	AT3G20500.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	10.1	8.3	1.8	5.4	0.63%	5.2
3748	AT1G30290.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:10670304-10672722 REVERSE | Aliases: F12P21.10, F12P21_10	6.2	4.8	1.4	5.4	0.63%	5.2
3750	AT4G38100.1 | expressed protein | chr4:17886864-17888198 REVERSE | Aliases: F20D10.220, F20D10_220	6.8	5.1	1.7	5.4	0.63%	5.2
3751	AT4G32540.1 | Symbol: YUC | flavin-containing monooxygenase / FMO (YUCCA), identical to gi:16555352 | chr4:15700910-15702876 FORWARD | Aliases: L23H3.20, L23H3_20, YUCCA	5.4	3.7	1.7	5.4	0.63%	5.1
3752	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	5.0	3.5	1.6	5.4	0.63%	5.1
3754	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	4.2	2.7	1.4	5.4	0.63%	5.2
3758	AT3G16570.1 | Symbol: RALFL23 | rapid alkalinization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316 | chr3:5644704-5645420 FORWARD | Aliases: MGL6.3, RALF LIKE 23	6.6	5.1	1.6	5.4	0.63%	5.2
3760	AT2G47580.1 | Symbol: U1A | small nuclear ribonucleoprotein U1A / spliceosomal protein U1A / U1snRNP-specific protein, identical to GB:Z49991 U1snRNP-specific protein (Arabidopsis thaliana)	8.0	5.6	2.4	5.4	0.63%	5.1
3761	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	8.1	5.9	2.2	5.4	0.63%	5.1
3762	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	9.7	8.1	1.6	5.4	0.63%	5.2
3763	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	6.5	4.2	2.4	5.4	0.64%	5.1
3764	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	4.8	3.5	1.3	5.4	0.64%	5.1
3766	AT5G04790.1 | expressed protein | chr5:1388156-1388320 REVERSE | Aliases: MUK11.11	7.0	4.6	2.4	5.4	0.64%	4.9
3770	AT1G72040.1 | deoxynucleoside kinase family, contains Pfam profile: PF01712 deoxynucleoside kinase | chr1:27115559-27118004 REVERSE | Aliases: F28P5.7, F28P5_7	6.9	4.6	2.2	5.4	0.64%	5.1
3771	AT2G01400.1 | expressed protein | chr2:174270-175616 FORWARD | Aliases: F10A8.4	4.1	2.9	1.3	5.4	0.64%	5.2
3773	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	4.1	3.4	0.7	5.4	0.64%	4.9
3774	AT2G42540.2 | Symbol: COR15A |	5.7	2.5	3.2	5.4	0.64%	5.0
3775	AT5G51545.1 | expressed protein | chr5:20953660-20954626 FORWARD | Aliases: None	6.1	4.4	1.6	5.4	0.64%	5.1

Rank	Description	Sync	Root	M	t	adj.q	B
3776	AT3G06740.1 | zinc finger (GATA type) family protein | chr3:2126425-2127473 FORWARD | Aliases: F3E22.12	6.5	4.4	2.1	5.4	0.64%	5.2
3778	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	7.7	5.7	2.0	5.4	0.64%	5.1
3779	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	9.5	6.6	2.9	5.4	0.64%	5.1
3782	AT3G49910.1 | 60S ribosomal protein L26 (RPL26A), 60S RIBOSOMAL PROTEIN L26, Brassica rapa, EMBL:BRD495 | chr3:18515241-18515952 FORWARD | Aliases: F3A4.4	9.2	7.5	1.8	5.4	0.64%	5.1
3783	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	7.2	5.8	1.4	5.4	0.64%	5.1
3785	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	6.6	4.8	1.7	5.4	0.65%	5.1
3787	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	9.5	6.9	2.7	5.4	0.65%	5.1
3788	AT5G35080.1 | expressed protein | chr5:13371503-13374047 REVERSE | Aliases: F7N22.4, F7N22_4	7.2	5.7	1.5	5.4	0.65%	5.1
3789	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	11.3	9.9	1.5	5.4	0.65%	5.1
3791	AT1G02700.1 | expressed protein, similar to hypothetical protein GB:CAB80707 GI:7268598 from (Arabidopsis thaliana) | chr1:588329-589480 FORWARD | Aliases: T14P4.2, T14P4_2	4.5	3.0	1.5	5.4	0.65%	5.1
3792	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	7.6	5.4	2.2	5.4	0.65%	5.1
3793	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	11.0	8.6	2.4	5.4	0.65%	5.1
3794	AT5G01370.1 | expressed protein | chr5:152529-154350 FORWARD | Aliases: T10O8.80, T10O8_80	6.2	4.4	1.8	5.4	0.65%	5.1
3797	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	7.2	5.8	1.4	5.4	0.65%	5.1
3798	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	8.3	6.1	2.1	5.4	0.65%	5.1
3799	AT2G35190.1 | Symbol: NPSN11 |	6.8	4.9	1.8	5.4	0.65%	5.1
3800	AT4G13750.1 | expressed protein | chr4:7978944-7987554 FORWARD | Aliases: F18A5.140, F18A5_140	4.7	3.4	1.2	5.4	0.65%	5.1
3801	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	9.5	6.4	3.1	5.4	0.65%	5.1
3802	AT1G03100.1 | pentatricopeptide (PPR) repeat-containing protein, low similarity to CRP1 (Zea mays) GI:3289002; contains Pfam profile PF01535: PPR repeat | chr1:744026-746407 REVERSE | Aliases: F10O3.8, F10O3_8	5.3	4.1	1.2	5.4	0.65%	5.1
3803	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	5.2	1.2	5.4	0.65%	5.1

Rank	Description	Sync	Root	M	t	adj.q	B
3804	AT5G17070.1 | expressed protein | chr5:5613371-5616141 REVERSE | Aliases: F2K13.220, F2K13_220	6.0	3.3	2.8	5.4	0.65%	5.1
3809	AT2G30150.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:12881783-12883199 FORWARD | Aliases: T27E13.11, T27E13_11	8.7	7.1	1.6	5.4	0.65%	5.1
3810	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)	6.9	5.2	1.7	5.4	0.65%	5.1
3812	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	4.7	3.3	1.4	5.4	0.65%	5.1
3813	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	5.5	1.5	5.4	0.65%	5.1
3814	AT2G27760.1 | Symbol: ATIPT2 |	6.9	5.5	1.5	5.4	0.65%	5.1
3819	AT3G47500.1 | Dof-type zinc finger domain-containing protein, identical to H-protein promoter binding factor-2a GI:3386546 from (Arabidopsis thaliana)	6.8	6.0	0.8	5.4	0.66%	5.1
3822	AT1G67850.2 | expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707) | chr1:25441633-25445782 FORWARD | Aliases: F12A21.2, F12A21_2	6.0	4.5	1.6	5.4	0.66%	5.1
3823	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	4.9	3.4	1.5	5.4	0.66%	5.1
3825	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	6.5	1.1	5.4	0.66%	5.1
3826	AT4G37660.1 | ribosomal protein L12 family protein, ribosomal protein L12, Liberobacter africanum, U09675 | chr4:17695490-17696264 FORWARD | Aliases: F19F18.150, F19F18_150	5.0	2.3	2.7	5.4	0.66%	4.9
3828	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)	8.2	6.8	1.4	5.4	0.66%	5.1
3829	AT5G05200.1 | ABC1 family protein, contains Pfam domain, PF03109: ABC1 family | chr5:1543606-1547138 REVERSE | Aliases: K2A11.7, K2A11_7	9.5	8.5	1.0	5.4	0.66%	5.0
3831	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	6.4	4.6	1.7	5.4	0.66%	5.1
3833	AT4G17010.1 | expressed protein | chr4:9575831-9577922 FORWARD | Aliases: DL4535W, FCAALL.229	6.7	4.1	2.5	5.4	0.66%	5.1
3834	AT1G10522.1 | expressed protein | chr1:3469637-3471880 FORWARD | Aliases: None	4.8	3.5	1.4	5.4	0.66%	5.1
3836	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	11.2	10.3	0.9	5.4	0.66%	4.9
3837	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	6.7	4.9	1.8	5.4	0.66%	5.0
3840	AT1G54110.1 | cation exchanger, putative (CAX10), Ca2+:Cation Antiporter (CaCA) Family member PMID:11500563 | chr1:20203086-20205363 FORWARD | Aliases: F15I1.20	5.5	4.3	1.2	5.4	0.66%	5.1
3843	AT2G38090.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr2:15951789-15954163 FORWARD | Aliases: F16M14.2, F16M14_2	6.1	4.9	1.2	5.4	0.66%	5.1
3844	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	6.8	5.1	1.7	5.4	0.66%	5.1
3847	AT1G20816.1 | expressed protein | chr1:7233757-7235117 FORWARD | Aliases: F2D10.33, F2D10_33	4.9	2.5	2.5	5.4	0.66%	4.8

Rank	Description	Sync	Root	M	t	adj.q	B
3848	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	3.8	1.7	5.4	0.66%	5.1
3849	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	11.0	9.8	1.2	5.4	0.66%	5.0
3852	AT3G15460.1 | brix domain-containing protein, contains Pfam domain, PF04427: Brix domain | chr3:5213343-5216268 REVERSE | Aliases: MJK13.12	6.7	5.1	1.6	5.4	0.67%	5.1
3853	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	12.3	11.2	1.1	5.4	0.67%	5.0
3854	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	12.3	11.2	1.1	5.4	0.67%	5.0
3855	AT2G28590.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:12256912-12258745 FORWARD | Aliases: T8O18.12, T8O18_12	5.3	4.0	1.2	5.4	0.67%	5.1
3856	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	11.0	9.3	1.7	5.4	0.67%	5.1
3857	AT1G17470.1 | Symbol: ATDRG1 |	9.6	8.0	1.6	5.4	0.67%	5.1
3859	AT1G64490.1 | expressed protein | chr1:23955801-23956376 FORWARD | Aliases: F1N19.6, F1N19_6	8.0	6.0	1.9	5.4	0.67%	5.1
3861	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:BAB93003.1); 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)	6.8	4.7	2.2	5.4	0.67%	5.1
3863	AT3G21750.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:7664352-7666202 FORWARD | Aliases: MSD21.8	5.4	3.4	2.1	5.4	0.67%	4.7
3865	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	4.6	1.3	5.4	0.67%	5.1
3868	AT4G19350.1 | Symbol: EMB3006 | expressed protein | chr4:10562034-10563768 REVERSE | Aliases: EMB3006, EMBRYO DEFECTIVE 3006, T5K18.130, T5K18_130	6.6	5.0	1.6	5.4	0.68%	5.1
3873	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	5.8	1.5	5.4	0.68%	5.0
3878	AT3G10670.1 | Symbol: ATNAP7 |	9.3	6.6	2.8	5.4	0.68%	5.1
3879	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	7.5	6.1	1.4	5.4	0.68%	5.1
3880	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	4.5	3.4	1.1	5.4	0.68%	5.1
3881	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	6.7	5.2	1.5	5.4	0.68%	5.1
3882	AT3G20680.1 | expressed protein | chr3:7230078-7231200 REVERSE | Aliases: F3H11.7	4.4	3.3	1.1	5.4	0.68%	5.1

Rank	Description	Sync	Root	M	t	adj.q	B
3883	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	10.7	6.3	4.3	5.4	0.68%	5.1
3884	AT3G54560.1 | histone H2A.F/Z, identical to GI:2407800	8.0	5.4	2.6	5.4	0.68%	5.1
3885	AT5G42240.1 | Symbol: SCPL42 |	4.5	3.3	1.2	5.4	0.68%	5.1
3887	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	6.4	5.2	1.3	5.3	0.69%	5.0
3891	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	6.5	5.0	1.6	5.3	0.69%	5.1
3892	AT1G23310.2 | Symbol: GGT1 | similar to glutamate:glyoxylate aminotransferase 2 (GGT2) [Arabidopsis thaliana] (TAIR:At1g70580.1); similar to glutamate:glyoxylate aminotransferase 2 (GGT2) [Arabidopsis thaliana] (TAIR:At1g70580.2); similar to alanine aminotransferase [Oryza sativa (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	9.0	1.3	5.3	0.69%	5.0
3896	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	5.0	3.6	1.4	5.3	0.69%	5.1
3897	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	5.9	4.0	2.0	5.3	0.69%	5.0
3902	AT1G54770.1 | expressed protein | chr1:20438329-20439675 FORWARD | Aliases: T22H22.18, T22H22_18	4.9	3.6	1.3	5.3	0.69%	5.1
3905	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	7.3	6.3	1.0	5.3	0.69%	5.0
3906	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	3.6	2.5	1.1	5.3	0.69%	5.0
3908	AT1G54570.1 | esterase/lipase/thioesterase family protein, contains Interpro entry IPR000379 | chr1:20384145-20388688 REVERSE | Aliases: T22H22.2, T22H22_2	7.1	5.8	1.3	5.3	0.69%	5.0
3909	AT5G04140.2 | Symbol: GLU1 | glutamate synthase (GLU1) / ferredoxin-dependent glutamate synthase (Fd-GOGAT 1), identical to ferredoxin-dependent glutamate synthase precursor (Arabidopsis thaliana) GI:3869251 | chr5:1130032-1138439 FORWARD | Aliases: F21E1.60, F21E1_60, FERREDOXIN DEPENDENT GLUAMATE SYNTHASE 1, GLS1, GLUAMATE SYNTHASE 1, GLUTAMATE SYNTHASE	6.3	4.5	1.8	5.3	0.69%	5.0
3912	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	10.8	8.9	1.9	5.3	0.70%	5.0
3913	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	6.1	1.0	5.3	0.70%	4.9
3914	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	6.1	1.0	5.3	0.70%	4.9
3916	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	9.7	8.6	1.0	5.3	0.70%	4.9
3918	AT1G12320.1 | expressed protein | chr1:4189353-4190340 FORWARD | Aliases: F5O11.5, F5O11_5	6.7	5.3	1.4	5.3	0.70%	5.0
3919	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)	6.2	4.8	1.4	5.3	0.70%	5.0

Rank	Description	Sync	Root	M	t	adj.q	B
3921	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	4.5	3.1	1.4	5.3	0.70%	5.0
3923	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	13.5	12.4	1.1	5.3	0.70%	4.4
3924	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	5.6	4.0	1.7	5.3	0.70%	5.0
3925	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	6.2	1.3	5.3	0.70%	5.0
3927	AT3G45590.1 | Symbol: ATSEN1 |	7.7	6.3	1.4	5.3	0.70%	5.0
3929	AT1G60230.1 | radical SAM domain-containing protein, contains Pfam profile PF04055: radical SAM domain protein | chr1:22215749-22218089 REVERSE | Aliases: T13D8.12, T13D8_12	4.9	3.4	1.5	5.3	0.71%	5.0
3930	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	4.3	2.8	1.5	5.3	0.71%	5.0
3931	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	10.9	8.6	2.4	5.3	0.71%	5.0
3932	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	11.7	8.2	3.6	5.3	0.71%	5.0
3933	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	8.3	6.7	1.6	5.3	0.71%	5.0
3934	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	9.6	7.2	2.4	5.3	0.71%	5.0
3935	AT3G02220.1 | expressed protein | chr3:412090-413611 REVERSE | Aliases: F14P3.13, F14P3_13	7.9	5.9	2.0	5.3	0.71%	5.0
3937	AT2G39730.3 | Symbol: RCA | ribulose bisphosphate carboxylase/oxygenase activase / RuBisCO activase, identical to SWISS-PROT:P10896 ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor (RuBisCO activase, RA)(Arabidopsis thaliana) | chr2:16577824-16580597 REVERSE | Aliases: RUBISCO ACTIVASE, T5I7.18	8.8	5.1	3.7	5.3	0.71%	5.0
3939	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	7.0	5.1	1.9	5.3	0.71%	5.0
3941	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	5.4	2.2	5.3	0.71%	4.9
3942	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	3.6	0.9	5.3	0.71%	5.0
3946	AT5G07330.1 | expressed protein | chr5:2315981-2316875 FORWARD | Aliases: T2I1.40, T2I1_40	4.2	2.3	1.9	5.3	0.71%	5.0
3948	AT2G17670.2 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:7681433-7683239 FORWARD | Aliases: T17A5.11, T17A5_11	7.0	5.8	1.2	5.3	0.71%	5.0

Rank	Description	Sync	Root	M	t	adj.q	B
3951	AT1G53290.1 | galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase ;contains similarity to Avr9 elicitor response protein GI:4138265 from (Nicotiana tabacum) | chr1:19874967-19877158 FORWARD | Aliases: F12M16.19, F12M16_19	8.8	6.8	2.0	5.3	0.71%	5.0
3954	AT5G20230.1 | Symbol: ATBCB | plastocyanin-like domain-containing protein | chr5:6826508-6827601 FORWARD | Aliases: ARABIDOPSIS BLUE COPPER BINDING PROTEIN, BCB, F5O24.120, F5O24_120	5.3	2.6	2.7	5.3	0.72%	5.0
3956	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	7.2	5.8	1.4	5.3	0.72%	5.0
3960	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	4.6	3.5	1.1	5.3	0.72%	5.0
3962	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	6.9	4.8	2.1	5.3	0.72%	5.0
3963	AT4G33780.1 | expressed protein | chr4:16201833-16203643 REVERSE | Aliases: T16L1.270, T16L1_270	8.5	6.9	1.6	5.3	0.72%	5.0
3966	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:P17606I {Sorghum bicolor}; contains InterPro entry IPR001236: Lactate/malate dehydrogenase | chr5:23596427-23599521 REVERSE | Aliases: MCK7.20, MCK7_20	8.1	5.5	2.6	5.3	0.72%	4.9
3970	ATCG00070.1 | Symbol: PSBK | PSII K protein | chrC:7017-7202 FORWARD | Aliases: PSBK	5.2	3.2	2.0	5.3	0.72%	5.0
3971	AT2G24790.2 | zinc finger (B-box type) family protein | chr2:10573977-10574702 FORWARD | Aliases: F27A10.10	7.0	5.4	1.6	5.3	0.73%	5.0
3972	AT3G57880.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr3:21441993-21445363 REVERSE | Aliases: T10K17.90	5.5	4.4	1.2	5.3	0.73%	5.0
3973	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) {Homo sapiens}; contains Pfam profile PF04719: hTAFII28-like protein conserved region | chr4:10953557-10954983 FORWARD | Aliases: F1C12.195, F1C12_195	7.4	6.3	1.1	5.3	0.73%	5.0
3974	AT5G19350.1 | RNA-binding protein 45 (RBP45), putative	8.9	7.9	1.0	5.3	0.73%	4.9
3975	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	8.8	7.2	1.7	5.3	0.73%	5.0
3976	AT1G07770.2 | Symbol: RPS15A |	11.3	10.5	0.9	5.3	0.73%	4.8
3977	AT1G07170.1 | expressed protein, contains Pfam domain PF03660: Uncharacterised protein family (UPF0123) | chr1:2200133-2201139 FORWARD | Aliases: F10K1.35	9.1	8.1	1.0	5.3	0.73%	4.9
3978	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	5.4	1.7	5.3	0.73%	4.9
3979	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	5.4	1.7	5.3	0.73%	4.9
3980	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	9.7	7.0	2.6	5.3	0.73%	5.0
3981	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	8.9	7.0	1.9	5.3	0.73%	5.0
3985	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	5.9	4.0	1.9	5.3	0.74%	4.7

Rank	Description	Sync	Root	M	t	adj.q	B
3986	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	10.1	8.2	1.9	5.3	0.74%	4.9
3988	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	9.7	6.9	2.7	5.3	0.74%	5.0
3991	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	9.3	8.1	1.2	5.3	0.74%	4.7
3992	AT2G02170.1 | remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region | chr2:556492-558797 REVERSE | Aliases: F5O4.6, F5O4_6	5.4	4.1	1.3	5.3	0.74%	5.0
3993	AT2G45600.1 | expressed protein, low similarity to PrMC3 (Pinus radiata) GI:5487873 | chr2:18796662-18798026 FORWARD | Aliases: F17K2.13	4.0	2.6	1.4	5.3	0.74%	5.0
3996	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)	5.7	4.2	1.4	5.3	0.74%	5.0
3998	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	8.1	7.2	0.9	5.3	0.74%	4.9
3999	AT1G07220.1 | expressed protein | chr1:2217072-2219378 REVERSE | Aliases: F10K1.7, F10K1_7	5.3	3.7	1.6	5.3	0.74%	5.0
4001	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	10.3	9.1	1.3	5.3	0.75%	5.0
4002	AT3G47450.2 | expressed protein | chr3:17494053-17497332 REVERSE | Aliases: T21L8.200	5.5	3.7	1.8	5.3	0.75%	4.8
4005	AT5G12890.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:4069580-4071230 REVERSE | Aliases: T24H18.60, T24H18_60	6.9	5.8	1.1	5.3	0.75%	4.8
4006	AT2G43500.1 | RWP-RK domain-containing protein, low similarity to nodule inception protein (Lotus japonicus) GI:6448579; contains Pfam profile: PF02042 RWP-RK domain | chr2:18069792-18073527 FORWARD | Aliases: T1O24.24	5.7	4.3	1.4	5.3	0.75%	5.0
4010	AT3G54110.1 | Symbol: ATPUMP1 | plant uncoupling mitochondrial protein (PUMP), identical to plant uncoupling mitochondrial protein (Arabidopsis thaliana) GI:3115108 | chr3:20049670-20052179 FORWARD | Aliases: F24B22.70, PUMP, UCP, UCP2, UNCOUPLING PROTEIN, UNCOUPLING PROTEIN PUMP2	10.9	8.6	2.3	5.3	0.75%	4.9
4011	AT5G06700.1 | expressed protein, strong similarity to unknown protein (emb:CAB82953.1)	8.4	6.7	1.7	5.3	0.75%	4.9
4012	AT1G53000.1 | cytidylyltransferase family, contains Pfam profile: PF02348 cytidylyltransferase	7.7	5.3	2.4	5.3	0.75%	4.9
4015	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	5.9	4.7	1.2	5.2	0.75%	4.9
4019	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	6.5	4.9	1.6	5.2	0.75%	4.9
4021	AT3G56290.1 | expressed protein | chr3:20889518-20890547 REVERSE | Aliases: F18O21.250	5.8	4.3	1.6	5.2	0.75%	4.9
4023	AT5G13470.1 | expressed protein | chr5:4318565-4319834 FORWARD | Aliases: T6I14.1	5.0	3.9	1.1	5.2	0.75%	4.9
4024	AT5G16440.1 | Symbol: IPP1 | similar to MutT/nudix family protein [Arabidopsis thaliana] (TAIR:At1g79690.1); similar to isopentenyl pyrophosphate:dimethyllallyl 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	7.0	3.6	3.5	5.2	0.75%	4.9
4026	AT3G20240.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier proteins | chr3:7057023-7058897 FORWARD | Aliases: MAL21.26	6.0	4.3	1.6	5.2	0.75%	4.9

Rank	Description	Sync	Root	M	t	adj.q	B
4027	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	4.2	1.8	5.2	0.76%	4.9
4029	AT5G48500.1 | expressed protein, similar to unknown protein (gb:AAD28645.1) | chr5:19670217-19671470 FORWARD | Aliases: MJE7.14, MJE7_14	5.0	3.8	1.2	5.2	0.76%	4.9
4031	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	6.6	4.6	2.0	5.2	0.76%	4.8
4032	AT2G39350.1 | ABC transporter family protein | chr2:16436774-16439635 REVERSE | Aliases: T16B24.1, T16B24_1	6.0	4.2	1.9	5.2	0.76%	4.9
4035	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	4.5	3.5	1.0	5.2	0.76%	4.9
4037	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	5.7	4.6	1.1	5.2	0.76%	4.9
4038	AT1G67040.1 | expressed protein, ; expression supported by MPSS | chr1:25022768-25025585 REVERSE | Aliases: F1O19.10, F1O19_10	4.1	3.0	1.1	5.2	0.76%	4.9
4039	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	4.4	3.5	0.9	5.2	0.76%	4.8
4040	AT1G21065.1 | expressed protein | chr1:7374199-7375778 FORWARD | Aliases: None	8.8	7.5	1.4	5.2	0.76%	4.7
4041	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	5.2	4.2	0.9	5.2	0.77%	4.9
4043	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	6.3	4.3	2.0	5.2	0.77%	4.9
4044	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	11.7	10.6	1.2	5.2	0.77%	4.5
4045	AT2G34357.1 | expressed protein | chr2:14506315-14512806 FORWARD | Aliases: None	6.3	4.6	1.8	5.2	0.77%	4.9
4051	AT2G02400.1 | cinnamoyl-CoA reductase family, similar to cinnamoyl-CoA reductase from Pinus taeda (GI:17978649), Eucalyptus gunnii (GI:2058311) | chr2:631266-632574 REVERSE | Aliases: T16F16.19, T16F16_19	7.6	5.8	1.7	5.2	0.77%	4.9
4052	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	7.5	4.3	3.2	5.2	0.77%	4.9
4053	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	8.5	6.7	1.8	5.2	0.78%	4.8
4055	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	10.6	8.3	2.3	5.2	0.78%	4.8
4057	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	3.2	1.1	5.2	0.78%	4.9
4058	AT5G38720.1 | expressed protein, predicted protein, Drosophila melanogaster | chr5:15525477-15527789 REVERSE | Aliases: MKD10.4, MKD10_4	7.3	5.4	1.9	5.2	0.78%	4.9
4064	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	6.9	5.8	1.0	5.2	0.78%	4.8
4066	AT5G53860.3 | Symbol: EMB2737 | expressed protein | chr5:21882494-21886068 FORWARD | Aliases: EMB2737, EMBRYO DEFECTIVE 2737, K6O8.3	6.9	5.6	1.3	5.2	0.79%	4.9

Rank	Description	Sync	Root	M	t	adj.q	B
4069	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	6.2	4.4	1.8	5.2	0.79%	4.8
4070	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	3.7	2.7	1.0	5.2	0.79%	4.9
4073	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	7.4	5.9	1.5	5.2	0.79%	4.9
4075	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	7.5	4.2	3.3	5.2	0.79%	4.8
4079	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	12.2	10.5	1.7	5.2	0.79%	4.7
4080	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}	12.2	10.5	1.7	5.2	0.79%	4.7
4084	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	9.7	7.1	2.6	5.2	0.80%	4.9
4087	AT1G63610.2 | expressed protein | chr1:23587190-23589386 REVERSE | Aliases: F2K11.3, F2K11_3	6.5	4.4	2.1	5.2	0.81%	4.9
4088	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	10.1	1.4	5.2	0.81%	4.6
4089	AT5G48910.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:19850098-19852160 REVERSE | Aliases: K19E20.2, K19E20_2	5.6	4.6	1.0	5.2	0.81%	4.8
4093	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	5.3	1.6	5.2	0.81%	4.9
4095	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	9.8	6.2	3.5	5.2	0.81%	4.9
4096	AT1G78580.1 | Symbol: ATTPS1 |	6.9	5.5	1.4	5.2	0.81%	4.8
4100	AT4G01570.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:679472-681940 FORWARD | Aliases: T15B16.21, T15B16_21	4.6	3.8	0.9	5.2	0.81%	4.8
4101	AT2G45520.1 | expressed protein | chr2:18761830-18763362 REVERSE | Aliases: F17K2.5	8.6	7.4	1.2	5.2	0.81%	4.9
4102	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	5.8	4.4	1.4	5.2	0.81%	4.9
4104	AT5G45020.1 | expressed protein | chr5:18185909-18187843 FORWARD | Aliases: K21C13.21, K21C13_21	5.6	4.8	0.8	5.2	0.81%	4.8
4107	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 LaI (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	7.7	6.4	1.4	5.2	0.81%	4.9
4112	AT3G13980.1 | expressed protein | chr3:4619045-4620269 REVERSE | Aliases: MDC16.10	4.2	3.3	0.9	5.2	0.81%	4.8
4113	AT4G29735.1 | expressed protein, contains Pfam domain PF05251: Uncharacterised protein family (UPF0197) | chr4:14562645-14564384 REVERSE | Aliases: None	10.7	8.9	1.8	5.2	0.82%	4.8

Rank	Description	Sync	Root	M	t	adj.q	B
4114	AT2G45790.1 | eukaryotic phosphomannomutase family protein, contains Pfam profile: PF03332 eukaryotic phosphomannomutase | chr2:18862853-18865442 FORWARD | Aliases: F4I18.23	10.3	8.7	1.6	5.2	0.82%	4.8
4115	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	6.6	3.3	3.2	5.2	0.82%	4.7
4116	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	5.0	3.6	1.4	5.2	0.82%	4.8
4117	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	10.5	1.0	5.2	0.82%	4.6
4119	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	10.2	8.5	1.7	5.2	0.82%	4.8
4121	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	5.4	3.9	1.4	5.2	0.82%	4.8
4123	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	9.1	6.1	2.9	5.2	0.83%	4.8
4124	AT1G74440.1 | expressed protein, similar to YGL010w-like protein GB:AAC32136 (Picea mariana) | chr1:27980163-27984065 REVERSE | Aliases: F1M20.12, F1M20_12	4.6	3.7	0.9	5.2	0.83%	4.8
4125	AT4G33400.1 | dem protein-related / defective embryo and meristems protein-related, identical to dem GI:2190419 from (Lycopersicon esculentum)	7.3	4.7	2.6	5.2	0.83%	4.8
4127	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	8.2	6.4	1.9	5.1	0.83%	4.8
4128	AT1G08200.1 | Symbol: AXS2 | expressed protein | chr1:2573857-2576709 REVERSE | Aliases: T23G18.6, T23G18_6, UDP D APIOSE/UDP D XYLOSE SYNTHASE 2	10.4	8.3	2.1	5.1	0.83%	4.7
4129	AT2G27860.1 | Symbol: AXS1 | expressed protein | chr2:11871470-11873975 REVERSE | Aliases: F15K20.4, F15K20_4, UDP D APIOSE/UDP D XYLOSE SYNTHASE 1	10.4	8.3	2.1	5.1	0.83%	4.7
4130	AT3G54400.1 | aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease | chr3:20151036-20153620 REVERSE | Aliases: T14E10.1	6.3	3.6	2.7	5.1	0.83%	4.8
4131	AT4G34360.1 | protease-related, similar to PIR:I46078 endothelin converting enzyme, Bos primigenius taurus | chr4:16431945-16433962 FORWARD | Aliases: F10M10.130, F10M10_130	3.9	2.8	1.1	5.1	0.83%	4.8
4133	AT2G30540.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	5.3	2.8	2.5	5.1	0.83%	4.8
4134	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	5.5	4.6	0.9	5.1	0.83%	4.8
4135	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	9.8	8.6	1.2	5.1	0.83%	4.8
4136	AT5G15320.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:4977541-4978897 FORWARD | Aliases: F8M21.210, F8M21_210	10.3	9.3	1.0	5.1	0.83%	4.7
4137	AT1G67950.4 | RNA recognition motif (RRM)-containing protein | chr1:25482030-25483839 REVERSE | Aliases: T23K23.20, T23K23_20	5.7	4.3	1.5	5.1	0.83%	4.8
4139	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	4.3	3.5	0.8	5.1	0.83%	4.7
4140	AT5G48470.1 | expressed protein | chr5:19658987-19661588 FORWARD | Aliases: MJE7.11, MJE7_11	5.1	4.1	1.0	5.1	0.83%	4.8
4142	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	8.4	5.6	2.8	5.1	0.83%	4.8

Rank	Description	Sync	Root	M	t	adj.q	B
4145	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	4.0	1.8	5.1	0.84%	4.7
4146	AT1G65230.1 | expressed protein | chr1:24232813-24234565 FORWARD | Aliases: T23K8.14, T23K8_14	3.6	2.5	1.1	5.1	0.84%	4.8
4148	AT5G25580.1 | expressed protein | chr5:8903508-8906314 FORWARD | Aliases: T14C9.120, T14C9_120	4.9	2.7	2.2	5.1	0.84%	4.7
4151	AT5G47570.1 | expressed protein | chr5:19309839-19311962 REVERSE | Aliases: MNJ7.16, MNJ7_16	12.2	11.0	1.2	5.1	0.84%	4.6
4152	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	7.9	6.6	1.3	5.1	0.84%	4.8
4154	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	8.1	5.3	2.7	5.1	0.84%	4.8
4155	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	4.6	2.8	1.8	5.1	0.84%	4.8
4156	AT5G28840.1 | NAD-dependent epimerase/dehydratase family protein, similar to sugar epimerase BlmG from Streptomyces verticillus GI:9937230; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family | chr5:10862177-10864906 REVERSE | Aliases: F7P1.20, F7P1_20	8.5	6.1	2.4	5.1	0.84%	4.8
4159	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	13.2	11.6	1.6	5.1	0.84%	4.3
4160	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	4.2	3.1	1.1	5.1	0.84%	4.8
4161	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}	10.5	9.2	1.3	5.1	0.84%	4.7
4162	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	7.0	5.4	1.6	5.1	0.84%	4.8
4164	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	5.4	4.2	1.2	5.1	0.84%	4.8
4168	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.	6.3	4.7	1.6	5.1	0.85%	4.8
4171	AT2G30320.1 | tRNA pseudouridine synthase family protein, similar to pseudouridine synthase (Schizosaccharomyces pombe) GI:6469502; contains Pfam profile PF01416: tRNA pseudouridine synthase	5.7	3.9	1.8	5.1	0.85%	4.8
4173	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	4.6	3.2	1.4	5.1	0.85%	4.8
4174	AT3G55430.1 | glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative, similar to beta-1,3 glucanase GI:7414433 from (Pisum sativum); contains Pfam profile PF00332: Glycosyl hydrolases family 17	8.6	7.0	1.7	5.1	0.85%	4.8
4176	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)	4.7	3.6	1.1	5.1	0.85%	4.7
4178	AT5G18250.1 | expressed protein, similar to unknown protein (dbj:BAA90342.1) | chr5:6033706-6035382 FORWARD | Aliases: MRG7.21, MRG7_21	5.1	3.5	1.6	5.1	0.86%	4.8
4179	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	4.5	3.2	1.3	5.1	0.86%	4.7
4180	AT4G11060.1 | single-strand-binding family protein, contains Pfam domain PF00436: Single-strand binding protein family	6.4	3.7	2.7	5.1	0.86%	4.6

Rank	Description	Sync	Root	M	t	adj.q	B
4181	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	10.3	9.5	0.9	5.1	0.86%	4.5
4185	AT5G25570.2 | expressed protein | chr5:8901758-8903219 FORWARD | Aliases: T14C9.110, T14C9_110	3.9	2.4	1.6	5.1	0.86%	4.8
4188	AT1G14345.1 | expressed protein, contains one transmembrane domain | chr1:4899141-4899974 FORWARD | Aliases: None	4.1	3.2	0.9	5.1	0.86%	4.6
4189	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	4.6	3.4	1.1	5.1	0.86%	4.8
4190	AT5G49210.2 | expressed protein | chr5:19967069-19968910 FORWARD | Aliases: K21P3.8, K21P3_8	6.7	5.5	1.2	5.1	0.86%	4.8
4192	AT1G69510.3 | expressed protein | chr1:26130049-26131596 FORWARD | Aliases: F10D13.16, F10D13_16	11.2	9.9	1.3	5.1	0.86%	4.4
4195	AT2G23560.1 | 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 | chr2:10036416-10037362 REVERSE | Aliases: F26B6.21, F26B6_21	8.1	6.6	1.5	5.1	0.86%	4.8
4196	AT3G12650.1 | expressed protein | chr3:4017837-4018638 REVERSE | Aliases: T2E22.4	8.9	8.0	0.9	5.1	0.86%	4.7
4199	AT5G64310.1 | Symbol: AGP1 | arabinogalactan-protein (AGP1), identical to gi:3883120 gb:AAC77823 | chr5:25739159-25739872 FORWARD | Aliases: ARABINOGALACTAN PROTEIN 1, MSJ1.15, MSJ1_15	9.8	7.9	1.9	5.1	0.86%	4.8
4200	AT5G46020.1 | expressed protein | chr5:18680104-18682054 REVERSE | Aliases: MCL19.6, MCL19_6	10.6	9.4	1.2	5.1	0.86%	4.7
4202	AT5G53650.1 | expressed protein | chr5:21808403-21809666 FORWARD | Aliases: MNC6.19, MNC6_19	8.4	7.0	1.4	5.1	0.86%	4.6
4203	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 methyl-transferase (MTase)) | chr4:6619480-6623347 REVERSE | Aliases: EMB1706, EMBRYO DEFECTIVE 1706, T12H20.6, T12H20_6	8.2	5.4	2.7	5.1	0.87%	4.7
4204	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	3.9	0.9	5.1	0.87%	4.6
4205	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	5.0	3.7	1.3	5.1	0.87%	4.8
4209	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	5.5	3.4	2.1	5.1	0.87%	4.8
4210	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	3.1	0.9	5.1	0.87%	4.6
4211	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	6.3	5.1	1.2	5.1	0.87%	4.7
4212	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	4.9	4.0	0.9	5.1	0.87%	4.6
4215	AT2G22860.1 | Symbol: ATPSK2 |	10.0	8.9	1.2	5.1	0.87%	4.7
4216	AT2G22870.1 | Symbol: EMB2001 | expressed protein | chr2:9746537-9748586 FORWARD | Aliases: EMB2001, EMBRYO DEFECTIVE 2001, T20K9.8, T20K9_8	6.3	5.0	1.4	5.1	0.87%	4.8

Rank	Description	Sync	Root	M	t	adj.q	B
4219	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	5.1	4.0	1.1	5.1	0.87%	4.8
4220	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	7.7	6.5	1.2	5.1	0.87%	4.8
4221	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	7.3	6.4	0.9	5.1	0.88%	4.7
4222	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	4.7	2.9	1.9	5.1	0.88%	4.6
4225	AT3G04760.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:1303581-1305884 REVERSE | Aliases: F7O18.25, F7O18_25	5.1	3.1	2.0	5.1	0.88%	4.6
4226	AT4G30700.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr4:14962499-14965020 REVERSE | Aliases: T10C21.50, T10C21_50	3.9	2.8	1.1	5.1	0.88%	4.7
4229	AT5G43260.1 | chaperone protein dnaJ-related, similar to Chaperone protein dnaJ (SP:Q9WZV3) (Thermotoga maritima) | chr5:17374615-17375310 REVERSE | Aliases: MNL12.8, MNL12_8	8.7	7.4	1.3	5.1	0.88%	4.7
4230	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	4.1	1.4	5.1	0.88%	4.7
4231	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	4.1	1.4	5.1	0.88%	4.7
4232	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	4.6	1.2	5.1	0.88%	4.7
4234	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	4.8	3.9	1.0	5.1	0.88%	4.7
4235	AT5G02740.2 | expressed protein | chr5:616492-618595 FORWARD | Aliases: F9G14.50, F9G14_50	6.1	4.2	1.9	5.1	0.89%	4.7
4236	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	10.6	7.9	2.7	5.1	0.89%	4.7
4239	AT2G47400.1 | Symbol: CP12 1 |	9.2	7.7	1.5	5.1	0.89%	4.7
4241	AT5G36950.1 | DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana) | chr5:14612211-14615570 FORWARD | Aliases: MLF18.70, MLF18_70	5.9	4.4	1.5	5.1	0.89%	4.7
4243	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	6.7	5.0	1.7	5.1	0.89%	4.7
4244	AT5G62650.1 | expressed protein | chr5:25169851-25173154 REVERSE | Aliases: MRG21.7, MRG21_7	7.0	5.9	1.1	5.1	0.89%	4.7
4245	AT1G71430.1 | expressed protein | chr1:26924102-26924801 FORWARD | Aliases: F3I17.24, F3I17_24	6.8	4.9	1.9	5.1	0.89%	4.6
4246	AT4G33100.1 | expressed protein, contains Pfam PF05254: Uncharacterised protein family (UPF0203) | chr4:15971177-15972492 FORWARD | Aliases: F4I10.30, F4I10_30	7.1	6.0	1.1	5.1	0.90%	4.7
4248	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	8.6	6.9	1.7	5.1	0.90%	4.7

Rank	Description	Sync	Root	M	t	adj.q	B
4249	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	5.1	3.9	1.2	5.1	0.90%	4.7
4250	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	7.2	5.5	1.7	5.1	0.90%	4.7
4251	AT5G23440.1 | 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	4.5	3.4	1.0	5.1	0.90%	4.7
4252	AT4G31985.1 | 60S ribosomal protein L39 (RPL39C) | chr4:15469901-15470565 FORWARD | Aliases: None	10.8	8.9	1.9	5.1	0.90%	4.4
4253	AT5G04000.1 | expressed protein | chr5:1079102-1079839 REVERSE | Aliases: F8F6.210, F8F6_210	5.2	3.0	2.2	5.1	0.90%	4.7
4254	AT1G15260.1 | expressed protein, EST gb:N65467 comes from this gene | chr1:5249755-5250568 FORWARD | Aliases: F9L1.20, F9L1_20	4.1	2.6	1.5	5.1	0.90%	4.7
4256	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	5.2	3.9	1.3	5.1	0.90%	4.7
4257	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	4.2	2.7	1.6	5.1	0.90%	4.7
4258	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	4.6	1.7	5.1	0.90%	4.7
4260	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)	4.4	3.5	1.0	5.1	0.91%	4.7
4261	AT5G55740.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr5:22579167-22581659 REVERSE | Aliases: MDF20.18, MDF20_18	3.8	2.6	1.2	5.1	0.91%	4.7
4268	AT3G49730.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:18453260-18458631 REVERSE | Aliases: T16K5.80	6.9	5.3	1.7	5.0	0.91%	4.7
4270	AT3G47250.3 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function | chr3:17410862-17412705 REVERSE | Aliases: F13I12.300	3.7	2.5	1.2	5.0	0.91%	4.7
4271	AT1G72520.1 | lipoxygenase, putative, similar to lipoxygenase gi:1495804 (Solanum tuberosum), gi:1654140 (Lycopersicon esculentum), GB:CAB56692 (Arabidopsis thaliana)	4.9	3.5	1.5	5.0	0.91%	4.7
4273	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	6.2	4.3	1.9	5.0	0.91%	4.6
4274	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	9.0	7.3	1.6	5.0	0.91%	4.6
4275	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	6.7	5.2	1.5	5.0	0.91%	4.7
4276	AT5G47435.2 | formyltetrahydrofolate deformylase, putative, similar to formyltetrahydrofolate deformylase (strain PCC 6803- Synechocystis sp.) SWISS-PROT:Q55135 | chr5:19258930-19261181 FORWARD | Aliases: None	11.0	9.9	1.1	5.0	0.91%	4.4
4277	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	7.1	5.7	1.5	5.0	0.91%	4.7

Rank	Description	Sync	Root	M	t	adj.q	B
4280	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	7.7	5.1	2.5	5.0	0.91%	4.7
4281	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	9.3	7.3	2.0	5.0	0.91%	4.7
4283	AT2G38550.1 | expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136) | chr2:16139092-16141493 FORWARD | Aliases: T6A23.25, T6A23_25	9.4	6.9	2.5	5.0	0.91%	4.7
4284	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 (Arabidopsis thaliana) | chr5:16421688-16423224 FORWARD | Aliases: MMG1.2, MMG1_2, TOM20, TRANSLOCASE OF OUTER MEMBRANE 20 4	10.2	8.5	1.7	5.0	0.91%	4.5
4285	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	9.8	8.4	1.5	5.0	0.91%	4.7
4286	AT1G53030.1 | cytochrome c oxidase copper chaperone family protein, contains Pfam domian, PF05051: Cytochrome C oxidase copper chaperone (COX17) | chr1:19763721-19765110 REVERSE | Aliases: F8L10.24, F8L10_24	6.3	4.6	1.7	5.0	0.92%	4.7
4287	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	5.1	1.1	5.0	0.92%	4.7
4288	AT3G60910.1 | expressed protein, low similarity to PIR:I46078 endothelin converting enzyme from Bos primigenius taurus	7.8	7.0	0.7	5.0	0.92%	4.5
4291	AT4G28230.1 | expressed protein | chr4:13995793-13997313 REVERSE | Aliases: F26K10.110, F26K10_110	7.7	5.8	2.0	5.0	0.92%	4.7
4292	AT5G10180.1 | Symbol: AST68 | sulfate transporter, identical to sulfate transporter (Arabidopsis thaliana) GI:2114104	7.1	4.7	2.3	5.0	0.92%	4.7
4295	AT1G77060.1 | mutase family protein, similar to carboxyvinyl-carboxyphosphonate phosphorylmutase GB:O49290 from (Arabidopsis thaliana); similar to carboxyphosphonoenolpyruvate mutase (GI:47149) (Streptomyces hygroscopicus); contains Prosite PS00161: Isocitrate lyase signature | chr1:28956579-28958374 REVERSE | Aliases: F22K20.14, F22K20_14	4.9	3.0	1.9	5.0	0.92%	4.7
4296	AT3G55040.1 | In2-1 protein, putative, similar to In2-1 protein, Zea mays, P49248 | chr3:20409695-20411282 REVERSE | Aliases: T15C9.60	5.2	4.2	1.1	5.0	0.92%	4.7
4299	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	6.5	5.1	1.4	5.0	0.92%	4.7
4300	AT5G28490.1 | expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640) | chr5:10454545-10455117 REVERSE | Aliases: F24J2.30, F24J2_30	3.5	2.7	0.9	5.0	0.92%	4.6
4301	AT3G48490.1 | expressed protein | chr3:17972274-17972890 FORWARD | Aliases: T29H11.260	4.3	3.1	1.2	5.0	0.93%	4.7
4302	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	5.7	4.7	1.1	5.0	0.93%	4.6
4303	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)	5.5	3.7	1.8	5.0	0.93%	4.7
4304	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	9.4	7.7	1.6	5.0	0.93%	4.7
4306	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	6.9	4.6	2.2	5.0	0.93%	4.6

<table>
<tr><th>Rank</th><th>Description</th><th>Sync</th><th>Root</th><th>M</th><th>t</th><th>adj.q</th><th>B</th></tr>
<tr><td>4309</td><td>AT4G33500.1 | protein phosphatase 2C-related / PP2C-related, YHR077c (NMD2,IFS1) protein -Saccharomyces cerevisiae,PID:g555939</td><td>6.3</td><td>5.1</td><td>1.2</td><td>5.0</td><td>0.93%</td><td>4.7</td></tr>
<tr><td>4310</td><td>AT1G44790.1 | ChaC-like family protein, contains Pfam profile: PF04752 ChaC-like protein | chr1:16914594-16916104 REVERSE | Aliases: T12C22.6, T12C22_6</td><td>6.7</td><td>4.4</td><td>2.2</td><td>5.0</td><td>0.93%</td><td>4.7</td></tr>
<tr><td>4311</td><td>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</td><td>10.7</td><td>9.1</td><td>1.5</td><td>5.0</td><td>0.93%</td><td>4.5</td></tr>
<tr><td>4313</td><td>AT1G53840.1 | Symbol: ATPME1 |</td><td>5.4</td><td>3.3</td><td>2.1</td><td>5.0</td><td>0.93%</td><td>4.6</td></tr>
<tr><td>4315</td><td>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</td><td>10.6</td><td>9.5</td><td>1.1</td><td>5.0</td><td>0.93%</td><td>4.5</td></tr>
<tr><td>4316</td><td>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}</td><td>8.3</td><td>7.3</td><td>1.0</td><td>5.0</td><td>0.94%</td><td>4.5</td></tr>
<tr><td>4319</td><td>AT5G10695.1 | expressed protein | chr5:3377664-3378222 FORWARD | Aliases: None</td><td>9.3</td><td>8.0</td><td>1.3</td><td>5.0</td><td>0.94%</td><td>4.6</td></tr>
<tr><td>4323</td><td>AT3G22680.1 | expressed protein | chr3:8019736-8020515 FORWARD | Aliases: MWI23.5</td><td>7.3</td><td>5.4</td><td>1.9</td><td>5.0</td><td>0.94%</td><td>4.7</td></tr>
<tr><td>4324</td><td>AT5G53060.1 | KH domain-containing protein | chr5:21532252-21535663 FORWARD | Aliases: MNB8.12, MNB8_12</td><td>5.3</td><td>4.1</td><td>1.2</td><td>5.0</td><td>0.94%</td><td>4.6</td></tr>
<tr><td>4326</td><td>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</td><td>10.7</td><td>8.5</td><td>2.2</td><td>5.0</td><td>0.94%</td><td>4.6</td></tr>
<tr><td>4327</td><td>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</td><td>4.6</td><td>3.2</td><td>1.4</td><td>5.0</td><td>0.94%</td><td>4.6</td></tr>
<tr><td>4329</td><td>AT3G13845.1 | expressed protein | chr3:4557333-4558586 REVERSE | Aliases: None</td><td>9.9</td><td>8.7</td><td>1.2</td><td>5.0</td><td>0.94%</td><td>4.5</td></tr>
<tr><td>4332</td><td>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</td><td>4.9</td><td>4.0</td><td>0.9</td><td>5.0</td><td>0.94%</td><td>4.6</td></tr>
<tr><td>4333</td><td>AT4G17420.1 | expressed protein, contains Pfam domain, PF01987: Protein of unknown function | chr4:9722451-9724652 REVERSE | Aliases: DL4745C, FCAALL.389</td><td>7.5</td><td>6.3</td><td>1.2</td><td>5.0</td><td>0.94%</td><td>4.7</td></tr>
<tr><td>4334</td><td>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</td><td>4.1</td><td>2.6</td><td>1.5</td><td>5.0</td><td>0.94%</td><td>4.7</td></tr>
<tr><td>4335</td><td>AT3G11050.1 | Symbol: ATFER2 |</td><td>6.4</td><td>4.4</td><td>2.0</td><td>5.0</td><td>0.94%</td><td>4.4</td></tr>
<tr><td>4336</td><td>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-acetylesterase (Digitalis lanata) GI:3688284; contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif | chr1:25434992-25436635 REVERSE | Aliases: F12A21.4, F12A21_4</td><td>5.6</td><td>4.5</td><td>1.1</td><td>5.0</td><td>0.94%</td><td>4.7</td></tr>
<tr><td>4338</td><td>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</td><td>8.3</td><td>7.2</td><td>1.1</td><td>5.0</td><td>0.94%</td><td>4.7</td></tr>
<tr><td>4341</td><td>AT1G64105.1 | Symbol: ANAC027 | no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain | chr1:23798713-23799305 FORWARD | Aliases: ANAC027</td><td>8.4</td><td>6.7</td><td>1.7</td><td>5.0</td><td>0.95%</td><td>4.7</td></tr>
<tr><td>4342</td><td>AT5G64680.2 | expressed protein | chr5:25871408-25872710 FORWARD | Aliases: MUB3.20, MUB3_20</td><td>5.8</td><td>4.6</td><td>1.2</td><td>5.0</td><td>0.95%</td><td>4.6</td></tr>
<tr><td>4344</td><td>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</td><td>10.4</td><td>9.6</td><td>0.8</td><td>5.0</td><td>0.95%</td><td>4.3</td></tr>
<tr><td>4347</td><td>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</td><td>4.0</td><td>2.6</td><td>1.3</td><td>5.0</td><td>0.95%</td><td>4.7</td></tr>
</table>

Rank	Description	Sync	Root	M	t	adj.q	B
4349	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 scienitific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497. | chr3:11923677-11926884 REVERSE | Aliases: T6J22.5	6.2	5.0	1.2	5.0	0.95%	4.6
4350	AT2G06010.1 | Symbol: ORG4 | expressed protein | chr2:2336815-2338899 FORWARD | Aliases: F5K7.23, F5K7_23, OBP3 RESPONSIVE GENE 4	5.0	4.0	0.9	5.0	0.96%	4.6
4351	AT1G16780.1 | Symbol: AVPL1 | vacuolar-type H+-translocating inorganic pyrophosphatase, putative, similar to vacuolar-type H+-translocating inorganic pyrophosphatase GI:6901676 from (Arabidopsis thaliana) | chr1:5739292-5743562 REVERSE | Aliases: AVPL1, F17F16.2, F17F16_2, VACUOLAR PYROPHOSPHATASE LIKE PROTEIN 1	5.9	4.4	1.5	5.0	0.96%	4.6
4354	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	10.7	9.2	1.5	5.0	0.96%	4.6
4355	AT4G24700.1 | expressed protein | chr4:12744632-12745323 REVERSE | Aliases: F22K18.100, F22K18_100	3.4	2.5	0.8	5.0	0.96%	4.5
4356	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	11.3	9.0	2.3	5.0	0.96%	4.5
4357	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	5.8	2.1	5.0	0.96%	4.6
4358	AT3G51140.1 | expressed protein | chr3:19008748-19010883 FORWARD | Aliases: F24M12.180	7.1	4.8	2.4	5.0	0.96%	4.6
4361	AT1G06720.1 | expressed protein, contains Pfam domain, PF04950: Protein of unknown function (DUF663) | chr1:2060443-2067322 REVERSE | Aliases: F4H5.19, F4H5_19	7.0	4.4	2.6	5.0	0.97%	4.6
4363	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	4.0	2.4	1.6	5.0	0.97%	4.6
4364	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	8.7	7.4	1.3	5.0	0.97%	4.6
4367	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	9.1	6.3	2.7	5.0	0.97%	4.6
4368	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	5.4	4.0	1.4	5.0	0.97%	4.6
4369	AT3G56510.2 | similar to unnamed protein product [Yarrowia lipolytica CLIB99] (GB:CAG82708.1) | chr3:20954907-20957640 REVERSE | Aliases: T5P19.160	9.3	8.2	1.1	5.0	0.97%	4.6
4372	AT1G18850.1 | expressed protein | chr1:6504797-6506412 REVERSE | Aliases: F6A14.6, F6A14_6	5.5	3.9	1.6	5.0	0.97%	4.6
4374	AT2G36835.1 | expressed protein | chr2:15456686-15458505 REVERSE | Aliases: None	7.7	5.4	2.4	5.0	0.97%	4.6
4375	AT5G13610.1 | expressed protein | chr5:4383016-4385032 FORWARD | Aliases: T6I14.13	7.3	5.9	1.4	5.0	0.98%	4.6
4377	AT1G11420.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr1:3844581-3846872 REVERSE | Aliases: T23J18.9, T23J18_9	5.5	3.3	2.2	5.0	0.98%	4.6
4378	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	9.0	7.1	1.9	5.0	0.98%	4.5
4379	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	8.0	6.0	2.0	5.0	0.98%	4.6
4381	AT3G53540.1 | expressed protein | chr3:19857478-19861946 REVERSE | Aliases: F4P12.240	5.5	4.6	1.0	5.0	0.98%	4.5

Rank	Description	Sync	Root	M	t	adj.q	B
4382	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	8.9	7.7	1.2	5.0	0.98%	4.6
4384	AT5G05160.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:1528001-1530063 FORWARD | Aliases: K2A11.3, K2A11_3	9.4	8.3	1.1	5.0	0.98%	4.5
4386	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	6.1	5.0	1.1	5.0	0.98%	4.6
4387	AT2G20480.1 | expressed protein | chr2:8837658-8838579 REVERSE | Aliases: T13C7.7, T13C7_7	3.3	2.4	0.9	5.0	0.99%	4.3
4389	AT3G13570.1 | Symbol: SCL30a |	6.5	5.0	1.5	5.0	0.99%	4.6
4390	AT5G10010.1 | expressed protein | chr5:3127907-3131721 FORWARD | Aliases: T31P16.7, T31P16_7	5.2	3.9	1.3	5.0	0.99%	4.6
4391	AT2G03350.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr2:1019576-1021183 REVERSE | Aliases: T4M8.22, T4M8_22	6.1	4.8	1.3	5.0	0.99%	4.6
4393	AT1G02160.1 | expressed protein | chr1:410785-411590 FORWARD | Aliases: T6A9.18	10.5	9.4	1.0	5.0	0.99%	4.3
4394	AT1G47400.1 | expressed protein | chr1:17388157-17388626 FORWARD | Aliases: T3F24.21, T3F24_21	4.1	3.0	1.1	5.0	0.99%	4.6
4396	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	8.2	6.5	1.7	5.0	0.99%	4.6
4397	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	6.4	4.7	1.7	5.0	0.99%	4.6
4399	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	9.8	8.0	1.9	5.0	0.99%	4.6
4401	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	7.8	6.5	1.3	5.0	1.00%	4.6
4402	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	3.9	0.7	5.0	1.00%	4.4
4403	AT4G10450.1 | 60S ribosomal protein L9 (RPL90D), ribosomal protein L9, cytosolic - garden pea, PIR2:S19978 | chr4:6462949-6464521 REVERSE | Aliases: F7L13.30, F7L13_30	5.8	4.4	1.4	5.0	1.00%	4.6
4405	AT3G09350.1 | armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat | chr3:2871051-2873318 FORWARD | Aliases: F3L24.22	5.2	3.1	2.1	4.9	1.00%	4.6
4406	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	6.4	4.6	1.8	4.9	1.00%	4.6
4409	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	2.7	0.7	4.9	1.00%	4.2
4412	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	4.7	3.4	1.4	4.9	1.01%	4.6
4413	AT3G18490.1 | aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease | chr3:6348761-6350674 REVERSE | Aliases: MYF24.39	9.4	7.9	1.5	4.9	1.01%	4.6

Rank	Description	Sync	Root	M	t	adj.q	B
4414	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)	5.8	4.2	1.6	4.9	1.01%	4.6
4416	AT5G65810.1 | expressed protein, similar to unknown protein (emb CAB66910.1) | chr5:26354895-26356963 REVERSE | Aliases: K22J17.2, K22J17_2	7.9	5.8	2.1	4.9	1.01%	4.6
4420	AT1G65500.1 | expressed protein | chr1:24361530-24362279 FORWARD | Aliases: F5I14.4, F5I14_4	5.1	2.6	2.5	4.9	1.01%	4.4
4421	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	3.8	2.5	1.3	4.9	1.01%	4.6
4422	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	12.1	10.6	1.6	4.9	1.01%	4.3
4424	AT5G66780.1 | expressed protein | chr5:26680799-26681629 FORWARD | Aliases: MUD21.2, MUD21_2	4.0	2.4	1.6	4.9	1.01%	4.5
4426	AT2G40550.1 | expressed protein | chr2:16941914-16945213 FORWARD | Aliases: T2P4.10, T2P4_10	6.2	3.5	2.7	4.9	1.01%	4.5
4428	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	8.8	6.8	2.0	4.9	1.01%	4.6
4429	AT4G32240.1 | expressed protein | chr4:15568306-15569194 FORWARD | Aliases: F10M6.120, F10M6_120	11.2	10.4	0.8	4.9	1.01%	3.9
4430	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	5.7	2.5	3.2	4.9	1.01%	4.6
4432	AT3G22290.1 | expressed protein | chr3:7881672-7885549 FORWARD | Aliases: AT3G22280, MCB17.1	7.9	7.2	0.7	4.9	1.01%	4.4
4433	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	8.3	6.6	1.8	4.9	1.01%	4.5
4434	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	7.1	5.8	1.3	4.9	1.01%	4.6
4437	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	9.7	6.4	3.3	4.9	1.02%	4.5
4438	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	8.0	6.4	1.6	4.9	1.02%	4.6
4440	AT5G02710.1 | expressed protein, contains Pfam PF03692: Uncharacterised protein family (UPF0153) | chr5:612606-614418 FORWARD | Aliases: F9G14.8	3.5	2.4	1.1	4.9	1.02%	4.5
4441	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	5.6	3.7	1.9	4.9	1.02%	4.6
4442	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	3.4	1.8	4.9	1.02%	4.6
4443	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	3.8	2.4	1.3	4.9	1.02%	4.5
4444	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	4.9	0.9	4.9	1.02%	4.5
4446	AT1G21350.3 | expressed protein | chr1:7476930-7479021 REVERSE | Aliases: F24J8.1, F24J8_1	4.3	3.2	1.1	4.9	1.02%	4.6

Rank	Description	Sync	Root	M	t	adj.q	B
4449	AT5G60960.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:24545476-24547237 REVERSE | Aliases: MSL3.8, MSL3_8	8.5	5.8	2.8	4.9	1.02%	4.6
4450	AT4G25730.1 | FtsJ-like methyltransferase family protein, contains Pfam profile: PF01728 FtsJ-like methyltransferase | chr4:13102688-13106789 REVERSE | Aliases: F14M19.10, F14M19_10	5.5	4.4	1.0	4.9	1.02%	4.5
4451	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	5.2	4.1	1.2	4.9	1.02%	4.5
4453	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	5.8	4.3	1.5	4.9	1.02%	4.6
4454	AT5G35360.2 | Symbol: CAC2 | similar to methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA) [Arabidopsis thaliana] (TAIR:At1g03090.2); similar to biotin carboxylase precursor [Glycine max] (GB:AAC23573.1); similar to biotin carboxylase precursor [Glycine max] (GB:AAC02267.1); similar to acetyl-CoA carboxylase [Glycine max] (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	10.8	9.7	1.0	4.9	1.02%	4.2
4457	AT5G40480.1 | Symbol: EMB3012 | expressed protein, ; expression supported by MPSS | chr5:16230589-16241210 FORWARD | Aliases: EMB3012, EMBRYO DEFECTIVE 3012, K21I16.30, K21I16_30	6.3	5.0	1.3	4.9	1.02%	4.6
4459	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	6.2	5.4	0.8	4.9	1.02%	4.4
4462	AT1G11120.1 | expressed protein | chr1:3715229-3719681 FORWARD | Aliases: T19D16.22, T19D16_22	5.3	3.7	1.6	4.9	1.03%	4.6
4466	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	6.1	4.4	1.7	4.9	1.03%	4.5
4469	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	4.3	3.1	1.2	4.9	1.03%	4.4
4470	AT2G15290.1 | expressed protein | chr2:6649408-6651117 REVERSE | Aliases: F27O10.6, F27O10_6	8.8	6.7	2.1	4.9	1.03%	4.6
4471	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	6.3	3.4	2.9	4.9	1.03%	4.4
4473	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	4.8	3.2	1.6	4.9	1.04%	4.5
4475	AT1G76130.1 | Symbol: ATAMY2 |	4.5	3.3	1.2	4.9	1.04%	4.5
4478	AT3G47930.1 | Symbol: ATGLDH |	8.4	6.6	1.8	4.9	1.04%	4.5
4479	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	5.8	3.6	2.2	4.9	1.04%	4.4
4485	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	7.7	5.0	2.7	4.9	1.05%	4.5
4487	AT4G35490.1 | ribosomal protein L11 family protein, several ribosomal proteins L11 | chr4:16855907-16856679 FORWARD | Aliases: F15J1.60, F15J1_60	9.5	7.1	2.4	4.9	1.05%	4.5
4492	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	4.1	3.1	1.0	4.9	1.05%	4.5
4494	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	6.3	5.0	1.3	4.9	1.06%	4.5

Rank	Description	Sync	Root	M	t	adj.q	B
4495	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	9.5	8.2	1.3	4.9	1.06%	4.5
4496	AT5G23130.1 | peptidoglycan-binding LysM domain-containing protein, contains Pfam profile PF01476: LysM domain	3.1	2.5	0.7	4.9	1.06%	4.2
4497	AT1G12250.1 | thylakoid lumenal protein-related, weak similarity to SP:O22160 Thylakoid lumenal 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	5.6	4.9	0.7	4.9	1.06%	4.3
4498	AT1G18250.2 | Symbol: ATLP 1 |	5.2	3.6	1.6	4.9	1.06%	4.4
4499	AT3G26090.1 | Symbol: RGS1 | expressed protein | chr3:9533985-9536866 FORWARD | Aliases: ATRGS1, MPE11.28, REGULATOR OF G PROTEIN SIGNALING 1	7.9	6.6	1.3	4.9	1.06%	4.5
4500	AT4G14150.1 | Symbol: PAKRP1 |	6.5	4.1	2.5	4.9	1.06%	4.5
4501	AT4G27520.1 | plastocyanin-like domain-containing protein, similar to PIR:JC7196 phytocyanin-related protein Pn14 {Ipomoea nil}; contains Pfam profile PF02298: Plastocyanin-like domain | chr4:13750446-13751911 REVERSE | Aliases: T29A15.10, T29A15_10	5.1	3.5	1.6	4.9	1.06%	4.5
4502	AT1G68430.1 | expressed protein | chr1:25658568-25659107 REVERSE | Aliases: T2E12.2, T2E12_2	4.3	3.2	1.1	4.9	1.06%	4.5
4507	AT5G39740.1 | 60S ribosomal protein L5 (RPL5B), ribosomal protein L5, rice | chr5:15920551-15922688 FORWARD | Aliases: MKM21.30, MKM21_30	8.8	5.6	3.2	4.9	1.07%	4.5
4508	AT4G30935.1 | WRKY family transcription factor, contains Pfam profile: PF03106	6.5	5.4	1.0	4.9	1.07%	4.5
4510	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	4.3	3.4	0.9	4.9	1.07%	4.4
4511	AT1G16750.1 | expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547 | chr1:5729090-5731863 REVERSE | Aliases: F19K19.16	7.0	4.8	2.2	4.9	1.07%	4.3
4512	AT4G34960.1 | peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, similar to cyclophilin (Arabidopsis thaliana) gi:2443755:gb:AAB71401	5.2	4.0	1.2	4.9	1.07%	4.5
4513	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	10.2	8.8	1.4	4.9	1.07%	4.4
4514	AT5G37360.1 | expressed protein | chr5:14822459-14825454 REVERSE | Aliases: MNJ8.18, MNJ8_18	6.5	5.4	1.1	4.9	1.07%	4.5
4515	AT5G25800.1 | exonuclease family protein, contains exonuclease domain, Pfam:PF00929 | chr5:8979625-8982876 REVERSE | Aliases: F18A17.50, F18A17_50	4.7	3.7	1.0	4.9	1.07%	4.5
4517	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	10.5	9.1	1.4	4.9	1.07%	4.2
4518	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	5.6	4.6	1.0	4.9	1.07%	4.5
4520	AT1G75110.1 | expressed protein | chr1:28197776-28199594 REVERSE | Aliases: F9E10.4, F9E10_4	3.8	2.9	0.9	4.9	1.07%	4.4
4522	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	6.0	4.3	1.7	4.9	1.07%	4.4
4524	AT3G57030.1 | strictosidine synthase family protein, similar to strictosidine synthase (Rauvolfia serpentina)(SP:P15324) | chr3:21112436-21114272 REVERSE | Aliases: F24I3.110	8.3	6.4	1.8	4.9	1.07%	4.5
4525	AT5G19260.1 | expressed protein, various predicted proteins | chr5:6479402-6480448 REVERSE | Aliases: F7K24.10, F7K24_10	4.8	3.5	1.3	4.9	1.07%	4.4
4528	AT4G21940.1 | Symbol: CPK15 | calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase (Nicotiana tabacum) gi:3283996:gb:AAC25423 | chr4:11640819-11643653 FORWARD | Aliases: F1N20.5	3.6	2.8	0.8	4.9	1.07%	4.3

Rank	Description	Sync	Root	M	t	adj.q	B
4529	AT5G20220.1 | zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle | chr5:6821992-6825983 FORWARD | Aliases: F5O24.110, F5O24_110	4.7	4.0	0.8	4.9	1.07%	4.4
4531	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) {Arabidopsis thaliana}; contains InterPro accession IPR003881: Isochorismatase | chr1:24252515-24254065 REVERSE | Aliases: T8F5.6, T8F5_6	10.6	9.1	1.5	4.9	1.08%	4.4
4532	AT3G13360.1 | expressed protein | chr3:4338366-4340403 REVERSE | Aliases: MDC11.20	8.0	6.2	1.8	4.9	1.08%	4.5
4534	AT1G61160.1 | expressed protein | chr1:22548684-22550022 REVERSE | Aliases: F11P17.19, F11P17_19	4.7	3.6	1.1	4.9	1.08%	4.5
4536	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	6.9	1.6	4.9	1.08%	4.5
4537	AT5G40040.1 | 60S acidic ribosomal protein P2 (RPP2E), acidic ribosomal protein P2, Parthenium argentatum,SWISSPROT:RLA2_PARAR	5.5	3.8	1.7	4.9	1.08%	4.4
4539	AT5G06360.1 | ribosomal protein S8e family protein, contains Pfam profile PF01201: Ribosomal protein S8e | chr5:1944772-1946725 FORWARD | Aliases: MHF15.12, MHF15_12	9.2	6.9	2.3	4.9	1.08%	4.5
4540	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	11.6	10.0	1.6	4.9	1.09%	4.3
4542	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	10.2	0.9	4.9	1.09%	4.3
4544	AT2G41600.2 | expressed protein | chr2:17352455-17353793 REVERSE | Aliases: T32G6.12, T32G6_12	5.7	4.2	1.5	4.9	1.10%	4.5
4545	AT4G16410.1 | expressed protein, contains Pfam PF05421: Protein of unknown function (DUF751) | chr4:9261708-9262614 REVERSE | Aliases: DL4233C, FCAALL.144	6.5	4.8	1.7	4.9	1.10%	4.5
4547	AT1G21600.2 | similar to putative tonoplast membrane integral protein [Oryza sativa (japonica cultivar-group)] (GB:BAD81369.1)	4.0	2.9	1.1	4.9	1.10%	4.2
4550	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	5.4	3.0	2.4	4.9	1.10%	4.0
4551	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	3.2	0.9	4.9	1.10%	4.4
4552	AT1G05055.1 | basic transcription factor 2, 44kD subunit-related, contains weak similarity to Swiss-Prot:Q13888 TFIIH basal transcription factor complex p44 subunit (Basic transcription factor 2 44 kDa subunit, BTF2-p44, General transcription factor IIH polypeptide 2) (Homo sapiens) | chr1:1448718-1450855 REVERSE | Aliases: AT1G05050	6.4	5.3	1.1	4.8	1.10%	4.4
4553	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	4.5	3.5	1.0	4.8	1.10%	4.4
4554	AT5G63040.2 | expressed protein, similar to unknown protein (emb:CAB81845.1) | chr5:25305372-25307638 FORWARD | Aliases: MJH22.10, MJH22_10	3.9	3.0	0.9	4.8	1.10%	4.4
4555	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	10.8	8.8	2.0	4.8	1.10%	4.2
4557	AT1G68680.1 | expressed protein | chr1:25789169-25790587 FORWARD | Aliases: F24J5.21, F24J5_21	7.8	6.3	1.6	4.8	1.11%	4.5
4558	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	3.7	2.6	1.0	4.8	1.11%	4.4
4559	AT5G16720.1 | expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593 | chr5:5494231-5496813 FORWARD | Aliases: F5E19.60, F5E19_60	4.3	3.5	0.8	4.8	1.11%	4.3

Rank	Description	Sync	Root	M	t	adj.q	B
4560	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)	8.1	5.0	3.1	4.8	1.11%	4.4
4561	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	5.5	1.8	4.8	1.11%	4.4
4562	AT5G15510.1 | expressed protein | chr5:5034123-5036798 FORWARD | Aliases: T20K14.120, T20K14_120	5.6	4.3	1.2	4.8	1.11%	4.5
4564	AT1G62780.1 | expressed protein | chr1:23252844-23254770 REVERSE | Aliases: F23N19.15, F23N19_15	4.1	2.5	1.6	4.8	1.11%	4.5
4566	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	4.0	1.1	4.8	1.11%	4.5
4567	AT1G48200.1 | expressed protein | chr1:17800524-17802006 REVERSE | Aliases: F21D18.7, F21D18_7	5.5	3.4	2.1	4.8	1.11%	4.4
4568	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	11.1	10.2	0.9	4.8	1.11%	4.1
4569	AT4G34260.1 | expressed protein | chr4:16398119-16401814 FORWARD | Aliases: F10M10.30, F10M10_30	6.0	4.8	1.2	4.8	1.11%	4.5
4570	AT1G73880.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr1:27788642-27790465 FORWARD | Aliases: F2P9.25, F2P9_25	10.4	7.4	3.0	4.8	1.11%	4.5
4572	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,	9.0	7.7	1.3	4.8	1.11%	4.5
4573	AT4G30020.1 | subtilase family protein, contains similarity to meiotic serine proteinase TMP GI:6468325 from (Lycopersicon esculentum)	6.7	5.6	1.1	4.8	1.11%	4.4
4580	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	6.1	1.5	4.8	1.12%	4.4
4583	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	8.1	6.2	1.9	4.8	1.13%	4.4
4584	AT3G09470.2 | expressed protein | chr3:2911521-2914505 REVERSE | Aliases: AT3G09460, F11F8.4	6.5	4.7	1.8	4.8	1.13%	4.3
4586	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	8.8	6.7	2.1	4.8	1.13%	4.4
4588	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	7.4	6.2	1.2	4.8	1.13%	4.4
4589	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	3.5	1.2	4.8	1.13%	4.4
4590	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	12.3	11.2	1.2	4.8	1.13%	4.0
4593	AT1G52280.1 | Ras-related GTP-binding protein, putative, similar to RAB7D GI:1370187 from (Lotus japonicus) (Plant J. 11 (2), 237-250 (1997)); contains Pfam PF00071: Ras family | chr1:19471638-19473255 REVERSE | Aliases: F19K6.10, F19K6_10	7.4	5.9	1.4	4.8	1.13%	4.3
4595	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	5.5	3.9	1.6	4.8	1.13%	4.4

Rank	Description	Sync	Root	M	t	adj.q	B
4596	AT4G39150.1 | DNAJ heat shock N-terminal domain-containing protein, similar to SP:P39101 CAJ1 protein, Saccharomyces cerevisiae, PIR2:S48085; contains Pfam profile PF00226 DnaJ domain | chr4:18233499-18236058 REVERSE | Aliases: T22F8.50, T22F8_50	8.1	7.0	1.0	4.8	1.14%	4.3
4597	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)	8.5	6.8	1.7	4.8	1.14%	4.4
4598	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	7.0	4.5	2.5	4.8	1.14%	4.3
4599	AT1G08450.2 | Symbol: CRT3 | calreticulin 3 (CRT3), identical to similar to SP:O04153 Calreticulin 3 precursor {Arabidopsis thaliana}	8.7	7.7	1.0	4.8	1.14%	4.2
4600	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	4.1	2.5	1.6	4.8	1.14%	4.4
4602	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	8.4	6.2	2.2	4.8	1.14%	4.4
4603	AT5G66550.1 | Maf family protein, contains Pfam domain PF02545: Maf-like protein | chr5:26576856-26578404 REVERSE | Aliases: K1F13.22, K1F13_22	5.4	4.3	1.1	4.8	1.14%	4.4
4605	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	7.1	4.9	2.2	4.8	1.14%	4.4
4608	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	4.9	3.7	1.2	4.8	1.14%	4.4
4611	AT5G48480.1 | expressed protein | chr5:19661901-19663103 FORWARD | Aliases: MJE7.12, MJE7_12	7.9	6.1	1.9	4.8	1.15%	4.4
4613	AT3G26710.1 | expressed protein | chr3:9814763-9815987 FORWARD | Aliases: MLJ15.10	6.5	5.3	1.2	4.8	1.15%	4.4
4617	AT1G06630.1 | F-box family protein, contains F-box domain Pfam:PF00646	4.4	3.6	0.8	4.8	1.15%	4.3
4620	AT2G20820.2 | expressed protein, . | chr2:8971430-8972505 FORWARD | Aliases: F5H14.21, F5H14_21	11.5	10.2	1.3	4.8	1.15%	4.3
4621	AT4G34760.1 | auxin-responsive family protein, auxin-induced protein X15, Glycine max, PIR2:JQ1097 | chr4:16582188-16582884 REVERSE | Aliases: F11I11.11	4.4	2.9	1.5	4.8	1.15%	4.3
4622	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	9.4	8.1	1.3	4.8	1.15%	4.3
4625	AT5G64010.1 | expressed protein | chr5:25635445-25637405 REVERSE | Aliases: MBM17.11, MBM17_11	7.1	5.9	1.3	4.8	1.16%	4.4
4627	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	6.4	1.2	4.8	1.16%	4.4
4628	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	8.9	6.2	2.7	4.8	1.16%	4.4
4629	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	5.9	4.2	1.8	4.8	1.16%	4.4
4633	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	5.8	4.5	1.4	4.8	1.17%	4.4
4635	AT5G27430.1 | signal peptidase subunit family protein, contains Pfam profile: PF04573 signal peptidase subunit | chr5:9687390-9689366 FORWARD | Aliases: F21A20.140, F21A20_140	5.6	3.9	1.6	4.8	1.17%	4.3
4637	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	5.5	4.2	1.3	4.8	1.17%	4.4

Rank	Description	Sync	Root	M	t	adj.q	B
4640	AT5G06240.1 | Symbol: EMB2735 | expressed protein | chr5:1888314-1889697 FORWARD | Aliases: EMB2735, EMBRYO DEFECTIVE 2735, MBL20.12, MBL20_12	6.1	5.2	0.9	4.8	1.17%	4.3
4641	AT3G50980.1 | dehydrin, putative, similar to dehydrin Xero 1 (Arabidopsis thaliana) SWISS-PROT:P25863 | chr3:18952957-18953846 FORWARD | Aliases: F24M12.20	5.5	4.0	1.5	4.8	1.17%	4.4
4643	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	6.5	4.8	1.7	4.8	1.17%	4.4
4645	AT1G58220.1 | myb family transcription factor, contains Pfam profile: PF00249: Myb-like DNA-binding domain | chr1:21561908-21566630 REVERSE | Aliases: F16M22.4, F16M22_4	5.3	4.1	1.2	4.8	1.18%	4.4
4646	AT1G03860.3 | Symbol: ATPHB2 |	8.1	5.4	2.7	4.8	1.18%	4.4
4648	AT3G43520.1 | expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136) | chr3:15417012-15418896 FORWARD | Aliases: T18D12.90	9.9	8.3	1.6	4.8	1.18%	4.3
4649	AT3G61110.1 | Symbol: ARS27A |	11.3	9.3	2.0	4.8	1.18%	4.0
4650	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	6.9	4.8	2.1	4.8	1.18%	4.4
4651	AT1G77230.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain | chr1:29021023-29022858 FORWARD | Aliases: T14N5.9, T14N5_9	5.6	3.9	1.7	4.8	1.18%	4.4
4653	AT5G09460.1 | expressed protein | chr5:2944438-2945418 REVERSE | Aliases: T5E8.260, T5E8_260	5.4	3.8	1.6	4.8	1.18%	4.4
4655	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	5.5	4.3	1.2	4.8	1.18%	4.4
4656	AT5G16240.1 | 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 | chr5:5306810-5309935 FORWARD | Aliases: T21H19.160, T21H19_160	4.9	3.8	1.1	4.8	1.18%	4.4
4657	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	4.0	2.7	1.4	4.8	1.18%	4.4
4658	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	7.9	1.3	4.8	1.18%	4.3
4662	AT3G28200.1 | peroxidase, putative, similar to peroxidase ATP26a GB:CAA72487 GI:1890317 (Arabidopsis thaliana)	5.7	4.8	1.0	4.8	1.18%	4.3
4666	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	2.9	0.9	4.8	1.18%	4.3
4668	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	4.5	2.7	1.8	4.8	1.18%	4.4
4669	AT5G45350.1 | proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965 | chr5:18399064-18400926 REVERSE | Aliases: MFC19.1, MFC19_1	9.0	6.9	2.2	4.8	1.18%	4.4
4670	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	5.8	4.9	0.9	4.8	1.18%	4.3
4671	AT1G31780.1 | similar to Component of oligomeric golgi complex 6 [Xenopus tropicalis] (GB:AAH75361.1) | chr1:11391210-11394729 FORWARD | Aliases: F5M6.21, F5M6_21	6.8	4.8	2.0	4.8	1.19%	4.4

<table>
<tr><th>Rank</th><th>Description</th><th>Sync</th><th>Root</th><th>M</th><th>t</th><th>adj.q</th><th>B</th></tr>
<tr><td>4674</td><td>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</td><td>12.3</td><td>11.2</td><td>1.1</td><td>4.8</td><td>1.19%</td><td>3.7</td></tr>
<tr><td>4675</td><td>AT2G42720.1 | F-box family protein, contains F-box domain Pfam:PF00646</td><td>4.0</td><td>3.2</td><td>0.9</td><td>4.8</td><td>1.19%</td><td>4.3</td></tr>
<tr><td>4676</td><td>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</td><td>7.0</td><td>5.9</td><td>1.2</td><td>4.8</td><td>1.19%</td><td>4.3</td></tr>
<tr><td>4678</td><td>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</td><td>8.4</td><td>6.4</td><td>2.0</td><td>4.8</td><td>1.19%</td><td>4.4</td></tr>
<tr><td>4679</td><td>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</td><td>5.0</td><td>3.9</td><td>1.0</td><td>4.8</td><td>1.19%</td><td>4.4</td></tr>
<tr><td>4680</td><td>AT5G03440.2 | expressed protein | chr5:856871-858404 REVERSE | Aliases: F12E4.200, F12E4_200</td><td>5.8</td><td>4.4</td><td>1.4</td><td>4.8</td><td>1.19%</td><td>4.3</td></tr>
<tr><td>4682</td><td>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</td><td>4.8</td><td>4.0</td><td>0.8</td><td>4.8</td><td>1.19%</td><td>4.2</td></tr>
<tr><td>4685</td><td>AT2G33430.1 | plastid developmental protein DAG, putative, similar to DAG protein, chloroplast precursor (Garden snapdragon) SWISS-PROT:Q38732</td><td>6.3</td><td>5.1</td><td>1.2</td><td>4.8</td><td>1.19%</td><td>4.4</td></tr>
<tr><td>4688</td><td>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</td><td>4.5</td><td>3.4</td><td>1.1</td><td>4.8</td><td>1.19%</td><td>4.4</td></tr>
<tr><td>4690</td><td>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</td><td>8.9</td><td>7.4</td><td>1.5</td><td>4.8</td><td>1.20%</td><td>4.2</td></tr>
<tr><td>4691</td><td>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</td><td>8.9</td><td>6.4</td><td>2.5</td><td>4.8</td><td>1.20%</td><td>4.4</td></tr>
<tr><td>4692</td><td>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</td><td>10.7</td><td>8.4</td><td>2.3</td><td>4.8</td><td>1.20%</td><td>4.3</td></tr>
<tr><td>4693</td><td>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</td><td>7.9</td><td>6.5</td><td>1.4</td><td>4.8</td><td>1.20%</td><td>4.2</td></tr>
<tr><td>4694</td><td>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</td><td>3.9</td><td>2.9</td><td>0.9</td><td>4.8</td><td>1.20%</td><td>4.3</td></tr>
<tr><td>4695</td><td>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</td><td>9.2</td><td>6.9</td><td>2.3</td><td>4.8</td><td>1.20%</td><td>4.4</td></tr>
<tr><td>4696</td><td>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</td><td>5.8</td><td>4.4</td><td>1.5</td><td>4.8</td><td>1.20%</td><td>4.4</td></tr>
<tr><td>4697</td><td>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</td><td>4.8</td><td>3.9</td><td>0.9</td><td>4.8</td><td>1.20%</td><td>4.3</td></tr>
<tr><td>4698</td><td>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</td><td>6.1</td><td>4.7</td><td>1.4</td><td>4.8</td><td>1.20%</td><td>4.4</td></tr>
<tr><td>4699</td><td>AT2G14460.1 | expressed protein | chr2:6161575-6162086 REVERSE | Aliases: T13P21.16, T13P21_16</td><td>7.1</td><td>4.6</td><td>2.5</td><td>4.8</td><td>1.20%</td><td>4.3</td></tr>
<tr><td>4701</td><td>AT2G29760.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:12719961-12722177 FORWARD | Aliases: T27A16.14, T27A16_14</td><td>4.7</td><td>3.9</td><td>0.8</td><td>4.8</td><td>1.20%</td><td>4.2</td></tr>
<tr><td>4703</td><td>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</td><td>9.5</td><td>7.7</td><td>1.8</td><td>4.8</td><td>1.21%</td><td>4.4</td></tr>
</table>

Rank	Description	Sync	Root	M	t	adj.q	B
4704	AT3G58670.1 | expressed protein | chr3:21714367-21717027 REVERSE | Aliases: T20N10.20	4.8	3.6	1.2	4.8	1.21%	4.3
4706	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	11.0	9.2	1.8	4.8	1.21%	4.1
4707	AT3G19480.1 | D-3-phosphoglycerate dehydrogenase, putative / 3-PGDH, putative, similar to SP:O04130 from (Arabidopsis thaliana) | chr3:6752537-6754791 FORWARD | Aliases: MLD14.34	4.1	2.8	1.3	4.7	1.21%	4.4
4708	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	7.2	5.9	1.3	4.7	1.21%	4.4
4710	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	6.3	4.8	1.6	4.7	1.22%	4.4
4711	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	3.9	1.5	4.7	1.22%	4.3
4713	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	7.1	4.6	2.6	4.7	1.22%	4.3
4714	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	5.5	4.0	1.5	4.7	1.22%	4.3
4715	AT3G57785.1 | expressed protein | chr3:21415551-21416194 REVERSE | Aliases: None	6.5	4.4	2.0	4.7	1.22%	4.3
4716	AT3G08630.1 | expressed protein | chr3:2620838-2622226 FORWARD | Aliases: F17O14.10	7.0	4.0	3.0	4.7	1.22%	4.3
4717	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	7.8	6.6	1.2	4.7	1.22%	4.3
4718	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	5.8	1.9	4.7	1.23%	4.3
4720	AT5G49520.1 | Symbol: WRKY48 |	4.2	2.3	1.9	4.7	1.23%	4.3
4722	AT1G02110.1 | proline-rich family protein, contains proline-rich domain, INTERPRO:IPR000694 | chr1:392939-395554 FORWARD | Aliases: T7I23.5, T7I23_5	5.6	4.4	1.2	4.7	1.23%	4.3
4723	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	4.0	3.3	0.7	4.7	1.23%	4.1
4724	AT4G29670.2 | thioredoxin family protein, contains Pfam profile PF00085: Thioredoxin | chr4:14535613-14537244 REVERSE | Aliases: T16L4.180, T16L4_180	7.3	6.2	1.1	4.7	1.23%	4.3
4725	AT1G15370.1 | expressed protein | chr1:5287057-5288506 FORWARD | Aliases: F9L1.32, F9L1_32	8.8	7.5	1.3	4.7	1.23%	4.2
4726	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	4.3	1.3	4.7	1.23%	4.3
4727	AT3G10940.1 | protein phosphatase-related, similar to protein phosphatase PTPKIS1 protein (GI:11595504) (Arabidopsis thaliana)	6.6	5.6	1.0	4.7	1.23%	4.3
4730	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	6.7	5.2	1.5	4.7	1.23%	4.3

Rank	Description	Sync	Root	M	t	adj.q	B
4732	AT3G46210.4 | similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At2g07110.1); similar to putative exosome component [Oryza sativa (japonica cultivar-group)] (GB:XP_470449.1); contains InterPro domain 3' exoribonuclease (InterPro:IPR001247) | chr3:16987739-16989877 REVERSE | Aliases: F12M12.180	5.6	4.3	1.2	4.7	1.23%	4.3
4733	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	5.5	4.3	1.3	4.7	1.23%	4.3
4735	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	7.1	5.7	1.4	4.7	1.23%	4.3
4739	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	6.0	4.3	1.7	4.7	1.23%	4.3
4741	AT2G36885.2 | expressed protein | chr2:15489090-15490785 REVERSE | Aliases: None	7.2	5.0	2.2	4.7	1.23%	4.3
4743	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	8.2	6.0	2.3	4.7	1.23%	4.3
4750	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	6.0	0.9	4.7	1.23%	4.3
4754	AT1G58160.1 | jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	3.8	3.0	0.8	4.7	1.24%	4.1
4760	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	8.8	6.9	1.9	4.7	1.25%	4.3
4763	AT1G69780.1 | Symbol: ATHB13 |	4.0	3.1	0.9	4.7	1.25%	4.2
4765	AT1G55130.1 | endomembrane protein 70, putative, similar to multispanning membrane protein GI:2276460 from (Homo sapiens) | chr1:20573321-20576060 FORWARD | Aliases: T7N22.7, T7N22_7	5.8	4.4	1.4	4.7	1.25%	4.3
4766	AT5G11910.1 | esterase/lipase/thioesterase family protein, low similarity to cinnamoyl ester hydrolase CinI (Butyrivibrio fibrisolvens) GI:1622732; contains Interpro entry IPR000379 | chr5:3836338-3838214 REVERSE | Aliases: F14F18.80, F14F18_80	8.2	7.1	1.2	4.7	1.25%	4.3
4767	AT5G39890.1 | expressed protein | chr5:15991621-15993498 FORWARD | Aliases: MYH19.8, MYH19_8	6.8	4.7	2.1	4.7	1.25%	4.3
4771	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	9.8	8.2	1.6	4.7	1.26%	4.3
4772	AT5G37055.1 | zinc finger (HIT type) family protein, contains Pfam profile: PF04438 HIT zinc finger | chr5:14658781-14659670 REVERSE | Aliases: None	5.1	4.3	0.8	4.7	1.26%	4.2
4773	AT3G01370.1 | expressed protein, contains Pfam domain, PF04581: Protein of unknown function (DUF578) | chr3:139018-143699 FORWARD | Aliases: T13O15.1, T13O15_1	5.6	4.3	1.3	4.7	1.26%	4.3
4775	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	5.7	4.8	0.9	4.7	1.26%	4.1
4777	AT5G42330.1 | expressed protein | chr5:16943887-16944716 FORWARD | Aliases: MDH9.2, MDH9_2	7.2	4.9	2.3	4.7	1.26%	4.0
4781	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	6.4	5.3	1.1	4.7	1.26%	4.3
4783	AT4G28025.1 | expressed protein | chr4:13935641-13937388 REVERSE | Aliases: None	8.5	7.5	0.9	4.7	1.26%	4.3
4786	AT1G61870.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:22868669-22870280 REVERSE | Aliases: F8K4.8, F8K4_8	7.1	5.2	1.9	4.7	1.27%	4.3
4788	AT2G40020.2 | expressed protein | chr2:16718064-16720148 FORWARD | Aliases: T28M21.18, T28M21_18	4.6	3.4	1.2	4.7	1.27%	4.3

Rank	Description	Sync	Root	M	t	adj.q	B
4789	AT1G04985.1 | expressed protein | chr1:1416342-1418438 REVERSE | Aliases: F13M7.2, F13M7_2	7.8	6.6	1.2	4.7	1.27%	4.3
4792	AT3G05130.1 | expressed protein, ; expression supported by MPSS | chr3:1433481-1435385 REVERSE | Aliases: T12H1.9, T12H1_9	5.0	3.7	1.3	4.7	1.27%	4.3
4794	AT5G07720.1 | galactosyl transferase GMA12/MNN10 family protein, very low similarity to alpha-1,2-galactosyltransferase, Schizosaccharomyces pombe (SP:Q09174)	4.4	2.9	1.5	4.7	1.27%	4.2
4795	AT4G01050.1 | hydroxyproline-rich glycoprotein family protein, contains a rhodanese homology domain. | chr4:455768-458510 FORWARD | Aliases: F2N1.31, F2N1_31	6.1	3.8	2.3	4.7	1.27%	4.3
4797	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	5.5	4.0	1.5	4.7	1.27%	4.3
4798	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	5.3	4.1	1.2	4.7	1.27%	4.3
4799	AT5G63000.1 | expressed protein | chr5:25297238-25298759 REVERSE | Aliases: MJH22.6, MJH22_6	10.4	9.0	1.4	4.7	1.28%	4.2
4806	AT1G52260.1 | Symbol: ATPDIL1 5 | Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	6.0	4.7	1.3	4.7	1.28%	4.3
4807	AT2G40935.2 | expressed protein, low similarity to PGPS/D12 (Petunia x hybrida) GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614	8.1	6.9	1.1	4.7	1.28%	4.3
4808	AT1G30960.1 | GTP-binding protein (ERG), identical to GTP-binding protein ERG SP:O82653 from (Arabidopsis thaliana) | chr1:11037635-11039982 REVERSE | Aliases: F17F8.15	4.9	3.4	1.5	4.7	1.28%	4.3
4811	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	5.0	3.2	1.9	4.7	1.29%	4.1
4816	AT1G09680.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:3134109-3135932 REVERSE | Aliases: F21M12.7, F21M12_7	5.4	4.2	1.2	4.7	1.29%	4.2
4817	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	4.0	3.2	0.7	4.7	1.29%	3.9
4818	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	10.9	8.2	2.6	4.7	1.29%	4.3
4819	AT3G03020.1 | expressed protein | chr3:680951-682006 FORWARD | Aliases: F13E7.3, F13E7_3	3.9	3.0	0.9	4.7	1.29%	4.2
4821	AT1G67350.1 | expressed protein, contains similarity to MHC class II antigen GI:9502037 from (Aotus nancymaae)	11.8	11.2	0.6	4.7	1.30%	3.5
4822	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	6.2	4.6	1.5	4.7	1.30%	4.2
4824	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	9.3	7.9	1.3	4.7	1.30%	4.0
4828	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	8.7	7.3	1.4	4.7	1.30%	4.2
4829	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)	5.9	4.5	1.4	4.7	1.30%	4.3
4830	AT4G17390.1 | 60S ribosomal protein L15 (RPL15B) | chr4:9714225-9715624 REVERSE | Aliases: DL4730C, FCAALL.32	10.9	9.9	1.0	4.7	1.30%	4.0
4835	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	4.0	1.2	4.7	1.31%	4.1

Rank	Description	Sync	Root	M	t	adj.q	B
4836	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	6.9	1.1	4.7	1.31%	4.2
4837	AT4G10500.1 | oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to hyoscyamine 6 beta-hydroxylase (Atropa belladona)(GI:4996123); contains PF03171 2OG-Fe(II) oxygenase superfamily domain | chr4:6491085-6492442 FORWARD | Aliases: F7L13.80, F7L13_80	2.7	2.3	0.4	4.7	1.31%	3.8
4838	AT3G23070.1 | expressed protein, contains Pfam domain, PF04581: Protein of unknown function (DUF578) | chr3:8203476-8208003 FORWARD | Aliases: MXC7.10	4.8	3.8	1.1	4.7	1.31%	4.2
4841	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	9.1	7.0	2.1	4.7	1.31%	4.3
4842	AT3G48500.1 | Symbol: PDE312 |	5.4	4.1	1.3	4.7	1.31%	4.2
4843	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	4.5	1.3	4.7	1.31%	4.2
4845	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 [Crocosphaera 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	7.4	6.1	1.2	4.7	1.31%	4.2
4846	AT4G27060.1 | Symbol: TOR1 | expressed protein | chr4:13581414-13585161 REVERSE | Aliases: CN, CONVOLUTA, SPIRAL 2, SPR2, T24A18.10, T24A18_10, TORTIFOLIA 1	7.0	6.0	1.0	4.7	1.31%	4.2
4847	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	10.1	7.9	2.2	4.7	1.32%	4.2
4849	AT5G62540.1 | ubiquitin-conjugating enzyme 3 (UBC3), E2; identical to gi:431261, SP:P42746 | chr5:25121160-25122845 FORWARD | Aliases: K19B1.15, K19B1_15	8.9	7.3	1.6	4.7	1.32%	4.2
4850	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	6.2	4.9	1.2	4.7	1.32%	4.2
4851	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	8.4	7.0	1.4	4.7	1.32%	4.2
4852	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	8.7	6.5	2.2	4.7	1.32%	4.2
4854	AT2G22610.1 | kinesin motor protein-related | chr2:9606630-9611827 FORWARD | Aliases: T9I22.5, T9I22_5	4.6	3.3	1.3	4.7	1.32%	4.2
4857	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	6.7	5.2	1.6	4.7	1.33%	4.2
4858	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	3.7	2.9	0.8	4.7	1.33%	4.0
4859	AT3G21580.2 | expressed protein | chr3:7601975-7603727 REVERSE | Aliases: MIL23.15	5.1	4.1	1.0	4.7	1.33%	4.2
4861	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	6.3	4.1	2.2	4.7	1.33%	4.2

Rank	Description	Sync	Root	M	t	adj.q	B
4862	AT1G52290.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr1:19473733-19476031 REVERSE | Aliases: F19K6.9, F19K6_9	4.3	3.3	1.0	4.7	1.33%	4.2
4864	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	10.4	9.0	1.4	4.7	1.33%	4.1
4865	AT4G27654.1 | expressed protein | chr4:13811651-13812132 FORWARD | Aliases: None	6.0	3.3	2.8	4.6	1.34%	4.2
4866	AT5G28500.1 | expressed protein, predicted proteins, Arabidopsis thaliana and Synechocystis sp. | chr5:10477775-10479388 FORWARD | Aliases: T26D3.4, T26D3_4	8.0	6.2	1.7	4.6	1.34%	4.2
4867	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	3.1	2.5	0.6	4.6	1.34%	3.9
4868	AT4G13520.1 | expressed protein | chr4:7864390-7864920 FORWARD | Aliases: T6G15.70, T6G15_70	10.9	9.8	1.1	4.6	1.34%	3.7
4869	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	5.5	3.8	1.7	4.6	1.34%	4.2
4872	AT4G17970.1 | expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	4.8	3.2	1.6	4.6	1.34%	4.1
4874	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)	4.5	3.8	0.8	4.6	1.34%	4.0
4878	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	4.6	2.8	1.8	4.6	1.34%	4.2
4879	AT2G21830.1 | DC1 domain-containing protein, contains Pfam profilePF03107: DC1 domain | chr2:9310793-9312977 FORWARD | Aliases: F7D8.15, F7D8_15	6.4	5.2	1.1	4.6	1.35%	4.2
4880	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	5.1	4.3	0.8	4.6	1.35%	4.0
4881	AT2G29180.1 | expressed protein | chr2:12550111-12551306 FORWARD | Aliases: F16P2.44, F16P2_44	6.3	4.5	1.7	4.6	1.35%	4.1
4887	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	4.9	3.7	1.2	4.6	1.35%	4.2
4888	AT1G11840.5 | Symbol: ATGLX1 |	11.8	10.3	1.6	4.6	1.35%	4.0
4889	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	5.4	4.2	1.2	4.6	1.35%	4.2
4890	AT5G20590.1 | expressed protein, various predicted proteins, Arabidopsis thaliana | chr5:6963440-6966607 FORWARD | Aliases: F7C8.180, F7C8_180	7.0	6.0	1.1	4.6	1.35%	4.2
4891	AT1G48380.1 | Symbol: RHL1 | root hair initiation protein root hairless 1 (RHL1) | chr1:17881081-17882938 REVERSE | Aliases: F11A17.7, F11A17_7, ROOT HAIRLESS 1	6.3	5.1	1.2	4.6	1.35%	4.2
4895	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	3.7	2.7	1.1	4.6	1.36%	4.2
4897	AT5G20130.1 | expressed protein | chr5:6797445-6798901 FORWARD | Aliases: F5O24.20, F5O24_20	6.5	5.4	1.0	4.6	1.36%	4.2
4899	AT3G17350.1 | expressed protein | chr3:5934100-5935042 FORWARD | Aliases: MGD8.19	5.1	3.7	1.4	4.6	1.36%	4.2
4902	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	4.7	3.1	1.7	4.6	1.36%	4.2
4903	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	6.5	4.4	2.2	4.6	1.36%	4.2

Rank	Description	Sync	Root	M	t	adj.q	B
4904	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	8.3	6.7	1.6	4.6	1.36%	4.1
4908	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	3.9	3.1	0.8	4.6	1.37%	4.1
4909	AT1G03687.2 | DTW domain-containing protein, contains Pfam PF03942: DTW domain	5.1	4.0	1.1	4.6	1.37%	4.2
4911	AT3G10640.2 | SNF7 family protein, contains Pfam domain, PF03357: SNF7 family | chr3:3323315-3325051 REVERSE | Aliases: F13M14.7	8.2	6.9	1.3	4.6	1.37%	4.1
4912	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	6.4	5.2	1.2	4.6	1.37%	4.1
4915	AT3G23620.1 | brix domain-containing protein, contains Pfam domain, PF04427: Brix domain | chr3:8480076-8482164 FORWARD | Aliases: MDB19.11	6.5	3.7	2.7	4.6	1.37%	4.1
4917	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	5.6	4.6	1.0	4.6	1.38%	4.2
4920	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	5.0	4.2	0.8	4.6	1.38%	4.1
4921	AT2G34510.1 | expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642 | chr2:14551076-14553886 REVERSE | Aliases: T31E10.15, T31E10_15	5.0	3.6	1.4	4.6	1.38%	4.2
4922	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	4.3	3.4	0.9	4.6	1.38%	4.1
4923	AT5G67130.1 | expressed protein | chr5:26808592-26811253 FORWARD | Aliases: K21H1.9, K21H1_9	6.6	5.5	1.0	4.6	1.38%	4.1
4924	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	2.7	1.0	4.6	1.38%	4.0
4927	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	9.3	8.4	0.9	4.6	1.39%	4.0
4928	AT1G14410.1 | DNA-binding protein-related, similar to DNA-binding protein p24 GI:9651810 from (Solanum tuberosum) | chr1:4929118-4930888 REVERSE | Aliases: F14L17.18, F14L17_18	6.1	4.7	1.4	4.6	1.39%	4.2
4933	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	8.9	7.4	1.5	4.6	1.39%	4.1
4934	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	6.5	4.4	2.1	4.6	1.39%	4.1
4935	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	9.6	7.4	2.2	4.6	1.39%	4.2
4936	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	8.1	6.3	1.9	4.6	1.39%	4.2
4937	AT3G46040.1 | 40S ribosomal protein S15A (RPS15aD), cytoplasmic ribosomal protein S15a, Arabidopsis thaliana, EMBL:ATAF1412 | chr3:16925554-16926744 FORWARD | Aliases: F12M12.10	10.4	9.2	1.1	4.6	1.39%	3.9
4938	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	4.6	3.4	1.2	4.6	1.39%	4.1

Rank	Description	Sync	Root	M	t	adj.q	B
4940	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	8.5	6.8	1.7	4.6	1.39%	4.1
4942	AT1G52550.1 | expressed protein | chr1:19576596-19577699 REVERSE | Aliases: F6D8.23, F6D8_23	3.8	2.8	1.0	4.6	1.39%	4.1
4944	AT5G16750.1 | Symbol: TOZ | transducin family protein / WD-40 repeat family protein, contains 8 WD-40 repeats (PF00400); similar to transducin homolog sazD - Homo sapiens, EMBL:U02609 | chr5:5504349-5509345 REVERSE | Aliases: F5E19.90, F5E19_90, TORMOZ, TORMOZEMBRYO DEFECTIVE	5.4	4.2	1.1	4.6	1.39%	4.1
4946	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	4.8	3.3	1.5	4.6	1.39%	4.2
4948	AT5G59850.1 | 40S ribosomal protein S15A (RPS15aF), cytoplasmic ribosomal protein S15a, Arabidopsis thaliana, EMBL:ATAF1412 | chr5:24129426-24130836 REVERSE | Aliases: MMN10.16	9.2	7.0	2.2	4.6	1.39%	4.2
4950	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	6.7	3.9	2.8	4.6	1.39%	4.2
4951	AT3G05430.1 | PWWP domain-containing protein, contains Pfam profile:PF00855 PWWP domain | chr3:1567631-1571078 FORWARD | Aliases: F22F7.12, F22F7_12	3.9	3.4	0.5	4.6	1.39%	3.8
4952	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	7.4	6.1	1.3	4.6	1.40%	4.2
4953	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	6.3	4.1	2.3	4.6	1.40%	4.2
4955	AT3G51010.1 | expressed protein | chr3:18957681-18959137 REVERSE | Aliases: F24M12.50	7.1	5.2	1.9	4.6	1.40%	4.2
4956	AT5G05610.2 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr5:1676941-1679105 REVERSE | Aliases: MOP10.15, MOP10_15	6.0	4.5	1.5	4.6	1.40%	4.1
4957	AT3G60830.1 | Symbol: ATARP7 |	7.2	6.1	1.2	4.6	1.40%	4.1
4959	AT1G07500.1 | expressed protein, ; expression supported by MPSS | chr1:2304763-2305028 REVERSE | Aliases: F22G5.11, F22G5_11	4.9	3.4	1.5	4.6	1.40%	4.1
4962	AT3G53430.1 | 60S ribosomal protein L12 (RPL12B), 60S RIBOSOMAL PROTEIN L12, Prunus armeniaca, SWISSPROT:RL12_PRUAR | chr3:19820665-19821447 REVERSE | Aliases: F4P12.130	10.2	8.2	2.0	4.6	1.40%	4.2
4965	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	7.3	6.2	1.1	4.6	1.41%	4.0
4966	AT4G32810.1 | Symbol: CCD8 | Encodes a protein with similarity to carotenoid cleaving deoxygenases. Involved in the production of a graft transmissable 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	4.3	2.3	2.0	4.6	1.41%	4.2
4969	AT5G59460.1 | scarecrow-like transcription factor 11 (SCL11), identical to cDNA scarecrow-like 11 (SCL11) mRNA, partial cds gi:4580526	5.1	3.7	1.3	4.6	1.41%	4.0
4970	AT5G27990.1 | expressed protein, predicted proteins, Saccharomyces cerevisiae and Schizosaccharomyces pombe | chr5:10017052-10018445 FORWARD | Aliases: F15F15.60, F15F15_60	6.7	5.5	1.2	4.6	1.41%	4.0
4971	AT5G13270.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr5:4246957-4249215 REVERSE | Aliases: T31B5.90, T31B5_90	3.0	2.5	0.5	4.6	1.41%	3.7
4974	AT3G21360.1 | expressed protein | chr3:7522810-7524586 FORWARD | Aliases: MHC9.4	6.5	5.4	1.1	4.6	1.42%	4.1
4975	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	5.4	4.2	1.2	4.6	1.42%	4.2

Rank	Description	Sync	Root	M	t	adj.q	B
4976	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	5.6	3.2	2.4	4.6	1.42%	4.1
4977	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	6.8	5.6	1.2	4.6	1.42%	4.1
4981	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	9.4	7.1	2.3	4.6	1.42%	4.1
4983	AT4G14100.1 | expressed protein | chr4:8120715-8122406 FORWARD | Aliases: DL3085W, FCAALL.191	4.9	3.7	1.2	4.6	1.43%	4.1
4984	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)	8.4	7.0	1.4	4.6	1.43%	4.1
4992	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)	4.7	3.9	0.9	4.6	1.43%	4.0
4998	AT1G29700.1 | expressed protein | chr1:10384967-10387427 REVERSE | Aliases: F15D2.25	4.2	3.0	1.1	4.6	1.44%	4.0
5000	AT2G37420.1 | kinesin motor protein-related | chr2:15707410-15712422 FORWARD | Aliases: F3G5.21, F3G5_21	4.9	3.0	1.8	4.6	1.44%	4.1
5003	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	6.1	5.4	0.7	4.6	1.44%	3.9
5008	AT2G33180.1 | expressed protein | chr2:14073545-14074544 FORWARD | Aliases: F25I18.8, F25I18_8	3.8	2.6	1.2	4.6	1.45%	4.1
5011	AT2G17250.1 | expressed protein, weak similarity to Ribosome biogenesis protein MAK21 (Swiss-Prot:Q12176) (Saccharomyces cerevisiae) | chr2:7506559-7510207 FORWARD | Aliases: T23A1.11, T23A1_11	7.1	5.9	1.1	4.6	1.45%	4.0
5012	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	5.0	1.2	4.6	1.45%	4.1
5013	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	7.6	5.3	2.3	4.6	1.45%	4.1
5014	AT1G28480.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	8.1	7.0	1.1	4.6	1.45%	4.0
5016	AT3G04830.2 | expressed protein | chr3:1326255-1329370 FORWARD | Aliases: T9J14.22, T9J14_22	8.7	6.5	2.2	4.6	1.45%	4.1
5017	AT4G22530.1 | embryo-abundant protein-related, similar to embryo-abundant protein (Picea glauca) GI:1350531 | chr4:11859015-11860159 REVERSE | Aliases: F7K2.110, F7K2_110	6.8	5.5	1.3	4.6	1.46%	4.1
5018	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	4.9	1.2	4.6	1.46%	4.1
5019	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	7.8	5.6	2.2	4.6	1.46%	4.1
5021	AT2G45640.1 | sin3 associated polypeptide p18 family protein, similar to Sin3 associated polypeptide p18 (2HOR0202) (Swiss-Prot:O00422) (Homo sapiens)	7.5	6.7	0.8	4.6	1.46%	4.0
5022	AT3G13490.1 | tRNA synthetase class II (D, K and N) family protein, similar to SP:Q9RHV9 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)	5.2	4.3	1.0	4.6	1.46%	3.9

Rank	Description	Sync	Root	M	t	adj.q	B
5024	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	9.0	6.8	2.3	4.6	1.46%	4.1
5025	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	6.2	1.2	4.6	1.46%	4.0
5026	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	4.9	3.5	1.4	4.6	1.46%	4.1
5027	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	3.6	2.8	0.8	4.6	1.46%	4.0
5028	AT2G32500.1 | expressed protein | chr2:13802337-13804259 REVERSE | Aliases: T26B15.6, T26B15_6	4.3	3.1	1.2	4.6	1.46%	4.1
5029	AT2G37890.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr2:15868766-15871087 REVERSE | Aliases: T8P21.20, T8P21_20	5.2	4.1	1.2	4.6	1.46%	4.1
5031	AT3G09650.1 | Symbol: HCF152 |	7.2	5.7	1.5	4.6	1.47%	4.1
5034	AT1G69230.2 | expressed protein | chr1:26029981-26031371 REVERSE | Aliases: F4N2.18	4.5	3.1	1.4	4.6	1.47%	4.1
5036	AT1G48460.1 | expressed protein | chr1:17915014-17916968 FORWARD | Aliases: T1N15.7, T1N15_7	5.0	3.8	1.2	4.6	1.47%	4.1
5037	AT3G02490.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:513532-515932 FORWARD | Aliases: F16B3.12, F16B3_12	7.0	5.8	1.2	4.6	1.47%	4.0
5038	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	4.4	3.6	0.8	4.5	1.47%	4.0
5043	AT4G38890.1 | dihydrouridine synthase family protein, contains Pfam domain, PF01207: Dihydrouridine synthase (Dus) | chr4:18135903-18139094 REVERSE | Aliases: F19H22.4	9.0	7.9	1.1	4.5	1.48%	4.1
5044	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	5.3	3.3	2.0	4.5	1.48%	4.1
5046	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	4.7	1.9	4.5	1.48%	4.1
5047	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	3.3	2.9	0.5	4.5	1.48%	3.6
5049	AT5G57850.1 | aminotransferase class IV family protein, contains Pfam profile: PF01063 aminotransferase class IV | chr5:23452528-23454552 REVERSE | Aliases: MTI20.10, MTI20_10	5.8	4.6	1.2	4.5	1.49%	4.1
5050	AT5G63530.1 | Symbol: ATFP3 | copper chaperone (CCH)-related, low similarity to copper homeostasis factor (GI:3168840); nearly identical to farnesylated protein ATFP3 (GI:4097547); contains Pfam profile PF00403: Heavy-metal-associated domain | chr5:25450469-25453060 FORWARD | Aliases: MLE2.16, MLE2_16	7.5	4.5	3.0	4.5	1.49%	4.1
5051	AT1G64355.2 | expressed protein, similar to hypothetical protein Tery02003428 [Trichodesmium erythraeum IMS101] (GB:ZP_00326379.1) | chr1:23889765-23890875 FORWARD | Aliases: None	3.8	2.9	0.8	4.5	1.49%	4.0
5052	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	5.9	4.7	1.2	4.5	1.49%	4.0
5057	AT5G27740.1 | expressed protein | chr5:9823744-9827068 FORWARD | Aliases: T1G16.70, T1G16_70	5.2	4.0	1.2	4.5	1.50%	4.1

Rank	Description	Sync	Root	M	t	adj.q	B
5059	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	5.0	3.8	1.1	4.5	1.50%	4.1
5061	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	5.4	4.6	0.8	4.5	1.50%	4.0
5062	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	6.4	4.9	1.5	4.5	1.50%	4.1
5063	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	7.8	1.3	4.5	1.50%	4.0
5065	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	4.4	1.5	4.5	1.50%	4.1
5066	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	10.5	9.2	1.4	4.5	1.50%	3.9
5067	AT3G18720.1 | F-box family protein, contains Pfam PF00646: F-box domain | chr3:6444373-6445765 REVERSE | Aliases: MVE11.8	2.7	2.3	0.4	4.5	1.50%	3.5
5069	AT3G17465.1 | Symbol: RPL3P | ribosomal protein L3 family protein | chr3:5977823-5979578 REVERSE | Aliases: MKP6.7, RIBOSOMAL PROTEIN L3 PLASTID	6.7	5.1	1.6	4.5	1.50%	4.1
5074	AT4G15830.1 | expressed protein | chr4:8995126-8996614 REVERSE | Aliases: DL3955C, FCAALL.419	8.2	6.7	1.5	4.5	1.51%	4.0
5077	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	5.6	4.5	1.1	4.5	1.52%	4.0
5078	AT2G24440.1 | expressed protein | chr2:10398169-10400326 FORWARD | Aliases: T28I24.17, T28I24_17	5.3	3.9	1.3	4.5	1.52%	4.1
5080	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	3.1	2.6	0.5	4.5	1.52%	3.6
5083	AT5G22790.1 | expressed protein | chr5:7599149-7601693 REVERSE | Aliases: K8E10.2, K8E10_2	7.4	6.2	1.3	4.5	1.52%	4.1
5084	AT1G04610.1 | flavin-containing monooxygenase / FMO (YUCCA3), identical to gi:16555356	6.5	4.5	2.0	4.5	1.52%	4.1
5089	AT3G49080.1 | ribosomal protein S9 family protein, contains Pfam profile PF00380: ribosomal protein S9	6.8	5.8	1.0	4.5	1.52%	4.0
5092	AT1G27385.1 | expressed protein | chr1:9510925-9512847 REVERSE | Aliases: None	7.4	6.4	1.0	4.5	1.53%	4.1
5093	AT2G23090.1 | expressed protein | chr2:9836530-9837490 REVERSE | Aliases: F21P24.15	12.0	10.9	1.1	4.5	1.53%	3.6
5094	AT3G17160.1 | expressed protein | chr3:5852158-5853694 FORWARD | Aliases: K14A17.24	8.4	6.7	1.7	4.5	1.53%	4.0
5097	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	6.1	4.2	1.9	4.5	1.53%	4.0
5099	AT2G31890.1 | expressed protein | chr2:13563222-13566844 REVERSE | Aliases: F20M17.7, F20M17_7	6.7	5.7	1.0	4.5	1.53%	4.0
5100	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	7.0	6.4	0.6	4.5	1.53%	3.6
5101	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	11.9	0.6	4.5	1.54%	3.6
5102	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	8.6	5.8	2.8	4.5	1.54%	4.1

Rank	Description	Sync	Root	M	t	adj.q	B
5103	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	6.6	5.2	1.5	4.5	1.54%	4.0
5105	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	7.2	5.7	1.5	4.5	1.54%	4.1
5106	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	6.2	4.7	1.5	4.5	1.54%	4.0
5109	AT5G53170.1 | Symbol: FTSH11 |	6.9	4.6	2.4	4.5	1.55%	4.0
5110	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	5.7	4.9	0.8	4.5	1.55%	3.8
5111	AT1G31817.1 | chloroplast 30S ribosomal protein S11, putative, contains Pfam profile: PF00411: Ribosomal protein S11 | chr1:11414730-11416418 REVERSE | Aliases: F5M6.25, F5M6_25	5.9	3.9	2.0	4.5	1.55%	4.1
5112	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	5.0	1.3	4.5	1.55%	4.0
5113	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	2.6	0.7	4.5	1.55%	3.8
5119	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	11.7	9.7	1.9	4.5	1.56%	3.8
5120	AT1G01725.1 | expressed protein | chr1:269794-270775 REVERSE | Aliases: None	8.1	6.5	1.6	4.5	1.56%	4.0
5121	AT5G67180.1 | AP2 domain-containing transcription factor, putative, similar to (SP:P47927) Floral homeotic protein APETALA2. (Mouse-ear cress) {Arabidopsis thaliana} | chr5:26819233-26821245 REVERSE | Aliases: K21H1.22, K21H1_22	3.8	3.0	0.8	4.5	1.56%	3.8
5122	AT4G09730.1 | DEAD/DEAH box helicase, putative, RNA helicase -Mus musculus,PIR2:I84741	4.0	2.9	1.0	4.5	1.56%	3.9
5125	AT3G55380.1 | ubiquitin-conjugating enzyme 14 (UBC14), E2; UbcAT3; identical to gi:2129757, S46656 | chr3:20542396-20544150 FORWARD | Aliases: T22E16.40	7.1	5.6	1.4	4.5	1.57%	4.0
5126	AT1G66330.2 | senescence-associated family protein, similar to senescence-associated protein (GI:12836895) (Ipomoea batatas) | chr1:24733292-24736125 REVERSE | Aliases: T27F4.8, T27F4_8	5.8	4.1	1.7	4.5	1.57%	4.0
5127	AT2G44525.1 | expressed protein | chr2:18389172-18390587 FORWARD | Aliases: None	8.4	6.9	1.5	4.5	1.57%	4.0
5128	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	7.2	4.6	2.6	4.5	1.57%	4.0
5129	AT4G33540.1 | metallo-beta-lactamase family protein | chr4:16130876-16133963 FORWARD | Aliases: T16L1.30, T16L1_30	8.5	6.4	2.0	4.5	1.57%	4.0
5130	AT2G39310.1 | jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	4.5	3.3	1.3	4.5	1.57%	4.0
5133	AT4G15940.1 | fumarylacetoacetate hydrolase family protein, contains Pfam domain, PF01557: fumarylacetoacetate hydrolase family protein | chr4:9038304-9040758 FORWARD | Aliases: DL4011W, FCAALL.203	9.5	7.9	1.6	4.5	1.58%	3.9
5139	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	6.8	5.1	1.8	4.5	1.58%	4.0

Rank	Description	Sync	Root	M	t	adj.q	B
5140	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	6.3	4.6	1.7	4.5	1.58%	4.0
5145	AT5G02280.1 | synbindin, putative, similar to Swiss-Prot:Q9ES56 synbindin (TRS23 homolog) (Mus musculus) | chr5:469324-470792 FORWARD | Aliases: T1E22.40, T1E22_40	7.7	6.4	1.3	4.5	1.58%	4.0
5148	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	5.3	4.5	0.8	4.5	1.58%	3.8
5150	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	9.2	1.0	4.5	1.59%	3.8
5151	ATCG01090.1 | Symbol: NDHI | Encodes subunit of the chloroplast NAD(P)H dehydrogenase complex	8.8	7.1	1.7	4.5	1.59%	4.0
5152	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	5.1	3.5	1.6	4.5	1.59%	4.0
5153	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	6.9	5.4	1.6	4.5	1.59%	4.0
5154	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	5.7	1.0	4.5	1.59%	3.9
5155	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	4.0	2.8	1.2	4.5	1.59%	4.0
5156	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	4.0	3.2	0.8	4.5	1.59%	3.8
5157	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	5.9	0.6	4.5	1.60%	3.7
5158	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	6.0	3.9	2.1	4.5	1.60%	4.0
5159	AT1G09910.1 | expressed protein | chr1:3220037-3224543 REVERSE | Aliases: F21M12.30, F21M12_30	7.2	6.2	1.0	4.5	1.60%	3.9
5164	AT3G27230.1 | expressed protein | chr3:10055166-10056928 FORWARD | Aliases: K17E12.5	7.7	6.1	1.6	4.5	1.60%	4.0
5165	AT3G57090.1 | expressed protein | chr3:21139509-21141167 FORWARD | Aliases: F24I3.170	9.0	7.4	1.6	4.5	1.60%	3.9
5166	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	10.7	7.8	2.9	4.5	1.60%	3.9
5168	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	3.6	3.1	0.6	4.5	1.60%	3.6
5171	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	7.0	1.5	4.5	1.61%	4.0
5173	AT2G25920.1 | expressed protein | chr2:11061369-11063120 REVERSE | Aliases: F17H15.5, F17H15_5	5.2	4.2	1.0	4.5	1.61%	3.9
5175	AT5G67440.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr5:26929933-26933306 REVERSE | Aliases: K8K14.18, K8K14_18	5.0	4.1	0.9	4.5	1.61%	3.8
5177	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	11.3	6.7	4.6	4.5	1.61%	4.0
5178	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)	11.3	6.7	4.6	4.5	1.61%	4.0

Rank	Description	Sync	Root	M	t	adj.q	B
5180	AT2G03670.1 | Symbol: CDC48B |	4.3	2.9	1.4	4.5	1.61%	3.9
5183	AT3G60380.1 | expressed protein | chr3:22327888-22330241 REVERSE | Aliases: T8B10.40	7.1	5.7	1.5	4.5	1.61%	3.9
5185	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	2.5	0.7	4.5	1.61%	3.7
5187	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	10.3	8.2	2.1	4.5	1.61%	4.0
5189	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	8.2	6.2	2.0	4.5	1.61%	3.9
5191	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	5.8	1.4	4.5	1.62%	4.0
5193	AT2G39050.1 | hydroxyproline-rich glycoprotein family protein, contains QXW lectin repeat domain, Pfam:PF00652	7.3	6.0	1.3	4.5	1.62%	4.0
5194	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	5.3	3.8	1.5	4.5	1.62%	4.0
5197	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	2.7	0.8	4.5	1.62%	3.8
5198	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	5.1	1.7	4.5	1.62%	4.0
5199	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	6.4	4.7	1.7	4.5	1.62%	4.0
5201	AT5G04590.1 | Symbol: SIR | sulfite reductase / ferredoxin (SIR), identical to sulfite reductase (Arabidopsis thaliana) GI:804953, GI:2584721	9.0	6.6	2.4	4.5	1.62%	4.0
5202	AT5G56580.1 | Symbol: ATMKK6 |	4.2	3.0	1.2	4.5	1.62%	3.9
5203	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	5.6	4.6	0.9	4.5	1.62%	4.0
5204	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	5.4	4.3	1.1	4.5	1.62%	4.0
5208	AT3G23805.1 | Symbol: RALFL24 | rapid alkalinization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316 | chr3:8586389-8587063 FORWARD | Aliases: RALF LIKE 24	6.1	4.9	1.2	4.4	1.63%	3.9
5210	AT5G51960.1 | expressed protein | chr5:21127929-21128574 FORWARD | Aliases: MSG15.4, MSG15_4	6.3	4.6	1.6	4.4	1.63%	3.9
5212	AT1G47720.1 | expressed protein, contains Pfam PF05329: Protein of unknown function (DUF731) | chr1:17563795-17565323 REVERSE | Aliases: T2E6.21	5.6	4.4	1.2	4.4	1.64%	4.0
5213	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	6.9	5.8	1.2	4.4	1.64%	3.9
5215	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	8.6	6.4	2.2	4.4	1.64%	4.0

Rank	Description	Sync	Root	M	t	adj.q	B
5218	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	4.9	3.9	1.0	4.4	1.65%	3.9
5219	AT2G36485.1 | expressed protein | chr2:15314035-15314869 REVERSE | Aliases: None	3.9	2.8	1.1	4.4	1.65%	3.9
5221	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	11.7	9.6	2.2	4.4	1.65%	3.6
5223	AT2G45440.1 | Symbol: DHDPS2 |	7.7	4.7	3.1	4.4	1.65%	3.9
5224	AT4G29070.2 | expressed protein | chr4:14321895-14323313 FORWARD | Aliases: F19B15.100, F19B15_100	6.2	5.0	1.2	4.4	1.65%	4.0
5225	AT5G55210.1 | expressed protein, similar to unknown protein (pir::T04913) | chr5:22413756-22414614 REVERSE | Aliases: MCO15.16, MCO15_16	4.4	3.2	1.2	4.4	1.65%	3.9
5226	AT5G16120.1 | 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 | chr5:5265957-5267982 FORWARD | Aliases: T21H19.40, T21H19_40	7.7	6.8	0.8	4.4	1.65%	3.8
5227	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	3.6	0.9	4.4	1.65%	3.9
5231	AT5G38730.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:15528131-15529921 FORWARD | Aliases: MKD10.5, MKD10_5	5.0	4.0	1.0	4.4	1.66%	3.8
5232	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	6.2	3.9	2.3	4.4	1.66%	3.9
5233	AT2G34710.1 | Symbol: PHB | homeobox-leucine zipper transcription factor (HB-14), identical to homeodomain transcription factor (ATHB-14)GP:3132474 GB:Y11122 (Arabidopsis thaliana);	6.8	5.9	0.9	4.4	1.66%	3.9
5234	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	6.4	4.9	1.5	4.4	1.66%	3.9
5238	AT5G10620.1 | expressed protein, contains Pfam profile PF02590: Uncharacterized ACR, COG1576 | chr5:3355467-3356616 REVERSE | Aliases: F12B17.30, F12B17_30	5.1	3.7	1.3	4.4	1.67%	4.0
5240	AT4G10620.1 | expressed protein | chr4:6564275-6566500 FORWARD | Aliases: T4F9.80, T4F9_80	6.9	5.9	1.0	4.4	1.67%	3.9
5241	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	7.2	2.2	4.4	1.67%	3.9
5242	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	5.8	4.6	1.2	4.4	1.67%	3.9
5243	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	5.1	3.9	1.2	4.4	1.67%	3.8
5244	AT4G05330.1 | zinc finger and C2 domain protein, putative, similar to zinc finger and C2 domain protein GI:9957238 from (Arabidopsis thaliana)	4.8	3.6	1.2	4.4	1.67%	4.0
5245	AT5G43640.1 | 40S ribosomal protein S15 (RPS15E) | chr5:17548529-17549597 FORWARD | Aliases: K9D7.14, K9D7_14	3.0	2.7	0.3	4.4	1.67%	3.1
5246	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	3.5	2.8	0.7	4.4	1.67%	3.8
5248	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	10.0	7.9	2.1	4.4	1.67%	3.9
5249	AT4G21865.1 | expressed protein | chr4:11601917-11603287 FORWARD | Aliases: None	5.7	3.6	2.1	4.4	1.67%	3.7

Rank	Description	Sync	Root	M	t	adj.q	B
5251	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	4.5	3.0	1.4	4.4	1.68%	3.9
5254	AT5G61770.3 | brix domain-containing protein, contains Pfam domain, PF04427: Brix domain | chr5:24832863-24834869 FORWARD | Aliases: MAC9.8, MAC9_8	5.8	4.2	1.6	4.4	1.68%	4.0
5255	AT2G29360.1 | tropinone reductase, putative / tropine dehydrogenase, putative, similar to tropinone reductase SP:P50165 from (Datura stramonium) | chr2:12610902-12612312 FORWARD | Aliases: F16P2.26, F16P2_26	3.4	2.6	0.7	4.4	1.68%	3.7
5256	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	4.7	3.8	0.9	4.4	1.68%	3.8
5257	AT1G15710.1 | prephenate dehydrogenase family protein, contains Pfam profile: PF02153 prephenate dehydrogenase	7.1	4.3	2.7	4.4	1.68%	3.9
5258	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	9.2	6.2	3.0	4.4	1.68%	3.9
5259	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	10.3	9.4	1.0	4.4	1.68%	3.8
5260	AT1G67660.1 | expressed protein | chr1:25367198-25368892 FORWARD | Aliases: F12A21.19, F12A21_19	5.1	4.1	1.0	4.4	1.68%	3.9
5262	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	4.4	3.2	1.2	4.4	1.68%	3.8
5263	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	4.4	0.7	4.4	1.68%	3.7
5264	AT1G55170.1 | expressed protein | chr1:20583990-20585642 FORWARD | Aliases: T7N22.12, T7N22_12	6.8	5.6	1.2	4.4	1.68%	3.9
5265	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	10.1	7.7	2.4	4.4	1.68%	4.0
5266	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	3.1	2.5	0.6	4.4	1.68%	3.7
5267	AT1G10660.4 | expressed protein | chr1:3532474-3535132 FORWARD | Aliases: F20B24.10, F20B24_10	6.8	4.5	2.2	4.4	1.69%	3.9
5269	AT2G43550.1 | Encodes a defensin-like (DEFL) family protein. | chr2:18080311-18080982 FORWARD | Aliases: T1O24.29	4.2	3.2	1.0	4.4	1.69%	3.9
5270	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	8.2	6.1	2.0	4.4	1.69%	3.9
5272	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	3.6	1.5	4.4	1.69%	3.9
5273	AT2G17270.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr2:7517182-7519469 FORWARD | Aliases: F5J6.3, F5J6_3	4.9	3.8	1.1	4.4	1.69%	3.9
5274	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	5.0	3.6	1.4	4.4	1.69%	3.9
5275	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	3.9	2.3	1.6	4.4	1.69%	3.9

Rank	Description	Sync	Root	M	t	adj.q	B
5278	AT5G50100.1 | expressed protein, contains Pfam domain PF04134: Protein of unknown function, DUF393 | chr5:20389079-20390667 FORWARD | Aliases: MPF21.11, MPF21_11	5.8	4.7	1.0	4.4	1.70%	3.9
5279	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	2.8	2.3	0.5	4.4	1.71%	3.4
5280	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	4.1	3.2	0.9	4.4	1.71%	3.9
5281	AT1G20330.1 | Symbol: SMT2 | S-adenosyl-methionine-sterol-C-methyltransferase, identical to sterol-C-methyltransferase GI:1061040 from (Arabidopsis thaliana)	7.0	5.1	1.9	4.4	1.71%	3.9
5286	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	7.5	5.4	2.1	4.4	1.72%	3.9
5287	AT1G32190.1 | expressed protein | chr1:11592935-11595962 REVERSE | Aliases: F3C3.3, F3C3_3	4.4	3.7	0.7	4.4	1.72%	3.7
5289	AT5G25470.2 | expressed protein | chr5:8865732-8867688 REVERSE | Aliases: T14C9.20, T14C9_20	5.0	3.5	1.5	4.4	1.72%	3.9
5290	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	4.7	3.6	1.1	4.4	1.72%	3.9
5291	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	5.0	3.9	1.1	4.4	1.72%	3.9
5292	AT3G02950.1 | expressed protein | chr3:665365-666910 REVERSE | Aliases: F13E7.10, F13E7_10	4.5	3.3	1.2	4.4	1.72%	3.8
5293	AT2G18940.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat | chr2:8210812-8213477 REVERSE | Aliases: F19F24.14, F19F24_14	5.1	3.8	1.4	4.4	1.72%	3.9
5296	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	11.3	10.4	0.9	4.4	1.72%	3.4
5297	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	11.3	10.4	0.9	4.4	1.72%	3.4
5300	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	10.1	8.1	2.1	4.4	1.73%	3.8
5304	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	6.3	0.9	4.4	1.73%	3.8
5305	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	6.5	4.7	1.7	4.4	1.73%	3.8
5306	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	5.6	4.3	1.3	4.4	1.73%	3.9
5308	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	10.5	8.9	1.6	4.4	1.73%	3.7
5309	AT5G12140.1 | Symbol: ATCYS1 |	12.0	10.8	1.1	4.4	1.73%	3.6
5310	AT4G34740.1 | Symbol: ATASE2 |	4.4	3.5	0.9	4.4	1.73%	3.8

Rank	Description	Sync	Root	M	t	adj.q	B
5311	AT1G20540.1 | transducin family protein / WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); similar to Rbap46 polypeptide (GI:9454362) (Gallus gallus) | chr1:7112611-7115810 FORWARD | Aliases: F5M15.14, F5M15_14	8.8	7.5	1.3	4.4	1.73%	3.8
5312	AT3G04860.1 | expressed protein | chr3:1339114-1340629 REVERSE | Aliases: T9J14.19, T9J14_19	5.7	4.5	1.2	4.4	1.73%	3.9
5313	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	8.7	7.0	1.7	4.4	1.73%	3.9
5316	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	4.7	3.8	1.0	4.4	1.74%	3.9
5317	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	6.7	5.1	1.6	4.4	1.74%	3.9
5318	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	3.3	2.7	0.6	4.4	1.74%	3.5
5322	AT1G09160.2 | protein phosphatase 2C-related / PP2C-related, similar to GB:AAC16260 | chr1:2952773-2955606 REVERSE | Aliases: T12M4.15, T12M4_15	6.4	5.3	1.1	4.4	1.74%	3.9
5323	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	11.2	10.4	0.8	4.4	1.74%	3.6
5325	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	8.3	6.8	1.5	4.4	1.74%	3.9
5326	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	3.7	3.0	0.7	4.4	1.75%	3.7
5327	AT2G40780.1 | hypothetical protein | chr2:17028953-17029826 FORWARD | Aliases: T7D17.4, T7D17_4	4.4	3.5	0.9	4.4	1.75%	3.8
5328	AT5G52440.1 | Symbol: HCF106 |	7.0	5.3	1.7	4.4	1.75%	3.9
5329	AT1G31920.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:11461835-11463782 REVERSE | Aliases: F5M6.8, F5M6_8	3.7	2.7	1.0	4.4	1.75%	3.7
5333	AT1G18090.2 | exonuclease, putative, similar to Swiss-Prot:P53695 exonuclease I (EXO I) (Schizosaccharomyces pombe) | chr1:6224497-6228233 FORWARD | Aliases: T10F20.10	3.8	3.0	0.8	4.4	1.76%	3.8
5334	AT1G12280.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.1	2.4	0.7	4.4	1.76%	3.6
5335	AT1G80860.2 | expressed protein | chr1:30393156-30394194 REVERSE | Aliases: F23A5.21, F23A5_21	7.1	6.1	1.1	4.4	1.76%	3.8
5340	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	8.2	7.4	0.8	4.4	1.76%	3.7
5344	AT1G69830.1 | Symbol: ATAMY3 |	7.1	5.0	2.2	4.4	1.76%	3.9
5345	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	6.6	5.5	1.1	4.4	1.77%	3.8
5347	AT2G27450.2 | Symbol: NLP1 | carbon-nitrogen hydrolase family protein, low similarity to beta-alanine synthase (Drosophila melanogaster) GI: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	10.6	8.7	1.9	4.4	1.77%	3.7

Rank	Description	Sync	Root	M	t	adj.q	B
5349	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	6.0	4.3	1.8	4.4	1.77%	3.9
5354	AT1G42480.1 | expressed protein | chr1:15938670-15941301 FORWARD | Aliases: T8D8.4, T8D8_4	6.1	5.2	0.8	4.4	1.77%	3.6
5355	AT5G51220.1 | ubiquinol-cytochrome C chaperone family protein, contains Pfam PF03981: Ubiquinol-cytochrome C chaperone	7.9	6.6	1.3	4.4	1.78%	3.8
5356	AT2G47720.1 | expressed protein | chr2:19563694-19564209 FORWARD | Aliases: F17A22.11	4.4	3.4	1.0	4.4	1.78%	3.8
5358	AT1G26460.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:9151719-9154727 FORWARD | Aliases: T1K7.17, T1K7_17	7.5	4.8	2.7	4.4	1.78%	3.9
5360	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 (Arabidopsis thaliana) | chr2:13389030-13390834 FORWARD | Aliases: STO HOMOLOG, T28P16.13, T28P16_13	3.9	2.7	1.2	4.4	1.78%	3.8
5365	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	5.0	4.4	0.6	4.4	1.79%	3.6
5366	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	5.5	4.7	0.8	4.4	1.79%	3.7
5367	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	3.6	2.9	0.7	4.4	1.79%	3.7
5368	AT5G64640.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:25853953-25856279 FORWARD | Aliases: MUB3.16, MUB3_16	4.6	3.7	0.9	4.4	1.79%	3.8
5370	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	5.5	0.9	4.4	1.79%	3.6
5376	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	4.8	1.2	4.4	1.79%	3.9
5377	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	3.4	2.7	0.7	4.4	1.79%	3.7
5379	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	2.5	2.1	0.4	4.4	1.79%	3.0
5381	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	5.9	4.8	1.1	4.4	1.80%	3.8
5382	AT4G18750.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr4:10304861-10307476 FORWARD | Aliases: F28A21.160, F28A21_160	3.1	2.6	0.5	4.4	1.80%	3.3
5383	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	7.6	6.2	1.4	4.4	1.80%	3.8
5384	AT5G27110.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr5:9538575-9540650 REVERSE | Aliases: T21B4.20, T21B4_20	5.5	4.4	1.0	4.4	1.80%	3.8
5386	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	5.0	1.0	4.4	1.80%	3.8

Rank	Description	Sync	Root	M	t	adj.q	B
5387	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	5.2	3.6	1.5	4.4	1.80%	3.8
5388	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	7.7	5.5	2.2	4.4	1.80%	3.9
5391	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	5.3	1.6	4.3	1.81%	3.8
5395	AT3G10090.1 | 40S ribosomal protein S28 (RPS28A), similar to ribosomal protein S28 GB:P34789 (Arabidopsis thaliana) | chr3:3108815-3110022 REVERSE | Aliases: T22K18.8	10.8	8.7	2.1	4.3	1.81%	3.5
5396	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	5.5	4.1	1.4	4.3	1.81%	3.8
5406	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	7.9	6.8	1.1	4.3	1.81%	3.7
5409	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	5.2	3.6	1.6	4.3	1.82%	3.9
5415	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	8.4	6.9	1.5	4.3	1.83%	3.8
5416	AT4G04180.1 | AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family | chr4:2020434-2023990 FORWARD | Aliases: T27D20.13, T27D20_13	4.7	3.7	1.0	4.3	1.83%	3.8
5417	AT5G64940.2 | Symbol: ATATH13 | ABC1 family protein, contains Pfam domain, PF03109: ABC1 family | chr5:25966199-25971048 FORWARD | Aliases: MXK3.17, MXK3_17	5.5	3.3	2.2	4.3	1.83%	3.8
5418	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	5.5	3.9	1.7	4.3	1.83%	3.8
5419	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	9.0	7.4	1.6	4.3	1.83%	3.8
5420	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	4.1	3.4	0.7	4.3	1.83%	3.7
5422	AT2G35790.1 | expressed protein | chr2:15047758-15049201 FORWARD | Aliases: T20F21.20	6.9	5.3	1.6	4.3	1.83%	3.8
5423	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	4.9	3.7	1.2	4.3	1.83%	3.8
5425	AT3G26740.1 | light responsive protein-related, similar to light regulated protein precursor SP:Q03200 (Oryza sativa) (Plant Mol. Biol. 22 (1), 165-170 (1993)), ccr protein GB:S52663 (Citrus X paradisi) (Plant Mol. Biol. 26 (1), 165-173 (1994)) | chr3:9829039-9829917 FORWARD | Aliases: MLJ15.9	3.4	2.4	1.0	4.3	1.83%	3.7
5428	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	5.4	3.7	1.7	4.3	1.84%	3.8
5429	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	4.8	3.6	1.3	4.3	1.84%	3.8
5430	AT1G04190.1 | tetratricopeptide repeat (TPR)-containing protein, low similarity to protein antigen LmSTI1 (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	8.0	6.4	1.6	4.3	1.84%	3.8

Rank	Description	Sync	Root	M	t	adj.q	B
5431	AT1G22570.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr1:7976609-7978562 REVERSE | Aliases: F12K8.8, F12K8_8	6.2	5.0	1.2	4.3	1.84%	3.8
5432	AT2G33220.1 | expressed protein | chr2:14085948-14087213 FORWARD | Aliases: F25I18.4, F25I18_4	10.1	9.0	1.2	4.3	1.84%	3.7
5434	AT4G32340.1 | expressed protein | chr4:15612597-15614259 REVERSE | Aliases: F8B4.40	6.8	5.4	1.4	4.3	1.84%	3.8
5436	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	10.4	9.3	1.1	4.3	1.84%	3.7
5438	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	4.7	3.7	1.0	4.3	1.85%	3.8
5440	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	6.2	4.4	1.8	4.3	1.85%	3.8
5442	AT4G15660.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	3.1	2.7	0.4	4.3	1.85%	3.2
5443	AT5G52380.1 | zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle | chr5:21278579-21280364 REVERSE | Aliases: K24M7.12, K24M7_12	6.0	4.8	1.2	4.3	1.85%	3.7
5445	AT5G64160.1 | expressed protein | chr5:25688156-25689689 FORWARD | Aliases: MHJ24.14, MHJ24_14	7.4	5.7	1.6	4.3	1.85%	3.8
5446	AT5G42670.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr5:17125490-17127463 FORWARD | Aliases: MJB21.4, MJB21_4	6.3	4.9	1.4	4.3	1.85%	3.8
5448	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	7.4	6.0	1.4	4.3	1.86%	3.8
5450	AT1G30530.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr1:10814641-10816565 FORWARD | Aliases: F26G16.15, F26G16_15	5.6	4.0	1.6	4.3	1.86%	3.8
5451	AT2G46100.1 | expressed protein | chr2:18960353-18962069 FORWARD | Aliases: T3F17.25	9.2	7.8	1.3	4.3	1.86%	3.8
5455	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	5.8	5.0	0.8	4.3	1.86%	3.6
5457	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	4.9	3.7	1.3	4.3	1.86%	3.8
5458	AT2G04230.1 | F-box family protein, contains F-box domain Pfam:PF00646	4.2	3.2	1.0	4.3	1.86%	3.7
5460	AT5G65250.1 | expressed protein | chr5:26095759-26097424 REVERSE | Aliases: MQN23.20, MQN23_20	6.1	4.4	1.6	4.3	1.87%	3.8
5461	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	2.9	2.3	0.6	4.3	1.87%	3.5
5463	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	6.8	2.2	4.3	1.87%	3.8
5465	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	3.4	2.4	1.0	4.3	1.87%	3.6
5466	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	9.2	7.2	2.0	4.3	1.87%	3.8
5467	AT1G15480.1 | DNA-binding protein, putative, similar to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile PF01535: PPR repeat | chr1:5318208-5320589 FORWARD | Aliases: F9L1.43, F9L1_43	4.7	3.7	1.0	4.3	1.87%	3.8

Rank	Description	Sync	Root	M	t	adj.q	B
5469	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	6.5	5.0	1.5	4.3	1.87%	3.8
5470	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	8.8	1.5	4.3	1.88%	3.6
5471	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	6.7	4.8	1.9	4.3	1.88%	3.8
5472	AT2G42530.1 | cold-responsive protein / cold-regulated protein (cor15b), nearly identical to cold-regulated gene cor15b (Arabidopsis thaliana) GI:456016; contains Pfam profile PF02987: Late embryogenesis abundant protein | chr2:17716114-17717023 REVERSE | Aliases: F14N22.20, F14N22_20	5.8	4.0	1.8	4.3	1.88%	3.8
5473	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	9.6	7.3	2.3	4.3	1.88%	3.8
5475	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	6.2	4.8	1.5	4.3	1.88%	3.8
5477	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	9.8	7.9	1.9	4.3	1.88%	3.7
5482	AT5G43810.1 | Symbol: ZLL | pinhead protein (PINHEAD) / zwille 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	5.4	3.5	1.9	4.3	1.89%	3.8
5485	AT5G03370.1 | acylphosphatase family, contains Pfam PF00708: Acylphosphatase | chr5:825572-827033 REVERSE | Aliases: F12E4.110, F12E4_110	5.4	4.5	0.8	4.3	1.89%	3.7
5486	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}	4.3	3.3	1.0	4.3	1.90%	3.7
5488	AT1G49170.1 | expressed protein | chr1:18186934-18188102 REVERSE | Aliases: F27J15.6, F27J15_6	3.7	2.6	1.1	4.3	1.90%	3.6
5490	AT5G27710.1 | expressed protein | chr5:9812992-9815424 FORWARD | Aliases: T1G16.40, T1G16_40	5.1	4.0	1.1	4.3	1.90%	3.7
5491	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	7.0	5.7	1.4	4.3	1.90%	3.8
5492	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	3.5	2.6	0.9	4.3	1.90%	3.6
5494	AT5G64980.1 | expressed protein | chr5:25978001-25980461 REVERSE | Aliases: MXK3.21, MXK3_21	3.8	2.9	0.9	4.3	1.90%	3.8
5495	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	3.2	1.0	4.3	1.90%	3.6
5496	AT1G16490.1 | myb family transcription factor (MYB58), contains PFAM profile: myb DNA binding domain PF00249 | chr1:5629648-5630988 REVERSE | Aliases: F3O9.29, F3O9_29	4.1	3.0	1.0	4.3	1.91%	3.7
5497	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	11.2	10.0	1.2	4.3	1.91%	3.5
5498	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	6.6	5.7	0.9	4.3	1.91%	3.8
5500	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	4.0	3.0	1.0	4.3	1.91%	3.7
5502	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	6.3	5.3	1.0	4.3	1.91%	3.8

Rank	Description	Sync	Root	M	t	adj.q	B
5503	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	6.8	5.9	0.9	4.3	1.91%	3.7
5504	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	6.1	4.8	1.3	4.3	1.92%	3.8
5505	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	5.0	1.1	4.3	1.93%	3.7
5506	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	5.3	1.0	4.3	1.93%	3.7
5510	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	5.2	3.7	1.6	4.3	1.93%	3.6
5512	AT1G48450.2 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g17800.1); similar to unknown [Brassica napus] (GB:AAK30572.1); contains InterPro domain Protein of unknown function DUF760 (InterPro:IPR008479) | chr1:17912171-17914113 REVERSE | Aliases: T1N15.6, T1N15_6	9.3	8.3	1.0	4.3	1.93%	3.6
5514	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	4.7	3.7	0.9	4.3	1.93%	3.6
5518	AT4G26410.1 | expressed protein | chr4:13346757-13349025 FORWARD | Aliases: M3E9.160, M3E9_160	9.3	8.1	1.2	4.3	1.95%	3.6
5520	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	5.0	3.9	1.0	4.3	1.95%	3.7
5521	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	5.7	4.7	1.0	4.3	1.95%	3.7
5524	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	5.3	4.4	0.9	4.3	1.95%	3.6
5526	AT1G43860.1 | expressed protein | chr1:16624508-16626909 REVERSE | Aliases: F28H19.11, F28H19_11	7.6	6.6	0.9	4.3	1.96%	3.7
5527	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	6.6	4.9	1.7	4.3	1.96%	3.7
5528	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	4.2	3.1	1.1	4.3	1.96%	3.7
5529	AT1G14310.1 | haloacid dehalogenase-like hydrolase family protein, contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	7.8	6.9	1.0	4.3	1.96%	3.7
5531	AT1G42960.1 | expressed protein localized to the inner membrane of the chloroplast. | chr1:16128235-16129727 FORWARD | Aliases: F13A11.2, F13A11_2	10.2	9.1	1.1	4.3	1.96%	3.5
5532	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	10.6	8.3	2.3	4.3	1.96%	3.7
5536	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	3.4	2.3	1.1	4.3	1.96%	3.8
5538	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	6.9	5.7	1.2	4.3	1.97%	3.7

Rank	Description	Sync	Root	M	t	adj.q	B
5541	AT1G19140.2 | expressed protein | chr1:6610774-6612458 REVERSE | Aliases: F14D16.30, F14D16_30	8.1	6.5	1.7	4.3	1.97%	3.7
5543	AT4G39300.2 | expressed protein | chr4:18286787-18288332 FORWARD | Aliases: T22F8.210, T22F8_210	4.7	3.1	1.6	4.3	1.97%	3.7
5544	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	6.0	4.9	1.1	4.3	1.97%	3.7
5545	AT2G40240.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:16818104-16819306 FORWARD | Aliases: T7M7.22	3.7	3.1	0.6	4.3	1.98%	3.4
5548	AT2G06255.1 | expressed protein | chr2:2457570-2459808 FORWARD | Aliases: None	3.6	3.1	0.5	4.3	1.98%	3.4
5554	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	8.3	6.8	1.5	4.3	1.99%	3.7
5555	AT1G02816.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr1:621461-622469 FORWARD | Aliases: None	6.5	4.7	1.8	4.3	1.99%	3.7
5557	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	7.7	6.7	1.0	4.3	2.00%	3.7
5558	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	2.8	2.3	0.5	4.3	2.00%	3.3
5559	AT4G30930.1 | Symbol: WRKY32 |	7.2	5.4	1.9	4.3	2.00%	3.7
5563	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	6.0	5.3	0.7	4.3	2.00%	3.6
5564	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	5.8	4.0	1.7	4.3	2.00%	3.6
5565	AT2G36970.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:15536085-15537828 FORWARD | Aliases: T1J8.15, T1J8_15	6.1	4.5	1.6	4.2	2.01%	3.7
5566	AT4G04020.1 | plastid-lipid associated protein PAP, putative / fibrillin, putative, strong similarity to plastid-lipid associated proteins PAP1 GI:14248554, PAP2 GI:14248556 from (Brassica rapa), fibrillin (Brassica napus) GI:4139097; contains Pfam profile PF04755: PAP_fibrillin | chr4:1932149-1933948 FORWARD | Aliases: T24H24.16, T24H24_16	8.0	4.0	4.0	4.2	2.01%	3.1
5567	AT4G22240.1 | plastid-lipid associated protein PAP, putative, similar to plastid-lipid associated proteins PAP2 (Brassica rapa) GI:14248550 GI:14248556; contains Pfam profile PF04755: PAP_fibrillin | chr4:11765815-11767316 REVERSE | Aliases: T10I14.70, T10I14_70	8.0	4.0	4.0	4.2	2.01%	3.1
5569	AT2G32580.1 | expressed protein | chr2:13834740-13836386 FORWARD | Aliases: T26B15.14, T26B15_14	8.6	6.1	2.6	4.2	2.01%	3.7
5570	AT3G51750.2 | expressed protein | chr3:19207482-19208313 REVERSE | Aliases: T18N14.130	4.4	2.9	1.5	4.2	2.01%	3.6
5571	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	4.2	3.0	1.2	4.2	2.01%	3.7
5573	AT1G60550.1 | naphthoate synthase, putative / dihydroxynaphthoic acid synthetase, putative / DHNA synthetase, putative, contains similarity to MENB from Escherichia coli (SP:P27290), Bacillus subtilis (SP:P23966); contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein | chr1:22309496-22311838 REVERSE | Aliases: F8A5.9, F8A5_9	6.1	4.1	2.0	4.2	2.01%	3.7
5575	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	6.0	5.2	0.8	4.2	2.01%	3.5
5576	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	9.2	6.4	2.8	4.2	2.01%	3.7
5579	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	6.4	5.4	1.0	4.2	2.01%	3.7

Rank	Description	Sync	Root	M	t	adj.q	B
5581	AT5G65390.1 | Symbol: AGP7 | arabinogalactan-protein (AGP7) | chr5:26145810-26146564 REVERSE | Aliases: MNA5.12, MNA5_12	6.9	5.7	1.2	4.2	2.01%	3.7
5586	AT2G25790.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:11007677-11011313 FORWARD | Aliases: F17H15.18, F17H15_18	7.6	6.4	1.3	4.2	2.01%	3.6
5588	AT2G01140.1 | fructose-bisphosphate aldolase, putative, similar to plastidic aldolase NPALDP1 from Nicotiana paniculata (GI:4827251); contains Pfam profile PF00274 Fructose-bisphosphate aldolase class-I | chr2:94810-96634 REVERSE | Aliases: F10A8.2, F10A8_2	11.3	9.8	1.5	4.2	2.02%	3.2
5593	AT5G51040.2 | expressed protein, contains InterPro domain Protein of unknown function DUF339 (InterPro:IPR005631) | chr5:20767886-20769250 FORWARD | Aliases: K3K7.22, K3K7_22	10.1	9.1	1.0	4.2	2.02%	3.5
5596	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	11.4	10.8	0.7	4.2	2.03%	3.1
5597	AT5G43750.1 | expressed protein | chr5:17597193-17598449 REVERSE | Aliases: MQD19.9, MQD19_9	4.5	2.9	1.6	4.2	2.03%	3.7
5598	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	12.6	12.1	0.5	4.2	2.03%	3.2
5599	AT3G60360.1 | expressed protein | chr3:22323285-22325375 REVERSE | Aliases: T8B10.20	6.4	4.7	1.7	4.2	2.03%	3.7
5601	AT5G21150.1 | PAZ domain-containing protein / piwi domain-containing protein, similar to SP:O04379 Argonaute protein (AGO1) {Arabidopsis thaliana}; contains Pfam profile: PF02170 PAZ (Piwi Argonaut and Zwille), PF02171 Piwi domain | chr5:7192242-7198327 FORWARD | Aliases: T10F18.180, T10F18_180	2.6	2.1	0.4	4.2	2.04%	3.1
5602	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)	8.1	6.5	1.6	4.2	2.04%	3.7
5604	AT3G62450.1 | expressed protein | chr3:23109120-23109606 FORWARD | Aliases: T12C14.150	9.1	8.3	0.8	4.2	2.04%	3.5
5605	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	5.2	4.5	0.7	4.2	2.04%	3.5
5606	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	7.2	5.3	1.9	4.2	2.04%	3.6
5607	AT2G18910.1 | hydroxyproline-rich glycoprotein family protein | chr2:8199790-8201420 REVERSE | Aliases: F19F24.21	6.4	5.0	1.4	4.2	2.04%	3.7
5608	AT1G14490.1 | DNA-binding protein-related, contains similarity to DNA-binding proteins	4.2	3.4	0.8	4.2	2.04%	3.6
5609	AT5G40770.1 | Symbol: ATPHB3 |	9.2	7.4	1.8	4.2	2.04%	3.7
5610	AT5G09990.1 | expressed protein | chr5:3124569-3125073 FORWARD | Aliases: MYH9.1	3.3	2.4	0.9	4.2	2.04%	3.3
5612	AT2G25830.1 | YebC-related, contains Pfam profile PF01709: Domain of unknown function; contains TIGRFAM TIGR01033: conserved hypothetical protein; similar to YebC (GI:5771432) (Legionella pneumophila) | chr2:11025846-11028768 REVERSE | Aliases: F17H15.14, F17H15_14	6.5	4.5	2.1	4.2	2.04%	3.7
5614	AT1G14710.2 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr1:5061861-5065097 REVERSE | Aliases: F10B6.11, F10B6_11	6.1	4.7	1.4	4.2	2.05%	3.6
5619	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	8.3	7.2	1.1	4.2	2.06%	3.6
5623	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	4.2	0.9	4.2	2.06%	3.6
5625	AT4G27720.1 | expressed protein, contains Pfam PF05631: Protein of unknown function (DUF791) | chr4:13831126-13833820 FORWARD | Aliases: T29A15.210, T29A15_210	6.2	4.4	1.8	4.2	2.06%	3.7
5626	AT2G39450.1 | cation efflux family protein, contains cation efflux family protein domain, Pfam:PF01545	7.5	5.7	1.9	4.2	2.06%	3.7

Rank	Description	Sync	Root	M	t	adj.q	B
5627	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	5.9	4.1	1.8	4.2	2.06%	3.7
5628	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	9.2	1.2	4.2	2.07%	3.5
5629	AT4G13140.1 | expressed protein | chr4:7650322-7651141 REVERSE | Aliases: F17N18.30, F17N18_30	8.3	7.0	1.3	4.2	2.07%	3.7
5631	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	8.5	7.3	1.2	4.2	2.07%	3.7
5633	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	7.3	6.2	1.1	4.2	2.07%	3.6
5636	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 GLUTAMYLCYSTEINE SYNTHETASE, GSH1, ROOT MERISTEMLESS 1	11.1	8.4	2.7	4.2	2.07%	3.7
5637	AT1G25420.3 | expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292 | chr1:8916086-8918175 FORWARD | Aliases: F2J7.16, F2J7_16	7.9	6.7	1.2	4.2	2.07%	3.6
5638	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	6.0	3.8	2.2	4.2	2.07%	3.7
5639	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	3.8	2.2	1.6	4.2	2.08%	3.6
5640	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	3.7	0.8	4.2	2.08%	3.6
5641	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	5.9	5.3	0.6	4.2	2.08%	3.4
5642	AT4G31830.1 | expressed protein | chr4:15400610-15401138 REVERSE | Aliases: F11C18.30, F11C18_30	2.9	2.5	0.4	4.2	2.08%	3.1
5645	AT4G30480.3 | expressed protein | chr4:14897352-14899127 FORWARD | Aliases: F17I23.180, F17I23_180	9.1	7.3	1.9	4.2	2.08%	3.5
5646	AT1G23790.1 | expressed protein | chr1:8409952-8412030 FORWARD | Aliases: F5O8.34, F5O8_34	3.6	2.8	0.8	4.2	2.08%	3.5
5649	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	5.5	4.4	1.1	4.2	2.09%	3.6
5650	AT5G01470.1 | expressed protein | chr5:190927-192610 FORWARD | Aliases: T10O8.180, T10O8_180	5.1	4.0	1.1	4.2	2.09%	3.7
5654	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	3.5	2.9	0.6	4.2	2.10%	3.4
5655	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	2.7	2.2	0.5	4.2	2.10%	3.0
5657	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	5.9	5.0	0.9	4.2	2.10%	3.6
5658	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	6.0	4.9	1.1	4.2	2.10%	3.6

Rank	Description	Sync	Root	M	t	adj.q	B
5659	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:At1g62590.1); 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	4.5	3.7	0.8	4.2	2.10%	3.5
5660	AT4G17960.1 | expressed protein | chr4:9970859-9972468 FORWARD | Aliases: T6K21.140, T6K21_140	5.9	4.3	1.6	4.2	2.10%	3.6
5663	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	12.1	10.3	1.9	4.2	2.11%	3.6
5665	AT3G60660.1 | expressed protein | chr3:22432385-22434452 FORWARD | Aliases: T4C21.70	3.1	2.4	0.7	4.2	2.11%	3.4
5666	AT2G23390.1 | expressed protein | chr2:9967452-9970699 REVERSE | Aliases: F26B6.4, F26B6_4	6.2	5.1	1.1	4.2	2.11%	3.6
5667	AT3G27520.1 | expressed protein | chr3:10193659-10194736 FORWARD | Aliases: MMJ24.7	3.1	2.6	0.5	4.2	2.11%	3.3
5668	AT3G22880.1 | Symbol: ATDMC1 |	8.4	6.3	2.0	4.2	2.11%	3.6
5670	AT3G27930.1 | expressed protein | chr3:10370536-10373673 REVERSE | Aliases: K24A2.1	6.5	5.8	0.7	4.2	2.12%	3.5
5672	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	8.2	6.5	1.7	4.2	2.12%	3.5
5674	AT1G11940.1 | expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266 | chr1:4031578-4034076 REVERSE | Aliases: F12F1.19, F12F1_19	4.9	3.8	1.1	4.2	2.12%	3.6
5675	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	7.0	5.5	1.5	4.2	2.12%	3.5
5681	ATCG00080.1 | Symbol: PSBI | PSII I protein | chrC:7583-7693 FORWARD | Aliases: PSBI	10.1	7.3	2.8	4.2	2.13%	3.4
5682	AT3G63090.1 | expressed protein | chr3:23324403-23325964 FORWARD | Aliases: T20O10.190	4.7	3.8	0.9	4.2	2.13%	3.6
5683	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	2.9	2.4	0.5	4.2	2.13%	3.2
5685	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	5.2	4.0	1.2	4.2	2.13%	3.7
5687	AT1G44890.1 | expressed protein | chr1:16965584-16967406 FORWARD | Aliases: T12C22.18, T12C22_18	7.0	5.7	1.3	4.2	2.13%	3.6
5689	AT1G19010.2 | expressed protein | chr1:6565774-6567515 FORWARD | Aliases: F14D16.16, F14D16_16	4.4	3.6	0.9	4.2	2.13%	3.6
5691	AT5G13970.1 | expressed protein | chr5:4506234-4507807 REVERSE | Aliases: MAC12.6, MAC12_6	7.6	6.4	1.2	4.2	2.14%	3.4
5692	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	6.9	4.9	2.0	4.2	2.14%	3.7
5693	AT3G26360.1 | ribosomal protein-related, similar to SP:Q9Z3S4 30S ribosomal protein S21 {Rhizobium meliloti} | chr3:9656519-9657610 REVERSE | Aliases: F20C19.8	7.4	6.3	1.1	4.2	2.14%	3.6
5695	AT2G25950.1 | expressed protein | chr2:11075729-11077738 FORWARD | Aliases: F17H15.2	9.4	7.3	2.0	4.2	2.14%	3.7
5696	AT3G22550.1 | senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana) | chr3:7991653-7993461 REVERSE | Aliases: F16J14.11	4.8	3.9	0.9	4.2	2.14%	3.6
5698	AT1G76170.1 | expressed protein, contains Pfam profile PF01171: PP-loop family | chr1:28589073-28591119 REVERSE | Aliases: T23E18.11, T23E18_11	4.1	3.4	0.7	4.2	2.14%	3.4

Rank	Description	Sync	Root	M	t	adj.q	B
5699	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	11.7	10.4	1.3	4.2	2.14%	3.1
5701	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	6.8	5.9	0.9	4.2	2.14%	3.5
5702	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	8.3	1.9	4.2	2.14%	3.5
5703	AT2G39080.1 | expressed protein | chr2:16316907-16319587 REVERSE | Aliases: T7F6.25, T7F6_25	6.4	5.9	0.6	4.2	2.14%	3.3
5705	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	9.3	6.8	2.5	4.2	2.15%	3.6
5706	AT5G45590.1 | expressed protein | chr5:18501734-18503505 REVERSE | Aliases: K2N11.6, K2N11_6	4.8	3.2	1.7	4.2	2.15%	3.6
5707	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	9.0	7.9	1.1	4.2	2.15%	3.6
5708	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	3.5	3.0	0.6	4.2	2.15%	3.1
5709	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	3.9	1.3	4.2	2.15%	3.6
5712	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	5.3	3.7	1.6	4.2	2.15%	3.6
5714	AT3G21780.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:7675058-7676353 REVERSE | Aliases: MSD21.11	3.6	2.5	1.1	4.2	2.16%	3.6
5715	AT1G05060.1 | expressed protein | chr1:1451057-1452871 REVERSE | Aliases: T7A14.7, T7A14_7	5.8	4.0	1.7	4.2	2.16%	3.7
5716	AT1G30880.1 | expressed protein, similar to ESTs gb:R30049 and gb:T46176 | chr1:10993215-10994100 REVERSE | Aliases: F17F8.25	8.7	6.9	1.8	4.2	2.16%	3.7
5717	AT2G34090.2 | expressed protein, similar to GP:1301832:gnl:PID:e239862:Z71287	3.8	3.0	0.8	4.2	2.16%	3.5
5723	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	10.0	6.1	3.9	4.2	2.16%	3.6
5725	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	5.1	3.6	1.4	4.2	2.16%	3.6
5727	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	8.2	6.9	1.3	4.2	2.16%	3.6
5732	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	7.3	6.1	1.2	4.2	2.16%	3.5
5734	AT1G61640.2 | ABC1 family protein, contains Pfam domain, PF03109: ABC1 family | chr1:22750066-22752849 REVERSE | Aliases: T25B24.1, T25B24_1	4.4	3.5	0.9	4.2	2.17%	3.5
5735	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	9.8	9.0	0.9	4.2	2.17%	3.3
5736	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	6.5	5.0	1.5	4.2	2.17%	3.6

Rank	Description	Sync	Root	M	t	adj.q	B
5737	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	6.6	5.0	1.6	4.2	2.17%	3.6
5738	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	5.7	4.7	1.0	4.2	2.17%	3.6
5739	AT1G28510.1 | expressed protein | chr1:10023875-10026281 FORWARD | Aliases: F3M18.5, F3M18_5	6.4	5.1	1.3	4.2	2.18%	3.5
5742	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	8.9	7.7	1.3	4.2	2.18%	3.6
5743	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	7.6	5.9	1.7	4.2	2.18%	3.6
5745	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	5.3	4.4	0.9	4.2	2.19%	3.4
5747	AT3G62310.1 | 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 | chr3:23068221-23071665 REVERSE | Aliases: T12C14.10	7.4	6.2	1.2	4.2	2.19%	3.5
5748	AT3G12260.1 | complex 1 family protein / LVR family protein, contains Pfam PF05347: Complex 1 protein (LYR family) | chr3:3908947-3910403 REVERSE | Aliases: F28J15.12	10.5	8.2	2.3	4.2	2.20%	3.5
5753	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) {Triticum aestivum}; contains Pfam profiles PF02854: MIF4G domain, PF02847: MA3 domain | chr2:10232305-10235718 REVERSE | Aliases: T29E15.25, T29E15_25	6.7	5.8	0.9	4.2	2.21%	3.4
5755	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	10.1	7.9	2.2	4.2	2.21%	3.6
5759	AT4G25550.1 | expressed protein | chr4:13048386-13051178 FORWARD | Aliases: M7J2.80, M7J2_80	7.3	5.4	1.9	4.2	2.21%	3.6
5760	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	5.3	3.9	1.4	4.2	2.21%	3.6
5761	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	3.5	2.8	0.7	4.2	2.21%	3.3
5762	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 annuum} | chr3:877951-880453 REVERSE | Aliases: O ACETYLSERINE (THIOL) LYASE, T12J13.9, T12J13_9	4.5	3.5	1.0	4.2	2.21%	3.5
5763	AT5G59980.1 | RNase P subunit p30 family protein, contains Pfam PF01876: RNase P subunit p30 | chr5:24164433-24166953 FORWARD | Aliases: MMN10.23, MMN10_23	3.3	2.6	0.7	4.2	2.21%	3.5
5764	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	3.3	1.1	4.2	2.22%	3.6
5765	AT3G61770.1 | expressed protein, contains Pfam domain, PF02681: Uncharacterized BCR, COG1963 | chr3:22875518-22877380 FORWARD | Aliases: F21F14.5	5.0	4.0	1.1	4.2	2.22%	3.6
5766	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	9.7	8.6	1.1	4.2	2.22%	3.3

Rank	Description	Sync	Root	M	t	adj.q	B
5769	AT5G04910.1 | expressed protein, ; expression supported by MPSS | chr5:1437696-1438771 FORWARD | Aliases: MUG13.24, MUG13_24	8.9	7.9	1.0	4.2	2.22%	3.3
5770	AT3G06530.1 | BAP28-related, similar to Protein BAP28 (Swiss-Prot:Q9H583) (Homo sapiens) | chr3:2022602-2033643 FORWARD | Aliases: F5E6.14, F5E6_14	4.4	3.7	0.7	4.2	2.22%	3.4
5772	AT3G04890.1 | expressed protein | chr3:1347652-1349205 FORWARD | Aliases: T9J14.16, T9J14_16	6.7	5.9	0.8	4.1	2.22%	3.5
5776	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	6.3	0.8	4.1	2.23%	3.4
5784	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	9.2	7.0	2.2	4.1	2.25%	3.5
5785	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	7.3	6.4	0.8	4.1	2.25%	3.5
5786	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	4.6	3.5	1.1	4.1	2.25%	3.5
5788	AT4G31120.2 | Skb1 methyltransferase family protein, contains Pfam profile: PF05185 Skb1 methyltransferase | chr4:15132125-15136624 REVERSE | Aliases: F6E21.40, F6E21_40	7.2	6.4	0.9	4.1	2.25%	3.4
5789	AT3G19240.1 | expressed protein | chr3:6664256-6666564 FORWARD | Aliases: MVI11.21	9.6	8.3	1.3	4.1	2.25%	3.6
5790	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	10.3	9.0	1.3	4.1	2.25%	3.6
5791	AT5G47455.6 | expressed protein | chr5:19267950-19269591 FORWARD | Aliases: None	4.5	3.3	1.1	4.1	2.26%	3.5
5792	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	4.8	1.4	4.1	2.26%	3.5
5795	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	5.8	4.4	1.3	4.1	2.26%	3.5
5798	AT3G12860.1 | nucleolar protein Nop56, putative, similar to XNop56 protein (Xenopus laevis) GI:14799394; contains Pfam profile PF01798: Putative snoRNA binding domain	6.4	5.1	1.3	4.1	2.27%	3.5
5799	AT1G26330.1 | expressed protein | chr1:9107612-9113507 FORWARD | Aliases: F28B23.2, F28B23_2	4.1	2.9	1.3	4.1	2.27%	3.6
5800	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	4.0	3.2	0.8	4.1	2.27%	3.5
5801	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	3.3	2.6	0.7	4.1	2.27%	3.4
5802	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	6.1	5.0	1.1	4.1	2.28%	3.6
5803	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	3.2	2.4	0.9	4.1	2.28%	3.2

Rank	Description	Sync	Root	M	t	adj.q	B
5805	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	3.9	3.2	0.7	4.1	2.28%	3.4
5807	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	3.1	2.5	0.6	4.1	2.29%	3.3
5809	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	6.7	4.9	1.8	4.1	2.30%	3.5
5811	AT4G01080.1 | expressed protein | chr4:466391-468293 REVERSE | Aliases: F2N1.14, F2N1_14	3.8	2.9	0.9	4.1	2.30%	3.5
5812	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	9.9	8.7	1.1	4.1	2.30%	3.4
5814	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	8.6	7.0	1.5	4.1	2.30%	3.5
5819	AT2G44640.1 | expressed protein | chr2:18424319-18426472 FORWARD | Aliases: F16B22.13	7.6	5.3	2.3	4.1	2.31%	3.6
5820	AT5G11310.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:3606403-3608608 FORWARD | Aliases: F2I11.200, F2I11_200	3.4	2.8	0.6	4.1	2.31%	3.1
5821	AT2G22370.1 | expressed protein | chr2:9507895-9509269 REVERSE | Aliases: F14M13.23, F14M13_23	6.8	5.7	1.2	4.1	2.31%	3.4
5822	AT5G16780.1 | SART-1 family protein, contains Pfam domain, PF03343: SART-1 family | chr5:5517528-5522261 REVERSE | Aliases: F5E19.120, F5E19_120	8.2	6.2	2.0	4.1	2.31%	3.6
5824	AT3G22790.1 | kinase interacting family protein, similar to kinase interacting protein 1 (GI:13936326) (Petunia integrifolia) | chr3:8052453-8057895 REVERSE | Aliases: MWI23.16	4.1	3.4	0.7	4.1	2.31%	3.4
5827	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 INITATION FACTOR 4E, F15J5.10, F15J5_10, LSP1	10.3	8.1	2.2	4.1	2.32%	3.5
5828	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	4.6	3.6	0.9	4.1	2.32%	3.5
5829	AT1G19960.1 | expressed protein | chr1:6928074-6928268 FORWARD | Aliases: T20H2.25, T20H2_25	6.7	4.6	2.1	4.1	2.32%	3.6
5830	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	4.3	3.5	0.8	4.1	2.32%	3.2
5831	AT3G13440.1 | expressed protein | chr3:4377104-4379582 FORWARD | Aliases: MRP15.19	7.3	6.2	1.1	4.1	2.32%	3.5
5833	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	9.0	7.7	1.3	4.1	2.32%	3.4
5835	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	6.3	5.5	0.8	4.1	2.33%	3.3
5837	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	10.4	8.9	1.5	4.1	2.33%	3.4
5841	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	3.4	0.6	4.1	2.34%	3.2

Rank	Description	Sync	Root	M	t	adj.q	B
5842	AT1G18800.1 | nucleosome assembly protein (NAP) family protein, similar to SP:Q01105:SET protein (HLA-DR associated protein II) (PHAPII) (Phosphatase 2A inhibitor I2PP2A) {Homo sapiens}; contains Pfam profile PF00956: Nucleosome assembly protein (NAP) | chr1:6481104-6483587 REVERSE | Aliases: F6A14.10, F6A14_10	3.6	2.5	1.1	4.1	2.34%	3.3
5843	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	9.0	7.6	1.5	4.1	2.34%	3.5
5844	AT3G21140.1 | expressed protein | chr3:7409463-7412231 REVERSE | Aliases: MSA6.18	6.3	5.1	1.2	4.1	2.35%	3.5
5846	AT2G03680.1 | Symbol: SPR1 | expressed protein, Alternative splicing exists based on EST evidence | chr2:1120797-1122004 FORWARD | Aliases: F19B11.13, F19B11_13, SKU6, SPIRAL1	11.8	10.7	1.1	4.1	2.35%	2.9
5847	AT3G56730.1 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537 | chr3:21025166-21026053 FORWARD | Aliases: T8M16.60	8.0	6.7	1.2	4.1	2.35%	3.4
5848	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	4.5	4.0	0.5	4.1	2.35%	2.9
5849	AT4G33865.1 | 40S ribosomal protein S29 (RPS29C) | chr4:16233214-16234201 REVERSE | Aliases: None	12.4	11.8	0.6	4.1	2.35%	3.0
5852	AT5G47520.1 | Ras-related GTP-binding protein, putative, similar to GTP-binding protein RAB11J GI:1370160 from (Lotus japonicus) | chr5:19294588-19295593 REVERSE | Aliases: MNJ7.11, MNJ7_11	7.2	6.2	1.1	4.1	2.36%	3.4
5855	AT1G68660.1 | expressed protein | chr1:25781514-25782824 REVERSE | Aliases: F24J5.10, F24J5_10	8.8	7.6	1.2	4.1	2.36%	3.5
5858	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	4.7	4.0	0.7	4.1	2.37%	3.3
5859	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	12.3	10.4	2.0	4.1	2.37%	3.4
5860	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	8.2	7.3	0.8	4.1	2.37%	3.2
5862	AT5G45600.1 | Symbol: GAS41 | YEATS family protein, contains Pfam domain PF03366: YEATS family | chr5:18505129-18507096 FORWARD | Aliases: K2N11.8, K2N11_8	7.9	6.4	1.5	4.1	2.37%	3.5
5865	AT2G30695.2 | expressed protein | chr2:13086184-13088427 REVERSE | Aliases: None	4.4	3.3	1.1	4.1	2.38%	3.5
5866	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	4.8	3.7	1.0	4.1	2.38%	3.5
5870	AT5G65490.1 | expressed protein, similar to unknown protein (dbj BAA75199.1) | chr5:26194728-26197542 REVERSE | Aliases: K19O4.5, K19O4_5	6.3	5.2	1.2	4.1	2.38%	3.5
5873	AT5G16010.1 | 3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein, similar to steroid 5alpha-reductase - Rattus norvegicus, PIR:A34239 (SP:24008); contains Pfam 3-oxo-5-alpha-steroid 4-dehydrogenase domain PF02544 | chr5:5227927-5229119 FORWARD | Aliases: F1N13.150, F1N13_150	8.6	6.6	2.0	4.1	2.39%	3.5
5875	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	5.2	4.4	0.8	4.1	2.39%	3.4
5876	AT1G05430.1 | expressed protein | chr1:1594056-1595817 REVERSE | Aliases: T25N20.8, T25N20_8	7.3	5.8	1.5	4.1	2.39%	3.5
5879	AT5G59830.2 | expressed protein | chr5:24122304-24124406 FORWARD | Aliases: MMN10.5, MMN10_5	8.0	7.3	0.7	4.1	2.40%	3.3
5880	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	4.8	3.4	1.4	4.1	2.40%	3.5

Rank	Description	Sync	Root	M	t	adj.q	B
5883	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	4.7	3.8	0.9	4.1	2.41%	3.4
5886	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	6.9	5.7	1.1	4.1	2.42%	3.5
5890	AT4G19230.2 | Symbol: CYP707A1 | cytochrome P450 family protein, cytochrome P450, Arabidopsis thaliana; supported by cDNA: gi_15293092_gb_AY050980.1_	5.5	4.2	1.3	4.1	2.42%	3.4
5891	AT1G10480.1 | Symbol: ZFP5 | zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type | chr1:3449692-3451227 FORWARD | Aliases: T10O24.9, T10O24_9, ZFP5, ZINC FINGER PROTEIN 5	5.1	4.3	0.9	4.1	2.42%	3.3
5893	AT1G14990.1 | expressed protein | chr1:5167147-5168238 REVERSE | Aliases: T15D22.3, T15D22_3	7.1	5.7	1.3	4.1	2.42%	3.4
5895	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	8.8	7.4	1.4	4.1	2.43%	3.5
5896	AT1G05590.1 | glycosyl hydrolase family 20 protein, similar to beta-hexosaminidase precursor SP:P43077 from (Candida albicans)	5.4	4.5	0.9	4.1	2.43%	3.4
5897	AT1G68560.1 | Symbol: XYL1 | alpha-xylosidase (XYL1), identical to alpha-xylosidase precursor GB:AAD05539 GI:4163997 from (Arabidopsis thaliana); contains Pfam profile PF01055: Glycosyl hydrolases family 31; identical to cDNA alpha-xylosidase precursor (XYL1) partial cds GI:4163996 | chr1:25737845-25741658 REVERSE | Aliases: F24J5.20, F24J5_20	3.9	2.5	1.4	4.1	2.43%	3.5
5899	AT5G10910.1 | mraW methylase family protein, contains Pfam profile PF01795: MraW methylase family | chr5:3439554-3441583 FORWARD | Aliases: T30N20.180, T30N20_180	5.6	4.3	1.4	4.1	2.43%	3.4
5902	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	5.8	4.5	1.3	4.1	2.43%	3.5
5904	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	7.7	6.5	1.2	4.1	2.43%	3.5
5905	AT5G16790.1 | expressed protein | chr5:5522499-5523914 REVERSE | Aliases: F5E19.130, F5E19_130	3.8	3.1	0.6	4.1	2.43%	3.3
5906	AT5G42070.1 | expressed protein, similar to unknown protein (dbj:BAA92898.1) | chr5:16836215-16837423 REVERSE | Aliases: MJC20.18, MJC20_18	4.9	3.4	1.4	4.1	2.44%	3.5
5908	AT4G17180.1 | glycosyl hydrolase family 17 protein, similar to 3-glucanase GI:18483232 from (Sorghum bicolor) | chr4:9646518-9648306 FORWARD | Aliases: DL4625W, FCAALL.368	4.6	3.7	0.9	4.1	2.44%	3.4
5909	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	5.2	4.1	1.1	4.1	2.44%	3.5
5910	AT1G74210.1 | glycerophosphoryl diester phosphodiesterase family protein, low similarity to glycerophosphodiester phosphodiesterase (Borrelia hermsii) GI:1399038; contains Pfam profile PF03009: Glycerophosphoryl diester phosphodiesterase family | chr1:27913979-27916602 FORWARD | Aliases: F1O17.12, F1O17_12	10.1	8.7	1.3	4.1	2.44%	3.4
5912	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	10.1	9.1	0.9	4.1	2.44%	3.4
5913	AT1G49840.1 | expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620) | chr1:18455738-18458026 FORWARD | Aliases: F10F5.2, F10F5_2	5.1	4.0	1.1	4.1	2.44%	3.5
5917	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	10.2	9.2	1.1	4.1	2.45%	3.3
5920	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	6.6	5.4	1.3	4.1	2.45%	3.5

Rank	Description	Sync	Root	M	t	adj.q	B
5922	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	4.3	3.1	1.2	4.1	2.45%	3.4
5923	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	9.8	8.4	1.4	4.1	2.45%	3.3
5924	AT2G15490.2 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:6768717-6770556 FORWARD | Aliases: F9O13.4	4.7	3.5	1.2	4.1	2.46%	3.4
5926	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	7.2	6.3	0.9	4.1	2.46%	3.2
5929	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	6.8	5.6	1.2	4.1	2.46%	3.4
5932	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	6.4	5.8	0.6	4.1	2.46%	3.0
5933	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	8.1	7.5	0.6	4.1	2.46%	3.3
5935	AT5G26940.4 | exonuclease family protein, contains exonuclease domain, Pfam:PF00929 | chr5:9480597-9482772 FORWARD | Aliases: F2P16.200, F2P16_200	7.3	6.0	1.3	4.1	2.46%	3.5
5937	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	5.7	4.5	1.2	4.1	2.46%	3.5
5938	AT2G11890.2 | expressed protein, contains InterPro domain Adenylate cyclase (InterPro:IPR008172) | chr2:4809865-4811457 FORWARD | Aliases: None	6.8	5.6	1.2	4.1	2.46%	3.5
5939	AT2G22425.1 | expressed protein, weak similarity to Swiss-Prot:Q9Y6A9 microsomal signal peptidase 12 kDa subunit (SPase 12 kDa subunit, SPC12, HSPC033) (Homo sapiens)	10.7	10.2	0.5	4.1	2.46%	2.8
5941	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	9.2	7.7	1.4	4.1	2.47%	3.4
5943	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	9.1	8.0	1.1	4.1	2.48%	3.3
5944	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:BAB32406.1); 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	3.9	3.2	0.7	4.1	2.48%	3.2
5945	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	6.8	6.0	0.7	4.1	2.48%	3.3
5946	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	4.8	3.4	1.3	4.1	2.48%	3.5
5947	AT1G51440.1 | lipase class 3 family protein, similar to DEFECTIVE IN ANTHER DEHISCENCE1 (Arabidopsis thaliana) GI:16215706, lipase (Dianthus caryophyllus) GI:4103627; contains Pfam profile PF01764: Lipase | chr1:19074585-19076362 FORWARD | Aliases: F5D21.19, F5D21_19	3.5	2.8	0.7	4.0	2.48%	3.3
5948	AT5G11980.1 | conserved oligomeric Golgi complex component-related / COG complex component-related, similar to SP:Q96MW5 Conserved oligomeric Golgi complex component 8 {Homo sapiens}; contains Pfam profile PF04124: Dor1-like family | chr5:3868653-3872270 REVERSE | Aliases: F14F18.150, F14F18_150	6.2	5.1	1.1	4.0	2.49%	3.4

Rank	Description	Sync	Root	M	t	adj.q	B
5952	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	6.7	5.5	1.2	4.0	2.49%	3.4
5953	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	4.9	4.1	0.7	4.0	2.49%	3.4
5955	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	4.9	4.0	0.9	4.0	2.49%	3.4
5957	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	3.6	2.7	0.9	4.0	2.50%	3.4
5959	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	6.4	1.1	4.0	2.50%	3.3
5960	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	5.9	4.9	1.0	4.0	2.50%	3.3
5961	AT3G02820.1 | zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle | chr3:611543-613390 FORWARD | Aliases: F13E7.24, F13E7_24	4.2	3.2	1.0	4.0	2.50%	3.3
5962	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	7.1	5.9	1.2	4.0	2.51%	3.4
5965	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	4.8	3.1	1.7	4.0	2.52%	3.4
5967	AT1G28390.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:9966614-9968272 REVERSE | Aliases: F3M18.17, F3M18_17	5.6	4.8	0.8	4.0	2.52%	3.4
5968	AT3G07150.1 | hypothetical protein | chr3:2263812-2264582 REVERSE | Aliases: T1B9.19	3.5	2.7	0.8	4.0	2.53%	3.3
5970	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	9.2	7.8	1.4	4.0	2.53%	3.4
5972	AT5G17210.2 | expressed protein | chr5:5656435-5658149 FORWARD | Aliases: MKP11.6, MKP11_6	7.2	5.4	1.8	4.0	2.53%	3.4
5976	AT1G24310.1 | expressed protein | chr1:8624050-8626394 FORWARD | Aliases: F3I6.25, F3I6_25	4.2	3.6	0.6	4.0	2.53%	3.2
5977	AT1G06500.2 | expressed protein | chr1:1989485-1990727 FORWARD | Aliases: F12K11.25, F12K11_25	7.4	6.1	1.3	4.0	2.53%	3.4
5981	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	5.2	4.4	0.9	4.0	2.54%	3.3
5982	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	4.6	3.5	1.1	4.0	2.54%	3.4
5984	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	11.0	9.2	1.8	4.0	2.54%	3.3
5985	AT1G23280.1 | MAK16 protein-related, contains similarity to MAK16 protein SP:P10962 from (Saccharomyces cerevisiae) | chr1:8260854-8262639 REVERSE | Aliases: F26F24.12, F26F24_12	5.7	3.7	2.0	4.0	2.54%	3.4
5986	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	6.9	5.4	1.5	4.0	2.54%	3.4
5987	AT5G12020.1 | 17.6 kDa	4.3	3.4	0.9	4.0	2.54%	3.4

Rank	Description	Sync	Root	M	t	adj.q	B
5988	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	4.7	4.0	0.7	4.0	2.55%	3.1
5990	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	4.1	2.5	1.6	4.0	2.55%	3.5
5991	AT1G10500.1 | Symbol: ATCPISCA | Involved in chloroplast Fe-S cluster	7.8	6.7	1.0	4.0	2.55%	3.4
5995	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	8.4	7.2	1.2	4.0	2.56%	3.2
5996	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	7.2	5.3	1.9	4.0	2.56%	3.4
5998	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	5.2	4.2	1.0	4.0	2.57%	3.3
6001	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	3.5	2.7	0.8	4.0	2.57%	3.2
6002	AT2G45100.1 | transcription factor IIB (TFIIB) family protein, contains Pfam domain, PF00382: Transcription factor TFIIB repeat | chr2:18602423-18605163 REVERSE | Aliases: T14P1.9	5.7	4.4	1.3	4.0	2.57%	3.4
6003	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	3.8	3.1	0.7	4.0	2.57%	3.1
6004	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	7.8	6.4	1.5	4.0	2.57%	3.3
6006	AT5G27830.2 | expressed protein | chr5:9861293-9862900 FORWARD | Aliases: T1G16.160, T1G16_160	7.9	6.1	1.8	4.0	2.57%	3.3
6007	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	3.1	2.5	0.7	4.0	2.57%	3.1
6008	AT1G26160.1 | metal-dependent phosphohydrolase HD domain-containing protein, contains Pfam profile PF01966: HD domain | chr1:9044428-9046966 REVERSE | Aliases: F28B23.16, F28B23_16	6.3	4.8	1.6	4.0	2.57%	3.4
6009	AT5G51200.1 | expressed protein | chr5:20822152-20836818 FORWARD | Aliases: MWD22.15, MWD22_15	6.3	5.0	1.3	4.0	2.57%	3.3
6010	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	6.1	2.9	4.0	2.57%	3.3
6011	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	5.4	4.5	0.8	4.0	2.57%	3.3
6012	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	6.5	4.8	1.7	4.0	2.58%	3.4
6014	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	4.4	3.3	1.1	4.0	2.58%	3.4
6017	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	6.7	5.4	1.3	4.0	2.59%	3.4
6018	AT1G03300.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr1:811033-813086 REVERSE | Aliases: F15K9.10, F15K9_10	4.0	3.4	0.7	4.0	2.59%	3.2

Rank	Description	Sync	Root	M	t	adj.q	B
6019	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	7.5	1.4	4.0	2.59%	3.4
6020	AT1G07970.1 | expressed protein | chr1:2469288-2472620 REVERSE | Aliases: T6D22.6, T6D22_6	5.2	4.4	0.8	4.0	2.59%	3.3
6023	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	3.6	1.4	4.0	2.59%	3.4
6026	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	5.1	3.3	1.9	4.0	2.60%	3.4
6029	AT3G58470.1 | expressed protein, several hypothetical proteins - Saccharomyces cerevisiae | chr3:21637648-21639546 REVERSE | Aliases: F14P22.60	6.2	4.3	1.9	4.0	2.60%	3.3
6030	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	3.1	1.2	4.0	2.61%	3.4
6031	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)	4.7	3.9	0.8	4.0	2.61%	3.2
6032	AT5G27620.1 | Symbol: CYCH;1 |	4.6	3.5	1.2	4.0	2.61%	3.3
6035	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	4.1	3.4	0.7	4.0	2.61%	3.3
6037	AT2G37330.1 | Symbol: ALS3 | expressed protein, and genefinder | chr2:15676217-15677744 FORWARD | Aliases: ALUMINUM SENSITIVE 3, F3G5.12, F3G5_12	6.7	5.4	1.3	4.0	2.62%	3.4
6041	AT5G20140.1 | SOUL heme-binding family protein, contains PFam profile PF04832: SOUL heme-binding protein | chr5:6798834-6800905 REVERSE | Aliases: F5O24.30, F5O24_30	5.1	4.4	0.7	4.0	2.62%	3.3
6042	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	7.8	6.0	1.8	4.0	2.63%	3.4
6043	AT3G15640.1 | cytochrome c oxidase family protein, contains Pfam domain, PF01215: Cytochrome c oxidase subunit Vb | chr3:5299117-5301752 FORWARD | Aliases: MSJ11.5	10.0	9.1	1.0	4.0	2.63%	3.2
6045	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	8.4	7.3	1.1	4.0	2.63%	3.2
6046	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	5.4	1.5	4.0	2.63%	3.3
6048	AT1G20770.1 | expressed protein | chr1:7215016-7216693 REVERSE | Aliases: F2D10.26, F2D10_26	7.5	5.5	2.0	4.0	2.64%	3.4
6051	AT1G69210.1 | expressed protein | chr1:26021765-26023721 REVERSE | Aliases: F4N2.17, F4N2_17	3.8	3.1	0.7	4.0	2.64%	3.1
6052	AT4G17310.2 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g47455.3) | chr4:9685190-9686940 REVERSE | Aliases: DL4690C, FCAALL.398	4.5	3.7	0.8	4.0	2.64%	3.2
6054	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	5.6	4.1	1.5	4.0	2.65%	3.4
6055	AT2G47840.1 | tic20 protein-related, similar to Tic20 (GI:3769673) (Pisum sativum) | chr2:19601257-19602071 REVERSE | Aliases: F17A22.23	7.8	7.2	0.7	4.0	2.65%	3.1
6059	AT5G02370.1 | kinesin motor protein-related, kinesin, Xenopus laevis, EMBL:XLA249840 | chr5:503406-506922 FORWARD | Aliases: T1E22.130, T1E22_130	4.7	3.7	1.0	4.0	2.65%	3.2
6063	AT4G39460.1 | mitochondrial substrate carrier family protein | chr4:18355987-18358887 REVERSE | Aliases: F23K16.90, F23K16_90	6.2	4.5	1.7	4.0	2.66%	3.4
6064	AT5G15070.1 | expressed protein | chr5:4876518-4885824 FORWARD | Aliases: F2G14.190, F2G14_190	4.4	3.5	0.9	4.0	2.66%	3.2

Rank	Description	Sync	Root	M	t	adj.q	B
6072	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: F17O7.16, F17O7_16, SPERMIDINE SYNTHASE 2	11.8	10.6	1.1	4.0	2.67%	3.0
6073	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	3.5	2.7	0.8	4.0	2.67%	3.2
6074	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	4.0	3.3	0.7	4.0	2.68%	3.1
6077	AT3G63490.2 | ribosomal protein L1 family protein, ribosomal protein L1, S.oleracea, EMBL:SORPL1 | chr3:23455190-23457820 FORWARD | Aliases: MAA21.120	5.9	4.8	1.1	4.0	2.68%	3.3
6078	AT5G09270.2 | expressed protein | chr5:2878885-2880817 FORWARD | Aliases: T2K12.7	6.8	5.9	0.8	4.0	2.68%	3.2
6082	AT3G22845.1 | emp24/gp25L/p24 protein-related, contains weak similarity to transmembrane protein (GI:1212965) (Homo sapiens) | chr3:8087314-8088754 FORWARD | Aliases: F5N5.1	8.9	7.7	1.2	4.0	2.69%	3.2
6083	AT5G02160.1 | expressed protein | chr5:426352-427252 FORWARD | Aliases: T7H20.210, T7H20_210	3.4	2.6	0.8	4.0	2.69%	3.2
6085	AT1G62690.1 | expressed protein | chr1:23214109-23215054 REVERSE | Aliases: F23N19.23, F23N19_23	4.0	3.1	0.8	4.0	2.69%	3.2
6086	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	6.1	5.0	1.0	4.0	2.69%	3.3
6087	AT5G56020.1 | expressed protein | chr5:22701715-22703595 FORWARD | Aliases: MDA7.6, MDA7_6	7.0	5.8	1.2	4.0	2.69%	3.3
6088	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	3.3	2.7	0.6	4.0	2.69%	3.1
6090	AT1G16460.3 | Symbol: ATRDH2 |	9.4	7.6	1.7	4.0	2.70%	3.2
6093	AT1G73240.1 | expressed protein | chr1:27545848-27548581 REVERSE | Aliases: T18K17.9, T18K17_9	3.9	2.9	1.1	4.0	2.70%	3.2
6096	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	3.6	2.7	0.9	4.0	2.71%	3.2
6098	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	10.0	6.9	3.1	4.0	2.71%	3.2
6099	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	10.0	6.9	3.1	4.0	2.71%	3.2
6101	AT1G66080.1 | expressed protein | chr1:24603881-24604820 REVERSE | Aliases: F15E12.12, F15E12_12	3.6	2.9	0.7	4.0	2.71%	3.2
6104	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	5.6	4.4	1.1	4.0	2.71%	3.4
6105	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	4.2	3.6	0.7	4.0	2.72%	3.2
6106	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	8.4	7.4	1.0	4.0	2.72%	3.3
6107	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	7.7	5.0	2.7	4.0	2.72%	3.4

Rank	Description	Sync	Root	M	t	adj.q	B
6112	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	3.9	2.4	1.5	4.0	2.73%	3.4
6113	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	3.9	3.2	0.7	4.0	2.73%	3.1
6115	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	2.5	2.2	4.0	2.73%	3.4
6117	AT3G56430.1 | expressed protein, unknown protein At2g40800 - Arabidopsis thaliana, EMBL:AC007660 | chr3:20934579-20936788 REVERSE | Aliases: T5P19.80	5.1	4.3	0.8	4.0	2.74%	3.2
6119	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	5.8	4.6	1.2	4.0	2.74%	3.4
6120	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	5.9	1.2	4.0	2.74%	3.3
6122	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	6.7	5.0	1.7	4.0	2.74%	3.4
6124	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	3.0	2.4	0.6	4.0	2.75%	3.0
6125	AT5G66540.1 | expressed protein, ; supported by full-Length cDNA gi:12057175 from (Arabidopsis thaliana) | chr5:26573576-26576653 REVERSE | Aliases: K1F13.21, K1F13_21	4.0	3.3	0.7	4.0	2.75%	3.1
6126	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	4.4	3.3	1.1	4.0	2.75%	3.3
6128	AT2G17300.1 | expressed protein | chr2:7529547-7530018 REVERSE | Aliases: F5J6.6, F5J6_6	3.9	3.3	0.6	4.0	2.75%	3.1
6129	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)	7.1	6.1	0.9	4.0	2.76%	3.1
6130	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	3.8	1.0	4.0	2.76%	3.2
6131	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	4.1	3.3	0.8	4.0	2.76%	3.2
6133	AT1G12180.1 | expressed protein | chr1:4130419-4131135 FORWARD | Aliases: T28K15.15, T28K15_15	4.5	3.0	1.5	4.0	2.76%	3.3
6134	AT5G64840.1 | Symbol: ATGCN5 |	8.2	6.4	1.7	4.0	2.76%	3.2
6135	AT3G13674.1 | expressed protein | chr3:4474784-4475888 REVERSE | Aliases: MMM17.23	3.3	2.4	0.9	4.0	2.76%	3.2
6136	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	6.8	5.6	1.3	4.0	2.77%	3.3
6139	AT1G13370.1 | histone H3, putative, strong similarity to Histone H3.2, minor Medicago sativa SP:P11105, histone H3 Rubus idaeus GI:10732809; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 | chr1:4587777-4588610 REVERSE | Aliases: T6J4.12, T6J4_12	4.0	2.4	1.6	3.9	2.77%	3.3
6141	AT5G20380.1 | transporter-related, low similarity to vesicular glutamate transporter 3 (Rattus norvegicus) GI:21685382	4.8	3.8	1.0	3.9	2.78%	3.2
6142	AT2G22900.1 | galactosyl transferase GMA12/MNN10 family protein, very low similarity to alpha-1,2-galactosyltransferase, Schizosaccharomyces pombe (SP:Q09174)	7.3	6.0	1.3	3.9	2.78%	3.1
6143	AT2G27290.1 | expressed protein | chr2:11685478-11686870 REVERSE | Aliases: F12K2.13, F12K2_13	5.1	4.2	0.8	3.9	2.78%	3.3

Rank	Description	Sync	Root	M	t	adj.q	B
6144	AT3G56040.1 | expressed protein | chr3:20803052-20808551 REVERSE | Aliases: F27K19.220	4.4	3.6	0.9	3.9	2.78%	3.2
6145	AT1G08640.1 | expressed protein | chr1:2748430-2751281 REVERSE | Aliases: F22O13.12, F22O13_12	6.5	5.2	1.4	3.9	2.78%	3.4
6148	AT2G43530.1 | Encodes a defensin-like (DEFL) family protein. | chr2:18077163-18077710 FORWARD | Aliases: T1O24.27	3.1	2.4	0.6	3.9	2.79%	3.1
6151	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	3.5	2.7	0.8	3.9	2.79%	3.2
6152	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	6.1	1.0	3.9	2.79%	3.0
6153	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	3.2	2.7	0.5	3.9	2.79%	2.9
6154	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	5.1	3.9	1.3	3.9	2.80%	3.3
6155	AT1G74870.1 | expressed protein, contains similarity to hypothetical proteins | chr1:28130754-28131936 FORWARD | Aliases: F25A4.16, F25A4_16	4.7	3.7	1.0	3.9	2.80%	3.3
6156	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	5.7	4.3	1.4	3.9	2.80%	3.3
6157	AT5G24600.1 | expressed protein, contains Pfam profile PF04654: Protein of unknown function, DUF599 | chr5:8421632-8423483 REVERSE | Aliases: K18P6.13, K18P6_13	4.8	3.8	1.0	3.9	2.80%	3.3
6159	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	4.8	3.2	1.6	3.9	2.80%	3.3
6161	AT5G20290.1 | 40S ribosomal protein S8 (RPS8A), ribosomal protein S8 - Zea mays, PIR:T04088 | chr5:6851483-6853065 REVERSE | Aliases: F5O24.180, F5O24_180	11.9	10.9	1.0	3.9	2.81%	3.1
6164	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	6.9	5.9	1.0	3.9	2.81%	3.2
6165	AT5G57345.1 | expressed protein | chr5:23246652-23247861 REVERSE | Aliases: None	4.6	3.9	0.8	3.9	2.81%	3.2
6166	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	7.3	6.0	1.2	3.9	2.82%	3.2
6169	AT4G03180.1 | expressed protein | chr4:1403201-1405570 FORWARD | Aliases: F4C21.10, F4C21_10	6.7	6.0	0.7	3.9	2.82%	3.1
6173	AT3G46940.1 | deoxyuridine 5'-triphosphate nucleotidohydrolase family, contains Pfam profile: PF00692 deoxyuridine 5'-triphosphate nucleotidohydrolase	6.6	5.3	1.3	3.9	2.82%	3.3
6176	AT5G18100.1 | Symbol: CSD3 | superoxide dismutase (Cu-Zn) / copper/zinc superoxide dismutase (CSD3), identical to copper/zinc superoxide dismutase GI:3273755	7.5	6.6	0.9	3.9	2.83%	3.1
6178	AT5G11070.1 | expressed protein | chr5:3516218-3516996 REVERSE | Aliases: T5K6.60, T5K6_60	7.1	5.7	1.4	3.9	2.83%	3.3
6180	AT5G06910.1 | Symbol: ATJ6 | DNAJ heat shock protein, putative (J6), identical to DnaJ homologue (Arabidopsis thaliana) GI:2689720; contains Pfam profile PF00226 DnaJ domain	7.5	5.8	1.7	3.9	2.83%	3.3
6181	AT1G80910.1 | expressed protein | chr1:30405628-30408934 FORWARD | Aliases: F23A5.27, F23A5_27	6.0	5.0	1.0	3.9	2.85%	3.2
6182	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	8.1	6.2	2.0	3.9	2.85%	3.2
6183	AT4G28190.1 | Symbol: ULT1 | expressed protein | chr4:13985476-13987267 FORWARD | Aliases: F26K10.70, F26K10_70, ULT, ULTRAPETALA, ULTRAPETALA1	7.3	6.0	1.3	3.9	2.85%	3.2

Rank	Description	Sync	Root	M	t	adj.q	B
6186	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	7.6	6.0	1.6	3.9	2.85%	3.3
6188	AT3G16250.1 | ferredoxin-related, contains Pfam profile: PF00111 2Fe-2S iron-sulfur cluster binding domains | chr3:5506268-5508420 REVERSE | Aliases: MYA6.6	2.8	2.2	0.6	3.9	2.86%	2.9
6190	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	4.3	3.3	0.9	3.9	2.86%	3.1
6191	AT5G66710.1 | protein kinase, putative, similar to protein kinase ATN1 GP:1054633 (Arabidopsis thaliana) | chr5:26653835-26655790 FORWARD | Aliases: MSN2.10, MSN2_10	4.0	3.2	0.8	3.9	2.86%	3.1
6193	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	11.3	9.3	2.0	3.9	2.86%	3.3
6194	AT5G47830.2 | expressed protein | chr5:19390124-19391557 REVERSE | Aliases: MCA23.17, MCA23_17	5.8	5.0	0.8	3.9	2.86%	3.2
6198	AT5G40650.1 | Symbol: SDH2 2 |	9.5	7.9	1.6	3.9	2.87%	3.1
6200	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	9.1	7.4	1.6	3.9	2.87%	3.2
6201	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	5.0	4.4	0.6	3.9	2.87%	3.0
6203	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	4.3	2.9	1.4	3.9	2.88%	3.2
6206	AT5G67070.1 | Symbol: RALFL34 | rapid alkalinization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316 | chr5:26785321-26786072 FORWARD | Aliases: K21H1.3, K21H1_3, RALF LIKE 34	4.8	3.7	1.1	3.9	2.89%	3.3
6207	AT5G13290.2 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:4252846-4254435 REVERSE | Aliases: T31B5.110, T31B5_110	5.9	5.0	0.8	3.9	2.89%	3.2
6209	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	5.6	4.3	1.3	3.9	2.89%	3.3
6210	AT1G77810.2 | galactosyltransferase family protein, contains Pfam profile PF01762: Galactosyltransferase | chr1:29265515-29267895 REVERSE | Aliases: T32E8.14	6.4	5.5	0.9	3.9	2.89%	3.2
6212	AT4G37510.1 | ribonuclease III family protein, contains Pfam profile PF00636 RNase3 domain | chr4:17626098-17628941 REVERSE | Aliases: F6G17.160, F6G17_160	5.5	4.2	1.2	3.9	2.89%	3.3
6213	AT4G16450.1 | expressed protein | chr4:9280104-9280740 FORWARD | Aliases: DL4250W, FCAALL.388	10.6	9.8	0.7	3.9	2.90%	2.9
6216	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	10.8	10.3	0.5	3.9	2.90%	2.8
6217	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	2.5	1.0	3.9	2.90%	3.2
6218	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	5.5	4.7	0.8	3.9	2.90%	3.1
6219	AT3G56870.1 | expressed protein | chr3:21063452-21066569 FORWARD | Aliases: T8M16.200	3.7	2.7	1.0	3.9	2.91%	3.3

Rank	Description	Sync	Root	M	t	adj.q	B
6220	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	4.9	4.2	0.7	3.9	2.91%	3.1
6222	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	6.4	5.6	0.8	3.9	2.91%	3.2
6224	AT2G24390.1 | similar to avirulence-responsive protein-related / avirulence induced gene (AIG) protein-related [Arabidopsis thaliana] (TAIR:At4g31310.1); similar to avrRpt2-induced protein 2-like [Oryza sativa (japonica cultivar-group)] (GB:XP_464100.1) | chr2:10380811-10382032 FORWARD | Aliases: T28I24.12, T28I24_12	3.6	3.0	0.6	3.9	2.91%	3.0
6225	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	4.6	1.0	3.9	2.91%	3.1
6226	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	6.9	6.0	0.8	3.9	2.91%	3.1
6232	AT5G60860.1 | Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303742 from (Pisum sativum)	5.0	3.8	1.2	3.9	2.92%	3.2
6233	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	5.3	4.3	1.0	3.9	2.93%	3.2
6235	AT3G58790.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8; general stress protein gspA, Bacillus subtilis, PIR:S16423 | chr3:21753048-21757301 REVERSE | Aliases: T20N10.140	4.7	3.9	0.9	3.9	2.93%	3.1
6236	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	3.0	2.3	0.7	3.9	2.93%	3.1
6237	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	4.7	3.9	0.8	3.9	2.93%	3.1
6238	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	5.2	4.1	1.2	3.9	2.93%	3.2
6241	AT4G31580.1 | Symbol: SRZ 22 |	7.4	6.2	1.2	3.9	2.93%	3.3
6243	AT1G10840.2 | Symbol: TIF3H1 |	8.7	7.5	1.2	3.9	2.93%	3.2
6245	AT5G42850.2 | expressed protein | chr5:17199108-17199807 REVERSE | Aliases: MBD2.4, MBD2_4	7.7	6.6	1.1	3.9	2.93%	3.0
6251	AT3G08640.1 | alphavirus core protein family, contains Pfam profile: PF00944 alphavirus core protein | chr3:2622886-2624314 FORWARD | Aliases: F17O14.11	8.3	6.1	2.2	3.9	2.95%	3.3
6252	AT3G08920.1 | rhodanese-like domain-containing protein, contains rhodanese-like domain PF:00581 | chr3:2712242-2713272 FORWARD | Aliases: T16O11.14	5.0	4.0	1.0	3.9	2.95%	3.2
6254	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	4.7	3.8	0.8	3.9	2.95%	3.2
6256	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	10.9	9.5	1.4	3.9	2.95%	3.1
6258	AT5G51720.1 | expressed protein | chr5:21026822-21027571 FORWARD | Aliases: MIO24.14, MIO24_14	6.1	4.1	2.0	3.9	2.96%	3.3

Rank	Description	Sync	Root	M	t	adj.q	B
6259	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	5.9	4.6	1.2	3.9	2.96%	3.3
6260	AT3G11400.1 | Symbol: EIF3G1 |	8.9	7.3	1.6	3.9	2.96%	3.2
6261	AT5G48090.1 | expressed protein, ; expression supported by MPSS | chr5:19502460-19505609 FORWARD | Aliases: MDN11.17, MDN11_17	3.0	2.5	0.4	3.9	2.96%	2.7
6262	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	4.6	3.8	0.7	3.9	2.96%	3.0
6263	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	3.5	2.2	1.3	3.9	2.96%	2.9
6264	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	10.2	9.2	1.1	3.9	2.96%	3.0
6265	AT3G52570.1 | expressed protein, contains Interpro entry IPR000379 | chr3:19512108-19513977 FORWARD | Aliases: F3C22.3	7.1	6.2	0.9	3.9	2.97%	3.0
6269	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	10.7	9.4	1.4	3.9	2.97%	2.9
6271	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)	2.8	2.4	0.5	3.9	2.97%	2.7
6272	AT4G34200.1 | D-3-phosphoglycerate dehydrogenase, putative / 3-PGDH, putative, similar to phosphoglycerate dehydrogenase, Arabidopsis thaliana, SP:O04130 | chr4:16373850-16376626 REVERSE | Aliases: F10M10.7	8.7	6.0	2.7	3.9	2.97%	3.3
6273	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	4.4	3.5	0.9	3.9	2.97%	3.2
6276	AT4G28450.1 | transducin family protein / WD-40 repeat family protein, SOF1 (involved in rRNA processing) protein-yeast | chr4:14061465-14064679 REVERSE | Aliases: F20O9.130, F20O9_130	5.6	4.6	1.0	3.9	2.97%	3.1
6278	AT3G62920.1 | expressed protein | chr3:23271692-23272268 FORWARD | Aliases: T20O10.20	4.9	4.1	0.7	3.9	2.98%	3.1
6280	AT1G31290.1 | PAZ domain-containing protein / piwi domain-containing protein, contains Pfam profiles PF02170: PAZ domain, PF02171: Piwi domain	4.5	3.2	1.3	3.9	2.98%	3.2
6282	AT2G35155.1 | expressed protein | chr2:14826073-14829044 REVERSE | Aliases: None	5.6	4.4	1.2	3.9	2.99%	3.2
6283	AT1G28100.3 | expressed protein | chr1:9801069-9804413 FORWARD | Aliases: F13K9.27, F13K9_27	8.3	7.2	1.1	3.9	2.99%	3.1
6284	AT3G62140.1 | similar to P0426D06.11 [Oryza sativa (japonica cultivar-group)] (GB:NP_908670.1)	8.3	7.1	1.3	3.9	2.99%	3.1
6287	AT1G19330.1 | expressed protein | chr1:6680558-6683498 REVERSE | Aliases: F18O14.5, F18O14_5	6.7	5.5	1.2	3.9	3.00%	3.3
6288	AT4G04190.2 | expressed protein | chr4:2024576-2026415 FORWARD | Aliases: T27D20.12, T27D20_12	5.0	4.0	1.0	3.9	3.00%	3.1
6291	AT5G50840.2 | expressed protein | chr5:20703046-20706144 FORWARD | Aliases: K7B16.6, K7B16_6	7.4	5.8	1.6	3.9	3.01%	3.1
6292	AT3G13910.1 | expressed protein | chr3:4590926-4591490 REVERSE | Aliases: MDC16.3	6.7	5.9	0.9	3.9	3.02%	3.2
6294	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	4.1	2.7	1.4	3.9	3.03%	3.3
6295	AT1G28530.2 | expressed protein | chr1:10031983-10035485 REVERSE | Aliases: F3M18.3	4.2	3.5	0.7	3.9	3.03%	3.1
6297	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	4.8	3.7	1.1	3.9	3.04%	3.2

Rank	Description	Sync	Root	M	t	adj.q	B
6298	AT1G63150.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:23423061-23425244 FORWARD | Aliases: F16M19.13, F16M19_13	3.1	2.6	0.4	3.9	3.04%	2.7
6299	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	5.0	4.1	1.0	3.9	3.04%	3.2
6300	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	5.5	4.5	1.0	3.9	3.04%	3.2
6301	AT1G29710.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:10387659-10389086 FORWARD | Aliases: T3M22.4, T3M22_4	3.3	2.9	0.4	3.9	3.04%	2.6
6302	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	6.8	1.0	3.9	3.04%	3.0
6303	AT4G24370.1 | expressed protein | chr4:12611038-12612141 REVERSE | Aliases: T22A6.200, T22A6_200	4.4	3.3	1.1	3.9	3.05%	3.1
6304	AT5G38150.1 | expressed protein | chr5:15240346-15242165 REVERSE | Aliases: MXA21.20, MXA21_20	4.5	3.3	1.2	3.9	3.05%	3.2
6306	AT5G65900.1 | DEAD/DEAH box helicase, putative, contains Pfam profiles	4.6	3.4	1.1	3.9	3.05%	3.1
6308	AT3G17120.2 | expressed protein | chr3:5841323-5843491 FORWARD | Aliases: K14A17.19	5.4	4.1	1.3	3.9	3.05%	3.3
6309	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	4.0	3.6	0.4	3.9	3.06%	2.5
6310	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	10.1	9.5	0.6	3.9	3.06%	3.0
6311	ATCG00750.1 | Symbol: RPS11 | 30S chloroplast ribosomal protein S11 | chrC:78960-79376 REVERSE | Aliases: RPS11	8.2	6.1	2.1	3.9	3.07%	3.2
6313	AT5G19140.2 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g43830.1); similar to hypothetical protein ARG10 - mung bean (GB:T07820)	7.0	5.3	1.7	3.9	3.09%	3.1
6315	AT5G41190.1 | expressed protein, ; expression supported by MPSS | chr5:16504856-16507240 REVERSE | Aliases: MEE6.26, MEE6_26	6.5	5.6	0.9	3.9	3.09%	3.1
6316	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	3.7	0.8	3.9	3.09%	3.1
6317	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	6.7	5.4	1.3	3.9	3.09%	3.1
6318	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	6.4	5.3	1.2	3.9	3.10%	3.2
6320	AT4G19540.1 | expressed protein | chr4:10657393-10659243 FORWARD | Aliases: F24J7.100, F24J7_100	6.0	5.2	0.8	3.9	3.10%	3.1
6321	AT3G21300.1 | RNA methyltransferase family protein, contains TIGRfam TIGR00479: RNA methyltransferase, TrmA family | chr3:7493445-7496295 REVERSE | Aliases: MXL8.18	3.0	2.5	0.5	3.9	3.10%	2.7
6322	AT5G63420.1 | Symbol: EMB2746 | metallo-beta-lactamase family protein	4.5	3.8	0.7	3.9	3.11%	3.0
6323	AT5G61040.1 | expressed protein | chr5:24579559-24582185 REVERSE | Aliases: MAF19.5, MAF19_5	4.8	4.2	0.6	3.9	3.11%	2.7
6325	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	8.3	6.9	1.4	3.8	3.11%	3.1

Rank	Description	Sync	Root	M	t	adj.q	B
6329	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	9.9	6.7	3.2	3.8	3.11%	3.2
6330	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	5.9	0.6	3.8	3.11%	2.8
6332	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	3.4	0.8	3.8	3.12%	3.1
6333	AT3G51500.1 | expressed protein, predicted protein, Oryza sativa, EMBL:AP000367 | chr3:19119113-19119866 FORWARD | Aliases: F26O13.140	4.3	3.4	0.9	3.8	3.12%	3.1
6335	AT1G64220.1 | preprotein translocase-related, similar to TOM7 protein (Solanum tuberosum) GI:3319774 | chr1:23836751-23836984 REVERSE | Aliases: F22C12.30, F22C12_30	2.9	2.5	0.4	3.8	3.13%	2.6
6336	AT3G55760.2 | expressed protein | chr3:20711414-20714035 FORWARD | Aliases: F1I16.170	6.7	5.0	1.7	3.8	3.13%	3.1
6337	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	9.2	7.1	2.1	3.8	3.13%	3.1
6340	AT4G33925.1 | expressed protein | chr4:16263242-16264229 FORWARD | Aliases: None	5.4	4.2	1.2	3.8	3.13%	3.2
6341	AT5G16620.2 | Symbol: PDE120 |	5.4	4.0	1.4	3.8	3.13%	3.2
6342	AT5G61300.1 | expressed protein | chr5:24668131-24670002 REVERSE | Aliases: MFB13.7, MFB13_7	5.1	4.3	0.8	3.8	3.14%	2.9
6344	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	5.9	4.9	1.1	3.8	3.14%	3.0
6346	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	5.3	4.6	0.6	3.8	3.15%	2.9
6348	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	5.3	4.4	0.9	3.8	3.15%	3.1
6349	AT3G24100.1 | four F5 family protein / 4F5 family protein, contains Pfam PF04419: 4F5 protein family | chr3:8703613-8704235 FORWARD | Aliases: MUJ8.7	7.9	7.0	0.9	3.8	3.15%	3.1
6350	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	8.0	1.1	3.8	3.15%	3.1
6351	AT4G14600.1 | expressed protein | chr4:8376396-8378331 FORWARD | Aliases: DL3340W, FCAALL.126	5.4	4.2	1.2	3.8	3.16%	3.1
6355	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	6.1	4.8	1.3	3.8	3.16%	3.2
6356	ATCG00720.1 | Symbol: PETB | Encodes the cytochrome b(6) subunit of the cytochrome b6f complex. | chrC:74841-76292 FORWARD | Aliases: PETB	8.5	6.7	1.8	3.8	3.16%	3.2
6358	AT2G38670.1 | ethanolamine-phosphate cytidylyltransferase, putative / phosphorylethanolamine transferase, putative / CTP:phosphoethanolamine cytidylyltransferase, putative, similar to SP:Q99447 Ethanolamine-phosphate cytidylyltransferase (EC 2.7.7.14) {Homo sapiens}; contains Pfam profile PF01467: Cytidylyltransferase | chr2:16175945-16178996 FORWARD | Aliases: T6A23.13, T6A23_13	7.6	6.0	1.6	3.8	3.16%	3.1
6361	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	4.7	4.0	0.8	3.8	3.16%	3.0
6364	AT2G40820.1 | proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965 | chr2:17041814-17046552 REVERSE | Aliases: T20B5.2, T20B5_2	4.7	4.0	0.8	3.8	3.17%	3.1

Rank	Description	Sync	Root	M	t	adj.q	B
6365	AT5G39900.1 | similar to GTP-binding protein LepA, putative [Arabidopsis thaliana] (TAIR:At5g08650.1); similar to hypothetical protein LOC231279 isoform a [Mus musculus] (GB:NP_766299.1); similar to PREDICTED: similar to Hypothetical protein FLJ13220 [Canis familiaris] (GB:XP_539246.1); similar to PREDICTED: similar to expressed sequence AA407526 isoform a [Rattus norvegicus] (GB:XP_223381.3); similar to unnamed protein product [Homo sapiens] (GB:BAB14507.1); similar to Hypothetical protein FLJ13220 [Homo sapiens] (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	3.6	3.1	0.5	3.8	3.17%	2.5
6366	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	8.9	6.4	2.6	3.8	3.17%	3.2
6367	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	8.0	5.9	2.1	3.8	3.17%	3.2
6370	AT5G63150.1 | expressed protein | chr5:25347426-25348070 FORWARD | Aliases: MDC12.12, MDC12_12	5.5	4.2	1.2	3.8	3.18%	3.1
6371	AT5G16930.1 | AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family | chr5:5568396-5571958 FORWARD | Aliases: F2K13.80, F2K13_80	3.1	2.5	0.5	3.8	3.18%	2.7
6372	AT2G34140.1 | Dof-type zinc finger domain-containing protein | chr2:14421120-14421805 REVERSE | Aliases: T14G11.26, T14G11_26	6.6	5.8	0.7	3.8	3.18%	3.0
6373	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	9.5	7.4	2.1	3.8	3.18%	3.1
6376	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	7.2	2.7	3.8	3.19%	3.2
6377	AT5G13100.1 | expressed protein | chr5:4156663-4158539 FORWARD | Aliases: T19L5.60, T19L5_60	5.8	4.8	1.0	3.8	3.19%	3.1
6380	AT5G01380.1 | expressed protein | chr5:155638-157521 REVERSE | Aliases: T10O8.90, T10O8_90	4.8	3.3	1.6	3.8	3.19%	3.2
6382	AT3G57180.1 | expressed protein | chr3:21174524-21177009 REVERSE | Aliases: F28O9.30	5.6	3.9	1.7	3.8	3.20%	3.2
6383	AT1G15960.1 | Symbol: NRAMP6 |	3.0	2.5	0.5	3.8	3.20%	2.5
6384	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	5.8	1.5	3.8	3.20%	3.2
6385	AT4G00860.1 | Symbol: ATOZI1 |	11.8	10.8	1.0	3.8	3.20%	2.6
6386	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	8.9	8.1	0.8	3.8	3.20%	2.9
6388	AT2G42690.1 | lipase, putative, similar to lipase (Dianthus caryophyllus) GI:4103627; contains Pfam profile PF01764: Lipase | chr2:17783318-17784794 REVERSE | Aliases: F14N22.2	6.5	4.9	1.6	3.8	3.20%	3.2
6389	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	6.5	1.9	3.8	3.21%	3.1
6390	AT3G26085.1 | CAAX amino terminal protease family protein, contains Pfam profile PF02517 CAAX amino terminal protease family protein | chr3:9532006-9533850 FORWARD | Aliases: None	5.6	4.9	0.7	3.8	3.21%	3.0
6393	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	3.7	0.8	3.8	3.21%	3.0
6394	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	8.4	7.6	0.8	3.8	3.22%	3.0
6396	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	11.6	10.0	1.5	3.8	3.23%	2.9
6398	AT4G26700.3 | Symbol: ATFIM1 |	6.4	5.2	1.3	3.8	3.23%	3.2

Rank	Description	Sync	Root	M	t	adj.q	B
6401	AT3G14750.1 | expressed protein, weak similarity to Septation ring formation regulator (Swiss-Prot:O34894) (Bacillus subtilis)	7.5	6.7	0.8	3.8	3.23%	2.8
6402	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	8.9	7.8	1.1	3.8	3.23%	2.9
6405	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	5.8	4.5	1.3	3.8	3.24%	3.2
6407	AT4G28330.1 | expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At4g28340.1) | chr4:14022393-14022993 REVERSE | Aliases: F20O9.10, F20O9_10	6.6	5.2	1.4	3.8	3.24%	3.2
6408	AT2G16390.1 | Symbol: DRD1 | SNF2 domain-containing protein / helicase domain-containing protein, low similarity to RAD54 (Drosophila melanogaster) GI: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	3.4	2.9	0.5	3.8	3.24%	2.7
6415	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	5.1	4.3	0.8	3.8	3.24%	3.1
6418	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	7.1	6.2	0.9	3.8	3.25%	2.9
6421	AT2G39830.1 | LIM domain-containing protein, contains Pfam profile PF00412: LIM domain	5.0	4.3	0.7	3.8	3.26%	3.0
6423	AT3G25990.1 | DNA-binding protein GT-1-related, similar to GT-1 GI:598073 from (Arabidopsis thaliana) | chr3:9505922-9507940 REVERSE | Aliases: MPE11.20	3.5	2.9	0.7	3.8	3.26%	2.9
6425	AT1G47420.1 | expressed protein, identical to hypothetical protein GB:AAD46040 GI:5668814 from (Arabidopsis thaliana) | chr1:17397958-17399693 REVERSE | Aliases: T3F24.12	12.5	10.4	2.1	3.8	3.27%	3.0
6427	AT1G15230.1 | expressed protein, ESTs gb:R30529, gb:Z48463, gb:Z48467, gb:AA597369 and gb:AA394772 come from this gene	6.3	5.3	0.9	3.8	3.27%	3.0
6428	AT1G28540.1 | expressed protein | chr1:10035650-10036927 FORWARD | Aliases: F3M18.29	7.6	6.6	1.0	3.8	3.27%	2.9
6429	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	3.4	2.7	0.6	3.8	3.28%	2.8
6430	AT2G41110.1 | Symbol: ATCAL4 |	9.0	6.9	2.2	3.8	3.28%	3.1
6431	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	2.7	0.4	3.8	3.28%	2.6
6432	AT5G54970.1 | expressed protein | chr5:22330436-22330990 FORWARD | Aliases: MBG8.24, MBG8_24	6.6	4.0	2.5	3.8	3.28%	3.2
6435	AT4G28200.1 | expressed protein | chr4:13987608-13990456 REVERSE | Aliases: F26K10.80, F26K10_80	6.6	5.5	1.1	3.8	3.29%	2.9
6436	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	6.1	5.2	1.0	3.8	3.29%	3.1
6437	AT4G18820.1 | expressed protein | chr4:10330382-10334279 FORWARD | Aliases: F28A21.230, F28A21_230	5.5	4.6	1.0	3.8	3.29%	3.0
6442	AT5G44420.1 | Symbol: PDF1.2 |	3.0	2.5	0.5	3.8	3.31%	2.8
6443	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	5.8	4.9	0.9	3.8	3.31%	3.0
6446	ATCG00120.1 | Symbol: ATPA | ATPase alpha subunit | chrC:9938-11461 REVERSE | Aliases: ATPA	6.9	5.1	1.8	3.8	3.31%	3.1

Rank	Description	Sync	Root	M	t	adj.q	B
6447	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	6.2	5.3	0.9	3.8	3.31%	3.0
6448	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	4.1	3.3	0.8	3.8	3.31%	3.0
6450	AT5G55140.1 | ribosomal protein L30 family protein, contains similarity to 50S ribosomal protein L30 | chr5:22398262-22399254 FORWARD | Aliases: MCO15.9, MCO15_9	6.2	4.7	1.5	3.8	3.31%	3.1
6452	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	7.0	6.2	0.8	3.8	3.31%	2.9
6454	AT3G05280.1 | integral membrane Yip1 family protein, contains Pfam domain, PF04893: Yip1 domain | chr3:1503764-1505648 REVERSE | Aliases: T12H1.25, T12H1_25	7.2	5.7	1.5	3.8	3.32%	3.1
6455	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	7.9	6.9	1.0	3.8	3.32%	3.1
6456	AT1G30480.1 | Symbol: DRT111 |	7.3	6.1	1.1	3.8	3.32%	3.0
6457	AT3G29330.1 | expressed protein | chr3:11258939-11260290 REVERSE | Aliases: MUO10.3	4.4	3.8	0.6	3.8	3.33%	2.9
6459	AT3G62630.1 | expressed protein | chr3:23174723-23176171 REVERSE | Aliases: F26K9.60	3.4	2.9	0.6	3.8	3.33%	2.8
6460	AT4G09760.3 | choline kinase, putative, similar to GmCK2p choline kinase gi:1438881:gb:AAC49375 | chr4:6148755-6151380 REVERSE | Aliases: F17A8.110, F17A8_110	5.9	4.8	1.1	3.8	3.33%	3.1
6464	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	3.6	2.9	0.7	3.8	3.33%	3.0
6465	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	7.6	6.7	0.9	3.8	3.33%	2.8
6466	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	10.0	7.8	2.2	3.8	3.33%	3.1
6467	AT5G18770.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.1	2.6	0.5	3.8	3.33%	2.6
6469	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	5.8	4.5	1.3	3.8	3.33%	3.1
6471	AT2G19460.1 | expressed protein | chr2:8438564-8439187 FORWARD | Aliases: F27F23.23	4.0	2.7	1.3	3.8	3.33%	3.0
6472	AT1G18600.1 | rhomboid family protein, contains Pfam profile PF01694: Rhomboid family | chr1:6400396-6402770 FORWARD | Aliases: F25I16.6, F25I16_6	8.2	5.7	2.5	3.8	3.34%	2.9
6474	AT3G12380.1 | Symbol: ATARP5 |	6.9	6.2	0.6	3.8	3.34%	2.8
6475	AT5G08570.1 | pyruvate kinase, putative, similar to pyruvate kinase, cytosolic isozyme (Glycine max) SWISS-PROT:Q42806	9.4	7.9	1.6	3.8	3.34%	2.9
6476	AT5G42000.1 | ORMDL family protein, contains Pfam domain PF04061: ORMDL family	5.6	4.1	1.5	3.8	3.34%	3.0
6477	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	3.5	0.5	3.8	3.34%	2.7
6478	AT3G06490.1 | Symbol: MYB108 |	4.0	3.2	0.8	3.8	3.34%	2.9

Rank	Description	Sync	Root	M	t	adj.q	B
6480	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	9.8	8.5	1.4	3.8	3.35%	3.0
6481	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	12.1	10.9	1.2	3.8	3.35%	2.9
6482	AT1G67620.1 | expressed protein, contains Pfam domain PF02410: Domain of unknown function DUF143 | chr1:25344239-25345605 FORWARD | Aliases: F12B7.17, F12B7_17	4.9	3.3	1.5	3.8	3.35%	3.1
6484	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	2.9	0.6	3.8	3.36%	2.8
6485	AT5G10460.1 | haloacid dehalogenase-like hydrolase family protein, contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	6.7	5.3	1.4	3.8	3.37%	3.0
6486	AT4G11600.1 | Symbol: ATGPX6 |	11.1	9.8	1.3	3.8	3.37%	2.8
6488	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	8.0	7.0	1.0	3.8	3.38%	3.0
6489	AT5G06400.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:1955960-1959052 FORWARD | Aliases: MHF15.8, MHF15_8	3.1	2.7	0.4	3.8	3.38%	2.5
6492	AT3G28500.1 | 60S acidic ribosomal protein P2 (RPP2C), similar to acidic ribosomal protein P2b (rpp2b) GB:U62753 GI:2431770 from (Zea mays) | chr3:10683334-10683968 FORWARD | Aliases: T20D4.1	6.1	4.9	1.2	3.8	3.38%	3.1
6493	AT4G32840.1 | phosphofructokinase family protein, similar to phosphofructokinase (Amycolatopsis methanolica) GI:17432243; contains Pfam profile PF00365: Phosphofructokinase | chr4:15844784-15848445 REVERSE | Aliases: T16I18.50, T16I18_50	5.0	4.2	0.9	3.8	3.38%	2.7
6496	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	6.2	2.9	3.8	3.38%	3.1
6498	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	5.2	4.4	0.7	3.8	3.39%	2.7
6500	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	10.4	8.8	1.7	3.8	3.39%	2.9
6501	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	7.8	6.2	1.7	3.8	3.39%	3.1
6502	AT1G30330.2 | Symbol: ARF6 | similar to auxin-responsive factor (ARF8) [Arabidopsis thaliana] (TAIR:At5g37020.1); similar to auxin response factor 6b [Oryza sativa] (GB:BAB85915.1); 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	5.5	4.6	0.9	3.8	3.40%	3.1
6503	AT4G35910.1 | expressed protein | chr4:17008584-17011454 REVERSE | Aliases: T19K4.40	6.4	5.2	1.2	3.8	3.40%	3.0
6504	AT1G20870.1 | expressed protein | chr1:7259091-7260764 REVERSE | Aliases: F9H16.15, F9H16_15	4.7	3.8	1.0	3.8	3.40%	3.1
6512	AT3G59110.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:21865697-21869181 FORWARD | Aliases: F17J16.160	4.8	4.1	0.7	3.8	3.43%	2.8
6513	AT4G25630.1 | Symbol: FIB2 | fibrillarin 2 (FIB2), identical to fibrillarin 2 GI:9965655 from (Arabidopsis thaliana) | chr4:13074142-13076432 FORWARD | Aliases: ATFIB2, FIBRILLARIN 2, L73G19.10, L73G19_10	8.1	6.9	1.2	3.8	3.44%	3.0
6516	AT3G22520.1 | expressed protein | chr3:7974769-7977597 FORWARD | Aliases: F16J14.8	5.1	4.1	1.1	3.8	3.45%	3.0

Rank	Description	Sync	Root	M	t	adj.q	B
6518	AT3G55510.1 | expressed protein | chr3:20589963-20593382 FORWARD | Aliases: T22E16.170	4.7	3.4	1.3	3.8	3.45%	3.1
6523	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	10.9	10.1	0.8	3.8	3.47%	2.9
6524	AT5G40600.1 | Symbol: EMB1875 | expressed protein | chr5:16272272-16273993 REVERSE | Aliases: EMB1875, EMBRYO DEFECTIVE 1875, MNF13.13, MNF13_13	3.7	3.1	0.5	3.8	3.47%	2.7
6526	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	3.9	0.7	3.8	3.47%	2.9
6527	AT1G01990.1 | expressed protein | chr1:343166-344319 REVERSE | Aliases: F22M8.12, F22M8_12	5.5	5.0	0.5	3.8	3.47%	2.6
6528	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	9.7	7.6	2.1	3.8	3.47%	3.0
6531	AT2G47610.1 | 60S ribosomal protein L7A (RPL7aA) | chr2:19536860-19538725 FORWARD | Aliases: T30B22.8	9.6	7.8	1.8	3.7	3.49%	2.9
6535	AT1G71850.1 | expressed protein, ; expression supported by MPSS | chr1:27028537-27029949 REVERSE | Aliases: F14O23.23, F14O23_23	4.9	4.0	0.9	3.7	3.51%	3.0
6536	AT4G22000.1 | expressed protein | chr4:11659650-11660916 REVERSE | Aliases: F1N20.100, F1N20_100	9.2	7.8	1.4	3.7	3.51%	3.0
6539	AT4G17430.1 | expressed protein, weak similarity to CigA protein (Mucor circinelloides) GI:9717020 | chr4:9724852-9726840 REVERSE | Aliases: DL4750C, FCAALL.1	4.9	4.2	0.7	3.7	3.51%	2.9
6540	AT5G66440.1 | expressed protein | chr5:26547461-26548323 REVERSE | Aliases: K1F13.9, K1F13_9	9.1	7.5	1.6	3.7	3.52%	3.0
6542	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	9.2	8.1	1.2	3.7	3.52%	2.8
6543	AT4G37080.2 | expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547 | chr4:17473266-17476946 FORWARD | Aliases: AP22.58, AP22_58	4.5	3.8	0.7	3.7	3.53%	2.8
6545	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	6.6	2.3	4.2	3.7	3.53%	3.1
6547	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	8.7	7.4	1.3	3.7	3.53%	3.0
6548	AT3G59480.1 | pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase | chr3:21993998-21995572 FORWARD | Aliases: T16L24.30	4.9	3.7	1.2	3.7	3.53%	3.1
6550	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	9.0	8.1	0.9	3.7	3.54%	2.9
6551	AT1G14680.1 | expressed protein | chr1:5040856-5041728 FORWARD | Aliases: F10B6.4, F10B6_4	4.2	2.9	1.4	3.7	3.55%	2.9
6552	AT5G18280.1 | Symbol: ATAPY2 |	5.4	4.7	0.7	3.7	3.55%	2.7
6555	AT4G17060.1 | expressed protein | chr4:9593548-9595268 REVERSE | Aliases: None	5.9	5.0	0.9	3.7	3.55%	2.9
6557	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	3.2	2.5	0.7	3.7	3.55%	2.8
6558	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	7.5	5.4	2.1	3.7	3.55%	3.0
6559	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	8.3	7.2	1.0	3.7	3.55%	2.9

Rank	Description	Sync	Root	M	t	adj.q	B
6562	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	3.3	2.8	0.6	3.7	3.55%	2.7
6563	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	6.2	4.7	1.5	3.7	3.56%	3.0
6564	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	6.9	6.2	0.8	3.7	3.56%	2.9
6566	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	5.4	4.5	0.8	3.7	3.56%	2.9
6567	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	3.5	2.6	1.0	3.7	3.56%	2.9
6568	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	8.9	7.2	1.6	3.7	3.57%	3.0
6569	AT4G10250.1 | Symbol: ATHSP22.0 | 22.0 kDa ER small heat shock protein (HSP22.0-ER), identical to endomembrane-localized small heat shock protein GI:511795 from (Arabidopsis thaliana) | chr4:6370339-6371286 FORWARD | Aliases: ATHSP22.0, T9A4.7	3.2	2.6	0.6	3.7	3.57%	2.8
6570	AT1G61340.1 | F-box family protein, contains Pfam PF00646: F-box domain; similar to late embryogenesis abundant protein GI:1350540 from (Picea glauca)	6.4	5.2	1.3	3.7	3.57%	3.0
6572	AT3G46460.1 | ubiquitin-conjugating enzyme 13 (UBC13), E2; identical to gi:992706 | chr3:17106886-17108437 REVERSE | Aliases: F18L15.180	7.5	6.2	1.3	3.7	3.57%	3.0
6574	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	11.6	10.3	1.2	3.7	3.58%	2.6
6575	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	5.4	0.7	3.7	3.58%	2.9
6576	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 scienitific 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	5.8	5.0	0.8	3.7	3.58%	2.9
6577	AT4G39690.1 | expressed protein | chr4:18417664-18421965 FORWARD | Aliases: T19P19.80, T19P19_80	7.6	5.9	1.7	3.7	3.58%	3.0
6578	AT2G46230.1 | expressed protein, contains Pfam profile: PF04900 protein of unknown function, DUF652 | chr2:18991045-18993032 REVERSE | Aliases: T3F17.12	8.2	7.0	1.2	3.7	3.58%	2.9
6579	AT3G22670.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:8017778-8019466 REVERSE | Aliases: MWI23.4	5.2	4.0	1.2	3.7	3.58%	3.0
6580	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	3.6	1.2	3.7	3.58%	3.0
6582	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	7.7	6.2	1.6	3.7	3.58%	3.0
6584	AT1G19525.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:6761511-6762769 FORWARD | Aliases: None	6.3	5.1	1.2	3.7	3.59%	2.9

Rank	Description	Sync	Root	M	t	adj.q	B
6585	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	5.4	3.8	1.5	3.7	3.59%	3.1
6586	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	10.5	8.8	1.7	3.7	3.59%	2.9
6588	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	7.7	6.5	1.2	3.7	3.59%	3.0
6592	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	10.1	9.5	0.6	3.7	3.60%	2.6
6595	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	8.7	7.1	1.6	3.7	3.60%	3.0
6598	AT1G03320.1 | expressed protein | chr1:817027-817767 FORWARD | Aliases: F15K9.8, F15K9_8	2.6	2.2	0.4	3.7	3.60%	2.4
6599	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	9.6	8.4	1.1	3.7	3.60%	3.0
6601	AT5G37510.2 | Symbol: EMB1467 | NADH-ubiquinone dehydrogenase, mitochondrial, putative, similar to NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial from Solanum tuberosum (SP:Q43644) | chr5:14914640-14917877 FORWARD | Aliases: EMB1467, EMBRYO DEFECTIVE 1467, MPA22.5, MPA22_5	11.1	8.7	2.4	3.7	3.60%	2.9
6603	AT4G31560.1 | expressed protein | chr4:15295207-15296233 FORWARD | Aliases: F3L17.130, F3L17_130	5.6	4.5	1.1	3.7	3.61%	3.1
6604	AT5G58790.1 | expressed protein, ; expression supported by MPSS | chr5:23762232-23763018 FORWARD | Aliases: MZN1.28	4.9	4.0	0.9	3.7	3.61%	2.7
6605	AT3G02530.1 | 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 | chr3:528581-532589 REVERSE | Aliases: F16B3.16, F16B3_16	8.4	6.4	2.0	3.7	3.62%	2.9
6606	AT4G23493.1 | expressed protein | chr4:12256192-12257049 REVERSE | Aliases: None	6.6	5.4	1.2	3.7	3.62%	2.9
6609	AT1G61990.1 | mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF | chr1:22914870-22916600 FORWARD | Aliases: F8K4.18, F8K4_18	5.1	3.7	1.4	3.7	3.63%	3.0
6610	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	10.9	9.3	1.7	3.7	3.63%	2.6
6611	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	4.5	3.8	0.7	3.7	3.63%	2.9
6612	AT1G53200.2 | expressed protein | chr1:19844044-19847071 REVERSE | Aliases: F12M16.11, F12M16_11	4.1	3.4	0.7	3.7	3.63%	2.8
6613	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	11.0	9.8	1.1	3.7	3.63%	2.8
6620	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	4.5	4.0	0.5	3.7	3.65%	2.6
6626	AT1G04980.1 | Symbol: ATPDIL2 2 | Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	6.0	5.2	0.9	3.7	3.66%	2.9
6628	AT5G36120.1 | YGGT family protein, contains Pfam profile PF02325: YGGT family (unknown function) | chr5:14215818-14216473 REVERSE | Aliases: MAB16.6, MAB16_6	4.2	3.6	0.6	3.7	3.66%	2.8

Rank	Description	Sync	Root	M	t	adj.q	B
6631	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	5.1	1.1	3.7	3.66%	3.0
6632	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	8.3	6.6	1.7	3.7	3.67%	2.9
6633	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	7.8	6.8	1.0	3.7	3.67%	2.9
6634	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	6.7	1.6	3.7	3.68%	2.9
6635	AT1G45332.1 | mitochondrial elongation factor, putative, similar to mitochondrial elongation factor GI:3917 from (Saccharomyces cerevisiae) | chr1:17174795-17179261 REVERSE | Aliases: AT1G45261, F2G19.2, F2G19_2	9.3	6.8	2.6	3.7	3.68%	3.0
6636	AT2G45030.1 | mitochondrial elongation factor, putative, similar to SP:P25039 Elongation factor G 1, mitochondrial precursor (mEF-G-1) {Saccharomyces cerevisiae}; 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	9.3	6.8	2.6	3.7	3.68%	3.0
6639	AT5G25170.1 | expressed protein | chr5:8693187-8695098 FORWARD | Aliases: F21J6.101, F21J6_101	5.9	4.7	1.1	3.7	3.69%	2.8
6640	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	6.1	5.1	1.0	3.7	3.69%	3.0
6641	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	8.9	7.5	1.3	3.7	3.69%	2.9
6642	AT4G27240.1 | zinc finger (C2H2 type) family protein, contains zinc finger, C2H2 type, domain, PROSITE:PS00028	5.5	3.8	1.7	3.7	3.69%	3.0
6643	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	10.7	9.5	1.3	3.7	3.70%	2.7
6645	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	10.6	8.7	2.0	3.7	3.71%	2.7
6646	AT3G15380.1 | choline transporter-related, contains weak similarity to CD92 protein (Homo sapiens) gi:16945323:emb:CAC82175 | chr3:5193235-5196596 FORWARD | Aliases: MJK13.4	4.8	4.0	0.9	3.7	3.71%	2.9
6648	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	4.3	0.7	3.7	3.71%	2.8
6650	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	5.0	0.8	3.7	3.71%	2.8
6651	AT2G46470.1 | OXA1 protein, putative, similar to Oxa1 protein (Arabidopsis thaliana) GI:10176922 | chr2:19079385-19082195 FORWARD | Aliases: F11C10.16	5.2	4.2	1.0	3.7	3.72%	3.0
6656	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	2.3	0.5	3.7	3.73%	2.6
6658	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	6.1	5.3	0.8	3.7	3.74%	2.7
6659	AT3G52860.1 | expressed protein | chr3:19602826-19603743 REVERSE | Aliases: F8J2.30	4.0	3.2	0.8	3.7	3.74%	2.8
6660	AT5G58575.1 | expressed protein | chr5:23691244-23692462 FORWARD | Aliases: None	4.9	3.7	1.3	3.7	3.74%	3.0

Rank	Description	Sync	Root	M	t	adj.q	B
6661	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	6.3	5.6	0.7	3.7	3.75%	2.7
6664	AT1G20230.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:7009561-7011843 FORWARD | Aliases: T20H2.1, T20H2_1	3.9	3.1	0.8	3.7	3.75%	2.9
6665	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	5.8	4.9	0.9	3.7	3.76%	2.8
6673	AT3G14650.1 | Symbol: CYP72A11 | cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus) | chr3:4922138-4924695 FORWARD | Aliases: MIE1.15	4.8	3.7	1.0	3.7	3.77%	2.8
6678	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	4.3	3.7	0.7	3.7	3.79%	2.7
6679	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	7.4	6.1	1.3	3.7	3.79%	2.8
6681	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	4.3	3.2	1.2	3.7	3.80%	3.0
6682	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	7.8	6.4	1.4	3.7	3.81%	2.8
6683	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	7.0	5.9	1.1	3.7	3.81%	2.9
6685	AT5G59440.2 | thymidylate kinase family protein, similar to thymidylate kinase GI:291900 | chr5:23988461-23990097 FORWARD | Aliases: F2O15.12, F2O15_12	6.1	4.9	1.2	3.7	3.81%	3.0
6689	AT3G25740.1 | Symbol: MAP1B | metallopeptidase M24 family protein, similar to SP:O33343 Methionine aminopeptidase (EC 3.4.11.18) (Peptidase M) {Mycobacterium tuberculosis}; contains Pfam profile PF00557: metallopeptidase family M24 | chr3:9399023-9400999 FORWARD | Aliases: K13N2.17, MAP1C, METHIONINE AMINOPEPTIDASE 1C	4.7	3.8	0.8	3.7	3.81%	2.7
6690	AT1G35340.3 | ATP-dependent protease La (LON) domain-containing protein, contains Pfam profile PF02190: ATP-dependent protease La (LON) domain	7.5	6.8	0.8	3.7	3.81%	2.8
6692	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	5.0	1.0	3.7	3.82%	2.8
6695	AT5G55540.1 | expressed protein | chr5:22513422-22517769 REVERSE | Aliases: MTE17.26, MTE17_26	6.2	5.4	0.8	3.7	3.83%	2.8
6696	AT1G34270.1 | exostosin family protein, contains Pfam profile: PF03016 Exostosin family | chr1:12492389-12494522 REVERSE | Aliases: F23M19.7, F23M19_7	4.4	3.7	0.7	3.7	3.83%	2.8
6701	AT4G28590.1 | expressed protein | chr4:14125286-14126841 REVERSE | Aliases: T5F17.40, T5F17_40	3.0	2.6	0.5	3.7	3.83%	2.4
6702	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	7.0	6.1	0.9	3.7	3.84%	2.8
6707	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	4.8	4.0	0.8	3.7	3.84%	2.8
6709	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	3.0	0.8	3.7	3.84%	2.7
6710	AT4G32920.1 | glycine-rich protein | chr4:15887578-15896009 REVERSE | Aliases: F26P21.40, F26P21_40	4.3	3.6	0.7	3.7	3.85%	2.8

Rank	Description	Sync	Root	M	t	adj.q	B
6711	AT1G48470.1 | Symbol: GLN1;5 |	5.7	4.3	1.3	3.7	3.85%	3.0
6714	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	6.1	5.2	0.8	3.7	3.85%	2.7
6715	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	7.0	6.0	1.0	3.7	3.85%	2.7
6717	AT1G18490.1 | expressed protein | chr1:6367061-6368842 FORWARD | Aliases: F15H18.26, F15H18_26	7.9	6.7	1.2	3.7	3.86%	2.8
6718	AT5G02550.1 | expressed protein | chr5:573052-573556 REVERSE | Aliases: T22P11.140, T22P11_140	4.1	3.0	1.1	3.7	3.86%	2.7
6720	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	4.5	3.1	1.3	3.7	3.87%	2.9
6722	AT4G14695.1 | expressed protein, contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041) | chr4:8419828-8420871 FORWARD | Aliases: None	3.1	2.4	0.7	3.7	3.87%	2.3
6726	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	6.0	5.3	0.7	3.7	3.88%	2.7
6727	AT2G34620.1 | mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF | chr2:14584275-14585367 FORWARD | Aliases: T31E10.4, T31E10_4	2.8	2.4	0.4	3.7	3.88%	2.3
6730	AT5G58500.1 | expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640) | chr5:23662761-23663309 REVERSE | Aliases: MQJ2.11, MQJ2_11	5.3	4.6	0.7	3.7	3.88%	2.7
6731	AT5G49650.2 | xylulose kinase, putative, similar to D-xylulokinase (Pichia stipitis) gi:8100400:gb:AAF72328 | chr5:20170007-20172994 FORWARD | Aliases: MNI5.3, MNI5_3	8.0	6.4	1.7	3.7	3.88%	2.9
6734	AT2G41550.1 | expressed protein | chr2:17335617-17338211 REVERSE | Aliases: T32G6.7, T32G6_7	5.2	4.3	0.9	3.7	3.89%	2.9
6737	AT1G78995.1 | expressed protein | chr1:29719972-29721004 REVERSE | Aliases: None	3.9	3.2	0.7	3.7	3.89%	2.6
6738	AT1G10990.2 | expressed protein, and genscan | chr1:3670278-3671187 REVERSE | Aliases: T19D16.27, T19D16_27	4.4	3.7	0.7	3.7	3.89%	2.5
6739	AT5G03390.1 | expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295) | chr5:834987-836750 FORWARD | Aliases: F12E4.130, F12E4_130	3.2	2.4	0.8	3.7	3.89%	2.8
6740	AT3G56010.1 | expressed protein | chr3:20799670-20800903 FORWARD | Aliases: F27K19.190	5.1	4.5	0.7	3.7	3.89%	2.8
6741	AT2G01710.1 | DNAJ heat shock N-terminal domain-containing protein, simlar to AHM1 (Triticum aestivum) GI:6691467; contains Pfam profile PF00226: DnaJ domain | chr2:315725-316992 FORWARD | Aliases: T8O11.12, T8O11_12	5.0	4.3	0.7	3.7	3.90%	2.6
6743	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	4.7	3.2	1.5	3.6	3.90%	3.0
6745	AT1G63220.1 | C2 domain-containing protein, similar to phloem protein RPP16 (Oryza sativa (japonica cultivar-group)) GI:21998839; contains Pfam profile PF00168: C2 domain | chr1:23452584-23454106 FORWARD | Aliases: F9N12.16, F9N12_16	7.4	5.6	1.9	3.6	3.90%	2.9
6746	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	6.0	4.7	1.3	3.6	3.91%	2.8
6749	AT1G62730.1 | expressed protein | chr1:23232724-23234401 REVERSE | Aliases: F23N19.9, F23N19_9	5.3	4.2	1.1	3.6	3.92%	2.8
6751	AT5G05670.2 | expressed protein | chr5:1695731-1698105 REVERSE | Aliases: MJJ3.7, MJJ3_7	5.5	4.4	1.1	3.6	3.92%	2.9

Rank	Description	Sync	Root	M	t	adj.q	B
6753	AT5G42990.1 | ubiquitin-conjugating enzyme 18 (UBC18), E2; identical to gi:2801448 | chr5:17261219-17263182 REVERSE | Aliases: MBD2.19, MBD2_19	6.9	6.0	0.9	3.6	3.93%	2.8
6754	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	3.7	3.1	0.7	3.6	3.93%	2.8
6755	AT5G65650.1 | expressed protein | chr5:26256728-26258741 FORWARD | Aliases: K21L13.17, K21L13_17	5.5	4.3	1.2	3.6	3.93%	2.8
6757	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	6.7	5.3	1.4	3.6	3.94%	2.9
6760	AT3G63160.1 | expressed protein | chr3:23344488-23345009 REVERSE | Aliases: F16M2.10	4.9	4.1	0.8	3.6	3.94%	2.7
6762	AT5G11100.1 | C2 domain-containing protein, similar to Ca2+-dependent lipid-binding protein (CLB1) GI:2789434 from (Lycopersicon esculentum) | chr5:3532403-3535222 FORWARD | Aliases: T5K6.90, T5K6_90	5.5	4.6	0.9	3.6	3.94%	2.9
6763	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	6.9	5.8	1.1	3.6	3.94%	2.9
6765	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	10.8	9.5	1.4	3.6	3.95%	2.7
6766	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	3.2	0.5	3.6	3.95%	2.6
6768	AT2G30960.1 | expressed protein | chr2:13183781-13185405 REVERSE | Aliases: F7F1.17, F7F1_17	7.4	5.9	1.6	3.6	3.95%	2.9
6770	AT2G18410.2 | expressed protein | chr2:7997847-7999856 FORWARD | Aliases: T30D6.8, T30D6_8	4.4	4.0	0.4	3.6	3.96%	2.4
6771	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	3.8	3.0	0.9	3.6	3.96%	2.6
6772	AT1G10770.1 | invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	4.6	3.8	0.8	3.6	3.96%	2.8
6773	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	4.0	2.7	1.2	3.6	3.97%	2.8
6775	AT2G06030.1 | expressed protein | chr2:2352158-2353770 REVERSE | Aliases: F5K7.21, F5K7_21	3.9	3.4	0.5	3.6	3.98%	2.6
6776	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	5.0	4.0	1.0	3.6	3.98%	2.9
6782	AT5G57500.1 | expressed protein | chr5:23303463-23304797 REVERSE | Aliases: MUA2.7, MUA2_7	2.8	2.4	0.5	3.6	3.99%	2.4
6786	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	8.0	6.7	1.2	3.6	4.00%	2.8
6787	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	6.1	1.1	3.6	4.00%	2.8
6788	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	4.1	3.3	0.8	3.6	4.01%	2.8
6791	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	5.2	3.4	3.6	4.01%	2.9
6793	AT1G21410.1 | F-box family protein, similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250	7.4	6.4	1.1	3.6	4.01%	2.8

Rank	Description	Sync	Root	M	t	adj.q	B
6795	AT5G63135.1 | expressed protein | chr5:25342205-25343705 REVERSE | Aliases: None	3.6	2.3	1.3	3.6	4.01%	2.7
6798	AT3G55330.1 | photosystem II reaction center PsbP family protein, contains Pfam profile PF01789: PsbP | chr3:20524870-20526328 REVERSE | Aliases: T26I12.210	5.0	4.0	1.1	3.6	4.02%	2.9
6804	AT3G12610.1 | Symbol: DRT100 |	4.0	3.0	1.1	3.6	4.03%	2.9
6806	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	7.5	6.5	1.1	3.6	4.03%	2.7
6807	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	3.9	3.0	0.9	3.6	4.03%	2.8
6808	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	9.4	8.1	1.3	3.6	4.03%	2.8
6812	AT4G10090.1 | expressed protein | chr4:6305439-6307514 FORWARD | Aliases: F28M11.10, F28M11_10	4.6	4.0	0.5	3.6	4.05%	2.5
6813	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	3.8	0.8	3.6	4.05%	2.7
6816	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	9.3	8.2	1.1	3.6	4.05%	2.9
6817	AT2G16270.1 | expressed protein, and genefinder; expression supported by MPSS	4.3	3.7	0.5	3.6	4.05%	2.6
6821	AT5G08280.1 | hydroxymethylbilane synthase / porphobilinogen deaminase, chloroplast / pre-uroporphyrinogen synthase, identical to SP:Q43316 | chr5:2663191-2665793 REVERSE | Aliases: F8L15.10, F8L15_10	5.8	4.1	1.6	3.6	4.07%	2.9
6822	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	5.5	4.5	1.0	3.6	4.07%	2.7
6823	AT4G11960.1 | expressed protein, hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057 | chr4:7174880-7177752 REVERSE | Aliases: F16J13.30, F16J13_30	6.8	5.7	1.1	3.6	4.07%	2.8
6824	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	6.7	5.3	1.4	3.6	4.08%	2.8
6827	AT5G52910.1 | Symbol: ATIM | timeless family protein, contains Pfam domains PF05029: Timeless protein C terminal region and PF04821: Timeless protein	4.3	3.7	0.6	3.6	4.08%	2.6
6828	AT2G42600.2 | Symbol: ATPPC2 |	8.1	7.2	0.9	3.6	4.10%	2.6
6829	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	7.2	5.9	1.2	3.6	4.10%	2.8
6830	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	6.4	5.0	1.4	3.6	4.10%	2.7
6832	AT2G27775.2 | expressed protein | chr2:11849812-11850370 REVERSE | Aliases: None	4.7	3.4	1.2	3.6	4.11%	2.5
6834	AT4G08280.1 | expressed protein, hypothetical protein ssr1391 - Synechocystis sp. (strain PCC 6803),PIR2:S75571 | chr4:5230323-5232128 FORWARD | Aliases: T12G13.120, T12G13_120	5.8	4.2	1.5	3.6	4.11%	2.8
6835	AT4G28020.1 | expressed protein, contains Pfam PF01980: Uncharacterised protein family	5.0	4.4	0.6	3.6	4.11%	2.7
6836	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	9.2	7.3	1.8	3.6	4.11%	2.9

Rank	Description	Sync	Root	M	t	adj.q	B
6837	AT3G11770.1 | expressed protein | chr3:3721334-3722652 REVERSE | Aliases: F26K24.6	8.3	7.5	0.8	3.6	4.11%	2.7
6839	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	4.8	3.8	1.0	3.6	4.12%	2.6
6843	AT1G68790.1 | expressed protein | chr1:25838372-25842982 REVERSE | Aliases: F14K14.10, F14K14_10	9.5	7.5	2.0	3.6	4.13%	2.7
6845	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	5.2	4.3	0.9	3.6	4.13%	2.7
6846	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	3.6	3.0	0.6	3.6	4.13%	2.6
6850	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	3.5	3.0	0.6	3.6	4.14%	2.6
6851	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	4.2	3.0	1.2	3.6	4.14%	2.9
6853	AT1G63210.1 | expressed protein, contains Pfam profile: PF04283 protein of unknown function (DUF439) | chr1:23447353-23451019 FORWARD | Aliases: F16M19.22, F16M19_22	3.5	2.9	0.6	3.6	4.14%	2.5
6854	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	11.0	8.5	2.5	3.6	4.14%	2.8
6855	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	6.2	5.0	1.3	3.6	4.14%	2.8
6858	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	4.0	3.4	0.6	3.6	4.15%	2.5
6859	AT1G50900.1 | expressed protein | chr1:18869874-18870872 FORWARD | Aliases: F8A12.12, F8A12_12	4.3	2.9	1.3	3.6	4.15%	2.8
6861	AT4G29830.1 | Symbol: VIP3 | transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); G protein beta subunit-like protein, Schistosoma mansoni, gb:U30261	7.7	6.8	0.9	3.6	4.15%	2.8
6862	AT2G45340.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:18698796-18701776 FORWARD | Aliases: F4L23.15	4.0	3.2	0.9	3.6	4.15%	2.7
6864	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	5.9	5.2	0.7	3.6	4.16%	2.6
6868	AT3G47630.2 | similar to Hypothetical protein CBG04116 [Caenorhabditis briggsae] (GB:CAE60498.1) | chr3:17574031-17576414 REVERSE | Aliases: F1P2.180	4.9	4.2	0.7	3.6	4.17%	2.7
6871	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	5.8	5.2	0.7	3.6	4.18%	2.6
6872	AT4G35230.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:16755123-16758096 REVERSE | Aliases: F23E12.210, F23E12_210	9.6	8.8	0.8	3.6	4.18%	2.5
6873	AT5G25590.1 | expressed protein, contains Pfam profile PF04783: Protein of unknown function (DUF630) | chr5:8906601-8909923 REVERSE | Aliases: T14C9.130, T14C9_130	3.7	3.2	0.5	3.6	4.18%	2.4
6874	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	5.0	1.5	3.6	4.19%	2.6

Rank	Description	Sync	Root	M	t	adj.q	B
6875	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	6.0	4.7	1.3	3.6	4.19%	2.9
6878	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	2.0	0.4	3.6	4.19%	2.2
6879	AT3G17310.2 | methyltransferase family protein, similar to cytosine methyltransferase (GI:7658293) (Arabidopsis thaliana) | chr3:5909007-5913248 REVERSE | Aliases: MGD8.15	5.0	4.1	0.9	3.6	4.20%	2.8
6880	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	7.0	5.1	2.0	3.6	4.20%	2.9
6883	AT1G77920.1 | bZIP family transcription factor, contains Pfam profile: PF00170 bZIP transcription factor | chr1:29303299-29305757 FORWARD | Aliases: F28K19.13, F28K19_13	7.7	7.0	0.7	3.6	4.22%	2.7
6885	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	5.5	4.3	1.2	3.6	4.22%	2.9
6889	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	4.6	4.0	0.7	3.6	4.23%	2.6
6893	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	2.8	2.3	0.5	3.6	4.23%	2.4
6897	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	6.5	5.3	1.1	3.6	4.24%	2.7
6898	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)	4.7	3.6	1.1	3.6	4.24%	2.7
6899	AT4G10890.1 | expressed protein | chr4:6688829-6693754 FORWARD | Aliases: None	4.2	3.5	0.7	3.6	4.24%	2.5
6901	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	3.3	2.8	0.4	3.6	4.24%	2.2
6903	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	3.0	1.1	3.6	4.25%	2.7
6904	AT4G08240.2 | expressed protein | chr4:5194672-5196758 FORWARD | Aliases: T12G13.80, T12G13_80	5.6	4.3	1.4	3.6	4.26%	2.7
6905	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	3.1	2.7	0.4	3.6	4.26%	2.3
6906	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	8.3	0.6	3.6	4.26%	2.4
6907	AT4G16140.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr4:9129058-9129853 FORWARD | Aliases: DL4110W, FCAALL.289	3.5	2.8	0.7	3.6	4.27%	2.7
6909	AT3G11745.1 | expressed protein | chr3:3713769-3714585 REVERSE | Aliases: None	4.1	3.4	0.7	3.6	4.27%	2.6
6910	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	7.8	0.8	3.6	4.27%	2.6

Rank	Description	Sync	Root	M	t	adj.q	B
6911	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	7.5	6.2	1.2	3.6	4.27%	2.7
6915	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	5.2	4.2	1.0	3.6	4.29%	2.8
6917	AT4G27700.1 | rhodanese-like domain-containing protein, contains rhodanese-like domain PF00581	6.0	5.4	0.7	3.6	4.30%	2.7
6918	AT1G09470.1 | expressed protein, ; expression supported by MPSS | chr1:3055393-3056933 REVERSE | Aliases: F14J9.13, F14J9_13	4.4	3.3	1.1	3.6	4.30%	2.8
6919	AT1G69070.1 | expressed protein | chr1:25970975-25975052 REVERSE | Aliases: F4N2.4, F4N2_4	4.2	3.6	0.6	3.6	4.30%	2.5
6921	AT3G07640.1 | expressed protein | chr3:2438144-2439847 FORWARD | Aliases: MLP3.9	6.3	4.8	1.4	3.6	4.30%	2.8
6922	AT1G74850.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:28122510-28125975 REVERSE | Aliases: F25A4.18, F25A4_18	4.3	3.8	0.5	3.6	4.30%	2.5
6925	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	8.8	1.9	3.6	4.32%	2.7
6926	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	4.1	1.0	3.6	4.32%	2.8
6927	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	3.8	0.4	3.6	4.32%	2.1
6929	AT1G02800.1 | Symbol: ATCEL2 |	4.7	3.7	1.0	3.6	4.33%	2.8
6930	AT3G12930.1 | expressed protein, contains Pfam domain PF02410: Domain of unknown function DUF143 | chr3:4128414-4129963 FORWARD | Aliases: MGH6.4	4.4	3.6	0.8	3.6	4.33%	2.8
6932	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	3.3	2.7	0.5	3.6	4.33%	2.5
6933	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	9.0	8.2	0.8	3.6	4.33%	2.6
6934	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	7.0	0.7	3.6	4.33%	2.6
6936	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	6.3	5.5	0.8	3.6	4.34%	2.7
6937	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	5.2	4.1	1.2	3.6	4.34%	2.7
6939	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	7.7	5.1	2.7	3.6	4.34%	2.8
6940	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	6.2	5.2	1.0	3.6	4.34%	2.7
6941	AT5G17610.1 | expressed protein | chr5:5803964-5805254 FORWARD | Aliases: K10A8.90, K10A8_90	7.7	7.1	0.6	3.6	4.35%	2.5
6942	AT4G39630.1 | expressed protein | chr4:18397589-18399381 REVERSE | Aliases: F23K16.7	4.6	3.8	0.9	3.6	4.35%	2.7
6943	AT1G61065.1 | expressed protein | chr1:22493909-22495126 REVERSE | Aliases: None	7.4	6.4	1.0	3.6	4.35%	2.7

Rank	Description	Sync	Root	M	t	adj.q	B
6946	AT5G57860.3 | ubiquitin family protein, contains Pfam profile PF00240: Ubiquitin family | chr5:23454871-23456538 FORWARD | Aliases: MTI20.11, MTI20_11	5.5	4.4	1.2	3.6	4.35%	2.4
6949	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	2.9	0.4	3.6	4.35%	2.1
6951	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	7.7	6.4	1.2	3.6	4.36%	2.8
6953	AT5G40960.1 | expressed protein | chr5:16429973-16430179 REVERSE | Aliases: MEE6.3, MEE6_3	8.7	7.4	1.3	3.6	4.36%	2.7
6954	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	6.5	5.7	0.9	3.6	4.36%	2.6
6955	AT3G62620.1 | sucrose-phosphatase-related, contains weak similarity to sucrose-phosphatase (Arabidopsis thaliana) gi:11127757:gb:AAG31075 | chr3:23170779-23172830 FORWARD | Aliases: F26K9.50	3.9	3.3	0.6	3.6	4.36%	2.5
6956	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	9.7	7.9	1.7	3.6	4.36%	2.7
6958	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	7.1	5.1	2.0	3.6	4.37%	2.8
6959	AT5G64620.1 | Symbol: C/VIF2 |	4.7	3.8	0.9	3.6	4.38%	2.8
6960	AT1G27310.1 | nuclear transport factor 2 (NTF2), putative, similar to Swiss-Prot:P33331 nuclear transport factor 2 (NTF-2) (Nuclear transport factor P10) (Saccharomyces cerevisiae) | chr1:9484338-9485883 REVERSE | Aliases: F17L21.10, F17L21_10	7.0	4.7	2.3	3.5	4.38%	2.8
6961	AT2G30160.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr2:12884915-12886726 FORWARD | Aliases: T27E13.10, T27E13_10	5.4	4.4	1.1	3.5	4.39%	2.8
6963	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	9.3	6.4	2.8	3.5	4.39%	2.8
6965	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	6.4	5.4	1.0	3.5	4.40%	2.6
6967	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	6.8	6.0	0.8	3.5	4.40%	2.7
6968	AT3G18870.1 | mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF | chr3:6508226-6509349 REVERSE | Aliases: MCB22.4	2.9	2.5	0.4	3.5	4.40%	2.3
6969	AT1G14060.1 | expressed protein | chr1:4817141-4818017 REVERSE | Aliases: None	5.8	4.9	0.9	3.5	4.40%	2.8
6971	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	4.6	3.5	1.1	3.5	4.41%	2.6
6973	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	7.0	2.2	3.5	4.41%	2.7
6975	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	6.9	6.0	1.0	3.5	4.41%	2.6

Rank	Description	Sync	Root	M	t	adj.q	B
6976	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	9.0	7.3	1.6	3.5	4.41%	2.7
6981	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	4.0	3.5	0.5	3.5	4.42%	2.3
6985	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	7.5	5.6	1.9	3.5	4.44%	2.7
6986	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	4.2	3.4	0.8	3.5	4.44%	2.7
6987	AT1G79150.1 | expressed protein, ; expression supported by MPSS | chr1:29779996-29782767 REVERSE | Aliases: YUP8H12R.24, YUP8H12R_24	7.2	5.8	1.5	3.5	4.44%	2.5
6988	AT3G16175.1 | thioesterase family protein, contains Pfam profile PF03061: thioesterase family protein | chr3:5480470-5482048 FORWARD | Aliases: None	3.4	2.7	0.7	3.5	4.44%	2.4
6989	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	5.8	4.8	1.0	3.5	4.44%	2.7
6990	AT4G31210.1 | DNA topoisomerase family protein, similar to DNA Topoisomerase I (SP:Q9X3X7) {Zymomonas mobilis}	4.6	3.7	0.9	3.5	4.45%	2.7
6991	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	5.3	4.7	0.6	3.5	4.45%	2.5
6992	AT1G08270.2 | expressed protein, low similarity to SP:P46467 SKD1 protein (Vacuolar sorting protein 4b) {Mus musculus}	3.8	3.4	0.4	3.5	4.45%	2.1
6993	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	4.9	4.0	0.9	3.5	4.45%	2.7
6999	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	3.7	3.0	0.7	3.5	4.46%	2.6
7000	AT1G16480.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:5625696-5628562 REVERSE | Aliases: F3O9.28, F3O9_28	3.3	2.8	0.5	3.5	4.47%	2.3
7001	AT5G18950.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:6328521-6329972 REVERSE | Aliases: F17K4.200, F17K4_200	6.2	5.3	0.8	3.5	4.47%	2.5
7003	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	4.5	3.7	0.8	3.5	4.48%	2.5
7005	AT2G41840.1 | 40S ribosomal protein S2 (RPS2C)	10.5	9.2	1.2	3.5	4.49%	2.5
7006	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	3.5	0.8	3.5	4.49%	2.6
7007	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	9.3	7.5	1.9	3.5	4.49%	2.7
7008	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	6.5	5.1	1.4	3.5	4.50%	2.8
7011	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	5.7	4.3	1.4	3.5	4.50%	2.6

Rank	Description	Sync	Root	M	t	adj.q	B
7013	AT2G17390.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr2:7562732-7565120 FORWARD | Aliases: F5J6.15, F5J6_15	11.1	10.4	0.7	3.5	4.50%	2.1
7014	AT2G21290.1 | expressed protein | chr2:9119937-9120411 FORWARD | Aliases: F3K23.5, F3K23_5	10.8	10.1	0.7	3.5	4.50%	2.1
7015	AT5G15050.1 | glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/I-Branching enzyme | chr5:4871642-4873601 REVERSE | Aliases: F2G14.170, F2G14_170	5.6	4.6	0.9	3.5	4.51%	2.6
7016	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	10.1	8.8	1.3	3.5	4.51%	2.6
7017	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	8.0	7.4	0.7	3.5	4.51%	2.5
7018	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	7.1	6.2	0.9	3.5	4.51%	2.6
7019	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	5.1	0.7	3.5	4.51%	2.5
7020	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	6.6	5.8	0.8	3.5	4.51%	2.7
7021	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	2.9	0.4	3.5	4.51%	2.2
7023	AT3G24570.1 | peroxisomal membrane 22 kDa family protein, contains Mpv17 / PMP22 family domain, Pfam:PF04117 | chr3:8966451-8968662 REVERSE | Aliases: MOB24.15	7.5	6.4	1.0	3.5	4.52%	2.5
7028	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	3.1	2.7	0.4	3.5	4.52%	2.2
7029	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	4.4	3.6	0.8	3.5	4.53%	2.6
7031	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	9.3	7.3	2.0	3.5	4.53%	2.6
7034	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	4.1	3.4	0.7	3.5	4.53%	2.5
7036	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	5.0	4.0	1.0	3.5	4.53%	2.7
7038	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	5.4	3.9	1.4	3.5	4.53%	2.8
7039	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	9.2	7.3	1.9	3.5	4.54%	2.7
7040	AT3G52230.1 | expressed protein | chr3:19382265-19383653 FORWARD | Aliases: T25B15.4	7.8	5.0	2.8	3.5	4.54%	2.7
7041	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	3.5	3.0	0.5	3.5	4.54%	2.4

Rank	Description	Sync	Root	M	t	adj.q	B
7044	AT1G23070.1 | expressed protein, contains Pfam profile PF03619: Domain of unknown function | chr1:8174000-8175747 REVERSE | Aliases: T26J12.15, T26J12_15	3.8	3.1	0.7	3.5	4.54%	2.4
7045	AT5G48730.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:19780378-19782362 FORWARD | Aliases: K24G6.6, K24G6_6	4.8	3.8	1.0	3.5	4.54%	2.7
7046	AT3G27050.1 | expressed protein | chr3:9979396-9980901 REVERSE | Aliases: MOJ10.12	8.4	7.4	1.0	3.5	4.54%	2.5
7047	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	6.3	5.5	0.8	3.5	4.54%	2.7
7049	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	2.8	0.9	3.5	4.54%	2.6
7050	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	9.2	8.8	0.4	3.5	4.54%	2.1
7051	AT3G61490.2 | 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 | chr3:22769363-22771167 FORWARD | Aliases: F2A19.90	5.6	5.1	0.5	3.5	4.54%	2.3
7052	AT1G43910.1 | AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 | chr1:16658044-16660096 REVERSE | Aliases: F9C16.7, F9C16_7	7.6	6.0	1.6	3.5	4.55%	2.6
7053	AT2G48120.1 | Symbol: PAC | pale cress protein (PAC), identical to PAC (Arabidopsis thaliana) gi:1483213:emb:CAA65334	3.3	2.7	0.5	3.5	4.55%	2.4
7055	AT1G49400.1 | Symbol: EMB1129 | ribosomal protein S17 family protein, similar to 40S ribosomal protein S17 GI:1620985 from (Nicotiana plumbaginifolia) | chr1:18286708-18287870 FORWARD | Aliases: EMB1129, EMBRYO DEFECTIVE 1129, F13F21.17, F13F21_17	5.6	3.4	2.1	3.5	4.55%	2.7
7056	AT1G07570.2 | Symbol: APK1A | protein kinase (APK1a), identical to Protein kinase APK1A from (Arabidopsis thaliana) SWISS-PROT:Q06548	4.7	4.0	0.7	3.5	4.55%	2.6
7057	AT4G02485.1 | oxidoreductase, 2OG-Fe(II) oxygenase family protein, contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily | chr4:1092681-1094595 FORWARD | Aliases: None	3.8	3.3	0.5	3.5	4.55%	2.4
7058	AT2G18780.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.9	2.8	1.1	3.5	4.55%	2.7
7059	AT3G03890.2 | expressed protein | chr3:999474-1002040 REVERSE | Aliases: F20H23.6, F20H23_6	8.3	6.8	1.5	3.5	4.55%	2.6
7064	AT1G14030.1 | ribulose-1,5 bisphosphate carboxylase oxygenase large subunit N-methyltransferase, putative, strong similarity to SP:P94026 Ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N- methyltransferase, chloroplast precursor (EC 2.1.1.127) ((Ribulose- bisphosphate-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	4.4	3.7	0.7	3.5	4.56%	2.6
7067	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)	5.1	3.5	1.6	3.5	4.58%	2.7
7069	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	4.8	0.8	3.5	4.59%	2.7
7072	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	4.3	3.6	0.7	3.5	4.60%	2.5
7073	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	6.4	1.0	3.5	4.60%	2.6

Rank	Description	Sync	Root	M	t	adj.q	B
7076	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	8.5	6.4	2.0	3.5	4.61%	2.7
7078	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	4.2	3.0	1.1	3.5	4.61%	2.7
7080	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	7.7	6.3	1.4	3.5	4.62%	2.6
7081	AT5G40550.1 | expressed protein | chr5:16258333-16260609 FORWARD | Aliases: MNF13.7, MNF13_7	3.8	3.1	0.7	3.5	4.62%	2.4
7084	AT1G77510.1 | Symbol: ATPDIL1 2 | Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	8.4	6.6	1.8	3.5	4.62%	2.6
7086	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	11.3	10.6	0.7	3.5	4.63%	2.1
7087	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	4.4	0.6	3.5	4.63%	2.5
7091	AT3G60420.1 | expressed protein | chr3:22345406-22346760 FORWARD | Aliases: T8B10.80	3.1	2.0	1.1	3.5	4.63%	2.5
7092	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	10.2	8.7	1.5	3.5	4.63%	2.6
7095	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	3.3	0.6	3.5	4.64%	2.5
7096	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	4.6	1.0	3.5	4.64%	2.7
7099	AT5G14960.1 | Symbol: DEL2/E2FD/E2L1 |	3.2	2.8	0.4	3.5	4.64%	2.1
7101	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	7.8	7.0	0.8	3.5	4.64%	2.7
7102	AT3G49850.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr3:18500030-18501981 FORWARD | Aliases: T16K5.200	5.1	4.1	1.0	3.5	4.65%	2.7
7103	AT3G08890.2 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr3:2706642-2708753 FORWARD | Aliases: T16O11.17	4.4	3.8	0.6	3.5	4.65%	2.4
7106	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	9.2	8.3	0.9	3.5	4.65%	2.4
7107	AT3G01610.1 | Symbol: CDC48C |	6.3	5.4	0.8	3.5	4.65%	2.4
7109	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 (Arabidopsis thaliana) | chr2:18231342-18233236 FORWARD | Aliases: COI1 SUPPRESSOR1, F6E13.18, F6E13.41, F6E13_41	6.4	5.0	1.4	3.5	4.66%	2.7
7111	AT1G79080.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:29751865-29753837 REVERSE | Aliases: YUP8H12R.30, YUP8H12R_30	4.3	3.2	1.1	3.5	4.66%	2.7
7113	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	5.8	4.0	1.8	3.5	4.66%	2.6

Rank	Description	Sync	Root	M	t	adj.q	B
7114	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	7.9	6.6	1.4	3.5	4.67%	2.7
7115	AT5G07880.1 | Symbol: SNAP29 |	3.4	2.7	0.7	3.5	4.68%	2.6
7117	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	3.8	0.6	3.5	4.68%	2.5
7118	AT2G30060.1 | Ran-binding protein 1b (RanBP1b), nearly identical to atranbp1b (Arabidopsis thaliana) GI:2058284 | chr2:12834036-12835996 FORWARD | Aliases: T27E13.20, T27E13_20	7.7	6.9	0.9	3.5	4.68%	2.3
7119	AT4G00010.1 | expressed protein | chr4:3894-5908 REVERSE | Aliases: T15P10.10, T15P10_10	4.2	3.2	0.9	3.5	4.69%	2.7
7120	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	8.7	8.1	0.6	3.5	4.70%	2.4
7122	AT1G10740.2 | expressed protein | chr1:3568191-3570761 REVERSE | Aliases: T16B5.12, T16B5_12	5.8	4.9	1.0	3.5	4.71%	2.6
7125	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	5.5	4.7	0.9	3.5	4.71%	2.6
7126	AT5G49100.1 | expressed protein | chr5:19914596-19916340 REVERSE | Aliases: K20J1.7, K20J1_7	6.7	4.9	1.8	3.5	4.72%	2.8
7127	AT5G50740.1 | copper chaperone (CCH)-related, low similarity to copper homeostasis factor (GI:3168840)(PMID: 9701579); similar to farnesylated protein ATFP3 (GI:4097547); contains Pfam profile PF00403: Heavy-metal-associated domain | chr5:20654374-20655086 REVERSE | Aliases: MFB16.14, MFB16_14	4.2	3.4	0.8	3.5	4.72%	2.5
7128	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	7.8	6.1	1.8	3.5	4.72%	2.7
7129	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	4.1	3.3	0.7	3.5	4.73%	2.6
7130	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	4.4	3.4	1.1	3.5	4.73%	2.6
7131	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	3.7	3.1	0.7	3.5	4.74%	2.4
7133	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	6.1	5.5	0.6	3.5	4.74%	2.3
7134	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 plumbaginifolia) | chr1:20263359-20265933 FORWARD | Aliases: F20D21.9, F20D21_9	9.7	8.6	1.1	3.5	4.74%	2.5
7135	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	6.0	4.8	1.2	3.5	4.74%	2.6
7136	AT5G58920.1 | expressed protein | chr5:23810355-23811471 FORWARD | Aliases: K19M22.6, K19M22_6	7.0	5.9	1.0	3.5	4.74%	2.6
7138	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	9.4	6.8	2.5	3.5	4.75%	2.4
7141	AT4G29870.1 | expressed protein, predicted protein, Arabidopsis thaliana, PIR2:T01282 | chr4:14606007-14606680 FORWARD | Aliases: F27B13.110, F27B13_110	6.1	5.3	0.8	3.5	4.76%	2.6
7142	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	8.8	7.8	1.0	3.5	4.76%	2.5

Rank	Description	Sync	Root	M	t	adj.q	B
7145	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	4.9	4.0	0.9	3.5	4.76%	2.7
7146	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	6.1	5.4	0.7	3.5	4.76%	2.5
7147	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	6.8	5.5	1.3	3.5	4.77%	2.6
7148	AT1G54680.1 | expressed protein | chr1:20416721-20418149 FORWARD | Aliases: T22H22.11, T22H22_11	8.9	7.7	1.2	3.5	4.77%	2.5
7149	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	4.6	3.5	1.1	3.5	4.77%	2.7
7153	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	4.5	3.5	1.0	3.5	4.78%	2.7
7154	AT1G79560.1 | Symbol: EMB1047/FTSH12 |	5.0	3.8	1.2	3.5	4.78%	2.5
7155	AT3G14900.1 | expressed protein | chr3:5013299-5015284 REVERSE | Aliases: K15M2.4	5.0	3.3	1.7	3.5	4.78%	2.6
7156	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).	9.5	7.9	1.6	3.5	4.78%	2.6
7158	AT4G18580.2 | expressed protein | chr4:10234421-10236028 REVERSE | Aliases: F28J12.240, F28J12_240	7.5	5.8	1.7	3.5	4.79%	2.6
7159	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	8.7	7.5	1.2	3.5	4.79%	2.6
7160	AT5G24390.1 | RabGAP/TBC domain-containing protein, similar to GTPase activating protein (Yarrowia lipolytica) GI:2370595; contains Pfam profile PF00566: TBC domain | chr5:8326003-8329466 REVERSE | Aliases: K16H17.10, K16H17_10	4.6	4.0	0.6	3.5	4.79%	2.4
7164	AT5G44670.1 | expressed protein, contains Pfam:PF01697 Domain of unknown function | chr5:18036132-18038612 REVERSE | Aliases: K15C23.12, K15C23_12	7.0	6.0	1.0	3.5	4.81%	2.6
7167	AT1G61620.1 | expressed protein, contains Pfam profile: PF01363 FYVE zinc finger | chr1:22741208-22743095 FORWARD | Aliases: T25B24.3, T25B24_3	8.3	7.1	1.3	3.5	4.83%	2.6
7168	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	5.2	4.6	0.6	3.5	4.83%	2.2
7169	AT3G25580.1 | thioredoxin-related, contains weak similarity to thioredoxin (Swiss-Prot:O17486) (Echinococcus granulosus) | chr3:9293725-9295584 FORWARD | Aliases: MWL2.25	5.1	4.2	0.9	3.5	4.84%	2.7
7170	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	8.3	7.1	1.2	3.5	4.84%	2.6
7172	AT1G21060.1 | expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547 | chr1:7371788-7374093 FORWARD | Aliases: T22I11.12, T22I11_12	3.9	3.1	0.8	3.5	4.85%	2.5
7173	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	6.1	4.4	1.7	3.5	4.85%	2.7
7176	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	7.4	5.4	2.0	3.5	4.85%	2.6
7177	AT5G10710.2 | expressed protein | chr5:3379145-3382780 FORWARD | Aliases: MAJ23.70, MAJ23_70	8.2	7.4	0.8	3.5	4.85%	2.4

Rank	Description	Sync	Root	M	t	adj.q	B
7179	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	2.5	0.6	3.5	4.85%	2.4
7180	AT3G27060.1 | ribonucleoside-diphosphate reductase small chain, putative / ribonucleotide reductase, putative, similar to ribonucleotide reductase R2 (Nicotiana tabacum) GI:1044912; contains Pfam profile PF00268: Ribonucleotide reductase, small chain | chr3:9981103-9982532 REVERSE | Aliases: MOJ10.15	7.4	5.9	1.5	3.5	4.85%	2.7
7183	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	6.8	5.8	1.0	3.5	4.87%	2.5
7185	AT1G76020.1 | expressed protein | chr1:28535786-28537218 REVERSE | Aliases: T4O12.23, T4O12_23	4.2	3.3	0.9	3.5	4.87%	2.4
7186	AT4G12840.1 | expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707) | chr4:7533618-7535830 REVERSE | Aliases: T20K18.190, T20K18_190	4.9	4.3	0.6	3.5	4.88%	2.3
7188	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	11.1	9.4	1.7	3.5	4.89%	2.4
7189	ATCG00420.1 | Symbol: NDHJ | NADH dehydrogenase subunit | chrC:48677-49153 REVERSE | Aliases: NDHJ	6.3	4.2	2.1	3.5	4.89%	2.7
7190	AT1G12120.1 | expressed protein, contains Pfam domain PF05904: Plant protein of unknown function (DUF863) | chr1:4114769-4117592 REVERSE | Aliases: T28K15.14, T28K15_14	7.7	6.7	1.0	3.5	4.89%	2.4
7196	AT1G74690.1 | calmodulin-binding family protein, low similarity to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif | chr1:28064275-28068286 REVERSE | Aliases: F25A4.33, F25A4_33	6.6	5.4	1.1	3.5	4.91%	2.7
7197	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	3.0	2.5	0.5	3.4	4.92%	2.2
7198	AT1G64680.1 | expressed protein | chr1:24039684-24041064 FORWARD | Aliases: F1N19.25, F1N19_25	5.2	4.3	0.9	3.4	4.92%	2.6
7199	AT5G67080.1 | Symbol: MAPKKK19 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:26789952-26790986 FORWARD | Aliases: K21H1.4, K21H1_4	3.7	3.0	0.8	3.4	4.92%	2.4
7200	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	6.2	5.2	1.0	3.4	4.92%	2.4
7201	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	7.9	6.2	1.7	3.4	4.92%	2.6
7202	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	3.5	2.7	0.8	3.4	4.93%	2.5
7203	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	9.4	8.2	1.2	3.4	4.93%	2.3
7205	AT5G15350.1 | plastocyanin-like domain-containing protein, contains plastocyanin-like domain Pfam:PF02298 | chr5:4984962-4986221 REVERSE | Aliases: F8M21.240, F8M21_240	8.5	6.8	1.8	3.4	4.93%	2.6
7206	AT5G11930.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	5.3	4.4	0.8	3.4	4.93%	2.6
7210	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	6.7	5.9	0.8	3.4	4.95%	2.5

Rank	Description	Sync	Root	M	t	adj.q	B
7211	AT1G32920.1 | expressed protein | chr1:11928787-11929281 FORWARD | Aliases: F9L11.25, F9L11_25	7.9	6.3	1.6	3.4	4.95%	2.6
7212	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	2.5	0.4	3.4	4.95%	2.1
7213	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	3.6	0.7	3.4	4.95%	2.5
7214	AT1G54030.1 | GDSL-motif lipase, putative, similar to myrosinase-associated proteins GI:1769968, GI:1769970, GI:1216391, GI:1216389 from (Brassica napus); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase | chr1:20171302-20173268 FORWARD | Aliases: F15I1.11, F15I1_11	7.8	5.9	1.9	3.4	4.96%	2.6
7218	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	9.3	7.6	1.7	3.4	4.97%	2.5
7220	AT3G19515.1 | expressed protein | chr3:6766674-6769032 REVERSE | Aliases: MLD14.38	8.3	6.9	1.4	3.4	4.98%	2.4
7223	AT4G35130.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:16721089-16723503 REVERSE | Aliases: T12J5.8	3.8	3.4	0.4	3.4	4.98%	1.9
7225	AT5G18920.1 | expressed protein | chr5:6310066-6310848 FORWARD | Aliases: F17K4.170, F17K4_170	4.0	3.3	0.7	3.4	4.99%	2.6
7227	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	4.3	3.4	0.9	3.4	5.00%	2.6
7228	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	11.0	9.5	1.5	3.4	5.00%	2.5
7230	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	4.1	3.4	0.6	3.4	5.00%	2.3
7231	AT5G66760.1 | Symbol: SDH1 1 |	10.5	9.1	1.4	3.4	5.00%	2.5

Rank	Description	Sync	Root	M	t	adj.q	B
1	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	2.6	11.6	-9.0	-57.3	1.3E-7	17.6
2	AT5G59090.3 | similar to subtilase family protein [Arabidopsis thaliana] (TAIR:At5g58820.1); similar to subtilase family protein [Arabidopsis thaliana] (TAIR:At5g59100.1); similar to subtilase family protein [Arabidopsis thaliana] (TAIR:At5g59130.1); similar to subtilase family protein [Arabidopsis thaliana] (TAIR:At5g58840.1); similar to subtilase family protein [Arabidopsis thaliana] (TAIR:At5g59120.1); similar to pre-pro-cucumisin [Cucumis melo] (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	12.1	-9.3	-56.8	1.3E-7	18.4
3	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 thalliana} | chr1:1529767-1531438 FORWARD | Aliases: PEROXIDASE PRECURSOR, RARE COLD INDUCIBLE GENE 3, RCI3A, YUP8H12.13, YUP8H12_13	2.9	11.9	-9.0	-44.1	3.1E-7	14.8
4	AT3G25930.1 | universal stress protein (USP) family protein, contains Pfam PF00582: universal stress protein family | chr3:9494082-9495154 REVERSE | Aliases: MPE11.10	3.1	10.9	-7.8	-44.0	3.1E-7	16.2
5	AT1G43160.1 | Symbol: RAP2.6 |	2.2	11.3	-9.1	-43.7	3.1E-7	15.2
6	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	3.3	11.0	-7.7	-42.9	3.1E-7	14.9
7	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	12.0	-10.0	-42.9	3.1E-7	14.8
8	AT2G16750.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr2:7278094-7281775 FORWARD | Aliases: T24I21.16, T24I21_16	2.5	10.9	-8.4	-42.8	3.1E-7	17.7
9	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	12.7	-9.3	-42.2	3.1E-7	13.3
10	AT1G74760.1 | zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	2.7	10.9	-8.2	-41.8	3.1E-7	14.5
11	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)	4.5	15.3	-10.8	-41.0	3.3E-7	12.1
12	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)	3.2	10.5	-7.3	-38.9	4.7E-7	15.1
13	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	3.5	12.4	-8.9	-36.6	7.0E-7	13.4
14	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	9.7	-7.3	-35.8	7.8E-7	14.0
15	AT1G18100.1 | Symbol: E12A11 |	2.3	9.8	-7.4	-35.4	8.1E-7	13.4
16	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	2.8	12.3	-9.4	-34.0	1.0E-6	12.7
17	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)	4.3	13.6	-9.2	-33.4	1.1E-6	13.0
19	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	2.9	10.6	-7.7	-32.2	1.4E-6	12.8
20	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	12.0	-8.5	-32.0	1.4E-6	13.7

Rank	Description	Sync	Root	M	t	adj.q	B
21	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	4.2	12.7	-8.5	-31.7	1.4E-6	13.2
22	AT3G53480.1 | ABC transporter family protein, PDR5-like ABC transporter, Spirodela polyrrhiza, EMBL:Z70524 | chr3:19836285-19842755 FORWARD | Aliases: F4P12.180	3.4	11.1	-7.7	-31.1	1.6E-6	14.7
24	AT2G28160.1 | basic helix-loop-helix (bHLH) family protein | chr2:12011785-12013199 FORWARD | Aliases: F24D13.5, F24D13_5	2.8	10.8	-8.1	-29.8	1.9E-6	12.9
25	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	3.6	12.2	-8.6	-29.8	1.9E-6	13.7
27	AT5G64100.1 | peroxidase, putative, identical to peroxidase ATP3a (Arabidopsis thaliana) gi:1546698:emb:CAA67340 | chr5:25667867-25669349 REVERSE | Aliases: MHJ24.8, MHJ24_8	3.2	11.8	-8.6	-29.7	1.9E-6	11.6
28	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	3.7	13.5	-9.8	-29.6	1.9E-6	10.2
29	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	9.2	-6.4	-29.3	2.0E-6	12.9
30	AT3G11340.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:3556713-3558275 FORWARD | Aliases: F11B9.23	3.0	10.5	-7.4	-28.8	2.1E-6	12.0
31	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	3.0	10.9	-7.9	-28.7	2.1E-6	13.8
32	AT4G11530.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr4:6985617-6989593 FORWARD | Aliases: F25E4.150, F25E4_150	3.0	8.7	-5.7	-28.6	2.1E-6	13.4
33	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	3.6	11.3	-7.7	-28.3	2.3E-6	13.1
34	AT5G09530.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr5:2959735-2961272 REVERSE | Aliases: T5E8.2	3.2	10.4	-7.2	-28.2	2.3E-6	14.9
35	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	4.4	13.0	-8.6	-28.0	2.3E-6	12.1
39	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	8.6	-5.7	-27.3	2.6E-6	14.2
41	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	3.8	11.4	-7.6	-27.0	2.6E-6	12.5
42	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	11.2	-8.7	-27.0	2.6E-6	10.3
43	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	2.9	11.0	-8.1	-26.9	2.7E-6	12.4
44	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	4.4	10.8	-6.5	-26.8	2.7E-6	12.4
45	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	3.1	10.2	-7.2	-26.7	2.7E-6	12.7
46	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	12.4	-9.0	-26.6	2.7E-6	12.6

Rank	Description	Sync	Root	M	t	adj.q	B
48	AT5G19890.1 | peroxidase, putative, identical to peroxidase (Arabidopsis thaliana) gi:1403134:emb:CAA67092 | chr5:6724117-6725925 REVERSE | Aliases: F28I16.40, F28I16_40	3.4	11.9	-8.5	-26.5	2.7E-6	13.6
49	AT4G11290.1 | peroxidase, putative, identical to peroxidase ATP19a (Arabidopsis thaliana) gi:1546692:emb:CAA67337 | chr4:6869959-6871657 FORWARD | Aliases: F8L21.80, F8L21_80	2.0	9.0	-7.0	-25.9	3.1E-6	12.3
50	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	3.9	12.4	-8.5	-25.6	3.3E-6	11.9
52	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	3.4	10.6	-7.2	-25.5	3.3E-6	12.1
53	AT5G26280.1 | 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 | chr5:9208715-9210575 FORWARD | Aliases: F9D12.7	4.5	11.4	-6.9	-25.2	3.6E-6	13.4
54	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 (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563 | chr1:3665089-3667139 REVERSE | Aliases: T19D16.11, T19D16_11, ZRT, IRT LIKE PROTEIN	4.8	11.4	-6.5	-25.2	3.6E-6	11.8
55	AT5G19970.1 | expressed protein, ; expression supported by MPSS | chr5:6747552-6748643 FORWARD | Aliases: F28I16.120, F28I16_120	3.3	10.2	-6.9	-25.1	3.6E-6	11.5
56	AT1G49500.1 | expressed protein | chr1:18325476-18325952 REVERSE | Aliases: F13F21.6, F13F21_6	4.4	10.9	-6.5	-25.0	3.7E-6	12.8
57	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	5.3	13.7	-8.4	-24.8	3.8E-6	10.2
58	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	3.7	11.0	-7.3	-24.8	3.8E-6	13.5
59	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	4.4	11.1	-6.7	-24.7	3.9E-6	11.2
60	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	4.1	11.4	-7.2	-24.6	3.9E-6	12.9
61	AT1G13300.1 | myb family transcription factor, contains Pfam domain, PF00249: Myb-like DNA-binding domain | chr1:4556889-4558705 FORWARD | Aliases: T6J4.6, T6J4_6	5.5	11.7	-6.2	-24.5	3.9E-6	12.4
62	AT5G54040.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	11.5	-8.9	-24.3	4.2E-6	15.0
63	AT3G61390.2 | U-box domain-containing protein, several hypothetical proteins - Arabidopsis thaliana | chr3:22727328-22729348 FORWARD | Aliases: F2A19.1	2.6	9.2	-6.6	-24.2	4.2E-6	14.7
64	AT1G44050.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.4	9.2	-6.8	-24.1	4.4E-6	14.6
65	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	4.3	12.0	-7.7	-24.0	4.4E-6	10.7
67	AT1G13110.1 | Symbol: CYP71B7 | cytochrome P450 71B7 (CYP71B7), identical to (SP:Q96514) cytochrome P450 71B7 (Arabidopsis thaliana);	2.9	9.9	-6.9	-24.0	4.4E-6	12.0
69	AT4G32650.3 | Symbol: ATKC1 | similar to inward rectifying potassium channel (KAT2) [Arabidopsis thaliana] (TAIR:At4g18290.1); similar to potassium channel [Daucus carota] (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)	2.8	10.0	-7.3	-23.4	5.0E-6	12.1
70	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	2.9	11.0	-8.0	-23.4	5.1E-6	13.1

Rank	Description	Sync	Root	M	t	adj.q	B
71	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 (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563 | chr1:22448988-22450810 REVERSE | Aliases: T7P1.10, T7P1_10	8.0	12.2	-4.2	-23.3	5.1E-6	13.6
72	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	10.0	-7.6	-23.2	5.3E-6	11.9
73	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	3.0	10.7	-7.6	-23.0	5.6E-6	10.4
74	AT2G35585.1 | expressed protein | chr2:14943745-14945042 FORWARD | Aliases: None	2.8	9.4	-6.7	-22.6	6.4E-6	12.0
75	AT1G30750.1 | expressed protein | chr1:10904889-10905691 REVERSE | Aliases: T5I8.20	2.6	9.4	-6.8	-22.5	6.5E-6	11.0
79	AT4G00700.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr4:286051-289514 FORWARD | Aliases: F6N23.8, F6N23_8	3.3	9.7	-6.4	-22.2	6.9E-6	11.0
80	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	2.9	10.7	-7.7	-22.1	7.0E-6	11.4
81	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	3.3	10.3	-7.0	-21.8	7.6E-6	12.6
82	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	2.8	8.7	-6.0	-21.7	7.9E-6	12.8
83	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	3.8	10.1	-6.3	-21.7	7.9E-6	12.4
86	AT5G58350.1 | Symbol: WNK4 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:23602401-23605027 FORWARD | Aliases: MCK7.22, MCK7_22, ZIK2	3.6	9.2	-5.6	-21.5	8.2E-6	13.3
87	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	5.0	11.0	-6.0	-21.4	8.2E-6	11.8
88	AT2G01880.1 | purple acid phosphatase (PAP7), identical to purple acid phosphatase (PAP7) GI:20257476 from (Arabidopsis thaliana); contains Pfam profile: PF00149 calcineurin-like phosphoesterase | chr2:391422-393999 REVERSE | Aliases: T23K3.7, T23K3_7	2.8	9.9	-7.1	-21.4	8.4E-6	11.7
89	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	7.9	-5.8	-21.2	8.5E-6	13.0
91	AT4G13580.1 | disease resistance-responsive family protein, contains similarity to pathogenesis-related protein (Pisum sativum) gi:4585273:gb:AAD25355	3.7	11.7	-8.0	-21.2	8.5E-6	9.5
92	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	3.8	11.5	-7.7	-21.1	8.5E-6	10.0
94	AT3G20960.1 | Symbol: CYP705A33 | cytochrome P450 family protein, similar to Cytochrome P450 93A1 (SP:Q42798)	2.8	8.5	-5.7	-21.1	8.5E-6	12.2
95	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	4.8	10.7	-5.9	-21.1	8.5E-6	10.8

Rank	Description	Sync	Root	M	t	adj.q	B
97	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:At2g13680.1); 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 alata] (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	6.2	11.9	-5.7	-21.0	8.8E-6	11.1
98	AT4G24130.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr4:12527785-12528602 FORWARD | Aliases: T19F6.120, T19F6_120	3.5	10.5	-7.0	-20.9	8.8E-6	11.7
100	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	12.0	-6.0	-20.7	9.4E-6	11.2
101	AT2G32150.1 | haloacid dehalogenase-like hydrolase family protein, contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	5.2	11.0	-5.8	-20.7	9.5E-6	11.3
102	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	3.3	10.5	-7.3	-20.6	9.6E-6	11.9
103	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	10.5	-7.7	-20.5	1.0E-5	9.8
105	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	6.0	13.4	-7.4	-20.4	1.0E-5	10.4
107	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	3.0	10.0	-6.9	-20.3	1.0E-5	10.7
108	AT1G30870.1 | cationic peroxidase, putative, similar to cationic peroxidase (gi:1232069); similar to EST gb:AI100412 | chr1:10991466-10993004 FORWARD | Aliases: T17H7.19	3.1	10.6	-7.4	-20.3	1.0E-5	12.2
109	AT4G15340.1 | Symbol: ATPEN1 |	2.3	8.6	-6.3	-20.3	1.0E-5	11.7
110	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	4.4	9.7	-5.2	-20.2	1.1E-5	11.2
111	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	3.0	10.7	-7.7	-20.1	1.1E-5	12.3
112	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	9.7	-6.8	-20.0	1.1E-5	9.9
113	AT5G43580.1 | protease inhibitor, putative, similar to SP:P19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}; contains Pfam profile PF00280: Potato inhibitor I family	3.5	9.8	-6.3	-20.0	1.1E-5	11.3
114	AT5G48290.2 | similar to heavy-metal-associated domain-containing protein [Arabidopsis thaliana] (TAIR:At3g07600.1); similar to OSJNBa0016O02.17 [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	9.5	-7.1	-20.0	1.1E-5	11.7
115	AT5G04730.1 | expressed protein, ; expression supported by MPSS | chr5:1364102-1365067 REVERSE | Aliases: MUK11.5	2.4	8.3	-5.9	-20.0	1.1E-5	11.6
116	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	9.9	-6.8	-19.9	1.1E-5	10.4
117	AT3G48360.1 | speckle-type POZ	3.3	9.7	-6.4	-19.8	1.1E-5	10.9

Rank	Description	Sync	Root	M	t	adj.q	B
118	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	4.3	10.1	-5.7	-19.8	1.2E-5	12.4
119	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 ATFP6 (GI:4097553); contains heavy-metal-associated domain PF00403 | chr4:16685725-16686708 REVERSE | Aliases: T12J5.12	3.3	9.8	-6.6	-19.8	1.2E-5	10.9
121	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	9.6	-6.3	-19.5	1.2E-5	10.0
122	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	4.0	12.1	-8.1	-19.4	1.3E-5	12.6
123	AT2G36380.1 | ABC transporter family protein, related to multi drug resistance proteins and P-glycoproteins | chr2:15264662-15270766 FORWARD | Aliases: F1O11.1, F1O11_1	6.1	10.9	-4.7	-19.4	1.3E-5	12.3
125	AT4G17215.1 | expressed protein | chr4:9655848-9656588 FORWARD | Aliases: None	3.8	9.8	-6.0	-19.3	1.3E-5	11.5
126	AT2G37750.1 | expressed protein | chr2:15838067-15838636 FORWARD | Aliases: T8P21.37	3.8	10.8	-7.0	-19.3	1.3E-5	9.5
127	AT3G43800.1 | Symbol: ATGSTU27 | glutathione S-transferase, putative, glutathione transferase, papaya, PIR:T09781 | chr3:15671846-15672912 FORWARD | Aliases: T28A8.90	5.1	10.6	-5.5	-19.3	1.3E-5	12.4
128	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	4.5	11.2	-6.7	-19.2	1.3E-5	10.0
129	AT3G14680.1 | Symbol: CYP72A14 | cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus) | chr3:4934428-4936570 FORWARD | Aliases: MIE1.1	3.4	10.1	-6.6	-19.2	1.3E-5	10.4
130	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 hosphatidylinositol/phophatidylcholine 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	10.4	-7.2	-19.2	1.3E-5	10.4
131	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	2.9	9.5	-6.6	-19.1	1.4E-5	10.5
132	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	9.3	-6.1	-18.8	1.6E-5	10.6
133	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	5.9	11.3	-5.4	-18.7	1.6E-5	11.7
136	AT3G16560.1 | protein phosphatase 2C-related / PP2C-related, contains protein phosphatase 2C domain | chr3:5635602-5638488 REVERSE | Aliases: MDC8.3	3.4	8.8	-5.5	-18.6	1.6E-5	10.2
138	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	4.1	9.4	-5.3	-18.6	1.6E-5	10.9
139	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	4.2	9.6	-5.4	-18.5	1.6E-5	11.4
141	AT3G47730.1 | Symbol: ATATH1 |	4.9	10.4	-5.5	-18.5	1.7E-5	11.5

Rank	Description	Sync	Root	M	t	adj.q	B
142	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	6.1	11.8	-5.7	-18.5	1.7E-5	10.3
143	AT5G50400.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	9.1	12.0	-2.9	-18.5	1.7E-5	13.4
144	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	3.6	9.0	-5.5	-18.4	1.7E-5	11.8
145	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	3.1	8.4	-5.2	-18.3	1.7E-5	10.4
147	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	6.4	13.3	-6.9	-18.2	1.8E-5	9.5
148	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	11.4	-4.8	-18.0	1.9E-5	11.7
150	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	2.8	9.4	-6.6	-18.0	2.0E-5	9.4
152	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	3.6	10.8	-7.2	-18.0	2.0E-5	9.5
153	AT3G44990.1 | Symbol: XTR8 | xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative | chr3:16457960-16459749 REVERSE | Aliases: ATXTR8, F14D17.60	6.4	12.1	-5.7	-17.9	2.0E-5	11.9
156	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	2.4	8.5	-6.1	-17.8	2.1E-5	9.9
157	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	2.7	8.5	-5.8	-17.7	2.1E-5	9.4
159	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	7.7	-5.0	-17.6	2.2E-5	10.6
160	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	2.8	8.4	-5.6	-17.6	2.2E-5	9.7
161	AT5G65530.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr5:26207823-26210192 REVERSE | Aliases: K21L13.3, K21L13_3	3.3	9.7	-6.4	-17.6	2.2E-5	10.3
163	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	3.2	9.8	-6.5	-17.4	2.4E-5	9.1
165	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	9.3	-5.8	-17.3	2.4E-5	9.7
167	AT1G78080.1 | Symbol: RAP2.4 |	3.8	8.9	-5.1	-17.3	2.5E-5	11.1
170	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	3.1	9.9	-6.7	-17.2	2.5E-5	8.5
171	AT3G04720.1 | Symbol: PR4 | hevein-like protein (HEL), identical to SP:P43082 Hevein-like protein precursor {Arabidopsis thaliana}; similar to SP:P09762 Wound-induced protein WIN2 precursor {Solanum tuberosum}; contains Pfam profile PF00187: Chitin recognition protein | chr3:1285573-1286568 REVERSE | Aliases: F7O18.21, F7O18_21, HEL, HEVEIN LIKE, PATHOGENESIS RELATED 4, PR 4	6.8	12.3	-5.6	-17.2	2.5E-5	9.6

Rank	Description	Sync	Root	M	t	adj.q	B
172	AT1G15670.1 | 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 | chr1:5389947-5391485 FORWARD | Aliases: F7H2.1, F7H2_1	3.7	9.8	-6.2	-17.2	2.5E-5	10.5
173	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	2.9	9.1	-6.2	-17.2	2.5E-5	9.5
174	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	5.7	9.6	-4.0	-17.2	2.5E-5	11.5
177	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	3.1	9.8	-6.7	-17.0	2.6E-5	12.3
178	AT2G45920.1 | U-box domain-containing protein, contains Pfam profile PF04564: U-box domain | chr2:18906288-18908376 FORWARD | Aliases: F4I18.10	4.3	9.9	-5.6	-17.0	2.7E-5	11.6
179	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	8.2	-5.6	-16.9	2.7E-5	11.0
180	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	2.7	9.0	-6.4	-16.9	2.7E-5	9.3
181	AT1G54370.1 | sodium proton exchanger, putative (NHX5), contains similarity to Na+/H+ 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	3.1	8.2	-5.0	-16.9	2.7E-5	10.2
182	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	3.3	7.9	-4.5	-16.9	2.7E-5	11.6
183	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	6.6	11.7	-5.1	-16.9	2.7E-5	11.7
184	AT5G61340.1 | expressed protein | chr5:24679230-24680343 REVERSE | Aliases: MFB13.11, MFB13_11	2.9	8.8	-5.9	-16.8	2.7E-5	10.7
185	AT5G35190.1 | proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr5:13451411-13452397 FORWARD | Aliases: T25C13.70, T25C13_70	3.6	10.0	-6.4	-16.8	2.7E-5	10.3
186	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	2.6	9.0	-6.4	-16.8	2.8E-5	10.7
188	AT1G68440.1 | expressed protein | chr1:25661696-25662936 FORWARD | Aliases: T2E12.1, T2E12_1	4.4	9.9	-5.5	-16.7	2.8E-5	10.6
191	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	2.8	8.5	-5.7	-16.7	2.8E-5	10.2
192	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)	4.6	8.8	-4.2	-16.7	2.8E-5	10.8
196	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	8.0	12.6	-4.5	-16.7	2.8E-5	11.3
197	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	5.3	9.0	-3.7	-16.7	2.8E-5	11.7
198	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	4.5	9.8	-5.3	-16.7	2.8E-5	11.5
204	AT3G23160.1 | expressed protein, contains Pfam domain PF05003: protein of unknown function (DUF668); expression supported by MPSS | chr3:8260066-8261634 REVERSE | Aliases: K14B15.5	4.5	8.8	-4.3	-16.6	2.8E-5	11.1

Rank	Description	Sync	Root	M	t	adj.q	B
207	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	10.8	-6.4	-16.5	2.9E-5	10.4
210	AT3G21710.2 | expressed protein | chr3:7648366-7649792 FORWARD | Aliases: MSD21.2	5.4	10.9	-5.5	-16.3	3.0E-5	9.2
211	AT5G04960.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:1461911-1463970 FORWARD | Aliases: MUG13.18, MUG13_18	2.9	9.8	-6.9	-16.3	3.1E-5	10.3
214	AT3G54590.1 | Symbol: ATHRGP1 | proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965	3.0	11.2	-8.2	-16.1	3.3E-5	8.4
215	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	3.8	8.8	-5.0	-16.1	3.4E-5	10.0
216	AT5G58900.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr5:23800349-23802560 REVERSE | Aliases: K19M22.10, K19M22_10	6.9	10.5	-3.6	-16.1	3.4E-5	11.2
217	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	2.9	7.2	-4.3	-16.1	3.4E-5	10.8
218	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	4.0	8.6	-4.6	-16.0	3.4E-5	10.6
219	AT1G29020.1 | calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain | chr1:10120483-10127054 REVERSE | Aliases: F28N24.34	3.2	8.0	-4.8	-16.0	3.5E-5	9.8
220	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	6.4	11.3	-4.9	-16.0	3.5E-5	11.2
221	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	3.2	8.9	-5.7	-15.9	3.6E-5	9.5
224	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	2.7	8.3	-5.6	-15.8	3.7E-5	10.2
225	AT1G64405.1 | expressed protein | chr1:23927395-23927999 FORWARD | Aliases: None	3.2	7.9	-4.7	-15.8	3.7E-5	11.3
226	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	5.0	9.1	-4.1	-15.8	3.7E-5	10.8
230	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	4.5	10.8	-6.3	-15.7	3.9E-5	11.0
231	AT4G27410.2 | Symbol: RD26 | no apical meristem (NAM) family protein (RD26), contains Pfam PF02365: No apical meristem (NAM) domain; Arabidopsis thaliana nap gene,PID:e1234813; identical to cDNA RD26 mRNA for NAM-like protein GI:15375403	7.2	11.8	-4.6	-15.7	3.9E-5	10.2
232	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	7.7	11.0	-3.3	-15.6	3.9E-5	11.5
234	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 (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563 | chr1:1545215-1547797 REVERSE | Aliases: YUP8H12.8, YUP8H12_8	4.0	10.3	-6.3	-15.5	4.0E-5	9.0
235	AT2G21100.1 | disease resistance-responsive protein-related / dirigent protein-related, similar to dirigent protein (Thuja plicata) gi:6694699:gb:AAF25360; similar to disease resistance response protein 206-d (Pisum sativum) gi:508844:gb:AAB18669	3.7	8.7	-5.1	-15.5	4.0E-5	9.6

Rank	Description	Sync	Root	M	t	adj.q	B
236	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	3.9	8.8	-4.9	-15.5	4.0E-5	11.6
237	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)	6.6	11.0	-4.4	-15.5	4.0E-5	10.7
238	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	9.7	-5.7	-15.5	4.0E-5	9.3
239	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	5.3	11.1	-5.8	-15.5	4.1E-5	8.9
245	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	3.5	8.2	-4.7	-15.4	4.2E-5	10.6
246	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	4.9	9.5	-4.6	-15.4	4.2E-5	10.9
247	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	2.7	8.5	-5.7	-15.3	4.2E-5	9.2
248	AT1G18910.1 | zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	3.8	8.8	-5.0	-15.3	4.2E-5	10.0
249	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	10.6	-7.4	-15.3	4.2E-5	8.8
251	AT3G61930.1 | expressed protein | chr3:22946485-22947156 FORWARD | Aliases: F21F14.100	4.2	10.6	-6.4	-15.3	4.3E-5	9.2
254	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	6.7	11.2	-4.5	-15.2	4.3E-5	10.9
256	AT1G78000.2 | Symbol: SULTR1;2 | sulfate transporter (Sultr1;2), identical to sulfate transporter Sultr1;2 (Arabidopsis thaliana) GI:7768660; contaisn 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	7.2	11.4	-4.2	-15.2	4.3E-5	10.6
257	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	3.9	10.5	-6.6	-15.2	4.5E-5	8.7
258	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	5.7	9.0	-3.3	-15.2	4.5E-5	11.0
260	AT5G25770.2 | expressed protein | chr5:8969219-8972049 REVERSE | Aliases: F18A17.20, F18A17_20	9.7	11.7	-2.1	-15.1	4.5E-5	12.3
261	AT4G21410.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr4:11402325-11405067 REVERSE | Aliases: F18E5.30	5.5	9.9	-4.4	-15.1	4.6E-5	10.3
262	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	4.3	9.1	-4.8	-15.1	4.6E-5	10.1
263	AT1G24440.1 | expressed protein, similar to MTD2 (Medicago truncatula) GI:9294812 | chr1:8662007-8663952 FORWARD | Aliases: F21J9.10	6.5	9.5	-2.9	-15.0	4.6E-5	11.3
264	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	9.8	-4.5	-15.0	4.6E-5	10.5
265	AT5G42250.1 | alcohol dehydrogenase, putative, similar to alcohol dehydrogenase ADH GI:7705214 from (Lycopersicon esculentum); contains Pfam zinc-binding dehydrogenase domain PF00107	4.1	10.5	-6.5	-15.0	4.7E-5	8.9
266	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	9.0	-5.6	-15.0	4.7E-5	9.5

Rank	Description	Sync	Root	M	t	adj.q	B
268	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	5.2	9.2	-4.0	-15.0	4.7E-5	10.7
270	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	7.3	9.5	-2.3	-15.0	4.7E-5	12.0
271	AT5G12170.1 | expressed protein, similar to unknown protein (pir::T09909) | chr5:3933503-3934962 FORWARD | Aliases: MXC9.13, MXC9_13	6.3	10.4	-4.1	-15.0	4.7E-5	10.1
272	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	8.3	-5.6	-15.0	4.7E-5	8.4
273	AT1G80180.1 | expressed protein | chr1:30161718-30162476 REVERSE | Aliases: F18B13.26, F18B13_26	6.7	11.2	-4.4	-15.0	4.7E-5	10.3
274	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	4.7	10.8	-6.1	-14.9	4.8E-5	10.6
275	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	4.4	8.7	-4.3	-14.9	4.8E-5	10.7
276	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	4.2	8.9	-4.7	-14.8	4.9E-5	10.0
278	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	3.1	8.5	-5.4	-14.8	5.0E-5	10.0
279	AT1G27030.1 | expressed protein | chr1:9381790-9383970 FORWARD | Aliases: T7N9.9, T7N9_9	5.2	9.5	-4.3	-14.8	5.0E-5	11.0
283	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	3.3	10.5	-7.2	-14.7	5.2E-5	10.7
285	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	3.1	9.6	-6.5	-14.7	5.2E-5	8.7
286	AT1G30700.1 | 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 | chr1:10892552-10894554 FORWARD | Aliases: T5I8.15, T5I8_15	2.9	8.2	-5.3	-14.6	5.4E-5	11.2
287	AT1G02900.1 | Symbol: RALFL1 |	6.2	11.1	-4.9	-14.6	5.4E-5	9.7
288	AT1G03850.2 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	4.5	10.0	-5.5	-14.5	5.6E-5	8.8
290	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	2.8	5.6	-2.7	-14.5	5.7E-5	11.6
291	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	2.9	7.7	-4.8	-14.4	5.9E-5	9.3
292	AT5G49770.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:20240086-20244493 FORWARD | Aliases: K2I5.14, K2I5_14	2.5	8.9	-6.5	-14.4	5.9E-5	9.8
294	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	9.7	-6.5	-14.4	5.9E-5	10.1
299	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	3.7	10.3	-6.7	-14.3	6.1E-5	8.7
302	AT3G19030.1 | expressed protein, contains similarity to phosphoserine aminotransferase GB:P19689 from (Yersinia enterocolitica) | chr3:6563985-6564430 REVERSE | Aliases: K13E13.14	3.5	9.5	-6.0	-14.2	6.3E-5	9.5

Rank	Description	Sync	Root	M	t	adj.q	B
303	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	6.4	12.0	-5.7	-14.2	6.3E-5	10.7
307	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	6.3	10.8	-4.5	-14.2	6.4E-5	10.0
308	AT4G39675.1 | expressed protein | chr4:18413769-18414232 FORWARD | Aliases: None	5.6	11.4	-5.7	-14.2	6.4E-5	11.3
311	AT5G66490.1 | expressed protein | chr5:26564453-26564994 REVERSE | Aliases: K1F13.15, K1F13_15	4.5	9.6	-5.1	-14.1	6.4E-5	10.5
312	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	5.3	-3.2	-14.1	6.5E-5	10.8
314	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	9.8	-6.9	-14.0	6.7E-5	8.8
316	AT1G55850.1 | Symbol: ATCSLE1 | cellulose synthase family protein, similar to cellulose synthase catalytic subunit (gi:13925881) from Nicotiana alata, cellulose synthase-5 (gi:9622882) from Zea mays | chr1:20880365-20883146 FORWARD | Aliases: CSLE1, F14J16.9, F14J16_9	7.3	10.9	-3.5	-14.0	6.7E-5	10.8
317	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)	5.5	9.0	-3.6	-14.0	6.7E-5	10.6
318	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	3.2	9.5	-6.4	-14.0	6.7E-5	7.7
319	AT2G20960.1 | Symbol: PEARLI4 | expressed protein, pEARLI 4 gene product (Arabidopsis thaliana) GI:871782 | chr2:9013729-9016844 FORWARD | Aliases: F26H11.28, F26H11_28, PEARLI4	4.3	7.4	-3.1	-14.0	6.7E-5	10.6
320	AT1G34040.1 | alliinase family protein, contains Pfam profiles: PF04864 allinase C-terminal domain, PF04863 alliinase EGF-like domain | chr1:12374413-12376159 FORWARD | Aliases: F12G12.14, F12G12_14	2.6	7.2	-4.7	-14.0	6.7E-5	9.1
321	AT1G34060.1 | alliinase family protein, contains Pfam profiles: PF04864 allinase C-terminal domain, PF04863 alliinase EGF-like domain | chr1:12396399-12398348 REVERSE | Aliases: F12G12.12, F12G12_12	2.6	7.2	-4.7	-14.0	6.7E-5	9.1
322	AT1G32450.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr1:11715130-11719935 REVERSE | Aliases: F5D14.23, F5D14_23	6.5	10.3	-3.9	-14.0	6.7E-5	10.1
324	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	5.3	10.5	-5.2	-14.0	6.7E-5	9.9
325	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	5.6	9.2	-3.5	-13.9	6.9E-5	10.4
327	AT4G19160.3 | expressed protein | chr4:10477307-10480150 FORWARD | Aliases: T18B16.130, T18B16_130	5.7	10.4	-4.7	-13.9	6.9E-5	10.3
328	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	4.7	9.0	-4.3	-13.9	7.1E-5	10.0
329	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	6.2	11.9	-5.7	-13.9	7.1E-5	10.1
332	AT2G25160.1 | Symbol: CYP82F1 | cytochrome P450, putative, similar to cytochrome p450(CYP82C1p) GI:2739004 from (Glycine max)	2.6	7.2	-4.6	-13.8	7.2E-5	8.8
333	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	6.0	11.3	-5.3	-13.8	7.3E-5	8.4
334	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	5.4	9.2	-3.7	-13.8	7.3E-5	10.3

Rank	Description	Sync	Root	M	t	adj.q	B
335	AT1G67730.1 | b-keto acyl reductase, putative (GLOSSY8), similar to b-keto acyl reductase GI:2586127 from (Hordeum vulgare) | chr1:25395123-25397273 FORWARD | Aliases: F12A21.14, F12A21_14	8.8	11.5	-2.7	-13.8	7.3E-5	11.4
337	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	8.5	-5.7	-13.7	7.5E-5	7.9
340	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	7.5	10.2	-2.7	-13.7	7.5E-5	10.9
344	AT3G61380.1 | expressed protein | chr3:22719459-22722254 REVERSE | Aliases: F2A19.4	4.6	7.8	-3.2	-13.6	7.9E-5	10.8
345	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	6.1	8.6	-2.5	-13.6	7.9E-5	11.3
346	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	6.8	10.4	-3.5	-13.6	7.9E-5	10.2
347	AT2G47890.2 | zinc finger (B-box type) family protein | chr2:19615066-19616702 FORWARD | Aliases: F17A22.28	6.1	10.1	-4.0	-13.6	7.9E-5	9.9
348	AT4G23700.1 | Symbol: ATCHX17 | cation/hydrogen exchanger, putative (CHX17), similar to Na+/H+-exchanging protein slr1595 - Synechocystis sp., EMBL:D90902; monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563	3.7	8.9	-5.2	-13.5	8.1E-5	9.7
349	AT5G07220.1 | BAG domain-containing protein, contains Pfam:PF02179 BAG domain | chr5:2265257-2266968 REVERSE | Aliases: T28J14.160, T28J14_160	5.4	9.5	-4.0	-13.5	8.3E-5	10.0
350	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	11.1	12.7	-1.5	-13.5	8.3E-5	11.7
352	AT1G12110.1 | Symbol: NRT1.1 |	7.8	11.4	-3.6	-13.5	8.3E-5	10.7
353	AT3G08760.1 | Symbol: ATSIK | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:2657924-2660833 REVERSE | Aliases: F17O14.23	4.5	8.0	-3.6	-13.5	8.3E-5	10.7
357	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	3.8	8.4	-4.6	-13.4	8.6E-5	10.4
358	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	5.6	9.1	-3.5	-13.4	8.6E-5	9.9
360	AT1G70780.1 | expressed protein | chr1:26698845-26700041 REVERSE | Aliases: F5A18.4, F5A18_4	10.2	11.8	-1.5	-13.4	8.7E-5	11.6
361	AT5G57740.1 | Symbol: XBAT32 |	3.2	5.9	-2.7	-13.3	8.8E-5	10.6
362	AT3G56980.1 | Symbol: ORG3 | basic helix-loop-helix (bHLH) family protein | chr3:21097525-21098473 REVERSE | Aliases: T8M16.8	4.8	9.8	-5.0	-13.3	8.9E-5	9.0
363	AT3G62040.1 | similar to haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] (TAIR:At5g59490.1); similar to expressed protein [Oryza sativa (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	3.8	9.6	-5.8	-13.3	8.9E-5	8.7
364	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	7.0	-4.0	-13.3	8.9E-5	9.3
367	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	9.5	-2.9	-13.3	8.9E-5	10.5
370	AT1G03660.1 | expressed protein, contains 2 predicted transmembrane domains; expression supported by MPSS | chr1:911435-911758 REVERSE | Aliases: F21B7.26, F21B7_26	3.8	8.0	-4.2	-13.2	9.3E-5	9.6

Rank	Description	Sync	Root	M	t	adj.q	B
371	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	3.7	9.0	-5.3	-13.2	9.3E-5	9.2
372	AT2G45830.2 | expressed protein | chr2:18873135-18875616 FORWARD | Aliases: F4I18.19	4.6	9.0	-4.4	-13.2	9.4E-5	10.3
374	AT3G25190.1 | nodulin, putative, similar to nodulin 21 (N-21) (Glycine max) SWISS-PROT:P16313 | chr3:9175694-9177013 FORWARD | Aliases: MJL12.26	4.8	9.7	-4.9	-13.2	9.4E-5	9.1
378	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	3.9	8.8	-4.9	-13.1	9.6E-5	9.4
382	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	3.8	8.6	-4.8	-13.0	9.9E-5	9.0
384	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	8.4	10.6	-2.2	-13.0	1.0E-4	10.9
385	AT5G44610.1 | DREPP plasma membrane polypeptide-related, contains Pfam profile: PF05558 DREPP plasma membrane polypeptide | chr5:18010792-18011895 REVERSE | Aliases: K15C23.5, K15C23_5	5.8	11.8	-5.9	-13.0	1.0E-4	8.9
392	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	2.8	8.4	-5.6	-13.0	1.0E-4	8.1
394	AT5G56080.1 | nicotianamine synthase, putative, similar to nicotianamine synthase (Lycopersicon esculentum)(GI:4753801), nicotianamine synthase 2 (Hordeum vulgare)(GI:4894912) | chr5:22728628-22729590 REVERSE | Aliases: MDA7.14, MDA7_14	2.6	8.5	-5.9	-12.9	1.0E-4	7.2
395	AT4G02090.1 | expressed protein | chr4:923100-923916 FORWARD | Aliases: T10M13.10, T10M13_10	3.7	8.8	-5.1	-12.9	1.0E-4	9.1
397	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	3.7	8.1	-4.4	-12.9	1.0E-4	9.4
399	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	5.8	8.9	-3.1	-12.9	1.0E-4	10.4
400	AT2G27920.3 | Symbol: SCPL51 |	3.7	8.2	-4.4	-12.9	1.0E-4	9.2
401	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	4.0	8.0	-4.0	-12.9	1.1E-4	9.5
402	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	3.3	8.5	-5.2	-12.8	1.1E-4	8.0
403	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	6.1	10.2	-4.1	-12.8	1.1E-4	10.9
404	AT2G17710.1 | expressed protein | chr2:7700678-7701828 FORWARD | Aliases: T17A5.17, T17A5_17	6.1	11.2	-5.1	-12.8	1.1E-4	9.5
409	AT4G30450.1 | glycine-rich protein | chr4:14886033-14886681 REVERSE | Aliases: F17I23.210, F17I23_210	8.4	10.8	-2.4	-12.8	1.1E-4	11.0
412	AT1G73920.2 | lipase family protein, similar to lipase GB:CAA74737 (SP:O46108) from (Drosophila melanogaster) | chr1:27794537-27798575 FORWARD | Aliases: F2P9.21, F2P9_21	6.1	9.8	-3.8	-12.7	1.1E-4	9.8
414	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	3.1	6.2	-3.1	-12.7	1.1E-4	10.1
416	AT1G54970.1 | Symbol: ATPRP1 |	3.0	9.0	-6.1	-12.7	1.1E-4	8.8

Rank	Description	Sync	Root	M	t	adj.q	B
418	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	7.4	9.6	-2.2	-12.7	1.1E-4	10.7
419	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	5.9	9.9	-4.0	-12.6	1.1E-4	9.1
420	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	4.5	8.2	-3.7	-12.6	1.1E-4	9.8
421	AT2G19060.1 | GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL6 GI:15054390, EXL1 GI:15054382, EXL2 GI:15054384 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	3.6	8.0	-4.5	-12.6	1.1E-4	9.0
424	AT5G58770.1 | dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative, similar to GI:796076 | chr5:23751602-23752860 FORWARD | Aliases: MZN1.21, MZN1_21	2.6	7.7	-5.1	-12.6	1.1E-4	8.0
425	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, METHYLTHIOALKYMALATE SYNTHASE LIKE, MYJ24.1, MYJ24_1	9.8	11.1	-1.3	-12.6	1.2E-4	11.2
427	AT1G56320.1 | expressed protein | chr1:21089213-21090124 REVERSE | Aliases: F14G9.7, F14G9_7	4.1	9.3	-5.2	-12.6	1.2E-4	8.9
430	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	8.1	10.3	-2.3	-12.6	1.2E-4	10.8
431	AT1G28130.2 | Symbol: GH3.17 |	4.2	6.7	-2.4	-12.6	1.2E-4	10.6
432	AT3G51440.1 | strictosidine synthase family protein, similar to hemomucin (Drosophila melanogaster)(GI:1280434), strictosidine synthase (Rauvolfia serpentina)(SP:P15324); contains strictosidine synthase domain PF03088 | chr3:19100060-19101618 FORWARD | Aliases: F26O13.80	5.5	9.0	-3.5	-12.6	1.2E-4	10.1
437	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	9.5	-4.1	-12.5	1.2E-4	10.3
442	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	5.6	8.4	-2.9	-12.5	1.2E-4	10.4
443	AT3G17790.1 | Symbol: ATACP5 |	3.6	8.7	-5.1	-12.5	1.2E-4	9.3
448	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)	5.5	7.2	-1.6	-12.4	1.2E-4	10.9
450	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	6.3	9.9	-3.6	-12.4	1.2E-4	10.2
451	AT5G10520.1 | protein kinase family protein, contains protein kinase domain, INTERPRO:IPR000719 | chr5:3320379-3322911 REVERSE | Aliases: F12B17.130, F12B17_130	3.3	7.9	-4.5	-12.4	1.2E-4	8.8
453	AT1G12750.1 | rhomboid family protein, contains PFAM domain PF01694, Rhomboid family | chr1:4344983-4348325 REVERSE | Aliases: T12C24.28, T12C24_28	4.8	8.5	-3.6	-12.4	1.3E-4	10.4
456	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	4.3	9.4	-5.2	-12.3	1.3E-4	9.1
458	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	6.2	9.3	-3.2	-12.3	1.3E-4	10.2
460	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	7.1	9.6	-2.5	-12.3	1.3E-4	10.3
461	AT3G20340.1 | expressed protein | chr3:7092906-7093428 REVERSE | Aliases: MQC12.8	2.4	7.8	-5.3	-12.2	1.3E-4	10.1

Rank	Description	Sync	Root	M	t	adj.q	B
464	AT1G69810.1 | Symbol: WRKY36 |	3.2	7.5	-4.3	-12.2	1.3E-4	9.6
465	AT2G29995.1 | expressed protein | chr2:12803987-12806496 REVERSE | Aliases: None	4.7	9.4	-4.6	-12.2	1.4E-4	9.2
467	AT1G44800.1 | 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	5.7	10.7	-5.1	-12.2	1.4E-4	8.6
470	AT1G15130.1 | hydroxyproline-rich glycoprotein family protein | chr1:5205997-5209910 REVERSE | Aliases: F9L1.7, F9L1_7	4.1	7.3	-3.2	-12.2	1.4E-4	10.2
471	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	6.6	-4.2	-12.2	1.4E-4	8.7
474	AT3G49210.1 | expressed protein | chr3:18249033-18252208 REVERSE | Aliases: F2K15.70	4.0	7.8	-3.7	-12.2	1.4E-4	9.3
476	AT1G49860.1 | Symbol: ATGSTF14 | glutathione S-transferase, putative, similar to GI:860955 from (Hyoscyamus muticus) (Plant Physiol. 109 (1), 253-260 (1995))	3.0	8.2	-5.1	-12.1	1.4E-4	8.1
477	AT5G02480.1 | expressed protein, p | chr5:547561-549910 FORWARD | Aliases: T22P11.70, T22P11_70	7.6	9.7	-2.1	-12.1	1.4E-4	10.7
478	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	7.8	-4.8	-12.1	1.4E-4	8.7
481	AT2G20630.2 | protein phosphatase 2C, putative / PP2C, putative | chr2:8903993-8906916 REVERSE | Aliases: F23N11.5, F23N11_5	6.1	9.0	-2.8	-12.1	1.4E-4	10.4
482	AT5G40690.1 | expressed protein | chr5:16307939-16308811 FORWARD | Aliases: MNF13.25, MNF13_25	3.3	7.1	-3.8	-12.1	1.4E-4	8.9
483	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	8.4	12.0	-3.5	-12.1	1.4E-4	10.5
486	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	3.0	7.2	-4.2	-12.1	1.4E-4	8.6
487	AT3G15630.1 | expressed protein | chr3:5296854-5297606 REVERSE | Aliases: MSJ11.3	3.8	7.7	-4.0	-12.1	1.4E-4	9.3
488	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	4.3	7.7	-3.4	-12.1	1.4E-4	9.4
490	AT1G29180.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.2	7.8	-4.5	-12.1	1.4E-4	9.2
491	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	6.4	9.1	-2.7	-12.0	1.4E-4	10.4
492	AT4G05070.1 | expressed protein | chr4:2593596-2594117 REVERSE | Aliases: C17L7.2	8.3	11.2	-2.8	-12.0	1.4E-4	10.3
494	AT4G38830.1 | protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain | chr4:18122320-18124937 FORWARD | Aliases: T9A14.110, T9A14_110	3.7	8.2	-4.5	-12.0	1.4E-4	8.4
498	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	6.9	-3.1	-12.0	1.5E-4	9.9
499	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	6.1	10.8	-4.7	-12.0	1.5E-4	9.6
500	AT3G14660.1 | Symbol: CYP72A13 | cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus) | chr3:4924784-4927441 FORWARD | Aliases: MIE1.16	6.8	9.5	-2.7	-12.0	1.5E-4	10.4
501	AT5G18780.1 | F-box family protein, contains F-box domain Pfam:PF00646	6.6	9.8	-3.2	-12.0	1.5E-4	9.9
502	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	3.6	8.4	-4.9	-12.0	1.5E-4	7.6

Rank	Description	Sync	Root	M	t	adj.q	B
503	AT5G37260.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr5:14768574-14770202 REVERSE | Aliases: MNJ8.4, MNJ8_4	3.8	8.7	-4.9	-11.9	1.5E-4	9.4
507	AT4G03500.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr4:1553090-1556569 FORWARD | Aliases: F9H3.13, F9H3_13	3.4	7.4	-4.0	-11.9	1.5E-4	8.4
509	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.	2.0	7.3	-5.4	-11.9	1.5E-4	7.2
513	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	5.9	-2.9	-11.9	1.5E-4	9.5
515	AT5G12420.1 | expressed protein | chr5:4024315-4026742 REVERSE | Aliases: None	2.5	6.6	-4.1	-11.9	0.02%	8.5
516	AT4G30670.1 | expressed protein | chr4:14957371-14957968 REVERSE | Aliases: T10C21.20, T10C21_20	2.9	8.8	-5.9	-11.8	0.02%	8.8
517	AT1G67920.1 | expressed protein | chr1:25477207-25477803 FORWARD | Aliases: T23K23.23, T23K23_23	4.4	9.4	-5.0	-11.8	0.02%	9.5
518	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	3.0	6.5	-3.5	-11.8	0.02%	8.9
519	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	3.1	7.0	-3.9	-11.8	0.02%	8.9
520	AT3G13760.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	4.9	8.2	-3.3	-11.8	0.02%	9.2
521	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	4.4	8.7	-4.3	-11.8	0.02%	9.0
522	AT5G57530.1 | xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to xyloglucan endotransglycosylase XTR9 GI:4218963 from (Arabidopsis thaliana) | chr5:23317547-23318831 REVERSE | Aliases: MUA2.10, MUA2_10	2.5	8.3	-5.8	-11.8	0.02%	8.1
523	AT1G54320.1 | LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein, Similar to GI:11994416; GI:4966357; GI:4835763; GI:9757735 from (Arabidopsis thaliana) | chr1:20279202-20281624 REVERSE | Aliases: F20D21.14, F20D21_14	10.2	11.9	-1.7	-11.8	0.02%	10.7
525	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	6.3	-2.9	-11.8	0.02%	10.0
526	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	4.9	10.3	-5.4	-11.8	0.02%	7.7
529	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	8.5	-3.1	-11.8	0.02%	9.8
532	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	4.5	8.6	-4.1	-11.7	0.02%	10.0
533	AT1G68850.1 | peroxidase, putative, identical to peroxidase ATP23a GB:CAA70035 (Arabidopsis thaliana) | chr1:25887279-25888896 REVERSE | Aliases: T6L1.4, T6L1_4	3.1	6.1	-3.0	-11.7	0.02%	9.6
539	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	5.0	9.5	-4.5	-11.7	0.02%	9.3
540	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	4.8	8.3	-3.5	-11.7	0.02%	9.4
541	AT1G55590.1 | F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250 | chr1:20772986-20775537 REVERSE | Aliases: F20N2.2	5.4	7.8	-2.3	-11.7	0.02%	9.9

Rank	Description	Sync	Root	M	t	adj.q	B
546	AT4G36380.1 | Symbol: ROT3 | cytochrome P450 90C1 (CYP90C1) / rotundifolia3 (ROT3), identical	3.3	8.2	-4.9	-11.6	0.02%	7.5
547	AT5G56540.1 | Symbol: AGP14 | arabinogalactan-protein (AGP14), identical to gi:10880505:gb:AAG24282 | chr5:22910377-22910868 FORWARD | Aliases: ARABINOGALACTAN PROTEIN 14, MKN22.5, MKN22_5	5.5	11.9	-6.3	-11.6	0.02%	8.8
548	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	7.3	-3.3	-11.6	0.02%	9.1
549	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	9.5	11.3	-1.8	-11.6	0.02%	10.5
552	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	3.1	7.5	-4.4	-11.6	0.02%	8.0
556	AT2G25090.1 | Symbol: CIPK16 |	3.0	8.4	-5.4	-11.6	0.02%	7.2
557	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	3.1	8.1	-5.0	-11.6	0.02%	9.3
558	AT1G64460.1 | phosphatidylinositol 3- and 4-kinase family protein, contains Pfam profile PF00454: Phosphatidylinositol 3- and 4-kinase	3.7	7.3	-3.6	-11.6	0.02%	9.6
559	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	3.2	7.5	-4.3	-11.5	0.02%	8.8
564	AT5G25440.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:8854842-8856761 REVERSE | Aliases: F18G18.180, F18G18_180	3.3	5.2	-1.9	-11.5	0.02%	10.2
565	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	4.9	9.0	-4.1	-11.5	0.02%	9.6
566	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	2.3	7.4	-5.1	-11.5	0.02%	7.1
568	AT4G32950.1 | protein phosphatase 2C, putative / PP2C, putative, phosphoprotein phosphatase, Arabidopsis thaliana, PIR2:S55457	5.9	10.0	-4.1	-11.5	0.02%	8.8
569	AT3G10500.1 | Symbol: ANAC053 | no apical meristem (NAM) family protein, similar to to NAC2 (GI:645671) (Arabidopsis thaliana); contains Pfam PF02365: No apical meristem (NAM) protein | chr3:3271617-3274035 FORWARD | Aliases: ANAC053, F13M14.22	7.2	10.5	-3.3	-11.5	0.02%	9.4
570	AT3G45710.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr3:16793629-16795720 FORWARD | Aliases: T6D9.40	3.1	7.4	-4.3	-11.5	0.02%	9.4
573	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	3.0	6.4	-3.5	-11.5	0.02%	8.7
574	AT1G55940.1 | Symbol: CYP708A1 | cytochrome P450, putative, similar to SP:Q42569 from (Arabidopsis thaliana) | chr1:20926133-20929284 REVERSE | Aliases: F14J16.21, F14J16_21	2.6	6.7	-4.1	-11.4	0.02%	9.0
576	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	3.1	7.4	-4.3	-11.4	0.02%	7.9
577	AT3G23090.1 | expressed protein | chr3:8214318-8217087 REVERSE | Aliases: MXC7.13	4.8	7.9	-3.1	-11.4	0.02%	9.8
578	AT3G57040.1 | Symbol: ARR9 | two-component responsive regulator / response reactor 4 (RR4), identical to responce 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	4.1	7.9	-3.9	-11.4	0.02%	9.4
580	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	2.7	6.9	-4.2	-11.4	0.02%	8.5

Rank	Description	Sync	Root	M	t	adj.q	B
581	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	4.7	6.6	-1.9	-11.4	0.02%	10.1
582	AT2G22620.1 | expressed protein | chr2:9611881-9617675 REVERSE | Aliases: T9I22.6, T9I22_6	3.2	6.7	-3.5	-11.4	0.02%	9.6
583	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	3.9	7.5	-3.6	-11.4	0.02%	8.8
585	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	4.2	8.1	-3.9	-11.4	0.02%	8.3
586	AT5G40730.1 | Symbol: AGP24 | arabinogalactan-protein (AGP24)	9.5	12.7	-3.2	-11.4	0.02%	10.3
587	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	2.9	7.4	-4.5	-11.4	0.02%	7.9
588	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	6.2	8.5	-2.3	-11.4	0.02%	9.8
590	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:BAB97268.1); similar to chloride channel [Oryza sativa (japonica cultivar-group)] (GB:BAB97267.1); similar to chloride channel Stclc1 [Solanum tuberosum] (GB:CAA71369.1); similar to C1C-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	6.3	9.2	-2.9	-11.4	0.02%	9.5
591	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	3.3	8.4	-5.0	-11.4	0.02%	8.2
592	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	6.3	10.0	-3.7	-11.4	0.02%	9.4
593	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	3.5	8.1	-4.6	-11.4	0.02%	7.9
595	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	6.5	9.2	-2.7	-11.3	0.02%	9.6
596	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	11.3	14.1	-2.7	-11.3	0.02%	10.3
597	AT4G38540.1 | monooxygenase, putative (MO2), identical to GI:3426064 | chr4:18023173-18025021 FORWARD | Aliases: F20M13.100, F20M13_100	7.4	9.8	-2.4	-11.3	0.02%	9.9
598	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	3.8	7.8	-3.9	-11.3	0.02%	8.2
600	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	7.9	10.6	-2.7	-11.3	0.02%	10.0
601	AT3G48450.1 | nitrate-responsive NOI protein, putative, similar to nitrate-induced NOI protein (Zea mays) GI:2642213 | chr3:17955017-17955873 REVERSE | Aliases: T29H11.30	3.9	6.9	-3.0	-11.3	0.02%	9.4
605	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	3.3	7.2	-3.9	-11.3	0.02%	8.4

Rank	Description	Sync	Root	M	t	adj.q	B
609	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	10.2	12.2	-2.0	-11.2	0.02%	10.2
613	AT3G49960.1 | peroxidase, putative, identical to peroxidase ATP21a (Arabidopsis thaliana) gi:1546696:emb:CAA67339 | chr3:18535069-18536672 REVERSE | Aliases: F3A4.40	3.0	8.0	-5.0	-11.2	0.02%	9.8
615	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	5.4	8.7	-3.3	-11.2	0.02%	8.7
617	AT3G25790.1 | myb family transcription factor, contains Pfam domain, PF00249: Myb-like DNA-binding domain | chr3:9414364-9416240 FORWARD | Aliases: K13N2.13	5.2	10.1	-4.9	-11.2	0.02%	8.4
619	AT4G18640.1 | leucine-rich repeat transmembrane protein kinase, putative | chr4:10259695-10263775 FORWARD | Aliases: F28A21.50, F28A21_50	3.9	7.4	-3.5	-11.1	0.02%	9.4
620	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	8.0	-4.8	-11.1	0.02%	7.4
626	AT1G08500.1 | plastocyanin-like domain-containing protein | chr1:2689057-2690048 FORWARD | Aliases: T27G7.18, T27G7_18	3.9	8.0	-4.1	-11.1	0.02%	8.2
627	AT3G44510.1 | expressed protein | chr3:16119094-16120345 REVERSE | Aliases: F14L2.60	3.0	6.5	-3.5	-11.1	0.02%	8.3
628	AT5G24080.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:8139256-8141125 REVERSE | Aliases: MZF18.3, MZF18_3	3.0	6.9	-3.9	-11.1	0.02%	8.3
634	AT2G16970.1 | expressed protein, ; expression supported by MPSS | chr2:7376631-7382610 FORWARD | Aliases: F12A24.15, F12A24_15	3.9	7.2	-3.3	-11.1	0.02%	8.8
635	AT1G30370.1 | lipase class 3 family protein, similar to DEFECTIVE IN ANTHER DEHISCENCE1 (Arabidopsis thaliana) GI:16215706; contains Pfam profile: PF01764: Lipase | chr1:10719151-10720740 REVERSE | Aliases: T4K22.3, T4K22_3	3.5	7.7	-4.3	-11.1	0.02%	7.8
636	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	4.3	7.7	-3.4	-11.0	0.02%	9.3
637	AT3G62860.1 | esterase/lipase/thioesterase family protein, similar to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162; contains Interpro entry IPR000379 | chr3:23250421-23253226 REVERSE | Aliases: F26K9.290	4.9	7.4	-2.5	-11.0	0.02%	9.3
638	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	5.3	9.1	-3.8	-11.0	0.02%	9.0
639	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	4.8	8.4	-3.6	-11.0	0.02%	9.3
645	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	7.7	-4.0	-11.0	0.02%	8.1
646	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	10.4	-2.8	-11.0	0.02%	9.3
648	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	7.0	10.4	-3.4	-11.0	0.02%	9.4
649	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	5.5	8.8	-3.3	-11.0	0.02%	8.8

Rank	Description	Sync	Root	M	t	adj.q	B
650	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	2.9	7.8	-4.9	-11.0	0.02%	7.7
652	AT1G21120.1 | O-methyltransferase, putative, similar to GI:2781394 | chr1:7395221-7396738 REVERSE | Aliases: T22I11.5, T22I11_5	4.0	7.4	-3.3	-11.0	0.02%	9.6
653	AT3G32040.1 | geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltranstransferase, 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	4.6	8.4	-3.8	-11.0	0.02%	9.1
654	AT1G07380.1 | ceramidase family protein, contains similarity to mitochondrial ceramidase (Homo sapiens) gi:9246993:gb:AAF86240	5.5	7.9	-2.4	-11.0	0.02%	9.6
656	AT3G06380.1 | F-box family protein / tubby family protein, similar to phosphodiesterase (GI: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) (GI: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	4.6	7.0	-2.4	-11.0	0.02%	9.8
657	AT1G22440.1 | alcohol dehydrogenase, putative, similar to alcohol dehydrogenase ADH GI:7705214 from (Lycopersicon esculentum); contains Pfam zinc-binding dehydrogenase domain PF00107	6.8	10.3	-3.5	-11.0	0.02%	9.7
659	AT3G53150.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:19708714-19710237 REVERSE | Aliases: T4D2.80	3.4	7.9	-4.5	-10.9	0.02%	8.3
660	AT5G66815.1 | expressed protein | chr5:26694591-26695091 FORWARD | Aliases: None	2.8	5.7	-3.0	-10.9	0.02%	9.3
665	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	5.3	8.1	-2.8	-10.9	0.02%	9.1
668	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)	5.9	9.4	-3.6	-10.9	0.02%	9.5
670	AT2G40080.1 | Symbol: ELF4 | expressed protein | chr2:16741372-16741990 REVERSE | Aliases: T28M21.24, T28M21_24	7.4	10.9	-3.5	-10.9	0.02%	9.4
672	AT4G31240.2 | expressed protein | chr4:15176461-15178514 REVERSE | Aliases: F8F16.60, F8F16_60	4.1	6.8	-2.7	-10.9	0.02%	9.2
673	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	4.3	8.9	-4.6	-10.9	0.02%	8.8
675	AT3G45640.1 | Symbol: ATMPK3 |	5.5	9.7	-4.2	-10.9	0.02%	9.8
677	AT2G27000.1 | Symbol: CYP705A8 | cytochrome P450 family protein | chr2:11530382-11532173 REVERSE | Aliases: T20P8.5, T20P8_5	4.3	7.8	-3.5	-10.9	0.02%	9.3
680	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	10.2	-2.5	-10.8	0.02%	9.6
681	AT3G01420.1 | Symbol: ALPHA DOX1 | pathogen-responsive alpha-dioxygenase, putative, similar to pathogen-inducible alpha-dioxygenase (Nicotiana attenuata) GI:12539609; contains Pfam profile PF03098: Animal haem peroxidase | chr3:159473-162844 REVERSE | Aliases: ALPHA DIOXYGENASE 1, T13O15.6, T13O15_6	3.9	8.5	-4.6	-10.8	0.02%	7.2
687	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	4.0	7.3	-3.3	-10.8	0.02%	8.6
689	AT5G16900.1 | 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 | chr5:5555257-5559718 FORWARD | Aliases: F2K13.50, F2K13_50	3.3	5.6	-2.3	-10.8	0.02%	9.4
691	AT1G04220.1 | beta-ketoacyl-CoA synthase, putative, Strong similarity to beta-keto-Coa synthase gb:U37088 from Simmondsia chinensis, GI:4091810 | chr1:1119359-1122525 REVERSE | Aliases: F20D22.1, F20D22_1	2.7	8.7	-6.0	-10.8	0.02%	6.7

Rank	Description	Sync	Root	M	t	adj.q	B
693	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)	6.9	9.9	-3.1	-10.8	0.02%	9.5
694	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	5.4	8.4	-3.0	-10.8	0.02%	9.2
697	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	5.0	9.1	-4.1	-10.7	0.02%	8.7
698	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	6.0	10.1	-4.1	-10.7	0.02%	8.9
699	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	6.7	10.0	-3.3	-10.7	0.02%	8.7
700	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	7.6	-4.3	-10.7	0.02%	8.3
701	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	6.8	-2.2	-10.7	0.02%	9.4
706	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	9.2	11.5	-2.3	-10.7	0.02%	9.8
707	AT1G54120.1 | expressed protein | chr1:20210688-20211208 FORWARD | Aliases: F15I1.22, F15I1_22	4.2	8.4	-4.3	-10.7	0.03%	8.0
710	AT1G70460.1 | protein kinase, putative, contains Pfam PF00069: Protein kinase domain | chr1:26559511-26562947 FORWARD | Aliases: F24J13.3, F24J13_3	3.5	7.2	-3.7	-10.7	0.03%	8.0
712	AT2G38470.1 | Symbol: WRKY33 |	5.1	10.3	-5.1	-10.7	0.03%	9.0
713	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	8.6	-4.9	-10.7	0.03%	6.8
714	AT1G11670.1 | MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI: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	3.9	7.3	-3.4	-10.7	0.03%	8.6
715	AT5G64930.1 | Symbol: CPR5 | CPR5 protein, putative, Constitutive expressor of Pathogensis 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	6.6	8.6	-2.0	-10.7	0.03%	9.7
717	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	8.6	-5.4	-10.7	0.03%	7.9
719	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	3.8	9.2	-5.4	-10.7	0.03%	7.0
721	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	7.0	-4.3	-10.7	0.03%	7.7
722	AT1G17090.1 | expressed protein, Pfam | chr1:5842209-5842875 REVERSE | Aliases: F20D23.31, F20D23_31	3.5	7.7	-4.2	-10.6	0.03%	8.4
723	AT1G30900.1 | vacuolar sorting receptor, putative, similar to BP-80 vacuolar sorting receptor (Pisum sativum) GI:1737222 | chr1:10997256-11000524 FORWARD | Aliases: F17F8.23	5.6	9.7	-4.1	-10.6	0.03%	8.7
726	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	3.2	7.9	-4.7	-10.6	0.03%	9.2

Rank	Description	Sync	Root	M	t	adj.q	B
727	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	3.6	8.3	-4.7	-10.6	0.03%	8.0
730	AT3G50740.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:18866142-18867865 REVERSE | Aliases: F18B3.20	3.1	9.4	-6.2	-10.6	0.03%	8.1
733	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	9.0	-3.3	-10.6	0.03%	8.8
738	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	7.5	-3.8	-10.6	0.03%	8.0
740	AT5G14120.1 | nodulin family protein, similar to nodulin-like protein (Arabidopsis thaliana) GI:3329368, nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366 | chr5:4555984-4559116 FORWARD | Aliases: MUA22.12, MUA22_12	6.9	10.1	-3.2	-10.6	0.03%	9.1
741	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	3.7	7.8	-4.2	-10.5	0.03%	7.8
743	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	4.8	10.1	-5.3	-10.5	0.03%	9.0
747	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	7.4	10.8	-3.3	-10.5	0.03%	9.4
751	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	7.3	-4.1	-10.5	0.03%	7.9
753	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	8.2	-3.3	-10.5	0.03%	8.2
755	AT2G42850.1 | Symbol: CYP718 |	3.3	8.1	-4.8	-10.5	0.03%	7.5
757	AT4G23270.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr4:12171113-12173935 FORWARD | Aliases: F21P8.160, F21P8_160	6.8	9.0	-2.2	-10.5	0.03%	9.6
759	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	6.2	-2.4	-10.5	0.03%	9.4
765	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	4.4	8.9	-4.5	-10.5	0.03%	8.7
766	AT3G21630.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:7615416-7618588 REVERSE | Aliases: MIL23.20	7.7	9.8	-2.1	-10.4	0.03%	9.6
768	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	4.0	9.1	-5.1	-10.4	0.03%	8.5
769	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	5.6	8.8	-3.2	-10.4	0.03%	9.3
770	AT4G14410.2 | basic helix-loop-helix (bHLH) family protein | chr4:8300072-8301663 FORWARD | Aliases: DL3245W, FCAALL.201	8.3	10.1	-1.7	-10.4	0.03%	9.7
771	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	5.3	10.3	-5.1	-10.4	0.03%	8.1
773	AT5G47040.1 | Lon protease homolog 1, mitochondrial (LON), identical to Lon protease homolog 1	5.5	8.9	-3.4	-10.4	0.03%	9.1
776	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	7.3	11.7	-4.5	-10.4	0.03%	8.6

Rank	Description	Sync	Root	M	t	adj.q	B
779	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	4.0	8.1	-4.1	-10.4	0.03%	8.4
780	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	4.2	8.4	-4.2	-10.4	0.03%	8.9
782	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	7.1	-3.6	-10.4	0.03%	8.1
783	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	7.5	11.1	-3.7	-10.4	0.03%	8.7
784	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	7.8	10.4	-2.7	-10.3	0.03%	9.3
792	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	6.3	8.7	-2.3	-10.3	0.03%	9.4
793	AT5G41990.1 | Symbol: WNK8 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:16811805-16815234 REVERSE | Aliases: MJC20.9, MJC20_9	7.5	10.2	-2.7	-10.3	0.03%	9.3
796	AT2G16980.2 | expressed protein | chr2:7383431-7388176 FORWARD | Aliases: F12A24.16, F12A24_16	4.6	8.6	-4.0	-10.3	0.03%	8.7
800	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	6.0	8.5	-2.5	-10.3	0.03%	9.0
802	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	5.6	8.9	-3.3	-10.3	0.03%	8.8
803	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	5.5	9.0	-3.5	-10.2	0.03%	8.1
808	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	9.4	-3.7	-10.2	0.03%	9.2
810	AT5G45800.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:18592809-18596324 REVERSE | Aliases: MRA19.24, MRA19_24	4.1	7.8	-3.7	-10.2	0.03%	9.1
813	AT1G54540.1 | expressed protein | chr1:20371369-20372088 REVERSE | Aliases: F20D21.35, F20D21_35	3.5	7.0	-3.5	-10.2	0.03%	7.8
819	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	6.8	-4.2	-10.2	0.03%	7.0
822	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	7.0	9.1	-2.1	-10.2	0.03%	9.4

Rank	Description	Sync	Root	M	t	adj.q	B
826	AT3G22750.1 | protein kinase, putative, similar to protein kinase ATMRK1 (Arabidopsis thaliana) gi:2351097:dbj:BAA22079 | chr3:8037223-8039910 REVERSE | Aliases: MWI23.12	5.0	7.5	-2.4	-10.2	0.03%	8.8
828	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	3.6	6.3	-2.8	-10.2	0.03%	8.8
829	AT3G02240.1 | expressed protein | chr3:418522-419158 FORWARD | Aliases: F14P3.11, F14P3_11	3.2	6.8	-3.7	-10.1	0.03%	8.0
833	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	3.9	6.5	-2.6	-10.1	0.03%	8.6
837	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	9.2	-3.0	-10.1	0.03%	9.1
838	AT3G12900.1 | oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to SP:P10967 1-aminocyclopropane-1-carboxylate oxidase homolog (Protein E8) {Lycopersicon esculentum}, desacetoxyvindoline-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	8.8	-5.4	-10.1	0.03%	7.9
840	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	2.4	5.9	-3.5	-10.1	0.03%	7.7
841	AT4G18780.1 | Symbol: CESA8 | cellulose synthase, catalytic subunit (IRX1), nearly identical to gi:12836997 | chr4:10312665-10316797 REVERSE | Aliases: ATCESA8, CELLULASE SYNTHASE 8, F28A21.190, F28A21_190, IRREGULAR XYLEM 1, IRX1, LEAF WILTING 2, LEW2	3.6	7.8	-4.2	-10.1	0.03%	7.9
842	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	8.3	10.2	-1.8	-10.1	0.03%	9.3
845	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	5.5	-2.4	-10.1	0.03%	8.9
846	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	10.3	12.8	-2.5	-10.1	0.03%	9.5
847	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	7.6	-2.5	-10.1	0.03%	8.8
849	AT1G23870.1 | Symbol: ATTPS9 |	3.3	8.2	-4.9	-10.1	0.03%	8.6
850	AT2G26510.1 | Symbol: PDE135 |	7.2	9.2	-2.0	-10.1	0.03%	9.3
851	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	3.4	7.0	-3.6	-10.1	0.03%	8.1
852	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	6.5	-3.8	-10.1	0.03%	7.6
861	AT1G44770.1 | expressed protein | chr1:16909979-16911903 REVERSE | Aliases: T12C22.4, T12C22_4	8.4	10.1	-1.7	-10.0	0.03%	9.4
863	AT1G75130.1 | Symbol: CYP721A1 | cytochrome P450 family protein, similar to Cytochrome P450 72A1 (SP:Q05047) (Catharanthus roseus) | chr1:28203636-28205611 REVERSE | Aliases: F22H5.19	5.3	7.0	-1.7	-10.0	0.03%	9.3
865	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	11.2	-2.8	-10.0	0.03%	9.4
868	AT5G17640.1 | expressed protein | chr5:5810189-5813286 REVERSE | Aliases: K10A8.120, K10A8_120	5.1	8.1	-3.0	-10.0	0.03%	8.8

Rank	Description	Sync	Root	M	t	adj.q	B
869	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	2.4	7.6	-5.1	-10.0	0.03%	7.8
872	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	2.9	8.9	-5.9	-10.0	0.03%	8.5
874	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	8.1	12.0	-3.8	-10.0	0.03%	9.2
875	AT5G58780.1 | dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative, similar to GI:796076 | chr5:23752855-23754561 REVERSE | Aliases: MZN1.33	2.9	6.6	-3.7	-10.0	0.03%	7.8
877	AT3G51540.1 | expressed protein, mucin 5AC, Homo sapiens, PIR:S53363 | chr3:19126321-19128189 FORWARD | Aliases: F26O13.180	3.0	5.9	-2.8	-10.0	0.03%	8.3
881	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	3.4	7.0	-3.6	-10.0	0.03%	7.9
882	AT3G20450.1 | expressed protein | chr3:7130668-7131280 REVERSE | Aliases: MQC12.24	4.1	6.9	-2.8	-10.0	0.04%	8.6
884	AT5G10580.2 | expressed protein, contains Pfam profile PF04654: Protein of unknown function, DUF599 | chr5:3347438-3350072 FORWARD | Aliases: F12B17.70, F12B17_70	5.0	8.5	-3.5	-9.9	0.04%	7.7
886	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	4.0	6.9	-2.9	-9.9	0.04%	8.8
887	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	9.6	-2.3	-9.9	0.04%	9.2
888	AT5G64410.1 | Symbol: ATOPT4 |	4.2	7.9	-3.7	-9.9	0.04%	7.7
890	AT3G17770.1 | dihydroxyacetone kinase family protein, contains Pfam domains, PF02733: DAK1 domain and PF02734: DAK2 domain | chr3:6081677-6085963 REVERSE | Aliases: MIG5.7	6.3	8.9	-2.6	-9.9	0.04%	9.0
898	AT1G20070.1 | expressed protein | chr1:6958001-6959114 REVERSE | Aliases: T20H2.15, T20H2_15	5.4	9.5	-4.1	-9.9	0.04%	7.9
899	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	9.8	-6.9	-9.9	0.04%	8.3
900	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	8.5	12.2	-3.7	-9.9	0.04%	8.3
903	AT2G39360.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:16444550-16447232 REVERSE | Aliases: F12L6.2, F12L6_2	4.4	8.2	-3.7	-9.9	0.04%	8.2
906	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	4.1	9.7	-5.6	-9.9	0.04%	8.3
912	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	6.5	9.4	-2.9	-9.8	0.04%	9.1
913	AT1G59520.3 | Symbol: CW7 | expressed protein (CW7) | chr1:21865049-21869855 FORWARD | Aliases: CW7, T30E16.4, T30E16_4	5.5	7.9	-2.3	-9.8	0.04%	9.1
915	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	5.5	8.8	-3.3	-9.8	0.04%	8.8
916	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	7.0	9.0	-2.1	-9.8	0.04%	9.1

Rank	Description	Sync	Root	M	t	adj.q	B
917	AT3G18170.1 | expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563) | chr3:6228348-6229668 FORWARD | Aliases: MRC8.17	4.6	9.6	-5.0	-9.8	0.04%	7.0
918	AT1G67330.1 | expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579) | chr1:25217515-25218834 FORWARD | Aliases: F1N21.15	3.9	9.0	-5.1	-9.8	0.04%	8.5
921	AT5G27930.2 | protein phosphatase 2C, putative / PP2C, putative, protein phosphatase-2C, Mesembryanthemum crystallinum, EMBL:AF075581 | chr5:9958102-9961170 REVERSE | Aliases: F15F15.3	4.6	7.0	-2.4	-9.8	0.04%	8.8
924	AT4G33300.2 | Symbol: ADR1 L1 | similar to disease resistance protein (NBS-LRR class), putative [Arabidopsis thaliana] (TAIR:At5g47280.1); similar to disease resistance protein (CC-NBS-LRR class), putative [Arabidopsis thaliana] (TAIR:At5g04720.1); similar to disease resistance protein (CC-NBS-LRR class), putative [Arabidopsis thaliana] (TAIR:At1g33560.1); similar to disease resistance protein-like protein MsR1 [Medicago sativa] (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	7.4	9.8	-2.5	-9.8	0.04%	8.9
925	AT4G13130.1 | DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain | chr4:7647385-7649827 FORWARD | Aliases: F17N18.20, F17N18_20	3.2	6.5	-3.4	-9.8	0.04%	8.4
926	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	5.9	8.7	-2.8	-9.8	0.04%	8.9
932	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	3.9	7.4	-3.5	-9.8	0.04%	8.1
933	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	3.4	7.2	-3.8	-9.8	0.04%	8.5
934	AT3G60520.1 | expressed protein | chr3:22372505-22373554 REVERSE | Aliases: T8B10.180	3.2	5.2	-2.0	-9.8	0.04%	9.0
936	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 scienitific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497. | chr3:2520780-2523114 FORWARD | Aliases: F17A17.24	3.6	7.0	-3.4	-9.7	0.04%	7.5
937	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	7.2	-4.6	-9.7	0.04%	7.0
939	AT5G48560.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.4	7.2	-3.8	-9.7	0.04%	8.6
943	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	3.5	7.7	-4.3	-9.7	0.04%	6.9
947	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	5.4	9.2	-3.8	-9.7	0.04%	7.8
949	AT5G10030.1 | Symbol: TGA4 | bZIP family transcription factor	4.5	7.6	-3.1	-9.7	0.04%	8.6
952	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	6.2	-4.0	-9.7	0.04%	7.8
954	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	3.4	7.8	-4.5	-9.7	0.04%	6.4
959	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	8.2	-4.5	-9.7	0.04%	7.3
961	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	5.0	8.8	-3.8	-9.6	0.04%	7.2
965	AT3G25640.1 | expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617 | chr3:9334956-9336041 FORWARD | Aliases: T5M7.9	3.8	6.9	-3.1	-9.6	0.04%	8.4

Rank	Description	Sync	Root	M	t	adj.q	B
966	AT1G34370.3 | similar to zinc finger (C2H2 type) family protein [Arabidopsis thaliana] (TAIR:At5g22890.1); similar to putative zinc finger protein [Oryza sativa (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	8.7	11.1	-2.4	-9.6	0.04%	9.0
968	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	4.2	7.8	-3.6	-9.6	0.04%	7.6
969	AT1G02810.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr1:618270-620480 FORWARD | Aliases: F22D16.20, F22D16_20	2.5	5.6	-3.0	-9.6	0.04%	8.1
972	AT1G73390.3 | expressed protein | chr1:27594477-27598803 REVERSE | Aliases: T9L24.40, T9L24_40	4.9	7.8	-3.0	-9.6	0.04%	8.3
974	AT5G01060.1 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr5:22739-24846 FORWARD | Aliases: F7J8.40, F7J8_40	3.8	7.0	-3.2	-9.6	0.04%	8.1
977	AT1G07730.2 | disease resistance-responsive family protein, contains Pfam PF03018: Plant disease resistance response protein | chr1:2397524-2398693 REVERSE | Aliases: None	4.7	8.9	-4.2	-9.6	0.04%	7.3
979	AT5G62150.1 | peptidoglycan-binding LysM domain-containing protein, contains Pfam profile PF01476: LysM domain	5.1	7.8	-2.6	-9.6	0.04%	8.2
981	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	6.5	9.6	-3.1	-9.6	0.04%	8.4
982	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	5.7	7.9	-2.2	-9.6	0.04%	8.6
984	AT2G34830.1 | Symbol: WRKY35 |	3.4	6.8	-3.4	-9.6	0.04%	7.8
986	AT5G66690.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:26642306-26644019 FORWARD | Aliases: MSN2.8, MSN2_8	5.5	9.5	-4.0	-9.6	0.04%	8.2
988	AT3G14060.1 | expressed protein | chr3:4657053-4657608 REVERSE | Aliases: MDC16.20	4.0	7.1	-3.0	-9.6	0.04%	8.2
991	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	4.7	7.3	-2.6	-9.6	0.04%	8.3
992	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	4.6	7.6	-3.0	-9.6	0.04%	8.5
993	AT5G19730.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:6670460-6673284 FORWARD | Aliases: T29J13.150, T29J13_150	4.1	8.5	-4.4	-9.6	0.04%	7.6
997	AT1G25230.1 | purple acid phosphatase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase; similar to purple acid phosphatase (GI:20257479) (Arabidopsis thaliana)	3.2	7.1	-4.0	-9.6	0.04%	7.6
998	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	4.0	8.5	-4.5	-9.5	0.04%	6.7
1000	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	8.6	-3.0	-9.5	0.04%	8.5
1001	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	6.2	-3.1	-9.5	0.04%	7.7
1007	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	7.6	9.7	-2.1	-9.5	0.04%	8.8

Rank	Description	Sync	Root	M	t	adj.q	B
1009	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	7.2	9.7	-2.5	-9.5	0.04%	8.9
1010	AT2G28940.2 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:12433348-12435762 REVERSE | Aliases: T9I4.2, T9I4_2	3.7	6.8	-3.1	-9.5	0.04%	7.9
1011	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	6.6	9.2	-2.6	-9.5	0.04%	8.8
1014	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	8.1	-4.6	-9.5	0.04%	6.7
1016	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	7.2	-2.2	-9.5	0.04%	8.5
1017	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	3.6	7.2	-3.6	-9.5	0.04%	7.1
1019	AT3G26470.1 | expressed protein | chr3:9687335-9688879 FORWARD | Aliases: F20C19.20	3.1	7.4	-4.2	-9.5	0.04%	6.7
1022	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	5.6	7.3	-1.8	-9.5	0.04%	9.0
1023	AT1G07240.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr1:2223690-2225447 FORWARD | Aliases: F10K1.5, F10K1_5	5.3	7.6	-2.3	-9.5	0.04%	8.6
1026	AT3G53780.2 | rhomboid family protein, contains PFAM domain PF01694, Rhomboid family | chr3:19935546-19938004 REVERSE | Aliases: F5K20.80	8.0	10.1	-2.1	-9.5	0.04%	8.8
1027	AT3G26720.1 | glycosyl hydrolase family 38 protein, similar to lysosomal alpha-mannosidase GI:3522867 from (Homo sapiens) | chr3:9817891-9824423 FORWARD | Aliases: MLJ15.19	7.8	10.9	-3.1	-9.5	0.04%	8.6
1029	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	2.8	8.7	-5.9	-9.5	0.04%	8.7
1031	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	6.8	-3.2	-9.5	0.04%	8.5
1032	AT1G27380.2 | Symbol: RIC2 | p21-rho-binding domain-containing protein, contains Pfam PF00786: P21-Rho-binding domain	3.0	5.5	-2.5	-9.4	0.04%	8.6
1038	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	6.4	9.3	-2.9	-9.4	0.04%	8.6
1040	AT1G68670.1 | myb family transcription factor, contains Pfam domain, PF00249: Myb-like DNA-binding domain | chr1:25785745-25787737 FORWARD | Aliases: F24J5.9, F24J5_9	6.4	8.1	-1.7	-9.4	0.04%	8.8
1043	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	6.3	-2.6	-9.4	0.05%	8.4
1045	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	4.2	9.2	-5.0	-9.4	0.05%	7.8
1046	AT1G27290.1 | expressed protein | chr1:9481546-9482899 FORWARD | Aliases: F17L21.8, F17L21_8	6.9	9.1	-2.2	-9.4	0.05%	8.9

Rank	Description	Sync	Root	M	t	adj.q	B
1051	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	7.0	-3.8	-9.4	0.05%	7.5
1056	AT5G07080.1 | transferase family protein, similar to 10-deacetylbaccatin 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	3.1	8.1	-5.0	-9.4	0.05%	7.9
1057	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	6.5	8.8	-2.3	-9.4	0.05%	8.5
1058	AT5G25640.1 | expressed protein, ; expression supported by MPSS | chr5:8949852-8950334 REVERSE | Aliases: T14C9.180, T14C9_180	5.2	7.3	-2.1	-9.4	0.05%	8.7
1059	AT3G07570.1 | membrane protein, putative, similar to membrane protein SDR2 (GI:1747306) (Mus musculus)	6.8	9.4	-2.6	-9.4	0.05%	8.4
1061	AT3G18560.1 | expressed protein | chr3:6393916-6394783 FORWARD | Aliases: K24M9.5	4.2	6.9	-2.7	-9.4	0.05%	7.9
1062	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	5.9	9.8	-4.0	-9.4	0.05%	8.3
1067	AT2G01450.4 | Symbol: ATMPK17 | 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	7.5	11.2	-3.7	-9.3	0.05%	8.2
1070	AT1G07870.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:2429696-2432018 REVERSE | Aliases: F24B9.4, F24B9_4	6.8	9.7	-2.9	-9.3	0.05%	8.4
1071	AT1G11540.1 | expressed protein, contains Pfam profile: PF01925 domain of unknown function DUF81 | chr1:3875160-3877155 REVERSE | Aliases: T23J18.20, T23J18_20	5.0	7.1	-2.2	-9.3	0.05%	8.5
1075	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	7.6	9.5	-1.9	-9.3	0.05%	8.8
1078	AT3G14280.1 | expressed protein | chr3:4760984-4762402 REVERSE | Aliases: MLN21.7	4.3	8.7	-4.4	-9.3	0.05%	7.3
1080	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	9.1	12.6	-3.6	-9.3	0.05%	8.4
1083	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	5.1	7.6	-2.5	-9.3	0.05%	8.3
1084	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	9.1	-2.6	-9.3	0.05%	8.6
1085	AT5G62420.1 | aldo/keto reductase family protein, similar to chalcone reductase (Sesbania rostrata)(GI:2792155); contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family | chr5:25082061-25083337 FORWARD | Aliases: K19B1.2, K19B1_2	3.2	8.1	-5.0	-9.3	0.05%	8.2
1086	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	6.2	9.1	-2.9	-9.3	0.05%	8.8

Rank	Description	Sync	Root	M	t	adj.q	B
1090	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	4.8	8.5	-3.8	-9.3	0.05%	8.1
1092	AT2G29900.1 | presenilin family protein, similar to presenilin (Drosophila melanogaster) GI:2062395; contains Pfam profile PF01080: Presenilin	5.8	7.2	-1.4	-9.3	0.05%	8.8
1093	AT3G23200.1 | expressed protein | chr3:8281370-8282785 FORWARD | Aliases: K14B15.11	6.2	9.0	-2.8	-9.3	0.05%	8.0
1094	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	3.4	7.5	-4.1	-9.3	0.05%	6.8
1097	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	5.5	8.5	-3.0	-9.3	0.05%	8.2
1098	AT2G25590.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr2:10898373-10900850 FORWARD | Aliases: F3N11.4, F3N11_4	6.6	9.4	-2.8	-9.3	0.05%	8.4
1099	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	5.1	8.6	-3.5	-9.3	0.05%	8.3
1100	AT1G20110.1 | zinc finger (FYVE type) family protein, contains Pfam profile: PF01363 FYVE zinc finger | chr1:6971476-6974812 FORWARD | Aliases: T20H2.10, T20H2_10	8.8	10.7	-1.9	-9.3	0.05%	8.8
1101	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	10.1	-3.3	-9.2	0.05%	8.4
1104	AT3G23880.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.5	7.4	-3.9	-9.2	0.05%	7.6
1105	AT5G66250.3 | kinectin-related, contains weak similarity to kinectin (GI:3766232) (Vulpes vulpes) | chr5:26485761-26487170 FORWARD | Aliases: K1L20.3, K1L20_3	6.6	8.9	-2.3	-9.2	0.05%	8.6
1110	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	4.6	8.8	-4.1	-9.2	0.05%	7.7
1115	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	5.7	8.3	-2.6	-9.2	0.05%	8.4
1116	AT5G50760.1 | auxin-responsive family protein, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana) | chr5:20661887-20662695 FORWARD | Aliases: MFB16.16, MFB16_16	2.7	6.6	-4.0	-9.2	0.05%	6.6
1119	AT4G31550.3 | Symbol: WRKY11 |	4.0	6.3	-2.3	-9.2	0.05%	8.3
1123	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	4.1	7.4	-3.2	-9.2	0.05%	7.9
1126	AT1G30130.2 | expressed protein, similar to hypothetical protein GI:1469227 from (Brassica oleracea) | chr1:10587587-10589606 FORWARD | Aliases: T2H7.7, T2H7_7	5.4	8.5	-3.2	-9.2	0.05%	8.4
1136	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	6.8	-3.7	-9.1	0.05%	7.0
1139	AT1G30400.2 | Symbol: ATMRP1 |	6.0	9.0	-3.0	-9.1	0.05%	8.4
1140	AT1G21360.1 | expressed protein | chr1:7481353-7483425 FORWARD | Aliases: F24J8.2, F24J8_2	2.6	7.8	-5.2	-9.1	0.05%	5.5
1142	AT1G56230.1 | expressed protein | chr1:21049699-21052690 REVERSE | Aliases: F14G9.16, F14G9_16	6.8	9.9	-3.0	-9.1	0.05%	8.5
1144	AT5G45480.1 | expressed protein, contains Pfam domain, PF04578: Protein of unknown function, DUF594 | chr5:18443331-18446317 REVERSE | Aliases: MFC19.15, MFC19_15	2.8	5.9	-3.1	-9.1	0.05%	7.6

Rank	Description	Sync	Root	M	t	adj.q	B
1146	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	4.6	7.9	-3.3	-9.1	0.05%	7.5
1147	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	3.1	6.6	-3.4	-9.1	0.05%	7.4
1148	AT3G52360.1 | expressed protein | chr3:19423098-19423896 FORWARD | Aliases: T25B15.130	6.8	9.6	-2.8	-9.1	0.05%	8.6
1149	AT5G55910.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr5:22657070-22659528 REVERSE | Aliases: MYN21.2, MYN21_2	5.3	7.7	-2.4	-9.1	0.05%	8.5
1150	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	4.2	7.4	-3.1	-9.1	0.05%	7.3
1151	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)	9.0	11.5	-2.5	-9.1	0.05%	8.6
1153	AT4G18700.1 | Symbol: CIPK12 |	8.5	10.2	-1.8	-9.1	0.05%	8.7
1155	AT4G15330.1 | Symbol: CYP705A1 | cytochrome P450 family protein | chr4:8751391-8753134 REVERSE | Aliases: DL3710C, FCAALL.270	3.3	7.8	-4.5	-9.1	0.05%	6.3
1157	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	7.3	9.4	-2.1	-9.1	0.05%	8.5
1161	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	5.6	-1.6	-9.1	0.05%	8.6
1162	AT4G10380.1 | major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230 | chr4:6431235-6434818 REVERSE | Aliases: F7L13.6	5.4	7.6	-2.2	-9.1	0.05%	8.6
1163	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	5.2	8.0	-2.8	-9.1	0.05%	8.2
1165	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	6.4	9.5	-3.1	-9.1	0.05%	8.5
1166	AT1G04440.1 | casein kinase, putative, similar to casein kinase I (Arabidopsis thaliana) gi:1103318:emb:CAA55395; contains protein kinase domain, Pfam:PF00069	5.6	9.3	-3.7	-9.1	0.05%	8.2
1167	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	7.0	9.4	-2.4	-9.1	0.05%	8.5
1171	AT4G13020.3 | Symbol: MHK | similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:At4g19110.1); similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:At4g19110.2); similar to putative Cdc2-related protein kinase CRK2 [Beta vulgaris] (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	5.5	8.1	-2.5	-9.0	0.05%	8.3
1172	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	8.0	-5.2	-9.0	0.05%	8.1
1175	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	4.5	-2.2	-9.0	0.05%	8.4
1180	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	6.4	9.1	-2.8	-9.0	0.06%	8.1

Rank	Description	Sync	Root	M	t	adj.q	B
1185	AT4G34500.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	4.9	7.1	-2.2	-9.0	0.06%	8.2
1188	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	3.7	-1.3	-9.0	0.06%	8.6
1189	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	5.8	8.0	-2.2	-9.0	0.06%	8.4
1190	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	5.9	9.2	-3.3	-9.0	0.06%	8.2
1192	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	4.4	8.3	-4.0	-9.0	0.06%	8.5
1193	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	12.5	14.3	-1.8	-9.0	0.06%	8.4
1194	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	6.7	-1.7	-9.0	0.06%	8.5
1196	AT1G22930.1 | T-complex protein 11, contains Pfam PF05794: T-complex protein 11 | chr1:8117386-8122116 FORWARD | Aliases: F19G10.11, F19G10_11	8.0	10.6	-2.6	-9.0	0.06%	8.2
1199	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	2.9	6.9	-4.0	-9.0	0.06%	6.3
1200	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	2.7	5.3	-2.5	-9.0	0.06%	8.0
1201	AT5G07250.1 | rhomboid family protein, contains PFAM domain PF01694, Rhomboid family | chr5:2273555-2275991 REVERSE | Aliases: T28J14.190, T28J14_190	5.4	7.9	-2.5	-9.0	0.06%	8.4
1203	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	3.5	8.1	-4.7	-9.0	0.06%	8.0
1205	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	6.8	9.3	-2.4	-9.0	0.06%	8.3
1207	AT1G70290.1 | Symbol: ATTPS8 |	6.3	8.6	-2.2	-9.0	0.06%	8.5
1210	AT4G18430.1 | Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303742 from (Pisum sativum)	3.0	5.7	-2.7	-9.0	0.06%	7.7
1211	AT5G61820.1 | expressed protein, MtN19, Medicago truncatula, EMBL:MTY15367 | chr5:24851544-24853917 REVERSE | Aliases: MAC9.6, MAC9_6	10.2	11.8	-1.6	-9.0	0.06%	8.6
1213	AT2G17440.1 | leucine-rich repeat family protein, contains Pfam PF00560: Leucine Rich Repeats | chr2:7578222-7580838 FORWARD | Aliases: F5J6.20, F5J6_20	4.0	6.9	-3.0	-9.0	0.06%	8.3
1215	AT3G18830.1 | Symbol: ATPLT5 |	6.4	8.1	-1.7	-8.9	0.06%	8.6
1223	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	5.3	7.7	-2.4	-8.9	0.06%	8.0
1224	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	8.3	10.9	-2.5	-8.9	0.06%	8.5

Rank	Description	Sync	Root	M	t	adj.q	B
1225	AT3G06650.1 | Symbol: ACLB 1 |	5.9	8.7	-2.8	-8.9	0.06%	8.2
1226	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	4.3	6.7	-2.4	-8.9	0.06%	8.2
1227	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	5.2	7.8	-2.7	-8.9	0.06%	8.1
1228	AT3G01470.1 | Symbol: ATHB 1 |	8.6	11.5	-2.9	-8.9	0.06%	8.3
1232	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	5.2	-2.7	-8.9	0.06%	7.7
1234	AT2G37090.1 | Symbol: IXR9 | Encodes a protein with similarity to glycosyltransferases. Mutants have irregular xylem phenotype suggesting a role in secondary cell wall biosynthesis.	4.0	7.2	-3.2	-8.9	0.06%	7.3
1237	AT5G15600.1 | expressed protein | chr5:5078203-5079094 FORWARD | Aliases: T20K14.210, T20K14_210	7.1	9.6	-2.5	-8.9	0.06%	7.9
1240	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	2.5	7.6	-5.1	-8.9	0.06%	7.7
1241	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	6.1	9.5	-3.4	-8.9	0.06%	8.3
1242	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	8.2	-2.2	-8.9	0.06%	8.3
1244	AT3G55850.2 | Symbol: LAF3.1 |	4.6	6.6	-2.1	-8.9	0.06%	8.3
1245	AT3G19660.1 | expressed protein | chr3:6825527-6826012 REVERSE | Aliases: MMB12.13	5.6	8.2	-2.6	-8.8	0.06%	8.2
1251	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	7.7	10.2	-2.5	-8.8	0.06%	8.4
1257	AT3G20370.1 | 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 | chr3:7105377-7107231 FORWARD | Aliases: MQC12.15	4.4	7.6	-3.2	-8.8	0.06%	7.6
1259	AT1G26440.4 | Symbol: ATUPS5 |	3.8	7.4	-3.6	-8.8	0.06%	7.3
1268	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	9.3	-5.0	-8.8	0.06%	7.9
1270	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	6.2	-1.8	-8.8	0.06%	8.3
1272	AT4G17280.1 | auxin-responsive family protein, similar to auxin-induced protein AIR12 (GI:11357190) (Arabidopsis thaliana) | chr4:9678541-9680401 REVERSE | Aliases: DL4675C, FCAALL.393	3.3	6.0	-2.7	-8.8	0.06%	7.8
1277	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	4.7	7.7	-3.1	-8.8	0.06%	7.1
1279	AT5G49900.1 | expressed protein, contains Pfam domain PF04685: Protein of unknown function, DUF608 | chr5:20314349-20319572 REVERSE | Aliases: K9P8.4, K9P8_4	8.0	9.7	-1.7	-8.8	0.06%	8.4

Rank	Description	Sync	Root	M	t	adj.q	B
1280	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)	7.7	9.4	-1.7	-8.8	0.06%	8.3
1283	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	3.2	6.8	-3.6	-8.8	0.06%	7.8
1284	AT3G21430.1 | expressed protein | chr3:7544634-7550830 REVERSE | Aliases: MHC9.11	5.4	7.6	-2.1	-8.8	0.06%	8.4
1286	AT3G11410.1 | protein phosphatase 2C, putative / PP2C, putative, identical to protein phosphatase 2C (PP2C) GB:P49598 (Arabidopsis thaliana); contains Pfam profile PF00481: Protein phosphatase 2C; identical to cDNA protein phosphatase 2C GI:633027 | chr3:3583889-3585796 REVERSE | Aliases: F24K9.8	5.9	8.0	-2.1	-8.8	0.06%	8.2
1287	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	5.2	8.3	-3.2	-8.7	0.06%	7.8
1288	AT2G23450.2 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:9995834-9998739 REVERSE | Aliases: F26B6.10, F26B6_10	4.9	7.3	-2.5	-8.7	0.06%	7.7
1289	AT3G54220.1 | Symbol: SCR | scarecrow transcription factor, putative, nearly identical to SCARECROW (Arabidopsis thaliana) GI:1497987	3.3	6.1	-2.8	-8.7	0.06%	7.9
1293	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	6.1	9.1	-3.0	-8.7	0.06%	7.7
1296	AT1G24320.1 | alpha-glucosidase, putative, similar to alpha-glucosidase I from GI:16506680 (Arabidopsis thaliana) | chr1:8626316-8630960 REVERSE | Aliases: F3I6.26, F3I6_26	3.3	6.6	-3.3	-8.7	0.06%	7.1
1297	AT4G22270.1 | expressed protein | chr4:11773340-11775984 FORWARD | Aliases: T10I14.100, T10I14_100	4.1	6.1	-2.0	-8.7	0.06%	8.1
1298	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	3.3	5.8	-2.6	-8.7	0.06%	7.8
1299	AT4G20860.1 | FAD-binding domain-containing protein, simlar 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	4.4	9.2	-4.7	-8.7	0.06%	7.7
1300	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	3.3	8.0	-4.7	-8.7	0.06%	7.6
1301	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	3.5	5.5	-2.0	-8.7	0.06%	8.2
1302	AT2G24550.1 | expressed protein, weak similarity to MTD1 (Medicago truncatula) GI:9294810 | chr2:10434936-10436301 REVERSE | Aliases: F25P17.15, F25P17_15	5.8	9.8	-4.0	-8.7	0.06%	8.2
1303	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	3.9	6.8	-2.9	-8.7	0.06%	7.8
1304	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	6.7	9.6	-2.8	-8.7	0.06%	8.4
1305	AT1G23040.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich domains, INTERPRO:IPR000694 | chr1:8164948-8165851 FORWARD | Aliases: F19G10.19	6.3	8.5	-2.2	-8.7	0.06%	8.0
1307	AT1G67340.1 | zinc finger (MYND type) family protein / F-box family protein | chr1:25233928-25235503 FORWARD | Aliases: F1N21.16	4.1	6.5	-2.5	-8.7	0.07%	8.2
1308	AT2G30040.1 | Symbol: MAPKKK14 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:12828787-12830246 FORWARD | Aliases: F23F1.4, F23F1_4	4.9	7.5	-2.6	-8.7	0.07%	7.9

Rank	Description	Sync	Root	M	t	adj.q	B
1309	AT3G58710.2 | Symbol: WRKY69 |	5.8	9.0	-3.2	-8.7	0.07%	8.1
1313	AT1G05575.1 | expressed protein | chr1:1661690-1662186 REVERSE | Aliases: None	2.4	6.6	-4.2	-8.7	0.07%	8.2
1314	AT5G62390.1 | calmodulin-binding family protein, contains IQ calmodulin-binding motif, Pfam:PF00612 | chr5:25069275-25071515 REVERSE | Aliases: MMI9.22, MMI9_22	7.0	10.1	-3.1	-8.7	0.07%	8.1
1315	AT1G29280.1 | Symbol: WRKY65 |	4.5	9.0	-4.5	-8.7	0.07%	6.8
1317	AT5G06570.2 | expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873 | chr5:2007601-2011042 REVERSE | Aliases: F15M7.10, F15M7_10	3.4	7.8	-4.4	-8.7	0.07%	7.6
1318	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	5.8	7.8	-2.0	-8.7	0.07%	8.0
1319	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	3.2	6.3	-3.1	-8.7	0.07%	8.1
1320	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	3.6	7.8	-4.2	-8.7	0.07%	7.0
1321	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	6.9	10.2	-3.3	-8.6	0.07%	8.1
1322	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	6.8	-3.8	-8.6	0.07%	6.5
1323	AT5G02420.1 | expressed protein | chr5:523387-524074 FORWARD | Aliases: T22P11.10, T22P11_10	3.0	6.6	-3.7	-8.6	0.07%	7.9
1328	AT1G21310.1 | Symbol: ATEXT3 |	4.3	11.0	-6.7	-8.6	0.07%	6.4
1329	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)	3.3	4.5	-1.2	-8.6	0.07%	8.3
1330	AT1G71090.1 | auxin efflux carrier family protein, contains auxin efflux carrier domain, Pfam:PF03547 | chr1:26815874-26817792 FORWARD | Aliases: F23N20.8, F23N20_8	7.0	9.4	-2.4	-8.6	0.07%	8.0
1332	AT1G31050.1 | expressed protein | chr1:11075634-11076180 REVERSE | Aliases: F17F8.3	5.7	9.9	-4.2	-8.6	0.07%	7.1
1333	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	4.8	-1.9	-8.6	0.07%	8.2
1334	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	5.8	-3.4	-8.6	0.07%	6.8
1341	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	4.3	6.9	-2.6	-8.6	0.07%	7.5
1343	AT5G11020.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:3486440-3488381 REVERSE | Aliases: None	3.3	6.5	-3.2	-8.6	0.07%	8.0
1345	AT1G33800.1 | expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579) | chr1:12261399-12262697 FORWARD | Aliases: F14M2.8, F14M2_8	2.8	6.7	-3.9	-8.6	0.07%	6.6
1346	AT5G22850.1 | aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease | chr5:7633440-7636570 REVERSE | Aliases: MRN17.8, MRN17_8	7.1	8.5	-1.4	-8.6	0.07%	8.3
1350	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	6.0	9.4	-3.4	-8.6	0.07%	7.9

Rank	Description	Sync	Root	M	t	adj.q	B
1352	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	3.8	7.5	-3.7	-8.6	0.07%	7.2
1356	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	5.9	9.4	-3.5	-8.6	0.07%	8.1
1357	AT1G69325.1 | remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region | chr1:26066868-26067399 FORWARD | Aliases: None	3.0	8.7	-5.7	-8.6	0.07%	6.6
1358	AT3G51550.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:19128563-19131840 REVERSE | Aliases: F26O13.190	5.2	8.0	-2.8	-8.6	0.07%	8.0
1361	AT3G01690.1 | expressed protein | chr3:256562-258554 FORWARD | Aliases: F4P13.23, F4P13_23	9.9	11.6	-1.6	-8.6	0.07%	8.2
1362	AT1G25400.1 | expressed protein, similar to unknown protein GI:6714347 from (Arabidopsis thaliana) | chr1:8911117-8912385 REVERSE | Aliases: F2J7.13, F2J7_13	4.4	6.7	-2.2	-8.6	0.07%	7.9
1363	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	4.1	8.4	-4.3	-8.6	0.07%	6.0
1364	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	5.7	7.7	-2.0	-8.5	0.07%	7.9
1365	AT4G22110.2 | alcohol dehydrogenase, putative, similar to alcohol dehydrogenase ADH GI:7705214 from (Lycopersicon esculentum); contains Pfam zinc-binding dehydrogenase domain PF00107	3.5	6.2	-2.7	-8.5	0.07%	7.6
1366	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	6.7	9.5	-2.8	-8.5	0.07%	8.2
1369	AT4G29500.1 | prolidase-related, contains similarity to prolidase GI:3114966 from (Suberites domuncula) | chr4:14490217-14491495 FORWARD | Aliases: T16L4.10, T16L4_10	7.8	9.4	-1.6	-8.5	0.07%	8.2
1371	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	2.5	5.9	-3.3	-8.5	0.07%	7.2
1372	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	4.2	7.2	-2.9	-8.5	0.07%	7.2
1374	AT4G31875.1 | expressed protein | chr4:15411707-15412295 REVERSE | Aliases: None	3.3	5.9	-2.6	-8.5	0.07%	7.5
1375	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	6.5	9.9	-3.5	-8.5	0.07%	7.6
1378	AT5G04470.1 | expressed protein | chr5:1266692-1267417 REVERSE | Aliases: T19N18.8	6.7	8.9	-2.2	-8.5	0.07%	8.1
1380	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	6.8	-3.2	-8.5	0.07%	7.8
1381	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	3.2	4.7	-1.5	-8.5	0.07%	8.2
1382	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	8.0	-1.9	-8.5	0.07%	8.2

Rank	Description	Sync	Root	M	t	adj.q	B
1383	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	4.9	7.2	-2.4	-8.5	0.07%	7.9
1387	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	4.8	-2.1	-8.5	0.07%	7.8
1388	AT5G43180.1 | expressed protein, contains Pfam profile PF04654: Protein of unknown function, DUF599 | chr5:17353566-17355080 REVERSE | Aliases: K24F5.2, K24F5_2	4.6	8.2	-3.6	-8.5	0.07%	7.4
1391	AT1G01660.1 | U-box domain-containing protein | chr1:240057-242608 REVERSE | Aliases: T1N6.4, T1N6_4	2.8	4.9	-2.0	-8.5	0.07%	7.9
1392	AT5G52060.1 | BAG domain-containing protein, contains Pfam:PF02179 BAG domain | chr5:21169454-21170919 REVERSE | Aliases: MSG15.15, MSG15_15	7.1	9.8	-2.7	-8.5	0.07%	7.9
1395	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	6.7	8.5	-1.8	-8.5	0.07%	8.1
1396	AT4G26140.2 | Symbol: BGAL12 |	2.6	5.7	-3.1	-8.5	0.07%	7.3
1397	AT3G08650.2 | metal transporter family protein, contains ZIP Zinc transporter domain, Pfam:PF02535 | chr3:2624467-2627376 REVERSE | Aliases: F17O14.12	8.0	9.9	-1.9	-8.5	0.07%	8.2
1399	AT4G30350.1 | heat shock protein-related, contains similarity to heat shock protein 101 (Triticum aestivum) gi:6013196:gb:AAF01280 | chr4:14847746-14851149 FORWARD | Aliases: F17I23.310, F17I23_310	5.2	9.4	-4.2	-8.5	0.07%	7.5
1400	AT5G40510.1 | expressed protein | chr5:16246416-16248326 FORWARD | Aliases: MNF13.5, MNF13_5	3.7	6.9	-3.2	-8.5	0.07%	7.5
1401	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	2.9	6.2	-3.3	-8.5	0.07%	6.8
1404	AT4G36790.1 | 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 | chr4:17336177-17338376 FORWARD | Aliases: AP22.91, AP22_91	6.0	7.4	-1.4	-8.5	0.08%	8.2
1408	AT3G27110.2 | peptidase M48 family protein, contains Pfam domain, PF01435: Peptidase family M48 | chr3:9999133-10001412 FORWARD | Aliases: MOJ10.19	4.1	7.1	-3.0	-8.4	0.08%	7.2
1409	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	5.3	6.8	-1.5	-8.4	0.08%	8.1
1410	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	4.5	7.9	-3.4	-8.4	0.08%	7.4
1414	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	3.7	6.3	-2.6	-8.4	0.08%	7.4
1415	AT1G43790.1 | expressed protein | chr1:16578335-16578857 FORWARD | Aliases: F28H19.19, F28H19_19	4.8	8.1	-3.3	-8.4	0.08%	7.2
1417	AT3G16350.1 | myb family transcription factor, ; contains Pfam profile: PF00249 Myb-like DNA-binding domain | chr3:5547724-5549666 FORWARD | Aliases: T2O4.10	5.2	7.1	-1.9	-8.4	0.08%	8.0
1419	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	8.6	10.5	-1.9	-8.4	0.08%	8.1
1422	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	3.3	6.5	-3.2	-8.4	0.08%	6.6

Rank	Description	Sync	Root	M	t	adj.q	B
1428	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	9.8	-2.4	-8.4	0.08%	8.0
1432	AT4G25390.2 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:12977351-12979578 FORWARD | Aliases: T30C3.60, T30C3_60	5.2	8.3	-3.0	-8.4	0.08%	7.8
1433	AT3G46130.2 | Symbol: MYB111 |	7.3	9.8	-2.5	-8.4	0.08%	7.8
1434	AT5G43560.2 | meprin 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 | chr5:17517656-17522873 FORWARD | Aliases: K9D7.6, K9D7_6	8.3	9.9	-1.6	-8.4	0.08%	8.1
1435	AT5G09520.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr5:2958293-2958857 REVERSE | Aliases: T5E8.1	2.8	4.6	-1.8	-8.4	0.08%	7.8
1436	AT5G22270.1 | expressed protein, similar to unknown protein (gb AAF02129.1) | chr5:7372236-7373105 REVERSE | Aliases: T6G21.5	4.2	9.8	-5.6	-8.4	0.08%	7.6
1437	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	8.7	-5.0	-8.4	0.08%	7.5
1440	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	3.1	7.0	-3.9	-8.4	0.08%	7.5
1441	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	4.6	6.5	-1.9	-8.4	0.08%	8.0
1444	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	6.3	-2.7	-8.4	0.08%	7.3
1446	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	7.1	-3.3	-8.3	0.08%	6.8
1450	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	5.7	8.8	-3.1	-8.3	0.08%	7.7
1451	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	7.6	8.8	-1.2	-8.3	0.08%	8.1
1452	AT4G05150.1 | octicosapeptide/Phox/Bem1p (PB1) domain-containing protein, various predicted proteins contains Pfam profile PF00564: PB1 domain	5.6	8.8	-3.2	-8.3	0.08%	7.6
1457	AT2G35930.1 | U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain | chr2:15089934-15091552 REVERSE | Aliases: F11F19.16, F11F19_16	5.5	8.7	-3.2	-8.3	0.08%	7.7
1459	AT3G28550.1 | proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr3:10701944-10705166 REVERSE | Aliases: MZN14.2	2.7	8.7	-6.0	-8.3	0.08%	8.0
1464	AT1G56720.2 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:21267093-21270033 REVERSE | Aliases: F25P12.84, F25P12_84	3.6	6.0	-2.4	-8.3	0.08%	7.9
1465	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	7.5	-1.1	-8.3	0.08%	8.0
1468	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	2.8	5.5	-2.8	-8.3	0.08%	7.4
1469	AT3G56360.1 | expressed protein, unknown protein 110K5.12 - Sorghum bicolor, TREMBL:AF124045_5	9.1	11.4	-2.2	-8.3	0.08%	7.8

Rank	Description	Sync	Root	M	t	adj.q	B
1475	AT5G26820.1 | ferroportin-related, low similarity to ferroportin1 (Danio rerio) GI:7109245 | chr5:9433622-9437103 FORWARD | Aliases: F2P16.6, F2P16_6	7.8	9.3	-1.5	-8.3	0.08%	8.0
1477	AT4G35600.1 | Symbol: CONNEXIN 32 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:16896242-16898881 FORWARD | Aliases: F8D20.110, F8D20_110	4.8	7.2	-2.4	-8.3	0.08%	7.9
1483	AT3G47210.1 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function | chr3:17396298-17398229 FORWARD | Aliases: F13I12.260	5.1	7.4	-2.2	-8.3	0.08%	7.5
1484	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	4.3	-1.7	-8.3	0.08%	7.9
1492	AT3G58990.1 | aconitase C-terminal domain-containing protein, contains Pfam profile PF00694: Aconitase C-terminal domain | chr3:21808035-21809280 REVERSE | Aliases: F17J16.40	3.9	6.9	-3.0	-8.3	0.08%	6.8
1493	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	5.2	8.4	-3.2	-8.3	0.08%	7.5
1494	AT5G20050.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:6774304-6775847 FORWARD | Aliases: F28I16.200, F28I16_200	7.6	9.9	-2.4	-8.3	0.08%	8.0
1496	AT4G36970.1 | remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region | chr4:17429739-17431680 REVERSE | Aliases: AP22.30, AP22_30	5.5	7.8	-2.3	-8.2	0.08%	7.8
1498	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	6.0	-2.4	-8.2	0.09%	7.5
1499	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	3.1	7.2	-4.1	-8.2	0.09%	7.8
1501	AT5G05400.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.4	5.8	-2.5	-8.2	0.09%	7.2
1502	AT2G27740.1 | expressed protein, contains Pfam profile PF04949: Family of unknown function (DUF662) | chr2:11829855-11830808 FORWARD | Aliases: F15K20.16, F15K20_16	3.6	6.1	-2.5	-8.2	0.09%	7.7
1504	AT3G29780.1 | Symbol: RALFL27 | expressed protein | chr3:11674220-11674668 FORWARD | Aliases: RALF LIKE 27, T26G12.18	3.0	7.1	-4.1	-8.2	0.09%	6.1
1506	AT1G18160.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr1:6248786-6254032 FORWARD | Aliases: T10F20.16	7.0	9.1	-2.2	-8.2	0.09%	7.7
1507	AT5G13580.1 | ABC transporter family protein | chr5:4370695-4373204 FORWARD | Aliases: T6I14.7	3.5	5.6	-2.1	-8.2	0.09%	7.6
1509	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	3.7	6.8	-3.1	-8.2	0.09%	7.1
1510	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	5.4	8.3	-2.9	-8.2	0.09%	7.7
1513	AT1G74790.1 | expressed protein, contains similarity to hedgehog-interacting protein GI:4868122 from (Mus musculus) | chr1:28102471-28105557 FORWARD | Aliases: F25A4.24, F25A4_24	5.3	7.2	-1.9	-8.2	0.09%	7.7
1515	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	2.7	7.0	-4.3	-8.2	0.09%	6.2

Rank	Description	Sync	Root	M	t	adj.q	B
1516	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	5.8	8.0	-2.2	-8.2	0.09%	7.8
1517	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	4.4	7.5	-3.2	-8.2	0.09%	7.3
1520	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	4.7	-1.6	-8.2	0.09%	7.9
1524	AT4G00360.1 | Symbol: CYP86A2 | cytochrome P450, putative | chr4:160768-163002 FORWARD | Aliases: A_IG005I10.21, A_IG005I10_21, F5I10.21, F5I10_21	4.0	6.9	-2.9	-8.2	0.09%	7.4
1525	AT5G05410.2 | Symbol: DREB2A |	6.5	9.9	-3.5	-8.2	0.09%	7.5
1526	AT3G56930.1 | zinc finger (DHHC type) family protein, low similarity to Golgi-specific DHHC zinc figer protein (Mus musculus) GI:21728103; contains Pfam profile PF01529: DHHC zinc finger domain | chr3:21084474-21087293 FORWARD | Aliases: T8M16.5	3.2	5.2	-2.0	-8.2	0.09%	7.6
1527	AT5G14690.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:4733802-4734550 REVERSE | Aliases: T9L3.3	3.2	6.0	-2.8	-8.2	0.09%	7.5
1528	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	2.4	6.0	-3.6	-8.2	0.09%	7.2
1529	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	8.3	-1.7	-8.2	0.09%	7.8
1530	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	8.7	9.5	-0.8	-8.2	0.09%	7.8
1534	AT5G18490.1 | expressed protein | chr5:6134154-6136767 REVERSE | Aliases: T28N17.2	4.5	6.7	-2.1	-8.2	0.09%	7.5
1535	AT5G16250.1 | expressed protein | chr5:5310100-5310954 REVERSE | Aliases: T21H19.170, T21H19_170	3.9	6.0	-2.1	-8.2	0.09%	7.5
1537	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	5.4	8.6	-3.2	-8.1	0.09%	7.5
1538	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	6.8	8.6	-1.8	-8.1	0.09%	7.8
1540	AT5G62720.2 | integral membrane HPP family protein, contains Pfam domain, PF04982: HPP family | chr5:25209086-25212181 FORWARD | Aliases: MQB2.4, MQB2_4	7.3	9.4	-2.1	-8.1	0.09%	7.6
1541	AT1G80310.1 | expressed protein | chr1:30199510-30201446 FORWARD | Aliases: F5I6.6, F5I6_6	6.9	8.9	-2.0	-8.1	0.09%	7.8
1542	AT4G10390.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:6441689-6443385 REVERSE | Aliases: F7L13.4	4.2	6.3	-2.1	-8.1	0.09%	7.6
1544	AT3G14940.1 | Symbol: ATPPC3 |	7.4	11.2	-3.8	-8.1	0.09%	7.7
1547	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	6.0	8.0	-2.0	-8.1	0.09%	7.8
1549	AT3G09540.1 | pectate lyase family protein, simliar to style development-specific protein 9612 SP:P24396 from (Lycopersicon esculentum) | chr3:2928875-2931234 REVERSE | Aliases: F11F8.12	3.8	6.0	-2.2	-8.1	0.09%	7.5
1554	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	7.5	9.1	-1.7	-8.1	0.09%	7.8
1555	AT2G31990.1 | exostosin family protein, contains Pfam profile: PF03016	3.9	6.6	-2.6	-8.1	0.09%	7.4
1561	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	4.7	-1.9	-8.1	0.09%	7.6

Rank	Description	Sync	Root	M	t	adj.q	B
1569	AT5G45510.1 | leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560 | chr5:18461884-18466673 FORWARD | Aliases: MFC19.18, MFC19_18	5.8	8.4	-2.6	-8.1	0.09%	7.6
1576	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	12.4	14.3	-1.9	-8.1	0.09%	7.3
1578	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	3.8	6.6	-2.8	-8.1	0.09%	7.2
1579	AT1G50590.1 | pirin, putative, similar to SP:O00625 Pirin {Homo sapiens}; contains Pfam profile PF02678: Pirin	3.7	6.2	-2.4	-8.1	0.09%	7.6
1585	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	6.3	-2.9	-8.1	0.09%	6.9
1586	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	7.0	8.9	-1.8	-8.1	0.09%	7.7
1587	AT1G10380.1 | expressed protein | chr1:3400607-3402325 FORWARD | Aliases: F14N23.27	3.5	7.0	-3.5	-8.1	0.10%	6.7
1588	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	7.2	-4.1	-8.1	0.10%	6.5
1590	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	6.8	9.4	-2.6	-8.1	0.10%	7.6
1591	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	2.8	4.6	-1.8	-8.1	0.10%	7.7
1592	AT2G48030.1 | endonuclease/exonuclease/phosphatase family protein, contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family | chr2:19654597-19657218 REVERSE | Aliases: T9J23.18	4.5	6.4	-1.9	-8.0	0.10%	7.6
1593	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	5.1	7.2	-2.1	-8.0	0.10%	7.7
1594	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	7.5	-3.8	-8.0	0.10%	7.5
1597	AT4G01720.1 | Symbol: WRKY47 |	2.7	5.1	-2.3	-8.0	0.10%	7.3
1598	AT3G07310.1 | expressed protein | chr3:2327824-2329787 REVERSE | Aliases: T1B9.2	4.7	6.9	-2.2	-8.0	0.10%	7.6
1599	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	4.3	6.7	-2.4	-8.0	0.10%	7.3
1600	AT4G24960.1 | Symbol: ATHVA22D | ABA-responsive protein (HVA22d), identical to AtHVA22d (Arabidopsis thaliana) GI:4884938 | chr4:12827947-12829249 FORWARD | Aliases: F13M23.100, F13M23_100	4.9	8.6	-3.8	-8.0	0.10%	7.2

Rank	Description	Sync	Root	M	t	adj.q	B
1605	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	5.0	-2.4	-8.0	0.10%	7.1
1606	AT3G57410.1 | Symbol: VLN3 | villin 3 (VLN3), nearly identical to villin 3 (VLN3) (Arabidopsis thaliana) GI:3415117 | chr3:21254113-21262077 REVERSE | Aliases: F28O9.1, VILLIN 3	4.0	6.4	-2.4	-8.0	0.10%	7.4
1607	AT2G26730.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:11395485-11398719 FORWARD | Aliases: F18A8.10, F18A8_10	4.3	6.3	-2.0	-8.0	0.10%	7.5
1608	AT1G49100.1 | 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 | chr1:18169815-18173773 REVERSE | Aliases: F27J15.13, F27J15_13	3.1	5.7	-2.6	-8.0	0.10%	7.2
1609	AT1G11310.1 | Symbol: MLO2 | seven transmembrane MLO family protein / MLO-like protein 2 (MLO2), idenctical 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	6.0	8.6	-2.6	-8.0	0.10%	7.6
1610	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	8.6	12.3	-3.7	-8.0	0.10%	7.4
1611	AT5G06800.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr5:2103172-2105899 FORWARD | Aliases: MPH15.16, MPH15_16	2.9	6.2	-3.3	-8.0	0.10%	7.1
1615	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	6.9	9.4	-2.5	-8.0	0.10%	7.7
1626	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	5.0	7.7	-2.6	-8.0	0.10%	7.3
1628	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	6.7	-2.5	-8.0	0.10%	7.2
1631	AT4G33666.1 | expressed protein | chr4:16169051-16169538 FORWARD | Aliases: None	3.1	6.5	-3.4	-8.0	0.10%	6.6
1634	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	3.7	5.3	-1.6	-8.0	0.10%	7.6
1635	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	7.3	-1.9	-8.0	0.10%	7.5
1636	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	2.9	4.9	-2.0	-8.0	0.10%	7.5
1637	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	8.2	9.8	-1.6	-8.0	0.10%	7.7
1639	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	4.4	7.6	-3.2	-8.0	0.10%	7.1
1641	AT1G27520.1 | glycoside hydrolase family 47 protein, Similar to gb:U04299 mannosyl-oligosaccharide alpha-1,2-mannosidase from Mus musculus. ESTs gb:R84145 and gb:AA394707 come from this gene	5.3	7.1	-1.8	-8.0	0.10%	7.7
1642	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: ARABINOGALACTAN PROTEIN 2, F14M13.13, F14M13_13	6.9	8.8	-1.9	-8.0	0.10%	7.7

Rank	Description	Sync	Root	M	t	adj.q	B
1645	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 Arabidosis Thaliana (GB:1TQ1); contains InterPro domain Rhodanese-like (InterPro:IPR001763) | chr5:26464874-26465953 FORWARD | Aliases: K2A18.25, K2A18_25	7.4	9.7	-2.3	-8.0	0.10%	7.6
1646	AT4G13030.2 | expressed protein | chr4:7607264-7609840 FORWARD | Aliases: F25G13.120, F25G13_120	5.8	7.8	-2.0	-8.0	0.10%	7.4
1650	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	5.0	10.1	-5.1	-8.0	0.10%	6.5
1651	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	6.1	-2.7	-8.0	0.10%	7.2
1652	AT3G15300.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr3:5147412-5148217 REVERSE | Aliases: K7L4.10	6.8	8.8	-2.0	-8.0	0.10%	7.3
1656	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	3.6	5.8	-2.2	-7.9	0.10%	7.3
1658	AT3G27470.1 | expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707) | chr3:10164286-10168111 FORWARD | Aliases: K1G2.18	3.6	5.8	-2.1	-7.9	0.10%	7.5
1659	AT4G40060.1 | Symbol: ATHB16 |	4.9	7.2	-2.3	-7.9	0.10%	7.4
1660	AT1G44170.2 | Symbol: ALDH3H1 | aldehyde dehydrogenase, putative (ALDH), similar to aldehyde dehydrogenase ALDH (Craterostigma plantagineum) gi:17065918:emb:CAC84900	6.5	10.0	-3.5	-7.9	0.10%	7.5
1661	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, PAPAIN TYPE CYSTEINE ENDOPEPTIDASE XCP2, XYLEM CYSTEINE PEPTIDASE 2	5.1	10.4	-5.3	-7.9	0.10%	7.0
1663	AT5G25280.2 | serine-rich protein-related, contains some similarity to serine-rich proteins | chr5:8773795-8776003 FORWARD | Aliases: F18G18.20, F18G18_20	5.3	8.4	-3.1	-7.9	0.10%	7.2
1667	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	3.7	5.8	-2.0	-7.9	0.10%	7.6
1668	AT1G08310.1 | esterase/lipase/thioesterase family protein, contains Interpro entry IPR000379 | chr1:2618683-2620408 FORWARD | Aliases: T23G18.18, T23G18_18	3.6	6.7	-3.2	-7.9	0.10%	7.3
1672	AT2G21540.2 | similar to SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [Arabidopsis thaliana] (TAIR:At4g34580.1); similar to SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [Arabidopsis thaliana] (TAIR:At4g39180.1); similar to SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [Arabidopsis thaliana] (TAIR:At4g36490.1); similar to SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [Arabidopsis thaliana] (TAIR:At2g18180.1); 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) | chr2:9227629-9231359 REVERSE | Aliases: F3K23.30	3.2	5.9	-2.6	-7.9	0.10%	7.2
1677	AT5G40020.1 | pathogenesis-related thaumatin family protein, similar to SP:P50699 Thaumatin-like protein precursor {Arabidopsis thaliana}, pathogenesis-related group 5 protein (Brassica rapa) GI:2749943; contains Pfam profile PF00314: Thaumatin family | chr5:16039990-16041544 REVERSE | Aliases: MYH19.180, MYH19_180	3.8	7.3	-3.4	-7.9	0.10%	6.2
1682	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	5.4	6.8	-1.5	-7.9	0.10%	7.7
1683	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	7.1	9.0	-1.9	-7.9	0.10%	7.7
1684	AT2G25680.1 | expressed protein, ; expression supported by MPSS | chr2:10940139-10941615 REVERSE | Aliases: F3N11.13, F3N11_13	4.8	7.9	-3.2	-7.9	0.10%	6.7
1688	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	4.2	7.0	-2.8	-7.9	0.10%	6.8

Rank	Description	Sync	Root	M	t	adj.q	B
1689	AT2G41705.1 | camphor resistance CrcB family protein, contains Pfam profile PF02537: CrcB-like protein	4.5	6.6	-2.1	-7.9	0.10%	7.4
1692	AT5G66420.2 | similar to transcriptional regulator [Clostridium tetani E88] (GB:NP_782382.1) | chr5:26538900-26542307 REVERSE | Aliases: K1F13.7, K1F13_7	7.7	9.7	-2.0	-7.9	0.11%	7.4
1697	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	3.2	5.8	-2.6	-7.9	0.11%	7.2
1700	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	2.7	5.2	-2.4	-7.9	0.11%	7.1
1705	AT2G45220.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr2:18651160-18653521 REVERSE | Aliases: F4L23.27	3.6	8.8	-5.2	-7.9	0.11%	7.0
1707	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	6.9	-3.7	-7.9	0.11%	7.1
1711	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	5.2	-1.7	-7.9	0.11%	7.5
1713	AT4G40010.1 | serine/threonine protein kinase, putative, similar to serine-threonine protein kinase (Triticum aestivum) gi:2055374:gb:AAB58348	4.7	9.2	-4.6	-7.8	0.11%	6.6
1714	AT1G29270.1 | expressed protein | chr1:10230305-10231128 FORWARD | Aliases: F28N24.5, F28N24_5	2.5	6.4	-4.0	-7.8	0.11%	6.6
1717	AT1G33840.1 | hypothetical protein, contains Pfam profile PF04525: Protein of unknown function (DUF567) | chr1:12283842-12285330 REVERSE | Aliases: F14M2.3, F14M2_3	2.7	5.3	-2.6	-7.8	0.11%	7.1
1719	AT4G32140.1 | expressed protein | chr4:15522905-15525433 REVERSE | Aliases: F10N7.50, F10N7_50	5.5	7.5	-1.9	-7.8	0.11%	7.5
1720	AT1G12290.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.6	3.9	-1.3	-7.8	0.11%	7.6
1722	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	6.7	10.3	-3.5	-7.8	0.11%	6.9
1723	AT1G12740.1 | Symbol: CYP87A2 | cytochrome P450 family protein, similar to Cytochrome P450 90A1 (SP:Q42569) (Arabidopsis thaliana) | chr1:4342460-4344615 FORWARD | Aliases: T12C24.27, T12C24_27	1.9	5.7	-3.8	-7.8	0.11%	6.8
1726	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	5.0	7.2	-2.1	-7.8	0.11%	7.5
1727	AT5G63930.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:25600232-25603725 FORWARD | Aliases: MBM17.3, MBM17_3	6.3	8.1	-1.8	-7.8	0.11%	7.5
1730	AT2G30360.1 | Symbol: CIPK11 |	7.1	10.2	-3.1	-7.8	0.11%	7.5
1732	AT3G11280.2 | myb family transcription factor, contains Pfam profile: PF00249 Myb-like DNA-binding domain | chr3:3533261-3534502 REVERSE | Aliases: F11B9.25	7.9	10.0	-2.1	-7.8	0.11%	7.6
1733	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: HOMEOBOX PROTEIN, T28I19.70, T28I19_70	4.4	8.6	-4.2	-7.8	0.11%	7.1
1735	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	7.3	9.1	-1.8	-7.8	0.11%	7.6
1736	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	8.7	12.1	-3.3	-7.8	0.11%	7.5
1737	AT2G05260.1 | lipase class 3 family protein, contains Pfam profile PF01764: Lipase | chr2:1918332-1920039 FORWARD | Aliases: F5G3.16, F5G3_16	6.4	8.0	-1.6	-7.8	0.11%	7.5

Rank	Description	Sync	Root	M	t	adj.q	B
1739	AT4G19680.2 | Symbol: IRT2 | similar to iron-responsive transporter (IRT1) [Arabidopsis thaliana] (TAIR:At4g19690.2); 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) | chr4:10703386-10704811 FORWARD | Aliases: T16H5.40, T16H5_40	3.1	8.4	-5.3	-7.8	0.11%	5.9
1740	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	2.4	3.6	-1.2	-7.8	0.11%	7.6
1743	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	4.7	7.6	-2.9	-7.8	0.11%	7.1
1745	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	7.6	-3.9	-7.8	0.11%	6.4
1750	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	3.6	7.3	-3.7	-7.8	0.11%	6.7
1755	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	8.6	9.7	-1.2	-7.8	0.11%	7.5
1760	AT5G19930.1 | integral membrane family protein, contains Pfam domain PF01940: Integral membrane protein | chr5:6737585-6739350 REVERSE | Aliases: F28I16.80, F28I16_80	6.9	9.6	-2.7	-7.8	0.11%	7.4
1761	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	5.7	-2.3	-7.8	0.11%	6.9
1764	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	2.6	5.7	-3.2	-7.8	0.11%	6.5
1765	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	2.8	3.9	-1.0	-7.8	0.11%	7.5
1766	AT2G02780.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:781846-784645 REVERSE | Aliases: T20F6.8, T20F6_8	2.9	4.3	-1.4	-7.8	0.11%	7.5
1767	AT3G22240.1 | expressed protein | chr3:7863684-7864586 REVERSE | Aliases: MMP21.2	9.3	11.8	-2.5	-7.8	0.11%	7.3
1768	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	4.3	5.9	-1.6	-7.8	0.11%	7.5
1770	AT1G72630.1 | expressed protein | chr1:27347932-27349238 FORWARD | Aliases: F28P22.18, F28P22_18	6.0	7.4	-1.4	-7.8	0.11%	7.5
1776	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	7.7	8.8	-1.1	-7.7	0.11%	7.5
1778	AT3G14340.1 | expressed protein | chr3:4782764-4783144 FORWARD | Aliases: MLN21.13	5.2	7.6	-2.5	-7.7	0.11%	7.0
1779	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	8.6	-4.0	-7.7	0.11%	6.7
1780	AT1G80380.2 | phosphoribulokinase/uridine kinase-related | chr1:30222157-30224863 FORWARD | Aliases: F5I6.13, F5I6_13	7.8	9.8	-2.0	-7.7	0.11%	7.2
1781	AT3G03380.1 | DegP protease, putative, contains similarity to degP GI:2623992 from (Bradyrhizobium japonicum) | chr3:799622-808529 FORWARD | Aliases: AT3G03390, T21P5.20, T21P5_20	5.0	6.4	-1.5	-7.7	0.11%	7.5
1782	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	5.9	-2.9	-7.7	0.12%	6.8
1786	AT1G45688.2 | expressed protein | chr1:17193844-17195598 FORWARD | Aliases: F2G19.25, F2G19_25	5.8	7.8	-2.0	-7.7	0.12%	7.3

Rank	Description	Sync	Root	M	t	adj.q	B
1788	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	8.7	10.8	-2.1	-7.7	0.12%	7.5
1790	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	5.5	-2.1	-7.7	0.12%	7.3
1791	AT3G47780.1 | Symbol: ATATH6 |	6.4	8.5	-2.1	-7.7	0.12%	7.3
1793	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) (Arabidopsis thaliana); similar to actinfilin (GI:21667852) (Rattus norvegicus) | chr2:19003041-19005706 FORWARD | Aliases: T3F17.9	6.0	7.6	-1.6	-7.7	0.12%	7.5
1796	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	8.2	11.6	-3.3	-7.7	0.12%	6.8
1799	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	4.4	7.6	-3.2	-7.7	0.12%	7.4
1801	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	6.8	-3.0	-7.7	0.12%	7.0
1805	AT3G17920.1 | leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560 | chr3:6137261-6142029 FORWARD | Aliases: MEB5.14	5.4	7.0	-1.6	-7.7	0.12%	7.5
1810	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	4.1	-1.9	-7.7	0.12%	7.3
1811	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	5.3	7.3	-1.9	-7.7	0.12%	7.2
1812	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	6.7	9.0	-2.3	-7.7	0.12%	7.0
1817	AT4G21230.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr4:11319196-11321689 REVERSE | Aliases: F7J7.170, F7J7_170	3.3	6.9	-3.6	-7.7	0.12%	6.2
1819	AT4G32440.2 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr4:15656691-15659754 FORWARD | Aliases: F8B4.140, F8B4_140	4.9	6.4	-1.5	-7.7	0.12%	7.4
1822	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	3.5	6.1	-2.5	-7.7	0.12%	7.1
1824	AT3G09270.1 | Symbol: ATGSTU8 | glutathione S-transferase, putative, similar to glutathione transferase GB:CAA71784 (Glycine max) | chr3:2848295-2849293 REVERSE | Aliases: F3L24.14	5.3	8.6	-3.3	-7.7	0.12%	7.1
1828	AT1G77280.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr1:29036362-29040776 REVERSE | Aliases: T14N5.13, T14N5_13	4.2	8.0	-3.7	-7.7	0.12%	7.0
1829	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	4.9	8.1	-3.3	-7.7	0.12%	6.7
1830	AT5G01740.1 | expressed protein, wound-inducible protein wun1 protein - Solanum tuberosum, PIR:JQ0398 | chr5:280719-281442 FORWARD | Aliases: T20L15.10, T20L15_10	4.2	6.7	-2.5	-7.7	0.12%	7.0

Rank	Description	Sync	Root	M	t	adj.q	B
1832	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	5.4	8.2	-2.8	-7.6	0.12%	7.3
1833	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	5.5	7.6	-2.1	-7.6	0.12%	7.4
1836	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	6.9	-1.2	-7.6	0.12%	7.4
1838	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	2.5	4.7	-2.2	-7.6	0.12%	6.8
1839	AT4G03560.1 | Symbol: ATTPC1 |	7.8	9.8	-2.0	-7.6	0.12%	7.4
1841	AT1G55020.1 | Symbol: LOX1 | lipoxygenase (LOX1), identical to SP:Q06327 | chr1:20529375-20533940 FORWARD | Aliases: LIPOXYGENASE	5.0	8.1	-3.1	-7.6	0.12%	7.2
1843	AT5G43030.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.3	3.8	-1.5	-7.6	0.12%	7.4
1844	AT5G04150.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain; PMID: 12679534	3.6	5.0	-1.4	-7.6	0.12%	7.4
1846	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	3.7	5.7	-2.0	-7.6	0.12%	7.4
1852	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	2.7	5.0	-2.3	-7.6	0.12%	7.3
1853	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	5.6	-2.9	-7.6	0.12%	6.5
1854	AT3G14430.1 | expressed protein | chr3:4824204-4824844 REVERSE | Aliases: MOA2.3	9.2	10.0	-0.8	-7.6	0.12%	7.2
1856	AT1G23720.1 | proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr1:8388644-8391529 FORWARD | Aliases: F5O8.27, F5O8_27	3.0	9.0	-5.9	-7.6	0.12%	6.1
1857	AT1G74770.1 | expressed protein | chr1:28094772-28098495 REVERSE | Aliases: F25A4.26, F25A4_26	3.0	8.7	-5.7	-7.6	0.12%	7.1
1858	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	4.5	8.0	-3.5	-7.6	0.12%	6.8
1860	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	2.6	6.1	-3.5	-7.6	0.12%	7.1
1862	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	3.1	6.9	-3.9	-7.6	0.12%	7.2
1863	AT1G78420.1 | expressed protein | chr1:29509426-29512379 FORWARD | Aliases: F3F9.7, F3F9_7	6.2	8.0	-1.8	-7.6	0.12%	7.2
1864	AT4G03340.1 | glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/I-Branching enzyme | chr4:1467749-1470062 REVERSE | Aliases: F4C21.27, F4C21_27	4.3	6.1	-1.8	-7.6	0.12%	7.3
1866	AT5G49080.1 | proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr5:19908010-19910035 REVERSE | Aliases: K20J1.5, K20J1_5	4.1	10.6	-6.6	-7.6	0.12%	6.2
1868	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	4.4	6.4	-2.0	-7.6	0.12%	7.2
1870	AT5G43230.1 | hypothetical protein | chr5:17367665-17369975 FORWARD | Aliases: MNL12.5, MNL12_5	2.6	3.6	-1.0	-7.6	0.13%	7.4
1871	AT1G31720.1 | expressed protein | chr1:11356083-11357062 FORWARD | Aliases: F27M3.8, F27M3_8	2.8	6.7	-3.8	-7.6	0.13%	5.4

Rank	Description	Sync	Root	M	t	adj.q	B
1877	AT3G07870.1 | F-box family protein, contains F-box domain Pfam:PF00646	5.6	6.8	-1.2	-7.6	0.13%	7.4
1878	AT1G18390.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:6327456-6329928 FORWARD | Aliases: F15H18.25, F15H18_25	4.2	5.7	-1.5	-7.6	0.13%	7.4
1880	AT5G07270.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr5:2280672-2283594 FORWARD | Aliases: T28J14.210, T28J14_210	3.4	5.4	-2.0	-7.6	0.13%	7.2
1883	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	2.6	6.2	-3.6	-7.6	0.13%	6.1
1884	AT5G25820.1 | exostosin family protein, contains Pfam profile: PF03016 exostosin family | chr5:8997186-9000318 REVERSE | Aliases: F18A17.70, F18A17_70	3.9	6.6	-2.6	-7.6	0.13%	6.6
1887	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	9.0	10.4	-1.4	-7.6	0.13%	7.4
1888	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) GI:1805654 Belongs to plant 2B ATPase??s with an N-terminal autoinhibitor. | chr3:21222455-21227353 REVERSE | Aliases: F28O9.180	6.4	7.6	-1.3	-7.6	0.13%	7.3
1889	AT2G38860.2 | Symbol: YLS5 | proteaseI (pfpI)-like protein (YLS5), contains Pfam profile PF01965: DJ-1/PfpI family; supporting cDNA gi:13122287:dbj:AB047808.1:; identical to proteaseI (pfpI)-like protein (Arabidopsis thaliana) GI:13122288, cDNA proteaseI (pfpI)-like protein GI:13122287 | chr2:16240522-16242309 REVERSE | Aliases: T7F6.3, T7F6_3	8.4	10.1	-1.7	-7.6	0.13%	7.3
1893	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	3.8	6.1	-2.3	-7.6	0.13%	7.0
1896	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	4.7	-1.8	-7.6	0.13%	7.2
1898	AT3G59940.1 | kelch repeat-containing F-box family protein, contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	3.5	6.5	-2.9	-7.6	0.13%	6.6
1904	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	2.8	6.4	-3.6	-7.5	0.13%	6.3
1906	AT1G66450.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.4	5.9	-2.4	-7.5	0.13%	7.2
1909	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	4.8	6.9	-2.0	-7.5	0.13%	7.1
1910	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	5.0	8.3	-3.2	-7.5	0.13%	7.2
1911	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	7.6	-2.7	-7.5	0.13%	6.8
1913	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	3.8	5.2	-1.4	-7.5	0.13%	7.3

Rank	Description	Sync	Root	M	t	adj.q	B
1914	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	4.0	5.5	-1.5	-7.5	0.13%	7.3
1915	AT2G24570.1 | Symbol: WRKY17 |	3.8	6.4	-2.6	-7.5	0.13%	7.1
1917	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	6.3	7.9	-1.6	-7.5	0.13%	7.2
1918	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	3.0	4.2	-1.3	-7.5	0.13%	7.3
1919	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	3.7	6.7	-3.0	-7.5	0.13%	7.2
1923	AT5G40850.1 | Symbol: UPM1 | urophorphyrin III methylase (UPM1), identical to urophorphyrin 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	7.6	9.8	-2.1	-7.5	0.13%	7.3
1924	AT1G34510.1 | peroxidase, putative, similar to peroxidase ATP13a GB:CAA67312 from (Arabidopsis thaliana) | chr1:12615711-12617010 REVERSE | Aliases: F12K21.18, F12K21_18	2.5	6.4	-3.9	-7.5	0.13%	6.5
1928	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	7.6	10.2	-2.6	-7.5	0.13%	7.0
1932	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	9.1	10.4	-1.2	-7.5	0.13%	7.2
1933	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	5.6	8.2	-2.7	-7.5	0.13%	6.8
1935	AT4G40050.1 | expressed protein | chr4:18560854-18563832 REVERSE | Aliases: T5J17.220, T5J17_220	3.3	5.6	-2.3	-7.5	0.13%	7.2
1939	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	7.7	9.5	-1.8	-7.5	0.13%	7.3
1941	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	8.7	-1.4	-7.5	0.13%	7.3
1942	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	7.8	-5.1	-7.5	0.13%	7.3
1943	AT5G02270.1 | Symbol: ATNAP9 |	10.4	12.0	-1.6	-7.5	0.13%	7.1
1945	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	6.8	-2.8	-7.5	0.13%	6.6

Rank	Description	Sync	Root	M	t	adj.q	B
1946	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	5.9	-2.4	-7.5	0.13%	7.0
1947	AT2G34070.1 | expressed protein | chr2:14394505-14397309 REVERSE | Aliases: T14G11.19, T14G11_19	5.1	6.6	-1.5	-7.5	0.13%	7.2
1950	AT3G05490.1 | Symbol: RALFL22 | rapid alkalinization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316 | chr3:1591283-1591989 FORWARD | Aliases: F22F7.6, F22F7_6, RALF LIKE 22	6.8	9.3	-2.5	-7.5	0.13%	7.2
1952	AT5G63370.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:25401132-25404450 REVERSE | Aliases: K9H21.10, K9H21_10	5.7	7.7	-2.0	-7.5	0.13%	7.2
1955	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	2.6	5.2	-2.7	-7.5	0.13%	6.6
1957	AT3G57380.1 | expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563) | chr3:21240779-21242706 FORWARD | Aliases: F28O9.230	4.1	6.1	-2.0	-7.5	0.13%	7.1
1959	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	8.3	-5.2	-7.5	0.13%	7.0
1963	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	4.1	6.9	-2.8	-7.5	0.13%	7.2
1969	AT1G22360.2 | Symbol: AT2 | similar to UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22380.1); similar to UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22340.1); similar to UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22400.1); similar to UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22370.2); similar to glycosyltransferase NTGT5a [Nicotiana tabacum] (GB:BAD93689.1); contains InterPro domain UDP-glucoronosyl/UDP-glucosyl transferase (InterPro:IPR002213) | chr1:7894847-7897580 REVERSE | Aliases: None	5.5	9.5	-4.0	-7.5	0.13%	6.5
1970	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	6.7	10.4	-3.7	-7.5	0.14%	7.1
1973	AT3G51830.1 | Symbol: ATG5 | phosphoinositide phosphatase family protein, contains similarity to phosphoinositide phosphatase SAC1 (Rattus norvegicus) gi:11095248:gb:AAG29810; contains Pfam domain, PF02383: SacI homology domain ; Contains nonconsensus AT/AA splice site at intron 7 | chr3:19231126-19236257 FORWARD | Aliases: ATEM1.8, TRANSMEMBRANE PROTEIN G5P	5.4	8.1	-2.7	-7.5	0.14%	7.2
1978	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	4.4	7.8	-3.4	-7.4	0.14%	7.0
1979	AT5G18650.1 | zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	7.5	9.9	-2.3	-7.4	0.14%	7.2
1980	AT5G27150.1 | Symbol: NHX1 | sodium proton exchanger / Na+/H+ antiporter (NHX1), identical to Na+/H+ 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+/H+ EXCHANGER, T21B4.60, T21B4_60	7.0	9.6	-2.6	-7.4	0.14%	7.0
1982	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	4.8	7.4	-2.6	-7.4	0.14%	7.1
1985	AT3G14090.1 | exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit; | chr3:4669260-4671560 REVERSE | Aliases: MAG2.5	4.2	6.0	-1.7	-7.4	0.14%	7.1
1988	AT4G38550.1 | expressed protein | chr4:18025653-18028794 FORWARD | Aliases: F20M13.110, F20M13_110	4.2	7.8	-3.6	-7.4	0.14%	7.0
1990	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	2.9	4.9	-2.1	-7.4	0.14%	7.0

Rank	Description	Sync	Root	M	t	adj.q	B
1991	AT2G25010.1 | expressed protein | chr2:10638649-10640736 FORWARD | Aliases: F27C12.7, F27C12_7	4.0	6.9	-3.0	-7.4	0.14%	6.8
1992	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	5.1	8.6	-3.5	-7.4	0.14%	6.9
1993	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	10.5	-2.6	-7.4	0.14%	7.2
1994	AT2G20670.1 | expressed protein, contains Pfam profile PF04720: Protein of unknown function (DUF506) | chr2:8918941-8920615 REVERSE | Aliases: F23N11.1	3.3	4.9	-1.6	-7.4	0.14%	7.2
1995	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	7.7	9.5	-1.8	-7.4	0.14%	7.2
1997	AT1G27740.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.8	6.1	-3.3	-7.4	0.14%	6.0
2000	AT3G07070.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:2237964-2240080 FORWARD | Aliases: F17A9.25	2.4	4.3	-1.9	-7.4	0.14%	7.0
2006	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	5.1	-1.9	-7.4	0.14%	6.9
2009	AT5G13080.1 | Symbol: WRKY75 |	3.8	6.7	-2.9	-7.4	0.14%	7.1
2010	AT1G48260.1 | Symbol: CIPK17 |	3.5	5.9	-2.4	-7.4	0.14%	6.7
2011	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	5.2	-2.2	-7.4	0.14%	6.9
2021	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	4.0	6.7	-2.7	-7.4	0.15%	6.4
2022	AT3G09960.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	3.5	5.3	-1.8	-7.4	0.15%	7.0
2023	AT5G49710.3 | expressed protein, similar to unknown protein (pir::T05575) | chr5:20212653-20214579 FORWARD | Aliases: K2I5.7, K2I5_7	5.0	7.6	-2.6	-7.3	0.15%	6.4
2025	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	7.5	-3.2	-7.3	0.15%	6.9
2027	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	3.5	5.2	-1.7	-7.3	0.15%	7.0
2029	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	2.8	5.4	-2.6	-7.3	0.15%	6.8
2031	AT3G55720.1 | expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620) | chr3:20690799-20692426 FORWARD | Aliases: F1I16.130	2.7	4.9	-2.2	-7.3	0.15%	6.7
2033	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	5.7	-2.4	-7.3	0.15%	6.9
2034	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	7.5	9.5	-2.0	-7.3	0.15%	7.1

Rank	Description	Sync	Root	M	t	adj.q	B
2035	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	9.1	-5.9	-7.3	0.15%	6.4
2038	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	4.3	8.0	-3.7	-7.3	0.15%	6.0
2039	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	4.9	7.5	-2.5	-7.3	0.15%	6.7
2040	AT2G40000.1 | expressed protein | chr2:16707588-16709106 REVERSE | Aliases: T28M21.16, T28M21_16	8.2	10.3	-2.1	-7.3	0.15%	7.1
2041	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	3.6	5.8	-2.2	-7.3	0.15%	6.7
2044	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	3.0	5.2	-2.2	-7.3	0.15%	6.7
2045	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	5.4	-2.4	-7.3	0.15%	7.0
2047	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	3.5	7.3	-3.8	-7.3	0.15%	5.8
2049	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	2.2	5.5	-3.3	-7.3	0.15%	6.4
2051	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	5.2	6.8	-1.7	-7.3	0.15%	7.1
2052	AT2G43210.2 | UBX domain-containing protein, contains Pfam profile PF00789: UBX domain	7.3	9.1	-1.8	-7.3	0.15%	7.0
2053	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	6.3	-1.6	-7.3	0.15%	7.0
2056	AT3G45900.1 | expressed protein | chr3:16885387-16887007 REVERSE | Aliases: F16L2.110	5.6	6.8	-1.3	-7.3	0.15%	7.1
2057	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	8.0	-2.2	-7.3	0.15%	6.9
2058	AT3G13690.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:4485799-4490238 FORWARD | Aliases: MMM17.11	3.6	5.9	-2.2	-7.3	0.15%	7.1
2059	AT4G35560.1 | expressed protein | chr4:16881567-16887024 FORWARD | Aliases: F8D20.70, F8D20_70	5.4	8.1	-2.7	-7.3	0.15%	6.9
2060	AT3G55910.1 | expressed protein, PA26, p53 regulated PA26-T3 nuclear protein, Homo sapiens, EMBL:AF033121 | chr3:20753878-20754458 FORWARD | Aliases: F27K19.90	3.8	5.9	-2.1	-7.3	0.15%	6.8
2066	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	5.2	6.4	-1.2	-7.3	0.15%	7.1
2070	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	4.7	7.0	-2.3	-7.3	0.15%	7.0
2071	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	6.2	7.8	-1.6	-7.3	0.15%	7.1

Rank	Description	Sync	Root	M	t	adj.q	B
2072	AT1G44970.1 | peroxidase, putative, similar to peroxidase GI:993004 from (Mercurialis annua) | chr1:17004652-17006124 FORWARD | Aliases: F27F5.6, F27F5_6	2.4	4.9	-2.5	-7.3	0.15%	6.4
2075	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	6.1	7.7	-1.6	-7.3	0.16%	7.0
2076	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	3.2	6.4	-3.2	-7.3	0.16%	6.6
2077	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	5.8	7.9	-2.1	-7.3	0.16%	6.8
2079	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	4.6	7.0	-2.5	-7.3	0.16%	7.1
2080	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	5.4	7.7	-2.3	-7.3	0.16%	6.8
2082	AT5G24880.1 | expressed protein, ; expression supported by MPSS | chr5:8552746-8554077 FORWARD | Aliases: F6A4.90, F6A4_90	3.5	8.5	-5.0	-7.3	0.16%	6.5
2085	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	4.0	6.5	-2.5	-7.3	0.16%	6.5
2086	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.	4.3	6.3	-2.0	-7.3	0.16%	6.8
2090	AT3G43230.1 | zinc finger (FYVE type) family protein, contains Pfam domain PF01363: FYVE zinc finger | chr3:15218355-15220813 FORWARD | Aliases: F7K15.80	8.2	9.7	-1.5	-7.2	0.16%	7.1
2091	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	2.5	7.1	-4.6	-7.2	0.16%	6.2
2094	AT2G19150.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr2:8312182-8314526 FORWARD | Aliases: T20K24.17, T20K24_17	3.3	6.6	-3.3	-7.2	0.16%	6.1
2095	AT1G58410.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.9	5.1	-2.2	-7.2	0.16%	6.8
2097	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	5.3	7.6	-2.3	-7.2	0.16%	7.0
2100	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	6.6	-3.4	-7.2	0.16%	6.9
2102	AT4G39870.1 | expressed protein, hypothetical protein, Schizosaccharomyces cerevisae, Z99168 | chr4:18501889-18504422 FORWARD | Aliases: T5J17.40, T5J17_40	5.1	6.7	-1.6	-7.2	0.16%	7.0
2107	AT1G54710.1 | expressed protein, contains 3 WD-40 repeats (PF00400) (1 weak) submitForm(); | chr1:20420437-20424702 REVERSE | Aliases: T22H22.14, T22H22_14	6.2	7.9	-1.7	-7.2	0.16%	7.0
2109	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	4.0	7.1	-3.1	-7.2	0.16%	6.0
2110	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	5.9	9.5	-3.6	-7.2	0.16%	6.9
2112	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	3.8	7.7	-3.8	-7.2	0.16%	6.4

Rank	Description	Sync	Root	M	t	adj.q	B
2113	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	3.1	5.0	-1.9	-7.2	0.16%	6.7
2118	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	8.4	-3.7	-7.2	0.16%	6.6
2123	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	3.8	6.4	-2.6	-7.2	0.16%	6.8
2124	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	5.6	11.2	-5.6	-7.2	0.16%	6.7
2125	AT3G01860.2 | expressed protein | chr3:303725-304473 FORWARD | Aliases: F28J7.19, F28J7_19	5.5	10.2	-4.8	-7.2	0.16%	6.4
2128	AT1G66440.1 | DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain | chr1:24785834-24788014 FORWARD | Aliases: F28G11.16, F28G11_16	3.5	6.3	-2.8	-7.2	0.16%	6.5
2129	AT4G22070.1 | Symbol: WRKY31 |	2.0	2.9	-0.9	-7.2	0.16%	7.0
2130	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	4.6	7.0	-2.4	-7.2	0.16%	6.7
2131	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	6.0	8.4	-2.4	-7.2	0.16%	6.8
2132	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	2.8	6.5	-3.7	-7.2	0.16%	5.9
2133	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	9.1	-1.4	-7.2	0.16%	7.0
2134	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	5.0	7.1	-2.2	-7.2	0.16%	6.7
2139	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	2.5	4.0	-1.4	-7.2	0.16%	7.0
2140	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	3.4	8.8	-5.4	-7.2	0.16%	6.4
2141	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	3.3	4.7	-1.4	-7.2	0.16%	7.0
2142	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	3.6	5.9	-2.3	-7.2	0.16%	6.9
2143	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	5.0	-1.7	-7.2	0.16%	6.9
2144	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	6.4	7.9	-1.5	-7.2	0.16%	7.0

Rank	Description	Sync	Root	M	t	adj.q	B
2145	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	7.8	-1.9	-7.2	0.16%	6.8
2146	AT4G28260.1 | expressed protein | chr4:14004491-14006976 FORWARD | Aliases: F26K10.140, F26K10_140	8.4	11.0	-2.6	-7.2	0.16%	7.0
2148	AT5G43520.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	5.7	-3.0	-7.2	0.16%	6.1
2150	AT2G16760.1 | expressed protein | chr2:7282783-7284314 FORWARD | Aliases: T24I21.17, T24I21_17	4.9	6.2	-1.4	-7.2	0.16%	7.0
2151	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	7.3	9.5	-2.2	-7.2	0.16%	7.0
2152	AT4G12070.1 | expressed protein | chr4:7231816-7234495 FORWARD | Aliases: F16J13.140, F16J13_140	4.7	6.2	-1.5	-7.2	0.16%	7.0
2154	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	5.8	-3.5	-7.2	0.16%	5.9
2158	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	6.0	7.8	-1.8	-7.2	0.16%	7.0
2159	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	7.1	10.4	-3.2	-7.2	0.16%	6.8
2168	AT3G48760.1 | zinc finger (DHHC type) family protein, contains Pfam profile PF01529: DHHC zinc finger domain | chr3:18086817-18089276 FORWARD | Aliases: T21J18.30	6.6	8.9	-2.2	-7.2	0.17%	6.9
2169	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	7.3	9.5	-2.1	-7.2	0.17%	7.0
2170	AT3G12360.1 | ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023 | chr3:3934085-3936701 FORWARD | Aliases: T2E22.31	8.5	9.8	-1.3	-7.2	0.17%	6.9
2172	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	4.7	8.3	-3.6	-7.2	0.17%	6.8
2173	AT1G12030.1 | expressed protein, contains Pfam profile PF04720: Protein of unknown function (DUF506) | chr1:4064749-4066317 REVERSE | Aliases: F12F1.10, F12F1_10	4.1	6.2	-2.0	-7.2	0.17%	6.9
2174	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	3.6	6.4	-2.8	-7.2	0.17%	6.3
2175	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	4.0	6.5	-2.5	-7.1	0.17%	6.4
2176	AT1G29760.1 | expressed protein | chr1:10422316-10424312 FORWARD | Aliases: F1N18.18, F1N18_18	6.5	8.8	-2.3	-7.1	0.17%	6.8
2177	AT5G08240.1 | expressed protein | chr5:2650838-2652387 REVERSE | Aliases: F8L15.11	3.1	7.3	-4.2	-7.1	0.17%	6.1
2178	AT1G71190.1 | Symbol: SAG18 | expressed protein | chr1:26837072-26838689 REVERSE | Aliases: F23N20.18, F23N20_18, TTN4	6.6	8.1	-1.5	-7.1	0.17%	7.0
2179	AT3G63010.1 | expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873 | chr3:23300400-23302459 FORWARD | Aliases: T20O10.110	3.9	5.2	-1.2	-7.1	0.17%	7.0
2181	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	8.1	-4.3	-7.1	0.17%	6.2

Rank	Description	Sync	Root	M	t	adj.q	B
2182	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	8.9	-1.4	-7.1	0.17%	6.9
2184	AT3G23800.1 | selenium-binding family protein, contains Pfam profile: PF05694 56kDa selenium binding protein (SBP56) | chr3:8581661-8583842 FORWARD | Aliases: MYM9.16	7.0	10.2	-3.2	-7.1	0.17%	6.7
2188	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	7.2	8.9	-1.7	-7.1	0.17%	6.9
2189	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	7.5	10.6	-3.1	-7.1	0.17%	6.9
2192	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	2.5	6.2	-3.6	-7.1	0.17%	6.4
2194	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	3.3	6.2	-2.9	-7.1	0.17%	6.7
2196	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	5.2	7.1	-1.8	-7.1	0.17%	6.9
2197	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	7.7	10.9	-3.2	-7.1	0.17%	6.9
2202	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	4.5	6.2	-1.7	-7.1	0.17%	6.9
2204	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	4.1	-1.2	-7.1	0.17%	6.9
2205	AT1G66020.1 | terpene synthase/cyclase family protein, contains Pfam profile: PF01397: Terpene synthase family	3.4	5.7	-2.4	-7.1	0.17%	6.6
2206	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	7.5	-2.3	-7.1	0.17%	6.6
2208	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	2.5	4.1	-1.6	-7.1	0.17%	6.8
2215	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	4.3	-1.8	-7.1	0.17%	6.8
2216	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	8.5	10.6	-2.2	-7.1	0.17%	6.8
2217	AT1G78960.1 | Symbol: ATLUP2 |	4.1	6.1	-1.9	-7.1	0.17%	6.8
2219	AT1G71740.1 | expressed protein | chr1:26990907-26991299 FORWARD | Aliases: F14O23.12, F14O23_12	3.9	6.8	-2.8	-7.1	0.18%	5.9
2221	AT3G21550.1 | expressed protein, contains Pfam profile PF05078: Protein of unknown function (DUF679) | chr3:7591489-7592328 REVERSE | Aliases: MIL23.12	3.4	6.0	-2.6	-7.1	0.18%	6.4
2222	AT2G42890.2 | Symbol: MEI2 | RNA recognition motif (RRM)-containing protein | chr2:17857639-17861607 FORWARD | Aliases: F7D19.11, F7D19_11	5.7	8.3	-2.6	-7.1	0.18%	6.5

Rank	Description	Sync	Root	M	t	adj.q	B
2223	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	3.1	5.8	-2.8	-7.1	0.18%	6.5
2224	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	7.4	9.0	-1.6	-7.1	0.18%	6.9
2225	AT4G21400.1 | protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain | chr4:11399142-11401720 REVERSE | Aliases: F18E5.20	5.1	7.7	-2.6	-7.1	0.18%	6.9
2226	AT5G04460.1 | expressed protein | chr5:1260010-1263846 FORWARD | Aliases: T19N18.3	3.9	5.4	-1.6	-7.1	0.18%	6.8
2230	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	3.1	4.7	-1.6	-7.1	0.18%	6.9
2234	AT5G02780.1 | In2-1 protein, putative, similar to In2-1 (Zea mays) EMBL:X58573	5.7	9.0	-3.4	-7.1	0.18%	6.7
2235	AT2G26890.1 | Symbol: GRV2 | DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226: DnaJ domain	6.7	8.6	-1.9	-7.0	0.18%	6.9
2240	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	3.3	5.6	-2.2	-7.0	0.18%	6.4
2246	AT4G00040.1 | chalcone and stilbene synthase family protein, similar to chalcone synthase homolog PrChS1, Pinus radiata, gb:U90341; similar to anther-specific protein (Nicotiana sylvestris)(GI:2326774), YY2 protein (Oryza sativa)(GI:2645170) | chr4:14627-16079 FORWARD | Aliases: F6N15.12, F6N15_12	6.2	8.5	-2.3	-7.0	0.18%	6.7
2248	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	3.1	6.9	-3.7	-7.0	0.18%	6.7
2249	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	6.9	9.8	-2.8	-7.0	0.18%	6.5
2255	AT4G12910.1 | Symbol: SCPL20 |	4.6	7.1	-2.5	-7.0	0.18%	6.7
2256	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	5.9	7.4	-1.4	-7.0	0.18%	6.8
2258	AT5G54730.1 | expressed protein | chr5:22251015-22254030 REVERSE | Aliases: K5F14.9, K5F14_9	6.5	8.5	-2.0	-7.0	0.18%	6.8
2260	AT5G40450.1 | expressed protein | chr5:16202027-16212756 REVERSE | Aliases: MPO12.160, MPO12_160	9.0	11.2	-2.2	-7.0	0.18%	6.8
2262	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	5.7	8.6	-2.9	-7.0	0.18%	6.7
2263	AT5G11090.1 | serine-rich protein-related, contains some similarity to serine-rich proteins | chr5:3524681-3525847 FORWARD | Aliases: T5K6.80, T5K6_80	5.0	7.5	-2.5	-7.0	0.18%	6.7
2264	AT5G05440.1 | expressed protein, low similarity to cytokinin-specific binding protein (Vigna radiata) GI:4190976 | chr5:1609251-1610447 FORWARD | Aliases: K18I23.25, K18I23_25	7.1	9.4	-2.3	-7.0	0.18%	6.6
2265	AT5G65910.1 | BSD domain-containing protein, contains Pfam profile PF03909: BSD domain	5.5	7.2	-1.7	-7.0	0.18%	6.8
2266	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	8.9	11.4	-2.5	-7.0	0.18%	6.8
2267	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	7.5	-2.2	-7.0	0.18%	6.8

Rank	Description	Sync	Root	M	t	adj.q	B
2271	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 Lycopersicon esculentum, proline-rich cell wall protein (Medicago sativa) 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	3.9	-1.3	-7.0	0.19%	6.8
2275	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	3.1	5.7	-2.7	-7.0	0.19%	5.9
2278	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	2.8	4.9	-2.1	-7.0	0.19%	6.5
2279	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	8.1	-3.3	-7.0	0.19%	6.3
2280	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	8.1	-3.3	-7.0	0.19%	6.3
2281	AT5G42840.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	4.1	-1.5	-7.0	0.19%	6.8
2284	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	4.8	-2.0	-7.0	0.19%	6.6
2285	AT3G25250.1 | Symbol: AGC2 1 |	4.2	5.9	-1.6	-7.0	0.19%	6.8
2287	AT5G62680.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr5:25182656-25185169 REVERSE | Aliases: MRG21.10, MRG21_10	3.1	6.4	-3.3	-7.0	0.19%	6.5
2288	AT5G05310.3 | expressed protein | chr5:1571272-1574580 FORWARD | Aliases: K18I23.11, K18I23_11	4.8	6.2	-1.4	-7.0	0.19%	6.8
2291	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	2.5	5.6	-3.0	-7.0	0.19%	6.5
2292	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	7.9	-2.3	-7.0	0.19%	6.7
2295	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	4.6	6.9	-2.3	-7.0	0.19%	6.5
2297	AT5G26310.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:9234688-9236388 FORWARD | Aliases: F9D12.4, F9D12_4	3.4	7.0	-3.6	-7.0	0.19%	6.6
2300	AT1G30850.1 | expressed protein | chr1:10985097-10985999 FORWARD | Aliases: T17H7.17, T17H7_17	2.6	4.1	-1.5	-7.0	0.19%	6.8
2303	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	4.1	6.9	-2.8	-7.0	0.19%	6.7
2308	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	5.1	6.2	-1.1	-7.0	0.19%	6.8
2310	AT1G64480.1 | Symbol: CBL8 | calcineurin B-like protein 8 (CBL8), identical to calcineurin B-like protein 8 (GI:15866276) (Arabidopsis thaliana); similar to CALCINEURIN B SUBUNIT GB:P25296 from (Saccharomyces cerevisiae) | chr1:23951691-23953414 REVERSE | Aliases: CALCINEURIN B LIKE PROTEIN 5, CBL8, F1N19.5, F1N19_5	2.5	4.7	-2.2	-7.0	0.19%	6.3
2317	AT1G11920.1 | pectate lyase family protein, similar to pectate lyase GI:14289169 from (Salix gilgiana)	2.7	4.5	-1.8	-6.9	0.19%	6.8
2318	AT5G19240.1 | expressed protein | chr5:6470131-6471064 FORWARD | Aliases: T24G5.140, T24G5_140	2.8	7.0	-4.2	-6.9	0.19%	6.3

Rank	Description	Sync	Root	M	t	adj.q	B
2321	AT2G03200.1 | aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease | chr2:966448-967915 REVERSE | Aliases: T18E12.13, T18E12_13	2.1	5.9	-3.7	-6.9	0.19%	6.5
2322	AT1G66930.1 | serine/threonine protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr1:24974186-24976732 FORWARD | Aliases: T4O24.2	2.8	4.7	-1.9	-6.9	0.19%	6.5
2326	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	6.1	-2.7	-6.9	0.19%	6.6
2327	AT1G53590.1 | C2 domain-containing protein | chr1:20000118-20003933 FORWARD | Aliases: F22G10.28	5.1	6.9	-1.8	-6.9	0.19%	6.7
2329	AT1G18150.2 | Symbol: ATMPK8 |	5.7	7.6	-1.9	-6.9	0.20%	6.7
2330	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	3.0	4.8	-1.8	-6.9	0.20%	6.7
2331	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	6.3	-2.4	-6.9	0.20%	6.2
2333	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	2.6	4.8	-2.2	-6.9	0.20%	6.3
2334	AT4G29900.1 | Symbol: ACA10 | calcium-transporting ATPase, plasma membrane-type, putative / Ca2+-ATPase, putative (ACA10), identical to SP:Q9SZR1 Potential calcium-transporting ATPase 10, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 10) {Arabidopsis thaliana}; similar to SP:Q9LF79 Calcium-transporting ATPase 8, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 8) {Arabidopsis thaliana} | chr4:14610889-14618781 REVERSE | Aliases: ATACA10, AUTOINHIBITED CA(2+) ATPASE, F27B13.140, F27B13_140	6.7	8.5	-1.8	-6.9	0.20%	6.7
2336	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	5.7	-2.7	-6.9	0.20%	6.0
2338	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	6.7	-1.4	-6.9	0.20%	6.7
2339	AT3G26300.1 | Symbol: CYP71B34 | cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450 | chr3:9640436-9642103 REVERSE | Aliases: F20C19.2	3.3	6.4	-3.1	-6.9	0.20%	6.0
2342	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	6.2	8.3	-2.1	-6.9	0.20%	6.6
2350	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	9.5	11.5	-2.0	-6.9	0.20%	6.7
2352	AT3G57420.1 | expressed protein, contains Pfam domain PF03385: Protein of unknown function, DUF288 | chr3:21263396-21266253 REVERSE | Aliases: T8H10.20	3.5	5.3	-1.9	-6.9	0.20%	6.7
2353	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	6.0	-2.0	-6.9	0.20%	6.6
2356	AT5G14540.1 | proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965 | chr5:4687150-4689677 REVERSE | Aliases: T15N1.30, T15N1_30	4.7	7.5	-2.8	-6.9	0.20%	6.6
2357	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	7.9	-1.7	-6.9	0.20%	6.7
2358	AT4G15400.1 | transferase family protein, similar to deacetylvindoline 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	2.7	4.8	-2.2	-6.9	0.20%	6.3
2362	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	5.3	7.2	-1.9	-6.9	0.20%	6.6

Rank	Description	Sync	Root	M	t	adj.q	B
2367	AT2G40160.1 | expressed protein | chr2:16784468-16786486 FORWARD | Aliases: T7M7.25, T7M7_25	3.4	6.2	-2.7	-6.9	0.20%	6.1
2368	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	6.8	7.8	-1.0	-6.9	0.20%	6.6
2370	AT1G70330.1 | Symbol: ENT1,AT | equilibrative nucleoside transporter family protein, contains similarity to SWISS-PROT:Q14542 equilibrative nucleoside transporter 2 (Equilibrative nitrobenzylmercaptopurine riboside-insensitive nucleoside transporter, Equilibrative NBMPR-insensitive nucleoside transporter, Nucleoside transporter, ei-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	7.0	10.5	-3.4	-6.9	0.20%	6.6
2371	AT2G30860.1 | Symbol: ATGSTF9 | glutathione S-transferase, putative, identical to GB:Y12295 | chr2:13146074-13147322 FORWARD | Aliases: ATGSTF7, F7F1.7, F7F1_7, GLUTTR	8.4	12.0	-3.7	-6.9	0.20%	6.5
2372	AT1G47530.1 | ripening-responsive protein, putative, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family | chr1:17454120-17456861 FORWARD | Aliases: F16N3.20, F16N3_20	4.8	6.4	-1.6	-6.9	0.20%	6.6
2373	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	4.8	7.1	-2.3	-6.9	0.20%	6.5
2375	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) (GI:559920) from (Nicotiana tabacum), which, due to scienitific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.	3.1	7.1	-4.0	-6.9	0.21%	6.4
2378	AT1G79380.1 | copine-related, low similarity to SP:Q99829 Copine I {Homo sapiens} | chr1:29865384-29868528 FORWARD | Aliases: T8K14.20, T8K14_20	6.5	9.7	-3.2	-6.9	0.21%	6.5
2381	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	4.0	5.5	-1.5	-6.8	0.21%	6.7
2382	AT4G17030.1 | Symbol: ATEXLB1 | expansin-related, identical to SWISS-PROT:O23547 expansin-related protein 1 precursor (At-EXPR1)(Arabidopsis thaliana); related to expansins, http://www.bio.psu.edu/expansins/ | chr4:9581605-9583309 REVERSE | Aliases: ARABIDOPSIS THALIANA EXPANSIN LIKE B1, AT EXPR, ATEXPR1, ATHEXP BETA 3.1, DL4545C, EXPR, FCAALL.341	3.1	5.3	-2.2	-6.8	0.21%	6.3
2386	AT5G23920.1 | expressed protein | chr5:8073227-8074173 REVERSE | Aliases: MRO11.4, MRO11_4	6.5	8.6	-2.0	-6.8	0.21%	6.6
2388	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	2.9	5.8	-2.9	-6.8	0.21%	6.4
2390	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	5.4	-2.8	-6.8	0.21%	6.3
2392	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	4.6	-2.3	-6.8	0.21%	6.4
2394	AT5G28630.1 | glycine-rich protein | chr5:10636635-10637253 FORWARD | Aliases: F4I4.10, F4I4_10	3.4	9.0	-5.6	-6.8	0.21%	6.5
2396	AT4G37445.1 | expressed protein | chr4:17604088-17604926 REVERSE | Aliases: None	3.0	4.7	-1.7	-6.8	0.21%	6.6
2397	AT5G06839.1 | bZIP family transcription factor, contains Pfam profile: PF00170 bZIP transcription factor | chr5:2120528-2126455 FORWARD | Aliases: None	2.9	6.3	-3.3	-6.8	0.21%	6.0
2398	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	6.9	-3.9	-6.8	0.21%	6.6
2400	AT2G01980.1 | Symbol: SOS1 | sodium proton exchanger, putative (NHX7) (SOS1), identical to putative Na+/H+ antiporter SOS1 (Arabidopsis thaliana) 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	5.6	7.1	-1.5	-6.8	0.21%	6.6
2401	AT4G28370.1 | zinc finger (C3HC4-type RING finger) family protein, contains Pfam PF00097: Zinc finger, C3HC4 type (RING finger) | chr4:14035616-14041672 FORWARD | Aliases: F20O9.50, F20O9_50	3.4	4.8	-1.4	-6.8	0.21%	6.6

Rank	Description	Sync	Root	M	t	adj.q	B
2402	AT2G30010.1 | expressed protein | chr2:12812801-12816462 FORWARD | Aliases: F23F1.7, F23F1_7	3.5	4.8	-1.3	-6.8	0.21%	6.6
2405	AT5G25110.1 | Symbol: CIPK25 |	5.5	9.2	-3.7	-6.8	0.21%	6.4
2408	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	6.8	8.2	-1.5	-6.8	0.21%	6.6
2410	AT3G08720.2 | Symbol: ATPK19 |	8.5	9.8	-1.3	-6.8	0.21%	6.6
2413	AT1G52910.1 | expressed protein | chr1:19711729-19712991 FORWARD | Aliases: F14G24.18, F14G24_18	4.5	6.4	-2.0	-6.8	0.21%	6.5
2415	AT3G10680.1 | heat shock protein-related, contains weak similarity to Pfam profile PF00011: Hsp20/alpha crystallin family | chr3:3337778-3339350 FORWARD | Aliases: T7M13.24	3.7	5.2	-1.5	-6.8	0.21%	6.6
2418	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	6.3	8.7	-2.3	-6.8	0.21%	6.6
2422	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	6.1	8.0	-1.9	-6.8	0.21%	6.6
2423	AT1G51790.1 | leucine-rich repeat protein kinase, putative, smilar 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	2.4	6.0	-3.7	-6.8	0.21%	6.5
2424	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	5.9	8.8	-2.9	-6.8	0.21%	6.5
2425	AT4G35190.1 | expressed protein, contains Pfam profile PF03641: decarboxylase family protein | chr4:16746604-16748266 FORWARD | Aliases: T12J5.60, T12J5_60	4.6	6.0	-1.4	-6.8	0.22%	6.6
2427	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	7.0	-1.5	-6.8	0.22%	6.6
2428	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	2.9	4.5	-1.6	-6.8	0.22%	6.5
2429	AT2G22920.2 | Symbol: SCPL12 |	3.6	5.9	-2.3	-6.8	0.22%	6.5
2430	AT3G62390.1 | expressed protein, several hypothetical proteins - Arabidopsis thaliana | chr3:23097996-23100166 REVERSE | Aliases: T12C14.90	4.3	6.0	-1.7	-6.8	0.22%	6.6
2433	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	9.2	11.7	-2.6	-6.8	0.22%	6.6
2434	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	3.6	5.1	-1.5	-6.8	0.22%	6.6
2435	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	8.7	10.0	-1.3	-6.8	0.22%	6.6
2438	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	5.0	8.5	-3.4	-6.8	0.22%	6.6
2439	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	6.0	7.8	-1.8	-6.8	0.22%	6.5
2440	AT1G66200.2 | Symbol: ATGSR2 |	9.0	12.5	-3.5	-6.8	0.22%	6.4
2441	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	4.3	5.7	-1.3	-6.8	0.22%	6.6

Rank	Description	Sync	Root	M	t	adj.q	B
2444	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	3.5	6.1	-2.5	-6.8	0.22%	6.4
2447	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	3.5	6.2	-2.6	-6.8	0.22%	6.2
2456	AT1G16860.1 | merozoite surface protein-related, contains weak similarity to merozoite surface protein (Plasmodium falciparum) gi:12043655:gb:AAG47601	4.2	5.7	-1.5	-6.8	0.22%	6.5
2457	AT3G22540.1 | expressed protein | chr3:7984097-7984634 REVERSE | Aliases: F16J14.10	4.7	7.6	-3.0	-6.8	0.22%	6.1
2459	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 simlar 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	7.0	-2.3	-6.7	0.22%	6.5
2461	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) (Arabidopsis thaliana) | chr2:9533175-9534910 REVERSE | Aliases: F14M13.17, F14M13_17	6.0	8.3	-2.3	-6.7	0.22%	6.4
2462	AT4G03330.1 | Symbol: SYP123 |	3.7	5.9	-2.2	-6.7	0.22%	6.3
2468	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	2.9	4.6	-1.7	-6.7	0.22%	6.5
2470	AT5G53320.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:21653295-21655622 REVERSE | Aliases: K19E1.12, K19E1_12	6.0	7.5	-1.4	-6.7	0.22%	6.5
2473	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	5.2	-2.1	-6.7	0.22%	6.5
2475	AT3G09410.3 | pectinacetylesterase family protein, similar to pectinacetylesterase precursor GB:CAA67728 (Vigna radiata); contains Pfam profile: PF03283 pectinacetylesterase | chr3:2897644-2900990 REVERSE | Aliases: F3L24.30	3.3	4.6	-1.2	-6.7	0.22%	6.6
2481	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	6.4	-2.4	-6.7	0.23%	6.1
2482	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	4.2	5.3	-1.0	-6.7	0.23%	6.5
2483	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	4.2	-1.7	-6.7	0.23%	6.4
2485	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	5.4	-2.2	-6.7	0.23%	6.5
2486	AT4G09990.1 | expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579) | chr4:6258877-6260061 REVERSE | Aliases: T5L19.120, T5L19_120	3.0	5.3	-2.3	-6.7	0.23%	6.3
2487	AT5G65480.1 | expressed protein | chr5:26193247-26195140 FORWARD | Aliases: MNA5.18	9.4	11.1	-1.7	-6.7	0.23%	6.5
2492	AT2G26290.1 | protein kinase, putative, similar to auxin-regulated dual specificity cytosolic kinase (Lycopersicon esculentum) gi:14484938:gb:AAK62821	3.2	5.9	-2.7	-6.7	0.23%	6.3
2496	AT5G40860.1 | hypothetical protein | chr5:16388659-16389213 FORWARD | Aliases: MHK7.9, MHK7_9	2.9	5.4	-2.6	-6.7	0.23%	6.1
2497	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	6.8	8.3	-1.5	-6.7	0.23%	6.5

Rank	Description	Sync	Root	M	t	adj.q	B
2498	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	3.6	5.2	-1.7	-6.7	0.23%	6.4
2502	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	4.4	6.0	-1.7	-6.7	0.23%	6.5
2504	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	4.4	-1.8	-6.7	0.23%	6.4
2505	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	3.8	5.6	-1.8	-6.7	0.23%	6.5
2507	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	6.5	9.0	-2.5	-6.7	0.23%	6.4
2508	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	5.7	7.1	-1.4	-6.7	0.23%	6.5
2513	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	4.4	7.1	-2.8	-6.7	0.23%	6.3
2515	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	4.7	6.0	-1.3	-6.7	0.23%	6.5
2516	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	6.8	8.1	-1.3	-6.7	0.23%	6.5
2517	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	6.6	-4.1	-6.7	0.24%	5.9
2519	AT1G10340.2 | ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023 | chr1:3390324-3392526 REVERSE | Aliases: F14N23.22, F14N23_22	3.3	4.8	-1.5	-6.7	0.24%	6.5
2520	AT2G04680.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	4.6	-1.8	-6.7	0.24%	6.4
2521	AT1G23560.1 | expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220 | chr1:8352604-8354251 REVERSE | Aliases: F28C11.32	4.8	7.0	-2.2	-6.7	0.24%	6.4
2522	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	2.6	3.8	-1.2	-6.7	0.24%	6.5
2523	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	5.1	7.3	-2.2	-6.7	0.24%	6.4
2525	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	5.4	-2.1	-6.7	0.24%	6.2
2529	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	1.7	2.6	-0.9	-6.7	0.24%	6.4
2531	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	6.3	9.8	-3.5	-6.7	0.24%	6.4

Rank	Description	Sync	Root	M	t	adj.q	B
2535	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	7.3	8.9	-1.6	-6.6	0.24%	6.5
2537	AT5G44130.1 | fasciclin-like arabinogalactan-protein, putative, similar to gi_13377784_gb_AAK20861 | chr5:17778317-17779230 FORWARD | Aliases: MLN1.5, MLN1_5	4.7	6.9	-2.1	-6.6	0.24%	6.3
2540	AT3G20040.1 | similar to hexokinase, putative [Arabidopsis thaliana] (TAIR:At1g50460.1); similar to putative hexokinase [Oryza sativa (japonica cultivar-group)] (GB:XP_463697.1); contains InterPro domain Hexokinase (InterPro:IPR001312) | chr3:6994900-6998177 FORWARD | Aliases: MAL21.4	4.3	6.2	-1.9	-6.6	0.24%	6.4
2542	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	12.3	-1.2	-6.6	0.24%	6.3
2544	AT5G45370.3 | nodulin-related / integral membrane family protein, contains Pfam profile:PF00892 integral membrane protein DUF6	4.4	6.1	-1.7	-6.6	0.24%	6.4
2545	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	5.3	-2.7	-6.6	0.24%	6.0
2546	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	4.3	6.0	-1.6	-6.6	0.24%	6.4
2547	AT3G16180.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr3:5481331-5485100 REVERSE | Aliases: MSL1.22	4.9	6.9	-2.0	-6.6	0.24%	6.4
2551	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	6.8	8.6	-1.8	-6.6	0.24%	6.5
2552	AT2G25980.1 | jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	3.1	4.5	-1.3	-6.6	0.24%	6.5
2554	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	6.1	8.5	-2.3	-6.6	0.24%	6.4
2555	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	8.2	9.3	-1.2	-6.6	0.24%	6.4
2556	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	5.6	-2.3	-6.6	0.24%	5.9
2559	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	4.6	6.2	-1.6	-6.6	0.24%	6.3
2565	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	5.9	7.8	-1.8	-6.6	0.24%	6.4
2566	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	3.9	5.5	-1.6	-6.6	0.24%	6.4
2567	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	5.9	8.7	-2.8	-6.6	0.24%	6.4
2569	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	4.5	6.8	-2.3	-6.6	0.25%	6.1

Rank	Description	Sync	Root	M	t	adj.q	B
2571	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	6.8	8.5	-1.8	-6.6	0.25%	6.4
2574	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	7.2	8.8	-1.7	-6.6	0.25%	6.3
2575	AT5G54700.1 | ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023 | chr5:22240322-22242735 REVERSE | Aliases: K5F14.4, K5F14_4	2.9	5.0	-2.0	-6.6	0.25%	6.3
2580	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	4.5	6.2	-1.7	-6.6	0.25%	6.4
2581	AT5G62900.1 | expressed protein | chr5:25266023-25267103 FORWARD | Aliases: MQB2.22, MQB2_22	5.4	7.7	-2.3	-6.6	0.25%	6.3
2585	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	6.2	8.4	-2.2	-6.6	0.25%	6.4
2586	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	6.9	9.2	-2.3	-6.6	0.25%	6.3
2587	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	4.2	-1.4	-6.6	0.25%	6.4
2588	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	5.9	10.3	-4.5	-6.6	0.25%	6.3
2592	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	6.4	-3.2	-6.6	0.25%	5.9
2594	AT1G70450.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:26556239-26558100 FORWARD | Aliases: F24J13.2, F24J13_2	3.7	7.8	-4.1	-6.6	0.25%	6.1
2597	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	5.6	8.0	-2.4	-6.6	0.25%	6.2
2598	AT1G15110.1 | phosphatidyl serine synthase family protein, contains Pfam profile: PF03034 phosphatidyl serine synthase	4.6	6.5	-1.9	-6.6	0.25%	6.4
2602	AT1G69600.1 | zinc finger homeobox family protein / ZF-HD homeobox family protein | chr1:26186133-26186861 FORWARD | Aliases: F24J1.29, F24J1_29	4.4	6.2	-1.8	-6.6	0.25%	6.2
2603	AT1G47480.1 | expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873 | chr1:17420019-17421872 FORWARD | Aliases: F16N3.25, F16N3_25	2.7	5.3	-2.5	-6.6	0.25%	6.2
2604	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; Ca2+:Cation Antiporter (CaCA) Family member PMID:11500563 | chr5:195588-198523 FORWARD | Aliases: ATCAX4, F7A7.10, F7A7_10	4.1	6.3	-2.3	-6.6	0.25%	6.3
2605	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	5.0	-2.1	-6.6	0.25%	6.3
2606	AT5G20270.1 | expressed protein, contains Pfam domain, PF03006: Uncharacterised protein family (Hly-III / UPF0073) | chr5:6840835-6842860 REVERSE | Aliases: F5O24.160, F5O24_160	3.0	5.5	-2.5	-6.6	0.25%	5.9
2607	AT5G14330.1 | expressed protein | chr5:4619800-4620554 REVERSE | Aliases: F18O22.120, F18O22_120	3.1	6.9	-3.8	-6.6	0.25%	4.6
2618	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	7.9	-3.0	-6.6	0.26%	5.8

Rank	Description	Sync	Root	M	t	adj.q	B
2623	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	5.1	7.8	-2.7	-6.6	0.26%	6.0
2626	AT5G07820.1 | expressed protein | chr5:2498750-2500547 REVERSE | Aliases: F13G24.20, F13G24_20	3.2	5.8	-2.6	-6.6	0.26%	6.1
2627	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	3.6	5.8	-2.2	-6.5	0.26%	5.9
2628	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	5.7	-2.5	-6.5	0.26%	6.3
2630	AT1G43710.1 | Symbol: EMB1075 | serine decarboxylase, identical to serine decarboxylase (Arabidopsis thaliana) GI:15011302; contains Pfam profile PF00282: Pyridoxal-dependent decarboxylase conserved domain	9.4	10.7	-1.4	-6.5	0.26%	6.3
2631	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	5.0	-2.0	-6.5	0.26%	6.1
2632	AT1G11440.1 | expressed protein | chr1:3849360-3850662 FORWARD | Aliases: T23J18.11, T23J18_11	4.9	6.7	-1.8	-6.5	0.26%	6.3
2633	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	3.5	5.8	-2.3	-6.5	0.26%	6.2
2634	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	3.1	5.7	-2.6	-6.5	0.26%	6.1
2639	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	3.1	4.6	-1.5	-6.5	0.26%	6.3
2646	AT5G54050.1 | DC1 domain-containing protein | chr5:21950849-21953221 REVERSE | Aliases: K19P17.23, K19P17_23	2.9	4.7	-1.8	-6.5	0.26%	6.4
2647	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)(Antirrhinum majus) | chr5:22424775-22428170 REVERSE | Aliases: MCO15.20, MCO15_20	2.8	5.5	-2.7	-6.5	0.26%	6.0
2650	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	5.4	-2.1	-6.5	0.26%	6.2
2652	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	3.8	6.4	-2.6	-6.5	0.26%	6.3
2653	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	9.2	10.6	-1.4	-6.5	0.26%	6.2
2657	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	5.9	8.1	-2.3	-6.5	0.26%	6.1
2660	AT4G00670.1 | similar to DNA-binding protein, putative [Arabidopsis thaliana] (TAIR:At2g45820.1); similar to OSJNBb0039L24.13 [Oryza sativa (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	4.2	6.8	-2.6	-6.5	0.26%	5.9
2661	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	7.1	8.8	-1.7	-6.5	0.26%	6.3
2663	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	5.5	7.2	-1.6	-6.5	0.26%	6.3

Rank	Description	Sync	Root	M	t	adj.q	B
2666	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	9.2	10.8	-1.7	-6.5	0.26%	6.3
2671	AT5G13990.1 | exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit; | chr5:4514570-4516894 REVERSE | Aliases: MAC12.17, MAC12_17	2.9	4.2	-1.4	-6.5	0.27%	6.3
2672	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	5.8	7.7	-1.9	-6.5	0.27%	6.3
2673	AT1G13970.1 | expressed protein | chr1:4779520-4782531 REVERSE | Aliases: F16A14.19	3.5	6.3	-2.9	-6.5	0.27%	5.8
2675	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)	2.7	3.7	-1.0	-6.5	0.27%	6.3
2677	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	8.9	10.9	-2.0	-6.5	0.27%	6.3
2678	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	8.3	-3.6	-6.5	0.27%	6.2
2679	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	4.2	-1.4	-6.5	0.27%	6.3
2686	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	6.8	7.8	-0.9	-6.5	0.27%	6.2
2688	AT5G25520.2 | transcription elongation factor-related, contains weak similarity to transcription elongation factors | chr5:8885091-8889623 FORWARD | Aliases: T14C9.60, T14C9_60	5.1	7.1	-2.0	-6.5	0.27%	6.3
2689	AT1G30650.1 | Symbol: WRKY14 |	2.4	5.0	-2.7	-6.5	0.27%	6.0
2690	AT1G25390.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:8906439-8908841 REVERSE | Aliases: F2J7.14, F2J7_14	5.2	7.0	-1.8	-6.5	0.27%	6.1
2691	AT2G30210.1 | laccase, putative / diphenol oxidase, putative, similar to laccase (Populus balsamifera subsp. trichocarpa)(GI:3805960) | chr2:12894523-12896904 REVERSE | Aliases: T9D9.2	3.8	7.2	-3.4	-6.5	0.27%	5.9
2692	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	4.1	5.7	-1.6	-6.5	0.27%	6.2
2695	AT5G14730.1 | expressed protein | chr5:4756221-4757660 FORWARD | Aliases: T9L3.30, T9L3_30	3.6	5.5	-1.9	-6.5	0.27%	6.2
2698	AT4G36520.1 | trichohyalin-related, low similarity to SP:Q07283 Trichohyalin {Homo sapiens} | chr4:17230592-17235438 REVERSE | Aliases: AP22.19, AP22_19	4.0	6.7	-2.7	-6.5	0.27%	6.0
2703	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	6.3	-2.6	-6.5	0.27%	6.0
2706	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	6.8	8.8	-2.0	-6.5	0.27%	6.2
2714	AT3G52480.1 | expressed protein | chr3:19463232-19464140 REVERSE | Aliases: F22O6.140	3.3	4.9	-1.6	-6.5	0.27%	6.1
2715	AT1G59580.2 | Symbol: ATMPK2 |	3.9	5.3	-1.4	-6.5	0.28%	6.2
2717	AT3G20570.1 | plastocyanin-like domain-containing protein | chr3:7186312-7187527 REVERSE | Aliases: K10D20.11	4.2	6.0	-1.8	-6.5	0.28%	6.1
2722	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	5.2	-1.6	-6.4	0.28%	6.2

Rank	Description	Sync	Root	M	t	adj.q	B
2724	AT3G05050.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr3:1408619-1411807 REVERSE | Aliases: T12H1.1, T12H1_1	5.1	6.5	-1.4	-6.4	0.28%	6.2
2727	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	8.3	9.9	-1.6	-6.4	0.28%	6.3
2734	AT5G26270.1 | expressed protein, ; expression supported by MPSS | chr5:9206511-9207515 FORWARD | Aliases: T19G15.120, T19G15_120	3.4	4.5	-1.1	-6.4	0.28%	6.2
2737	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	4.1	7.1	-3.0	-6.4	0.28%	5.2
2740	AT1G27090.1 | glycine-rich protein | chr1:9403898-9406243 REVERSE | Aliases: T7N9.15, T7N9_15	5.4	7.5	-2.1	-6.4	0.28%	6.2
2742	AT5G67480.2 | TAZ zinc finger family protein / BTB/POZ domain-containing protein, contains Pfam PF00651 : BTB/POZ domain; contains Pfam PF02135 : TAZ zinc finger; simiar 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	5.3	7.0	-1.7	-6.4	0.28%	6.2
2747	AT1G80360.1 | aminotransferase class I and II family protein, low similarity to GI:14278621 Aromatic Aminotransferase from Pyrococcus horikoshii | chr1:30213391-30215579 REVERSE | Aliases: F5I6.11, F5I6_11	8.1	9.9	-1.8	-6.4	0.28%	6.2
2748	AT3G14560.1 | expressed protein | chr3:4889079-4890166 FORWARD | Aliases: MIE1.6	3.7	6.8	-3.2	-6.4	0.28%	5.9
2752	AT5G47950.1 | transferase family protein, similar to deacetylvindoline 4-O-acetyltransferase (Catharanthus roseus)(GI:4091808)(PMID:9681034), acetyl-CoA:benzylalcohol acetyltranferase (Clarkia concinna)(GI:6166328)(PMID:10588064)	3.8	6.1	-2.3	-6.4	0.28%	6.0
2753	AT2G31790.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:13525288-13527441 FORWARD | Aliases: F20M17.17, F20M17_17	6.1	7.8	-1.6	-6.4	0.28%	6.2
2754	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	6.2	-1.4	-6.4	0.28%	6.2
2757	AT5G02350.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	4.6	-1.9	-6.4	0.28%	6.2
2764	AT2G18690.1 | expressed protein | chr2:8104504-8105909 FORWARD | Aliases: MSF3.7, MSF3_7	4.9	6.7	-1.7	-6.4	0.29%	6.2
2766	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	3.6	8.4	-4.9	-6.4	0.29%	6.1
2767	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	3.7	5.7	-2.0	-6.4	0.29%	6.1
2768	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	5.0	-1.6	-6.4	0.29%	6.2
2769	AT5G03170.1 | Symbol: FLA11 | fasciclin-like arabinogalactan-protein (FLA11) | chr5:752775-753656 REVERSE | Aliases: F15A17.200, F15A17_200	3.2	5.4	-2.2	-6.4	0.29%	6.1
2772	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)	7.6	10.4	-2.8	-6.4	0.29%	6.2
2774	AT5G57785.1 | expressed protein | chr5:23426122-23426648 REVERSE | Aliases: None	3.3	5.8	-2.5	-6.4	0.29%	5.6
2775	AT5G57910.1 | expressed protein, similar to unknown protein (emb:CAB79781.1) | chr5:23468375-23469828 REVERSE | Aliases: MTI20.17, MTI20_17	5.5	6.9	-1.4	-6.4	0.29%	6.2
2777	AT3G29630.1 | glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	3.3	5.6	-2.3	-6.4	0.29%	5.8
2780	AT4G21850.2 | methionine sulfoxide reductase domain-containing protein / SeIR 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: SeIR domain | chr4:11591128-11592250 REVERSE | Aliases: T8O5.60, T8O5_60	4.6	7.2	-2.6	-6.4	0.29%	6.0

Rank	Description	Sync	Root	M	t	adj.q	B
2781	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	2.9	4.9	-2.1	-6.4	0.29%	5.9
2782	AT1G73120.1 | expressed protein | chr1:27500847-27501611 REVERSE | Aliases: T18K17.22, T18K17_22	3.9	7.4	-3.6	-6.4	0.29%	5.9
2783	AT5G45810.1 | Symbol: CIPK19 |	4.3	6.1	-1.8	-6.4	0.29%	6.1
2784	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	4.6	6.7	-2.1	-6.4	0.29%	6.1
2786	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	4.5	-1.1	-6.4	0.29%	6.2
2788	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	7.3	8.7	-1.4	-6.4	0.29%	6.2
2789	AT1G79270.1 | expressed protein, contains Pfam profile PF04146: YT521-B-like family | chr1:29820399-29824585 FORWARD | Aliases: YUP8H12R.13, YUP8H12R_13	6.3	8.9	-2.6	-6.4	0.29%	6.1
2790	AT5G09880.1 | RNA recognition motif (RRM)-containing protein | chr5:3081458-3085255 REVERSE | Aliases: MYH9.9, MYH9_9	6.5	8.5	-2.0	-6.4	0.29%	6.2
2792	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	3.9	6.3	-2.4	-6.4	0.29%	6.1
2793	AT1G70850.3 | similar to Bet v I allergen family protein [Arabidopsis thaliana] (TAIR:At1g70830.1); similar to Bet v I allergen family protein [Arabidopsis thaliana] (TAIR:At1g70830.2); similar to Csf-2 [Cucumis sativus] (GB:BAA83470.1); contains InterPro domain Bet v I allergen (InterPro:IPR000916) | chr1:26718528-26720445 REVERSE | Aliases: F15H11.10, F15H11_10	4.7	6.3	-1.6	-6.4	0.29%	6.2
2796	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	5.4	-2.0	-6.4	0.29%	5.9
2802	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 (Nicotiana tabacum), which, due to scienitific 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	5.1	-2.3	-6.4	0.30%	6.0
2803	AT3G52900.1 | expressed protein, contains Pfam profile PF04949: Family of unknown function (DUF662) | chr3:19624098-19625005 FORWARD | Aliases: F8J2.70	3.6	6.8	-3.1	-6.4	0.30%	5.5
2806	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	6.4	7.5	-1.1	-6.4	0.30%	6.2
2810	AT2G42280.2 | basic helix-loop-helix (bHLH) family protein | chr2:17618361-17620565 REVERSE | Aliases: T24P15.19, T24P15_19	3.0	4.7	-1.6	-6.3	0.30%	6.1
2815	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	3.7	5.8	-2.1	-6.3	0.30%	6.0
2818	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	3.9	5.7	-1.8	-6.3	0.30%	6.1
2821	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	10.1	11.5	-1.3	-6.3	0.30%	6.1
2823	AT5G53850.3 | haloacid dehalogenase-like hydrolase family protein, low similarity to enolase-phosphatase E-1 enzyme (Klebsiella oxytoca) GI:401712; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase | chr5:21878223-21882133 REVERSE | Aliases: K19P17.1, K19P17_1	9.2	10.5	-1.2	-6.3	0.30%	6.1
2824	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	2.7	4.7	-2.0	-6.3	0.30%	5.8

Rank	Description	Sync	Root	M	t	adj.q	B
2826	AT1G24170.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8 | chr1:8557205-8558821 REVERSE | Aliases: F3I6.10, F3I6_10	7.3	8.1	-0.8	-6.3	0.30%	6.0
2828	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	4.8	-1.0	-6.3	0.30%	6.1
2829	AT5G25560.1 | zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	7.2	8.8	-1.6	-6.3	0.30%	6.1
2832	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	5.9	7.7	-1.8	-6.3	0.30%	6.1
2837	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) {Bacillus subtilis}; contains Pfam profile PF00857: isochorismatase family protein | chr5:7819819-7820679 REVERSE | Aliases: MKD15.8, MKD15_8	2.7	5.3	-2.7	-6.3	0.31%	5.3
2838	AT2G24170.1 | endomembrane protein 70, putative, similar to MURA transposase of maize Mutator transposon | chr2:10281224-10284066 REVERSE | Aliases: F27D4.8, F27D4_8	5.1	6.6	-1.5	-6.3	0.31%	6.1
2840	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	6.1	7.5	-1.4	-6.3	0.31%	6.1
2843	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	7.9	9.6	-1.6	-6.3	0.31%	6.1
2844	AT1G33560.1 | Symbol: ADR1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.6	5.1	-1.5	-6.3	0.31%	6.1
2845	AT1G70230.1 | expressed protein | chr1:26453983-26455608 FORWARD | Aliases: F20P5.5, F20P5_5	4.2	6.6	-2.4	-6.3	0.31%	5.9
2846	AT3G01720.1 | expressed protein | chr3:262258-265912 REVERSE | Aliases: F4P13.27	7.6	9.8	-2.2	-6.3	0.31%	6.1
2847	AT2G15830.1 | expressed protein | chr2:6901200-6901633 FORWARD | Aliases: F19G14.17, F19G14_17	3.2	7.2	-4.0	-6.3	0.31%	4.8
2848	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	3.8	-1.1	-6.3	0.31%	6.1
2849	AT3G45040.1 | phosphatidate cytidylyltransferase family protein, weak similarity to SP:P20048 Dolichol kinase (EC 2.7.1.108) {Saccharomyces cerevisiae}; contains Pfam profile: PF01148 phosphatidate cytidylyltransferase | chr3:16483647-16486738 REVERSE | Aliases: F14D17.110	7.0	8.2	-1.2	-6.3	0.31%	6.1
2850	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	2.4	4.4	-2.0	-6.3	0.31%	5.7
2851	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	3.8	6.8	-3.0	-6.3	0.31%	6.1
2853	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	6.3	7.7	-1.4	-6.3	0.31%	6.0
2854	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	2.7	4.1	-1.4	-6.3	0.31%	6.1
2855	AT1G23120.1 | major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:294060); Location of EST gb:T88564 ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family	5.4	7.0	-1.6	-6.3	0.31%	6.1
2864	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	6.5	7.7	-1.2	-6.3	0.31%	6.1

Rank	Description	Sync	Root	M	t	adj.q	B
2865	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	4.4	6.8	-2.5	-6.3	0.31%	6.0
2866	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	6.1	7.7	-1.6	-6.3	0.32%	6.1
2868	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	4.9	6.0	-1.1	-6.3	0.32%	6.1
2869	AT5G02620.1 | ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023 | chr5:589525-591675 FORWARD | Aliases: T22P11.210, T22P11_210	4.4	5.5	-1.1	-6.3	0.32%	6.1
2870	AT2G36910.1 | Symbol: ATPGP1 |	8.6	10.1	-1.5	-6.3	0.32%	6.1
2872	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	6.4	-1.1	-6.3	0.32%	6.0
2875	AT3G11690.1 | expressed protein | chr3:3694994-3696484 FORWARD | Aliases: T19F11.9	4.2	5.7	-1.5	-6.3	0.32%	6.0
2877	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	7.7	-1.1	-6.3	0.32%	6.1
2879	AT3G57630.2 | exostosin family protein, contains Pfam profile: PF03016	5.2	6.8	-1.7	-6.3	0.32%	6.0
2880	AT3G53100.1 | GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382) (Arabidopsis thaliana), SP:P40603 Anther-specific proline-rich protein APG {Brassica napus}; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family | chr3:19695725-19697575 REVERSE | Aliases: T4D2.30	2.2	4.4	-2.2	-6.3	0.32%	6.1
2882	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	7.9	10.2	-2.3	-6.3	0.32%	6.0
2884	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	4.0	-1.7	-6.3	0.32%	6.1
2885	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	5.3	9.4	-4.1	-6.3	0.32%	6.0
2889	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	5.6	7.0	-1.4	-6.3	0.32%	6.1
2893	AT4G11300.1 | expressed protein | chr4:6872182-6873537 REVERSE | Aliases: F8L21.90, F8L21_90	4.2	6.3	-2.1	-6.3	0.32%	6.0
2894	AT3G52400.1 | Symbol: SYP122 |	5.2	7.5	-2.2	-6.2	0.32%	6.0
2895	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	8.4	-1.5	-6.2	0.32%	6.1
2896	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	8.4	-1.5	-6.2	0.32%	6.1

Rank	Description	Sync	Root	M	t	adj.q	B
2897	AT1G58100.1 | TCP family transcription factor, putative, similar to auxin-induced basic helix-loop-helix transcription factor GI:5731257 from (Gossypium hirsutum) | chr1:21516112-21517592 REVERSE | Aliases: T15M6.11	6.1	7.5	-1.3	-6.2	0.32%	6.0
2898	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	4.4	-1.1	-6.2	0.32%	6.1
2899	AT4G13660.1 | pinoresinol-lariciresinol reductase, putative, similar to pinoresinol-lariciresinol reductase TH1 (Tsuga heterophylla)(GI:7578915); contains isoflavone reductase domain PF02716	8.7	11.0	-2.3	-6.2	0.32%	6.0
2900	AT2G39340.1 | SAC3/GANP family protein, contains Pfam profile: PF03399 SAC3/GANP family | chr2:16430719-16437679 FORWARD | Aliases: T16B24.2, T16B24_2	5.0	6.2	-1.2	-6.2	0.32%	6.0
2901	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	3.4	5.6	-2.2	-6.2	0.32%	5.9
2903	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	5.5	8.2	-2.6	-6.2	0.32%	6.0
2904	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	9.4	-1.0	-6.2	0.32%	6.0
2905	AT1G15740.1 | leucine-rich repeat family protein | chr1:5410929-5415297 FORWARD | Aliases: F7H2.8, F7H2_8	6.6	9.7	-3.0	-6.2	0.32%	6.0
2911	AT5G54020.1 | expressed protein | chr5:21939090-21940760 REVERSE | Aliases: K19P17.19, K19P17_19	2.8	5.8	-3.0	-6.2	0.33%	5.6
2912	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	4.0	6.0	-2.0	-6.2	0.33%	5.8
2915	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	9.2	10.7	-1.4	-6.2	0.33%	6.0
2925	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	5.6	7.9	-2.3	-6.2	0.33%	6.0
2927	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	3.9	-1.2	-6.2	0.33%	6.0
2931	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	3.5	5.2	-1.7	-6.2	0.33%	6.0
2933	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	6.1	8.8	-2.7	-6.2	0.33%	6.0
2936	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	7.9	9.7	-1.8	-6.2	0.33%	6.0
2937	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	8.5	9.9	-1.4	-6.2	0.33%	6.0

Rank	Description	Sync	Root	M	t	adj.q	B
2938	AT2G32260.1 | cholinephosphate cytidylyltransferase, putative / phosphorylcholine transferase, putative / CTP:phosphocholine cytidylyltransferase, putative, strong similarity to CTP:phosphocholine cytidylyltransferase (Brassica napus) GI:1418125; contains Pfam profile PF01467: Cytidylyltransferase | chr2:13704593-13707718 FORWARD | Aliases: T32F6.22, T32F6_22	7.7	9.7	-2.0	-6.2	0.34%	6.0
2949	AT1G18860.1 | Symbol: WRKY61 |	2.6	4.2	-1.6	-6.2	0.34%	6.0
2950	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	2.8	4.5	-1.8	-6.2	0.34%	6.0
2951	AT4G24740.2 | Symbol: AFC2 | protein kinase (AFC2), identical to protein kinase AFC2 (Arabidopsis thaliana) SWISS-PROT:P51567	6.8	8.3	-1.5	-6.2	0.34%	6.0
2953	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	5.9	7.5	-1.5	-6.2	0.34%	6.0
2954	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	5.7	-1.4	-6.2	0.34%	6.0
2957	AT1G16670.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069; similar to receptor-like serine/threonine kinase GI:2465923 from (Arabidopsis thaliana) | chr1:5697332-5699762 FORWARD | Aliases: F19K19.4, F19K19_4	5.9	7.5	-1.5	-6.2	0.34%	6.0
2959	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	4.2	-0.9	-6.2	0.34%	5.9
2960	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	6.5	7.8	-1.3	-6.2	0.34%	6.0
2963	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	9.1	10.2	-1.2	-6.2	0.34%	5.9
2965	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	3.9	6.9	-3.0	-6.2	0.34%	5.9
2970	AT3G50950.2 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	4.6	6.4	-1.8	-6.2	0.34%	5.9
2972	AT4G05190.1 | Symbol: ATK5 | kinesin-like protein A, putative, kinesin like protein A, Arabidopsis thaliana, gb:Q07970 | chr4:2675136-2679480 FORWARD | Aliases: ARABIDOPSIS THALIANA KINESIN 5, C17L7.110, C17L7_110	2.3	3.3	-0.9	-6.2	0.35%	5.9
2973	AT1G71820.1 | expressed protein | chr1:27013307-27020770 FORWARD | Aliases: F14O23.20, F14O23_20	4.3	5.7	-1.4	-6.2	0.35%	5.9
2976	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	4.7	6.2	-1.5	-6.2	0.35%	5.9
2977	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	3.4	4.9	-1.5	-6.2	0.35%	5.9
2978	AT1G45976.1 | Symbol: SBP1 | expressed protein | chr1:17201791-17203173 FORWARD | Aliases: F2G19.22, F2G19_22, S RIBONUCLEASE BINDING PROTEIN 1	7.4	8.8	-1.4	-6.2	0.35%	5.9
2983	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	4.7	6.2	-1.5	-6.2	0.35%	6.0
2984	AT5G19120.1 | expressed protein, low similarity to extracellular dermal glycoprotein EDGP precursor (Daucus carota) GI:285741, SP:P13917 Basic 7S globulin precursor {Glycine max} | chr5:6414564-6415807 FORWARD | Aliases: T24G5.20, T24G5_20	6.5	8.7	-2.2	-6.2	0.35%	5.9

Rank	Description	Sync	Root	M	t	adj.q	B
2985	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	7.6	9.2	-1.6	-6.2	0.35%	6.0
2986	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	5.4	6.6	-1.3	-6.1	0.35%	5.9
2988	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	7.0	8.2	-1.1	-6.1	0.35%	5.9
2989	AT2G26480.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:11271041-11272762 FORWARD | Aliases: T9J22.15, T9J22_15	2.8	4.5	-1.7	-6.1	0.35%	5.9
2990	AT3G13590.1 | DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain | chr3:4435323-4437341 REVERSE | Aliases: K20M4.3	3.1	4.2	-1.1	-6.1	0.35%	5.9
3005	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	4.9	6.5	-1.6	-6.1	0.35%	5.9
3006	AT1G19530.1 | expressed protein | chr1:6763906-6764944 FORWARD | Aliases: F18O14.29, F18O14_29	5.8	8.8	-3.0	-6.1	0.35%	5.8
3007	AT4G28300.2 | hydroxyproline-rich glycoprotein family protein | chr4:14014679-14017074 FORWARD | Aliases: F26K10.180, F26K10_180	3.8	6.0	-2.1	-6.1	0.35%	5.7
3008	AT4G26050.1 | leucine-rich repeat family protein, contains Pfam PF00560: Leucine Rich Repeat domains; | chr4:13210468-13213443 FORWARD | Aliases: F20B18.160, F20B18_160	2.8	4.6	-1.8	-6.1	0.35%	5.9
3009	AT4G27435.1 | expressed protein | chr4:13723824-13725143 FORWARD | Aliases: None	2.8	4.2	-1.4	-6.1	0.35%	5.9
3013	AT4G38060.2 | expressed protein | chr4:17873003-17874801 REVERSE | Aliases: F20D10.180, F20D10_180	7.1	9.8	-2.7	-6.1	0.35%	5.9
3017	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	6.0	7.7	-1.7	-6.1	0.35%	5.9
3018	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	5.3	-2.8	-6.1	0.36%	5.4
3024	AT2G02630.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	3.9	-1.1	-6.1	0.36%	5.9
3028	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	7.1	-1.8	-6.1	0.36%	5.9
3029	AT1G53270.1 | ABC transporter family protein, contains similarity to ABC transporter GI:10280532 from (Homo sapiens) | chr1:19866546-19868318 FORWARD | Aliases: F12M16.17, F12M16_17	2.5	3.6	-1.1	-6.1	0.36%	5.9
3030	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	8.3	10.9	-2.6	-6.1	0.36%	5.9
3031	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	6.2	7.9	-1.7	-6.1	0.36%	5.9
3034	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	3.6	5.7	-2.1	-6.1	0.36%	5.6
3038	AT5G35580.1 | protein kinase, putative, similar to auxin-regulated dual specificity cytosolic kinase (Lycopersicon esculentum) gi:14484938:gb:AAK62821	6.1	8.0	-1.9	-6.1	0.37%	5.9

Rank	Description	Sync	Root	M	t	adj.q	B
3039	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	4.7	-0.9	-6.1	0.37%	5.8
3045	AT1G53180.1 | expressed protein | chr1:19835109-19836510 FORWARD | Aliases: F12M16.8, F12M16_8	2.5	4.7	-2.3	-6.1	0.37%	5.8
3046	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	3.4	4.4	-1.0	-6.1	0.37%	5.8
3047	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	2.1	6.9	-4.7	-6.1	0.37%	5.4
3048	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	9.9	10.9	-1.0	-6.1	0.37%	5.8
3049	AT5G05250.1 | expressed protein | chr5:1557038-1557999 REVERSE | Aliases: K18I23.5, K18I23_5	8.1	10.6	-2.5	-6.1	0.37%	5.9
3050	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	5.6	7.9	-2.3	-6.1	0.37%	5.9
3052	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	5.1	-0.7	-6.1	0.37%	5.6
3053	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	5.1	7.3	-2.3	-6.1	0.37%	5.9
3056	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	7.6	-2.8	-6.1	0.37%	5.4
3059	AT3G20130.1 | Symbol: CYP705A22 | cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450 | chr3:7026935-7028842 FORWARD | Aliases: MAL21.17	2.4	3.3	-0.9	-6.1	0.37%	5.8
3065	AT1G09170.1 | kinesin motor protein-related, similar to GB:AAB61066 | chr1:2956591-2962209 REVERSE | Aliases: T12M4.14, T12M4_14	2.7	4.1	-1.4	-6.1	0.38%	5.8
3067	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	4.5	6.1	-1.6	-6.1	0.38%	5.9
3069	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	6.1	8.8	-2.7	-6.1	0.38%	5.7
3071	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	6.1	7.8	-1.7	-6.1	0.38%	5.8
3074	AT2G36650.1 | expressed protein | chr2:15366994-15368407 FORWARD | Aliases: F13K3.5, F13K3_5	3.7	6.0	-2.3	-6.1	0.38%	5.7
3075	AT2G42060.1 | CHP-rich zinc finger protein, putative | chr2:17555268-17556078 FORWARD | Aliases: T6D20.5, T6D20_5	2.3	4.0	-1.7	-6.0	0.38%	5.8
3076	AT4G01910.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	5.0	6.6	-1.6	-6.0	0.38%	5.8
3079	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	4.8	-0.9	-6.0	0.38%	5.7
3083	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	5.5	7.5	-2.0	-6.0	0.39%	5.8
3086	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	5.7	-1.3	-6.0	0.39%	5.8

Rank	Description	Sync	Root	M	t	adj.q	B
3087	AT2G20650.2 | zinc finger (C3HC4-type RING finger) family protein | chr2:8910718-8914363 REVERSE | Aliases: F23N11.3	4.4	5.9	-1.5	-6.0	0.39%	5.8
3088	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 Geobacillus stearothermophilus (GI:16753175), cadmium resistance protein B from Staphylococcus aureus (GI:14020985) | chr4:14720259-14724583 REVERSE | Aliases: F6G3.140, F6G3_140	4.7	6.8	-2.1	-6.0	0.39%	5.8
3089	AT4G35500.2 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr4:16857358-16859608 FORWARD | Aliases: F8D20.10, F8D20_10	4.5	6.1	-1.6	-6.0	0.39%	5.8
3093	AT5G52830.1 | Symbol: WRKY27 |	4.3	6.7	-2.4	-6.0	0.39%	5.8
3096	AT5G26200.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr5:9157145-9158780 FORWARD | Aliases: F9D12.12	4.8	6.9	-2.1	-6.0	0.39%	5.4
3098	AT5G38770.1 | hypothetical protein | chr5:15543344-15543637 FORWARD | Aliases: MKD10.70, MKD10_70	2.7	3.6	-0.9	-6.0	0.39%	5.7
3102	AT4G12760.1 | expressed protein, ; expression supported by MPSS | chr4:7504873-7506088 FORWARD | Aliases: T20K18.110, T20K18_110	7.2	8.6	-1.4	-6.0	0.40%	5.8
3105	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	9.0	10.1	-1.1	-6.0	0.40%	5.7
3106	AT3G13100.1 | Symbol: ATMRP7 |	3.7	6.2	-2.5	-6.0	0.40%	5.7
3110	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	6.7	-1.8	-6.0	0.40%	5.8
3111	AT3G46930.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:17296628-17299017 FORWARD | Aliases: F13I12.1	4.3	6.4	-2.1	-6.0	0.40%	5.8
3112	AT5G10210.1 | expressed protein | chr5:3206237-3206830 FORWARD | Aliases: F18D22.2	3.9	6.2	-2.3	-6.0	0.40%	5.8
3113	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	4.5	6.4	-2.0	-6.0	0.40%	5.8
3120	AT2G38320.1 | expressed protein | chr2:16062367-16065058 FORWARD | Aliases: T19C21.19, T19C21_19	3.1	5.3	-2.2	-6.0	0.40%	5.5
3123	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	6.5	7.8	-1.3	-6.0	0.40%	5.8
3125	AT4G26060.1 | expressed protein | chr4:13214755-13216470 REVERSE | Aliases: F20B18.170, F20B18_170	8.0	9.4	-1.4	-6.0	0.40%	5.8
3126	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	5.5	7.2	-1.7	-6.0	0.40%	5.8
3128	AT5G44700.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:18050091-18054121 REVERSE | Aliases: K23L20.3, K23L20_3	2.1	3.0	-0.9	-6.0	0.40%	5.5
3129	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	3.9	6.5	-2.5	-6.0	0.40%	5.8
3131	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	5.4	-1.5	-6.0	0.40%	5.7
3134	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	7.3	8.7	-1.4	-6.0	0.40%	5.8
3137	AT3G27350.1 | expressed protein | chr3:10127272-10129192 FORWARD | Aliases: K1G2.6	6.0	7.3	-1.4	-6.0	0.41%	5.8

Rank	Description	Sync	Root	M	t	adj.q	B
3138	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	4.1	-1.4	-6.0	0.41%	5.7
3139	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	5.5	6.9	-1.4	-6.0	0.41%	5.8
3140	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	5.6	7.1	-1.5	-6.0	0.41%	5.8
3142	AT4G34138.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr4:16348110-16349986 REVERSE | Aliases: None	5.8	8.3	-2.5	-6.0	0.41%	5.8
3143	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	2.9	3.9	-1.0	-6.0	0.41%	5.7
3145	AT5G66810.1 | expressed protein, similar to unknown protein (gb:AAB71479.1:) | chr5:26690152-26693821 FORWARD | Aliases: MUD21.5, MUD21_5	4.1	5.5	-1.3	-6.0	0.41%	5.8
3147	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	4.3	7.0	-2.7	-6.0	0.41%	5.7
3149	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	3.9	5.6	-1.7	-6.0	0.41%	5.6
3151	AT5G62600.1 | transportin-SR-related, contains weak similarity to transportin-SR (GI:5052414) (Homo sapiens) | chr5:25140537-25149893 REVERSE | Aliases: K19B1.1, K19B1_1	5.8	7.6	-1.8	-6.0	0.41%	5.7
3152	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	4.6	-1.4	-6.0	0.41%	5.7
3154	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	2.9	4.9	-1.9	-6.0	0.41%	5.5
3157	AT2G37040.1 | Symbol: PAL1 | phenylalanine ammonia-lyase 1 (PAL1), nearly identical to SP:P35510 | chr2:15564455-15567442 REVERSE | Aliases: CI0004, T1J8.22, T1J8_22	8.4	11.0	-2.5	-6.0	0.41%	5.7
3158	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	5.6	7.0	-1.4	-5.9	0.41%	5.7
3160	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	7.3	8.8	-1.6	-5.9	0.42%	5.7
3162	AT4G37460.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain | chr4:17608371-17615770 REVERSE | Aliases: F6G17.110, F6G17_110	7.0	8.5	-1.5	-5.9	0.42%	5.7
3166	AT2G33830.2 | dormancy/auxin associated family protein, contains Pfam profile: PF05564 dormancy/auxin associated protein | chr2:14316600-14317417 REVERSE | Aliases: T1B8.13, T1B8_13	7.7	9.9	-2.3	-5.9	0.42%	5.7
3169	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	3.5	5.4	-1.9	-5.9	0.42%	5.5
3176	AT1G17145.1 | expressed protein | chr1:5860112-5862672 REVERSE | Aliases: None	6.6	7.9	-1.3	-5.9	0.42%	5.7
3177	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	2.7	6.2	-3.6	-5.9	0.42%	5.7

Rank	Description	Sync	Root	M	t	adj.q	B
3178	AT2G15480.1 | similar to UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At4g34131.1); similar to UDP-glucoronosyl/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-glucoronosyl/UDP-glucosyl transferase (InterPro:IPR002213) | chr2:6765763-6767715 FORWARD | Aliases: F9O13.3	5.1	7.1	-1.9	-5.9	0.42%	5.7
3180	AT3G46690.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:17208614-17210322 REVERSE | Aliases: T6H20.280	3.9	6.1	-2.2	-5.9	0.42%	5.5
3182	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	3.4	5.4	-2.0	-5.9	0.42%	5.4
3183	AT4G39270.2 | leucine-rich repeat transmembrane protein kinase, putative, receptor protein kinase erecta, Arabidopsis thaliana	4.5	9.2	-4.7	-5.9	0.42%	5.6
3187	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	6.5	7.8	-1.3	-5.9	0.42%	5.7
3188	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	10.6	12.7	-2.0	-5.9	0.42%	5.5
3190	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	3.6	5.2	-1.7	-5.9	0.42%	5.7
3191	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 GI:13122291	6.7	8.0	-1.4	-5.9	0.42%	5.7
3198	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	5.7	-1.9	-5.9	0.43%	5.6
3199	AT2G27660.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.8	7.2	-3.3	-5.9	0.43%	5.5
3203	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)	4.8	6.4	-1.6	-5.9	0.43%	5.7
3205	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	4.4	-1.7	-5.9	0.43%	5.6
3206	AT5G16660.1 | expressed protein | chr5:5465490-5467066 REVERSE | Aliases: MTG13.11, MTG13_11	8.2	9.4	-1.2	-5.9	0.43%	5.7
3208	AT5G45940.1 | MutT/nudix family protein, contains Pfam profile PF00293: NUDIX domain | chr5:18646279-18647884 REVERSE | Aliases: K15I22.14, K15I22_14	4.8	6.2	-1.4	-5.9	0.43%	5.7
3209	AT4G32020.1 | expressed protein, NuLL | chr4:15487950-15489456 FORWARD | Aliases: F10N7.170, F10N7_170	2.4	6.2	-3.8	-5.9	0.43%	5.6
3211	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	7.2	9.5	-2.3	-5.9	0.43%	5.7
3214	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	7.1	8.9	-1.8	-5.9	0.43%	5.7
3218	AT1G01240.3 | expressed protein | chr1:99894-101834 FORWARD | Aliases: F633.5, F633_5, F6F3.27	6.7	8.1	-1.4	-5.9	0.43%	5.6
3223	AT3G12920.1 | expressed protein | chr3:4121890-4123503 REVERSE | Aliases: MGH6.3	9.8	10.5	-0.8	-5.9	0.43%	5.6
3226	AT5G19410.1 | ABC transporter family protein, white membrane transporter, Bactrocera tryoni, EMBL:U97104 | chr5:6545239-6547113 REVERSE | Aliases: F7K24.160, F7K24_160	2.7	4.7	-2.0	-5.9	0.44%	5.5

Rank	Description	Sync	Root	M	t	adj.q	B
3231	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	5.4	6.2	-0.9	-5.9	0.44%	5.5
3237	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:At3g56000.1); similar to glycosyl transferase family 2 protein [Arabidopsis thaliana] (TAIR:At4g13410.1); 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	3.3	4.9	-1.6	-5.9	0.44%	5.6
3240	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	5.8	7.0	-1.2	-5.9	0.44%	5.7
3242	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	5.1	-2.8	-5.9	0.44%	5.4
3246	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	5.2	-0.7	-5.9	0.44%	5.5
3250	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	4.7	6.5	-1.8	-5.9	0.45%	5.6
3252	AT2G41560.1 | Symbol: ACA4 | calcium-transporting ATPase 4, plasma membrane-type / Ca2+-ATPase, isoform 4 (ACA4), identical to SP:O22218 Calcium-transporting ATPase 4, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-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	5.2	6.5	-1.3	-5.9	0.45%	5.6
3254	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	10.2	11.1	-0.9	-5.9	0.45%	5.5
3255	AT4G13390.1 | proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr4:7783814-7785322 FORWARD | Aliases: T9E8.130, T9E8_130	2.9	6.0	-3.1	-5.9	0.45%	4.6
3256	AT2G21520.1 | similar to SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [Arabidopsis thaliana] (TAIR:At4g39170.1); similar to putative hosphatidylinositol/phophatidylcholine 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)	7.2	9.3	-2.2	-5.9	0.45%	5.6
3257	AT4G16640.1 | matrix metalloproteinase, putative, metalloproteinase (Arabidopsis thaliana) GI:3128477; contains InterPro accession IPR001818: Matrixin	2.8	3.9	-1.0	-5.9	0.45%	5.6
3258	AT1G33050.2 | expressed protein | chr1:11968897-11971001 REVERSE | Aliases: T9L6.12, T9L6_12	5.5	7.3	-1.8	-5.9	0.45%	5.6
3262	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	6.0	-1.3	-5.8	0.45%	5.6
3271	AT5G57150.3 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	5.1	7.3	-2.2	-5.8	0.46%	5.6
3272	AT3G20650.2 | mRNA capping enzyme family protein, contains Pfam PF03291: mRNA capping enzyme, large subunit | chr3:7220887-7224034 REVERSE | Aliases: F3H11.3	3.7	4.8	-1.1	-5.8	0.46%	5.6
3273	AT1G09430.1 | Symbol: ACLA 3 |	8.7	10.3	-1.6	-5.8	0.46%	5.5
3278	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	6.2	8.4	-2.2	-5.8	0.46%	5.6
3281	AT1G63310.1 | expressed protein, similar to unknown protein GB:AAC69930 from (Arabidopsis thaliana) | chr1:23489982-23490750 REVERSE | Aliases: F9N12.7, F9N12_7	2.5	4.9	-2.4	-5.8	0.46%	5.0

Rank	Description	Sync	Root	M	t	adj.q	B
3282	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	3.8	-0.9	-5.8	0.46%	5.6
3284	AT1G22540.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr1:7964031-7966425 FORWARD | Aliases: F12K8.12, F12K8_12	5.7	6.9	-1.2	-5.8	0.46%	5.6
3286	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	2.6	4.1	-1.5	-5.8	0.46%	5.5
3287	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	5.6	6.7	-1.2	-5.8	0.46%	5.6
3289	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	3.0	4.1	-1.1	-5.8	0.46%	5.6
3290	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	6.3	8.3	-2.0	-5.8	0.46%	5.6
3297	AT3G22260.2 | OTU-like cysteine protease family protein, contains Pfam profile PF02338: OTU-like cysteine protease | chr3:7871015-7873572 FORWARD | Aliases: MMP21.4	4.9	6.3	-1.4	-5.8	0.46%	5.6
3299	AT2G46620.1 | AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 | chr2:19145871-19147817 REVERSE | Aliases: F13A10.15	3.7	5.0	-1.3	-5.8	0.46%	5.6
3302	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	9.0	-2.2	-5.8	0.47%	5.6
3304	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	5.1	6.7	-1.6	-5.8	0.47%	5.6
3311	AT5G10740.1 | protein phosphatase 2C-related / PP2C-related, protein phosphatase 2C, alfalfa, PIR:T09640 | chr5:3393570-3396177 REVERSE | Aliases: MAJ23.3	6.9	8.0	-1.1	-5.8	0.47%	5.5
3312	AT1G15400.2 | expressed protein, ESTs gb:H37295 and gb:R64895 come from this gene | chr1:5296220-5296897 REVERSE | Aliases: F9L1.35, F9L1_35	8.4	9.7	-1.4	-5.8	0.47%	5.6
3313	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	5.0	6.4	-1.4	-5.8	0.47%	5.6
3316	AT5G47635.1 | expressed protein | chr5:19324280-19325121 REVERSE | Aliases: None	3.0	4.6	-1.6	-5.8	0.47%	5.5
3320	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 (GI:13374061) (Flaveria bidentis) | chr1:28051237-28051788 REVERSE | Aliases: F1M20.34, F1M20_34	5.1	7.4	-2.3	-5.8	0.47%	5.6
3321	AT4G35030.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr4:16676134-16677541 FORWARD | Aliases: M4E13.90, M4E13_90	3.1	7.1	-4.0	-5.8	0.47%	3.9
3324	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	3.9	6.6	-2.7	-5.8	0.47%	5.4
3325	AT3G04350.1 | expressed protein | chr3:1153734-1156783 REVERSE | Aliases: T6K12.3, T6K12_3	5.0	6.2	-1.2	-5.8	0.47%	5.5
3327	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	2.7	3.6	-0.9	-5.8	0.47%	5.5
3329	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	4.1	5.6	-1.5	-5.8	0.47%	5.6

Rank	Description	Sync	Root	M	t	adj.q	B
3330	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	11.3	12.2	-0.9	-5.8	0.47%	5.3
3331	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	3.5	-1.0	-5.8	0.47%	5.5
3332	AT2G22330.1 | Symbol: CYP79B3 | cytochrome P450, putative, similar to cytochrome P450 79B2 (SP:O81346) (Arabidopsis thaliana)	3.6	4.8	-1.1	-5.8	0.47%	5.6
3333	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	5.4	-1.5	-5.8	0.47%	5.5
3337	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	5.4	6.9	-1.5	-5.8	0.47%	5.6
3338	AT3G03040.1 | F-box family protein, contains F-box domain Pfam:PF00646	4.2	5.4	-1.2	-5.8	0.48%	5.5
3340	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	2.8	4.6	-1.8	-5.8	0.48%	5.6
3342	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	6.6	8.3	-1.7	-5.8	0.48%	5.5
3348	AT3G15050.1 | calmodulin-binding family protein, similar to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif | chr3:5066886-5067967 REVERSE | Aliases: K15M2.19	2.9	3.8	-0.9	-5.8	0.48%	5.5
3349	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	3.0	5.0	-2.0	-5.8	0.48%	5.4
3351	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)	7.8	9.3	-1.5	-5.8	0.48%	5.5
3353	AT5G35180.1 | expressed protein | chr5:13441648-13450248 FORWARD | Aliases: T25C13.60, T25C13_60	6.7	9.0	-2.3	-5.8	0.49%	5.5
3355	AT2G41660.1 | expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617 | chr2:17374900-17376267 FORWARD | Aliases: T32G6.18, T32G6_18	3.6	7.1	-3.6	-5.8	0.49%	5.3
3356	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	4.4	6.8	-2.4	-5.8	0.49%	5.5
3359	AT2G17590.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.3	3.2	-0.8	-5.8	0.49%	5.4
3360	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	4.5	-1.9	-5.8	0.49%	5.3
3364	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	4.8	6.3	-1.4	-5.7	0.49%	5.5
3367	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	6.0	8.1	-2.1	-5.7	0.49%	5.5
3371	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	5.6	-3.1	-5.7	0.49%	5.2

Rank	Description	Sync	Root	M	t	adj.q	B
3375	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	6.8	-2.0	-5.7	0.50%	5.5
3377	AT3G07600.1 | heavy-metal-associated domain-containing protein, identical to residues 23 to 179 of farnesylated protein ATFP4 (putative metal-binding protein) GB:AAD09508 (Arabidopsis thaliana); contains Pfam profile PF00403: Heavy-metal-associated domain | chr3:2424123-2425028 REVERSE | Aliases: MLP3.5	3.2	5.6	-2.4	-5.7	0.50%	5.5
3378	AT1G13590.1 | Symbol: ATPSK1 |	4.9	7.9	-3.0	-5.7	0.50%	5.2
3381	AT2G01180.2 | Symbol: ATPAP1 |	4.8	6.2	-1.4	-5.7	0.50%	5.5
3382	AT2G22080.1 | expressed protein | chr2:9393621-9395263 FORWARD | Aliases: T16B14.7, T16B14_7	8.0	10.3	-2.3	-5.7	0.50%	5.5
3385	AT5G52510.1 | scarecrow-like transcription factor 8 (SCL8) | chr5:21324275-21326528 FORWARD | Aliases: T4M5.2, T4M5_2	5.4	7.2	-1.8	-5.7	0.50%	5.5
3387	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	5.1	-1.2	-5.7	0.50%	5.5
3388	AT5G51160.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr5:20809506-20811000 FORWARD | Aliases: MWD22.10, MWD22_10	3.7	6.7	-3.0	-5.7	0.50%	5.5
3389	AT5G46340.1 | O-acetyltransferase-related, similar to O-acetyltransferase (Homo sapiens) GI:17016934 | chr5:18813153-18817321 REVERSE | Aliases: MPL12.14, MPL12_14	4.3	5.9	-1.5	-5.7	0.50%	5.5
3390	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	9.1	-1.2	-5.7	0.50%	5.4
3391	AT3G58640.2 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr3:21697718-21704818 REVERSE | Aliases: F14P22.230	6.1	7.0	-0.8	-5.7	0.50%	5.4
3393	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	4.7	-1.8	-5.7	0.50%	5.5
3394	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	5.7	-2.7	-5.7	0.50%	5.1
3395	AT1G20980.1 | Symbol: SPL14 | SPL1-Related2 protein (SPL1R2), strong similarity to SPL1-Related2 protein (Arabidopsis thaliana) GI:6006427; contains Pfam profile PF03110: SBP domain	6.3	7.7	-1.5	-5.7	0.50%	5.5
3396	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	6.6	-0.9	-5.7	0.50%	5.4
3397	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	3.7	6.4	-2.7	-5.7	0.50%	5.3
3398	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	5.4	-1.7	-5.7	0.50%	5.5
3400	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	5.4	8.5	-3.1	-5.7	0.50%	5.5
3401	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	8.0	-3.3	-5.7	0.50%	5.4
3403	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	5.0	5.9	-1.0	-5.7	0.50%	5.4
3409	AT5G59590.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:24026209-24027875 REVERSE | Aliases: F2O15.19, F2O15_19	3.5	6.1	-2.5	-5.7	0.50%	5.3

Rank	Description	Sync	Root	M	t	adj.q	B
3411	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	8.1	-3.7	-5.7	0.50%	5.5
3412	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	6.6	8.6	-2.0	-5.7	0.51%	5.5
3413	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	4.1	-1.2	-5.7	0.51%	5.5
3419	AT4G17110.1 | expressed protein, ; expression supported by MPSS | chr4:9613629-9615510 REVERSE | Aliases: DL4590C, FCAALL.359	5.5	7.7	-2.2	-5.7	0.51%	5.4
3420	AT2G23320.2 | Symbol: WRKY15 |	5.5	6.9	-1.5	-5.7	0.51%	5.5
3421	AT5G36260.1 | aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease | chr5:14302185-14305563 REVERSE | Aliases: T30G6.12, T30G6_12	2.8	4.0	-1.2	-5.7	0.51%	5.5
3422	AT1G70500.1 | polygalacturonase, putative / pectinase, putative, similar to polygalacturonase (Cucumis sativus) GI:6624205; contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)	3.0	4.2	-1.2	-5.7	0.51%	5.4
3423	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	3.0	-0.6	-5.7	0.51%	5.2
3426	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	6.5	8.2	-1.7	-5.7	0.51%	5.5
3427	AT4G17230.1 | scarecrow-like transcription factor 13 (SCL13) | chr4:9660996-9663782 REVERSE | Aliases: DL4650C, FCAALL.225	4.1	6.0	-1.8	-5.7	0.51%	5.4
3434	AT3G19340.1 | expressed protein | chr3:6701279-6704232 REVERSE | Aliases: MLD14.7	7.2	8.7	-1.4	-5.7	0.51%	5.5
3439	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	6.2	9.4	-3.2	-5.7	0.51%	5.4
3442	AT1G27300.1 | expressed protein | chr1:9483250-9484576 FORWARD | Aliases: F17L21.9, F17L21_9	6.9	8.2	-1.3	-5.7	0.51%	5.5
3446	AT3G03180.1 | Got1-like family protein, contains Pfam profile: PF04178 Got1-like family | chr3:733394-734434 FORWARD | Aliases: T17B22.13, T17B22_13	5.8	6.6	-0.8	-5.7	0.51%	5.4
3447	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	2.7	4.8	-2.1	-5.7	0.51%	5.4
3449	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	5.4	6.6	-1.2	-5.7	0.51%	5.4
3450	AT2G32280.1 | expressed protein | chr2:13720137-13721086 FORWARD | Aliases: T32F6.20, T32F6_20	3.5	4.7	-1.2	-5.7	0.51%	5.4
3451	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	6.1	-0.9	-5.7	0.51%	5.2
3452	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	7.0	-1.1	-5.7	0.51%	5.4
3455	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	7.5	10.6	-3.1	-5.7	0.52%	5.3
3456	AT4G10770.1 | Symbol: ATOPT7 |	3.0	4.2	-1.3	-5.7	0.52%	5.4
3457	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	5.6	-2.9	-5.7	0.52%	5.4

Rank	Description	Sync	Root	M	t	adj.q	B
3458	AT4G02180.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.4	5.5	-2.1	-5.7	0.52%	5.4
3459	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	5.4	7.4	-2.0	-5.7	0.52%	5.4
3461	AT1G07990.1 | SIT4 phosphatase-associated family protein, contains Pfam profile: PF04499 SIT4 phosphatase-associated protein | chr1:2477155-2483135 FORWARD | Aliases: T6D22.8, T6D22_8	3.8	5.3	-1.6	-5.7	0.52%	5.4
3466	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	2.6	4.0	-1.4	-5.7	0.52%	5.4
3469	AT5G45840.1 | leucine-rich repeat transmembrane protein kinase, putative, and genscan+ | chr5:18611307-18614448 REVERSE | Aliases: K15I22.4, K15I22_4	2.4	3.5	-1.1	-5.7	0.52%	5.4
3471	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	5.3	7.4	-2.0	-5.7	0.52%	5.4
3473	AT1G27210.1 | expressed protein | chr1:9455455-9458013 REVERSE | Aliases: T7N9.27, T7N9_27	4.5	6.8	-2.3	-5.7	0.52%	5.4
3474	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	3.7	-1.1	-5.7	0.52%	5.4
3475	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	3.8	5.3	-1.5	-5.7	0.52%	5.4
3477	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	3.4	5.5	-2.1	-5.7	0.52%	5.4
3478	AT1G13750.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	5.3	6.6	-1.3	-5.7	0.52%	5.4
3482	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	6.8	9.0	-2.2	-5.7	0.52%	5.4
3486	AT1G02360.1 | chitinase, putative, similar to chitinase precursor GI:5880845 from (Petroselinum crispum) | chr1:471990-473140 REVERSE | Aliases: T6A9.5, T6A9_5	5.1	8.7	-3.6	-5.7	0.53%	5.3
3487	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	8.7	10.4	-1.8	-5.7	0.53%	5.2
3488	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	6.5	-2.0	-5.7	0.53%	5.4
3489	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	2.6	-0.5	-5.7	0.53%	5.0
3493	AT2G28120.1 | nodulin family protein, similar to nodulin-like protein (Arabidopsis thaliana) GI:3329368, nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366 | chr2:11992764-11994815 FORWARD | Aliases: F24D13.9, F24D13_9	4.5	5.7	-1.2	-5.7	0.53%	5.4
3494	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	6.6	8.5	-1.9	-5.7	0.53%	5.4
3497	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)	4.6	6.5	-1.9	-5.6	0.53%	5.4

Rank	Description	Sync	Root	M	t	adj.q	B
3498	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	4.8	7.2	-2.4	-5.6	0.53%	5.3
3501	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	5.3	7.4	-2.1	-5.6	0.53%	5.1
3504	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	7.4	-1.6	-5.6	0.53%	5.4
3508	AT4G18425.1 | expressed protein, contains Pfam profile PF05078: Protein of unknown function (DUF679) | chr4:10181345-10182151 REVERSE | Aliases: None	2.9	6.1	-3.2	-5.6	0.53%	5.1
3513	AT2G42150.1 | DNA-binding bromodomain-containing protein, contains Pfam domains, PF00439: Bromodomain and PF00249: Myb-like DNA-binding domain	4.0	5.8	-1.8	-5.6	0.54%	5.4
3515	AT2G02610.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain | chr2:710711-712818 FORWARD | Aliases: T8K22.9, T8K22_9	2.8	4.2	-1.4	-5.6	0.54%	5.3
3517	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	9.4	11.2	-1.8	-5.6	0.54%	5.4
3520	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	7.8	-1.2	-5.6	0.55%	5.3
3521	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	5.0	6.4	-1.5	-5.6	0.55%	5.3
3526	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	6.8	-2.8	-5.6	0.55%	5.0
3528	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	7.0	8.4	-1.4	-5.6	0.55%	5.3
3529	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	7.7	9.4	-1.7	-5.6	0.55%	5.3
3530	AT1G69526.2 | similar to UbiE/COQ5 methyltransferase family protein [Arabidopsis thaliana] (TAIR:At1g69523.1); similar to COG0500: SAM-dependent methyltransferases [Nostoc punctiforme 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)	2.9	4.8	-1.9	-5.6	0.55%	5.3
3531	AT1G31470.1 | nodulin-related, weak similarity to nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366 | chr1:11262918-11264817 REVERSE | Aliases: T8E3.15, T8E3_15	6.0	7.2	-1.3	-5.6	0.55%	5.3
3532	AT4G36500.1 | expressed protein | chr4:17225915-17226613 REVERSE | Aliases: AP22.75, AP22_75	3.7	5.5	-1.8	-5.6	0.56%	5.3
3533	AT2G20010.1 | expressed protein | chr2:8644828-8648555 REVERSE | Aliases: T2G17.19, T2G17_19	5.0	7.1	-2.2	-5.6	0.56%	5.3
3535	AT5G03545.1 | expressed protein, No ATG start, annotated according to PMID:11123795 | chr5:894705-895399 FORWARD | Aliases: None	8.2	11.8	-3.6	-5.6	0.56%	4.2
3536	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	4.5	-1.1	-5.6	0.56%	5.3
3540	AT5G58300.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:23589105-23592587 FORWARD | Aliases: MCK7.17, MCK7_17	4.4	6.3	-1.9	-5.6	0.56%	5.3
3541	AT5G51310.1 | gibberellin 20-oxidase-related, low similarity to GI:9791186, GI:1109695	2.9	4.1	-1.3	-5.6	0.56%	5.3

Rank	Description	Sync	Root	M	t	adj.q	B
3542	AT3G27210.1 | expressed protein | chr3:10046423-10048580 REVERSE | Aliases: K17E12.3	4.2	5.6	-1.4	-5.6	0.56%	5.3
3544	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	6.4	7.7	-1.3	-5.6	0.56%	5.3
3549	AT5G58200.1 | expressed protein | chr5:23566860-23569278 FORWARD | Aliases: MCK7.7, MCK7_7	7.4	9.0	-1.6	-5.6	0.56%	5.3
3551	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	5.7	-2.5	-5.6	0.56%	5.3
3552	AT5G48310.1 | expressed protein | chr5:19592187-19597588 REVERSE | Aliases: K23F3.3, K23F3_3	5.8	6.9	-1.1	-5.6	0.56%	5.3
3554	AT5G56180.2 | Symbol: ATARP8 |	4.9	5.8	-0.8	-5.6	0.56%	5.2
3555	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	5.1	6.8	-1.7	-5.6	0.56%	5.3
3557	AT1G49960.2 | xanthine/uracil permease family protein, contains Pfam profile: PF00860 permease family | chr1:18502308-18505554 FORWARD | Aliases: F2J10.15, F2J10_15	3.4	5.2	-1.8	-5.6	0.56%	5.3
3559	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	5.4	-2.2	-5.6	0.56%	5.2
3561	AT5G49270.1 | phytochelatin synthetase-related, contains Pfam PF04833: Phytochelatin synthetase-like conserved region | chr5:19989138-19991670 REVERSE | Aliases: K21P3.15, K21P3_15	3.7	5.8	-2.2	-5.6	0.57%	5.1
3562	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, F18O21.200	9.1	10.7	-1.6	-5.6	0.57%	5.3
3567	AT3G51520.1 | diacylglycerol acyltransferase family, contains Pfam PF03982: Diacylglycerol acyltransferase | chr3:19121628-19123739 FORWARD | Aliases: F26O13.160	6.2	8.7	-2.5	-5.6	0.57%	5.3
3568	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	4.3	-1.2	-5.6	0.57%	5.3
3569	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	6.1	8.8	-2.7	-5.6	0.57%	5.3
3571	AT1G80870.1 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr1:30397025-30399275 FORWARD | Aliases: F23A5.23, F23A5_23	5.5	7.3	-1.8	-5.6	0.57%	5.3
3572	AT3G12870.1 | expressed protein | chr3:4094424-4095044 REVERSE | Aliases: MJM20.1	5.0	7.7	-2.8	-5.6	0.57%	5.0
3573	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	2.0	2.5	-0.5	-5.6	0.57%	4.8
3575	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	5.3	7.1	-1.8	-5.6	0.57%	5.3
3576	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	5.7	7.0	-1.4	-5.6	0.57%	5.3

Rank	Description	Sync	Root	M	t	adj.q	B
3577	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	7.4	9.2	-1.7	-5.6	0.57%	5.3
3578	AT4G31410.2 | expressed protein | chr4:15243743-15245767 FORWARD | Aliases: F3L17.5	6.0	7.0	-1.1	-5.6	0.57%	5.3
3581	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	5.0	-1.2	-5.6	0.57%	5.3
3582	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	3.8	6.5	-2.8	-5.6	0.57%	5.1
3584	AT5G47390.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr5:19244017-19246085 FORWARD | Aliases: MQL5.25, MQL5_25	5.4	7.7	-2.3	-5.6	0.57%	5.3
3586	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	4.2	-0.9	-5.6	0.57%	5.2
3588	AT5G06610.1 | expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620) | chr5:2029898-2033724 FORWARD | Aliases: F15M7.14, F15M7_14	5.1	7.2	-2.0	-5.6	0.57%	5.3
3594	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	4.8	-1.2	-5.6	0.58%	5.3
3597	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	9.2	11.0	-1.9	-5.6	0.58%	5.2
3598	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	4.9	7.3	-2.4	-5.6	0.58%	5.2
3600	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	5.2	6.6	-1.4	-5.6	0.58%	5.3
3601	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	5.5	7.4	-1.9	-5.6	0.58%	5.3
3604	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	2.7	4.0	-1.3	-5.6	0.58%	5.3
3606	AT4G22212.1 | Encodes a defensin-like (DEFL) family protein. | chr4:11753998-11754700 FORWARD | Aliases: None	10.0	11.4	-1.4	-5.6	0.58%	5.1
3607	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	4.6	6.0	-1.4	-5.6	0.58%	5.3
3609	AT2G47860.2 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr2:19607018-19609262 FORWARD | Aliases: F17A22.25	2.6	3.7	-1.1	-5.6	0.58%	5.2
3612	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	4.6	6.6	-1.9	-5.5	0.58%	5.3
3613	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	9.3	-2.2	-5.5	0.58%	5.3
3615	AT2G36950.1 | heavy-metal-associated domain-containing protein, nearly identical to farnesylated protein ATFP2 (GI:4097545) Pfam profile PF00403: Heavy-metal-associated domain | chr2:15522212-15524010 FORWARD | Aliases: T1J8.13, T1J8_13	9.6	11.6	-2.0	-5.5	0.58%	5.3

Rank	Description	Sync	Root	M	t	adj.q	B
3626	AT1G27150.1 | expressed protein | chr1:9429044-9432235 FORWARD | Aliases: T7N9.21, T7N9_21	9.0	9.9	-0.8	-5.5	0.58%	5.1
3627	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	7.7	-4.0	-5.5	0.58%	5.2
3629	AT5G39590.1 | expressed protein | chr5:15868639-15871194 FORWARD | Aliases: MIJ24.8, MIJ24_8	7.2	9.7	-2.5	-5.5	0.59%	5.3
3630	AT1G09250.1 | expressed protein | chr1:2989380-2990352 FORWARD | Aliases: T12M4.4, T12M4_4	4.2	5.7	-1.4	-5.5	0.59%	5.3
3632	AT1G19230.1 | respiratory burst oxidase protein E (RbohE) / NADPH oxidase, nearly identical to respiratory burst oxidase protein E GI:3242787 (gi:3242787) from (Arabidopsis thaliana)	2.9	4.6	-1.7	-5.5	0.59%	5.2
3634	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	5.6	8.3	-2.7	-5.5	0.59%	5.3
3637	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	7.6	9.1	-1.5	-5.5	0.59%	5.3
3640	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	8.7	9.8	-1.1	-5.5	0.59%	5.2
3642	AT3G20080.3 | Symbol: CYP705A15 | cytochrome P450 family protein, similar to Cytochrome P450 93A1 (SP:Q42798)	3.6	4.8	-1.2	-5.5	0.59%	5.3
3645	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	3.8	6.0	-2.2	-5.5	0.59%	5.1
3647	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	6.9	9.1	-2.1	-5.5	0.59%	5.3
3648	AT5G60950.1 | phytochelatin synthetase-related, contains Pfam profile PF04833: Phytochelatin synthetase-like conserved region | chr5:24544383-24545232 REVERSE | Aliases: MSL3.7, MSL3_7	4.2	6.5	-2.3	-5.5	0.59%	5.2
3651	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	6.5	10.8	-4.3	-5.5	0.59%	5.2
3653	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	6.2	7.4	-1.2	-5.5	0.59%	5.3
3654	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	3.2	-0.8	-5.5	0.59%	5.1
3655	AT2G41120.1 | expressed protein | chr2:17147973-17149497 REVERSE | Aliases: T3K9.11, T3K9_11	3.7	4.9	-1.2	-5.5	0.59%	5.3
3656	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	4.3	5.7	-1.5	-5.5	0.59%	5.3
3658	AT3G45190.1 | SIT4 phosphatase-associated family protein, contains Pfam profile: PF04499 SIT4 phosphatase-associated protein | chr3:16552979-16559146 REVERSE | Aliases: T14D3.130	2.9	3.7	-0.7	-5.5	0.59%	5.0
3662	AT1G70470.1 | expressed protein | chr1:26563022-26563697 REVERSE | Aliases: F24J13.4, F24J13_4	2.8	6.1	-3.3	-5.5	0.60%	5.2
3664	AT3G15040.1 | expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584 | chr3:5064711-5066697 REVERSE | Aliases: K15M2.18	6.0	7.0	-1.0	-5.5	0.60%	5.2
3667	AT4G39670.1 | expressed protein | chr4:18410166-18410994 FORWARD | Aliases: T19P19.60, T19P19_60	3.9	6.0	-2.1	-5.5	0.60%	5.2
3669	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	5.6	7.1	-1.4	-5.5	0.60%	5.2

Rank	Description	Sync	Root	M	t	adj.q	B
3670	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	6.0	8.1	-2.1	-5.5	0.60%	5.2
3671	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	7.0	8.1	-1.1	-5.5	0.60%	5.2
3673	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	3.5	5.1	-1.5	-5.5	0.60%	5.2
3677	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	6.8	-3.6	-5.5	0.60%	5.2
3679	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	5.9	7.2	-1.3	-5.5	0.60%	5.2
3682	AT5G12010.1 | expressed protein | chr5:3877813-3879540 REVERSE | Aliases: F14F18.180, F14F18_180	7.9	9.3	-1.4	-5.5	0.60%	5.0
3683	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	10.0	11.3	-1.3	-5.5	0.61%	5.0
3684	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	4.7	7.8	-3.1	-5.5	0.61%	5.1
3685	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	6.4	-3.7	-5.5	0.61%	4.9
3686	AT5G16520.1 | expressed protein | chr5:5394656-5397458 REVERSE | Aliases: MQK4.27, MQK4_27	4.6	6.1	-1.5	-5.5	0.61%	5.2
3687	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: F17O7.5, F17O7_5	7.8	9.4	-1.6	-5.5	0.61%	5.2
3690	AT5G05880.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:1769649-1771516 FORWARD | Aliases: K18J17.3, K18J17_3	3.8	5.0	-1.2	-5.5	0.61%	5.2
3691	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	5.7	-1.9	-5.5	0.61%	5.1
3693	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	5.7	-2.0	-5.5	0.61%	5.2
3694	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	2.8	-0.9	-5.5	0.61%	5.1
3696	AT4G13530.2 | expressed protein, predicted protein, Arabidopsis thaliana | chr4:7866780-7868716 FORWARD | Aliases: T6G15.80, T6G15_80	8.4	9.9	-1.6	-5.5	0.61%	5.2
3697	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	5.4	-2.0	-5.5	0.61%	5.2
3698	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	3.7	4.9	-1.2	-5.5	0.61%	5.2
3699	AT3G06620.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr3:2062212-2067422 REVERSE | Aliases: F5E6.5, F5E6_5	2.7	3.2	-0.5	-5.5	0.61%	4.8

Rank	Description	Sync	Root	M	t	adj.q	B
3701	AT1G03550.1 | secretory carrier membrane protein (SCAMP) family protein, contains Pfam domain, PF04144: SCAMP family | chr1:885623-887956 REVERSE | Aliases: F21B7.17, F21B7_17	4.4	6.4	-2.0	-5.5	0.61%	5.2
3702	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	4.1	-1.2	-5.5	0.62%	5.2
3703	AT2G47930.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr2:19624045-19624751 REVERSE | Aliases: T9J23.8, T9J23_8	3.0	4.6	-1.6	-5.5	0.62%	5.2
3704	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	3.3	4.2	-0.9	-5.5	0.62%	5.2
3705	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	8.2	9.1	-0.8	-5.5	0.62%	5.1
3715	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	5.3	-2.2	-5.5	0.62%	5.2
3716	AT3G09940.1 | monodehydroascorbate reductase, putative, similar to monodehydroascorbate reductase (NADH) GB:JU0182 (Cucumis sativus) | chr3:3056384-3059153 REVERSE | Aliases: F8A24.20	3.3	4.6	-1.3	-5.5	0.62%	5.2
3717	AT1G48300.1 | expressed protein | chr1:17851024-17852466 FORWARD | Aliases: F11A17.15, F11A17_15	9.1	11.7	-2.6	-5.5	0.62%	5.1
3719	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	2.1	4.7	-2.6	-5.5	0.62%	5.1
3720	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 (Lycopersicon esculentum) | chr1:458133-460696 REVERSE | Aliases: T6A9.1, T6A9_1	3.9	5.0	-1.1	-5.5	0.62%	5.2
3725	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	4.7	6.1	-1.4	-5.5	0.62%	5.2
3732	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	4.9	8.2	-3.4	-5.5	0.63%	5.2
3734	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	3.4	-0.7	-5.5	0.63%	4.9
3735	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	3.4	-1.4	-5.5	0.63%	5.2
3736	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	3.2	4.7	-1.5	-5.5	0.63%	5.2
3739	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	6.1	8.7	-2.6	-5.5	0.63%	5.2
3741	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	4.8	-1.2	-5.5	0.63%	5.1
3742	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	6.3	-3.2	-5.5	0.63%	5.2
3744	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	4.9	-1.0	-5.4	0.63%	5.2

Rank	Description	Sync	Root	M	t	adj.q	B
3746	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	4.0	5.7	-1.7	-5.4	0.63%	5.1
3749	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	4.6	-1.4	-5.4	0.63%	5.2
3753	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	2.2	4.7	-2.5	-5.4	0.63%	5.2
3755	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	2.7	3.2	-0.5	-5.4	0.63%	4.8
3756	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	8.1	-2.6	-5.4	0.63%	5.2
3757	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	2.9	-0.7	-5.4	0.63%	5.0
3759	AT2G35610.1 | expressed protein | chr2:14954444-14958326 REVERSE | Aliases: T20F21.19, T20F21_19	5.2	6.8	-1.6	-5.4	0.63%	5.2
3765	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	5.5	-1.2	-5.4	0.64%	5.1
3767	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	4.6	-2.0	-5.4	0.64%	5.1
3768	AT1G55265.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr1:20620980-20621668 FORWARD | Aliases: None	4.3	5.5	-1.2	-5.4	0.64%	5.2
3769	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	7.6	-1.5	-5.4	0.64%	5.2
3772	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	4.7	6.5	-1.8	-5.4	0.64%	5.1
3777	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	3.5	4.2	-0.7	-5.4	0.64%	5.0
3780	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	6.5	7.5	-1.1	-5.4	0.64%	5.1
3781	AT5G35750.1 | Symbol: AHK2 | histidine kinase (AHK2), identical to histidine kinase AHK2 (Arabidopsis thaliana) gi:13537196:dbj:BAB40774 | chr5:13928601-13933567 REVERSE | Aliases: ARABIDOPSIS HISTIDINE KINASE 2, MXH1.16, MXH1_16	4.0	5.7	-1.7	-5.4	0.64%	5.1
3784	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	7.2	-1.4	-5.4	0.64%	5.2
3786	AT4G02540.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	6.8	9.3	-2.5	-5.4	0.65%	5.1
3790	AT5G47560.1 | Symbol: ATSDAT/ATTDT | Encodes a tonoplast malate/fumarate transporter.	2.9	4.4	-1.5	-5.4	0.65%	5.1
3795	AT5G53010.1 | calcium-transporting ATPase, putative | chr5:21505716-21513763 REVERSE | Aliases: MNB8.7, MNB8_7	2.8	4.3	-1.5	-5.4	0.65%	5.1
3796	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	3.2	4.2	-1.0	-5.4	0.65%	5.1

Rank	Description	Sync	Root	M	t	adj.q	B
3805	AT5G46050.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr5:18692262-18696373 REVERSE | Aliases: MCL19.10, MCL19_10	2.9	4.3	-1.4	-5.4	0.65%	5.1
3806	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	4.9	-1.1	-5.4	0.65%	5.1
3807	AT2G28305.1 | expressed protein, contains Pfam profile PF03641: decarboxylase family protein | chr2:12088190-12091741 FORWARD | Aliases: T1B3.18	2.6	3.1	-0.6	-5.4	0.65%	4.8
3808	AT1G12950.1 | MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: MatE | chr1:4419768-4422632 FORWARD | Aliases: F13K23.21, F13K23_21	3.1	4.4	-1.3	-5.4	0.65%	5.1
3811	AT4G14280.1 | expressed protein | chr4:8222513-8225069 FORWARD | Aliases: DL3180W, FCAALL.154	2.4	3.2	-0.8	-5.4	0.65%	5.0
3815	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	7.3	-1.2	-5.4	0.65%	5.1
3816	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	9.1	10.6	-1.5	-5.4	0.66%	5.1
3817	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	6.3	8.6	-2.3	-5.4	0.66%	5.1
3818	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	5.2	6.3	-1.1	-5.4	0.66%	5.1
3820	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	6.0	7.8	-1.8	-5.4	0.66%	5.1
3821	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	5.7	-1.3	-5.4	0.66%	5.1
3824	AT4G28770.1 | expressed protein | chr4:14211328-14213677 REVERSE | Aliases: F16A16.120, F16A16_120	7.5	9.2	-1.7	-5.4	0.66%	5.0
3827	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	5.7	7.2	-1.5	-5.4	0.66%	5.1
3830	AT4G31840.1 | plastocyanin-like domain-containing protein | chr4:15401646-15402623 FORWARD | Aliases: F11C18.40, F11C18_40	4.2	5.8	-1.5	-5.4	0.66%	5.1
3832	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	8.2	10.0	-1.8	-5.4	0.66%	5.1
3835	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	3.4	-0.7	-5.4	0.66%	4.7
3838	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	5.0	8.0	-3.0	-5.4	0.66%	4.7
3839	AT4G21310.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr4:11339058-11340080 REVERSE | Aliases: T6K22.40, T6K22_40	4.1	5.6	-1.5	-5.4	0.66%	5.1
3841	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	7.0	8.8	-1.8	-5.4	0.66%	5.1
3842	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	6.0	7.6	-1.5	-5.4	0.66%	5.1

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3845	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	7.5	9.4	-1.9	-5.4	0.66%	5.1
3846	AT4G24170.1 | kinesin motor family protein, contains Pfam domain, PF00225: Kinesin motor domain | chr4:12543216-12546815 FORWARD | Aliases: T19F6.1	2.3	3.2	-0.9	-5.4	0.66%	4.9
3850	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	8.7	-1.3	-5.4	0.67%	5.1
3851	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	4.2	5.4	-1.3	-5.4	0.67%	5.1
3858	AT3G23590.1 | expressed protein | chr3:8467456-8473626 FORWARD | Aliases: MDB19.7	5.8	6.9	-1.1	-5.4	0.67%	5.0
3860	AT1G11050.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:3681888-3684169 FORWARD | Aliases: T19D16.6, T19D16_6	4.2	5.9	-1.7	-5.4	0.67%	5.1
3862	AT3G09010.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:2749958-2752281 FORWARD | Aliases: T16O11.3	3.8	4.8	-1.0	-5.4	0.67%	5.1
3864	AT2G16900.1 | expressed protein | chr2:7330697-7333303 REVERSE | Aliases: F12A24.8, F12A24_8	5.6	6.7	-1.1	-5.4	0.67%	5.0
3866	AT1G06000.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains similarity to UDPG glucosyltransferase GB:AAB62270 GI:2232354 from (Solanum berthaultii) | chr1:1820307-1821892 REVERSE | Aliases: T21E18.5, T21E18_5	6.8	8.2	-1.4	-5.4	0.67%	5.0
3867	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	3.7	5.0	-1.3	-5.4	0.67%	5.0
3869	AT2G22930.1 | glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	3.0	4.2	-1.2	-5.4	0.68%	5.1
3870	AT5G48060.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr5:19492522-19496228 FORWARD | Aliases: MDN11.14, MDN11_14	3.1	4.1	-1.0	-5.4	0.68%	5.1
3871	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	3.0	4.1	-1.1	-5.4	0.68%	5.1
3872	AT5G50900.1 | armadillo/beta-catenin repeat family protein, armadillo/beta-catenin-like repeats, Pfam:PF00514 | chr5:20722030-20724004 REVERSE | Aliases: K3K7.4, K3K7_4	8.1	9.2	-1.1	-5.4	0.68%	5.0
3874	AT3G52740.1 | expressed protein | chr3:19557352-19557942 REVERSE | Aliases: F3C22.140	7.0	8.2	-1.2	-5.4	0.68%	5.1
3875	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	6.4	7.4	-1.0	-5.4	0.68%	5.0
3876	AT2G47630.1 | esterase/lipase/thioesterase family protein, similar to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162; contains Interpro entry IPR000379 | chr2:19541573-19544073 FORWARD | Aliases: F17A22.2	6.9	9.0	-2.1	-5.4	0.68%	5.0
3877	AT1G73750.1 | expressed protein, contains Pfam profile: PF00561 alpha/beta hydrolase fold | chr1:27740291-27742740 FORWARD | Aliases: F25P22.17, F25P22_17	4.5	6.1	-1.7	-5.4	0.68%	5.1
3886	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	5.5	-2.0	-5.3	0.68%	5.1
3888	AT1G31710.1 | copper amine oxidase, putative, similar to copper amine oxidase (Lens culinaris) gi:15451834:gb:AAB34918	3.9	4.8	-0.9	-5.3	0.69%	5.0
3889	AT5G40340.1 | PWWP domain-containing protein, KED, Nicotiana tabacum, EMBL:AB009883 | chr5:16148882-16151908 REVERSE | Aliases: MPO12.6, MPO12_6	4.0	7.1	-3.1	-5.3	0.69%	5.0
3890	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	8.0	9.4	-1.5	-5.3	0.69%	5.0

Rank	Description	Sync	Root	M	t	adj.q	B
3893	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) (BRI1-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	6.4	8.7	-2.4	-5.3	0.69%	5.1
3894	AT2G40230.1 | transferase family protein, similar to taxadienol acetyl transferase from Taxus cuspidata (gi:6978038); contains Pfam transferase family domain PF002458	3.8	5.1	-1.3	-5.3	0.69%	5.0
3895	AT5G54500.1 | Symbol: FQR1 | quinone reductase, putative, similar to 1,4-benzoquinone reductase (Phanerochaete chrysosporium)(GI:4454993); contains flavodoxin domain PF00258	9.0	10.3	-1.3	-5.3	0.69%	5.0
3898	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	5.3	7.1	-1.8	-5.3	0.69%	5.1
3899	AT3G03560.1 | expressed protein | chr3:853976-856493 REVERSE | Aliases: T21P5.2	4.0	5.0	-1.0	-5.3	0.69%	5.0
3900	AT1G63720.1 | expressed protein, similar to putative protein GB:CAA18164 (Arabidopsis thaliana) | chr1:23639519-23641178 REVERSE | Aliases: F24D7.9, F24D7_9	3.8	4.6	-0.8	-5.3	0.69%	5.0
3901	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	3.5	6.9	-3.4	-5.3	0.69%	5.0
3903	AT1G18570.1 | Symbol: MYB51 | myb family transcription factor (MYB51), contains PFAM profile: PF00249	3.0	4.5	-1.5	-5.3	0.69%	5.1
3904	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	4.0	6.2	-2.2	-5.3	0.69%	4.9
3907	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	5.1	6.5	-1.3	-5.3	0.69%	5.0
3910	AT2G31880.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:13561973-13564054 FORWARD | Aliases: F20M17.8, F20M17_8	5.0	6.7	-1.7	-5.3	0.69%	5.0
3911	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	7.3	9.3	-2.0	-5.3	0.70%	5.0
3915	AT3G20150.1 | kinesin motor family protein, contains Pfam domain, PF00225: Kinesin motor domain | chr3:7031418-7036505 FORWARD | Aliases: MAL21.18	2.8	3.9	-1.1	-5.3	0.70%	5.0
3917	AT3G27390.1 | expressed protein | chr3:10134450-10137730 REVERSE | Aliases: K1G2.10	3.6	5.1	-1.6	-5.3	0.70%	5.0
3920	AT5G20610.1 | expressed protein | chr5:6968692-6972997 FORWARD | Aliases: T1M15.10, T1M15_10	4.9	6.9	-2.0	-5.3	0.70%	5.0
3922	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	3.3	-0.8	-5.3	0.70%	4.9
3926	AT4G33960.1 | expressed protein | chr4:16277371-16277784 FORWARD | Aliases: F17I5.150, F17I5_150	5.1	7.3	-2.2	-5.3	0.70%	4.9
3928	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 (Brassica napus) | chr1:18294712-18299493 FORWARD | Aliases: F13F21.14, F13F21_14, LONG CHAIN ACYL COA SYNTHETASE 2	3.0	4.5	-1.5	-5.3	0.70%	5.0
3936	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	6.0	-0.9	-5.3	0.71%	4.9
3938	AT1G32100.1 | pinoresinol-lariciresinol reductase, putative, similar to pinoresinol-lariciresinol reductase TH1 (Tsuga heterophylla)(GI:7578915); contains isoflavone reductase domain PF02716	5.9	9.1	-3.2	-5.3	0.71%	5.0

Rank	Description	Sync	Root	M	t	adj.q	B
3940	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	6.6	-1.6	-5.3	0.71%	5.0
3943	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	5.8	-2.6	-5.3	0.71%	4.8
3944	AT5G05140.1 | transcription elongation factor-related, low similarity to transcription elongation factor TFIIS.h (Mus musculus) GI:3288547, elongin A (Mus musculus) GI:6009624 | chr5:1519914-1522668 FORWARD | Aliases: MUG13.28	4.0	5.7	-1.7	-5.3	0.71%	5.0
3945	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	4.3	5.9	-1.7	-5.3	0.71%	5.0
3947	AT1G09155.1 | Symbol: ATPP2 B15 | SKP1 interacting partner 3-related, low similarity to SKP1 interacting partner 3 (Arabidopsis thaliana) GI:10716951	2.7	6.3	-3.6	-5.3	0.71%	4.8
3949	AT1G75190.1 | expressed protein | chr1:28223043-28223888 FORWARD | Aliases: F22H5.8, F22H5_8	3.3	5.9	-2.6	-5.3	0.71%	5.0
3950	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	5.0	6.4	-1.4	-5.3	0.71%	5.0
3952	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	6.6	8.7	-2.1	-5.3	0.71%	5.0
3953	AT1G17860.1 | trypsin and protease inhibitor family protein / Kunitz family protein, similar to LeMir (miraculin homolog) GI:2654440 from (Lycopersicon esculentum), tumor-related protein (Nicotiana tabacum) GI:1762933; contains Pfam profile PF00197: Trypsin and protease inhibitor | chr1:6149294-6150031 FORWARD | Aliases: F2H15.9, F2H15_9	6.8	10.0	-3.1	-5.3	0.72%	5.0
3955	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	3.9	5.1	-1.3	-5.3	0.72%	5.0
3957	AT4G15500.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr4:8857093-8858520 REVERSE | Aliases: DL3790C, FCAALL.307	4.4	7.2	-2.8	-5.3	0.72%	4.9
3958	AT1G49050.1 | aspartyl protease family protein, contains Pfam PF00026: Eukaryotic aspartyl protease; contains similarity to nucellin GI:2290203 from (Hordeum vulgare)	6.8	9.2	-2.3	-5.3	0.72%	5.0
3959	AT1G30640.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr1:10861279-10864682 FORWARD | Aliases: T5I8.9, T5I8_9	5.2	6.8	-1.6	-5.3	0.72%	5.0
3961	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	3.7	6.1	-2.4	-5.3	0.72%	4.8
3964	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	4.0	5.5	-1.5	-5.3	0.72%	5.0
3965	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 plumbaginifolia] (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	4.1	6.2	-2.1	-5.3	0.72%	5.0
3967	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	3.1	4.0	-0.9	-5.3	0.72%	4.9
3968	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	4.7	-1.1	-5.3	0.72%	5.0
3969	AT2G36810.1 | expressed protein | chr2:15432818-15443960 REVERSE | Aliases: F13K3.21, F13K3_21	3.4	5.7	-2.4	-5.3	0.72%	5.0
3982	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	8.1	-1.1	-5.3	0.73%	4.9
3983	AT2G34910.1 | expressed protein | chr2:14733979-14735126 FORWARD | Aliases: F19I3.14, F19I3_14	3.4	5.7	-2.4	-5.3	0.73%	4.6

Rank	Description	Sync	Root	M	t	adj.q	B
3984	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	4.9	6.6	-1.6	-5.3	0.73%	4.9
3987	AT2G31090.1 | expressed protein | chr2:13263215-13263788 FORWARD | Aliases: T16B12.10, T16B12_10	9.6	10.8	-1.2	-5.3	0.74%	4.8
3989	AT2G42760.1 | expressed protein | chr2:17803061-17804308 REVERSE | Aliases: F7D19.24, F7D19_24	8.2	9.9	-1.7	-5.3	0.74%	4.9
3990	AT5G23530.1 | expressed protein, contains similarity to PrMC3 (Pinus radiata) GI:5487873 | chr5:7932969-7934439 REVERSE | Aliases: MQM1.21, MQM1_21	3.1	4.4	-1.2	-5.3	0.74%	5.0
3994	AT3G27270.1 | expressed protein | chr3:10074517-10075397 FORWARD | Aliases: K17E12.9	4.4	5.7	-1.3	-5.3	0.74%	5.0
3995	AT2G28780.1 | expressed protein | chr2:12347111-12350498 REVERSE | Aliases: F8N16.7, F8N16_7	3.6	4.9	-1.4	-5.3	0.74%	5.0
3997	AT1G60010.1 | expressed protein | chr1:22099025-22100242 REVERSE | Aliases: T2K10.6, T2K10_6	4.7	6.7	-1.9	-5.3	0.74%	4.9
4000	AT2G19710.1 | expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292 | chr2:8513216-8517163 FORWARD | Aliases: F6F22.26, F6F22_26	4.0	5.0	-1.0	-5.3	0.75%	4.9
4003	AT5G57670.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:23377626-23379690 REVERSE | Aliases: MRI1.2, MRI1_2	2.1	2.4	-0.4	-5.3	0.75%	4.3
4004	AT2G20740.3 | expressed protein | chr2:8943759-8944591 FORWARD | Aliases: AT2G20730, F5H14.29, F5H14_29	5.7	6.9	-1.1	-5.3	0.75%	4.9
4007	AT5G45380.1 | sodium:solute symporter family protein, contains Pfam profile: PF00474 sodium:solute symporter family | chr5:18408351-18413053 FORWARD | Aliases: MFC19.5, MFC19_5	4.7	6.5	-1.8	-5.3	0.75%	4.9
4008	AT2G13650.2 | Symbol: GONST1 |	5.7	8.1	-2.4	-5.3	0.75%	5.0
4009	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	8.6	10.1	-1.4	-5.3	0.75%	4.8
4013	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	3.6	5.6	-1.9	-5.3	0.75%	4.9
4014	AT1G12680.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:4319884-4322943 REVERSE | Aliases: T12C24.32, T12C24_32	5.3	6.6	-1.3	-5.2	0.75%	4.9
4016	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	6.0	-3.5	-5.2	0.75%	4.9
4017	AT3G16920.1 | glycoside hydrolase family 19 protein, similar to class I chitinase GI:7798670 from (Arabis microphylla)	2.8	6.9	-4.1	-5.2	0.75%	4.9
4018	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	6.2	7.3	-1.1	-5.2	0.75%	4.8
4020	AT3G11370.1 | DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain | chr3:3561105-3562886 FORWARD | Aliases: F11B9.29	2.1	4.6	-2.5	-5.2	0.75%	4.9
4022	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	7.7	9.0	-1.3	-5.2	0.75%	4.8
4025	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	5.5	6.7	-1.2	-5.2	0.75%	4.9
4028	AT3G53510.1 | ABC transporter family protein, breast cancer resistance protein (BCRP), Homo sapiens, EMBL:AF098951 | chr3:19848191-19850840 REVERSE | Aliases: F4P12.210	2.5	3.5	-1.0	-5.2	0.76%	4.9
4030	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	3.2	5.8	-2.7	-5.2	0.76%	4.9

Rank	Description	Sync	Root	M	t	adj.q	B
4033	AT5G60720.1 | expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547 | chr5:24435455-24439460 REVERSE | Aliases: MUP24.14, MUP24_14	3.2	5.1	-1.9	-5.2	0.76%	4.9
4034	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	2.9	3.9	-1.0	-5.2	0.76%	4.9
4036	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	5.8	-2.1	-5.2	0.76%	4.9
4042	AT2G45210.1 | auxin-responsive protein-related, weakly similar to small auxin up RNA (GI:546362) {Arabidopsis thaliana} | chr2:18648640-18649778 FORWARD | Aliases: F4L23.28	4.7	6.3	-1.6	-5.2	0.77%	4.9
4046	AT5G49830.1 | expressed protein | chr5:20267712-20272215 REVERSE | Aliases: K21G20.4, K21G20_4	4.1	5.0	-0.9	-5.2	0.77%	4.9
4047	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	9.4	10.7	-1.3	-5.2	0.77%	4.9
4048	AT1G10090.1 | expressed protein | chr1:3290059-3296181 REVERSE | Aliases: T27I1.11, T27I1_11	4.4	5.1	-0.7	-5.2	0.77%	4.8
4049	AT4G23496.1 | expressed protein | chr4:12257689-12258421 REVERSE | Aliases: None	3.4	4.3	-0.9	-5.2	0.77%	4.8
4050	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	3.0	4.2	-1.1	-5.2	0.77%	4.8
4054	AT2G35770.1 | Symbol: SCPL28 |	2.1	3.8	-1.7	-5.2	0.78%	4.9
4056	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	4.3	5.2	-0.8	-5.2	0.78%	4.8
4059	AT5G43880.1 | expressed protein | chr5:17657202-17660817 REVERSE | Aliases: F6B6.2, F6B6_2	2.8	3.7	-0.9	-5.2	0.78%	4.7
4060	AT3G09320.1 | zinc finger (DHHC type) family protein, similar to Golgi-specific DHHC zinc figer protein (Mus musculus) GI:21728103; contains Pfam profile PF01529: DHHC zinc finger domain | chr3:2861749-2864251 REVERSE | Aliases: F3L24.19	5.4	6.9	-1.5	-5.2	0.78%	4.9
4061	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	4.3	6.3	-2.0	-5.2	0.78%	4.9
4062	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	5.8	6.9	-1.1	-5.2	0.78%	4.9
4063	AT4G26320.1 | Symbol: AGP13 | arabinogalactan-protein (AGP13), identical to gi:10880503:gb:AAG24281 | chr4:13317109-13317479 REVERSE | Aliases: ARABINOGALACTAN PROTEIN 13, T25K17.130, T25K17_130	6.1	8.4	-2.3	-5.2	0.78%	4.9
4065	AT1G14780.1 | expressed protein | chr1:5090985-5094147 FORWARD | Aliases: F10B6.18, F10B6_18	3.5	5.5	-2.0	-5.2	0.78%	4.9
4067	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	2.9	3.6	-0.7	-5.2	0.79%	4.6
4068	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	3.6	6.0	-2.4	-5.2	0.79%	4.9
4071	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	4.7	6.5	-1.8	-5.2	0.79%	4.9
4072	AT2G32430.1 | galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase | chr2:13778373-13781579 FORWARD | Aliases: T32F6.5, T32F6_5	5.4	6.5	-1.1	-5.2	0.79%	4.8

Rank	Description	Sync	Root	M	t	adj.q	B
4074	AT3G45840.1 | similar to DC1 domain-containing protein / UV-B light-insensitive protein, putative [Arabidopsis thaliana] (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)	3.0	7.3	-4.2	-5.2	0.79%	4.9
4076	NA	3.7	7.1	-3.4	-5.2	0.79%	4.9
4077	AT2G39380.1 | exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit; | chr2:16454084-16456161 REVERSE | Aliases: F12L6.4, F12L6_4	3.3	4.9	-1.6	-5.2	0.79%	4.9
4078	AT4G34600.1 | expressed protein | chr4:16529230-16530191 FORWARD | Aliases: T4L20.180, T4L20_180	6.6	8.1	-1.5	-5.2	0.79%	4.8
4081	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	4.2	-0.9	-5.2	0.79%	4.8
4082	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	5.3	6.0	-0.7	-5.2	0.79%	4.6
4083	AT2G27830.1 | expressed protein | chr2:11867295-11868552 FORWARD | Aliases: F15K20.7, F15K20_7	3.7	5.8	-2.1	-5.2	0.79%	4.7
4085	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 HSFB1, ATHSF4, HEAT SHOCK FACTOR 4, HEAT SHOCK TRANSCRIPTION FACTOR 4, HSFB1	8.6	11.3	-2.7	-5.2	0.80%	4.8
4086	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	3.4	4.4	-0.9	-5.2	0.80%	4.8
4090	AT1G49660.1 | expressed protein | chr1:18382365-18383467 REVERSE | Aliases: F14J22.11, F14J22_11	7.1	9.5	-2.4	-5.2	0.81%	4.8
4091	AT3G59900.1 | expressed protein, hypothetical protein At2g44080 - Arabidopsis thaliana, EMBL:AC004005 | chr3:22140703-22141434 FORWARD | Aliases: F24G16.170	6.1	8.7	-2.6	-5.2	0.81%	4.9
4092	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	3.6	-1.4	-5.2	0.81%	4.9
4094	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	6.3	7.5	-1.2	-5.2	0.81%	4.9
4097	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	8.2	9.1	-0.9	-5.2	0.81%	4.7
4098	AT1G03380.1 | expressed protein | chr1:835825-840891 FORWARD | Aliases: F21B7.1	5.0	6.3	-1.3	-5.2	0.81%	4.8
4099	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	4.2	5.3	-1.2	-5.2	0.81%	4.8
4103	AT5G47620.3 | heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative | chr5:19319496-19321316 REVERSE | Aliases: MNJ7.21, MNJ7_21	9.9	10.8	-0.9	-5.2	0.81%	4.7
4105	AT5G06850.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr5:2126976-2129325 REVERSE | Aliases: MOJ9.2, MOJ9_2	3.9	5.3	-1.4	-5.2	0.81%	4.9
4106	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	4.7	6.0	-1.3	-5.2	0.81%	4.8
4108	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	2.5	3.3	-0.8	-5.2	0.81%	4.7
4109	AT1G35780.1 | expressed protein | chr1:13278486-13281472 REVERSE | Aliases: F14D7.8, F14D7_8	5.5	6.6	-1.1	-5.2	0.81%	4.8

Rank	Description	Sync	Root	M	t	adj.q	B
4110	AT1G75390.1 | bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor | chr1:28295426-28296669 FORWARD | Aliases: F1B16.8, F1B16_8	7.4	8.9	-1.5	-5.2	0.81%	4.8
4111	AT1G01420.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr1:154566-156011 REVERSE | Aliases: F6F3.22, F6F3_22	3.4	4.1	-0.8	-5.2	0.81%	4.7
4118	AT3G61630.1 | AP2 domain-containing transcription factor, putative, transcription factor Pti6 - Lycopersicon esculentum, PIR:T07728 | chr3:22816155-22817499 FORWARD | Aliases: F15G16.20	2.3	3.0	-0.8	-5.2	0.82%	4.7
4120	AT1G74080.1 | Symbol: MYB122 |	2.7	4.0	-1.3	-5.2	0.82%	4.8
4122	AT5G48110.1 | terpene synthase/cyclase family protein | chr5:19518383-19521583 REVERSE | Aliases: MDN11.20, MDN11_20	2.8	4.3	-1.5	-5.2	0.82%	4.8
4126	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	7.3	-1.1	-5.1	0.83%	4.8
4132	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	7.5	-1.6	-5.1	0.83%	4.7
4138	AT1G29970.1 | expressed protein, similar to GI:3128228 from (Arabidopsis thaliana) (Nature 402 (6763), 761-768 (1999))	6.7	7.5	-0.8	-5.1	0.83%	4.7
4141	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	3.8	-0.8	-5.1	0.83%	4.7
4143	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	4.6	-0.8	-5.1	0.83%	4.6
4144	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	2.8	3.4	-0.6	-5.1	0.84%	4.6
4147	AT4G08620.1 | Symbol: SULTR1;1 | sulfate transporter, identical to sulfate transporter (Arabidopsis thaliana) GI:3777483 | chr4:5500310-5506262 FORWARD | Aliases: SULTR1.2	3.3	5.0	-1.6	-5.1	0.84%	4.8
4149	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	4.6	6.2	-1.5	-5.1	0.84%	4.8
4150	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	5.7	-1.2	-5.1	0.84%	4.8
4153	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	9.0	10.1	-1.2	-5.1	0.84%	4.8
4157	AT4G32410.1 | Symbol: CESA1 | cellulose synthase, catalytic subunit, putative, similar to cellulose synthase-1 (gi:9622874) and -2 (gi:9622876) from Zea mays	6.6	7.9	-1.3	-5.1	0.84%	4.7
4158	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	2.9	4.9	-2.0	-5.1	0.84%	4.7
4163	AT1G21050.1 | expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617 | chr1:7366764-7367667 FORWARD | Aliases: T22I11.13, T22I11_13	4.4	6.4	-2.0	-5.1	0.84%	4.8
4165	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	2.4	3.1	-0.7	-5.1	0.85%	4.5
4166	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	2.6	4.0	-1.4	-5.1	0.85%	4.7
4167	AT5G43040.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.1	3.7	-0.7	-5.1	0.85%	4.5

Rank	Description	Sync	Root	M	t	adj.q	B
4169	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	6.2	7.3	-1.2	-5.1	0.85%	4.8
4170	AT5G25270.1 | expressed protein | chr5:8757786-8762005 REVERSE | Aliases: F21J6.3	4.3	7.2	-2.9	-5.1	0.85%	4.7
4172	AT5G40470.1 | expressed protein | chr5:16225237-16227125 REVERSE | Aliases: K21I16.4, K21I16_4	5.5	7.2	-1.8	-5.1	0.85%	4.8
4175	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	4.0	-1.0	-5.1	0.85%	4.7
4177	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 inductor), 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 translocalized 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	8.5	9.7	-1.2	-5.1	0.86%	4.7
4182	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	5.5	-1.0	-5.1	0.86%	4.7
4183	AT1G49310.1 | expressed protein | chr1:18241531-18242030 REVERSE | Aliases: F13F21.30, F13F21_30	4.4	7.3	-2.9	-5.1	0.86%	4.8
4184	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	5.8	7.0	-1.2	-5.1	0.86%	4.7
4186	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	7.6	-1.1	-5.1	0.86%	4.8
4187	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	4.4	-1.2	-5.1	0.86%	4.8
4191	AT5G65640.1 | basic helix-loop-helix (bHLH) family protein | chr5:26254285-26256310 FORWARD | Aliases: K21L13.16, K21L13_16	3.9	5.4	-1.5	-5.1	0.86%	4.8
4193	AT2G29750.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:12716804-12718773 FORWARD | Aliases: T27A16.15, T27A16_15	3.7	5.6	-1.9	-5.1	0.86%	4.8
4194	AT1G55430.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	3.4	-0.6	-5.1	0.86%	4.5
4197	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	6.9	7.8	-0.9	-5.1	0.86%	4.7
4198	AT3G62160.1 | transferase family protein, low similarity to Taxus cuspidata transferases: 10-deacetylbaccatin III-10-O-acetyl transferase GI:6746554, taxadienol acetyl transferase GI:6978038, 2-debenzoyl-7,13-diacetylbaccatin III-2-O-benzoyl transferase GI:11559716; contains Pfam profile PF02458 transferase family | chr3:23025183-23026814 REVERSE | Aliases: T17J13.120	3.1	4.7	-1.6	-5.1	0.86%	4.7
4201	AT5G46780.2 | VQ motif-containing protein, contains PF05678: VQ motif | chr5:18996204-18997283 FORWARD | Aliases: MZA15.20, MZA15_20	5.6	8.0	-2.4	-5.1	0.86%	4.8
4206	AT3G27610.1 | expressed protein | chr3:10226779-10229428 REVERSE | Aliases: MGF10.2	4.9	6.9	-1.9	-5.1	0.87%	4.8
4207	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	5.9	6.9	-1.0	-5.1	0.87%	4.7
4208	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	6.8	9.8	-3.0	-5.1	0.87%	4.7
4213	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	8.8	-1.1	-5.1	0.87%	4.5

Rank	Description	Sync	Root	M	t	adj.q	B
4214	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	4.2	5.2	-1.0	-5.1	0.87%	4.7
4217	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	2.7	3.9	-1.2	-5.1	0.87%	4.7
4218	AT1G58070.1 | expressed protein | chr1:21506570-21507739 FORWARD | Aliases: T15M6.8, T15M6_8	2.9	4.3	-1.3	-5.1	0.87%	4.8
4223	AT2G46225.1 | Symbol: ABI1L1 |	4.0	5.1	-1.1	-5.1	0.88%	4.8
4224	AT1G12080.2 | expressed protein | chr1:4084203-4085041 FORWARD | Aliases: F12F1.4, F12F1_4	4.0	7.1	-3.2	-5.1	0.88%	4.5
4227	AT4G30850.2 | expressed protein, contains Pfam domain, PF03006: Uncharacterised protein family (Hly-III / UPF0073) | chr4:15020188-15022451 REVERSE | Aliases: F6I18.240, F6I18_240	7.5	8.7	-1.2	-5.1	0.88%	4.7
4228	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	4.9	7.2	-2.3	-5.1	0.88%	4.7
4233	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	11.5	12.3	-0.7	-5.1	0.88%	4.3
4237	AT5G26240.1 | Symbol: CLC D | chloride channel protein (CLC-d), identical to CLC-d chloride channel protein (Arabidopsis thaliana) GI:1742959	3.6	5.1	-1.5	-5.1	0.89%	4.7
4238	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	4.5	6.0	-1.5	-5.1	0.89%	4.7
4240	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	9.5	10.5	-1.0	-5.1	0.89%	4.3
4242	AT4G17785.1 | myb family transcription factor (MYB39), contains Pfam profile: PF00249 myb-like DNA-binding domain | chr4:9881648-9883445 REVERSE | Aliases: None	2.3	2.8	-0.5	-5.1	0.89%	4.1
4247	AT5G13810.1 | glutaredoxin family protein | chr5:4455354-4457022 FORWARD | Aliases: MAC12.24, MAC12_24	6.4	7.7	-1.4	-5.1	0.90%	4.6
4255	AT1G52240.1 | member of KPP-like gene family, homologs of KPP (kinase partner protein) gene in tomato.	2.8	4.1	-1.3	-5.1	0.90%	4.7
4259	AT1G50290.1 | expressed protein | chr1:18631227-18632102 REVERSE | Aliases: F14I3.24, F14I3_24	3.1	4.1	-1.0	-5.1	0.91%	4.7
4262	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	4.6	7.7	-3.0	-5.1	0.91%	4.7
4263	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	5.2	-1.3	-5.0	0.91%	4.7
4264	AT5G01610.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr5:231042-232198 FORWARD | Aliases: F7A7.130, F7A7_130	4.1	5.7	-1.6	-5.0	0.91%	4.7
4265	AT2G19410.1 | protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain | chr2:8411983-8416094 REVERSE | Aliases: F27F23.21, F27F23_21	2.6	3.5	-0.9	-5.0	0.91%	4.6
4266	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	3.4	4.2	-0.8	-5.0	0.91%	4.6
4267	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	6.9	8.3	-1.5	-5.0	0.91%	4.7
4269	AT2G44010.1 | expressed protein | chr2:18223760-18224514 FORWARD | Aliases: F6E13.14	3.5	7.9	-4.3	-5.0	0.91%	4.6

Rank	Description	Sync	Root	M	t	adj.q	B
4272	AT5G18970.1 | AWPM-19-like membrane family protein, contains Pfam profile: PF05512 AWPM-19-like family	2.9	5.1	-2.2	-5.0	0.91%	4.6
4278	AT1G07690.1 | expressed protein | chr1:2378073-2378997 FORWARD | Aliases: F24B9.22, F24B9_22	3.1	3.8	-0.7	-5.0	0.91%	4.4
4279	AT1G01190.1 | Symbol: CYP78A8 | cytochrome P450, putative, similar to cytochrome P450 SP:O48927 from (Glycine max) | chr1:83045-84864 REVERSE | Aliases: F6F3.25	3.6	5.1	-1.5	-5.0	0.91%	4.7
4282	AT1G75160.1 | expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620) | chr1:28213098-28215465 FORWARD | Aliases: F22H5.11, F22H5_11	2.1	2.6	-0.5	-5.0	0.91%	4.3
4289	AT3G19970.1 | expressed protein | chr3:6958654-6961466 FORWARD | Aliases: MZE19.2	4.3	5.5	-1.2	-5.0	0.92%	4.7
4290	AT3G16220.1 | expressed protein, similar to CGI-18 protein GB:AAD27727 (Homo sapiens) | chr3:5497620-5499241 FORWARD | Aliases: MYA6.3	5.2	6.7	-1.6	-5.0	0.92%	4.6
4293	AT2G29620.1 | expressed protein | chr2:12670277-12672880 REVERSE | Aliases: T27A16.28, T27A16_28	2.5	3.2	-0.7	-5.0	0.92%	4.4
4294	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	3.3	5.2	-1.9	-5.0	0.92%	4.6
4297	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	10.9	11.9	-1.0	-5.0	0.92%	4.5
4298	AT4G16563.1 | aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease | chr4:9329679-9331545 REVERSE | Aliases: None	3.7	5.7	-2.0	-5.0	0.92%	4.6
4305	AT5G53980.1 | homeobox-leucine zipper family protein, contains Pfam PF00046: Homeobox domain; similar to homeobox protein PpHB5 (GI:7415622) (Physcomitrella patens) | chr5:21931271-21931965 FORWARD | Aliases: K19P17.15, K19P17_15	2.7	3.8	-1.1	-5.0	0.93%	4.6
4307	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	3.8	-1.0	-5.0	0.93%	4.7
4308	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	3.1	4.0	-0.8	-5.0	0.93%	4.6
4312	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	5.4	7.1	-1.7	-5.0	0.93%	4.7
4314	AT1G69240.1 | hydrolase, alpha/beta fold family protein, low similarity to SP:Q40708 PIR7A protein {Oryza sativa}, polyneuridine aldehyde esterase GI:6651393 from (Rauvolfia serpentina), ethylene-induced esterase (Citrus sinensis) GI:14279437; contains Pfam profile PF00561: hydrolase, alpha/beta fold family | chr1:26031639-26033897 REVERSE | Aliases: F4N2.19, F4N2_19	2.3	3.2	-0.8	-5.0	0.93%	4.6
4317	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	5.1	6.5	-1.4	-5.0	0.94%	4.7
4318	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	5.5	6.9	-1.4	-5.0	0.94%	4.6
4320	AT1G51170.1 | protein kinase family protein | chr1:18957126-18958560 REVERSE | Aliases: F23H24.1	4.3	6.0	-1.7	-5.0	0.94%	4.7
4321	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	2.8	3.8	-1.1	-5.0	0.94%	4.6
4322	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	2.6	4.3	-1.7	-5.0	0.94%	4.6
4325	AT5G58520.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:23672476-23675388 FORWARD | Aliases: MQJ2.14, MQJ2_14	5.9	7.2	-1.2	-5.0	0.94%	4.7
4328	AT3G48020.1 | expressed protein | chr3:17735578-17735985 FORWARD | Aliases: T17F15.110	4.3	5.6	-1.3	-5.0	0.94%	4.6

Rank	Description	Sync	Root	M	t	adj.q	B
4330	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	5.5	-0.7	-5.0	0.94%	4.4
4331	AT1G32740.1 | expressed protein | chr1:11844857-11846482 FORWARD | Aliases: F6N18.12, F6N18_12	4.5	6.8	-2.3	-5.0	0.94%	4.7
4337	AT3G45700.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr3:16789698-16792183 FORWARD | Aliases: T6D9.30	4.0	5.6	-1.6	-5.0	0.94%	4.7
4339	AT5G08250.1 | cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450 | chr5:2653581-2655727 REVERSE | Aliases: F8L15.12	2.4	3.5	-1.1	-5.0	0.94%	4.5
4340	AT1G11080.1 | Symbol: SCPL31 |	2.5	3.9	-1.4	-5.0	0.94%	4.7
4343	AT5G41810.2 | expressed protein | chr5:16755290-16756891 FORWARD | Aliases: K16L22.9, K16L22_9	3.4	5.1	-1.7	-5.0	0.95%	4.6
4345	AT1G70530.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr1:26592413-26595042 REVERSE | Aliases: F24J13.10, F24J13_10	4.7	6.1	-1.4	-5.0	0.95%	4.6
4346	AT5G20300.3 | similar to chloroplast outer membrane protein, putative [Arabidopsis thaliana] (TAIR:At3g16620.1); similar to chloroplast Toc125 [Physcomitrella patens] (GB:AAS47583.1)	6.6	8.2	-1.6	-5.0	0.95%	4.5
4348	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	4.4	6.0	-1.6	-5.0	0.95%	4.6
4352	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	7.3	8.3	-0.9	-5.0	0.96%	4.4
4353	AT2G31820.1 | ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023 | chr2:13537427-13539639 FORWARD | Aliases: F20M17.14, F20M17_14	7.9	8.7	-0.8	-5.0	0.96%	4.3
4359	AT5G19050.1 | expressed protein | chr5:6369269-6371901 FORWARD | Aliases: T16G12.90, T16G12_90	6.0	7.7	-1.8	-5.0	0.96%	4.6
4360	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	9.2	-1.1	-5.0	0.96%	4.4
4362	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	5.7	7.0	-1.3	-5.0	0.97%	4.6
4365	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	8.6	9.9	-1.3	-5.0	0.97%	4.4
4366	AT3G19190.1 | expressed protein | chr3:6639717-6648242 FORWARD | Aliases: MVI11.11	4.6	6.2	-1.6	-5.0	0.97%	4.6
4370	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	2.6	-0.3	-5.0	0.97%	3.8
4371	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	5.0	6.3	-1.4	-5.0	0.97%	4.6
4373	AT1G08590.1 | similar to CLV1-like leucine rich repeat transmembrane receptor-like protein kinase (Ipomoea nil) (U77888) | chr1:2718781-2722224 FORWARD | Aliases: F22O13.7, F22O13_7	3.4	4.4	-1.0	-5.0	0.97%	4.6
4376	AT2G43820.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:18159304-18160985 FORWARD | Aliases: F18O19.7	4.4	7.0	-2.6	-5.0	0.98%	4.6
4380	AT5G63080.1 | transcription factor jumonji (jmjC) domain-containing protein, contains Pfam domain PF02373: jmjC domain	5.5	6.8	-1.3	-5.0	0.98%	4.6
4383	AT3G47770.1 | Symbol: ATATH5 |	2.8	3.6	-0.8	-5.0	0.98%	4.4

Rank	Description	Sync	Root	M	t	adj.q	B
4385	AT3G52800.1 | zinc finger (AN1-like) family protein, contains Pfam domain, PF01428: AN1-like Zinc finger | chr3:19580289-19581660 FORWARD | Aliases: F3C22.200	6.2	7.8	-1.6	-5.0	0.98%	4.6
4388	AT1G80240.1 | expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642 | chr1:30176249-30177718 REVERSE | Aliases: F18B13.30, F18B13_30	2.8	3.8	-1.1	-5.0	0.99%	4.6
4392	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	6.8	8.0	-1.2	-5.0	0.99%	4.6
4395	AT3G46730.1 | disease resistance protein (CC-NBS class), putative, domain signature CC-NBS exists, suggestive of a disease resistance protein.	2.3	3.3	-1.0	-5.0	0.99%	4.5
4398	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	4.7	-1.1	-5.0	0.99%	4.6
4400	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	4.3	-1.3	-5.0	1.00%	4.6
4404	AT3G10550.1 | expressed protein | chr3:3292904-3296874 REVERSE | Aliases: F13M14.17	5.6	6.9	-1.3	-4.9	1.00%	4.5
4407	AT5G65660.1 | hydroxyproline-rich glycoprotein family protein | chr5:26262475-26263605 REVERSE | Aliases: K21L13.18, K21L13_18	9.6	10.8	-1.2	-4.9	1.00%	4.6
4408	AT3G07990.1 | Symbol: SCPL27 |	2.8	3.6	-0.8	-4.9	1.00%	4.5
4410	AT2G26670.1 | Symbol: HY1 | heme oxygenase 1 (HO1) (HY1), identical to plastid heme oxygenase (HY1) (Arabidopsis thaliana) GI:4877362, heme oxygenase 1 (Arabidopsis thaliana) GI: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	8.0	10.0	-2.0	-4.9	1.00%	4.6
4411	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	5.2	6.7	-1.5	-4.9	1.00%	4.6
4415	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	6.7	7.8	-1.1	-4.9	1.01%	4.6
4417	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	4.0	5.5	-1.5	-4.9	1.01%	4.6
4418	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	7.3	8.8	-1.5	-4.9	1.01%	4.5
4419	AT3G49590.2 | expressed protein | chr3:18388545-18391269 FORWARD | Aliases: T9C5.180	5.3	6.9	-1.5	-4.9	1.01%	4.6
4423	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	5.0	6.8	-1.8	-4.9	1.01%	4.6
4425	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	5.2	6.7	-1.5	-4.9	1.01%	4.6
4427	AT3G01730.1 | expressed protein | chr3:266565-266994 FORWARD | Aliases: F4P13.28	3.2	5.0	-1.8	-4.9	1.01%	4.6
4431	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	4.8	6.8	-2.0	-4.9	1.01%	4.6
4435	AT5G19040.1 | Symbol: ATIPT5 |	3.9	5.5	-1.6	-4.9	1.01%	4.6

Rank	Description	Sync	Root	M	t	adj.q	B
4436	AT5G03550.1 | hypothetical protein | chr5:895812-896144 REVERSE | Aliases: F12E4.340, F12E4_340	2.4	3.0	-0.7	-4.9	1.01%	4.2
4439	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	5.4	6.9	-1.5	-4.9	1.02%	4.6
4445	AT5G37070.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr5:14668321-14669377 FORWARD | Aliases: MJG14.7, MJG14_7	6.8	7.6	-0.8	-4.9	1.02%	4.5
4447	AT3G05620.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr3:1629664-1631772 REVERSE | Aliases: F18C1.11, F18C1_11	2.8	4.7	-1.8	-4.9	1.02%	4.4
4448	AT3G52460.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr3:19457948-19458850 FORWARD | Aliases: F22O6.160	5.1	6.0	-0.9	-4.9	1.02%	4.4
4452	AT5G61350.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:24685199-24687727 FORWARD | Aliases: MFB13.1, MFB13_1	2.6	3.8	-1.2	-4.9	1.02%	4.6
4455	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	5.4	6.9	-1.5	-4.9	1.02%	4.5
4456	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	5.1	-2.6	-4.9	1.02%	4.6
4458	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)	6.7	7.8	-1.2	-4.9	1.02%	4.5
4460	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	4.9	5.8	-0.9	-4.9	1.02%	4.5
4461	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	4.2	5.4	-1.2	-4.9	1.03%	4.5
4463	AT1G08315.1 | armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat | chr1:2620334-2621542 REVERSE | Aliases: None	6.0	7.0	-1.0	-4.9	1.03%	4.5
4464	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	2.9	3.8	-0.9	-4.9	1.03%	4.4
4465	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	5.2	-1.4	-4.9	1.03%	4.6
4467	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	10.9	12.2	-1.2	-4.9	1.03%	4.3
4468	AT5G24230.1 | expressed protein | chr5:8228895-8230967 FORWARD | Aliases: MOP9.4, MOP9_4	2.4	3.3	-1.0	-4.9	1.03%	4.5
4472	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	5.0	-0.9	-4.9	1.03%	4.5
4474	AT4G28500.1 | Symbol: ANAC073 | no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; | chr4:14083020-14084272 FORWARD | Aliases: ANAC073, F20O9.190, F20O9_190	3.7	5.0	-1.3	-4.9	1.04%	4.5
4476	AT5G47980.1 | transferase family protein, similar to alcohol acyltransferase (Fragaria x ananassa)(GI:10121328)(PMID:10810141), deacetylvindoline 4-O-acetyltransferase (Catharanthus roseus)(GI:4091808)(PMID:9681034) | chr5:19446114-19447702 FORWARD | Aliases: MDN11.1	3.3	4.5	-1.1	-4.9	1.04%	4.5
4477	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	4.4	-1.0	-4.9	1.04%	4.5

Rank	Description	Sync	Root	M	t	adj.q	B
4480	AT2G18730.1 | diacylglycerol kinase, putative, contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain | chr2:8125912-8129003 FORWARD | Aliases: MSF3.11, MSF3_11	4.6	5.5	-0.8	-4.9	1.04%	4.4
4481	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	3.3	5.5	-2.2	-4.9	1.04%	4.5
4482	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	7.0	8.6	-1.7	-4.9	1.04%	4.5
4483	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	3.7	5.7	-1.9	-4.9	1.05%	4.5
4484	AT5G56140.1 | KH domain-containing protein | chr5:22742688-22745569 FORWARD | Aliases: MDA7.20, MDA7_20	4.0	5.6	-1.6	-4.9	1.05%	4.5
4486	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	7.2	9.0	-1.9	-4.9	1.05%	4.5
4488	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	4.3	-1.1	-4.9	1.05%	4.5
4489	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	4.5	5.4	-0.9	-4.9	1.05%	4.4
4490	AT1G67050.1 | expressed protein | chr1:25032290-25033451 REVERSE | Aliases: F1O19.11, F1O19_11	4.2	6.3	-2.1	-4.9	1.05%	4.5
4491	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	3.2	4.0	-0.8	-4.9	1.05%	4.4
4493	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	5.4	6.9	-1.5	-4.9	1.05%	4.5
4503	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	4.1	-1.1	-4.9	1.06%	4.5
4504	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	7.0	8.2	-1.3	-4.9	1.06%	4.5
4505	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	4.3	6.0	-1.7	-4.9	1.07%	4.5
4506	AT4G00755.2 | F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250 | chr4:324994-326964 FORWARD | Aliases: None	5.5	6.3	-0.7	-4.9	1.07%	4.3
4509	AT1G47655.1 | Dof-type zinc finger domain-containing protein | chr1:17527805-17528746 FORWARD | Aliases: None	3.9	5.1	-1.1	-4.9	1.07%	4.5
4516	AT3G52820.1 | purple acid phosphatase (PAP22), identical to purple acid phosphatase (PAP22)GI:20257494 from (Arabidopsis thaliana) | chr3:19584922-19587955 REVERSE | Aliases: F3C22.220	2.4	3.3	-0.8	-4.9	1.07%	4.4
4519	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	3.7	4.5	-0.8	-4.9	1.07%	4.2
4521	AT3G46760.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:17233012-17234025 FORWARD | Aliases: T6H20.210	2.7	3.9	-1.1	-4.9	1.07%	4.5
4523	AT3G45870.1 | integral membrane family protein / nodulin MtN21-related, simlar to MtN21 GI:2598575 (root nodule development) Medicago truncatula, EMBL:MTY15293 | chr3:16878187-16879911 FORWARD | Aliases: F16L2.80	3.1	3.9	-0.8	-4.9	1.07%	4.3
4526	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	3.3	4.2	-0.9	-4.9	1.07%	4.5

Rank	Description	Sync	Root	M	t	adj.q	B
4527	AT5G64905.1 | expressed protein | chr5:25956800-25957285 FORWARD | Aliases: None	3.0	4.1	-1.1	-4.9	1.07%	4.4
4530	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	4.0	4.9	-1.0	-4.9	1.08%	4.5
4533	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	5.2	7.6	-2.4	-4.9	1.08%	4.5
4535	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	4.9	-1.4	-4.9	1.08%	4.5
4538	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	5.7	7.8	-2.1	-4.9	1.08%	4.5
4541	AT5G12880.1 | proline-rich family protein, similar to hydroxyproline-rich glycoprotein gi:169345:gb:AAA33763 | chr5:4068522-4068965 REVERSE | Aliases: T24H18.50, T24H18_50	3.2	7.1	-3.9	-4.9	1.09%	4.5
4543	AT2G17130.2 | Symbol: IDH2 | isocitrate dehydrogenase subunit 2 / NAD+ isocitrate dehydrogenase subunit 2, nearly identical to NAD+ dependent isocitrate dehydrogenase subunit 2 (Arabidopsis thaliana) GI:1766048 | chr2:7467896-7469636 REVERSE | Aliases: F6P23.14, F6P23_14, ISOCITRATE DEHYDROGENASE SUBUNIT 2, NAD+ DEPENDENT ISOCITRATE DEHYDROGENASE SUBUNIT 2	9.2	10.7	-1.5	-4.9	1.09%	4.4
4546	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	4.6	-0.8	-4.9	1.10%	4.4
4548	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	5.8	-1.3	-4.9	1.10%	4.5
4549	AT4G08410.1 | proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; | chr4:5339083-5341206 REVERSE | Aliases: T28D5.100, T28D5_100	3.6	8.4	-4.8	-4.9	1.10%	3.9
4556	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	3.7	7.1	-3.4	-4.8	1.10%	4.4
4563	AT1G78100.1 | F-box family protein, contains F-box domain Pfam:PF00646	7.1	8.4	-1.3	-4.8	1.11%	4.3
4565	AT3G54870.1 | armadillo/beta-catenin repeat family protein / kinesin motor family protein, kinesin, Syncephalastrum racemosum, AJ225894 | chr3:20341784-20347695 FORWARD | Aliases: F28P10.150	3.4	4.5	-1.0	-4.8	1.11%	4.3
4571	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	4.4	-0.8	-4.8	1.11%	4.3
4574	AT3G09830.2 | protein kinase, putative, similar to protein kinase (Lophopyrum elongatum) gi:13022177:gb:AAK11674 | chr3:3016545-3018988 FORWARD | Aliases: F8A24.12	4.8	6.1	-1.3	-4.8	1.12%	4.4
4575	AT3G55700.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, glucuronosyl transferase homolog, Lycopersicon esculentum, PIR:S39507 ;contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:20682094-20684351 FORWARD | Aliases: F1I16.110	2.8	3.7	-0.9	-4.8	1.12%	4.3
4576	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	4.9	-1.3	-4.8	1.12%	4.5
4577	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	5.8	7.1	-1.3	-4.8	1.12%	4.3
4578	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	5.4	7.4	-2.0	-4.8	1.12%	4.4

Rank	Description	Sync	Root	M	t	adj.q	B
4579	AT5G27450.2 | mevalonate kinase (MK), identical to mevalonate kinase (Arabidopsis thaliana) SWISS-PROT:P46086 | chr5:9690745-9693227 FORWARD | Aliases: F21A20.160, F21A20_160	6.9	8.3	-1.4	-4.8	1.12%	4.5
4581	AT4G11670.1 | expressed protein, contains Pfam PF05664: Protein of unknown function (DUF810) | chr4:7044395-7053085 REVERSE | Aliases: T5C23.100, T5C23_100	5.1	6.4	-1.3	-4.8	1.12%	4.4
4582	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	4.0	-1.1	-4.8	1.12%	4.4
4585	AT4G12480.1 | Symbol: PEARLI 1 1 | protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, identical 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 | chr4:7406102-7406934 REVERSE | Aliases: T1P17.70, T1P17_70	2.3	3.4	-1.1	-4.8	1.13%	4.4
4587	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	6.0	7.4	-1.4	-4.8	1.13%	4.3
4591	AT1G42470.1 | patched family protein, similar to SP:O15118 Niemann-Pick C1 protein precursor from Homo sapiens (GB:AAB63982) (GI:2276463); contains Pfam profile PF02460 Patched family | chr1:15929427-15937648 FORWARD | Aliases: F7F22.1, F7F22_1	7.3	8.7	-1.4	-4.8	1.13%	4.3
4592	AT3G06440.1 | galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase | chr3:1972628-1975760 REVERSE | Aliases: F24P17.7, F24P17_7	4.4	5.2	-0.8	-4.8	1.13%	4.3
4594	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	7.0	7.8	-0.8	-4.8	1.13%	4.2
4601	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	6.8	8.0	-1.2	-4.8	1.14%	4.4
4604	AT2G44370.1 | DC1 domain-containing protein, highly similar to GP:2435515:AF024504 | chr2:18329070-18330197 REVERSE | Aliases: F4I1.18	2.7	4.1	-1.4	-4.8	1.14%	4.4
4606	AT2G44260.2 | expressed protein | chr2:18302914-18304943 FORWARD | Aliases: F4I1.7	3.0	3.9	-0.9	-4.8	1.14%	4.4
4607	AT2G07360.1 | SH3 domain-containing protein, contains Pfam profile PF00018: SH3 domain	4.4	5.0	-0.6	-4.8	1.14%	4.1
4609	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	5.4	-1.2	-4.8	1.14%	4.4
4610	AT5G23340.1 | expressed protein | chr5:7856195-7859280 FORWARD | Aliases: MKD15.20, MKD15_20	3.7	5.5	-1.8	-4.8	1.15%	4.4
4612	AT1G06620.1 | 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 | chr1:2025600-2027270 FORWARD | Aliases: F12K11.24, F12K11_24	2.6	3.5	-0.9	-4.8	1.15%	4.4
4614	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	8.9	10.1	-1.2	-4.8	1.15%	4.2
4615	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	4.9	6.7	-1.9	-4.8	1.15%	4.4
4616	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	7.0	-1.2	-4.8	1.15%	4.4
4618	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	4.4	-1.3	-4.8	1.15%	4.4
4619	AT3G11820.2 | Symbol: SYP121 |	6.0	7.6	-1.6	-4.8	1.15%	4.4

Rank	Description	Sync	Root	M	t	adj.q	B
4623	AT1G21210.1 | Symbol: WAK4 | wall-associated kinase 4	2.8	3.4	-0.6	-4.8	1.16%	4.1
4624	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	9.3	11.8	-2.4	-4.8	1.16%	4.4
4626	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	7.4	8.5	-1.1	-4.8	1.16%	4.3
4630	AT5G24890.1 | expressed protein, weak similarity to MTD1 (Medicago truncatula) GI:9294810 | chr5:8558207-8559409 REVERSE | Aliases: F6A4.100, F6A4_100	5.5	7.9	-2.4	-4.8	1.16%	4.4
4631	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 potasium 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	4.2	5.0	-0.8	-4.8	1.16%	4.2
4632	AT3G54010.2 | Symbol: PAS1 | peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative / pasticcino 1-D (PAS1-D), nearly identical to pasticcino 1-D (Arabidopsis thaliana) GI:3080740 | chr3:20011867-20016161 FORWARD | Aliases: F5K20.310, PASTICCINO 1	9.1	10.2	-1.1	-4.8	1.16%	4.2
4634	AT4G23880.1 | expressed protein | chr4:12415729-12416460 REVERSE | Aliases: T32A16.50, T32A16_50	3.5	4.5	-1.0	-4.8	1.17%	4.4
4636	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	5.9	8.3	-2.4	-4.8	1.17%	4.4
4638	AT1G70100.3 | expressed protein | chr1:26406746-26409751 FORWARD | Aliases: F20P5.17, F20P5_17	2.7	3.0	-0.3	-4.8	1.17%	3.6
4639	AT5G42870.1 | lipin family protein, contains Pfam profile: PF04571 lipin, N-terminal conserved region | chr5:17202691-17206909 REVERSE | Aliases: MBD2.6, MBD2_6	3.2	4.9	-1.7	-4.8	1.17%	4.3
4642	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	7.4	-0.8	-4.8	1.17%	4.0
4644	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	9.3	10.5	-1.2	-4.8	1.17%	4.2
4647	AT1G04400.2 | Symbol: CRY2 | cryptochrome 2 apoprotein (CRY2) / blue light photoreceptor (PHH1), 97% identical to photolysase (PHH1)	6.8	8.3	-1.5	-4.8	1.18%	4.3
4652	AT4G35580.1 | no apical meristem (NAM) family protein, similar to TIP (Arabidopsis thaliana) GI:9408601; contains Pfam profile PF02365: No apical meristem (NAM) protein | chr4:16888410-16890772 REVERSE | Aliases: F8D20.90, F8D20_90	5.1	6.3	-1.2	-4.8	1.18%	4.4
4654	AT3G53180.1 | glutamine synthetase, putative, similar to glutamine synthetase (glutamate--ammonia ligase) (Bacillus subtilis) SWISS-PROT:P12425 | chr3:19717872-19722393 FORWARD | Aliases: T4D2.110	5.6	6.9	-1.2	-4.8	1.18%	4.3
4659	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	5.4	6.3	-1.0	-4.8	1.18%	4.3
4660	AT4G20210.1 | terpene synthase/cyclase family protein, (+)-delta-cadinene synthase isozyme XC14, Gossypiumarboreum, PIR2:S68366 | chr4:10913623-10918292 REVERSE | Aliases: F1C12.130, F1C12_130	3.5	4.6	-1.1	-4.8	1.18%	4.3
4661	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	3.7	5.1	-1.4	-4.8	1.18%	4.4

Rank	Description	Sync	Root	M	t	adj.q	B
4663	AT5G40590.1 | DC1 domain-containing protein, predicted protein, Arabidopsis thaliana | chr5:16268665-16269546 REVERSE | Aliases: MNF13.11, MNF13_11	2.7	5.2	-2.6	-4.8	1.18%	4.2
4664	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	4.7	5.8	-1.2	-4.8	1.18%	4.4
4665	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	5.3	6.5	-1.2	-4.8	1.18%	4.4
4667	AT4G37180.2 | myb family transcription factor, contains Pfam domain, PF00249: Myb-like DNA-binding domain | chr4:17504558-17506361 FORWARD | Aliases: AP22.100, AP22_100	3.3	4.2	-0.9	-4.8	1.18%	4.3
4672	AT4G01920.1 | DC1 domain-containing protein, similar to A. thaliana CHP-rich proteins | chr4:828890-831200 REVERSE | Aliases: T7B11.18, T7B11_18	2.9	3.7	-0.8	-4.8	1.19%	4.3
4673	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	5.9	7.2	-1.4	-4.8	1.19%	4.4
4677	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	3.1	-0.5	-4.8	1.19%	3.9
4681	AT1G21780.1 | BTB/POZ domain-containing protein. Contains similarity to gb:AJ000644 SPOP (speckle-type POZ protein) from Homo sapiens 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	4.0	5.2	-1.2	-4.8	1.19%	4.3
4683	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	5.5	7.3	-1.8	-4.8	1.19%	4.4
4684	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	2.3	3.6	-1.3	-4.8	1.19%	4.4
4686	AT3G54380.2 | SAC3/GANP family protein, contains Pfam profile: PF03399 SAC3/GANP family | chr3:20144872-20147769 REVERSE | Aliases: T14E10.7	5.6	6.4	-0.7	-4.8	1.19%	3.9
4687	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	3.1	3.9	-0.8	-4.8	1.19%	4.2
4689	AT5G04840.1 | bZIP protein | chr5:1405306-1407935 FORWARD | Aliases: MUK11.16, MUK11_16	3.9	5.0	-1.2	-4.8	1.20%	4.4
4700	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	8.6	9.5	-0.9	-4.8	1.20%	4.3
4702	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	4.2	6.7	-2.4	-4.8	1.21%	4.4
4705	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	4.6	-1.9	-4.8	1.21%	4.4
4709	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	2.2	3.0	-0.8	-4.7	1.21%	4.2
4712	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	5.8	6.7	-0.9	-4.7	1.22%	4.2

Rank	Description	Sync	Root	M	t	adj.q	B
4719	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	4.9	5.9	-1.0	-4.7	1.23%	4.3
4721	AT1G67060.1 | expressed protein | chr1:25040279-25043029 FORWARD | Aliases: F1O19.19, F1O19_19	3.4	4.7	-1.3	-4.7	1.23%	4.3
4728	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	7.3	-1.4	-4.7	1.23%	4.2
4729	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	2.6	3.3	-0.7	-4.7	1.23%	4.1
4731	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	5.8	7.1	-1.3	-4.7	1.23%	4.3
4734	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	6.4	8.4	-2.0	-4.7	1.23%	4.3
4736	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	3.3	-0.9	-4.7	1.23%	4.1
4737	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	4.6	5.9	-1.3	-4.7	1.23%	4.3
4738	AT5G20680.1 | expressed protein, predicted proteins, Arabidopsis thaliana | chr5:6998105-7001912 FORWARD | Aliases: T1M15.80, T1M15_80	5.0	5.5	-0.6	-4.7	1.23%	4.0
4740	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	8.6	9.4	-0.8	-4.7	1.23%	4.2
4742	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.	2.9	4.7	-1.8	-4.7	1.23%	4.2
4744	AT4G32290.1 | expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266 | chr4:15589680-15591170 REVERSE | Aliases: F10M6.70, F10M6_70	4.5	5.7	-1.2	-4.7	1.23%	4.3
4745	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	5.9	7.1	-1.2	-4.7	1.23%	4.3
4746	AT5G15890.1 | expressed protein | chr5:5187690-5189351 REVERSE | Aliases: F1N13.30, F1N13_30	2.6	3.6	-0.9	-4.7	1.23%	4.3
4747	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	5.3	8.0	-2.7	-4.7	1.23%	4.3
4748	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	5.3	-1.3	-4.7	1.23%	4.3
4749	AT4G04990.1 | expressed protein, contains Pfam domain PF05553: Cotton fiber expressed protein | chr4:2555088-2557044 FORWARD | Aliases: C17L7.3	3.0	4.3	-1.2	-4.7	1.23%	4.3
4751	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	3.0	6.7	-3.7	-4.7	1.23%	4.3

Rank	Description	Sync	Root	M	t	adj.q	B
4752	AT4G31910.1 | transferase family protein, low similarity to anthranilate N-hydroxycinnamoyl/benzoyltransferase Dianthus caryophyllus GI:3288180, 10-deacetylbaccatin III-10-O-acetyl transferase Taxus cuspidata GI:6746554; contains Pfam profile PF02458 transferase family | chr4:15441088-15443906 FORWARD | Aliases: F11C18.110, F11C18_110	6.6	8.6	-2.0	-4.7	1.24%	4.3
4753	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	3.7	6.6	-2.9	-4.7	1.24%	4.3
4755	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	3.9	-1.0	-4.7	1.24%	4.3
4756	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	4.7	-1.2	-4.7	1.24%	4.3
4757	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	6.3	7.2	-0.8	-4.7	1.24%	4.3
4758	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	5.4	6.5	-1.1	-4.7	1.24%	4.3
4759	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	11.5	12.2	-0.7	-4.7	1.25%	3.9
4761	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	9.2	-0.6	-4.7	1.25%	3.8
4762	AT3G17420.1 | Symbol: GPK1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	6.0	7.8	-1.8	-4.7	1.25%	4.3
4764	AT5G20110.1 | 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 | chr5:6791489-6793348 REVERSE | Aliases: F28I16.260, F28I16_260	4.2	6.8	-2.6	-4.7	1.25%	4.3
4768	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	4.7	6.8	-2.1	-4.7	1.25%	4.3
4769	AT5G12370.3 | similar to Brain secretory protein SEC10P [Homo sapiens] (GB:AAH41126.1)	5.1	5.8	-0.7	-4.7	1.25%	4.1
4770	AT3G27820.1 | monodehydroascorbate reductase, putative, similar to cytosolic monodehydroascorbate reductase GB:BAA77214 (Oryza sativa)	7.8	8.8	-1.0	-4.7	1.25%	4.1
4774	AT5G06630.1 | proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr5:2036362-2037844 REVERSE | Aliases: F15M7.16, F15M7_16	3.5	8.2	-4.7	-4.7	1.26%	4.0
4776	AT3G20860.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	3.6	6.6	-2.9	-4.7	1.26%	4.2
4778	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	6.5	7.9	-1.3	-4.7	1.26%	4.2
4779	AT1G28050.1 | zinc finger (B-box type) family protein | chr1:9775515-9777797 REVERSE | Aliases: F13K9.15, F13K9_15	4.9	5.9	-0.9	-4.7	1.26%	4.2
4780	AT4G27860.1 | integral membrane family protein, contains Pfam PF01988: Integral membrane protein | chr4:13873803-13876532 FORWARD | Aliases: T27E11.100, T27E11_100	2.5	3.3	-0.7	-4.7	1.26%	4.2
4782	AT3G56410.2 | expressed protein | chr3:20927151-20932185 REVERSE | Aliases: T5P19.60	3.5	5.1	-1.7	-4.7	1.26%	4.3
4784	AT3G01350.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr3:135031-137467 FORWARD | Aliases: T13O15.11	4.1	5.2	-1.1	-4.7	1.26%	4.3
4785	AT2G01580.1 | expressed protein, and genefinder | chr2:265043-265904 REVERSE | Aliases: F2I9.20, F2I9_20	5.0	6.8	-1.8	-4.7	1.27%	4.3

Rank	Description	Sync	Root	M	t	adj.q	B
4787	AT5G58510.1 | expressed protein, KIAA0066, Homo sapiens, EMBL:HSORFKG1O | chr5:23665379-23671778 REVERSE | Aliases: MQJ2.13, MQJ2_13	5.5	6.5	-1.1	-4.7	1.27%	4.2
4790	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	4.8	6.1	-1.3	-4.7	1.27%	4.3
4791	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	8.0	9.4	-1.5	-4.7	1.27%	4.2
4793	AT3G52060.2 | expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266 | chr3:19321511-19323264 REVERSE | Aliases: F4F15.170	4.8	6.4	-1.6	-4.7	1.27%	4.2
4796	AT5G60490.1 | Symbol: FLA12 | fasciclin-like arabinogalactan-protein (FLA12) | chr5:24342953-24343928 REVERSE | Aliases: MUF9.12, MUF9_12	3.7	4.5	-0.8	-4.7	1.27%	4.1
4800	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	2.5	3.3	-0.8	-4.7	1.28%	4.1
4801	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	5.1	6.2	-1.1	-4.7	1.28%	4.3
4802	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	13.1	13.6	-0.5	-4.7	1.28%	3.2
4803	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	3.6	5.2	-1.6	-4.7	1.28%	4.3
4804	AT1G24100.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr1:8525424-8527076 REVERSE | Aliases: F3I6.2, F3I6_2	7.2	9.2	-1.9	-4.7	1.28%	4.1
4805	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	5.9	-1.2	-4.7	1.28%	4.2
4809	AT5G16490.1 | Symbol: RIC4 | p21-rho-binding domain-containing protein, contains Pfam PF00786: P21-Rho-binding domain	3.2	5.0	-1.8	-4.7	1.28%	4.3
4810	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	3.1	4.8	-1.7	-4.7	1.29%	4.2
4812	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	7.7	-3.3	-4.7	1.29%	4.3
4813	AT4G35040.1 | bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor | chr4:16680419-16682098 FORWARD | Aliases: M4E13.100, M4E13_100	8.2	9.4	-1.2	-4.7	1.29%	4.1
4814	AT3G03210.1 | expressed protein | chr3:740777-742316 FORWARD | Aliases: T17B22.10, T17B22_10	5.9	7.2	-1.3	-4.7	1.29%	4.2
4815	AT5G01710.1 | expressed protein | chr5:263516-265613 REVERSE | Aliases: F7A7.230, F7A7_230	8.8	9.6	-0.9	-4.7	1.29%	4.0
4820	AT1G13600.1 | bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor | chr1:4650784-4651466 REVERSE | Aliases: F21F23.3	3.6	5.0	-1.3	-4.7	1.30%	4.3
4823	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	3.1	-0.8	-4.7	1.30%	4.1
4825	AT4G25835.1 | AAA-type ATPase family protein, contains Pfam profile: PF00004 ATPase family | chr4:13136116-13137739 FORWARD | Aliases: None	3.1	5.7	-2.6	-4.7	1.30%	4.3
4826	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	7.4	-0.8	-4.7	1.30%	4.1
4827	AT4G38640.1 | choline transporter-related, contains weak similarity to CD92 protein (Homo sapiens) gi:16945323:emb:CAC82175 | chr4:18059647-18062283 REVERSE | Aliases: T9A14.3	5.4	6.9	-1.5	-4.7	1.30%	4.2

Rank	Description	Sync	Root	M	t	adj.q	B
4831	AT2G25060.1 | plastocyanin-like domain-containing protein | chr2:10669331-10670177 FORWARD | Aliases: F13D4.2	3.8	5.0	-1.2	-4.7	1.30%	4.3
4832	AT5G23210.2 | Symbol: SCPL34 |	2.5	3.2	-0.7	-4.7	1.30%	4.1
4833	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	2.4	3.2	-0.7	-4.7	1.31%	4.1
4834	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	7.1	8.6	-1.5	-4.7	1.31%	4.2
4839	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	5.2	-1.2	-4.7	1.31%	4.2
4840	AT5G02020.2 | expressed protein | chr5:386079-388120 REVERSE | Aliases: T7H20.70, T7H20_70	5.5	7.0	-1.5	-4.7	1.31%	4.3
4844	AT5G66100.1 | La domain-containing protein, similar to SP:P40796 La protein homolog (La ribonucleoprotein) (La autoantigen homolog) {Drosophila melanogaster}; contains Pfam profile PF05383: La domain | chr5:26444715-26447232 FORWARD | Aliases: K2A18.18, K2A18_18	3.9	4.6	-0.6	-4.7	1.31%	4.0
4848	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	6.5	-0.9	-4.7	1.32%	4.1
4853	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	3.8	-1.1	-4.7	1.32%	4.2
4855	AT5G54790.1 | expressed protein | chr5:22272356-22272715 REVERSE | Aliases: MBG8.5, MBG8_5	2.7	3.5	-0.8	-4.7	1.32%	4.0
4856	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	4.8	-0.8	-4.7	1.33%	4.1
4860	AT1G48500.1 | expressed protein, ; expression supported by MPSS | chr1:17936665-17938101 FORWARD | Aliases: T1N15.11, T1N15_11	3.2	4.6	-1.4	-4.7	1.33%	4.2
4863	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	6.5	-1.7	-4.7	1.33%	4.2
4870	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	5.7	8.3	-2.6	-4.6	1.34%	4.2
4871	AT2G35710.3 | glycogenin glucosyltransferase (glycogenin)-related, low similarity to glycogenin-2 from Homo sapiens (SP:O15488) | chr2:15020656-15021226 REVERSE | Aliases: T20F21.27	4.0	4.6	-0.6	-4.6	1.34%	3.8
4873	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	5.2	5.9	-0.7	-4.6	1.34%	4.0
4875	AT1G43700.1 | Symbol: VIP1 | VirE2-interacting protein (VIP1), identical to VirE2-interacting protein VIP1 GB:AAF37279 GI:7258340 from (Arabidopsis thaliana)	7.5	9.0	-1.4	-4.6	1.34%	4.2
4876	AT1G63530.1 | expressed protein | chr1:23567317-23568899 FORWARD | Aliases: F2K11.11, F2K11_11	2.6	3.0	-0.4	-4.6	1.34%	3.7
4877	AT2G14095.1 | expressed protein | chr2:5939477-5940873 REVERSE | Aliases: None	3.6	5.1	-1.5	-4.6	1.34%	4.2
4882	AT5G26660.1 | Symbol: ATMYB4 |	2.6	3.5	-0.9	-4.6	1.35%	4.1
4883	AT1G68450.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr1:25665164-25665902 REVERSE | Aliases: T2E12.4	4.0	6.8	-2.7	-4.6	1.35%	4.1
4884	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	4.8	5.8	-1.0	-4.6	1.35%	4.2
4885	AT5G15730.1 | serine/threonine protein kinase, putative, similar to protein-serine/threonine kinase (Nicotiana tabacum) gi:505146:dbj:BAA06538	5.1	6.1	-0.9	-4.6	1.35%	4.1

Rank	Description	Sync	Root	M	t	adj.q	B
4886	AT1G20840.1 | transporter-related, low similarity to D-xylose proton-symporter (Lactobacillus brevis) GI:2895856; contains Pfam profile PF00083: major facilitator superfamily protein	4.3	5.1	-0.8	-4.6	1.35%	4.1
4892	AT2G26190.1 | calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif | chr2:11154717-11157588 REVERSE | Aliases: T1D16.17, T1D16_17	5.2	8.6	-3.4	-4.6	1.35%	4.2
4893	AT1G49180.1 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr1:18188322-18191197 REVERSE | Aliases: F27J15.5, F27J15_5	2.8	3.8	-0.9	-4.6	1.36%	4.2
4894	AT5G64110.1 | peroxidase, putative, similar to peroxidase ATP3a (Arabidopsis thaliana) gi:1546698:emb:CAA67340	2.3	2.8	-0.5	-4.6	1.36%	3.6
4896	AT3G47050.1 | glycosyl hydrolase family 3 protein, beta-D-glucan exohydrolase, Nicotiana tabacum, TREMBL:AB017502_1 | chr3:17339020-17341874 REVERSE | Aliases: F13I12.100	3.4	4.5	-1.1	-4.6	1.36%	4.1
4898	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	5.8	7.4	-1.6	-4.6	1.36%	4.2
4900	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}	5.7	6.9	-1.3	-4.6	1.36%	4.2
4901	AT1G75180.3 | expressed protein | chr1:28219134-28222046 REVERSE | Aliases: F22H5.9, F22H5_9	4.8	5.7	-0.9	-4.6	1.36%	3.9
4905	AT1G21390.1 | Symbol: EMB2170 | expressed protein | chr1:7489140-7490726 REVERSE | Aliases: EMB2170, EMBRYO DEFECTIVE 2170, F24J8.30, F24J8_30	4.0	5.3	-1.3	-4.6	1.37%	4.2
4906	AT1G68000.1 | Symbol: ATPIS1 |	5.2	7.6	-2.4	-4.6	1.37%	4.2
4907	AT1G64000.1 | Symbol: WRKY56 |	2.4	2.9	-0.5	-4.6	1.37%	3.5
4910	AT3G55260.1 | glycosyl hydrolase family 20 protein, similar to beta-hexosaminidase A SP:P13723 from (Dictyostelium discoideum)	7.1	8.5	-1.4	-4.6	1.37%	4.2
4913	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	4.6	5.5	-0.9	-4.6	1.37%	4.1
4914	AT3G14770.1 | nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula) | chr3:4957363-4959709 REVERSE | Aliases: T21E2.6	2.5	3.3	-0.8	-4.6	1.37%	4.1
4916	AT5G04080.1 | expressed protein | chr5:1104706-1105389 FORWARD | Aliases: F21E1.3	3.0	4.7	-1.7	-4.6	1.37%	4.2
4918	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	6.2	-2.7	-4.6	1.38%	4.1
4919	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	2.8	5.1	-2.4	-4.6	1.38%	4.2
4925	AT1G72230.1 | plastocyanin-like domain-containing protein, similar to blue copper protein SP:Q41001 from (Pisum sativum) | chr1:27191728-27192906 FORWARD | Aliases: T9N14.17, T9N14_17	5.8	8.3	-2.5	-4.6	1.38%	4.2
4926	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	6.8	8.3	-1.5	-4.6	1.39%	4.2
4929	AT2G17940.1 | expressed protein, contains Pfam PF05701: Plant protein of unknown function (DUF827) | chr2:7809907-7811029 FORWARD | Aliases: T27K22.19, T27K22_19	3.3	4.1	-0.8	-4.6	1.39%	4.0
4930	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	3.5	4.7	-1.2	-4.6	1.39%	4.0
4931	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	5.3	6.8	-1.5	-4.6	1.39%	4.2

Rank	Description	Sync	Root	M	t	adj.q	B
4932	AT5G47580.1 | expressed protein, strong similarity to unknown protein (pir::E71441) | chr5:19312072-19314644 REVERSE | Aliases: MNJ7.17, MNJ7_17	5.5	6.5	-0.9	-4.6	1.39%	4.1
4939	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	7.8	9.3	-1.5	-4.6	1.39%	4.1
4941	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)	6.0	8.0	-2.1	-4.6	1.39%	4.1
4943	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	4.6	5.6	-1.1	-4.6	1.39%	4.1
4945	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	4.6	-1.3	-4.6	1.39%	4.1
4947	AT3G51890.1 | expressed protein, protein At2g40060 - Arabidopsis thaliana, EMBL:AF002109 | chr3:19260457-19261942 REVERSE | Aliases: ATEM1.14	6.6	8.2	-1.5	-4.6	1.39%	4.2
4949	AT1G05805.1 | basic helix-loop-helix (bHLH) family protein | chr1:1744773-1747692 FORWARD | Aliases: None	4.2	5.1	-0.9	-4.6	1.39%	4.1
4954	AT1G06780.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8 | chr1:2083423-2086961 FORWARD | Aliases: F4H5.13, F4H5_13	9.2	10.9	-1.7	-4.6	1.40%	3.9
4958	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	4.0	5.4	-1.4	-4.6	1.40%	4.1
4960	AT2G01930.2 | expressed protein | chr2:427116-428682 REVERSE | Aliases: F23I14.2, F23I14_2	4.8	6.0	-1.2	-4.6	1.40%	4.0
4961	AT3G20810.3 | similar to transcription factor jumonji (jmjC) 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, jmjC (InterPro:IPR003347) | chr3:7275712-7278326 FORWARD | Aliases: MOE17.12	4.8	6.0	-1.2	-4.6	1.40%	4.2
4963	AT4G03030.1 | kelch repeat-containing F-box family protein, contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	7.3	8.7	-1.4	-4.6	1.41%	4.1
4964	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	3.8	5.7	-1.9	-4.6	1.41%	4.2
4967	AT1G59850.1 | expressed protein | chr1:22032174-22033872 REVERSE | Aliases: F23H11.17, F23H11_17	3.0	4.0	-0.9	-4.6	1.41%	4.1
4968	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	10.6	11.3	-0.7	-4.6	1.41%	3.8
4972	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	3.8	-1.1	-4.6	1.41%	4.1
4973	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	4.2	5.7	-1.5	-4.6	1.42%	4.2
4978	AT2G29660.1 | zinc finger (C2H2 type) family protein, contains zinc finger, C2H2 type, domain, PROSITE:PS00028	6.2	7.3	-1.0	-4.6	1.42%	4.0
4979	AT3G01670.1 | expressed protein | chr3:247241-250477 FORWARD | Aliases: F4P13.21, F4P13_21	3.0	4.4	-1.3	-4.6	1.42%	4.2
4980	AT1G03730.1 | expressed protein, similar to ESTs gb:AA605440 and gb:H37232 | chr1:930828-931895 REVERSE | Aliases: F21B7.33	6.0	6.9	-0.9	-4.6	1.42%	4.0
4982	AT1G08520.1 | Symbol: PDE166 |	7.1	7.9	-0.7	-4.6	1.43%	3.9
4985	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	6.5	7.9	-1.4	-4.6	1.43%	4.1
4986	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;	7.1	7.9	-0.8	-4.6	1.43%	4.1

Rank	Description	Sync	Root	M	t	adj.q	B
4987	AT5G11000.1 | expressed protein | chr5:3479030-3480426 REVERSE | Aliases: T30N20.270, T30N20_270	7.2	8.8	-1.7	-4.6	1.43%	4.0
4988	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	6.2	8.3	-2.1	-4.6	1.43%	4.1
4989	AT4G24020.1 | RWP-RK domain-containing protein, similar to nodule inception protein (Lotus japonicus) GI:6448579; contains Pfam profile: PF02042 RWP-RK domain	4.5	5.9	-1.4	-4.6	1.43%	4.1
4990	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	4.3	5.7	-1.4	-4.6	1.43%	4.1
4991	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	5.1	-1.2	-4.6	1.43%	3.9
4993	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	8.3	9.3	-1.0	-4.6	1.43%	4.0
4994	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	3.5	3.9	-0.4	-4.6	1.43%	3.6
4995	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	3.4	4.6	-1.2	-4.6	1.43%	3.9
4996	AT1G22480.1 | plastocyanin-like domain-containing protein | chr1:7934158-7935371 REVERSE | Aliases: F12K8.17, F12K8_17	2.7	3.4	-0.8	-4.6	1.43%	4.0
4997	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	6.4	-0.8	-4.6	1.43%	3.8
4999	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	4.8	6.6	-1.8	-4.6	1.44%	4.1
5001	AT5G12900.1 | expressed protein | chr5:4071922-4074622 REVERSE | Aliases: T24H18.70, T24H18_70	3.9	4.8	-0.9	-4.6	1.44%	3.9
5002	AT5G63130.1 | octicosapeptide/Phox/Bem1p (PB1) domain-containing protein, contains Pfam profile PF00564: PB1 domain | chr5:25340335-25341498 FORWARD | Aliases: MDC12.9, MDC12_9	3.4	4.7	-1.3	-4.6	1.44%	4.1
5004	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	7.6	8.9	-1.4	-4.6	1.44%	3.8
5005	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	6.9	8.2	-1.3	-4.6	1.44%	4.1
5006	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	6.4	-1.1	-4.6	1.44%	4.0
5007	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	3.5	4.6	-1.1	-4.6	1.45%	4.1
5009	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	4.6	5.7	-1.1	-4.6	1.45%	3.9
5010	AT3G13040.2 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr3:4172149-4175255 REVERSE | Aliases: MGH6.22	8.5	9.7	-1.2	-4.6	1.45%	4.0

Rank	Description	Sync	Root	M	t	adj.q	B
5015	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	5.0	6.9	-1.9	-4.6	1.45%	4.1
5020	AT3G59370.1 | expressed protein, hypothetical protein F12F1.4 - Arabidopsis thaliana, EMBL:AC002131 | chr3:21952849-21953509 REVERSE | Aliases: F25L23.230	2.3	5.5	-3.2	-4.6	1.46%	4.1
5023	AT4G38090.2 | expressed protein, contains Pfam PF01205: Uncharacterized protein family UPF0029	6.3	7.5	-1.2	-4.6	1.46%	4.1
5030	AT1G08350.1 | endomembrane protein 70 family protein, KNOLLE; similar to putative endosomal protein GB:AAD20090 GI:4406780 from (Arabidopsis thaliana)	4.7	5.4	-0.7	-4.6	1.47%	3.9
5032	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	3.3	7.0	-3.7	-4.6	1.47%	4.1
5033	AT3G10760.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr3:3369585-3371232 FORWARD | Aliases: T7M13.16	3.5	4.9	-1.4	-4.6	1.47%	4.1
5035	AT1G68580.2 | agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein, contains Pfam profile PF01426: BAH domain and PF05641: Agenet domain	4.3	5.8	-1.5	-4.6	1.47%	4.0
5039	AT4G01330.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	4.0	4.8	-0.8	-4.5	1.47%	4.0
5040	AT5G52070.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr5:21178537-21182251 FORWARD | Aliases: MSG15.17, MSG15_17	3.2	5.4	-2.2	-4.5	1.47%	4.1
5041	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	6.1	8.0	-1.9	-4.5	1.48%	4.1
5042	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	4.7	6.1	-1.4	-4.5	1.48%	4.1
5045	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	2.7	3.4	-0.7	-4.5	1.48%	3.8
5048	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	2.7	3.3	-0.6	-4.5	1.49%	3.8
5053	AT1G77770.2 | expressed protein | chr1:29251099-29252921 REVERSE | Aliases: T32E8.10, T32E8_10	6.4	7.6	-1.2	-4.5	1.49%	3.9
5054	AT1G03010.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr1:693480-696382 FORWARD | Aliases: F10O3.17, F10O3_17	2.3	2.8	-0.6	-4.5	1.49%	3.7
5055	AT3G49690.1 | myb family transcription factor, contains PFAM profile: myb DNA binding domain PF00249 | chr3:18438821-18440186 FORWARD | Aliases: T16K5.40	5.5	7.3	-1.9	-4.5	1.50%	4.1
5056	AT2G23200.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:9886356-9888988 FORWARD | Aliases: T20D16.17, T20D16_17	3.7	4.6	-0.8	-4.5	1.50%	4.0
5058	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	3.2	5.8	-2.6	-4.5	1.50%	4.1
5060	AT2G28690.1 | expressed protein | chr2:12313967-12315705 REVERSE | Aliases: T8O18.2, T8O18_2	2.9	3.9	-1.0	-4.5	1.50%	3.9
5064	AT3G61300.1 | C2 domain-containing protein, anthranilate phosphoribosyltransferase (fragment) - Pisum sativum, PIR:T06460 | chr3:22698545-22701978 FORWARD | Aliases: T20K12.200	4.3	7.1	-2.8	-4.5	1.50%	4.0

Rank	Description	Sync	Root	M	t	adj.q	B
5068	AT4G19110.2 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr4:10454540-10459309 REVERSE | Aliases: T18B16.80, T18B16_80	6.0	8.4	-2.4	-4.5	1.50%	4.1
5070	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	2.5	3.1	-0.6	-4.5	1.50%	3.8
5071	AT1G07520.1 | scarecrow transcription factor family protein, similar to GB:AAD24412 from (Arabidopsis thaliana) (Plant J. 18 (1), 111-119 (1999)); contains Pfam profile: PF03514 GRAS family transcription factor | chr1:2309561-2311802 REVERSE | Aliases: F22G5.41, F22G5_41	3.5	4.2	-0.7	-4.5	1.51%	3.7
5072	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	5.3	-1.6	-4.5	1.51%	4.0
5073	AT2G25000.1 | Symbol: WRKY60 |	3.4	4.2	-0.8	-4.5	1.51%	4.0
5075	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	8.5	10.0	-1.5	-4.5	1.51%	4.1
5076	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	5.6	7.4	-1.8	-4.5	1.51%	4.0
5079	AT1G78090.1 | Symbol: ATTPPB |	4.3	5.9	-1.6	-4.5	1.52%	4.1
5081	AT3G47740.1 | Symbol: ATATH2 |	2.2	3.2	-1.0	-4.5	1.52%	4.0
5082	AT5G11570.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr5:3715944-3718277 REVERSE | Aliases: F15N18.160, F15N18_160	2.7	3.5	-0.9	-4.5	1.52%	4.0
5085	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	5.5	-1.5	-4.5	1.52%	3.9
5086	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	4.1	5.3	-1.2	-4.5	1.52%	4.1
5087	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	3.1	-0.7	-4.5	1.52%	3.9
5088	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	4.3	5.2	-0.9	-4.5	1.52%	4.0
5090	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	6.1	7.9	-1.8	-4.5	1.52%	4.0
5091	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	5.4	6.4	-1.0	-4.5	1.53%	4.0
5095	AT2G37820.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	3.8	-1.1	-4.5	1.53%	4.0
5096	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	5.3	6.3	-1.0	-4.5	1.53%	4.0
5098	ATMG00110.1 | Symbol: CCB206 |	3.4	5.3	-1.9	-4.5	1.53%	4.0
5104	AT1G74680.1 | exostosin family protein, contains Pfam profile: PF03016 Exostosin family | chr1:28062849-28064872 FORWARD | Aliases: F25A4.34, F25A4_34	7.2	7.9	-0.7	-4.5	1.54%	3.9

Rank	Description	Sync	Root	M	t	adj.q	B
5107	AT4G14010.1 | Symbol: RALFL32 | rapid alkalinization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316 | chr4:8092832-8093377 REVERSE | Aliases: DL3045C, FCAALL.140, RALF LIKE 32	8.6	9.8	-1.1	-4.5	1.54%	3.8
5108	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	3.5	4.6	-1.1	-4.5	1.54%	4.0
5114	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	6.4	-0.7	-4.5	1.55%	3.8
5115	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	4.0	6.0	-2.1	-4.5	1.55%	4.1
5116	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	6.3	-1.5	-4.5	1.55%	4.0
5117	AT5G50140.1 | ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023 | chr5:20413082-20415423 FORWARD | Aliases: MPF21.16, MPF21_16	3.0	4.3	-1.3	-4.5	1.55%	4.0
5118	AT3G19370.1 | expressed protein | chr3:6710797-6713656 FORWARD | Aliases: MLD14.10	6.4	8.3	-2.0	-4.5	1.56%	4.0
5123	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	5.4	-1.4	-4.5	1.57%	4.0
5124	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 OSJNBb0103I08.15 [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	6.8	8.1	-1.3	-4.5	1.57%	4.0
5131	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	6.3	7.3	-1.0	-4.5	1.57%	3.9
5132	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	2.2	2.6	-0.4	-4.5	1.58%	3.5
5134	AT4G37900.1 | glycine-rich protein | chr4:17821731-17824439 REVERSE | Aliases: F20D10.20, F20D10_20	5.0	6.3	-1.3	-4.5	1.58%	4.0
5135	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	5.6	6.4	-0.8	-4.5	1.58%	3.9
5136	AT2G21120.1 | expressed protein | chr2:9058829-9061694 REVERSE | Aliases: F26H11.12, F26H11_12	5.5	6.9	-1.4	-4.5	1.58%	4.0
5137	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	6.9	8.0	-1.1	-4.5	1.58%	4.0
5138	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	4.6	-1.6	-4.5	1.58%	4.0
5141	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	3.5	4.6	-1.0	-4.5	1.58%	4.0
5142	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	8.0	9.0	-1.0	-4.5	1.58%	3.9

Rank	Description	Sync	Root	M	t	adj.q	B
5143	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	3.3	-0.8	-4.5	1.58%	3.9
5144	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	6.3	7.3	-1.0	-4.5	1.58%	3.9
5146	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	3.1	-0.7	-4.5	1.58%	3.7
5147	AT1G59590.1 | Symbol: ZCF37 | expressed protein | chr1:21891417-21892457 FORWARD | Aliases: T30E16.15, T30E16_15, ZCF37	4.0	5.7	-1.7	-4.5	1.58%	4.0
5149	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	7.9	-1.5	-4.5	1.59%	3.9
5160	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	5.0	6.9	-1.9	-4.5	1.60%	4.0
5161	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	3.6	5.3	-1.7	-4.5	1.60%	4.0
5162	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	3.1	4.3	-1.2	-4.5	1.60%	4.0
5163	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	3.9	5.9	-1.9	-4.5	1.60%	4.0
5167	AT3G49790.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr3:18479036-18480748 REVERSE | Aliases: T16K5.140	3.3	4.4	-1.1	-4.5	1.60%	3.7
5169	AT1G79600.1 | ABC1 family protein, contains Pfam domain, PF03109: ABC1 family | chr1:29954839-29957583 REVERSE | Aliases: F20B17.3, F20B17_3	6.0	7.1	-1.0	-4.5	1.60%	3.9
5170	AT3G10250.2 | expressed protein | chr3:3167956-3170908 REVERSE | Aliases: F14P13.15	3.4	5.2	-1.7	-4.5	1.60%	4.0
5172	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	5.9	7.6	-1.7	-4.5	1.61%	4.0
5174	AT3G57570.1 | expressed protein | chr3:21323475-21331276 FORWARD | Aliases: T8H10.170	3.5	4.2	-0.7	-4.5	1.61%	3.8
5176	AT1G25550.1 | myb family transcription factor, contains Pfam domain, PF00249: Myb-like DNA-binding domain | chr1:8976525-8978080 FORWARD | Aliases: F2J7.21, F2J7_21	7.0	7.9	-1.0	-4.5	1.61%	3.7
5179	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 ENDOTRANSGLUCOSYLASE/HYDROLASE 18	3.3	5.0	-1.7	-4.5	1.61%	3.9
5181	AT3G46220.1 | expressed protein | chr3:16990060-16995776 FORWARD | Aliases: F12M12.190	6.5	7.6	-1.2	-4.5	1.61%	4.0
5182	AT5G02890.1 | transferase family protein, contains Pfam profile PF02458: Transferase family | chr5:670063-671467 REVERSE | Aliases: F9G14.200, F9G14_200	3.0	4.0	-1.0	-4.5	1.61%	3.9
5184	AT5G58375.1 | expressed protein | chr5:23613500-23614186 FORWARD | Aliases: None	9.2	10.8	-1.6	-4.5	1.61%	4.0
5186	AT5G13090.1 | expressed protein, predicted proteins - Arabidopsis thaliana | chr5:4153589-4154675 REVERSE | Aliases: T19L5.50, T19L5_50	5.5	6.5	-1.0	-4.5	1.61%	3.9
5188	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	8.6	10.8	-2.2	-4.5	1.61%	4.0
5190	AT5G55500.1 | Symbol: AtXylT |	5.4	6.3	-0.9	-4.5	1.61%	3.9

Rank	Description	Sync	Root	M	t	adj.q	B
5192	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	5.9	6.6	-0.7	-4.5	1.62%	3.8
5195	AT1G19835.1 | expressed protein, contains Pfam PF05911: Plant protein of unknown function (DUF869) | chr1:6855943-6860323 REVERSE | Aliases: F14P1.24, F14P1_24	9.0	9.9	-1.0	-4.5	1.62%	3.8
5196	AT5G66650.1 | expressed protein, contains Pfam domain, PF04678: Protein of unknown function, DUF607 | chr5:26620229-26621602 REVERSE | Aliases: MSN2.3, MSN2_3	3.5	4.5	-1.1	-4.5	1.62%	4.0
5200	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	2.5	3.0	-0.6	-4.5	1.62%	3.7
5205	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	7.8	9.1	-1.3	-4.5	1.63%	3.8
5206	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 (GI:6492344) (Xenopus laevis) | chr2:268817-272609 FORWARD | Aliases: F2I9.22, F2I9_22	4.7	6.5	-1.8	-4.5	1.63%	4.0
5207	AT2G23300.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:9921688-9924210 FORWARD | Aliases: T20D16.7, T20D16_7	3.4	5.0	-1.6	-4.4	1.63%	4.0
5209	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	2.7	3.5	-0.7	-4.4	1.63%	3.8
5211	AT3G53260.1 | Symbol: PAL2 | phenylalanine ammonia-lyase 2 (PAL2), nearly identical to SP:P45724 | chr3:19755029-19757758 REVERSE | Aliases: T4D2.190	8.1	10.4	-2.3	-4.4	1.64%	3.8
5214	AT2G30250.1 | Symbol: WRKY25 |	3.3	4.5	-1.3	-4.4	1.64%	4.0
5216	AT3G16690.1 | nodulin MtN3 family protein, contains Pfam PF03083 MtN3/saliva family | chr3:5684386-5686496 REVERSE | Aliases: MGL6.16	3.3	4.7	-1.4	-4.4	1.64%	3.9
5217	AT3G06670.1 | expressed protein | chr3:2105465-2113421 REVERSE | Aliases: T8E24.10	3.7	4.6	-0.9	-4.4	1.65%	3.9
5220	AT3G17340.1 | importin-related, contains Pfam profile PF03810: Importin-beta N-terminal domain	2.8	3.5	-0.7	-4.4	1.65%	3.8
5222	AT1G60610.2 | expressed protein | chr1:22331577-22333941 REVERSE | Aliases: F8A5.13, F8A5_13	6.3	7.2	-0.9	-4.4	1.65%	3.7
5228	AT1G17060.1 | Symbol: CYP72C1 | cytochrome P450, putative, 41% identical to Cytochrome P450 (Catharanthus roseus) (gi:404690)	3.0	3.6	-0.6	-4.4	1.65%	3.7
5229	AT4G22640.1 | expressed protein, various predicted proteins, Arabidopsis thaliana | chr4:11911611-11912019 FORWARD | Aliases: T12H17.30	3.9	5.8	-1.9	-4.4	1.65%	3.9
5230	AT5G57160.1 | Symbol: ATLIG4 |	6.1	7.3	-1.2	-4.4	1.65%	3.8
5235	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	4.0	-1.1	-4.4	1.66%	3.9
5236	AT5G47230.1 | Symbol: ATERF 5/ATERF5 |	3.8	5.2	-1.5	-4.4	1.67%	4.0
5237	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	7.5	-1.3	-4.4	1.67%	3.9
5239	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	4.9	5.6	-0.7	-4.4	1.67%	3.7
5247	AT1G13920.1 | remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region | chr1:4758185-4759751 FORWARD | Aliases: F16A14.13	2.8	3.8	-0.9	-4.4	1.67%	3.9
5250	AT5G56220.1 | expressed protein | chr5:22772097-22775146 FORWARD | Aliases: K24C1.3, K24C1_3	5.0	5.6	-0.6	-4.4	1.67%	3.7

Rank	Description	Sync	Root	M	t	adj.q	B
5252	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	5.9	-0.8	-4.4	1.68%	3.5
5253	AT2G30340.1 | LOB domain protein 13 / lateral organ boundaries domain protein 13 (LBD13), identical to LOB DOMAIN 13 (Arabidopsis thaliana) GI:17227158 SP:Q9AT61 | chr2:12938321-12939659 REVERSE | Aliases: T9D9.15, T9D9_15	2.2	3.2	-1.1	-4.4	1.68%	3.8
5261	AT3G16230.1 | expressed protein, similar to ASC-1 complex subunit P50 (GI:12061189) (Homo sapiens) | chr3:5500562-5503549 FORWARD | Aliases: MYA6.4	7.5	8.4	-0.8	-4.4	1.68%	3.9
5268	AT1G32640.1 | Symbol: ATMYC2 |	6.1	7.4	-1.3	-4.4	1.69%	3.9
5271	AT1G27430.1 | GYF domain-containing protein, contains Pfam profile: PF02213 GYF domain	4.7	5.8	-1.0	-4.4	1.69%	3.8
5276	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	3.6	5.0	-1.5	-4.4	1.70%	3.9
5277	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	5.9	7.2	-1.3	-4.4	1.70%	3.9
5282	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)	2.8	3.8	-1.0	-4.4	1.72%	3.9
5283	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	5.6	-0.9	-4.4	1.72%	3.8
5284	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	3.2	-0.8	-4.4	1.72%	3.7
5285	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	5.5	6.3	-0.8	-4.4	1.72%	3.7
5288	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	3.8	-0.6	-4.4	1.72%	3.5
5294	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	3.8	5.3	-1.5	-4.4	1.72%	3.9
5295	AT1G19180.2 | expressed protein | chr1:6622105-6623611 FORWARD | Aliases: T29M8.5, T29M8_5	5.8	7.5	-1.8	-4.4	1.72%	3.9
5298	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	6.0	-0.8	-4.4	1.73%	3.8
5299	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	6.6	7.7	-1.0	-4.4	1.73%	3.8
5301	AT5G25240.1 | expressed protein | chr5:8746608-8747200 REVERSE | Aliases: F21J6.107, F21J6_107	4.9	6.5	-1.6	-4.4	1.73%	3.8
5302	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	2.8	4.1	-1.3	-4.4	1.73%	3.9
5303	AT1G08100.1 | Symbol: ATNRT2.2 | high-affinity nitrate transporter (ACH2), identical to high-affinity nitrate transporter ACH2 (Arabidopsis thaliana) GI:3608364 | chr1:2527167-2529117 REVERSE | Aliases: ACH2, NITRATE TRANSPORTER 2, NRT2;2AT, T6D22.18, T6D22_18	3.2	4.3	-1.1	-4.4	1.73%	3.9
5307	AT1G55330.1 | Symbol: AGP21 | arabinogalactan-protein (AGP21)	9.2	10.7	-1.6	-4.4	1.73%	3.5
5314	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	6.6	7.6	-1.0	-4.4	1.73%	3.8

Rank	Description	Sync	Root	M	t	adj.q	B
5315	AT5G43190.1 | F-box family protein (FBX6), contains similarity to unusual floral organs (UFO) GI:4376159 from (Arabidopsis thaliana) | chr5:17357367-17358740 REVERSE | Aliases: MNL12.1, MNL12_1	5.5	6.1	-0.6	-4.4	1.74%	3.6
5319	AT5G49460.1 | Symbol: ACLB 2 |	5.8	7.7	-1.9	-4.4	1.74%	3.8
5320	AT1G75400.1 | expressed protein | chr1:28300580-28303347 FORWARD | Aliases: F1B16.7, F1B16_7	3.6	4.8	-1.3	-4.4	1.74%	3.9
5321	AT5G58540.3 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr5:23680362-23682905 FORWARD | Aliases: MQJ2.16, MQJ2_16	3.1	3.8	-0.8	-4.4	1.74%	3.8
5324	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	4.9	6.8	-1.9	-4.4	1.74%	3.9
5330	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	7.7	-1.1	-4.4	1.75%	3.9
5331	AT3G15890.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:5374254-5376281 FORWARD | Aliases: MVC8.1	4.7	5.8	-1.1	-4.4	1.75%	3.7
5332	AT1G80450.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr1:30248847-30249580 REVERSE | Aliases: T21F11.22, T21F11_22	2.0	2.4	-0.5	-4.4	1.76%	3.0
5336	AT3G30720.1 | expressed protein | chr3:12351626-12352205 FORWARD | Aliases: F21A17.18	3.4	4.9	-1.5	-4.4	1.76%	3.9
5337	AT2G18440.1 | Symbol: GUT15 | expressed protein | chr2:8002811-8004000 REVERSE | Aliases: GENE WITH UNSTABLE TRANSCRIPT 15, GUT15, T30D6.5, T30D6_5	8.1	9.8	-1.7	-4.4	1.76%	3.8
5338	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	2.6	3.5	-0.9	-4.4	1.76%	3.8
5339	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	4.3	5.6	-1.4	-4.4	1.76%	3.9
5341	AT5G60410.4 | Symbol: ATSIZ1 |	4.5	5.1	-0.6	-4.4	1.76%	3.6
5342	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	3.5	-0.7	-4.4	1.76%	3.7
5343	AT4G01650.2 | expressed protein | chr4:704407-706965 REVERSE | Aliases: T15B16.3, T15B16_3	3.5	4.4	-0.9	-4.4	1.76%	3.8
5346	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	5.8	7.2	-1.4	-4.4	1.77%	3.8
5348	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	6.0	7.0	-1.0	-4.4	1.77%	3.7
5350	AT3G62650.2 | expressed protein, putative mitochondrial carrier protein At2g47490 - Arabidopsis thaliana, EMBL:AC002535 | chr3:23179037-23180163 FORWARD | Aliases: F26K9.80	8.1	9.2	-1.1	-4.4	1.77%	3.8
5351	AT2G43220.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	4.3	5.2	-0.9	-4.4	1.77%	3.6
5352	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	5.3	6.5	-1.2	-4.4	1.77%	3.9
5353	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)	4.9	6.5	-1.6	-4.4	1.77%	3.9
5357	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	4.0	-0.8	-4.4	1.78%	3.6
5359	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	9.1	10.4	-1.3	-4.4	1.78%	3.8

Rank	Description	Sync	Root	M	t	adj.q	B
5361	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	3.1	4.1	-1.0	-4.4	1.78%	3.8
5362	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	5.4	-1.0	-4.4	1.78%	3.7
5363	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	4.1	-1.0	-4.4	1.79%	3.8
5364	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	3.4	-0.7	-4.4	1.79%	3.5
5369	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	4.0	4.7	-0.7	-4.4	1.79%	3.7
5371	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	6.0	6.8	-0.8	-4.4	1.79%	3.7
5372	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	12.3	12.9	-0.5	-4.4	1.79%	3.0
5373	AT4G35460.1 | Symbol: NTR1 | thioredoxin reductase 1 / NADPH-dependent thioredoxin reductase 1 (NTR1), identical to SP:Q39243	12.3	12.9	-0.5	-4.4	1.79%	3.0
5374	AT2G32800.1 | protein kinase family protein, contains dual protein kinase domains, Pfam:PF00069 | chr2:13923529-13926629 FORWARD | Aliases: F24L7.6, F24L7_6	4.7	6.2	-1.4	-4.4	1.79%	3.8
5375	AT2G29130.1 | laccase, putative / diphenol oxidase, putative, similar to laccase (Liriodendron tulipifera)(GI:1621467)	2.9	3.5	-0.6	-4.4	1.79%	3.5
5378	AT5G64880.1 | expressed protein | chr5:25949516-25951373 FORWARD | Aliases: MXK3.11, MXK3_11	4.7	5.8	-1.1	-4.4	1.79%	3.8
5380	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	2.6	3.4	-0.8	-4.4	1.80%	3.7
5385	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	4.4	5.4	-1.0	-4.4	1.80%	3.8
5389	AT5G24313.1 | expressed protein | chr5:8276788-8277405 REVERSE | Aliases: None	2.7	3.7	-1.0	-4.4	1.80%	3.7
5390	AT1G73630.1 | calcium-binding protein, putative, similar to calcium binding protein GI:14589311 from (Sesbania rostrata); contains Pfam profile: PF00036 EF hand (4 copies) | chr1:27688397-27689114 FORWARD | Aliases: F25P22.4, F25P22_4	2.6	3.3	-0.7	-4.3	1.81%	3.7
5392	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	4.2	-0.7	-4.3	1.81%	3.6
5393	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	8.5	10.5	-2.1	-4.3	1.81%	3.7
5394	AT3G12500.1 | Symbol: ATHCHIB | basic endochitinase, identical to basic endochitinase precursor SP:P19171 from (Arabidopsis thaliana)	5.7	8.4	-2.7	-4.3	1.81%	3.8
5397	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	4.1	5.1	-1.0	-4.3	1.81%	3.8
5398	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	5.6	-2.0	-4.3	1.81%	3.8

Rank	Description	Sync	Root	M	t	adj.q	B
5399	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 ENDOTRANSGLUCOSYLASE/HYDROLASE 17	2.6	3.9	-1.2	-4.3	1.81%	3.9
5400	AT2G20780.1 | mannitol transporter, putative, similar to mannitol transporter (Apium graveolens var. dulce) GI:12004316; contains Pfam profile PF00083: major facilitator superfamily protein	5.1	5.8	-0.7	-4.3	1.81%	3.7
5401	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	5.1	-0.9	-4.3	1.81%	3.7
5402	AT5G47020.1 | glycine-rich protein, strong similarity to unknown protein (emb:CAB87688.1) | chr5:19099232-19107244 FORWARD | Aliases: MQD22.16, MQD22_16	8.0	9.1	-1.0	-4.3	1.81%	3.6
5403	AT3G13782.1 | nucleosome assembly protein (NAP) family protein, similar to nucleosome assembly protein 1 (Glycine max) GI:1161252; contains Pfam profile PF00956: Nucleosome assembly protein (NAP) | chr3:4526667-4528405 FORWARD | Aliases: MMM17.24	3.4	5.9	-2.4	-4.3	1.81%	3.9
5404	AT1G06800.2 | lipase class 3 family protein, similar to DEFECTIVE IN ANTHER DEHISCENCE1 (Arabidopsis thaliana) GI:16215706; contains Pfam profile PF01764: Lipase | chr1:2090040-2091685 REVERSE | Aliases: F4H5.11, F4H5_11	3.6	4.4	-0.8	-4.3	1.81%	3.6
5405	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	4.8	5.8	-1.0	-4.3	1.81%	3.8
5407	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	5.0	6.0	-1.0	-4.3	1.82%	3.7
5408	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	4.7	-1.0	-4.3	1.82%	3.8
5410	AT5G59960.1 | expressed protein | chr5:24159240-24162559 REVERSE | Aliases: MMN10.21, MMN10_21	5.4	6.6	-1.3	-4.3	1.82%	3.8
5411	AT1G64200.1 | Symbol: VHA E3 |	5.8	7.1	-1.2	-4.3	1.82%	3.8
5412	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	3.3	4.4	-1.1	-4.3	1.82%	3.8
5413	AT2G40260.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr2:16823896-16825551 REVERSE | Aliases: T7M7.13	3.1	3.8	-0.7	-4.3	1.82%	3.6
5414	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	4.1	-0.6	-4.3	1.82%	3.5
5421	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	4.8	5.9	-1.1	-4.3	1.83%	3.8
5424	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	4.9	-0.7	-4.3	1.83%	3.7
5426	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	5.2	6.9	-1.7	-4.3	1.83%	3.8
5427	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	2.7	3.3	-0.6	-4.3	1.83%	3.5
5433	AT1G73860.1 | kinesin motor protein-related, similar to kinesin-C GB:AAF04841 from (Strongylocentrotus purpuratus) | chr1:27774647-27780518 REVERSE | Aliases: F2P9.27, F2P9_27	3.0	3.7	-0.8	-4.3	1.84%	3.6
5435	AT3G25950.1 | expressed protein | chr3:9497593-9498348 FORWARD | Aliases: MPE11.12	4.6	5.2	-0.6	-4.3	1.84%	3.5

Rank	Description	Sync	Root	M	t	adj.q	B
5437	AT1G15640.1 | expressed protein | chr1:5379072-5380022 FORWARD | Aliases: T16N11.15, T16N11_15	3.8	4.9	-1.1	-4.3	1.84%	3.8
5439	AT2G37480.2 | expressed protein | chr2:15744961-15746926 FORWARD | Aliases: F3G5.27, F3G5_27	4.9	5.8	-1.0	-4.3	1.85%	3.6
5441	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	8.3	-3.0	-4.3	1.85%	3.8
5444	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	8.0	9.2	-1.2	-4.3	1.85%	3.8
5447	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	5.1	5.6	-0.5	-4.3	1.86%	3.5
5449	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	3.4	4.6	-1.3	-4.3	1.86%	3.8
5452	AT4G16400.1 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g13175.1) | chr4:9260587-9263019 FORWARD | Aliases: DL4230W, FCAALL.356	4.3	5.8	-1.5	-4.3	1.86%	3.8
5453	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	5.4	6.4	-1.0	-4.3	1.86%	3.7
5454	AT2G47500.1 | kinesin motor protein-related | chr2:19500065-19505226 FORWARD | Aliases: T30B22.20	3.9	4.9	-1.0	-4.3	1.86%	3.8
5456	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	6.0	7.3	-1.3	-4.3	1.86%	3.8
5459	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	4.2	-0.8	-4.3	1.87%	3.6
5462	AT4G38260.1 | expressed protein, contains Pfam PF05742: Protein of unknown function (DUF833) | chr4:17936342-17938266 REVERSE | Aliases: F22I13.30, F22I13_30	5.6	7.8	-2.2	-4.3	1.87%	3.8
5464	AT3G63300.2 | expressed protein | chr3:23395963-23398817 FORWARD | Aliases: MAA21.9	4.0	5.4	-1.4	-4.3	1.87%	3.8
5468	AT5G19000.1 | Symbol: ATBPM1 |	6.6	8.0	-1.4	-4.3	1.87%	3.8
5474	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	6.8	7.8	-1.0	-4.3	1.88%	3.8
5476	AT2G28570.1 | expressed protein | chr2:12248847-12249806 FORWARD | Aliases: T17D12.13, T17D12_13	2.7	4.8	-2.1	-4.3	1.88%	3.8
5478	AT3G25570.1 | adenosylmethionine decarboxylase family protein, contains Pfam profile: PF01536 adenosylmethionine decarboxylase	3.4	4.7	-1.4	-4.3	1.88%	3.7
5479	AT1G29520.1 | AWPM-19-like membrane family protein, contains Pfam profile: PF05512 AWPM-19-like family	2.5	3.5	-0.9	-4.3	1.88%	3.8
5480	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	3.4	4.6	-1.2	-4.3	1.89%	3.7
5481	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.	3.2	4.2	-1.0	-4.3	1.89%	3.8
5483	AT3G52830.1 | expressed protein, MobA, Pseudomonas alcaligenes, EMBL:PAU88088 | chr3:19588983-19589243 FORWARD | Aliases: F8J2.1	2.7	3.4	-0.7	-4.3	1.89%	2.9

Rank	Description	Sync	Root	M	t	adj.q	B
5484	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	3.6	6.9	-3.2	-4.3	1.89%	3.8
5487	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	4.6	-0.8	-4.3	1.90%	3.6
5489	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	4.7	6.2	-1.5	-4.3	1.90%	3.8
5493	AT3G48860.2 | expressed protein | chr3:18128471-18133015 FORWARD | Aliases: T21J18.130	6.8	8.2	-1.4	-4.3	1.90%	3.7
5499	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	5.2	5.9	-0.8	-4.3	1.91%	3.7
5501	AT1G71970.1 | expressed protein | chr1:27096690-27097689 FORWARD | Aliases: F17M19.12, F17M19_12	4.6	5.7	-1.1	-4.3	1.91%	3.8
5507	AT2G43050.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr2:17909563-17911520 FORWARD | Aliases: ATPMEPCRD, MFL8.9	3.1	4.5	-1.4	-4.3	1.93%	3.7
5508	AT3G11600.1 | expressed protein, weak similarity to B-type cyclin (GI:849074) (Nicotiana tabacum) | chr3:3667235-3667985 FORWARD | Aliases: F24K9.6	3.3	4.8	-1.6	-4.3	1.93%	3.7
5509	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	3.4	4.3	-0.9	-4.3	1.93%	3.6
5511	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	6.4	8.0	-1.6	-4.3	1.93%	3.8
5513	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	8.6	9.6	-1.0	-4.3	1.93%	3.5
5515	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	5.2	6.2	-1.0	-4.3	1.93%	3.7
5516	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	3.8	4.8	-0.9	-4.3	1.94%	3.7
5517	AT2G35736.1 | expressed protein, ; expression supported by MPSS | chr2:15030163-15030333 REVERSE | Aliases: None	5.4	6.6	-1.2	-4.3	1.94%	3.8
5519	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	9.6	11.4	-1.9	-4.3	1.95%	3.4
5522	AT2G27390.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr2:11727562-11727966 REVERSE | Aliases: F12K2.3, F12K2_3	2.4	2.9	-0.6	-4.3	1.95%	3.4
5523	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	4.8	6.1	-1.3	-4.3	1.95%	3.6
5525	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	2.7	-0.7	-4.3	1.96%	3.6
5530	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	3.3	-0.5	-4.3	1.96%	3.2
5533	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	4.9	-0.8	-4.3	1.96%	3.6

Rank	Description	Sync	Root	M	t	adj.q	B
5534	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	7.2	7.9	-0.7	-4.3	1.96%	3.6
5535	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	8.9	10.2	-1.3	-4.3	1.96%	3.5
5537	AT5G42400.1 | SET domain-containing protein (TXR7), contains Pfam profile PF00856: SET domain | chr5:16971697-16977899 REVERSE | Aliases: MDH9.9, MDH9_9	5.0	5.9	-1.0	-4.3	1.97%	3.6
5539	AT4G17130.1 | expressed protein | chr4:9624275-9627621 REVERSE | Aliases: DL4600C, FCAALL.361	4.0	6.3	-2.3	-4.3	1.97%	3.7
5540	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	7.7	8.7	-1.1	-4.3	1.97%	3.7
5542	AT3G18260.1 | reticulon family protein (RTNLB9), weak similarity to RTN2-C (Homo sapiens) GI:3435090; contains Pfam profile PF02453: Reticulon	2.8	3.6	-0.7	-4.3	1.97%	3.4
5546	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	6.7	8.4	-1.7	-4.3	1.98%	3.7
5547	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	7.9	-0.7	-4.3	1.98%	3.5
5549	AT4G17490.1 | Symbol: ATERF6 |	4.2	6.3	-2.1	-4.3	1.98%	3.8
5550	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	3.1	-0.8	-4.3	1.98%	3.5
5551	AT1G55640.1 | 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) | chr1:20797437-20798000 FORWARD | Aliases: F20N2.7	3.2	4.2	-0.9	-4.3	1.98%	3.6
5552	AT5G46410.1 | NLI interacting factor (NIF) family protein, contains Pfam profile PF03031: NLI interacting factor | chr5:18842330-18846448 FORWARD | Aliases: MPL12.21, MPL12_21	5.1	6.0	-0.9	-4.3	1.98%	3.7
5553	AT3G02640.1 | expressed protein | chr3:564891-565715 REVERSE | Aliases: F16B3.27, F16B3_27	3.7	4.4	-0.7	-4.3	1.98%	3.5
5556	AT5G20170.1 | expressed protein | chr5:6807392-6810800 REVERSE | Aliases: F5O24.60, F5O24_60	6.1	6.9	-0.8	-4.3	2.00%	3.3
5560	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	5.3	-0.9	-4.3	2.00%	3.6
5561	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	4.9	6.1	-1.1	-4.3	2.00%	3.6
5562	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	6.2	7.7	-1.5	-4.3	2.00%	3.7
5568	AT5G06270.1 | expressed protein | chr5:1912551-1913675 FORWARD | Aliases: MHF15.21, MHF15_21	3.5	4.4	-0.9	-4.2	2.01%	3.6
5572	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	5.6	-1.4	-4.2	2.01%	3.7
5574	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	4.5	6.0	-1.5	-4.2	2.01%	3.7
5577	AT2G20625.1 | expressed protein | chr2:8903235-8904299 REVERSE | Aliases: F23N11.15, F23N11_15	2.9	4.2	-1.3	-4.2	2.01%	3.7
5578	AT3G22380.1 | expressed protein | chr3:7913126-7919491 FORWARD | Aliases: None	5.9	7.1	-1.1	-4.2	2.01%	3.7
5580	AT2G48040.1 | expressed protein | chr2:19658266-19659835 REVERSE | Aliases: T9J23.19	5.8	7.1	-1.2	-4.2	2.01%	3.7

Rank	Description	Sync	Root	M	t	adj.q	B
5582	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	3.3	6.1	-2.8	-4.2	2.01%	3.7
5583	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	10.5	11.8	-1.3	-4.2	2.01%	3.5
5584	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	5.8	6.5	-0.7	-4.2	2.01%	3.6
5585	AT1G05790.1 | lipase class 3 family protein, contains Pfam profile PF01764: Lipase | chr1:1733038-1737484 FORWARD | Aliases: T20M3.5, T20M3_5	6.3	7.6	-1.3	-4.2	2.01%	3.7
5587	AT5G37580.1 | expressed protein | chr5:14944543-14946800 REVERSE | Aliases: K12B20.4, K12B20_4	5.3	6.4	-1.0	-4.2	2.02%	3.7
5589	AT1G23530.1 | expressed protein | chr1:8345824-8346637 FORWARD | Aliases: F28C11.16	3.0	3.7	-0.7	-4.2	2.02%	3.5
5590	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	10.1	-0.9	-4.2	2.02%	3.4
5591	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	4.4	5.4	-1.0	-4.2	2.02%	3.6
5592	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	5.0	5.8	-0.8	-4.2	2.02%	3.6
5594	AT2G42980.1 | aspartyl protease family protein, contains pfam profile: PF00026 eukaryotic aspartyl protease | chr2:17882082-17883665 REVERSE | Aliases: F23E6.3, F23E6_3	2.6	3.1	-0.5	-4.2	2.02%	3.1
5595	AT1G75020.2 | Symbol: LPAT4 | phospholipid/glycerol acyltransferase family protein, contains Pfam profile: PF01553 Acyltransferase | chr1:28174786-28177087 FORWARD | Aliases: F25A4.2, F25A4_2, LPAT4	6.3	8.1	-1.7	-4.2	2.02%	3.7
5600	AT1G26820.1 | Symbol: RNS3 | ribonuclease 3 (RNS3), identical to ribonuclease SP:P42815 Ribonuclease 3 precursor (EC 3.1.27.1) {Arabidopsis thaliana}	3.8	5.3	-1.6	-4.2	2.04%	3.7
5603	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-acetylesterase (Digitalis lanata) GI:3688284; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family	3.1	4.8	-1.7	-4.2	2.04%	3.7
5611	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	5.5	6.2	-0.8	-4.2	2.04%	3.6
5613	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	5.4	6.9	-1.6	-4.2	2.05%	3.7
5615	AT2G46940.1 | expressed protein | chr2:19293846-19294650 REVERSE | Aliases: F14M4.23	3.3	4.5	-1.2	-4.2	2.05%	3.7
5616	AT1G14740.1 | expressed protein | chr1:5075208-5077786 REVERSE | Aliases: F10B6.14, F10B6_14	4.6	5.7	-1.1	-4.2	2.05%	3.4
5617	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	3.4	-1.2	-4.2	2.05%	3.7
5618	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	6.9	-1.8	-4.2	2.05%	3.7

Rank	Description	Sync	Root	M	t	adj.q	B
5620	AT5G12050.1 | expressed protein | chr5:3890105-3891514 FORWARD | Aliases: F14F18.220, F14F18_220	2.3	2.7	-0.4	-4.2	2.06%	2.9
5621	AT4G28540.1 | casein kinase, putative, similar to casein kinase I (Arabidopsis thaliana) gi:1103318:emb:CAA55395; contains protein kinase domain, Pfam:PF00069	7.0	8.1	-1.1	-4.2	2.06%	3.7
5622	AT3G01680.1 | expressed protein | chr3:251988-255520 FORWARD | Aliases: F4P13.22, F4P13_22	3.4	5.9	-2.5	-4.2	2.06%	3.7
5624	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	2.6	3.3	-0.7	-4.2	2.06%	3.4
5630	AT4G18050.1 | ABC transporter family protein, contains Pfam profile: PF00005 ABC transporter; similar to multidrug-resistant protein CjMDR1 GI:14715462 from (Coptis japonica)	2.7	3.4	-0.7	-4.2	2.07%	3.4
5632	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	4.1	4.9	-0.8	-4.2	2.07%	3.6
5634	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	3.5	5.3	-1.8	-4.2	2.07%	3.7
5635	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	3.3	-0.6	-4.2	2.07%	3.4
5643	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	5.2	6.9	-1.7	-4.2	2.08%	3.6
5644	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	4.3	-0.9	-4.2	2.08%	3.4
5647	AT2G43840.2 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:18164715-18166252 FORWARD | Aliases: F18O19.5	5.7	7.0	-1.2	-4.2	2.09%	3.4
5648	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	5.0	5.8	-0.8	-4.2	2.09%	3.6
5651	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	6.0	7.1	-1.1	-4.2	2.10%	3.6
5652	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	4.2	6.2	-2.0	-4.2	2.10%	3.7
5653	AT4G14760.1 | M protein repeat-containing protein, contains Pfam profile: PF02370 M protein repeat | chr4:8475964-8481089 FORWARD | Aliases: DL3420W, FCAALL.305	6.1	7.4	-1.3	-4.2	2.10%	3.7
5656	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	3.8	4.6	-0.8	-4.2	2.10%	3.5
5661	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	4.2	-1.2	-4.2	2.10%	3.6
5662	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	8.1	-0.7	-4.2	2.11%	3.4
5664	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	6.8	7.8	-1.1	-4.2	2.11%	3.5
5669	AT3G28850.1 | glutaredoxin family protein | chr3:10849906-10851359 FORWARD | Aliases: T19N8.15	6.4	7.5	-1.1	-4.2	2.11%	3.5
5671	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	7.5	8.5	-0.9	-4.2	2.12%	3.4

Rank	Description	Sync	Root	M	t	adj.q	B
5673	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	2.8	3.4	-0.7	-4.2	2.12%	3.4
5676	AT1G76970.1 | VHS domain-containing protein / GAT domain-containing protein, weak similarity to HGF-regulated tyrosine kinase substrate (Mus musculus) GI:1089781; contains Pfam profiles PF00790: VHS domain, PF03127: GAT domain | chr1:28927560-28930298 REVERSE | Aliases: F22K20.7, F22K20_7	3.2	4.6	-1.3	-4.2	2.12%	3.6
5677	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	4.6	-0.9	-4.2	2.12%	3.5
5678	AT5G48175.1 | expressed protein, contains weak similarity to thioglucoside glucohydrolase (GI:5524767) (Arabidopsis thaliana) | chr5:19556422-19557007 FORWARD | Aliases: None	3.0	4.1	-1.1	-4.2	2.12%	3.4
5679	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	7.2	-2.3	-4.2	2.13%	3.7
5680	AT1G13990.1 | expressed protein | chr1:4794761-4796594 FORWARD | Aliases: F7A19.8, F7A19_8	6.6	7.7	-1.1	-4.2	2.13%	3.6
5684	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	3.4	4.7	-1.4	-4.2	2.13%	3.6
5686	AT4G18140.2 | similar to NLI interacting factor (NIF) family protein [Arabidopsis thaliana] (TAIR:At5g46410.1)	4.2	5.0	-0.8	-4.2	2.13%	3.6
5688	AT2G25810.1 | tonoplast intrinsic protein, putative, similar to tonoplast intrinsic protein GI:4584429 from (Nicotiana tabacum) | chr2:11019679-11021071 FORWARD | Aliases: F17H15.16, F17H15_16	2.7	3.6	-0.9	-4.2	2.13%	3.5
5690	AT5G06930.1 | expressed protein | chr5:2145140-2148040 FORWARD | Aliases: MOJ9.10, MOJ9_10	3.4	4.3	-0.9	-4.2	2.14%	3.6
5694	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	3.0	3.9	-0.9	-4.2	2.14%	3.5
5697	AT3G46600.2 | scarecrow transcription factor family protein, scarecrow-like 11 - Arabidopsis thaliana, EMBL:AF036307 | chr3:17168929-17170950 FORWARD | Aliases: F12A12.120	5.1	5.7	-0.6	-4.2	2.14%	3.4
5700	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	3.7	-0.9	-4.2	2.14%	3.6
5704	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	3.1	4.0	-0.9	-4.2	2.15%	3.6
5710	AT5G46040.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr5:18688624-18690778 REVERSE | Aliases: MCL19.9, MCL19_9	2.7	3.3	-0.7	-4.2	2.15%	3.4
5711	AT5G16210.1 | HEAT repeat-containing protein, contains Pfam profile PF02985: HEAT repeat | chr5:5290870-5297977 REVERSE | Aliases: T21H19.130, T21H19_130	5.4	6.1	-0.7	-4.2	2.15%	3.5
5713	AT1G09790.1 | phytochelatin synthetase-related, contains Pfam profile PF04833: Phytochelatin synthetase-like conserved region | chr1:3168484-3170821 REVERSE | Aliases: F21M12.17, F21M12_17	3.7	5.0	-1.3	-4.2	2.16%	3.5
5718	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	7.5	-1.3	-4.2	2.16%	3.6
5719	AT1G68795.1 | Symbol: CLE12 | CLE12, CLAVATA3/ESR-Related 12 | chr1:25844518-25845315 REVERSE | Aliases: CLAVATA3/ESR RELATED 12	2.9	4.0	-1.0	-4.2	2.16%	3.3
5720	AT3G21700.3 | expressed protein | chr3:7644482-7646362 FORWARD | Aliases: MSD21.1	3.1	3.9	-0.9	-4.2	2.16%	3.4
5721	AT5G66880.1 | serine/threonine protein kinase, putative, similar to serine-threonine protein kinase (Triticum aestivum) gi:2055374:gb:AAB58348	6.1	7.9	-1.7	-4.2	2.16%	3.6

Rank	Description	Sync	Root	M	t	adj.q	B
5722	AT1G24560.1 | expressed protein | chr1:8702372-8705835 FORWARD | Aliases: F21J9.22	8.0	9.1	-1.1	-4.2	2.16%	3.6
5724	AT5G15130.1 | Symbol: WRKY72 |	2.5	3.7	-1.2	-4.2	2.16%	3.6
5726	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	4.1	4.9	-0.9	-4.2	2.16%	3.5
5728	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	3.7	4.5	-0.8	-4.2	2.16%	3.5
5729	AT3G09290.1 | zinc finger (C2H2 type) family protein, ; contains Pfam profile: PF00096 Zinc finger, C2H2 type | chr3:2856147-2856665 FORWARD | Aliases: F3L24.16	3.2	4.9	-1.7	-4.2	2.16%	3.6
5730	AT3G03370.1 | expressed protein | chr3:797126-798480 REVERSE | Aliases: T21P5.21, T21P5_21	2.7	3.3	-0.6	-4.2	2.16%	3.3
5731	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	7.7	9.2	-1.5	-4.2	2.16%	3.5
5733	AT5G26600.2 | expressed protein, weak similarity to SP:P18549 Isopenicillin N epimerase (EC 5.-.-) {Streptomyces clavuligerus} | chr5:9377405-9379800 FORWARD | Aliases: None	7.3	8.0	-0.7	-4.2	2.17%	3.4
5740	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	9.5	-0.5	-4.2	2.18%	3.0
5741	AT1G34630.1 | expressed protein | chr1:12685178-12687710 FORWARD | Aliases: F12K21.3	5.6	7.2	-1.6	-4.2	2.18%	3.6
5744	AT1G17140.2 | tropomyosin-related, similar to Tropomyosin 1. (Baker's yeast)(SP:P17536) {Saccharomyces cerevisiae} | chr1:5856257-5858525 REVERSE | Aliases: F20D23.32	3.1	4.8	-1.8	-4.2	2.18%	3.6
5746	AT3G01810.1 | expressed protein | chr3:288580-292762 FORWARD | Aliases: F28J7.14, F28J7_14	4.9	6.5	-1.6	-4.2	2.19%	3.6
5749	AT3G01175.1 | expressed protein | chr3:59478-60852 FORWARD | Aliases: None	2.2	2.6	-0.3	-4.2	2.20%	2.7
5750	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	6.3	-0.8	-4.2	2.20%	3.4
5751	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	3.9	5.3	-1.4	-4.2	2.21%	3.6
5752	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	4.2	5.6	-1.3	-4.2	2.21%	3.6
5754	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	9.1	10.3	-1.3	-4.2	2.21%	3.3
5756	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	5.7	7.3	-1.5	-4.2	2.21%	3.6
5757	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	9.1	-0.7	-4.2	2.21%	3.5
5758	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	5.7	7.1	-1.4	-4.2	2.21%	3.6

Rank	Description	Sync	Root	M	t	adj.q	B
5767	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, HOMEOBOX PROTEIN GLABRA 2	2.9	3.7	-0.8	-4.2	2.22%	3.5
5768	AT5G24165.1 | expressed protein | chr5:8188563-8189279 FORWARD | Aliases: None	6.6	7.9	-1.3	-4.2	2.22%	3.5
5771	AT5G62550.1 | expressed protein | chr5:25122864-25125177 REVERSE | Aliases: K19B1.16, K19B1_16	4.2	6.4	-2.1	-4.1	2.22%	3.6
5773	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	2.2	2.9	-0.7	-4.1	2.22%	3.3
5774	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	3.3	5.4	-2.1	-4.1	2.23%	3.6
5775	AT3G50930.1 | AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 | chr3:18940507-18942820 FORWARD | Aliases: F18B3.210	3.3	3.7	-0.4	-4.1	2.23%	2.9
5777	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	6.8	7.8	-1.0	-4.1	2.23%	3.6
5778	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	5.6	7.7	-2.1	-4.1	2.23%	3.5
5779	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	8.3	-1.4	-4.1	2.24%	3.5
5780	AT5G45970.1 | Symbol: ARAC2 | Rac-like GTP-binding protein (ARAC2), identical to RAC-like GTP binding protein ARAC2 SP:Q38903	2.8	3.5	-0.7	-4.1	2.24%	3.4
5781	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	5.1	6.1	-1.0	-4.1	2.24%	3.3
5782	AT4G23870.1 | expressed protein, predicted proteins, Arabidopsis thaliana | chr4:12414240-12415059 FORWARD | Aliases: T32A16.40, T32A16_40	3.6	4.9	-1.3	-4.1	2.24%	3.5
5783	AT5G02640.1 | expressed protein, predicted proteins, Arabidopsis thaliana and Oryza sativa | chr5:594177-594865 REVERSE | Aliases: T22P11.230, T22P11_230	3.8	4.5	-0.6	-4.1	2.24%	3.3
5787	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	10.0	10.7	-0.8	-4.1	2.25%	3.4
5793	AT2G37940.1 | expressed protein | chr2:15883878-15886733 FORWARD | Aliases: T8P21.15, T8P21_15	5.6	6.6	-0.9	-4.1	2.26%	3.4
5794	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	6.5	7.8	-1.3	-4.1	2.26%	3.5
5796	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	3.5	4.6	-1.1	-4.1	2.26%	3.5
5797	AT1G16540.1 | Symbol: ABA3/LOS5/SIR3 |	3.3	4.2	-0.9	-4.1	2.27%	3.4
5804	AT3G51470.1 | protein phosphatase 2C, putative / PP2C, putative, protein phosphatase-2C, Mesembryanthemum crystallinum, EMBL:AF075580 | chr3:19108766-19110254 REVERSE | Aliases: F26O13.110	3.2	3.8	-0.6	-4.1	2.28%	3.3

Rank	Description	Sync	Root	M	t	adj.q	B
5806	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	4.8	6.5	-1.7	-4.1	2.29%	3.5
5808	AT3G51350.1 | aspartyl protease family protein, contains Eukaryotic and viral aspartyl proteases active site, PROSITE:PS00141 | chr3:19071301-19074489 REVERSE | Aliases: F26O13.3	2.9	4.3	-1.5	-4.1	2.29%	3.5
5810	AT5G37450.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:14870031-14874328 REVERSE | Aliases: T25O11.15, T25O11_15	2.7	3.3	-0.6	-4.1	2.30%	3.3
5813	AT1G47240.1 | Symbol: NRAMP2 |	6.6	7.7	-1.1	-4.1	2.30%	3.5
5815	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	2.9	3.6	-0.7	-4.1	2.30%	3.3
5816	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	3.7	-0.9	-4.1	2.30%	3.5
5817	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	3.7	4.3	-0.6	-4.1	2.31%	3.2
5818	AT4G02370.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr4:1042338-1043206 FORWARD | Aliases: T14P8.18, T14P8_18	8.0	9.7	-1.7	-4.1	2.31%	3.5
5823	AT5G03540.1 | exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit | chr5:889565-894155 FORWARD | Aliases: F12E4.330, F12E4_330	6.6	8.2	-1.6	-4.1	2.31%	3.6
5825	AT3G15940.1 | glycosyl transferase family 1 protein, contains Pfam profile:PF00534 Glycosyl transferases group 1 | chr3:5393519-5396765 REVERSE | Aliases: MVC8.8	6.0	7.0	-1.0	-4.1	2.32%	3.4
5826	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	3.9	5.5	-1.5	-4.1	2.32%	3.4
5832	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	6.5	7.7	-1.2	-4.1	2.32%	3.5
5834	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	4.6	5.4	-0.9	-4.1	2.32%	3.5
5836	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	5.1	-0.7	-4.1	2.33%	3.4
5838	AT2G31940.1 | expressed protein | chr2:13587677-13588189 FORWARD | Aliases: F20M17.26	2.7	3.5	-0.8	-4.1	2.33%	3.2
5839	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	5.8	6.8	-1.0	-4.1	2.34%	3.5
5840	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	3.7	-1.3	-4.1	2.34%	3.5
5845	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	7.2	8.0	-0.9	-4.1	2.35%	3.4
5850	AT1G51720.1 | glutamate dehydrogenase, putative, similar to NADP-specific glutatamate dehydrogenase (NADP-GDH) SP:P28724 (Giardia lamblia (Giardia intestinalis)) | chr1:19184440-19190200 FORWARD | Aliases: F19C24.7, F19C24_7	8.1	8.7	-0.7	-4.1	2.36%	3.2
5851	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	4.3	6.0	-1.7	-4.1	2.36%	3.5

Rank	Description	Sync	Root	M	t	adj.q	B
5853	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	2.2	3.1	-0.8	-4.1	2.36%	3.5
5854	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	4.9	5.8	-1.0	-4.1	2.36%	3.5
5856	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	5.5	6.3	-0.8	-4.1	2.36%	3.4
5857	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	4.6	5.3	-0.6	-4.1	2.37%	3.3
5861	AT3G24670.1 | pectate lyase family protein, similar to pectate lyase GP:14531296 from (Fragaria x ananassa) | chr3:9006212-9008808 REVERSE | Aliases: MSD24.10	5.3	7.2	-1.9	-4.1	2.37%	3.5
5863	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	3.8	5.9	-2.2	-4.1	2.37%	3.5
5864	AT5G39020.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:15634147-15636588 FORWARD | Aliases: MXF12.30, MXF12_30	2.7	3.9	-1.2	-4.1	2.38%	3.4
5867	AT2G20950.4 | expressed protein | chr2:9010220-9013019 FORWARD | Aliases: F26H11.29	5.7	8.0	-2.2	-4.1	2.38%	3.5
5868	AT3G10080.1 | germin-like protein, putative, similar to germin-like protein 2 (Oryza sativa) GI:2655287 | chr3:3107281-3108182 REVERSE | Aliases: T22K18.9	3.7	4.6	-1.0	-4.1	2.38%	3.5
5869	AT1G04330.1 | expressed protein, EST gb:H76414 comes from this gene | chr1:1161310-1161885 REVERSE | Aliases: F19P19.24, F19P19_24	2.5	3.1	-0.6	-4.1	2.38%	3.2
5871	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	2.6	3.2	-0.6	-4.1	2.39%	3.0
5872	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	5.5	6.2	-0.7	-4.1	2.39%	3.3
5874	AT3G62780.1 | C2 domain-containing protein, contains similarity to shock protein SRC2 (Glycine max) gi:2055230:dbj:BAA19769 ; contains Pfam profile PF00168:C2 domain | chr3:23233004-23233916 REVERSE | Aliases: F26K9.210	2.6	3.5	-0.9	-4.1	2.39%	3.1
5877	AT3G61690.1 | expressed protein | chr3:22839324-22845011 FORWARD | Aliases: F15G16.80	5.3	6.2	-0.9	-4.1	2.40%	3.4
5878	AT3G51630.1 | Symbol: WNK5 | protein kinase family protein, contains Pfam profile: PF00069 protein kinase domain | chr3:19159886-19163172 FORWARD | Aliases: T18N14.10, ZIK1	6.5	7.2	-0.7	-4.1	2.40%	3.3
5881	AT4G16447.1 | expressed protein | chr4:9278809-9279411 FORWARD | Aliases: None	3.4	6.1	-2.7	-4.1	2.40%	3.5
5882	AT2G43250.1 | expressed protein, and genefinder | chr2:17984305-17986685 FORWARD | Aliases: F14B2.19	4.1	4.9	-0.8	-4.1	2.40%	3.2
5884	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	4.8	6.2	-1.5	-4.1	2.41%	3.5
5885	AT4G10510.1 | subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa) | chr4:6495951-6499006 FORWARD | Aliases: F7L13.90, F7L13_90	2.6	3.2	-0.7	-4.1	2.41%	3.3
5887	AT1G35290.1 | thioesterase family protein, contains Pfam profile PF03061: thioesterase family protein | chr1:12947522-12948819 REVERSE | Aliases: T9I1.6, T9I1_6	2.5	3.5	-1.0	-4.1	2.42%	3.5
5888	AT1G02000.1 | Symbol: GAE2 | 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	5.7	6.7	-1.0	-4.1	2.42%	3.2

Rank	Description	Sync	Root	M	t	adj.q	B
5889	AT1G26970.1 | protein kinase, putative, similar to protein kinase (Arabidopsis thaliana) gi:2852449:dbj:BAA24695; contains protein kinase domain, Pfam:PF00069	3.3	4.2	-0.9	-4.1	2.42%	3.4
5892	AT3G53810.1 | 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 | chr3:19943970-19946212 REVERSE | Aliases: F5K20.110	4.2	5.1	-0.9	-4.1	2.42%	3.3
5894	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	5.2	6.7	-1.5	-4.1	2.42%	3.4
5898	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	2.9	3.4	-0.5	-4.1	2.43%	3.2
5900	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	3.5	-0.9	-4.1	2.43%	3.2
5901	AT5G03640.1 | protein kinase family protein, contains serine/threonine protein kinase domain, INTERPRO:IPR002290 | chr5:927914-930780 FORWARD | Aliases: F17C15.60, F17C15_60	2.7	3.3	-0.6	-4.1	2.43%	3.3
5903	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	7.8	10.4	-2.6	-4.1	2.43%	3.5
5907	AT3G44550.1 | acyl CoA reductase, putative, similar to acyl CoA reductase (Simmondsia chinensis) GI:5020215; contains Pfam profile PF03015: Male sterility protein | chr3:16149004-16151325 FORWARD | Aliases: F14L2.100	3.0	4.4	-1.3	-4.1	2.44%	3.4
5911	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	6.6	7.9	-1.2	-4.1	2.44%	3.4
5914	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	7.2	-1.0	-4.1	2.44%	3.3
5915	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	6.5	7.9	-1.3	-4.1	2.45%	3.4
5916	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	3.3	4.1	-0.8	-4.1	2.45%	3.4
5918	AT3G53670.1 | expressed protein | chr3:19901399-19903380 FORWARD | Aliases: AT3G53660, F4P12.370	4.9	5.5	-0.6	-4.1	2.45%	3.1
5919	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	3.5	-0.6	-4.1	2.45%	3.2
5921	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	8.9	10.4	-1.5	-4.1	2.45%	3.4
5925	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	3.8	4.8	-1.0	-4.1	2.46%	3.4
5927	AT5G27320.1 | expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873 | chr5:9629095-9631213 FORWARD | Aliases: F21A20.30, F21A20_30	4.2	5.2	-1.0	-4.1	2.46%	3.3
5928	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	6.9	8.6	-1.7	-4.1	2.46%	3.5
5930	AT5G41000.1 | oligopeptide transporter OPT family protein, contains Pfam profile PF03169: OPT oligopeptide transporter protein	4.0	5.1	-1.1	-4.1	2.46%	3.4
5931	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	5.7	-2.6	-4.1	2.46%	3.4

Rank	Description	Sync	Root	M	t	adj.q	B
5934	AT1G15800.1 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g80610.1) | chr1:5441077-5443653 REVERSE | Aliases: F7H2.14, F7H2_14	4.8	6.4	-1.6	-4.1	2.46%	3.5
5936	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	5.6	6.3	-0.7	-4.1	2.46%	3.2
5940	AT3G10340.1 | phenylalanine ammonia-lyase, putative, similar to phenylalanine ammonia-lyase GB:S48726 (Petroselinum crispum) | chr3:3204018-3208027 FORWARD | Aliases: F14P13.6	4.8	6.2	-1.4	-4.1	2.47%	3.5
5942	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	3.7	4.6	-0.9	-4.1	2.47%	3.4
5949	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	4.4	5.7	-1.4	-4.0	2.49%	3.4
5950	AT1G22335.1 | expressed protein, ; expression supported by MPSS | chr1:7888300-7889230 FORWARD | Aliases: None	2.7	3.6	-0.9	-4.0	2.49%	3.4
5951	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	7.0	7.8	-0.8	-4.0	2.49%	3.3
5954	AT1G29230.1 | Symbol: CIPK18 |	3.9	4.9	-1.0	-4.0	2.49%	3.4
5956	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	2.9	-0.4	-4.0	2.50%	2.8
5958	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	2.9	3.7	-0.8	-4.0	2.50%	3.3
5963	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	2.7	-0.3	-4.0	2.51%	2.6
5964	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	3.9	-0.7	-4.0	2.52%	3.3
5966	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	2.9	4.2	-1.4	-4.0	2.52%	3.4
5969	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	3.4	-0.8	-4.0	2.53%	3.3
5971	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	3.9	5.2	-1.3	-4.0	2.53%	3.3
5973	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	4.7	5.8	-1.1	-4.0	2.53%	3.4
5974	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	4.2	5.2	-0.9	-4.0	2.53%	3.4
5975	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	2.8	3.8	-1.0	-4.0	2.53%	3.3
5978	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	9.8	10.6	-0.8	-4.0	2.53%	3.2

Rank	Description	Sync	Root	M	t	adj.q	B
5979	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	5.8	7.5	-1.8	-4.0	2.53%	3.5
5980	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	8.5	-1.5	-4.0	2.53%	3.4
5983	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	5.2	-0.8	-4.0	2.54%	3.3
5989	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	3.3	-0.4	-4.0	2.55%	2.7
5992	AT4G12690.1 | expressed protein | chr4:7480804-7481867 FORWARD | Aliases: T20K18.40, T20K18_40	3.5	4.2	-0.7	-4.0	2.55%	3.2
5993	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	4.0	5.0	-1.0	-4.0	2.55%	3.2
5994	AT1G36640.1 | expressed protein | chr1:13854388-13854899 REVERSE | Aliases: T15P17.13, T15P17_13	2.6	5.5	-2.9	-4.0	2.55%	3.5
5997	AT2G22980.2 | Symbol: SCPL13 |	2.9	3.6	-0.7	-4.0	2.56%	2.9
5999	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	4.4	-1.5	-4.0	2.57%	3.4
6000	AT5G35960.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr5:14125754-14127766 REVERSE | Aliases: MEE13.6, MEE13_6	3.0	3.6	-0.6	-4.0	2.57%	2.9
6005	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	7.3	-0.8	-4.0	2.57%	3.3
6013	AT3G49840.1 | proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965 | chr3:18495527-18499283 FORWARD | Aliases: T16K5.190	3.1	3.6	-0.5	-4.0	2.58%	2.9
6015	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	5.3	6.6	-1.3	-4.0	2.58%	3.3
6016	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	3.9	-0.7	-4.0	2.58%	3.1
6021	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	4.8	6.3	-1.5	-4.0	2.59%	3.3
6022	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	5.1	6.1	-1.1	-4.0	2.59%	3.3
6024	AT5G65500.1 | protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain | chr5:26198319-26201223 REVERSE | Aliases: K19O4.3, K19O4_3	3.3	3.8	-0.5	-4.0	2.59%	2.8
6025	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	4.2	5.1	-0.9	-4.0	2.59%	3.4
6027	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	6.9	-0.7	-4.0	2.60%	3.1
6028	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	3.1	4.0	-0.8	-4.0	2.60%	2.9

Rank	Description	Sync	Root	M	t	adj.q	B
6033	AT3G54580.1 | proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr3:20211666-20214760 REVERSE | Aliases: T14E10.150	3.0	4.7	-1.7	-4.0	2.61%	3.3
6034	AT2G18170.1 | Symbol: ATMPK7 |	2.7	4.0	-1.3	-4.0	2.61%	3.2
6036	AT5G40010.1 | AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 | chr5:16037446-16038990 REVERSE | Aliases: MYH19.21, MYH19_21	3.1	4.3	-1.2	-4.0	2.61%	3.3
6038	AT1G33055.1 | expressed protein | chr1:11972220-11972570 REVERSE | Aliases: None	5.4	8.5	-3.1	-4.0	2.62%	3.4
6039	AT1G20100.1 | expressed protein | chr1:6969098-6970947 REVERSE | Aliases: T20H2.11, T20H2_11	7.5	9.4	-1.8	-4.0	2.62%	3.4
6040	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	4.1	5.7	-1.6	-4.0	2.62%	3.4
6044	AT5G05860.1 | Symbol: UGT76C2 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:1765508-1767456 FORWARD | Aliases: MJJ3.28, MJJ3_28	5.4	6.6	-1.2	-4.0	2.63%	3.4
6047	AT5G57630.1 | Symbol: CIPK21 |	4.3	5.7	-1.4	-4.0	2.64%	3.4
6049	AT1G14550.1 | anionic peroxidase, putative, similar to anionic peroxidase GI:170202 from (Nicotiana sylvestris) | chr1:4979023-4980319 FORWARD | Aliases: F14L17.33, F14L17_33	2.7	3.6	-0.8	-4.0	2.64%	3.3
6050	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	6.7	7.9	-1.2	-4.0	2.64%	3.4
6053	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	4.5	-0.9	-4.0	2.65%	3.3
6056	AT1G75810.1 | expressed protein | chr1:28465326-28466007 FORWARD | Aliases: T4O12.4, T4O12_4	6.0	7.1	-1.1	-4.0	2.65%	3.3
6057	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	4.7	5.4	-0.7	-4.0	2.65%	3.1
6058	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	5.1	6.4	-1.3	-4.0	2.65%	3.4
6060	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	2.5	3.3	-0.8	-4.0	2.65%	3.1
6061	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	4.2	-1.0	-4.0	2.66%	3.0
6062	AT1G34670.1 | myb family transcription factor, similar to myb-related protein mixta GI:485867 from (Antirrhinum majus)	2.8	3.9	-1.1	-4.0	2.66%	3.3
6065	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	7.9	8.9	-1.1	-4.0	2.66%	3.4
6066	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	7.3	8.2	-0.9	-4.0	2.66%	3.2
6067	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	5.9	-2.5	-4.0	2.66%	3.4
6068	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	4.7	5.6	-0.9	-4.0	2.66%	3.2
6069	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	5.3	6.1	-0.8	-4.0	2.66%	3.0

Rank	Description	Sync	Root	M	t	adj.q	B
6070	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	4.3	-1.4	-4.0	2.66%	3.3
6071	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	4.3	-1.4	-4.0	2.66%	3.3
6075	AT4G35540.1 | expressed protein, transcription factor IIIB chain BRF1, Saccharomycescerevisiae, PIR2:A44072 | chr4:16873840-16875603 FORWARD | Aliases: F8D20.50, F8D20_50	5.7	7.0	-1.3	-4.0	2.68%	3.3
6076	AT3G01560.1 | proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965 | chr3:219589-221886 FORWARD | Aliases: F4P13.11, F4P13_11	5.2	6.0	-0.8	-4.0	2.68%	3.3
6079	AT1G15890.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.3	4.5	-1.2	-4.0	2.68%	3.2
6080	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	6.4	8.0	-1.6	-4.0	2.69%	3.4
6081	AT2G26240.1 | expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136) | chr2:11174335-11175535 REVERSE | Aliases: T1D16.12, T1D16_12	9.2	9.9	-0.7	-4.0	2.69%	3.2
6084	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	3.2	3.7	-0.4	-4.0	2.69%	2.7
6089	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	5.4	7.3	-1.9	-4.0	2.69%	3.3
6091	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	2.9	3.7	-0.8	-4.0	2.70%	3.3
6092	AT3G03870.2 | expressed protein, predicted using genefinder | chr3:995224-997417 FORWARD | Aliases: F20H23.8, F20H23_8	4.9	5.7	-0.8	-4.0	2.70%	3.3
6094	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	2.9	3.8	-0.9	-4.0	2.70%	3.2
6095	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	3.2	-0.5	-4.0	2.70%	2.6
6097	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	4.6	-0.9	-4.0	2.71%	3.3
6100	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	2.9	-0.5	-4.0	2.71%	2.9
6102	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	5.7	6.9	-1.3	-4.0	2.71%	3.4
6103	AT5G19950.3 | expressed protein | chr5:6741111-6743775 REVERSE | Aliases: F28I16.100, F28I16_100	3.4	4.2	-0.9	-4.0	2.71%	3.2
6108	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	4.7	-1.4	-4.0	2.72%	3.4
6109	AT1G63580.1 | protein kinase-related | chr1:23580996-23581917 FORWARD | Aliases: F2K11.6, F2K11_6	2.6	3.1	-0.5	-4.0	2.72%	3.0
6110	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	4.1	5.2	-1.2	-4.0	2.72%	3.3
6111	AT5G43550.1 | expressed protein | chr5:17515120-17515491 FORWARD | Aliases: K9D7.5, K9D7_5	2.3	2.6	-0.4	-4.0	2.72%	2.5

Rank	Description	Sync	Root	M	t	adj.q	B
6114	AT5G03670.1 | expressed protein | chr5:947145-950170 FORWARD | Aliases: F17C15.90, F17C15_90	2.4	2.9	-0.5	-4.0	2.73%	2.8
6116	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	2.6	3.1	-0.5	-4.0	2.73%	2.8
6118	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	3.7	4.3	-0.6	-4.0	2.74%	3.0
6121	AT5G56100.1 | glycine-rich protein / oleosin, contains Pfam PF01277: Oleosin domain | chr5:22734341-22734977 FORWARD | Aliases: MDA7.16, MDA7_16	7.2	9.3	-2.1	-4.0	2.74%	3.3
6123	AT5G18470.1 | curculin-like (mannose-binding) lectin family protein, contains Pfam profile: PF01453 lectin (probable mannose binding) | chr5:6127799-6129679 FORWARD | Aliases: T28N17.6	4.2	5.1	-0.9	-4.0	2.74%	3.2
6127	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	5.7	-1.1	-4.0	2.75%	3.3
6132	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	4.5	5.5	-1.0	-4.0	2.76%	3.2
6137	AT2G23510.1 | transferase family protein, low similarity to EIG-I24 from Nicotiana tabacum (gi:10798748), 10-deacetylbaccatin 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	3.5	-0.8	-4.0	2.77%	3.1
6138	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	3.8	-0.7	-4.0	2.77%	3.0
6140	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	7.4	8.9	-1.5	-3.9	2.78%	3.2
6146	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	9.4	11.2	-1.8	-3.9	2.78%	3.1
6147	AT5G38790.1 | expressed protein, predicted protein, Arabidopsis thaliana; expression supported by MPSS	3.0	6.8	-3.8	-3.9	2.79%	3.3
6149	AT1G51620.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:19143798-19145455 FORWARD | Aliases: F19C24.15, F19C24_15	2.4	2.7	-0.4	-3.9	2.79%	2.6
6150	AT1G76560.1 | CP12 domain-containing protein, contains Pfam domain PF02672: CP12 domain | chr1:28733147-28733747 FORWARD | Aliases: F14G6.16, F14G6_16	6.9	8.3	-1.4	-3.9	2.79%	3.3
6158	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	7.1	8.5	-1.4	-3.9	2.80%	3.3
6160	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 (Arabidopsis thaliana); 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	3.9	4.6	-0.7	-3.9	2.81%	3.0
6162	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	7.2	8.6	-1.4	-3.9	2.81%	3.2
6163	AT5G28770.3 | Symbol: BZO2H3 |	4.1	5.4	-1.3	-3.9	2.81%	3.3
6167	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	4.0	-0.8	-3.9	2.82%	3.0
6168	AT1G72470.1 | exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit; | chr1:27287355-27289557 FORWARD | Aliases: T10D10.6, T10D10_6	4.4	5.2	-0.8	-3.9	2.82%	3.1

Rank	Description	Sync	Root	M	t	adj.q	B
6170	AT4G36160.1 | Symbol: ANAC076 | no apical meristem (NAM) family protein, similar to NAC2 (GI:6456751)	2.8	3.2	-0.4	-3.9	2.82%	2.5
6171	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	5.4	6.2	-0.8	-3.9	2.82%	3.2
6172	AT4G36980.1 | expressed protein | chr4:17433639-17437057 REVERSE | Aliases: AP22.35, AP22_35	6.6	8.4	-1.9	-3.9	2.82%	3.2
6174	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	5.2	-1.2	-3.9	2.83%	3.3
6175	AT3G10320.1 | expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563) | chr3:3195319-3197351 REVERSE | Aliases: F14P13.8	3.2	4.2	-0.9	-3.9	2.83%	3.2
6177	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	3.6	4.3	-0.7	-3.9	2.83%	3.1
6179	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	3.9	4.6	-0.7	-3.9	2.83%	3.1
6184	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	3.3	-0.5	-3.9	2.85%	2.9
6185	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	7.2	7.7	-0.5	-3.9	2.85%	2.9
6187	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	3.7	4.8	-1.1	-3.9	2.85%	3.2
6189	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	5.6	6.3	-0.7	-3.9	2.86%	3.1
6192	AT4G32450.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:15661098-15662711 FORWARD | Aliases: F8B4.150, F8B4_150	3.4	5.8	-2.5	-3.9	2.86%	3.2
6195	AT5G24290.2 | integral membrane family protein, contains Pfam domain PF01988: Integral membrane protein | chr5:8263135-8265658 REVERSE | Aliases: MOP9.11, MOP9_11	3.8	4.6	-0.8	-3.9	2.87%	3.1
6196	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	6.1	7.1	-1.0	-3.9	2.87%	3.3
6197	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	6.1	-2.3	-3.9	2.87%	3.3
6199	AT5G44820.1 | expressed protein, similar to unknown protein (pir::T04881) | chr5:18112940-18114812 REVERSE | Aliases: K23L20.17, K23L20_17	2.7	2.9	-0.3	-3.9	2.87%	2.4
6202	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	3.1	3.7	-0.5	-3.9	2.87%	2.9
6204	AT3G51920.1 | Symbol: CAM9 | calmodulin-9 (CAM9), identical to calmodulin 9 GI:5825602 from (Arabidopsis thaliana); contains Pfam profile PF00036: EF hand | chr3:19279026-19280366 REVERSE | Aliases: CALMODULIN 9, F4F15.30	9.4	10.2	-0.8	-3.9	2.88%	3.1
6205	AT5G60930.1 | chromosome-associated kinesin, putative, microtubule-associated motor KIF4 , Mus musculus, PIR:A54803 | chr5:24532624-24539737 REVERSE | Aliases: MSL3.50, MSL3_50	3.9	4.8	-0.8	-3.9	2.88%	3.0

Rank	Description	Sync	Root	M	t	adj.q	B
6208	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	2.7	-0.3	-3.9	2.89%	2.5
6211	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	3.0	4.8	-1.8	-3.9	2.89%	3.2
6214	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	6.4	7.2	-0.7	-3.9	2.90%	2.9
6215	AT5G25130.1 | Symbol: CYP71B12 | cytochrome P450 family protein, CYTOCHROME P450 71B1 - Thlaspi arvense, EMBL:L24438 | chr5:8668302-8670107 FORWARD | Aliases: F21J6.2	3.2	3.9	-0.7	-3.9	2.90%	3.1
6221	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	3.9	-0.5	-3.9	2.91%	2.8
6223	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	5.6	-1.3	-3.9	2.91%	3.2
6227	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	7.9	9.2	-1.2	-3.9	2.92%	3.1
6228	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	6.3	-1.4	-3.9	2.92%	3.3
6229	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	2.7	3.4	-0.6	-3.9	2.92%	3.0
6230	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	6.9	-0.6	-3.9	2.92%	3.0
6231	AT5G55620.1 | expressed protein, similar to unknown protein (gb:AAF04428.1) | chr5:22547430-22548165 FORWARD | Aliases: MDF20.6, MDF20_6	2.6	3.0	-0.3	-3.9	2.92%	2.5
6234	AT3G05120.1 | expressed protein, low similarity to PrMC3 (Pinus radiata) GI:5487873 | chr3:1430483-1432784 FORWARD | Aliases: T12H1.8, T12H1_8	5.2	6.0	-0.7	-3.9	2.93%	3.1
6239	AT5G08480.2 | VQ motif-containing protein, contains PF05678: VQ motif | chr5:2743621-2745112 FORWARD | Aliases: F8L15.9	2.1	2.5	-0.4	-3.9	2.93%	2.6
6240	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	7.9	9.0	-1.1	-3.9	2.93%	3.1
6242	AT1G15460.1 | anion exchange family protein, member of the PF:00955 Anion exchanger family | chr1:5309996-5313424 REVERSE | Aliases: F9L1.41, F9L1_41	2.4	2.9	-0.5	-3.9	2.93%	2.8
6244	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	3.5	4.2	-0.6	-3.9	2.93%	3.0
6246	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)	5.5	6.6	-1.1	-3.9	2.93%	3.1
6247	AT5G65160.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain | chr5:26048419-26051040 REVERSE | Aliases: MQN23.9, MQN23_9	4.2	5.1	-0.9	-3.9	2.93%	3.1
6248	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	7.3	-0.8	-3.9	2.94%	3.0
6249	AT1G15280.2 | glycine-rich protein | chr1:5252332-5256746 FORWARD | Aliases: F9L1.22, F9L1_22	3.6	4.2	-0.6	-3.9	2.94%	3.0

Rank	Description	Sync	Root	M	t	adj.q	B
6250	AT1G68230.1 | reticulon family protein (RTNLB14), contains Pfam profile PF02453: Reticulon | chr1:25575848-25576584 FORWARD | Aliases: T22E19.14, T22E19_14	3.2	3.9	-0.8	-3.9	2.95%	3.2
6253	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)	3.6	5.0	-1.4	-3.9	2.95%	3.3
6255	AT5G07100.2 | Symbol: WRKY26 |	3.1	4.6	-1.4	-3.9	2.95%	3.0
6257	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	2.7	3.4	-0.7	-3.9	2.96%	3.0
6266	AT3G25655.1 | expressed protein | chr3:9338769-9339302 REVERSE | Aliases: None	3.0	4.3	-1.3	-3.9	2.97%	3.2
6267	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	3.6	-0.4	-3.9	2.97%	2.6
6268	AT5G17040.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, similar to UDP glucose:flavonoid 3-o-glucosyltransferase GI:13620861 from (Vitis vinifera); contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:5605287-5606973 REVERSE | Aliases: F2K13.190, F2K13_190	3.4	4.3	-0.9	-3.9	2.97%	3.1
6270	AT5G23390.1 | expressed protein, contains Pfam profile: PF04842 plant protein of unknown function (DUF639) | chr5:7870516-7874508 REVERSE | Aliases: T32G24.2, T32G24_2	5.9	7.6	-1.8	-3.9	2.97%	3.2
6274	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	7.1	8.4	-1.3	-3.9	2.97%	3.1
6275	AT2G21180.1 | expressed protein | chr2:9081741-9082461 REVERSE | Aliases: F26H11.6, F26H11_6	6.1	6.8	-0.7	-3.9	2.97%	3.0
6277	AT1G61080.1 | proline-rich family protein | chr1:22496859-22500684 REVERSE | Aliases: T7P1.21, T7P1_21	2.6	3.2	-0.6	-3.9	2.98%	2.9
6279	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	4.1	5.5	-1.5	-3.9	2.98%	3.2
6281	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)	3.4	4.7	-1.3	-3.9	2.99%	3.1
6285	AT3G27100.1 | expressed protein | chr3:9995832-9997249 REVERSE | Aliases: MOJ10.18	7.9	9.1	-1.2	-3.9	3.00%	3.2
6286	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	4.4	5.0	-0.6	-3.9	3.00%	3.0
6289	AT3G07780.1 | expressed protein | chr3:2484476-2487030 FORWARD | Aliases: MLP3.23	8.3	9.7	-1.4	-3.9	3.01%	3.0
6290	AT2G43535.1 | Encodes a defensin-like (DEFL) family protein. | chr2:18078050-18078739 FORWARD | Aliases: None	4.2	6.1	-1.9	-3.9	3.01%	3.2
6293	AT4G31750.1 | protein phosphatase 2C, putative / PP2C, putative, protein phosphatase 2C, Medicago sativa, PID:g2582800	8.2	8.9	-0.8	-3.9	3.02%	2.9
6296	AT1G72180.1 | leucine-rich repeat transmembrane protein kinase, putative, similar to GI:3641252 from (Malus x domestica) (Plant Mol. Biol. 40 (6), 945-957 (1999)) | chr1:27166482-27171092 FORWARD | Aliases: T9N14.3, T9N14_3	4.4	5.3	-0.9	-3.9	3.04%	3.1
6305	AT3G52240.1 | expressed protein | chr3:19383880-19386858 REVERSE | Aliases: T25B15.10	4.4	5.0	-0.6	-3.9	3.05%	3.0
6307	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	3.3	-0.5	-3.9	3.05%	2.7
6312	AT3G58050.1 | expressed protein | chr3:21503516-21508134 FORWARD | Aliases: T10K17.260	4.5	5.1	-0.6	-3.9	3.08%	2.9
6314	AT1G80830.1 | Symbol: NRAMP1 |	9.2	10.5	-1.3	-3.9	3.09%	2.7

Rank	Description	Sync	Root	M	t	adj.q	B
6319	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	3.3	5.2	-1.9	-3.9	3.10%	3.2
6324	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	7.7	9.3	-1.6	-3.8	3.11%	3.1
6326	AT3G03690.1 | glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/I-Branching enzyme | chr3:911245-913684 REVERSE | Aliases: T12J13.3, T12J13_3	3.0	3.5	-0.5	-3.8	3.11%	2.8
6327	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	6.4	-1.1	-3.8	3.11%	3.1
6328	AT5G18590.2 | kelch repeat-containing protein, identical to RanGAP1 interacting protein (GI: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	7.1	8.0	-0.8	-3.8	3.11%	2.8
6331	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	3.0	3.9	-1.0	-3.8	3.11%	3.0
6334	AT4G31320.1 | auxin-responsive protein, putative / small auxin up RNA (SAUR_C), similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesnerian); similar to auxin-induced protein 15A (SP:P33081) from (Glycine max) | chr4:15193999-15194568 REVERSE | Aliases: F8F16.140, F8F16_140	2.8	3.8	-1.0	-3.8	3.12%	3.0
6338	AT3G52070.2 | expressed protein | chr3:19323731-19324444 FORWARD | Aliases: F4F15.180	4.9	6.4	-1.4	-3.8	3.13%	3.2
6339	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	3.6	-0.8	-3.8	3.13%	2.9
6343	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	4.2	5.3	-1.1	-3.8	3.14%	3.2
6345	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	3.0	3.5	-0.4	-3.8	3.14%	2.7
6347	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	4.2	5.2	-1.0	-3.8	3.15%	3.1
6352	AT1G61560.1 | Symbol: MLO6 | seven transmembrane MLO family protein / MLO-like protein 6 (MLO6), idenctical to membrane protein Mlo6 (Arabidopsis thaliana) gi:14091582:gb:AAK53799; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 (Hordeum vulgare)(Barley); contains Pfam profile	2.6	3.1	-0.4	-3.8	3.16%	2.7
6353	AT3G47980.1 | integral membrane HPP family protein, contains Pfam domain, PF04982: HPP family | chr3:17721462-17723786 FORWARD | Aliases: T17F15.150	3.9	4.5	-0.6	-3.8	3.16%	2.8
6354	AT2G25710.2 | Symbol: HCS1 | holocarboxylase synthetase 1 (HCS1), identical to holocarboxylase synthetase 1 (hcs1) (Arabidopsis thaliana) GI:19698365	5.2	6.8	-1.6	-3.8	3.16%	3.2
6357	AT2G25735.1 | expressed protein | chr2:10982138-10982837 REVERSE | Aliases: None	2.8	3.7	-0.9	-3.8	3.16%	3.1
6359	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	5.4	6.3	-0.9	-3.8	3.16%	2.9
6360	AT1G07260.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr1:2227593-2229318 REVERSE | Aliases: F10K1.3, F10K1_3	5.1	6.0	-0.9	-3.8	3.16%	3.0
6362	AT3G09850.1 | D111/G-patch domain-containing protein, contains Pfam profile PF01585: G-patch domain | chr3:3023216-3025856 REVERSE | Aliases: F8A24.10	8.3	8.9	-0.7	-3.8	3.17%	3.0
6363	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	3.0	3.6	-0.6	-3.8	3.17%	2.8

Rank	Description	Sync	Root	M	t	adj.q	B
6368	AT1G32690.1 | expressed protein, similar to hypothetical protein GB:AAC61817 GI:3668085 from (Arabidopsis thaliana) | chr1:11820888-11821690 REVERSE | Aliases: F6N18.23, F6N18_23	5.7	6.7	-1.0	-3.8	3.18%	3.1
6369	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	3.7	5.0	-1.4	-3.8	3.18%	3.1
6374	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	2.5	3.8	-1.3	-3.8	3.19%	3.2
6375	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	9.1	10.0	-0.9	-3.8	3.19%	2.9
6378	AT1G22070.1 | Symbol: TGA3 | bZIP family transcription factor (TGA3), identical to transcription factor GI:304113 from (Arabidopsis thaliana)	6.9	7.8	-0.9	-3.8	3.19%	2.9
6379	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	6.6	7.6	-1.0	-3.8	3.19%	2.9
6381	AT5G04040.1 | patatin-related, contains Patatin domain PF01734	6.0	7.0	-0.9	-3.8	3.20%	3.1
6387	AT1G10800.1 | expressed protein | chr1:3598159-3598592 REVERSE | Aliases: T16B5.6	5.1	5.8	-0.7	-3.8	3.20%	2.9
6391	AT1G78260.2 | RNA recognition motif (RRM)-containing protein, similar to RNA recognition motif-containing protein SEB-4 GI:8895698 from (Xenopus laevis); contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) | chr1:29451878-29455297 FORWARD | Aliases: F3F9.20, F3F9_20	3.7	5.1	-1.4	-3.8	3.21%	3.2
6392	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	5.9	-0.7	-3.8	3.21%	2.9
6395	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	3.5	-0.7	-3.8	3.22%	2.8
6397	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	3.9	4.7	-0.8	-3.8	3.23%	3.0
6399	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	3.9	5.3	-1.4	-3.8	3.23%	3.1
6400	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	3.3	-0.7	-3.8	3.23%	2.9
6403	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	3.5	-0.7	-3.8	3.24%	2.9
6404	AT2G22310.1 | Symbol: ATUBP4 |	6.2	7.0	-0.8	-3.8	3.24%	3.0
6406	AT1G48840.1 | expressed protein, contains Pfam profile: PF04842 plant protein of unknown function (DUF639) | chr1:18065203-18068948 FORWARD | Aliases: T24P22.6, T24P22_6	4.5	5.3	-0.8	-3.8	3.24%	3.0
6409	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	3.2	-0.6	-3.8	3.24%	2.8
6410	NA	11.3	12.0	-0.7	-3.8	3.24%	1.9
6411	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	3.2	4.1	-0.9	-3.8	3.24%	2.8
6412	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	3.7	-0.7	-3.8	3.24%	2.9

Rank	Description	Sync	Root	M	t	adj.q	B
6413	AT4G27430.1 | Symbol: CIP7 | COP1-interacting protein 7 (CIP7), identical to COP1-Interacting Protein 7 (CIP7) GI:3327868 from (Arabidopsis thaliana)	4.4	5.4	-0.9	-3.8	3.24%	3.0
6414	AT1G48110.1 | expressed protein, contains Pfam profile PF04146: YT521-B-like family | chr1:17772787-17777120 REVERSE | Aliases: F21D18.17, F21D18_17	4.6	5.4	-0.8	-3.8	3.24%	2.9
6416	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	8.1	9.6	-1.5	-3.8	3.24%	2.7
6417	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	8.2	9.2	-1.0	-3.8	3.25%	3.0
6419	AT2G35870.1 | expressed protein | chr2:15068888-15069190 REVERSE | Aliases: F11F19.22, F11F19_22	2.9	3.4	-0.5	-3.8	3.26%	2.6
6420	AT3G50190.1 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g50130.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g50140.1); similar to hypothetical protein [Oryza sativa (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	4.1	-1.3	-3.8	3.26%	3.0
6422	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	4.1	5.2	-1.1	-3.8	3.26%	3.1
6424	AT1G53340.1 | DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain | chr1:19902596-19904599 REVERSE | Aliases: F12M16.24, F12M16_24	4.4	6.4	-2.0	-3.8	3.27%	3.1
6426	AT3G29760.1 | NLI interacting factor (NIF) family protein, contains Pfam profile PF03031: NLI interacting factor | chr3:11591984-11594312 REVERSE | Aliases: MOD1.21	4.5	5.4	-0.9	-3.8	3.27%	3.0
6433	AT5G55590.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:22537137-22538925 FORWARD | Aliases: MDF20.3, MDF20_3	3.3	4.6	-1.2	-3.8	3.29%	3.1
6434	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	3.9	4.5	-0.6	-3.8	3.29%	2.9
6438	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	4.7	5.8	-1.1	-3.8	3.30%	3.0
6439	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	6.5	8.5	-1.9	-3.8	3.30%	3.1
6440	AT1G59650.1 | Symbol: CW14 | expressed protein, ; supporting cDNA gi:6520232:dbj:AB028233.1: | chr1:21923410-21926588 FORWARD | Aliases: CW14, T30E16.22, T30E16_22	7.4	8.0	-0.6	-3.8	3.30%	2.9
6441	AT2G38790.1 | expressed protein | chr2:16221269-16222342 REVERSE | Aliases: F13I13.2	4.0	5.0	-1.0	-3.8	3.31%	3.0
6444	AT1G56020.1 | expressed protein | chr1:20955811-20957077 FORWARD | Aliases: F14J16.33	3.6	4.5	-0.9	-3.8	3.31%	3.1
6445	AT4G12020.1 | Symbol: WRKY19 |	3.4	5.5	-2.1	-3.8	3.31%	3.0
6449	AT2G34180.1 | Symbol: CIPK13 |	2.8	3.5	-0.7	-3.8	3.31%	3.0
6451	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	4.1	5.7	-1.5	-3.8	3.31%	3.0
6453	AT2G31750.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:13504310-13507763 FORWARD | Aliases: F20M17.21, F20M17_21	3.7	4.8	-1.1	-3.8	3.32%	3.1
6458	AT3G53990.2 | universal stress protein (USP) family protein, contains Pfam PF00582: universal stress protein family | chr3:20000315-20002084 REVERSE | Aliases: F5K20.290, F5K20_290	6.3	8.2	-1.9	-3.8	3.33%	2.9
6461	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	6.9	7.8	-0.8	-3.8	3.33%	2.6

Rank	Description	Sync	Root	M	t	adj.q	B
6462	AT1G53680.1 | Symbol: ATGSTU28 | glutathione S-transferase, putative, similar to GI:2853219 from (Carica papaya) | chr1:20042026-20042785 FORWARD | Aliases: F22G10.22, F22G10_22	3.6	4.7	-1.1	-3.8	3.33%	2.9
6463	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	3.6	4.7	-1.1	-3.8	3.33%	3.1
6468	AT1G69790.1 | protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) SWISS-PROT:Q06548 | chr1:26270422-26272646 FORWARD | Aliases: T6C23.1, T6C23_1	3.7	5.4	-1.6	-3.8	3.33%	3.1
6470	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	4.5	6.5	-2.0	-3.8	3.33%	3.1
6473	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	10.7	11.6	-0.9	-3.8	3.34%	2.5
6479	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	4.6	6.7	-2.2	-3.8	3.35%	3.1
6483	AT5G11700.1 | glycine-rich protein, predicted protein, Arabidopsis thaliana | chr5:3762467-3771124 REVERSE | Aliases: T22P22.90, T22P22_90	3.6	4.6	-1.0	-3.8	3.36%	3.0
6487	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	3.9	4.6	-0.7	-3.8	3.38%	2.9
6490	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	2.9	3.6	-0.7	-3.8	3.38%	2.9
6491	AT5G49780.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:20245813-20250321 FORWARD | Aliases: K2I5.15, K2I5_15	3.5	4.6	-1.1	-3.8	3.38%	3.0
6494	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	3.3	-0.7	-3.8	3.38%	2.9
6495	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	8.2	-2.1	-3.8	3.38%	3.0
6497	AT3G20310.1 | Symbol: ATERF 7/ATERF7 |	6.0	7.4	-1.4	-3.8	3.39%	3.0
6499	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	8.2	10.1	-1.9	-3.8	3.39%	3.1
6505	AT5G27950.1 | kinesin motor protein-related, kinesin heavy chain-like protein, potato, PIR:T07397 | chr5:9984055-9987994 FORWARD | Aliases: F15F15.20, F15F15_20	3.1	4.2	-1.1	-3.8	3.41%	2.8
6506	AT1G21200.1 | expressed protein | chr1:7421206-7423132 FORWARD | Aliases: F16F4.11, F16F4_11	3.1	4.6	-1.5	-3.8	3.41%	3.0
6507	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	5.2	-0.7	-3.8	3.42%	2.9
6508	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	7.2	-0.6	-3.8	3.42%	2.8
6509	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	6.5	7.6	-1.2	-3.8	3.42%	2.8
6510	AT5G33390.1 | glycine-rich protein, similar to nuclear antigen EBNA-1 (GI:3342234) {Cercopithecine herpesvirus 15} | chr5:12679019-12680050 FORWARD | Aliases: None	5.4	6.5	-1.0	-3.8	3.43%	3.1

Rank	Description	Sync	Root	M	t	adj.q	B
6511	AT2G46550.1 | expressed protein | chr2:19119061-19121224 REVERSE | Aliases: F13A10.8	6.8	7.8	-0.9	-3.8	3.43%	2.9
6514	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	7.4	9.5	-2.2	-3.8	3.44%	3.1
6515	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	4.0	4.6	-0.6	-3.8	3.45%	2.7
6517	AT2G28460.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.2	4.8	-1.6	-3.8	3.45%	3.1
6519	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	6.4	7.2	-0.8	-3.8	3.45%	2.9
6520	AT3G14690.1 | Symbol: CYP72A15 | cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus) | chr3:4937386-4939472 FORWARD | Aliases: MIE1.19	7.0	8.8	-1.8	-3.8	3.46%	3.0
6521	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	3.8	-1.0	-3.8	3.46%	2.8
6522	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	6.0	6.8	-0.8	-3.8	3.47%	2.9
6525	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	2.8	-0.3	-3.8	3.47%	2.3
6529	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	4.8	6.1	-1.3	-3.8	3.47%	3.0
6530	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	6.4	7.5	-1.0	-3.7	3.48%	2.8
6532	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	4.9	5.9	-0.9	-3.7	3.49%	2.9
6533	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	3.1	-0.6	-3.7	3.49%	2.7
6534	AT3G26700.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:9811187-9813901 FORWARD | Aliases: MLJ15.17	3.1	3.7	-0.6	-3.7	3.49%	2.8
6537	AT2G37300.1 | expressed protein, and genefinder | chr2:15669678-15670524 REVERSE | Aliases: F3G5.9, F3G5_9	2.9	3.5	-0.5	-3.7	3.51%	2.7
6538	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	3.7	4.6	-0.9	-3.7	3.51%	2.9
6541	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	2.8	3.2	-0.4	-3.7	3.52%	2.2
6544	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	3.0	-0.6	-3.7	3.53%	2.6
6546	AT5G15680.1 | expressed protein | chr5:5101191-5110796 REVERSE | Aliases: F14F8.60, F14F8_60	3.8	4.3	-0.6	-3.7	3.53%	2.7
6549	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	2.7	-0.4	-3.7	3.54%	2.4

Rank	Description	Sync	Root	M	t	adj.q	B
6553	AT3G44700.1 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function; expression supported by MPSS | chr3:16247330-16248723 REVERSE | Aliases: T18B22.100	2.2	2.6	-0.5	-3.7	3.55%	2.2
6554	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	3.3	4.3	-1.0	-3.7	3.55%	3.0
6556	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	2.6	4.0	-1.4	-3.7	3.55%	2.8
6560	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	4.7	-1.3	-3.7	3.55%	2.9
6561	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	4.8	6.5	-1.7	-3.7	3.55%	3.0
6565	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	5.6	-0.9	-3.7	3.56%	3.0
6571	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	3.8	4.5	-0.7	-3.7	3.57%	2.9
6573	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	5.9	6.6	-0.6	-3.7	3.57%	2.8
6581	AT1G65180.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.5	3.1	-0.7	-3.7	3.58%	2.7
6583	AT2G34610.1 | expressed protein | chr2:14582471-14583596 FORWARD | Aliases: T31E10.5, T31E10_5	3.8	4.4	-0.6	-3.7	3.58%	2.6
6587	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	2.5	3.2	-0.7	-3.7	3.59%	2.7
6589	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	3.6	-0.9	-3.7	3.60%	2.9
6590	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	2.9	-0.5	-3.7	3.60%	2.7
6591	AT5G44580.1 | expressed protein | chr5:17996538-17997634 FORWARD | Aliases: K15C23.2, K15C23_2	2.7	3.3	-0.6	-3.7	3.60%	2.5
6593	AT1G08180.1 | expressed protein | chr1:2564738-2565073 REVERSE | Aliases: T23G18.4, T23G18_4	3.0	4.0	-1.0	-3.7	3.60%	2.8
6594	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	7.2	9.4	-2.2	-3.7	3.60%	2.9
6596	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	4.3	5.1	-0.8	-3.7	3.60%	2.9
6597	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	3.1	3.6	-0.6	-3.7	3.60%	2.7
6600	AT5G51500.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:20935155-20937064 REVERSE | Aliases: K17N15.5, K17N15_5	2.5	3.0	-0.5	-3.7	3.60%	2.5
6602	AT2G42270.1 | U5 small nuclear ribonucleoprotein helicase, putative | chr2:17611408-17618411 FORWARD | Aliases: T24P15.18, T24P15_18	5.7	6.8	-1.2	-3.7	3.61%	2.7
6607	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	4.5	-1.1	-3.7	3.62%	2.7

Rank	Description	Sync	Root	M	t	adj.q	B
6608	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	7.2	-1.0	-3.7	3.62%	2.9
6614	AT2G38500.1 | expressed protein | chr2:16124505-16126177 REVERSE | Aliases: T6A23.30	4.2	4.7	-0.5	-3.7	3.63%	2.5
6615	AT3G46810.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	3.5	-0.8	-3.7	3.63%	2.6
6616	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	3.6	5.6	-2.0	-3.7	3.64%	2.9
6617	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	4.9	6.4	-1.5	-3.7	3.64%	3.0
6618	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	6.5	-0.8	-3.7	3.64%	2.7
6619	AT1G26650.1 | expressed protein | chr1:9210076-9211547 FORWARD | Aliases: T24P13.3, T24P13_3	5.5	6.4	-0.9	-3.7	3.65%	2.8
6621	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	4.1	4.8	-0.7	-3.7	3.66%	2.7
6622	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	7.1	8.1	-1.0	-3.7	3.66%	2.8
6623	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	4.7	6.2	-1.5	-3.7	3.66%	3.0
6624	AT1G13310.1 | expressed protein | chr1:4561067-4562295 REVERSE | Aliases: T6J4.7, T6J4_7	2.6	3.1	-0.5	-3.7	3.66%	2.4
6625	AT4G16850.1 | expressed protein | chr4:9480100-9481757 FORWARD | Aliases: DL4450W, FCAALL.194	5.0	5.5	-0.5	-3.7	3.66%	2.5
6627	AT4G36060.2 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.5	2.9	-0.4	-3.7	3.66%	2.5
6629	AT2G17990.1 | expressed protein | chr2:7834004-7835836 FORWARD | Aliases: T27K22.14, T27K22_14	8.6	9.5	-0.9	-3.7	3.66%	2.8
6630	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	3.2	4.0	-0.8	-3.7	3.66%	2.8
6637	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	3.4	4.5	-1.1	-3.7	3.68%	2.9
6638	AT3G20770.1 | Symbol: EIN3 | ethylene-insensitive 3 (EIN3), identical to ethylene-insensitive3 GI:2224933 from (Arabidopsis thaliana)	7.1	8.5	-1.4	-3.7	3.68%	2.9
6644	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	6.8	-2.9	-3.7	3.71%	3.0
6647	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	8.2	-0.9	-3.7	3.71%	2.9
6649	AT1G63910.1 | Symbol: ATMYB103 | myb family transcription factor (MYB103), contains Pfam profile: PF00249 myb-like DNA-binding domain	2.3	2.7	-0.4	-3.7	3.71%	2.3
6652	AT2G18640.1 | Symbol: GGPS4 | geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltranstransferase, putative, similar to gi:1944371; contains GB:L22347 | chr2:8090822-8091970 REVERSE | Aliases: F24H14.2, GERANYLGERANYL PYROPHOSPHATE SYNTHASE 4	2.6	3.0	-0.4	-3.7	3.72%	2.3
6653	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	5.2	6.0	-0.8	-3.7	3.73%	2.8
6654	AT5G42630.1 | myb family transcription factor (KAN4), contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to	2.2	2.6	-0.4	-3.7	3.73%	2.3

Rank	Description	Sync	Root	M	t	adj.q	B
6655	AT1G25540.1 | Symbol: PFT1 | phytochrome and flowering time regulatory protein (PFT1), PMID: 12815435	5.4	6.2	-0.8	-3.7	3.73%	2.8
6657	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	3.7	-0.6	-3.7	3.73%	2.7
6662	AT1G65690.1 | harpin-induced protein-related / HIN1-related / harpin-responsive protein-related, similar to hin1 homolog (GI:13122296) (Arabidopsis thaliana); similar to hin1 (GI:22830759) (Nicotiana tabacum); contains 1 transmembrane domain; | chr1:24435096-24436616 REVERSE | Aliases: F1E22.7, F1E22_7	3.3	3.9	-0.5	-3.7	3.75%	2.6
6663	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	5.9	6.9	-1.0	-3.7	3.75%	2.9
6666	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	5.9	6.6	-0.7	-3.7	3.76%	2.9
6667	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 profilePF01019: Gamma-glutamyltranspeptidase	3.8	4.4	-0.7	-3.7	3.77%	2.7
6668	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	4.0	5.1	-1.1	-3.7	3.77%	2.9
6669	AT3G51580.1 | expressed protein | chr3:19141813-19144259 REVERSE | Aliases: T18N14.6	6.4	7.0	-0.6	-3.7	3.77%	2.7
6670	AT4G31330.1 | expressed protein, contains Pfam profile PF04654: Protein of unknown function, DUF599 | chr4:15202302-15203437 FORWARD | Aliases: F8F16.150, F8F16_150	5.4	6.5	-1.0	-3.7	3.77%	2.8
6671	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	5.3	6.1	-0.7	-3.7	3.77%	2.9
6672	AT4G26770.1 | phosphatidate cytidylyltransferase, putative / CDP-diglyceride synthetase, putative, similar to CDP-diacylglycerol synthetase GI:2182104 from (Solanum tuberosum) | chr4:13482082-13484846 FORWARD | Aliases: F10M23.110, F10M23_110	2.6	3.0	-0.5	-3.7	3.77%	2.4
6674	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	3.7	4.1	-0.5	-3.7	3.78%	2.5
6675	AT5G66950.1 | expressed protein | chr5:26750559-26753372 FORWARD | Aliases: K8A10.2, K8A10_2	6.1	7.2	-1.2	-3.7	3.78%	2.9
6676	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)	6.3	7.2	-1.0	-3.7	3.79%	2.8
6677	AT3G13090.1 | Symbol: ATMRP8 |	3.8	4.5	-0.7	-3.7	3.79%	2.6
6680	AT3G61010.1 | glycosyl hydrolase family protein 85, hypothetical protein F9F8.14 - Arabidopsis thaliana, EMBL:AC009991	4.1	5.1	-1.0	-3.7	3.80%	2.8
6684	AT5G65460.1 | kinesin motor protein-related, contains similarity to kinesin heavy chain | chr5:26179057-26186227 REVERSE | Aliases: MNA5.20, MNA5_20	3.4	4.2	-0.8	-3.7	3.81%	2.6
6686	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	2.6	-0.5	-3.7	3.81%	2.5
6687	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	4.4	5.1	-0.7	-3.7	3.81%	2.5
6688	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	8.0	9.1	-1.1	-3.7	3.81%	2.8
6691	AT2G15300.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:6656712-6659092 FORWARD | Aliases: F27O10.5, F27O10_5	3.0	3.5	-0.5	-3.7	3.81%	2.5

Rank	Description	Sync	Root	M	t	adj.q	B
6693	AT5G01990.1 | auxin efflux carrier family protein, contains auxin efflux carrier domain, Pfam:PF03547 | chr5:377228-379908 REVERSE | Aliases: T7H20.40, T7H20_40	5.2	5.9	-0.7	-3.7	3.82%	2.7
6694	AT1G23830.1 | expressed protein | chr1:8422949-8424077 REVERSE | Aliases: F5O8.39, F5O8_39	4.9	6.0	-1.1	-3.7	3.83%	2.9
6697	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	4.3	5.5	-1.2	-3.7	3.83%	3.0
6698	AT4G39330.2 | similar to mannitol dehydrogenase, putative [Arabidopsis thaliana] (TAIR:At2g21730.1); similar to mannitol dehydrogenase, putative [Arabidopsis thaliana] (TAIR:At2g21890.1); similar to putative sinapyl alcohol dehydrogenase [Populus tremula x Populus tremuloides] (GB:AAM95578.1); contains InterPro domain Zinc-containing alcohol dehydrogenase superfamily (InterPro:IPR002085)	3.5	4.2	-0.7	-3.7	3.83%	2.6
6699	AT4G24560.1 | Symbol: UBP16 | ubiquitin-specific protease 16, putative (UBP16), similar to ubiquitin-specific protease 16 GI:11993477 (Arabidopsis thaliana) | chr4:12679220-12684949 REVERSE | Aliases: F22K18.240, F22K18_240, UBIQUITIN SPECIFIC PROTEASE 16	4.8	6.0	-1.2	-3.7	3.83%	2.9
6700	AT5G64120.1 | peroxidase, putative, identical to peroxidase (Arabidopsis thaliana) gi:1483222:emb:CAA67551 | chr5:25676532-25678228 REVERSE | Aliases: MHJ24.10, MHJ24_10	3.3	5.4	-2.0	-3.7	3.83%	2.9
6703	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	4.3	6.4	-2.0	-3.7	3.84%	2.8
6704	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	7.4	8.4	-1.0	-3.7	3.84%	2.7
6705	AT5G51770.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:21048256-21050220 FORWARD | Aliases: MIO24.10, MIO24_10	5.1	6.3	-1.2	-3.7	3.84%	2.9
6706	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	3.7	4.3	-0.6	-3.7	3.84%	2.5
6708	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	2.6	3.0	-0.4	-3.7	3.84%	2.4
6712	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	9.5	10.7	-1.2	-3.7	3.85%	2.7
6713	AT5G28040.1 | expressed protein, contains Pfam profile: PF04504 protein of unknown function, DUF573 | chr5:10037273-10039005 REVERSE | Aliases: F15F15.110, F15F15_110	5.9	7.1	-1.2	-3.7	3.85%	2.7
6716	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	4.4	-1.0	-3.7	3.86%	2.7
6719	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	4.7	5.8	-1.0	-3.7	3.86%	2.7
6721	AT5G43730.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.9	4.9	-2.1	-3.7	3.87%	2.7
6723	AT1G05710.4 | ethylene-responsive protein, putative, similar to ethylene-inducible ER33 protein (Lycopersicon esculentum) gi:5669656:gb:AAD46413; identical to bHLH transcription factor (bHLH-alpha gene) | chr1:1715779-1717243 FORWARD | Aliases: F3F20.16, F3F20_16	6.2	7.1	-0.9	-3.7	3.87%	2.8
6724	AT5G37550.1 | expressed protein | chr5:14936131-14937022 REVERSE | Aliases: MPA22.10, MPA22_10	5.7	6.9	-1.1	-3.7	3.88%	2.9
6725	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	7.7	9.6	-1.9	-3.7	3.88%	2.9
6728	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	9.2	10.2	-1.0	-3.7	3.88%	2.7

Rank	Description	Sync	Root	M	t	adj.q	B
6729	AT2G46650.1 | Symbol: B5 #1 | cytochrome b5, putative, similar to cytochome b5 GI:2695711 from (Olea europaea) | chr2:19158723-19159663 FORWARD | Aliases: T3A4.3, T3A4_3	4.5	6.5	-2.0	-3.7	3.88%	3.0
6732	AT4G33610.1 | glycine-rich protein | chr4:16146264-16146996 FORWARD | Aliases: T16L1.100, T16L1_100	3.7	4.6	-0.9	-3.7	3.88%	2.7
6733	AT4G36480.2 | Symbol: ATLCB1 |	4.4	5.4	-1.0	-3.7	3.88%	2.8
6735	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	4.7	5.6	-1.0	-3.7	3.89%	2.9
6736	AT2G39580.1 | expressed protein | chr2:16517503-16524151 FORWARD | Aliases: F12L6.24, F12L6_24	3.6	4.9	-1.3	-3.7	3.89%	2.7
6742	AT2G47270.1 | expressed protein | chr2:19418630-19419221 REVERSE | Aliases: T8I13.11	2.6	3.3	-0.7	-3.7	3.90%	2.5
6744	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	4.2	-0.7	-3.6	3.90%	2.6
6747	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)	2.6	3.8	-1.1	-3.6	3.91%	2.8
6748	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	5.1	5.7	-0.6	-3.6	3.91%	2.7
6750	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	3.0	-0.4	-3.6	3.92%	2.3
6752	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	7.1	9.0	-1.9	-3.6	3.92%	2.8
6756	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	4.5	-0.7	-3.6	3.93%	2.7
6758	AT3G12480.1 | transcription factor, putative | chr3:3957844-3960479 FORWARD | Aliases: T2E22.20	8.2	9.1	-0.9	-3.6	3.94%	2.5
6759	AT1G65510.1 | expressed protein | chr1:24363116-24363532 FORWARD | Aliases: F5I14.24, F5I14_24	3.0	4.7	-1.7	-3.6	3.94%	2.9
6761	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	5.3	6.2	-0.8	-3.6	3.94%	2.7
6764	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	7.5	-1.8	-3.6	3.95%	2.8
6767	AT3G20110.1 | Symbol: CYP705A20 | cytochrome P450 family protein, similar to Cytochrome P450 93A1 (SP:Q42798)	2.7	3.1	-0.4	-3.6	3.95%	2.3
6769	AT1G28240.1 | expressed protein | chr1:9868303-9872198 REVERSE | Aliases: F3H9.11, F3H9_11	4.0	4.8	-0.8	-3.6	3.96%	2.5
6774	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	5.3	-1.1	-3.6	3.98%	2.8
6777	AT3G04640.1 | glycine-rich protein, predicted proteins, Arabidopsis thaliana | chr3:1260912-1261689 REVERSE | Aliases: F7O18.12, F7O18_12	5.5	6.8	-1.3	-3.6	3.98%	2.9
6778	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	2.8	-0.5	-3.6	3.98%	2.2
6779	AT5G38380.2 | expressed protein | chr5:15362890-15365657 FORWARD | Aliases: MXI10.5, MXI10_5	4.8	5.4	-0.7	-3.6	3.98%	2.7

Rank	Description	Sync	Root	M	t	adj.q	B
6780	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	4.9	5.8	-0.9	-3.6	3.99%	2.7
6781	AT1G33440.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr1:12127454-12130369 REVERSE | Aliases: F10C21.11, F10C21_11	3.0	3.5	-0.6	-3.6	3.99%	2.6
6783	AT1G60890.1 | 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 | chr1:22415911-22420898 REVERSE | Aliases: T7P1.4, T7P1_4	4.2	5.4	-1.2	-3.6	3.99%	2.9
6784	AT3G21890.1 | zinc finger (B-box type) family protein, contains Pfam profile: PF01760 CONSTANS family zinc finger | chr3:7709187-7709740 REVERSE | Aliases: MZN24.1	5.4	7.0	-1.6	-3.6	3.99%	2.9
6785	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	6.5	7.6	-1.1	-3.6	4.00%	2.8
6789	AT4G00400.1 | phospholipid/glycerol acyltransferase family protein | chr4:174072-176837 REVERSE | Aliases: A_IG005I10.4, A_IG005I10_4, F5I10.4, F5I10_4	2.9	3.3	-0.4	-3.6	4.01%	2.3
6790	AT2G18970.1 | expressed protein | chr2:8236198-8236837 FORWARD | Aliases: F19F24.17, F19F24_17	3.4	4.3	-0.9	-3.6	4.01%	2.6
6792	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	3.4	4.3	-0.8	-3.6	4.01%	2.8
6794	AT1G52180.1 | major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230 | chr1:19428613-19429597 REVERSE | Aliases: F9I5.3, F9I5_3	3.0	3.8	-0.8	-3.6	4.01%	2.8
6796	AT3G50690.1 | leucine-rich repeat family protein | chr3:18845948-18848078 REVERSE | Aliases: T3A5.70	7.7	9.2	-1.5	-3.6	4.02%	2.7
6797	AT1G51140.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	5.2	6.2	-1.0	-3.6	4.02%	2.8
6799	AT3G25855.1 | expressed protein | chr3:9460658-9461532 REVERSE | Aliases: None	2.4	2.7	-0.3	-3.6	4.02%	2.0
6800	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	4.1	5.2	-1.1	-3.6	4.02%	2.8
6801	AT1G61930.1 | expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584 | chr1:22896766-22897635 FORWARD | Aliases: F8K4.12, F8K4_12	5.8	7.1	-1.3	-3.6	4.03%	2.8
6802	AT3G59120.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	3.6	-0.7	-3.6	4.03%	2.6
6803	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	5.1	6.5	-1.3	-3.6	4.03%	2.9
6805	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	2.8	-0.4	-3.6	4.03%	2.1
6809	AT4G26890.1 | Symbol: MAPKKK16 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:13511845-13513412 FORWARD | Aliases: F10M23.230, F10M23_230	3.7	4.8	-1.0	-3.6	4.03%	2.9
6810	AT2G01410.1 | expressed protein | chr2:174777-176398 REVERSE | Aliases: F10A8.30	6.5	7.1	-0.6	-3.6	4.04%	2.3
6811	AT1G24600.1 | expressed protein | chr1:8720295-8720707 FORWARD | Aliases: None	3.5	4.3	-0.8	-3.6	4.04%	2.7

Rank	Description	Sync	Root	M	t	adj.q	B
6814	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	4.9	6.6	-1.7	-3.6	4.05%	2.9
6815	AT5G49320.1 | expressed protein | chr5:20012251-20013440 REVERSE | Aliases: K21P3.22, K21P3_22	4.7	5.5	-0.9	-3.6	4.05%	2.7
6818	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	2.4	3.0	-0.7	-3.6	4.06%	2.6
6819	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	4.1	5.5	-1.4	-3.6	4.06%	2.8
6820	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	5.6	7.0	-1.4	-3.6	4.06%	2.6
6825	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	3.7	-0.6	-3.6	4.08%	2.6
6826	AT3G14205.1 | 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 2 (SAC2) GI:31415720 | chr3:4715755-4720958 REVERSE | Aliases: None	6.0	7.7	-1.7	-3.6	4.08%	2.7
6831	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	4.7	5.5	-0.8	-3.6	4.11%	2.8
6833	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	3.5	-0.5	-3.6	4.11%	2.6
6838	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	8.3	9.0	-0.7	-3.6	4.11%	2.6
6840	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	4.6	-0.7	-3.6	4.12%	2.6
6841	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	6.0	7.1	-1.1	-3.6	4.12%	2.7
6842	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	3.1	-0.5	-3.6	4.13%	2.4
6844	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	3.7	4.4	-0.7	-3.6	4.13%	2.5
6847	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	4.7	5.4	-0.6	-3.6	4.13%	2.7
6848	AT2G39440.1 | expressed protein | chr2:16471796-16477549 REVERSE | Aliases: F12L6.10, F12L6_10	3.8	4.3	-0.5	-3.6	4.13%	2.5
6849	AT3G43940.1 | expressed protein | chr3:15775252-15776358 REVERSE | Aliases: T15B3.80	3.2	3.8	-0.6	-3.6	4.14%	2.5
6852	AT2G18060.1 | Symbol: ANAC037 | no apical meristem (NAM) family protein, similar to NAC2 (GI:6456751)	2.9	3.6	-0.7	-3.6	4.14%	2.7
6856	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	4.2	5.1	-0.9	-3.6	4.15%	2.8

Rank	Description	Sync	Root	M	t	adj.q	B
6857	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	4.3	4.8	-0.5	-3.6	4.15%	2.4
6860	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	5.3	7.0	-1.7	-3.6	4.15%	2.9
6863	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	3.8	4.9	-1.1	-3.6	4.15%	2.9
6865	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	3.7	5.2	-1.5	-3.6	4.16%	2.8
6866	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	5.7	6.6	-0.9	-3.6	4.17%	2.7
6867	AT4G15840.1 | expressed protein | chr4:8997042-9001045 FORWARD | Aliases: DL3960W, FCAALL.399	6.3	7.0	-0.7	-3.6	4.17%	2.5
6869	AT4G32750.1 | expressed protein | chr4:15795990-15798245 REVERSE | Aliases: F4D11.50, F4D11_50	4.7	5.3	-0.6	-3.6	4.17%	2.6
6870	AT5G03860.1 | malate synthase, putative, strong similarity to glyoxysomal malate synthase from Brassica napus (SP:P13244) | chr5:1032103-1034569 REVERSE | Aliases: MED24.5	3.0	3.5	-0.5	-3.6	4.18%	2.4
6876	AT1G03520.1 | glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein, contains Pfam profile PF02485: Core-2/I-Branching enzyme | chr1:877863-880159 REVERSE | Aliases: F21B7.14	5.4	6.1	-0.6	-3.6	4.19%	2.6
6877	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	4.2	-1.1	-3.6	4.19%	2.7
6881	AT2G43570.1 | chitinase, putative, similar to chitinase class IV GI:722272 from (Brassica napus) | chr2:18083301-18084539 REVERSE | Aliases: F18O19.32	3.9	5.0	-1.2	-3.6	4.22%	2.8
6882	AT2G37840.2 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:15858968-15863379 FORWARD | Aliases: AT2G37850, T8P21.25, T8P21_25	4.6	5.7	-1.1	-3.6	4.22%	2.6
6884	AT1G34320.1 | expressed protein, contains Pfam domain PF05003: protein of unknown function (DUF668) | chr1:12520691-12524341 FORWARD | Aliases: F23M19.3, F23M19_3	4.2	5.1	-0.9	-3.6	4.22%	2.8
6886	AT5G54030.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	3.3	-0.5	-3.6	4.23%	2.2
6887	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)	5.7	6.6	-0.9	-3.6	4.23%	2.7
6888	AT4G34690.1 | expressed protein | chr4:16555468-16556102 REVERSE | Aliases: T4L20.270, T4L20_270	2.6	3.0	-0.5	-3.6	4.23%	2.3
6890	AT1G53100.1 | similar to glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein [Arabidopsis thaliana] (TAIR:At3g15350.1); similar to glycosyltransferase family 14 protein / core-2/I-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	3.7	-0.6	-3.6	4.23%	2.5
6891	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	4.8	5.6	-0.8	-3.6	4.23%	2.6
6892	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	5.7	-0.7	-3.6	4.23%	2.6
6894	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	5.8	7.0	-1.2	-3.6	4.23%	2.7

Rank	Description	Sync	Root	M	t	adj.q	B
6895	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	9.6	-0.5	-3.6	4.24%	2.2
6896	AT2G41140.1 | Symbol: CRK1 | calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium/calmodulin-dependent protein kinase CaMK3 (Nicotiana tabacum) gi:16904226:gb:AAL30820 | chr2:17157465-17160768 FORWARD | Aliases: CDPK RELATED KINASE 1, T3K9.9, T3K9_9	5.4	6.3	-0.9	-3.6	4.24%	2.7
6900	AT2G37360.1 | ABC transporter family protein | chr2:15680634-15682999 REVERSE | Aliases: F3G5.15, F3G5_15	2.4	3.2	-0.8	-3.6	4.24%	2.7
6902	NA	12.5	13.1	-0.5	-3.6	4.25%	1.7
6908	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	3.0	3.7	-0.6	-3.6	4.27%	2.5
6912	AT1G07250.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, similar to UDP-glucose glucosyltransferase GI:453245 from (Manihot esculenta) | chr1:2225899-2227565 FORWARD | Aliases: F10K1.4, F10K1_4	8.2	9.0	-0.8	-3.6	4.27%	2.3
6913	AT5G05190.1 | expressed protein, similar to unknown protein (emb:CAB88044.1) | chr5:1541522-1544365 FORWARD | Aliases: K2A11.6, K2A11_6	4.7	5.3	-0.6	-3.6	4.27%	2.6
6914	AT1G27670.1 | expressed protein | chr1:9627559-9628483 REVERSE | Aliases: T22C5.12, T22C5_12	2.8	3.3	-0.5	-3.6	4.29%	2.4
6916	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	6.2	8.2	-2.0	-3.6	4.30%	2.7
6920	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	2.9	3.3	-0.4	-3.6	4.30%	2.3
6923	AT3G49930.1 | zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type | chr3:18521231-18521948 FORWARD | Aliases: F3A4.10	3.7	4.5	-0.8	-3.6	4.31%	2.7
6924	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	6.6	-1.4	-3.6	4.31%	2.7
6928	AT4G30630.1 | expressed protein | chr4:14950644-14952382 FORWARD | Aliases: F17I23.30, F17I23_30	4.4	5.6	-1.2	-3.6	4.33%	2.6
6931	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	3.3	-0.5	-3.6	4.33%	2.1
6935	AT3G08490.1 | expressed protein | chr3:2574111-2575131 REVERSE | Aliases: T8G24.9	3.4	4.2	-0.8	-3.6	4.33%	2.7
6938	AT2G25510.1 | expressed protein | chr2:10863505-10864234 FORWARD | Aliases: F13B15.17, F13B15_17	2.6	3.1	-0.5	-3.6	4.34%	2.0
6944	AT1G80690.1 | expressed protein | chr1:30333961-30335695 REVERSE | Aliases: F23A5.4, F23A5_4	5.3	6.1	-0.8	-3.6	4.35%	2.6
6945	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	2.5	-0.3	-3.6	4.35%	1.9
6947	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	4.2	5.2	-1.0	-3.6	4.35%	2.7
6948	AT4G34140.1 | D111/G-patch domain-containing protein, contains Pfam PF01585: G-patch domain | chr4:16350736-16354258 FORWARD | Aliases: F28A23.100, F28A23_100	3.5	4.8	-1.3	-3.6	4.35%	2.7
6950	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	3.5	-0.6	-3.6	4.36%	2.5
6952	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	6.0	7.8	-1.8	-3.6	4.36%	2.8

Rank	Description	Sync	Root	M	t	adj.q	B
6957	AT3G56100.1 | Symbol: MRLK | leucine-rich repeat transmembrane protein kinase, putative, hypothetical proteins - Arabidopsis thaliana	3.3	4.0	-0.7	-3.6	4.37%	2.6
6962	AT5G51390.1 | expressed protein, similar to unknown protein (gb:AAB68039.1) | chr5:20895193-20895690 REVERSE | Aliases: MFG13.10, MFG13_10	3.2	4.4	-1.2	-3.5	4.39%	2.5
6964	AT5G20790.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:7039913-7040656 REVERSE | Aliases: T1M15.190, T1M15_190	4.2	5.3	-1.1	-3.5	4.39%	2.8
6966	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	5.7	-0.9	-3.5	4.40%	2.6
6970	AT5G16320.1 | Symbol: FRL1 | expressed protein | chr5:5344505-5346022 FORWARD | Aliases: FRIGIDA LIKE 1, MQK4.4, MQK4_4	4.0	4.5	-0.6	-3.5	4.40%	2.3
6972	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	5.3	5.9	-0.7	-3.5	4.41%	2.5
6974	AT1G21370.2 | expressed protein | chr1:7483772-7486311 FORWARD | Aliases: F24J8.26, F24J8_26	6.9	7.7	-0.8	-3.5	4.41%	2.5
6977	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	5.2	7.2	-2.0	-3.5	4.42%	2.7
6978	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	2.5	2.9	-0.4	-3.5	4.42%	2.2
6979	AT5G51420.1 | long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein, contains similarity to wax synthase wax synthase - Simmondsia chinensis, PID:g5020219 similar to wax synthase (gi:5020219) from Simmondsia chinensis | chr5:20902645-20903952 REVERSE | Aliases: MFG13.13, MFG13_13	3.3	3.9	-0.6	-3.5	4.42%	2.4
6980	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	2.7	-0.3	-3.5	4.42%	1.7
6982	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	4.1	-0.7	-3.5	4.43%	2.5
6983	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	3.5	-0.3	-3.5	4.43%	1.8
6984	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	9.6	10.5	-0.9	-3.5	4.43%	2.3
6994	AT4G26180.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr4:13260272-13262044 REVERSE | Aliases: T25K17.6	4.4	5.0	-0.6	-3.5	4.46%	2.3
6995	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	6.8	7.9	-1.1	-3.5	4.46%	2.6
6996	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	4.8	5.7	-0.9	-3.5	4.46%	2.8
6997	AT4G24990.1 | Symbol: ATGP4 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr4:12849719-12851643 REVERSE | Aliases: F13M23.130, F13M23_130	9.1	10.1	-1.0	-3.5	4.46%	2.5
6998	AT1G30140.1 | expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At5g27260.1) | chr1:10598611-10599680 FORWARD | Aliases: T2H7.6, T2H7_6	3.1	3.5	-0.4	-3.5	4.46%	2.1
7002	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	7.2	-1.0	-3.5	4.48%	2.3

Rank	Description	Sync	Root	M	t	adj.q	B
7004	AT4G08380.1 | proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr4:5311090-5312403 REVERSE | Aliases: T28D5.70, T28D5_70	3.2	4.2	-1.0	-3.5	4.48%	2.7
7009	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	3.5	-0.6	-3.5	4.50%	2.4
7010	AT3G22160.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr3:7817864-7818992 REVERSE | Aliases: MKA23.7	3.6	4.1	-0.5	-3.5	4.50%	2.1
7012	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.	6.4	7.5	-1.1	-3.5	4.50%	2.6
7022	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	9.3	10.6	-1.3	-3.5	4.52%	2.2
7024	AT4G33490.1 | similar to nucellin protein, putative [Arabidopsis thaliana] (TAIR:At1g44130.1); similar to nucellin-like aspartic protease [Oryza sativa (japonica cultivar-group)] (GB:AAY23257.1); contains InterPro domain Aspartic protease A1, pepsin (InterPro:IPR001461)	4.2	5.0	-0.8	-3.5	4.52%	2.6
7025	AT1G63500.1 | protein kinase-related, low similarity to protein kinase (Arabidopsis thaliana); contains Pfam profile: PF00069 Eukaryotic protein kinase domain	3.5	4.1	-0.6	-3.5	4.52%	2.5
7026	AT2G18680.1 | expressed protein | chr2:8101976-8102861 FORWARD | Aliases: MSF3.6, MSF3_6	3.4	4.2	-0.8	-3.5	4.52%	2.5
7027	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	3.9	-0.8	-3.5	4.52%	2.6
7030	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	3.8	5.0	-1.2	-3.5	4.53%	2.8
7032	AT5G45280.2 | pectinacetylesterase, putative, similar to pectinacetylesterase precursor GI:1431629 from (Vigna radiata) | chr5:18362822-18366919 FORWARD | Aliases: K9E15.6, K9E15_6	5.1	5.8	-0.6	-3.5	4.53%	2.5
7033	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	5.5	-0.7	-3.5	4.53%	2.3
7035	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	3.7	4.6	-0.8	-3.5	4.53%	2.7
7037	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	4.4	5.5	-1.2	-3.5	4.53%	2.6
7042	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	7.1	-1.1	-3.5	4.54%	2.5
7043	AT3G49880.1 | glycosyl hydrolase family protein 43, contains similarity to xylanase GI:2645416 from (Caldicellulosiruptor saccharolyticus) | chr3:18507234-18509698 FORWARD | Aliases: T16K5.230	4.4	5.1	-0.7	-3.5	4.54%	2.6
7048	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	5.2	5.9	-0.7	-3.5	4.54%	2.5
7054	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	3.1	4.1	-1.0	-3.5	4.55%	2.6
7060	AT4G34590.1 | Symbol: GBF6 | bZIP transcription factor family protein, similar to common plant regulatory factor 7 GI:9650828 from (Petroselinum crispum) | chr4:16521866-16523235 FORWARD | Aliases: T4L20.170, T4L20_170	7.0	8.6	-1.7	-3.5	4.55%	2.7
7061	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	3.5	-0.6	-3.5	4.55%	2.4

Rank	Description	Sync	Root	M	t	adj.q	B
7062	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	3.4	-0.4	-3.5	4.55%	1.9
7063	AT5G18760.1 | zinc finger (C3HC4-type RING finger) family protein, predicted proteins, Arabidopsis thaliana ; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger) | chr5:6258300-6260882 REVERSE | Aliases: F17K4.10, F17K4_10	3.8	4.2	-0.5	-3.5	4.56%	2.3
7065	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	3.7	-0.9	-3.5	4.57%	2.2
7066	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	4.3	4.9	-0.6	-3.5	4.57%	2.5
7068	AT3G58650.1 | expressed protein | chr3:21707223-21709828 REVERSE | Aliases: F14P22.240	2.9	3.2	-0.3	-3.5	4.58%	1.9
7070	AT3G56500.1 | serine-rich protein-related, contains some similarity to serine-rich proteins | chr3:20954617-20954949 FORWARD | Aliases: T5P19.150	2.7	3.3	-0.6	-3.5	4.60%	2.4
7071	AT3G12730.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr3:4047079-4048621 REVERSE | Aliases: MBK21.11	2.2	2.5	-0.3	-3.5	4.60%	2.1
7074	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)	3.5	4.4	-1.0	-3.5	4.60%	2.4
7075	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	3.5	-0.4	-3.5	4.60%	2.1
7077	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	6.4	7.8	-1.3	-3.5	4.61%	2.6
7079	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	7.7	-1.2	-3.5	4.62%	2.4
7082	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	6.4	8.0	-1.6	-3.5	4.62%	2.7
7083	AT1G70660.1 | 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 | chr1:26644258-26645810 FORWARD | Aliases: F5A18.16, F5A18_16	8.1	9.1	-1.0	-3.5	4.62%	2.7
7085	AT3G47060.1 | Symbol: FTSH7 | encodes an FtsH protease that is localized to the chloroplast | chr3:17343970-17347951 FORWARD | Aliases: F13I12.110, FTSH7	4.8	5.7	-0.8	-3.5	4.62%	2.6
7088	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	3.7	4.3	-0.6	-3.5	4.63%	2.5
7089	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	3.1	4.0	-0.9	-3.5	4.63%	2.6
7090	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	3.2	-0.3	-3.5	4.63%	1.8
7093	AT5G42440.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:16990532-16991802 REVERSE | Aliases: MDH9.13, MDH9_13	3.6	4.1	-0.5	-3.5	4.64%	2.2
7094	AT2G23700.1 | expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547 | chr2:10083449-10087312 REVERSE | Aliases: F27L4.12, F27L4_12	3.7	4.9	-1.1	-3.5	4.64%	2.4
7097	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	4.5	5.3	-0.8	-3.5	4.64%	2.3

Rank	Description	Sync	Root	M	t	adj.q	B
7098	AT1G56660.1 | expressed protein | chr1:21241553-21244223 FORWARD | Aliases: F25P12.91, F25P12_91	6.4	8.5	-2.0	-3.5	4.64%	2.6
7100	AT2G46330.2 | Symbol: AGP16 | arabinogalactan-protein (AGP16), identical to gi:10880509:gb:AAG24284 | chr2:19025581-19026328 REVERSE | Aliases: ARABINOGALACTAN PROTEIN 16, F11C10.2	9.0	10.2	-1.2	-3.5	4.64%	2.6
7104	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	9.5	10.3	-0.8	-3.5	4.65%	2.5
7105	AT2G24130.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:10265228-10268300 FORWARD | Aliases: F27D4.4, F27D4_4	3.1	3.6	-0.5	-3.5	4.65%	2.0
7108	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	3.3	3.8	-0.5	-3.5	4.66%	2.2
7110	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	5.5	6.9	-1.4	-3.5	4.66%	2.7
7112	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)	5.6	6.4	-0.7	-3.5	4.66%	2.4
7116	AT2G25730.1 | expressed protein | chr2:10963380-10979807 REVERSE | Aliases: F3N11.1, F3N11_1	7.2	7.9	-0.7	-3.5	4.68%	2.3
7121	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	6.3	8.0	-1.6	-3.5	4.71%	2.6
7123	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	3.7	-0.7	-3.5	4.71%	2.4
7124	AT3G18670.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023 | chr3:6424141-6426477 REVERSE | Aliases: MVE11.3	3.1	3.6	-0.5	-3.5	4.71%	2.2
7132	AT5G24170.1 | expressed protein | chr5:8189489-8191394 REVERSE | Aliases: K12G2.6, K12G2_6	4.3	5.0	-0.7	-3.5	4.74%	2.5
7137	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	3.8	4.6	-0.8	-3.5	4.75%	2.4
7139	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	2.4	2.8	-0.4	-3.5	4.75%	1.9
7140	AT2G25620.1 | protein phosphatase 2C, putative / PP2C, putative | chr2:10910021-10912323 REVERSE | Aliases: F3N11.7, F3N11_7	4.5	5.5	-1.0	-3.5	4.76%	2.6
7143	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	2.5	3.1	-0.6	-3.5	4.76%	2.3
7144	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	3.5	4.1	-0.6	-3.5	4.76%	2.3
7150	AT3G03570.1 | expressed protein, similar to hypothetical protein GB:CAB38918 (Arabidopsis thaliana) | chr3:856903-860476 FORWARD | Aliases: T12J13.15, T12J13_15	3.7	4.3	-0.6	-3.5	4.78%	2.5
7151	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	7.6	8.8	-1.3	-3.5	4.78%	2.6
7152	AT2G27590.1 | expressed protein | chr2:11784714-11786928 REVERSE | Aliases: F10A12.26, F10A12_26	4.9	5.6	-0.7	-3.5	4.78%	2.4
7157	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	2.5	3.1	-0.5	-3.5	4.79%	2.1
7161	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	5.0	-1.3	-3.5	4.80%	2.6

Rank	Description	Sync	Root	M	t	adj.q	B
7162	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	6.3	7.4	-1.2	-3.5	4.80%	2.7
7163	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	6.2	7.4	-1.2	-3.5	4.80%	2.4
7165	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	6.6	7.5	-0.9	-3.5	4.82%	2.6
7166	AT1G17580.1 | Symbol: MYA1 | myosin, putative, similar to myosin GI:433663 from (Arabidopsis thaliana) | chr1:6039296-6049549 FORWARD | Aliases: ATMYA1, F1L3.28, F1L3_28	5.7	6.5	-0.8	-3.5	4.83%	2.6
7171	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	6.9	7.6	-0.8	-3.5	4.84%	2.5
7174	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	3.3	6.2	-2.9	-3.5	4.85%	2.5
7175	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	3.3	6.2	-2.9	-3.5	4.85%	2.5
7178	AT4G14020.1 | rapid alkalinization factor (RALF) family protein | chr4:8095210-8095731 REVERSE | Aliases: DL3050C, FCAALL.138	4.1	5.2	-1.1	-3.5	4.85%	2.7
7181	AT3G06780.1 | glycine-rich protein | chr3:2143494-2144527 FORWARD | Aliases: F3E22.8	4.7	5.2	-0.5	-3.5	4.85%	2.3
7182	AT5G01620.2 | expressed protein, several hypothetical proteins - Arabidopsis thaliana | chr5:232732-234878 FORWARD | Aliases: F7A7.140, F7A7_140	6.7	7.8	-1.0	-3.5	4.86%	2.4
7184	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	5.6	6.9	-1.3	-3.5	4.87%	2.5
7187	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	4.9	6.8	-1.8	-3.5	4.88%	2.5
7191	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	5.6	-0.9	-3.5	4.89%	2.7
7192	AT1G07680.1 | hypothetical protein | chr1:2376059-2376990 FORWARD | Aliases: F24B9.23, F24B9_23	3.5	4.3	-0.9	-3.5	4.90%	2.5
7193	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	9.7	-2.1	-3.5	4.90%	2.5
7194	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	3.6	4.7	-1.1	-3.5	4.91%	2.6
7195	AT4G25160.1 | protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain | chr4:12903308-12907348 REVERSE | Aliases: F24A6.13	3.2	3.9	-0.6	-3.5	4.91%	2.4
7204	AT1G47410.1 | expressed protein, identical to hypothetical protein GB:AAD46041 GI:5668815 from (Arabidopsis thaliana) | chr1:17397258-17397948 FORWARD | Aliases: T3F24.15	5.5	6.8	-1.3	-3.4	4.93%	2.7
7207	AT2G43590.1 | chitinase, putative, similar to basic endochitinase CHB4 precursor SP:Q06209 from (Brassica napus) | chr2:18088408-18089826 REVERSE | Aliases: F18O19.30	4.3	4.8	-0.5	-3.4	4.94%	2.3
7208	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	4.1	-0.6	-3.4	4.95%	2.2
7209	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	3.3	-0.8	-3.4	4.95%	2.4

Rank	Description	Sync	Root	M	t	adj.q	B
7215	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	4.8	5.8	-1.0	-3.4	4.96%	2.7
7216	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	4.1	4.9	-0.8	-3.4	4.97%	2.6
7217	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	4.3	5.5	-1.2	-3.4	4.97%	2.7
7219	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	11.8	12.4	-0.6	-3.4	4.97%	1.8
7221	AT5G53110.1 | expressed protein | chr5:21546248-21546970 FORWARD | Aliases: MFH8.3, MFH8_3	3.0	3.7	-0.7	-3.4	4.98%	2.4
7222	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	2.7	3.1	-0.4	-3.4	4.98%	2.1
7224	AT1G05030.1 | hexose transporter, putative, similar to hexose transporters from Nicotiana tabacum (GI:8347244), Solanum tuberosum (GI:8347246), Arabidopsis thaliana (GI:8347250); contains Pfam profile PF00083: major facilitator superfamily protein | chr1:1438151-1441416 REVERSE | Aliases: T7A14.10, T7A14_10	5.6	6.8	-1.2	-3.4	4.98%	2.5
7226	AT4G38240.2 | Symbol: CGL1 | alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase, putative, similar to N-acetylglucosaminyltransferase I from Arabidopsis thaliana (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	5.0	-1.0	-3.4	4.99%	2.3
7229	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	8.3	10.6	-2.4	-3.4	5.00%	2.6

Rank	Description	Sync	Root	M	t	adj.q	B
7232	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	5.5	4.6	0.9	3.4	5.0%	2.4
7233	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	3.3	-0.4	-3.4	5.0%	2.0
7234	AT1G49160.2 | Symbol: WNK7 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:18182972-18185535 REVERSE | Aliases: F27J15.7, F27J15_7	5.0	6.3	-1.3	-3.4	5.0%	2.5
7235	AT1G23880.1 | NHL repeat-containing protein, contains Pfam profile PF01436: NHL repeat	3.8	3.4	0.4	3.4	5.0%	2.1
7236	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	4.3	-0.6	-3.4	5.0%	2.2
7237	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	4.0	3.3	0.6	3.4	5.0%	2.3
7238	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	2.5	-0.4	-3.4	5.0%	1.8
7239	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	6.3	7.9	-1.5	-3.4	5.0%	2.6
7240	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	3.3	4.0	-0.7	-3.4	5.0%	2.5
7241	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)	5.7	4.6	1.1	3.4	5.0%	2.7
7242	AT5G44780.1 | expressed protein, low similarity to SP:Q38732 DAG protein, chloroplast precursor {Antirrhinum majus} | chr5:18085327-18087868 FORWARD | Aliases: K23L20.12, K23L20_12	3.8	3.0	0.8	3.4	5.0%	2.4
7243	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	7.3	5.7	1.6	3.4	5.0%	2.6
7244	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	4.8	4.0	0.8	3.4	5.0%	2.5
7245	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	2.8	-0.4	-3.4	5.0%	2.1
7246	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	5.8	0.9	3.4	5.0%	2.4
7247	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	5.5	4.5	1.0	3.4	5.0%	2.5
7248	AT1G51580.1 | KH domain-containing protein | chr1:19129251-19131827 FORWARD | Aliases: F5D21.23, F5D21_23	6.4	5.5	0.9	3.4	5.0%	2.6
7249	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	6.9	5.9	1.1	3.4	5.0%	2.4
7250	AT1G01300.1 | aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease | chr1:116943-118764 FORWARD | Aliases: F6F3.10, F6F3_10	6.2	4.4	1.9	3.4	5.0%	2.7

Rank	Description	Sync	Root	M	t	adj.q	B
7251	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: ATAHL, F24B18.1, F24B18_1, HAL2 LIKE	7.3	5.7	1.6	3.4	5.0%	2.5
7252	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) (Oryctolagus cuniculus); contains Pfam domain, PF01603: Protein phosphatase 2A regulatory B subunit (B56 family) | chr5:8882471-8884837 REVERSE | Aliases: T14C9.50, T14C9_50	5.1	4.3	0.8	3.4	5.1%	2.5
7253	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	9.2	7.6	1.6	3.4	5.1%	2.6
7254	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	5.0	-2.2	-3.4	5.1%	2.5
7255	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	11.2	9.1	2.1	3.4	5.1%	2.5
7256	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	3.4	-0.3	-3.4	5.1%	2.0
7257	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	6.4	-0.8	-3.4	5.1%	2.4
7258	AT5G14370.1 | expressed protein | chr5:4631894-4633716 REVERSE | Aliases: F18O22.160, F18O22_160	3.5	2.8	0.7	3.4	5.1%	2.5
7259	AT1G49700.1 | expressed protein, ; expression supported by MPSS | chr1:18392460-18393976 REVERSE | Aliases: F14J22.9, F14J22_9	3.4	2.8	0.5	3.4	5.1%	2.2
7260	AT5G49550.1 | expressed protein | chr5:20123879-20124417 REVERSE | Aliases: K6M13.19	7.6	6.9	0.6	3.4	5.1%	2.4
7261	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	8.0	-1.8	-3.4	5.1%	2.3
7262	AT5G59510.1 | expressed protein | chr5:24007300-24007922 FORWARD | Aliases: F2O15.21, F2O15_21	2.3	2.5	-0.3	-3.4	5.1%	1.7
7263	AT5G22700.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.5	4.3	-0.9	-3.4	5.1%	2.1
7264	AT5G40150.1 | peroxidase, putative, identical to peroxidase ATP26a {Arabidopsis thaliana} GP:1890317:emb:CAA72487 | chr5:16076737-16078271 REVERSE | Aliases: MSN9.50, MSN9_50	3.9	3.5	0.5	3.4	5.1%	2.1
7265	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	10.1	8.8	1.3	3.4	5.1%	2.5
7266	AT3G46720.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:17221840-17223333 REVERSE | Aliases: T6H20.250	4.1	4.7	-0.6	-3.4	5.1%	2.1
7267	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	2.6	-0.4	-3.4	5.1%	1.8
7268	ATCG00480.1 | Symbol: ATPB | chloroplast-encoded gene for beta subunit of ATP synthase | chrC:52660-54156 REVERSE | Aliases: ATPB	9.4	7.6	1.7	3.4	5.1%	2.5
7269	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}	11.0	10.5	0.4	3.4	5.1%	2.1
7270	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	4.8	5.8	-1.0	-3.4	5.1%	2.5

Rank	Description	Sync	Root	M	t	adj.q	B
7271	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	6.0	6.7	-0.7	-3.4	5.1%	2.3
7272	AT4G26500.1 | Symbol: EMB1374 | BolA-like family protein / Fe-S metabolism associated domain-containing protein, similar to SufE protein (Erwinia chrysanthemi) GI: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	6.6	5.9	0.7	3.4	5.1%	2.5
7273	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	7.0	-1.7	-3.4	5.1%	2.7
7274	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	8.0	8.8	-0.8	-3.4	5.1%	2.2
7275	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	2.9	3.3	-0.4	-3.4	5.1%	2.0
7276	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	7.5	6.9	0.6	3.4	5.1%	2.3
7277	AT1G79975.2 | expressed protein | chr1:30089065-30090457 FORWARD | Aliases: None	5.2	6.0	-0.8	-3.4	5.1%	2.5
7278	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	3.1	3.6	-0.5	-3.4	5.1%	2.0
7279	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	4.1	-0.5	-3.4	5.1%	2.3
7280	AT1G02820.1 | late embryogenesis abundant 3 family protein / LEA3 family protein, similar to late embryogenis 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	3.9	3.2	0.6	3.4	5.1%	2.3
7281	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	4.9	5.6	-0.6	-3.4	5.1%	2.4
7282	AT2G36350.1 | protein kinase, putative, similar to protein kinase KIPK (KCBP-interacting protein kinase) (Arabidopsis thaliana) gi:7716430:gb:AAF68383	4.5	3.7	0.7	3.4	5.1%	2.5
7283	AT4G32150.1 | Symbol: VAMP7C |	7.1	7.8	-0.7	-3.4	5.1%	2.4
7284	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	2.8	3.4	-0.6	-3.4	5.1%	2.4
7285	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	6.2	7.4	-1.2	-3.4	5.1%	2.5
7286	AT1G28380.1 | expressed protein | chr1:9963579-9966306 FORWARD | Aliases: F3M18.18, F3M18_18	5.3	6.1	-0.8	-3.4	5.1%	2.4
7287	AT3G47680.1 | expressed protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana) | chr3:17588468-17589376 REVERSE | Aliases: T23J7.10	3.9	5.5	-1.6	-3.4	5.2%	2.6
7288	AT3G08510.2 | Symbol: ATPLC2 |	5.2	6.4	-1.2	-3.4	5.2%	2.4
7289	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	5.0	0.5	3.4	5.2%	2.1
7290	AT2G42840.2 | Symbol: PDF1 | protodermal factor 1 (PDF1), identical to protodermal factor 1 (Arabidopsis thaliana) gi:4929130:gb:AAD33869 | chr2:17833078-17834560 REVERSE | Aliases: F7D19.16, F7D19_16, PROTODERMAL FACTOR 1	2.9	3.6	-0.6	-3.4	5.2%	2.0
7291	AT1G26630.1 | eukaryotic translation initiation factor 5A, putative / eIF-5A, putative, strong similariy to SP:Q9AXQ6 Eukaryotic translation initiation factor 5A-1 (eIF-5A 1) {Lycopersicon esculentum} | chr1:9205823-9207402 FORWARD | Aliases: T24P13.1, T24P13_1	11.4	9.7	1.7	3.4	5.2%	2.5

Rank	Description	Sync	Root	M	t	adj.q	B
7292	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	6.6	8.0	-1.3	-3.4	5.2%	2.2
7293	AT2G26170.2 | Symbol: CYP711A1 | thromboxane-A synthase, putative / cytochrome P450 family protein, simiar 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	9.5	8.6	0.9	3.4	5.2%	2.3
7294	AT2G42700.1 | expressed protein | chr2:17785429-17789167 FORWARD | Aliases: F14N22.4	6.2	5.4	0.8	3.4	5.2%	2.5
7295	AT2G40970.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr2:17104628-17105773 REVERSE | Aliases: T20B5.17, T20B5_17	6.9	5.8	1.1	3.4	5.2%	2.4
7296	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	3.5	-0.4	-3.4	5.2%	2.0
7297	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	4.5	3.8	0.7	3.4	5.2%	2.3
7298	AT4G24100.1 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr4:12515086-12519851 FORWARD | Aliases: T19F6.90, T19F6_90	3.0	3.9	-0.9	-3.4	5.2%	2.5
7299	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	3.9	-0.5	-3.4	5.2%	2.2
7300	AT5G05480.1 | expressed protein | chr5:1622071-1624270 REVERSE | Aliases: MOP10.2, MOP10_2	6.6	7.6	-1.0	-3.4	5.2%	2.5
7301	AT3G63270.1 | expressed protein | chr3:23386592-23388448 REVERSE | Aliases: F16M2.120	3.0	3.4	-0.4	-3.4	5.2%	1.9
7302	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	11.1	9.4	1.7	3.4	5.2%	2.3
7303	AT1G03270.1 | expressed protein, contains Pfam profile PF01595: Domain of unknown function | chr1:799191-802436 FORWARD | Aliases: F15K9.13, F15K9_13	5.4	3.8	1.6	3.4	5.2%	2.6
7304	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	2.9	2.4	0.4	3.4	5.2%	2.0
7305	AT5G59410.1 | expressed protein | chr5:23976815-23978032 REVERSE | Aliases: F2O15.9, F2O15_9	8.3	7.5	0.8	3.4	5.2%	2.4
7306	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	10.2	0.8	3.4	5.2%	2.3
7307	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	6.8	5.6	1.2	3.4	5.2%	2.4
7308	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	4.7	1.1	3.4	5.2%	2.5
7309	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	11.4	10.7	0.7	3.4	5.2%	2.2
7310	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	3.6	-0.8	-3.4	5.2%	2.3
7311	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	2.5	-0.4	-3.4	5.2%	2.1
7312	AT3G51290.1 | proline-rich family protein | chr3:19050959-19053548 FORWARD | Aliases: F24M12.330	3.6	3.0	0.6	3.4	5.2%	2.3

Rank	Description	Sync	Root	M	t	adj.q	B
7313	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	3.5	-0.3	-3.4	5.2%	1.9
7314	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	2.6	3.3	-0.6	-3.4	5.2%	2.0
7315	AT5G50730.1 | expressed protein, ; expression supported by MPSS | chr5:20653209-20653628 REVERSE | Aliases: MFB16.13, MFB16_13	6.7	4.9	1.9	3.4	5.2%	2.6
7316	AT1G80940.2 | expressed protein | chr1:30415667-30417021 FORWARD | Aliases: F23A5.30, F23A5_30	4.7	5.7	-1.0	-3.4	5.2%	2.5
7317	AT4G24430.1 | expressed protein | chr4:12630729-12633085 FORWARD | Aliases: T22A6.260, T22A6_260	2.6	3.2	-0.6	-3.4	5.2%	2.0
7318	AT1G79610.1 | sodium proton exchanger, putative (NHX6), identical to Na+/H+ exchanger 6 (Arabidopsis thaliana) gi:19919848:gb:AAM08407 (Plant J. (2002) In press); contains similarity to Na+/H+ antiporter GI:1655701 from (Xenopus laevis); 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	7.2	-0.8	-3.4	5.2%	2.5
7319	AT2G25240.1 | serpin, putative / serine protease inhibitor, putative, similar to phloem serpin-1 (Cucurbita maxima) GI:9937311; contains Pfam profile PF00079: Serpin (serine protease inhibitor) | chr2:10758847-10760206 REVERSE | Aliases: T22F11.17, T22F11_17	5.0	5.7	-0.7	-3.4	5.2%	2.3
7320	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	4.1	3.2	0.9	3.4	5.2%	2.6
7321	AT4G30996.1 | expressed protein | chr4:15101366-15102690 FORWARD | Aliases: None	7.6	6.6	1.0	3.4	5.2%	2.2
7322	AT1G19690.1 | expressed protein, similar to (SP:P76370) Protein yeeZ precursor. {Escherichia coli O157:H7} | chr1:6807706-6809560 REVERSE | Aliases: F14P1.35, F14P1_35	6.5	5.4	1.1	3.4	5.2%	2.6
7323	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	5.5	4.4	1.2	3.4	5.2%	2.5
7324	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	7.9	9.2	-1.3	-3.4	5.2%	2.3
7325	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	5.0	7.0	-2.0	-3.4	5.2%	2.6
7326	AT2G18350.1 | zinc finger homeobox family protein / ZF-HD homeobox family protein | chr2:7978099-7979163 REVERSE | Aliases: T30D6.14, T30D6_14	3.8	4.7	-0.9	-3.4	5.2%	2.5
7327	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	6.2	1.7	3.4	5.2%	2.6
7328	AT3G52030.1 | F-box family protein / WD-40 repeat family protein | chr3:19312850-19315205 FORWARD | Aliases: F4F15.140	6.7	7.5	-0.8	-3.4	5.2%	2.0
7329	AT2G38310.1 | expressed protein, low similarity to early flowering protein 1 (Asparagus officinalis) GI:1572683, SP:P80889 Ribonuclease 1 (EC 3.1.-.-) {Panax ginseng}	8.2	9.4	-1.2	-3.4	5.2%	2.4
7330	AT1G22150.1 | Symbol: SULTR1;3 | sulfate transporter (Sultr1;3), identical to sulfate tansporter 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 TANSPORTER SULTR1;3	4.0	3.3	0.7	3.4	5.2%	2.4
7331	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	5.4	4.0	1.4	3.4	5.2%	2.5
7332	AT5G25080.1 | expressed protein | chr5:8643675-8647061 FORWARD | Aliases: T11H3.90, T11H3_90	4.5	3.2	1.3	3.4	5.2%	2.3

Rank	Description	Sync	Root	M	t	adj.q	B
7333	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	4.4	3.8	0.6	3.4	5.2%	2.3
7334	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	6.2	-3.6	-3.4	5.2%	2.5
7335	AT3G12720.1 | myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA binding domain | chr3:4043317-4044616 REVERSE | Aliases: MBK21.26	2.2	2.6	-0.4	-3.4	5.2%	1.5
7336	AT3G13060.2 | expressed protein, contains Pfam profile PF04146: YT521-B-like family | chr3:4180582-4183982 FORWARD | Aliases: MGH6.21	7.5	6.7	0.8	3.4	5.2%	2.4
7337	AT1G66160.2 | U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain | chr1:24640859-24642271 FORWARD | Aliases: F15E12.6, F15E12_6	4.7	5.8	-1.0	-3.4	5.2%	2.4
7338	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	6.9	5.2	1.7	3.4	5.2%	2.6
7339	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	11.0	12.7	-1.7	-3.4	5.2%	2.2
7340	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	3.7	-0.7	-3.4	5.2%	2.4
7341	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	3.9	-0.6	-3.4	5.2%	2.2
7342	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	9.7	8.8	0.9	3.4	5.3%	2.6
7343	AT2G36220.1 | expressed protein | chr2:15199559-15200777 FORWARD | Aliases: F2H17.17, F2H17_17	3.2	4.1	-1.0	-3.4	5.3%	2.6
7344	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	7.6	9.6	-2.0	-3.4	5.3%	2.6
7345	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 MICROSPOROCYTES1, EXS, EXTRA SPOROGENOUS CELL, T28J14.220, T28J14_220	3.0	3.8	-0.8	-3.4	5.3%	2.3
7346	AT5G48760.1 | 60S ribosomal protein L13A (RPL13aD) | chr5:19788364-19789948 REVERSE | Aliases: K24G6.9, K24G6_9	6.9	5.6	1.3	3.4	5.3%	2.5
7347	AT5G15980.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:5213084-5215623 FORWARD | Aliases: F1N13.120, F1N13_120	6.2	5.1	1.1	3.4	5.3%	2.4
7348	AT5G04650.1 | hypothetical protein, predicted protein, Arabidopsi thaliana | chr5:1334404-1334957 FORWARD | Aliases: T1E3.10, T1E3_10	4.4	5.8	-1.4	-3.4	5.3%	2.4
7349	NA	11.6	12.2	-0.6	-3.4	5.3%	1.2
7350	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	9.0	7.3	1.7	3.4	5.3%	2.5
7351	AT4G34490.1 | Symbol: ATCAP1 |	8.5	7.7	0.8	3.4	5.3%	2.3
7352	AT5G24100.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:8149219-8151311 FORWARD | Aliases: MZF18.1, MZF18_1	2.5	3.0	-0.4	-3.4	5.3%	2.1
7353	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	7.8	5.8	2.1	3.4	5.3%	2.6

Rank	Description	Sync	Root	M	t	adj.q	B
7354	AT1G03170.1 | expressed protein | chr1:769632-770684 FORWARD | Aliases: F15K9.22, F15K9_22	3.8	3.2	0.6	3.4	5.3%	2.4
7355	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	4.0	-0.8	-3.4	5.3%	2.5
7356	AT5G52410.2 | expressed protein | chr5:21293182-21296669 FORWARD | Aliases: K24M7.15, K24M7_15	4.2	2.8	1.4	3.4	5.3%	2.5
7357	AT5G38690.1 | expressed protein | chr5:15496407-15500291 REVERSE | Aliases: MBB18.24, MBB18_24	4.3	3.6	0.7	3.4	5.3%	2.3
7358	AT3G15060.1 | Ras-related GTP-binding family protein, similar to GTP-binding protein GI:303742 from (Pisum sativum); contains Pfam profile: PF00071 ras family	4.6	3.7	0.9	3.4	5.3%	2.4
7359	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	6.5	7.1	-0.7	-3.4	5.3%	2.3
7360	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	3.6	3.2	0.4	3.4	5.3%	2.1
7361	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	4.8	-1.2	-3.4	5.3%	2.4
7362	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	9.4	10.8	-1.3	-3.4	5.3%	2.4
7363	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	5.0	5.6	-0.6	-3.4	5.3%	2.1
7364	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	3.6	-0.7	-3.4	5.3%	2.4
7365	AT5G64890.1 | expressed protein | chr5:25951798-25952735 FORWARD | Aliases: MXK3.12, MXK3_12	4.2	5.8	-1.5	-3.4	5.3%	2.5
7366	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	3.4	2.9	0.5	3.4	5.3%	2.1
7367	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	3.0	3.8	-0.8	-3.4	5.3%	2.3
7368	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	4.4	3.6	0.7	3.4	5.3%	2.4
7369	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	2.2	0.3	3.4	5.3%	1.8
7370	AT3G51940.1 | expressed protein | chr3:19284472-19286247 REVERSE | Aliases: F4F15.50	5.5	7.6	-2.1	-3.4	5.3%	2.6
7371	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	6.4	7.8	-1.5	-3.4	5.3%	2.4
7372	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	4.1	3.7	0.4	3.4	5.3%	2.0

Rank	Description	Sync	Root	M	t	adj.q	B
7373	AT5G12470.1 | expressed protein | chr5:4044625-4047439 REVERSE | Aliases: None	10.6	9.6	1.0	3.4	5.3%	2.1
7374	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	7.0	5.8	1.2	3.4	5.4%	2.4
7375	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	11.4	0.9	3.4	5.4%	1.9
7376	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	5.1	4.0	1.1	3.4	5.4%	2.3
7377	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	5.4	4.7	0.7	3.4	5.4%	2.0
7378	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	7.9	6.4	1.6	3.4	5.4%	2.6
7379	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	4.1	4.9	-0.8	-3.4	5.4%	2.3
7380	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)	10.9	9.0	1.9	3.4	5.4%	2.4
7381	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	7.6	8.9	-1.3	-3.4	5.4%	2.3
7382	AT1G12310.1 | calmodulin, putative, similar to calmodulin SP:P04465 from (Trypanosoma brucei gambiense) | chr1:4187163-4188054 REVERSE | Aliases: F5O11.35, F5O11_35	7.3	5.7	1.7	3.4	5.4%	2.4
7383	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	9.4	1.0	3.4	5.4%	2.1
7384	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:BAB63916; identical to cDNA ERD7 partial cds GI:15320411 | chr2:7762687-7764934 REVERSE | Aliases: EARLY RESPONSIVE TO DEHYDRATION 7, T13L16.14, T13L16_14	8.0	9.5	-1.5	-3.4	5.4%	2.4
7385	AT4G32960.1 | expressed protein | chr4:15908621-15910183 REVERSE | Aliases: F26P21.80, F26P21_80	7.8	6.5	1.3	3.4	5.4%	2.3
7386	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	7.6	4.8	2.8	3.4	5.4%	2.5
7387	AT4G15140.1 | expressed protein | chr4:8639422-8640292 REVERSE | Aliases: DL3615C, FCAALL.236	3.2	2.5	0.7	3.4	5.4%	2.2
7388	AT1G64980.1 | expressed protein | chr1:24141180-24142924 REVERSE | Aliases: F13O11.28, F13O11_28	6.5	5.8	0.7	3.4	5.4%	2.2
7389	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	7.6	6.0	1.6	3.4	5.4%	2.6
7390	AT3G45260.1 | zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type | chr3:16607366-16609683 REVERSE | Aliases: F18N11.20	2.9	3.8	-0.8	-3.4	5.4%	2.2

Rank	Description	Sync	Root	M	t	adj.q	B
7391	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	4.2	4.9	-0.7	-3.4	5.4%	2.3
7392	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	7.6	8.5	-0.9	-3.4	5.4%	2.3
7393	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	3.3	2.4	0.9	3.4	5.4%	2.3
7394	AT4G11870.1 | expressed protein | chr4:7140489-7140713 REVERSE | Aliases: T26M18.80, T26M18_80	4.1	2.7	1.3	3.4	5.4%	2.2
7395	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	7.1	8.5	-1.4	-3.4	5.4%	2.4
7396	AT3G08610.1 | expressed protein | chr3:2615432-2616809 REVERSE | Aliases: F17O14.8	12.5	11.9	0.6	3.4	5.4%	1.3
7397	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	6.4	4.5	1.9	3.4	5.4%	2.4
7398	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	3.1	2.7	0.4	3.4	5.4%	2.0
7399	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	4.2	3.6	0.6	3.4	5.4%	2.3
7400	AT1G16170.1 | expressed protein | chr1:5538731-5539790 REVERSE | Aliases: T24D18.25, T24D18_25	9.1	9.6	-0.5	-3.4	5.4%	1.9
7401	AT2G39120.1 | expressed protein | chr2:16328872-16330035 FORWARD | Aliases: T7F6.29, T7F6_29	3.9	3.3	0.6	3.4	5.4%	2.2
7402	AT3G21790.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:7676934-7678421 REVERSE | Aliases: MSD21.15	5.8	4.3	1.5	3.4	5.4%	2.6
7403	AT2G41380.1 | embryo-abundant protein-related, similar to embryo-abundant protein (Picea glauca) GI:1350531 | chr2:17259019-17260135 FORWARD | Aliases: F13H10.7, F13H10_7	3.7	3.2	0.5	3.4	5.4%	2.1
7404	AT1G21670.1 | expressed protein, similar to TolB protein precursor (SP:P50601) {Pseudomonas aeruginosa} | chr1:7610387-7612671 FORWARD | Aliases: F8K7.9, F8K7_9	8.8	6.7	2.1	3.4	5.4%	2.4
7405	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	2.5	2.8	-0.3	-3.4	5.4%	1.8
7406	AT1G64790.1 | translational activator family protein, similar to HsGCN1 (Homo sapiens) GI:2282576 | chr1:24068600-24085571 REVERSE | Aliases: F13O11.35, F13O11_35	5.7	5.0	0.7	3.4	5.4%	2.3
7407	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	5.7	6.5	-0.8	-3.4	5.4%	2.4
7408	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	4.1	3.3	0.7	3.4	5.4%	2.0
7409	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	4.5	-0.4	-3.4	5.4%	1.9
7410	AT1G80190.1 | expressed protein | chr1:30164368-30166007 FORWARD | Aliases: F18B13.27, F18B13_27	5.0	3.9	1.2	3.4	5.4%	2.5
7411	AT2G15630.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:6821603-6823486 FORWARD | Aliases: F9O13.18	4.2	3.3	0.9	3.4	5.5%	2.5

Rank	Description	Sync	Root	M	t	adj.q	B
7412	AT3G57540.1 | remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region | chr3:21312374-21314038 REVERSE | Aliases: T8H10.140	8.2	9.7	-1.6	-3.4	5.5%	2.3
7413	AT4G25480.1 | Symbol: DREB1A |	3.2	3.9	-0.8	-3.4	5.5%	2.3
7414	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	5.5	4.5	0.9	3.4	5.5%	2.5
7415	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	3.2	-0.5	-3.4	5.5%	1.8
7416	AT4G31430.3 | similar to nucleoporin-related [Arabidopsis thaliana] (TAIR:At5g20200.1); similar to OSJNBa0071I13.9 [Oryza sativa (japonica cultivar-group)] (GB:CAE03408.3) | chr4:15248462-15252843 FORWARD | Aliases: F3L17.8	2.7	3.2	-0.5	-3.4	5.5%	1.9
7417	AT5G26140.1 | lysine decarboxylase family protein, contains Pfam profile PF03641: decarboxylase family protein	2.4	2.9	-0.5	-3.4	5.5%	1.8
7418	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	3.3	-0.5	-3.4	5.5%	2.0
7419	AT3G21200.1 | expressed protein | chr3:7436078-7438419 FORWARD | Aliases: MXL8.5	8.3	7.2	1.0	3.4	5.5%	2.4
7420	AT1G74320.1 | choline kinase, putative, similar to GmCK2p choline kinase gi:1438881:gb:AAC49375 | chr1:27944334-27946865 FORWARD | Aliases: F1O17.1, F1O17_1	4.0	2.8	1.2	3.4	5.5%	2.3
7421	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	3.4	3.9	-0.5	-3.4	5.5%	2.1
7422	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	3.0	-0.5	-3.4	5.5%	2.2
7423	AT5G51670.1 | expressed protein, contains Pfam domain PF05003: protein of unknown function (DUF668) | chr5:21010786-21012322 FORWARD | Aliases: K10D11.2, K10D11_2	3.4	5.0	-1.6	-3.4	5.5%	2.5
7424	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	3.3	4.1	-0.8	-3.4	5.5%	2.5
7425	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	4.0	2.3	3.4	5.5%	2.5
7426	AT4G26690.1 | glycerophosphoryl diester phosphodiesterase family protein, weak similarity to glycerophosphodiester phosphodiesterase (Borrelia hermsii) GI:1399038; contains Pfam profile PF03009: Glycerophosphoryl diester phosphodiesterase family | chr4:13456034-13460025 REVERSE | Aliases: F10M23.30, F10M23_30	3.5	4.3	-0.7	-3.4	5.5%	2.1
7427	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	3.7	2.8	0.9	3.4	5.5%	2.5
7428	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	3.6	4.3	-0.8	-3.4	5.5%	2.4
7429	AT3G21470.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:7563614-7565254 FORWARD | Aliases: MIL23.2	2.8	2.4	0.3	3.4	5.5%	1.8
7430	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	4.5	5.8	-1.3	-3.4	5.5%	2.4
7431	AT5G40380.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr5:16169375-16172405 FORWARD | Aliases: MPO12.90, MPO12_90	2.4	2.1	0.2	3.4	5.5%	1.5
7432	AT2G32240.1 | expressed protein, contains Pfam profile: PF04508 viral A-type inclusion protein repeat | chr2:13691376-13695401 REVERSE | Aliases: F22D22.1, F22D22_1	9.3	10.3	-1.1	-3.4	5.5%	2.2

Rank	Description	Sync	Root	M	t	adj.q	B
7433	AT2G05890.1 | expressed protein, includes At2g05890, At4g07450, At3g30630, At3g43100, At2g09960, At3g30550, At1g39430, At2g10460, At4g03640, At5g35250	2.1	2.7	-0.6	-3.4	5.5%	1.9
7434	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	6.1	4.9	1.2	3.3	5.5%	2.6
7435	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)	5.1	5.7	-0.6	-3.3	5.5%	2.3
7436	AT4G29170.1 | Mnd1 family protein, contains Pfam PF03962: Mnd1 family | chr4:14382845-14385381 FORWARD | Aliases: F19B15.200, F19B15_200	3.8	2.9	0.9	3.3	5.5%	2.3
7437	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	5.6	4.6	1.0	3.3	5.5%	2.4
7438	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	7.7	6.3	1.4	3.3	5.5%	2.5
7439	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	2.6	-0.4	-3.3	5.6%	1.9
7440	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	2.7	3.2	-0.5	-3.3	5.6%	2.2
7441	AT1G08720.1 | Symbol: EDR1 | mitogen-activated protein kinase kinase kinase (MAPKKK) (EDR1), identical to EDR1, a MAP kinase kinase kinase (Arabidopsis thaliana) gi:11127925:gb:AAG31143 | chr1:2774033-2779300 FORWARD | Aliases: ENHANCED DISEASE RESISTANCE 1, F22O13.20, F22O13_20, MAPKK KINASE EDR1	4.1	4.7	-0.6	-3.3	5.6%	2.1
7442	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	5.8	4.7	1.1	3.3	5.6%	2.4
7443	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	4.4	5.2	-0.8	-3.3	5.6%	2.3
7444	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	5.4	-0.6	-3.3	5.6%	2.0
7445	AT1G18380.1 | expressed protein | chr1:6325869-6326621 FORWARD | Aliases: F15H18.27, F15H18_27	3.1	3.7	-0.6	-3.3	5.6%	2.1
7446	AT3G61600.2 | Symbol: ATPOB1 |	7.5	8.4	-0.9	-3.3	5.6%	2.1
7447	AT5G41880.1 | DNA primase small subunit family, contains Pfam profile: PF01896 DNA primase small subunit | chr5:16778299-16781011 FORWARD | Aliases: K16L22.17, K16L22_17	5.5	4.3	1.2	3.3	5.6%	2.5
7448	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	3.2	0.5	3.3	5.6%	2.1
7449	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	5.8	4.8	1.0	3.3	5.6%	2.3
7450	AT2G47180.1 | galactinol synthase, putative, similar to galactinol synthase, isoform GolS-1 GI:5608497 from (Ajuga reptans) | chr2:19375868-19377511 REVERSE | Aliases: T8I13.2	4.6	3.8	0.8	3.3	5.6%	2.4
7451	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	4.7	4.1	0.6	3.3	5.6%	2.2
7452	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	5.7	5.0	0.6	3.3	5.6%	2.2

Rank	Description	Sync	Root	M	t	adj.q	B
7453	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	4.0	3.0	1.0	3.3	5.6%	2.3
7454	AT4G32560.3 | similar to MGC89046 protein [Xenopus tropicalis] (GB:AAH82492.1)	4.9	4.2	0.7	3.3	5.6%	2.2
7455	AT3G14960.1 | galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase | chr3:5035903-5038014 REVERSE | Aliases: K15M2.10	5.2	4.1	1.1	3.3	5.6%	2.4
7456	AT1G21880.2 | peptidoglycan-binding LysM domain-containing protein, contains Pfam profile PF01476: LysM domain	5.9	4.3	1.6	3.3	5.6%	2.4
7457	AT5G62280.1 | expressed protein | chr5:25034308-25035472 FORWARD | Aliases: MMI9.11, MMI9_11	3.7	4.3	-0.6	-3.3	5.6%	2.2
7458	AT5G43140.1 | peroxisomal membrane 22 kDa family protein, contains Mpv17 / PMP22 family domain, Pfam:PF04117 | chr5:17338773-17340633 FORWARD | Aliases: MMG4.17, MMG4_17	5.3	4.5	0.8	3.3	5.6%	2.4
7459	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	9.4	10.4	-1.1	-3.3	5.6%	2.1
7460	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.	6.2	5.3	0.9	3.3	5.6%	2.4
7461	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	10.1	10.7	-0.6	-3.3	5.6%	2.1
7462	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	8.2	7.1	1.1	3.3	5.6%	2.4
7463	AT1G18080.1 | Symbol: ATARCA |	9.1	5.8	3.3	3.3	5.6%	2.6
7464	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	3.7	0.9	3.3	5.6%	2.5
7465	AT5G08060.1 | expressed protein, sigma factor F inhibitor spoIIAB, Bacillus megaterium, PIR:B48402 | chr5:2580538-2582565 FORWARD | Aliases: T22D6.4	6.4	4.1	2.3	3.3	5.6%	2.5
7466	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	5.4	4.2	1.2	3.3	5.6%	2.6
7467	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	8.8	9.5	-0.7	-3.3	5.6%	2.1
7468	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	5.7	4.7	1.0	3.3	5.6%	2.5
7469	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	4.8	4.0	0.8	3.3	5.6%	2.4
7470	AT5G65120.1 | expressed protein | chr5:26030108-26031866 FORWARD | Aliases: MQN23.5, MQN23_5	3.7	3.2	0.5	3.3	5.6%	2.2
7471	AT5G03080.1 | phosphatidic acid phosphatase-related / PAP2-related, contains Pfam profile PF01569: PAP2 superfamily | chr5:721866-723399 FORWARD | Aliases: F15A17.110, F15A17_110	5.2	6.1	-0.9	-3.3	5.6%	2.2
7472	AT1G20300.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat | chr1:7029619-7031525 FORWARD | Aliases: F14O10.10, F14O10_10	6.0	5.2	0.7	3.3	5.6%	2.3
7473	AT3G21390.1 | mitochondrial substrate carrier family protein | chr3:7531408-7534544 FORWARD | Aliases: MHC9.7	7.9	6.9	1.0	3.3	5.6%	2.4

Rank	Description	Sync	Root	M	t	adj.q	B
7474	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	5.8	6.3	-0.5	-3.3	5.6%	2.1
7475	NA	12.0	12.6	-0.5	-3.3	5.6%	1.2
7476	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	9.2	-1.7	-3.3	5.7%	2.4
7477	AT1G63240.1 | expressed protein | chr1:23459686-23462301 REVERSE | Aliases: F9N12.14, F9N12_14	3.0	2.3	0.7	3.3	5.7%	2.0
7478	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	6.5	-1.0	-3.3	5.7%	2.5
7479	AT5G60640.2 | Symbol: ATPDIL1 4 | thioredoxin family protein, similar to protein disulfide isomerase GI:5902592 from (Volvox carteri f. nagariensis), GI:2708314 from Chlamydomonas reinhardtii; contains Pfam profile: PF00085 Thioredoxin | chr5:24388186-24391264 REVERSE | Aliases: ATPDIL1 4, MUP24.6, MUP24_6, PDI LIKE 1 4	11.6	11.1	0.4	3.3	5.7%	1.6
7480	AT2G25080.1 | Symbol: ATGPX1 |	7.7	6.0	1.7	3.3	5.7%	2.4
7481	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	3.8	4.5	-0.7	-3.3	5.7%	2.2
7482	AT1G15510.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:5329106-5331706 FORWARD | Aliases: T16N11.2, T16N11_2	4.8	3.9	0.9	3.3	5.7%	2.4
7483	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	4.8	3.8	0.9	3.3	5.7%	2.5
7484	AT4G27620.2 | expressed protein | chr4:13788827-13790964 REVERSE | Aliases: T29A15.110, T29A15_110	3.4	3.1	0.4	3.3	5.7%	1.9
7485	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	4.4	3.8	0.5	3.3	5.7%	2.2
7486	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	5.1	5.6	-0.5	-3.3	5.7%	2.1
7487	AT4G27010.1 | expressed protein, ; expression supported by MPSS | chr4:13558472-13568302 FORWARD | Aliases: F10M23.350, F10M23_350	4.2	3.4	0.9	3.3	5.7%	2.3
7488	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	9.4	11.5	-2.1	-3.3	5.7%	2.1
7489	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	7.6	-0.8	-3.3	5.7%	2.3
7490	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	5.9	-1.8	-3.3	5.7%	2.5
7491	AT5G11990.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr5:3872652-3873197 REVERSE | Aliases: F14F18.160, F14F18_160	3.0	3.6	-0.6	-3.3	5.7%	2.2
7492	AT3G58080.1 | expressed protein | chr3:21521283-21521539 REVERSE | Aliases: F9D24.3	3.3	3.9	-0.6	-3.3	5.7%	2.0
7493	AT4G19960.1 | potassium transporter family protein, similar to potassium transporter (Arabidopsis thaliana) 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	5.4	-0.7	-3.3	5.7%	2.3

Rank	Description	Sync	Root	M	t	adj.q	B
7494	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	4.2	-0.5	-3.3	5.7%	2.0
7495	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	5.2	4.5	0.8	3.3	5.7%	2.2
7496	AT5G55710.1 | expressed protein | chr5:22572104-22572876 REVERSE | Aliases: MDF20.15, MDF20_15	5.2	4.3	0.9	3.3	5.7%	2.4
7497	AT5G20090.1 | expressed protein, contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041) | chr5:6787004-6788656 REVERSE | Aliases: F28I16.240, F28I16_240	11.7	11.0	0.7	3.3	5.7%	1.9
7498	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	4.1	-1.0	-3.3	5.7%	2.0
7499	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	3.2	-0.4	-3.3	5.7%	1.9
7500	AT5G57700.2 | BNR/Asp-box repeat family protein, contains Pfam PF02012: BNR/Asp-box repeat | chr5:23392100-23394348 FORWARD | Aliases: MRI1.6, MRI1_6	7.3	6.4	1.0	3.3	5.7%	2.2
7501	AT1G43590.1 | expressed protein, contains Pfam domain, PF04827: Protein of unknown function (DUF635) | chr1:16416561-16417067 FORWARD | Aliases: T10P12.13, T10P12_13	2.4	2.6	-0.3	-3.3	5.7%	1.5
7502	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	7.2	6.6	0.6	3.3	5.7%	2.3
7503	AT1G14770.2 | expressed protein | chr1:5086625-5088621 REVERSE | Aliases: F10B6.17, F10B6_17	4.0	3.5	0.5	3.3	5.7%	2.1
7504	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	8.6	7.9	0.7	3.3	5.7%	2.3
7505	AT2G25200.1 | expressed protein | chr2:10743659-10744723 REVERSE | Aliases: F13D4.4	6.2	5.0	1.2	3.3	5.7%	2.5
7506	AT4G09890.1 | expressed protein | chr4:6218393-6218923 FORWARD | Aliases: T5L19.20, T5L19_20	6.5	5.5	1.0	3.3	5.7%	2.4
7507	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	9.6	8.8	0.9	3.3	5.7%	2.2
7508	AT3G17740.1 | expressed protein | chr3:6067765-6072845 REVERSE | Aliases: MIG5.4	5.1	6.0	-0.9	-3.3	5.7%	2.3
7509	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}	10.3	8.4	1.9	3.3	5.7%	2.4
7510	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	3.1	3.6	-0.5	-3.3	5.7%	2.0
7511	AT3G53950.1 | glyoxal oxidase-related, contains similarity to glyoxal oxidase precursor (Phanerochaete chrysosporium) gi:1050302:gb:AAA87594 | chr3:19986597-19988417 FORWARD | Aliases: F5K20.250	5.9	5.0	0.8	3.3	5.7%	2.1
7512	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	4.6	5.2	-0.6	-3.3	5.7%	2.3
7513	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	4.3	5.4	-1.1	-3.3	5.7%	2.4
7514	AT4G15270.1 | glucosyltransferase-related, contains some similarity to glucosyltransferase GI:14349251 from (Nicotiana tabacum) | chr4:8716601-8717796 REVERSE | Aliases: DL3680C, FCAALL.253	5.1	6.2	-1.1	-3.3	5.7%	2.4
7515	AT1G79520.1 | cation efflux family protein, contains cation efflux family protein domain, Pfam:PF01545	3.9	3.0	1.0	3.3	5.7%	2.4

Rank	Description	Sync	Root	M	t	adj.q	B
7516	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	10.7	10.0	0.6	3.3	5.7%	1.9
7517	AT1G76250.1 | expressed protein | chr1:28611344-28614022 REVERSE | Aliases: T23E18.18, T23E18_18	2.6	3.6	-1.0	-3.3	5.7%	2.2
7518	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	7.4	8.2	-0.8	-3.3	5.7%	2.3
7519	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	4.9	5.7	-0.8	-3.3	5.7%	2.4
7520	AT1G01920.2 | similar to ribulose-1,5 bisphosphate 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	5.3	4.4	0.8	3.3	5.7%	2.4
7521	AT3G16990.1 | TENA/THI-4 family protein, contains Pfam profile: PF03070 TENA/THI-4 family | chr3:5795845-5796811 REVERSE | Aliases: K14A17.22	7.7	7.1	0.5	3.3	5.7%	1.9
7522	AT1G65820.1 | microsomal glutathione s-transferase, putative, similar to MGST3_HUMAN SP:O14880	10.5	11.4	-0.9	-3.3	5.7%	1.7
7523	AT1G19580.1 | bacterial transferase hexapeptide repeat-containing protein, contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats) | chr1:6774754-6777438 FORWARD | Aliases: None	6.9	5.0	1.9	3.3	5.7%	2.5
7524	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	11.9	9.6	2.3	3.3	5.8%	2.1
7525	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	4.3	-0.6	-3.3	5.8%	2.3
7526	AT5G18210.1 | short-chain dehydrogenase/reductase (SDR) family protein, similar to short-chain type dehydrogenase/reductase SP:Q08632 (Picea abies) | chr5:6017867-6019995 FORWARD | Aliases: MRG7.17, MRG7_17	4.9	4.4	0.4	3.3	5.8%	1.8
7527	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	10.0	9.5	0.5	3.3	5.8%	2.0
7528	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	13.5	12.3	1.2	3.3	5.8%	1.1
7529	AT5G53300.2 | Symbol: UBC10 | ubiquitin-conjugating enzyme 10 (UBC10), E2; identical to gi:297877, SP:P35133 | chr5:21649740-21651389 REVERSE | Aliases: None	13.5	12.3	1.2	3.3	5.8%	1.1
7530	AT1G66230.1 | Symbol: MYB20 | myb family transcription factor (MYB20), similar to myb-related transcription factor GI:1430846 from (Lycopersicon esculentum); contains PFAM profile: Myb DNA binding domain PF00249 | chr1:24680817-24682078 FORWARD | Aliases: MYB20, T6J19.5, T6J19_5	4.7	3.9	0.8	3.3	5.8%	2.4
7531	AT3G05780.1 | Lon protease, putative, similar to Lon protease homolog 2 SP:P93655 | chr3:1714947-1719614 REVERSE | Aliases: F10A16.7, F10A16_7	2.6	3.0	-0.4	-3.3	5.8%	1.8
7532	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	4.2	2.9	1.3	3.3	5.8%	2.3
7533	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	3.4	4.8	-1.4	-3.3	5.8%	2.3
7534	AT2G41610.1 | expressed protein | chr2:17354235-17355317 FORWARD | Aliases: T32G6.13, T32G6_13	3.4	4.2	-0.9	-3.3	5.8%	2.4

Rank	Description	Sync	Root	M	t	adj.q	B
7535	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	2.8	-0.4	-3.3	5.8%	1.7
7536	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	11.2	9.9	1.3	3.3	5.8%	2.2
7537	AT5G15900.1 | expressed protein, several hypothetical proteins - Arabidopsis thaliana | chr5:5189494-5192073 REVERSE | Aliases: F1N13.40, F1N13_40	2.3	2.6	-0.3	-3.3	5.8%	1.8
7538	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	7.7	6.5	1.3	3.3	5.8%	2.3
7539	AT1G71730.1 | expressed protein | chr1:26989750-26990571 REVERSE | Aliases: F14O23.11, F14O23_11	5.3	3.9	1.3	3.3	5.8%	2.4
7540	AT5G04810.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat | chr5:1390038-1393931 FORWARD | Aliases: MUK11.12	5.6	4.7	0.9	3.3	5.8%	2.3
7541	AT4G37300.1 | expressed protein | chr4:17554749-17555855 FORWARD | Aliases: F6G17.14	6.8	4.2	2.7	3.3	5.8%	2.4
7542	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	7.4	5.9	1.5	3.3	5.8%	2.3
7543	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	3.3	0.8	3.3	5.8%	2.2
7544	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	6.1	-0.8	-3.3	5.8%	2.2
7545	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)	2.6	3.0	-0.4	-3.3	5.8%	1.8
7546	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	5.5	4.4	1.1	3.3	5.9%	2.3
7547	AT5G25540.1 | Symbol: CID6 | Expressed protein contains PAM2 PABC interacting domain.	6.7	7.3	-0.6	-3.3	5.9%	2.1
7548	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	5.2	-0.3	-3.3	5.9%	1.7
7549	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	8.4	7.3	1.1	3.3	5.9%	2.3
7550	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	5.3	-0.7	-3.3	5.9%	1.9
7551	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	4.9	5.6	-0.6	-3.3	5.9%	2.1
7552	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	4.4	4.9	-0.5	-3.3	5.9%	2.0
7553	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	4.2	3.2	1.0	3.3	5.9%	2.4
7554	AT1G71870.1 | MATE efflux family protein, contains Pfam profile PF01554: Uncharacterized membrane protein family | chr1:27036118-27038557 REVERSE | Aliases: F14O23.25, F14O23_25	3.7	4.6	-0.9	-3.3	5.9%	2.3

Rank	Description	Sync	Root	M	t	adj.q	B
7555	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	4.2	3.2	1.1	3.3	5.9%	2.4
7556	AT3G09720.1 | DEAD/DEAH box helicase, putative, similar to RNA helicase involved in rRNA processing GB:6321267 from (Saccharomyces cerevisiae)c, ontains DEAD and DEAH box domain | chr3:2980236-2983578 REVERSE | Aliases: F11F8.31	4.3	3.8	0.5	3.3	5.9%	2.0
7557	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	5.7	-0.7	-3.3	5.9%	2.0
7558	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	2.7	0.4	3.3	5.9%	2.0
7559	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	3.1	-0.5	-3.3	5.9%	1.6
7560	AT5G42750.1 | expressed protein | chr5:17160048-17161388 REVERSE | Aliases: MJB21.13, MJB21_13	3.2	4.3	-1.1	-3.3	5.9%	2.4
7561	AT1G69760.1 | expressed protein | chr1:26242923-26244371 REVERSE | Aliases: T6C23.4, T6C23_4	4.0	4.9	-0.9	-3.3	5.9%	2.2
7562	AT1G31335.1 | expressed protein | chr1:11216895-11217374 REVERSE | Aliases: None	5.0	6.2	-1.1	-3.3	5.9%	2.4
7563	AT1G50930.1 | expressed protein | chr1:18880566-18881374 FORWARD | Aliases: F8A12.15, F8A12_15	2.4	3.7	-1.3	-3.3	5.9%	2.3
7564	AT1G75420.1 | glycosyl transferase family 1 protein, contains Pfam glycosyl transferase, group 1 family protein domain PF00534	4.1	4.8	-0.7	-3.3	5.9%	2.2
7565	AT1G30230.1 | elongation factor 1-beta / EF-1-beta, identical to SP:P48006 Elongation factor 1-beta (EF-1-beta) {Arabidopsis thaliana}	9.9	8.2	1.7	3.3	5.9%	2.4
7566	AT2G18110.1 | elongation factor 1-beta, putative / EF-1-beta, putative, nearly identical to eEF-1beta (Arabidopsis thaliana) GI:398606	9.9	8.2	1.7	3.3	5.9%	2.4
7567	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	3.7	2.9	0.7	3.3	5.9%	2.2
7568	AT1G73340.1 | cytochrome P450 family protein, similar to Cytochrome P450 90A1 (SP:Q42569) (Arabidopsis thaliana); contains Pfam profile: PF00067 cytochrome P450 | chr1:27576797-27578934 FORWARD | Aliases: T9L24.44, T9L24_44	2.6	3.0	-0.4	-3.3	5.9%	1.9
7569	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	2.7	3.1	-0.4	-3.3	5.9%	1.9
7570	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	9.2	10.1	-0.9	-3.3	5.9%	2.0
7571	AT5G15190.2 | expressed protein | chr5:4932823-4933539 REVERSE | Aliases: F8M21.80, F8M21_80	2.7	3.6	-0.9	-3.3	5.9%	2.0
7572	AT4G25970.1 | Symbol: PSD2 | similar to phosphatidylserine decarboxylase, putative [Arabidopsis thaliana] (TAIR:At5g57190.1); similar to putative phosphatidylserine decarboxylase [Oryza sativa (japonica 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	8.3	-1.3	-3.3	5.9%	2.3
7573	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	3.8	6.0	-2.2	-3.3	5.9%	2.4
7574	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	4.5	1.0	3.3	5.9%	2.4
7575	AT4G35410.2 | clathrin adaptor complex small chain family protein, contains Pfam profile: PF01217 clathrin adaptor complex small chain	4.7	4.0	0.7	3.3	5.9%	2.2

Rank	Description	Sync	Root	M	t	adj.q	B
7576	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	8.2	7.0	1.2	3.3	5.9%	2.4
7577	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	4.9	6.1	-1.2	-3.3	5.9%	2.5
7578	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	4.8	-0.9	-3.3	5.9%	2.4
7579	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	6.4	4.9	1.5	3.3	5.9%	2.3
7580	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	4.1	4.9	-0.8	-3.3	5.9%	2.2
7581	AT5G63940.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr5:25605324-25608684 FORWARD | Aliases: MBM17.4, MBM17_4	6.1	4.6	1.4	3.3	5.9%	2.4
7582	AT2G32590.1 | barren family protein, low similarity to SP:Q9Y7R3 Condensin complex subunit 2 (p105) {Schizosaccharomyces pombe}; contains Pfam profile PF05786: Barren protein	4.6	3.6	1.0	3.3	5.9%	2.1
7583	AT5G28610.1 | expressed protein | chr5:10610963-10611351 FORWARD | Aliases: T10I18.2, T10I18_2	2.7	4.2	-1.5	-3.3	5.9%	2.4
7584	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	4.5	5.5	-1.0	-3.3	5.9%	2.4
7585	AT1G13950.1 | Symbol: EIF 5A |	5.9	4.7	1.2	3.3	6.0%	2.3
7586	AT1G75980.1 | expressed protein | chr1:28526215-28527963 REVERSE | Aliases: T4O12.20, T4O12_20	6.2	5.3	0.9	3.3	6.0%	2.2
7587	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	2.5	3.0	-0.5	-3.3	6.0%	2.1
7588	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	2.5	-0.2	-3.3	6.0%	1.3
7589	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	5.8	6.8	-1.0	-3.3	6.0%	2.3
7590	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	7.8	5.6	2.2	3.3	6.0%	2.3
7591	AT5G61865.1 | expressed protein | chr5:24864553-24867018 FORWARD | Aliases: None	3.6	3.1	0.5	3.3	6.0%	2.0
7592	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	6.4	-0.8	-3.3	6.0%	2.2
7593	AT1G51670.1 | expressed protein | chr1:19160810-19162417 FORWARD | Aliases: F19C24.12, F19C24_12	2.9	2.4	0.4	3.3	6.0%	1.8
7594	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	5.7	6.2	-0.5	-3.3	6.0%	2.1
7595	AT3G63170.1 | expressed protein | chr3:23345327-23347732 FORWARD | Aliases: F16M2.20	7.0	6.1	0.9	3.3	6.0%	2.2

Rank	Description	Sync	Root	M	t	adj.q	B
7596	AT2G02680.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.1	4.5	-2.4	-3.3	6.0%	2.4
7597	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	9.4	-0.7	-3.3	6.0%	2.1
7598	AT2G01220.2 | expressed protein | chr2:123275-126426 FORWARD | Aliases: AT2G01230, F10A8.10, F10A8_10	6.6	7.1	-0.5	-3.3	6.0%	1.8
7599	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	3.9	4.7	-0.8	-3.3	6.0%	2.3
7600	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	8.2	8.9	-0.7	-3.3	6.0%	2.1
7601	AT2G47200.1 | expressed protein | chr2:19384799-19385401 REVERSE | Aliases: T8I13.4	3.2	4.4	-1.2	-3.3	6.0%	2.5
7602	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	3.3	-0.7	-3.3	6.0%	2.1
7603	AT1G54200.1 | expressed protein | chr1:20239379-20240732 FORWARD | Aliases: F20D21.2, F20D21_2	3.7	3.1	0.6	3.3	6.0%	2.2
7604	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	3.5	-0.5	-3.3	6.0%	1.7
7605	AT1G53400.1 | expressed protein | chr1:19928439-19930268 FORWARD | Aliases: F12M16.29, F12M16_29	9.3	10.0	-0.7	-3.3	6.0%	2.3
7606	AT1G65270.3 | expressed protein | chr1:24245411-24248615 FORWARD | Aliases: T8F5.4, T8F5_4	7.9	6.8	1.1	3.3	6.0%	2.2
7607	AT3G06035.1 | expressed protein | chr3:1823105-1824188 REVERSE | Aliases: None	8.9	8.1	0.8	3.3	6.0%	2.3
7608	AT5G58650.1 | expressed protein | chr5:23716934-23717452 REVERSE | Aliases: MZN1.10, MZN1_10	7.5	6.6	0.8	3.3	6.0%	2.2
7609	AT1G76220.1 | hypothetical protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function | chr1:28602424-28603194 REVERSE | Aliases: T23E18.15, T23E18_15	3.0	3.4	-0.4	-3.3	6.0%	1.9
7610	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	6.8	-0.8	-3.3	6.0%	2.1
7611	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) {Arabidopsis thaliana} | chr5:17567460-17568808 FORWARD | Aliases: IAA4, MQD19.3, MQD19_3	5.2	5.5	-0.3	-3.3	6.0%	1.6
7612	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	7.1	5.8	1.2	3.3	6.0%	2.5
7613	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	5.3	4.4	0.9	3.3	6.0%	2.4
7614	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	8.5	1.2	3.3	6.0%	2.3
7615	AT5G53410.1 | hypothetical protein, similar to unknown protein (gb AAC73044.1)	3.7	4.6	-1.0	-3.3	6.0%	2.1
7616	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	5.4	6.3	-0.9	-3.3	6.1%	2.2
7617	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	3.7	-0.6	-3.3	6.1%	2.1
7618	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	5.7	4.7	1.0	3.3	6.1%	2.4

Rank	Description	Sync	Root	M	t	adj.q	B
7619	AT4G26940.2 | galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase | chr4:13529431-13532681 REVERSE | Aliases: F10M23.280, F10M23_280	5.7	6.4	-0.8	-3.3	6.1%	2.3
7620	AT4G14380.1 | expressed protein | chr4:8285767-8286768 FORWARD | Aliases: DL3230W, FCAALL.187	4.0	4.9	-0.9	-3.3	6.1%	2.2
7621	AT4G01970.1 | similar to raffinose synthase family protein [Arabidopsis thaliana] (TAIR:At5g40390.1); similar to raffinose synthase [Cucumis sativus] (GB:AAD02832.1); similar to galactinol-raffinose galactosyltransferase [Vigna angularis] (GB:CAB64363.1); similar to putative alkaline alpha galactosidase I [Oryza sativa (japonica cultivar-group)] (GB:XP_550270.1); similar to putative raffinose synthase [Oryza sativa (japonica cultivar-group)] (GB:NP_909442.1); similar to stachyose synthase [Pisum sativum] (GB:CAD55555.1); contains InterPro domain Raffinose synthase (InterPro:IPR008811) | chr4:853927-857358 REVERSE | Aliases: T7B11.23, T7B11_23	3.1	3.6	-0.6	-3.3	6.1%	2.0
7622	AT2G46130.2 | Symbol: WRKY43 |	2.4	3.1	-0.7	-3.3	6.1%	1.9
7623	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	8.7	9.8	-1.1	-3.3	6.1%	2.0
7624	AT4G10280.1 | expressed protein | chr4:6374742-6376107 REVERSE | Aliases: T9A4.15	5.0	3.8	1.2	3.3	6.1%	2.3
7625	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	8.9	-1.1	-3.3	6.1%	2.3
7626	AT4G19185.1 | integral membrane family protein, contains Pfam profile:PF00892 integral membrane protein DUF6 | chr4:10489096-10491668 REVERSE | Aliases: None	7.0	7.8	-0.8	-3.3	6.1%	2.1
7627	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	2.4	2.8	-0.4	-3.3	6.1%	1.8
7628	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	5.2	-0.7	-3.3	6.1%	2.0
7629	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 Methanothrix 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	7.3	8.1	-0.8	-3.3	6.1%	2.1
7630	AT5G01950.1 | leucine-rich repeat transmembrane protein kinase, putative, receptor protein kinases | chr5:364899-370079 REVERSE | Aliases: T20L15.220, T20L15_220	5.9	7.2	-1.3	-3.3	6.1%	2.1
7631	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	6.9	-1.2	-3.3	6.1%	2.4
7632	AT1G70620.2 | cyclin-related, contains weak similarity to Swiss-Prot:P35662 cylicin I (Multiple-band polypeptide I) (Bos taurus) | chr1:26630297-26634767 FORWARD | Aliases: F5A18.20, F5A18_20	5.3	8.2	-2.9	-3.3	6.1%	2.5
7633	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	7.7	5.7	2.0	3.3	6.1%	2.2
7634	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	2.9	-0.4	-3.3	6.1%	1.7
7635	NA	12.2	12.9	-0.6	-3.3	6.1%	1.1
7636	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	6.3	5.4	0.9	3.3	6.1%	2.1
7637	AT4G28240.1 | wound-responsive protein-related, wound-induced protein - tomato (fragment), PIR2:S19773	8.0	9.0	-0.9	-3.3	6.1%	2.1
7638	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	4.0	3.6	0.4	3.3	6.1%	1.9

Rank	Description	Sync	Root	M	t	adj.q	B
7639	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	6.5	7.3	-0.9	-3.3	6.1%	2.1
7640	AT2G35480.1 | expressed protein | chr2:14917489-14919127 FORWARD | Aliases: T32F12.14, T32F12_14	4.3	3.6	0.7	3.3	6.1%	2.3
7641	AT2G40150.1 | expressed protein | chr2:16782520-16784321 FORWARD | Aliases: T7M7.4, T7M7_4	6.6	7.4	-0.8	-3.3	6.1%	2.1
7642	AT5G65050.1 | Symbol: AGL31 | MADS-box protein (MAF2)	5.0	4.3	0.7	3.3	6.1%	2.3
7643	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	5.0	4.3	0.7	3.3	6.1%	2.3
7644	AT3G25480.1 | rhodanese-like domain-containing protein, contains Rhodanese-like domain PF:00581 | chr3:9236435-9237844 REVERSE | Aliases: MWL2.9	3.9	3.4	0.5	3.3	6.1%	2.0
7645	AT1G07020.1 | expressed protein | chr1:2154900-2156007 REVERSE | Aliases: F10K1.34, F10K1_34	6.2	7.0	-0.8	-3.3	6.1%	2.2
7646	AT1G29050.1 | expressed protein, similar to hypothetical protein GB:AAB67625 GI:2342727 from (Arabidopsis thaliana) | chr1:10136217-10139194 REVERSE | Aliases: F28N24.24, F28N24_24	7.5	8.1	-0.6	-3.3	6.1%	2.0
7647	AT3G54620.1 | Symbol: BZO2H4 |	5.0	6.5	-1.5	-3.3	6.1%	2.4
7648	AT1G67500.1 | Symbol: ATREV3 |	7.0	7.9	-0.9	-3.3	6.2%	2.1
7649	AT1G06580.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:2014439-2016053 REVERSE | Aliases: F12K11.8, F12K11_8	4.9	3.9	1.0	3.3	6.2%	2.2
7650	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	6.5	5.4	1.1	3.3	6.2%	2.2
7651	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	4.5	3.6	0.8	3.3	6.2%	2.4
7652	AT5G47800.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr5:19371053-19373526 FORWARD | Aliases: MCA23.12, MCA23_12	3.4	3.0	0.4	3.3	6.2%	1.8
7653	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	8.2	6.8	1.5	3.3	6.2%	2.3
7654	AT3G28720.1 | expressed protein | chr3:10783513-10785684 FORWARD | Aliases: T19N8.1	8.5	7.1	1.4	3.3	6.2%	2.2
7655	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	3.4	2.9	0.5	3.3	6.2%	1.7
7656	AT2G35733.1 | expressed protein | chr2:15029755-15029946 REVERSE | Aliases: None	5.4	6.3	-0.8	-3.3	6.2%	2.1
7657	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	4.6	3.6	1.1	3.3	6.2%	2.1
7658	AT3G10920.2 | Symbol: MSD1 | similar to superoxide dismutase (Mn), putative / manganese superoxide dismutase, putative [Arabidopsis thaliana] (TAIR:At3g56350.1); similar to superoxide dismutase [Raphanus sativus] (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	7.1	2.1	3.3	6.2%	2.2
7659	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	4.7	5.4	-0.7	-3.3	6.2%	2.2
7660	AT2G32920.1 | Symbol: ATPDIL2 3 | Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	5.6	3.4	2.2	3.3	6.2%	2.3

Rank	Description	Sync	Root	M	t	adj.q	B
7661	AT3G47110.1 | leucine-rich repeat transmembrane protein kinase, putative, protein kinase Xa21 receptor type precursor, Oryza sativa, PIR:A57676 | chr3:17358088-17361281 REVERSE | Aliases: F13I12.160	3.2	3.8	-0.6	-3.3	6.2%	2.1
7662	AT4G20300.2 | expressed protein | chr4:10955448-10959223 FORWARD | Aliases: F1C12.211, F1C12_211	4.5	6.9	-2.5	-3.3	6.2%	2.3
7663	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)	6.7	5.8	0.9	3.3	6.2%	2.2
7664	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	3.0	-0.4	-3.3	6.2%	2.0
7665	AT4G25070.1 | expressed protein, ; expression supported by MPSS | chr4:12872492-12876478 FORWARD | Aliases: F24A6.14	4.7	6.6	-1.9	-3.3	6.2%	2.3
7666	AT1G60860.1 | ARF GTPase-activating domain-containing protein | chr1:22404909-22411304 REVERSE | Aliases: F23C21.2, F23C21_2	5.5	6.8	-1.3	-3.3	6.2%	2.2
7667	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	3.1	-0.6	-3.3	6.2%	2.1
7668	AT3G59400.1 | Symbol: GUN4 | expressed protein | chr3:21959694-21960687 REVERSE | Aliases: F25L23.260	3.2	2.4	0.8	3.3	6.2%	2.3
7669	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	5.3	-1.8	-3.3	6.2%	2.4
7670	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	8.4	5.7	2.7	3.3	6.2%	2.4
7671	AT1G75710.1 | zinc finger (C2H2 type) family protein, contains zinc finger, C2H2 type, domain, PROSITE:PS00028	5.1	6.2	-1.1	-3.3	6.2%	2.3
7672	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	2.4	0.4	3.3	6.2%	1.4
7673	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	6.0	4.7	1.3	3.3	6.2%	2.3
7674	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	3.8	3.1	0.7	3.3	6.2%	2.3
7675	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	4.3	-0.8	-3.3	6.2%	2.2
7676	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	6.8	1.0	3.3	6.2%	2.3
7677	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	5.7	4.3	1.4	3.3	6.2%	2.3
7678	AT2G02510.1 | expressed protein | chr2:673304-674738 FORWARD | Aliases: T8K22.19, T8K22_19	9.7	9.1	0.6	3.3	6.2%	1.8
7679	AT3G01970.1 | Symbol: WRKY45 |	5.4	4.5	0.9	3.2	6.2%	2.3
7680	AT1G06820.1 | Symbol: CRTISO |	5.5	6.2	-0.7	-3.2	6.2%	2.1
7681	AT3G61090.1 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537 | chr3:22620069-22620797 REVERSE | Aliases: T27I15.180	3.8	3.3	0.5	3.2	6.2%	2.1
7682	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	3.8	4.9	-1.1	-3.2	6.2%	2.2
7683	AT3G01820.1 | adenylate kinase family protein, contains Pfam profile: PF00406 adenylate kinase	5.3	4.1	1.2	3.2	6.2%	2.4
7684	AT3G25805.1 | expressed protein | chr3:9427513-9429426 REVERSE | Aliases: None	4.4	3.7	0.7	3.2	6.2%	2.2

Rank	Description	Sync	Root	M	t	adj.q	B
7685	AT5G26930.1 | zinc finger (GATA type) family protein, various predicted proteins, Arabidopsis thaliana	3.9	4.5	-0.6	-3.2	6.2%	2.0
7686	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	4.5	3.8	0.7	3.2	6.3%	2.3
7687	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	4.4	5.2	-0.8	-3.2	6.3%	1.9
7688	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	6.9	6.0	0.8	3.2	6.3%	2.1
7689	AT2G22060.1 | expressed protein | chr2:9388072-9389225 FORWARD | Aliases: T16B14.9, T16B14_9	4.3	5.1	-0.8	-3.2	6.3%	2.0
7690	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	9.6	8.8	0.8	3.2	6.3%	2.0
7691	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	6.1	1.1	3.2	6.3%	2.3
7692	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	11.8	-1.3	-3.2	6.3%	2.0
7693	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	7.3	4.9	2.4	3.2	6.3%	2.4
7694	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	4.8	5.9	-1.0	-3.2	6.3%	2.2
7695	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	3.9	2.7	1.1	3.2	6.3%	2.4
7696	AT4G26250.1 | galactinol synthase, putative, similar to galactinol synthase, isoform GolS-1 (Ajuga reptans) GI:5608497; contains Pfam profile: PF01501 glycosyl transferase family 8 | chr4:13289650-13291093 FORWARD | Aliases: T25K17.60, T25K17_60	2.4	2.7	-0.3	-3.2	6.3%	1.4
7697	AT4G21430.1 | similar to transcription factor jumonji (jmjC) domain-containing protein [Arabidopsis thaliana] (TAIR:At1g62310.1); similar to putative DNA-binding protein PD3, chloroplast [Oryza sativa (japonica cultivar-group)] (GB:XP_468520.1); contains InterPro domain Transcription factor jumonji, jmjC (InterPro:IPR003347)	5.6	5.0	0.7	3.2	6.3%	2.0
7698	AT3G06090.1 | hypothetical protein | chr3:1840779-1841018 FORWARD | Aliases: F28L1.2, F28L1_2	3.4	3.9	-0.5	-3.2	6.3%	1.7
7699	AT2G20020.1 | expressed protein | chr2:8651467-8654272 FORWARD | Aliases: T2G17.18, T2G17_18	3.6	3.1	0.5	3.2	6.3%	1.8
7700	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	2.5	2.8	-0.4	-3.2	6.3%	1.7
7701	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	4.7	3.2	1.5	3.2	6.3%	2.4
7702	AT4G01030.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr4:448336-449838 REVERSE | Aliases: F3I3.50, F3I3_50	3.2	2.8	0.4	3.2	6.3%	1.6
7703	AT5G23650.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr5:7969815-7971022 FORWARD | Aliases: MQM1.9, MQM1_9	2.5	2.8	-0.3	-3.2	6.3%	1.5
7704	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	5.6	6.4	-0.8	-3.2	6.3%	2.1

Rank	Description	Sync	Root	M	t	adj.q	B
7705	AT3G50940.1 | AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 | chr3:18944744-18946592 FORWARD | Aliases: F18B3.220	3.0	2.5	0.4	3.2	6.3%	1.7
7706	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	3.6	-1.1	-3.2	6.3%	1.8
7707	AT2G38530.1 | Symbol: LTP2 | nonspecific lipid transfer protein 2 (LTP2), identical to nonspecific lipid-transfer protein 2 from Arabidopsis thaliana (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	2.7	3.3	-0.6	-3.2	6.3%	1.7
7708	AT4G10780.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.3	2.7	-0.4	-3.2	6.3%	1.6
7709	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)	3.8	3.3	0.5	3.2	6.3%	1.7
7710	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	3.3	-0.7	-3.2	6.3%	2.0
7711	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	6.8	5.9	0.8	3.2	6.3%	2.3
7712	AT2G47910.2 | expressed protein | chr2:19621768-19622839 FORWARD | Aliases: F17A22.30, F17A22.40, F17A22_30, F17A22_40	4.0	3.5	0.5	3.2	6.3%	2.0
7713	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	6.9	6.0	0.9	3.2	6.3%	2.3
7714	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	2.9	3.7	-0.8	-3.2	6.3%	2.0
7715	AT2G20080.2 | expressed protein | chr2:8670011-8672107 REVERSE | Aliases: T2G17.12, T2G17_12	2.5	2.7	-0.3	-3.2	6.3%	1.4
7716	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	6.0	-0.9	-3.2	6.3%	2.3
7717	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	2.9	2.5	0.4	3.2	6.3%	1.7
7718	AT1G77870.1 | expressed protein, similar to geranylgeranylated protein ATGP4 (GI:4097567) | chr1:29289974-29290783 FORWARD | Aliases: F28K19.8, F28K19_8	2.6	3.0	-0.4	-3.2	6.3%	1.7
7719	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	2.9	-0.3	-3.2	6.3%	1.5
7720	AT3G04650.1 | expressed protein | chr3:1262018-1264628 FORWARD | Aliases: F7O18.13, F7O18_13	4.9	4.4	0.5	3.2	6.3%	2.0
7721	AT2G04280.1 | expressed protein | chr2:1479815-1482086 REVERSE | Aliases: T23O15.9, T23O15_9	7.8	6.9	1.0	3.2	6.3%	2.0
7722	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	4.7	1.2	3.2	6.3%	2.2
7723	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	3.9	0.6	3.2	6.3%	2.1
7724	AT4G09340.1 | SPla/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	6.5	5.1	1.4	3.2	6.3%	2.2

Rank	Description	Sync	Root	M	t	adj.q	B
7725	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	8.4	6.9	1.5	3.2	6.3%	2.3
7726	AT1G10180.1 | expressed protein | chr1:3338305-3341573 REVERSE | Aliases: F14N23.6, F14N23_6	7.7	6.8	0.8	3.2	6.3%	2.2
7727	AT5G52950.1 | expressed protein, ; expression supported by MPSS | chr5:21491113-21494165 REVERSE | Aliases: MXC20.3, MXC20_3	4.9	3.0	1.9	3.2	6.3%	2.3
7728	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	3.3	2.7	0.5	3.2	6.3%	2.0
7729	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	3.5	3.1	0.4	3.2	6.3%	1.9
7730	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	7.3	5.5	1.8	3.2	6.3%	2.3
7731	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	3.8	-0.6	-3.2	6.4%	2.0
7732	AT5G08420.1 | expressed protein | chr5:2713414-2716180 FORWARD | Aliases: F8L15.150, F8L15_150	7.1	5.6	1.5	3.2	6.4%	2.3
7733	AT3G12300.1 | expressed protein | chr3:3921537-3923162 REVERSE | Aliases: F28J15.10	4.9	4.1	0.7	3.2	6.4%	2.1
7734	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	10.5	9.7	0.8	3.2	6.4%	2.1
7735	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	9.6	1.5	3.2	6.4%	1.6
7736	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	4.8	5.5	-0.7	-3.2	6.4%	2.2
7737	AT4G22830.1 | expressed protein | chr4:11990149-11991379 REVERSE | Aliases: F7H19.1	3.0	2.5	0.5	3.2	6.4%	2.1
7738	AT1G64160.1 | disease resistance-responsive family protein / dirigent family protein, similar to dirigent protein GB:AAF25365 GI:6694709 from (Thuja plicata); similar to pathogenesis-related protein (Pisum sativum) gi:4585273 gb:AAD25355 | chr1:23817726-23818274 FORWARD | Aliases: F22C12.8, F22C12_8	2.4	2.0	0.4	3.2	6.4%	1.8
7739	AT2G46505.1 | Symbol: SDH4 | expressed protein | chr2:19096801-19097621 REVERSE | Aliases: None	8.9	7.2	1.6	3.2	6.4%	2.3
7740	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	6.2	1.9	3.2	6.4%	2.3
7741	AT4G01220.2 | expressed protein | chr4:513773-515853 REVERSE | Aliases: F2N1.35, F2N1_35	4.4	3.7	0.6	3.2	6.4%	2.1
7742	AT5G11720.1 | alpha-glucosidase 1 (AGLU1), identical to alpha-glucosidase 1 (Arabidopsis thaliana) GI:2323344 | chr5:3776815-3780129 FORWARD | Aliases: T22P22.110, T22P22_110	6.1	6.8	-0.7	-3.2	6.4%	2.1
7743	AT2G36210.1 | auxin-responsive family protein, similar to auxin-induced protein SAUR-AC1 (GI:546362) (PIR:T06084) (Arabidopsis thaliana) | chr2:15193119-15193883 REVERSE | Aliases: F2H17.18, F2H17_18	3.3	4.4	-1.1	-3.2	6.4%	2.3
7744	AT4G31870.1 | Symbol: ATGPX7 |	3.8	3.2	0.5	3.2	6.4%	2.0
7745	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	3.6	-0.4	-3.2	6.4%	1.9
7746	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	4.8	-0.8	-3.2	6.4%	2.1

Rank	Description	Sync	Root	M	t	adj.q	B
7747	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	3.9	5.1	-1.2	-3.2	6.4%	2.3
7748	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	5.6	4.2	1.4	3.2	6.4%	2.4
7749	AT4G35710.1 | hypothetical protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function | chr4:16925306-16926157 FORWARD | Aliases: F8D20.220, F8D20_220	4.3	5.0	-0.7	-3.2	6.4%	2.0
7750	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	10.8	0.6	3.2	6.4%	1.7
7751	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	3.7	0.8	3.2	6.4%	2.1
7752	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	4.1	0.7	3.2	6.4%	2.2
7753	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	4.1	1.1	3.2	6.4%	2.2
7754	AT4G11480.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr4:6971403-6973794 FORWARD | Aliases: F25E4.100, F25E4_100	3.2	2.7	0.5	3.2	6.4%	1.9
7755	AT4G27530.1 | expressed protein | chr4:13752646-13753236 FORWARD | Aliases: T29A15.20, T29A15_20	3.1	2.7	0.4	3.2	6.4%	1.7
7756	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	8.8	6.1	2.6	3.2	6.4%	2.3
7757	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	6.4	5.5	0.8	3.2	6.4%	2.1
7758	AT4G03150.1 | expressed protein | chr4:1393614-1394574 REVERSE | Aliases: F4C21.13	3.8	3.5	0.3	3.2	6.4%	1.5
7759	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	9.1	7.5	1.5	3.2	6.4%	2.3
7760	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	6.2	6.9	-0.8	-3.2	6.4%	2.1
7761	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	7.0	6.0	1.0	3.2	6.4%	2.3
7762	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	4.6	3.8	0.8	3.2	6.5%	2.1
7763	AT4G33460.1 | Symbol: ATNAP13 | ABC transporter family protein, ABC-type transport protein sll1623 -Synechocystis,PIR2:S74812	5.8	4.8	1.0	3.2	6.5%	2.2
7764	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	4.2	3.5	0.7	3.2	6.5%	2.0
7765	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	8.3	9.3	-0.9	-3.2	6.5%	2.2
7766	AT5G47050.1 | expressed protein | chr5:19123567-19125575 FORWARD | Aliases: MQD22.19, MQD22_19	7.8	8.5	-0.7	-3.2	6.5%	1.9

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7767	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	11.0	9.8	1.3	3.2	6.5%	2.2
7768	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	5.9	4.9	1.0	3.2	6.5%	2.3
7769	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	3.5	4.6	-1.0	-3.2	6.5%	2.1
7770	ATCG00570.1 | Symbol: PSBF | PSII cytochrome b559 | chrC:63942-64061 REVERSE | Aliases: PSBF	9.1	7.3	1.8	3.2	6.5%	2.3
7771	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	9.8	8.7	1.0	3.2	6.5%	2.1
7772	AT1G78310.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr1:29468549-29469946 REVERSE | Aliases: F3F9.15, F3F9_15	3.3	4.1	-0.8	-3.2	6.5%	2.2
7773	AT1G54880.1 | hypothetical protein | chr1:20464705-20465225 REVERSE | Aliases: F14C21.36, F14C21_36	3.1	3.4	-0.3	-3.2	6.5%	1.6
7774	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	3.9	-0.8	-3.2	6.5%	2.2
7775	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	3.3	3.8	-0.5	-3.2	6.5%	2.0
7776	AT1G25560.1 | AP2 domain-containing transcription factor, putative, similar to DNA-binding protein RAV2 GI:3868859 from (Arabidopsis thaliana)	4.9	5.5	-0.6	-3.2	6.5%	2.0
7777	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	5.9	4.9	0.9	3.2	6.5%	2.0
7778	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	5.8	4.3	1.5	3.2	6.5%	2.3
7779	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	3.0	2.6	0.4	3.2	6.5%	1.8
7780	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	3.4	4.0	-0.6	-3.2	6.5%	2.0
7781	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	3.1	-0.6	-3.2	6.5%	1.8
7782	AT4G19600.1 | cyclin family protein, similar to cyclin T2a (Homo sapiens) GI:2981198; contains Pfam profile PF00134: Cyclin, N-terminal domain	7.5	6.3	1.2	3.2	6.5%	2.1
7783	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	6.2	-1.5	-3.2	6.5%	2.3
7784	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	7.9	0.9	3.2	6.5%	2.2
7785	AT3G50110.1 | phosphatase-related, similar to PTEN1 GI:5566292 from (Drosophila melanogaster); contains prosite evidence: PS00383: Tyrosine specific protein phosphatases active site | chr3:18591592-18595518 REVERSE | Aliases: F3A4.190	5.6	4.7	0.9	3.2	6.5%	2.2
7786	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	3.5	3.0	0.5	3.2	6.5%	2.0

Rank	Description	Sync	Root	M	t	adj.q	B
7787	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	5.4	6.7	-1.3	-3.2	6.5%	2.3
7788	AT2G43100.1 | aconitase C-terminal domain-containing protein, contains Pfam profile PF00694: Aconitase C-terminal domain | chr2:17927737-17928766 FORWARD | Aliases: MFL8.14	4.4	5.3	-0.9	-3.2	6.5%	2.1
7789	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	2.8	0.7	3.2	6.5%	2.2
7790	AT2G45060.1 | expressed protein | chr2:18591427-18593851 REVERSE | Aliases: T14P1.13	5.3	3.6	1.6	3.2	6.5%	2.3
7791	AT1G72800.1 | nuM1-related, contains similarity with nuM1 GI:1279563 from (Medicago sativa) | chr1:27400878-27402162 FORWARD | Aliases: F28P22.1, F28P22_1	5.3	6.7	-1.4	-3.2	6.5%	2.3
7792	AT1G68185.1 | ubiquitin-related, similar to ubiquitin-like protein smt3/pmt3 SP:O13351 from (Fission yeast) | chr1:25560121-25562179 FORWARD | Aliases: None	4.6	3.7	0.8	3.2	6.5%	2.2
7793	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	5.4	6.2	-0.8	-3.2	6.5%	2.0
7794	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	4.4	5.1	-0.6	-3.2	6.5%	2.1
7795	AT3G10525.1 | expressed protein | chr3:3281367-3282037 REVERSE | Aliases: None	3.0	4.2	-1.2	-3.2	6.5%	2.2
7796	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	3.9	-0.6	-3.2	6.5%	1.8
7797	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	4.9	4.2	0.8	3.2	6.6%	2.2
7798	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	3.6	4.1	-0.4	-3.2	6.6%	1.7
7799	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	6.7	5.5	1.2	3.2	6.6%	2.3
7800	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	7.8	7.2	0.5	3.2	6.6%	2.0
7801	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.	7.0	6.0	1.0	3.2	6.6%	2.2
7802	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	4.9	0.7	3.2	6.6%	2.1
7803	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	9.2	7.3	2.0	3.2	6.6%	2.2
7804	AT5G41260.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:16521140-16524703 FORWARD | Aliases: K1O13.5, K1O13_5	3.2	3.8	-0.6	-3.2	6.6%	2.0
7805	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	4.2	3.7	0.5	3.2	6.6%	2.0
7806	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	6.5	-0.7	-3.2	6.6%	2.1

Rank	Description	Sync	Root	M	t	adj.q	B
7807	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	6.3	7.0	-0.7	-3.2	6.6%	2.1
7808	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	3.4	3.8	-0.4	-3.2	6.6%	1.7
7809	AT1G10690.1 | expressed protein | chr1:3549993-3550633 REVERSE | Aliases: T16B5.17, T16B5_17	3.5	2.8	0.7	3.2	6.6%	1.9
7810	AT3G09730.1 | expressed protein | chr3:2984023-2986265 FORWARD | Aliases: F11F8.32	3.0	2.5	0.5	3.2	6.6%	1.9
7811	AT5G41280.1 | expressed protein, contains Pfam profile: PF01657 domain of unknown function | chr5:16526760-16527957 FORWARD | Aliases: K1O13.8, K1O13_8	2.7	3.0	-0.4	-3.2	6.6%	1.8
7812	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	3.3	2.9	0.4	3.2	6.6%	1.8
7813	AT5G22950.1 | SNF7 family protein, contains Pfam domain, PF03357: SNF7 family | chr5:7681308-7682906 FORWARD | Aliases: MRN17.18, MRN17_18	7.5	8.4	-0.9	-3.2	6.6%	2.1
7814	AT1G33860.1 | expressed protein | chr1:12294374-12295285 FORWARD | Aliases: T3M13.25	4.9	3.7	1.1	3.2	6.6%	2.3
7815	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	10.5	-0.4	-3.2	6.6%	1.6
7816	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	5.4	-2.5	-3.2	6.6%	2.2
7817	AT3G04660.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.5	3.0	0.5	3.2	6.6%	1.8
7818	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	7.4	-0.9	-3.2	6.6%	2.0
7819	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	4.9	5.7	-0.7	-3.2	6.6%	2.2
7820	AT1G26300.2 | BSD domain-containing protein, contains Pfam profile PF03909: BSD domain	4.8	4.5	0.4	3.2	6.6%	1.6
7821	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	8.5	7.1	1.4	3.2	6.6%	2.0
7822	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	4.2	0.9	3.2	6.6%	2.3
7823	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	6.0	4.8	1.2	3.2	6.6%	2.0
7824	AT1G03350.1 | BSD domain-containing protein, contains Pfam profile PF03909: BSD domain	7.2	7.7	-0.5	-3.2	6.6%	1.9
7825	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	6.7	6.1	0.6	3.2	6.6%	2.0
7826	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	3.7	-0.7	-3.2	6.6%	2.1
7827	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	4.7	-0.5	-3.2	6.6%	2.0
7828	AT1G31660.1 | bystin family, contains Pfam profile: PF05291 Bystin | chr1:11331157-11333519 REVERSE | Aliases: F27M3.14, F27M3_14	4.6	3.9	0.7	3.2	6.7%	2.0
7829	AT2G37560.2 | Symbol: ATORC2 |	3.9	3.1	0.7	3.2	6.7%	2.1

Rank	Description	Sync	Root	M	t	adj.q	B
7830	AT2G37080.1 | myosin heavy chain-related, low similarity to myosin heavy chain (Rana catesbeiana) GI:4249701 | chr2:15588486-15592265 REVERSE | Aliases: T2N18.16, T2N18_16	6.8	5.5	1.2	3.2	6.7%	2.1
7831	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	4.9	5.8	-1.0	-3.2	6.7%	2.2
7832	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	5.3	-0.5	-3.2	6.7%	1.9
7833	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	7.5	6.7	0.8	3.2	6.7%	2.0
7834	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	5.0	-1.0	-3.2	6.7%	2.3
7835	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	4.2	3.3	0.9	3.2	6.7%	2.1
7836	AT2G28080.1 | glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	5.9	6.4	-0.6	-3.2	6.7%	1.7
7837	AT1G09770.1 | Symbol: ATCDC5 |	9.0	7.7	1.3	3.2	6.7%	2.0
7838	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	3.5	4.7	-1.1	-3.2	6.7%	2.2
7839	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	7.2	6.1	1.0	3.2	6.7%	2.1
7840	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	7.1	-1.1	-3.2	6.7%	2.1
7841	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	5.7	0.8	3.2	6.7%	2.0
7842	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	9.3	10.1	-0.7	-3.2	6.7%	2.1
7843	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	3.2	2.7	0.5	3.2	6.7%	1.7
7844	AT4G13630.1 | expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593 | chr4:7933904-7936025 REVERSE | Aliases: F18A5.20, F18A5_20	5.9	6.4	-0.5	-3.2	6.7%	1.8
7845	AT1G36980.1 | expressed protein | chr1:14027484-14029382 FORWARD | Aliases: T32E20.29, T32E20_29	10.0	10.5	-0.5	-3.2	6.7%	1.5
7846	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	3.4	-0.4	-3.2	6.7%	1.6
7847	AT3G06590.2 | expressed protein | chr3:2052699-2055413 REVERSE | Aliases: F5E6.8, F5E6_8	3.9	5.0	-1.1	-3.2	6.7%	2.2
7848	AT1G11915.1 | expressed protein | chr1:4021823-4023290 FORWARD | Aliases: None	2.9	3.2	-0.3	-3.2	6.7%	1.3
7849	AT3G58840.1 | expressed protein | chr3:21768289-21769749 REVERSE | Aliases: T20N10.190	8.3	6.9	1.4	3.2	6.7%	2.2
7850	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	5.7	4.9	0.8	3.2	6.7%	2.1

Rank	Description	Sync	Root	M	t	adj.q	B
7851	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	6.4	4.8	1.5	3.2	6.7%	2.2
7852	AT3G02890.1 | PHD finger protein-related, contains low similarity to PHD-finger domain proteins | chr3:641050-645310 FORWARD | Aliases: F13E7.16, F13E7_16	3.8	3.0	0.8	3.2	6.7%	2.2
7853	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	2.9	-0.5	-3.2	6.7%	1.8
7854	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	3.9	4.7	-0.7	-3.2	6.7%	2.2
7855	AT1G78940.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:29685750-29688855 REVERSE | Aliases: YUP8H12R.45, YUP8H12R_45	2.6	2.3	0.3	3.2	6.7%	1.3
7856	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	3.8	4.8	-1.0	-3.2	6.7%	2.1
7857	AT2G43290.1 | Symbol: MSS3 | calmodulin-like protein (MSS3), identical to calmodulin-like MSS3 from GI:9965747 (Arabidopsis thaliana)	4.2	3.6	0.7	3.2	6.7%	2.1
7858	AT3G29200.1 | Symbol: CM1 | chorismate mutase, chloroplast (CM1), identical to chorismate mutase GB:Z26519 (SP:P42738) (Arabidopsis thaliana)	5.7	6.6	-0.9	-3.2	6.7%	2.0
7859	AT3G51990.1 | protein kinase family protein, contains protein kinase domain, PF00069 | chr3:19298856-19300308 FORWARD | Aliases: F4F15.100	6.3	7.0	-0.7	-3.2	6.7%	2.0
7860	AT1G70990.1 | proline-rich family protein | chr1:26770959-26771738 REVERSE | Aliases: F15H11.18, F15H11_18	4.1	4.6	-0.6	-3.2	6.7%	1.9
7861	AT5G44660.1 | expressed protein, similar to unknown protein (pir::T05327) | chr5:18033037-18034404 FORWARD | Aliases: K15C23.11, K15C23_11	2.6	3.1	-0.5	-3.2	6.7%	1.8
7862	AT1G18620.1 | expressed protein | chr1:6410025-6414443 FORWARD | Aliases: F25I16.3, F25I16_3	3.9	5.2	-1.3	-3.2	6.7%	2.3
7863	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	9.4	10.6	-1.1	-3.2	6.7%	2.1
7864	AT3G01015.1 | expressed protein, ; expression supported by MPSS | chr3:1805-4024 REVERSE | Aliases: TEL3N.1, TEL3N_1	2.7	2.4	0.3	3.2	6.7%	1.4
7865	AT5G66930.2 | expressed protein, similar to unknown protein (pir::T38383) | chr5:26743168-26744977 FORWARD | Aliases: MUD21.19, MUD21_19	4.7	5.9	-1.2	-3.2	6.7%	2.2
7866	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	5.8	1.9	3.2	6.8%	2.2
7867	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	6.6	7.7	-1.1	-3.2	6.8%	2.2
7868	AT3G28340.1 | galactinol synthase, putative | chr3:10590184-10591776 REVERSE | Aliases: MZF16.17	5.2	6.0	-0.7	-3.2	6.8%	2.1
7869	AT3G48120.1 | expressed protein | chr3:17783122-17785724 FORWARD | Aliases: T24C20.2	4.5	3.7	0.8	3.2	6.8%	2.1
7870	AT1G04390.1 | expressed protein | chr1:1179362-1183703 REVERSE | Aliases: F19P19.16, F19P19_16	3.4	4.0	-0.7	-3.2	6.8%	2.0
7871	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	8.9	8.4	0.5	3.2	6.8%	1.9
7872	AT1G68700.1 | expressed protein | chr1:25796481-25796786 FORWARD | Aliases: F24J5.7, F24J5_7	3.4	4.1	-0.7	-3.2	6.8%	2.1

Rank	Description	Sync	Root	M	t	adj.q	B
7873	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	7.1	0.6	3.2	6.8%	2.0
7874	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	6.6	5.4	1.2	3.2	6.8%	2.1
7875	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	2.1	0.2	3.2	6.8%	1.1
7876	AT5G25460.1 | expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642 | chr5:8863393-8865680 FORWARD | Aliases: F18G18.200, F18G18_200	2.3	2.7	-0.4	-3.2	6.8%	1.7
7877	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	2.4	2.8	-0.3	-3.2	6.8%	1.5
7878	AT5G52540.1 | expressed protein, contains PF05684: Protein of unknown function (DUF819) | chr5:21338654-21341006 REVERSE | Aliases: F6N7.1, F6N7_1	9.6	7.4	2.2	3.2	6.8%	2.0
7879	AT1G71380.1 | glycosyl hydrolase family 9 protein, similar to beta-glucanase GB:AAB72171 | chr1:26903446-26905451 REVERSE | Aliases: F3I17.16, F3I17_16	2.7	2.4	0.3	3.2	6.8%	1.5
7880	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	3.7	-0.5	-3.2	6.8%	1.9
7881	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	10.0	10.5	-0.4	-3.2	6.8%	1.5
7882	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	4.3	-0.6	-3.2	6.8%	2.0
7883	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	3.5	-0.6	-3.2	6.8%	1.8
7884	AT5G18190.1 | protein kinase family protein, contains Pfam domains, PF00069: Protein kinase domain | chr5:6009969-6013726 REVERSE | Aliases: MRG7.15, MRG7_15	4.6	5.4	-0.8	-3.2	6.8%	2.0
7885	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	3.6	-0.7	-3.2	6.8%	2.2
7886	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	9.8	8.7	1.1	3.2	6.8%	1.9
7887	AT3G06150.1 | expressed protein | chr3:1861803-1864122 REVERSE | Aliases: F28L1.9, F28L1_9	5.0	4.6	0.4	3.2	6.8%	1.7
7888	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	5.1	-0.7	-3.2	6.8%	2.0
7889	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	6.3	5.6	0.7	3.2	6.9%	1.9
7890	AT3G05830.1 | Encodes alpha-helical IF (intermediate filament)-like protein. | chr3:1736686-1738670 FORWARD | Aliases: F10A16.12, F10A16_12	3.7	4.8	-1.1	-3.2	6.9%	2.1
7891	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	8.0	7.4	0.6	3.2	6.9%	2.0
7892	AT4G03990.1 | hypothetical protein, similar to At2g04970, At2g15200, At1g32830, At2g14140, At3g30450, At5g34895, At3g47270, At2g02200 | chr4:1916459-1917814 REVERSE | Aliases: T24H24.2, T24H24_2	2.8	3.1	-0.3	-3.2	6.9%	1.2
7893	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	4.0	3.4	0.6	3.2	6.9%	2.0

Rank	Description	Sync	Root	M	t	adj.q	B
7894	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) (Podospora anserina) | chr5:22739778-22742311 REVERSE | Aliases: MDA7.19, MDA7_19	6.2	4.8	1.4	3.2	6.9%	2.2
7895	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	3.2	-0.5	-3.2	6.9%	1.9
7896	AT5G58210.3 | hydroxyproline-rich glycoprotein family protein | chr5:23569339-23571572 FORWARD | Aliases: MCK7.8, MCK7_8	4.2	3.7	0.5	3.2	6.9%	1.9
7897	AT3G27180.1 | expressed protein | chr3:10028074-10031306 REVERSE | Aliases: MYF5.5	3.9	3.2	0.7	3.2	6.9%	2.2
7898	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	6.4	7.2	-0.8	-3.2	6.9%	2.2
7899	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	3.5	4.0	-0.6	-3.2	6.9%	1.8
7900	AT1G60650.2 | glycine-rich RNA-binding protein, putative, similar to RNA binding protein(RZ-1) GI:1435061 from (Nicotiana sylvestris); contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) | chr1:22343552-22346002 FORWARD | Aliases: F8A5.17, F8A5_17	6.3	5.5	0.8	3.2	6.9%	2.1
7901	AT4G29210.2 | gamma-glutamyltranspeptidase family protein, similar to SP:P07314 Gamma-glutamyltranspeptidase precursor (EC 2.3.2.2) (Gamma-glutamyltransferase) (GGT) {Rattus norvegicus}; contains Pfam profilePF01019: Gamma-glutamyltranspeptidase	5.7	6.6	-0.9	-3.2	6.9%	2.1
7902	AT1G29610.1 | hypothetical protein | chr1:10345749-10346229 FORWARD | Aliases: F15D2.18, F15D2_18	2.4	2.8	-0.3	-3.2	6.9%	1.4
7903	AT3G14180.1 | expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189 | chr3:4707120-4708855 REVERSE | Aliases: MAG2.16	4.6	5.5	-0.9	-3.2	6.9%	2.1
7904	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	6.7	5.3	1.4	3.2	6.9%	2.1
7905	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	3.7	3.3	0.4	3.2	6.9%	1.6
7906	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)	3.6	4.3	-0.7	-3.2	6.9%	2.0
7907	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	9.8	6.6	3.2	3.2	6.9%	2.3
7908	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	4.2	3.6	0.5	3.2	6.9%	1.9
7909	AT3G43210.1 | Symbol: TES | kinesin motor family protein (NACK2), contains Pfam profile: PF00225 kinesin motor domain	5.2	4.7	0.5	3.2	6.9%	1.9
7910	AT3G53930.1 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr3:19977330-19981791 FORWARD | Aliases: F5K20.230	4.9	5.6	-0.8	-3.2	6.9%	2.1
7911	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, HOMOGENTISATE PHYTYLTRANSFERASE, HOMOGENTISATE PHYTYLTRANSFERASE 1, HPT, TOCOPHEROL PHYTYLTRANSFERASE, TOCOPHEROL POLYPRENYLTRANSFERASE, TPT1, VITAMIN E 2, VTE2	4.9	3.9	1.0	3.2	6.9%	2.2
7912	AT4G17570.1 | zinc finger (GATA type) family protein | chr4:9783897-9787433 REVERSE | Aliases: DL4820C, FCAALL.45	4.6	5.1	-0.5	-3.2	6.9%	1.7
7913	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	2.7	0.8	3.2	6.9%	2.0

Rank	Description	Sync	Root	M	t	adj.q	B
7914	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	6.7	5.7	1.0	3.2	6.9%	2.3
7915	AT1G63120.1 | rhomboid family protein, contains PFAM domain PF01694, Rhomboid family | chr1:23412541-23414480 REVERSE | Aliases: F16M19.4, F16M19_4	6.1	7.5	-1.5	-3.2	6.9%	2.0
7916	AT2G15820.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profiles PF01535: PPR repeat, PF03161 LAGLIDADG DNA endonuclease family	4.0	3.5	0.5	3.2	6.9%	1.7
7917	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	4.6	-1.1	-3.2	6.9%	2.0
7918	AT4G10810.1 | expressed protein | chr4:6645712-6646332 REVERSE | Aliases: F25I24.20, F25I24_20	6.9	5.5	1.4	3.2	7.0%	2.2
7919	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	3.5	3.1	0.4	3.2	7.0%	1.8
7920	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	3.3	-0.4	-3.2	7.0%	1.8
7921	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	3.8	4.4	-0.6	-3.2	7.0%	2.0
7922	AT2G39950.1 | expressed protein | chr2:16683620-16687567 REVERSE | Aliases: T28M21.11, T28M21_11	3.7	4.2	-0.5	-3.2	7.0%	1.9
7923	AT3G20260.1 | expressed protein | chr3:7064080-7066504 REVERSE | Aliases: MQC12.1	3.4	2.8	0.6	3.2	7.0%	1.9
7924	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	5.8	6.5	-0.7	-3.2	7.0%	2.2
7925	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	8.8	8.1	0.8	3.2	7.0%	2.0
7926	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	7.8	8.5	-0.7	-3.2	7.0%	2.1
7927	AT5G45610.1 | expressed protein | chr5:18513538-18516900 REVERSE | Aliases: MRA19.1, MRA19_1	4.4	3.8	0.6	3.2	7.0%	1.9
7928	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	4.9	0.8	3.2	7.0%	2.0
7929	AT3G61810.1 | glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase precursor GI:4097948 from (Oryza sativa); contains Pfam profile PF00332: Glycosyl hydrolases family 17 | chr3:22888143-22889444 FORWARD | Aliases: F21F14.9	3.2	4.1	-0.9	-3.2	7.0%	2.1
7930	AT4G23810.1 | Symbol: WRKY53 |	3.9	5.3	-1.4	-3.2	7.0%	2.2
7931	AT3G55710.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:20684826-20686925 FORWARD | Aliases: F1I16.120	2.8	3.3	-0.5	-3.2	7.0%	1.7
7932	AT4G33040.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	5.6	5.0	0.6	3.1	7.0%	1.8
7933	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){Arabidopsis thaliana}; strong similarity to phosphoethanolamine N-methyltransferase from (Spinacia oleracea) GI:7407189, (Triticum aestivum) GI:17887465; contains Pfam profile PF01209: methlytransferase, UbiE/COQ5 family | chr3:6154369-6157558 FORWARD | Aliases: AT3G17990, MEB5.22, N METHYLTRANSFERASE 1, S ADENOSYLMETHIONINE:PHOSPHO ETHANOLAMINE	4.5	3.9	0.6	3.1	7.0%	2.0
7934	AT3G14980.1 | PHD finger transcription factor, putative, contains Pfam profile: PF00628 PHD-finger | chr3:5039938-5044818 REVERSE | Aliases: K15M2.12	5.3	4.6	0.8	3.1	7.0%	2.1

Rank	Description	Sync	Root	M	t	adj.q	B
7935	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	6.5	5.9	0.7	3.1	7.0%	1.9
7936	AT5G23170.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:7798414-7799451 REVERSE | Aliases: MKD15.3, MKD15_3	4.7	6.0	-1.3	-3.1	7.0%	2.2
7937	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	6.6	5.4	1.2	3.1	7.0%	2.2
7938	AT2G01740.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:326135-327814 REVERSE | Aliases: T8O11.9, T8O11_9	4.4	3.6	0.8	3.1	7.0%	2.0
7939	AT3G59040.2 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:21832326-21835289 REVERSE | Aliases: F17J16.90	5.6	4.7	0.9	3.1	7.0%	2.0
7940	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	4.1	4.8	-0.7	-3.1	7.1%	2.0
7941	AT2G31930.1 | expressed protein | chr2:13584632-13585325 FORWARD | Aliases: F20M17.3, F20M17_3	2.5	3.1	-0.5	-3.1	7.1%	1.8
7942	AT2G04400.1 | indole-3-glycerol phosphate synthase (IGPS), nearly identical to SP:P49572 | chr2:1531159-1534041 FORWARD | Aliases: T1O3.19, T1O3_19	8.7	7.4	1.3	3.1	7.1%	2.1
7943	AT3G16010.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:5434020-5436270 FORWARD | Aliases: MSL1.5	4.8	3.7	1.1	3.1	7.1%	2.0
7944	AT3G50240.1 | Symbol: KICP 02 | kinesin motor protein-related, KINESIN-LIKE PROTEIN KIF4, Homo sapiens, EMBL:AF179308	4.5	3.8	0.7	3.1	7.1%	2.1
7945	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	2.6	3.1	-0.5	-3.1	7.1%	1.7
7946	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	5.6	0.8	3.1	7.1%	2.1
7947	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	4.7	-0.7	-3.1	7.1%	1.8
7948	AT1G69360.1 | expressed protein | chr1:26075947-26079917 REVERSE | Aliases: F10D13.5, F10D13_5	5.2	6.1	-0.9	-3.1	7.1%	2.1
7949	AT5G43870.1 | expressed protein | chr5:17649573-17653125 REVERSE | Aliases: F6B6.1, F6B6_1	3.9	3.1	0.8	3.1	7.1%	2.1
7950	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	6.5	-1.5	-3.1	7.1%	2.1
7951	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	4.3	-0.4	-3.1	7.1%	1.6
7952	AT5G01890.1 | leucine-rich repeat transmembrane protein kinase, putative, leucine-rich receptor-like protein (LRPKm1) - Malus domestica, EMBL:AF053127	5.8	6.5	-0.6	-3.1	7.1%	2.0
7953	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	7.1	5.9	1.2	3.1	7.1%	1.9
7954	AT1G12020.1 | expressed protein | chr1:4062460-4063335 REVERSE | Aliases: F12F1.11, F12F1_11	3.7	4.1	-0.4	-3.1	7.1%	1.7
7955	AT5G11670.1 | malate oxidoreductase, putative, similar to NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (SP:P12628) {Phaseolus vulgaris}	10.7	11.4	-0.7	-3.1	7.1%	1.6

Rank	Description	Sync	Root	M	t	adj.q	B
7956	AT5G26080.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr5:9108000-9108425 FORWARD | Aliases: T1N24.105, T1N24_105	2.3	2.8	-0.5	-3.1	7.1%	1.7
7957	AT2G05755.1 | integral membrane family protein, contains Pfam PF00892: Integral membrane protein domain | chr2:2170890-2173757 FORWARD | Aliases: None	5.3	5.8	-0.5	-3.1	7.1%	1.9
7958	AT5G46680.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:18958196-18959789 FORWARD | Aliases: MZA15.9, MZA15_9	5.7	4.3	1.4	3.1	7.1%	2.1
7959	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	3.4	4.0	-0.7	-3.1	7.1%	1.9
7960	AT3G07210.1 | expressed protein, predicted using genefinder | chr3:2292804-2295458 REVERSE | Aliases: T1B9.12	3.6	3.0	0.6	3.1	7.1%	2.0
7961	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'	5.5	4.4	1.1	3.1	7.1%	2.0
7962	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	6.1	5.4	0.7	3.1	7.1%	2.0
7963	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	8.2	1.0	3.1	7.1%	1.9
7964	AT1G63450.1 | exostosin family protein, contains Pfam profile: PF03016	2.7	3.1	-0.5	-3.1	7.1%	1.7
7965	AT5G02800.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:635230-637480 REVERSE | Aliases: F9G14.110, F9G14_110	3.3	4.0	-0.8	-3.1	7.1%	1.9
7966	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	4.4	5.4	-1.0	-3.1	7.1%	2.1
7967	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	4.0	1.9	2.2	3.1	7.1%	2.0
7968	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	7.5	6.6	0.9	3.1	7.2%	2.0
7969	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	4.4	3.7	0.7	3.1	7.2%	2.1
7970	AT5G14520.1 | pescadillo-related, similar to pescadillo (Zebrafish, Danio rerio) SWISS-PROT:P79741 | chr5:4680792-4684333 REVERSE | Aliases: T15N1.10, T15N1_10	7.9	7.3	0.6	3.1	7.2%	1.8
7971	AT3G62240.1 | zinc finger (C2H2 type) family protein, contains Pfam PF00096: Zinc finger, C2H2 type | chr3:23044417-23047740 REVERSE | Aliases: T17J13.200	7.2	8.3	-1.1	-3.1	7.2%	2.1
7972	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	3.1	0.9	3.1	7.2%	1.8
7973	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	9.2	0.4	3.1	7.2%	1.6
7974	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	3.4	3.8	-0.4	-3.1	7.2%	1.7
7975	AT3G50380.1 | expressed protein | chr3:18697424-18711514 REVERSE | Aliases: F11C1.220	5.3	6.3	-1.1	-3.1	7.2%	2.0
7976	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}	10.8	9.9	0.8	3.1	7.2%	1.8

Rank	Description	Sync	Root	M	t	adj.q	B
7977	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	4.6	4.1	0.6	3.1	7.2%	1.9
7978	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	10.4	9.9	0.5	3.1	7.2%	1.1
7979	AT5G22840.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:7630720-7633226 REVERSE | Aliases: MRN17.7, MRN17_7	4.7	3.9	0.8	3.1	7.2%	2.0
7980	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	3.4	3.0	0.5	3.1	7.2%	1.8
7981	AT3G54640.1 | Symbol: TSA1 | tryptophan synthase, alpha subunit (TSA1), identical to gi:619753 | chr3:20234137-20236501 REVERSE | Aliases: TRP3, TRYPTOPHAN SYNTHASE ALPHA CHAIN	9.2	7.5	1.7	3.1	7.2%	2.0
7982	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	10.8	10.4	0.4	3.1	7.2%	1.4
7983	NA	12.8	13.2	-0.4	-3.1	7.2%	1.0
7984	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	3.1	-0.6	-3.1	7.2%	1.9
7985	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	7.8	1.7	3.1	7.2%	2.1
7986	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	6.6	8.1	-1.5	-3.1	7.2%	2.1
7987	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)	3.8	4.7	-0.8	-3.1	7.2%	2.2
7988	AT1G18200.1 | Ras-related GTP-binding family protein, contains Pfam profile: PF00071 Ras family | chr1:6264240-6266652 REVERSE | Aliases: T10F20.21	3.5	3.0	0.5	3.1	7.2%	1.9
7989	AT2G25430.1 | epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain;	5.8	6.8	-1.0	-3.1	7.2%	2.0
7990	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	3.9	-0.8	-3.1	7.2%	2.1
7991	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;	5.5	4.6	0.8	3.1	7.3%	2.1
7992	AT5G60680.1 | expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584 | chr5:24403371-24404202 FORWARD | Aliases: MUP24.10, MUP24_10	4.9	5.8	-0.9	-3.1	7.3%	2.0
7993	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	7.5	6.2	1.2	3.1	7.3%	2.1
7994	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	3.5	-0.6	-3.1	7.3%	1.9

Rank	Description	Sync	Root	M	t	adj.q	B
7995	AT3G22800.1 | leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycsimilar 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	3.5	4.3	-0.8	-3.1	7.3%	2.1
7996	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	2.5	2.9	-0.4	-3.1	7.3%	1.5
7997	AT5G18400.2 | expressed protein, contains Pfam profile PF05093: Protein of unknown function (DUF689) | chr5:6092684-6094996 REVERSE | Aliases: F20L16.120, F20L16_120	7.8	6.7	1.0	3.1	7.3%	2.0
7998	AT5G51170.1 | expressed protein | chr5:20811024-20812625 REVERSE | Aliases: MWD22.11, MWD22_11	6.3	5.1	1.2	3.1	7.3%	2.1
7999	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	9.8	10.6	-0.7	-3.1	7.3%	1.4
8000	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	6.2	-0.7	-3.1	7.3%	2.0
8001	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	3.9	5.0	-1.1	-3.1	7.3%	2.1
8002	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	3.5	0.7	3.1	7.3%	1.9
8003	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	9.1	6.7	2.4	3.1	7.3%	2.2
8004	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	6.8	6.0	0.9	3.1	7.3%	1.9
8005	AT1G77630.1 | peptidoglycan-binding LysM domain-containing protein, contains Pfam profile PF01476: LysM domain	3.3	2.6	0.7	3.1	7.3%	1.9
8006	AT5G61990.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:24916832-24920343 REVERSE | Aliases: MTG10.2, MTG10_2	3.5	3.9	-0.3	-3.1	7.3%	1.6
8007	AT3G01080.1 | Symbol: WRKY58 |	3.8	4.4	-0.6	-3.1	7.3%	1.9
8008	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)	5.8	4.6	1.1	3.1	7.3%	2.0
8009	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	3.9	0.8	3.1	7.3%	1.9
8010	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	4.5	3.8	0.8	3.1	7.3%	2.0
8011	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	3.3	4.6	-1.3	-3.1	7.3%	2.2
8012	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	2.2	2.5	-0.3	-3.1	7.3%	1.3
8013	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	9.9	-1.1	-3.1	7.3%	1.9
8014	AT1G73380.2 | expressed protein | chr1:27592693-27594540 FORWARD | Aliases: T9L24.41, T9L24_41	6.3	5.5	0.7	3.1	7.3%	2.0

Rank	Description	Sync	Root	M	t	adj.q	B
8015	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	4.3	5.1	-0.8	-3.1	7.4%	1.9
8016	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	2.4	-0.3	-3.1	7.4%	1.0
8017	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	4.5	3.7	0.7	3.1	7.4%	2.0
8018	AT2G20230.1 | expressed protein | chr2:8732622-8735101 FORWARD | Aliases: F11A3.22, F11A3_22	8.6	10.1	-1.5	-3.1	7.4%	1.9
8019	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	9.6	10.6	-1.0	-3.1	7.4%	1.7
8020	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	8.2	7.6	0.6	3.1	7.4%	1.5
8021	AT5G04740.1 | ACT domain-containing protein, contains Pfam profile PF01842: ACT domain	9.5	10.7	-1.2	-3.1	7.4%	2.0
8022	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	5.0	4.3	0.8	3.1	7.4%	2.2
8023	AT2G21185.1 | expressed protein | chr2:9083518-9084129 REVERSE | Aliases: None	7.2	6.3	0.9	3.1	7.4%	2.2
8024	AT5G63100.1 | expressed protein | chr5:25331363-25332654 REVERSE | Aliases: MDC12.6, MDC12_6	3.3	2.8	0.5	3.1	7.4%	1.7
8025	AT5G47090.1 | expressed protein | chr5:19144486-19145996 FORWARD | Aliases: K14A3.4, K14A3_4	8.5	6.7	1.8	3.1	7.4%	2.2
8026	AT2G43390.1 | expressed protein | chr2:18027427-18027938 REVERSE | Aliases: T1O24.13	2.9	3.7	-0.8	-3.1	7.4%	1.9
8027	AT5G01030.2 | expressed protein | chr5:9933-13234 FORWARD | Aliases: F7J8.10, F7J8_10	7.1	6.2	0.9	3.1	7.4%	2.1
8028	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	3.1	2.5	0.6	3.1	7.4%	1.6
8029	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	4.2	5.0	-0.8	-3.1	7.4%	2.0
8030	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	9.0	10.0	-1.0	-3.1	7.4%	2.1
8031	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	2.6	-0.3	-3.1	7.4%	1.3
8032	AT1G22850.1 | expressed protein | chr1:8080191-8082864 REVERSE | Aliases: F19G10.23	6.4	5.2	1.2	3.1	7.4%	2.1
8033	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	7.7	-0.8	-3.1	7.4%	1.8
8034	AT4G19980.1 | expressed protein, ; expression supported by MPSS | chr4:10828163-10828546 REVERSE | Aliases: F18F4.80, F18F4_80	2.2	2.6	-0.4	-3.1	7.4%	1.5
8035	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	3.3	2.9	0.4	3.1	7.4%	1.6
8036	AT3G30660.1 | hypothetical protein | chr3:12209587-12209820 FORWARD | Aliases: MED16.2	2.1	2.5	-0.4	-3.1	7.4%	1.7
8037	AT5G19300.1 | expressed protein, contains Pfam profile PF02598: Uncharacterized ACR, COG2106 | chr5:6495581-6498216 FORWARD | Aliases: F7K24.50, F7K24_50	5.4	4.2	1.2	3.1	7.4%	2.3

Rank	Description	Sync	Root	M	t	adj.q	B
8038	AT5G57480.1 | AAA-type ATPase family protein, contains Pfam profile: PF00004 ATPase family | chr5:23296632-23298194 REVERSE | Aliases: MUA2.5, MUA2_5	6.4	8.1	-1.7	-3.1	7.4%	2.0
8039	AT1G23650.1 | expressed protein, ; expression supported by MPSS | chr1:8371009-8371095 REVERSE | Aliases: F5O8.41, F5O8_41	2.9	3.7	-0.8	-3.1	7.4%	1.4
8040	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	3.3	5.0	-1.7	-3.1	7.4%	2.0
8041	AT3G51130.1 | expressed protein, contains Pfam PF03676: Uncharacterised protein family (UPF0183) | chr3:19005120-19008568 FORWARD | Aliases: F24M12.170	7.2	8.2	-1.0	-3.1	7.4%	1.7
8042	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	3.8	-0.4	-3.1	7.5%	1.3
8043	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	5.2	4.2	1.0	3.1	7.5%	2.2
8044	AT1G26180.1 | expressed protein | chr1:9054738-9056837 FORWARD | Aliases: F28B23.14, F28B23_14	5.7	4.7	1.0	3.1	7.5%	2.2
8045	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	3.6	3.1	0.5	3.1	7.5%	1.8
8046	AT1G64560.1 | expressed protein | chr1:23977487-23977840 FORWARD | Aliases: F1N19.29, F1N19_29	5.3	7.0	-1.7	-3.1	7.5%	1.8
8047	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	4.8	4.3	0.5	3.1	7.5%	1.8
8048	AT2G37320.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:15674302-15675804 FORWARD | Aliases: F3G5.11, F3G5_11	3.2	2.9	0.3	3.1	7.5%	1.4
8049	AT2G19790.1 | clathrin adaptor complex small chain family protein, contains Pfam profile: PF01217 clathrin adaptor complex small chain	9.2	7.2	2.0	3.1	7.5%	2.2
8050	AT4G02130.3 | similar to glycosyl transferase family 8 protein [Arabidopsis thaliana] (TAIR:At1g02720.2); similar to glycosyl transferase family 8 protein [Arabidopsis thaliana] (TAIR:At1g02720.1); similar to putative glycosyltransferase [Oryza sativa (japonica cultivar-group)] (GB:XP_479332.1); similar to OSJNBa0074L08.24 [Oryza sativa (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	4.4	4.9	-0.5	-3.1	7.5%	1.9
8051	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	3.9	-0.6	-3.1	7.5%	1.9
8052	AT3G52210.3 | similar to mRNA capping enzyme family protein [Arabidopsis thaliana] (TAIR:At3g20650.1); similar to hypothetical protein DDB0188046 [Dictyostelium discoideum] (GB:EAL63113.1); contains InterPro domain mRNA capping enzyme, large subunit (InterPro:IPR004971)	3.0	2.4	0.7	3.1	7.5%	1.9
8053	AT1G53035.1 | expressed protein | chr1:19765368-19766219 REVERSE | Aliases: None	5.4	6.0	-0.6	-3.1	7.5%	1.8
8054	AT5G07950.1 | expressed protein, ferredoxin (2Fe-2S), Arabidopsis thaliana, PIR:B71412	4.1	3.7	0.4	3.1	7.5%	1.6
8055	AT3G05170.1 | phosphoglycerate/bisphosphoglycerate mutase family protein, contains Pfam profile PF00300: phosphoglycerate mutase family | chr3:1466579-1468406 FORWARD | Aliases: T12H1.14, T12H1_14	4.7	6.2	-1.5	-3.1	7.5%	2.2
8056	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	3.7	0.9	3.1	7.5%	2.1
8057	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	3.1	4.1	-1.1	-3.1	7.5%	1.9
8058	AT5G11760.1 | expressed protein | chr5:3789293-3790453 FORWARD | Aliases: T22P22.150, T22P22_150	7.5	6.3	1.2	3.1	7.5%	2.1
8059	AT5G62100.2 | BAG domain-containing protein, similar to BAG domain containing proteins (At5g07220, At5g52060) | chr5:24957622-24959200 FORWARD | Aliases: MTG10.13, MTG10_13	3.0	3.9	-0.9	-3.1	7.5%	1.9

Rank	Description	Sync	Root	M	t	adj.q	B
8060	AT5G45550.1 | mob1/phocein family protein, contains Pfam profile: PF03637 Mob1/phocein family | chr5:18479444-18482248 FORWARD | Aliases: MFC19.22, MFC19_22	7.5	4.8	2.6	3.1	7.5%	2.2
8061	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	5.6	6.5	-1.0	-3.1	7.5%	2.0
8062	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	6.5	7.6	-1.1	-3.1	7.5%	2.1
8063	AT4G38530.1 | Symbol: ATPLC1 |	2.9	3.4	-0.5	-3.1	7.5%	1.6
8064	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	7.7	2.4	3.1	7.5%	2.2
8065	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	8.3	7.1	1.3	3.1	7.5%	2.0
8066	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	2.9	3.8	-0.9	-3.1	7.6%	1.8
8067	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	3.8	2.8	0.9	3.1	7.6%	2.1
8068	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	4.9	5.8	-0.9	-3.1	7.6%	2.0
8069	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	3.3	3.8	-0.5	-3.1	7.6%	1.7
8070	AT3G18380.2 | expressed protein | chr3:6310742-6313305 REVERSE | Aliases: MYF24.10	5.6	4.6	1.0	3.1	7.6%	2.0
8071	AT4G10170.2 | synaptobrevin-related family protein, similar to Vesicle-associated membrane protein 722	6.7	7.9	-1.2	-3.1	7.6%	2.0
8072	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	5.4	4.6	0.8	3.1	7.6%	2.0
8073	AT1G49560.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr1:18346252-18348005 FORWARD | Aliases: F14J22.20, F14J22_20	3.8	3.3	0.5	3.1	7.6%	1.9
8074	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	3.1	4.1	-1.0	-3.1	7.6%	1.9
8075	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	2.7	3.3	-0.6	-3.1	7.6%	1.7
8076	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	2.7	3.6	-0.9	-3.1	7.6%	1.9
8077	AT2G21870.2 | expressed protein | chr2:9327278-9329814 REVERSE | Aliases: F7D8.19, F7D8_19	10.5	8.9	1.6	3.1	7.6%	2.1
8078	AT5G17980.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr5:5953598-5956747 FORWARD | Aliases: MCM23.5, MCM23_5	4.1	3.5	0.6	3.1	7.6%	1.9
8079	AT2G03390.1 | uvrB/uvrC motif-containing protein, contains Pfam profile PF02151: UvrB/uvrC motif | chr2:1030399-1032619 REVERSE | Aliases: T4M8.18, T4M8_18	5.4	5.0	0.4	3.1	7.6%	1.6

Rank	Description	Sync	Root	M	t	adj.q	B
8080	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	5.0	3.9	1.1	3.1	7.6%	2.0
8081	AT1G72960.1 | root hair defective 3 GTP-binding (RHD3) family protein, contains Pfam profile: PF05879 root hair defective 3 GTP-binding protein (RHD3)	2.4	2.8	-0.4	-3.1	7.6%	1.6
8082	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	2.8	3.3	-0.5	-3.1	7.6%	1.8
8083	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	10.6	-1.3	-3.1	7.6%	2.0
8084	AT5G16050.1 | Symbol: GRF5 | 14-3-3 protein GF14 upsilon (GRF5), identical to 14-3-3 protein GF14 upsilon GI:2232148 from (Arabidopsis thaliana) | chr5:5243748-5245814 REVERSE | Aliases: F1N13.190, F1N13_190, GF14 UPSILON, GF14 UPSILON CHAIN	9.6	7.7	1.9	3.1	7.6%	1.9
8085	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	2.7	-0.4	-3.1	7.6%	1.5
8086	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	3.5	-0.3	-3.1	7.6%	1.4
8087	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	5.9	5.3	0.6	3.1	7.6%	1.9
8088	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	7.1	5.7	1.3	3.1	7.6%	2.2
8089	AT3G07190.1 | expressed protein | chr3:2285811-2287161 REVERSE | Aliases: T1B9.14	5.9	5.0	0.8	3.1	7.6%	2.1
8090	AT1G63520.1 | expressed protein | chr1:23563550-23565806 FORWARD | Aliases: F2K11.12, F2K11_12	2.5	2.9	-0.4	-3.1	7.6%	1.5
8091	AT1G52710.1 | cytochrome c oxidase-related, similar to SP:P00428 Cytochrome c oxidase polypeptide Vb (EC 1.9.3.1) (VI) (Bovine) {Bos taurus} | chr1:19641999-19643891 REVERSE | Aliases: F6D8.4, F6D8_4	6.9	7.7	-0.8	-3.1	7.6%	2.1
8092	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	9.3	7.4	2.0	3.1	7.6%	2.1
8093	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	6.1	4.6	1.5	3.1	7.6%	2.2
8094	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	7.6	8.3	-0.7	-3.1	7.7%	1.8
8095	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	5.1	6.0	-0.9	-3.1	7.7%	1.9
8096	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	6.2	2.1	3.1	7.7%	2.0
8097	AT1G04170.1 | Symbol: EIF2 GAMMA | eukaryotic translation initiation factor 2 subunit 3, putative / eIF2S3, putative / eIF-2-gamma, putative, similar to gb:U37354 from S. pombe. ESTs gb:T41979, gb:N37284 and gb:N37529 come from this gene	6.9	5.2	1.7	3.1	7.7%	2.0
8098	AT4G29910.1 | origin recognition complex subunit 5-related (ORC5), contains weak similarity to Origin recognition complex subunit 5 (Swiss-Prot:Q9WUV0) (Mus musculus)	4.8	4.0	0.8	3.1	7.7%	2.1

Rank	Description	Sync	Root	M	t	adj.q	B
8099	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	4.5	4.9	-0.5	-3.1	7.7%	1.6
8100	AT3G04790.1 | ribose 5-phosphate isomerase-related, similar to ribose-5-phosphate isomerase GI:18654317 from (Spinacia oleracea) | chr3:1313324-1314369 FORWARD | Aliases: F7O18.28, F7O18_28	9.3	8.3	1.1	3.1	7.7%	1.9
8101	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	2.5	-0.3	-3.1	7.7%	1.3
8102	AT3G60980.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:22576284-22577720 REVERSE | Aliases: T27I15.70	6.4	5.8	0.5	3.1	7.7%	1.8
8103	AT2G37590.1 | Dof-type zinc finger domain-containing protein | chr2:15776222-15777697 FORWARD | Aliases: F13M22.9, F13M22_9	3.5	4.0	-0.5	-3.1	7.7%	1.7
8104	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	7.9	7.3	0.6	3.1	7.7%	1.9
8105	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	5.4	4.4	0.9	3.1	7.7%	1.8
8106	AT4G12990.1 | expressed protein | chr4:7595041-7595445 REVERSE | Aliases: F25G13.80, F25G13_80	6.0	7.7	-1.7	-3.1	7.7%	2.1
8107	AT5G64150.1 | methylase family protein, contains TIGRfam TIGR00536: modification methylase, HemK family | chr5:25686057-25688444 REVERSE | Aliases: MHJ24.13, MHJ24_13	4.9	4.3	0.5	3.1	7.7%	1.8
8108	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	4.0	0.6	3.1	7.7%	1.8
8109	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	6.0	5.1	1.0	3.1	7.7%	1.9
8110	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	4.0	3.3	0.7	3.1	7.8%	2.0
8111	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	3.6	-0.8	-3.1	7.8%	2.0
8112	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	3.2	-0.9	-3.1	7.8%	1.7
8113	AT3G04670.2 | Symbol: WRKY39 |	6.1	7.0	-0.9	-3.1	7.8%	1.7
8114	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	5.2	5.7	-0.5	-3.1	7.8%	1.9
8115	AT4G20160.1 | expressed protein, ; expression supported by MPSS | chr4:10890993-10894981 FORWARD | Aliases: F1C12.80, F1C12_80	3.0	3.4	-0.4	-3.1	7.8%	1.5
8116	AT2G31010.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:13201288-13207205 FORWARD | Aliases: F7F1.22, F7F1_22	3.3	2.9	0.4	3.1	7.8%	1.5
8117	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	8.2	7.1	1.1	3.1	7.8%	1.9
8118	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	3.8	3.3	0.5	3.1	7.8%	1.8

Rank	Description	Sync	Root	M	t	adj.q	B
8119	AT1G09520.1 | expressed protein | chr1:3070907-3072052 REVERSE | Aliases: F14J9.18, F14J9_18	5.5	4.6	0.9	3.1	7.8%	2.1
8120	AT2G23270.1 | expressed protein, ; similar to GP:2464853:gnl:PID:e353149:Z99707 | chr2:9910295-9910925 FORWARD | Aliases: T20D16.10, T20D16_10	3.8	4.9	-1.1	-3.1	7.8%	1.8
8121	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	3.8	3.2	0.5	3.1	7.8%	1.8
8122	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)	7.5	5.1	2.4	3.1	7.8%	2.1
8123	AT2G36390.1 | Symbol: SBE2.1 |	7.9	6.9	1.0	3.1	7.8%	1.8
8124	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	3.3	3.8	-0.5	-3.1	7.8%	1.7
8125	AT4G01010.1 | Symbol: ATCNGC13 | cyclic nucleotide-regulated ion channel, putative (CNGC13), similar to CaM-regulated potassium ion channel (ACBK1) GI:8515883 from (Arabidopsis thaliana) | chr4:434569-437242 REVERSE | Aliases: CNGC13, F3I3.1, F3I3_1	3.7	4.6	-0.9	-3.1	7.9%	1.9
8126	AT5G52420.1 | expressed protein | chr5:21298999-21300507 FORWARD | Aliases: K24M7.17, K24M7_17	5.3	4.7	0.6	3.1	7.9%	1.9
8127	AT3G23740.1 | expressed protein | chr3:8551779-8554737 REVERSE | Aliases: MYM9.8	2.9	2.6	0.4	3.1	7.9%	1.4
8128	AT3G17410.1 | serine/threonine protein kinase, putative, similar to Pto kinase interactor 1 GB:AAC61805 from (Lycopersicon esculentum)	7.0	8.2	-1.2	-3.1	7.9%	2.0
8129	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	3.7	0.9	3.1	7.9%	2.1
8130	AT5G01280.1 | expressed protein | chr5:114010-116236 REVERSE | Aliases: T10O8.1	2.7	3.3	-0.6	-3.1	7.9%	1.9
8131	AT1G11740.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023 | chr1:3963277-3966824 REVERSE | Aliases: F25C20.11, F25C20_11	3.8	4.7	-0.9	-3.1	7.9%	2.1
8132	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	4.0	1.0	3.1	7.9%	1.9
8133	AT1G49000.1 | expressed protein | chr1:18127227-18127789 REVERSE | Aliases: F27J15.21, F27J15_21	3.5	4.6	-1.1	-3.1	7.9%	2.1
8134	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	4.3	3.8	0.6	3.1	7.9%	1.8
8135	AT1G69010.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	5.6	4.1	1.5	3.1	7.9%	1.9
8136	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	5.5	4.9	0.6	3.1	7.9%	1.9
8137	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	5.4	0.5	3.1	7.9%	1.7
8138	AT4G17650.1 | aromatic-rich family protein, contains Pfam PF03654: Aromatic-Rich Protein Family | chr4:9827532-9829668 FORWARD | Aliases: DL4860W, FCAALL.381	4.8	3.7	1.1	3.1	7.9%	1.9
8139	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	5.6	6.5	-0.9	-3.1	7.9%	2.0
8140	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	2.7	-0.5	-3.1	7.9%	1.4
8141	AT5G02860.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:654100-656559 FORWARD | Aliases: F9G14.170, F9G14_170	3.8	3.3	0.4	3.1	7.9%	1.6

Rank	Description	Sync	Root	M	t	adj.q	B
8142	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	6.8	4.7	2.0	3.1	7.9%	2.1
8143	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	4.9	4.3	0.6	3.1	7.9%	1.7
8144	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	3.8	-0.5	-3.1	7.9%	1.7
8145	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	3.8	-0.5	-3.1	7.9%	1.6
8146	AT2G39650.1 | expressed protein, contains Pfam profile PF04720: Protein of unknown function (DUF506) | chr2:16534922-16536352 REVERSE | Aliases: F12L6.31, F12L6_31	4.1	4.7	-0.5	-3.1	7.9%	1.7
8147	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	3.4	3.0	0.4	3.1	7.9%	1.5
8148	AT4G22850.1 | expressed protein | chr4:11994054-11996240 FORWARD | Aliases: F7H19.30	4.2	4.5	-0.4	-3.1	8.0%	1.5
8149	AT1G16830.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:5758870-5762612 FORWARD | Aliases: F17F16.24	4.0	3.5	0.5	3.0	8.0%	1.6
8150	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	4.1	3.1	1.0	3.0	8.0%	1.8
8151	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	4.1	3.6	0.5	3.0	8.0%	1.6
8152	AT5G03260.1 | laccase, putative / diphenol oxidase, putative, similar to laccase (Pinus taeda)(GI:13661207) | chr5:777020-779423 REVERSE | Aliases: F15A17.290, F15A17_290	4.0	5.0	-1.0	-3.0	8.0%	1.9
8153	AT1G73000.1 | expressed protein | chr1:27466753-27467382 FORWARD | Aliases: F3N23.20, F3N23_20	2.9	3.2	-0.3	-3.0	8.0%	1.2
8154	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	8.5	7.1	1.5	3.0	8.0%	1.9
8155	AT3G14330.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:4779695-4782459 REVERSE | Aliases: MLN21.12	3.4	2.9	0.5	3.0	8.0%	1.6
8156	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	4.2	3.2	1.0	3.0	8.0%	1.8
8157	AT3G44200.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	5.0	5.7	-0.7	-3.0	8.0%	2.0
8158	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	3.1	4.0	-0.9	-3.0	8.0%	2.0
8159	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	4.6	-0.7	-3.0	8.0%	1.8
8160	AT3G46740.1 | Symbol: TOC75 | chloroplast outer envelope protein, putative, similar to chloroplastic outer envelope membrane protein (OEP75) (Pisum sativum) GI:633607; contains Pfam profile PF01103: outer membrane protein, OMP85 family | chr3:17226798-17230328 REVERSE | Aliases: T6H20.230, TOC75 III	6.7	5.7	1.0	3.0	8.0%	1.9
8161	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	2.8	3.1	-0.4	-3.0	8.0%	1.5

Rank	Description	Sync	Root	M	t	adj.q	B
8162	AT4G31030.1 | expressed protein | chr4:15111223-15111605 REVERSE | Aliases: F6I18.60, F6I18_60	7.3	6.9	0.4	3.0	8.0%	1.4
8163	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	5.4	4.6	0.7	3.0	8.0%	2.0
8164	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	4.9	4.0	0.8	3.0	8.0%	1.9
8165	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	4.2	4.7	-0.5	-3.0	8.0%	1.5
8166	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	6.5	5.7	0.9	3.0	8.0%	2.0
8167	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	7.1	8.4	-1.3	-3.0	8.0%	1.9
8168	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	3.7	3.1	0.6	3.0	8.0%	1.6
8169	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	4.4	5.2	-0.8	-3.0	8.0%	2.0
8170	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	4.1	-1.2	-3.0	8.0%	1.8
8171	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	3.6	3.1	0.5	3.0	8.0%	1.6
8172	AT2G21380.1 | kinesin motor protein-related | chr2:9148711-9156389 FORWARD | Aliases: F3K23.14, F3K23_14	4.9	3.9	1.1	3.0	8.0%	1.9
8173	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	11.9	10.7	1.2	3.0	8.0%	1.7
8174	AT5G64950.1 | mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF | chr5:25971070-25972386 FORWARD | Aliases: MXK3.18, MXK3_18	6.2	5.6	0.7	3.0	8.1%	1.9
8175	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	8.8	6.9	2.0	3.0	8.1%	2.1
8176	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	4.0	5.0	-1.1	-3.0	8.1%	2.0
8177	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 (Arabidopsis thaliana) gi:19421998:gb:AAL87850; identical to far-red elongated hypocotyl protein 1 (Arabidopsis thaliana) gi:17148773:gb:AAL35819 | chr2:15808899-15812593 REVERSE | Aliases: F13M22.18, F13M22_18, PAT3	6.3	7.3	-1.0	-3.0	8.1%	2.2
8178	AT3G20200.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:7047587-7051266 FORWARD | Aliases: MAL21.21	2.9	2.5	0.3	3.0	8.1%	1.3
8179	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	4.4	3.6	0.8	3.0	8.1%	2.0

Rank	Description	Sync	Root	M	t	adj.q	B
8180	AT3G13650.1 | disease resistance response 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 | chr3:4462899-4463879 FORWARD | Aliases: MMM17.15	5.7	7.0	-1.3	-3.0	8.1%	2.1
8181	AT3G06890.1 | expressed protein | chr3:2176862-2177592 FORWARD | Aliases: F17A9.4	5.0	5.9	-0.9	-3.0	8.1%	1.9
8182	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	5.1	6.8	-1.7	-3.0	8.1%	2.1
8183	AT5G19540.1 | expressed protein | chr5:6595704-6597891 FORWARD | Aliases: T20D1.60, T20D1_60	7.8	6.5	1.2	3.0	8.1%	2.0
8184	AT3G54150.1 | embryo-abundant protein-related, similar to embryo-abundant protein (Picea glauca) GI:1350531 | chr3:20061622-20063759 REVERSE | Aliases: F24B22.110	3.5	3.0	0.5	3.0	8.1%	1.6
8185	AT2G15960.1 | expressed protein | chr2:6954391-6954770 FORWARD | Aliases: F19G14.4, F19G14_4	3.9	5.1	-1.2	-3.0	8.1%	2.0
8186	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	4.4	5.2	-0.7	-3.0	8.1%	1.9
8187	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	7.6	8.7	-1.1	-3.0	8.1%	2.0
8188	AT1G30440.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr1:10759457-10762376 FORWARD | Aliases: F26G16.2, F26G16_2	6.6	7.1	-0.5	-3.0	8.1%	1.7
8189	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	5.1	4.6	0.5	3.0	8.1%	1.5
8190	AT3G29180.1 | expressed protein | chr3:11149452-11152797 FORWARD | Aliases: MUO22.2	8.7	8.1	0.7	3.0	8.1%	1.7
8191	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	6.9	8.0	-1.1	-3.0	8.1%	1.8
8192	AT3G52500.1 | aspartyl protease family protein, contains Pfam PF00026: eukaryotic aspartyl protease | chr3:19476477-19478364 REVERSE | Aliases: F22O6.120	6.9	5.4	1.5	3.0	8.1%	1.9
8193	AT5G14930.2 | Symbol: SAG101 |	3.9	5.2	-1.3	-3.0	8.1%	2.0
8194	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	7.4	6.0	1.4	3.0	8.1%	1.9
8195	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	4.9	4.3	0.6	3.0	8.2%	1.8
8196	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	2.5	-0.5	-3.0	8.2%	1.3
8197	AT5G18525.1 | WD-40 repeat family protein, contains Pfam profile PF00400: WD domain, G-beta repeat | chr5:6146760-6149757 REVERSE | Aliases: None	4.3	4.9	-0.5	-3.0	8.2%	1.5
8198	AT3G49820.1 | expressed protein | chr3:18492222-18492707 FORWARD | Aliases: T16K5.170	2.2	2.7	-0.5	-3.0	8.2%	1.4
8199	AT5G03230.1 | expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584 | chr5:769513-770384 FORWARD | Aliases: F15A17.260, F15A17_260	2.7	4.0	-1.3	-3.0	8.2%	1.8
8200	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	2.4	2.8	-0.4	-3.0	8.2%	1.5

Rank	Description	Sync	Root	M	t	adj.q	B
8201	AT5G22870.1 | harpin-induced protein-related / HIN1-related / harpin-responsive protein-related, weak similarity to hin1 (Nicotiana tabacum) GI:1619321 | chr5:7647059-7647682 REVERSE | Aliases: MRN17.10, MRN17_10	2.3	2.7	-0.4	-3.0	8.2%	1.6
8202	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	8.7	7.8	0.9	3.0	8.2%	1.9
8203	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	5.6	6.7	-1.1	-3.0	8.2%	1.8
8204	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	11.9	11.2	0.7	3.0	8.2%	1.6
8205	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	3.2	3.8	-0.6	-3.0	8.2%	1.7
8206	AT5G16860.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:5543837-5546389 FORWARD | Aliases: F2K13.10, F2K13_10	2.8	2.5	0.3	3.0	8.2%	1.1
8207	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	5.4	4.7	0.7	3.0	8.2%	1.7
8208	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	3.7	4.4	-0.7	-3.0	8.2%	1.7
8209	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	5.1	5.7	-0.6	-3.0	8.2%	1.9
8210	AT3G25690.1 | Symbol: CHUP1 | hydroxyproline-rich glycoprotein family protein, Common family members: At4g18570, At4g04980, At5g61090 (Arabidopsis thaliana);	5.6	4.5	1.2	3.0	8.2%	2.1
8211	AT1G22400.1 | Symbol: UGT85A1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr1:7903649-7906662 REVERSE | Aliases: F12K8.26, F12K8_26, UGT85A1	3.4	4.2	-0.8	-3.0	8.2%	1.9
8212	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	4.1	3.7	0.4	3.0	8.2%	1.6
8213	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	2.7	3.0	-0.3	-3.0	8.2%	1.2
8214	AT3G50340.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr3:18676076-18677654 REVERSE | Aliases: F11C1.180	7.1	6.6	0.6	3.0	8.2%	1.7
8215	AT3G66652.1 | fip1 motif-containing protein, contains Pfam profile PF05182: Fip1 motif	5.0	3.7	1.2	3.0	8.2%	1.9
8216	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	4.3	1.1	3.0	8.2%	2.0
8217	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	6.2	5.6	0.6	3.0	8.2%	1.9
8218	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	10.2	9.2	0.9	3.0	8.2%	1.8
8219	AT1G17950.1 | Symbol: MYB52 | myb family transcription factor (MYB52), similar to myb-like protein GI:6979341 from (Oryza sativa) | chr1:6177610-6179282 FORWARD | Aliases: ATMYB52, BW52, F2H15.17, F2H15_17, MYB52	2.7	3.2	-0.5	-3.0	8.2%	1.4
8220	AT3G61340.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.8	2.4	0.4	3.0	8.2%	1.5

Rank	Description	Sync	Root	M	t	adj.q	B
8221	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	4.7	4.0	0.6	3.0	8.2%	1.9
8222	AT4G27120.2 | expressed protein | chr4:13602096-13604375 REVERSE | Aliases: T24A18.70, T24A18_70	8.3	9.2	-0.8	-3.0	8.3%	1.8
8223	AT3G01650.1 | copine-related, low similarity to SP:Q99829 Copine I {Homo sapiens} | chr3:242018-245275 FORWARD | Aliases: F4P13.19, F4P13_19	5.4	6.0	-0.5	-3.0	8.3%	1.8
8224	AT5G37210.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.7	4.3	-0.6	-3.0	8.3%	1.7
8225	AT5G54220.1 | Encodes a defensin-like (DEFL) family protein. | chr5:22028575-22028981 FORWARD | Aliases: MDK4.4, MDK4_4	2.9	3.7	-0.8	-3.0	8.3%	1.8
8226	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	5.3	4.2	1.1	3.0	8.3%	2.1
8227	AT1G33250.1 | fringe-related protein, + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.	5.3	6.1	-0.8	-3.0	8.3%	1.6
8228	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	8.6	7.8	0.7	3.0	8.3%	1.9
8229	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	3.5	-0.4	-3.0	8.3%	1.5
8230	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)	4.7	4.1	0.6	3.0	8.3%	1.9
8231	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	3.5	4.1	-0.5	-3.0	8.3%	1.7
8232	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	11.0	1.0	3.0	8.3%	1.5
8233	AT3G25165.1 | Symbol: RALFL25 | rapid alkalinization factor (RALF) family protein | chr3:9163347-9163900 REVERSE | Aliases: RALF LIKE 25	2.2	2.4	-0.2	-3.0	8.3%	0.7
8234	AT4G01110.1 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g46300.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD72426.1) | chr4:479501-481160 REVERSE | Aliases: F2N1.3, F2N1_3	3.3	3.9	-0.7	-3.0	8.3%	1.8
8235	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	4.6	4.1	0.5	3.0	8.3%	1.7
8236	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	4.7	4.1	0.6	3.0	8.3%	1.8
8237	AT1G62150.1 | mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF | chr1:22973694-22975429 REVERSE | Aliases: F19K23.9, F19K23_9	5.6	4.8	0.8	3.0	8.3%	2.0
8238	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	9.5	1.0	3.0	8.3%	1.2
8239	AT3G01180.1 | glycogen synthase, putative, similar to glycogen synthase Q43847 from (Solanum tuberosum) | chr3:62252-65852 REVERSE | Aliases: T4P13.13, T4P13_13	6.7	5.3	1.4	3.0	8.3%	1.9
8240	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	3.0	-0.4	-3.0	8.3%	1.4

Rank	Description	Sync	Root	M	t	adj.q	B
8241	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	5.0	5.7	-0.6	-3.0	8.4%	1.7
8242	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	2.6	-0.3	-3.0	8.4%	0.9
8243	AT5G41100.2 | expressed protein | chr5:16464450-16468109 FORWARD | Aliases: MEE6.17, MEE6_17	4.3	5.0	-0.7	-3.0	8.4%	1.8
8244	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	6.4	7.1	-0.7	-3.0	8.4%	1.7
8245	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	2.7	3.2	-0.5	-3.0	8.4%	1.4
8246	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	4.8	4.3	0.5	3.0	8.4%	1.7
8247	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	7.0	6.3	0.7	3.0	8.4%	1.7
8248	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	3.2	-0.5	-3.0	8.4%	1.7
8249	AT2G18980.1 | peroxidase, putative, identical to peroxidase ATP22a (Arabidopsis thaliana) gi:1620369:emb:CAA70034 | chr2:8240417-8242394 REVERSE | Aliases: F19F24.18, F19F24_18	2.7	3.0	-0.3	-3.0	8.4%	1.3
8250	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	3.2	-0.4	-3.0	8.4%	1.3
8251	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	10.3	11.1	-0.8	-3.0	8.4%	1.5
8252	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	4.7	3.7	1.0	3.0	8.4%	1.8
8253	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	5.6	7.1	-1.5	-3.0	8.4%	2.0
8254	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	9.6	7.7	1.9	3.0	8.4%	1.9
8255	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	6.5	5.3	1.1	3.0	8.4%	1.9
8256	AT1G21850.1 | Symbol: SKS8 | multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)(Brassica napus); contains Pfam profile: PF00394 Multicopper oxidase | chr1:7667792-7670519 REVERSE | Aliases: SKS8, T26F17.6, T26F17_6	2.8	3.3	-0.4	-3.0	8.4%	1.6
8257	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	6.0	6.7	-0.6	-3.0	8.4%	1.7
8258	AT5G45320.1 | expressed protein, ; expression supported by MPSS | chr5:18379581-18380280 REVERSE | Aliases: K9E15.10, K9E15_10	2.7	3.2	-0.4	-3.0	8.4%	1.4
8259	AT3G01160.1 | expressed protein | chr3:54548-57469 REVERSE | Aliases: T4P13.15, T4P13_15	5.0	3.8	1.2	3.0	8.4%	2.0

Rank	Description	Sync	Root	M	t	adj.q	B
8260	AT4G28290.1 | expressed protein | chr4:14011875-14012589 REVERSE | Aliases: F26K10.170, F26K10_170	4.9	6.2	-1.2	-3.0	8.4%	1.9
8261	AT1G13880.1 | ELM2 domain-containing protein, contains Pfam profile: PF01448 ELM2 domain | chr1:4748926-4751208 FORWARD | Aliases: F16A14.9, F16A14_9	4.5	5.9	-1.3	-3.0	8.4%	1.9
8262	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	8.4	8.9	-0.5	-3.0	8.4%	1.5
8263	AT5G53560.1 | Symbol: ATB5 A |	12.6	12.1	0.5	3.0	8.4%	1.0
8264	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	5.9	0.7	3.0	8.4%	1.9
8265	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)	7.6	8.7	-1.1	-3.0	8.5%	1.8
8266	AT1G23710.1 | expressed protein | chr1:8385240-8386415 FORWARD | Aliases: F5O8.26, F5O8_26	4.8	6.4	-1.6	-3.0	8.5%	2.0
8267	AT2G04890.1 | Symbol: SCL21 | scarecrow-like transcription factor 21 (SCL21) | chr2:1719778-1722378 REVERSE | Aliases: F1O13.2, F1O13_2, SCARECROW LIKE 21, SCL21	6.1	5.3	0.8	3.0	8.5%	1.8
8268	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	7.7	6.5	1.2	3.0	8.5%	1.8
8269	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	3.1	2.8	0.3	3.0	8.5%	1.1
8270	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	6.6	8.7	-2.1	-3.0	8.5%	2.0
8271	AT3G12940.1 | expressed protein | chr3:4130014-4132474 REVERSE | Aliases: MGH6.5	2.8	3.2	-0.4	-3.0	8.5%	1.5
8272	AT5G48720.1 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g01990.1); similar to P0413C03.27 [Oryza sativa (japonica cultivar-group)] (GB:NP_914850.1)	3.9	3.3	0.6	3.0	8.5%	1.7
8273	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	5.0	-0.6	-3.0	8.5%	1.6
8274	AT1G35250.1 | thioesterase family protein, contains Pfam profile PF03061: thioesterase family protein | chr1:12932923-12934457 REVERSE | Aliases: T9I1.4, T9I1_4	3.5	4.2	-0.7	-3.0	8.5%	1.7
8275	AT2G18876.2 | expressed protein | chr2:8176630-8179605 FORWARD | Aliases: None	4.5	5.9	-1.4	-3.0	8.5%	2.1
8276	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	3.9	3.3	0.5	3.0	8.5%	1.6
8277	AT1G49750.1 | leucine-rich repeat family protein, contains leucine-rich repeats, Pfam:PF00560 | chr1:18414597-18416469 REVERSE | Aliases: F14J22.4, F14J22_4	3.4	2.8	0.6	3.0	8.5%	1.7
8278	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	3.7	0.4	3.0	8.5%	1.5
8279	AT1G05530.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr1:1636495-1637862 REVERSE | Aliases: T25N20.18	3.5	4.1	-0.7	-3.0	8.5%	1.8

Rank	Description	Sync	Root	M	t	adj.q	B
8280	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	4.9	-0.6	-3.0	8.5%	1.5
8281	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	4.7	1.1	3.0	8.5%	2.0
8282	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	3.3	2.8	0.5	3.0	8.5%	1.6
8283	AT4G19370.1 | expressed protein | chr4:10566274-10567546 REVERSE | Aliases: T5K18.150, T5K18_150	4.6	3.9	0.6	3.0	8.5%	1.9
8284	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	2.5	-0.3	-3.0	8.5%	1.2
8285	AT1G20530.1 | expressed protein | chr1:7108360-7110367 REVERSE | Aliases: F5M15.15, F5M15_15	3.3	2.9	0.4	3.0	8.5%	1.5
8286	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	5.5	0.8	3.0	8.5%	1.7
8287	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	4.5	4.0	0.5	3.0	8.6%	1.6
8288	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	4.2	5.3	-1.1	-3.0	8.6%	1.8
8289	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	11.2	10.1	1.2	3.0	8.6%	1.6
8290	AT1G28630.1 | expressed protein, ; expression supported by MPSS | chr1:10061209-10063438 REVERSE | Aliases: F1K23.14, F1K23_14	2.6	3.0	-0.4	-3.0	8.6%	1.4
8291	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	4.6	4.1	0.5	3.0	8.6%	1.7
8292	AT2G20500.1 | expressed protein | chr2:8842201-8843125 REVERSE | Aliases: T13C7.9, T13C7_9	2.6	3.0	-0.4	-3.0	8.6%	1.4
8293	AT4G29810.2 | Symbol: ATMKK2 |	7.6	6.5	1.1	3.0	8.6%	1.7
8294	AT2G28910.1 | Symbol: CXIP4 | CAX-interacting protein 4 (CAXIP4), contains Pfam domain PF00098: Zinc knuckle; identical to cDNA CAX-interacting protein 4 GI:27651998	12.0	12.7	-0.7	-3.0	8.6%	1.2
8295	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	8.6	7.4	1.2	3.0	8.6%	1.6
8296	AT1G55160.1 | expressed protein | chr1:20582084-20583677 FORWARD | Aliases: T7N22.11	6.2	7.0	-0.8	-3.0	8.6%	1.9
8297	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	2.7	3.4	-0.7	-3.0	8.6%	1.5
8298	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	2.2	0.3	3.0	8.6%	1.1
8299	AT3G62930.1 | glutaredoxin family protein, contains glutaredoxin domain, INTERPRO:IPR002109 | chr3:23272513-23272821 REVERSE | Aliases: T20O10.30	3.1	3.6	-0.5	-3.0	8.6%	1.4
8300	AT1G06930.1 | expressed protein, ; expression supported by MPSS | chr1:2129162-2129671 FORWARD | Aliases: F4H5.24, F4H5_24	3.0	3.6	-0.5	-3.0	8.6%	1.5
8301	AT2G22590.1 | glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	3.8	3.0	0.8	3.0	8.6%	1.9

Rank	Description	Sync	Root	M	t	adj.q	B
8302	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	3.8	-0.5	-3.0	8.6%	1.6
8303	AT2G41420.1 | proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965 | chr2:17273555-17275102 REVERSE | Aliases: F13H10.3, F13H10_3	6.5	4.7	1.7	3.0	8.6%	1.9
8304	AT5G62950.1 | expressed protein | chr5:25279458-25281047 REVERSE | Aliases: MQB2.27, MQB2_27	5.8	6.4	-0.7	-3.0	8.6%	1.8
8305	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	6.0	5.4	0.5	3.0	8.6%	1.8
8306	AT3G22890.1 | Symbol: APS1 | sulfate adenylyltransferase 1 / ATP-sulfurylase 1 (APS1), nearly identical to ATP sulfurylase (APS1) (Arabidopsis thaliana) GI:6606509 | chr3:8112730-8114996 FORWARD | Aliases: F5N5.7	8.9	10.4	-1.4	-3.0	8.6%	1.8
8307	AT5G53530.1 | vacuolar protein sorting-associated protein 26, putative / VPS26, putative, similar to vacuolar sorting protein 26 (Homo sapiens) GI:9622852; contains Pfam profile PF03643: Vacuolar protein sorting-associated protein 26 | chr5:21763269-21765790 REVERSE | Aliases: MNC6.7, MNC6_7	6.9	7.7	-0.8	-3.0	8.6%	1.8
8308	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	10.8	9.9	0.9	3.0	8.6%	1.7
8309	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	5.8	-1.0	-3.0	8.7%	1.9
8310	AT4G33140.1 | expressed protein | chr4:15981408-15984354 FORWARD | Aliases: F4I10.70, F4I10_70	5.3	4.4	0.9	3.0	8.7%	1.7
8311	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	3.0	3.5	-0.5	-3.0	8.7%	1.5
8312	AT3G30280.1 | transferase family protein, similar to deacetylvindoline 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	4.5	-1.1	-3.0	8.7%	2.1
8313	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	7.4	0.9	3.0	8.7%	1.8
8314	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	6.8	-0.9	-3.0	8.7%	1.7
8315	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	3.2	-0.3	-3.0	8.7%	1.1
8316	AT1G24575.1 | expressed protein | chr1:8711023-8711515 REVERSE | Aliases: None	2.4	2.6	-0.3	-3.0	8.7%	0.8
8317	AT1G18450.1 | Symbol: ATARP4 |	6.2	5.5	0.7	3.0	8.7%	1.7
8318	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 MOdifier) | chr2:5551263-5563546 REVERSE | Aliases: F14O4.6, F14O4_6	6.1	7.3	-1.2	-3.0	8.7%	2.0
8319	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	2.3	0.2	3.0	8.7%	0.5
8320	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	3.6	4.7	-1.0	-3.0	8.7%	2.0

Rank	Description	Sync	Root	M	t	adj.q	B
8321	AT3G47790.1 | Symbol: ATATH7 |	2.7	3.5	-0.9	-3.0	8.7%	1.8
8322	AT2G22410.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:9516097-9518311 FORWARD | Aliases: F14M13.19, F14M13_19	4.4	3.6	0.8	3.0	8.7%	1.9
8323	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	5.8	6.5	-0.6	-3.0	8.7%	1.7
8324	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	3.8	3.2	0.6	3.0	8.7%	1.7
8325	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	2.6	3.0	-0.4	-3.0	8.7%	1.3
8326	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	5.7	6.6	-0.9	-3.0	8.7%	1.8
8327	AT1G66250.1 | glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase GI:15150341 from (Camellia sinensis)	5.1	4.3	0.8	3.0	8.7%	1.9
8328	AT1G09810.1 | expressed protein, contains Pfam profile PF04146: YT521-B-like family | chr1:3180964-3182832 REVERSE | Aliases: F21M12.20, F21M12_20	4.6	3.8	0.8	3.0	8.7%	1.9
8329	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	5.5	-0.5	-3.0	8.7%	1.5
8330	AT1G09900.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:3218135-3219931 FORWARD | Aliases: F21M12.38, F21M12_38	3.5	3.1	0.4	3.0	8.7%	1.4
8331	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	6.8	7.5	-0.7	-3.0	8.7%	1.7
8332	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	3.1	-0.3	-3.0	8.7%	1.2
8333	AT5G52980.1 | expressed protein | chr5:21499386-21500889 REVERSE | Aliases: MNB8.4, MNB8_4	5.6	5.1	0.5	3.0	8.7%	1.5
8334	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	7.2	6.1	1.1	3.0	8.7%	1.8
8335	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	3.0	-0.3	-3.0	8.7%	1.0
8336	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	6.1	-0.7	-3.0	8.7%	1.6
8337	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	6.9	6.0	0.9	3.0	8.7%	1.8
8338	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	7.6	0.9	3.0	8.8%	1.7
8339	AT3G02930.1 | expressed protein, ; expression supported by MPSS | chr3:655313-658326 FORWARD | Aliases: F13E7.12, F13E7_12	6.6	4.5	2.1	3.0	8.8%	2.0
8340	AT5G62070.1 | calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif | chr5:24947145-24949802 REVERSE | Aliases: MTG10.10, MTG10_10	4.1	4.6	-0.4	-3.0	8.8%	1.4
8341	AT4G10470.1 | expressed protein | chr4:6476010-6478339 FORWARD | Aliases: F7L13.50, F7L13_50	3.2	2.9	0.3	3.0	8.8%	1.3

Rank	Description	Sync	Root	M	t	adj.q	B
8342	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	5.7	5.0	0.6	3.0	8.8%	1.8
8343	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	4.7	0.6	3.0	8.8%	1.4
8344	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	5.8	4.9	0.9	3.0	8.8%	1.8
8345	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	8.5	7.5	1.1	3.0	8.8%	1.7
8346	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	3.2	-0.3	-3.0	8.8%	1.2
8347	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	4.3	-0.7	-3.0	8.8%	1.7
8348	AT4G20020.2 | expressed protein | chr4:10844141-10846133 REVERSE | Aliases: F18F4.120, F18F4_120	5.2	4.6	0.5	3.0	8.8%	1.4
8349	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	4.4	3.8	0.6	3.0	8.8%	1.6
8350	AT3G59390.2 | expressed protein, protein CG15643 - Drosophila melanogaster, EMBL:AE003499 | chr3:21957095-21959273 FORWARD | Aliases: F25L23.250	5.4	4.8	0.6	3.0	8.8%	1.7
8351	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	5.1	-0.7	-3.0	8.8%	1.8
8352	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	7.9	9.0	-1.1	-3.0	8.8%	1.8
8353	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	4.2	-0.6	-3.0	8.8%	1.7
8354	AT3G10850.1 | Symbol: GLX2 2 |	8.7	7.0	1.7	3.0	8.8%	1.8
8355	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	2.8	3.3	-0.5	-3.0	8.9%	1.6
8356	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	9.6	10.9	-1.3	-3.0	8.9%	1.7
8357	AT5G47480.1 | expressed protein | chr5:19274647-19280651 FORWARD | Aliases: MNJ7.7, MNJ7_7	8.2	9.6	-1.4	-3.0	8.9%	1.5
8358	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	7.8	8.4	-0.6	-3.0	8.9%	1.5
8359	AT1G09440.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:3045515-3047395 REVERSE | Aliases: F14J9.10, F14J9_10	3.8	4.5	-0.8	-3.0	8.9%	1.5
8360	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	4.6	6.1	-1.5	-3.0	8.9%	2.0
8361	AT3G49900.1 | BTB/POZ domain-containing protein, contains BTB/POZ domain, INTERPRO:IPR000210 | chr3:18511620-18513599 REVERSE | Aliases: T16K5.250	3.1	2.7	0.4	3.0	8.9%	1.3

Rank	Description	Sync	Root	M	t	adj.q	B
8362	AT2G24290.1 | expressed protein | chr2:10345759-10347201 FORWARD | Aliases: T28I24.2, T28I24_2	5.2	4.1	1.1	3.0	8.9%	1.8
8363	AT3G45050.4 | expressed protein | chr3:16486964-16488948 FORWARD | Aliases: F14D17.120	3.9	3.1	0.8	3.0	8.9%	1.9
8364	AT2G39640.1 | glycosyl hydrolase family 17 protein | chr2:16532164-16534090 REVERSE | Aliases: F12L6.1	2.6	3.2	-0.6	-3.0	8.9%	1.6
8365	AT3G47010.1 | glycosyl hydrolase family 3 protein, beta-D-glucan exohydrolase, Nicotiana tabacum, TREMBL:AB017502_1 | chr3:17327645-17330450 REVERSE | Aliases: F13I12.60	7.2	6.2	1.0	3.0	8.9%	1.9
8366	ATCG00550.1 | Symbol: PSBJ | PSII component | chrC:63538-63660 REVERSE | Aliases: PSBJ	10.9	10.3	0.6	3.0	8.9%	1.4
8367	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	2.8	2.5	0.3	3.0	8.9%	1.1
8368	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	4.6	-0.6	-3.0	8.9%	1.8
8369	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}	4.0	3.5	0.5	3.0	8.9%	1.5
8370	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	3.3	-0.7	-3.0	8.9%	1.6
8371	AT3G46290.1 | protein kinase, putative, similar to receptor-like protein kinase (Catharanthus roseus) gi:1644291:emb:CAA97692 | chr3:17023994-17026772 FORWARD | Aliases: F12M12.260	2.7	3.1	-0.3	-3.0	8.9%	1.3
8372	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	6.3	4.7	1.6	3.0	8.9%	1.7
8373	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 domian PF04280: Mitochondrial import inner membrane, translocase subunit TIM44 | chr2:15151926-15155169 REVERSE | Aliases: F11F19.2, F11F19_2	5.5	4.1	1.3	3.0	8.9%	1.9
8374	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	7.6	6.3	1.3	3.0	8.9%	1.7
8375	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	8.0	7.2	0.8	3.0	8.9%	1.8
8376	AT5G18200.1 | expressed protein | chr5:6015229-6016782 FORWARD | Aliases: MRG7.16, MRG7_16	6.0	4.7	1.3	3.0	8.9%	1.8
8377	AT5G50360.1 | expressed protein | chr5:20522406-20523564 REVERSE | Aliases: MXI22.7, MXI22_7	6.5	5.5	1.0	3.0	8.9%	2.0
8378	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	3.6	-0.5	-3.0	9.0%	1.4
8379	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	3.1	-0.3	-3.0	9.0%	1.2
8380	AT2G40030.1 | Symbol: NRPD1b |	3.8	3.4	0.4	3.0	9.0%	1.4
8381	AT1G12620.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat | chr1:4294592-4297082 REVERSE | Aliases: T12C24.15, T12C24_15	5.0	4.1	0.9	3.0	9.0%	1.9
8382	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	4.6	5.2	-0.6	-3.0	9.0%	1.8

Rank	Description	Sync	Root	M	t	adj.q	B
8383	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	3.2	-0.4	-3.0	9.0%	1.5
8384	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	5.7	6.3	-0.6	-3.0	9.0%	1.7
8385	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	3.0	-0.5	-3.0	9.0%	1.5
8386	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	6.1	7.8	-1.7	-3.0	9.0%	1.9
8387	AT2G15890.1 | expressed protein | chr2:6927451-6929084 REVERSE | Aliases: F19G14.11, F19G14_11	5.8	6.4	-0.6	-3.0	9.0%	1.7
8388	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	7.8	-0.9	-3.0	9.0%	1.8
8389	AT2G01950.1 | leucine-rich repeat transmembrane protein kinase, putative, similar to brassinosteroid insensitive protein | chr2:440635-444275 REVERSE | Aliases: F14H20.2, F14H20_2	4.6	5.5	-0.9	-3.0	9.0%	1.7
8390	AT3G15810.1 | expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567) | chr3:5347833-5349295 REVERSE | Aliases: MSJ11.21	6.8	7.4	-0.6	-2.9	9.0%	1.6
8391	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	3.0	-0.4	-2.9	9.0%	1.4
8392	AT1G15810.1 | ribosomal protein S15 family protein, contains similarity to ribosomal protein S15 | chr1:5444413-5447229 FORWARD | Aliases: F7H2.15, F7H2_15	6.2	5.0	1.2	2.9	9.0%	1.8
8393	AT5G61280.1 | remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region | chr5:24660851-24662136 REVERSE | Aliases: MFB13.5, MFB13_5	2.7	3.4	-0.7	-2.9	9.0%	1.7
8394	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	3.6	3.9	-0.3	-2.9	9.0%	1.2
8395	NA	5.0	6.2	-1.2	-2.9	9.0%	1.6
8396	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	2.8	-0.4	-2.9	9.1%	1.3
8397	AT3G13772.1 | endomembrane protein 70, putative, TM4 family; | chr3:4521540-4524401 REVERSE | Aliases: MMM17.22	9.0	9.9	-0.8	-2.9	9.1%	1.5
8398	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	4.3	3.6	0.7	2.9	9.1%	1.8
8399	AT4G30580.1 | Symbol: ATS2 | phospholipid/glycerol acyltransferase family protein | chr4:14932347-14934525 REVERSE | Aliases: EMB1995, EMBRYO DEFECTIVE 1995, F17I23.80, F17I23_80	6.4	5.8	0.6	2.9	9.1%	1.6
8400	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	7.1	6.6	0.6	2.9	9.1%	1.6
8401	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	5.3	4.8	0.5	2.9	9.1%	1.3
8402	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	3.0	3.9	-0.9	-2.9	9.1%	1.7

Rank	Description	Sync	Root	M	t	adj.q	B
8403	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	6.3	5.6	0.7	2.9	9.1%	1.5
8404	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	4.1	4.8	-0.7	-2.9	9.1%	1.7
8405	AT2G02800.2 | Symbol: APK2B | protein kinase (APK2b), identical to protein kinase APK2b (Arabidopsis thaliana) gi:2852449:dbj:BAA24695 | chr2:795514-799441 REVERSE | Aliases: PROTEIN KINASE 2B, T20F6.6, T20F6_6	8.6	9.7	-1.2	-2.9	9.1%	1.7
8406	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	10.0	8.9	1.0	2.9	9.1%	1.7
8407	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	8.3	6.6	1.7	2.9	9.1%	1.9
8408	AT1G77370.1 | glutaredoxin, putative, similar to glutaredoxin (Ricinus communis) gi:1732424:emb:CAA89699 | chr1:29078741-29079683 FORWARD | Aliases: F2P24.8, F2P24_8	9.6	10.3	-0.7	-2.9	9.1%	1.4
8409	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	3.8	-0.5	-2.9	9.1%	1.6
8410	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	5.7	0.8	2.9	9.1%	1.7
8411	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	7.1	6.1	1.0	2.9	9.1%	1.8
8412	AT4G20230.1 | terpene synthase/cyclase family protein, vetispiradiene synthase, Hyoscyamus muticus, PATX:G763421 | chr4:10924221-10926761 REVERSE | Aliases: F1C12.150, F1C12_150	2.6	3.1	-0.5	-2.9	9.1%	1.4
8413	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	9.0	7.9	1.1	2.9	9.1%	1.8
8414	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	5.0	4.5	0.6	2.9	9.1%	1.7
8415	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	5.6	6.5	-0.8	-2.9	9.1%	1.6
8416	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:ubiquinoe oxidoreductase NDUFB7 subunit (GI:9651635) (Homo sapiens)	10.4	9.1	1.2	2.9	9.1%	1.3
8417	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	6.7	7.5	-0.8	-2.9	9.1%	1.4
8418	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	6.5	7.1	-0.7	-2.9	9.1%	1.8
8419	AT3G14760.1 | expressed protein | chr3:4956356-4957262 FORWARD | Aliases: T21E2.1	2.5	2.7	-0.2	-2.9	9.1%	0.8
8420	AT4G32280.1 | Symbol: IAA29 | auxin-responsive AUX/IAA family protein, contains Pfam profile: PF02309: AUX/IAA family	2.3	2.8	-0.5	-2.9	9.2%	1.5
8421	AT4G20350.1 | similar to LOC495973 protein [Xenopus laevis] (GB:AAH87349.1) | chr4:10988405-10989851 FORWARD | Aliases: F9F13.6, F9F13_6	3.6	3.2	0.4	2.9	9.2%	1.4

Rank	Description	Sync	Root	M	t	adj.q	B
8422	AT5G40530.2 | expressed protein, contains Pfam profile PF05148: Protein of unknown function (DUF691) | chr5:16251740-16253450 FORWARD | Aliases: MNF13.4, MNF13_4	5.8	4.9	1.0	2.9	9.2%	1.6
8423	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	3.8	3.1	0.6	2.9	9.2%	1.7
8424	AT4G24760.1 | expressed protein | chr4:12761293-12763791 REVERSE | Aliases: F22K18.40, F22K18_40	5.5	4.5	1.0	2.9	9.2%	1.8
8425	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	7.4	5.8	1.5	2.9	9.2%	1.7
8426	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	9.6	7.8	1.8	2.9	9.2%	1.7
8427	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)	4.9	4.4	0.5	2.9	9.2%	1.5
8428	AT2G41730.1 | expressed protein | chr2:17416541-17417015 FORWARD | Aliases: T11A7.17, T11A7_17	3.5	2.8	0.7	2.9	9.2%	1.7
8429	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	6.9	6.3	0.7	2.9	9.2%	1.6
8430	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	4.5	3.4	1.0	2.9	9.2%	2.0
8431	AT5G47880.2 | Symbol: ERF1 1 |	6.8	7.6	-0.8	-2.9	9.2%	1.6
8432	AT1G32210.1 | Symbol: ATDAD1 |	9.8	8.9	0.9	2.9	9.2%	1.6
8433	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	3.5	-0.5	-2.9	9.2%	1.5
8434	AT5G55930.1 | Symbol: ATOPT1 |	3.9	3.2	0.7	2.9	9.3%	1.9
8435	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	7.4	-1.3	-2.9	9.3%	1.8
8436	AT1G73060.1 | expressed protein | chr1:27482661-27487376 FORWARD | Aliases: F3N23.26, F3N23_26	3.7	3.4	0.4	2.9	9.3%	1.3
8437	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	7.4	6.3	1.1	2.9	9.3%	2.0
8438	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	3.0	2.6	0.3	2.9	9.3%	1.2
8439	AT3G03680.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr3:907507-910814 FORWARD | Aliases: T12J13.4, T12J13_4	3.9	3.2	0.7	2.9	9.3%	1.8
8440	AT4G37740.1 | Symbol: AtGRF2 |	4.1	3.0	1.0	2.9	9.3%	1.8
8441	AT3G63360.1 | Encodes a defensin-like (DEFL) family protein. | chr3:23412232-23412566 REVERSE | Aliases: MAA21.5	2.9	3.5	-0.6	-2.9	9.3%	1.3

Rank	Description	Sync	Root	M	t	adj.q	B
8442	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	4.6	3.7	0.9	2.9	9.3%	2.0
8443	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	9.7	8.9	0.8	2.9	9.3%	1.8
8444	AT3G47240.1 | expressed protein | chr3:17404846-17405973 REVERSE | Aliases: F13I12.290	2.1	2.3	-0.2	-2.9	9.3%	0.6
8445	AT3G22435.1 | XS domain-containing protein, contains Pfam profile PF03468: XS domain | chr3:7956255-7957891 FORWARD | Aliases: None	3.5	4.3	-0.8	-2.9	9.3%	1.5
8446	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	5.7	6.7	-1.0	-2.9	9.3%	1.8
8447	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	9.5	8.6	1.0	2.9	9.3%	1.3
8448	AT1G59740.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr1:21971736-21976076 FORWARD | Aliases: F23H11.6, F23H11_6	7.0	6.1	0.8	2.9	9.3%	1.6
8449	AT2G14800.1 | expressed protein | chr2:6362264-6364061 FORWARD | Aliases: F26C24.6, F26C24_6	5.4	3.8	1.7	2.9	9.3%	2.0
8450	AT1G27960.1 | expressed protein, contains Pfam profile PF04146: YT521-B-like family | chr1:9742193-9745721 REVERSE | Aliases: F13K9.7, F13K9_7	4.2	5.2	-1.0	-2.9	9.3%	1.8
8451	AT5G57690.1 | diacylglycerol kinase, putative, contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain | chr5:23389289-23391695 REVERSE | Aliases: MRI1.5, MRI1_5	4.0	3.5	0.5	2.9	9.3%	1.5
8452	AT4G14390.1 | ankyrin repeat family protein, contains Pfam profile: PF00023 ankyrin repeat | chr4:8289640-8292079 FORWARD | Aliases: DL3235W, FCAALL.188	3.3	3.9	-0.6	-2.9	9.3%	1.6
8453	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	2.9	0.5	2.9	9.3%	1.6
8454	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	4.2	3.6	0.7	2.9	9.3%	1.7
8455	AT1G78530.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:29544167-29545574 REVERSE | Aliases: T30F21.14, T30F21_14	2.9	3.5	-0.7	-2.9	9.3%	1.7
8456	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	3.2	3.9	-0.7	-2.9	9.4%	1.7
8457	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	4.1	3.6	0.5	2.9	9.4%	1.6
8458	AT3G56880.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr3:21070894-21071944 FORWARD | Aliases: T8M16.210	8.9	8.1	0.8	2.9	9.4%	1.6
8459	AT5G22340.2 | expressed protein | chr5:7394476-7396878 FORWARD | Aliases: MWD9.13, MWD9_13	5.6	4.9	0.7	2.9	9.4%	1.7
8460	AT2G24330.1 | expressed protein | chr2:10354240-10356905 REVERSE | Aliases: T28I24.6, T28I24_6	4.8	2.8	2.0	2.9	9.4%	1.8
8461	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	2.8	3.4	-0.5	-2.9	9.4%	1.2
8462	AT3G45010.1 | Symbol: SCPL48 |	9.2	10.2	-1.0	-2.9	9.4%	1.1
8463	AT5G11870.1 | expressed protein | chr5:3825533-3827242 FORWARD | Aliases: F14F18.40, F14F18_40	3.3	3.9	-0.5	-2.9	9.4%	1.6
8464	AT5G07400.1 | forkhead-associated domain-containing protein / FHA domain-containing protein | chr5:2340643-2345453 FORWARD | Aliases: T2I1.110, T2I1_110	4.5	5.1	-0.6	-2.9	9.4%	1.4

Rank	Description	Sync	Root	M	t	adj.q	B
8465	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	5.2	6.5	-1.3	-2.9	9.4%	1.8
8466	AT1G64930.1 | Symbol: CYP89A7 | cytochrome P450, putative, similar to cytochrome P450 CYP89 (SP:Q42602)(Arabidopsis thaliana); similar to cytochrome p450 GI:438242 from (Solanum melongena) | chr1:24124589-24126124 FORWARD | Aliases: F13O11.23, F13O11_23	3.0	4.0	-1.0	-2.9	9.4%	1.8
8467	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	5.0	5.8	-0.8	-2.9	9.4%	1.9
8468	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	3.2	-0.4	-2.9	9.4%	1.2
8469	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	3.3	-0.3	-2.9	9.4%	1.1
8470	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	4.7	5.2	-0.5	-2.9	9.4%	1.5
8471	AT4G37020.1 | expressed protein | chr4:17445691-17447394 FORWARD | Aliases: AP22.69, AP22_69	5.2	4.5	0.7	2.9	9.4%	1.7
8472	AT5G01810.2 | Symbol: CIPK15 |	7.5	8.8	-1.4	-2.9	9.5%	1.6
8473	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	2.6	0.3	2.9	9.5%	1.1
8474	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	3.8	-0.5	-2.9	9.5%	1.4
8475	AT1G27450.2 | Symbol: APT1 | adenine phosphoribosyltransferase 1 (APT1), nearly identical to SP:P31166 Adenine phosphoribosyltransferase 1 (EC 2.4.2.7) (APRT) {Arabidopsis thaliana}	9.5	7.4	2.1	2.9	9.5%	2.0
8476	AT1G73320.2 | similar to Expressed protein [Arabidopsis thaliana] (TAIR:At1g08125.1); similar to P0684C02.12 [Oryza sativa (japonica cultivar-group)] (GB:NP_915768.1)	4.4	3.6	0.8	2.9	9.5%	1.8
8477	AT2G03800.1 | Symbol: GEK1 | expressed protein | chr2:1156774-1158930 FORWARD | Aliases: F19B11.25, F19B11_25, GEKO1	7.0	6.0	0.9	2.9	9.5%	1.7
8478	AT5G55390.1 | Symbol: EDM2 | hydroxyproline-rich glycoprotein family protein | chr5:22465192-22471640 REVERSE | Aliases: MTE17.10, MTE17_10	4.8	6.0	-1.2	-2.9	9.5%	1.7
8479	AT2G22000.1 | expressed protein | chr2:9369406-9370082 FORWARD | Aliases: F7D8.32, F7D8_32	2.9	4.1	-1.3	-2.9	9.5%	1.6
8480	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	4.4	0.5	2.9	9.5%	1.5
8481	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	2.9	-0.3	-2.9	9.5%	1.1
8482	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	2.8	3.8	-1.0	-2.9	9.5%	1.6
8483	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	6.3	5.2	1.1	2.9	9.5%	1.8

Rank	Description	Sync	Root	M	t	adj.q	B
8484	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	4.8	6.8	-2.0	-2.9	9.5%	1.8
8485	AT3G15500.1 | Symbol: ATNAC3 |	4.3	4.9	-0.6	-2.9	9.5%	1.7
8486	AT2G02650.1 | reverse transcriptase-related, similar to reverse transcriptase (Arabidopsis thaliana) GI:976278	2.3	2.7	-0.4	-2.9	9.5%	1.1
8487	AT2G37610.1 | hypothetical protein | chr2:15783947-15784751 REVERSE | Aliases: F13M22.11, F13M22_11	2.5	2.8	-0.3	-2.9	9.5%	0.8
8488	AT2G25760.2 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:10991886-10996002 REVERSE | Aliases: AT2G25750, F17H15.21, F17H15_21	4.9	5.3	-0.3	-2.9	9.5%	1.1
8489	AT3G12080.1 | Symbol: EMB2738 | GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function	6.4	5.7	0.7	2.9	9.5%	1.7
8490	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	6.1	6.9	-0.8	-2.9	9.5%	1.6
8491	AT5G65520.1 | expressed protein | chr5:26206951-26207817 REVERSE | Aliases: K21L13.2, K21L13_2	3.9	3.4	0.5	2.9	9.5%	1.2
8492	AT1G47330.1 | expressed protein, contains Pfam profile PF01595: Domain of unknown function | chr1:17353490-17356733 FORWARD | Aliases: T3F24.6, T3F24_6	7.5	8.9	-1.4	-2.9	9.5%	1.6
8493	AT5G67290.1 | FAD-dependent oxidoreductase family protein, contains Pfam profile PF01266: FAD dependent oxidoreductase	5.1	5.6	-0.5	-2.9	9.5%	1.5
8494	AT3G14000.2 | expressed protein | chr3:4630879-4633923 REVERSE | Aliases: MDC16.13	3.6	3.1	0.5	2.9	9.6%	1.6
8495	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 sylvestris}; contains Pfam profile PF00670: S-adenosyl-L-homocysteine hydrolase, NAD binding domain | chr3:8587671-8589720 REVERSE | Aliases: MYM9.17, SAHH2	5.6	7.3	-1.7	-2.9	9.6%	1.9
8496	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	2.8	2.6	0.3	2.9	9.6%	0.9
8497	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	4.3	3.8	0.5	2.9	9.6%	1.6
8498	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	5.2	0.5	2.9	9.6%	1.3
8499	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	6.3	6.8	-0.6	-2.9	9.6%	1.5
8500	AT5G49680.1 | cell expansion protein, putative, similar to SABRE (Arabidopsis thaliana) GI:719291 | chr5:20199258-20205533 FORWARD | Aliases: K2I5.4, K2I5_4	4.0	5.7	-1.8	-2.9	9.6%	1.8
8501	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	4.5	0.5	2.9	9.6%	1.5
8502	AT5G51270.1 | protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain | chr5:20852363-20855488 REVERSE | Aliases: MWD22.22, MWD22_22	3.0	3.6	-0.5	-2.9	9.6%	1.5
8503	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	2.5	-0.3	-2.9	9.6%	0.8
8504	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	7.5	-0.9	-2.9	9.6%	1.6
8505	AT5G65960.1 | expressed protein | chr5:26402574-26404630 FORWARD | Aliases: K2A18.2, K2A18_2	6.2	7.0	-0.8	-2.9	9.6%	1.7

Rank	Description	Sync	Root	M	t	adj.q	B
8506	AT1G80760.1 | Symbol: NIP6;1 |	3.3	4.0	-0.6	-2.9	9.6%	1.6
8507	AT2G45180.1 | 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 | chr2:18633413-18633951 FORWARD | Aliases: F4L23.31	3.2	3.6	-0.4	-2.9	9.6%	1.4
8508	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	5.0	5.7	-0.7	-2.9	9.6%	1.6
8509	AT3G28080.2 | nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula) | chr3:10452778-10456466 FORWARD | Aliases: MMG15.13	2.3	2.7	-0.4	-2.9	9.6%	1.0
8510	AT1G05170.1 | galactosyltransferase family protein | chr1:1491110-1494218 REVERSE | Aliases: YUP8H12.22, YUP8H12_22	3.0	3.4	-0.4	-2.9	9.6%	1.5
8511	AT4G28100.1 | expressed protein | chr4:13965114-13966837 REVERSE | Aliases: T13J8.210, T13J8_210	2.9	3.6	-0.7	-2.9	9.6%	1.6
8512	AT5G62130.1 | Per1-like protein-related | chr5:24967543-24970417 REVERSE | Aliases: MTG10.16, MTG10_16	2.7	3.4	-0.7	-2.9	9.6%	1.6
8513	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	8.1	6.6	1.5	2.9	9.6%	1.7
8514	AT2G38970.1 | zinc finger (C3HC4-type RING finger) family protein, very 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	5.1	4.5	0.7	2.9	9.6%	1.7
8515	AT2G20930.1 | expressed protein | chr2:9007700-9008818 REVERSE | Aliases: F5H14.10, F5H14_10	6.8	6.1	0.7	2.9	9.7%	1.5
8516	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	4.7	5.5	-0.7	-2.9	9.7%	1.7
8517	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	10.1	10.8	-0.7	-2.9	9.7%	1.4
8518	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	5.4	6.2	-0.9	-2.9	9.7%	1.8
8519	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	3.5	3.9	-0.4	-2.9	9.7%	1.3
8520	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	4.3	-0.7	-2.9	9.7%	1.5
8521	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	9.3	1.5	2.9	9.7%	1.7
8522	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	3.2	-0.5	-2.9	9.7%	1.6
8523	AT1G27330.1 | expressed protein, similar to EST gb:AA650671 and gb:T20610 | chr1:9492965-9494051 FORWARD | Aliases: F17L21.12, F17L21_12	10.9	10.4	0.6	2.9	9.7%	1.3
8524	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	10.4	0.6	2.9	9.7%	1.3
8525	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	2.5	-0.3	-2.9	9.7%	0.7
8526	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	3.6	-0.4	-2.9	9.7%	1.2

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8527	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	7.4	-1.1	-2.9	9.7%	1.8
8528	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	6.9	5.8	1.1	2.9	9.7%	1.8
8529	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	5.6	6.1	-0.5	-2.9	9.7%	1.5
8530	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	3.0	0.5	2.9	9.7%	1.2
8531	AT1G60130.1 | jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	3.1	3.6	-0.5	-2.9	9.7%	1.3
8532	AT2G02640.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain | chr2:732387-734270 FORWARD | Aliases: T8K22.6, T8K22_6	2.7	3.0	-0.4	-2.9	9.7%	1.0
8533	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	3.8	4.5	-0.6	-2.9	9.7%	1.6
8534	AT3G61780.1 | Symbol: EMB1703 | expressed protein, ; expression supported by MPSS | chr3:22878789-22882437 REVERSE | Aliases: EMB1703, EMBRYO DEFECTIVE 1703, F21F14.1	3.3	2.9	0.4	2.9	9.8%	1.2
8535	AT2G31810.3 | acetolactate synthase small subunit, putative, similar to gi:5931761 from Nicotiana plumbaginifolia | chr2:13531299-13535578 FORWARD | Aliases: F20M17.15, F20M17_15	9.0	7.6	1.3	2.9	9.8%	1.8
8536	AT1G56260.1 | expressed protein | chr1:21067944-21069242 REVERSE | Aliases: F14G9.13, F14G9_13	4.3	3.6	0.7	2.9	9.8%	1.7
8537	AT1G52050.1 | jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	2.8	3.2	-0.4	-2.9	9.8%	1.2
8538	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	4.9	4.2	0.7	2.9	9.8%	1.7
8539	AT3G02120.1 | hydroxyproline-rich glycoprotein family protein | chr3:377104-377720 FORWARD | Aliases: F1C9.2	3.7	4.5	-0.8	-2.9	9.8%	1.6
8540	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	2.8	-0.4	-2.9	9.8%	1.4
8541	AT3G48410.1 | hydrolase, alpha/beta fold family protein, low simiilarity to 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (Rhodococcus sp. RHA1) GI:8978311, SP:Q59695:ACOC_PSEPU Dihydrolipoamide acetyltransferase component of acetoin cleaving system (EC 2.3.1.12) (Acetoin dehydrogenase E2 component) {Pseudomonas putida}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family | chr3:17936687-17939173 REVERSE | Aliases: T29H11.70	4.7	5.8	-1.1	-2.9	9.8%	1.6
8542	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	9.2	8.2	1.0	2.9	9.8%	1.8
8543	AT5G62020.1 | Symbol: AT HSFB2A | 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: HSFB2A, MTG10.7, MTG10_7	5.1	5.7	-0.5	-2.9	9.8%	1.6
8544	AT4G14920.1 | PHD finger transcription factor, putative | chr4:8531153-8535838 REVERSE | Aliases: DL3500C, FCAALL.143	4.5	4.0	0.5	2.9	9.8%	1.5
8545	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	2.4	0.3	2.9	9.8%	1.2

Rank	Description	Sync	Root	M	t	adj.q	B
8546	AT4G02320.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr4:1022725-1026118 REVERSE | Aliases: T14P8.1, T14P8_1	2.4	2.7	-0.3	-2.9	9.8%	0.9
8547	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	3.4	3.1	0.3	2.9	9.8%	0.9
8548	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	8.9	8.0	0.9	2.9	9.8%	1.5
8549	AT2G39480.1 | ABC transporter family protein, related to multi drug resistance proteins and P-glycoproteins | chr2:16484870-16492117 REVERSE | Aliases: F12L6.14, F12L6_14	3.4	4.1	-0.7	-2.9	9.8%	1.5
8550	AT2G42900.1 | expressed protein | chr2:17861676-17862506 FORWARD | Aliases: F23E6.13	2.9	3.3	-0.3	-2.9	9.8%	1.0
8551	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	9.7	10.2	-0.5	-2.9	9.8%	1.4
8552	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	4.8	3.4	1.4	2.9	9.8%	1.8
8553	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	5.2	1.0	2.9	9.8%	1.7
8554	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	4.1	2.9	1.2	2.9	9.9%	1.7
8555	AT3G63260.2 | Symbol: ATMRK1 |	5.7	6.5	-0.8	-2.9	9.9%	1.6
8556	AT4G29200.1 | expressed protein | chr4:14398060-14400204 REVERSE | Aliases: F17A13.20, F17A13_20	2.1	2.3	-0.2	-2.9	9.9%	0.5
8557	AT3G54970.2 | expressed protein | chr3:20379199-20381066 REVERSE | Aliases: T15C9.1	4.5	3.9	0.6	2.9	9.9%	1.6
8558	AT3G19320.1 | leucine-rich repeat family protein, contains leucine-rich repeats, Pfam:PF00560;	2.3	2.5	-0.2	-2.9	9.9%	0.7
8559	AT2G12400.1 | expressed protein | chr2:5012025-5015304 REVERSE | Aliases: F24C20.8, F24C20_8	6.5	7.0	-0.6	-2.9	9.9%	1.5
8560	AT5G25090.1 | plastocyanin-like domain-containing protein | chr5:8647059-8647820 REVERSE | Aliases: T11H3.100, T11H3_100	2.7	3.1	-0.4	-2.9	9.9%	1.3
8561	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	7.0	6.2	0.7	2.9	9.9%	1.8
8562	AT1G64140.1 | expressed protein, similar to putative disease resistance protein GB:CAB40943 GI:4586107 from (Arabidopsis thaliana); weak similarity to Loricrin (Swiss-Prot:P23490) (Homo sapiens) | chr1:23807456-23810822 REVERSE | Aliases: F22C12.10, F22C12_10	6.8	7.9	-1.1	-2.9	9.9%	1.8
8563	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	6.0	6.5	-0.5	-2.9	9.9%	1.5
8564	AT3G26125.1 | Symbol: CYP86C2 | cytochrome P450, putative | chr3:9553049-9554674 FORWARD | Aliases: MJL14.4	2.9	3.7	-0.8	-2.9	9.9%	1.7
8565	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	6.1	6.7	-0.5	-2.9	9.9%	1.5
8566	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	5.0	4.3	0.7	2.9	9.9%	1.5

Rank	Description	Sync	Root	M	t	adj.q	B
8567	AT2G01680.1 | ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023 | chr2:306384-308629 FORWARD | Aliases: T8O11.15, T8O11_15	7.0	7.7	-0.7	-2.9	9.9%	1.6
8568	AT4G01660.1 | Symbol: ABC1At |	7.4	8.1	-0.7	-2.9	9.9%	1.5
8569	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	3.8	0.8	2.9	9.9%	1.6
8570	AT4G20470.1 | expressed protein | chr4:11032343-11032765 REVERSE | Aliases: F9F13.120, F9F13_120	3.6	4.3	-0.7	-2.9	9.9%	1.5
8571	AT1G43980.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:16688272-16691942 REVERSE | Aliases: F9C16.15, F9C16_15	2.8	2.5	0.3	2.9	9.9%	1.0
8572	AT2G22500.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr2:9570304-9571831 REVERSE | Aliases: F14M13.10, F14M13_10	6.7	7.8	-1.1	-2.9	9.9%	1.4
8573	AT3G56140.1 | expressed protein, At2g40400 - Arabidopsis thaliana, EMBL:AC007020 | chr3:20840325-20843813 FORWARD | Aliases: F18O21.100	7.6	7.0	0.5	2.9	9.9%	1.6
8574	AT2G25310.1 | expressed protein | chr2:10784187-10786289 REVERSE | Aliases: T22F11.10, T22F11_10	7.0	6.2	0.8	2.9	9.9%	1.7
8575	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	4.2	3.4	0.8	2.9	9.9%	1.8
8576	AT3G07930.3 | HhH-GPD base excision DNA repair family protein | chr3:2526636-2528639 FORWARD | Aliases: F17A17.27	3.8	4.2	-0.4	-2.9	10.0%	1.2
8577	AT3G22090.1 | expressed protein | chr3:7782965-7783564 FORWARD | Aliases: MZN24.30	3.5	3.0	0.5	2.9	10.0%	1.5
8578	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	7.6	8.9	-1.3	-2.9	10.0%	1.8
8579	AT5G64470.2 | expressed protein, similar to unknown protein (gb:AAD15463.1) | chr5:25793251-25795189 FORWARD | Aliases: T12B11.6, T12B11_6	4.5	4.1	0.5	2.9	10.0%	1.4
8580	AT2G45560.2 | Symbol: CYP76C1 | cytochrome P450 family protein | chr2:18784299-18785448 REVERSE | Aliases: F17K2.9	2.8	2.6	0.3	2.9	10.0%	1.1
8581	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	2.9	-0.3	-2.9	10.0%	0.9
8582	AT1G55325.1 | expressed protein | chr1:20641103-20650885 FORWARD | Aliases: None	2.8	3.2	-0.3	-2.9	10.0%	1.2
8583	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	5.7	7.4	-1.7	-2.9	10.0%	1.7
8584	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	4.1	-0.4	-2.9	10.0%	1.2
8585	AT1G60770.1 | pentatricopeptide (PPR) repeat-containing protein, low similarity to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile PF01535: PPR repeat | chr1:22370366-22372379 REVERSE | Aliases: F8A5.28, F8A5_28	4.0	3.2	0.7	2.9	10.0%	1.5
8586	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	11.0	10.2	0.8	2.9	10.0%	1.4
8587	AT1G53570.3 | Symbol: MAP3KA |	3.0	3.8	-0.7	-2.9	10.0%	1.6
8588	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	3.0	3.5	-0.5	-2.9	10.0%	1.4
8589	AT4G04450.1 | Symbol: WRKY42 |	2.8	3.1	-0.4	-2.9	10.1%	1.1

Rank	Description	Sync	Root	M	t	adj.q	B
8590	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	4.1	4.7	-0.6	-2.9	10.1%	1.4
8591	AT1G71310.3 | expressed protein | chr1:26882239-26883673 REVERSE | Aliases: F3I17.4, F3I17_4	4.7	3.7	1.0	2.9	10.1%	1.5
8592	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)	3.7	3.2	0.5	2.9	10.1%	1.4
8593	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	6.1	7.0	-0.9	-2.9	10.1%	1.9
8594	AT5G66180.3 | similar to NOL1/NOP2/sun family protein [Arabidopsis thaliana] (TAIR:At1g06560.1); similar to phosphate/phosphoenolpyruvate translocator-like [Oryza sativa (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	6.9	5.8	1.1	2.9	10.1%	1.8
8595	AT2G37070.1 | expressed protein | chr2:15586065-15588387 FORWARD | Aliases: T2N18.17, T2N18_17	3.5	4.1	-0.6	-2.9	10.1%	1.3
8596	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	3.4	3.8	-0.4	-2.9	10.1%	1.2
8597	AT3G51040.2 | expressed protein, contains Pfam PF05608: Protein of unknown function (DUF778) | chr3:18963125-18964661 REVERSE | Aliases: F24M12.80	7.3	7.9	-0.7	-2.9	10.1%	1.3
8598	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	8.6	6.2	2.4	2.9	10.1%	1.7
8599	AT5G53280.1 | expressed protein | chr5:21624733-21626560 FORWARD | Aliases: K19E1.8, K19E1_8	3.4	2.7	0.6	2.9	10.1%	1.5
8600	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	6.0	4.3	1.7	2.9	10.1%	1.8
8601	AT5G02530.1 | RNA and export factor-binding protein, putative, BcDNA.LD24793, Drosophila melanogaster, EMBL:AF172637 | chr5:564084-565856 REVERSE | Aliases: T22P11.120, T22P11_120	7.5	6.4	1.1	2.9	10.1%	1.7
8602	AT1G13960.2 | Symbol: WRKY4 | WRKY family transcription factor, similar to WKRY DNA-binding protein GB:AAD17441 | chr1:4776460-4779347 FORWARD | Aliases: F16A14.18	5.0	5.8	-0.8	-2.9	10.1%	1.6
8603	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	5.6	6.5	-0.9	-2.9	10.1%	1.8
8604	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	4.6	4.9	-0.4	-2.9	10.1%	1.3
8605	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	6.2	5.2	1.0	2.9	10.1%	1.7
8606	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	7.5	8.5	-1.0	-2.9	10.1%	1.4
8607	AT1G31460.1 | expressed protein | chr1:11261522-11263345 REVERSE | Aliases: T8E3.13, T8E3_13	5.5	5.9	-0.4	-2.9	10.1%	1.5
8608	AT1G64530.1 | RWP-RK domain-containing protein, similar to nodule inception protein (Lotus japonicus) GI:6448579; contains Pfam profile: PF02042 RWP-RK domain	4.8	5.5	-0.7	-2.9	10.1%	1.5
8609	AT1G14850.1 | Symbol: NUP155 |	4.6	3.6	0.9	2.9	10.1%	1.7

Rank	Description	Sync	Root	M	t	adj.q	B
8610	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	5.4	-0.5	-2.9	10.1%	1.3
8611	AT5G54530.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr5:22169951-22171651 FORWARD | Aliases: MRB17.3, MRB17_3	3.5	4.5	-1.0	-2.9	10.1%	1.8
8612	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	6.2	5.2	1.0	2.9	10.1%	1.8
8613	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	10.8	-0.5	-2.9	10.2%	1.2
8614	AT2G24950.1 | expressed protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function | chr2:10620184-10622642 FORWARD | Aliases: F27C12.13, F27C12_13	3.9	4.6	-0.7	-2.9	10.2%	1.5
8615	AT5G22450.1 | expressed protein | chr5:7437148-7442937 REVERSE | Aliases: MWD9.25, MWD9_25	7.5	9.2	-1.7	-2.9	10.2%	1.7
8616	AT1G06080.1 | Symbol: ADS1 | delta 9 desaturase (ADS1), identical to delta 9 acyl-lipid desaturase (ADS1) GB:BAA25180 GI:2970034 from (Arabidopsis thaliana) | chr1:1843569-1846299 FORWARD | Aliases: DELTA 9 DESATURASE, DELTA 9 DESATURASE 1, T21E18.13, T21E18_13	2.8	3.4	-0.6	-2.9	10.2%	1.2
8617	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	6.0	6.5	-0.5	-2.9	10.2%	1.6
8618	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	4.0	3.3	0.7	2.9	10.2%	1.7
8619	AT5G11780.1 | expressed protein | chr5:3793929-3796142 FORWARD | Aliases: T22P22.170, T22P22_170	3.3	2.9	0.4	2.9	10.2%	1.2
8620	AT3G58120.1 | bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor ;supported by cDNA gi:15100054:gb:AF401300.1:AF401300	2.9	2.5	0.4	2.9	10.2%	1.3
8621	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	4.7	3.8	0.9	2.9	10.2%	1.7
8622	AT1G02813.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr1:620678-621289 FORWARD | Aliases: None	2.3	2.6	-0.3	-2.9	10.2%	0.8
8623	AT4G11020.1 | expressed protein | chr4:6734685-6736071 REVERSE | Aliases: T22B4.3	2.5	2.9	-0.4	-2.9	10.2%	1.0
8624	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	5.1	6.2	-1.2	-2.9	10.2%	1.8
8625	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	6.1	6.7	-0.6	-2.9	10.2%	1.3
8626	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	9.6	8.4	1.3	2.9	10.2%	1.5
8627	AT1G27440.1 | exostosin family protein, contains Pfam profile: PF03016	3.2	3.7	-0.5	-2.9	10.2%	1.5
8628	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	5.8	5.4	0.4	2.9	10.2%	1.2
8629	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	4.9	5.7	-0.8	-2.9	10.2%	1.5

Rank	Description	Sync	Root	M	t	adj.q	B
8630	AT3G26935.1 | zinc finger (DHHC type) family protein, contains Pfam profile PF01529: DHHC zinc finger domain | chr3:9934238-9936455 REVERSE | Aliases: None	2.9	3.3	-0.4	-2.9	10.2%	1.4
8631	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	3.4	-0.5	-2.9	10.2%	1.3
8632	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	5.3	4.4	0.9	2.9	10.2%	1.8
8633	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	7.9	6.5	1.4	2.9	10.2%	1.7
8634	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	3.0	2.6	0.4	2.9	10.2%	1.2
8635	AT1G43580.1 | expressed protein | chr1:16412974-16415168 REVERSE | Aliases: T10P12.6, T10P12_6	7.7	8.4	-0.7	-2.9	10.2%	1.6
8636	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	7.7	9.6	-2.0	-2.8	10.3%	1.7
8637	AT1G54510.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	5.2	5.9	-0.7	-2.8	10.3%	1.4
8638	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:	5.1	4.3	0.7	2.8	10.3%	1.6
8639	AT4G24610.1 | expressed protein | chr4:12700607-12707909 REVERSE | Aliases: F22K18.190, F22K18_190	5.8	4.8	1.0	2.8	10.3%	1.7
8640	AT2G31480.1 | expressed protein, contains Pfam profile PF03754: Domain of unknown function (DUF313) | chr2:13416055-13418076 REVERSE | Aliases: T28P16.3, T28P16_3	3.3	3.9	-0.6	-2.8	10.3%	1.5
8641	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	6.6	6.0	0.6	2.8	10.3%	1.6
8642	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	4.7	0.4	2.8	10.3%	1.2
8643	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	4.2	3.7	0.5	2.8	10.3%	1.5
8644	AT4G36420.1 | ribosomal protein L12 family protein | chr4:17203034-17204315 REVERSE | Aliases: AP22.77, AP22_77	3.3	2.9	0.4	2.8	10.3%	1.3
8645	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	7.6	8.5	-0.9	-2.8	10.3%	1.4
8646	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	3.4	2.6	0.8	2.8	10.3%	1.8
8647	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	6.0	1.5	2.8	10.3%	1.8
8648	AT4G39900.1 | expressed protein | chr4:18508364-18510547 REVERSE | Aliases: T5J17.70, T5J17_70	5.9	4.8	1.0	2.8	10.3%	1.7
8649	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	3.7	-0.5	-2.8	10.3%	1.5
8650	AT4G17070.1 | expressed protein | chr4:9595404-9598191 REVERSE | Aliases: DL4565C, FCAALL.192	7.4	8.4	-1.0	-2.8	10.3%	1.7

Rank	Description	Sync	Root	M	t	adj.q	B
8651	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	3.6	4.4	-0.8	-2.8	10.3%	1.6
8652	AT1G07340.1 | Symbol: ATSTP2 |	2.5	2.9	-0.4	-2.8	10.3%	1.1
8653	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	3.2	2.8	0.4	2.8	10.3%	1.3
8654	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	3.1	2.8	0.4	2.8	10.3%	1.1
8655	AT5G42580.1 | Symbol: CYP705A12 | cytochrome P450 family protein, similar to Cytochrome P450 93A1 (SP:Q42798)	3.0	3.6	-0.5	-2.8	10.4%	1.5
8656	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 SUPRESSOR OF IRA1	7.1	6.1	1.0	2.8	10.4%	1.6
8657	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	3.2	4.3	-1.1	-2.8	10.4%	1.6
8658	AT1G55990.1 | glycine-rich protein, predicted proteins, Arabidopsis thaliana | chr1:20946152-20946616 REVERSE | Aliases: F14J16.30, F14J16_30	2.7	3.1	-0.4	-2.8	10.4%	1.0
8659	AT5G33290.1 | exostosin family protein, contains Pfam profile: PF03016 Exostosin family | chr5:12575486-12579250 FORWARD | Aliases: F19N2.10, F19N2_10	6.0	6.6	-0.6	-2.8	10.4%	1.5
8660	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	3.6	4.2	-0.5	-2.8	10.4%	1.4
8661	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	2.8	3.3	-0.4	-2.8	10.4%	1.4
8662	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	6.0	4.6	1.4	2.8	10.4%	1.7
8663	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	4.0	3.6	0.4	2.8	10.4%	1.1
8664	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	4.8	4.3	0.5	2.8	10.4%	1.4
8665	AT1G03510.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:876259-877548 REVERSE | Aliases: F21B7.13	3.5	3.2	0.3	2.8	10.4%	0.9
8666	AT1G22015.1 | galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase | chr1:7750991-7753508 REVERSE | Aliases: None	3.0	3.5	-0.5	-2.8	10.4%	1.3
8667	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	3.2	2.8	0.4	2.8	10.5%	1.3
8668	AT3G51320.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:19060832-19062480 REVERSE | Aliases: F24M12.360	5.5	4.9	0.6	2.8	10.5%	1.7
8669	AT1G71210.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:26841951-26845152 REVERSE | Aliases: F23N20.20, F23N20_20	3.0	2.7	0.3	2.8	10.5%	1.0
8670	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	6.1	1.9	2.8	10.5%	1.8

Rank	Description	Sync	Root	M	t	adj.q	B
8671	AT3G45490.1 | expressed protein | chr3:16698051-16698823 REVERSE | Aliases: F9K21.70	3.5	3.9	-0.4	-2.8	10.5%	1.2
8672	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	9.1	10.2	-1.1	-2.8	10.5%	1.5
8673	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	6.5	5.3	1.2	2.8	10.5%	1.8
8674	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)	4.5	4.0	0.5	2.8	10.5%	1.5
8675	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	6.4	7.1	-0.8	-2.8	10.5%	1.5
8676	AT3G49190.1 | condensation domain-containing protein, contains Pfam profile PF00668: Condensation domain | chr3:18242861-18245370 REVERSE | Aliases: F2K15.50	3.2	3.5	-0.4	-2.8	10.5%	1.0
8677	AT5G44060.1 | expressed protein, similar to unknown protein (gb:AAD10670.1) | chr5:17748232-17749132 FORWARD | Aliases: MRH10.17, MRH10_17	4.4	5.3	-0.9	-2.8	10.5%	1.6
8678	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	6.5	5.4	1.1	2.8	10.5%	1.8
8679	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	2.9	-0.3	-2.8	10.5%	1.1
8680	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	3.3	3.7	-0.4	-2.8	10.5%	1.3
8681	AT4G17895.1 | ubiquitin-specific protease 20, putative (UBP20), identical to ubiquitin-specific protease 20 GI:11993480 (Arabidopsis thaliana)	4.3	5.3	-0.9	-2.8	10.5%	1.5
8682	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	6.5	7.2	-0.7	-2.8	10.5%	1.4
8683	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	5.7	-0.9	-2.8	10.6%	1.4
8684	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	9.7	0.5	2.8	10.6%	1.3
8685	AT4G30460.1 | glycine-rich protein | chr4:14888986-14889808 REVERSE | Aliases: F17I23.200, F17I23_200	6.3	7.4	-1.1	-2.8	10.6%	1.7
8686	AT3G04540.1 | Encodes a defensin-like (DEFL) family protein. | chr3:1223356-1223720 FORWARD | Aliases: F7O18.19	2.8	3.4	-0.6	-2.8	10.6%	1.5
8687	AT1G01690.1 | expressed protein | chr1:249141-259171 FORWARD | Aliases: T1N6.6, T1N6_6	2.6	2.9	-0.4	-2.8	10.6%	1.0
8688	AT5G23520.1 | expressed protein | chr5:7929594-7931299 REVERSE | Aliases: MQM1.22, MQM1_22	3.9	4.4	-0.5	-2.8	10.6%	1.5
8689	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	4.5	5.2	-0.7	-2.8	10.6%	1.5
8690	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	3.4	-0.5	-2.8	10.6%	1.3
8691	AT3G22530.1 | expressed protein, contains Pfam profile:PF00011 HSP20:Hsp20/alpha crystallin family | chr3:7977611-7978642 REVERSE | Aliases: F16J14.9	6.2	5.7	0.4	2.8	10.6%	1.1
8692	AT5G43790.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:17609234-17610708 REVERSE | Aliases: MQD19.14, MQD19_14	4.7	4.2	0.5	2.8	10.6%	1.4

Rank	Description	Sync	Root	M	t	adj.q	B
8693	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	6.9	0.9	2.8	10.6%	1.7
8694	AT2G22970.2 | Symbol: SCPL11 |	2.8	3.1	-0.3	-2.8	10.7%	0.8
8695	AT3G26920.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.8	3.4	0.4	2.8	10.7%	1.1
8696	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	9.8	9.3	0.6	2.8	10.7%	1.3
8697	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	4.1	4.5	-0.4	-2.8	10.7%	1.3
8698	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	3.6	3.1	0.6	2.8	10.7%	1.3
8699	AT5G41560.1 | expressed protein | chr5:16638481-16639884 REVERSE | Aliases: MBK23.8, MBK23_8	7.0	6.2	0.9	2.8	10.7%	1.2
8700	AT5G22940.1 | exostosin family protein, contains Pfam profile: PF03016	3.5	3.9	-0.4	-2.8	10.7%	1.3
8701	AT1G04780.1 | ankyrin repeat family protein, contains Pfam PF00023: Ankyrin repeat | chr1:1340668-1343583 REVERSE | Aliases: F13M7.23	7.5	8.7	-1.2	-2.8	10.7%	1.7
8702	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	5.3	6.0	-0.8	-2.8	10.7%	1.7
8703	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	2.8	0.3	2.8	10.7%	1.0
8704	AT1G13050.1 | expressed protein | chr1:4450566-4451519 FORWARD | Aliases: F3F19.7, F3F19_7	2.6	2.3	0.3	2.8	10.7%	0.8
8705	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	3.9	1.0	2.8	10.7%	1.5
8706	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	2.7	2.4	0.3	2.8	10.7%	0.9
8707	AT4G16240.1 | expressed protein | chr4:9192351-9192583 REVERSE | Aliases: DL4160C, FCAALL.320	10.6	9.8	0.9	2.8	10.7%	1.4
8708	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	2.9	3.1	-0.2	-2.8	10.7%	0.7
8709	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	3.5	3.0	0.4	2.8	10.7%	1.4
8710	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	6.8	5.3	1.5	2.8	10.7%	1.7
8711	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	4.4	3.2	1.2	2.8	10.7%	1.5
8712	AT5G26610.2 | D111/G-patch domain-containing protein, contains Pfam PF01585: G-patch domain | chr5:9375256-9377128 FORWARD | Aliases: None	8.7	9.4	-0.7	-2.8	10.7%	1.2
8713	ATMG00120.1 | Symbol: ORF143 |	2.0	4.5	-2.5	-2.8	10.7%	1.6

Rank	Description	Sync	Root	M	t	adj.q	B
8714	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	3.5	2.9	0.6	2.8	10.7%	1.4
8715	AT2G22350.1 | RNase H domain-containing protein, low similarity to reverse transcriptase (Arabidopsis thaliana) GI:976278; contains Pfam profile PF00075: RNase H | chr2:9503156-9504121 FORWARD | Aliases: F14M13.25, F14M13_25	3.7	4.4	-0.7	-2.8	10.7%	1.3
8716	AT3G07480.1 | expressed protein | chr3:2388958-2389817 FORWARD | Aliases: F21O3.19	8.7	6.9	1.8	2.8	10.7%	1.6
8717	AT2G34530.2 | expressed protein | chr2:14556168-14557320 REVERSE | Aliases: T31E10.13, T31E10_13	2.7	3.1	-0.4	-2.8	10.8%	1.1
8718	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	7.8	8.3	-0.5	-2.8	10.8%	1.1
8719	AT2G10340.1 | expressed protein | chr2:3991114-3991371 REVERSE | Aliases: F12P23.15, F12P23_15	2.2	2.5	-0.3	-2.8	10.8%	1.0
8720	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	5.7	6.2	-0.5	-2.8	10.8%	1.3
8721	AT3G58970.1 | magnesium transporter CorA-like family protein, contains Pfam profile PF01544: CorA-like Mg2+ transporter protein | chr3:21800491-21802336 REVERSE | Aliases: F17J16.20	7.2	7.7	-0.4	-2.8	10.8%	1.2
8722	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	6.1	5.6	0.5	2.8	10.8%	1.4
8723	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	8.8	7.1	1.6	2.8	10.8%	1.8
8724	AT3G31350.1 | expressed protein | chr3:12705066-12705701 FORWARD | Aliases: T22B15.44	2.0	2.2	-0.2	-2.8	10.8%	0.8
8725	AT1G10520.1 | DNA polymerase lambda (POLL), identical to DNA polymerase lambda GI:12053869 from (Arabidopsis thaliana)	2.6	2.3	0.3	2.8	10.8%	1.0
8726	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	2.9	-0.4	-2.8	10.8%	1.1
8727	AT2G31040.1 | ATP synthase protein I -related, contains weaks similarity to Swiss-Prot:P08443 ATP synthase protein I (Synechococcus sp.) | chr2:13215983-13218162 REVERSE | Aliases: T16B12.15, T16B12_15	8.7	8.0	0.8	2.8	10.8%	1.6
8728	AT2G32860.2 | glycosyl hydrolase family 1 protein | chr2:13947264-13950878 FORWARD | Aliases: T21L14.20, T21L14_20	2.4	2.7	-0.2	-2.8	10.8%	0.6
8729	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	6.9	7.5	-0.6	-2.8	10.8%	1.3
8730	AT1G63800.1 | ubiquitin-conjugating enzyme 5 (UBC5), E2; identical to gi:431269, SP:P42749 | chr1:23671279-23672743 REVERSE | Aliases: T12P18.18, T12P18_18	9.3	10.3	-1.0	-2.8	10.8%	1.4
8731	AT5G24740.1 | expressed protein | chr5:8469954-8489706 REVERSE | Aliases: T4C12.10	5.5	6.4	-0.9	-2.8	10.8%	1.5
8732	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	8.4	7.3	1.1	2.8	10.8%	1.7
8733	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	3.1	-0.5	-2.8	10.8%	1.1
8734	AT4G16760.1 | Symbol: ACX1 | acyl-CoA oxidase (ACX1), identical to acyl-CoA oxidase (Arabidopsis thaliana) GI:3044214	8.1	9.5	-1.4	-2.8	10.8%	1.7

Rank	Description	Sync	Root	M	t	adj.q	B
8735	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	9.6	9.9	-0.4	-2.8	10.8%	1.1
8736	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	3.2	-0.3	-2.8	10.9%	0.8
8737	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	3.7	3.2	0.5	2.8	10.9%	1.3
8738	AT5G29050.1 | hypothetical protein, predicted protein, Arabidopsis thaliana | chr5:11111696-11112287 FORWARD | Aliases: F23C8.20, F23C8_20	2.2	2.5	-0.2	-2.8	10.9%	0.6
8739	AT1G47940.1 | expressed protein | chr1:17671954-17673382 FORWARD | Aliases: T6B12.6, T6B12_6	2.8	3.2	-0.4	-2.8	10.9%	1.1
8740	AT3G19990.1 | expressed protein | chr3:6965653-6967254 FORWARD | Aliases: MZE19.4	8.0	8.8	-0.8	-2.8	10.9%	1.4
8741	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	6.6	5.4	1.2	2.8	10.9%	1.6
8742	AT3G57780.1 | expressed protein | chr3:21410743-21413303 REVERSE | Aliases: F15B8.30	3.1	2.7	0.4	2.8	10.9%	1.2
8743	AT1G51920.1 | expressed protein | chr1:19297898-19298248 FORWARD | Aliases: T14L22.80, T14L22_80	3.1	4.0	-0.9	-2.8	10.9%	1.5
8744	AT4G10220.1 | expressed protein, IB1C3-1 protein, Arabidopsis thaliana, AJ011845 | chr4:6362185-6365075 FORWARD | Aliases: T9A4.9	2.2	2.6	-0.3	-2.8	10.9%	1.1
8745	AT5G22280.1 | expressed protein | chr5:7373998-7375722 REVERSE | Aliases: T6G21.7	6.1	5.0	1.1	2.8	10.9%	1.7
8746	AT2G23120.1 | expressed protein | chr2:9849123-9849714 FORWARD | Aliases: F21P24.18, F21P24_18	11.8	12.4	-0.6	-2.8	10.9%	0.7
8747	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	4.1	0.3	2.8	10.9%	1.2
8748	AT5G37600.1 | Symbol: ATGSR1 |	12.7	13.4	-0.7	-2.8	10.9%	1.1
8749	AT1G16810.2 | similar to CGI-144-like protein [Lycopersicon esculentum] (GB:CAC81814.1) | chr1:5755610-5756888 FORWARD | Aliases: F17F16.25	10.5	10.0	0.5	2.8	10.9%	1.2
8750	AT4G32915.1 | expressed protein | chr4:15885523-15886954 FORWARD | Aliases: None	4.7	4.3	0.4	2.8	10.9%	1.2
8751	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	7.3	0.7	2.8	10.9%	1.5
8752	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	4.6	3.8	0.8	2.8	10.9%	1.7
8753	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	3.0	-0.3	-2.8	10.9%	1.0
8754	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.	5.3	6.0	-0.7	-2.8	10.9%	1.6
8755	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	3.6	3.2	0.5	2.8	10.9%	1.3
8756	AT5G03900.2 | expressed protein, predicted protein, Synechocystis sp., PIR:S74969 | chr5:1048294-1052385 FORWARD | Aliases: F8F6.110	3.7	3.2	0.5	2.8	10.9%	1.2
8757	AT3G49000.1 | RNA polymerase III subunit RPC82 family protein, contains Pfam profile: PF05645 RNA polymerase III subunit RPC82	5.7	5.1	0.5	2.8	11.0%	1.5

Rank	Description	Sync	Root	M	t	adj.q	B
8758	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	3.4	-0.3	-2.8	11.0%	0.8
8759	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	3.6	4.1	-0.5	-2.8	11.0%	1.4
8760	AT5G35300.1 | expressed protein | chr5:13535547-13536179 FORWARD | Aliases: T26D22.30, T26D22_30	3.5	4.1	-0.6	-2.8	11.0%	1.3
8761	AT2G05120.1 | expressed protein | chr2:1841906-1846855 REVERSE | Aliases: F5G3.2, F5G3_2	3.5	3.1	0.4	2.8	11.0%	1.3
8762	AT5G52630.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:21367601-21369367 FORWARD | Aliases: F6N7.12, F6N7_12	4.6	3.8	0.8	2.8	11.0%	1.6
8763	AT1G24430.1 | transferase family protein, similar to deacetylvindoline 4-O-acetyltransferase from Catharanthus roseus GI:4091808 GB:AAC99311, acetyl CoA: benzylalcohol acetyltransferase Clarkia breweri GI:3170250, acetyl-CoA:benzylalcohol acetyltranferase Clarkia concinna GI:6166328; contains Pfam profile PF02458 transferase family | chr1:8657992-8659494 REVERSE | Aliases: F21J9.9	3.9	4.4	-0.5	-2.8	11.0%	1.3
8764	AT1G53165.1 | protein kinase, putative, similar to serine/threonine protein kinase 24 (Homo sapiens) SWISS-PROT:Q9Y6E0	4.8	5.6	-0.7	-2.8	11.0%	1.4
8765	AT2G28680.1 | cupin family protein, similar to legumin (11S-globulin) from Ginkgo biloba (GI:949869), 11S globulin from Avena sativa (GI:472867); contains a 11-S plant seed storage protein signature (PS00305) | chr2:12310040-12311876 REVERSE | Aliases: T8O18.3, T8O18_3	3.6	4.3	-0.7	-2.8	11.0%	1.5
8766	AT3G25545.1 | expressed protein | chr3:9278130-9279866 FORWARD | Aliases: None	4.4	3.8	0.6	2.8	11.0%	1.3
8767	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: F20O9.150, F20O9_150	8.8	8.1	0.7	2.8	11.0%	1.7
8768	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	10.6	11.4	-0.9	-2.8	11.0%	1.3
8769	AT3G23400.1 | plastid-lipid associated protein PAP / fibrillin family protein, contains Pfam profile PF04755: PAP_fibrillin | chr3:8376454-8378307 REVERSE | Aliases: MLM24.13	8.9	7.6	1.3	2.8	11.0%	1.5
8770	ATCG00020.1 | Symbol: PSBA | Encodes chlorophyll binding protein D1, a part of the photosystem II reaction center core | chrC:383-1444 REVERSE | Aliases: PSBA	11.5	9.4	2.1	2.8	11.0%	1.8
8771	AT3G16740.1 | F-box family protein, contains F-box domain Pfam:PF00646	4.8	5.2	-0.4	-2.8	11.0%	1.2
8772	AT2G22230.1 | beta-hydroxyacyl-ACP dehydratase, putative, similar to beta-hydroxyacyl-ACP dehydratase from Toxoplasma gondii (GI:3850997); contains Pfam profile PF01377 Thioester dehydratase	5.7	4.8	0.9	2.8	11.0%	1.7
8773	AT3G16530.1 | legume lectin family protein, contains Pfam domain, PF00139: Legume lectins beta domain | chr3:5624383-5625476 REVERSE | Aliases: MDC8.19	3.2	2.8	0.5	2.8	11.0%	1.4
8774	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	3.3	2.8	0.4	2.8	11.1%	1.3
8775	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	4.5	4.0	0.6	2.8	11.1%	1.6
8776	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	9.9	1.2	2.8	11.1%	1.2

Rank	Description	Sync	Root	M	t	adj.q	B
8777	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	4.7	4.0	0.7	2.8	11.1%	1.4
8778	AT1G22885.1 | expressed protein | chr1:8101554-8102364 FORWARD | Aliases: None	5.9	4.3	1.5	2.8	11.1%	1.7
8779	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	9.9	9.3	0.6	2.8	11.1%	1.3
8780	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	4.1	3.2	0.9	2.8	11.1%	1.4
8781	AT5G27280.1 | zinc finger (DNL type) family protein, contains Pfam profile PF05180: DNL zinc finger | chr5:9617489-9618484 FORWARD | Aliases: F21A20.2	6.3	6.8	-0.5	-2.8	11.1%	1.4
8782	AT4G31770.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	3.3	2.8	0.5	2.8	11.1%	1.4
8783	AT5G29070.1 | expressed protein | chr5:11132179-11133520 REVERSE | Aliases: F23C8.40, F23C8_40	2.2	2.4	-0.2	-2.8	11.1%	0.7
8784	AT5G49050.1 | hypothetical protein | chr5:19901155-19901607 FORWARD | Aliases: K19E20.20, K19E20_20	3.2	3.6	-0.4	-2.8	11.1%	1.1
8785	AT5G06370.1 | NC domain-containing protein, contains Pfam domain, PF04970: NC domain | chr5:1947140-1948574 REVERSE | Aliases: MHF15.11, MHF15_11	7.6	6.9	0.7	2.8	11.1%	1.5
8786	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	3.8	-0.5	-2.8	11.2%	1.3
8787	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	2.5	2.8	-0.3	-2.8	11.2%	0.9
8788	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	8.3	10.1	-1.8	-2.8	11.2%	1.4
8789	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	8.3	10.1	-1.8	-2.8	11.2%	1.4
8790	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	10.5	9.7	0.7	2.8	11.2%	1.5
8791	AT1G27060.1 | regulator of chromosome condensation (RCC1) family protein, low similiarity to UVB-resistance protein UVR8 (Arabidopsis thaliana) GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)	4.2	3.6	0.6	2.8	11.2%	1.5
8792	AT1G76960.1 | expressed protein | chr1:28925351-28925850 REVERSE | Aliases: F22K20.6, F22K20_6	2.2	2.3	-0.2	-2.8	11.2%	0.4
8793	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	12.3	11.4	0.9	2.8	11.2%	1.0
8794	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	9.3	0.7	2.8	11.2%	1.6
8795	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	4.5	5.0	-0.5	-2.8	11.2%	1.2

Rank	Description	Sync	Root	M	t	adj.q	B
8796	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	2.7	3.1	-0.4	-2.8	11.2%	1.0
8797	AT4G30390.1 | expressed protein | chr4:14862015-14863191 REVERSE | Aliases: F17I23.270, F17I23_270	6.5	5.4	1.1	2.8	11.2%	1.6
8798	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	3.5	0.6	2.8	11.2%	1.5
8799	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	7.7	6.8	0.9	2.8	11.2%	1.5
8800	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	4.3	3.4	0.9	2.8	11.2%	1.7
8801	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	2.8	3.1	-0.3	-2.8	11.2%	1.0
8802	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	3.3	-0.4	-2.8	11.2%	1.0
8803	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	3.9	0.5	2.8	11.2%	1.2
8804	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	4.3	3.1	1.2	2.8	11.3%	1.5
8805	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	3.3	2.8	0.5	2.8	11.3%	1.1
8806	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	4.9	5.7	-0.8	-2.8	11.3%	1.4
8807	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	2.6	2.3	0.3	2.8	11.3%	0.7
8808	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	5.4	0.6	2.8	11.3%	1.6
8809	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	8.2	7.0	1.1	2.8	11.3%	1.5
8810	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	2.8	0.4	2.8	11.3%	1.2
8811	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	9.7	8.9	0.8	2.8	11.3%	1.3
8812	AT2G46735.1 | expressed protein | chr2:19211255-19212182 FORWARD | Aliases: None	4.2	3.7	0.5	2.8	11.3%	1.4
8813	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	3.8	5.4	-1.6	-2.8	11.3%	1.5

Rank	Description	Sync	Root	M	t	adj.q	B
8814	AT3G20320.2 | mce-related family protein, contains Pfam PF02470: mce related protein | chr3:7087479-7089838 REVERSE | Aliases: MQC12.6	6.2	5.3	1.0	2.8	11.3%	1.4
8815	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	5.2	4.5	0.7	2.8	11.3%	1.4
8816	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	5.7	4.1	1.6	2.8	11.3%	1.8
8817	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	5.7	4.1	1.6	2.8	11.3%	1.8
8818	AT3G42310.1 | expressed protein | chr3:14470804-14472483 FORWARD | Aliases: T14K23.20	5.1	3.8	1.3	2.8	11.3%	1.9
8819	AT2G27260.1 | expressed protein | chr2:11676733-11677722 FORWARD | Aliases: F12K2.16, F12K2_16	6.5	5.9	0.5	2.8	11.4%	1.5
8820	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	10.1	9.3	0.8	2.8	11.4%	1.0
8821	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	6.4	5.6	0.7	2.8	11.4%	1.5
8822	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	3.8	3.1	0.8	2.8	11.4%	1.3
8823	AT2G36470.1 | expressed protein | chr2:15306441-15308069 REVERSE | Aliases: F1O11.10, F1O11_10	2.9	3.4	-0.5	-2.8	11.4%	1.3
8824	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	6.2	5.4	0.8	2.8	11.4%	1.6
8825	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	5.6	-0.9	-2.8	11.4%	1.6
8826	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	4.2	5.1	-0.9	-2.8	11.4%	1.4
8827	AT5G58030.1 | transport protein particle (TRAPP) component Bet3 family protein, very strong similarity to SPP30 (Solanum pollinated pistil) (Solanum chacoense) GI:4959712; contains Pfam profile PF04051: Transport protein particle (TRAPP) component, Bet3 | chr5:23504042-23505833 REVERSE | Aliases: K21L19.2	7.4	6.5	0.8	2.8	11.4%	1.2
8828	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	2.7	3.1	-0.4	-2.8	11.4%	0.9
8829	AT2G39980.1 | transferase family protein, contains Pfam profile PF02458 transferase family | chr2:16695379-16697034 REVERSE | Aliases: T28M21.14, T28M21_14	5.8	7.2	-1.4	-2.8	11.4%	1.6
8830	AT3G05530.1 | Symbol: RPT5A | 26S proteasome AAA-ATPase subunit (RPT5a), identical to GB:AAF22525 GI: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	9.1	7.9	1.2	2.8	11.4%	1.6
8831	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	4.1	3.3	0.8	2.8	11.4%	1.3
8832	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	8.7	7.7	1.0	2.8	11.4%	1.5
8833	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	4.5	5.5	-1.0	-2.8	11.4%	1.7

Rank	Description	Sync	Root	M	t	adj.q	B
8834	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	4.7	4.1	0.5	2.8	11.4%	1.4
8835	AT3G49890.1 | expressed protein, lea32, Arabidopsis thaliana, EMBL:ATH131342 | chr3:18510221-18511705 FORWARD | Aliases: T16K5.240	5.3	4.1	1.2	2.8	11.4%	1.5
8836	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	5.1	6.0	-0.8	-2.8	11.4%	1.4
8837	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	3.4	-0.4	-2.8	11.4%	1.2
8838	AT5G11290.1 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function | chr5:3599002-3600473 FORWARD | Aliases: F2I11.180, F2I11_180	2.7	3.0	-0.3	-2.8	11.4%	1.0
8839	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	5.5	6.2	-0.7	-2.8	11.4%	1.4
8840	AT1G69280.1 | expressed protein | chr1:26048823-26050333 REVERSE | Aliases: F4N2.23, F4N2_23	3.6	4.6	-1.0	-2.8	11.4%	1.2
8841	AT4G15100.1 | Symbol: SCPL30 |	2.6	2.9	-0.3	-2.8	11.4%	0.8
8842	AT4G16780.1 | Symbol: ATHB 2 |	3.7	4.3	-0.6	-2.8	11.4%	1.3
8843	AT3G55840.1 | expressed protein | chr3:20727974-20729845 REVERSE | Aliases: F27K19.20	4.0	3.2	0.8	2.8	11.4%	1.3
8844	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 INSENSTITIVE 5, SUN6, T7M7.16	3.3	3.6	-0.3	-2.8	11.4%	0.9
8845	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	3.7	3.3	0.4	2.8	11.5%	1.1
8846	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	3.3	0.3	2.8	11.5%	1.0
8847	AT5G52660.2 | myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA-binding domain | chr5:21376285-21379384 REVERSE | Aliases: F6N7.15, F6N7_15	3.6	4.3	-0.7	-2.8	11.5%	1.5
8848	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	4.6	-0.4	-2.8	11.5%	0.8
8849	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	8.1	7.6	0.5	2.8	11.5%	1.4
8850	AT5G14230.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr5:4593810-4595967 FORWARD | Aliases: F18O22.20, F18O22_20	4.2	4.9	-0.7	-2.8	11.5%	1.3
8851	AT1G01830.1 | armadillo/beta-catenin repeat family protein, armadillo/beta-catenin-like repeats, Pfam:PF00514 | chr1:298535-300729 REVERSE | Aliases: T1N6.25, T1N6_25	3.7	4.1	-0.4	-2.8	11.5%	1.2
8852	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	4.2	4.8	-0.6	-2.8	11.5%	1.5
8853	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	4.4	5.1	-0.7	-2.8	11.5%	1.7
8854	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	3.6	3.1	0.5	2.8	11.5%	1.4

Rank	Description	Sync	Root	M	t	adj.q	B
8855	AT4G29790.1 | expressed protein | chr4:14582994-14590581 FORWARD | Aliases: F27B13.30, F27B13_30	3.5	5.0	-1.4	-2.8	11.5%	1.6
8856	AT3G18040.2 | Symbol: ATMPK9 |	4.6	4.0	0.6	2.8	11.5%	1.2
8857	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	4.1	0.5	2.8	11.5%	1.5
8858	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	8.6	9.2	-0.5	-2.8	11.5%	1.3
8859	AT1G26795.1 | self-incompatibility protein-related, similar to S3 self-incompatibility protein (Papaver rhoeas) GI:1107841 | chr1:9276368-9276941 FORWARD | Aliases: None	3.2	3.6	-0.3	-2.8	11.5%	0.8
8860	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	4.8	5.5	-0.7	-2.8	11.5%	1.5
8861	AT4G18740.2 | expressed protein | chr4:10303425-10304583 REVERSE | Aliases: F28A21.150, F28A21_150	3.2	2.7	0.5	2.8	11.5%	1.2
8862	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	2.9	3.9	-1.0	-2.8	11.5%	1.4
8863	AT1G11970.1 | hypothetical protein | chr1:4044368-4044667 FORWARD | Aliases: F12F1.16, F12F1_16	2.6	2.9	-0.3	-2.8	11.6%	0.7
8864	AT5G53690.1 | hypothetical protein | chr5:21817713-21817943 FORWARD | Aliases: MGN6.4, MGN6_4	2.4	2.8	-0.4	-2.8	11.6%	0.5
8865	AT4G28430.1 | reticulon family protein, contains Pfam profile PF02453: Reticulon | chr4:14057798-14059865 FORWARD | Aliases: F20O9.110, F20O9_110	4.4	4.0	0.4	2.8	11.6%	1.3
8866	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	3.8	4.4	-0.6	-2.8	11.6%	1.4
8867	AT5G03420.1 | dentin sialophosphoprotein-related, contains weak similarity to Swiss-Prot:Q9NZW4 dentin sialophosphoprotein precursor (Homo sapiens) | chr5:845640-848601 FORWARD | Aliases: F12E4.170, F12E4_170	6.1	5.4	0.7	2.8	11.6%	1.2
8868	AT3G12950.1 | expressed protein | chr3:4132535-4135140 REVERSE | Aliases: MGH6.6	6.1	6.8	-0.7	-2.8	11.6%	1.5
8869	AT5G60630.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:24386876-24387630 REVERSE | Aliases: MUP24.5, MUP24_5	5.1	4.2	0.9	2.8	11.6%	1.6
8870	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)	8.0	5.6	2.4	2.8	11.6%	1.7
8871	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	2.4	2.8	-0.4	-2.8	11.6%	1.0
8872	AT4G11090.1 | expressed protein, other hypothetical proteins - Arabidopsis thaliana | chr4:6764533-6766264 REVERSE | Aliases: T22B4.70, T22B4_70	5.5	4.8	0.6	2.8	11.6%	1.3
8873	AT5G02690.1 | expressed protein | chr5:607358-607608 FORWARD | Aliases: F9G14.2	3.8	4.5	-0.7	-2.8	11.6%	1.5
8874	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	4.4	3.5	0.8	2.8	11.6%	1.6
8875	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	5.3	5.8	-0.6	-2.8	11.6%	1.5
8876	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	3.4	-0.4	-2.8	11.6%	1.0

Rank	Description	Sync	Root	M	t	adj.q	B
8877	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	4.6	4.1	0.5	2.8	11.6%	1.2
8878	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	3.0	0.4	2.8	11.6%	1.0
8879	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	2.1	2.4	-0.3	-2.8	11.6%	0.5
8880	AT3G29270.2 | expressed protein | chr3:11235551-11237669 FORWARD | Aliases: MMF24.2	5.2	4.4	0.8	2.8	11.6%	1.5
8881	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	4.7	4.3	0.4	2.8	11.6%	1.1
8882	AT5G46080.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:18706769-18708084 REVERSE | Aliases: MCL19.13, MCL19_13	2.8	3.4	-0.6	-2.7	11.6%	1.2
8883	AT2G34670.1 | proline-rich family protein, contains proline-rich region, INTERPRO:IPR000694 | chr2:14619665-14622812 REVERSE | Aliases: T29F13.12, T29F13_12	4.2	3.7	0.5	2.7	11.6%	1.3
8884	AT5G18070.1 | Symbol: DRT101 |	6.3	5.7	0.6	2.7	11.6%	1.4
8885	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	5.3	5.9	-0.7	-2.7	11.6%	1.3
8886	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	7.7	8.7	-1.0	-2.7	11.7%	1.5
8887	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	2.4	-0.2	-2.7	11.7%	0.3
8888	AT2G41700.2 | similar to ABC transporter family protein [Arabidopsis thaliana] (TAIR:At5g61730.1); similar to ATP-binding cassette, sub-family A member 3 [Homo sapiens] (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 [Mus musculus] (GB:NP_038883.1); similar to Abca3 protein [Mus musculus] (GB:AAH42663.1); similar to PREDICTED: similar to ATP-binding cassette, sub-family A member 3; ATP-binding cassette 3; ABC transporter 3, partial [Gallus gallus] (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	7.5	8.4	-0.9	-2.7	11.7%	1.4
8889	AT3G59870.1 | expressed protein, hypothetical protein F6E13.7 - Arabidopsis thaliana, PIR:T00674 | chr3:22127138-22129218 REVERSE | Aliases: F24G16.140	3.3	3.6	-0.3	-2.7	11.7%	1.0
8890	AT2G30400.1 | ovate family protein, 57% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	3.8	4.7	-0.9	-2.7	11.7%	1.6
8891	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	3.6	-0.4	-2.7	11.7%	1.0
8892	AT5G52750.1 | heavy-metal-associated domain-containing protein, Pfam profile PF00403: Heavy-metal-associated domain | chr5:21401269-21402150 FORWARD | Aliases: F6N7.24, F6N7_24	3.1	2.8	0.3	2.7	11.7%	1.0
8893	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	5.8	4.6	1.2	2.7	11.7%	1.6
8894	AT1G13290.1 | zinc finger (C2H2 type) family protein, contains Pfam domian PF00096: Zinc finger, C2H2 type | chr1:4550150-4551617 REVERSE | Aliases: T6J4.5, T6J4_5	3.6	3.9	-0.3	-2.7	11.7%	0.7
8895	AT5G06180.2 | expressed protein, similar to unknown protein (sp:Q9ZE28) | chr5:1873166-1876045 FORWARD | Aliases: MBL20.6, MBL20_6	4.8	4.3	0.5	2.7	11.7%	1.3

Rank	Description	Sync	Root	M	t	adj.q	B
8896	AT5G63810.1 | Symbol: BGAL10 |	4.6	4.1	0.5	2.7	11.7%	1.4
8897	AT5G38080.1 | expressed protein | chr5:15208945-15209875 REVERSE | Aliases: F16F17.9, F16F17_9	2.2	2.4	-0.2	-2.7	11.7%	0.3
8898	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	4.2	3.8	0.3	2.7	11.7%	1.1
8899	AT4G22320.1 | expressed protein | chr4:11792970-11794738 REVERSE | Aliases: T10I14.150, T10I14_150	4.2	3.4	0.7	2.7	11.7%	1.4
8900	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	6.0	5.0	1.0	2.7	11.7%	1.6
8901	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	2.4	-0.2	-2.7	11.7%	0.6
8902	AT5G04660.1 | Symbol: CYP77A4 | cytochrome P450, putative, cytochrome P450 77A3p, Glycine max., PIR:T05948 | chr5:1335996-1337671 FORWARD | Aliases: T1E3.20, T1E3_20	4.4	3.9	0.5	2.7	11.7%	1.4
8903	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	4.1	3.4	0.8	2.7	11.7%	1.4
8904	AT4G30790.1 | expressed protein | chr4:14993092-14997791 REVERSE | Aliases: T10C21.140, T10C21_140	6.0	7.3	-1.3	-2.7	11.7%	1.5
8905	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	2.7	-0.3	-2.7	11.8%	1.0
8906	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	4.6	3.6	0.9	2.7	11.8%	1.7
8907	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	4.6	3.6	0.9	2.7	11.8%	1.7
8908	AT4G36170.1 | expressed protein | chr4:17113875-17119837 FORWARD | Aliases: F23E13.60, F23E13_60	2.3	2.5	-0.2	-2.7	11.8%	0.4
8909	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	9.8	7.4	2.4	2.7	11.8%	1.4
8910	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	9.8	7.4	2.4	2.7	11.8%	1.4
8911	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	5.4	4.4	0.9	2.7	11.8%	1.6
8912	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	3.7	0.4	2.7	11.8%	1.0
8913	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	3.6	4.5	-0.9	-2.7	11.8%	1.5
8914	AT4G31860.2 | protein phosphatase 2C, putative / PP2C, putative, protein phosphatase 2C, Schizosaccharomyces pombe, PIR2:S54297 | chr4:15405953-15408997 REVERSE | Aliases: F11C18.60, F11C18_60	7.7	8.5	-0.8	-2.7	11.8%	1.2
8915	AT1G77400.1 | expressed protein | chr1:29090705-29091737 FORWARD | Aliases: F2P24.15, F2P24_15	3.1	2.7	0.4	2.7	11.8%	1.3
8916	AT4G07450.1 | expressed protein, includes At2g05890, At4g07450, At3g30630, At3g43100, At2g09960, At3g30550, At1g39430, At2g10460, At4g03640, At5g35250	2.4	4.0	-1.6	-2.7	11.8%	1.8

Rank	Description	Sync	Root	M	t	adj.q	B
8917	AT5G11500.1 | expressed protein, contains Pfam profile PF05670: Domain of unknown function (DUF814) | chr5:3676641-3679347 FORWARD | Aliases: F15N18.90, F15N18_90	11.0	10.3	0.7	2.7	11.8%	0.9
8918	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	6.3	5.5	0.8	2.7	11.8%	1.4
8919	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,	10.4	10.8	-0.4	-2.7	11.8%	0.9
8920	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	6.0	5.3	0.7	2.7	11.8%	1.5
8921	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)	3.0	3.6	-0.6	-2.7	11.8%	1.3
8922	AT3G21180.1 | Symbol: ACA9 | calcium-transporting ATPase, plasma membrane-type, putative / Ca2+-ATPase, putative (ACA9), identical to SP:Q9LU41 Potential calcium-transporting ATPase 9, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 9) {Arabidopsis thaliana} | chr3:7425525-7432204 FORWARD | Aliases: ATACA9, AUTOINHIBITED CA(2+) ATPASE, MXL8.3	3.0	3.6	-0.5	-2.7	11.8%	1.3
8923	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	2.9	3.5	-0.6	-2.7	11.8%	1.1
8924	AT5G13260.1 | expressed protein | chr5:4243031-4246880 FORWARD | Aliases: T31B5.80, T31B5_80	5.8	6.9	-1.1	-2.7	11.8%	1.5
8925	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	5.4	4.9	0.5	2.7	11.9%	1.3
8926	AT3G52710.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr3:19545563-19546996 FORWARD | Aliases: F3C22.110	2.6	3.1	-0.5	-2.7	11.9%	1.1
8927	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	2.5	-0.2	-2.7	11.9%	0.6
8928	AT1G76600.1 | expressed protein | chr1:28751782-28752739 FORWARD | Aliases: F14G6.20, F14G6_20	6.2	5.7	0.6	2.7	11.9%	1.4
8929	AT5G03530.1 | Symbol: ATRAB ALPHA | Ras-related GTP-binding family protein, contains Pfam profile: PF00071 Ras family	4.6	5.3	-0.7	-2.7	11.9%	1.2
8930	AT1G72020.1 | expressed protein | chr1:27112954-27114093 REVERSE | Aliases: F28P5.9, F28P5_9	10.5	9.2	1.2	2.7	11.9%	1.4
8931	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	8.1	6.9	1.2	2.7	11.9%	1.6
8932	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	11.0	9.8	1.2	2.7	11.9%	1.3
8933	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	5.0	5.7	-0.7	-2.7	12.0%	1.2
8934	AT4G33130.2 | expressed protein, weak similarity to Max-interacting transcriptional repressor (Mus musculus) GI:1184157 | chr4:15979053-15980658 REVERSE | Aliases: F4I10.60, F4I10_60	4.2	3.9	0.3	2.7	12.0%	0.9
8935	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 (GI:6463666) (Homo sapiens) | chr2:7955417-7957235 REVERSE | Aliases: T30D6.20, T30D6_20	7.4	6.9	0.5	2.7	12.0%	1.3
8936	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	8.7	9.2	-0.6	-2.7	12.0%	1.1

Rank	Description	Sync	Root	M	t	adj.q	B
8937	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	4.4	3.8	0.6	2.7	12.0%	1.5
8938	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	4.0	0.9	2.7	12.0%	1.5
8939	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	5.6	7.4	-1.9	-2.7	12.0%	1.7
8940	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	11.3	10.1	1.2	2.7	12.0%	1.1
8941	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	6.9	5.9	0.9	2.7	12.0%	1.3
8942	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	8.8	0.5	2.7	12.0%	1.1
8943	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	8.1	6.6	1.5	2.7	12.0%	1.4
8944	AT2G30790.1 | photosystem II oxygen-evolving complex 23, putative, expression not detected; similar to SP:O49344 (GI:28800560 (OEC23) Arabidopsis; 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	3.3	2.9	0.4	2.7	12.0%	1.2
8945	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	6.1	5.5	0.6	2.7	12.0%	1.4
8946	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	4.9	-0.8	-2.7	12.0%	1.2
8947	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	3.5	4.0	-0.5	-2.7	12.0%	1.3
8948	AT3G10985.1 | wound-responsive protein-related, similar to SP:P20144 Wound-induced protein 1 {Solanum tuberosum} | chr3:3442534-3443451 FORWARD | Aliases: None	4.2	5.2	-1.0	-2.7	12.0%	1.7
8949	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	8.0	6.9	1.1	2.7	12.0%	1.6
8950	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	6.3	5.4	0.9	2.7	12.0%	1.5
8951	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	3.8	-0.7	-2.7	12.0%	1.6
8952	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	5.2	4.6	0.6	2.7	12.0%	1.5
8953	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	10.3	8.1	2.1	2.7	12.0%	1.4

Rank	Description	Sync	Root	M	t	adj.q	B
8954	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	3.9	4.7	-0.9	-2.7	12.0%	1.5
8955	AT2G01070.1 | expressed protein, similar to membrane protein PTM1 precursor isolog GB:AAB65479	4.8	4.2	0.6	2.7	12.1%	1.4
8956	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	5.0	4.5	0.5	2.7	12.1%	1.4
8957	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	3.6	0.4	2.7	12.1%	1.2
8958	AT5G50330.1 | ABC1 family protein, contains Pfam domain, PF03109: ABC1 family | chr5:20502452-20505789 REVERSE | Aliases: MXI22.4, MXI22_4	2.9	3.5	-0.6	-2.7	12.1%	1.1
8959	AT2G28410.1 | expressed protein | chr2:12163207-12164006 FORWARD | Aliases: T1B3.7, T1B3_7	3.3	3.9	-0.6	-2.7	12.1%	1.3
8960	AT3G46880.1 | expressed protein, ; expression supported by MPSS | chr3:17276278-17277251 FORWARD | Aliases: T6H20.90	3.5	3.9	-0.4	-2.7	12.1%	0.9
8961	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	7.9	7.1	0.9	2.7	12.1%	1.4
8962	AT4G12930.1 | expressed protein | chr4:7573278-7573703 REVERSE | Aliases: F25G13.20, F25G13_20	2.3	2.6	-0.3	-2.7	12.1%	0.8
8963	AT2G18990.1 | expressed protein | chr2:8245773-8247077 REVERSE | Aliases: F19F24.19, F19F24_19	4.4	3.8	0.7	2.7	12.1%	1.5
8964	AT4G15950.1 | expressed protein | chr4:9040758-9041898 FORWARD | Aliases: DL4012W, FCAALL.240	3.8	3.2	0.5	2.7	12.1%	1.4
8965	AT5G02230.2 | haloacid dehalogenase-like hydrolase family protein, contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	3.8	4.7	-1.0	-2.7	12.1%	1.4
8966	AT1G77890.1 | expressed protein | chr1:29297017-29301054 FORWARD | Aliases: AT1G77900, F28K19.10, F28K19_10	4.2	4.9	-0.7	-2.7	12.1%	1.3
8967	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	4.3	4.8	-0.5	-2.7	12.1%	1.3
8968	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	2.6	2.9	-0.3	-2.7	12.1%	0.8
8969	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)	7.6	6.6	1.0	2.7	12.1%	1.5
8970	AT1G65860.1 | flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenase FMO3 (dimethylaniline monoxygenase (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	3.2	3.5	-0.4	-2.7	12.1%	0.8
8971	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	3.4	-0.4	-2.7	12.2%	1.0
8972	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	2.4	-0.2	-2.7	12.2%	0.7
8973	AT4G16610.1 | zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type | chr4:9354343-9355309 REVERSE | Aliases: DL4330C, FCAALL.418	3.7	3.2	0.5	2.7	12.2%	1.3
8974	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	2.2	0.4	2.7	12.2%	0.4
8975	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	4.9	4.3	0.6	2.7	12.2%	1.5

Rank	Description	Sync	Root	M	t	adj.q	B
8976	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	6.6	5.9	0.7	2.7	12.2%	1.3
8977	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	6.0	6.6	-0.5	-2.7	12.2%	1.2
8978	AT3G56810.1 | expressed protein | chr3:21047739-21049926 REVERSE | Aliases: T8M16.140	3.7	4.3	-0.6	-2.7	12.2%	1.3
8979	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	5.9	6.8	-1.0	-2.7	12.2%	1.4
8980	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	6.7	5.4	1.3	2.7	12.2%	1.5
8981	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	3.7	2.9	0.8	2.7	12.2%	1.3
8982	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	3.6	-0.4	-2.7	12.2%	0.9
8983	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	10.4	9.6	0.7	2.7	12.2%	1.3
8984	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	3.2	4.0	-0.8	-2.7	12.2%	1.4
8985	AT4G02800.1 | expressed protein, similar to A. thaliana hypothetical protein T6B20.12 (1946366) | chr4:1250077-1251681 FORWARD | Aliases: T5J8.12, T5J8_12	3.4	3.7	-0.4	-2.7	12.2%	1.0
8986	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	5.3	1.1	2.7	12.2%	1.5
8987	AT5G03560.1 | expressed protein | chr5:900462-902740 REVERSE | Aliases: F12E4.360, F12E4_360	5.8	5.0	0.7	2.7	12.3%	1.5
8988	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	3.8	3.2	0.6	2.7	12.3%	1.4
8989	AT5G08535.2 | D111/G-patch domain-containing protein, contains Pfam profile PF01585: G-patch domain; contains a 2nt micro-exon, as identified using GeneSeqer.	8.8	9.4	-0.5	-2.7	12.3%	0.9
8990	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	4.3	3.8	0.5	2.7	12.3%	1.3
8991	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	8.4	6.5	1.9	2.7	12.3%	1.6
8992	AT1G05950.1 | expressed protein | chr1:1804572-1807470 REVERSE | Aliases: T21E18.2, T21E18_2	4.3	3.5	0.7	2.7	12.3%	1.6
8993	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	4.6	4.0	0.6	2.7	12.3%	1.3
8994	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	6.0	6.7	-0.7	-2.7	12.3%	1.3
8995	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	6.0	6.7	-0.7	-2.7	12.3%	1.5
8996	AT5G02520.1 | expressed protein | chr5:562392-564004 FORWARD | Aliases: T22P11.110, T22P11_110	4.5	3.7	0.8	2.7	12.3%	1.3

Rank	Description	Sync	Root	M	t	adj.q	B
8997	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	3.1	2.8	0.4	2.7	12.3%	0.8
8998	ATCG00180.1 | Symbol: RPOC1 | RNA polymerase beta' subunit-1 | chrC:20251-23084 REVERSE | Aliases: RPOC1	7.6	5.6	1.9	2.7	12.3%	1.5
8999	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	2.4	-0.2	-2.7	12.3%	0.5
9000	AT4G09680.1 | expressed protein | chr4:6116759-6123301 FORWARD | Aliases: F17A8.30, F17A8_30	4.9	5.4	-0.5	-2.7	12.3%	1.2
9001	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	4.8	-0.7	-2.7	12.3%	1.3
9002	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	5.2	4.5	0.7	2.7	12.3%	1.5
9003	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	2.5	-0.2	-2.7	12.3%	0.3
9004	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	8.7	9.1	-0.5	-2.7	12.3%	1.1
9005	AT5G11600.1 | expressed protein | chr5:3733685-3735016 REVERSE | Aliases: T22P22.2	6.2	5.6	0.6	2.7	12.3%	1.2
9006	AT5G45310.1 | expressed protein | chr5:18376502-18378245 REVERSE | Aliases: K9E15.9, K9E15_9	4.0	3.6	0.4	2.7	12.4%	1.2
9007	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	6.2	6.6	-0.5	-2.7	12.4%	0.9
9008	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 anther 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	6.9	8.0	-1.2	-2.7	12.4%	1.4
9009	AT1G61010.3 | similar to metallo-beta-lactamase family protein [Arabidopsis thaliana] (TAIR:At2g01730.1); similar to Cleavage and Polyadenylation Specifity 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	4.8	4.4	0.4	2.7	12.4%	0.9
9010	AT5G22310.1 | expressed protein | chr5:7383632-7385737 REVERSE | Aliases: MWD9.9, MWD9_9	4.2	5.0	-0.8	-2.7	12.4%	1.3
9011	AT4G36000.1 | pathogenesis-related thaumatin family protein, similar to thaumatin-like protein precursor (Pyrus pyrifolia) GI:3241854; contains Pfam profile PF00314: Thaumatin family	3.3	3.7	-0.3	-2.7	12.4%	0.8
9012	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	5.4	1.0	2.7	12.4%	1.5
9013	ATCG00440.1 | Symbol: NDHC | Encodes NADH dehydrogenase D3 subunit of the chloroplast NAD(P)H dehydrogenase complex | chrC:50001-50363 REVERSE | Aliases: NDHC	10.9	9.9	1.0	2.7	12.4%	1.0
9014	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	3.7	4.3	-0.5	-2.7	12.4%	1.0
9015	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	2.8	3.3	-0.5	-2.7	12.4%	1.0

Rank	Description	Sync	Root	M	t	adj.q	B
9016	AT5G19450.2 | Symbol: CDPK19 |	7.7	8.6	-0.9	-2.7	12.4%	1.4
9017	AT2G37975.1 | expressed protein | chr2:15898931-15900717 REVERSE | Aliases: None	8.4	7.3	1.1	2.7	12.4%	1.3
9018	AT1G31670.1 | copper amine oxidase, putative, similar to amine oxidase (copper-containing) precursor (Pisum sativum) SWISS-PROT:Q43077	2.7	3.1	-0.4	-2.7	12.4%	1.2
9019	AT3G17840.1 | Symbol: RLK902 |	3.4	3.9	-0.5	-2.7	12.4%	1.3
9020	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)	7.3	9.2	-1.8	-2.7	12.4%	1.4
9021	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	7.3	9.2	-1.8	-2.7	12.4%	1.4
9022	AT4G24200.1 | expressed protein, hypothetical protein - Arabidopsis thaliana,PIR2:T06677 | chr4:12556666-12560883 REVERSE | Aliases: T22A6.30, T22A6_30	3.5	4.2	-0.7	-2.7	12.4%	1.5
9023	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	2.9	-0.3	-2.7	12.5%	0.6
9024	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	2.2	2.4	-0.2	-2.7	12.5%	0.5
9025	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}	11.6	10.9	0.7	2.7	12.5%	0.9
9026	AT5G10560.1 | glycosyl hydrolase family 3 protein, beta-xylosidase, Aspergllus nidulans, EMBL:ANXLND | chr5:3336256-3339367 REVERSE | Aliases: F12B17.90, F12B17_90	6.2	7.1	-0.9	-2.7	12.5%	1.5
9027	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	3.7	-0.6	-2.7	12.5%	1.4
9028	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	7.4	6.3	1.2	2.7	12.5%	1.3
9029	AT3G07050.1 | GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function | chr3:2229608-2232352 REVERSE | Aliases: F17A9.21	7.5	5.5	2.0	2.7	12.5%	1.5
9030	AT5G38970.3 | Symbol: BR6OX | cytochrome P450, putative, similar to Cytochrome P450 85 (SP:Q43147) {Lycopersicon esculentum};	2.3	2.5	-0.3	-2.7	12.5%	0.6
9031	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	7.6	8.0	-0.5	-2.7	12.5%	1.2
9032	AT5G16160.1 | expressed protein | chr5:5275515-5276609 REVERSE | Aliases: T21H19.80, T21H19_80	3.0	2.7	0.3	2.7	12.5%	0.7
9033	AT2G41770.1 | expressed protein, contains Pfam domain PF03385: Protein of unknown function, DUF288 | chr2:17431436-17434360 REVERSE | Aliases: T11A7.13, T11A7_13	5.3	6.6	-1.4	-2.7	12.5%	1.4
9034	AT1G62030.1 | DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain | chr1:22927915-22930263 REVERSE | Aliases: F8K4.22, F8K4_22	3.3	3.7	-0.5	-2.7	12.5%	1.0
9035	AT4G19550.1 | expressed protein | chr4:10659391-10661109 REVERSE | Aliases: F24J7.110, F24J7_110	3.7	3.0	0.7	2.7	12.5%	1.2
9036	AT3G18440.1 | expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	4.7	5.5	-0.7	-2.7	12.5%	1.3
9037	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	8.6	7.9	0.7	2.7	12.5%	1.2

Rank	Description	Sync	Root	M	t	adj.q	B
9038	AT5G26190.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.9	3.3	-0.5	-2.7	12.6%	1.2
9039	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	5.7	7.1	-1.4	-2.7	12.6%	1.6
9040	AT3G59490.1 | expressed protein | chr3:21995608-21997244 REVERSE | Aliases: T16L24.40	3.4	2.7	0.7	2.7	12.6%	0.9
9041	AT4G18010.2 | Symbol: IP5PII |	5.3	6.2	-0.9	-2.7	12.6%	1.4
9042	AT1G09400.1 | 12-oxophytodienoate reductase, putative, similar to OPR1 (GI:3882355) and OPR2 (GI:3882356) | chr1:3033603-3035038 REVERSE | Aliases: F14J9.6, F14J9_6	2.6	3.0	-0.4	-2.7	12.6%	0.9
9043	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	5.2	4.7	0.5	2.7	12.6%	1.0
9044	AT4G03670.1 | expressed protein | chr4:1626627-1627735 FORWARD | Aliases: T5L23.17, T5L23_17	2.6	2.8	-0.3	-2.7	12.6%	0.6
9045	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	4.7	5.4	-0.7	-2.7	12.6%	1.4
9046	AT3G47640.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.8	4.3	-0.4	-2.7	12.6%	1.2
9047	AT4G16170.1 | expressed protein | chr4:9165289-9167452 REVERSE | Aliases: DL4125C, FCAALL.293	8.0	8.7	-0.7	-2.7	12.6%	1.1
9048	AT2G47960.1 | expressed protein | chr2:19632684-19636180 FORWARD | Aliases: F17A22.35	6.3	5.5	0.7	2.7	12.6%	1.3
9049	AT5G62770.1 | expressed protein | chr5:25227721-25228833 FORWARD | Aliases: MQB2.9, MQB2_9	3.3	3.6	-0.3	-2.7	12.6%	1.0
9050	AT4G37730.1 | bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor | chr4:17723660-17724909 FORWARD | Aliases: T28I19.10, T28I19_10	4.7	4.2	0.5	2.7	12.7%	1.3
9051	AT3G06870.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr3:2167853-2168966 REVERSE | Aliases: F17A9.2	2.5	2.7	-0.2	-2.7	12.7%	0.5
9052	AT3G11910.1 | ubiquitin-specific protease, putative, strong similarity to ubiquitin-specific protease 12 (UBP12) (Arabidopsis thaliana) GI:11993471; contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF00917: MATH domain | chr3:3761394-3770391 REVERSE | Aliases: F26K24.20	8.1	7.4	0.7	2.7	12.7%	1.2
9053	AT5G53620.2 | expressed protein | chr5:21798226-21802438 FORWARD | Aliases: MNC6.16, MNC6_16	4.9	3.8	1.1	2.7	12.7%	1.5
9054	AT5G56850.2 | expressed protein | chr5:23002419-23004255 REVERSE | Aliases: MIK19.5, MIK19_5	4.9	4.4	0.5	2.7	12.7%	1.1
9055	AT4G28150.2 | expressed protein | chr4:13977309-13979012 REVERSE | Aliases: F26K10.30, F26K10_30	3.5	3.9	-0.5	-2.7	12.7%	1.2
9056	AT2G33520.1 | expressed protein | chr2:14203828-14204782 FORWARD | Aliases: F4P9.29, F4P9_29	4.5	3.7	0.8	2.7	12.7%	1.5
9057	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	6.1	5.6	0.5	2.7	12.7%	1.2
9058	AT4G18720.1 | transcription elongation factor-related, contains weak similarity to transcription elongation factors | chr4:10299956-10301239 FORWARD | Aliases: F28A21.130, F28A21_130	3.9	4.2	-0.4	-2.7	12.7%	0.9
9059	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	6.5	5.5	0.9	2.7	12.7%	1.3
9060	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	7.9	9.6	-1.7	-2.7	12.7%	1.4

Rank	Description	Sync	Root	M	t	adj.q	B
9061	AT2G21430.1 | cysteine proteinase A494, putative / thiol protease, putative, identical to SP:P43295 Probable cysteine proteinase A494 precursor (Arabidopsis thaliana); strong similarity to cysteine proteinase RD19A (thiol protease) GI:435618, SP:P43296 from (Arabidopsis thaliana) | chr2:9178971-9180399 REVERSE | Aliases: F3K23.19, F3K23_19	4.9	5.8	-0.9	-2.7	12.7%	1.6
9062	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	7.2	5.7	1.5	2.7	12.7%	1.5
9063	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	4.9	4.2	0.6	2.7	12.7%	1.3
9064	AT1G33980.1 | Smg-4/UPF3 family protein, contains Pfam PF03467: Smg-4/UPF3 family; similar to hUPF3B (GI:12232324) (Homo sapiens) | chr1:12351573-12355003 FORWARD | Aliases: F12G12.20, F12G12_20	4.5	5.4	-0.9	-2.7	12.7%	1.6
9065	AT1G73170.1 | expressed protein | chr1:27515331-27518458 REVERSE | Aliases: T18K17.17, T18K17_17	7.0	7.6	-0.6	-2.7	12.7%	1.4
9066	AT3G13810.1 | zinc finger (C2H2 type) family protein, similar to finger protein pcp1 GB:S48856 from (Solanum tuberosum) contains Pfam domain, PF00096: Zinc finger, C2H2 type	2.9	3.4	-0.4	-2.7	12.8%	1.0
9067	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	2.6	0.3	2.7	12.8%	0.8
9068	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	5.6	-0.4	-2.7	12.8%	1.0
9069	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	6.0	5.6	0.4	2.7	12.8%	1.0
9070	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	5.8	5.4	0.5	2.7	12.8%	1.2
9071	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	5.8	6.3	-0.5	-2.7	12.8%	1.0
9072	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	5.9	5.1	0.8	2.7	12.8%	1.1
9073	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	7.1	-0.7	-2.7	12.8%	1.1
9074	AT1G71950.1 | expressed protein, similar to Pi starvation-induced protein GB:BAA06151 from (Nicotiana tabacum)	8.5	7.8	0.7	2.7	12.8%	1.3
9075	AT4G05640.1 | hypothetical protein | chr4:3022681-3023682 FORWARD | Aliases: F21I2.30, F21I2_30	2.4	2.8	-0.4	-2.7	12.8%	1.1
9076	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	2.4	-0.2	-2.7	12.8%	0.5
9077	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	2.6	-0.3	-2.7	12.8%	0.7
9078	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	6.6	7.1	-0.5	-2.7	12.8%	1.1
9079	AT3G50130.1 | expressed protein, ; expression supported by MPSS | chr3:18600094-18602205 REVERSE | Aliases: F3A4.210	2.2	2.4	-0.2	-2.7	12.8%	0.3

Rank	Description	Sync	Root	M	t	adj.q	B
9080	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	4.7	5.2	-0.5	-2.7	12.9%	1.2
9081	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	3.4	-0.4	-2.7	12.9%	1.0
9082	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	5.8	5.3	0.4	2.7	12.9%	1.1
9083	AT2G31305.1 | expressed protein | chr2:13357499-13358541 FORWARD | Aliases: None	4.4	4.0	0.4	2.7	12.9%	1.0
9084	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	10.4	10.9	-0.5	-2.7	12.9%	1.0
9085	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	3.6	4.4	-0.8	-2.7	12.9%	1.5
9086	AT3G61360.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:22715279-22717113 REVERSE | Aliases: T20K12.260	3.9	3.4	0.6	2.7	12.9%	1.4
9087	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	4.2	4.6	-0.4	-2.7	12.9%	1.0
9088	AT3G08020.1 | PHD finger protein-related, contains low similarity to PHD-finger domain proteins | chr3:2557759-2561540 REVERSE | Aliases: F17A17.36	3.4	2.9	0.5	2.7	12.9%	1.1
9089	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	3.6	3.1	0.4	2.7	12.9%	0.9
9090	AT5G38560.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:15456479-15460394 FORWARD | Aliases: MBB18.10, MBB18_10	7.6	7.1	0.5	2.7	12.9%	1.2
9091	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	4.6	-0.7	-2.7	12.9%	1.3
9092	AT5G61210.1 | Symbol: SNAP33 |	10.5	9.3	1.2	2.7	12.9%	1.4
9093	AT3G11150.1 | expressed protein | chr3:3492873-3494655 REVERSE | Aliases: F11B9.8	3.5	4.0	-0.4	-2.7	12.9%	1.1
9094	AT2G39370.1 | expressed protein | chr2:16451208-16452344 REVERSE | Aliases: F12L6.3, F12L6_3	4.9	5.3	-0.4	-2.7	13.0%	1.1
9095	AT5G56170.1 | expressed protein, contains similarity to GPI-anchored protein | chr5:22753195-22754512 FORWARD | Aliases: MDA7.23, MDA7_23	8.9	9.5	-0.6	-2.7	13.0%	0.8
9096	AT4G25170.1 | expressed protein | chr4:12909585-12911590 FORWARD | Aliases: F24A6.10, F24A6_10	6.6	7.5	-0.9	-2.7	13.0%	1.4
9097	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	6.4	5.8	0.6	2.7	13.0%	1.2
9098	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	5.5	4.5	1.0	2.7	13.0%	1.5
9099	AT1G68490.1 | expressed protein | chr1:25697112-25699139 FORWARD | Aliases: T26J14.6, T26J14_6	6.7	7.9	-1.2	-2.7	13.0%	1.3
9100	AT5G49960.1 | expressed protein, ; expression supported by MPSS | chr5:20341399-20344913 REVERSE | Aliases: K9P8.10, K9P8_10	5.4	6.2	-0.8	-2.7	13.0%	1.4
9101	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	3.9	3.4	0.6	2.7	13.0%	1.4

Rank	Description	Sync	Root	M	t	adj.q	B
9102	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	3.9	3.4	0.6	2.7	13.0%	1.4
9103	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	3.9	3.4	0.6	2.7	13.0%	1.4
9104	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	6.9	7.7	-0.8	-2.7	13.0%	1.2
9105	AT4G30490.1 | AFG1-like ATPase family protein, contains Pfam profile: PF03969 AFG1-like ATPase	7.9	9.0	-1.1	-2.7	13.0%	1.3
9106	AT1G71340.1 | glycerophosphoryl diester phosphodiesterase family protein, contains Pfam profile PF03009: Glycerophosphoryl diester phosphodiesterase family | chr1:26889162-26892000 REVERSE | Aliases: F3I17.1, F3I17_1	6.3	7.6	-1.2	-2.7	13.0%	1.3
9107	AT5G24750.1 | expressed protein | chr5:8490575-8494590 REVERSE | Aliases: T4C12.20	5.4	4.9	0.5	2.7	13.0%	1.3
9108	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	5.4	-0.3	-2.7	13.0%	0.8
9109	AT2G37800.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.5	2.9	-0.3	-2.7	13.0%	0.7
9110	AT1G29530.1 | expressed protein | chr1:10324731-10326721 REVERSE | Aliases: F15D2.11, F15D2_11	5.1	4.3	0.7	2.7	13.0%	1.5
9111	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	5.1	4.3	0.7	2.7	13.0%	1.1
9112	AT3G53190.1 | pectate lyase family protein, similar to pectate lyase 2 GP:6606534 from (Musa acuminata) | chr3:19725019-19728568 FORWARD | Aliases: T4D2.120	7.0	6.5	0.6	2.7	13.0%	1.3
9113	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	4.5	4.1	0.5	2.7	13.1%	1.2
9114	AT4G18490.1 | hypothetical protein | chr4:10205298-10208208 FORWARD | Aliases: F28J12.150, F28J12_150	2.6	2.9	-0.3	-2.7	13.1%	0.7
9115	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	3.5	-0.4	-2.7	13.1%	0.9
9116	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	6.3	5.6	0.7	2.7	13.1%	1.4
9117	AT4G26850.1 | Symbol: VTC2 | expressed protein | chr4:13499016-13501654 REVERSE | Aliases: F10M23.190, F10M23_190, VITAMIN C DEFECTIVE 2	8.2	7.2	1.0	2.7	13.1%	1.4
9118	AT1G52980.1 | GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function | chr1:19741161-19744016 FORWARD | Aliases: F14G24.25, F14G24_25	7.5	6.7	0.8	2.7	13.1%	1.5
9119	AT3G15390.1 | expressed protein, low similarity to PRLI-interacting factor N (Arabidopsis thaliana) GI:11139276 | chr3:5196696-5199538 REVERSE | Aliases: MJK13.5	3.0	3.3	-0.2	-2.7	13.1%	0.6
9120	AT1G70900.1 | expressed protein | chr1:26735523-26737537 FORWARD | Aliases: F15H11.13, F15H11_13	6.0	5.4	0.6	2.7	13.1%	1.3
9121	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	7.1	6.0	1.1	2.7	13.1%	1.4
9122	AT5G23800.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr5:8022219-8024692 REVERSE | Aliases: MRO11.16, MRO11_16	3.2	2.9	0.3	2.7	13.1%	0.7

Rank	Description	Sync	Root	M	t	adj.q	B
9123	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	11.7	11.1	0.6	2.7	13.1%	0.9
9124	AT3G30320.1 | hypothetical protein | chr3:11933766-11937173 FORWARD | Aliases: T6J22.7	3.3	3.6	-0.3	-2.7	13.1%	0.7
9125	AT5G66985.1 | expressed protein | chr5:26760505-26761034 FORWARD | Aliases: None	5.8	7.0	-1.2	-2.7	13.1%	1.5
9126	AT5G58740.1 | nuclear movement family protein, contains Pfam profile: PF03593 nuclear movement protein	10.6	9.9	0.7	2.7	13.1%	1.1
9127	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	7.9	0.7	2.7	13.1%	1.1
9128	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)	3.8	3.1	0.6	2.7	13.1%	1.4
9129	AT4G11450.1 | expressed protein | chr4:6958676-6962041 REVERSE | Aliases: F25E4.70, F25E4_70	3.2	2.9	0.3	2.7	13.1%	0.8
9130	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	4.0	-0.5	-2.7	13.1%	1.0
9131	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	9.6	8.9	0.7	2.7	13.1%	1.0
9132	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	3.7	3.2	0.4	2.7	13.2%	1.1
9133	AT1G10610.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	5.4	4.4	0.9	2.7	13.2%	1.4
9134	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	3.4	2.8	0.5	2.7	13.2%	1.0
9135	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	4.6	4.1	0.5	2.7	13.2%	1.2
9136	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	10.5	8.7	1.7	2.7	13.2%	1.2
9137	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	5.2	4.6	0.7	2.7	13.2%	1.1
9138	AT3G18300.1 | expressed protein, ; expression supported by MPSS | chr3:6283402-6284226 FORWARD | Aliases: MYF24.2	3.7	4.6	-0.9	-2.7	13.2%	1.2
9139	AT5G59340.1 | Symbol: WOX2 | similar to homeobox-leucine zipper transcription factor family protein [Arabidopsis thaliana] (TAIR:At3g18010.1); similar to putative homeodomain transcripition 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	3.6	-0.4	-2.7	13.2%	1.0
9140	AT2G42110.1 | expressed protein | chr2:17569312-17569811 REVERSE | Aliases: T24P15.2	3.4	3.7	-0.3	-2.7	13.2%	0.9
9141	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	8.1	8.7	-0.6	-2.7	13.2%	1.3
9142	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	2.4	2.6	-0.3	-2.7	13.2%	0.6

Rank	Description	Sync	Root	M	t	adj.q	B
9143	AT4G38360.2 | expressed protein, contains Pfam profile PF03619: Domain of unknown function | chr4:17967101-17969952 FORWARD | Aliases: F22I13.130, F22I13_130	3.7	4.8	-1.1	-2.6	13.2%	1.2
9144	AT2G38290.2 | Symbol: ATAMT2 |	4.5	5.0	-0.5	-2.6	13.2%	1.3
9145	AT4G18590.1 | expressed protein | chr4:10236256-10237196 FORWARD | Aliases: F28J12.250, F28J12_250	6.3	5.7	0.6	2.6	13.2%	1.3
9146	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	9.5	8.9	0.6	2.6	13.3%	0.9
9147	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	5.5	4.9	0.6	2.6	13.3%	1.1
9148	AT4G25450.2 | Symbol: ATNAP8 |	6.1	5.6	0.5	2.6	13.3%	1.2
9149	AT5G20030.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr5:6764729-6766671 REVERSE | Aliases: F28I16.180, F28I16_180	5.2	5.9	-0.8	-2.6	13.3%	1.3
9150	AT3G01750.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr3:270236-272873 FORWARD | Aliases: F28J7.8	3.7	3.2	0.5	2.6	13.3%	1.2
9151	AT3G30380.1 | expressed protein, ; expression supported by MPSS | chr3:11976903-11979050 FORWARD | Aliases: T6J22.18	4.2	5.3	-1.1	-2.6	13.3%	1.1
9152	AT1G63690.2 | protease-associated (PA) domain-containing protein, contains protease associated (PA) domain, Pfam:PF02225 | chr1:23622041-23626059 FORWARD | Aliases: F24D7.12, F24D7_12	7.4	7.9	-0.5	-2.6	13.3%	1.2
9153	AT3G49070.1 | expressed protein, similar to At14a (GI:11994571 and GI:11994573) (Arabidopsis thaliana)	3.4	3.7	-0.4	-2.6	13.3%	1.1
9154	AT2G15270.1 | expressed protein | chr2:6644960-6646501 FORWARD | Aliases: F27O10.8, F27O10_8	7.8	6.4	1.3	2.6	13.3%	1.4
9155	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	3.8	-0.4	-2.6	13.3%	0.9
9156	AT2G27820.1 | prephenate dehydratase family protein | chr2:11863845-11865365 FORWARD | Aliases: F15K20.8, F15K20_8	5.4	5.9	-0.5	-2.6	13.3%	1.1
9157	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	5.1	4.1	1.0	2.6	13.3%	1.2
9158	AT3G29800.1 | AAA-type ATPase family, contains Pfam profile: ATPase family PF00004 | chr3:11722575-11724582 FORWARD | Aliases: K17E7.10	2.7	3.1	-0.4	-2.6	13.3%	1.0
9159	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	6.7	8.0	-1.4	-2.6	13.3%	1.4
9160	AT5G04320.1 | expressed protein | chr5:1209236-1212547 FORWARD | Aliases: T19N18.50, T19N18_50	5.0	5.6	-0.7	-2.6	13.3%	1.3
9161	AT4G19200.1 | proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965 | chr4:10498887-10500733 FORWARD | Aliases: T18B16.170, T18B16_170	8.3	6.2	2.1	2.6	13.3%	1.5
9162	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	6.6	5.8	0.8	2.6	13.4%	1.6
9163	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	5.7	4.7	1.0	2.6	13.4%	1.6
9164	AT1G31060.1 | expressed protein, similar to EST gb:T43267 | chr1:11078801-11079160 REVERSE | Aliases: F17F8.2	2.4	3.2	-0.8	-2.6	13.4%	1.0
9165	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	3.5	-0.5	-2.6	13.4%	1.2

Rank	Description	Sync	Root	M	t	adj.q	B
9166	AT3G15357.1 | expressed protein | chr3:5187123-5187717 FORWARD | Aliases: None	3.1	2.9	0.3	2.6	13.4%	0.7
9167	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	3.3	-0.4	-2.6	13.4%	0.8
9168	AT2G41870.1 | remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region | chr2:17477944-17480014 REVERSE | Aliases: T11A7.3, T11A7_3	5.5	6.1	-0.6	-2.6	13.4%	1.0
9169	AT4G18230.1 | expressed protein, predicted gene M02B7.4, Caenorhabditis elegans, PID:G1572781 | chr4:10080368-10081950 REVERSE | Aliases: T9A21.80, T9A21_80	4.5	5.3	-0.7	-2.6	13.4%	1.4
9170	AT4G01840.1 | Symbol: KCO5 | outward rectifying potassium channel, putative (KCO5), identical to KCO5 protein (Arabidopsis thaliana) gi:6522947:emb:CAB62162; similar to kco1 (Arabidopsis thaliana) gi:2230761:emb:CAA69158; member of the 2 pore, 4 transmembrane (2P/4TM) K+ channel family, PMID:11500563	4.7	5.7	-1.0	-2.6	13.4%	1.1
9171	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	4.3	3.8	0.5	2.6	13.4%	1.0
9172	AT1G65950.1 | ABC1 family protein, contains Pfam domain, PF03109: ABC1 family | chr1:24550367-24554807 REVERSE | Aliases: F12P19.11, F12P19_11	4.8	5.5	-0.7	-2.6	13.4%	1.3
9173	AT2G17110.1 | expressed protein | chr2:7450062-7453147 REVERSE | Aliases: F6P23.12, F6P23_12	3.9	4.7	-0.8	-2.6	13.4%	1.4
9174	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	7.8	5.5	2.3	2.6	13.4%	1.5
9175	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	6.2	1.2	2.6	13.4%	1.3
9176	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	4.6	-0.6	-2.6	13.4%	1.3
9177	AT3G14300.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr3:4766912-4769905 REVERSE | Aliases: ATPMEPCRC, MLN21.8	2.6	3.0	-0.4	-2.6	13.5%	0.8
9178	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	3.6	2.7	0.9	2.6	13.5%	1.0
9179	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	4.2	4.8	-0.6	-2.6	13.5%	1.2
9180	AT1G79790.2 | haloacid dehalogenase-like hydrolase family protein, contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	6.7	6.1	0.6	2.6	13.5%	1.2
9181	AT1G67410.1 | exostosin family protein, contains Pfam profile: PF03016	2.9	3.3	-0.4	-2.6	13.5%	1.0
9182	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	4.7	4.3	0.4	2.6	13.5%	1.1
9183	AT3G54660.1 | Symbol: GR | gluthatione 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	7.4	6.2	1.2	2.6	13.5%	1.5
9184	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	4.5	4.1	0.4	2.6	13.5%	1.0

Rank	Description	Sync	Root	M	t	adj.q	B
9185	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	8.1	0.9	2.6	13.5%	1.4
9186	AT1G67670.1 | expressed protein | chr1:25369136-25369330 FORWARD | Aliases: F12A21.18, F12A21_18	3.5	3.9	-0.4	-2.6	13.5%	0.9
9187	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	4.0	3.7	0.3	2.6	13.5%	0.9
9188	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	5.4	4.4	1.0	2.6	13.5%	1.5
9189	AT5G35460.1 | expressed protein | chr5:13689769-13691969 FORWARD | Aliases: MOK9.4, MOK9_4	7.2	8.7	-1.5	-2.6	13.5%	1.3
9190	AT1G16130.1 | Symbol: WAKL2 | wall-associated kinase, putative, similar to putative serine/threonine-specific protein kinase GI:7270012 from (Arabidopsis thaliana) | chr1:5525485-5528206 FORWARD | Aliases: T24D18.21, T24D18_21, WALL ASSOCIATED KINASE LIKE 2	3.8	4.4	-0.6	-2.6	13.5%	1.1
9191	AT3G18370.1 | C2 domain-containing protein, contains Pfam profile: PF00168 C2 domain | chr3:6305981-6310626 FORWARD | Aliases: MYF24.9	4.9	5.9	-1.0	-2.6	13.5%	1.3
9192	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	3.4	-0.5	-2.6	13.6%	1.0
9193	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	9.5	8.3	1.2	2.6	13.6%	1.2
9194	AT5G47250.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	4.9	4.3	0.6	2.6	13.6%	1.4
9195	AT2G42040.1 | expressed protein | chr2:17550112-17552308 FORWARD | Aliases: T6D20.7, T6D20_7	6.4	7.7	-1.3	-2.6	13.6%	1.5
9196	AT1G70160.1 | expressed protein, similar to hypothetical protein GI:4455225 from (Arabidopsis thaliana) | chr1:26423612-26426188 FORWARD | Aliases: F20P5.12, F20P5_12	8.6	9.7	-1.1	-2.6	13.6%	1.3
9197	AT1G76660.1 | expressed protein | chr1:28773774-28776260 REVERSE | Aliases: F28O16.3, F28O16_3	4.2	3.7	0.5	2.6	13.6%	1.0
9198	AT5G42880.1 | expressed protein, contains Pfam profile PF05701: Plant protein of unknown function (DUF827) | chr5:17208986-17211319 FORWARD | Aliases: MBD2.7, MBD2_7	5.2	6.2	-1.0	-2.6	13.6%	1.2
9199	AT3G26880.1 | self-incompatibility protein-related, similar to S1 self-incompatibility protein (Papaver rhoeas) GI:452430 | chr3:9907571-9907972 REVERSE | Aliases: MDJ14.22	2.8	3.3	-0.5	-2.6	13.6%	1.0
9200	AT3G48550.1 | expressed protein, putative zinc-finger protein - Arabidopsis thaliana,PID:g4406777 | chr3:18004984-18005677 FORWARD | Aliases: T8P19.60	3.4	2.9	0.4	2.6	13.6%	1.1
9201	AT4G40000.1 | NOL1/NOP2/sun family protein, contains Pfam profile PF01189: NOL1/NOP2/sun family | chr4:18543348-18547517 REVERSE | Aliases: T5J17.170, T5J17_170	3.8	3.2	0.6	2.6	13.6%	1.1
9202	AT4G17880.1 | basic helix-loop-helix (bHLH) family protein, bHLH protein, Arabidopsis thaliana, PATCHX:E255557	4.8	5.5	-0.7	-2.6	13.6%	1.3
9203	AT4G15700.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	2.0	2.3	-0.2	-2.6	13.6%	0.2
9204	AT2G42310.1 | expressed protein | chr2:17632290-17632967 FORWARD | Aliases: MHK10.3, MHK10_3	8.5	7.4	1.0	2.6	13.6%	1.3
9205	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	6.8	6.0	0.7	2.6	13.6%	1.1
9206	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	4.1	4.6	-0.5	-2.6	13.6%	1.0
9207	AT2G46900.1 | expressed protein, contains Pfam profile PF04910: Protein of unknown function, DUF654 | chr2:19276646-19279236 FORWARD | Aliases: F14M4.27	7.0	7.7	-0.7	-2.6	13.7%	1.3

Rank	Description	Sync	Root	M	t	adj.q	B
9208	AT2G02410.1 | expressed protein | chr2:632639-634831 FORWARD | Aliases: AT2G02420, T16F16.20, T16F16_20	3.7	4.7	-1.0	-2.6	13.7%	1.1
9209	AT5G07430.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:2352460-2354203 FORWARD | Aliases: T2I1.140, T2I1_140	2.1	2.3	-0.2	-2.6	13.7%	0.3
9210	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	2.6	-0.2	-2.6	13.7%	0.5
9211	AT2G26600.2 | glycosyl hydrolase family 17 protein | chr2:11323530-11325561 FORWARD | Aliases: T9J22.27, T9J22_27	7.3	7.8	-0.5	-2.6	13.7%	1.0
9212	AT3G49250.1 | expressed protein | chr3:18269246-18271983 REVERSE | Aliases: F2K15.110	4.6	4.1	0.5	2.6	13.7%	1.3
9213	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	8.8	1.1	2.6	13.7%	1.4
9214	AT2G21150.1 | XAP5 family protein, contains Pfam profile: PF04921 XAP5 protein	6.7	7.2	-0.5	-2.6	13.7%	1.1
9215	AT5G59240.1 | 40S ribosomal protein S8 (RPS8B), 40S ribosomal protein S8, Prunus armeniaca, EMBL:AF071889 | chr5:23919697-23920959 REVERSE | Aliases: MNC17.7, MNC17_7	4.9	4.5	0.4	2.6	13.7%	1.0
9216	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)	4.3	3.7	0.5	2.6	13.7%	1.2
9217	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}	4.6	5.6	-1.0	-2.6	13.7%	1.5
9218	AT2G43430.2 | Symbol: GLX2 1 |	7.5	8.3	-0.7	-2.6	13.7%	1.1
9219	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	5.8	6.3	-0.5	-2.6	13.7%	1.0
9220	AT3G17780.1 | expressed protein | chr3:6086954-6088342 FORWARD | Aliases: MIG5.8	9.2	8.2	1.0	2.6	13.7%	0.9
9221	AT5G63180.1 | pectate lyase family protein, similar to pectate lyase GP:14289169 from (Salix gilgiana)	2.4	2.7	-0.3	-2.6	13.7%	0.8
9222	AT3G60700.1 | expressed protein | chr3:22449377-22450180 FORWARD | Aliases: T4C21.110	3.0	3.4	-0.4	-2.6	13.7%	0.9
9223	AT3G22450.1 | expressed protein, ; expression supported by MPSS | chr3:7962450-7963385 FORWARD | Aliases: F16J14.2	3.7	3.3	0.4	2.6	13.7%	1.0
9224	AT1G31130.1 | expressed protein | chr1:11114682-11116176 REVERSE | Aliases: F28K20.6, F28K20_6	5.9	7.0	-1.1	-2.6	13.7%	1.4
9225	AT3G49380.1 | calmodulin-binding family protein | chr3:18322894-18324475 REVERSE | Aliases: F2K15.240	2.9	3.4	-0.5	-2.6	13.8%	1.1
9226	AT5G42960.1 | expressed protein | chr5:17252320-17253886 FORWARD | Aliases: MBD2.16, MBD2_16	6.1	5.4	0.7	2.6	13.8%	1.4
9227	AT2G26350.1 | Symbol: PEX10 | zinc-binding peroxisomal integral membrane protein (PEX10), identical to zinc-binding peroxisomal integral membrane protein GI:4337011 from (Arabidopsis thaliana) | chr2:11224570-11227511 REVERSE | Aliases: PEX10, T9J22.2	4.1	4.5	-0.5	-2.6	13.8%	1.1
9228	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	3.6	4.0	-0.4	-2.6	13.8%	1.0
9229	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	5.9	5.3	0.6	2.6	13.8%	1.2
9230	AT4G25760.1 | expressed protein | chr4:13116085-13116847 FORWARD | Aliases: F14M19.40, F14M19_40	4.5	3.8	0.7	2.6	13.8%	1.4
9231	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	7.6	6.3	1.2	2.6	13.8%	1.3

Rank	Description	Sync	Root	M	t	adj.q	B
9232	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	6.6	5.6	1.0	2.6	13.8%	1.4
9233	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	2.5	-0.3	-2.6	13.8%	0.4
9234	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	3.8	4.5	-0.6	-2.6	13.8%	1.3
9235	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	2.9	3.2	-0.2	-2.6	13.8%	0.6
9236	AT3G16860.1 | phytochelatin synthetase-related, contains Pfam PF04833: Phytochelatin synthetase-like conserved region | chr3:5759381-5762241 REVERSE | Aliases: MUH15.2	3.6	4.0	-0.4	-2.6	13.8%	1.0
9237	AT4G00990.1 | transcription factor jumonji (jmjC) domain-containing protein, contains Pfam domain, PF02373: jmjC domain | chr4:426944-431821 FORWARD | Aliases: F3I3.10	5.7	5.3	0.4	2.6	13.8%	1.0
9238	AT4G29020.1 | glycine-rich protein, supporting cDNA gi:20465684:gb:AY096677.1:	6.3	7.0	-0.8	-2.6	13.8%	1.1
9239	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	5.6	4.8	0.8	2.6	13.8%	1.5
9240	AT1G63930.1 | expressed protein, ; expression supported by MPSS | chr1:23731590-23732837 FORWARD | Aliases: T12P18.5, T12P18_5	3.6	4.5	-0.9	-2.6	13.9%	1.3
9241	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	6.3	7.3	-1.0	-2.6	13.9%	1.2
9242	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	2.7	0.2	2.6	13.9%	0.6
9243	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	2.7	-0.4	-2.6	13.9%	0.7
9244	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	7.5	8.2	-0.8	-2.6	13.9%	1.4
9245	AT5G48650.1 | nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein | chr5:19743960-19746880 FORWARD | Aliases: K15N18.17, K15N18_17	4.3	3.5	0.8	2.6	13.9%	1.2
9246	AT5G58910.1 | laccase, putative / diphenol oxidase, putative, similar to diphenol oxidase (Nicotiana tabacum)(GI:1685087) | chr5:23806748-23808907 REVERSE | Aliases: K19M22.11, K19M22_11	2.5	2.8	-0.4	-2.6	13.9%	0.8
9247	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	2.8	-0.4	-2.6	13.9%	0.7
9248	AT5G58870.1 | Symbol: FTSH9 | encodes an FtsH protease that is localized to the chloroplast | chr5:23787038-23791006 REVERSE | Aliases: FTSH9, K19M22.17, K19M22_17	7.0	7.6	-0.7	-2.6	13.9%	0.9
9249	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	5.2	5.9	-0.7	-2.6	13.9%	1.4
9250	AT3G07470.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr3:2386903-2388477 REVERSE | Aliases: F21O3.18	5.9	5.4	0.5	2.6	13.9%	1.1

Rank	Description	Sync	Root	M	t	adj.q	B
9251	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	5.6	4.9	0.7	2.6	13.9%	1.4
9252	AT2G42080.1 | DNAJ heat shock N-terminal domain-containing protein, low similarity to SP:Q9QYI7 DnaJ homolog subfamily B member 8 (mDJ6) {Mus musculus}; contains Pfam profile PF00226: DnaJ domain | chr2:17560326-17562565 REVERSE | Aliases: T6D20.3, T6D20_3	5.7	5.3	0.5	2.6	13.9%	1.1
9253	AT3G32930.1 | expressed protein | chr3:13493231-13494548 FORWARD | Aliases: T13O13.1	6.8	6.3	0.4	2.6	13.9%	1.0
9254	AT5G16610.2 | expressed protein | chr5:5444967-5448316 REVERSE | Aliases: MTG13.5, MTG13_5	5.1	5.4	-0.3	-2.6	13.9%	0.8
9255	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	4.9	4.5	0.5	2.6	13.9%	1.0
9256	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	5.2	0.7	2.6	13.9%	1.4
9257	AT5G19020.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:6352773-6357085 REVERSE | Aliases: T16G12.60, T16G12_60	3.7	3.3	0.4	2.6	13.9%	0.8
9258	AT1G26450.1 | beta-1,3-glucanase-related, similar to beta-1,3-glucanase GI:15150341 from (Camellia sinensis); C-terminal homology only	2.9	3.5	-0.6	-2.6	13.9%	1.3
9259	AT1G64570.1 | expressed protein | chr1:23982531-23987588 FORWARD | Aliases: F1N19.14, F1N19_14	3.2	3.5	-0.3	-2.6	13.9%	0.7
9260	AT2G41800.1 | expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642 | chr2:17443607-17445106 REVERSE | Aliases: T11A7.10, T11A7_10	4.7	5.3	-0.6	-2.6	13.9%	1.3
9261	AT1G61150.3 | expressed protein, similar to Protein C20orf11 (Swiss-Prot:Q9NWU2) (Homo sapiens) | chr1:22546221-22549281 FORWARD | Aliases: F11P17.12, F11P17_12	4.1	5.1	-1.0	-2.6	14.0%	1.4
9262	AT5G66230.1 | expressed protein | chr5:26479821-26481357 FORWARD | Aliases: K2A18.31, K2A18_31	3.7	4.4	-0.7	-2.6	14.0%	1.3
9263	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	4.9	-0.5	-2.6	14.0%	0.7
9264	AT1G11700.1 | expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584 | chr1:3945737-3946613 FORWARD | Aliases: F25C20.15, F25C20_15	4.4	5.0	-0.6	-2.6	14.0%	1.0
9265	AT1G30580.1 | expressed protein | chr1:10831655-10835520 REVERSE | Aliases: T5I8.3, T5I8_3	7.5	5.6	1.9	2.6	14.0%	1.4
9266	AT4G34215.2 | expressed protein | chr4:16379607-16381230 REVERSE | Aliases: None	5.3	4.8	0.5	2.6	14.0%	1.2
9267	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	2.9	3.2	-0.4	-2.6	14.0%	0.5
9268	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	4.7	4.2	0.5	2.6	14.0%	1.1
9269	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	5.0	4.5	0.5	2.6	14.0%	1.1
9270	AT3G16330.1 | expressed protein | chr3:5535202-5536069 FORWARD | Aliases: MYA6.13	4.0	3.3	0.7	2.6	14.0%	1.2
9271	AT3G49580.1 | expressed protein | chr3:18386254-18386762 REVERSE | Aliases: T9C5.170	8.6	6.3	2.3	2.6	14.0%	1.6

Rank	Description	Sync	Root	M	t	adj.q	B
9272	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	5.0	5.5	-0.5	-2.6	14.0%	1.0
9273	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	4.1	3.4	0.7	2.6	14.0%	1.2
9274	AT3G24560.3 | Symbol: RSY3 | expressed protein, contains Pfam profile PF01171: PP-loop family | chr3:8963767-8966968 FORWARD | Aliases: MOB24.14, RASPBERRY 3	3.0	2.5	0.5	2.6	14.0%	1.1
9275	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	2.3	2.6	-0.3	-2.6	14.0%	0.6
9276	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	4.6	5.0	-0.4	-2.6	14.1%	0.6
9277	AT5G13830.1 | FtsJ-like methyltransferase family protein, contains Pfam profile: PF01728 FtsJ-like methyltransferase | chr5:4467366-4468490 FORWARD | Aliases: MAC12.22, MAC12_22	4.2	3.8	0.4	2.6	14.1%	1.0
9278	AT2G46250.1 | myosin heavy chain-related, contains weak similarity to Myosin heavy chain, muscle (Swiss-Prot:P05661) (Drosophila melanogaster)	3.4	3.0	0.4	2.6	14.1%	0.7
9279	AT3G16890.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:5768407-5770386 REVERSE | Aliases: K14A17.14	2.7	2.5	0.2	2.6	14.1%	0.4
9280	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	3.3	4.1	-0.8	-2.6	14.1%	1.3
9281	AT3G20480.1 | tetraacyldisaccharide 4'-kinase family protein, contains Pfam PF02606: tetraacyldisaccharide-1-P 4'-kinase | chr3:7151433-7153398 REVERSE | Aliases: K10D20.2	3.7	3.3	0.3	2.6	14.1%	0.8
9282	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	9.7	10.2	-0.5	-2.6	14.1%	0.9
9283	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	8.6	7.3	1.3	2.6	14.1%	1.4
9284	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	3.0	3.6	-0.7	-2.6	14.1%	1.2
9285	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	3.3	2.6	0.7	2.6	14.1%	1.0
9286	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	4.4	3.6	0.8	2.6	14.1%	1.3
9287	AT4G32400.1 | mitochondrial substrate carrier family protein | chr4:15638631-15640471 FORWARD | Aliases: F8B4.100, F8B4_100	7.3	6.0	1.4	2.6	14.1%	1.3
9288	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	4.7	0.3	2.6	14.1%	0.7
9289	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)	7.3	8.5	-1.2	-2.6	14.1%	1.3
9290	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	11.9	10.7	1.2	2.6	14.1%	1.1
9291	AT1G35430.1 | expressed protein | chr1:13030531-13031130 REVERSE | Aliases: F12A4.3, F12A4_3	5.7	6.5	-0.8	-2.6	14.1%	1.2

Rank	Description	Sync	Root	M	t	adj.q	B
9292	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	3.3	3.0	0.3	2.6	14.1%	0.9
9293	AT3G20030.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.9	-0.4	-2.6	14.2%	0.6
9294	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	5.6	6.2	-0.6	-2.6	14.2%	1.3
9295	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	4.3	-0.3	-2.6	14.2%	0.6
9296	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	7.5	6.4	1.1	2.6	14.2%	1.1
9297	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)	5.1	4.4	0.7	2.6	14.2%	1.3
9298	AT5G20700.1 | senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana); | chr5:7005860-7007119 REVERSE | Aliases: T1M15.100, T1M15_100	7.4	8.2	-0.8	-2.6	14.2%	1.0
9299	AT3G14620.1 | Symbol: CYP72A8 | cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus) | chr3:4914921-4917083 FORWARD | Aliases: MIE1.12	4.8	4.0	0.8	2.6	14.2%	1.4
9300	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	3.5	2.7	0.8	2.6	14.2%	0.7
9301	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	7.4	8.0	-0.6	-2.6	14.2%	1.0
9302	AT4G22980.1 | expressed protein, ; expression supported by MPSS | chr4:12043985-12045664 REVERSE | Aliases: F7H19.160, F7H19_160	2.8	3.1	-0.3	-2.6	14.2%	0.6
9303	AT4G34220.1 | leucine-rich repeat transmembrane protein kinase, putative, protein kinase TMKL1, Arabidopsis thaliana, PID:E353150 | chr4:16381510-16384198 REVERSE | Aliases: F10M10.12	3.2	2.9	0.4	2.6	14.2%	0.9
9304	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	4.2	1.0	2.6	14.2%	1.1
9305	AT4G18970.1 | 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	3.2	3.5	-0.3	-2.6	14.2%	0.6
9306	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	7.1	7.6	-0.5	-2.6	14.2%	1.1
9307	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	4.9	-0.6	-2.6	14.2%	1.1
9308	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	4.4	3.9	0.5	2.6	14.2%	1.0
9309	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	5.3	4.6	0.8	2.6	14.2%	1.3

Rank	Description	Sync	Root	M	t	adj.q	B
9310	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	3.8	3.2	0.7	2.6	14.2%	1.0
9311	AT1G64640.1 | plastocyanin-like domain-containing protein, contains InterPro:IPR003245 plastocyanin-like domain | chr1:24025387-24026820 REVERSE | Aliases: F1N19.21, F1N19_21	2.8	3.0	-0.3	-2.6	14.3%	0.4
9312	AT5G38530.1 | tryptophan synthase-related, low similarity to tryptophan synthases, beta subunit, from Lactococcus lactis (SP:Q01998), Pyrococcus kodakaraensis (SP:Q9YGB0), Thermus thermophilus (SP:P16609); contains Pfam pyridoxal-phosphate dependent enzyme domain PF00291 | chr5:15441269-15443700 FORWARD | Aliases: MBB18.6, MBB18_6	9.4	8.2	1.2	2.6	14.3%	1.1
9313	AT5G55120.1 | expressed protein, strong similarity to unknown protein (pir::T04808) | chr5:22386321-22389093 FORWARD | Aliases: MCO15.7, MCO15_7	5.0	4.5	0.5	2.6	14.3%	1.0
9314	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	6.2	-0.9	-2.6	14.3%	1.2
9315	AT3G48690.1 | expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873 | chr3:18047382-18049219 REVERSE | Aliases: T8P19.200	7.0	6.1	0.9	2.6	14.3%	1.2
9316	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	7.8	6.2	1.6	2.6	14.3%	1.5
9317	AT5G57060.2 | expressed protein | chr5:23107424-23109196 FORWARD | Aliases: MHM17.20, MHM17_20	5.8	5.1	0.7	2.6	14.3%	1.2
9318	ATMG00510.1 | Symbol: NAD7 | NADH dehydrogenase subunit 7 | chrM:132071-138153 FORWARD | Aliases: NAD7	3.4	4.2	-0.8	-2.6	14.3%	1.2
9319	AT2G03830.1 | expressed protein | chr2:1171169-1172349 FORWARD | Aliases: T18C20.3, T18C20_3	2.0	2.2	-0.2	-2.6	14.3%	0.1
9320	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	5.7	4.7	1.0	2.6	14.3%	1.2
9321	AT1G79800.1 | plastocyanin-like domain-containing protein | chr1:30023442-30024110 FORWARD | Aliases: F20B17.22, F20B17_22	2.7	3.2	-0.5	-2.6	14.3%	0.9
9322	AT3G22920.1 | peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, similar to peptidyl-prolyl cis-trans isomerase PPIase (cyclophilin, cyclosporin A-binding protein) (Tomato) SWISS-PROT:P21568 | chr3:8122720-8123418 REVERSE | Aliases: F5N5.9	3.7	4.1	-0.4	-2.6	14.3%	0.8
9323	AT5G21130.1 | expressed protein | chr5:7185971-7186816 FORWARD | Aliases: T10F18.160, T10F18_160	3.0	3.4	-0.4	-2.6	14.3%	0.8
9324	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	9.4	11.1	-1.7	-2.6	14.3%	1.0
9325	AT2G23690.1 | expressed protein | chr2:10079357-10083049 FORWARD | Aliases: F27L4.13, F27L4_13	7.2	8.0	-0.9	-2.6	14.3%	1.1
9326	AT5G62750.1 | expressed protein, predicted proteins, Caenorhabditis elegans | chr5:25220675-25221343 REVERSE | Aliases: MQB2.7, MQB2_7	2.6	2.8	-0.2	-2.6	14.3%	0.1
9327	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	5.5	6.0	-0.5	-2.6	14.3%	1.2
9328	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	3.7	3.2	0.4	2.6	14.3%	1.1
9329	AT1G05310.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr1:1550614-1552433 REVERSE | Aliases: YUP8H12.7, YUP8H12_7	4.3	5.6	-1.3	-2.6	14.3%	1.3
9330	AT1G34570.1 | expressed protein | chr1:12654918-12656464 REVERSE | Aliases: F12K21.27	3.5	2.5	1.0	2.6	14.3%	1.5
9331	AT3G15750.1 | expressed protein | chr3:5335232-5336483 FORWARD | Aliases: MSJ11.15	3.5	2.5	1.0	2.6	14.3%	1.5

Rank	Description	Sync	Root	M	t	adj.q	B
9332	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	3.8	3.5	0.3	2.6	14.3%	0.8
9333	AT5G11420.1 | expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642 | chr5:3644599-3647296 FORWARD | Aliases: F15N18.10, F15N18_10	3.9	3.5	0.4	2.6	14.3%	1.0
9334	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	7.9	7.0	0.9	2.6	14.3%	1.5
9335	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	3.3	-0.7	-2.6	14.3%	0.9
9336	AT1G51450.1 | SPla/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	4.0	-0.4	-2.6	14.3%	1.0
9337	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	2.7	-0.3	-2.6	14.4%	0.6
9338	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	8.6	9.4	-0.8	-2.6	14.4%	0.8
9339	AT5G04550.1 | expressed protein, contains Pfam domain PF05003: protein of unknown function (DUF668) | chr5:1303181-1306117 REVERSE | Aliases: T32M21.140, T32M21_140	3.4	3.8	-0.4	-2.6	14.4%	0.8
9340	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	7.8	8.5	-0.7	-2.6	14.4%	1.3
9341	AT5G40940.1 | expressed protein | chr5:16423884-16425158 REVERSE | Aliases: MMG1.3, MMG1_3	2.3	2.1	0.2	2.6	14.4%	0.2
9342	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	2.5	2.8	-0.3	-2.6	14.4%	0.7
9343	AT5G63340.1 | expressed protein | chr5:25396120-25396900 FORWARD | Aliases: K9H21.7, K9H21_7	2.3	2.6	-0.2	-2.6	14.4%	0.5
9344	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	4.4	3.5	0.8	2.6	14.4%	1.4
9345	AT5G58360.1 | ovate family protein, 69% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	2.4	2.7	-0.4	-2.6	14.4%	0.8
9346	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	5.1	5.7	-0.6	-2.6	14.4%	1.2
9347	AT1G73930.2 | similar to FLJ00229 protein [Homo sapiens] (GB:BAB84982.1) | chr1:27798781-27801642 REVERSE | Aliases: F2P9.20, F2P9_20	6.1	5.6	0.4	2.6	14.4%	1.0
9348	AT2G19480.1 | nucleosome assembly protein (NAP), putative, similar to nucleosome assembly protein 1 (Glycine max) GI:1161252; contains Pfam profile PF00956: Nucleosome assembly protein (NAP)	8.1	9.0	-0.9	-2.6	14.4%	0.9
9349	AT3G24540.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:8952910-8955628 FORWARD | Aliases: MOB24.4	2.7	3.3	-0.6	-2.6	14.4%	0.8
9350	AT1G10470.1 | Symbol: ARR4 | two-component responsive regulator / response regulator 4 (ARR4), identical to responce 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	6.5	7.3	-0.8	-2.6	14.4%	1.3

Rank	Description	Sync	Root	M	t	adj.q	B
9351	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	9.1	7.2	2.0	2.6	14.4%	1.5
9352	AT1G53640.1 | expressed protein, ; expression supported by MPSS | chr1:20024553-20029129 REVERSE | Aliases: F22G10.8	5.7	6.3	-0.6	-2.6	14.4%	1.2
9353	AT4G18790.1 | Symbol: NRAMP5 |	3.9	4.2	-0.3	-2.6	14.4%	0.8
9354	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	5.5	7.1	-1.6	-2.6	14.4%	1.3
9355	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	3.1	4.0	-0.8	-2.6	14.4%	1.5
9356	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	8.9	8.1	0.8	2.6	14.4%	1.2
9357	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	2.9	-0.3	-2.6	14.4%	0.7
9358	AT1G30840.1 | Symbol: ATPUP4 |	4.8	5.4	-0.5	-2.6	14.4%	1.0
9359	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	3.4	3.0	0.4	2.6	14.4%	0.8
9360	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	3.2	2.8	0.4	2.6	14.4%	0.9
9361	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 Sybl1, Mus musculus, EMBL:MMU133536 | chr5:3546355-3548112 REVERSE | Aliases: F2I11.40, F2I11_40, VAMP713	5.9	5.3	0.6	2.6	14.4%	1.2
9362	AT1G22275.1 | expressed protein | chr1:7867234-7872055 FORWARD | Aliases: None	3.5	3.1	0.3	2.6	14.4%	0.8
9363	AT3G47620.1 | TCP family transcription factor, putative, auxin-induced basic helix-loop-helix transcription factor - Gossypium hirsutum, EMBL:AF165924	7.5	8.1	-0.6	-2.6	14.5%	1.2
9364	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	4.2	5.6	-1.4	-2.6	14.5%	1.2
9365	AT5G24510.1 | 60s acidic ribosomal protein P1, putative | chr5:8369298-8369869 REVERSE | Aliases: K18P6.3, K18P6_3	2.6	2.9	-0.3	-2.6	14.5%	0.7
9366	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	5.4	7.1	-1.7	-2.6	14.5%	1.5
9367	AT1G66460.1 | protein kinase family protein, contains Pfam profile: PF00069: Eukaryotic protein kinase domain | chr1:24793398-24795651 REVERSE | Aliases: F28G11.10, F28G11_10	2.5	2.8	-0.3	-2.6	14.5%	0.5
9368	AT5G51850.1 | expressed protein, similar to unknown protein (emb:CAB81354.1) | chr5:21096478-21098704 FORWARD | Aliases: MIO24.1, MIO24_1	2.2	2.4	-0.2	-2.6	14.5%	0.2
9369	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	5.2	4.4	0.8	2.6	14.5%	1.3
9370	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	5.1	1.1	2.6	14.5%	1.5
9371	AT5G11630.1 | expressed protein | chr5:3740461-3742140 FORWARD | Aliases: T22P22.20, T22P22_20	4.7	4.1	0.6	2.6	14.5%	1.1

Rank	Description	Sync	Root	M	t	adj.q	B
9372	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	9.1	8.0	1.1	2.6	14.5%	0.9
9373	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	4.0	0.9	2.6	14.5%	1.2
9374	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	12.1	11.8	0.3	2.6	14.5%	0.4
9375	AT3G24010.1 | PHD finger family protein, contains Pfam profile: PF00628 PHD-finger | chr3:8675965-8678227 REVERSE | Aliases: F14O13.20	9.0	8.5	0.5	2.6	14.5%	1.1
9376	AT1G72250.1 | kinesin motor protein-related | chr1:27196564-27201976 FORWARD | Aliases: T9N14.6, T9N14_6	3.0	2.6	0.4	2.6	14.5%	0.8
9377	AT5G60070.1 | ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023 | chr5:24207666-24209796 REVERSE | Aliases: MGO3.5, MGO3_5	3.5	3.9	-0.4	-2.6	14.5%	0.5
9378	AT1G79390.1 | expressed protein | chr1:29867946-29869214 REVERSE | Aliases: T8K14.19, T8K14_19	7.7	7.1	0.6	2.6	14.5%	1.0
9379	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	2.9	3.3	-0.4	-2.6	14.5%	0.7
9380	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	3.8	3.2	0.6	2.6	14.5%	1.1
9381	AT4G30770.1 | expressed protein | chr4:14986146-14986619 REVERSE | Aliases: T10C21.120, T10C21_120	1.9	2.1	-0.2	-2.6	14.5%	-0.0
9382	AT3G08880.1 | expressed protein | chr3:2703175-2703598 FORWARD | Aliases: T16O11.19	3.2	3.0	0.3	2.6	14.6%	0.5
9383	AT3G15350.2 | glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/I-Branching enzyme | chr3:5166249-5169527 FORWARD | Aliases: K7L4.15	4.1	3.7	0.4	2.6	14.6%	1.0
9384	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	5.6	6.4	-0.8	-2.6	14.6%	1.0
9385	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	4.6	5.3	-0.7	-2.6	14.6%	1.2
9386	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	5.3	4.9	0.5	2.6	14.6%	1.2
9387	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	5.9	4.9	1.1	2.6	14.6%	1.0
9388	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	6.9	-1.1	-2.6	14.6%	1.2
9389	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	5.6	4.7	0.9	2.6	14.6%	1.1
9390	AT1G35820.1 | hypothetical protein | chr1:13309331-13310469 REVERSE | Aliases: F10O5.1, F10O5_1	2.3	2.6	-0.3	-2.6	14.6%	0.7
9391	AT3G22710.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.8	-0.3	-2.6	14.6%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
9392	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	2.2	2.5	-0.3	-2.6	14.6%	0.8
9393	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	3.5	-0.3	-2.6	14.6%	0.5
9394	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	3.9	4.6	-0.7	-2.6	14.6%	1.2
9395	AT3G46240.1 | protein kinase-related, similar to light repressible receptor protein kinase (GI:1321686) (Arabidopsis thaliana)	3.2	3.6	-0.5	-2.6	14.6%	0.9
9396	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	5.2	6.2	-1.0	-2.6	14.6%	1.2
9397	AT2G04860.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:1706784-1708532 REVERSE | Aliases: F28I8.8, F28I8_8	3.8	4.6	-0.7	-2.6	14.6%	1.0
9398	AT3G29300.1 | expressed protein | chr3:11248248-11248889 FORWARD | Aliases: MMF24.5	2.2	2.5	-0.3	-2.6	14.6%	0.1
9399	AT5G09840.1 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537 | chr5:3058998-3061971 FORWARD | Aliases: MYH9.5, MYH9_5	2.5	2.3	0.2	2.6	14.6%	0.3
9400	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	11.4	10.9	0.5	2.6	14.6%	0.8
9401	AT2G07000.1 | expressed protein | chr2:2901867-2902287 REVERSE | Aliases: T4E14.11, T4E14_11	4.8	5.8	-1.0	-2.6	14.7%	1.3
9402	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 toSP: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}	8.2	7.5	0.7	2.6	14.7%	1.1
9403	AT4G32080.1 | expressed protein, ; expression supported by MPSS | chr4:15508439-15508774 REVERSE | Aliases: F10N7.110, F10N7_110	2.2	2.5	-0.2	-2.6	14.7%	0.2
9404	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	3.6	3.2	0.4	2.6	14.7%	1.0
9405	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	3.2	-0.3	-2.6	14.7%	0.7
9406	AT5G11890.1 | expressed protein | chr5:3831665-3832945 FORWARD | Aliases: F14F18.60, F14F18_60	3.7	2.9	0.8	2.6	14.7%	1.2
9407	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	6.0	7.0	-1.0	-2.6	14.7%	1.1
9408	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	10.4	8.5	1.9	2.6	14.7%	1.0
9409	AT3G01410.1 | RNase H domain-containing protein, low similarity to GAG-POL precursor (Oryza sativa (japonica cultivar-group)) GI:5902445; contains Pfam profile: PF00075 RNase H | chr3:153446-155606 REVERSE | Aliases: T13O15.5, T13O15_5	5.5	4.9	0.6	2.6	14.7%	1.3
9410	AT1G06410.1 | Symbol: ATTPS7 |	8.4	9.0	-0.6	-2.6	14.7%	0.8
9411	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	2.7	-0.3	-2.6	14.7%	0.6
9412	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	4.6	5.4	-0.8	-2.6	14.7%	1.0
9413	AT3G15140.1 | exonuclease family protein, contains exonuclease domain, Pfam:PF00929 | chr3:5099539-5101788 REVERSE | Aliases: F4B12.5	3.8	3.4	0.4	2.6	14.7%	0.8

Rank	Description	Sync	Root	M	t	adj.q	B
9414	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	6.1	-0.6	-2.6	14.7%	1.0
9415	AT3G03580.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:860519-863359 REVERSE | Aliases: T12J13.14, T12J13_14	3.9	3.4	0.5	2.6	14.8%	1.0
9416	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	4.3	3.8	0.6	2.6	14.8%	1.2
9417	AT1G73090.1 | expressed protein | chr1:27491878-27494427 FORWARD | Aliases: F3N23.29, F3N23_29	3.8	3.4	0.3	2.6	14.8%	0.7
9418	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	4.6	4.1	0.5	2.6	14.8%	1.2
9419	AT3G53310.1 | transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain | chr3:19777642-19779396 REVERSE | Aliases: F4P12.10	2.6	2.3	0.3	2.6	14.8%	0.5
9420	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	10.9	10.5	0.5	2.6	14.8%	0.5
9421	AT1G79160.1 | expressed protein | chr1:29784614-29785599 REVERSE | Aliases: YUP8H12R.23, YUP8H12R_23	4.2	4.7	-0.5	-2.6	14.8%	1.1
9422	AT3G51460.1 | phosphoinositide phosphatase family protein, contains similarity to phosphoinositide phosphatase SAC1 (Rattus norvegicus) 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	5.5	6.4	-0.9	-2.6	14.8%	1.2
9423	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	3.0	3.5	-0.4	-2.6	14.8%	0.8
9424	AT1G14687.1 | zinc finger homeobox family protein / ZF-HD homeobox family protein | chr1:5047798-5048607 FORWARD | Aliases: None	3.8	3.3	0.5	2.6	14.8%	1.1
9425	AT2G04025.1 | expressed protein | chr2:1276774-1277731 REVERSE | Aliases: F3C11.1, F3C11_1	2.6	2.9	-0.3	-2.6	14.8%	0.4
9426	AT3G29310.1 | calmodulin-binding protein-related | chr3:11250889-11253057 FORWARD | Aliases: MUO10.1	4.2	6.7	-2.5	-2.6	14.8%	1.3
9427	AT4G27900.2 | expressed protein | chr4:13890670-13893079 FORWARD | Aliases: T13J8.10, T13J8_10	5.6	5.0	0.6	2.6	14.9%	1.3
9428	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	3.9	4.7	-0.7	-2.6	14.9%	1.1
9429	AT4G28180.1 | expressed protein | chr4:13982917-13983687 REVERSE | Aliases: F26K10.60, F26K10_60	3.1	2.8	0.3	2.6	14.9%	0.6
9430	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	3.4	-0.6	-2.6	14.9%	0.9
9431	AT4G22010.1 | Symbol: SKS4 | multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)(Brassica napus); contains Pfam profile: PF00394 Multicopper oxidase | chr4:11663336-11666727 FORWARD | Aliases: F1N20.110, F1N20_110, SKS4	3.0	2.4	0.6	2.6	14.9%	1.2
9432	AT4G03120.1 | proline-rich family protein, similar to U1 small nuclear ribonucleoprotein C; contains proline rich extensin domains, INTERPRO:IPR002965	5.0	4.3	0.7	2.6	14.9%	1.2
9433	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.	6.3	7.0	-0.7	-2.6	14.9%	1.1
9434	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	3.2	3.7	-0.5	-2.6	14.9%	1.2
9435	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	2.6	3.0	-0.4	-2.6	14.9%	0.7

Rank	Description	Sync	Root	M	t	adj.q	B
9436	AT4G13160.1 | expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593 | chr4:7653651-7654921 FORWARD | Aliases: F17N18.50, F17N18_50	4.8	5.5	-0.7	-2.6	14.9%	1.0
9437	AT3G50670.2 | Symbol: U1 70K |	7.7	8.8	-1.1	-2.6	14.9%	1.2
9438	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)	5.1	4.4	0.7	2.6	14.9%	1.1
9439	AT5G10750.1 | expressed protein | chr5:3398952-3400157 FORWARD | Aliases: MAJ23.2	5.7	6.4	-0.6	-2.6	14.9%	1.2
9440	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	5.1	5.8	-0.7	-2.6	15.0%	1.1
9441	AT3G46700.1 | similar to UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At3g46680.1); similar to UDP-glucoronosyl/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-glucoronosyl/UDP-glucosyl transferase (InterPro:IPR002213) | chr3:17211304-17212874 REVERSE | Aliases: T6H20.270	3.2	3.6	-0.4	-2.6	15.0%	0.9
9442	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	5.4	5.8	-0.5	-2.6	15.0%	0.8
9443	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	4.4	5.0	-0.6	-2.6	15.0%	1.1
9444	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	5.1	-0.9	-2.6	15.0%	1.2
9445	AT5G46115.1 | expressed protein | chr5:18718547-18718967 FORWARD | Aliases: None	3.0	3.4	-0.4	-2.6	15.0%	0.7
9446	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	11.0	10.4	0.7	2.6	15.0%	0.9
9447	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	3.6	-0.5	-2.6	15.0%	1.0
9448	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	9.7	-0.3	-2.5	15.0%	0.4
9449	AT2G22180.1 | hydroxyproline-rich glycoprotein family protein | chr2:9436049-9436924 FORWARD | Aliases: T26C19.16, T26C19_16	2.7	3.0	-0.3	-2.5	15.0%	0.4
9450	AT3G15250.1 | similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:At1g53165.1); contains domain SER_RICH (PS50324) | chr3:5136269-5137202 REVERSE | Aliases: K7L4.5	2.0	2.2	-0.2	-2.5	15.0%	0.2
9451	AT2G40120.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:16762086-16764535 REVERSE | Aliases: T7M7.1, T7M7_1	4.5	5.4	-0.8	-2.5	15.0%	1.4
9452	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	3.7	3.2	0.5	2.5	15.0%	1.1
9453	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	2.5	-0.2	-2.5	15.0%	0.4
9454	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	5.4	4.8	0.6	2.5	15.0%	1.1
9455	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	2.8	-0.3	-2.5	15.0%	0.7

Rank	Description	Sync	Root	M	t	adj.q	B
9456	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	5.3	4.6	0.6	2.5	15.1%	1.0
9457	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	8.2	0.8	2.5	15.1%	1.2
9458	AT5G05550.2 | expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189	2.8	2.5	0.3	2.5	15.1%	0.7
9459	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	2.8	-0.3	-2.5	15.1%	0.7
9460	AT3G44210.1 | hypothetical protein | chr3:15927257-15928319 FORWARD | Aliases: F26G5.160	2.4	2.6	-0.2	-2.5	15.1%	0.1
9461	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	7.8	-0.7	-2.5	15.1%	1.0
9462	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	3.9	-0.7	-2.5	15.1%	1.1
9463	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	4.9	5.7	-0.8	-2.5	15.1%	1.2
9464	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	2.8	-0.3	-2.5	15.1%	0.8
9465	AT5G59600.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr5:24028227-24030251 REVERSE | Aliases: F2O15.13, F2O15_13	3.6	3.2	0.4	2.5	15.1%	1.0
9466	NA	5.5	3.4	2.1	2.5	15.1%	1.3
9467	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	6.2	0.9	2.5	15.1%	1.3
9468	AT5G42660.1 | expressed protein, contains Pfam profile PF04765: Protein of unknown function (DUF616) | chr5:17120152-17123192 REVERSE | Aliases: MJB21.3, MJB21_3	4.0	4.6	-0.6	-2.5	15.1%	1.1
9469	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	7.0	7.9	-1.0	-2.5	15.1%	1.1
9470	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	5.5	4.9	0.6	2.5	15.2%	1.0
9471	AT2G32970.1 | expressed protein | chr2:13998661-14002826 REVERSE | Aliases: T21L14.9, T21L14_9	3.8	4.5	-0.7	-2.5	15.2%	1.2
9472	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	3.0	-0.3	-2.5	15.2%	0.5
9473	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	4.5	3.8	0.7	2.5	15.2%	1.2
9474	AT5G62960.1 | expressed protein | chr5:25286508-25288867 FORWARD | Aliases: MJH22.1, MJH22_1	3.7	4.4	-0.7	-2.5	15.2%	1.1
9475	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	6.6	1.4	2.5	15.2%	1.2

Rank	Description	Sync	Root	M	t	adj.q	B
9476	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	3.1	3.5	-0.4	-2.5	15.2%	0.9
9477	AT2G31270.1 | hydroxyproline-rich glycoprotein family protein | chr2:13336092-13338907 FORWARD | Aliases: F16D14.11, F16D14_11	3.3	2.8	0.5	2.5	15.2%	1.0
9478	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	6.2	7.1	-0.9	-2.5	15.2%	1.2
9479	AT2G35810.1 | expressed protein | chr2:15056229-15057324 FORWARD | Aliases: F11F19.28, F11F19_28	10.5	9.1	1.4	2.5	15.2%	1.4
9480	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	3.7	3.2	0.4	2.5	15.2%	0.9
9481	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	3.7	4.5	-0.8	-2.5	15.2%	1.3
9482	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.	6.0	6.6	-0.6	-2.5	15.3%	0.9
9483	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	10.8	10.2	0.6	2.5	15.3%	0.8
9484	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	2.9	-0.4	-2.5	15.3%	0.7
9485	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 scienitific 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	3.6	-0.3	-2.5	15.3%	0.7
9486	AT5G40160.1 | Symbol: EMB506 |	3.3	3.0	0.3	2.5	15.3%	0.7
9487	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	3.0	0.7	2.5	15.4%	1.1
9488	AT3G08620.1 | KH domain-containing protein | chr3:2617774-2620579 FORWARD | Aliases: F17O14.9	4.3	3.7	0.5	2.5	15.4%	1.2
9489	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	3.9	-0.4	-2.5	15.4%	0.8
9490	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	4.7	5.4	-0.6	-2.5	15.4%	1.1
9491	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	2.7	2.4	0.4	2.5	15.4%	0.6
9492	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	6.5	-0.8	-2.5	15.4%	1.1
9493	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	2.4	-0.2	-2.5	15.4%	0.2
9494	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	4.4	4.1	0.3	2.5	15.4%	0.8

Rank	Description	Sync	Root	M	t	adj.q	B
9495	AT3G05740.1 | DNA helicase (RECQl1), identical to DNA Helicase (Arabidopsis thaliana) GI:10944747 | chr3:1698118-1701405 FORWARD | Aliases: F18C1.21	4.3	3.3	0.9	2.5	15.4%	1.3
9496	AT5G13220.3 | expressed protein | chr5:4218920-4220770 FORWARD | Aliases: T31B5.40, T31B5_40	3.3	1.6	1.7	2.5	15.4%	0.8
9497	AT5G10900.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	2.5	2.7	-0.2	-2.5	15.4%	0.4
9498	AT1G67080.1 | expressed protein | chr1:25048888-25050523 REVERSE | Aliases: F1O19.13, F1O19_13	7.9	7.1	0.8	2.5	15.4%	1.0
9499	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	6.0	5.1	0.9	2.5	15.5%	1.2
9500	AT3G42820.1 | expressed protein, hypothetical proteins - Arabidopsis thaliana | chr3:14932025-14938020 REVERSE | Aliases: T21C14.40	3.9	4.2	-0.3	-2.5	15.5%	0.5
9501	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	10.7	11.3	-0.6	-2.5	15.5%	0.9
9502	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	6.0	5.6	0.4	2.5	15.5%	0.9
9503	AT1G76930.2 | Symbol: ATEXT4 |	8.7	6.8	1.9	2.5	15.5%	0.7
9504	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	2.7	-0.2	-2.5	15.5%	0.3
9505	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	2.7	-0.2	-2.5	15.5%	0.3
9506	AT3G58800.1 | expressed protein, proline-rich protein A41R, Chlorella virus PBCV-1, PIR:T17531	3.9	3.4	0.6	2.5	15.5%	1.2
9507	AT4G14990.1 | expressed protein | chr4:8565618-8569810 REVERSE | Aliases: DL3535C, FCAALL.26	5.0	5.8	-0.8	-2.5	15.5%	1.4
9508	AT2G33360.1 | expressed protein | chr2:14147058-14150194 FORWARD | Aliases: F4P9.13, F4P9_13	4.4	4.1	0.3	2.5	15.5%	0.6
9509	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	3.1	-0.4	-2.5	15.5%	0.5
9510	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	7.2	6.8	0.4	2.5	15.5%	0.9
9511	AT3G62080.1 | SNF7 family protein, contains Pfam domain, PF03357: SNF7 family | chr3:22997151-22999743 FORWARD | Aliases: T17J13.40	2.8	3.3	-0.5	-2.5	15.5%	0.6
9512	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	4.6	-0.8	-2.5	15.6%	0.9
9513	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	7.2	6.3	0.9	2.5	15.6%	1.2
9514	AT4G11800.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	6.8	7.4	-0.6	-2.5	15.6%	0.9
9515	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) {Arabidopsis thaliana}; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor | chr3:17468780-17469555 FORWARD | Aliases: T21L8.130	3.3	2.9	0.4	2.5	15.6%	0.9
9516	AT3G53550.1 | expressed protein, various predicted proteins, Arabidopsis thaliana | chr3:19867848-19869286 FORWARD | Aliases: F4P12.250	2.2	2.4	-0.2	-2.5	15.6%	0.1
9517	AT2G17640.1 | Symbol: AtSerat3;1 | serine O-acetyltransferase, putative (SAT-106), similar to Arabidopsis thaliana serine acetyltransferase GI:905391	8.9	8.3	0.6	2.5	15.6%	0.8
9518	AT3G53610.2 | Symbol: ATRAB8 |	6.3	6.8	-0.5	-2.5	15.6%	1.2

Rank	Description	Sync	Root	M	t	adj.q	B
9519	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}	8.4	7.7	0.8	2.5	15.6%	1.3
9520	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	4.9	5.5	-0.6	-2.5	15.6%	1.2
9521	AT2G26070.1 | expressed protein | chr2:11112750-11114233 REVERSE | Aliases: T19L18.12, T19L18_12	7.8	7.0	0.8	2.5	15.6%	1.2
9522	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	5.0	4.2	0.8	2.5	15.6%	1.1
9523	AT3G63050.1 | expressed protein | chr3:23308866-23309364 REVERSE | Aliases: T20O10.150	4.0	4.4	-0.5	-2.5	15.6%	0.9
9524	AT4G23070.1 | rhomboid family protein, contains PFAM domain PF01694, Rhomboid family | chr4:12090701-12092088 REVERSE | Aliases: F7H19.260, F7H19_260	3.1	3.6	-0.5	-2.5	15.6%	0.5
9525	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	5.0	-1.1	-2.5	15.6%	1.2
9526	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	2.5	-0.2	-2.5	15.6%	0.0
9527	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	2.4	2.7	-0.3	-2.5	15.6%	0.4
9528	AT2G38650.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8 | chr2:16168886-16172804 REVERSE | Aliases: T6A23.15, T6A23_15	5.7	5.3	0.4	2.5	15.7%	0.9
9529	AT4G19420.2 | pectinacetylesterase family protein, contains Pfam profile: PF03283 pectinacetylesterase	3.6	4.1	-0.5	-2.5	15.7%	0.9
9530	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	7.5	6.1	1.4	2.5	15.7%	1.3
9531	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	10.3	9.1	1.2	2.5	15.7%	1.1
9532	AT1G09320.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr1:3009943-3012354 REVERSE | Aliases: T31J12.4, T31J12_4	4.8	3.9	0.8	2.5	15.7%	1.2
9533	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	4.1	3.7	0.4	2.5	15.7%	0.9
9534	AT4G00130.1 | hypothetical protein, contains Pfam profile PF04504: Protein of unknown function, DUF573	3.5	4.0	-0.4	-2.5	15.7%	0.7
9535	AT1G71900.1 | expressed protein | chr1:27065150-27068158 FORWARD | Aliases: F17M19.5, F17M19_5	5.8	4.8	1.0	2.5	15.7%	1.1
9536	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	4.1	3.4	0.7	2.5	15.7%	1.3
9537	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	3.4	-0.4	-2.5	15.7%	0.9
9538	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	8.6	7.3	1.3	2.5	15.7%	1.2
9539	AT4G28460.1 | expressed protein | chr4:14066004-14066550 FORWARD | Aliases: F20O9.140, F20O9_140	5.4	6.4	-1.0	-2.5	15.7%	1.1

Rank	Description	Sync	Root	M	t	adj.q	B
9540	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	4.1	3.8	0.3	2.5	15.8%	0.6
9541	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	3.1	-0.4	-2.5	15.8%	0.5
9542	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	3.7	3.3	0.4	2.5	15.8%	0.9
9543	AT4G09620.1 | expressed protein, hypothetical protein F6E13.15 - Arabidopsis thaliana,PIR2:T00682 | chr4:6076989-6078959 REVERSE | Aliases: T25P22.60, T25P22_60	6.2	5.9	0.3	2.5	15.8%	0.6
9544	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	9.4	-1.3	-2.5	15.8%	1.2
9545	AT5G65870.1 | Symbol: ATPSK5 |	5.3	4.6	0.7	2.5	15.8%	1.2
9546	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	3.4	0.4	2.5	15.8%	0.8
9547	AT2G39760.2 | Symbol: ATBPM3 |	5.5	4.0	1.5	2.5	15.8%	1.2
9548	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	7.7	9.1	-1.4	-2.5	15.8%	1.2
9549	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	3.8	4.5	-0.7	-2.5	15.8%	1.1
9550	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 profilePF05042: Caleosin related protein | chr1:8252744-8254610 REVERSE | Aliases: F26F24.33, F26F24_33	2.8	3.1	-0.3	-2.5	15.8%	0.6
9551	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	6.1	-1.3	-2.5	15.9%	1.0
9552	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	12.5	12.0	0.5	2.5	15.9%	0.6
9553	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	4.3	-0.4	-2.5	15.9%	0.9
9554	AT5G48970.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr5:19873702-19876989 REVERSE | Aliases: K19E20.10, K19E20_10	6.3	5.6	0.6	2.5	15.9%	1.0
9555	AT3G49490.1 | expressed protein | chr3:18355729-18359665 REVERSE | Aliases: T9C5.90	8.5	8.9	-0.4	-2.5	15.9%	0.8
9556	AT4G05300.1 | hypothetical protein | chr4:2705668-2708156 FORWARD | Aliases: C17L7.220, C17L7_220	3.4	3.6	-0.2	-2.5	15.9%	0.4
9557	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	2.4	2.7	-0.3	-2.5	16.0%	0.3
9558	AT1G52320.2 | expressed protein, contains Pfam profile: PF04782 protein of unknown function (DUF632) | chr1:19489368-19491102 FORWARD | Aliases: F19K6.7, F19K6_7	5.8	6.5	-0.7	-2.5	16.0%	1.1
9559	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	8.3	8.8	-0.6	-2.5	16.0%	0.8

Rank	Description	Sync	Root	M	t	adj.q	B
9560	AT5G17350.1 | expressed protein | chr5:5718774-5719610 FORWARD | Aliases: MKP11.31, MKP11_31	4.9	4.2	0.7	2.5	16.0%	1.3
9561	AT2G47940.1 | Symbol: DEGP2 | DegP2 protease (DEGP2), identical to DegP2 protease GI:13172275 from (Arabidopsis thaliana); identical to cDNA DegP2 protease (DEGP2) nuclear gene for chloroplast product GI:13172274	4.8	3.9	1.0	2.5	16.0%	1.2
9562	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	5.5	6.7	-1.2	-2.5	16.0%	1.2
9563	AT1G13670.1 | expressed protein | chr1:4688173-4688875 FORWARD | Aliases: F21F23.11, F21F23_11	3.7	4.0	-0.3	-2.5	16.0%	0.5
9564	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	2.9	-0.3	-2.5	16.0%	0.6
9565	AT2G39705.1 | expressed protein | chr2:16563934-16564655 FORWARD | Aliases: None	6.1	7.5	-1.4	-2.5	16.0%	1.1
9566	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	5.2	0.6	2.5	16.0%	1.1
9567	ATCG01080.1 | Symbol: NDHG | NADH dehydrogenase ND6 | chrC:118377-118907 REVERSE | Aliases: NDHG	4.5	6.1	-1.6	-2.5	16.0%	1.2
9568	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)	6.6	5.9	0.8	2.5	16.1%	1.3
9569	AT2G31710.1 | expressed protein | chr2:13488870-13490182 REVERSE | Aliases: T9H9.23, T9H9_23	5.8	5.1	0.7	2.5	16.1%	0.9
9570	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	3.4	3.1	0.3	2.5	16.1%	0.6
9571	AT1G21480.2 | exostosin family protein, contains Pfam profile: PF03016 Exostosin family | chr1:7518980-7521461 REVERSE | Aliases: F24J8.10, F24J8_10	5.8	5.4	0.5	2.5	16.1%	0.8
9572	AT3G47130.1 | F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain;	2.4	2.7	-0.3	-2.5	16.1%	0.3
9573	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	4.3	3.8	0.4	2.5	16.1%	0.9
9574	AT4G17350.1 | expressed protein | chr4:9701144-9703838 FORWARD | Aliases: DL4710W, FCAALL.415	7.6	7.1	0.5	2.5	16.1%	0.9
9575	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	5.2	5.7	-0.5	-2.5	16.1%	1.1
9576	AT1G04960.1 | expressed protein | chr1:1407800-1410867 REVERSE | Aliases: F13M7.5, F13M7_5	7.9	8.5	-0.6	-2.5	16.1%	0.9
9577	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	3.2	-0.3	-2.5	16.1%	0.5
9578	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	8.1	7.6	0.6	2.5	16.1%	0.9
9579	AT2G39870.1 | expressed protein | chr2:16650621-16652455 FORWARD | Aliases: T28M21.3, T28M21_3	3.5	3.2	0.3	2.5	16.1%	0.7
9580	AT2G01735.1 | Symbol: RIE1 | zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger) domain	6.2	6.9	-0.7	-2.5	16.1%	1.2
9581	AT1G05330.1 | expressed protein, ; expression supported by MPSS | chr1:1558169-1558582 FORWARD | Aliases: YUP8H12.5, YUP8H12_5	2.4	2.6	-0.3	-2.5	16.1%	0.2
9582	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 profilesPF03893: Lipase 3 N-terminal region, PF01764: Lipase	4.3	5.7	-1.4	-2.5	16.1%	1.3

Rank	Description	Sync	Root	M	t	adj.q	B
9583	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	6.0	0.8	2.5	16.1%	0.8
9584	AT3G09310.1 | expressed protein | chr3:2860246-2861338 REVERSE | Aliases: F3L24.18	3.9	3.3	0.6	2.5	16.1%	0.8
9585	AT3G28580.1 | AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 | chr3:10716860-10718566 FORWARD | Aliases: MZN14.6	2.9	3.5	-0.6	-2.5	16.1%	0.5
9586	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	5.5	0.8	2.5	16.1%	0.9
9587	AT4G25330.1 | expressed protein | chr4:12957844-12958719 FORWARD | Aliases: T30C3.2	2.5	2.9	-0.4	-2.5	16.1%	0.5
9588	AT3G06960.2 | Symbol: PDE320 |	6.3	5.7	0.6	2.5	16.1%	1.0
9589	AT1G32370.4 | Symbol: TOM2B | expressed protein | chr1:11676941-11678427 FORWARD | Aliases: F5D14.14, F5D14_14, TTM1	4.8	4.3	0.5	2.5	16.1%	1.0
9590	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	9.7	8.3	1.5	2.5	16.1%	1.1
9591	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	6.2	5.7	0.5	2.5	16.1%	1.0
9592	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	2.9	-0.3	-2.5	16.1%	0.6
9593	AT3G46630.1 | expressed protein, contains similarity to defective chloroplasts and leaves protein SP:Q42463 from (Lycopersicon esculentum) | chr3:17191919-17193414 REVERSE | Aliases: F12A12.150	7.0	6.4	0.6	2.5	16.1%	1.0
9594	AT4G20050.1 | Symbol: QRT3 | expressed protein, C65DMY30S | chr4:10849792-10853356 REVERSE | Aliases: F18F4.150, F18F4_150, QUARTET 3	3.8	4.3	-0.5	-2.5	16.1%	0.9
9595	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	3.3	-0.4	-2.5	16.1%	0.8
9596	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	3.4	2.7	0.7	2.5	16.1%	0.9
9597	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	3.7	3.4	0.4	2.5	16.2%	0.7
9598	AT4G33770.1 | inositol 1,3,4-trisphosphate 5/6-kinase family protein, contains Pfam doamin 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	4.6	5.2	-0.6	-2.5	16.2%	1.1
9599	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	3.6	-0.5	-2.5	16.2%	0.8
9600	AT1G14350.1 | Symbol: MYB124 |	2.4	2.8	-0.3	-2.5	16.2%	0.7
9601	ATMG01360.1 | Symbol: COX1 | cytochrome c oxidase subunit 1 | chrM:349830-351413 REVERSE | Aliases: COX1	7.8	9.7	-1.9	-2.5	16.2%	0.9
9602	AT3G23490.1 | Symbol: CYN | cyanate lyase family, contains Pfam profile: PF02560 cyanate lyase C-terminal domain | chr3:8423042-8424659 REVERSE | Aliases: CYANASE, MEE5.3	7.1	5.8	1.3	2.5	16.2%	1.3
9603	AT2G33500.2 | zinc finger (B-box type) family protein | chr2:14195063-14197330 REVERSE | Aliases: F4P9.27, F4P9_27	4.4	3.9	0.4	2.5	16.2%	1.0
9604	AT2G36670.2 | aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease | chr2:15371867-15375237 REVERSE | Aliases: F13K3.7, F13K3_7	4.7	4.3	0.4	2.5	16.2%	0.8
9605	AT5G09830.1 | BolA-like family protein, contains Pfam profile: PF01722 BolA-like protein | chr5:3057658-3058822 REVERSE | Aliases: MYH9.4, MYH9_4	9.5	9.0	0.5	2.5	16.2%	1.0

Rank	Description	Sync	Root	M	t	adj.q	B
9606	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	10.0	10.6	-0.5	-2.5	16.2%	0.6
9607	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	5.4	5.9	-0.5	-2.5	16.2%	1.0
9608	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	4.0	3.5	0.5	2.5	16.2%	1.1
9609	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	7.8	8.9	-1.1	-2.5	16.2%	1.0
9610	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	8.0	7.0	1.0	2.5	16.3%	1.1
9611	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	3.9	-0.6	-2.5	16.3%	0.9
9612	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	4.2	-0.3	-2.5	16.3%	0.7
9613	AT3G32940.1 | expressed protein | chr3:13494664-13497497 REVERSE | Aliases: T13O13.2	5.4	6.4	-1.1	-2.5	16.3%	1.1
9614	AT3G02390.1 | expressed protein | chr3:489066-489478 FORWARD | Aliases: F11A12.8, F11A12_8	3.3	4.1	-0.7	-2.5	16.3%	0.9
9615	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)	3.7	4.4	-0.7	-2.5	16.3%	1.1
9616	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	2.5	-0.2	-2.5	16.3%	0.4
9617	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	4.2	3.6	0.6	2.5	16.3%	1.0
9618	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	7.5	6.7	0.8	2.5	16.3%	0.9
9619	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	4.0	-0.6	-2.5	16.3%	1.2
9620	AT2G41620.1 | nucleoporin interacting component family protein, contains Pfam profile PF04097: Nucleoporin interacting component | chr2:17357223-17362126 REVERSE | Aliases: T32G6.14, T32G6_14	5.8	4.8	1.0	2.5	16.3%	1.1
9621	AT5G44740.2 | UMUC-like DNA repair family protein, low similarity to DNA polymerase eta (Homo sapiens) GI:11463971; contains Pfam profile PF00817: ImpB/MucB/SamB family | chr5:18065011-18069102 REVERSE | Aliases: K23L20.8, K23L20_8	3.3	2.9	0.4	2.5	16.3%	0.8
9622	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	2.6	-0.2	-2.5	16.4%	0.2
9623	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	3.8	4.2	-0.5	-2.5	16.4%	1.0
9624	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	3.6	4.1	-0.5	-2.5	16.4%	1.0

Rank	Description	Sync	Root	M	t	adj.q	B
9625	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	4.2	3.7	0.5	2.5	16.4%	0.9
9626	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	6.0	6.7	-0.6	-2.5	16.4%	1.1
9627	AT5G20950.2 | glycosyl hydrolase family 3 protein, beta-D-glucan exohydrolase, Nicotiana tabacum, EMBL:AB017502 | chr5:7107378-7111311 REVERSE | Aliases: F22D1.120, F22D1_120	6.0	4.3	1.8	2.5	16.4%	1.3
9628	AT1G09290.1 | expressed protein, This gene is continued on the 5' end of BAC T12M14 | chr1:3001519-3003764 REVERSE | Aliases: T12M4.20	4.3	3.8	0.4	2.5	16.4%	1.0
9629	AT5G06550.1 | similar to transcription factor jumonji (jmjC) 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, jmjC (InterPro:IPR003347) | chr5:2001147-2003076 REVERSE | Aliases: F15M7.8, F15M7_8	4.7	4.2	0.5	2.5	16.4%	1.0
9630	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	6.7	6.2	0.5	2.5	16.4%	1.0
9631	AT3G49060.1 | protein kinase family protein / U-box domain-containing protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain	5.1	5.7	-0.7	-2.5	16.4%	0.9
9632	AT4G13180.1 | short-chain dehydrogenase/reductase (SDR) family protein, similar to short-chain type dehydrogenase/reductase SP:Q08632 (Picea abies) | chr4:7657192-7658193 REVERSE | Aliases: F17N18.70, F17N18_70	10.1	8.0	2.1	2.5	16.4%	1.3
9633	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	2.0	2.4	-0.3	-2.5	16.4%	0.4
9634	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	2.1	2.4	-0.3	-2.5	16.4%	0.3
9635	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	3.7	4.1	-0.4	-2.5	16.4%	0.8
9636	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	9.1	-0.6	-2.5	16.4%	0.8
9637	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	4.1	-0.5	-2.5	16.4%	0.8
9638	AT3G48000.1 | Symbol: ALDH2B4 | aldehyde dehydrogenase (ALDH2), identical to aldehyde dehydrogenase (Arabidopsis thaliana) GI:8574427; similar to mitochondrial aldehyde dehydrogenase (Arabidopsis thaliana) gi:19850249:gb:AAL99612; identical to cDNA aldehyde dehydrogenase AtALDH2a GI:20530140 | chr3:17727852-17730999 REVERSE | Aliases: ALDEHYDE DEHYDROGENASE 2, ALDH2, T17F15.130	11.5	10.7	0.8	2.5	16.5%	1.0
9639	AT4G27080.1 | Symbol: ATPDIL5 4 | Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	6.9	5.7	1.2	2.5	16.5%	1.0
9640	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	8.6	8.0	0.6	2.5	16.5%	1.2
9641	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	4.9	0.7	2.5	16.5%	1.0
9642	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)	5.0	4.1	0.9	2.5	16.5%	1.2

Rank	Description	Sync	Root	M	t	adj.q	B
9643	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	3.1	-0.3	-2.5	16.5%	0.6
9644	AT1G04900.1 | expressed protein, contains Pfam PF02636: Uncharacterized ACR, COG1565 | chr1:1383840-1388520 FORWARD | Aliases: F13M7.11, F13M7_11	4.4	3.8	0.6	2.5	16.5%	1.0
9645	AT2G36710.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr2:15396545-15398328 REVERSE | Aliases: F13K3.11, F13K3_11	3.1	3.4	-0.3	-2.5	16.5%	0.6
9646	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	4.8	6.1	-1.3	-2.5	16.5%	1.2
9647	AT5G24655.1 | expressed protein | chr5:8440698-8441221 REVERSE | Aliases: None	8.3	7.6	0.7	2.5	16.6%	0.9
9648	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	5.2	5.8	-0.6	-2.5	16.6%	1.0
9649	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	3.4	3.0	0.4	2.5	16.6%	0.8
9650	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	3.7	1.1	2.5	16.6%	1.5
9651	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	3.7	1.1	2.5	16.6%	1.5
9652	AT1G77800.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr1:29258290-29265511 FORWARD | Aliases: T32E8.13, T32E8_13	6.0	6.5	-0.5	-2.5	16.6%	1.0
9653	AT3G13920.2 | Symbol: EIF4A1 |	9.0	7.6	1.5	2.5	16.6%	1.2
9654	AT5G67020.1 | expressed protein | chr5:26767076-26768475 FORWARD | Aliases: K8A10.9, K8A10_9	3.9	4.3	-0.3	-2.5	16.6%	0.7
9655	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	4.9	-0.4	-2.5	16.6%	0.9
9656	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	3.4	3.1	0.3	2.5	16.6%	0.8
9657	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)	4.6	5.8	-1.2	-2.5	16.6%	1.1
9658	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	6.2	7.0	-0.8	-2.5	16.6%	1.3
9659	AT4G25270.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr4:12937263-12938846 REVERSE | Aliases: F24A6.110, F24A6_110	3.6	4.2	-0.7	-2.5	16.6%	0.9
9660	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	4.5	-0.4	-2.5	16.7%	0.8
9661	AT4G29520.1 | expressed protein | chr4:14493920-14495735 REVERSE | Aliases: T16L4.30, T16L4_30	6.1	5.3	0.8	2.5	16.7%	1.1
9662	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	5.3	-0.7	-2.5	16.7%	0.8
9663	AT5G66320.2 | zinc finger (GATA type) family protein | chr5:26513181-26514903 REVERSE | Aliases: K1L20.10, K1L20_10	3.1	3.4	-0.4	-2.5	16.7%	0.6
9664	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	7.1	8.4	-1.2	-2.5	16.7%	1.1

Rank	Description	Sync	Root	M	t	adj.q	B
9665	AT1G53050.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr1:19775713-19779415 FORWARD | Aliases: F8L10.9, F8L10_9	6.3	5.5	0.8	2.5	16.7%	1.1
9666	AT5G61450.1 | 2-phosphoglycerate kinase-related, contains weak similarity to 2-phosphoglycerate kinase (GI:467751) (Methanothermus fervidus) | chr5:24727259-24730171 REVERSE | Aliases: MCI2.1	6.1	6.7	-0.6	-2.5	16.7%	1.1
9667	AT5G19840.1 | transcription factor jumonji (jmjC) domain-containing protein, low similarity to PASS1 (Homo sapiens) GI:21591407; contains Pfam profile PF02373: jmjC domain | chr5:6705374-6709794 FORWARD | Aliases: T29J13.260, T29J13_260	2.4	2.7	-0.3	-2.5	16.7%	0.5
9668	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	3.4	-0.4	-2.5	16.7%	0.8
9669	AT3G42460.1 | expressed protein, several hypothetical proteins - Arabidopsis thaliana | chr3:14601277-14602206 REVERSE | Aliases: T32A11.30	2.7	2.9	-0.2	-2.5	16.7%	0.3
9670	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	4.9	5.5	-0.6	-2.5	16.7%	0.8
9671	AT5G26210.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr5:9157982-9160357 REVERSE | Aliases: T19G15.60, T19G15_60	5.4	5.9	-0.5	-2.5	16.7%	1.0
9672	AT5G24450.1 | transcription factor-related, low similarity to transcription factor IIIC63 (Homo sapiens) GI:5281316 | chr5:8348783-8353298 FORWARD | Aliases: T31K7.3, T31K7_3	6.0	7.3	-1.2	-2.5	16.7%	1.1
9673	AT5G14070.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	3.5	4.2	-0.6	-2.5	16.7%	1.1
9674	AT2G26550.1 | Symbol: HO2 | heme oxygenase 2 (HO2), similar to heme oxygenase 2 (Arabidopsis thaliana) gi:4530595:gb:AAD22109	4.9	4.5	0.4	2.5	16.7%	0.8
9675	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	8.4	10.1	-1.7	-2.5	16.7%	1.1
9676	AT4G02680.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain | chr4:1181051-1184930 REVERSE | Aliases: T10P11.24, T10P11_24	8.2	7.2	1.0	2.5	16.7%	1.1
9677	AT3G32270.1 | expressed protein, similar to putative replication protein A1 GB:AAC95163 GI:4006821 from (Arabidopsis thaliana)	4.4	5.1	-0.7	-2.5	16.7%	1.1
9678	AT3G15560.1 | expressed protein | chr3:5268599-5270125 FORWARD | Aliases: MQD17.1	3.0	3.2	-0.2	-2.5	16.8%	0.2
9679	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	3.2	-0.2	-2.5	16.8%	0.3
9680	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	4.6	4.0	0.6	2.5	16.8%	1.0
9681	AT1G11240.1 | expressed protein | chr1:3766754-3768294 REVERSE | Aliases: T28P6.24, T28P6_24	9.1	7.8	1.3	2.5	16.8%	1.1
9682	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	3.1	2.9	0.2	2.5	16.8%	0.1
9683	AT2G46490.1 | expressed protein (APS2), identical to cDNA Aps2, partial cds GI:4519894	8.7	7.4	1.3	2.5	16.8%	1.2
9684	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	2.7	-0.2	-2.5	16.8%	0.2
9685	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	3.1	3.5	-0.3	-2.5	16.8%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
9686	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	5.7	-0.8	-2.5	16.8%	1.0
9687	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	6.2	5.3	0.9	2.5	16.8%	1.2
9688	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)	3.6	3.1	0.6	2.5	16.8%	0.9
9689	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	5.5	4.5	1.1	2.5	16.8%	1.1
9690	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: methlytransferase, UbiE/COQ5 family | chr1:8295174-8296912 REVERSE | Aliases: F26F24.24, F26F24_24	7.6	6.8	0.8	2.5	16.8%	1.2
9691	AT2G28620.1 | kinesin motor protein-related | chr2:12272244-12277097 REVERSE | Aliases: T8O18.9, T8O18_9	4.1	4.7	-0.6	-2.5	16.8%	1.0
9692	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	4.3	-0.3	-2.5	16.8%	0.6
9693	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)	2.4	2.6	-0.2	-2.5	16.8%	-0.2
9694	AT4G31290.1 | ChaC-like family protein, contains Pfam profile: PF04752 ChaC-like protein | chr4:15185997-15188490 FORWARD | Aliases: F8F16.110, F8F16_110	6.0	6.8	-0.7	-2.5	16.8%	1.0
9695	AT2G04305.1 | magnesium transporter CorA-like protein-related | chr2:1501405-1503782 REVERSE | Aliases: T23O15.7, T23O15_7	3.6	3.2	0.3	2.5	16.8%	0.6
9696	AT3G06260.1 | galactinol synthase, putative, contains Pfam profile: PF01501 glycosyl transferase family 8 | chr3:1893810-1894865 REVERSE | Aliases: F28L1.20, F28L1_20	2.8	3.1	-0.2	-2.5	16.9%	0.2
9697	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	9.0	8.5	0.5	2.5	16.9%	0.8
9698	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	6.2	4.9	1.4	2.5	16.9%	1.2
9699	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	3.5	-0.3	-2.5	16.9%	0.6
9700	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	3.8	-1.0	-2.5	16.9%	1.0
9701	AT3G51270.1 | RIO1 family protein, contains Pfam profile PF01163: RIO1 family | chr3:19044830-19047751 FORWARD | Aliases: F24M12.310	7.4	6.6	0.8	2.5	16.9%	1.1
9702	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	5.7	0.6	2.5	16.9%	0.9
9703	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: T1O3.15, T1O3_15	3.2	3.6	-0.4	-2.5	16.9%	0.5
9704	AT5G03780.1 | Symbol: TRFL10 |	4.5	3.8	0.7	2.5	16.9%	1.0
9705	AT3G15095.1 | expressed protein | chr3:5081961-5084057 FORWARD | Aliases: K15M2.25	4.9	4.2	0.8	2.5	16.9%	1.2
9706	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	5.5	4.7	0.8	2.5	16.9%	1.1

Rank	Description	Sync	Root	M	t	adj.q	B
9707	AT3G60260.3 | similar to phagocytosis and cell motility protein ELMO1-related [Arabidopsis thaliana] (TAIR:At2g44770.1); similar to OSJNBb0038F03.14 [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	6.4	5.8	0.7	2.5	16.9%	0.8
9708	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/PfpI (InterPro:IPR002818); contains InterPro domain DJ-1 protein (InterPro:IPR006287) | chr3:5047407-5049884 FORWARD | Aliases: K15M2.13, K15M2_13	12.7	11.8	0.9	2.5	17.0%	0.7
9709	AT5G58070.1 | lipocalin, putative, similar to temperature stress-induced lipocalin (Triticum aestivum) GI:18650668 | chr5:23517287-23518435 REVERSE | Aliases: K21L19.9, K21L19_9	10.7	9.1	1.6	2.5	17.0%	1.2
9710	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	2.4	-0.2	-2.5	17.0%	0.3
9711	AT5G57260.1 | Symbol: CYP71B10 | cytochrome P450 71B10, identical to cytochrome P450 71B10 (SP:Q9LVD2) (Arabidopsis thaliana)	3.1	3.4	-0.3	-2.5	17.0%	0.3
9712	AT3G09670.1 | PWWP domain-containing protein | chr3:2966435-2968973 FORWARD | Aliases: F11F8.26	4.1	3.6	0.5	2.5	17.0%	0.5
9713	AT1G60810.1 | Symbol: ACLA 2 |	9.5	8.5	1.0	2.5	17.0%	0.9
9714	AT3G59920.1 | Symbol: ATGDI2 |	10.7	9.6	1.0	2.5	17.0%	1.0
9715	AT5G67350.1 | expressed protein | chr5:26885516-26886712 REVERSE | Aliases: K8K14.7, K8K14_7	3.8	4.2	-0.5	-2.5	17.0%	0.9
9716	AT3G30340.1 | nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula) | chr3:11959080-11961577 FORWARD | Aliases: T6J22.10	3.5	3.9	-0.4	-2.5	17.0%	0.4
9717	AT1G53710.1 | similar to putative cell division control protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470871.1); contains InterPro domain Metallo-phosphoesterase (InterPro:IPR004843) | chr1:20056829-20060064 REVERSE | Aliases: F22G10.25, F22G10_25	4.9	5.2	-0.2	-2.5	17.0%	0.3
9718	AT3G20430.1 | expressed protein | chr3:7121486-7123179 FORWARD | Aliases: MQC12.22	7.7	7.0	0.7	2.5	17.0%	0.9
9719	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	7.1	5.9	1.2	2.5	17.0%	1.2
9720	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	5.4	4.9	0.6	2.5	17.0%	0.9
9721	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	8.9	9.2	-0.3	-2.5	17.0%	0.7
9722	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	3.6	0.5	2.5	17.0%	0.8
9723	AT5G41170.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:16495714-16497810 REVERSE | Aliases: MEE6.24, MEE6_24	3.3	3.6	-0.3	-2.4	17.1%	0.5
9724	AT1G64410.1 | expressed protein | chr1:23930056-23935866 REVERSE | Aliases: F15H21.18, F15H21_18	3.9	4.8	-0.9	-2.4	17.1%	0.8
9725	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	6.5	7.2	-0.7	-2.4	17.1%	1.1
9726	AT2G46000.1 | expressed protein | chr2:18928030-18929240 REVERSE | Aliases: F4I18.48	3.5	2.9	0.5	2.4	17.1%	1.0
9727	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	7.5	6.9	0.6	2.4	17.1%	0.8

Rank	Description	Sync	Root	M	t	adj.q	B
9728	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	11.2	11.8	-0.6	-2.4	17.1%	0.5
9729	AT4G27657.1 | expressed protein | chr4:13813050-13813522 FORWARD | Aliases: None	4.0	2.9	1.0	2.4	17.1%	0.6
9730	AT5G19880.1 | peroxidase, putative, similar to peroxidase (Lycopersicon esculentum) gi:296910:emb:CAA50597 | chr5:6720386-6722477 REVERSE | Aliases: F28I16.30, F28I16_30	3.4	2.6	0.8	2.4	17.1%	1.0
9731	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	5.1	4.6	0.6	2.4	17.1%	1.1
9732	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	2.7	-0.3	-2.4	17.1%	0.5
9733	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	3.3	-0.3	-2.4	17.1%	0.3
9734	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	6.1	5.2	0.9	2.4	17.1%	1.1
9735	AT5G51210.1 | glycine-rich protein / oleosin | chr5:20837327-20838117 FORWARD | Aliases: MWD22.16, MWD22_16	4.0	3.7	0.3	2.4	17.2%	0.7
9736	AT3G62410.1 | Symbol: CP12 2 |	5.6	4.7	1.0	2.4	17.2%	1.3
9737	AT4G38590.1 | Symbol: BGAL14 |	3.5	3.9	-0.4	-2.4	17.2%	0.6
9738	AT1G10720.1 | BSD domain-containing protein, contains Pfam profile PF03909: BSD domain	3.3	3.7	-0.4	-2.4	17.2%	0.8
9739	AT2G03520.1 | Symbol: ATUPS4 |	2.2	2.5	-0.3	-2.4	17.2%	0.3
9740	AT1G11880.1 | expressed protein, contains Pfam profile PF04188: Protein of unknown function (DUF409) | chr1:4007704-4010432 REVERSE | Aliases: F12F1.28, F12F1_28	3.0	3.4	-0.5	-2.4	17.2%	0.7
9741	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	3.1	0.5	2.4	17.2%	0.9
9742	AT4G16090.1 | hypothetical protein, contains Pfam profile PF03478: Protein of unknown function (DUF295) | chr4:9103090-9103968 FORWARD | Aliases: DL4085W, FCAALL.276	3.5	3.9	-0.4	-2.4	17.2%	0.6
9743	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	3.3	3.6	-0.3	-2.4	17.2%	0.4
9744	AT5G37480.1 | expressed protein | chr5:14901561-14903198 REVERSE | Aliases: MPA22.2, MPA22_2	7.6	8.2	-0.6	-2.4	17.2%	0.9
9745	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	3.9	4.6	-0.7	-2.4	17.2%	0.6
9746	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	3.3	0.5	2.4	17.2%	0.9
9747	AT3G14370.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:4797852-4799511 REVERSE | Aliases: MLN21.22	2.9	3.4	-0.5	-2.4	17.2%	1.0
9748	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	7.3	8.1	-0.9	-2.4	17.2%	0.9

Rank	Description	Sync	Root	M	t	adj.q	B
9749	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	7.3	8.1	-0.9	-2.4	17.2%	0.9
9750	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 ATFP7 (GI:4097555); contains heavy-metal-associated domain PF00403 | chr1:8139154-8140191 FORWARD | Aliases: F19G10.25	5.4	6.7	-1.2	-2.4	17.2%	1.0
9751	AT5G09230.6 | transcriptional regulator Sir2 family protein, contains Pfam domain PF02146: transcriptional regulator, Sir2 family; | chr5:2871379-2873785 FORWARD | Aliases: T2K12.8	8.1	8.4	-0.3	-2.4	17.2%	0.5
9752	AT3G53500.2 | Symbol: RSZ32 | zinc knuckle (CCHC-type) family protein, contains Pfam domain PF00098: Zinc knuckle | chr3:19845324-19847976 REVERSE | Aliases: F4P12.200, RSZ32	8.5	7.8	0.7	2.4	17.2%	1.1
9753	AT3G09550.1 | ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023 | chr3:2932468-2934359 FORWARD | Aliases: F11F8.13	3.1	3.5	-0.4	-2.4	17.2%	0.5
9754	AT4G21780.1 | expressed protein | chr4:11567142-11567711 FORWARD | Aliases: F17L22.240, F17L22_240	4.7	5.4	-0.7	-2.4	17.2%	1.1
9755	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	10.6	9.8	0.8	2.4	17.3%	0.8
9756	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	2.6	3.0	-0.4	-2.4	17.3%	0.6
9757	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	7.1	7.7	-0.6	-2.4	17.3%	0.9
9758	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	6.2	5.8	0.5	2.4	17.3%	0.9
9759	AT1G34355.1 | forkhead-associated domain-containing protein / FHA domain-containing protein | chr1:12536475-12541869 FORWARD | Aliases: None	3.1	2.8	0.3	2.4	17.3%	0.5
9760	AT1G05470.1 | endonuclease/exonuclease/phosphatase family protein, simlar 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	2.3	2.7	-0.3	-2.4	17.3%	0.1
9761	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	4.8	4.1	0.7	2.4	17.3%	1.2
9762	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	3.5	3.9	-0.4	-2.4	17.3%	0.8
9763	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	2.4	2.7	-0.4	-2.4	17.3%	0.3
9764	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	3.5	4.1	-0.6	-2.4	17.3%	1.0
9765	AT3G54140.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr3:20056641-20059550 REVERSE | Aliases: F24B22.100	4.1	4.6	-0.4	-2.4	17.3%	0.8
9766	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	3.4	3.0	0.4	2.4	17.3%	0.8
9767	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	7.2	0.6	2.4	17.3%	1.0
9768	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	7.1	6.8	0.3	2.4	17.3%	0.4

Rank	Description	Sync	Root	M	t	adj.q	B
9769	AT5G07290.1 | RNA recognition motif (RRM)-containing protein, Mei2-like protein - Arabidopsis thaliana, EMBL:D86122 | chr5:2293373-2298976 FORWARD | Aliases: T28J14.230, T28J14_230	3.5	4.2	-0.6	-2.4	17.4%	0.9
9770	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	5.0	5.4	-0.4	-2.4	17.4%	0.7
9771	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	5.3	6.0	-0.8	-2.4	17.4%	0.9
9772	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	3.2	0.4	2.4	17.4%	0.6
9773	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	3.9	-0.5	-2.4	17.4%	0.6
9774	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	5.0	6.0	-0.9	-2.4	17.4%	1.0
9775	AT1G62250.2 | expressed protein | chr1:22999169-23001221 REVERSE | Aliases: F19K23.17, F19K23_17	6.3	7.1	-0.8	-2.4	17.4%	1.0
9776	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	3.5	3.1	0.4	2.4	17.4%	0.8
9777	AT4G30050.1 | expressed protein, ; expression supported by MPSS | chr4:14687212-14688757 REVERSE | Aliases: F6G3.80, F6G3_80	2.5	2.9	-0.3	-2.4	17.4%	0.5
9778	AT5G14680.1 | universal stress protein (USP) family protein, similar to ER6 protein (Lycopersicon esculentum) GI:5669654; contains Pfam profile PF00582: universal stress protein family | chr5:4730910-4733084 REVERSE | Aliases: T15N1.170, T15N1_170	7.8	7.3	0.5	2.4	17.4%	0.8
9779	AT2G07520.1 | hypothetical protein | chr2:3135109-3135777 FORWARD | Aliases: F9A16.11, F9A16_11	2.1	2.2	-0.1	-2.4	17.4%	-0.3
9780	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	8.5	7.7	0.8	2.4	17.4%	1.0
9781	AT1G69050.1 | expressed protein | chr1:25965587-25966011 FORWARD | Aliases: F4N2.3	2.2	2.4	-0.3	-2.4	17.5%	0.2
9782	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	3.3	-0.3	-2.4	17.5%	0.4
9783	AT3G46100.1 | Symbol: ATHRS1 |	6.7	6.3	0.4	2.4	17.5%	0.8
9784	AT1G67280.1 | lactoylglutathione lyase, putative / glyoxalase I, putative, similar to putative lactoylglutathione lyase SP:Q39366, GI:2494843 from (Brassica oleracea)	9.0	8.0	1.0	2.4	17.5%	0.9
9785	AT1G63350.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.7	3.0	-0.4	-2.4	17.5%	0.4
9786	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	5.5	5.0	0.5	2.4	17.5%	0.6
9787	AT4G33310.1 | expressed protein | chr4:16056160-16056420 FORWARD | Aliases: F17M5.70, F17M5_70	4.5	5.1	-0.6	-2.4	17.5%	1.0
9788	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) (4CL 3) (4-coumaroyl-CoA synthase 3) {Arabidopsis thaliana} | chr1:24170890-24175165 REVERSE | Aliases: 4 COUMARATE:COA LIGASE, F16G16.6, F16G16_6	5.3	4.5	0.8	2.4	17.5%	1.0
9789	AT4G17330.1 | Symbol: ATG2484 1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr4:9688900-9693875 REVERSE | Aliases: DL4700C, FCAALL.411	7.3	8.1	-0.8	-2.4	17.5%	0.7
9790	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	2.9	-0.3	-2.4	17.5%	0.6

Rank	Description	Sync	Root	M	t	adj.q	B
9791	AT1G78180.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr1:29421821-29423868 FORWARD | Aliases: T11I11.12, T11I11_12	4.2	4.6	-0.4	-2.4	17.5%	0.8
9792	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	4.4	3.7	0.7	2.4	17.5%	1.1
9793	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 (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563 | chr2:12845807-12847189 REVERSE | Aliases: T27E13.18, T27E13_18	6.8	7.7	-0.9	-2.4	17.5%	1.1
9794	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	3.0	3.4	-0.4	-2.4	17.5%	0.9
9795	AT1G63680.1 | Symbol: PDE316 |	3.9	3.4	0.5	2.4	17.5%	0.8
9796	AT5G57510.1 | expressed protein | chr5:23306390-23306782 REVERSE | Aliases: MUA2.8, MUA2_8	3.1	3.4	-0.3	-2.4	17.6%	0.5
9797	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	2.8	3.1	-0.3	-2.4	17.6%	0.4
9798	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	3.4	0.8	2.4	17.6%	1.2
9799	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	7.2	-1.2	-2.4	17.6%	0.7
9800	AT3G10990.1 | F-box family protein, contains TIGRfam:TIGR01640 F-box protein interaction domain | chr3:3446468-3447001 REVERSE | Aliases: F9F8.19	2.9	3.2	-0.3	-2.4	17.6%	0.5
9801	AT2G20180.2 | Symbol: PIL5 | basic helix-loop-helix (bHLH) family protein, contains Pfam domain, PF00010: Helix-loop-helix DNA-binding domain	2.2	2.5	-0.3	-2.4	17.6%	0.3
9802	AT1G29820.1 | expressed protein | chr1:10437646-10440770 FORWARD | Aliases: F1N18.14, F1N18_14	7.1	6.6	0.5	2.4	17.6%	0.9
9803	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	2.8	-0.3	-2.4	17.6%	0.4
9804	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	6.9	6.4	0.5	2.4	17.6%	1.0
9805	AT1G19020.1 | expressed protein | chr1:6568064-6568569 FORWARD | Aliases: F14D16.17, F14D16_17	6.9	7.6	-0.7	-2.4	17.6%	0.9
9806	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	11.5	11.0	0.5	2.4	17.6%	0.4
9807	AT4G08370.1 | proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr4:5301959-5303311 REVERSE | Aliases: T28D5.60, T28D5_60	2.4	2.7	-0.4	-2.4	17.6%	0.1
9808	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	3.1	-0.3	-2.4	17.6%	0.4
9809	AT1G56200.1 | Symbol: EMB1303 | expressed protein | chr1:21034480-21035721 FORWARD | Aliases: EMB1303, EMBRYO DEFECTIVE 1303, F14G9.26, F14G9_26	9.2	8.6	0.6	2.4	17.6%	0.8
9810	AT3G47170.1 | transferase family protein, low similarity to 10-deacetylbaccatin III-10-O-acetyl transferase Taxus cuspidata GI:6746554; contains Pfam profile PF02458 transferase family | chr3:17379657-17381479 REVERSE | Aliases: F13I12.220	3.2	3.5	-0.4	-2.4	17.7%	0.4
9811	AT2G37310.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:15672181-15674154 REVERSE | Aliases: F3G5.10, F3G5_10	3.3	2.9	0.3	2.4	17.7%	0.6

Rank	Description	Sync	Root	M	t	adj.q	B
9812	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	3.1	-0.3	-2.4	17.7%	0.6
9813	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	4.7	-0.4	-2.4	17.7%	0.6
9814	AT1G28190.1 | expressed protein | chr1:9846871-9847910 REVERSE | Aliases: F3H9.15, F3H9_15	3.1	3.6	-0.5	-2.4	17.7%	0.7
9815	AT3G52170.1 | expressed protein | chr3:19357884-19360491 REVERSE | Aliases: T25B15.1	5.1	4.0	1.0	2.4	17.7%	1.1
9816	AT1G33490.1 | expressed protein | chr1:12150675-12152374 REVERSE | Aliases: F10C21.22, F10C21_22	6.0	4.9	1.1	2.4	17.7%	0.9
9817	AT5G05930.2 | guanylyl cyclase-related (GC1), similar to guanylyl cyclase (GC1) GI:21436486 from (Arabidopsis thaliana); identical to cDNA putative guanylate cyclase GI:21436486 | chr5:1780013-1783379 REVERSE | Aliases: K18J17.8, K18J17_8	5.1	5.5	-0.4	-2.4	17.7%	0.9
9818	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	8.7	9.7	-1.0	-2.4	17.7%	0.5
9819	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:At4g29220.1); 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	6.4	0.5	2.4	17.7%	0.8
9820	AT3G10040.1 | expressed protein, est match | chr3:3096420-3098076 REVERSE | Aliases: T22K18.13	6.5	5.5	1.0	2.4	17.7%	1.1
9821	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	3.1	2.8	0.3	2.4	17.7%	0.4
9822	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	4.5	3.9	0.6	2.4	17.7%	0.8
9823	ATCG00160.1 | Symbol: RPS2 | Chloroplast ribosomal protein S2	7.1	6.2	0.9	2.4	17.7%	0.9
9824	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	6.4	5.7	0.7	2.4	17.7%	1.1
9825	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	3.0	-0.3	-2.4	17.7%	0.5
9826	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	6.1	-0.6	-2.4	17.7%	1.0
9827	AT4G16630.1 | DEAD/DEAH box helicase, putative (RH28), identical to cDNA DEAD box RNA helicase, RH28 GI:3776026 | chr4:9362011-9366770 REVERSE | Aliases: DL4340C, FCAALL.424	4.7	3.4	1.3	2.4	17.7%	1.3
9828	AT4G35760.1 | expressed protein | chr4:16942326-16944665 REVERSE | Aliases: F4B14.2	5.4	4.7	0.7	2.4	17.7%	0.9
9829	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	10.1	9.3	0.7	2.4	17.7%	0.9
9830	AT1G12810.1 | proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965 | chr1:4367306-4368800 FORWARD | Aliases: F13K23.6, F13K23_6	5.2	4.4	0.8	2.4	17.7%	0.9
9831	AT1G53790.1 | F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	4.2	4.7	-0.5	-2.4	17.8%	0.9

Rank	Description	Sync	Root	M	t	adj.q	B
9832	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	3.7	3.2	0.5	2.4	17.8%	1.0
9833	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	3.2	0.3	2.4	17.8%	0.6
9834	AT3G13235.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr3:4271343-4274436 REVERSE | Aliases: None	4.7	5.2	-0.5	-2.4	17.8%	0.7
9835	AT5G61370.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:24689022-24690883 REVERSE | Aliases: MFB13.15, MFB13_15	6.1	5.2	1.0	2.4	17.8%	1.1
9836	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 β-oxidation steps of jasmonic acid biosynthesis. | chr5:25404637-25407289 REVERSE | Aliases: K9H21.11, K9H21_11	6.9	6.2	0.6	2.4	17.8%	0.9
9837	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	4.4	4.0	0.4	2.4	17.8%	0.7
9838	AT4G32105.1 | expressed protein | chr4:15513226-15514093 REVERSE | Aliases: None	2.9	3.3	-0.4	-2.4	17.8%	0.6
9839	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	4.1	-0.3	-2.4	17.8%	0.5
9840	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	4.9	4.3	0.7	2.4	17.8%	1.1
9841	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	5.7	4.6	1.1	2.4	17.8%	1.1
9842	AT5G19860.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr5:6714266-6715877 REVERSE | Aliases: T29J13.3	9.0	10.2	-1.2	-2.4	17.8%	1.0
9843	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	6.5	7.0	-0.6	-2.4	17.8%	1.0
9844	AT3G11950.1 | UbiA prenyltransferase family protein, contains Pfam profile PF01040: UbiA prenyltransferase family | chr3:3779845-3785104 REVERSE | Aliases: MEC18.6	6.9	5.7	1.2	2.4	17.8%	1.0
9845	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	5.7	5.3	0.4	2.4	17.8%	0.7
9846	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	4.0	-0.5	-2.4	17.8%	0.8
9847	AT5G02180.1 | amino acid transporter family protein, belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II	2.8	3.1	-0.3	-2.4	17.8%	0.4
9848	AT5G50920.1 | Symbol: CLPC | Similar to ATP-dependent Clp protease ATP-binding subunit / ClpC, almost identical to ClpC GI:2921158 from (Arabidopsis thaliana); 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	9.3	8.8	0.5	2.4	17.8%	0.9
9849	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	4.5	5.0	-0.5	-2.4	17.9%	0.9
9850	AT4G37290.1 | expressed protein | chr4:17549678-17550251 REVERSE | Aliases: F6G17.7	3.6	4.1	-0.5	-2.4	17.9%	0.7
9851	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	3.0	2.8	0.2	2.4	17.9%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
9852	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), Arabidopsis thaliana | chr5:5574284-5575913 REVERSE | Aliases: F2K13.110, F2K13_110	4.3	3.7	0.6	2.4	17.9%	1.0
9853	AT3G44430.1 | expressed protein | chr3:16079244-16080737 FORWARD | Aliases: T22K7.110	3.3	2.8	0.5	2.4	17.9%	0.7
9854	AT1G64500.1 | glutaredoxin family protein | chr1:23956896-23958155 FORWARD | Aliases: F1N19.7, F1N19_7	4.8	5.3	-0.5	-2.4	17.9%	0.7
9855	AT4G16660.1 | heat shock protein 70, putative / HSP70, putative | chr4:9376773-9381529 FORWARD | Aliases: DL4355W, FCAALL.64	5.5	4.5	1.1	2.4	17.9%	1.1
9856	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	4.7	-0.4	-2.4	17.9%	0.5
9857	AT5G19220.1 | Symbol: ADG2 | Encodes the large subunit of ADP-glucose pyrophosphorylase which catalyzes the first, rate limiting step in starch biosynthesis.	2.8	3.2	-0.3	-2.4	17.9%	0.6
9858	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	4.3	5.2	-0.9	-2.4	17.9%	0.8
9859	AT1G71780.1 | expressed protein | chr1:26998748-27000312 REVERSE | Aliases: F14O23.16, F14O23_16	7.1	5.7	1.4	2.4	17.9%	1.1
9860	AT5G13640.1 | Symbol: ATPDAT |	6.8	7.5	-0.6	-2.4	17.9%	0.7
9861	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	3.0	0.4	2.4	18.0%	0.8
9862	AT1G01670.1 | U-box domain-containing protein | chr1:242844-245988 REVERSE | Aliases: T1N6.28, T1N6_28	4.8	5.4	-0.6	-2.4	18.0%	1.0
9863	AT2G41020.2 | WW domain-containing protein, contains Pfam domain PF00397: WW domain | chr2:17124412-17128166 FORWARD | Aliases: AT2G41030, T3K9.21, T3K9_21	3.9	4.2	-0.3	-2.4	18.0%	0.4
9864	AT1G06050.1 | expressed protein | chr1:1830604-1832552 REVERSE | Aliases: T21E18.10, T21E18_10	5.9	6.6	-0.7	-2.4	18.0%	1.1
9865	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	4.9	5.4	-0.5	-2.4	18.0%	0.9
9866	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	8.0	1.0	2.4	18.0%	1.2
9867	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	3.2	3.6	-0.4	-2.4	18.0%	0.9
9868	AT4G14820.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:8507789-8510033 REVERSE | Aliases: DL3450C, FCAALL.330	4.7	4.3	0.4	2.4	18.0%	0.7
9869	AT5G49555.1 | amine oxidase-related, contains Pfam profile PF01593: amine oxidase, flavin-containing | chr5:20124455-20127862 REVERSE | Aliases: None	6.6	5.4	1.2	2.4	18.0%	0.9
9870	NA	8.2	8.8	-0.6	-2.4	18.0%	0.0
9871	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	2.6	2.3	0.2	2.4	18.0%	0.3
9872	AT2G44230.1 | expressed protein | chr2:18293601-18295476 FORWARD | Aliases: F4I1.4	3.1	3.4	-0.3	-2.4	18.1%	0.5
9873	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	7.7	7.2	0.5	2.4	18.1%	0.8

Rank	Description	Sync	Root	M	t	adj.q	B
9874	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	5.5	7.2	-1.6	-2.4	18.1%	0.9
9875	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	2.7	-0.3	-2.4	18.1%	0.3
9876	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	4.6	4.3	0.4	2.4	18.1%	0.7
9877	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	3.5	3.9	-0.4	-2.4	18.1%	0.5
9878	AT4G18000.1 | expressed protein | chr4:9989765-9990148 REVERSE | Aliases: T6K21.180, T6K21_180	3.3	4.0	-0.6	-2.4	18.1%	0.7
9879	AT5G56790.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:22985165-22988756 FORWARD | Aliases: MIK19.26, MIK19_26	7.1	7.6	-0.5	-2.4	18.1%	0.8
9880	AT1G25340.2 | Symbol: MYB116 |	2.8	3.2	-0.3	-2.4	18.1%	0.5
9881	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:AI099566	4.7	5.4	-0.7	-2.4	18.1%	1.0
9882	AT3G30480.1 | hypothetical protein | chr3:12116931-12117470 FORWARD | Aliases: MSJ3.12	2.2	2.4	-0.2	-2.4	18.1%	0.0
9883	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	7.1	6.5	0.6	2.4	18.1%	0.7
9884	AT3G63000.1 | NPL4 family protein, contains Pfam domain, PF05021: NPL4 family | chr3:23294584-23296515 FORWARD | Aliases: T20O10.100	9.2	9.8	-0.6	-2.4	18.1%	0.9
9885	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	6.2	-0.6	-2.4	18.1%	0.7
9886	AT4G14050.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr4:8103640-8105516 REVERSE | Aliases: DL3066C, FCAALL.80	2.7	2.5	0.2	2.4	18.1%	0.3
9887	AT1G52400.2 | Symbol: BGL1 | similar to glycosyl hydrolase family 1 protein [Arabidopsis thaliana] (TAIR:At3g21370.1); similar to glycosyl hydrolase family 1 protein [Arabidopsis thaliana] (TAIR:At3g09260.1); similar to glycosyl hydrolase family 1 protein / anther-specific protein ATA27 [Arabidopsis thaliana] (TAIR:At1g75940.1); similar to beta-glucosidase [Brassica nigra] (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	3.4	2.9	0.4	2.4	18.1%	0.6
9888	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	3.1	2.6	0.5	2.4	18.1%	0.7
9889	AT1G52720.1 | expressed protein | chr1:19644567-19645333 FORWARD | Aliases: F6D8.3, F6D8_3	6.7	5.9	0.8	2.4	18.1%	1.0
9890	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) {Arabidopsis thaliana}; 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	8.9	8.3	0.6	2.4	18.1%	1.0
9891	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	2.7	3.3	-0.6	-2.4	18.1%	0.4
9892	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	6.0	6.6	-0.7	-2.4	18.1%	0.9
9893	AT5G16080.1 | expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873 | chr5:5252318-5253621 REVERSE | Aliases: F1N13.220, F1N13_220	3.5	4.1	-0.6	-2.4	18.2%	1.0

Rank	Description	Sync	Root	M	t	adj.q	B
9894	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	10.1	11.1	-1.0	-2.4	18.2%	1.0
9895	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	10.9	9.3	1.6	2.4	18.2%	0.6
9896	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	4.6	5.2	-0.6	-2.4	18.2%	0.8
9897	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	4.6	-0.8	-2.4	18.2%	0.9
9898	AT5G08210.1 | expressed protein | chr5:2641265-2641761 REVERSE | Aliases: F8L15.6	4.0	4.6	-0.6	-2.4	18.2%	0.7
9899	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	3.5	3.1	0.5	2.4	18.2%	0.8
9900	AT1G06560.1 | NOL1/NOP2/sun family protein, contains Pfam profile PF01189: NOL1/NOP2/sun family | chr1:2007629-2012200 FORWARD | Aliases: F12K11.10, F12K11_10	5.0	4.4	0.6	2.4	18.2%	1.0
9901	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	7.6	6.8	0.7	2.4	18.2%	0.7
9902	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	5.3	4.5	0.8	2.4	18.2%	0.7
9903	AT3G56670.1 | expressed protein, hypothetical proteins - Arabidopsis thaliana | chr3:21000014-21000974 REVERSE | Aliases: T5P19.320	2.2	2.3	-0.1	-2.4	18.2%	-0.2
9904	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	5.0	4.4	0.6	2.4	18.2%	0.8
9905	AT5G45530.1 | expressed protein, contains Pfam domain, PF04578: Protein of unknown function, DUF594 | chr5:18471543-18474504 REVERSE | Aliases: MFC19.20, MFC19_20	3.3	3.8	-0.5	-2.4	18.2%	0.6
9906	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	3.5	3.1	0.4	2.4	18.2%	0.8
9907	AT5G54910.1 | DEAD/DEAH box helicase, putative	5.5	4.4	1.1	2.4	18.2%	1.1
9908	AT1G70540.1 | invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	2.8	3.0	-0.2	-2.4	18.2%	0.1
9909	AT4G32730.2 | Symbol: PC MYB1 | myb family transcription factor, identical to PC-MYB1 GI:5678826 from (Arabidopsis thaliana);	3.7	4.1	-0.4	-2.4	18.3%	0.4
9910	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	3.0	-0.3	-2.4	18.3%	0.4
9911	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	2.8	2.4	0.4	2.4	18.3%	0.6
9912	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	7.1	7.9	-0.8	-2.4	18.3%	0.6
9913	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	3.4	3.0	0.3	2.4	18.3%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
9914	AT3G19530.1 | expressed protein | chr3:6775271-6775555 REVERSE | Aliases: T31J18.3	2.8	3.2	-0.4	-2.4	18.3%	0.4
9915	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	3.6	3.2	0.4	2.4	18.3%	0.8
9916	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	3.4	-0.5	-2.4	18.3%	0.8
9917	AT5G18310.2 | expressed protein, predicted proteins, Drosophila melanogaster | chr5:6061734-6063024 FORWARD | Aliases: F20L16.30, F20L16_30	9.4	10.0	-0.6	-2.4	18.3%	0.3
9918	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	2.9	-0.2	-2.4	18.3%	0.3
9919	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)	3.9	4.5	-0.5	-2.4	18.3%	0.8
9920	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	5.2	4.7	0.6	2.4	18.3%	0.9
9921	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	6.4	5.5	0.9	2.4	18.4%	1.0
9922	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	3.2	-0.3	-2.4	18.4%	0.6
9923	AT1G76210.1 | expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function | chr1:28599844-28600776 REVERSE | Aliases: T23E18.14, T23E18_14	2.9	3.4	-0.5	-2.4	18.4%	0.7
9924	AT4G37320.1 | Symbol: CYP81D5 | cytochrome P450 family protein | chr4:17559574-17561690 REVERSE | Aliases: F6G17.8	7.7	8.1	-0.5	-2.4	18.4%	0.6
9925	AT4G19140.1 | expressed protein | chr4:10469675-10472152 FORWARD | Aliases: T18B16.110, T18B16_110	7.2	7.6	-0.4	-2.4	18.4%	0.7
9926	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	3.4	3.8	-0.4	-2.4	18.4%	0.6
9927	AT3G44050.1 | kinesin motor protein-related, KLP2 protein, Xenopus laevis, PIR:T30335 | chr3:15829725-15835848 FORWARD | Aliases: F26G5.1	5.1	4.4	0.6	2.4	18.4%	0.7
9928	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	5.7	6.6	-0.9	-2.4	18.4%	0.8
9929	AT1G30810.1 | transcription factor jumonji (jmj) 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: jmjN domain and PF02373: jmjC domain; intron between exons 6 and 7 was required to circumvent a frameshift. There could be an underlying sequence error.	4.1	4.6	-0.5	-2.4	18.5%	0.8
9930	AT3G51610.1 | expressed protein | chr3:19150536-19153057 REVERSE | Aliases: T18N14.2	8.0	7.1	0.9	2.4	18.5%	1.0
9931	AT5G03700.1 | PAN domain-containing protein, contains Pfam profile: PF00024 PAN domain	5.0	5.5	-0.5	-2.4	18.5%	0.9
9932	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	4.4	-0.4	-2.4	18.5%	0.5
9933	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	3.2	-0.5	-2.4	18.5%	0.3

Rank	Description	Sync	Root	M	t	adj.q	B
9934	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	9.9	-0.5	-2.4	18.5%	0.4
9935	AT5G55960.1 | expressed protein | chr5:22679802-22682259 FORWARD | Aliases: MYN21.7, MYN21_7	3.6	4.0	-0.5	-2.4	18.5%	0.7
9936	AT3G54030.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:20021931-20024671 FORWARD | Aliases: F5K20.330	4.7	5.3	-0.6	-2.4	18.5%	0.6
9937	AT1G03900.1 | Symbol: ATNAP4 |	7.4	8.0	-0.5	-2.4	18.5%	0.9
9938	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	2.2	0.3	2.4	18.5%	0.5
9939	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	5.4	4.3	1.1	2.4	18.5%	0.9
9940	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	4.6	0.6	2.4	18.5%	1.1
9941	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	8.2	6.0	2.1	2.4	18.5%	1.1
9942	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	6.5	7.1	-0.6	-2.4	18.5%	0.7
9943	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	7.3	8.4	-1.1	-2.4	18.5%	0.8
9944	AT1G15430.2 | expressed protein | chr1:5304454-5306007 FORWARD | Aliases: F9L1.39, F9L1_39	7.5	6.4	1.1	2.4	18.6%	1.0
9945	AT2G29390.3 | Symbol: SMO2 1 |	6.7	5.4	1.3	2.4	18.6%	1.0
9946	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	3.7	4.1	-0.4	-2.4	18.6%	0.5
9947	AT4G08820.1 | hypothetical protein | chr4:5621761-5623206 FORWARD | Aliases: T32A17.130, T32A17_130	3.7	4.2	-0.5	-2.4	18.6%	0.5
9948	AT1G77360.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:29076877-29078322 REVERSE | Aliases: F2P24.7, F2P24_7	4.3	3.7	0.5	2.4	18.6%	0.7
9949	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	3.1	-0.3	-2.4	18.6%	0.3
9950	AT3G28740.1 | cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450 | chr3:10789935-10791790 REVERSE | Aliases: T19N8.17	6.2	5.6	0.6	2.4	18.6%	0.7
9951	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	6.2	5.6	0.6	2.4	18.6%	0.8
9952	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	9.1	7.8	1.3	2.4	18.7%	1.0
9953	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	8.2	9.0	-0.8	-2.4	18.7%	0.6
9954	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	3.3	-0.3	-2.4	18.7%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
9955	AT5G58950.1 | protein kinase family protein, concontains protein kinase domain, Pfam:PF00069 | chr5:23818154-23820868 REVERSE | Aliases: K19M22.20, K19M22_20	8.3	8.8	-0.6	-2.4	18.7%	0.8
9956	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	3.7	-0.4	-2.4	18.7%	0.4
9957	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	2.6	0.3	2.4	18.7%	0.2
9958	AT5G44150.1 | expressed protein | chr5:17780911-17782328 REVERSE | Aliases: MLN1.7, MLN1_7	5.8	5.3	0.6	2.4	18.7%	0.9
9959	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	3.4	3.8	-0.4	-2.4	18.7%	0.4
9960	NA	9.4	7.3	2.2	2.4	18.7%	1.2
9961	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	2.2	0.3	2.4	18.7%	0.3
9962	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	9.2	10.0	-0.7	-2.4	18.7%	0.6
9963	AT2G47700.1 | zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type(RING finger)	4.6	5.5	-0.9	-2.4	18.8%	0.9
9964	AT2G25540.1 | Symbol: CESA10 |	2.9	3.3	-0.4	-2.4	18.8%	0.4
9965	AT4G14900.1 | hydroxyproline-rich glycoprotein family protein | chr4:8521517-8523700 REVERSE | Aliases: DL3490C, FCAALL.410	5.8	6.7	-0.9	-2.4	18.8%	0.8
9966	AT3G30350.1 | expressed protein | chr3:11962896-11964265 REVERSE | Aliases: T6J22.14	2.8	3.1	-0.3	-2.4	18.8%	-0.0
9967	AT1G75310.1 | Symbol: AUL1 | DNAJ 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	5.7	6.2	-0.5	-2.4	18.8%	0.9
9968	AT2G17033.2 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:7408275-7410728 FORWARD | Aliases: None	4.2	3.6	0.5	2.4	18.8%	0.9
9969	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	3.1	3.8	-0.7	-2.4	18.8%	0.6
9970	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	3.9	-0.8	-2.4	18.8%	0.9
9971	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	3.8	3.3	0.6	2.4	18.8%	1.0
9972	AT5G25860.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.5	3.9	-0.4	-2.4	18.8%	0.6
9973	AT4G17810.1 | similar to zinc finger (C2H2 type) family protein [Arabidopsis thaliana] (TAIR:At2g37740.1); similar to OSJNBa0086O06.19 [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	2.5	2.9	-0.4	-2.4	18.8%	0.4
9974	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	3.1	3.6	-0.5	-2.4	18.8%	0.7
9975	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	8.3	9.2	-0.9	-2.4	18.8%	0.6
9976	AT4G05570.1 | expressed protein | chr4:2839609-2840634 REVERSE | Aliases: T1J24.5, T1J24_5	3.0	3.3	-0.3	-2.4	18.8%	0.3

Rank	Description	Sync	Root	M	t	adj.q	B
9977	AT5G54880.1 | DTW domain-containing protein, contains Pfam domain, PF03942: DTW domain	3.5	3.1	0.4	2.4	18.9%	0.6
9978	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	8.1	8.7	-0.6	-2.4	18.9%	0.7
9979	AT2G44710.1 | RNA recognition motif (RRM)-containing protein | chr2:18439794-18444207 FORWARD | Aliases: F16B22.20	3.3	3.6	-0.3	-2.4	18.9%	0.3
9980	AT2G17750.1 | hypothetical protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function | chr2:7716320-7718233 REVERSE | Aliases: T17A5.3, T17A5_3	2.3	2.5	-0.2	-2.4	18.9%	-0.1
9981	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	3.5	-0.6	-2.4	18.9%	0.8
9982	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	3.2	-0.5	-2.4	18.9%	0.5
9983	ATCG00820.1 | Symbol: RPS19 | Encodes a 6.8-kDa protein of the small ribosomal subunit. | chrC:84005-84283 REVERSE | Aliases: RPS19	11.4	9.7	1.7	2.4	18.9%	0.6
9984	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	7.9	-1.0	-2.4	18.9%	1.1
9985	AT5G17160.1 | expressed protein | chr5:5639648-5642515 REVERSE | Aliases: F2K13.310, F2K13_310	4.3	4.8	-0.5	-2.4	18.9%	0.8
9986	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	9.5	9.1	0.4	2.4	19.0%	0.5
9987	AT1G50730.1 | expressed protein | chr1:18798943-18806931 FORWARD | Aliases: F4M15.4, F4M15_4	4.6	5.2	-0.6	-2.4	19.0%	1.0
9988	AT3G19460.1 | reticulon family protein (RTNLB11), weak similarity to neuroendocrine-specific protein C (Homo sapiens) GI:307311; identical to cDNA RTNLB11 GI:32331878	5.6	5.2	0.4	2.4	19.0%	0.7
9989	AT1G11200.1 | expressed protein, contains Pfam profile PF03619: Domain of unknown function | chr1:3753365-3755638 FORWARD | Aliases: T28P6.25	5.8	5.1	0.6	2.4	19.0%	0.8
9990	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	2.1	-0.2	-2.4	19.0%	-0.3
9991	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	2.4	2.6	-0.2	-2.4	19.0%	0.2
9992	AT1G69260.1 | expressed protein | chr1:26042825-26044751 FORWARD | Aliases: F4N2.22, F4N2_22	7.6	8.5	-0.9	-2.4	19.0%	0.9
9993	AT1G51540.1 | kelch repeat-containing protein, contains Pfam profile PF01344: Kelch motif | chr1:19117052-19121734 FORWARD | Aliases: F5D21.24, F5D21_24	6.5	6.0	0.5	2.4	19.0%	0.7
9994	AT2G21620.2 | Symbol: RD2 | universal stress protein (USP) family protein / responsive to dessication 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	8.8	9.9	-1.1	-2.4	19.0%	0.9
9995	AT5G24440.1 | Symbol: CID13 | RNA-binding protein, putative. Contains PAM2, PABC binding domain. | chr5:8345405-8347779 REVERSE | Aliases: CID13, T31K7.2, T31K7_2	3.1	3.5	-0.4	-2.4	19.0%	0.4
9996	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	3.5	2.7	0.8	2.4	19.0%	0.7
9997	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	9.4	8.6	0.8	2.4	19.0%	0.9
9998	AT1G35610.1 | DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain | chr1:13143128-13144966 REVERSE | Aliases: F15O4.27	3.3	3.7	-0.3	-2.4	19.0%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
9999	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	4.4	-0.6	-2.4	19.0%	1.0
10000	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	11.6	10.4	1.2	2.4	19.1%	0.6
10001	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	4.1	3.4	0.7	2.4	19.1%	1.0
10002	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	2.7	3.0	-0.3	-2.4	19.1%	0.3
10003	AT1G71080.1 | expressed protein | chr1:26813503-26815427 REVERSE | Aliases: F23N20.7, F23N20_7	8.4	7.4	1.0	2.4	19.1%	0.9
10004	AT3G23310.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr3:8339044-8343639 FORWARD | Aliases: MLM24.2	4.6	4.1	0.5	2.4	19.1%	0.7
10005	AT4G25200.1 | Symbol: ATHSP23.6 MITO |	3.6	3.0	0.5	2.4	19.1%	0.9
10006	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)	7.5	6.2	1.4	2.4	19.1%	1.2
10007	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	2.8	-0.4	-2.4	19.1%	0.4
10008	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	4.1	5.0	-0.9	-2.4	19.1%	1.1
10009	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	2.9	3.3	-0.4	-2.4	19.1%	0.5
10010	AT3G10310.1 | kinesin motor protein-related, similar to carboxy-terminal kinesin 2 GB:P79955 (Xenopus laevis) | chr3:3190213-3195010 FORWARD | Aliases: F14P13.9	2.6	2.8	-0.2	-2.4	19.1%	0.1
10011	AT1G75550.1 | glycine-rich protein | chr1:28373098-28373601 REVERSE | Aliases: F10A5.23, F10A5_23	3.6	4.3	-0.7	-2.4	19.1%	0.7
10012	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	4.1	4.9	-0.8	-2.4	19.1%	0.9
10013	AT3G63220.2 | kelch repeat-containing F-box family protein, contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	5.4	5.9	-0.5	-2.4	19.1%	0.8
10014	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	3.5	3.0	0.5	2.4	19.2%	0.3
10015	AT1G27640.1 | expressed protein | chr1:9614450-9614893 REVERSE | Aliases: T22C5.9	4.3	4.9	-0.6	-2.4	19.2%	0.7
10016	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	5.4	4.8	0.6	2.4	19.2%	1.0
10017	AT5G37040.1 | F-box family protein, contains Pfam profile: PF00646 F-box domain | chr5:14656365-14657164 FORWARD | Aliases: MJG14.2, MJG14_2	3.8	4.4	-0.6	-2.4	19.2%	0.8
10018	AT2G17660.1 | nitrate-responsive NOI protein, putative, similar to nitrate-induced NOI protein (Zea mays) GI:2642213 | chr2:7680364-7680794 FORWARD | Aliases: T17A5.20, T17A5_20	3.8	4.8	-1.0	-2.4	19.2%	0.9
10019	AT5G10840.1 | endomembrane protein 70, putative, TM4 family; | chr5:3424911-3427835 REVERSE | Aliases: T30N20.110, T30N20_110	7.7	6.4	1.3	2.4	19.2%	1.0
10020	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	3.7	4.2	-0.5	-2.4	19.2%	0.7

Rank	Description	Sync	Root	M	t	adj.q	B
10021	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	2.7	-0.5	-2.4	19.2%	0.8
10022	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	2.5	-0.2	-2.4	19.2%	-0.1
10023	AT3G18160.2 | peroxin-3 family protein, contains Pfam domain, PF04882: Peroxin-3 | chr3:6220632-6223079 FORWARD | Aliases: MRC8.15	5.4	5.0	0.5	2.4	19.2%	0.5
10024	AT3G50570.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich protein domains, INTERPRO:IPR000694 | chr3:18777730-18778510 REVERSE | Aliases: T20E23.170	2.8	3.0	-0.2	-2.4	19.2%	-0.2
10025	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	3.6	-0.4	-2.4	19.2%	0.6
10026	AT3G58620.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain | chr3:21691303-21694112 FORWARD | Aliases: F14P22.210	5.5	6.2	-0.7	-2.4	19.3%	0.9
10027	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	2.6	-0.3	-2.4	19.3%	-0.0
10028	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	4.0	-0.3	-2.4	19.3%	0.6
10029	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	3.5	-0.6	-2.4	19.3%	0.4
10030	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	3.1	-0.4	-2.4	19.3%	0.3
10031	AT1G05600.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat | chr1:1672098-1673747 FORWARD | Aliases: F3F20.5, F3F20_5	6.5	5.7	0.7	2.4	19.3%	1.0
10032	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	6.0	5.1	0.9	2.4	19.3%	0.9
10033	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	4.1	3.4	0.7	2.3	19.3%	0.7
10034	AT5G24630.1 | expressed protein, ; expression supported by MPSS | chr5:8432526-8436173 REVERSE | Aliases: K18P6.17, K18P6_17	5.3	4.2	1.2	2.3	19.3%	1.0
10035	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	4.9	0.5	2.3	19.4%	0.7
10036	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	3.8	0.3	2.3	19.4%	0.5
10037	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	2.6	2.9	-0.3	-2.3	19.4%	0.4
10038	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	4.3	5.5	-1.1	-2.3	19.4%	1.1
10039	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	2.6	-0.3	-2.3	19.4%	0.3

Rank	Description	Sync	Root	M	t	adj.q	B
10040	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 pI (InterPro:IPR005795); contains InterPro domain Expansin/Lol pI (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	7.1	6.3	0.9	2.3	19.4%	0.7
10041	AT2G44870.1 | expressed protein | chr2:18510213-18511755 FORWARD | Aliases: T13E15.12	6.8	6.2	0.6	2.3	19.4%	0.7
10042	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	4.7	5.2	-0.5	-2.3	19.4%	0.9
10043	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	10.4	9.6	0.8	2.3	19.4%	0.7
10044	AT5G14940.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr5:4831751-4834315 REVERSE | Aliases: F2G14.60, F2G14_60	5.2	5.7	-0.6	-2.3	19.4%	0.7
10045	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	6.3	5.2	1.1	2.3	19.4%	1.1
10046	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	3.3	-0.3	-2.3	19.4%	0.4
10047	AT1G53560.1 | expressed protein | chr1:19988423-19989649 REVERSE | Aliases: F22G10.10	5.5	6.1	-0.6	-2.3	19.4%	0.8
10048	AT1G79660.1 | expressed protein | chr1:29980756-29981666 FORWARD | Aliases: F20B17.9, F20B17_9	10.5	9.7	0.8	2.3	19.5%	0.2
10049	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	9.3	8.6	0.8	2.3	19.5%	0.7
10050	AT3G03840.1 | auxin-responsive protein, putative, similar to auxin-inducible SAUR (Small Auxin Up RNAs) (GI:3043536) (Raphanus sativus) | chr3:981079-981805 FORWARD | Aliases: F20H23.14, F20H23_14	2.1	2.2	-0.1	-2.3	19.5%	-0.5
10051	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	4.2	-0.5	-2.3	19.5%	0.6
10052	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.	5.3	6.0	-0.7	-2.3	19.5%	1.0
10053	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	4.5	-0.7	-2.3	19.5%	1.0
10054	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	4.9	4.5	0.4	2.3	19.5%	0.5
10055	AT2G32640.2 | expressed protein | chr2:13853996-13857978 REVERSE | Aliases: T26B15.22	3.1	2.8	0.3	2.3	19.5%	0.5
10056	AT1G76580.1 | similar to squamosa promoter-binding protein-like 1 (SPL1) [Arabidopsis thaliana] (TAIR:At2g47070.1); similar to putative SBP-domain protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470314.1); contains domain SER_RICH (PS50324) | chr1:28740222-28743811 FORWARD | Aliases: F14G6.18, F14G6_18	4.0	4.3	-0.3	-2.3	19.5%	0.3
10057	AT2G11010.1 | hypothetical protein | chr2:4368951-4373001 FORWARD | Aliases: F15K19.8, F15K19_8	2.6	2.9	-0.2	-2.3	19.5%	0.2
10058	AT3G57940.1 | expressed protein, contains Pfam profile PF05127: Putative ATPase (DUF699) | chr3:21460275-21466938 FORWARD | Aliases: T10K17.150	4.4	3.7	0.7	2.3	19.5%	1.1
10059	AT3G47530.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:17528367-17530142 REVERSE | Aliases: F1P2.80	5.0	4.6	0.4	2.3	19.5%	0.7

Rank	Description	Sync	Root	M	t	adj.q	B
10060	AT1G45160.1 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr1:17086006-17092717 REVERSE | Aliases: F27F5.23, F27F5_23	6.0	6.7	-0.7	-2.3	19.5%	0.8
10061	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	4.1	3.6	0.5	2.3	19.5%	0.5
10062	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	5.3	6.8	-1.5	-2.3	19.5%	1.0
10063	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)	2.9	2.7	0.3	2.3	19.5%	0.3
10064	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	4.5	4.0	0.5	2.3	19.5%	0.6
10065	AT5G35890.1 | expressed protein | chr5:14043093-14043956 REVERSE | Aliases: MIK22.20, MIK22_20	2.0	2.2	-0.2	-2.3	19.5%	-0.2
10066	NA	3.3	3.9	-0.6	-2.3	19.5%	0.6
10067	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	11.2	0.4	2.3	19.6%	0.2
10068	AT1G79720.1 | aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease | chr1:30002020-30003938 REVERSE | Aliases: F19K16.30, F19K16_30	3.6	3.3	0.3	2.3	19.6%	0.6
10069	AT1G77690.1 | amino acid permease, putative, similar to AUX1 (regulator of root gravitropism, putative permease) GI:1531758 GB:CAA67308 from (Arabidopsis thaliana); contains Pfam profile PF01490: Transmembrane amino acid transporter protein | chr1:29205835-29208234 REVERSE | Aliases: T32E8.2, T32E8_2	5.6	6.5	-0.9	-2.3	19.6%	0.8
10070	AT5G25070.1 | expressed protein | chr5:8641001-8643494 REVERSE | Aliases: T11H3.80, T11H3_80	6.0	6.6	-0.7	-2.3	19.6%	0.9
10071	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	6.8	5.9	0.8	2.3	19.6%	0.7
10072	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	6.3	-0.8	-2.3	19.6%	0.9
10073	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	3.4	0.4	2.3	19.6%	0.6
10074	AT2G24430.2 | no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;	2.6	2.9	-0.3	-2.3	19.6%	0.4
10075	AT5G22580.1 | expressed protein | chr5:7502681-7503448 FORWARD | Aliases: MQJ16.12, MQJ16_12	2.9	3.3	-0.4	-2.3	19.6%	0.5
10076	AT4G21060.1 | galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase | chr4:11240741-11244871 FORWARD | Aliases: T13K14.220, T13K14_220	4.7	5.6	-1.0	-2.3	19.6%	1.0
10077	AT5G02040.2 | prenylated rab acceptor (PRA1) family protein, contains Pfam PF03208: PRA1 family protein | chr5:400896-402873 FORWARD | Aliases: T7H20.90, T7H20_90	4.3	5.0	-0.7	-2.3	19.6%	0.9
10078	AT3G19870.1 | expressed protein | chr3:6907487-6911239 FORWARD | Aliases: MPN9.11	5.0	5.5	-0.5	-2.3	19.6%	0.7
10079	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: T27I1.9, T27I1_9	4.6	3.8	0.9	2.3	19.6%	1.1
10080	AT4G18610.1 | expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640) | chr4:10250709-10251553 FORWARD | Aliases: F28A21.20, F28A21_20	5.4	5.9	-0.5	-2.3	19.6%	0.9
10081	AT5G28240.1 | expressed protein, predicted proteins, Arabidopsis thaliana | chr5:10216257-10216787 FORWARD | Aliases: T8M17.10, T8M17_10	2.8	3.1	-0.3	-2.3	19.6%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
10082	AT1G61350.1 | armadillo/beta-catenin repeat family protein, armadillo/beta-catenin-like repeats, Pfam:PF00514 | chr1:22637547-22639559 FORWARD | Aliases: T1F9.16, T1F9_16	5.3	4.7	0.6	2.3	19.6%	1.0
10083	AT1G60030.1 | xanthine/uracil permease family protein, contains Pfam profile: PF00860 permease family | chr1:22117531-22120510 REVERSE | Aliases: T2K10.8, T2K10_8	3.6	4.1	-0.4	-2.3	19.6%	0.6
10084	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	2.6	-0.2	-2.3	19.6%	-0.0
10085	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	2.6	2.4	0.2	2.3	19.6%	0.2
10086	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	6.7	0.4	2.3	19.6%	0.7
10087	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	3.5	-0.4	-2.3	19.6%	0.7
10088	AT2G04420.1 | expressed protein | chr2:1535486-1536247 FORWARD | Aliases: T1O3.17, T1O3_17	2.1	2.4	-0.2	-2.3	19.7%	-0.4
10089	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	6.7	5.8	0.9	2.3	19.7%	0.9
10090	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	6.4	6.9	-0.6	-2.3	19.7%	0.5
10091	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	2.7	3.0	-0.3	-2.3	19.7%	0.1
10092	AT2G22570.2 | isochorismatase hydrolase family protein, contains Pfam profile PF00857: isochorismatase family protein | chr2:9596629-9597937 REVERSE | Aliases: F14M13.1	5.3	5.9	-0.5	-2.3	19.7%	0.9
10093	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	3.6	-0.3	-2.3	19.7%	0.4
10094	AT5G50990.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr5:20756972-20758507 FORWARD | Aliases: K3K7.15, K3K7_15	4.9	4.3	0.7	2.3	19.8%	0.9
10095	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	5.9	5.3	0.7	2.3	19.8%	1.0
10096	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 scienitific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.	2.7	3.1	-0.4	-2.3	19.8%	0.4
10097	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	6.5	5.7	0.9	2.3	19.8%	0.9
10098	AT2G44660.1 | ALG6, ALG8 glycosyltransferase family protein, similar to SP:P40351 Dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase (EC 2.4.1.-) (Dolichyl-P-Glc:Glc1Man9GlcNAc2-PP-dolichyl glucosyltransferase) {Saccharomyces cerevisiae}; contains Pfam profile PF03155: ALG6, ALG8 glycosyltransferase family | chr2:18428171-18429902 REVERSE | Aliases: F16B22.15	3.8	3.3	0.5	2.3	19.8%	0.4
10099	AT1G19000.2 | myb family transcription factor, similar to MybSt1 GI:7705206 from (Solanum tuberosum) | chr1:6560783-6562772 REVERSE | Aliases: F14D16.15, F14D16_15	6.7	7.9	-1.2	-2.3	19.8%	0.9

Rank	Description	Sync	Root	M	t	adj.q	B
10100	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)	6.3	5.6	0.7	2.3	19.8%	0.9
10101	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	6.3	5.6	0.7	2.3	19.8%	0.9
10102	AT4G02810.1 | expressed protein | chr4:1256173-1257212 FORWARD | Aliases: T5J8.13, T5J8_13	4.9	5.7	-0.8	-2.3	19.8%	1.0
10103	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	8.8	8.0	0.8	2.3	19.8%	0.8
10104	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	2.5	2.7	-0.2	-2.3	19.8%	0.1
10105	AT3G63510.1 | nitrogen regulation family protein, contains Pfam domain PF01207: Dihydrouridine synthase (Dus); similar to (SP:P45672) NIFR3-like protein (SP:P45672) (Azospirillum brasilense)	3.6	3.3	0.3	2.3	19.8%	0.5
10106	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	4.4	3.9	0.6	2.3	19.9%	0.8
10107	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	3.4	0.5	2.3	19.9%	0.8
10108	AT2G44250.1 | expressed protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function | chr2:18300533-18302612 FORWARD | Aliases: F4I1.6	2.1	2.2	-0.1	-2.3	19.9%	-0.3
10109	AT4G33550.1 | similar to protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] (TAIR:At4g30880.1); similar to seed specific protein Bn15D18B [Brassica napus] (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	4.8	5.6	-0.8	-2.3	19.9%	1.0
10110	AT5G53510.1 | Symbol: ATOPT9 |	2.9	3.3	-0.4	-2.3	19.9%	0.5
10111	AT4G34310.2 | expressed protein | chr4:16414117-16419732 FORWARD | Aliases: F10M10.80, F10M10_80	3.5	4.0	-0.5	-2.3	19.9%	0.8
10112	AT2G41230.1 | expressed protein | chr2:17202004-17202752 REVERSE | Aliases: F13H10.22, F13H10_22	7.6	8.3	-0.8	-2.3	19.9%	0.6
10113	AT5G41050.1 | expressed protein | chr5:16450545-16451546 REVERSE | Aliases: MEE6.12, MEE6_12	2.9	3.4	-0.5	-2.3	19.9%	0.6
10114	AT5G58530.1 | glutaredoxin family protein | chr5:23677612-23678575 FORWARD | Aliases: MQJ2.15, MQJ2_15	4.6	4.3	0.3	2.3	19.9%	0.2
10115	AT5G13760.1 | expressed protein, similar to unknown protein (gb AAF63775.1) | chr5:4442017-4444938 FORWARD | Aliases: MXE10.1, MXE10_1	4.3	3.6	0.7	2.3	19.9%	0.9
10116	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	6.3	5.2	1.1	2.3	19.9%	0.8
10117	AT4G17120.1 | expressed protein | chr4:9615997-9624221 REVERSE | Aliases: DL4595C, FCAALL.360	3.5	3.8	-0.3	-2.3	19.9%	0.2
10118	AT5G46850.1 | expressed protein, ; expression supported by MPSS | chr5:19027941-19029237 FORWARD | Aliases: MSD23.3, MSD23_3	4.8	4.3	0.4	2.3	19.9%	0.8
10119	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	3.6	3.3	0.3	2.3	19.9%	0.3
10120	AT1G08030.1 | expressed protein | chr1:2490951-2491919 REVERSE | Aliases: T6D22.29, T6D22_29	3.5	3.9	-0.4	-2.3	19.9%	0.4
10121	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	5.5	4.8	0.7	2.3	19.9%	1.1

Rank	Description	Sync	Root	M	t	adj.q	B
10122	AT5G45960.1 | GDSL-motif lipase/hydrolase family protein | chr5:18654250-18657585 REVERSE | Aliases: K15I22.16, K15I22_16	2.4	2.7	-0.3	-2.3	20.0%	-0.1
10123	AT1G80000.2 | expressed protein, identical to unknown protein GB:AAD55481 (Arabidopsis thaliana) | chr1:30097822-30102058 FORWARD | Aliases: F19K16.3, F19K16_3	3.4	3.9	-0.5	-2.3	20.0%	0.7
10124	AT2G42910.1 | ribose-phosphate pyrophosphokinase 4 / phosphoribosyl diphosphate synthetase 4 (PRS4), identical to phosphoribosyl diphosphate synthase (prs4) (Arabidopsis thaliana) GI:4902472	8.7	6.8	1.9	2.3	20.0%	1.1
10125	AT1G24450.1 | ribonuclease III family protein, contains similarity to Swiss-Prot:P51837 ribonuclease III (EC 3.1.26.3) (RNase III) (Coxiella burnetii)	5.7	4.8	0.9	2.3	20.0%	0.9
10126	AT3G46800.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.4	2.7	-0.2	-2.3	20.1%	0.2
10127	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	4.9	4.3	0.6	2.3	20.1%	0.6
10128	AT3G13740.1 | URF 4-related, similar to URF 4 (GI:49224) (Swiss-Prot:Q05370)(Synechococcus sp.) | chr3:4504278-4506243 FORWARD | Aliases: MMM17.16	5.0	4.5	0.6	2.3	20.1%	0.9
10129	AT2G20240.1 | expressed protein | chr2:8734713-8737581 REVERSE | Aliases: F11A3.21, F11A3_21	2.8	2.6	0.3	2.3	20.1%	0.3
10130	AT1G35210.1 | expressed protein | chr1:12896630-12897380 REVERSE | Aliases: T32G9.25, T32G9_25	3.5	3.8	-0.3	-2.3	20.1%	0.3
10131	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	3.3	0.3	2.3	20.1%	0.1
10132	AT5G64290.1 | oxoglutarate/malate translocator, putative, similar to SWISS-PROT:Q41364 2-oxoglutarate/malate translocator, chloroplast precursor. (Spinach){Spinacia oleracea}	7.6	5.7	1.9	2.3	20.1%	1.0
10133	AT5G23550.1 | expressed protein | chr5:7939614-7941631 REVERSE | Aliases: MQM1.18, MQM1_18	4.8	4.0	0.8	2.3	20.1%	0.7
10134	AT3G42910.1 | expressed protein, ; expression supported by MPSS | chr3:14985091-14988749 REVERSE | Aliases: F18P9.70	2.5	2.8	-0.3	-2.3	20.1%	0.1
10135	AT2G24620.1 | S-locus glycoprotein family protein, contains Pfam profile: PF00954 S-locus glycoprotein family | chr2:10470155-10470628 REVERSE | Aliases: F25P17.8, F25P17_8	2.7	3.0	-0.3	-2.3	20.1%	-0.0
10136	AT2G06390.1 | expressed protein | chr2:2516583-2516709 REVERSE | Aliases: F18P14.18, F18P14_18	1.5	3.0	-1.5	-2.3	20.1%	1.0
10137	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.	4.7	4.1	0.6	2.3	20.1%	1.1
10138	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	4.7	4.2	0.6	2.3	20.1%	0.7
10139	AT1G44030.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	3.1	-0.3	-2.3	20.1%	0.5
10140	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	5.9	6.4	-0.5	-2.3	20.1%	0.4
10141	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	2.2	2.5	-0.3	-2.3	20.1%	0.1
10142	AT5G39950.1 | Symbol: ATTRX2 |	11.0	10.1	0.9	2.3	20.1%	0.8
10143	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	6.6	7.2	-0.6	-2.3	20.1%	0.7
10144	AT3G55350.1 | expressed protein | chr3:20529450-20531792 FORWARD | Aliases: T22E16.10	4.0	3.6	0.3	2.3	20.1%	0.4

Rank	Description	Sync	Root	M	t	adj.q	B
10145	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	7.4	8.1	-0.7	-2.3	20.2%	0.7
10146	AT2G24230.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:10308897-10311892 REVERSE | Aliases: F27D4.14, F27D4_14	3.7	3.4	0.3	2.3	20.2%	0.6
10147	AT1G77720.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:29215415-29218973 FORWARD | Aliases: T32E8.5, T32E8_5	2.7	2.5	0.2	2.3	20.2%	0.1
10148	AT3G02740.1 | aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease | chr3:590517-593174 FORWARD | Aliases: F13E7.32, F13E7_32	9.2	9.7	-0.4	-2.3	20.2%	0.4
10149	AT3G54750.2 | expressed protein | chr3:20275683-20279726 REVERSE | Aliases: T5N23.110	6.6	5.6	1.0	2.3	20.2%	1.0
10150	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	2.9	-0.2	-2.3	20.2%	0.2
10151	AT1G79110.2 | expressed protein | chr1:29764079-29765597 FORWARD | Aliases: YUP8H12R.27, YUP8H12R_27	5.1	6.0	-0.9	-2.3	20.2%	0.8
10152	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	3.3	-0.3	-2.3	20.2%	0.4
10153	AT1G79140.1 | expressed protein | chr1:29777505-29778801 REVERSE | Aliases: YUP8H12R.47, YUP8H12R_47	3.2	2.8	0.4	2.3	20.2%	0.5
10154	AT4G08230.1 | glycine-rich protein | chr4:5187853-5189637 REVERSE | Aliases: T12G13.70, T12G13_70	7.9	8.4	-0.5	-2.3	20.2%	0.8
10155	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	10.5	11.1	-0.6	-2.3	20.2%	0.8
10156	AT5G46910.1 | transcription factor jumonji (jmj) family protein, contains Pfam domains PF02375: jmjN domain and PF02373: jmjC domain | chr5:19065007-19068107 FORWARD | Aliases: MQD22.4, MQD22_4	4.5	5.3	-0.8	-2.3	20.2%	0.9
10157	AT1G19730.1 | Symbol: ATTRX4 |	5.9	5.5	0.4	2.3	20.2%	0.7
10158	AT5G60550.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:24356455-24359719 FORWARD | Aliases: MUF9.13, MUF9_13	6.8	7.8	-1.1	-2.3	20.2%	1.0
10159	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	9.9	9.6	0.3	2.3	20.2%	0.2
10160	AT3G54680.1 | proteophosphoglycan-related, contains similarity to proteophosphoglycan (Leishmania major) gi:5420389:emb:CAB46680 | chr3:20255367-20257051 FORWARD | Aliases: T5N23.40	3.2	3.6	-0.4	-2.3	20.2%	0.5
10161	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	6.3	5.3	1.0	2.3	20.2%	1.0
10162	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	2.7	-0.2	-2.3	20.2%	-0.0
10163	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	3.8	3.5	0.3	2.3	20.2%	0.6
10164	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	3.2	0.5	2.3	20.2%	0.6

Rank	Description	Sync	Root	M	t	adj.q	B
10165	AT3G54310.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr3:20122131-20123922 REVERSE | Aliases: F24B22.270	2.9	3.2	-0.3	-2.3	20.2%	0.1
10166	AT4G32130.1 | expressed protein | chr4:15520037-15522589 REVERSE | Aliases: F10N7.60, F10N7_60	4.8	2.8	2.0	2.3	20.2%	1.2
10167	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	4.4	-0.6	-2.3	20.2%	0.7
10168	AT2G42610.2 | expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640) | chr2:17754994-17757517 FORWARD | Aliases: F14N22.12, F14N22_12	2.9	2.6	0.3	2.3	20.2%	0.2
10169	AT5G50300.1 | xanthine/uracil/vitamin C permease family protein, contains Pfam profile PF00860: Permease family | chr5:20483294-20485350 REVERSE | Aliases: K6A12.16, K6A12_16	3.7	4.2	-0.5	-2.3	20.2%	0.5
10170	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	9.4	10.2	-0.8	-2.3	20.2%	0.7
10171	AT1G50160.1 | hypothetical protein, similar to putative non-LTR retrolelement reverse transcriptase GB:AAD25836 GI:4587608 from (Arabidopsis thaliana)	2.5	2.8	-0.3	-2.3	20.2%	-0.1
10172	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	3.9	3.4	0.4	2.3	20.2%	0.8
10173	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	7.5	6.8	0.7	2.3	20.3%	0.8
10174	AT1G63080.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:23392549-23394393 REVERSE | Aliases: F16M19.17, F16M19_17	5.6	5.2	0.4	2.3	20.3%	0.3
10175	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	4.8	4.1	0.6	2.3	20.3%	0.9
10176	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	3.4	3.1	0.4	2.3	20.3%	0.6
10177	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	5.8	6.1	-0.3	-2.3	20.3%	0.5
10178	AT5G61620.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr5:24789609-24790733 FORWARD | Aliases: K11J9.15, K11J9_15	3.0	3.3	-0.3	-2.3	20.3%	0.5
10179	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	6.5	7.2	-0.6	-2.3	20.3%	0.9
10180	AT4G27040.1 | expressed protein | chr4:13572444-13575544 REVERSE | Aliases: F10M23.380, F10M23_380	8.7	9.2	-0.4	-2.3	20.3%	0.7
10181	AT4G17660.1 | protein kinase, putative, similar to protein kinase (Lophopyrum elongatum) gi:13022177:gb:AAK11674 | chr4:9831372-9833019 FORWARD | Aliases: DL4865W, FCAALL.77	2.8	2.5	0.3	2.3	20.3%	0.3
10182	AT1G76380.3 | DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487 | chr1:28656048-28659474 REVERSE | Aliases: F15M4.12, F15M4_12	5.1	4.6	0.5	2.3	20.3%	0.8
10183	AT4G08940.1 | expressed protein | chr4:5730400-5732183 REVERSE | Aliases: T3H13.12, T3H13_12	3.7	3.2	0.5	2.3	20.3%	0.6
10184	AT1G03250.1 | expressed protein | chr1:793353-795338 REVERSE | Aliases: F15K9.15, F15K9_15	5.3	4.7	0.6	2.3	20.3%	0.8
10185	AT3G45120.1 | expressed protein | chr3:16522715-16523035 REVERSE | Aliases: T14D3.60	3.9	4.9	-1.0	-2.3	20.4%	1.1
10186	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	7.7	8.2	-0.4	-2.3	20.4%	0.6

Rank	Description	Sync	Root	M	t	adj.q	B
10187	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	3.1	3.5	-0.4	-2.3	20.4%	0.5
10188	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	3.6	4.0	-0.4	-2.3	20.4%	0.7
10189	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	9.7	8.8	0.8	2.3	20.4%	0.6
10190	AT3G02200.2 | proteasome family protein, contains Pfam domain, PF01399: PCI domain | chr3:406609-409169 FORWARD | Aliases: F1C9.1	6.6	5.1	1.4	2.3	20.4%	1.1
10191	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	4.0	4.4	-0.4	-2.3	20.4%	0.4
10192	AT3G16490.1 | calmodulin-binding family protein, contains IQ calmodulin-binding motif, Pfam:PF00612 | chr3:5603968-5605637 REVERSE | Aliases: MDC8.12	3.6	4.1	-0.5	-2.3	20.4%	0.5
10193	AT5G44350.1 | ethylene-responsive nuclear protein -related, contains weak similarity to ethylene-regulated nuclear protein ERT2 (Arabidopsis thaliana) gi:2765442:emb:CAA75349	5.1	5.6	-0.5	-2.3	20.4%	0.6
10194	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	5.5	6.0	-0.5	-2.3	20.4%	0.7
10195	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	3.3	-0.4	-2.3	20.4%	0.3
10196	AT1G07030.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr1:2158419-2160808 REVERSE | Aliases: F10K1.26, F10K1_26	5.3	4.9	0.4	2.3	20.4%	0.5
10197	AT4G27390.1 | expressed protein, hypothetical protein, Synechocystis sp., PIR2:S77328 | chr4:13703145-13704699 REVERSE | Aliases: F27G19.8	4.1	3.8	0.3	2.3	20.4%	0.5
10198	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	7.5	6.9	0.6	2.3	20.4%	0.7
10199	AT1G16850.1 | expressed protein | chr1:5764800-5765644 REVERSE | Aliases: F17F16.17, F6I1.15, F6I1_15	4.7	5.2	-0.5	-2.3	20.4%	0.7
10200	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	7.2	5.9	1.3	2.3	20.4%	1.0
10201	AT3G14360.1 | lipase class 3 family protein, low similarity to Chain A, Lipase Ii From Rhizopus Niveus GI:1942798; contains Pfam profile PF01764: Lipase | chr3:4791596-4794445 FORWARD | Aliases: MLN21.14	5.4	5.8	-0.4	-2.3	20.4%	0.2
10202	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	2.4	2.7	-0.3	-2.3	20.4%	-0.1
10203	AT2G22400.1 | NOL1/NOP2/sun family protein, contains Pfam profile PF01189: NOL1/NOP2/sun family | chr2:9511739-9515955 REVERSE | Aliases: F14M13.20, F14M13_20	6.7	5.8	0.9	2.3	20.4%	0.8
10204	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	4.3	0.5	2.3	20.5%	0.9
10205	AT3G30650.1 | expressed protein | chr3:12203280-12204656 FORWARD | Aliases: MQP15.6	2.3	2.5	-0.3	-2.3	20.5%	-0.0
10206	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	10.8	11.7	-0.9	-2.3	20.5%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
10207	AT4G01890.1 | glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase (Lycopersicon esculentum) GI:7381227; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases) | chr4:816210-818428 FORWARD | Aliases: T7B11.15, T7B11_15	3.9	4.7	-0.8	-2.3	20.5%	0.8
10208	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	3.3	3.7	-0.4	-2.3	20.5%	0.6
10209	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	2.6	-0.3	-2.3	20.5%	-0.0
10210	AT4G02880.1 | expressed protein | chr4:1274512-1278165 FORWARD | Aliases: T5J8.20, T5J8_20	4.4	3.9	0.4	2.3	20.5%	0.8
10211	AT1G26540.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr1:9167576-9170921 REVERSE | Aliases: T1K7.9, T1K7_9	3.3	2.9	0.4	2.3	20.6%	0.3
10212	AT5G11560.1 | PQQ enzyme repeat-containing protein, contains Pfam profile PF01011: PQQ enzyme repeat | chr5:3709482-3714042 REVERSE | Aliases: F15N18.150, F15N18_150	8.8	9.6	-0.8	-2.3	20.6%	0.6
10213	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	7.5	-1.2	-2.3	20.6%	1.0
10214	AT4G24790.1 | expressed protein, ; expression supported by MPSS | chr4:12778232-12781041 FORWARD | Aliases: F6I7.13	3.1	2.8	0.3	2.3	20.6%	0.3
10215	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	4.7	4.2	0.5	2.3	20.6%	0.5
10216	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	3.2	3.4	-0.3	-2.3	20.6%	0.3
10217	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	9.3	10.0	-0.7	-2.3	20.6%	0.6
10218	AT5G48020.1 | expressed protein | chr5:19479884-19482183 REVERSE | Aliases: MDN11.10, MDN11_10	8.8	8.0	0.8	2.3	20.6%	1.0
10219	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	11.8	10.9	0.9	2.3	20.6%	0.6
10220	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	10.3	-0.9	-2.3	20.6%	-0.1
10221	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	10.3	-0.9	-2.3	20.6%	-0.1
10222	AT5G43220.1 | hypothetical protein, similar to unknown protein (gb:AAF03435.1)	2.7	3.2	-0.5	-2.3	20.6%	0.5
10223	AT1G58150.1 | expressed protein | chr1:21533768-21534123 FORWARD | Aliases: T15M6.2	5.9	4.9	0.9	2.3	20.6%	0.9
10224	AT3G27550.1 | group II intron splicing factor CRS1-related, contains weak similarity to CRS1 (Zea mays) gi:9837550:gb:AAG00595	3.2	2.9	0.3	2.3	20.6%	0.3
10225	AT2G30430.1 | hypothetical protein | chr2:12975253-12975489 FORWARD | Aliases: T6B20.26, T6B20_26	2.2	2.4	-0.2	-2.3	20.6%	-0.3
10226	AT5G02850.1 | hydroxyproline-rich glycoprotein family protein | chr5:652108-653671 FORWARD | Aliases: F9G14.160, F9G14_160	3.9	3.3	0.6	2.3	20.6%	0.5
10227	AT1G43780.1 | Symbol: SCPL44 |	2.5	2.9	-0.4	-2.3	20.6%	0.7
10228	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	2.8	0.3	2.3	20.6%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
10229	AT1G19680.1 | expressed protein | chr1:6805450-6808126 FORWARD | Aliases: F14P1.21, F14P1_21	6.8	6.4	0.4	2.3	20.6%	0.5
10230	AT1G11690.1 | hypothetical protein | chr1:3941469-3942212 FORWARD | Aliases: F25C20.16, F25C20_16	3.6	4.0	-0.4	-2.3	20.6%	0.4
10231	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	4.0	-0.4	-2.3	20.6%	0.6
10232	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	5.2	-0.6	-2.3	20.6%	1.0
10233	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	3.7	4.6	-0.8	-2.3	20.6%	0.9
10234	AT4G31790.2 | diphthine synthase, putative (DPH5), similar to	4.2	3.5	0.7	2.3	20.6%	1.0
10235	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	4.0	5.5	-1.5	-2.3	20.6%	0.8
10236	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	4.0	4.9	-0.8	-2.3	20.6%	0.8
10237	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	10.4	9.1	1.4	2.3	20.7%	0.8
10238	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	6.5	5.8	0.6	2.3	20.7%	0.7
10239	AT1G68650.1 | expressed protein, contains Pfam profile PF01169: Uncharacterized protein family UPF0016	7.3	6.5	0.8	2.3	20.7%	1.0
10240	AT3G59260.1 | pirin, putative, similar to SP:O00625 Pirin {Homo sapiens}; contains Pfam profile PF02678: Pirin	2.5	2.7	-0.2	-2.3	20.7%	0.0
10241	AT4G28570.1 | alcohol oxidase-related, low similarity to long chain fatty alcohol oxidase from Candida cloacae (GI:6983581), Candida tropicalis (GI:6983594) | chr4:14119460-14122093 FORWARD | Aliases: T5F17.20, T5F17_20	7.6	8.5	-0.9	-2.3	20.7%	0.6
10242	AT1G34220.2 | expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292 | chr1:12462442-12465978 REVERSE | Aliases: F23M19.10, F23M19_10	5.3	4.7	0.6	2.3	20.7%	0.6
10243	AT2G46930.1 | pectinacetylesterase, putative, similar to pectinacetylesterase precursor GI:1431629 from (Vigna radiata) | chr2:19290588-19293416 FORWARD | Aliases: F14M4.24	7.3	6.5	0.8	2.3	20.8%	0.9
10244	AT3G25960.1 | pyruvate kinase, putative, similar to pyruvate kinase, cytosolic isozyme (Nicotiana tabacum) SWISS-PROT:Q42954 | chr3:9499676-9501169 FORWARD | Aliases: MPE11.9	3.1	3.6	-0.5	-2.3	20.8%	0.6
10245	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	4.7	0.5	2.3	20.8%	0.8
10246	AT2G01590.1 | expressed protein | chr2:266648-267797 FORWARD | Aliases: F2I9.21, F2I9_21	3.5	3.9	-0.4	-2.3	20.8%	0.4
10247	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	8.6	7.2	1.4	2.3	20.8%	1.0
10248	AT1G57550.1 | hydrophobic protein, putative / low temperature and salt responsive protein, putative, similar to SP:Q9ARD5 Low-temperature induced protein lt101.2 {Hordeum vulgare}, SP:Q9ZNQ7 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	4.7	-0.5	-2.3	20.8%	0.4
10249	AT3G56080.1 | dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase | chr3:20821288-20824015 REVERSE | Aliases: F18O21.40	3.7	4.2	-0.5	-2.3	20.8%	0.7
10250	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	5.3	4.5	0.8	2.3	20.8%	0.7

Rank	Description	Sync	Root	M	t	adj.q	B
10251	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	4.9	5.5	-0.6	-2.3	20.8%	0.6
10252	AT5G28930.1 | expressed protein, various predicted proteins, Arabidopsis thaliana | chr5:10968251-10972491 FORWARD | Aliases: F3F24.30, F3F24_30	2.6	2.8	-0.2	-2.3	20.8%	0.1
10253	AT2G31130.1 | expressed protein | chr2:13270758-13273637 REVERSE | Aliases: T16B12.6, T16B12_6	5.8	6.4	-0.6	-2.3	20.8%	0.9
10254	AT2G30910.2 | Symbol: ARPC1A |	6.7	6.0	0.7	2.3	20.8%	1.0
10255	AT2G31300.1 | Symbol: ARPC1b |	6.7	6.0	0.7	2.3	20.8%	1.0
10256	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	3.8	0.5	2.3	20.8%	0.8
10257	AT2G14160.1 | RNA recognition motif (RRM)-containing protein | chr2:5983547-5983883 REVERSE | Aliases: T22C12.9, T22C12_9	2.6	2.9	-0.3	-2.3	20.8%	0.1
10258	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	6.2	5.5	0.7	2.3	20.8%	0.9
10259	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	6.2	5.5	0.7	2.3	20.8%	0.9
10260	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	5.2	5.9	-0.7	-2.3	20.9%	0.8
10261	AT1G22340.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase; similar to UDP-glucose glucosyltransferase GI:3928543 from (Arabidopsis thaliana) | chr1:7890453-7892079 REVERSE | Aliases: T16E15.5, T16E15_5	5.4	5.9	-0.5	-2.3	20.9%	0.6
10262	AT2G16600.1 | Symbol: ROC3 | peptidyl-prolyl cis-trans isomerase, cytosolic / cyclophilin / rotamase (ROC3), identical to cytosolic cyclophilin (Arabidopsis thaliana) GI:1305455 | chr2:7207889-7208650 FORWARD | Aliases: CYCLOPHILIN, T24I21.1, T24I21_1	9.1	7.4	1.7	2.3	20.9%	1.1
10263	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	4.2	-0.6	-2.3	20.9%	1.0
10264	AT2G22780.1 | Symbol: PMDH1 | malate dehydrogenase, glyoxysomal, putative, strong similarity to glyoxysomal malate dehydrogenase (EC 1.1.1.37) SP:P19446 {Citrullus 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	8.5	6.6	1.9	2.3	20.9%	0.9
10265	AT1G62530.1 | expressed protein | chr1:23149997-23150961 REVERSE | Aliases: T3P18.9, T3P18_9	2.6	2.4	0.2	2.3	20.9%	0.0
10266	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	3.5	-0.5	-2.3	20.9%	0.5
10267	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	3.3	-0.3	-2.3	20.9%	-0.1
10268	AT1G55700.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	3.3	-0.6	-2.3	21.0%	0.5
10269	AT1G50890.1 | expressed protein | chr1:18865839-18869707 REVERSE | Aliases: F8A12.11, F8A12_11	4.3	4.6	-0.4	-2.3	21.0%	0.7
10270	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	3.9	-0.5	-2.3	21.0%	0.5
10271	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	4.7	-0.3	-2.3	21.0%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
10272	AT2G43620.1 | chitinase, putative, similar to basic endochitinase CHB4 precursor SP:Q06209 from (Brassica napus) | chr2:18100847-18102102 REVERSE | Aliases: F18O19.27	3.6	3.0	0.6	2.3	21.0%	0.7
10273	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	2.4	-0.2	-2.3	21.0%	-0.1
10274	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	3.2	3.7	-0.4	-2.3	21.1%	0.7
10275	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	3.6	4.2	-0.6	-2.3	21.1%	0.9
10276	AT3G56610.1 | expressed protein | chr3:20982616-20983063 REVERSE | Aliases: T5P19.260	2.6	2.9	-0.3	-2.3	21.1%	0.0
10277	AT2G34330.1 | expressed protein | chr2:14493706-14494380 FORWARD | Aliases: F13P17.17, F13P17_17	3.6	4.0	-0.4	-2.3	21.1%	0.5
10278	AT3G60200.1 | expressed protein, hypothetical proteins At2g44600 - Arabidopsis thaliana, EMBL:AAC27462	4.2	4.5	-0.3	-2.3	21.1%	0.4
10279	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	3.0	2.8	0.2	2.3	21.1%	-0.0
10280	AT1G75680.1 | glycosyl hydrolase family 9 protein, similar to endo-beta-1,4-glucanase GB:AAC12685 GI:3025470 from (Pinus radiata) | chr1:28420713-28423190 REVERSE | Aliases: F10A5.13, F10A5_13	9.0	9.5	-0.4	-2.3	21.1%	0.3
10281	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	5.6	4.7	0.8	2.3	21.1%	0.9
10282	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	3.0	3.3	-0.3	-2.3	21.1%	0.0
10283	AT2G17510.1 | ribonuclease II family protein, similar to SP:P37202 Mitotic control protein dis3 {Schizosaccharomyces pombe}; contains Pfam profile PF00773: RNB-like protein | chr2:7616352-7623049 REVERSE | Aliases: MJB20.7, MJB20_7	4.8	5.4	-0.6	-2.3	21.1%	0.8
10284	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	2.9	0.2	2.3	21.1%	0.1
10285	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	3.0	-0.2	-2.3	21.1%	0.0
10286	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	2.5	-0.2	-2.3	21.2%	-0.2
10287	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	6.2	7.0	-0.8	-2.3	21.2%	0.7
10288	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	2.2	-0.2	-2.3	21.2%	-0.4
10289	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	11.6	10.5	1.1	2.3	21.2%	0.7
10290	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	11.6	10.5	1.1	2.3	21.2%	0.7
10291	AT5G54480.1 | expressed protein | chr5:22135230-22137392 FORWARD | Aliases: F24B18.10, F24B18_10	2.9	3.2	-0.3	-2.3	21.2%	-0.0
10292	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	7.9	8.2	-0.3	-2.3	21.2%	0.4

Rank	Description	Sync	Root	M	t	adj.q	B
10293	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	5.2	4.7	0.5	2.3	21.2%	0.9
10294	AT4G23540.1 | expressed protein, probable membrane protein YPL012w, Saccharomyces cerevisiae, PIR2:S59681 | chr4:12279918-12284693 REVERSE | Aliases: F16G20.240, F16G20_240	4.7	4.0	0.7	2.3	21.2%	0.7
10295	AT3G43530.1 | hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287 | chr3:15438133-15441064 REVERSE | Aliases: T18D12.100	3.6	4.0	-0.5	-2.3	21.2%	0.2
10296	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	8.7	9.5	-0.8	-2.3	21.2%	0.8
10297	AT3G53270.4 | expressed protein, endopeptidase Clp ATP-binding chain C, Chlamydia pneumoniae, PIR:G72079 | chr3:19761025-19764083 REVERSE | Aliases: T4D2.1	5.0	5.3	-0.3	-2.3	21.2%	0.4
10298	AT2G23990.2 | plastocyanin-like domain-containing protein | chr2:10213915-10214991 REVERSE | Aliases: T29E15.19, T29E15_19	2.8	3.1	-0.3	-2.3	21.2%	0.3
10299	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	6.0	6.8	-0.7	-2.3	21.2%	0.7
10300	AT3G61250.1 | myb family transcription factor (MYB17), contains PFAM profile: Myb-like DNA-binding domain PF00249 | chr3:22681977-22683713 FORWARD | Aliases: T20K12.150	3.0	2.7	0.3	2.3	21.2%	0.3
10301	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	4.4	4.7	-0.3	-2.3	21.3%	0.3
10302	AT2G19300.1 | expressed protein | chr2:8375122-8375301 REVERSE | Aliases: F27F23.10, F27F23_10	2.7	2.9	-0.2	-2.3	21.3%	-0.1
10303	AT2G28810.1 | Dof-type zinc finger domain-containing protein, similar to zinc finger protein OBP2 GI:5059394 from (Arabidopsis thaliana) | chr2:12370707-12372454 FORWARD | Aliases: F8N16.10, F8N16_10	4.4	4.8	-0.3	-2.3	21.3%	0.5
10304	AT1G32980.1 | subtilisin-like serine protease-related, similar to subtilase SP1 (Oryza sativa) GI:9957714 | chr1:11954258-11955342 REVERSE | Aliases: F9L11.33, F9L11_33	2.9	3.2	-0.3	-2.3	21.3%	0.3
10305	ATCG00650.1 | Symbol: RPS18 | chloroplast-encoded ribosomal protein S18 | chrC:67917-68222 FORWARD | Aliases: RPS18	6.8	5.3	1.5	2.3	21.3%	0.9
10306	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	2.8	-0.4	-2.3	21.3%	0.4
10307	AT3G23960.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.7	2.9	-0.3	-2.3	21.3%	0.2
10308	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	2.6	-0.2	-2.3	21.3%	-0.2
10309	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	2.8	0.2	2.3	21.3%	0.2
10310	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	5.1	6.0	-0.9	-2.3	21.3%	0.9
10311	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	2.3	-0.2	-2.3	21.3%	-0.3
10312	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	3.1	-0.3	-2.3	21.4%	0.3

Rank	Description	Sync	Root	M	t	adj.q	B
10313	AT5G14890.1 | NHL repeat-containing protein, contains Pfam profile PF01436: NHL repeat	3.5	3.9	-0.4	-2.3	21.4%	0.4
10314	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	4.2	4.8	-0.7	-2.3	21.4%	0.5
10315	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	8.1	9.1	-1.0	-2.3	21.4%	0.8
10316	AT5G44270.1 | expressed protein | chr5:17850863-17852967 FORWARD | Aliases: K9L2.2, K9L2_2	2.4	2.7	-0.2	-2.3	21.4%	-0.1
10317	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	4.0	5.0	-1.0	-2.3	21.4%	0.8
10318	AT2G19170.1 | Symbol: SLP3 | subtilase family protein, contains similarity to meiotic serine proteinase TMP GI:6468325 from (Lycopersicon esculentum)	3.6	3.3	0.3	2.3	21.5%	0.3
10319	AT5G16870.1 | expressed protein | chr5:5546814-5548739 REVERSE | Aliases: F2K13.20, F2K13_20	3.9	3.4	0.4	2.3	21.5%	0.4
10320	AT5G45430.1 | protein kinase, putative, contains similarity to male germ cell-associated kinase (Homo sapiens) gi:23268497:gb:AAN16405	5.6	6.4	-0.8	-2.3	21.5%	0.9
10321	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	4.5	4.9	-0.4	-2.3	21.5%	0.6
10322	AT5G54060.1 | glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	4.4	5.1	-0.6	-2.3	21.5%	0.6
10323	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	3.1	-0.3	-2.3	21.5%	0.3
10324	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	3.5	3.9	-0.4	-2.3	21.5%	0.4
10325	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	2.4	-0.2	-2.3	21.5%	-0.3
10326	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	3.2	3.6	-0.4	-2.3	21.5%	0.6
10327	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	10.0	8.9	1.1	2.3	21.5%	0.7
10328	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.	2.7	2.4	0.3	2.3	21.5%	0.2
10329	AT3G55960.1 | NLI interacting factor (NIF) family protein, contains Pfam profile PF03031: NLI interacting factor | chr3:20771436-20774012 REVERSE | Aliases: F27K19.140	7.1	8.2	-1.1	-2.3	21.5%	0.8
10330	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	2.9	-0.4	-2.3	21.5%	0.4
10331	AT2G23440.1 | expressed protein | chr2:9986485-9986899 FORWARD | Aliases: F26B6.9, F26B6_9	2.8	3.0	-0.2	-2.3	21.6%	-0.1
10332	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	9.6	8.6	1.0	2.3	21.6%	0.9

Rank	Description	Sync	Root	M	t	adj.q	B
10333	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	3.8	-0.5	-2.3	21.6%	0.4
10334	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	4.5	5.3	-0.8	-2.3	21.6%	0.6
10335	AT5G50910.1 | hypothetical protein | chr5:20725635-20726508 REVERSE | Aliases: K3K7.5, K3K7_5	2.1	2.3	-0.2	-2.3	21.6%	-0.4
10336	AT5G24140.1 | Symbol: SQP2 | squalene monooxygenase 2 / squalene epoxidase 2 (SQP2), identical to SP:O65403 | chr5:8164359-8167676 REVERSE | Aliases: MLE8.6, MLE8_6	2.3	2.4	-0.1	-2.3	21.6%	-0.3
10337	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	6.7	4.8	1.9	2.3	21.6%	0.9
10338	AT3G19310.1 | expressed protein, similar to GB:CAB16796 from (Arabidopsis thaliana) | chr3:6694266-6696220 FORWARD | Aliases: MLD14.39	3.1	3.4	-0.3	-2.3	21.6%	0.1
10339	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	9.2	8.4	0.8	2.3	21.6%	0.9
10340	AT1G05210.1 | expressed protein | chr1:1510138-1511678 FORWARD | Aliases: YUP8H12.18, YUP8H12_18	5.3	4.9	0.4	2.3	21.6%	0.5
10341	NA	10.0	10.5	-0.4	-2.3	21.6%	-0.3
10342	AT3G13225.1 | similar to PREDICTED: similar to mKIAA1014 protein [Gallus gallus] (GB:XP_424260.1); contains InterPro domain WW/Rsp5/WWP domain (InterPro:IPR001202) | chr3:4258777-4262903 REVERSE | Aliases: MJH23.2	2.8	3.1	-0.3	-2.3	21.6%	0.2
10343	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	3.6	4.0	-0.4	-2.3	21.6%	0.2
10344	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	3.8	-0.4	-2.3	21.6%	0.1
10345	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	2.3	-0.2	-2.3	21.6%	-0.5
10346	AT4G00780.1 | meprin 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	2.4	2.6	-0.2	-2.3	21.6%	-0.1
10347	AT1G67580.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:25330802-25335042 REVERSE | Aliases: F12B7.13, F12B7_13	5.5	6.3	-0.8	-2.3	21.6%	0.8
10348	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	6.9	6.4	0.5	2.3	21.6%	0.6
10349	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	9.1	8.1	1.0	2.3	21.6%	1.0
10350	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	9.1	8.1	1.0	2.3	21.6%	1.0
10351	AT3G62480.1 | expressed protein | chr3:23122259-23122849 REVERSE | Aliases: T12C14.180	2.4	2.6	-0.2	-2.3	21.6%	-0.3
10352	AT2G05590.2 | expressed protein, similar to nucleolar protein C7C (GI:13540302) (Rattus norvegicus) | chr2:2067094-2069203 FORWARD | Aliases: T20G20.6, T20G20_6	4.6	5.2	-0.6	-2.3	21.7%	0.7

Rank	Description	Sync	Root	M	t	adj.q	B
10353	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	8.0	7.5	0.6	2.3	21.7%	0.6
10354	AT5G26970.1 | expressed protein | chr5:9487063-9487389 REVERSE | Aliases: F2P16.230, F2P16_230	2.7	3.0	-0.3	-2.3	21.7%	0.1
10355	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	3.9	-0.6	-2.3	21.7%	0.6
10356	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	4.0	3.7	0.3	2.3	21.7%	0.2
10357	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	4.3	3.8	0.5	2.3	21.7%	0.7
10358	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	3.1	-0.3	-2.3	21.7%	0.3
10359	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	2.4	0.3	2.3	21.7%	0.2
10360	AT1G74950.1 | expressed protein | chr1:28152236-28154055 REVERSE | Aliases: F25A4.8, F25A4_8	6.2	4.9	1.3	2.3	21.7%	1.0
10361	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	5.0	4.3	0.7	2.3	21.7%	0.5
10362	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	2.9	3.3	-0.4	-2.3	21.7%	0.3
10363	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	6.5	1.0	2.3	21.7%	0.9
10364	AT5G14310.1 | expressed protein, low similarity to PrMC3 (Pinus radiata) GI:5487873 | chr5:4615321-4617618 FORWARD | Aliases: F18O22.100, F18O22_100	4.5	5.2	-0.8	-2.3	21.7%	0.4
10365	AT5G04440.1 | expressed protein | chr5:1254949-1256954 FORWARD | Aliases: T19N18.1	6.7	6.1	0.6	2.3	21.7%	0.7
10366	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 nitrobenzylmercaptopurine 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	3.8	3.2	0.6	2.3	21.8%	1.0
10367	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 nitrobenzylmercaptopurine 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	3.8	3.2	0.6	2.3	21.8%	1.0
10368	AT5G18130.2 | expressed protein, similar to unknown protein (gb:AAF00631.1) | chr5:5995482-5997400 FORWARD | Aliases: MRG7.9, MRG7_9	5.8	6.2	-0.5	-2.3	21.8%	0.6
10369	AT1G13130.1 | glycosyl hydrolase family 5 protein / cellulase family protein | chr1:4474718-4477939 FORWARD | Aliases: F3F19.15, F3F19_15	2.5	3.0	-0.4	-2.3	21.8%	0.1
10370	AT4G01690.2 | Symbol: PPOX | protoporphyrinogen oxidase (PPOX), identical to SP:P55826 | chr4:729892-732734 FORWARD | Aliases: PROTOPORPHYRINOGEN OXIDASE, T15B16.13, T15B16_13	8.1	7.1	1.0	2.3	21.8%	0.8
10371	AT1G23350.1 | invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	2.6	2.9	-0.3	-2.3	21.8%	0.1
10372	ATMG01330.1 | Symbol: ORF107H | hypothetical protein | chrM:329082-329465 REVERSE | Aliases: ORF107H	2.8	3.5	-0.7	-2.3	21.8%	0.1

Rank	Description	Sync	Root	M	t	adj.q	B
10373	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	5.5	4.7	0.8	2.3	21.8%	0.6
10374	AT4G08460.2 | expressed protein | chr4:5377140-5380615 REVERSE | Aliases: T15F16.1, T15F16_1	5.8	6.2	-0.4	-2.3	21.8%	0.5
10375	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	3.2	-0.3	-2.3	21.9%	0.4
10376	AT5G41730.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr5:16702142-16704373 REVERSE | Aliases: MUF8.1, MUF8_1	2.5	3.1	-0.5	-2.3	21.9%	0.4
10377	AT2G07260.1 | hypothetical protein | chr2:3019653-3021695 REVERSE | Aliases: T13E11.3, T13E11_3	2.1	2.4	-0.3	-2.3	21.9%	-0.1
10378	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	9.6	-0.5	-2.3	21.9%	0.4
10379	AT3G06180.1 | expressed protein | chr3:1871694-1873751 FORWARD | Aliases: F28L1.12, F28L1_12	6.8	6.3	0.5	2.3	21.9%	0.4
10380	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 ('A'TPases 'A'ssociated with diverse cellular 'A'ctivities) | chr3:502714-505237 REVERSE | Aliases: F16B3.8, F16B3_8	5.1	4.7	0.4	2.2	21.9%	0.6
10381	AT4G22050.1 | aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease | chr4:11683877-11685656 FORWARD | Aliases: F1N20.150, F1N20_150	3.1	2.5	0.6	2.2	21.9%	0.9
10382	AT1G17750.1 | leucine-rich repeat transmembrane protein kinase, putative, similar to receptor-like protein kinase INRPK1 GI:1684913 from (Ipomoea nil)	3.6	3.9	-0.3	-2.2	21.9%	0.3
10383	AT5G63030.1 | glutaredoxin, putative, similar to glutaredoxin (Ricinus communis) gi:1732424:emb:CAA89699 | chr5:25303511-25304906 FORWARD | Aliases: MJH22.9, MJH22_9	9.7	9.3	0.4	2.2	22.0%	0.4
10384	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) GI:2749943; contains Pfam profile: PF00314 thaumatin family | chr1:27685069-27686790 FORWARD | Aliases: F25P22.3, F25P22_3	2.8	2.5	0.3	2.2	22.0%	0.3
10385	AT4G35210.1 | expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function | chr4:16751433-16752185 FORWARD | Aliases: T12J5.80, T12J5_80	3.4	3.8	-0.4	-2.2	22.0%	0.2
10386	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	6.3	6.8	-0.6	-2.2	22.0%	0.5
10387	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	7.3	6.8	0.5	2.2	22.0%	0.6
10388	AT1G27690.1 | expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620) | chr1:9636581-9638564 FORWARD | Aliases: T22C5.14, T22C5_14	5.0	4.6	0.4	2.2	22.0%	0.5
10389	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	3.9	3.5	0.4	2.2	22.0%	0.6
10390	ATCG00730.1 | Symbol: PETD | A chloroplast gene encoding subunit IV of the cytochrome b6/f complex | chrC:76481-77672 FORWARD | Aliases: PETD	3.2	4.4	-1.1	-2.2	22.0%	0.8
10391	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	3.1	-0.2	-2.2	22.0%	-0.2
10392	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	5.3	4.5	0.7	2.2	22.0%	0.4
10393	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	3.3	-0.3	-2.2	22.0%	0.2
10394	AT3G49650.1 | kinesin motor protein-related, several kinesin-like proteins | chr3:18416245-18420387 REVERSE | Aliases: T9C5.240	2.7	3.0	-0.3	-2.2	22.0%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
10395	AT3G12470.1 | expressed protein | chr3:3956064-3956834 REVERSE | Aliases: T2E22.21	2.8	3.0	-0.2	-2.2	22.0%	0.1
10396	AT2G42630.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:17765609-17767786 REVERSE | Aliases: F14N22.10, F14N22_10	4.1	4.5	-0.5	-2.2	22.0%	0.5
10397	AT1G06240.1 | expressed protein, contains Pfam domain, PF04305: Protein of unknown function (DUF455) | chr1:1911121-1913179 FORWARD | Aliases: F9P14.10, F9P14_10	4.7	4.1	0.6	2.2	22.0%	0.8
10398	AT5G22590.1 | hypothetical protein | chr5:7504539-7505841 FORWARD | Aliases: MDJ22.1, MDJ22_1	2.8	3.0	-0.2	-2.2	22.0%	-0.3
10399	AT2G09910.1 | expressed protein | chr2:3760479-3764291 FORWARD | Aliases: F7B19.5, F7B19_5	3.4	3.9	-0.5	-2.2	22.0%	0.6
10400	AT4G15690.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	2.5	2.7	-0.2	-2.2	22.1%	-0.2
10401	AT5G10780.1 | expressed protein, HSPC184, Homo sapiens, EMBL:AF151018 | chr5:3408347-3410044 FORWARD | Aliases: T30N20.50, T30N20_50	9.4	8.2	1.2	2.2	22.1%	0.9
10402	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	3.3	3.5	-0.3	-2.2	22.1%	0.1
10403	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	5.7	4.9	0.8	2.2	22.1%	0.9
10404	AT4G14090.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl 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	4.7	0.4	2.2	22.1%	0.6
10405	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	3.7	3.4	0.4	2.2	22.1%	0.4
10406	AT1G60400.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.0	3.5	-0.5	-2.2	22.1%	0.3
10407	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	3.7	3.4	0.3	2.2	22.1%	0.3
10408	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	6.9	8.3	-1.3	-2.2	22.1%	0.9
10409	AT2G24120.2 | Symbol: PDE319 |	4.0	3.7	0.3	2.2	22.1%	0.5
10410	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	8.1	-0.7	-2.2	22.1%	0.3
10411	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	4.1	-0.5	-2.2	22.1%	0.6
10412	AT2G40700.1 | DEAD/DEAH box helicase, putative (RH17), identical to GB:CAA09207, contains a DEAD/DEAH box family ATP-dependent helicas signature; identical to cDNA DEAD box RNA helicase, RH17 GI:3776008 | chr2:16983861-16986636 FORWARD | Aliases: T7D17.12, T7D17_12	4.0	3.5	0.5	2.2	22.1%	0.5
10413	AT4G16840.1 | expressed protein | chr4:9474904-9475542 FORWARD | Aliases: DL4445W, FCAALL.92	4.0	3.6	0.4	2.2	22.2%	0.7
10414	AT5G24810.1 | ABC1 family protein, contains Pfam domain, PF03109: ABC1 family | chr5:8516638-8522770 REVERSE | Aliases: F6A4.20, F6A4_20	8.0	8.6	-0.6	-2.2	22.2%	0.7
10415	AT1G64370.1 | expressed protein | chr1:23892583-23893324 FORWARD | Aliases: F15H21.1, F15H21_1	3.8	4.3	-0.6	-2.2	22.2%	0.7
10416	AT1G41770.1 | hypothetical protein | chr1:15539662-15539973 FORWARD | Aliases: F9M8.10	3.9	4.7	-0.8	-2.2	22.2%	0.6

Rank	Description	Sync	Root	M	t	adj.q	B
10417	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	2.4	-0.1	-2.2	22.2%	-0.4
10418	AT5G15280.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:4962296-4966143 FORWARD | Aliases: F8M21.170, F8M21_170	3.9	4.3	-0.4	-2.2	22.2%	0.5
10419	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	2.6	-0.2	-2.2	22.2%	0.0
10420	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) (Crypthecodinium cohnii) | chr1:18358488-18360310 FORWARD | Aliases: F14J22.17, F14J22_17	5.3	4.7	0.6	2.2	22.2%	0.7
10421	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	6.2	4.9	1.3	2.2	22.2%	1.0
10422	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	7.1	6.6	0.5	2.2	22.2%	0.8
10423	AT1G52420.1 | glycosyl transferase family 1 protein, contains Pfam profile: PF00534 Glycosyl transferases group 1 | chr1:19531518-19534956 FORWARD | Aliases: F19K6.13	9.4	9.0	0.4	2.2	22.2%	0.5
10424	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	2.7	3.2	-0.5	-2.2	22.2%	0.2
10425	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	4.3	3.6	0.7	2.2	22.2%	0.9
10426	AT1G23680.1 | hypothetical protein, contains Pfam profile PF02713: Domain of unknown function DUF220 | chr1:8376676-8377145 REVERSE | Aliases: F5O8.23, F5O8_23	3.3	3.9	-0.6	-2.2	22.2%	0.5
10427	AT1G44990.1 | expressed protein | chr1:17009982-17010248 REVERSE | Aliases: F27F5.38, F27F5_38	6.2	7.0	-0.8	-2.2	22.3%	0.7
10428	AT3G44770.1 | expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626) | chr3:16327067-16330445 FORWARD | Aliases: T32N15.6	3.2	3.7	-0.5	-2.2	22.3%	0.4
10429	AT1G48290.1 | expressed protein, ; expression supported by MPSS | chr1:17846336-17848575 FORWARD | Aliases: F11A17.26, F11A17_26	3.2	3.7	-0.4	-2.2	22.3%	0.4
10430	ATCG01040.1 | Symbol: YCF5 | hypothetical protein | chrC:114461-115447 FORWARD | Aliases: YCF5	10.4	9.0	1.4	2.2	22.3%	0.5
10431	AT5G47940.1 | expressed protein | chr5:19426468-19429119 REVERSE | Aliases: K16F13.3, K16F13_3	4.4	4.8	-0.5	-2.2	22.3%	0.7
10432	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	2.9	-0.3	-2.2	22.3%	0.1
10433	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	2.9	3.1	-0.2	-2.2	22.3%	-0.0
10434	AT3G16540.1 | DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana) | chr3:5626296-5628863 REVERSE | Aliases: MDC8.17	3.4	3.8	-0.5	-2.2	22.4%	0.5
10435	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	7.6	8.0	-0.4	-2.2	22.4%	0.5
10436	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	4.5	0.7	2.2	22.4%	0.7

Rank	Description	Sync	Root	M	t	adj.q	B
10437	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	2.3	2.6	-0.4	-2.2	22.4%	0.1
10438	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	4.2	3.8	0.4	2.2	22.4%	0.6
10439	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	4.8	5.4	-0.6	-2.2	22.4%	0.6
10440	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	2.7	0.4	2.2	22.4%	0.1
10441	AT5G08110.1 | DEAD/DEAH box helicase, putative, several putative ATP-dependent helicases | chr5:2594971-2600115 REVERSE | Aliases: T22D6.50, T22D6_50	4.5	4.1	0.3	2.2	22.4%	0.4
10442	AT5G28820.1 | hypothetical protein | chr5:10831803-10832536 FORWARD | Aliases: T32B20.110, T32B20_110	2.7	2.9	-0.2	-2.2	22.5%	-0.1
10443	AT5G48600.1 | Symbol: ATSMC3 |	4.2	3.4	0.8	2.2	22.5%	0.8
10444	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	3.3	-0.3	-2.2	22.5%	0.4
10445	AT1G06420.1 | expressed protein, ; expression supported by MPSS | chr1:1958986-1959651 FORWARD | Aliases: T2D23.12, T2D23_12	4.5	3.4	1.1	2.2	22.5%	0.8
10446	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	5.7	6.4	-0.7	-2.2	22.5%	0.7
10447	AT1G63000.1 | Symbol: NRS/ER |	6.3	7.2	-0.9	-2.2	22.5%	0.7
10448	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	4.4	0.4	2.2	22.5%	0.5
10449	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	4.0	-0.5	-2.2	22.5%	0.5
10450	AT1G11400.3 | similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAG03976.1) | chr1:3838016-3840207 FORWARD | Aliases: T23J18.7, T23J18_7	7.0	6.4	0.7	2.2	22.5%	0.7
10451	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	6.9	7.3	-0.4	-2.2	22.5%	0.5
10452	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	4.3	0.8	2.2	22.5%	0.8
10453	AT4G05440.1 | temperature sensing protein-related, contains weak similarity to D123 (GI:1236114) (Rattus norvegicus) | chr4:2757211-2758272 FORWARD | Aliases: C6L9.120, C6L9_120	5.3	4.9	0.3	2.2	22.5%	0.5
10454	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	6.6	7.4	-0.8	-2.2	22.6%	0.6
10455	AT2G28070.1 | ABC transporter family protein | chr2:11963509-11966859 FORWARD | Aliases: F24D13.14, F24D13_14	4.8	5.2	-0.4	-2.2	22.6%	0.4

Rank	Description	Sync	Root	M	t	adj.q	B
10456	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	7.2	5.7	1.5	2.2	22.6%	0.9
10457	AT5G30490.1 | expressed protein | chr5:11629213-11631760 FORWARD | Aliases: None	5.1	4.6	0.4	2.2	22.6%	0.4
10458	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	5.8	5.0	0.8	2.2	22.6%	0.9
10459	AT2G43580.1 | chitinase, putative, similar to basic endochitinase CHB4 precursor SP:Q06209 from (Brassica napus) | chr2:18085726-18087105 REVERSE | Aliases: F18O19.31	2.0	2.1	-0.2	-2.2	22.6%	-0.3
10460	AT5G28650.1 | Symbol: WRKY74 |	5.3	4.8	0.5	2.2	22.6%	0.6
10461	AT4G22280.2 | F-box family protein, contains Pfam profile PF00646: F-box domain | chr4:11776025-11778131 REVERSE | Aliases: T10I14.110, T10I14_110	3.2	2.9	0.3	2.2	22.6%	0.2
10462	AT5G17630.1 | glucose-6-phosphate/phosphate translocator, putative, similar to glucose-6-phosphate/phosphate-translocator precursor (Solanum tuberosum) gi:2997593:gb:AAC08526	6.3	4.8	1.5	2.2	22.6%	0.8
10463	AT1G79710.1 | integral membrane transporter family protein, similar to high affinity folic acid/methotrexate transporter 5 (GI:21898554) (Leishmania tarentolae); Interpro IPR001991/ PR00173 Sodium:dicarboxylater symporter family | chr1:30000030-30001881 FORWARD | Aliases: F19K16.31, F19K16_31	5.3	5.9	-0.7	-2.2	22.6%	0.6
10464	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	4.0	4.6	-0.6	-2.2	22.6%	0.5
10465	AT5G56780.1 | expressed protein, contains similarity to transcription repressor | chr5:22981491-22983467 REVERSE | Aliases: MIK19.25, MIK19_25	3.6	3.3	0.3	2.2	22.6%	0.3
10466	AT1G03960.2 | calcium-binding EF hand family protein, contains Pfam profile: PF00036 EF hand | chr1:1013714-1017901 FORWARD | Aliases: F21M11.11, F21M11_11	2.5	2.8	-0.3	-2.2	22.6%	0.2
10467	AT1G61780.1 | postsynaptic protein-related, similar to postsynaptic protein CRIPT GI:3098551 from (Rattus norvegicus) | chr1:22816280-22817806 REVERSE | Aliases: T13M11.14, T13M11_14	10.8	10.4	0.4	2.2	22.6%	0.1
10468	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	2.1	0.1	2.2	22.6%	-0.7
10469	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	3.3	-0.6	-2.2	22.6%	0.5
10470	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	3.4	-0.5	-2.2	22.6%	0.1
10471	AT5G38310.1 | expressed protein | chr5:15327911-15328477 REVERSE | Aliases: MSI17.4, MSI17_4	3.3	2.9	0.4	2.2	22.7%	0.6
10472	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	2.8	-0.2	-2.2	22.7%	-0.1
10473	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	6.9	6.0	0.9	2.2	22.7%	0.8
10474	AT5G62400.1 | expressed protein | chr5:25071840-25072832 REVERSE | Aliases: MMI9.23, MMI9_23	2.5	2.7	-0.2	-2.2	22.7%	-0.1
10475	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	3.7	4.0	-0.3	-2.2	22.7%	0.3
10476	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	2.4	2.8	-0.4	-2.2	22.7%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
10477	AT2G45990.4 | expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_477679.1) | chr2:18926436-18928302 FORWARD | Aliases: F4I18.49	9.1	8.3	0.8	2.2	22.7%	0.8
10478	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	7.4	6.8	0.6	2.2	22.7%	0.8
10479	AT1G10670.2 | Symbol: ACLA 1 |	11.3	10.6	0.7	2.2	22.7%	0.3
10480	AT3G63080.1 | Symbol: ATGPX5 |	7.0	8.4	-1.4	-2.2	22.7%	0.8
10481	AT1G07750.1 | cupin family protein, similar to legumin (11S-globulin) from Ginkgo biloba (GI:949869), 11S globulin from Avena sativa (GI:472867) | chr1:2404034-2405939 REVERSE | Aliases: F24B9.13, F24B9_13	9.0	8.2	0.8	2.2	22.8%	0.6
10482	AT5G57680.1 | expressed protein | chr5:23379971-23380920 REVERSE | Aliases: MRI1.3, MRI1_3	2.4	2.7	-0.3	-2.2	22.8%	-0.0
10483	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	5.0	6.6	-1.5	-2.2	22.8%	1.0
10484	AT4G11690.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:7056248-7057948 FORWARD | Aliases: T5C23.120, T5C23_120	3.1	2.7	0.3	2.2	22.8%	0.1
10485	AT1G32660.1 | F-box family protein, contains Pfam profile: PF00646 F-box domain | chr1:11811020-11812360 FORWARD | Aliases: F6N18.5, F6N18_5	2.9	3.2	-0.3	-2.2	22.8%	0.2
10486	AT5G51980.2 | similar to WD-40 repeat family protein / zfwd1 protein (ZFWD1) [Arabidopsis thaliana] (TAIR:At4g25440.1); similar to Putative zfwd1 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	6.5	-0.6	-2.2	22.8%	0.7
10487	AT4G24030.1 | expressed protein | chr4:12486257-12486643 REVERSE | Aliases: T19F6.20, T19F6_20	3.6	4.3	-0.7	-2.2	22.8%	0.7
10488	AT5G63440.2 | expressed protein, contains Pfam PF02594: Uncharacterized ACR, YggU family COG1872 | chr5:25423551-25425631 FORWARD | Aliases: MLE2.7, MLE2_7	4.5	4.2	0.3	2.2	22.8%	0.3
10489	AT4G36020.1 | cold-shock DNA-binding family protein, contains Pfam domains, PF00313: 'Cold-shock' DNA-binding domain and PF00098: Zinc knuckle	9.3	8.7	0.6	2.2	22.8%	0.6
10490	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	5.1	4.0	1.1	2.2	22.8%	0.7
10491	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	3.9	4.4	-0.4	-2.2	22.8%	0.5
10492	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	3.3	2.9	0.3	2.2	22.8%	0.4
10493	AT5G01970.1 | expressed protein | chr5:372724-374951 REVERSE | Aliases: T7H20.20, T7H20_20	4.3	4.8	-0.5	-2.2	22.8%	0.6
10494	AT3G49220.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr3:18260769-18264824 FORWARD | Aliases: F2K15.80, F2K15_80	7.3	6.5	0.8	2.2	22.8%	0.8
10495	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	7.8	8.4	-0.6	-2.2	22.8%	0.5
10496	AT3G02140.1 | expressed protein | chr3:385324-386545 REVERSE | Aliases: F1C9.7	7.4	8.1	-0.8	-2.2	22.8%	0.7

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10497	AT3G07360.3 | similar to armadillo/beta-catenin repeat family protein / U-box domain-containing protein [Arabidopsis thaliana] (TAIR:At5g18320.1); similar to OSJNBa0020I02.15 [Oryza sativa (japonica cultivar-group)] (GB:XP_472015.1); contains InterPro domain Armadillo repeat (InterPro:IPR000225) | chr3:2354725-2356845 FORWARD | Aliases: F21O3.7	5.0	5.4	-0.4	-2.2	22.8%	0.3
10498	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	6.0	-1.3	-2.2	22.8%	0.8
10499	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	7.7	-0.3	-2.2	22.8%	0.2
10500	AT5G02650.1 | expressed protein | chr5:598774-599784 FORWARD | Aliases: T22P11.240, T22P11_240	4.3	3.9	0.4	2.2	22.9%	0.6
10501	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	3.4	4.0	-0.6	-2.2	22.9%	0.6
10502	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	10.7	10.1	0.6	2.2	22.9%	0.2
10503	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	6.2	7.4	-1.2	-2.2	22.9%	0.6
10504	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	5.0	5.9	-0.9	-2.2	22.9%	0.9
10505	AT4G30010.1 | expressed protein | chr4:14672877-14673225 FORWARD | Aliases: F6G3.40, F6G3_40	10.7	9.9	0.8	2.2	22.9%	0.1
10506	AT1G51360.1 | expressed protein | chr1:19047852-19048568 FORWARD | Aliases: F11M15.22, F11M15_22	3.2	2.9	0.4	2.2	22.9%	0.2
10507	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	7.7	6.7	1.0	2.2	22.9%	0.8
10508	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	2.7	-0.3	-2.2	23.0%	-0.2
10509	AT2G43540.1 | expressed protein | chr2:18079448-18080040 FORWARD | Aliases: T1O24.28	6.0	6.6	-0.6	-2.2	23.0%	0.5
10510	AT3G04630.3 | Symbol: WDL1 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g54460.1); similar to BRI1-KD interacting protein 116 [Oryza sativa (japonica cultivar-group)] (GB:BAD11344.1) | chr3:1258804-1260824 FORWARD | Aliases: F7O18.11, F7O18_11	4.3	5.2	-0.9	-2.2	23.0%	0.6
10511	AT4G12970.1 | expressed protein | chr4:7586140-7586827 REVERSE | Aliases: F25G13.60, F25G13_60	3.1	3.3	-0.2	-2.2	23.0%	-0.5
10512	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	6.5	5.2	1.3	2.2	23.0%	0.6
10513	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	2.8	-0.3	-2.2	23.0%	0.1
10514	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	6.5	5.3	1.1	2.2	23.0%	0.6
10515	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	4.3	3.9	0.4	2.2	23.0%	0.5

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10516	AT5G53660.1 | Symbol: AtGRF7 |	3.3	3.8	-0.5	-2.2	23.0%	0.5
10517	AT5G39380.1 | calmodulin-binding protein-related, has weak similarity to calmodulin-binding proteins | chr5:15775945-15777914 REVERSE | Aliases: MUL8.6, MUL8_6	3.9	4.3	-0.4	-2.2	23.0%	0.3
10518	AT3G57770.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr3:21408519-21409830 FORWARD | Aliases: F15B8.40	3.8	3.2	0.7	2.2	23.0%	0.8
10519	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	4.9	4.3	0.6	2.2	23.0%	0.6
10520	AT1G65350.1 | Symbol: UBQ13 | polyubiquitin, putative, similar to polyubiquitin GI:248337 from (Zea mays) | chr1:24280054-24280938 REVERSE | Aliases: T8F5.13, T8F5_13	4.8	5.3	-0.4	-2.2	23.0%	0.7
10521	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	2.4	2.6	-0.2	-2.2	23.0%	0.0
10522	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	4.0	0.4	2.2	23.0%	0.4
10523	AT1G33240.1 | Symbol: AT GTL1 | trihelix DNA-binding protein, putative, similar to GTL1 (Arabidopsis thaliana) GI:2664198 | chr1:12051451-12054526 REVERSE | Aliases: T9L6.10, T9L6_10	6.4	5.3	1.1	2.2	23.1%	0.8
10524	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	2.3	-0.3	-2.2	23.1%	-0.7
10525	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	2.9	3.4	-0.5	-2.2	23.1%	0.4
10526	AT1G16040.1 | expressed protein, similar To Phosphatidylinositol-glycan biosynthesis, class F protein (PIG-F). (Mouse) (SP:O09101) (Mus musculus); contains six transmembrane domains;	5.1	4.7	0.4	2.2	23.1%	0.1
10527	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	5.5	-0.6	-2.2	23.1%	0.8
10528	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	4.8	-0.8	-2.2	23.1%	0.7
10529	ATCG00340.1 | Symbol: PSAB | Encodes the D1 subunit of photosystem I and II reaction centers. | chrC:37375-39579 REVERSE | Aliases: PSAB	11.3	10.5	0.8	2.2	23.1%	0.5
10530	AT3G57990.1 | expressed protein | chr3:21480979-21482463 REVERSE | Aliases: T10K17.200	6.8	6.1	0.7	2.2	23.1%	0.7
10531	AT1G69770.1 | Symbol: CMT3 | chromomethylase 3 (CMT3), nearly identical to chromomethylase CMT3 (Arabidopsis thaliana) GI:14583092, GI:14647157 | chr1:26251990-26257248 REVERSE | Aliases: CHROMOMETHYLASE 3, T6C23.3, T6C23_3	4.6	3.9	0.7	2.2	23.1%	0.8
10532	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	7.1	-0.5	-2.2	23.2%	0.6
10533	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	8.5	9.5	-1.0	-2.2	23.2%	1.0
10534	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	8.5	9.5	-1.0	-2.2	23.2%	1.0
10535	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	3.7	4.3	-0.6	-2.2	23.2%	0.6
10536	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	3.9	-0.4	-2.2	23.2%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
10537	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	2.8	3.2	-0.3	-2.2	23.2%	0.1
10538	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	4.3	3.8	0.5	2.2	23.2%	0.6
10539	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	4.2	4.8	-0.6	-2.2	23.2%	0.4
10540	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	4.8	4.4	0.4	2.2	23.2%	0.1
10541	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	6.4	7.0	-0.6	-2.2	23.2%	0.8
10542	AT3G12230.1 | Symbol: SCPL14 |	2.6	3.4	-0.8	-2.2	23.2%	0.7
10543	AT3G12240.1 | Symbol: SCPL15 |	2.6	3.4	-0.8	-2.2	23.2%	0.7
10544	AT1G17390.1 | expressed protein | chr1:5958694-5959512 REVERSE | Aliases: F28G4.15	2.1	2.2	-0.2	-2.2	23.2%	-0.6
10545	AT5G37790.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:15025402-15028382 REVERSE | Aliases: K22F20.5, K22F20_5	6.0	5.5	0.5	2.2	23.2%	0.3
10546	AT1G15600.1 | expressed protein | chr1:5368918-5369756 FORWARD | Aliases: T16N11.10, T16N11_10	4.4	4.9	-0.5	-2.2	23.2%	0.4
10547	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	5.5	5.0	0.5	2.2	23.2%	0.6
10548	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	3.5	4.1	-0.6	-2.2	23.3%	0.6
10549	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	6.8	8.0	-1.2	-2.2	23.3%	0.6
10550	AT3G01070.1 | plastocyanin-like domain-containing protein | chr3:19599-20726 FORWARD | Aliases: T4P13.25, T4P13_25	3.4	3.8	-0.4	-2.2	23.3%	0.5
10551	AT5G43680.1 | expressed protein | chr5:17561256-17562979 FORWARD | Aliases: MQO24.4, MQO24_4	3.8	3.5	0.3	2.2	23.3%	0.3
10552	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	5.3	4.9	0.4	2.2	23.3%	0.6
10553	AT5G65710.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:26309598-26312666 FORWARD | Aliases: MPA24.6, MPA24_6	6.2	5.5	0.7	2.2	23.3%	0.9
10554	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	4.5	3.9	0.6	2.2	23.3%	0.7
10555	AT3G29750.1 | expressed protein | chr3:11581604-11583079 REVERSE | Aliases: MOD1.18	2.5	2.7	-0.2	-2.2	23.3%	0.1
10556	NA	5.9	6.7	-0.7	-2.2	23.3%	0.2
10557	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	3.2	-0.3	-2.2	23.3%	0.3
10558	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	4.9	-0.8	-2.2	23.3%	0.6

Rank	Description	Sync	Root	M	t	adj.q	B
10559	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	9.0	8.2	0.8	2.2	23.3%	0.2
10560	AT1G05860.1 | expressed protein | chr1:1769013-1771114 FORWARD | Aliases: T20M3.13, T20M3_13	3.7	3.4	0.2	2.2	23.3%	-0.0
10561	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	5.3	6.0	-0.7	-2.2	23.3%	0.6
10562	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	5.6	4.4	1.2	2.2	23.3%	0.9
10563	AT3G30450.1 | hypothetical protein, similar to At2g04970, At2g15200, At1g32830, At2g14140, At4g03990, At5g34895, At3g47270, At2g02200 | chr3:12086105-12089910 FORWARD | Aliases: MSJ3.6	1.9	2.2	-0.2	-2.2	23.3%	-0.7
10564	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	6.5	6.0	0.5	2.2	23.3%	0.4
10565	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	4.8	4.3	0.5	2.2	23.3%	0.4
10566	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	2.3	2.2	0.2	2.2	23.3%	-0.2
10567	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	2.9	3.2	-0.3	-2.2	23.4%	-0.1
10568	AT3G04310.1 | expressed protein | chr3:1141588-1142535 REVERSE | Aliases: T6K12.7, T6K12_7	4.9	4.3	0.5	2.2	23.4%	0.4
10569	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	3.4	3.8	-0.4	-2.2	23.4%	0.4
10570	AT2G42190.1 | expressed protein, ; similar to GP:9826:X07453 | chr2:17589947-17591272 FORWARD | Aliases: T24P15.10, T24P15_10	7.8	6.5	1.3	2.2	23.4%	0.7
10571	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	3.4	-0.4	-2.2	23.4%	0.4
10572	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	4.4	-0.3	-2.2	23.4%	0.3
10573	AT4G32050.1 | neurochondrin family protein, contains Pfam PF05536: Neurochondrin | chr4:15496543-15500849 FORWARD | Aliases: F10N7.130, F10N7_130	2.8	2.6	0.2	2.2	23.4%	-0.2
10574	AT3G25600.1 | calmodulin, putative, similar to calmodulin GI:239841 from (Paramecium tetraurelia) | chr3:9308491-9309199 FORWARD | Aliases: T5M7.6	7.0	7.7	-0.7	-2.2	23.4%	0.7
10575	AT5G55480.1 | glycerophosphoryl diester phosphodiesterase family protein, contains Pfam PF03009 : Glycerophosphoryl diester phosphodiesterase family; similar to Glycerophosphoryl diester phosphodiesterase precursor	4.3	3.7	0.6	2.2	23.4%	0.4
10576	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	9.1	8.8	0.4	2.2	23.4%	0.2
10577	AT3G07340.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.0	3.3	-0.3	-2.2	23.4%	0.1
10578	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	5.8	4.7	1.1	2.2	23.4%	0.7

Rank	Description	Sync	Root	M	t	adj.q	B
10579	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	4.3	4.8	-0.4	-2.2	23.4%	0.5
10580	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	4.9	4.3	0.6	2.2	23.4%	0.6
10581	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	3.9	3.3	0.5	2.2	23.5%	0.8
10582	AT1G27700.1 | expressed protein | chr1:9640185-9641853 REVERSE | Aliases: T22C5.15, T22C5_15	3.9	3.6	0.3	2.2	23.5%	0.3
10583	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	7.0	6.4	0.6	2.2	23.5%	0.7
10584	AT5G09995.3 | expressed protein | chr5:3125047-3126377 REVERSE | Aliases: None	3.7	3.1	0.6	2.2	23.5%	0.6
10585	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	4.4	4.0	0.4	2.2	23.5%	0.5
10586	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	5.3	4.9	0.3	2.2	23.5%	0.5
10587	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	6.5	6.9	-0.5	-2.2	23.5%	0.6
10588	AT1G49010.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr1:18136313-18137593 FORWARD | Aliases: F27J15.20	3.8	3.5	0.4	2.2	23.5%	0.4
10589	AT1G20690.1 | expressed protein | chr1:7174428-7176367 FORWARD | Aliases: F2D10.18, F2D10_18	2.2	2.5	-0.3	-2.2	23.5%	-0.2
10590	AT5G65440.1 | expressed protein | chr5:26168668-26174324 FORWARD | Aliases: MNA5.17, MNA5_17	5.3	4.7	0.5	2.2	23.5%	0.4
10591	AT2G04460.1 | expressed protein | chr2:1547685-1548254 REVERSE | Aliases: T1O3.13, T1O3_13	2.7	2.9	-0.2	-2.2	23.5%	-0.0
10592	AT2G31840.1 | expressed protein | chr2:13544989-13546835 REVERSE | Aliases: F20M17.12, F20M17_12	5.9	5.3	0.6	2.2	23.5%	0.6
10593	AT2G16910.1 | Symbol: AMS | basic helix-loop-helix (bHLH) family protein | chr2:7338803-7341815 FORWARD | Aliases: ABORTED MICROSPORES, F12A24.9, F12A24_9	3.2	3.6	-0.4	-2.2	23.5%	0.2
10594	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	4.6	5.5	-0.8	-2.2	23.5%	0.7
10595	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	5.4	6.2	-0.8	-2.2	23.5%	0.6
10596	AT1G23060.2 | expressed protein, Location of EST gb:T22158 and gb:AA395675 | chr1:8170796-8172473 REVERSE | Aliases: T26J12.16, T26J12_16	3.7	4.0	-0.3	-2.2	23.5%	0.1
10597	AT1G70740.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:26677294-26679543 REVERSE | Aliases: F5A18.8, F5A18_8	4.4	3.9	0.5	2.2	23.6%	0.3
10598	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	5.2	5.6	-0.4	-2.2	23.6%	0.5
10599	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	5.5	-0.7	-2.2	23.6%	0.7

Rank	Description	Sync	Root	M	t	adj.q	B
10600	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	4.8	-0.7	-2.2	23.6%	0.7
10601	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	4.6	5.1	-0.6	-2.2	23.6%	0.7
10602	AT2G18450.1 | Symbol: SDH1 2 |	5.0	6.1	-1.1	-2.2	23.7%	0.8
10603	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	2.7	-0.2	-2.2	23.7%	-0.1
10604	AT1G18220.1 | Symbol: ATPUP9 |	2.7	3.1	-0.4	-2.2	23.7%	0.1
10605	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	2.8	0.5	2.2	23.7%	0.5
10606	AT4G35200.1 | expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function | chr4:16749147-16749908 REVERSE | Aliases: T12J5.70, T12J5_70	2.7	3.2	-0.4	-2.2	23.7%	0.3
10607	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	3.2	-0.2	-2.2	23.7%	-0.3
10608	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	7.9	6.8	1.1	2.2	23.7%	0.7
10609	AT5G53370.1 | pectinesterase family protein | chr5:21666758-21668819 REVERSE | Aliases: ATPMEPCRF, K19E1.17, K19E1_17	7.3	8.7	-1.4	-2.2	23.7%	0.9
10610	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	10.1	9.5	0.6	2.2	23.7%	0.0
10611	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}	4.4	4.0	0.4	2.2	23.7%	0.5
10612	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	2.3	2.5	-0.2	-2.2	23.7%	-0.1
10613	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	4.3	4.0	0.3	2.2	23.8%	0.3
10614	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	3.9	4.7	-0.8	-2.2	23.8%	0.8
10615	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	3.3	-0.4	-2.2	23.8%	0.2
10616	AT2G27395.1 | cysteine protease-related, contains similarity to senescence-specific cysteine protease GI:5823018 from (Brassica napus)	3.0	3.4	-0.4	-2.2	23.8%	0.1
10617	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	2.7	3.0	-0.3	-2.2	23.8%	0.3
10618	AT2G36200.1 | kinesin motor protein-related | chr2:15186802-15192293 REVERSE | Aliases: F2H17.19, F2H17_19	4.8	4.3	0.5	2.2	23.8%	0.7
10619	AT1G54210.1 | autophagy 12a (APG12a), identical to autophagy 12a (Arabidopsis thaliana) GI:19912169 | chr1:20244912-20246230 FORWARD | Aliases: F20D21.38, F20D21_38	5.0	4.5	0.5	2.2	23.8%	0.5
10620	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	3.4	-0.5	-2.2	23.8%	0.3

Rank	Description	Sync	Root	M	t	adj.q	B
10621	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	7.3	7.9	-0.6	-2.2	23.8%	0.8
10622	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	2.7	3.0	-0.3	-2.2	23.9%	-0.0
10623	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	3.0	2.7	0.2	2.2	23.9%	-0.1
10624	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	2.9	-0.3	-2.2	23.9%	-0.0
10625	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	6.7	7.0	-0.3	-2.2	23.9%	0.2
10626	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	3.2	4.1	-0.9	-2.2	23.9%	0.8
10627	AT3G29430.1 | geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltranstransferase, putative, similar to gi:413730; similar to geranylgeranyl pyrophosphate synthase, chloroplast precursor GB:P34802 from (Arabidopsis thaliana) | chr3:11312593-11314029 FORWARD | Aliases: MUO10.10	3.9	4.2	-0.3	-2.2	23.9%	0.2
10628	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	3.5	-0.4	-2.2	23.9%	0.4
10629	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	3.9	4.5	-0.6	-2.2	23.9%	0.6
10630	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	3.1	2.8	0.3	2.2	24.0%	-0.0
10631	AT3G04560.1 | expressed protein | chr3:1226624-1229414 REVERSE | Aliases: F7O18.3, F7O18_3	9.1	8.7	0.4	2.2	24.0%	0.5
10632	AT3G20070.2 | Symbol: TTN9 | expressed protein | chr3:7004678-7006888 REVERSE | Aliases: MAL21.7, TITAN9	3.9	3.5	0.4	2.2	24.0%	0.4
10633	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	2.3	-0.1	-2.2	24.0%	-0.7
10634	AT3G26850.2 | expressed protein | chr3:9896779-9899243 REVERSE | Aliases: MDJ14.17	4.0	3.8	0.2	2.2	24.0%	-0.2
10635	AT4G27370.1 | Symbol: VIIIB | myosin family protein, contains Pfam profiles: PF00063 myosin head (motor domain), PF00612 IQ calmodulin-binding motif | chr4:13694887-13700786 REVERSE | Aliases: F27G19.14, TVIIIB	4.2	3.8	0.4	2.2	24.0%	0.3
10636	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	2.7	-0.2	-2.2	24.0%	-0.4
10637	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	8.5	9.8	-1.3	-2.2	24.0%	0.7
10638	AT1G10980.1 | expressed protein, ; expression supported by MPSS | chr1:3667531-3669821 REVERSE | Aliases: T19D16.10, T19D16_10	3.4	3.1	0.3	2.2	24.0%	0.1
10639	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	3.9	4.4	-0.6	-2.2	24.0%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
10640	AT3G24170.2 | similar to gluthatione 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	10.8	9.8	1.0	2.2	24.0%	0.5
10641	AT4G39120.1 | inositol monophosphatase family protein, low similarity to Mono-phosphatase (Streptomyces anulatus) GI:1045231; contains Pfam profile PF00459: Inositol monophosphatase family | chr4:18225572-18227901 REVERSE | Aliases: T22F8.20, T22F8_20	3.8	3.4	0.4	2.2	24.0%	0.5
10642	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	8.8	8.0	0.8	2.2	24.0%	0.8
10643	AT1G27000.1 | bZIP family transcription factor	7.1	8.3	-1.2	-2.2	24.1%	0.5
10644	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	5.0	4.6	0.4	2.2	24.1%	0.5
10645	AT2G31740.1 | expressed protein | chr2:13497985-13502187 REVERSE | Aliases: F20M17.22, F20M17_22	7.1	6.7	0.4	2.2	24.1%	0.5
10646	AT5G61800.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:24847213-24848779 REVERSE | Aliases: MAC9.12, MAC9_12	4.7	4.2	0.5	2.2	24.1%	0.3
10647	AT3G20900.1 | expressed protein | chr3:7323990-7324676 REVERSE | Aliases: MFD22.2	4.3	4.9	-0.6	-2.2	24.1%	0.5
10648	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	4.1	3.6	0.5	2.2	24.1%	0.1
10649	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	5.0	4.4	0.5	2.2	24.1%	0.7
10650	AT5G14040.1 | mitochondrial phosphate transporter, identical to mitochondrial phosphate transporter GI:3318617 from (Arabidopsis thaliana) | chr5:4530645-4533072 REVERSE | Aliases: MUA22.4, MUA22_4	9.3	7.9	1.5	2.2	24.1%	0.8
10651	AT1G05840.1 | aspartyl protease family protein, contains Pfam PF00026: Eukaryotic aspartyl protease | chr1:1762767-1766280 REVERSE | Aliases: T20M3.11, T20M3_11	7.6	8.0	-0.5	-2.2	24.1%	0.6
10652	AT5G19875.1 | expressed protein | chr5:6718343-6718997 FORWARD | Aliases: None	6.8	7.4	-0.6	-2.2	24.1%	0.6
10653	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	3.1	2.7	0.4	2.2	24.1%	0.4
10654	AT1G12260.1 | Symbol: ANAC007/EMB2749 | no apical meristem (NAM) family protein, similar to NAC2 (GI:6456751)	2.6	2.9	-0.2	-2.2	24.1%	-0.1
10655	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	4.6	-0.3	-2.2	24.1%	0.3
10656	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	6.5	6.0	0.5	2.2	24.1%	0.7
10657	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	2.6	-0.3	-2.2	24.1%	0.1

Rank	Description	Sync	Root	M	t	adj.q	B
10658	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	3.6	0.3	2.2	24.1%	0.2
10659	NA	4.0	4.8	-0.8	-2.2	24.2%	0.3
10660	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	3.6	4.1	-0.5	-2.2	24.2%	0.4
10661	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	4.8	1.3	2.2	24.2%	0.7
10662	AT5G01075.1 | expressed protein | chr5:26881-27448 REVERSE | Aliases: None	2.2	2.4	-0.2	-2.2	24.2%	-0.5
10663	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)	2.5	2.3	0.2	2.2	24.2%	-0.2
10664	AT4G24110.1 | expressed protein | chr4:12519942-12520823 REVERSE | Aliases: T19F6.100, T19F6_100	7.0	5.3	1.8	2.2	24.2%	1.0
10665	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	6.6	7.4	-0.8	-2.2	24.2%	0.5
10666	AT4G11130.1 | Symbol: RDR2 | RNA-dependent RNA polymerase, putative, similar to RNA-directed RNA polymerase (Lycopersicon esculentum) gi:4038592:emb:CAA71421	4.6	4.2	0.4	2.2	24.2%	0.1
10667	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	8.3	7.7	0.5	2.2	24.2%	0.3
10668	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	3.6	-0.3	-2.2	24.2%	-0.0
10669	AT2G14570.1 | SWIM zinc finger family protein | chr2:6228862-6230999 REVERSE | Aliases: T13P21.5, T13P21_5	4.4	4.1	0.3	2.2	24.2%	0.1
10670	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	8.6	7.0	1.7	2.2	24.2%	0.8
10671	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	3.1	-0.3	-2.2	24.2%	0.2
10672	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	3.4	4.0	-0.6	-2.2	24.2%	0.2
10673	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	3.4	-0.2	-2.2	24.2%	-0.2
10674	AT4G30970.1 | expressed protein | chr4:15069272-15074594 REVERSE | Aliases: F6I18.120, F6I18_120	3.8	4.0	-0.2	-2.2	24.2%	-0.1
10675	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	4.8	5.3	-0.5	-2.2	24.2%	0.6
10676	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	3.8	-0.3	-2.2	24.2%	0.0
10677	AT1G09280.2 | expressed protein, contains Pfam profile: PF03959 domain of unknown function (DUF341) | chr1:2997552-3001296 REVERSE | Aliases: T12M4.1, T12M4_1	7.2	6.8	0.4	2.2	24.2%	0.1
10678	AT3G49990.1 | expressed protein | chr3:18543308-18545257 REVERSE | Aliases: F3A4.70	6.2	5.4	0.8	2.2	24.2%	0.5
10679	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	2.6	-0.3	-2.2	24.2%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
10680	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	4.0	4.7	-0.7	-2.2	24.3%	0.4
10681	AT4G37650.1 | Symbol: SHR | short-root transcription factor (SHR) | chr4:17691780-17693754 FORWARD | Aliases: F19F18.140, F19F18_140, SGR7, SHORT ROOT	5.3	5.8	-0.5	-2.2	24.3%	0.6
10682	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	3.8	3.0	0.8	2.2	24.3%	0.8
10683	AT5G37130.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain | chr5:14698608-14703914 FORWARD | Aliases: MJG14.18, MJG14_18	4.2	5.2	-1.0	-2.2	24.3%	0.8
10684	AT3G05880.1 | Symbol: RCI2A | hydrophobic protein (RCI2A) / low temperature and salt responsive protein (LTI6A), identical to SP:Q9ZNQ7 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	11.1	11.6	-0.5	-2.2	24.3%	0.2
10685	AT2G17210.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:7492480-7494684 REVERSE | Aliases: T23A1.7, T23A1_7	3.4	3.7	-0.3	-2.2	24.3%	-0.0
10686	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	3.6	3.9	-0.3	-2.2	24.3%	0.2
10687	AT3G28670.1 | expressed protein | chr3:10745060-10748400 FORWARD | Aliases: MZN14.14	7.1	6.7	0.5	2.2	24.3%	0.6
10688	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	2.5	2.7	-0.2	-2.2	24.3%	-0.4
10689	AT2G20840.1 | secretory carrier membrane protein (SCAMP) family protein, contains Pfam domain, PF04144: SCAMP family | chr2:8978843-8981551 REVERSE | Aliases: F5H14.19, F5H14_19	5.0	4.6	0.4	2.2	24.3%	0.4
10690	AT4G22750.1 | zinc finger (DHHC type) family protein, contains DHHC zinc finger domain PF01529	6.9	7.9	-1.0	-2.2	24.4%	0.7
10691	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	5.8	0.7	2.2	24.4%	0.9
10692	AT2G34600.1 | expressed protein | chr2:14580251-14580899 FORWARD | Aliases: T31E10.6, T31E10_6	2.9	2.2	0.7	2.2	24.4%	0.1
10693	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	4.3	3.5	0.8	2.2	24.4%	0.7
10694	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	2.5	-0.3	-2.2	24.4%	-0.3
10695	AT5G67270.1 | Symbol: ATEB1C |	4.5	3.8	0.7	2.2	24.4%	0.6
10696	AT5G09670.2 | loricrin-related, contains weak similarity to Loricrin (Swiss-Prot:P23490) (Homo sapiens) | chr5:2995913-2998917 REVERSE | Aliases: F17I14.140, F17I14_140	7.7	8.2	-0.5	-2.2	24.4%	0.5
10697	AT5G59020.1 | expressed protein | chr5:23844262-23846829 REVERSE | Aliases: K19M22.16, K19M22_16	4.2	3.7	0.5	2.2	24.4%	0.6
10698	AT4G36760.2 | Symbol: ATAPP1 |	7.2	8.0	-0.9	-2.2	24.4%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
10699	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	7.1	6.7	0.4	2.2	24.5%	0.5
10700	AT5G05760.1 | Symbol: SYP31 | syntaxin 31 (SYP31) / SED5, identical to SP:Q9FFK1 Syntaxin 31 (AtSYP31) (AtSED5) {Arabidopsis thaliana} | chr5:1727473-1731022 REVERSE | Aliases: ATSED5, ATSYP31, MJJ3.17, MJJ3_17, T SNARE SED 5	4.3	3.7	0.6	2.2	24.5%	0.6
10701	AT3G49780.1 | Symbol: ATPSK3 |	4.2	4.9	-0.7	-2.2	24.5%	0.8
10702	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	7.3	6.6	0.6	2.2	24.5%	0.5
10703	AT5G54620.1 | ankyrin repeat family protein, contains Pfam domain, PF00023: Ankyrin repeat | chr5:22204987-22206972 REVERSE | Aliases: MRB17.12, MRB17_12	2.4	2.6	-0.2	-2.2	24.5%	-0.2
10704	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	8.5	7.5	1.0	2.2	24.5%	0.5
10705	AT4G22400.1 | expressed protein | chr4:11816841-11817824 FORWARD | Aliases: F7K2.5, F7K2_5	2.8	3.1	-0.3	-2.2	24.6%	0.1
10706	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	4.0	3.6	0.5	2.2	24.6%	0.6
10707	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)	5.6	4.9	0.7	2.2	24.6%	0.6
10708	AT5G16920.1 | expressed protein | chr5:5567014-5568131 FORWARD | Aliases: F2K13.70, F2K13_70	2.0	2.1	-0.1	-2.2	24.6%	-0.7
10709	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	5.1	4.6	0.4	2.2	24.6%	0.6
10710	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	5.0	5.3	-0.4	-2.2	24.6%	0.3
10711	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	6.0	5.5	0.5	2.2	24.6%	0.3
10712	AT3G53440.2 | expressed protein | chr3:19821766-19823648 FORWARD | Aliases: F4P12.140	3.5	3.3	0.3	2.2	24.6%	0.1
10713	AT5G49820.1 | Symbol: EMB1879 | expressed protein, contains Pfam domain, PF04884: Protein of unknown function, DUF647	6.3	6.9	-0.6	-2.2	24.6%	0.6
10714	AT5G25140.1 | Symbol: CYP71B13 | cytochrome P450 family protein, CYTOCHROME P450 71B1 - Thlaspi arvense, EMBL:L24438 | chr5:8672427-8674632 FORWARD | Aliases: F21J6.4	2.9	3.1	-0.3	-2.2	24.6%	0.1
10715	AT2G47820.1 | expressed protein | chr2:19594478-19597892 FORWARD | Aliases: F17A22.21	2.8	3.1	-0.3	-2.2	24.6%	0.1
10716	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}	6.0	5.5	0.5	2.2	24.6%	0.6
10717	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	3.1	2.8	0.3	2.2	24.6%	0.1
10718	AT5G01090.1 | legume lectin family protein, contains Pfam domain, PF00139: Legume lectins beta domain | chr5:32831-34325 FORWARD | Aliases: F7J8.70, F7J8_70	7.0	6.5	0.5	2.2	24.6%	0.6
10719	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	9.8	9.3	0.5	2.2	24.6%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
10720	AT3G13480.1 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g55475.1); similar to P0415C01.14 [Oryza sativa (japonica cultivar-group)] (GB:NP_917459.1)	7.2	8.0	-0.8	-2.2	24.7%	0.4
10721	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	3.4	-0.3	-2.2	24.7%	-0.1
10722	AT5G67200.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:26830951-26833792 REVERSE | Aliases: K21H1.16, K21H1_16	3.8	3.4	0.4	2.2	24.7%	0.4
10723	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)	4.1	4.5	-0.4	-2.2	24.7%	0.2
10724	AT3G47270.1 | expressed protein, similar to At2g04970, At2g15200, At1g32830, At2g14140, At3g30450, At4g03990, At5g34895, At2g02200 | chr3:17420777-17424798 FORWARD | Aliases: T21L8.20	2.0	2.4	-0.3	-2.2	24.7%	-0.6
10725	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	10.4	9.5	0.9	2.2	24.7%	0.4
10726	AT2G02580.1 | Symbol: CYP71B9 | cytochrome P450 family protein | chr2:701945-703769 FORWARD | Aliases: T8K22.12, T8K22_12	2.8	3.0	-0.2	-2.2	24.7%	-0.1
10727	AT4G34560.1 | expressed protein | chr4:16507640-16508759 FORWARD | Aliases: T4L20.140, T4L20_140	2.5	2.8	-0.3	-2.2	24.7%	0.0
10728	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	4.6	5.2	-0.6	-2.2	24.7%	0.6
10729	AT5G35320.1 | expressed protein | chr5:13539049-13540655 FORWARD | Aliases: T26D22.2, T26D22_2	4.4	3.9	0.5	2.2	24.8%	0.3
10730	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	3.6	4.2	-0.6	-2.2	24.8%	0.6
10731	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	6.0	5.2	0.8	2.2	24.8%	0.4
10732	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	2.4	-0.2	-2.2	24.8%	-0.5
10733	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	4.8	5.4	-0.6	-2.1	24.8%	0.5
10734	AT5G02990.1 | kelch repeat-containing F-box family protein, contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	4.9	5.4	-0.5	-2.1	24.8%	0.4
10735	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, Arabidopdis 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	7.0	6.5	0.5	2.1	24.8%	0.4
10736	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	2.6	2.8	-0.2	-2.1	24.8%	-0.2
10737	AT3G21865.1 | expressed protein | chr3:7701139-7703328 REVERSE | Aliases: MSD21.24, MSD21_24	9.6	9.2	0.4	2.1	24.8%	0.3
10738	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	3.3	-0.3	-2.1	24.9%	-0.1
10739	AT5G12450.1 | expressed protein, similarity to predicted proteins, Arabidopsis thaliana | chr5:4040940-4041131 FORWARD | Aliases: None	3.3	3.8	-0.4	-2.1	24.9%	-0.1
10740	AT3G29080.1 | expressed protein | chr3:11070589-11072613 FORWARD | Aliases: MXE2.4	2.9	3.7	-0.8	-2.1	24.9%	0.7
10741	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: HOMEOBOX PROTEIN, T8B10.50	3.6	4.1	-0.4	-2.1	24.9%	0.4
10742	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	10.2	9.3	0.9	2.1	24.9%	0.6

Rank	Description	Sync	Root	M	t	adj.q	B
10743	AT3G62610.1 | myb family transcription factor, similar to myb-like transcription factor GI:168590 from (Zea mays) | chr3:23165734-23167561 FORWARD | Aliases: F26K9.40	3.3	3.8	-0.5	-2.1	24.9%	0.3
10744	AT1G51570.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr1:19125844-19128356 REVERSE | Aliases: F19C24.20, F19C24_20	5.5	4.9	0.6	2.1	24.9%	0.6
10745	AT4G02630.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	6.1	5.4	0.7	2.1	24.9%	0.6
10746	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	6.4	6.8	-0.4	-2.1	24.9%	0.3
10747	AT5G22320.1 | leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560 | chr5:7388007-7390454 REVERSE | Aliases: MWD9.11, MWD9_11	7.7	6.4	1.3	2.1	24.9%	0.6
10748	AT4G26620.1 | sucrase-related | chr4:13427417-13429965 REVERSE | Aliases: T15N24.70, T15N24_70	7.8	7.3	0.5	2.1	24.9%	0.4
10749	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	5.3	0.6	2.1	24.9%	0.5
10750	AT1G11730.1 | galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase | chr1:3957473-3960113 FORWARD | Aliases: F25C20.12, F25C20_12	3.8	4.3	-0.5	-2.1	24.9%	0.4
10751	AT5G13590.1 | expressed protein | chr5:4374721-4378478 REVERSE | Aliases: T6I14.8	3.2	3.9	-0.7	-2.1	24.9%	0.4
10752	AT1G02790.1 | Symbol: PGA4 | exopolygalacturonase / galacturan 1,4-alpha-galacturonidase (PGA3) / pectinase, identical to SP:P49062 Exopolygalacturonase 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	3.2	-0.3	-2.1	25.0%	0.1
10753	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	4.4	3.9	0.5	2.1	25.0%	0.5
10754	AT4G00280.1 | expressed protein | chr4:122409-122851 REVERSE | Aliases: A_IG005I10.10, A_IG005I10_10, F5I10.10, F5I10_10	4.0	4.3	-0.3	-2.1	25.0%	-0.1
10755	AT5G19680.1 | leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560 | chr5:6649610-6651937 FORWARD | Aliases: T29J13.100, T29J13_100	6.9	5.9	1.0	2.1	25.0%	0.5
10756	AT4G20480.1 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537 | chr4:11034283-11035885 REVERSE | Aliases: F9F13.130, F9F13_130	8.1	8.8	-0.7	-2.1	25.0%	0.5
10757	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	5.1	4.7	0.3	2.1	25.0%	0.3
10758	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	3.2	-0.3	-2.1	25.0%	0.2
10759	AT3G08000.1 | RNA-binding protein, putative, similar to RNA-binding protein from (Nicotiana tabacum) GI:15822703, (Nicotiana sylvestris) 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	3.8	0.3	2.1	25.0%	0.2
10760	AT4G28410.1 | aminotransferase-related, similar to nicotianamine aminotransferase (Hordeum vulgare subsp. vulgare) GI:6469090 | chr4:14052252-14055018 FORWARD | Aliases: F20O9.90, F20O9_90	3.0	3.3	-0.3	-2.1	25.0%	0.2
10761	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	4.6	5.4	-0.8	-2.1	25.1%	0.6
10762	AT5G14420.4 | copine-related, low similarity to SP:Q99829 Copine I {Homo sapiens} | chr5:4648115-4650793 REVERSE | Aliases: F18O22.210, F18O22_210	4.8	5.3	-0.5	-2.1	25.1%	0.3
10763	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	3.9	3.5	0.4	2.1	25.1%	0.3

Rank	Description	Sync	Root	M	t	adj.q	B
10764	AT4G32910.1 | expressed protein | chr4:15881259-15885390 FORWARD | Aliases: F26P21.30, F26P21_30	8.7	8.1	0.6	2.1	25.1%	0.5
10765	AT2G21940.2 | shikimate kinase, putative, similar to shikimate kinase precursor from Lycopersicon esculentum (SP:Q00497); contains Pfam shikimate kinase domain PF01202 | chr2:9357926-9360235 FORWARD | Aliases: F7D8.26, F7D8_26	5.7	6.5	-0.8	-2.1	25.1%	0.5
10766	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	5.2	-0.5	-2.1	25.1%	0.2
10767	ATMG00630.1 | Symbol: ORF110B | hypothetical protein | chrM:183111-183443 FORWARD | Aliases: ORF110B	4.4	6.5	-2.2	-2.1	25.1%	0.7
10768	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	3.8	3.5	0.3	2.1	25.1%	0.1
10769	AT5G25500.1 | expressed protein, ; expression supported by MPSS | chr5:8881121-8882383 FORWARD | Aliases: T14C9.40, T14C9_40	5.3	4.8	0.5	2.1	25.1%	0.7
10770	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	3.6	4.1	-0.4	-2.1	25.1%	0.3
10771	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	2.3	-0.2	-2.1	25.1%	-0.2
10772	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	3.2	2.6	0.6	2.1	25.1%	0.3
10773	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	3.7	-0.3	-2.1	25.1%	0.2
10774	AT4G21150.1 | ribophorin II (RPN2) family protein, contains Pfam domain PF05817: Ribophorin II (RPN2) | chr4:11278439-11283858 FORWARD | Aliases: F7J7.90, F7J7_90	6.7	5.8	0.9	2.1	25.2%	0.7
10775	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	4.4	4.1	0.3	2.1	25.2%	0.3
10776	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	3.1	-0.3	-2.1	25.2%	0.1
10777	AT1G49110.1 | expressed protein | chr1:18175263-18176118 FORWARD | Aliases: F27J15.12, F27J15_12	4.5	5.0	-0.5	-2.1	25.2%	0.5
10778	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	4.0	3.4	0.6	2.1	25.2%	0.4
10779	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	3.1	3.4	-0.2	-2.1	25.2%	-0.2
10780	AT4G09970.2 | expressed protein | chr4:6245958-6248159 FORWARD | Aliases: T5L19.100, T5L19_100	4.8	4.3	0.5	2.1	25.2%	0.5
10781	AT5G12340.1 | expressed protein, ; expression supported by MPSS | chr5:3992949-3993611 REVERSE | Aliases: None	3.7	4.2	-0.6	-2.1	25.2%	0.5
10782	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	6.9	-0.8	-2.1	25.3%	0.5
10783	AT5G18540.2 | expressed protein, contains InterPro domain Bipartite nuclear localization signal (InterPro:IPR001472) | chr5:6153871-6156168 FORWARD | Aliases: T28N17.20, T28N17_20	5.2	4.4	0.8	2.1	25.3%	0.6
10784	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	8.4	9.1	-0.7	-2.1	25.3%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
10785	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	8.6	9.2	-0.6	-2.1	25.3%	0.3
10786	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	3.8	-0.3	-2.1	25.3%	0.1
10787	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	3.5	3.1	0.4	2.1	25.3%	0.5
10788	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	7.5	6.4	1.1	2.1	25.3%	0.5
10789	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	3.2	3.4	-0.2	-2.1	25.3%	-0.1
10790	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	2.4	-0.1	-2.1	25.3%	-0.8
10791	AT3G46270.1 | receptor protein kinase-related, contains weak similarity to light repressible receptor protein kinase (GI:1321686) (Arabidopsis thaliana) | chr3:17011699-17015222 REVERSE | Aliases: F12M12.240	2.0	2.1	-0.1	-2.1	25.3%	-0.6
10792	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	3.1	2.8	0.3	2.1	25.3%	0.2
10793	AT1G65440.1 | Symbol: GTB1 | glycine-rich protein | chr1:24310330-24318236 REVERSE | Aliases: GLOBAL TRANSCRIPTION FACTOR GROUP B, T8F5.22, T8F5_22	7.6	8.1	-0.6	-2.1	25.3%	0.4
10794	AT2G04870.1 | expressed protein | chr2:1716165-1716383 REVERSE | Aliases: F28I8.6, F28I8_6	3.6	4.0	-0.4	-2.1	25.3%	0.2
10795	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)	4.3	3.9	0.4	2.1	25.3%	0.5
10796	AT2G40090.1 | Symbol: ATATH9 |	5.3	4.8	0.5	2.1	25.3%	0.4
10797	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	5.5	5.1	0.4	2.1	25.3%	0.1
10798	AT5G51650.1 | hypothetical protein | chr5:20995429-20996475 REVERSE | Aliases: K17N15.20, K17N15_20	3.0	3.2	-0.2	-2.1	25.3%	-0.0
10799	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	2.8	3.2	-0.4	-2.1	25.4%	0.1
10800	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	3.2	-0.3	-2.1	25.4%	-0.1
10801	AT1G25370.1 | expressed protein | chr1:8897744-8899089 REVERSE | Aliases: F4F7.1	5.4	5.8	-0.4	-2.1	25.4%	0.1
10802	AT2G06700.1 | expressed protein | chr2:2671715-2672368 REVERSE | Aliases: T14A4.14, T14A4_14	4.7	5.3	-0.6	-2.1	25.4%	0.7
10803	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	2.1	-0.1	-2.1	25.4%	-0.7
10804	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	7.5	6.2	1.2	2.1	25.5%	0.7

Rank	Description	Sync	Root	M	t	adj.q	B
10805	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	4.9	5.5	-0.5	-2.1	25.5%	0.4
10806	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	3.5	3.8	-0.4	-2.1	25.5%	0.3
10807	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	6.1	5.3	0.8	2.1	25.5%	0.3
10808	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	7.7	9.4	-1.7	-2.1	25.5%	0.9
10809	AT1G52390.1 | expressed protein | chr1:19515637-19515903 REVERSE | Aliases: F19K6.2, F19K6_2	3.1	3.3	-0.2	-2.1	25.5%	-0.4
10810	AT1G32430.1 | F-box family protein, contains F-box domain Pfam:PF00646	4.6	5.0	-0.5	-2.1	25.5%	0.3
10811	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	6.1	-0.4	-2.1	25.5%	0.2
10812	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	6.7	6.0	0.7	2.1	25.5%	0.6
10813	AT2G14560.2 | expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567) | chr2:6221054-6221870 FORWARD | Aliases: T13P21.6, T13P21_6	3.1	3.3	-0.3	-2.1	25.5%	-0.0
10814	AT4G02750.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr4:1221116-1223461 REVERSE | Aliases: T5J8.5, T5J8_5	5.0	4.2	0.8	2.1	25.5%	0.8
10815	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	2.5	2.7	-0.2	-2.1	25.5%	-0.1
10816	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)	4.1	4.6	-0.5	-2.1	25.5%	0.6
10817	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	2.9	-0.2	-2.1	25.5%	-0.6
10818	AT2G07290.1 | expressed protein | chr2:3029558-3030032 FORWARD | Aliases: T13E11.6, T13E11_6	3.0	3.3	-0.3	-2.1	25.5%	0.1
10819	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	6.5	5.5	1.0	2.1	25.5%	0.7
10820	AT3G61720.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr3:22853986-22856373 REVERSE | Aliases: F21F14.8	3.4	3.9	-0.5	-2.1	25.5%	0.1
10821	AT3G24210.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023 | chr3:8753481-8756072 REVERSE | Aliases: MUJ8.11	3.3	3.7	-0.4	-2.1	25.5%	0.3
10822	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	6.1	-0.5	-2.1	25.5%	0.4
10823	AT5G17190.1 | expressed protein, similar to unknown protein (gb:AAF26109.1) | chr5:5652225-5652985 FORWARD | Aliases: MKP11.4, MKP11_4	9.5	8.5	1.0	2.1	25.6%	0.4
10824	AT1G51480.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.5	2.8	-0.2	-2.1	25.6%	-0.2
10825	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	4.9	4.3	0.6	2.1	25.6%	0.5
10826	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.	6.6	6.1	0.5	2.1	25.6%	0.3

Rank	Description	Sync	Root	M	t	adj.q	B
10827	AT4G31270.1 | expressed protein | chr4:15183235-15184967 REVERSE | Aliases: F8F16.90, F8F16_90	5.3	4.7	0.6	2.1	25.6%	0.5
10828	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	2.7	3.0	-0.3	-2.1	25.6%	0.0
10829	AT3G05670.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr3:1653270-1657165 FORWARD | Aliases: F18C1.6, F18C1_6	5.3	6.1	-0.8	-2.1	25.6%	0.6
10830	AT2G22720.3 | expressed protein | chr2:9664567-9667856 FORWARD | Aliases: T9I22.16, T9I22_16	4.8	5.1	-0.3	-2.1	25.6%	0.2
10831	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	3.0	3.3	-0.3	-2.1	25.6%	0.2
10832	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	4.8	5.2	-0.4	-2.1	25.6%	0.3
10833	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	8.1	8.6	-0.5	-2.1	25.6%	0.3
10834	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	4.7	4.3	0.4	2.1	25.6%	0.4
10835	AT2G40420.1 | amino acid transporter family protein, similar to neuronal glutamine transporter (Rattus norvegicus) GI:6978016; contains Pfam profile PF01490: Transmembrane amino acid transporter protein | chr2:16884318-16886292 FORWARD | Aliases: T3G21.19, T3G21_19	4.6	5.2	-0.6	-2.1	25.7%	0.5
10836	AT4G18975.2 | similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At4g21190.1); contains InterPro domain PPR repeat (InterPro:IPR002885)	4.8	4.3	0.6	2.1	25.7%	0.5
10837	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	3.7	3.2	0.4	2.1	25.7%	0.1
10838	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	9.2	8.6	0.6	2.1	25.7%	0.4
10839	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	12.3	12.7	-0.4	-2.1	25.7%	-0.5
10840	AT5G02210.1 | expressed protein, ; expression supported by MPSS | chr5:439251-439872 REVERSE | Aliases: T7H20.260, T7H20_260	4.2	3.5	0.7	2.1	25.7%	0.7
10841	AT4G04770.1 | Symbol: ATABC1 |	9.4	8.8	0.6	2.1	25.7%	0.2
10842	AT3G03300.1 | Symbol: DCL2 | DEAD/DEAH box helicase carpel factory-related, similar to RNA helicase GB:AAF03534 | chr3:768027-774834 REVERSE | Aliases: T17B22.28	5.0	5.8	-0.8	-2.1	25.7%	0.2
10843	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 nitrobenzylmercaptopurine 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	3.5	-0.5	-2.1	25.7%	0.2
10844	AT4G02330.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr4:1032413-1035037 FORWARD | Aliases: ATPMEPCRB, T14P8.14, T14P8_14	4.9	5.6	-0.8	-2.1	25.7%	0.6
10845	AT1G11260.1 | glucose transporter (STP1), nearly identical to glucose transporter GB:P23586 SP:P23586 from (Arabidopsis thaliana) | chr1:3777329-3780337 FORWARD | Aliases: T28P6.9, T28P6_9	6.4	7.2	-0.9	-2.1	25.7%	0.5
10846	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	2.9	2.6	0.3	2.1	25.8%	-0.2
10847	AT4G09470.1 | expressed protein | chr4:6010994-6012217 REVERSE | Aliases: T15G18.110, T15G18_110	3.0	3.7	-0.7	-2.1	25.8%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
10848	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	9.2	8.6	0.6	2.1	25.8%	0.3
10849	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	2.8	2.5	0.3	2.1	25.8%	0.0
10850	AT3G43140.1 | hypothetical protein, predicted proteins, Arabidopsis thaliana | chr3:15123419-15123833 FORWARD | Aliases: F7M19.150	3.3	3.8	-0.4	-2.1	25.8%	0.2
10851	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) (Oryctolagus cuniculus) | chr3:20947077-20950609 REVERSE | Aliases: T5P19.130	2.4	2.8	-0.4	-2.1	25.8%	-0.2
10852	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	3.2	3.6	-0.4	-2.1	25.8%	0.1
10853	AT5G46400.1 | expressed protein | chr5:18837259-18841877 FORWARD | Aliases: MPL12.20, MPL12_20	3.2	3.0	0.2	2.1	25.8%	-0.1
10854	AT4G16970.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:9551478-9555839 REVERSE | Aliases: DL4515C, FCAALL.319	3.7	3.3	0.4	2.1	25.8%	0.5
10855	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}	8.3	7.8	0.4	2.1	25.8%	0.2
10856	AT5G15880.1 | expressed protein | chr5:5185791-5188050 FORWARD | Aliases: F1N13.20, F1N13_20	6.9	6.5	0.4	2.1	25.8%	0.2
10857	AT2G29940.1 | ABC transporter family protein, similar to ABC1 protein GI:14331118 from (Nicotiana plumbaginifolia) | chr2:12767216-12773700 FORWARD | Aliases: F23F1.14, F23F1_14	2.8	2.9	-0.1	-2.1	25.8%	-0.6
10858	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	5.9	5.4	0.5	2.1	25.8%	0.6
10859	AT5G65550.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase ;similar to flavonol 3-O-glucosyltransferase (anthocyanin rhamnosyl transferase) from Petunia hybrida (SP:Q43716)	3.8	4.3	-0.4	-2.1	25.8%	0.3
10860	AT3G56750.1 | expressed protein | chr3:21029068-21031410 REVERSE | Aliases: T8M16.80	3.1	2.7	0.4	2.1	25.8%	0.2
10861	AT1G12970.1 | leucine-rich repeat family protein | chr1:4423638-4425787 FORWARD | Aliases: F13K23.23, F13K23_23	3.7	4.0	-0.3	-2.1	25.8%	-0.0
10862	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	9.5	8.9	0.7	2.1	25.8%	0.4
10863	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	7.3	6.3	1.0	2.1	25.8%	0.6
10864	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	2.9	-0.3	-2.1	25.8%	-0.0
10865	AT3G54080.1 | expressed protein | chr3:20036245-20038000 FORWARD | Aliases: F24B22.40	6.3	5.7	0.5	2.1	25.9%	0.4
10866	AT1G04200.1 | expressed protein, Contains similarity to gb:Z69902 from C. elegans | chr1:1109489-1114049 FORWARD | Aliases: F20D22.3, F20D22_3	5.1	5.7	-0.6	-2.1	25.9%	0.5
10867	AT1G68980.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:25936686-25938545 FORWARD | Aliases: T6L1.16, T6L1_16	4.4	4.1	0.4	2.1	25.9%	0.3
10868	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)	3.6	3.1	0.5	2.1	25.9%	0.4
10869	AT1G09310.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr1:3009057-3009882 FORWARD | Aliases: T31J12.3, T31J12_3	3.0	2.8	0.2	2.1	25.9%	-0.0

Rank	Description	Sync	Root	M	t	adj.q	B
10870	AT2G31190.1 | expressed protein, contains Pfam domain, PF04884: Protein of unknown function, DUF647 | chr2:13298303-13300839 REVERSE | Aliases: F16D14.3, F16D14_3	5.7	5.2	0.5	2.1	25.9%	0.5
10871	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	2.8	-0.3	-2.1	25.9%	-0.0
10872	AT1G67855.1 | expressed protein, hypothetical protein | chr1:25445809-25447019 REVERSE | Aliases: F12A21.1, F12A21_1	2.4	2.5	-0.2	-2.1	26.0%	-0.6
10873	AT3G16730.1 | expressed protein, ; expression supported by MPSS | chr3:5695639-5698869 REVERSE | Aliases: MGL6.20	3.7	3.4	0.3	2.1	26.0%	0.2
10874	AT4G33630.2 | expressed protein | chr4:16155506-16159938 FORWARD | Aliases: T16L1.120, T16L1_120	4.0	4.3	-0.3	-2.1	26.0%	0.2
10875	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	3.0	0.3	2.1	26.0%	0.3
10876	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	2.0	2.1	-0.1	-2.1	26.0%	-0.5
10877	AT2G41960.1 | expressed protein | chr2:17521131-17526371 REVERSE | Aliases: T6D20.15, T6D20_15	5.2	5.6	-0.4	-2.1	26.1%	0.5
10878	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	3.0	3.2	-0.2	-2.1	26.1%	-0.2
10879	AT5G52780.1 | expressed protein, similar to unknown protein (pir::T04431) | chr5:21408099-21408700 REVERSE | Aliases: F6N7.27, F6N7_27	2.3	2.1	0.2	2.1	26.1%	-0.4
10880	AT5G61400.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:24698776-24700740 FORWARD | Aliases: MFB13.18, MFB13_18	3.5	3.2	0.2	2.1	26.1%	0.0
10881	AT1G64650.1 | expressed protein | chr1:24027161-24030058 REVERSE | Aliases: F1N19.22, F1N19_22	6.0	5.5	0.5	2.1	26.1%	0.6
10882	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	6.5	5.8	0.7	2.1	26.1%	0.7
10883	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	6.6	5.1	1.5	2.1	26.1%	0.8
10884	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	5.3	4.8	0.5	2.1	26.1%	0.6
10885	AT2G31160.1 | expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640) | chr2:13284888-13285822 FORWARD | Aliases: T16B12.3, T16B12_3	2.7	3.0	-0.3	-2.1	26.1%	0.2
10886	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	6.8	6.0	0.9	2.1	26.2%	0.7
10887	AT3G54240.1 | hydrolase, alpha/beta fold family protein, low similarity to SP:P22862:ESTE_PSEFL Arylesterase (EC 3.1.1.2) (Aryl-ester hydrolase) {Pseudomonas fluorescens}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family | chr3:20091904-20093123 FORWARD | Aliases: F24B22.200	2.9	3.2	-0.3	-2.1	26.2%	0.1
10888	AT3G12040.1 | DNA-3-methyladenine glycosylase (MAG), identical to DNA-3-methlyadenine glycosylase (MAG) SP:Q39147 from (Arabidopsis thaliana); contains Pfam profile: PF02245 methylpurine-DNA glycosylase (MPG) | chr3:3835135-3836802 REVERSE | Aliases: MEC18.4	3.6	4.0	-0.4	-2.1	26.2%	0.4
10889	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	4.3	3.5	0.8	2.1	26.2%	0.7
10890	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	5.5	5.8	-0.3	-2.1	26.2%	-0.0
10891	AT1G14340.1 | RNA recognition motif (RRM)-containing protein | chr1:4897341-4898956 FORWARD | Aliases: F14L17.11, F14L17_11	7.2	7.8	-0.6	-2.1	26.2%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
10892	AT2G40620.1 | bZIP transcription factor family protein, identical to b-Zip DNA binding protein GI:2246376 from (Arabidopsis thaliana); contains a bZIP transcription factor basic domain signature (PDOC00036)	3.1	3.4	-0.3	-2.1	26.3%	0.1
10893	AT5G02390.1 | expressed protein, ; expression supported by MPSS | chr5:508762-511708 REVERSE | Aliases: T1E22.150, T1E22_150	2.5	2.8	-0.3	-2.1	26.3%	-0.1
10894	AT1G23200.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr1:8227167-8229571 FORWARD | Aliases: F26F24.2	2.9	3.2	-0.2	-2.1	26.3%	-0.0
10895	AT3G54350.2 | Symbol: EMB1967 | forkhead-associated domain-containing protein / FHA domain-containing protein, MSP58 - nucleolar protein, Mus musculus, EMBL:AF015309	6.5	6.2	0.3	2.1	26.3%	0.3
10896	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	6.5	6.1	0.4	2.1	26.3%	0.2
10897	AT1G68620.1 | expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873 | chr1:25769610-25770903 FORWARD | Aliases: F24J5.14, F24J5_14	3.9	3.5	0.4	2.1	26.3%	0.3
10898	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	3.5	-0.5	-2.1	26.3%	0.3
10899	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	2.7	0.3	2.1	26.3%	-0.0
10900	AT1G47900.1 | expressed protein | chr1:17650813-17654704 REVERSE | Aliases: T6B12.1, T6B12_1	6.4	7.0	-0.6	-2.1	26.3%	0.5
10901	AT5G46795.1 | expressed protein | chr5:19004215-19005424 REVERSE | Aliases: None	2.4	2.6	-0.2	-2.1	26.3%	-0.2
10902	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	7.6	8.6	-1.0	-2.1	26.3%	0.3
10903	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	3.4	-0.3	-2.1	26.4%	0.1
10904	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	2.5	-0.2	-2.1	26.4%	-0.3
10905	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	3.2	3.6	-0.4	-2.1	26.4%	0.3
10906	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	4.0	4.8	-0.7	-2.1	26.4%	0.7
10907	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	6.5	5.6	0.8	2.1	26.4%	0.6
10908	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	5.6	6.1	-0.5	-2.1	26.4%	0.5
10909	AT1G14180.2 | expressed protein | chr1:4847159-4849200 FORWARD | Aliases: F7A19.26	3.5	3.1	0.4	2.1	26.4%	0.3
10910	AT3G49450.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.6	-0.1	-2.1	26.4%	-0.5
10911	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	5.5	4.9	0.6	2.1	26.5%	0.5
10912	AT1G54560.1 | Symbol: XIE | myosin, putative, similar to myosin GI:433663 from (Arabidopsis thaliana)	3.5	3.9	-0.4	-2.1	26.5%	0.4
10913	AT5G65020.1 | Symbol: ANNAT2 |	12.5	11.7	0.8	2.1	26.5%	0.4
10914	AT5G57770.1 | expressed protein | chr5:23417967-23420338 REVERSE | Aliases: MRI1.13, MRI1_13	3.1	3.5	-0.3	-2.1	26.5%	0.1
10915	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	2.3	2.6	-0.3	-2.1	26.5%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
10916	AT5G57340.2 | expressed protein | chr5:23244526-23246429 FORWARD | Aliases: MJB24.15, MJB24_15	5.4	6.5	-1.2	-2.1	26.5%	0.4
10917	AT3G55005.1 | Symbol: TON1B | tonneau 1b (TON1b), identical to tonneau 1b (TON1b) GI:11494366 from (Arabidopsis thaliana) | chr3:20394979-20397355 FORWARD | Aliases: TONNEAU 1B	4.4	4.0	0.3	2.1	26.5%	0.3
10918	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	3.6	4.0	-0.4	-2.1	26.5%	0.2
10919	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	3.6	4.0	-0.4	-2.1	26.5%	0.3
10920	AT2G33460.1 | Symbol: RIC1 | p21-rho-binding domain-containing protein, contains Pfam PF00786: P21-Rho-binding domain	4.5	5.0	-0.5	-2.1	26.5%	0.2
10921	AT3G25710.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.3	2.5	-0.1	-2.1	26.6%	-0.6
10922	AT5G03360.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	3.0	-0.3	-2.1	26.6%	0.2
10923	AT3G62730.1 | expressed protein, DESSICATION-RELATED PROTEIN PCC13-62 PRECURSOR - Craterostigma plantagineum, PIR:E45509 | chr3:23218830-23220446 REVERSE | Aliases: F26K9.160	3.0	3.3	-0.3	-2.1	26.6%	-0.1
10924	AT4G25280.1 | adenylate kinase family protein, contains Pfam profile: PF00406 adenylate kinase	6.9	7.5	-0.6	-2.1	26.6%	0.4
10925	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	7.6	8.3	-0.7	-2.1	26.6%	0.5
10926	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	2.3	2.5	-0.2	-2.1	26.7%	-0.3
10927	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	2.5	-0.2	-2.1	26.7%	-0.3
10928	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	3.5	0.4	2.1	26.7%	0.3
10929	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	3.0	-0.3	-2.1	26.7%	-0.1
10930	AT4G39000.1 | glycosyl hydrolase family 9 protein, endo-1,4-beta-glucanase precursor - Fragariax ananassa, PID:g3549291 | chr4:18171716-18173791 REVERSE | Aliases: F19H22.100, F19H22_100	2.7	3.0	-0.3	-2.1	26.7%	0.2
10931	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	6.9	5.6	1.3	2.1	26.7%	0.7
10932	AT3G58000.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr3:21485927-21486454 FORWARD | Aliases: T10K17.210	2.7	3.0	-0.3	-2.1	26.7%	-0.0
10933	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)	9.7	9.0	0.7	2.1	26.7%	0.1
10934	AT2G43140.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile PF00010: Helix-loop-helix DNA-binding domain	3.3	2.9	0.4	2.1	26.8%	0.2
10935	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	7.1	6.4	0.8	2.1	26.8%	0.4
10936	AT1G77010.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:28947604-28949691 FORWARD | Aliases: F22K20.11, F22K20_11	4.4	3.9	0.4	2.1	26.8%	0.2
10937	ATCG00040.1 | Symbol: MATK | Encodes a maturase located in the trnK intron in the chloroplast genome.	10.3	8.9	1.5	2.1	26.8%	0.3
10938	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	2.8	-0.2	-2.1	26.8%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
10939	AT4G20060.1 | Symbol: EMB1895 | expressed protein, ; expression supported by MPSS | chr4:10854800-10859340 REVERSE | Aliases: EMB1895, EMBRYO DEFECTIVE 1895, F18F4.160, F18F4_160	3.9	4.3	-0.4	-2.1	26.8%	-0.1
10940	AT5G59950.3 | RNA and export factor-binding protein, putative | chr5:24157421-24159084 FORWARD | Aliases: MMN10.26, MMN10_26	6.8	7.3	-0.5	-2.1	26.8%	0.3
10941	AT3G18050.1 | expressed protein | chr3:6180865-6182860 FORWARD | Aliases: MRC8.3	2.7	2.4	0.3	2.1	26.8%	-0.1
10942	AT3G53160.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:19713434-19714954 REVERSE | Aliases: T4D2.90	3.4	3.0	0.4	2.1	26.8%	0.3
10943	AT4G15680.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	4.3	3.9	0.4	2.1	26.8%	0.2
10944	AT2G43310.1 | expressed protein | chr2:18003158-18003599 FORWARD | Aliases: F14B2.31	2.6	2.4	0.2	2.1	26.8%	-0.4
10945	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	6.2	5.4	0.7	2.1	26.8%	0.7
10946	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	2.5	2.8	-0.3	-2.1	26.8%	-0.2
10947	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	3.2	3.6	-0.4	-2.1	26.9%	0.1
10948	AT1G10410.1 | expressed protein, similar to ESTs gb:N96021 and gb:N96863 | chr1:3416686-3419640 REVERSE | Aliases: F14N23.31, F14N23_31	7.4	7.9	-0.5	-2.1	26.9%	0.2
10949	AT1G78890.1 | expressed protein | chr1:29661470-29662958 FORWARD | Aliases: F9K20.6, F9K20_6	6.5	5.4	1.1	2.1	26.9%	0.6
10950	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	2.5	2.7	-0.2	-2.1	27.0%	-0.3
10951	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	6.6	6.2	0.4	2.1	27.0%	0.3
10952	AT3G09000.1 | proline-rich family protein | chr3:2745649-2748464 FORWARD | Aliases: T16O11.4	5.3	5.7	-0.4	-2.1	27.0%	0.1
10953	AT1G44085.1 | glycine-rich protein, similar to glycine-rich protein GI:18147 from (Chenopodium rubrum)	3.3	3.6	-0.3	-2.1	27.0%	-0.1
10954	AT4G24730.2 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	6.1	5.7	0.4	2.1	27.0%	0.4
10955	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	3.6	0.3	2.1	27.0%	-0.0
10956	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	2.7	-0.3	-2.1	27.0%	-0.0
10957	AT3G56270.1 | expressed protein, contains Pfam PF05701: Plant protein of unknown function (DUF827) | chr3:20880979-20883028 FORWARD | Aliases: F18O21.230	4.0	3.6	0.4	2.1	27.0%	0.2
10958	AT1G74860.1 | expressed protein | chr1:28126980-28129543 FORWARD | Aliases: F25A4.17, F25A4_17	4.6	5.1	-0.6	-2.1	27.0%	0.4
10959	AT4G27350.1 | expressed protein | chr4:13690827-13692800 REVERSE | Aliases: F27G19.7, M4I22.160, M4I22_160	7.0	6.6	0.4	2.1	27.0%	0.2
10960	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	10.2	9.5	0.6	2.1	27.0%	0.1
10961	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	8.5	9.3	-0.8	-2.1	27.1%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
10962	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	5.5	5.9	-0.5	-2.1	27.1%	0.3
10963	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	10.3	9.2	1.1	2.1	27.1%	0.6
10964	AT4G17000.1 | expressed protein | chr4:9567065-9569932 REVERSE | Aliases: DL4530C, FCAALL.326	3.9	3.5	0.4	2.1	27.1%	0.5
10965	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	5.1	4.7	0.5	2.1	27.1%	0.5
10966	AT5G15000.1 | expressed protein | chr5:4853467-4855174 FORWARD | Aliases: F2G14.120, F2G14_120	2.3	2.5	-0.2	-2.1	27.1%	-0.5
10967	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	3.2	3.6	-0.3	-2.1	27.1%	0.0
10968	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	2.2	-0.1	-2.1	27.1%	-0.6
10969	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: F20O9.100, F20O9_100	3.0	3.2	-0.2	-2.1	27.1%	-0.1
10970	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	10.7	0.6	2.1	27.1%	-0.2
10971	AT3G25970.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:9501353-9503293 REVERSE | Aliases: MPE11.14	3.4	3.2	0.2	2.1	27.1%	-0.3
10972	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	6.4	5.8	0.6	2.1	27.1%	0.5
10973	ATCG00150.1 | Symbol: ATPI | ATPase a subunit	2.8	3.9	-1.1	-2.1	27.1%	0.2
10974	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: T22J18.1	3.2	3.6	-0.4	-2.1	27.1%	0.2
10975	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	9.4	9.0	0.4	2.1	27.1%	0.1
10976	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	2.6	-0.2	-2.1	27.1%	-0.3
10977	AT1G26620.1 | expressed protein, ; expression supported by MPSS | chr1:9195825-9198706 REVERSE | Aliases: T1K7.1, T1K7_1	3.4	4.2	-0.8	-2.1	27.1%	0.5
10978	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	3.7	-0.4	-2.1	27.2%	0.2
10979	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	6.2	5.7	0.5	2.1	27.2%	0.3
10980	AT1G58420.1 | expressed protein | chr1:21711044-21711783 FORWARD | Aliases: F9K23.5, F9K23_5	3.0	3.5	-0.5	-2.1	27.2%	0.5
10981	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	7.4	6.8	0.6	2.1	27.2%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
10982	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	4.8	4.4	0.4	2.1	27.2%	0.3
10983	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	4.6	5.2	-0.6	-2.1	27.2%	0.5
10984	AT5G29000.2 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr5:11022087-11024279 REVERSE | Aliases: F3F24.100, F3F24_100	5.0	5.5	-0.5	-2.1	27.2%	0.5
10985	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	3.5	-0.2	-2.1	27.2%	-0.5
10986	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	7.2	-0.6	-2.1	27.2%	0.5
10987	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	2.8	-0.3	-2.1	27.2%	-0.1
10988	AT5G17280.1 | expressed protein, similar to unknown protein (pir::T41692) | chr5:5686301-5686889 FORWARD | Aliases: MKP11.13, MKP11_13	6.4	5.7	0.7	2.1	27.2%	0.5
10989	AT2G01240.1 | reticulon family protein (RTNLB15), contains PFam profile PF02453: Reticulon | chr2:128439-129255 REVERSE | Aliases: F10A8.12, F10A8_12	2.7	3.0	-0.3	-2.1	27.2%	0.1
10990	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	2.9	-0.4	-2.1	27.2%	-0.2
10991	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 GI:5231145 from (Arabidopsis thaliana) | chr2:968332-970015 REVERSE | Aliases: ATFUT2, T18E12.12, T18E12_12	3.2	3.6	-0.5	-2.1	27.2%	0.1
10992	AT5G49670.1 | expressed protein | chr5:20193611-20198897 FORWARD | Aliases: K2I5.3, K2I5_3	3.1	3.4	-0.3	-2.1	27.3%	-0.1
10993	AT3G24280.1 | expressed protein | chr3:8798941-8799408 REVERSE | Aliases: K7M2.4	2.3	2.4	-0.1	-2.1	27.3%	-0.6
10994	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	11.6	0.5	2.1	27.4%	-0.5
10995	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	6.7	5.2	1.6	2.1	27.4%	0.7
10996	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	3.9	4.4	-0.5	-2.1	27.4%	0.3
10997	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	3.4	3.0	0.4	2.1	27.4%	0.2
10998	NA	12.3	12.7	-0.3	-2.1	27.4%	-0.1
10999	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	6.2	5.7	0.6	2.1	27.4%	0.6
11000	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	2.3	-0.2	-2.1	27.4%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
11001	AT3G47700.1 | chromosome structural maintenance protein-related, contains weak similarity to RAD50-interacting protein 1 (Homo sapiens) gi:11967435:gb:AAG42101 | chr3:17594586-17597609 REVERSE | Aliases: T23J7.30	6.3	6.9	-0.6	-2.1	27.4%	0.4
11002	AT3G23080.2 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g14500.1); similar to putative nodule membrane protein [Medicago sativa] (GB:AAL57201.1); contains InterPro domain Lipid-binding START (InterPro:IPR002913)	5.3	5.8	-0.5	-2.1	27.4%	0.3
11003	AT3G59340.1 | expressed protein, identical to anthocyanin-related membrane protein 3 (GI:16416387) (Arabidopsis thaliana) | chr3:21939741-21942547 REVERSE | Aliases: F25L23.200	2.2	2.5	-0.3	-2.1	27.4%	-0.2
11004	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	7.6	8.1	-0.5	-2.1	27.4%	0.6
11005	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	3.5	3.9	-0.4	-2.1	27.4%	0.3
11006	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	2.9	-0.2	-2.1	27.4%	-0.3
11007	AT4G30825.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:15009611-15012325 FORWARD | Aliases: None	3.4	3.1	0.3	2.1	27.4%	0.1
11008	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	6.5	-0.5	-2.1	27.4%	0.3
11009	AT3G46360.1 | expressed protein | chr3:17053200-17054485 REVERSE | Aliases: F18L15.80	3.8	4.4	-0.6	-2.1	27.5%	0.2
11010	AT1G48330.1 | expressed protein, similar to hypothetical protein GI:9294146 from (Arabidopsis thaliana) | chr1:17867513-17868054 FORWARD | Aliases: F11A17.11, F11A17_11	3.1	3.3	-0.2	-2.1	27.5%	-0.4
11011	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 (petH) GI:5730138 | chr5:26467983-26470388 REVERSE | Aliases: K2A18.27, K2A18_27	5.3	4.9	0.4	2.1	27.5%	0.2
11012	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	6.6	0.4	2.1	27.5%	0.3
11013	AT3G07800.1 | thymidine kinase, putative, similar to thymidine kinase (Oryza sativa) SWISS-PROT:O81263	8.7	7.9	0.8	2.1	27.5%	0.3
11014	AT5G41310.1 | kinesin motor protein-related | chr5:16533862-16539620 REVERSE | Aliases: K1O13.11, K1O13_11	2.9	3.2	-0.3	-2.1	27.5%	-0.1
11015	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	4.2	-0.4	-2.1	27.5%	0.2
11016	AT1G71460.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:26931646-26933978 REVERSE | Aliases: F26A9.16	3.7	3.5	0.3	2.1	27.5%	0.0
11017	AT2G04740.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr2:1657118-1659669 FORWARD | Aliases: F28I8.22, F28I8_22	5.5	5.0	0.5	2.1	27.6%	0.4
11018	AT1G72080.1 | expressed protein | chr1:27124069-27126423 REVERSE | Aliases: F28P5.14, F28P5_14	3.6	3.9	-0.3	-2.1	27.6%	-0.1
11019	AT1G22030.1 | expressed protein | chr1:7759153-7760545 REVERSE | Aliases: F2E2.8, F2E2_8	6.2	6.9	-0.6	-2.1	27.6%	0.5
11020	AT5G16380.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr5:5359413-5360713 REVERSE | Aliases: MQK4.11, MQK4_11	3.0	2.6	0.5	2.1	27.6%	0.2
11021	AT5G42860.1 | expressed protein | chr5:17200294-17202144 REVERSE | Aliases: MBD2.5, MBD2_5	6.1	6.5	-0.4	-2.1	27.6%	0.4
11022	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)	2.5	2.3	0.2	2.1	27.6%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
11023	AT1G62085.1 | mitochondrial transcription termination factor family protein / mTERF family protein, contains Pfam profile PF02536: mTERF | chr1:22952422-22953807 REVERSE | Aliases: None	2.8	2.6	0.2	2.1	27.6%	-0.3
11024	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	2.9	3.1	-0.1	-2.1	27.6%	-0.6
11025	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	3.3	-0.3	-2.1	27.6%	-0.1
11026	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	7.0	7.4	-0.4	-2.1	27.6%	0.1
11027	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	5.3	4.9	0.4	2.1	27.7%	0.2
11028	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	2.4	-0.2	-2.1	27.7%	-0.8
11029	AT1G15860.1 | expressed protein | chr1:5455050-5456926 FORWARD | Aliases: F7H2.19, F7H2_19	4.8	4.2	0.6	2.1	27.7%	0.4
11030	AT2G33170.1 | leucine-rich repeat transmembrane protein kinase, putative, similar to receptor protein kinase (Pinus sylvestris) 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	3.6	0.4	2.1	27.7%	0.0
11031	AT3G18840.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:6496204-6498946 FORWARD | Aliases: MCB22.1	3.7	4.0	-0.4	-2.1	27.7%	0.1
11032	AT2G27510.1 | ferredoxin, putative, similar to non-photosynthetic ferredoxin from Citrus sinensis (GI:1360725), Ferredoxin, root R-B2 from Raphanus sativus (SP:P14937); contains Pfam profile PF00111 2Fe-2S iron-sulfur cluster binding domain | chr2:11765157-11766554 REVERSE | Aliases: F10A12.19, F10A12_19	11.6	11.2	0.4	2.1	27.7%	0.1
11033	AT1G07120.1 | expressed protein | chr1:2184758-2186579 REVERSE | Aliases: F10K1.18, F10K1_18	2.9	3.2	-0.3	-2.1	27.7%	-0.0
11034	AT5G03960.1 | calmodulin-binding family protein | chr5:1068275-1069977 REVERSE | Aliases: F8F6.170, F8F6_170	4.5	5.2	-0.7	-2.1	27.7%	0.6
11035	AT3G17800.1 | expressed protein | chr3:6090467-6093157 REVERSE | Aliases: MEB5.2	8.3	8.9	-0.6	-2.1	27.7%	0.2
11036	AT2G05500.1 | expressed protein, ; expression supported by MPSS | chr2:2014365-2015403 REVERSE | Aliases: T20G20.15, T20G20_15	2.3	2.5	-0.2	-2.1	27.7%	-0.9
11037	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	4.6	-0.4	-2.1	27.7%	0.3
11038	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 scienitific 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	5.1	4.5	0.6	2.1	27.7%	0.5
11039	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	4.0	4.6	-0.6	-2.1	27.8%	0.6
11040	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	2.2	-0.2	-2.1	27.8%	-0.7
11041	AT5G19340.1 | expressed protein | chr5:6515094-6516207 REVERSE | Aliases: F7K24.90, F7K24_90	3.0	3.2	-0.3	-2.1	27.8%	-0.2
11042	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	3.4	-0.5	-2.1	27.8%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11043	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	10.6	9.9	0.7	2.1	27.8%	0.2
11044	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	5.6	6.5	-0.9	-2.1	27.8%	0.4
11045	AT3G52880.1 | monodehydroascorbate reductase, putative, monodehydroascorbate reductase (NADH), Lycoperison esculentum, PIR:T06407 | chr3:19612190-19615431 REVERSE | Aliases: F8J2.50	10.7	9.6	1.0	2.1	27.8%	0.4
11046	AT1G12600.1 | expressed protein | chr1:4286412-4288860 REVERSE | Aliases: F5O11.33, F5O11_33	3.1	3.4	-0.3	-2.1	27.8%	0.0
11047	AT3G19380.1 | U-box domain-containing protein, contains similarity to immediate-early fungal elicitor protein CMPG1 GI:14582200 (Petroselinum crispum); contains Pfam profile PF04564: U-box domain | chr3:6714398-6716105 REVERSE | Aliases: MLD14.11	3.2	3.4	-0.3	-2.1	27.8%	0.0
11048	AT3G63470.1 | Symbol: SCPL40 |	2.8	3.0	-0.2	-2.1	27.8%	-0.2
11049	AT2G16940.1 | RNA recognition motif (RRM)-containing protein | chr2:7349723-7354490 REVERSE | Aliases: F12A24.12, F12A24_12	6.2	5.6	0.6	2.1	27.9%	0.4
11050	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	3.1	3.5	-0.4	-2.1	27.9%	0.2
11051	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	3.9	3.5	0.4	2.1	27.9%	0.5
11052	AT5G63880.1 | SNF7 family protein, contains Pfam domain, PF03357: SNF7 family | chr5:25580964-25583175 FORWARD | Aliases: MGI19.8, MGI19_8	8.3	8.0	0.4	2.1	27.9%	0.2
11053	AT2G37720.1 | expressed protein | chr2:15825160-15828373 FORWARD | Aliases: F13M22.22, F13M22_22	2.1	2.3	-0.2	-2.1	27.9%	-0.4
11054	AT3G01880.1 | hypothetical protein | chr3:307789-309567 FORWARD | Aliases: F1C9.34	3.1	3.5	-0.3	-2.1	27.9%	-0.1
11055	AT1G18290.1 | expressed protein | chr1:6297429-6297959 FORWARD | Aliases: F15H18.19	3.0	3.3	-0.3	-2.1	27.9%	0.1
11056	AT2G03540.1 | expressed protein, ; expression supported by MPSS | chr2:1073756-1074512 FORWARD | Aliases: T4M8.2, T4M8_2	3.5	4.0	-0.6	-2.1	27.9%	0.3
11057	AT2G01620.1 | expressed protein | chr2:278126-279295 FORWARD | Aliases: T8O11.21, T8O11_21	7.6	7.1	0.5	2.1	27.9%	0.4
11058	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	2.8	3.1	-0.3	-2.1	27.9%	0.0
11059	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	3.3	-0.2	-2.1	27.9%	-0.3
11060	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-conensus AT-AC splice sites at intron 5 | chr5:2716701-2720213 FORWARD | Aliases: F8L15.160, F8L15_160	7.4	7.9	-0.5	-2.1	27.9%	0.0
11061	AT5G17240.1 | SET domain-containing protein, contains Pfam profile PF00856: SET domain	2.7	2.5	0.3	2.1	27.9%	-0.2
11062	AT3G01770.1 | DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487 | chr3:275418-278792 REVERSE | Aliases: F28J7.10	10.2	9.7	0.5	2.1	27.9%	0.2
11063	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	2.7	-0.3	-2.1	27.9%	-0.2
11064	AT1G55830.1 | expressed protein, similar to M-type 9 protein (GI:507127) (Streptococcus pyogenes) | chr1:20871584-20873871 REVERSE | Aliases: F20N2.20	5.4	6.3	-0.8	-2.1	27.9%	0.6

Rank	Description	Sync	Root	M	t	adj.q	B
11065	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	10.2	10.5	-0.3	-2.1	27.9%	-0.2
11066	AT3G45670.1 | protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr3:16776305-16777444 FORWARD | Aliases: T6D9.3	3.2	3.5	-0.3	-2.1	28.0%	-0.1
11067	AT3G51050.1 | FG-GAP repeat-containing protein	5.9	6.6	-0.7	-2.1	28.0%	0.3
11068	AT1G50740.1 | expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136) | chr1:18811340-18812667 FORWARD | Aliases: F4M15.3, F4M15_3	7.9	7.5	0.4	2.1	28.0%	0.1
11069	AT2G45320.1 | expressed protein | chr2:18691190-18693219 REVERSE | Aliases: F4L23.17	6.7	7.1	-0.3	-2.1	28.0%	0.2
11070	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	4.2	3.7	0.5	2.1	28.0%	0.2
11071	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	4.6	4.3	0.3	2.1	28.0%	0.2
11072	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	6.0	6.4	-0.4	-2.1	28.0%	0.2
11073	AT3G06990.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.3	3.8	-0.4	-2.1	28.0%	0.2
11074	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	4.3	4.8	-0.4	-2.1	28.0%	0.3
11075	AT1G76070.1 | expressed protein | chr1:28551276-28552505 FORWARD | Aliases: T23E18.1, T23E18_1	3.1	3.5	-0.4	-2.1	28.0%	0.4
11076	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)	3.8	4.4	-0.6	-2.1	28.0%	0.6
11077	AT5G02260.1 | Symbol: ATEXPA9 | expansin, putative (EXP9), similar to expansin precursor GI:4138914 from (Lycopersicon esculentum); alpha-expansin gene family, PMID:11641069	2.7	2.4	0.3	2.1	28.0%	-0.1
11078	AT5G10660.1 | calmodulin-binding protein-related, contains weak similarity to calmodulin-binding proteins | chr5:3370554-3371777 FORWARD | Aliases: MAJ23.20, MAJ23_20	3.1	3.3	-0.2	-2.1	28.0%	-0.3
11079	AT2G19200.1 | expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626) | chr2:8340300-8341703 FORWARD | Aliases: T20K24.25, T20K24_25	2.5	2.8	-0.2	-2.1	28.0%	-0.1
11080	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	2.7	3.1	-0.4	-2.1	28.0%	-0.2
11081	AT3G05980.1 | expressed protein | chr3:1795345-1796453 FORWARD | Aliases: F2O10.6, F2O10_6	3.4	3.8	-0.3	-2.1	28.1%	-0.3
11082	AT2G13680.1 | glycosyl transferase family 48 protein, contains Pfam profile: PF02364 1,3-beta-glucan synthase | chr2:5702206-5713216 FORWARD | Aliases: None	3.0	3.2	-0.2	-2.1	28.1%	-0.5
11083	AT1G52060.1 | jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	4.0	4.4	-0.4	-2.1	28.1%	0.3
11084	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	5.2	4.6	0.6	2.0	28.1%	0.4
11085	AT1G31000.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.8	3.1	-0.3	-2.0	28.1%	0.0

Rank	Description	Sync	Root	M	t	adj.q	B
11086	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 HOMEOBOX PROTEIN, KNOTTED1 LIKE HOMEOBOX GENE 3	6.4	5.8	0.6	2.0	28.1%	0.4
11087	AT1G65380.1 | Symbol: CLV2 | receptor-like protein CLAVATA2 (CLV2), identical to receptor-like protein CLAVATA2 (Arabidopsis thaliana) gi:6049566:gb:AAF02654contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; | chr1:24290489-24292912 FORWARD | Aliases: CLAVATA 2, T8F5.16, T8F5_16	4.4	4.1	0.4	2.0	28.1%	-0.0
11088	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	8.6	7.4	1.2	2.0	28.2%	0.5
11089	AT3G29240.2 | expressed protein, similar to At1g33780 (Arabidopsis thaliana); contains Pfam profile PF02622: Uncharacterized ACR, COG1678 | chr3:11192843-11194223 FORWARD | Aliases: MXO21.9	7.3	6.9	0.4	2.0	28.2%	0.3
11090	AT5G45980.1 | Symbol: WOX8 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g33880.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAT77402.1); contains InterPro domain Homeobox (InterPro:IPR001356) | chr5:18666136-18668063 FORWARD | Aliases: MCL19.2, MCL19_2	2.5	2.7	-0.2	-2.0	28.2%	-0.3
11091	AT3G25170.1 | Symbol: RALFL26 | rapid alkalinization factor (RALF) family protein | chr3:9165758-9166260 REVERSE | Aliases: MJL12.13, RALF LIKE 26	3.9	4.1	-0.2	-2.0	28.2%	-0.2
11092	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	3.8	4.1	-0.3	-2.0	28.2%	0.2
11093	AT5G53990.1 | glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	4.0	4.7	-0.7	-2.0	28.2%	0.6
11094	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	2.4	2.6	-0.2	-2.0	28.2%	-0.2
11095	AT1G56360.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	2.3	2.5	-0.2	-2.0	28.2%	-0.5
11096	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	4.2	3.3	0.8	2.0	28.2%	0.7
11097	AT4G24880.1 | expressed protein | chr4:12808530-12811383 FORWARD | Aliases: F13M23.20, F13M23_20	5.9	5.4	0.5	2.0	28.2%	0.4
11098	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	3.4	3.1	0.3	2.0	28.2%	-0.1
11099	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	7.4	0.9	2.0	28.2%	0.3
11100	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	9.9	9.1	0.7	2.0	28.2%	0.5
11101	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	2.7	-0.2	-2.0	28.2%	-0.4
11102	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	4.4	3.5	1.0	2.0	28.2%	0.6
11103	AT2G45870.1 | expressed protein, contains Pfam profile PF05249: Uncharacterised protein family (UPF0187) | chr2:18882968-18884551 FORWARD | Aliases: F4I18.15	2.8	2.4	0.3	2.0	28.2%	0.0
11104	AT3G15351.2 | expressed protein | chr3:5176066-5177644 FORWARD | Aliases: None	5.8	6.4	-0.7	-2.0	28.2%	0.2
11105	AT2G20515.1 | expressed protein | chr2:8845935-8846768 REVERSE | Aliases: None	2.3	2.6	-0.3	-2.0	28.2%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11106	AT3G14630.1 | Symbol: CYP72A9 | cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus) | chr3:4917505-4919416 FORWARD | Aliases: MIE1.13	2.9	3.2	-0.3	-2.0	28.2%	0.0
11107	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	7.4	7.1	0.3	2.0	28.2%	0.3
11108	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	2.5	-0.2	-2.0	28.2%	-0.4
11109	AT5G05270.2 | chalcone-flavanone isomerase family protein, contains very low similarity to chalcone-flavonone isomerase (chalcone isomerase), GI:1705761 from Vitis vinifera; contains Pfam profile PF02431: Chalcone-flavanone isomerase | chr5:1563431-1565007 FORWARD | Aliases: K18I23.7, K18I23_7	4.4	4.8	-0.4	-2.0	28.3%	0.4
11110	AT3G14400.1 | Symbol: UBP25 | ubiquitin-specific protease 25 (UBP25), similar to GI:11993490 | chr3:4811539-4815504 REVERSE | Aliases: MLN21.18, UBIQUITIN SPECIFIC PROTEASE 25	4.7	5.7	-1.1	-2.0	28.3%	0.5
11111	AT2G36820.1 | expressed protein | chr2:15445489-15447772 REVERSE | Aliases: F13K3.22, F13K3_22	3.3	3.9	-0.6	-2.0	28.3%	0.5
11112	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	3.5	0.3	2.0	28.3%	0.1
11113	AT5G46440.1 | expressed protein | chr5:18851870-18852380 FORWARD | Aliases: K11I1.3, K11I1_3	3.1	3.4	-0.3	-2.0	28.3%	-0.3
11114	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	2.3	-0.3	-2.0	28.3%	-0.0
11115	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	3.0	2.8	0.2	2.0	28.3%	-0.3
11116	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	8.6	7.4	1.2	2.0	28.3%	0.5
11117	AT5G56800.1 | expressed protein | chr5:22990215-22991434 FORWARD | Aliases: MIK19.27, MIK19_27	2.5	2.8	-0.3	-2.0	28.3%	-0.3
11118	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	9.4	8.4	1.0	2.0	28.3%	0.6
11119	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	9.7	-0.7	-2.0	28.4%	0.1
11120	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	5.5	5.0	0.4	2.0	28.4%	0.3
11121	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	3.6	3.2	0.4	2.0	28.4%	0.4
11122	AT3G20830.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:7284969-7286266 REVERSE | Aliases: MOE17.13	4.4	4.7	-0.3	-2.0	28.4%	0.1
11123	AT1G31620.1 | expressed protein | chr1:11316922-11317875 FORWARD | Aliases: F27M3.18, F27M3_18	2.7	3.0	-0.3	-2.0	28.4%	-0.1
11124	AT5G26350.1 | expressed protein | chr5:9253111-9253640 REVERSE | Aliases: F9D12.102, F9D12_102	3.4	4.0	-0.6	-2.0	28.4%	0.2
11125	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	5.2	4.5	0.7	2.0	28.4%	0.4
11126	AT3G14067.1 | subtilase family protein, contains similarity to cucumisin-like serine protease GI:3176874 from (Arabidopsis thaliana) | chr3:4658428-4660761 REVERSE | Aliases: MAG2.15	3.8	5.3	-1.6	-2.0	28.4%	0.5
11127	AT1G67940.1 | Symbol: ATNAP3 |	8.2	8.5	-0.3	-2.0	28.4%	0.0

Rank	Description	Sync	Root	M	t	adj.q	B
11128	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	3.4	-0.3	-2.0	28.4%	-0.1
11129	AT5G60130.1 | transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain | chr5:24229097-24230184 REVERSE | Aliases: MGO3.11, MGO3_11	2.4	2.7	-0.2	-2.0	28.5%	-0.5
11130	AT1G23540.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr1:8346931-8349775 REVERSE | Aliases: F28C11.17	2.5	2.7	-0.2	-2.0	28.5%	-0.1
11131	AT1G47340.1 | F-box family protein, contains F-box domain Pfam:PF00646	6.1	5.0	1.1	2.0	28.5%	0.5
11132	AT4G10370.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	3.1	-0.3	-2.0	28.5%	-0.2
11133	AT1G21500.1 | expressed protein | chr1:7529871-7531014 REVERSE | Aliases: F24J8.11, F24J8_11	3.5	3.1	0.4	2.0	28.5%	0.1
11134	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	3.5	-0.3	-2.0	28.6%	-0.2
11135	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	5.9	-0.6	-2.0	28.6%	0.4
11136	AT1G50090.1 | aminotransferase class IV family protein, contains Pfam profile: PF01063 aminotransferase class IV | chr1:18558309-18560462 REVERSE | Aliases: F2J10.5, F2J10_5	3.5	3.9	-0.4	-2.0	28.6%	0.0
11137	AT1G54923.1 | expressed protein | chr1:20479424-20480235 REVERSE | Aliases: F14C21.35, F14C21_35	2.3	2.4	-0.1	-2.0	28.6%	-0.7
11138	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	6.8	7.2	-0.4	-2.0	28.6%	0.2
11139	AT1G42630.1 | zinc knuckle (CCHC-type) family protein,	2.7	3.3	-0.5	-2.0	28.6%	0.5
11140	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	10.2	9.6	0.6	2.0	28.6%	0.3
11141	AT4G20770.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:11130773-11132995 REVERSE | Aliases: F21C20.120, F21C20_120	2.9	3.1	-0.2	-2.0	28.6%	-0.4
11142	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	2.9	2.7	0.2	2.0	28.6%	-0.3
11143	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	4.7	-0.3	-2.0	28.6%	-0.0
11144	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	3.2	3.7	-0.5	-2.0	28.6%	0.5
11145	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	2.9	2.6	0.3	2.0	28.6%	-0.1
11146	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	5.1	4.6	0.5	2.0	28.6%	0.4
11147	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	5.2	-0.4	-2.0	28.6%	0.2
11148	AT3G18650.1 | MADS-box family protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana) | chr3:6417350-6418510 REVERSE | Aliases: MVE11.1	2.6	3.0	-0.3	-2.0	28.6%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11149	AT3G02010.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:337972-340449 FORWARD | Aliases: F1C9.21	4.2	3.9	0.3	2.0	28.6%	0.0
11150	AT4G09460.1 | Symbol: ATMYB6 |	5.8	6.3	-0.5	-2.0	28.7%	0.4
11151	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	4.1	4.5	-0.4	-2.0	28.7%	0.1
11152	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	6.1	5.4	0.7	2.0	28.7%	0.4
11153	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	8.4	9.2	-0.8	-2.0	28.7%	0.2
11154	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	7.8	6.9	0.9	2.0	28.7%	0.5
11155	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	4.1	3.7	0.4	2.0	28.7%	0.3
11156	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	2.8	3.1	-0.3	-2.0	28.7%	-0.0
11157	AT5G37620.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	3.1	-0.3	-2.0	28.7%	0.1
11158	AT2G22440.1 | expressed protein | chr2:9535990-9536997 FORWARD | Aliases: F14M13.16, F14M13_16	2.8	3.0	-0.2	-2.0	28.7%	-0.4
11159	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	3.1	3.8	-0.7	-2.0	28.7%	0.3
11160	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	3.4	3.0	0.5	2.0	28.7%	0.4
11161	AT2G16365.2 | F-box family protein, contains Pfam:PF00646 F-box domain	5.7	6.3	-0.6	-2.0	28.7%	0.4
11162	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	10.8	0.3	2.0	28.7%	-0.1
11163	AT1G80060.1 | expressed protein | chr1:30121195-30122417 REVERSE | Aliases: F18B13.35, F18B13_35	4.1	3.5	0.6	2.0	28.7%	0.4
11164	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	10.1	8.5	1.6	2.0	28.7%	0.5
11165	AT1G31010.1 | expressed protein, contains Pfam PF05329: Protein of unknown function (DUF731) | chr1:11054733-11056859 REVERSE | Aliases: F17F8.7	4.8	4.5	0.3	2.0	28.8%	-0.1
11166	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	9.4	8.2	1.1	2.0	28.8%	0.3
11167	AT2G04480.1 | expressed protein | chr2:1554279-1555511 REVERSE | Aliases: T1O3.11, T1O3_11	3.0	3.3	-0.3	-2.0	28.9%	-0.1
11168	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	3.8	3.5	0.3	2.0	28.9%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11169	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	6.6	5.9	0.7	2.0	28.9%	0.5
11170	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	9.1	8.3	0.8	2.0	28.9%	0.2
11171	AT5G64710.2 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537 | chr5:25887071-25889455 FORWARD | Aliases: MVP7.3, MVP7_3	3.3	3.0	0.3	2.0	28.9%	0.0
11172	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	5.6	0.4	2.0	28.9%	0.3
11173	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	5.5	6.2	-0.7	-2.0	28.9%	0.5
11174	AT5G04110.1 | DNA topoisomerase II family protein, siimilar 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	3.7	3.9	-0.2	-2.0	28.9%	-0.6
11175	AT1G15320.1 | expressed protein | chr1:5272463-5273694 REVERSE | Aliases: F9L1.26, F9L1_26	2.4	2.2	0.2	2.0	28.9%	-0.5
11176	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)	3.6	3.9	-0.3	-2.0	28.9%	-0.1
11177	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	7.1	6.6	0.4	2.0	28.9%	-0.0
11178	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	3.3	3.6	-0.3	-2.0	28.9%	0.1
11179	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	6.1	5.4	0.7	2.0	28.9%	0.6
11180	AT4G03750.1 | hypothetical protein | chr4:1667202-1668886 FORWARD | Aliases: T5L23.27, T5L23_27	3.5	4.1	-0.6	-2.0	28.9%	0.3
11181	AT5G66310.1 | kinesin motor family protein, contains Pfam domain, PF00225: Kinesin motor domain | chr5:26502911-26508608 REVERSE | Aliases: K1L20.9, K1L20_9	3.9	4.2	-0.3	-2.0	28.9%	-0.1
11182	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	6.9	6.4	0.5	2.0	29.0%	0.3
11183	AT5G19760.1 | dicarboxylate/tricarboxylate carrier (DTC), identical to dicarboxylate/tricarboxylate carrier (Arabidopsis thaliana) GI:19913113	11.3	10.5	0.8	2.0	29.0%	0.2
11184	AT2G45550.1 | Symbol: CYP76C4 | cytochrome P450 family protein | chr2:18780615-18782728 REVERSE | Aliases: F17K2.8	2.9	3.3	-0.4	-2.0	29.0%	-0.1
11185	AT1G22210.1 | trehalose-6-phosphate phosphatase, putative, similar to trehalose-6-phosphate phosphatase (AtTPPB) GI:2944180 from (Arabidopsis thaliana); contains Pfam profile PF02358: Trehalose-phosphatase | chr1:7841507-7844045 FORWARD | Aliases: F16L1.6, F16L1_6	2.5	2.8	-0.3	-2.0	29.0%	-0.2
11186	AT2G32100.1 | ovate protein-related, contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568 | chr2:13654929-13655862 FORWARD | Aliases: F22D22.15, F22D22_15	2.4	2.7	-0.2	-2.0	29.0%	-0.2
11187	AT4G02640.2 | Symbol: BZO2H1 |	6.7	7.5	-0.8	-2.0	29.0%	0.5
11188	AT4G04930.1 | Symbol: DES 1 LIKE | fatty acid desaturase family protein, similar to D. melanogaster 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	2.8	3.1	-0.2	-2.0	29.0%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11189	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	3.6	-0.4	-2.0	29.0%	0.1
11190	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	3.4	0.3	2.0	29.0%	0.1
11191	AT1G57906.1 | expressed protein | chr1:21439092-21440475 FORWARD | Aliases: F13D13.1, F13D13_1	3.6	3.9	-0.4	-2.0	29.0%	0.1
11192	AT4G11740.1 | Symbol: SAY1 | ara4-interacting protein, putative (SAY1), similar to Ara4-interacting protein (Arabidopsis thaliana) GI:13160609; contains Pfam profiles PF00789: UBX domain, PF02809: Ubiquitin interaction motif | chr4:7071854-7075495 FORWARD | Aliases: T5C23.170, T5C23_170	6.9	7.4	-0.5	-2.0	29.0%	0.3
11193	AT2G20430.1 | Symbol: RIC6 | p21-rho-binding domain-containing protein, contains Pfam PF00786: P21-Rho-binding domain	3.4	3.8	-0.4	-2.0	29.0%	-0.1
11194	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	2.8	3.0	-0.2	-2.0	29.0%	-0.3
11195	AT5G48270.1 | expressed protein | chr5:19581970-19582938 REVERSE | Aliases: MIF21.16, MIF21_16	2.7	3.1	-0.3	-2.0	29.0%	-0.2
11196	AT2G37585.1 | glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/I-Branching enzyme | chr2:15772862-15774956 FORWARD | Aliases: None	4.1	4.4	-0.4	-2.0	29.0%	-0.0
11197	AT1G71470.1 | hypothetical protein | chr1:26934448-26935075 FORWARD | Aliases: F26A9.15	3.6	4.0	-0.4	-2.0	29.0%	0.1
11198	AT1G55080.1 | expressed protein | chr1:20556685-20557881 REVERSE | Aliases: T7N22.3, T7N22_3	3.6	3.0	0.6	2.0	29.1%	0.2
11199	AT3G45680.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr3:16781922-16784015 FORWARD | Aliases: T6D9.10	3.2	3.7	-0.5	-2.0	29.1%	0.2
11200	AT2G42440.1 | LOB domain protein 17 / lateral organ boundaries domain protein 17 (LBD17), nearly identical to SP:Q9SLB6 LOB domain protein 17 {Arabidopsis thaliana}; identical to ASYMMETRIC LEAVES2-like protein 15 (Arabidopsis thaliana) GI:19919001 | chr2:17675920-17676794 REVERSE | Aliases: MHK10.16, MHK10_16	4.3	4.0	0.3	2.0	29.1%	0.1
11201	AT5G48590.1 | expressed protein | chr5:19715647-19717173 FORWARD | Aliases: K15N18.6, K15N18_6	5.9	5.5	0.3	2.0	29.1%	-0.1
11202	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	4.8	4.4	0.4	2.0	29.1%	0.2
11203	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	6.3	7.2	-0.8	-2.0	29.1%	0.4
11204	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	2.5	0.2	2.0	29.1%	-0.4
11205	AT1G50120.1 | expressed protein | chr1:18565497-18569804 FORWARD | Aliases: F2J10.3, F2J10_3	7.2	6.5	0.7	2.0	29.1%	0.4
11206	AT1G70420.1 | expressed protein | chr1:26543237-26544425 REVERSE | Aliases: F17O7.4, F17O7_4	4.6	5.2	-0.6	-2.0	29.1%	-0.1
11207	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	6.3	5.5	0.8	2.0	29.2%	0.4
11208	AT3G48210.1 | expressed protein | chr3:17860344-17862663 FORWARD | Aliases: T24C20.90	3.1	2.8	0.3	2.0	29.2%	-0.2
11209	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	2.5	2.6	-0.2	-2.0	29.2%	-0.6
11210	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	2.7	3.0	-0.3	-2.0	29.2%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11211	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	2.6	-0.2	-2.0	29.2%	-0.6
11212	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	3.5	3.2	0.3	2.0	29.2%	-0.1
11213	AT3G60580.1 | zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type | chr3:22404914-22406019 FORWARD | Aliases: T8B10.240	2.8	2.5	0.2	2.0	29.2%	-0.3
11214	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	4.8	-0.6	-2.0	29.2%	0.5
11215	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	3.1	-0.2	-2.0	29.2%	-0.4
11216	AT1G11370.1 | pectinesterase family protein, similar to pectin methylesterase GI:1279597 from (Nicotiana plumbaginifolia); contains Pfam profile: PF01095 pectinesterase | chr1:3828098-3830945 REVERSE | Aliases: T23J18.3, T23J18_3	2.1	2.3	-0.1	-2.0	29.2%	-0.6
11217	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	4.9	-0.5	-2.0	29.2%	0.2
11218	AT4G32270.1 | UDP-sugar transporter-related, contains weak similarity to Swiss-Prot:Q95YI5 UDP-sugar transporter UST74c (Drosophila melanogaster) | chr4:15575021-15579695 REVERSE | Aliases: F10M6.90, F10M6_90	4.8	4.3	0.4	2.0	29.2%	0.1
11219	AT4G14180.1 | expressed protein, ; expression supported by MPSS | chr4:8178325-8183510 FORWARD | Aliases: DL3130W, FCAALL.114	2.3	2.2	0.1	2.0	29.2%	-0.6
11220	AT3G45500.1 | expressed protein | chr3:16699403-16700678 REVERSE | Aliases: F9K21.80	2.8	3.1	-0.3	-2.0	29.3%	-0.1
11221	AT3G18180.1 | expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563) | chr3:6230276-6231884 FORWARD | Aliases: MRC8.18	2.5	2.8	-0.3	-2.0	29.3%	0.1
11222	AT4G15250.1 | zinc finger (B-box type) family protein | chr4:8709942-8711106 REVERSE | Aliases: DL3670C, FCAALL.247	2.7	2.9	-0.2	-2.0	29.3%	-0.2
11223	ATMG00150.1 | Symbol: ORF116 |	2.7	2.5	0.2	2.0	29.3%	-0.5
11224	AT2G30550.2 | lipase class 3 family protein, similar to DEFECTIVE IN ANTHER DEHISCENCE1 (Arabidopsis thaliana) GI:16215706; contains Pfam profile PF01764: Lipase | chr2:13021925-13024230 FORWARD | Aliases: T6B20.10, T6B20_10	6.6	7.4	-0.8	-2.0	29.3%	0.4
11225	AT5G25840.1 | expressed protein | chr5:9010727-9011501 REVERSE | Aliases: F18A17.90, F18A17_90	2.4	2.6	-0.2	-2.0	29.4%	-0.4
11226	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	7.3	7.8	-0.4	-2.0	29.4%	0.3
11227	AT4G15120.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr4:8634722-8635558 FORWARD | Aliases: DL3605W, FCAALL.67	3.2	3.6	-0.4	-2.0	29.4%	0.2
11228	AT2G10380.1 | hypothetical protein | chr2:4005622-4006571 FORWARD | Aliases: F12P23.11, F12P23_11	3.0	3.3	-0.2	-2.0	29.4%	-0.2
11229	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	9.3	6.1	3.2	2.0	29.4%	-0.1
11230	AT5G17920.1 | Symbol: ATCIMS |	9.3	6.1	3.2	2.0	29.4%	-0.1
11231	AT1G26350.1 | expressed protein | chr1:9115997-9116768 REVERSE | Aliases: F28B23.28	2.7	2.9	-0.2	-2.0	29.4%	-0.3
11232	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	3.6	3.8	-0.2	-2.0	29.4%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11233	AT2G36870.1 | xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to cellulase (xyloglucan endo-transglycosylase) GI:311835 from (Tropaeolum majus) | chr2:15479724-15481760 REVERSE | Aliases: T1J8.5, T1J8_5	3.2	3.7	-0.5	-2.0	29.4%	0.2
11234	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	4.7	4.2	0.5	2.0	29.4%	0.3
11235	AT1G04750.2 | Symbol: VAMP7B |	10.1	9.0	1.1	2.0	29.4%	0.5
11236	AT4G15240.1 | fringe-related protein, + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.	4.2	4.8	-0.6	-2.0	29.4%	0.5
11237	AT1G79060.1 | expressed protein | chr1:29746641-29748493 FORWARD | Aliases: YUP8H12R.32, YUP8H12R_32	2.4	2.6	-0.2	-2.0	29.5%	-0.4
11238	AT2G42950.1 | expressed protein | chr2:17870896-17873564 FORWARD | Aliases: F7D19.5, F7D19_5	6.9	7.2	-0.3	-2.0	29.5%	-0.0
11239	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	5.3	5.8	-0.5	-2.0	29.5%	0.3
11240	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	10.2	9.7	0.5	2.0	29.5%	0.2
11241	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	4.0	4.7	-0.6	-2.0	29.5%	0.4
11242	AT5G65840.1 | expressed protein | chr5:26360956-26363289 REVERSE | Aliases: K14B20.1, K14B20_1	4.0	3.7	0.3	2.0	29.5%	0.2
11243	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	4.0	4.3	-0.4	-2.0	29.5%	0.2
11244	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	4.9	3.9	1.0	2.0	29.5%	0.4
11245	AT5G55030.2 | expressed protein | chr5:22344421-22347072 REVERSE | Aliases: K13P22.3, K13P22_3	4.4	4.8	-0.4	-2.0	29.5%	0.1
11246	AT1G10950.1 | endomembrane protein 70, putative | chr1:3659216-3663984 FORWARD | Aliases: T19D16.13, T19D16_13	9.5	8.9	0.6	2.0	29.5%	0.1
11247	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	5.3	0.3	2.0	29.5%	0.2
11248	AT5G47410.1 | expressed protein | chr5:19249442-19249813 FORWARD | Aliases: MQL5.27, MQL5_27	7.3	6.4	0.9	2.0	29.5%	0.3
11249	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	3.6	-0.4	-2.0	29.5%	-0.1
11250	AT4G16120.1 | Symbol: ATSEB1 |	5.9	5.2	0.8	2.0	29.5%	0.5
11251	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	3.5	-0.4	-2.0	29.5%	0.1
11252	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	3.3	-0.3	-2.0	29.5%	-0.3
11253	AT1G08620.1 | 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 | chr1:2737557-2743673 FORWARD | Aliases: F22O13.10, F22O13_10	5.0	6.2	-1.2	-2.0	29.5%	0.3
11254	AT3G26230.1 | Symbol: CYP71B24 | cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450 | chr3:9599437-9601140 REVERSE | Aliases: MTC11.22	2.9	3.0	-0.2	-2.0	29.5%	-0.7

Rank	Description	Sync	Root	M	t	adj.q	B
11255	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	6.2	0.6	2.0	29.5%	0.5
11256	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	6.4	0.3	2.0	29.5%	0.1
11257	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	2.9	-0.3	-2.0	29.5%	-0.1
11258	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	11.7	10.6	1.0	2.0	29.6%	0.4
11259	AT1G42700.1 | hypothetical protein | chr1:16069371-16070032 FORWARD | Aliases: F8D11.10	3.2	3.5	-0.2	-2.0	29.6%	-0.3
11260	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	3.2	-0.4	-2.0	29.6%	0.0
11261	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	6.7	6.1	0.6	2.0	29.6%	0.4
11262	AT2G02760.1 | Symbol: ATUBC2 |	11.4	11.0	0.4	2.0	29.6%	-0.2
11263	AT2G20690.1 | lumazine-binding family protein, SP:P50854 Riboflavin synthase alpha chain (EC 2.5.1.9) {Actinobacillus pleuropneumoniae}; contains Pfam profile PF00677: Lumazine binding domain | chr2:8930386-8932052 FORWARD | Aliases: F5H14.34, F5H14_34	5.1	4.6	0.4	2.0	29.7%	0.1
11264	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	2.2	-0.3	-2.0	29.7%	-0.8
11265	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	3.2	-0.4	-2.0	29.7%	-0.1
11266	AT3G07350.1 | expressed protein, contains Pfam profile PF04720: Protein of unknown function (DUF506) | chr3:2347474-2348797 FORWARD | Aliases: F21O3.6	5.4	5.8	-0.5	-2.0	29.7%	0.2
11267	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	6.8	-1.1	-2.0	29.7%	0.4
11268	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	2.3	2.1	0.2	2.0	29.7%	-0.6
11269	AT3G06080.2 | expressed protein, identical to unknown protein GB:AAF30301 from (Arabidopsis thaliana) | chr3:1834713-1837990 REVERSE | Aliases: F24F17.6, F24F17_6	3.0	3.2	-0.2	-2.0	29.7%	-0.5
11270	AT2G44200.1 | expressed protein | chr2:18283286-18285703 FORWARD | Aliases: F4I1.1, F4I1_1	7.5	8.6	-1.0	-2.0	29.8%	0.3
11271	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	5.1	5.7	-0.6	-2.0	29.8%	0.6
11272	AT1G64470.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr1:23948448-23949435 REVERSE | Aliases: F1N19.30, F1N19_30	3.2	3.7	-0.4	-2.0	29.8%	0.0
11273	AT5G27970.1 | expressed protein | chr5:10004724-10015672 FORWARD | Aliases: F15F15.40, F15F15_40	3.5	4.1	-0.6	-2.0	29.8%	0.1
11274	AT2G36720.1 | PHD finger transcription factor, putative | chr2:15400150-15406497 FORWARD | Aliases: F13K3.12, F13K3_12	5.5	6.0	-0.5	-2.0	29.8%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11275	AT1G07420.2 | Symbol: SMO2 2 |	4.6	5.6	-1.0	-2.0	29.8%	0.5
11276	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	3.6	4.0	-0.5	-2.0	29.8%	0.1
11277	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	3.6	-0.3	-2.0	29.8%	0.0
11278	AT2G13610.1 | ABC transporter family protein | chr2:5680770-5682913 REVERSE | Aliases: T10F5.15, T10F5_15	3.4	3.6	-0.3	-2.0	29.8%	-0.1
11279	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	8.9	8.3	0.5	2.0	29.8%	0.4
11280	AT2G01860.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:388054-390248 FORWARD | Aliases: T23K3.5, T23K3_5	4.1	3.6	0.5	2.0	29.8%	0.3
11281	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	3.3	-0.3	-2.0	29.8%	-0.1
11282	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	3.6	4.1	-0.5	-2.0	29.8%	0.4
11283	AT5G50915.2 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.4	2.6	-0.2	-2.0	29.8%	-0.5
11284	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	8.5	8.9	-0.4	-2.0	29.8%	-0.0
11285	AT5G24250.1 | expressed protein | chr5:8233699-8234655 REVERSE | Aliases: MOP9.6, MOP9_6	2.3	2.5	-0.2	-2.0	29.8%	-0.6
11286	AT1G47300.1 | F-box family protein, similar to hypothetical protein GB:AAD22295 GI:4544385 from (Arabidopsis thaliana)	2.3	2.5	-0.2	-2.0	29.9%	-0.8
11287	AT5G57570.1 | expressed protein | chr5:23331010-23331420 REVERSE | Aliases: MUA2.15, MUA2_15	3.4	3.1	0.4	2.0	29.9%	0.0
11288	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	2.8	2.6	0.2	2.0	29.9%	-0.2
11289	AT3G55420.1 | expressed protein | chr3:20558694-20559744 FORWARD | Aliases: T22E16.80	5.5	4.9	0.6	2.0	29.9%	0.1
11290	AT1G16020.2 | expressed protein | chr1:5498159-5501352 FORWARD | Aliases: T24D18.12, T24D18_12	5.1	4.7	0.4	2.0	29.9%	0.3
11291	AT1G67470.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:25275845-25277239 FORWARD | Aliases: T1F15.6	4.4	4.0	0.4	2.0	29.9%	0.3
11292	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	3.5	3.2	0.3	2.0	29.9%	-0.0
11293	AT4G36560.1 | hypothetical protein | chr4:17252662-17252994 FORWARD | Aliases: AP22.48, AP22_48	2.6	2.8	-0.2	-2.0	29.9%	-0.6
11294	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	3.3	-0.3	-2.0	29.9%	-0.4
11295	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	6.8	6.3	0.4	2.0	29.9%	0.2
11296	AT3G53940.1 | mitochondrial substrate carrier family protein | chr3:19981997-19984747 REVERSE | Aliases: F5K20.240	4.1	3.7	0.4	2.0	29.9%	0.4
11297	AT5G51840.1 | expressed protein | chr5:21089195-21091664 FORWARD | Aliases: MIO24.2, MIO24_2	5.7	5.0	0.7	2.0	29.9%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11298	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	5.5	4.7	0.8	2.0	29.9%	0.6
11299	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	3.3	3.6	-0.3	-2.0	29.9%	-0.1
11300	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	6.9	8.2	-1.3	-2.0	30.0%	0.5
11301	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	4.0	3.5	0.4	2.0	30.0%	0.3
11302	AT4G28740.1 | expressed protein | chr4:14200995-14202651 FORWARD | Aliases: F16A16.150, F16A16_150	7.8	8.3	-0.5	-2.0	30.0%	0.2
11303	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	8.9	7.9	1.0	2.0	30.0%	0.3
11304	AT2G42710.1 | ribosomal protein L1 family protein | chr2:17789385-17792140 FORWARD | Aliases: F14N22.3	4.6	4.3	0.3	2.0	30.0%	0.1
11305	AT5G49370.1 | hypothetical protein | chr5:20041228-20041756 FORWARD | Aliases: K7J8.4, K7J8_4	2.1	2.2	-0.1	-2.0	30.0%	-1.0
11306	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	2.9	-0.2	-2.0	30.0%	-0.7
11307	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	9.7	9.1	0.6	2.0	30.0%	0.1
11308	AT4G23260.1 | protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain | chr4:12167433-12169904 REVERSE | Aliases: F21P8.150, F21P8_150	3.0	2.6	0.4	2.0	30.0%	-0.1
11309	AT3G52610.1 | expressed protein | chr3:19521459-19523636 FORWARD | Aliases: F3C22.10	6.1	5.8	0.3	2.0	30.1%	0.2
11310	AT5G46500.1 | expressed protein | chr5:18873681-18875014 FORWARD | Aliases: K11I1.9, K11I1_9	2.5	2.7	-0.2	-2.0	30.1%	-0.6
11311	AT5G09740.1 | histone acetyltransferase, putative, similar to histone acetyltransferase (Homo sapiens) gi:8317213:gb:AAF72665 | chr5:3021981-3024726 REVERSE | Aliases: F17I14.70, F17I14_70	4.7	4.1	0.5	2.0	30.1%	-0.1
11312	AT4G29780.1 | expressed protein | chr4:14579710-14581706 FORWARD | Aliases: F27B13.20, F27B13_20	6.3	6.9	-0.6	-2.0	30.1%	0.5
11313	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	5.5	6.2	-0.8	-2.0	30.1%	0.5
11314	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:AAC78591 | chr1:25835466-25837507 REVERSE | Aliases: F14K14.11, F14K14_11	2.4	2.6	-0.2	-2.0	30.1%	-0.4
11315	NA	5.5	6.2	-0.7	-2.0	30.1%	-0.1
11316	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	2.9	3.1	-0.3	-2.0	30.1%	-0.2
11317	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	4.4	4.9	-0.5	-2.0	30.1%	0.4
11318	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	3.4	-0.3	-2.0	30.2%	0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11319	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	2.3	2.5	-0.2	-2.0	30.2%	-0.6
11320	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	9.2	9.8	-0.6	-2.0	30.2%	0.4
11321	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	4.1	3.8	0.4	2.0	30.2%	0.1
11322	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	3.7	3.2	0.4	2.0	30.2%	0.3
11323	AT4G28110.1 | myb family transcription factor (MYB41), contains PFAM profile: myb DNA binding protein PF00249 | chr4:13968035-13969390 REVERSE | Aliases: T13J8.220, T13J8_220	3.9	4.3	-0.4	-2.0	30.2%	0.2
11324	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	3.4	-0.2	-2.0	30.2%	-0.3
11325	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	3.0	-0.3	-2.0	30.2%	-0.4
11326	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	4.9	4.3	0.6	2.0	30.3%	0.2
11327	ATMG01370.1 | Symbol: ORF111D | hypothetical protein | chrM:360717-361052 REVERSE | Aliases: ORF111D	6.7	5.3	1.4	2.0	30.3%	0.6
11328	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	4.5	4.2	0.3	2.0	30.3%	0.2
11329	AT1G05290.1 | expressed protein | chr1:1539151-1540545 REVERSE | Aliases: YUP8H12.10, YUP8H12_10	2.8	3.0	-0.2	-2.0	30.3%	-0.5
11330	AT3G50170.1 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function | chr3:18612840-18614721 REVERSE | Aliases: F11C1.10	2.5	2.6	-0.2	-2.0	30.3%	-0.6
11331	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	7.2	-0.7	-2.0	30.3%	0.4
11332	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	4.3	-0.4	-2.0	30.4%	0.3
11333	AT1G05750.1 | Symbol: PDE247 |	2.7	2.5	0.2	2.0	30.4%	-0.5
11334	AT3G43760.1 | expressed protein | chr3:15659200-15660409 REVERSE | Aliases: T28A8.50	2.8	3.0	-0.2	-2.0	30.4%	-0.3
11335	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	3.7	-0.4	-2.0	30.4%	-0.1
11336	AT1G74160.1 | expressed protein | chr1:27890797-27895084 FORWARD | Aliases: F9E11.1, F9E11_1	4.1	4.5	-0.4	-2.0	30.4%	0.3
11337	AT1G47970.1 | expressed protein | chr1:17690940-17692485 FORWARD | Aliases: T2J15.12, T2J15_12	7.7	8.2	-0.5	-2.0	30.4%	-0.1
11338	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	3.8	4.2	-0.4	-2.0	30.4%	0.1
11339	AT5G63140.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	3.0	2.8	0.2	2.0	30.4%	-0.2
11340	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	5.5	5.1	0.4	2.0	30.4%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11341	AT4G26980.1 | expressed protein | chr4:13548552-13550721 REVERSE | Aliases: F10M23.320, F10M23_320	3.8	3.5	0.3	2.0	30.4%	0.1
11342	AT4G36630.2 | Symbol: EMB2754 | expressed protein | chr4:17271834-17276622 REVERSE | Aliases: AP22.59, AP22_59, EMB2754, EMBRYO DEFECTIVE 2754	5.1	5.5	-0.5	-2.0	30.4%	0.1
11343	AT3G25130.1 | expressed protein | chr3:9152411-9153878 FORWARD | Aliases: MJL12.7	3.8	3.3	0.6	2.0	30.4%	0.5
11344	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	6.9	7.4	-0.4	-2.0	30.4%	0.1
11345	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	5.2	4.4	0.7	2.0	30.4%	0.6
11346	AT2G24600.3 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr2:10459238-10461603 REVERSE | Aliases: F25P17.10, F25P17_10	3.2	3.6	-0.3	-2.0	30.5%	0.0
11347	AT1G48280.1 | hydroxyproline-rich glycoprotein family protein | chr1:17838756-17841385 FORWARD | Aliases: F11A17.16, F11A17_16	4.5	4.0	0.5	2.0	30.5%	0.3
11348	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	5.8	-0.6	-2.0	30.5%	0.1
11349	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 8 (TOPP8) [Arabidopsis thaliana] (TAIR:At5g27840.1); 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	5.8	-0.5	-2.0	30.5%	0.3
11350	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	4.2	3.8	0.4	2.0	30.5%	0.1
11351	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	9.3	8.5	0.8	2.0	30.5%	0.2
11352	AT4G13990.1 | exostosin family protein, contains Pfam profile: PF03016	4.1	3.7	0.4	2.0	30.5%	0.2
11353	AT4G23040.1 | UBX domain-containing protein, similar to Ara4-interacting protein (Arabidopsis thaliana) GI:13160609; contains Pfam profile PF00789: UBX domain	5.1	5.6	-0.5	-2.0	30.5%	0.5
11354	AT4G38010.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:17859576-17861255 REVERSE | Aliases: F20D10.130, F20D10_130	3.9	3.7	0.2	2.0	30.5%	-0.1
11355	AT4G31570.1 | expressed protein | chr4:15297067-15306042 FORWARD | Aliases: F28M20.240, F28M20_240	2.8	3.1	-0.3	-2.0	30.5%	-0.3
11356	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	3.4	-0.3	-2.0	30.5%	0.0
11357	AT1G24938.1 | expressed protein | chr1:8789363-8792067 REVERSE | Aliases: None	2.7	3.1	-0.4	-2.0	30.5%	0.2
11358	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	5.5	5.9	-0.4	-2.0	30.5%	0.0
11359	AT2G11910.2 | expressed protein | chr2:4812767-4814399 REVERSE | Aliases: F23M2.7, F23M2_7	8.1	7.4	0.7	2.0	30.5%	0.3
11360	AT2G01690.2 | expressed protein | chr2:308701-313804 REVERSE | Aliases: T8O11.14, T8O11_14	4.0	4.8	-0.8	-2.0	30.5%	0.3
11361	AT1G21090.1 | hydroxyproline-rich glycoprotein family protein | chr1:7384618-7386547 FORWARD | Aliases: T22I11.8, T22I11_8	2.8	2.6	0.2	2.0	30.5%	-0.3

Rank	Description	Sync	Root	M	t	adj.q	B
11362	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	3.0	3.3	-0.3	-2.0	30.6%	-0.2
11363	AT5G17760.2 | AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 | chr5:5860423-5862424 REVERSE | Aliases: MVA3.110, MVA3_110	3.0	3.2	-0.2	-2.0	30.6%	-0.3
11364	AT5G04290.1 | KOW domain-containing transcription factor family protein | chr5:1196070-1202654 FORWARD | Aliases: T19N18.20, T19N18_20	8.3	9.1	-0.7	-2.0	30.6%	-0.2
11365	AT5G19660.1 | subtilase family protein, contains Pfam profile: PF00082 subtilase family | chr5:6642006-6646532 REVERSE | Aliases: T29J13.80, T29J13_80	5.5	6.3	-0.8	-2.0	30.6%	0.3
11366	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	5.4	6.2	-0.7	-2.0	30.6%	0.6
11367	AT5G52460.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.9	-0.3	-2.0	30.6%	-0.3
11368	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	4.2	3.7	0.4	2.0	30.6%	0.3
11369	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	5.0	5.3	-0.3	-2.0	30.6%	0.1
11370	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	10.8	10.3	0.6	2.0	30.6%	0.1
11371	AT3G56840.1 | FAD-dependent oxidoreductase family protein, contains Pfam profile PF01266 FAD dependent oxidoreductase | chr3:21055296-21057293 FORWARD | Aliases: T8M16.170	5.7	6.1	-0.4	-2.0	30.6%	0.2
11372	NA	7.8	8.6	-0.8	-2.0	30.6%	0.1
11373	AT5G43745.1 | phosphotransferase-related, similar to streptomycin-3'-phosphotransferase (Streptomyces griseus) GI:153164 | chr5:17586374-17592198 REVERSE | Aliases: None	3.6	3.4	0.3	2.0	30.6%	0.0
11374	AT5G13950.1 | expressed protein | chr5:4495973-4500683 REVERSE | Aliases: MAC12.8, MAC12_8	4.1	4.5	-0.4	-2.0	30.6%	0.3
11375	AT4G09390.1 | hypothetical protein, various predicted proteins -Arabidopsis thaliana | chr4:5951913-5952885 FORWARD | Aliases: T15G18.190, T15G18_190	2.5	2.8	-0.2	-2.0	30.6%	-0.2
11376	AT5G35670.1 | calmodulin-binding family protein, contains IQ calmodulin-binding motif, Pfam:PF00612 | chr5:13873345-13875756 FORWARD | Aliases: MXH1.1, MXH1_1	3.4	3.0	0.5	2.0	30.6%	0.2
11377	AT3G45000.1 | SNF7 family protein, contains Pfam profile PF03357: SNF7 family | chr3:16471333-16472392 FORWARD | Aliases: F14D17.70	2.8	2.6	0.2	2.0	30.6%	-0.5
11378	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	7.4	6.2	1.2	2.0	30.6%	0.4
11379	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	4.3	3.4	0.9	2.0	30.6%	0.2
11380	AT5G26680.1 | endonuclease, putative, similar to Swiss-Prot:P39748 FLAP endonuclease-1 (Maturation factor 1) (MF1) (Homo sapiens) | chr5:9311885-9315478 REVERSE | Aliases: None	4.1	3.6	0.5	2.0	30.6%	0.5
11381	AT1G31940.1 | expressed protein | chr1:11470039-11471320 REVERSE | Aliases: F5M6.6	6.2	5.6	0.7	2.0	30.6%	0.2
11382	AT1G68750.1 | Symbol: ATPPC4 |	3.3	3.0	0.3	2.0	30.6%	-0.1
11383	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	3.0	3.3	-0.3	-2.0	30.6%	-0.3

Rank	Description	Sync	Root	M	t	adj.q	B
11384	AT3G09980.1 | expressed protein, contains Pfam profile PF04949: Family of unknown function (DUF662) | chr3:3069236-3071412 FORWARD | Aliases: T22K18.21	8.2	6.9	1.4	2.0	30.6%	0.5
11385	AT2G34320.1 | hypothetical protein | chr2:14492038-14492916 FORWARD | Aliases: F13P17.16, F13P17_16	2.9	3.2	-0.3	-2.0	30.6%	-0.2
11386	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	2.7	3.1	-0.4	-2.0	30.7%	0.1
11387	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	6.1	7.8	-1.7	-2.0	30.7%	0.3
11388	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	4.6	0.5	2.0	30.7%	-0.0
11389	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	3.6	-0.4	-2.0	30.7%	0.1
11390	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	7.5	6.7	0.7	2.0	30.7%	0.5
11391	AT1G53830.1 | Symbol: ATPME2 |	3.4	3.7	-0.3	-2.0	30.7%	0.1
11392	AT1G12660.1 | expressed protein | chr1:4308941-4311499 FORWARD | Aliases: T12C24.19, T12C24_19	2.7	3.0	-0.3	-2.0	30.7%	-0.4
11393	AT1G80245.2 | expressed protein | chr1:30179070-30180434 FORWARD | Aliases: None	4.1	3.5	0.5	2.0	30.7%	0.1
11394	AT1G52840.1 | expressed protein | chr1:19678208-19679779 FORWARD | Aliases: F14G24.11, F14G24_11	2.2	2.4	-0.2	-2.0	30.7%	-0.5
11395	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	10.7	9.9	0.8	2.0	30.7%	-0.0
11396	AT1G31430.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:11253917-11255718 REVERSE | Aliases: T8E3.8, T8E3_8	2.9	2.5	0.3	2.0	30.7%	-0.1
11397	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	7.0	-0.5	-2.0	30.7%	0.2
11398	AT1G65910.1 | Symbol: ANAC028 | no apical meristem (NAM) family protein, similar to jasmonic acid 2 GI:6175246 from (Lycopersicon esculentum); similar to NAC2 (GI:6456751) {Arabidopsis thaliana} | chr1:24524454-24527827 REVERSE | Aliases: ANAC028, F12P19.8, F12P19_8	2.6	2.9	-0.2	-2.0	30.8%	-0.4
11399	AT1G23400.1 | expressed protein | chr1:8312065-8314733 REVERSE | Aliases: F26F24.27, F26F24_27	4.5	4.2	0.3	2.0	30.8%	-0.0
11400	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	3.1	2.9	0.2	2.0	30.8%	-0.5
11401	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	2.5	2.8	-0.2	-2.0	30.8%	-0.3
11402	AT5G14020.1 | expressed protein | chr5:4523524-4525865 REVERSE | Aliases: MAC12.31, MAC12_31	2.7	2.9	-0.2	-2.0	30.8%	-0.5
11403	AT5G25340.1 | expressed protein | chr5:8793021-8794787 FORWARD | Aliases: F18G18.80, F18G18_80	3.6	4.2	-0.5	-2.0	30.8%	-0.0

Rank	Description	Sync	Root	M	t	adj.q	B
11404	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	5.9	0.3	2.0	30.8%	0.2
11405	AT2G41690.1 | Symbol: AT HSFB3 | heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain | chr2:17388801-17389655 FORWARD | Aliases: HSFB3, T32G6.21, T32G6_21	3.5	3.2	0.3	2.0	30.8%	-0.0
11406	AT1G68460.1 | Symbol: ATIPT1 |	3.3	2.9	0.4	2.0	30.9%	0.3
11407	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	8.4	7.1	1.3	2.0	30.9%	0.5
11408	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	3.3	-0.3	-2.0	30.9%	0.0
11409	AT1G34010.1 | expressed protein | chr1:12359529-12361169 REVERSE | Aliases: F12G12.17, F12G12_17	5.5	4.9	0.5	2.0	30.9%	0.5
11410	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	4.7	0.4	2.0	30.9%	0.1
11411	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	4.5	3.9	0.5	2.0	30.9%	0.3
11412	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	2.2	2.4	-0.2	-2.0	30.9%	-0.2
11413	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	6.7	6.0	0.7	2.0	30.9%	0.3
11414	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	3.3	-0.3	-2.0	30.9%	-0.2
11415	AT4G31115.1 | expressed protein, supported by full length cDNA gi:21436034 from (Arabidopsis thaliana)	3.0	2.6	0.4	2.0	30.9%	-0.3
11416	AT3G57710.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:21396936-21398376 REVERSE | Aliases: F15B8.100	4.3	4.0	0.3	2.0	31.0%	-0.1
11417	AT4G30230.1 | expressed protein | chr4:14806382-14807164 FORWARD | Aliases: F9N11.80, F9N11_80	2.2	2.4	-0.2	-2.0	31.0%	-0.6
11418	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	3.0	2.8	0.2	2.0	31.0%	-0.2
11419	AT4G04210.1 | Symbol: pux4 | UBX domain-containing protein, similar to XY40 protein (Rattus norvegicus) GI:2547025; contains Pfam profile PF00789: UBX domain	7.4	6.9	0.5	2.0	31.0%	0.0
11420	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	3.3	0.3	2.0	31.1%	-0.1
11421	AT4G37330.1 | Symbol: CYP81D4 | cytochrome P450 family protein | chr4:17562339-17564590 REVERSE | Aliases: F6G17.5	5.7	6.4	-0.7	-2.0	31.1%	0.1
11422	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	2.4	-0.1	-2.0	31.1%	-0.8
11423	AT1G15040.2 | glutamine amidotransferase-related | chr1:5179617-5181369 REVERSE | Aliases: T15D22.12, T15D22_12	3.5	3.9	-0.4	-2.0	31.1%	-0.1
11424	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	8.9	8.3	0.6	2.0	31.1%	0.4
11425	AT5G47460.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:19269690-19271420 REVERSE | Aliases: MNJ7.5, MNJ7_5	4.8	4.3	0.5	2.0	31.1%	0.1
11426	AT3G49600.1 | Symbol: UBP26 | ubiquitin-specific protease 26 (UBP26), similar to GI:11993492; RNA binding protein - Homo sapiens, EMBL:AB016089 (N-terminus), several ubiquitin carboxyl-terminal hydrolases from aa pos. 712	3.8	3.4	0.4	2.0	31.1%	0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11427	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	3.5	-0.3	-2.0	31.1%	-0.2
11428	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)	5.3	4.8	0.5	2.0	31.1%	0.4
11429	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	8.7	8.4	0.3	2.0	31.1%	0.1
11430	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	2.3	2.6	-0.2	-2.0	31.1%	-0.5
11431	AT3G63040.1 | expressed protein, predicted protein, C.elegans | chr3:23307621-23308184 REVERSE | Aliases: T20O10.140	2.2	2.1	0.1	2.0	31.1%	-0.8
11432	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	5.9	6.5	-0.6	-2.0	31.1%	0.4
11433	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	2.6	-0.2	-2.0	31.1%	-0.2
11434	AT3G19490.1 | Symbol: ATNHD1 |	9.1	8.6	0.5	2.0	31.1%	0.2
11435	AT3G42940.1 | expressed protein | chr3:15017601-15018182 FORWARD | Aliases: F18P9.100	2.6	2.9	-0.3	-2.0	31.1%	-0.2
11436	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	10.5	10.0	0.5	2.0	31.1%	-0.1
11437	AT4G32430.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:15652898-15655480 FORWARD | Aliases: F8B4.130, F8B4_130	3.0	3.3	-0.3	-2.0	31.1%	-0.2
11438	AT5G28570.1 | hypothetical protein | chr5:10574625-10575163 FORWARD | Aliases: T10I18.4, T10I18_4	4.0	4.2	-0.3	-2.0	31.1%	-0.4
11439	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	2.5	2.8	-0.2	-2.0	31.1%	-0.2
11440	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	5.3	5.8	-0.5	-2.0	31.2%	-0.2
11441	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	9.3	-0.8	-2.0	31.2%	-0.2
11442	AT3G02600.1 | Symbol: LPP3 | Encodes phosphatidic acid phosphatase. Expressed during germination. | chr3:551358-554678 FORWARD | Aliases: ATLPP3, F16B3.23, F16B3_23, LPP3	4.9	5.4	-0.5	-2.0	31.2%	0.1
11443	AT4G03940.1 | expressed protein | chr4:1873622-1875231 FORWARD | Aliases: T24M8.7, T24M8_7	4.7	5.3	-0.5	-2.0	31.2%	0.2
11444	AT3G21670.1 | nitrate transporter (NTP3), nearly identical to nitrate transporter (Arabidopsis thaliana) GI:4490323; contains Pfam profile: PF00854 POT family	4.6	4.0	0.6	2.0	31.2%	0.3
11445	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	3.9	3.6	0.4	2.0	31.2%	0.1
11446	AT1G46768.1 | Symbol: RAP2.1 |	3.8	4.2	-0.4	-2.0	31.2%	0.3
11447	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	5.2	4.7	0.4	2.0	31.2%	0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11448	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	9.4	10.7	-1.3	-2.0	31.2%	0.5
11449	AT1G75380.3 | wound-responsive protein-related, similar to wound inducive gene GI:8096273 from (Nicotiana tabacum) | chr1:28285050-28287694 REVERSE | Aliases: F1B16.9, F1B16_9	9.4	10.7	-1.3	-2.0	31.2%	0.5
11450	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	6.5	-0.5	-2.0	31.2%	0.1
11451	AT5G47170.1 | expressed protein, similar to unknown protein (gb AAF26469.1) | chr5:19175735-19176187 REVERSE | Aliases: MQL5.2, MQL5_2	3.4	3.0	0.4	2.0	31.2%	0.0
11452	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	3.4	4.3	-0.9	-2.0	31.2%	0.5
11453	AT5G54590.2 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr5:22197706-22199924 FORWARD | Aliases: MRB17.9, MRB17_9	3.9	4.3	-0.3	-2.0	31.3%	-0.0
11454	AT5G44080.1 | bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor | chr5:17755879-17757098 REVERSE | Aliases: MRH10.19, MRH10_19	6.0	6.5	-0.6	-2.0	31.3%	0.1
11455	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	2.9	0.2	2.0	31.3%	-0.4
11456	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	3.8	0.4	2.0	31.3%	0.3
11457	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	7.2	6.5	0.7	2.0	31.3%	0.3
11458	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	6.1	5.4	0.7	2.0	31.3%	0.5
11459	AT5G43010.1 | Symbol: RPT4A | 26S proteasome AAA-ATPase subunit (RPT4a), gb:AAF22524.1 | chr5:17265606-17268362 REVERSE | Aliases: MBD2.21, MBD2_21	8.0	7.1	0.9	2.0	31.3%	0.2
11460	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	8.5	8.0	0.5	2.0	31.3%	0.1
11461	AT1G62700.1 | Symbol: ANAC026 | no apical meristem (NAM) family protein, similar to NAC2 (GI:6456751)	2.5	2.6	-0.2	-2.0	31.4%	-0.5
11462	AT4G09830.1 | expressed protein | chr4:6188764-6190850 FORWARD | Aliases: F17A8.180, F17A8_180	8.9	8.4	0.5	2.0	31.4%	0.0
11463	AT3G62010.1 | expressed protein | chr3:22975652-22982754 FORWARD | Aliases: F21F14.180	5.9	5.4	0.5	2.0	31.4%	0.1
11464	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	6.0	4.8	1.2	2.0	31.4%	0.4
11465	AT1G28070.1 | expressed protein, ; expression supported by MPSS | chr1:9783069-9783851 FORWARD | Aliases: F13K9.17, F13K9_17	5.7	5.2	0.5	2.0	31.4%	0.3
11466	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	5.6	1.0	2.0	31.4%	0.3

Rank	Description	Sync	Root	M	t	adj.q	B
11467	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	2.4	-0.2	-2.0	31.4%	-0.4
11468	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	7.5	6.9	0.5	2.0	31.5%	0.3
11469	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	5.8	5.0	0.8	2.0	31.5%	0.6
11470	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	2.4	2.7	-0.3	-2.0	31.5%	-0.2
11471	AT5G22910.1 | Symbol: ATCHX9 |	3.1	3.5	-0.4	-2.0	31.5%	-0.2
11472	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	3.0	-0.3	-2.0	31.5%	-0.3
11473	AT5G02670.1 | expressed protein | chr5:602720-604604 REVERSE | Aliases: T22P11.260, T22P11_260	2.5	2.7	-0.2	-2.0	31.5%	-0.5
11474	AT5G16680.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr5:5467537-5473504 REVERSE | Aliases: MTG13.4, MTG13_4	6.9	7.7	-0.8	-2.0	31.5%	0.1
11475	AT5G57400.1 | expressed protein | chr5:23280048-23280443 REVERSE | Aliases: MSF19.6, MSF19_6	2.8	2.9	-0.2	-2.0	31.5%	-0.5
11476	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}	6.4	7.2	-0.8	-2.0	31.5%	0.3
11477	AT4G13740.1 | Symbol: EMB2597 | expressed protein | chr4:7975184-7977362 FORWARD | Aliases: EMB2597, EMBRYO DEFECTIVE 2597, F18A5.130, F18A5_130	3.2	3.8	-0.6	-2.0	31.6%	-0.1
11478	AT2G25220.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:10749793-10752202 REVERSE | Aliases: T22F11.19	3.2	3.5	-0.4	-2.0	31.6%	0.1
11479	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	2.7	2.9	-0.2	-2.0	31.6%	-0.5
11480	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	6.6	6.2	0.4	2.0	31.6%	0.1
11481	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	8.0	8.4	-0.4	-2.0	31.6%	0.2
11482	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	4.7	4.2	0.5	2.0	31.6%	0.3
11483	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	3.5	-0.3	-2.0	31.6%	-0.4
11484	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)	4.5	3.9	0.5	2.0	31.6%	0.5
11485	AT1G67290.1 | glyoxal oxidase-related, contains similarity to glyoxal oxidase precursor (Phanerochaete chrysosporium) gi:1050302:gb:AAA87594 | chr1:25194684-25196900 REVERSE | Aliases: F1N21.11	3.0	3.3	-0.3	-2.0	31.6%	0.0
11486	AT5G60590.2 | yrdC protein-related | chr5:24374251-24375976 FORWARD | Aliases: MUP24.1	2.6	2.4	0.2	2.0	31.6%	-0.3
11487	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	3.6	-0.4	-2.0	31.6%	-0.0
11488	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	4.3	0.3	2.0	31.7%	0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11489	AT2G38010.2 | ceramidase family protein, contains Pfam domain, PF04734: Neutral/alkaline nonlysosomal ceramidase | chr2:15913940-15917009 FORWARD | Aliases: T8P21.8, T8P21_8	6.9	6.5	0.4	2.0	31.7%	0.0
11490	AT3G17860.2 | expressed protein | chr3:6121059-6123017 FORWARD | Aliases: MEB5.8	4.4	4.7	-0.3	-1.9	31.7%	0.2
11491	AT4G22190.1 | expressed protein | chr4:11741867-11743330 REVERSE | Aliases: T10I14.20, T10I14_20	5.5	6.0	-0.5	-1.9	31.7%	-0.0
11492	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	3.0	-0.2	-1.9	31.7%	-0.3
11493	AT3G28350.1 | hypothetical protein | chr3:10609596-10611901 FORWARD | Aliases: MFJ20.3	2.6	2.4	0.2	1.9	31.7%	-0.6
11494	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	3.5	3.8	-0.2	-1.9	31.7%	-0.3
11495	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 NAPTHOIC ACID PHYTYLTRANSFERASE, ABC4, ABERRANT CHLORPLAST DEVELOPMENT4, F8A5.36, F8A5_36	3.1	2.8	0.3	1.9	31.7%	-0.2
11496	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	8.2	7.2	1.0	1.9	31.7%	0.1
11497	AT1G25290.1 | rhomboid family protein, contains PFAM domain PF01694, Rhomboid family | chr1:8867144-8869079 FORWARD | Aliases: F4F7.32, F4F7_32	4.8	4.6	0.2	1.9	31.7%	-0.1
11498	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	8.0	7.4	0.6	1.9	31.7%	0.5
11499	AT3G15530.2 | expressed protein | chr3:5252882-5254465 REVERSE | Aliases: MJK13.19	7.2	7.7	-0.5	-1.9	31.7%	0.2
11500	AT5G57830.1 | expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593 | chr5:23446517-23448222 REVERSE | Aliases: MTI20.7, MTI20_7	4.6	5.2	-0.6	-1.9	31.7%	0.4
11501	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	2.6	-0.2	-1.9	31.7%	-0.7
11502	AT5G54120.1 | expressed protein | chr5:21980126-21980954 FORWARD | Aliases: MJP23.10, MJP23_10	3.2	3.6	-0.5	-1.9	31.7%	0.1
11503	AT2G38760.1 | Symbol: ANNAT3 |	3.9	3.6	0.3	1.9	31.8%	0.1
11504	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	7.6	6.9	0.7	1.9	31.8%	0.3
11505	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	3.1	3.3	-0.3	-1.9	31.8%	-0.5
11506	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	2.7	0.4	1.9	31.8%	0.1
11507	AT5G54630.1 | zinc finger protein-related, contains Prosite:PS00028 Zinc finger, C2H2 type, domain | chr5:22209725-22211534 REVERSE | Aliases: MRB17.13, MRB17_13	4.2	4.6	-0.4	-1.9	31.8%	-0.2
11508	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	6.8	7.4	-0.7	-1.9	31.8%	0.4
11509	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	2.6	-0.3	-1.9	31.8%	-0.6

Rank	Description	Sync	Root	M	t	adj.q	B
11510	AT1G19150.1 | Symbol: LHCA2*1 | chlorophyll A-B binding protein, putative / LHCI 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	3.5	3.0	0.6	1.9	31.9%	0.4
11511	AT4G12000.1 | expressed protein | chr4:7193264-7195146 REVERSE | Aliases: F16J13.70, F16J13_70	4.7	5.3	-0.6	-1.9	31.9%	0.2
11512	AT2G29790.1 | expressed protein | chr2:12727961-12729532 REVERSE | Aliases: T27A16.11, T27A16_11	2.4	2.7	-0.2	-1.9	31.9%	-0.5
11513	AT5G55980.1 | serine-rich protein-related, contains some similarity to serine-rich proteins | chr5:22687527-22687868 FORWARD | Aliases: MDA7.2, MDA7_2	2.6	2.8	-0.2	-1.9	31.9%	-0.5
11514	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	4.1	4.5	-0.4	-1.9	31.9%	-0.2
11515	AT4G07530.1 | expressed protein | chr4:4365347-4368612 REVERSE | Aliases: T3E15.23, T3E15_23	3.6	4.2	-0.6	-1.9	31.9%	0.2
11516	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	3.4	-0.3	-1.9	31.9%	-0.2
11517	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	4.2	4.8	-0.6	-1.9	31.9%	0.2
11518	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	7.3	6.5	0.8	1.9	32.0%	0.3
11519	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	2.6	-0.2	-1.9	32.0%	-0.5
11520	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	2.8	-0.2	-1.9	32.0%	-0.7
11521	AT1G23610.1 | expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220 | chr1:8362904-8363215 REVERSE | Aliases: F28C11.24	3.1	3.7	-0.5	-1.9	32.0%	0.0
11522	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	5.0	-0.5	-1.9	32.0%	0.1
11523	AT4G21890.1 | expressed protein | chr4:11611855-11612915 REVERSE | Aliases: T8O5.100, T8O5_100	3.4	3.7	-0.3	-1.9	32.0%	-0.2
11524	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	3.5	4.0	-0.5	-1.9	32.0%	0.2
11525	AT3G26110.1 | expressed protein | chr3:9542720-9543351 FORWARD | Aliases: MPE11.5	3.4	3.6	-0.2	-1.9	32.0%	-0.4
11526	AT4G22650.1 | hypothetical protein, various predicted proteins, Arabidopsis thaliana | chr4:11913568-11914038 FORWARD | Aliases: T12H17.40	2.5	2.7	-0.2	-1.9	32.0%	-0.6
11527	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	3.7	4.0	-0.3	-1.9	32.0%	-0.0
11528	AT4G05270.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr4:2694937-2695326 FORWARD | Aliases: C17L7.190, C17L7_190	2.4	2.6	-0.2	-1.9	32.0%	-0.7
11529	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	3.0	-0.3	-1.9	32.1%	-0.1
11530	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	9.4	8.6	0.8	1.9	32.1%	-0.0

Rank	Description	Sync	Root	M	t	adj.q	B
11531	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	6.5	-0.5	-1.9	32.1%	0.3
11532	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	2.8	3.0	-0.2	-1.9	32.1%	-0.6
11533	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	5.1	0.5	1.9	32.1%	0.4
11534	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	3.8	4.6	-0.8	-1.9	32.1%	0.3
11535	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	9.3	8.4	0.9	1.9	32.1%	-0.1
11536	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	4.3	4.7	-0.4	-1.9	32.1%	-0.2
11537	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	2.7	2.9	-0.3	-1.9	32.1%	-0.2
11538	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	2.9	-0.2	-1.9	32.1%	-0.4
11539	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	3.2	-0.2	-1.9	32.1%	-0.5
11540	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	6.8	6.2	0.6	1.9	32.1%	0.4
11541	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	2.7	-0.2	-1.9	32.1%	-0.3
11542	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	3.0	-0.4	-1.9	32.2%	-0.1
11543	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	3.4	3.8	-0.4	-1.9	32.2%	-0.0
11544	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	2.8	-0.2	-1.9	32.2%	-0.6
11545	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	3.5	0.2	1.9	32.2%	-0.2
11546	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	4.5	4.2	0.3	1.9	32.2%	-0.1
11547	AT4G26240.1 | expressed protein | chr4:13286786-13288980 REVERSE | Aliases: T25K17.50, T25K17_50	6.3	5.9	0.4	1.9	32.2%	0.1
11548	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	3.7	-0.5	-1.9	32.2%	0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11549	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	3.4	-0.4	-1.9	32.2%	0.1
11550	AT5G48810.1 | Symbol: ATB5 B |	11.5	11.1	0.4	1.9	32.2%	0.0
11551	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) {Arabidopsis thaliana}; contains Pfam profile PF01717: Methionine synthase, vitamin-B12 independent | chr5:7124116-7128361 REVERSE | Aliases: F22D1.150, F22D1_150	4.6	4.2	0.5	1.9	32.2%	0.0
11552	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	7.0	7.9	-0.9	-1.9	32.2%	0.4
11553	AT2G37010.1 | Symbol: ATNAP12 | ABC transporter family protein, contains ABC transporter domain, Pfam:PF00005	2.5	2.8	-0.3	-1.9	32.2%	-0.2
11554	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	2.6	2.9	-0.2	-1.9	32.2%	-0.3
11555	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	6.5	7.3	-0.8	-1.9	32.2%	0.2
11556	AT5G05800.1 | expressed protein | chr5:1743087-1745246 REVERSE | Aliases: MJJ3.22, MJJ3_22	5.7	5.4	0.4	1.9	32.2%	0.1
11557	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	6.2	5.2	1.1	1.9	32.3%	0.3
11558	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	11.4	11.1	0.3	1.9	32.3%	-0.4
11559	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	4.3	4.7	-0.4	-1.9	32.4%	0.2
11560	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	4.1	-0.2	-1.9	32.4%	-0.2
11561	AT2G30530.1 | expressed protein | chr2:13015993-13018140 FORWARD | Aliases: T6B20.12, T6B20_12	6.7	6.3	0.5	1.9	32.4%	0.1
11562	AT5G62360.1 | invertase/pectin methylesterase inhibitor family protein, similar to pectinesterase from Arabidosis 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	3.6	-0.3	-1.9	32.4%	-0.2
11563	AT3G50780.1 | expressed protein | chr3:18886380-18888505 REVERSE | Aliases: F18B3.60	4.8	5.2	-0.4	-1.9	32.4%	0.2
11564	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	6.3	0.7	1.9	32.4%	0.4
11565	AT2G34080.1 | cysteine proteinase, putative, contains similarity to cysteine protease SPCP1 GI:13491750 from (Ipomoea batatas)	3.4	3.8	-0.4	-1.9	32.4%	0.1
11566	AT2G02220.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:584097-587123 REVERSE | Aliases: T16F16.1	3.2	3.5	-0.3	-1.9	32.4%	-0.3
11567	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	7.4	-0.4	-1.9	32.4%	0.1
11568	AT1G06060.1 | RanBPM-related, similar to RANBPM {GI:13194576)(Homo sapiens) | chr1:1832942-1835576 FORWARD | Aliases: T21E18.11, T21E18_11	3.7	4.0	-0.3	-1.9	32.4%	0.0
11569	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	5.1	5.6	-0.5	-1.9	32.4%	0.0
11570	AT5G01510.1 | expressed protein, contains Pfam domain, PF04884: Protein of unknown function, DUF647 | chr5:201605-205380 FORWARD | Aliases: F7A7.30, F7A7_30	3.7	3.4	0.3	1.9	32.5%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11571	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	5.9	0.9	1.9	32.5%	0.3
11572	AT1G48090.2 | C2 domain-containing protein, contains Pfam profile: PF00168 C2 domain | chr1:17739966-17761639 REVERSE | Aliases: F21D18.22	5.1	5.9	-0.9	-1.9	32.5%	0.4
11573	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	2.4	2.7	-0.3	-1.9	32.5%	-0.1
11574	AT5G63070.1 | 40S ribosomal protein S15, putative | chr5:25316404-25316886 REVERSE | Aliases: MDC12.3, MDC12_3	3.6	3.3	0.3	1.9	32.5%	0.0
11575	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	4.2	-0.4	-1.9	32.5%	-0.0
11576	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	5.1	5.5	-0.3	-1.9	32.6%	-0.0
11577	AT3G44560.1 | acyl CoA reductase, putative, similar to acyl CoA reductase (Simmondsia chinensis) GI:5020215; contains Pfam profile PF03015: Male sterility protein | chr3:16162164-16165384 FORWARD | Aliases: F14L2.110	2.0	2.2	-0.1	-1.9	32.6%	-1.1
11578	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	4.6	5.3	-0.7	-1.9	32.7%	0.2
11579	ATCG00210.1 | Symbol: YCF6 | hypothetical protein | chrC:28089-28178 FORWARD | Aliases: YCF6	6.0	7.5	-1.5	-1.9	32.7%	0.2
11580	AT1G08940.1 | phosphoglycerate/bisphosphoglycerate mutase family protein, contains Pfam profile PF00300: phosphoglycerate mutase family | chr1:2877695-2879172 FORWARD | Aliases: F7G19.18, F7G19_18	7.9	8.4	-0.5	-1.9	32.7%	-0.1
11581	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	5.5	6.3	-0.8	-1.9	32.7%	0.2
11582	AT5G35390.1 | leucine-rich repeat transmembrane protein kinase, putative, receptor-like protein kinase PRK1, Lycopersicon esculentum, PIR:T07865 | chr5:13614148-13616206 FORWARD | Aliases: T26D22.9, T26D22_9	2.8	3.1	-0.3	-1.9	32.7%	-0.2
11583	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	2.7	-0.3	-1.9	32.7%	-0.4
11584	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	2.0	0.1	1.9	32.8%	-1.0
11585	AT1G24420.1 | transferase family protein, similar to deacetylvindoline 4-O-acetyltransferase (Catharanthus roseus)(GI:4091808)(PMID:9681034), acetyl-CoA:benzylalcohol acetyltranferase (Clarkia concinna)(GI:6166330)(PMID:10588064) | chr1:8656676-8657986 FORWARD | Aliases: F21J9.8	2.4	2.7	-0.2	-1.9	32.8%	-0.4
11586	AT4G39720.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr4:18429886-18430858 REVERSE | Aliases: T19P19.110, T19P19_110	4.0	3.8	0.3	1.9	32.8%	-0.2
11587	AT3G07700.2 | ABC1 family protein, contains Pfam domain, PF03109: ABC1 family | chr3:2459497-2463648 REVERSE | Aliases: MLP3.15	4.1	4.6	-0.5	-1.9	32.8%	0.1
11588	AT3G54390.1 | expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189 | chr3:20148719-20150120 REVERSE | Aliases: T14E10.5	5.3	4.9	0.5	1.9	32.8%	0.2
11589	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	3.5	3.9	-0.4	-1.9	32.8%	0.0
11590	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	3.4	3.7	-0.3	-1.9	32.8%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11591	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	9.5	8.5	1.0	1.9	32.8%	0.4
11592	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	3.3	3.6	-0.3	-1.9	32.8%	-0.2
11593	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	5.3	0.4	1.9	32.8%	0.2
11594	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	7.4	6.8	0.6	1.9	32.8%	0.0
11595	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	2.2	-0.1	-1.9	32.8%	-0.7
11596	AT1G71690.1 | expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579) | chr1:26951439-26952726 FORWARD | Aliases: F14O23.3, F14O23_3	3.6	3.2	0.5	1.9	32.8%	0.2
11597	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	2.9	2.6	0.3	1.9	32.8%	-0.1
11598	AT5G48390.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain | chr5:19629304-19632589 FORWARD | Aliases: MJE7.2, MJE7_2	2.4	2.2	0.2	1.9	32.8%	-0.5
11599	AT2G22960.1 | serine carboxypeptidase S10 family protein, contains Pfam profile: PF00450 serine carboxypeptidase ;similar to sinapoylglucose:malate sinapoyltransferase GI:8699619 from (Arabidopsis thaliana)	2.5	2.7	-0.2	-1.9	32.8%	-0.8
11600	AT4G07515.1 | expressed protein | chr4:4314954-4315507 REVERSE | Aliases: None	3.2	3.5	-0.3	-1.9	32.8%	-0.3
11601	AT5G18510.1 | expressed protein | chr5:6141780-6143888 REVERSE | Aliases: T28N17.4	3.2	2.9	0.3	1.9	32.8%	-0.3
11602	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	3.8	-0.6	-1.9	32.8%	-0.0
11603	AT1G35663.1 | hypothetical protein | chr1:13199210-13199749 REVERSE | Aliases: F15O4.65, F15O4_65	2.2	2.4	-0.2	-1.9	32.9%	-0.9
11604	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	4.1	-0.4	-1.9	32.9%	0.0
11605	AT2G28270.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	2.9	-0.2	-1.9	32.9%	-0.7
11606	AT3G47460.1 | Symbol: ATSMC2 |	3.8	3.4	0.4	1.9	32.9%	-0.1
11607	AT4G31980.1 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function | chr4:15464911-15469210 FORWARD | Aliases: F11C18.13	3.6	4.3	-0.7	-1.9	32.9%	0.1
11608	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	3.1	2.8	0.3	1.9	32.9%	-0.2
11609	AT3G27590.1 | expressed protein | chr3:10222384-10222952 FORWARD | Aliases: MMJ24.15	2.6	2.9	-0.3	-1.9	32.9%	-0.1
11610	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	6.1	5.2	0.8	1.9	32.9%	0.4
11611	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	3.6	-0.3	-1.9	32.9%	-0.2
11612	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	4.1	-0.4	-1.9	32.9%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11613	AT4G14870.1 | expressed protein | chr4:8517187-8517897 FORWARD | Aliases: DL3475W, FCAALL.408	6.0	5.6	0.4	1.9	32.9%	0.0
11614	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	3.7	4.2	-0.5	-1.9	33.0%	0.2
11615	AT4G05580.1 | hypothetical protein | chr4:2841645-2841995 FORWARD | Aliases: T1J24.6, T1J24_6	2.4	2.6	-0.2	-1.9	33.0%	-0.9
11616	AT1G16880.2 | uridylyltransferase-related, similar to (Protein-PII) uridylyltransferase (PII uridylyl- transferase) (Uridylyl removing enzyme) (UTase)(SP:Q9AC53) (Caulobacter crescentus) | chr1:5773671-5775497 FORWARD | Aliases: F17F16.13	7.9	7.1	0.9	1.9	33.0%	0.4
11617	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	3.1	0.4	1.9	33.0%	0.1
11618	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	3.1	2.8	0.3	1.9	33.0%	-0.1
11619	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	2.7	3.0	-0.4	-1.9	33.0%	-0.5
11620	AT3G47540.1 | chitinase, putative, similar to basic endochitinase CHB4 precursor SP:Q06209 from (Brassica napus) | chr3:17532014-17533254 FORWARD | Aliases: F1P2.90	6.3	5.8	0.5	1.9	33.0%	-0.0
11621	AT5G05890.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:1772544-1774088 FORWARD | Aliases: K18J17.4, K18J17_4	4.8	5.2	-0.4	-1.9	33.0%	0.1
11622	AT3G07580.1 | expressed protein | chr3:2420975-2422667 REVERSE | Aliases: MLP3.3	4.3	4.0	0.3	1.9	33.0%	0.2
11623	AT5G46760.1 | basic helix-loop-helix (bHLH) family protein | chr5:18991458-18993236 FORWARD | Aliases: MZA15.18, MZA15_18	5.4	5.9	-0.5	-1.9	33.0%	0.0
11624	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	3.4	3.6	-0.2	-1.9	33.1%	-0.4
11625	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	5.7	6.3	-0.6	-1.9	33.1%	0.1
11626	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	5.1	5.6	-0.5	-1.9	33.1%	0.4
11627	AT4G10060.1 | expressed protein, contains Pfam domain PF04685: Protein of unknown function, DUF608 | chr4:6288850-6295398 FORWARD | Aliases: F28M11.3	4.0	4.5	-0.5	-1.9	33.1%	0.1
11628	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	2.4	-0.2	-1.9	33.1%	-0.6
11629	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	2.8	2.6	0.2	1.9	33.1%	-0.3
11630	AT1G22600.1 | expressed protein | chr1:7987297-7989176 REVERSE | Aliases: F12K8.5, F12K8_5	3.2	2.6	0.6	1.9	33.1%	0.1
11631	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	3.2	3.6	-0.3	-1.9	33.1%	-0.4
11632	AT5G22550.2 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function | chr5:7483876-7485461 REVERSE | Aliases: MQJ16.9, MQJ16_9	2.4	2.6	-0.2	-1.9	33.1%	-0.6
11633	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	5.7	5.1	0.5	1.9	33.1%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11634	AT5G15570.1 | expressed protein, hypothetical protein F14P3.19 - Arabidopsis thaliana, EMBL:AC009755 | chr5:5066854-5067999 FORWARD | Aliases: T20K14.180, T20K14_180	4.0	3.4	0.5	1.9	33.1%	0.1
11635	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	2.6	2.9	-0.3	-1.9	33.1%	-0.2
11636	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	6.6	6.1	0.5	1.9	33.2%	0.2
11637	AT2G38890.1 | expressed protein, and genefinder | chr2:16248312-16249995 FORWARD | Aliases: T7F6.6, T7F6_6	2.0	2.1	-0.1	-1.9	33.2%	-1.1
11638	AT1G50650.1 | stigma-specific Stig1 family protein, low similarity to stigma-specific protein STIG1 (Nicotiana tabacum) GI:496647; contains Pfam profile PF04885: Stigma-specific protein, Stig1 | chr1:18767441-18767965 REVERSE | Aliases: F11F12.3, F11F12_3	3.0	3.3	-0.2	-1.9	33.2%	-0.3
11639	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	2.9	-0.3	-1.9	33.2%	-0.1
11640	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	3.0	3.3	-0.3	-1.9	33.2%	-0.1
11641	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	3.1	0.2	1.9	33.3%	-0.3
11642	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	4.4	0.3	1.9	33.3%	0.0
11643	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}	12.0	11.4	0.6	1.9	33.3%	-0.2
11644	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	4.4	5.3	-0.9	-1.9	33.3%	0.3
11645	AT1G44222.1 | expressed protein | chr1:16823799-16824056 FORWARD | Aliases: T18F15.14, T18F15_14	3.1	3.5	-0.4	-1.9	33.3%	-0.0
11646	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	4.1	-0.3	-1.9	33.3%	-0.2
11647	AT5G51460.3 | Symbol: ATTPPA |	3.6	4.0	-0.3	-1.9	33.3%	-0.1
11648	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	3.0	-0.3	-1.9	33.3%	-0.4
11649	AT4G37295.1 | expressed protein | chr4:17553554-17554099 FORWARD | Aliases: None	5.0	5.6	-0.6	-1.9	33.3%	0.1
11650	AT3G12190.1 | expressed protein | chr3:3886190-3886999 FORWARD | Aliases: F28J15.4	2.8	3.0	-0.2	-1.9	33.3%	-0.7
11651	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	7.7	8.5	-0.8	-1.9	33.3%	0.2
11652	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	6.6	7.3	-0.7	-1.9	33.4%	-0.1
11653	AT5G05100.1 | expressed protein | chr5:1505123-1507203 REVERSE | Aliases: MUG13.4, MUG13_4	9.5	9.8	-0.3	-1.9	33.4%	-0.5
11654	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	9.8	10.1	-0.3	-1.9	33.4%	-0.4
11655	AT3G59440.1 | calcium-binding protein, putative, similar to calcium-binding protein (Lotus japonicus) GI:18413495 | chr3:21981332-21982099 FORWARD | Aliases: F25L23.300	3.2	3.5	-0.3	-1.9	33.4%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11656	AT2G23290.1 | myb family transcription factor | chr2:9911867-9913000 REVERSE | Aliases: T20D16.8, T20D16_8	6.1	7.3	-1.2	-1.9	33.4%	-0.0
11657	AT4G25570.1 | Symbol: ACYB 2 |	8.3	10.0	-1.7	-1.9	33.4%	0.4
11658	AT3G45720.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr3:16796031-16797930 FORWARD | Aliases: T6D9.50	2.8	3.1	-0.3	-1.9	33.4%	-0.2
11659	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	4.1	-0.4	-1.9	33.4%	0.2
11660	AT3G12685.1 | expressed protein, contains Pfam domain, PF02681: Uncharacterized BCR, COG1963 | chr3:4029190-4030362 REVERSE | Aliases: None	3.7	3.3	0.4	1.9	33.4%	0.2
11661	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	3.1	-0.2	-1.9	33.5%	-0.4
11662	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	3.2	2.9	0.3	1.9	33.5%	-0.2
11663	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	4.3	5.3	-1.0	-1.9	33.5%	0.4
11664	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	2.5	2.8	-0.2	-1.9	33.5%	-0.5
11665	AT3G29791.1 | expressed protein | chr3:11698235-11699250 FORWARD | Aliases: K17E7.5	3.0	3.1	-0.2	-1.9	33.5%	-0.6
11666	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	4.4	4.8	-0.4	-1.9	33.5%	-0.1
11667	AT1G56210.1 | copper chaperone (CCH)-related, low similarity to copper homeostasis factor (GI:3168840)(PMID:9701579) and farnesylated proteins ATFP3 (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	3.7	0.4	1.9	33.5%	0.2
11668	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	3.1	3.4	-0.3	-1.9	33.5%	-0.3
11669	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	4.4	4.2	0.2	1.9	33.6%	-0.2
11670	AT5G01450.1 | expressed protein | chr5:183329-186444 REVERSE | Aliases: T10O8.160, T10O8_160	5.4	6.1	-0.7	-1.9	33.6%	0.2
11671	AT3G04510.1 | expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640) | chr3:1215818-1216423 REVERSE | Aliases: T27C4.16, T27C4_16	2.5	2.8	-0.3	-1.9	33.6%	-0.1
11672	AT5G47900.1 | expressed protein | chr5:19409209-19411387 FORWARD | Aliases: MCA23.24, MCA23_24	3.8	4.1	-0.3	-1.9	33.6%	-0.0
11673	AT4G33600.1 | expressed protein | chr4:16144453-16145867 REVERSE | Aliases: T16L1.90, T16L1_90	2.9	3.1	-0.3	-1.9	33.6%	-0.4
11674	AT2G21610.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr2:9252241-9254105 REVERSE | Aliases: F2G1.12, F2G1_12	2.9	3.2	-0.3	-1.9	33.6%	-0.4
11675	AT5G19990.1 | Symbol: ATSUG1 |	10.4	8.7	1.6	1.9	33.6%	0.7
11676	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	8.7	1.6	1.9	33.6%	0.7

Rank	Description	Sync	Root	M	t	adj.q	B
11677	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	5.5	5.1	0.4	1.9	33.6%	0.1
11678	AT5G43020.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:17272540-17274970 REVERSE | Aliases: MMG4.2, MMG4_2	2.8	3.1	-0.3	-1.9	33.6%	-0.3
11679	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	8.7	8.3	0.4	1.9	33.6%	-0.4
11680	AT5G04760.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr5:1373531-1374736 REVERSE | Aliases: MUK11.7	6.7	7.2	-0.5	-1.9	33.6%	0.3
11681	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	11.8	0.4	1.9	33.6%	-0.6
11682	AT5G66610.1 | LIM domain-containing protein, contains Pfam profile PF00412: LIM domain	2.9	3.2	-0.3	-1.9	33.6%	-0.2
11683	AT3G13840.1 | scarecrow transcription factor family protein | chr3:4555312-4556844 REVERSE | Aliases: MCP4.6	2.8	3.1	-0.3	-1.9	33.7%	-0.0
11684	AT2G05350.1 | expressed protein | chr2:1950452-1954737 FORWARD | Aliases: F16J10.10, F16J10_10	2.2	2.5	-0.2	-1.9	33.7%	-0.7
11685	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	2.9	3.1	-0.2	-1.9	33.7%	-0.4
11686	AT4G13850.2 | Symbol: ATGRP2 |	7.6	6.6	1.1	1.9	33.7%	0.5
11687	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	2.7	2.5	0.2	1.9	33.7%	-0.4
11688	AT5G14390.1 | expressed protein | chr5:4637315-4639759 REVERSE | Aliases: F18O22.180, F18O22_180	5.7	6.2	-0.4	-1.9	33.7%	0.1
11689	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	2.9	-0.2	-1.9	33.7%	-0.4
11690	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	3.5	-0.2	-1.9	33.7%	-0.5
11691	AT5G24350.1 | expressed protein, weak similarity to neuroblastoma-amplified protein (Homo sapiens) GI:4337460 | chr5:8301540-8310898 FORWARD | Aliases: K16H17.4, K16H17_4	5.2	5.7	-0.5	-1.9	33.7%	0.1
11692	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	5.0	4.2	0.7	1.9	33.7%	0.5
11693	AT4G04840.1 | methionine sulfoxide reductase domain-containing protein / SeIR 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	3.9	-0.4	-1.9	33.7%	0.1
11694	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	2.5	-0.2	-1.9	33.7%	-0.9
11695	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	2.8	2.6	0.2	1.9	33.7%	-0.5
11696	AT5G01910.1 | expressed protein | chr5:357947-358652 REVERSE | Aliases: T20L15.180, T20L15_180	2.6	2.8	-0.2	-1.9	33.7%	-0.4
11697	AT3G30180.1 | Symbol: BR6OX2/CYP85A2 |	3.0	3.2	-0.3	-1.9	33.7%	-0.2
11698	AT2G20875.1 | expressed protein | chr2:8990260-8990660 REVERSE | Aliases: None	3.7	4.0	-0.3	-1.9	33.7%	-0.1
11699	AT4G36460.1 | expressed protein | chr4:17212665-17213102 REVERSE | Aliases: AP22.6, AP22_6	2.9	3.2	-0.3	-1.9	33.8%	-0.3

Rank	Description	Sync	Root	M	t	adj.q	B
11700	AT4G16820.1 | lipase class 3 family protein, similar to DEFECTIVE IN ANTHER DEHISCENCE1 (Arabidopsis thaliana) GI:16215706; contains Pfam profile PF01764: Lipase | chr4:9467582-9469135 FORWARD | Aliases: DL4435W, FCAALL.42	3.6	2.9	0.7	1.9	33.8%	0.2
11701	AT2G20360.1 | expressed protein | chr2:8793096-8796554 FORWARD | Aliases: F11A3.9, F11A3_9	9.5	7.9	1.5	1.9	33.8%	0.5
11702	AT1G54230.1 | expressed protein | chr1:20254621-20255894 FORWARD | Aliases: F20D21.5, F20D21_5	2.5	2.7	-0.2	-1.9	33.8%	-0.5
11703	AT1G30270.2 | Symbol: CIPK23 |	5.2	6.0	-0.7	-1.9	33.8%	0.2
11704	AT3G10930.1 | expressed protein | chr3:3420135-3420837 REVERSE | Aliases: F9F8.25	6.7	5.6	1.2	1.9	33.8%	0.2
11705	AT1G32340.1 | Symbol: NHL8 | zinc finger (C3HC4-type RING finger) family protein, contains a Zinc finger, C3HC4 type (RING finger) signature, PROSITE:PS00518	6.7	7.2	-0.5	-1.9	33.8%	-0.1
11706	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	9.1	7.8	1.4	1.9	33.8%	-0.0
11707	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	9.4	0.6	1.9	33.8%	0.2
11708	AT5G08220.1 | expressed protein | chr5:2642281-2642992 REVERSE | Aliases: F8L15.7	2.8	2.6	0.2	1.9	33.8%	-0.6
11709	AT2G18250.1 | cytidylyltransferase 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: Cytidylyltransferase | chr2:7947107-7948581 FORWARD | Aliases: T30D6.24, T30D6_24	8.3	7.3	1.0	1.9	33.8%	0.3
11710	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	2.9	0.2	1.9	33.8%	-0.3
11711	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	7.4	7.9	-0.4	-1.9	33.8%	-0.1
11712	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	5.9	6.2	-0.3	-1.9	33.8%	-0.1
11713	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	2.7	-0.2	-1.9	33.8%	-0.4
11714	AT2G07300.1 | expressed protein | chr2:3030795-3031771 FORWARD | Aliases: T13E11.7, T13E11_7	2.5	2.7	-0.2	-1.9	33.8%	-0.4
11715	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	2.5	2.4	0.2	1.9	33.8%	-0.7
11716	AT4G17090.1 | Symbol: CT BMY |	3.3	3.1	0.3	1.9	33.9%	-0.1
11717	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	2.6	-0.2	-1.9	33.9%	-0.8
11718	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	2.3	2.6	-0.3	-1.9	33.9%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
11719	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	4.5	4.1	0.4	1.9	33.9%	-0.1
11720	AT1G50970.1 | membrane trafficking VPS53 family protein, contains Pfam domain PF04100: Vps53-like, N-terminal | chr1:18899991-18903936 FORWARD | Aliases: F8A12.19, F8A12_19	2.6	2.9	-0.2	-1.9	33.9%	-0.6
11721	AT4G26820.1 | hypothetical protein | chr4:13493459-13494187 REVERSE | Aliases: F10M23.160, F10M23_160	3.4	3.6	-0.3	-1.9	33.9%	-0.5
11722	AT1G14510.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr1:4961882-4964420 REVERSE | Aliases: F14L17.29, F14L17_29	7.1	7.7	-0.6	-1.9	33.9%	0.2
11723	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	2.7	-0.2	-1.9	33.9%	-1.1
11724	AT4G33750.1 | expressed protein | chr4:16188358-16188927 FORWARD | Aliases: T16L1.240, T16L1_240	5.3	6.5	-1.3	-1.9	33.9%	0.2
11725	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	3.1	2.9	0.2	1.9	33.9%	-0.3
11726	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.	3.6	3.2	0.4	1.9	33.9%	0.1
11727	AT4G36660.1 | expressed protein | chr4:17286711-17287285 REVERSE | Aliases: AP22.12, AP22_12	7.1	6.4	0.6	1.9	33.9%	0.1
11728	AT1G27590.1 | expressed protein, similar to hypothetical protein GB:AAD45997 GI:5668770 from (Arabidopsis thaliana) | chr1:9592149-9593949 FORWARD | Aliases: T22C5.2	3.2	3.0	0.3	1.9	33.9%	-0.1
11729	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	2.6	2.8	-0.2	-1.9	34.0%	-0.5
11730	AT1G19340.1 | methyltransferase MT-A70 family protein, contains Pfam profile PF05063: MT-A70 (S-adenosylmethionine-binding subunit of human mRNA:m6A methyl-transferase (MTase)) | chr1:6684742-6687107 FORWARD | Aliases: F18O14.6, F18O14_6	2.9	2.6	0.2	1.9	34.0%	-0.3
11731	AT1G49510.1 | Symbol: EMB1273 | expressed protein | chr1:18330586-18332229 FORWARD | Aliases: EMB1273, EMBRYO DEFECTIVE 1273, F13F21.5, F13F21_5	4.0	3.7	0.3	1.9	34.0%	-0.1
11732	AT2G43950.3 | expressed protein | chr2:18207400-18209746 REVERSE | Aliases: F6E13.8	5.0	4.5	0.4	1.9	34.0%	-0.2
11733	AT2G22750.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.2	2.4	-0.2	-1.9	34.0%	-0.6
11734	AT1G16290.1 | expressed protein | chr1:5570747-5573532 REVERSE | Aliases: F3O9.9, F3O9_9	3.9	3.5	0.3	1.9	34.0%	-0.1
11735	AT3G26450.1 | 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 | chr3:9682535-9684605 REVERSE | Aliases: F20C19.24	3.8	4.1	-0.3	-1.9	34.0%	-0.1
11736	AT3G16930.1 | hypothetical protein | chr3:5778882-5779369 FORWARD | Aliases: K14A17.28	2.6	2.9	-0.3	-1.9	34.1%	-0.2
11737	AT2G16410.1 | hypothetical protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277 | chr2:7120727-7121341 FORWARD | Aliases: F16F14.9, F16F14_9	3.6	4.2	-0.5	-1.9	34.1%	0.2
11738	AT2G03820.1 | nonsense-mediated mRNA decay NMD3 family protein, contains Pfam profile: PF04981 NMD3 family | chr2:1164954-1167026 REVERSE | Aliases: T18C20.2, T18C20_2	7.0	6.3	0.7	1.9	34.1%	0.1
11739	AT3G17030.1 | expressed protein | chr3:5804515-5808468 REVERSE | Aliases: K14A17.10	4.3	3.9	0.4	1.9	34.1%	-0.0
11740	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	3.8	3.5	0.2	1.9	34.1%	-0.2
11741	AT3G22430.1 | expressed protein | chr3:7953267-7954490 FORWARD | Aliases: MCB17.18	5.0	5.5	-0.5	-1.9	34.1%	0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11742	AT5G45690.1 | expressed protein | chr5:18552226-18553542 REVERSE | Aliases: MRA19.8, MRA19_8	2.7	2.9	-0.2	-1.9	34.2%	-0.4
11743	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	9.8	9.2	0.6	1.9	34.2%	0.1
11744	AT1G01260.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	4.7	5.0	-0.4	-1.9	34.2%	0.1
11745	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	2.8	3.0	-0.2	-1.9	34.2%	-0.5
11746	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	3.8	3.4	0.3	1.9	34.2%	-0.2
11747	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	3.5	-0.3	-1.9	34.2%	-0.2
11748	AT3G17180.1 | Symbol: SCPL33 |	3.4	3.8	-0.5	-1.9	34.2%	-0.0
11749	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	3.5	-0.2	-1.9	34.2%	-0.4
11750	AT4G15350.1 | Symbol: CYP705A2 | cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450 | chr4:8762953-8764594 FORWARD | Aliases: DL3720W, FCAALL.274	2.7	2.9	-0.2	-1.9	34.2%	-0.7
11751	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	6.8	6.2	0.6	1.9	34.2%	0.2
11752	AT2G47550.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr2:19516050-19519205 FORWARD | Aliases: T30B22.15	3.7	3.1	0.6	1.9	34.2%	0.3
11753	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	6.1	6.7	-0.6	-1.9	34.2%	-0.0
11754	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	2.7	-0.2	-1.9	34.2%	-0.5
11755	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	2.7	3.0	-0.3	-1.9	34.3%	-0.5
11756	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	3.2	-0.2	-1.9	34.3%	-0.6
11757	AT3G01140.1 | Symbol: MYB106 |	3.1	3.5	-0.3	-1.9	34.3%	-0.3
11758	AT4G02190.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	3.0	-0.3	-1.9	34.3%	-0.7
11759	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	7.7	7.0	0.6	1.9	34.3%	0.1
11760	AT5G67300.1 | myb family transcription factor, contains PFAM profile: myb DNA binding domain PF00249 | chr5:26871248-26872464 FORWARD | Aliases: K8K14.2, K8K14_2	7.6	8.8	-1.1	-1.9	34.3%	0.3
11761	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	8.4	9.3	-0.9	-1.9	34.4%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11762	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	2.0	-0.1	-1.9	34.4%	-0.8
11763	AT3G12770.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:4056837-4059200 REVERSE | Aliases: MBK21.13	4.0	3.5	0.5	1.9	34.4%	0.1
11764	AT3G11000.1 | expressed protein | chr3:3447592-3450517 FORWARD | Aliases: F9F8.18	3.1	2.8	0.3	1.9	34.4%	-0.2
11765	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	2.3	2.4	-0.1	-1.9	34.4%	-1.0
11766	AT4G04920.1 | expressed protein | chr4:2497929-2504798 FORWARD | Aliases: T1J1.2, T1J1_2	3.9	4.2	-0.2	-1.9	34.4%	-0.3
11767	AT5G61020.2 | YT521-B-like family protein, contains Pfam profile PF04146: YT521-B-like family | chr5:24574427-24577105 REVERSE | Aliases: MAF19.3, MAF19_3	7.4	6.4	0.9	1.9	34.4%	0.6
11768	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	3.5	-0.3	-1.9	34.4%	-0.6
11769	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	2.9	3.2	-0.2	-1.9	34.4%	-0.4
11770	AT1G67890.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr1:25460842-25466455 FORWARD | Aliases: T23K23.26, T23K23_26	5.8	6.6	-0.7	-1.9	34.5%	0.2
11771	AT2G17150.2 | similar to RWP-RK domain-containing protein [Arabidopsis thaliana] (TAIR:At4g35270.1); similar to Putataive nodule inception protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470173.1) | chr2:7475164-7478340 REVERSE | Aliases: F6P23.15, F6P23_15	6.0	6.3	-0.3	-1.9	34.5%	0.1
11772	AT3G20400.1 | Symbol: EMB2743 | hypothetical protein | chr3:7114409-7114720 FORWARD | Aliases: EMB2743, EMBRYO DEFECTIVE 2743, MQC12.19	2.6	2.9	-0.3	-1.9	34.5%	-0.5
11773	AT5G18060.1 | auxin-responsive protein, putative, similar to auxin-inducible SAUR (Small Auxin Up RNAs) GI:3043536 from radish (Raphanus sativus) | chr5:5975964-5976498 FORWARD | Aliases: MCM23.16, MCM23_16	2.8	3.1	-0.3	-1.9	34.5%	-0.1
11774	AT3G24820.1 | BSD domain-containing protein, contains Pfam profile PF03909: BSD domain	5.7	5.3	0.4	1.9	34.5%	0.1
11775	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	3.0	3.3	-0.3	-1.9	34.6%	-0.4
11776	AT5G55780.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	3.1	-0.3	-1.9	34.6%	-0.3
11777	AT3G26020.2 | similar to serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative [Arabidopsis thaliana] (TAIR:At3g21650.1); similar to serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative [Arabidopsis thaliana] (TAIR:At1g13460.1); similar to serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative [Arabidopsis thaliana] (TAIR:At1g13460.2); similar to serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'gamma) [Arabidopsis thaliana] (TAIR:At4g15415.2); similar to serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'gamma) [Arabidopsis thaliana] (TAIR:At4g15415.1); similar to putative protein phosphatase PP2A0 B' subunit gamma isoform [Oryza sativa (japonica cultivar-group)] (GB:XP_477422.1); similar to putative B' regulatory subunit of PP2A (AtB'gamma) [Oryza sativa (japonica cultivar-group)] (GB:XP_479842.1); similar to putative B' regulatory subunit of protein phosphatase [Oryza sativa (japonica 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	5.1	-0.6	-1.9	34.6%	0.2
11778	AT1G34440.1 | expressed protein | chr1:12591326-12592715 REVERSE | Aliases: F12K21.23, F12K21_23	3.3	3.6	-0.3	-1.9	34.6%	-0.3
11779	AT3G51240.1 | Symbol: F3H | naringenin 3-dioxygenase / flavanone 3-hydroxylase (F3H), identical to GI:3790548	8.0	7.3	0.7	1.9	34.6%	-0.1
11780	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	2.7	-0.2	-1.9	34.6%	-0.6
11781	AT1G05577.1 | expressed protein | chr1:1662642-1664287 REVERSE | Aliases: None	2.4	2.7	-0.2	-1.9	34.7%	-0.6

Rank	Description	Sync	Root	M	t	adj.q	B
11782	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	7.7	7.1	0.5	1.9	34.7%	-0.1
11783	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.	5.5	5.0	0.6	1.9	34.7%	0.1
11784	AT3G13240.1 | hypothetical protein | chr3:4275767-4276247 FORWARD | Aliases: MDC11.17	3.2	2.9	0.3	1.9	34.7%	-0.5
11785	AT4G01120.1 | Symbol: GBF2 | G-box binding factor 2 (GBF2), identical to G-box binding factor 2 (GBF2) SP:P42775 from (Arabidopsis thaliana);contains Pfam profile: PF00170 bZIP transcription factor	7.3	8.0	-0.7	-1.9	34.7%	0.1
11786	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	5.5	0.6	1.9	34.8%	-0.1
11787	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	4.4	4.0	0.4	1.9	34.8%	-0.1
11788	AT4G33980.1 | expressed protein | chr4:16282801-16285063 REVERSE | Aliases: F17I5.170, F17I5_170	6.2	7.6	-1.4	-1.9	34.8%	0.2
11789	AT3G14730.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:4949392-4951353 REVERSE | Aliases: MIE1.23	3.7	3.5	0.3	1.9	34.8%	-0.2
11790	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	3.8	4.2	-0.4	-1.9	34.8%	-0.1
11791	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	8.2	0.5	1.9	34.8%	0.2
11792	AT1G28520.1 | expressed protein | chr1:10029179-10031969 FORWARD | Aliases: F3M18.4, F3M18_4	4.4	4.2	0.3	1.9	34.8%	-0.2
11793	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	2.1	0.2	1.9	34.9%	-0.7
11794	AT3G61350.1 | Symbol: SKIP4 | SKP1 interacting partner 4 (SKIP4), almost idential 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	5.6	6.2	-0.6	-1.9	34.9%	0.0
11795	AT3G50140.1 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function | chr3:18603455-18605547 REVERSE | Aliases: F3A4.220	2.4	2.6	-0.2	-1.9	34.9%	-0.7
11796	AT4G17790.1 | expressed protein | chr4:9891064-9892807 FORWARD | Aliases: DL4930W, FCAALL.62	8.8	9.2	-0.4	-1.9	34.9%	-0.1
11797	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	3.3	-0.2	-1.9	34.9%	-0.3
11798	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	2.9	-0.2	-1.9	34.9%	-0.7
11799	AT5G56370.2 | F-box family protein, contains F-box domain Pfam:PF00646	2.2	2.3	-0.2	-1.9	34.9%	-0.8
11800	AT5G56240.1 | expressed protein | chr5:22777029-22781728 REVERSE | Aliases: K24C1.5, K24C1_5	5.1	5.6	-0.6	-1.9	34.9%	0.1
11801	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	4.8	4.3	0.5	1.9	34.9%	0.1
11802	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	4.7	-0.5	-1.9	35.0%	-0.2
11803	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	3.7	3.4	0.2	1.9	35.0%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
11804	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	5.6	5.3	0.3	1.9	35.0%	-0.3
11805	AT5G36900.1 | expressed protein | chr5:14564154-14565433 FORWARD | Aliases: MLF18.2, MLF18_2	3.4	3.8	-0.4	-1.9	35.0%	-0.2
11806	AT4G29820.1 | expressed protein | chr4:14595686-14597487 REVERSE | Aliases: F27B13.60, F27B13_60	4.2	3.9	0.4	1.9	35.0%	-0.1
11807	AT3G50200.1 | expressed protein, ; expression supported by MPSS | chr3:18623445-18624306 REVERSE | Aliases: F11C1.40	2.8	3.1	-0.3	-1.9	35.0%	-0.3
11808	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	3.7	3.3	0.4	1.9	35.0%	0.1
11809	AT1G43730.1 | expressed protein | chr1:16511163-16512224 REVERSE | Aliases: F2J6.21, F2J6_21	2.7	2.9	-0.2	-1.9	35.0%	-0.7
11810	AT2G10930.1 | expressed protein | chr2:4310363-4311049 REVERSE | Aliases: F16G22.1, F16G22_1	5.0	5.5	-0.5	-1.9	35.0%	-0.2
11811	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	6.7	6.1	0.6	1.9	35.0%	0.2
11812	AT5G25360.1 | expressed protein | chr5:8799713-8802649 REVERSE | Aliases: F18G18.100, F18G18_100	6.8	6.0	0.8	1.9	35.1%	0.2
11813	AT4G32120.1 | galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase | chr4:15516790-15519861 REVERSE | Aliases: F10N7.70, F10N7_70	6.4	6.0	0.4	1.9	35.1%	0.0
11814	AT1G08610.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:2733791-2735470 REVERSE | Aliases: F22O13.9, F22O13_9	4.3	3.8	0.4	1.9	35.1%	0.1
11815	AT1G09550.1 | pectinacetylesterase, putative, similar to pectinacetylesterase precursor GI:1431629 from (Vigna radiata) | chr1:3089735-3092329 REVERSE | Aliases: F14J9.21, F14J9_21	2.6	2.8	-0.3	-1.9	35.1%	-0.5
11816	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	2.7	2.5	0.3	1.9	35.1%	-0.3
11817	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	7.8	0.7	1.9	35.1%	-0.0
11818	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	6.7	6.2	0.5	1.9	35.1%	-0.1
11819	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	5.6	5.3	0.3	1.9	35.1%	-0.2
11820	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	8.5	8.8	-0.3	-1.9	35.2%	-0.1
11821	AT2G48070.2 | expressed protein | chr2:19669920-19671535 FORWARD | Aliases: T9J23.22	3.4	3.2	0.2	1.9	35.2%	-0.4
11822	AT3G52550.1 | expressed protein | chr3:19503354-19503890 REVERSE | Aliases: F3C22.7	3.1	3.3	-0.2	-1.9	35.2%	-0.6
11823	AT3G30750.1 | expressed protein | chr3:12423035-12423472 FORWARD | Aliases: MIF6.12	2.1	2.2	-0.1	-1.9	35.2%	-1.1
11824	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	4.0	0.3	1.9	35.2%	-0.2
11825	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	8.8	8.3	0.6	1.9	35.2%	0.2
11826	AT5G17130.1 | hypothetical protein | chr5:5636975-5637537 FORWARD | Aliases: F2K13.280, F2K13_280	3.7	4.1	-0.4	-1.9	35.3%	-0.3

Rank	Description	Sync	Root	M	t	adj.q	B
11827	AT5G55760.1 | transcriptional regulator Sir2 family protein, contains Pfam domain PF02146: transcriptional regulator, Sir2 family | chr5:22584448-22588189 FORWARD | Aliases: MDF20.20, MDF20_20	6.0	5.6	0.4	1.9	35.3%	0.0
11828	AT5G54350.1 | expressed protein, ; expression supported by MPSS | chr5:22087361-22088452 FORWARD | Aliases: MDK4.17, MDK4_17	3.0	3.3	-0.3	-1.9	35.3%	-0.2
11829	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	4.6	5.7	-1.1	-1.9	35.3%	-0.1
11830	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	5.5	5.1	0.4	1.9	35.3%	0.1
11831	AT5G13230.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:4222517-4224985 FORWARD | Aliases: T31B5.50, T31B5_50	3.5	3.9	-0.4	-1.9	35.3%	-0.2
11832	AT1G79900.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr1:30056972-30058624 REVERSE | Aliases: F19K16.14, F19K16_14	4.3	3.8	0.4	1.9	35.3%	0.2
11833	AT4G32460.2 | expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642 | chr4:15662272-15664954 REVERSE | Aliases: F8B4.160, F8B4_160	5.4	4.9	0.5	1.9	35.3%	0.2
11834	AT3G07860.1 | expressed protein | chr3:2507886-2509515 FORWARD | Aliases: F17A17.20	4.5	4.1	0.4	1.9	35.3%	-0.0
11835	AT5G47420.1 | expressed protein, contains Pfam domain, PF01987: Protein of unknown function | chr5:19250063-19252286 FORWARD | Aliases: MQL5.28, MQL5_28	5.5	4.9	0.7	1.9	35.3%	0.4
11836	AT2G35100.1 | exostosin family protein, contains Pfam profile: PF03016	5.9	5.5	0.4	1.9	35.4%	0.1
11837	AT2G44270.1 | expressed protein, contains Pfam profile PF01171: PP-loop family | chr2:18305154-18307229 REVERSE | Aliases: F4I1.8	6.0	5.6	0.4	1.9	35.4%	-0.1
11838	AT5G15610.2 | proteasome family protein, contains Pfam domain, PF01399: PCI domain | chr5:5079516-5082208 FORWARD | Aliases: T20K14.220, T20K14_220	6.3	5.9	0.4	1.9	35.4%	0.2
11839	AT2G30620.1 | histone H1.2, nearly identical to SP:P26569 Histone H1.2 {Arabidopsis thaliana} | chr2:13052008-13053588 FORWARD | Aliases: T6B20.3, T6B20_3	10.2	9.7	0.5	1.9	35.4%	-0.0
11840	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	5.6	5.1	0.5	1.9	35.4%	0.4
11841	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	8.4	8.9	-0.5	-1.9	35.4%	-0.2
11842	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	4.9	4.4	0.5	1.9	35.4%	0.3
11843	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	2.9	2.7	0.2	1.9	35.4%	-0.4
11844	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	2.6	2.8	-0.3	-1.9	35.4%	-0.4
11845	AT4G32970.1 | expressed protein, low similarity to SP:Q13061 Triadin {Homo sapiens} | chr4:15910348-15914328 REVERSE | Aliases: F26P21.90, F26P21_90	5.4	4.7	0.7	1.9	35.4%	0.5
11846	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	3.2	-0.2	-1.9	35.4%	-0.6
11847	AT2G21140.1 | Symbol: ATPRP2 |	3.0	3.4	-0.4	-1.9	35.4%	-0.1
11848	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	2.9	-0.4	-1.9	35.4%	0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11849	AT4G09840.1 | expressed protein | chr4:6190250-6191661 REVERSE | Aliases: F17A8.190, F17A8_190	6.1	6.9	-0.8	-1.9	35.5%	0.0
11850	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	4.4	0.5	1.9	35.5%	0.2
11851	AT4G21700.1 | expressed protein | chr4:11529968-11532856 FORWARD | Aliases: F17L22.160, F17L22_160	4.2	4.0	0.2	1.9	35.5%	-0.4
11852	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	2.7	2.8	-0.2	-1.9	35.5%	-0.7
11853	AT5G47360.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:19231672-19233105 REVERSE | Aliases: MQL5.22, MQL5_22	6.1	5.5	0.6	1.9	35.5%	0.2
11854	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	3.7	3.4	0.3	1.9	35.5%	-0.4
11855	AT4G19210.1 | Symbol: ATRLI2 |	8.2	7.0	1.3	1.9	35.5%	0.2
11856	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	5.8	6.4	-0.6	-1.9	35.5%	0.1
11857	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	2.7	2.9	-0.2	-1.9	35.6%	-0.6
11858	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	5.6	5.1	0.5	1.9	35.6%	0.0
11859	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	4.7	5.1	-0.3	-1.9	35.6%	-0.1
11860	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	5.7	5.2	0.6	1.9	35.6%	-0.0
11861	AT1G03610.1 | expressed protein | chr1:900886-903002 FORWARD | Aliases: F21B7.22	4.9	5.4	-0.4	-1.9	35.6%	0.1
11862	AT5G61130.1 | glycosyl hydrolase family protein 17, similar to beta-1,3-glucanase GI:15150341 from (Camellia sinensis); C-terminal homology only | chr5:24604456-24606806 REVERSE | Aliases: MAF19.13, MAF19_13	4.1	3.6	0.4	1.9	35.6%	0.1
11863	AT1G01730.1 | expressed protein | chr1:270967-272021 FORWARD | Aliases: T1N6.14, T1N6_14	7.5	7.2	0.3	1.9	35.6%	-0.2
11864	AT1G53860.1 | remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region | chr1:20110775-20113160 REVERSE | Aliases: T18A20.9, T18A20_9	2.7	3.0	-0.3	-1.9	35.6%	-0.5
11865	AT5G15580.1 | expressed protein, unknown protein F14P3.18 - Arabidopsis thaliana, EMBL:AC009755 | chr5:5068304-5072495 REVERSE | Aliases: T20K14.190, T20K14_190	3.7	3.3	0.4	1.9	35.7%	-0.0
11866	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	4.7	5.3	-0.6	-1.9	35.7%	0.2
11867	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	2.7	3.0	-0.3	-1.9	35.7%	-0.6
11868	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	6.4	5.6	0.8	1.9	35.8%	0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11869	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	4.7	4.3	0.3	1.9	35.8%	-0.1
11870	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	4.9	5.1	-0.2	-1.9	35.8%	-0.6
11871	AT1G70700.2 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g48500.1) | chr1:26658445-26660726 FORWARD | Aliases: F5A18.12, F5A18_12	2.5	2.4	0.2	1.9	35.8%	-0.8
11872	AT5G09450.1 | pentatricopeptide (PPR) repeat-containing protein, low similiarity to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile: PF01535 PPR repeat | chr5:2941813-2943669 FORWARD | Aliases: T5E8.250, T5E8_250	6.1	5.3	0.8	1.9	35.8%	0.1
11873	AT2G22840.1 | Symbol: AtGRF1 |	3.4	4.1	-0.7	-1.9	35.8%	0.0
11874	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	2.7	-0.3	-1.9	35.8%	-0.3
11875	AT5G64230.1 | expressed protein | chr5:25709679-25711279 FORWARD | Aliases: MSJ1.7, MSJ1_7	4.1	4.5	-0.4	-1.8	35.8%	0.0
11876	AT1G23510.2 | expressed protein | chr1:8341438-8342732 REVERSE | Aliases: F28C11.14, F28C11_14	2.8	3.0	-0.2	-1.8	35.8%	-0.5
11877	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	4.6	5.4	-0.8	-1.8	35.8%	0.3
11878	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	8.2	0.5	1.8	35.8%	0.1
11879	AT5G47920.1 | expressed protein, similar to unknown protein (emb:CAB67623.1) | chr5:19420399-19421314 REVERSE | Aliases: MCA23.26, MCA23_26	3.2	3.0	0.2	1.8	35.8%	-0.2
11880	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	2.2	-0.3	-1.8	35.9%	-0.0
11881	AT1G53020.1 | ubiquitin-conjugating enzyme family protein, similar to ubiquitin-conjugating enzyme GB:3319990 from (Mus musculus); contains Pfam profile PF00179: Ubiquitin-conjugating enzyme	3.5	3.9	-0.3	-1.8	35.9%	-0.3
11882	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	3.3	-0.3	-1.8	35.9%	-0.2
11883	AT3G50320.1 | hypothetical protein | chr3:18664818-18665665 REVERSE | Aliases: F11C1.160	2.4	2.5	-0.2	-1.8	35.9%	-0.7
11884	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	5.8	6.5	-0.7	-1.8	35.9%	0.3
11885	AT2G36550.1 | expressed protein | chr2:15334626-15335881 FORWARD | Aliases: F1O11.18, F1O11_18	3.0	3.2	-0.2	-1.8	35.9%	-0.5
11886	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	8.8	8.2	0.7	1.8	35.9%	0.1
11887	AT5G43500.2 | Symbol: ATARP9 |	3.8	3.5	0.3	1.8	35.9%	-0.1
11888	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	3.9	3.5	0.4	1.8	35.9%	0.1
11889	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	11.9	11.4	0.5	1.8	35.9%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
11890	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	3.8	-0.3	-1.8	36.0%	-0.1
11891	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	3.6	3.2	0.3	1.8	36.0%	-0.2
11892	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)	4.0	3.4	0.6	1.8	36.0%	-0.0
11893	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	3.7	0.4	1.8	36.0%	-0.1
11894	AT3G61200.1 | thioesterase family protein, contains Pfam profile PF03061: thioesterase family protein | chr3:22668430-22669365 REVERSE | Aliases: T20K12.100	9.0	8.5	0.4	1.8	36.0%	-0.1
11895	AT2G13960.1 | myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA binding domain | chr2:5866667-5868393 FORWARD | Aliases: F9B22.7, F9B22_7	4.9	4.2	0.7	1.8	36.0%	0.5
11896	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	4.9	4.2	0.7	1.8	36.0%	0.5
11897	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: ATSCL33, F7A10.26, F7A10.27, F7A10_26, SCL33	5.6	6.3	-0.7	-1.8	36.0%	0.3
11898	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	2.5	-0.2	-1.8	36.0%	-1.1
11899	AT3G25880.1 | auxin-resistance protein, putative, similar to Swiss-Prot:P42744 auxin-resistance protein AXR1 (Arabidopsis thaliana) | chr3:9470950-9471270 REVERSE | Aliases: MPE11.3	2.7	2.9	-0.2	-1.8	36.1%	-0.6
11900	AT3G02110.1 | Symbol: SCPL25 |	3.6	3.3	0.4	1.8	36.1%	0.1
11901	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	3.1	3.3	-0.2	-1.8	36.1%	-0.6
11902	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	5.7	5.1	0.6	1.8	36.1%	0.4
11903	AT3G48710.1 | expressed protein, putative protein - Arabidopsis thaliana, EMBL:AL078465.1 | chr3:18051962-18055173 FORWARD | Aliases: T8P19.220	6.0	4.9	1.1	1.8	36.2%	0.3
11904	AT1G44478.1 | hypothetical protein | chr1:16854781-16855678 REVERSE | Aliases: T18F15.6, T18F15_6	2.5	2.8	-0.3	-1.8	36.2%	-0.0
11905	AT1G44930.1 | expressed protein | chr1:16987550-16988109 FORWARD | Aliases: T12C22.25, T12C22_25	4.8	5.7	-0.8	-1.8	36.3%	0.2
11906	AT4G08780.1 | peroxidase, putative, similar to peroxidase isozyme (Armoracia rusticana) gi:217932:dbj:BAA14143	4.8	4.2	0.6	1.8	36.3%	0.2
11907	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	3.2	-0.3	-1.8	36.3%	-0.7
11908	AT2G30110.1 | Symbol: ATUBA1 |	7.5	6.8	0.7	1.8	36.3%	-0.2
11909	AT4G15480.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr4:8848849-8850514 REVERSE | Aliases: DL3780C, FCAALL.304	3.8	4.1	-0.3	-1.8	36.4%	-0.2
11910	AT4G02990.1 | mitochondrial transcription termination factor family protein / mTERF family protein, weak similarity to mtDBP protein (Paracentrotus lividus) GI:4584695; contains Pfam profile PF02536: mTERF | chr4:1321859-1324004 FORWARD | Aliases: T4I9.13, T4I9_13	4.0	3.7	0.4	1.8	36.4%	-0.0
11911	AT1G09350.1 | galactinol synthase, putative, contains Pfam profile: PF01501 glycosyl transferase family 8 | chr1:3019821-3021443 FORWARD | Aliases: F14J9.1, F14J9_1	2.8	3.1	-0.3	-1.8	36.4%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11912	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	5.6	6.1	-0.5	-1.8	36.4%	0.1
11913	AT4G31130.1 | expressed protein | chr4:15136941-15138801 REVERSE | Aliases: F6E21.50, F6E21_50	6.6	7.2	-0.6	-1.8	36.4%	0.0
11914	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	3.5	4.0	-0.6	-1.8	36.5%	-0.2
11915	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	5.9	5.4	0.5	1.8	36.5%	-0.0
11916	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	4.4	4.0	0.5	1.8	36.5%	-0.1
11917	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	2.9	-0.3	-1.8	36.5%	-0.5
11918	AT5G44790.1 | Symbol: RAN1 | copper-exporting ATPase / responsive-to-antagonist 1 / copper-transporting ATPase (RAN1), identical to SP:Q9S7J8	9.0	9.7	-0.7	-1.8	36.5%	-0.0
11919	AT5G43120.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain | chr5:17329830-17331596 FORWARD | Aliases: MMG4.15, MMG4_15	3.4	3.2	0.2	1.8	36.6%	-0.5
11920	AT2G35110.2 | Symbol: GRL/NAP1/NAPP | similar to similar to Mus musculus (Mouse). Similar to NCK-associated protein 1 [Dictyostelium discoideum] (GB:AAO52562.1) | chr2:14802794-14811009 REVERSE | Aliases: GRL, NAP1, NAPP, T4C15.22, T4C15_22	4.8	5.2	-0.4	-1.8	36.6%	-0.1
11921	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	5.7	5.2	0.5	1.8	36.6%	-0.0
11922	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-acetylesterase (Digitalis lanata) GI:3688284; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family	3.0	3.2	-0.2	-1.8	36.6%	-0.4
11923	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	3.7	3.5	0.2	1.8	36.6%	-0.3
11924	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	6.0	5.5	0.5	1.8	36.6%	0.1
11925	AT3G09050.1 | expressed protein | chr3:2764656-2766092 FORWARD | Aliases: MZB10.8	3.6	3.3	0.2	1.8	36.6%	-0.3
11926	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	3.2	-0.2	-1.8	36.6%	-0.6
11927	AT2G42140.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr2:17575755-17576605 REVERSE | Aliases: T24P15.5, T24P15_5	2.7	2.8	-0.2	-1.8	36.7%	-0.8
11928	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	7.6	7.1	0.5	1.8	36.7%	0.1
11929	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	3.1	3.4	-0.3	-1.8	36.7%	-0.2
11930	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	2.6	-0.2	-1.8	36.7%	-0.7

Rank	Description	Sync	Root	M	t	adj.q	B
11931	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	7.1	6.2	0.9	1.8	36.7%	0.2
11932	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	3.1	-0.2	-1.8	36.7%	-0.6
11933	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	4.5	4.2	0.3	1.8	36.7%	-0.1
11934	AT5G35290.1 | hypothetical protein | chr5:13535117-13535536 REVERSE | Aliases: T26D22.20, T26D22_20	3.7	4.0	-0.3	-1.8	36.8%	-0.5
11935	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	2.7	-0.2	-1.8	36.8%	-0.5
11936	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	2.5	2.7	-0.2	-1.8	36.8%	-0.5
11937	AT3G02940.1 | Symbol: MYB107 |	1.9	2.0	-0.1	-1.8	36.8%	-1.3
11938	AT1G80520.1 | expressed protein | chr1:30281373-30281951 FORWARD | Aliases: T21F11.15, T21F11_15	4.0	3.7	0.3	1.8	36.8%	-0.1
11939	AT3G31430.1 | expressed protein, low similarity to zinc finger protein (Arabidopsis thaliana) GI:976277 | chr3:12798340-12799350 REVERSE | Aliases: T22C2.102	2.2	2.5	-0.3	-1.8	36.8%	-0.8
11940	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	5.7	5.3	0.4	1.8	36.8%	-0.1
11941	AT3G43630.1 | nodulin, putative, similar to nodulin 21 (N-21) (Glycine max) SWISS-PROT:P16313 | chr3:15549804-15550406 FORWARD | Aliases: F22J12.3	4.7	5.2	-0.6	-1.8	36.8%	-0.0
11942	AT1G21100.1 | O-methyltransferase, putative, similar to GI:2781394 | chr1:7386828-7388417 REVERSE | Aliases: T22I11.7, T22I11_7	3.6	3.2	0.3	1.8	36.8%	-0.6
11943	ATCG00500.1 | Symbol: ACCD | carboxytransferase beta subunit | chrC:57075-58541 FORWARD | Aliases: ACCD	6.8	8.0	-1.2	-1.8	36.8%	0.0
11944	AT1G04000.1 | expressed protein, Location of ESTs 203I24T7, gb:H76794 and 203I24XP, gb:AA605510 | chr1:1028105-1029118 REVERSE | Aliases: F21M11.6, F21M11_6	3.6	3.9	-0.3	-1.8	36.8%	-0.2
11945	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	6.4	6.0	0.4	1.8	36.8%	0.0
11946	AT3G23170.1 | expressed protein | chr3:8267949-8268742 REVERSE | Aliases: K14B15.6	4.6	4.0	0.5	1.8	36.8%	0.3
11947	AT4G26570.2 | Symbol: ATCBL3 |	8.5	8.0	0.6	1.8	36.8%	-0.2
11948	AT3G17490.1 | F-box family protein, similar to F-box protein family, AtFBX9 (GI:20197985) (Arabidopsis thaliana); contains Pfam PF00646: F-box domain and TIGRFAM TIGR01640: F-box protein interaction domain | chr3:5984833-5985999 FORWARD | Aliases: MKP6.4	3.5	3.7	-0.2	-1.8	36.8%	-0.6
11949	AT5G55800.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.2	3.5	-0.3	-1.8	36.9%	-0.4
11950	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	5.0	5.3	-0.4	-1.8	36.9%	-0.0
11951	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	4.8	4.3	0.5	1.8	36.9%	0.2
11952	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)	11.6	11.1	0.5	1.8	36.9%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
11953	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	6.1	5.6	0.5	1.8	36.9%	0.2
11954	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	3.0	-0.2	-1.8	36.9%	-0.6
11955	AT5G20900.1 | expressed protein | chr5:7090751-7092541 FORWARD | Aliases: F22D1.70, F22D1_70	9.3	8.5	0.9	1.8	36.9%	-0.1
11956	AT2G14580.1 | Symbol: ATPRB1 |	3.3	3.6	-0.3	-1.8	36.9%	-0.7
11957	ATMG00160.1 | Symbol: COX2 | cytochrome c oxidase subunit 2 | chrM:40502-42628 REVERSE | Aliases: COX2	3.7	4.3	-0.5	-1.8	36.9%	-0.0
11958	AT2G43520.1 | Symbol: ATTI2 | Encodes a defensin-like (DEFL) family protein. | chr2:18075638-18076219 FORWARD | Aliases: T1O24.26	3.0	3.3	-0.3	-1.8	37.0%	-0.5
11959	AT5G04640.1 | MADS-box family protein, SLM3 MADS-box protein, S.latifolia, EMBL:SLSLM3	2.6	2.8	-0.2	-1.8	37.0%	-0.9
11960	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	3.5	-0.2	-1.8	37.0%	-0.4
11961	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	3.7	-0.3	-1.8	37.0%	-0.3
11962	AT3G31300.1 | hypothetical protein | chr3:12676906-12677097 FORWARD | Aliases: T22B15.1	2.2	2.3	-0.1	-1.8	37.0%	-1.2
11963	AT3G59430.3 | expressed protein | chr3:21975042-21977324 REVERSE | Aliases: F25L23.290	2.5	2.3	0.2	1.8	37.0%	-0.6
11964	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	4.4	4.8	-0.4	-1.8	37.0%	0.0
11965	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	4.0	0.6	1.8	37.1%	0.4
11966	AT1G06440.1 | expressed protein | chr1:1963379-1965050 REVERSE | Aliases: F12K11.21, F12K11_21	2.4	2.5	-0.1	-1.8	37.1%	-0.8
11967	AT2G23410.1 | Symbol: ACPT | dehydrodolichyl diphosphate synthase / DEDOL-PP synthase (DPS), identical to dehydrodolichyl diphosphate synthase (Arabidopsis thaliana) GI:7960765 | chr2:9973210-9974850 REVERSE | Aliases: None	2.3	2.6	-0.3	-1.8	37.1%	-0.6
11968	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	4.7	3.9	0.8	1.8	37.1%	0.0
11969	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	5.7	6.5	-0.8	-1.8	37.1%	0.0
11970	AT2G28605.1 | expressed protein | chr2:12261965-12262914 FORWARD | Aliases: T8O18.1, T8O18_1	3.0	2.7	0.2	1.8	37.2%	-0.5
11971	AT5G60210.1 | cytoplasmic linker protein-related, contains weak similarity to cytoplasmic linker protein CLIP-170 (GI:2905649) (Gallus gallus)	4.3	3.7	0.6	1.8	37.2%	0.2
11972	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	4.1	3.4	0.7	1.8	37.2%	0.1

Rank	Description	Sync	Root	M	t	adj.q	B
11973	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	2.7	-0.2	-1.8	37.2%	-0.5
11974	AT5G48860.1 | hypothetical protein | chr5:19828877-19830091 REVERSE | Aliases: K24G6.20, K24G6_20	2.2	2.3	-0.2	-1.8	37.2%	-0.8
11975	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	2.4	0.4	1.8	37.2%	0.0
11976	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	3.9	4.5	-0.6	-1.8	37.2%	0.0
11977	AT5G23690.1 | 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 | chr5:7987543-7990550 FORWARD | Aliases: MQM1.4, MQM1_4	4.5	4.1	0.3	1.8	37.2%	-0.3
11978	AT3G50160.1 | hypothetical protein, contains Pfam profile PF03140: Plant protein of unknown function | chr3:18609642-18611886 REVERSE | Aliases: F3A4.240	2.7	2.9	-0.2	-1.8	37.3%	-0.6
11979	AT5G08510.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:2753100-2755102 FORWARD | Aliases: F8L15.21	4.3	3.9	0.4	1.8	37.3%	-0.1
11980	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	3.0	3.3	-0.3	-1.8	37.3%	-0.2
11981	AT1G68160.1 | expressed protein | chr1:25549471-25552557 REVERSE | Aliases: T22E19.21, T22E19_21	5.1	4.8	0.3	1.8	37.3%	-0.1
11982	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	3.7	4.1	-0.3	-1.8	37.3%	-0.0
11983	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	3.7	4.2	-0.5	-1.8	37.3%	0.1
11984	AT3G51090.1 | expressed protein | chr3:18988968-18990983 REVERSE | Aliases: F24M12.130	3.9	3.7	0.2	1.8	37.3%	-0.5
11985	AT1G63460.1 | glutathione peroxidase, putative, contains Pfam profile: PF00255 glutathione peroxidases	10.0	9.7	0.3	1.8	37.4%	-0.2
11986	AT2G24220.1 | Symbol: ATPUP5 |	4.0	3.5	0.4	1.8	37.4%	0.1
11987	AT2G01310.1 | expressed protein | chr2:152480-152641 REVERSE | Aliases: F10A8.19, F10A8_19	3.0	3.2	-0.2	-1.8	37.4%	-0.7
11988	AT5G52490.1 | fibrillarin, putative, similar to fibrillarin from {Xenopus laevis} SP:P22232, {Mus musculus} SP:P35550, {Homo sapiens} SP:P22087 | chr5:21316083-21317465 FORWARD | Aliases: K24M7.24, K24M7_24	3.1	3.5	-0.4	-1.8	37.4%	-0.2
11989	AT3G02440.1 | expressed protein | chr3:500811-502236 REVERSE | Aliases: F16B3.7, F16B3_7	2.7	3.0	-0.2	-1.8	37.4%	-0.6
11990	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	3.0	3.4	-0.3	-1.8	37.4%	-0.3
11991	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	2.4	-0.2	-1.8	37.4%	-0.7
11992	AT4G20250.1 | expressed protein | chr4:10938000-10940538 REVERSE | Aliases: F1C12.170, F1C12_170	2.9	3.1	-0.2	-1.8	37.4%	-0.8
11993	AT3G08780.2 | similar to P0458H05.113 [Oryza sativa (japonica cultivar-group)] (GB:XP_478579.1) | chr3:2666447-2667539 REVERSE | Aliases: F17O14.25	5.5	5.1	0.3	1.8	37.4%	-0.0

Rank	Description	Sync	Root	M	t	adj.q	B
11994	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	3.7	3.1	0.6	1.8	37.4%	0.0
11995	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	4.4	4.8	-0.4	-1.8	37.4%	0.0
11996	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	3.9	-0.3	-1.8	37.5%	-0.5
11997	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	2.8	-0.2	-1.8	37.5%	-0.8
11998	AT4G04730.1 | expressed protein | chr4:2401925-2402347 REVERSE | Aliases: T4B21.14, T4B21_14	1.9	2.1	-0.1	-1.8	37.5%	-1.1
11999	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	4.4	0.3	1.8	37.5%	-0.2
12000	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	3.2	-0.2	-1.8	37.5%	-0.8
12001	AT2G01390.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:172255-174136 FORWARD | Aliases: F10A8.29	2.6	2.8	-0.2	-1.8	37.5%	-0.6
12002	AT5G64520.3 | Symbol: XRCC2 | similar to LOC443613 protein [Xenopus laevis] (GB:AAH73049.1) | chr5:25805260-25807536 FORWARD | Aliases: MUB3.4, MUB3_4	4.2	3.4	0.8	1.8	37.5%	0.4
12003	AT3G57120.1 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr3:21149884-21151589 FORWARD | Aliases: F24I3.200	4.8	5.0	-0.2	-1.8	37.5%	-0.5
12004	AT2G07760.1 | zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle | chr2:3584417-3586275 REVERSE | Aliases: T12J2.8, T12J2_8	2.6	2.8	-0.2	-1.8	37.5%	-0.5
12005	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	5.8	5.2	0.5	1.8	37.5%	0.2
12006	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	4.4	4.8	-0.3	-1.8	37.5%	-0.2
12007	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	6.5	5.7	0.8	1.8	37.6%	0.4
12008	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	3.0	-0.3	-1.8	37.6%	-0.5
12009	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	3.5	-0.4	-1.8	37.6%	-0.2
12010	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	2.6	-0.2	-1.8	37.7%	-0.8
12011	AT5G53440.1 | expressed protein | chr5:21700905-21705196 REVERSE | Aliases: MYN8.5, MYN8_5	8.6	8.3	0.3	1.8	37.7%	-0.3
12012	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	5.6	5.9	-0.3	-1.8	37.7%	-0.4
12013	AT2G18100.1 | expressed protein | chr2:7874910-7878724 FORWARD | Aliases: T27K22.3, T27K22_3	4.6	4.2	0.3	1.8	37.7%	-0.0

Rank	Description	Sync	Root	M	t	adj.q	B
12014	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) {Arabidopsis thaliana}, DEF (deficient in photosynthesis) protein (Arabidopsis thaliana) 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	8.0	0.6	1.8	37.7%	-0.2
12015	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	5.6	-0.4	-1.8	37.7%	-0.1
12016	AT3G44040.1 | expressed protein | chr3:15823362-15824941 FORWARD | Aliases: T15B3.180	2.8	3.0	-0.2	-1.8	37.7%	-0.7
12017	ATMG00720.1 | Symbol: ORF107D | hypothetical protein | chrM:209499-209822 FORWARD | Aliases: ORF107D	2.4	2.6	-0.2	-1.8	37.7%	-0.6
12018	AT5G02100.1 | oxysterol-binding family protein, similar to SWH1 (Saccharomyces cerevisiae) GI:402658; contains Pfam profile PF01237: Oxysterol-binding protein	8.2	8.7	-0.5	-1.8	37.7%	-0.1
12019	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	6.9	-0.5	-1.8	37.7%	0.2
12020	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	3.3	-0.2	-1.8	37.8%	-0.6
12021	AT3G29010.1 | expressed protein, ; expression supported by MPSS | chr3:11008477-11009214 FORWARD | Aliases: K5K13.4	4.1	3.8	0.4	1.8	37.8%	-0.0
12022	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}	6.2	5.6	0.7	1.8	37.8%	0.3
12023	AT2G41480.1 | peroxidase, putative, similar to peroxidase (Spinacia oleracea) gi:1781334:emb:CAA71494 | chr2:17303890-17305805 REVERSE | Aliases: T26J13.7, T26J13_7	5.7	6.2	-0.6	-1.8	37.8%	0.4
12024	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	2.7	2.9	-0.2	-1.8	37.8%	-0.9
12025	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	5.4	4.9	0.4	1.8	37.8%	0.2
12026	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	9.0	8.7	0.3	1.8	37.8%	-0.4
12027	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	5.4	4.9	0.5	1.8	37.8%	0.2
12028	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	7.2	6.4	0.8	1.8	37.8%	0.2
12029	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	2.9	3.3	-0.4	-1.8	37.9%	-0.0
12030	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	7.2	7.5	-0.4	-1.8	37.9%	-0.1
12031	AT1G48070.1 | expressed protein | chr1:17734160-17734791 REVERSE | Aliases: T2J15.15	2.7	2.9	-0.2	-1.8	37.9%	-0.6
12032	AT5G43080.1 | Symbol: CYCA3;1 | cyclin, putative, similar to A-type cyclins from (Nicotiana tabacum) GI:1064931, (Catharanthus roseus) 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	4.2	3.8	0.4	1.8	37.9%	0.2
12033	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	3.3	-0.4	-1.8	37.9%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
12034	AT5G26020.1 | hypothetical protein | chr5:9093598-9094880 REVERSE | Aliases: T1N24.102, T1N24_102	3.7	4.2	-0.6	-1.8	37.9%	0.1
12035	AT5G66820.1 | expressed protein | chr5:26706285-26708340 FORWARD | Aliases: MUD21.8, MUD21_8	6.5	7.1	-0.6	-1.8	37.9%	0.3
12036	AT3G26670.3 | expressed protein | chr3:9799223-9802280 REVERSE | Aliases: MLJ15.6	5.1	5.6	-0.5	-1.8	37.9%	0.1
12037	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	3.0	-0.2	-1.8	37.9%	-0.7
12038	AT3G24130.1 | pectinesterase family protein, contains Pfam profile: PF01095 Pectinesterase | chr3:8711670-8713368 REVERSE | Aliases: MUJ8.16	2.5	2.8	-0.3	-1.8	38.0%	-0.4
12039	ATMG00070.1 | Symbol: NAD9 | NADH dehydrogenase subunit 9 | chrM:23663-24235 REVERSE | Aliases: NAD9	3.6	4.5	-0.9	-1.8	38.0%	-0.1
12040	AT3G60680.1 | expressed protein, contains Pfam profile PF04859: Plant protein of unknown function (DUF641 | chr3:22440935-22443017 FORWARD | Aliases: T4C21.90	4.1	4.5	-0.4	-1.8	38.0%	-0.0
12041	AT5G51020.1 | expressed protein, similar to unknown protein (pir::S76207) | chr5:20762680-20764472 REVERSE | Aliases: K3K7.20, K3K7_20	8.4	8.0	0.4	1.8	38.0%	-0.2
12042	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	2.7	-0.2	-1.8	38.0%	-0.7
12043	AT5G18910.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:6306830-6309421 REVERSE | Aliases: F17K4.160, F17K4_160	2.9	3.0	-0.1	-1.8	38.1%	-1.0
12044	AT1G36920.1 | expressed protein | chr1:13984724-13986502 FORWARD | Aliases: F1O3.6, F1O3_6	2.5	2.7	-0.2	-1.8	38.1%	-0.9
12045	AT5G06440.3 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g11720.1) | chr5:1964469-1966956 REVERSE | Aliases: MHF15.4, MHF15_4	5.3	5.9	-0.5	-1.8	38.1%	-0.1
12046	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	3.1	-0.3	-1.8	38.1%	-0.6
12047	AT2G30890.1 | membrane protein, putative, similar to membrane protein SDR2 (GI:1747306) (Mus musculus)	2.5	2.3	0.2	1.8	38.1%	-0.4
12048	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	5.0	-0.4	-1.8	38.1%	-0.0
12049	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	3.8	-0.2	-1.8	38.1%	-0.8
12050	AT2G34370.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:14517561-14518970 FORWARD | Aliases: F13P17.21, F13P17_21	3.3	3.5	-0.2	-1.8	38.1%	-0.5
12051	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	3.4	0.3	1.8	38.2%	-0.3
12052	AT5G40740.1 | expressed protein | chr5:16319142-16323641 REVERSE | Aliases: MNF13.29, MNF13_29	2.9	2.7	0.2	1.8	38.2%	-0.8
12053	AT5G55020.1 | Symbol: MYB120 |	2.2	2.4	-0.2	-1.8	38.2%	-0.6
12054	AT5G35470.1 | hypothetical protein | chr5:13699706-13699978 REVERSE | Aliases: MOK9.5, MOK9_5	2.2	2.3	-0.1	-1.8	38.2%	-1.0
12055	AT3G16750.1 | expressed protein, ; expression supported by MPSS | chr3:5701151-5702019 REVERSE | Aliases: MGL6.22	2.8	3.1	-0.3	-1.8	38.2%	-0.3
12056	AT1G25410.1 | Symbol: ATIPT6 |	3.4	3.1	0.3	1.8	38.2%	-0.2
12057	AT1G10680.1 | P-glycoprotein, putative, similar to P-glycoprotein GI:4204793 from (Solanum tuberosum) | chr1:3538471-3543783 REVERSE | Aliases: F20B24.12, F20B24_12	2.9	2.6	0.3	1.8	38.2%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
12058	AT5G44470.1 | expressed protein | chr5:17935966-17936391 FORWARD | Aliases: MFC16.13, MFC16_13	2.5	2.7	-0.2	-1.8	38.2%	-0.8
12059	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	3.0	0.3	1.8	38.2%	-0.3
12060	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	5.8	0.5	1.8	38.2%	-0.0
12061	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	3.4	3.6	-0.2	-1.8	38.3%	-0.7
12062	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	8.8	8.3	0.5	1.8	38.3%	-0.1
12063	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	8.0	7.4	0.6	1.8	38.3%	0.2
12064	AT2G03360.1 | expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563) | chr2:1022284-1023465 REVERSE | Aliases: T4M8.21, T4M8_21	3.5	3.7	-0.3	-1.8	38.3%	-0.5
12065	AT3G10880.1 | hypothetical protein | chr3:3406300-3407136 FORWARD | Aliases: T7M13.4	3.3	3.0	0.3	1.8	38.3%	-0.2
12066	AT3G45850.1 | kinesin motor protein-related, kinesin-related protein TKRP125, Nicotiana tabacum, PIR:T02017 | chr3:16866597-16871935 REVERSE | Aliases: F16L2.60	4.4	4.0	0.3	1.8	38.4%	-0.4
12067	AT3G18690.1 | Symbol: MKS1 | VQ motif-containing protein, contains PF05678: VQ motif | chr3:6429540-6430508 REVERSE | Aliases: MVE11.5	5.6	6.0	-0.4	-1.8	38.4%	-0.1
12068	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	10.7	9.9	0.8	1.8	38.4%	-0.0
12069	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	2.8	3.2	-0.3	-1.8	38.4%	-0.2
12070	AT4G34120.1 | CBS domain-containing protein, contains Pfam profile PF00571: CBS domain	7.6	8.2	-0.5	-1.8	38.4%	0.2
12071	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	3.8	1.2	1.8	38.4%	0.0
12072	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	3.7	4.1	-0.4	-1.8	38.4%	-0.1
12073	AT2G34780.1 | Symbol: EMB1611 | expressed protein | chr2:14675732-14680686 FORWARD | Aliases: EMB1611, EMBRYO DEFECTIVE 1611, F19I3.1, F19I3_1	4.8	4.4	0.4	1.8	38.4%	-0.2
12074	AT2G31420.1 | expressed protein, contains Pfam profile PF03754: Domain of unknown function (DUF313) | chr2:13400441-13401070 REVERSE | Aliases: T28P16.9, T28P16_9	3.5	3.8	-0.3	-1.8	38.4%	-0.3
12075	AT3G15930.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:5387450-5389696 FORWARD | Aliases: MVC8.5	2.8	3.0	-0.2	-1.8	38.4%	-0.6
12076	AT3G14230.3 | Symbol: RAP2.2 |	5.2	6.1	-0.9	-1.8	38.4%	0.1
12077	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	3.2	3.7	-0.5	-1.8	38.4%	0.1

Rank	Description	Sync	Root	M	t	adj.q	B
12078	AT4G08760.1 | hypothetical protein | chr4:5584736-5591130 REVERSE | Aliases: T32A17.70, T32A17_70	3.2	3.7	-0.5	-1.8	38.4%	0.1
12079	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	3.4	-0.2	-1.8	38.4%	-0.4
12080	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	3.8	3.4	0.4	1.8	38.4%	0.0
12081	AT5G06280.3 | expressed protein, similar to unknown protein (pir::T08447) | chr5:1918282-1918897 REVERSE | Aliases: MHF15.20, MHF15_20	5.0	5.5	-0.5	-1.8	38.5%	-0.1
12082	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	7.4	7.9	-0.5	-1.8	38.5%	-0.4
12083	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	7.7	6.5	1.3	1.8	38.5%	0.3
12084	AT2G35880.1 | expressed protein | chr2:15070067-15072930 REVERSE | Aliases: F11F19.21, F11F19_21	8.6	9.3	-0.7	-1.8	38.5%	-0.3
12085	AT1G33540.1 | Symbol: SCPL18 |	2.7	2.9	-0.2	-1.8	38.5%	-0.5
12086	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	2.6	-0.3	-1.8	38.5%	-0.7
12087	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 scienitific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497. | chr1:13071143-13074927 FORWARD | Aliases: F15O4.45	3.8	3.5	0.3	1.8	38.5%	-0.2
12088	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	2.9	3.1	-0.2	-1.8	38.5%	-0.9
12089	AT3G49310.1 | expressed protein, contains PF05631: Protein of unknown function (DUF791) | chr3:18295849-18299037 REVERSE | Aliases: F2K15.170	4.2	4.6	-0.4	-1.8	38.5%	-0.3
12090	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	8.8	7.7	1.1	1.8	38.5%	0.3
12091	AT5G01480.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.2	3.7	-0.5	-1.8	38.5%	-0.1
12092	AT1G54470.1 | expressed protein | chr1:20348405-20348743 FORWARD | Aliases: F20D21.44, F20D21_44	2.3	2.5	-0.2	-1.8	38.6%	-0.6
12093	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	6.3	0.6	1.8	38.6%	0.0
12094	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	2.5	-0.1	-1.8	38.6%	-0.9
12095	AT3G28190.1 | expressed protein | chr3:10513472-10514294 FORWARD | Aliases: MIG10.9	2.6	2.8	-0.2	-1.8	38.6%	-0.8
12096	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	2.6	-0.2	-1.8	38.6%	-0.7
12097	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	3.9	4.3	-0.3	-1.8	38.6%	-0.4
12098	AT2G01190.1 | octicosapeptide/Phox/Bem1p (PB1) domain-containing protein, Pfam profile PF00564: PB1 domain | chr2:114974-117639 FORWARD | Aliases: F10A8.7, F10A8_7	5.0	5.3	-0.3	-1.8	38.6%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
12099	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	2.9	-0.5	-1.8	38.6%	-0.6
12100	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	12.4	11.8	0.6	1.8	38.6%	-0.9
12101	AT4G23900.1 | nucleoside diphosphate kinase 4 (NDK4), contains Pfam PF00334 : Nucleoside diphosphate kinase domain; identical to nucleoside diphosphate kinase 4 (GI:11990430)	5.5	5.2	0.4	1.8	38.6%	0.1
12102	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	2.7	0.3	1.8	38.7%	-0.1
12103	AT4G23000.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	2.7	2.9	-0.2	-1.8	38.7%	-0.6
12104	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	3.9	4.2	-0.3	-1.8	38.7%	-0.1
12105	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	8.1	7.4	0.6	1.8	38.7%	0.1
12106	AT1G06320.1 | expressed protein | chr1:1930601-1931448 FORWARD | Aliases: T2D23.15, T2D23_15	2.3	2.5	-0.2	-1.8	38.7%	-1.0
12107	AT5G60350.1 | expressed protein | chr5:24294956-24296340 FORWARD | Aliases: K9B18.6, K9B18_6	2.6	2.8	-0.3	-1.8	38.7%	-0.6
12108	AT1G77050.1 | DEAD/DEAH box helicase, putative, similar to RNA helicase GI:3776027 from (Arabidopsis thaliana)	2.9	2.6	0.3	1.8	38.7%	-0.6
12109	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	3.6	4.0	-0.4	-1.8	38.7%	-0.3
12110	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	3.5	4.2	-0.7	-1.8	38.7%	0.1
12111	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	2.6	-0.2	-1.8	38.7%	-1.0
12112	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)	3.7	4.0	-0.3	-1.8	38.7%	-0.1
12113	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	2.4	2.6	-0.2	-1.8	38.8%	-0.7
12114	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	3.8	3.5	0.3	1.8	38.8%	-0.2
12115	AT5G05010.2 | similar to coatomer delta subunit [Oryza sativa (japonica 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	7.2	0.5	1.8	38.8%	-0.2
12116	AT4G39130.1 | dehydrin family protein, contains Pfam domain, PF00257: Dehydrin	2.3	2.6	-0.3	-1.8	38.8%	-0.5
12117	AT2G41710.2 | ovule development protein, putative, similar to ovule development protein AINTEGUMENTA (GI:1209099) (Arabidopsis thaliana);Pfam domain (PF00847)	5.8	5.3	0.5	1.8	38.8%	0.1
12118	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	9.0	8.2	0.8	1.8	38.8%	0.0

Rank	Description	Sync	Root	M	t	adj.q	B
12119	AT4G09520.1 | 2,3-biphosphoglycerate-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	4.7	4.1	0.6	1.8	38.8%	0.0
12120	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	2.4	0.1	1.8	38.8%	-0.8
12121	AT1G31380.1 | hypothetical protein | chr1:11240432-11241080 REVERSE | Aliases: T8E3.3	2.8	3.0	-0.2	-1.8	38.8%	-0.8
12122	AT5G55770.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.5	2.8	-0.3	-1.8	38.8%	-0.6
12123	AT2G14530.1 | expressed protein | chr2:6194503-6197462 FORWARD | Aliases: T13P21.9, T13P21_9	3.8	3.6	0.3	1.8	38.9%	-0.4
12124	AT3G04970.2 | zinc finger (DHHC type) family protein, similar to Golgi-specific DHHC zinc figer protein (Mus musculus) GI:21728103; contains Pfam profile PF01529: DHHC zinc finger domain | chr3:1376182-1378506 FORWARD | Aliases: T9J14.8, T9J14_8	3.1	3.3	-0.2	-1.8	38.9%	-0.5
12125	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	3.6	-0.4	-1.8	38.9%	0.0
12126	AT4G31150.2 | endonuclease V family protein, contains Pfam PF04493: Endonuclease V | chr4:15143548-15145605 REVERSE | Aliases: F6E21.70, F6E21_70	4.2	4.6	-0.4	-1.8	38.9%	-0.1
12127	AT5G41490.1 | F-box family protein, contains Pfam profile: PF00646 F-box domain | chr5:16617673-16618836 FORWARD | Aliases: MYC6.19, MYC6_19	2.3	2.4	-0.2	-1.8	38.9%	-1.0
12128	AT5G61320.1 | Symbol: CYP89A3 | cytochrome P450, putative, Similar to	2.9	3.2	-0.3	-1.8	38.9%	-0.7
12129	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	2.7	-0.2	-1.8	38.9%	-0.5
12130	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	6.1	6.7	-0.6	-1.8	38.9%	-0.4
12131	AT1G64920.1 | glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	2.6	2.8	-0.2	-1.8	38.9%	-0.7
12132	AT3G47960.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr3:17708927-17711754 REVERSE | Aliases: T17F15.170	3.8	4.2	-0.4	-1.8	38.9%	-0.0
12133	AT5G64850.1 | expressed protein | chr5:25938670-25940580 FORWARD | Aliases: MXK3.7, MXK3_7	3.9	3.4	0.5	1.8	38.9%	-0.0
12134	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	2.5	-0.2	-1.8	38.9%	-0.8
12135	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	4.6	5.1	-0.5	-1.8	39.0%	-0.1
12136	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	3.0	3.4	-0.4	-1.8	39.0%	-0.2
12137	AT1G29480.1 | hypothetical protein | chr1:10317922-10318697 FORWARD | Aliases: F15D2.6, F15D2_6	2.2	2.3	-0.1	-1.8	39.0%	-1.2
12138	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	9.9	10.4	-0.4	-1.8	39.0%	-0.2
12139	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	4.6	-0.4	-1.8	39.0%	-0.2
12140	AT4G00500.2 | lipase class 3 family protein / calmodulin-binding heat-shock protein-related | chr4:224992-227195 REVERSE | Aliases: F6N23.21, F6N23_21	4.3	4.6	-0.4	-1.8	39.0%	0.0

Rank	Description	Sync	Root	M	t	adj.q	B
12141	AT1G19380.1 | expressed protein | chr1:6698051-6698788 FORWARD | Aliases: F18O14.10, F18O14_10	6.5	7.0	-0.5	-1.8	39.0%	-0.1
12142	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	4.8	-0.4	-1.8	39.0%	-0.2
12143	AT2G10440.1 | expressed protein | chr2:4020835-4025129 REVERSE | Aliases: F12P23.5, F12P23_5	2.2	2.3	-0.1	-1.8	39.1%	-1.1
12144	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	3.5	3.2	0.3	1.8	39.1%	-0.1
12145	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	4.6	4.2	0.5	1.8	39.1%	0.1
12146	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	2.7	-0.2	-1.8	39.1%	-0.6
12147	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	2.6	-0.2	-1.8	39.1%	-1.0
12148	AT5G36910.1 | Symbol: THI2.2.2 | thionin (THI2.2), identical to thionin (Arabidopsis thaliana) gi:1181533:gb:AAC41679	3.3	3.8	-0.5	-1.8	39.1%	-0.2
12149	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	4.4	4.7	-0.3	-1.8	39.1%	-0.1
12150	AT4G33800.1 | expressed protein | chr4:16210017-16211414 REVERSE | Aliases: T16L1.290, T16L1_290	2.6	2.8	-0.2	-1.8	39.1%	-0.8
12151	AT3G56950.1 | small basic membrane integral family protein, contains similarity to small basic membrane integral protein ZmSIP2-1 (GI:13447817) (Zea mays) | chr3:21088985-21090810 REVERSE | Aliases: T8M16.9	9.0	8.4	0.6	1.8	39.1%	-0.1
12152	AT2G24960.1 | expressed protein, ; expression supported by MPSS | chr2:10624342-10627113 FORWARD | Aliases: F27C12.12, F27C12_12	4.6	5.0	-0.4	-1.8	39.1%	-0.3
12153	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	3.0	0.2	1.8	39.2%	-0.6
12154	AT1G67790.1 | expressed protein | chr1:25421205-25423762 REVERSE | Aliases: F12A21.8, F12A21_8	2.5	2.7	-0.2	-1.8	39.2%	-0.7
12155	AT4G35220.1 | cyclase family protein, contains Pfam profile: PF04199 putative cyclase | chr4:16752618-16754310 FORWARD | Aliases: F23E12.220, F23E12_220	9.1	8.3	0.8	1.8	39.2%	0.2
12156	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	4.4	-0.4	-1.8	39.2%	-0.0
12157	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	4.0	4.4	-0.4	-1.8	39.2%	-0.1
12158	AT5G01850.1 | protein kinase, putative, similar to protein kinase (Arabidopsis thaliana) gi:1054633:emb:CAA63387; contains protein kinase domain, Pfam:PF00069	4.0	4.4	-0.4	-1.8	39.2%	-0.1
12159	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	3.6	3.3	0.4	1.8	39.2%	0.1
12160	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	3.3	3.7	-0.4	-1.8	39.2%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
12161	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	5.1	5.9	-0.7	-1.8	39.2%	0.1
12162	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	2.7	2.9	-0.2	-1.8	39.2%	-0.7
12163	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	5.1	4.5	0.6	1.8	39.3%	0.3
12164	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	7.4	8.6	-1.2	-1.8	39.3%	-0.0
12165	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	5.6	5.0	0.6	1.8	39.3%	-0.1
12166	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	4.1	3.7	0.4	1.8	39.3%	-0.0
12167	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	3.6	3.2	0.3	1.8	39.3%	-0.1
12168	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	4.3	-0.4	-1.8	39.3%	-0.2
12169	AT1G62840.1 | expressed protein | chr1:23275146-23276072 FORWARD | Aliases: F23N19.19, F23N19_19	5.4	6.0	-0.7	-1.8	39.3%	0.0
12170	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	2.7	-0.3	-1.8	39.4%	-0.6
12171	AT2G18245.1 | expressed protein | chr2:7944369-7946680 FORWARD | Aliases: None	3.3	3.1	0.2	1.8	39.4%	-0.3
12172	AT2G12880.1 | zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle | chr2:5298605-5298964 FORWARD | Aliases: T18E17.4	2.6	2.7	-0.2	-1.8	39.4%	-1.0
12173	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	12.1	11.6	0.5	1.8	39.4%	-0.6
12174	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	3.9	3.5	0.4	1.8	39.4%	0.1
12175	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	10.2	9.5	0.6	1.8	39.5%	-0.1
12176	AT3G47080.1 | expressed protein | chr3:17349091-17351363 REVERSE | Aliases: F13I12.130	4.6	4.3	0.4	1.8	39.5%	-0.1
12177	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	3.6	-0.4	-1.8	39.5%	-0.5
12178	AT3G57430.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:21266612-21269457 REVERSE | Aliases: T8H10.30	3.3	3.0	0.3	1.8	39.5%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
12179	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	5.8	6.6	-0.8	-1.8	39.5%	0.2
12180	AT5G12400.1 | PHD finger transcription factor, putative, similarity to predicted proteins, Arabidopsis thaliana | chr5:4013814-4020910 FORWARD | Aliases: None	2.9	3.3	-0.4	-1.8	39.5%	-0.2
12181	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 GI:5668790 from (Arabidopsis thaliana) | chr1:17566371-17567546 REVERSE | Aliases: T2E6.20	2.6	2.8	-0.2	-1.8	39.5%	-1.1
12182	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	2.9	2.5	0.4	1.8	39.5%	-0.3
12183	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	6.2	6.5	-0.4	-1.8	39.5%	-0.0
12184	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	3.9	3.6	0.3	1.8	39.5%	-0.3
12185	AT5G11820.1 | expressed protein, self-incompatibility protein S3 precursor, Papaver rhoeas cv., PIR:S69186 | chr5:3810650-3811177 REVERSE | Aliases: F14F18.2	2.0	2.1	-0.1	-1.8	39.5%	-1.0
12186	AT4G24640.1 | Symbol: APPB1 | invertase/pectin methylesterase inhibitor family protein, annotation temporarily based on supporting cDNA gi:4097527:gb:U63898.1:U63898	2.3	2.5	-0.2	-1.8	39.5%	-0.6
12187	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	6.1	6.6	-0.5	-1.8	39.5%	0.1
12188	AT3G29420.1 | geranylgeranyl pyrophosphate synthase-related / GGPP synthetase-related / farnesyltranstransferase-related, fragment similar to farnesyltranstransferase precursor GB:T10452 from (Sinapis alba)	2.9	3.2	-0.4	-1.8	39.5%	-0.3
12189	AT3G09180.1 | expressed protein | chr3:2819123-2821430 FORWARD | Aliases: MZB10.22	5.6	5.2	0.4	1.8	39.6%	0.0
12190	AT5G62180.1 | expressed protein, similar to PrMC3, Pinus radiata, GI:5487873 | chr5:24996070-24997075 REVERSE | Aliases: MMI9.26	3.8	4.0	-0.2	-1.8	39.6%	-0.4
12191	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	7.4	-0.5	-1.8	39.6%	-0.2
12192	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	3.7	3.3	0.4	1.8	39.6%	-0.2
12193	AT2G44000.1 | expressed protein | chr2:18221400-18222647 FORWARD | Aliases: F6E13.13	2.2	2.3	-0.1	-1.8	39.6%	-1.1
12194	AT5G40640.1 | expressed protein | chr5:16294270-16297652 FORWARD | Aliases: MNF13.19, MNF13_19	4.0	3.7	0.3	1.8	39.6%	-0.3
12195	AT2G18470.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr2:8012367-8014849 REVERSE | Aliases: T30D6.2	2.6	2.8	-0.2	-1.8	39.6%	-0.7
12196	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	2.8	-0.2	-1.8	39.7%	-0.8
12197	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	4.4	4.9	-0.5	-1.8	39.7%	0.1
12198	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}	10.2	9.3	0.8	1.8	39.7%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
12199	AT1G34470.1 | permease-related, low similarity to purine permease (Arabidopsis thaliana) GI:7620007 | chr1:12604278-12607011 FORWARD | Aliases: F12K21.21, F12K21_21	5.8	5.5	0.3	1.8	39.7%	-0.2
12200	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	4.5	0.3	1.8	39.7%	-0.2
12201	AT4G37310.1 | Symbol: CYP81H1 | cytochrome P450, putative | chr4:17555921-17558887 REVERSE | Aliases: F6G17.6	5.2	6.0	-0.8	-1.8	39.7%	0.4
12202	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	7.4	6.8	0.6	1.8	39.7%	0.0
12203	AT4G18630.1 | expressed protein, contains Pfam profile: PF05097 protein of unknown function (DUF688) | chr4:10257089-10258954 FORWARD | Aliases: F28A21.40, F28A21_40	3.4	3.1	0.3	1.8	39.7%	-0.1
12204	AT3G24830.1 | 60S ribosomal protein L13A (RPL13aB), similar to 60S RIBOSOMAL PROTEIN L13A GB:P35427 from (Rattus norvegicus) | chr3:9064570-9066089 FORWARD | Aliases: K7P8.13	10.5	9.9	0.6	1.8	39.7%	-0.2
12205	AT5G14240.1 | expressed protein | chr5:4595607-4597657 REVERSE | Aliases: F18O22.30, F18O22_30	6.7	6.0	0.7	1.8	39.7%	0.0
12206	AT3G25905.1 | Symbol: CLE27 | CLE27, putative, CLAVATA3/ESR-Related 27 (CLE27) | chr3:9487405-9488008 REVERSE | Aliases: CLAVATA3/ESR RELATED 27	2.6	2.9	-0.3	-1.8	39.7%	-0.5
12207	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	3.0	-0.2	-1.8	39.7%	-0.3
12208	AT3G44720.1 | prephenate dehydratase family protein, similar to bacterial PheA gene products | chr3:16282639-16284331 FORWARD | Aliases: T32N15.11	7.2	6.4	0.8	1.8	39.8%	0.1
12209	AT1G26100.1 | cytochrome B561 family protein, contains Pfam domain, PF03188: Cytochrome b561 | chr1:9022588-9024068 REVERSE | Aliases: F14G11.7, F14G11_7	5.7	5.9	-0.2	-1.8	39.8%	-0.3
12210	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	5.3	5.7	-0.4	-1.8	39.8%	-0.0
12211	AT1G32670.1 | expressed protein | chr1:11815644-11815956 FORWARD | Aliases: F6N18.7, F6N18_7	2.6	2.9	-0.2	-1.8	39.8%	-0.9
12212	AT5G48830.1 | expressed protein | chr5:19817340-19820241 REVERSE | Aliases: K24G6.16, K24G6_16	3.9	3.5	0.4	1.8	39.8%	-0.2
12213	AT3G06600.1 | expressed protein, ; expression supported by MPSS | chr3:2059564-2060464 REVERSE | Aliases: F5E6.7, F5E6_7	3.2	3.0	0.3	1.8	39.8%	-0.3
12214	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	3.5	3.0	0.4	1.8	39.8%	-0.1
12215	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	6.7	5.9	0.8	1.8	39.8%	-0.1
12216	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	2.8	3.0	-0.2	-1.8	39.8%	-0.6
12217	AT5G66980.1 | transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain | chr5:26758789-26760052 FORWARD | Aliases: K8A10.5, K8A10_5	3.2	2.9	0.3	1.8	39.8%	-0.5
12218	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	4.2	-0.3	-1.8	39.8%	-0.3
12219	AT1G72480.1 | expressed protein | chr1:27289727-27292001 REVERSE | Aliases: T10D10.5, T10D10_5	4.9	4.5	0.4	1.8	39.8%	0.0
12220	AT2G44240.1 | expressed protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function | chr2:18296900-18299421 FORWARD | Aliases: F4I1.5	3.1	3.3	-0.2	-1.8	39.8%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
12221	AT5G19380.1 | expressed protein | chr5:6526830-6530594 REVERSE | Aliases: F7K24.130, F7K24_130	6.1	5.7	0.4	1.8	39.8%	0.1
12222	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	8.4	7.5	0.9	1.8	39.8%	0.0
12223	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	3.3	-0.2	-1.8	39.8%	-0.5
12224	AT1G02300.1 | cathepsin B-like cysteine protease, putative, similar to cathepsin B-like cysteine proteinase GI:609175 from (Nicotiana rustica)	6.2	6.8	-0.6	-1.8	39.8%	-0.0
12225	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, F20O9.210, F20O9_210	2.7	3.0	-0.3	-1.8	39.9%	-0.3
12226	AT3G57070.1 | glutaredoxin family protein, contains Pfam profile PF00462: Glutaredoxin	4.2	4.4	-0.2	-1.8	39.9%	-0.4
12227	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	3.3	2.9	0.4	1.8	39.9%	-0.1
12228	AT1G50020.1 | expressed protein | chr1:18522758-18525363 REVERSE | Aliases: F2J10.10, F2J10_10	6.7	6.1	0.6	1.8	39.9%	0.1
12229	AT1G75140.1 | expressed protein | chr1:28205827-28207940 REVERSE | Aliases: F22H5.14, F22H5_14	4.2	4.5	-0.3	-1.8	40.0%	-0.3
12230	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	4.6	5.0	-0.4	-1.8	40.0%	-0.2
12231	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	4.1	-0.4	-1.8	40.0%	-0.2
12232	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	4.9	5.4	-0.5	-1.8	40.0%	0.1
12233	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	4.1	3.7	0.4	1.8	40.0%	-0.3
12234	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	7.6	8.1	-0.5	-1.8	40.0%	-0.1
12235	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	5.5	5.0	0.5	1.8	40.0%	-0.0
12236	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	2.8	2.6	0.2	1.8	40.0%	-0.5
12237	AT5G09310.1 | expressed protein | chr5:2887194-2888528 REVERSE | Aliases: T5E8.110, T5E8_110	7.5	6.8	0.7	1.8	40.0%	0.1
12238	AT1G34065.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr1:12398696-12400861 REVERSE | Aliases: None	4.0	4.3	-0.3	-1.8	40.0%	-0.4
12239	AT4G31880.1 | expressed protein | chr4:15419410-15424189 REVERSE | Aliases: F11C18.80, F11C18_80	5.5	5.1	0.4	1.8	40.0%	-0.0
12240	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	3.1	-0.4	-1.8	40.1%	-0.1
12241	AT3G05320.1 | expressed protein | chr3:1513456-1514688 REVERSE | Aliases: T12H1.29, T12H1_29	5.0	5.7	-0.7	-1.8	40.1%	-0.0
12242	AT1G13190.1 | RNA recognition motif (RRM)-containing protein | chr1:4498893-4501973 FORWARD | Aliases: F3F19.21, F3F19_21	6.4	6.9	-0.4	-1.8	40.1%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
12243	AT3G45360.1 | expressed protein, several hypothetical proteins - Arabidopsis thaliana | chr3:16652604-16652984 FORWARD | Aliases: F18N11.120	2.6	2.8	-0.1	-1.8	40.1%	-1.1
12244	AT1G04230.1 | expressed protein | chr1:1125571-1128167 FORWARD | Aliases: F19P19.34	4.9	4.5	0.3	1.8	40.1%	-0.1
12245	AT3G54840.1 | Symbol: ARA6 | Rab GTPase (ARA6), identical to small GTPase Ara6 (Arabidopsis thaliana) GI:13160603 | chr3:20329480-20331970 FORWARD | Aliases: F28P10.180	8.7	7.5	1.2	1.8	40.1%	0.0
12246	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	3.0	3.3	-0.3	-1.8	40.1%	-0.4
12247	AT3G20865.1 | arabinogalactan-protein, putative (AGP), similar to gi:10880503:gb:AAG24281 | chr3:7308510-7308968 REVERSE | Aliases: None	2.9	3.4	-0.4	-1.8	40.1%	-0.2
12248	AT1G22960.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:8128075-8130231 REVERSE | Aliases: F19G10.9, F19G10_9	3.0	2.8	0.2	1.8	40.1%	-0.7
12249	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	3.3	-0.3	-1.8	40.1%	-0.4
12250	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	4.9	5.5	-0.6	-1.8	40.1%	-0.1
12251	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	5.6	5.1	0.5	1.8	40.2%	0.1
12252	AT1G66480.1 | expressed protein | chr1:24809433-24811129 REVERSE | Aliases: F28G11.8, F28G11_8	4.1	4.4	-0.3	-1.8	40.2%	-0.2
12253	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: F10O3.15, F10O3_15	6.7	5.8	0.9	1.8	40.2%	0.1
12254	AT1G44000.1 | expressed protein | chr1:16710509-16712153 REVERSE | Aliases: F9C16.20, F9C16_20	7.3	7.0	0.4	1.8	40.2%	0.0
12255	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	3.7	3.4	0.3	1.8	40.2%	-0.1
12256	AT3G48040.1 | Symbol: ROP10 | Rac-like GTP-binding protein (ARAC8), identical to rac GTP binding protein Arac8 GI:3702966 from (Arabidopsis thaliana)	4.6	4.3	0.3	1.8	40.2%	-0.2
12257	AT4G12110.1 | Symbol: SMO1 1 |	4.8	4.1	0.7	1.8	40.3%	-0.1
12258	AT4G15870.1 | Symbol: ATTS1 | terpene synthase/cyclase family protein	2.8	3.2	-0.3	-1.8	40.3%	-0.4
12259	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	3.3	-0.2	-1.8	40.3%	-0.7
12260	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	4.6	4.1	0.5	1.8	40.3%	0.0
12261	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	3.0	2.7	0.3	1.8	40.3%	-0.3
12262	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	6.1	5.9	0.2	1.8	40.3%	-0.4
12263	AT1G78840.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.0	3.4	-0.4	-1.8	40.3%	-0.3
12264	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	6.0	6.8	-0.8	-1.8	40.3%	-0.0
12265	AT3G50370.1 | expressed protein | chr3:18687041-18694926 REVERSE | Aliases: F11C1.210	3.5	4.6	-1.2	-1.8	40.3%	0.1

Rank	Description	Sync	Root	M	t	adj.q	B
12266	AT3G44250.1 | Symbol: CYP71B38 | cytochrome P450 family protein, CYTOCHROME P450 71B7 - Arabidopsis thaliana, EMBL:X97864 | chr3:15959492-15961211 REVERSE | Aliases: T10D17.40	3.1	3.5	-0.3	-1.8	40.3%	-0.2
12267	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	4.2	-0.4	-1.8	40.4%	-0.5
12268	AT5G50340.1 | DNA repair protein-related, similar to RadA (Pseudomonas aeruginosa) GI:1881700 | chr5:20508643-20512982 REVERSE | Aliases: MXI22.5, MXI22_5	3.9	3.6	0.3	1.8	40.4%	-0.2
12269	AT2G31680.1 | Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:289370 from (Brassica napus) | chr2:13480671-13482129 REVERSE | Aliases: T9H9.20, T9H9_20	4.5	4.8	-0.3	-1.8	40.4%	-0.4
12270	AT5G11030.1 | Symbol: ALF4 | expressed protein | chr5:3490834-3495095 REVERSE | Aliases: ABERRANT LATERAL ROOT FORMATION 4, T5K6.20, T5K6_20	4.6	5.1	-0.4	-1.7	40.4%	0.0
12271	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	3.1	-0.3	-1.7	40.4%	-0.4
12272	AT5G58890.1 | MADS-box family protein, various predicted proteins, Oryza sativa and Arabidopsis thaliana | chr5:23798058-23798942 FORWARD | Aliases: K19M22.9, K19M22_9	2.7	3.0	-0.3	-1.7	40.4%	-0.4
12273	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	6.1	-0.8	-1.7	40.5%	-0.0
12274	AT2G24180.1 | Symbol: CYP71B6 | cytochrome P450 family protein | chr2:10288927-10290815 FORWARD | Aliases: CYTOCHROME P450 71B6, CYTOCHROME P450 MONOOXYGENASE 71B6, F27D4.9, F27D4_9	7.6	7.2	0.5	1.7	40.5%	-0.1
12275	AT2G44020.1 | mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF | chr2:18224635-18226461 REVERSE | Aliases: F6E13.15	5.3	5.0	0.3	1.7	40.5%	-0.2
12276	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	2.6	2.8	-0.2	-1.7	40.5%	-0.6
12277	AT5G40830.2 | Symbol: ATRAD3 |	5.3	4.4	0.9	1.7	40.5%	0.2
12278	AT1G12330.1 | expressed protein | chr1:4194656-4196735 FORWARD | Aliases: F5O11.6, F5O11_6	5.3	5.9	-0.6	-1.7	40.5%	0.1
12279	AT3G16660.1 | expressed protein | chr3:5676835-5677921 FORWARD | Aliases: MGL6.12	5.7	6.3	-0.6	-1.7	40.5%	0.0
12280	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	2.8	-0.2	-1.7	40.5%	-0.8
12281	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	3.9	4.4	-0.5	-1.7	40.5%	0.2
12282	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)	3.9	4.4	-0.5	-1.7	40.5%	0.2
12283	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	7.1	7.7	-0.6	-1.7	40.5%	-0.2
12284	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	4.1	0.8	1.7	40.5%	-0.0
12285	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	7.4	0.5	1.7	40.6%	-0.2

Rank	**Description**	**Sync**	**Root**	**M**	**t**	**adj.q**	**B**
12286	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	6.2	5.6	0.6	1.7	40.6%	-0.1
12287	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	7.0	6.0	1.0	1.7	40.6%	0.2
12288	AT3G05290.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr3:1505897-1507706 REVERSE | Aliases: T12H1.26, T12H1_26	8.2	7.9	0.4	1.7	40.6%	-0.3
12289	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	3.5	3.3	0.3	1.7	40.6%	-0.3
12290	AT1G24010.1 | expressed protein | chr1:8498792-8499488 REVERSE | Aliases: T23E23.27, T23E23_27	2.9	2.7	0.2	1.7	40.6%	-0.5
12291	AT1G55440.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.5	2.7	-0.2	-1.7	40.6%	-0.5
12292	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	4.6	4.3	0.3	1.7	40.6%	-0.5
12293	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	2.6	-0.2	-1.7	40.6%	-0.7
12294	AT1G75720.1 | hypothetical protein | chr1:28438309-28438979 REVERSE | Aliases: F10A5.8, F10A5_8	3.6	3.9	-0.3	-1.7	40.6%	-0.3
12295	AT1G01150.1 | expressed protein, ; expression supported by MPSS | chr1:70115-71998 REVERSE | Aliases: F6F3.30	2.2	2.1	0.1	1.7	40.6%	-1.3
12296	AT1G77270.1 | expressed protein | chr1:29032672-29036122 FORWARD | Aliases: T14N5.12, T14N5_12	2.7	2.6	0.1	1.7	40.6%	-1.0
12297	AT1G66370.1 | Symbol: MYB113 |	3.1	3.4	-0.3	-1.7	40.6%	-0.3
12298	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	2.4	2.3	0.1	1.7	40.6%	-1.1
12299	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	3.3	2.8	0.4	1.7	40.6%	0.1
12300	AT5G04820.1 | ovate family protein, 62% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	4.7	5.1	-0.4	-1.7	40.6%	-0.2
12301	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	1.9	0.1	1.7	40.6%	-1.5
12302	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	4.7	4.3	0.4	1.7	40.6%	-0.1
12303	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	3.1	-0.2	-1.7	40.6%	-0.9
12304	ATCG01100.1 | Symbol: NDHA | NADH dehydrogenase ND1 | chrC:119847-122009 REVERSE | Aliases: NDHA	6.0	4.7	1.3	1.7	40.7%	0.2
12305	AT5G54110.1 | Symbol: ATMAMI |	6.7	7.0	-0.3	-1.7	40.7%	-0.3
12306	AT4G04800.1 | methionine sulfoxide reductase domain-containing protein / SeIR 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: SeIR domain | chr4:2439548-2441203 FORWARD | Aliases: T4B21.6, T4B21_6	5.8	6.1	-0.3	-1.7	40.7%	-0.3
12307	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	2.7	2.9	-0.2	-1.7	40.7%	-0.6

Rank	Description	Sync	Root	M	t	adj.q	B
12308	AT5G28470.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr5:10429817-10432361 FORWARD | Aliases: F24J2.10, F24J2_10	2.6	2.8	-0.2	-1.7	40.7%	-0.6
12309	AT2G02150.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:547260-552228 REVERSE | Aliases: F5O4.8, F5O4_8	4.7	4.3	0.5	1.7	40.7%	0.0
12310	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	5.9	5.5	0.4	1.7	40.7%	-0.2
12311	AT3G30730.1 | hypothetical protein | chr3:12359875-12360078 REVERSE | Aliases: T4A2.2	2.6	2.7	-0.1	-1.7	40.7%	-1.1
12312	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	2.7	-0.2	-1.7	40.8%	-0.6
12313	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	3.8	0.3	1.7	40.8%	-0.2
12314	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	4.2	3.8	0.4	1.7	40.8%	0.0
12315	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	6.6	6.4	0.3	1.7	40.8%	-0.4
12316	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	2.4	-0.1	-1.7	40.8%	-1.1
12317	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	2.9	-0.2	-1.7	40.8%	-0.6
12318	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	3.5	-0.4	-1.7	40.8%	-0.4
12319	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	6.5	5.4	1.1	1.7	40.8%	0.2
12320	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	2.8	-0.2	-1.7	40.8%	-0.6
12321	AT5G47690.1 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g77600.1); similar to P0677H08.21 [Oryza sativa (japonica cultivar-group)] (GB:NP_915668.1)	4.8	5.8	-1.0	-1.7	40.9%	0.2
12322	AT1G03160.1 | expressed protein, similar to hypothetical protein DDB0187425 [Dictyostelium discoideum] (GB:EAL63733.1)	3.1	3.3	-0.2	-1.7	40.9%	-0.6
12323	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	3.4	-0.2	-1.7	40.9%	-0.6
12324	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	2.9	-0.2	-1.7	40.9%	-0.8
12325	AT1G53170.1 | Symbol: ATERF 8/ATERF8 |	4.2	4.6	-0.4	-1.7	40.9%	0.0
12326	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	7.5	8.1	-0.6	-1.7	40.9%	-0.1
12327	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	2.3	-0.1	-1.7	40.9%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
12328	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	3.5	-0.2	-1.7	40.9%	-0.9
12329	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	8.0	8.4	-0.4	-1.7	40.9%	-0.7
12330	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	12.4	11.6	0.8	1.7	40.9%	-0.3
12331	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	4.7	4.4	0.3	1.7	40.9%	-0.2
12332	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	3.8	0.4	1.7	40.9%	-0.0
12333	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	4.5	4.1	0.4	1.7	40.9%	-0.1
12334	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	6.3	5.6	0.6	1.7	41.0%	0.0
12335	AT3G28460.1 | expressed protein, contains Pfam PF03602: Conserved hypothetical protein 95 | chr3:10673303-10675632 REVERSE | Aliases: MFJ20.15	4.1	3.8	0.3	1.7	41.0%	-0.3
12336	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	2.6	2.9	-0.4	-1.7	41.0%	-0.4
12337	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	3.2	0.2	1.7	41.0%	-0.5
12338	AT2G34540.2 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g34530.1) | chr2:14557737-14559308 FORWARD | Aliases: T31E10.12, T31E10_12	3.0	3.2	-0.2	-1.7	41.0%	-0.7
12339	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	7.8	7.1	0.7	1.7	41.1%	0.1
12340	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	4.5	3.9	0.6	1.7	41.1%	-0.1
12341	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	4.8	-0.8	-1.7	41.1%	0.0
12342	AT4G03153.1 | kinase interacting family protein, similar to kinase interacting protein 1 (GI:13936326) (Petunia integrifolia) | chr4:1394845-1395588 REVERSE | Aliases: None	2.2	2.3	-0.2	-1.7	41.1%	-0.9
12343	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	2.3	-0.2	-1.7	41.1%	-1.2
12344	AT3G06070.1 | expressed protein | chr3:1831063-1831929 REVERSE | Aliases: F24F17.5, F24F17_5	2.3	2.5	-0.2	-1.7	41.1%	-1.0
12345	AT1G62950.1 | leucine-rich repeat transmembrane protein kinase, putative, contains protein kinase domains | chr1:23318959-23321726 FORWARD | Aliases: F16P17.10, F16P17_10	4.5	4.2	0.3	1.7	41.2%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
12346	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	2.7	-0.2	-1.7	41.2%	-0.9
12347	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	7.0	0.5	1.7	41.2%	-0.2
12348	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	2.8	-0.2	-1.7	41.2%	-0.7
12349	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	3.1	3.3	-0.2	-1.7	41.2%	-0.7
12350	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	6.9	7.5	-0.6	-1.7	41.2%	-0.0
12351	AT2G31945.1 | expressed protein | chr2:13588658-13589203 FORWARD | Aliases: None	3.5	3.8	-0.3	-1.7	41.3%	-0.2
12352	AT1G22980.1 | expressed protein | chr1:8132679-8134154 REVERSE | Aliases: F19G10.7	3.4	3.1	0.3	1.7	41.3%	-0.1
12353	AT1G29150.1 | Symbol: ATS9 | 26S proteasome regulatory subunit, putative (RPN6), similar to 19S proteosome subunit 9 GB:AAC34120 GI:3450889 from (Arabidopsis thaliana) | chr1:10180505-10182689 FORWARD | Aliases: 19S PROTEOSOME SUBUNIT 9, F28N24.15, F28N24_15, RPN6	10.6	9.8	0.8	1.7	41.3%	-0.4
12354	AT1G56690.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:21257482-21259596 FORWARD | Aliases: F25P12.87, F25P12_87	2.7	2.6	0.2	1.7	41.3%	-0.7
12355	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	3.4	3.8	-0.4	-1.7	41.3%	-0.4
12356	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	3.0	-0.2	-1.7	41.3%	-0.7
12357	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	2.7	-0.3	-1.7	41.3%	-0.3
12358	AT3G21720.1 | isocitrate lyase, putative, similar to isocitrate lyase GI:167144 from (Brassica napus) | chr3:7652511-7655950 REVERSE | Aliases: MSD21.4	4.6	4.9	-0.3	-1.7	41.3%	-0.4
12359	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	3.2	3.5	-0.3	-1.7	41.3%	-0.4
12360	AT3G26390.1 | hypothetical protein | chr3:9664687-9665187 REVERSE | Aliases: F20C19.11	2.8	3.0	-0.2	-1.7	41.3%	-0.8
12361	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	6.1	6.6	-0.6	-1.7	41.3%	-0.1
12362	AT2G23210.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:9889087-9890477 REVERSE | Aliases: T20D16.16, T20D16_16	3.0	3.2	-0.2	-1.7	41.3%	-0.8
12363	AT4G29960.1 | expressed protein | chr4:14660608-14662393 REVERSE | Aliases: F27B13.200, F27B13_200	6.6	6.0	0.7	1.7	41.4%	-0.1
12364	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	3.1	-0.2	-1.7	41.4%	-0.6
12365	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	2.3	2.5	-0.1	-1.7	41.4%	-1.3
12366	AT2G44100.1 | Symbol: ATGDI1 |	11.0	10.2	0.8	1.7	41.4%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
12367	AT2G25460.1 | expressed protein | chr2:10839838-10842561 REVERSE | Aliases: F13B15.12, F13B15_12	4.0	4.3	-0.3	-1.7	41.4%	-0.5
12368	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	3.4	3.2	0.2	1.7	41.4%	-0.4
12369	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	6.5	6.0	0.5	1.7	41.4%	-0.0
12370	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	5.9	5.4	0.5	1.7	41.4%	-0.2
12371	AT3G02350.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8 | chr3:479013-481481 FORWARD | Aliases: F11A12.4, F11A12_4	6.0	5.3	0.7	1.7	41.4%	0.1
12372	AT3G07610.1 | transcription factor jumonji (jmjC) domain-containing protein, contains Pfam domain, PF02373: jmjC domain | chr3:2426154-2432882 FORWARD | Aliases: MLP3.6	3.9	3.6	0.3	1.7	41.4%	-0.3
12373	AT2G28130.1 | expressed protein | chr2:11995753-11998694 FORWARD | Aliases: F24D13.8, F24D13_8	4.8	4.5	0.3	1.7	41.4%	-0.4
12374	AT5G20770.1 | hypothetical protein | chr5:7034190-7034885 REVERSE | Aliases: T1M15.170, T1M15_170	2.5	2.7	-0.3	-1.7	41.5%	-0.5
12375	AT3G06980.1 | DEAD/DEAH box helicase, putative, contains Pfam profile: PF00270 DEAD/DEAH box helicase | chr3:2201473-2204839 FORWARD | Aliases: F17A9.13	5.4	5.1	0.3	1.7	41.5%	-0.4
12376	AT2G48060.1 | expressed protein | chr2:19665165-19669751 REVERSE | Aliases: T9J23.21	3.7	4.0	-0.3	-1.7	41.5%	-0.4
12377	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	6.9	6.2	0.7	1.7	41.5%	0.1
12378	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	2.5	-0.2	-1.7	41.5%	-1.0
12379	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	3.9	4.4	-0.5	-1.7	41.5%	0.3
12380	AT5G56460.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr5:22882336-22885222 FORWARD | Aliases: MCD7.23, MCD7_23	4.3	3.8	0.5	1.7	41.5%	0.0
12381	AT5G44180.1 | homeobox transcription factor, putative, similar to homeobox transcription factor Hox7/homeotic protein Hox7 (GI:19486)	6.7	8.2	-1.5	-1.7	41.5%	0.2
12382	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	2.8	-0.2	-1.7	41.5%	-0.8
12383	AT3G02100.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:368847-370491 REVERSE | Aliases: F1C9.11, F1C9_11	3.4	3.8	-0.4	-1.7	41.5%	-0.3
12384	AT4G16100.1 | expressed protein | chr4:9105731-9108169 FORWARD | Aliases: DL4090W, FCAALL.70	5.3	5.7	-0.4	-1.7	41.5%	-0.3
12385	AT1G62045.1 | expressed protein | chr1:22938353-22939008 REVERSE | Aliases: None	5.8	6.4	-0.6	-1.7	41.6%	0.1
12386	AT1G44414.1 | expressed protein | chr1:16850221-16850526 FORWARD | Aliases: T18F15.8, T18F15_8	3.4	3.0	0.3	1.7	41.6%	-0.2
12387	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	5.2	4.9	0.3	1.7	41.6%	-0.2
12388	AT5G62140.1 | expressed protein | chr5:24971732-24972610 REVERSE | Aliases: MTG10.17, MTG10_17	3.5	3.2	0.3	1.7	41.6%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
12389	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	6.0	6.7	-0.7	-1.7	41.6%	0.0
12390	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	5.5	6.0	-0.6	-1.7	41.6%	-0.3
12391	AT3G28520.1 | AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 | chr3:10689560-10690996 FORWARD | Aliases: T20D4.3	3.7	4.1	-0.4	-1.7	41.6%	-0.4
12392	AT3G01040.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8 | chr3:8964-12429 FORWARD | Aliases: T4P13.28, T4P13_28	4.6	4.2	0.4	1.7	41.6%	-0.1
12393	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	4.5	-0.5	-1.7	41.7%	-0.2
12394	AT3G23040.1 | hypothetical protein | chr3:8186087-8186897 FORWARD | Aliases: MXC7.7	4.0	4.5	-0.5	-1.7	41.7%	-0.0
12395	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	7.3	6.8	0.5	1.7	41.7%	-0.1
12396	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	5.9	6.3	-0.4	-1.7	41.7%	-0.1
12397	AT1G75580.1 | auxin-responsive protein, putative, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana) | chr1:28381122-28381839 FORWARD | Aliases: F10A5.21, F10A5_21	2.7	2.9	-0.2	-1.7	41.7%	-0.8
12398	AT3G18230.1 | octicosapeptide/Phox/Bem1p (PB1) domain-containing protein, contains Pfam profile PF00564: PB1 domain | chr3:6251489-6254227 FORWARD | Aliases: MIE15.2	5.7	6.0	-0.3	-1.7	41.7%	-0.2
12399	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	2.9	-0.2	-1.7	41.8%	-0.8
12400	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	-0.1	-1.7	41.8%	-1.3
12401	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	4.5	4.2	0.3	1.7	41.8%	-0.1
12402	AT4G09580.1 | expressed protein | chr4:6052349-6054382 REVERSE | Aliases: T25P22.20, T25P22_20	3.0	3.2	-0.2	-1.7	41.8%	-0.6
12403	AT3G01550.1 | triose phosphate/phosphate translocator, putative, similar to SWISS-PROT:P52178 triose phosphate/phosphate translocator (Cauliflower){Brassica oleracea}	2.6	2.9	-0.2	-1.7	41.8%	-0.8
12404	AT3G05800.1 | expressed protein | chr3:1727347-1728246 FORWARD | Aliases: F10A16.9, F10A16_9	3.8	4.2	-0.5	-1.7	41.8%	0.0
12405	AT1G32540.2 | Symbol: LOL1 | zinc finger protein, putative, similar to zinc-finger protein Lsd1 (Arabidopsis thaliana) gi:1872521:gb:AAC49660	2.3	2.5	-0.2	-1.7	41.8%	-0.7
12406	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	2.4	0.2	1.7	41.8%	-1.0
12407	AT3G44760.1 | expressed protein | chr3:16316635-16317204 FORWARD | Aliases: T32N15.7	2.7	2.9	-0.2	-1.7	41.8%	-0.7
12408	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	10.7	9.5	1.2	1.7	41.9%	-0.1
12409	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	2.5	2.7	-0.2	-1.7	41.9%	-0.7
12410	AT2G38350.1 | expressed protein | chr2:16075419-16076386 FORWARD | Aliases: T19C21.16, T19C21_16	2.2	2.4	-0.2	-1.7	41.9%	-0.7

Rank	Description	Sync	Root	M	t	adj.q	B
12411	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)	6.9	7.3	-0.5	-1.7	41.9%	-0.3
12412	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	3.7	3.9	-0.3	-1.7	41.9%	-0.5
12413	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	3.5	0.2	1.7	41.9%	-0.7
12414	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	3.5	3.8	-0.3	-1.7	41.9%	-0.5
12415	AT5G08360.1 | expressed protein | chr5:2689714-2690973 FORWARD | Aliases: F8L15.90, F8L15_90	4.1	3.6	0.5	1.7	41.9%	0.2
12416	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	3.2	-0.2	-1.7	41.9%	-0.6
12417	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	8.0	8.7	-0.7	-1.7	42.0%	-0.0
12418	AT4G03000.2 | expressed protein, contains similarity to hypothetical proteins | chr4:1324136-1327520 FORWARD | Aliases: T4I9.12, T4I9_12	6.9	7.4	-0.5	-1.7	42.0%	-0.3
12419	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	3.2	3.8	-0.6	-1.7	42.0%	-0.1
12420	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	3.5	4.0	-0.5	-1.7	42.0%	0.1
12421	AT5G61560.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:24770094-24773944 FORWARD | Aliases: K11J9.9, K11J9_9	4.9	4.5	0.4	1.7	42.0%	-0.1
12422	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	4.4	3.9	0.6	1.7	42.0%	0.1
12423	AT4G32170.1 | Symbol: CYP96A2 | cytochrome P450, putative, cytochrome p450, Arabidopsis thaliana, PID:G2252844 | chr4:15533778-15535339 FORWARD | Aliases: F10M6.190	3.0	3.3	-0.4	-1.7	42.0%	-0.7
12424	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	2.9	-0.2	-1.7	42.0%	-0.8
12425	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	3.0	-0.2	-1.7	42.1%	-0.5
12426	AT1G70630.1 | expressed protein | chr1:26634895-26637759 FORWARD | Aliases: F24J13.20, F24J13_20	2.2	2.1	0.1	1.7	42.1%	-1.1
12427	AT3G54070.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023 | chr3:20032308-20034581 REVERSE | Aliases: F24B22.30	2.2	2.3	-0.1	-1.7	42.1%	-1.3
12428	AT3G50850.1 | expressed protein | chr3:18912323-18913334 REVERSE | Aliases: F18B3.130	4.5	4.2	0.3	1.7	42.1%	-0.3
12429	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	4.1	-0.3	-1.7	42.1%	-0.2
12430	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	4.1	-0.3	-1.7	42.1%	-0.5
12431	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	8.8	7.1	1.7	1.7	42.2%	0.3

Rank	Description	Sync	Root	M	t	adj.q	B
12432	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	2.6	-0.2	-1.7	42.2%	-1.0
12433	AT4G13600.1 | glycosyl hydrolase family protein 17, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum) | chr4:7911175-7912774 REVERSE | Aliases: T6G15.150, T6G15_150	2.5	2.7	-0.2	-1.7	42.2%	-0.5
12434	AT4G14970.1 | expressed protein | chr4:8553851-8561661 FORWARD | Aliases: DL3525W, FCAALL.148	2.8	2.6	0.2	1.7	42.2%	-0.5
12435	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	4.2	3.7	0.5	1.7	42.2%	-0.0
12436	AT4G33890.2 | expressed protein | chr4:16249727-16251384 FORWARD | Aliases: F17I5.80, F17I5_80	5.2	5.6	-0.4	-1.7	42.2%	-0.1
12437	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	5.5	5.0	0.5	1.7	42.2%	-0.2
12438	AT4G27550.1 | Symbol: ATTPS4 |	3.3	3.6	-0.3	-1.7	42.2%	-0.2
12439	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	3.3	3.6	-0.2	-1.7	42.2%	-0.6
12440	AT1G15780.1 | expressed protein | chr1:5430178-5435916 REVERSE | Aliases: F7H2.12, F7H2_12	7.7	8.3	-0.5	-1.7	42.2%	-0.2
12441	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	3.6	3.9	-0.3	-1.7	42.2%	-0.3
12442	AT3G62640.1 | expressed protein | chr3:23177265-23177876 REVERSE | Aliases: F26K9.70	2.3	2.5	-0.2	-1.7	42.3%	-0.9
12443	AT1G07060.1 | expressed protein | chr1:2167106-2168396 REVERSE | Aliases: F10K1.23, F10K1_23	3.5	3.8	-0.3	-1.7	42.3%	-0.4
12444	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	2.9	0.3	1.7	42.3%	-0.4
12445	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	2.7	-0.2	-1.7	42.3%	-0.6
12446	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	2.8	-0.2	-1.7	42.3%	-0.9
12447	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	2.7	2.9	-0.2	-1.7	42.3%	-0.4
12448	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	5.3	4.7	0.6	1.7	42.4%	0.2
12449	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) {Homo sapiens} | chr4:16812122-16814750 REVERSE | Aliases: F23E12.80, F23E12_80	8.1	7.2	0.9	1.7	42.4%	-0.2
12450	AT1G78030.1 | expressed protein | chr1:29347051-29348718 FORWARD | Aliases: F28K19.25, F28K19_25	2.5	2.2	0.2	1.7	42.4%	-0.4
12451	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	5.0	4.3	0.7	1.7	42.4%	0.1
12452	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	4.6	5.0	-0.4	-1.7	42.4%	-0.0

Rank	Description	Sync	Root	M	t	adj.q	B
12453	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	3.4	-0.3	-1.7	42.4%	-0.3
12454	AT1G63490.1 | transcription factor jumonji (jmjC) 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: jmjC domain | chr1:23548321-23555695 REVERSE | Aliases: F2K11.14, F2K11_14	4.3	4.8	-0.4	-1.7	42.5%	-0.0
12455	AT5G60610.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.8	2.5	0.3	1.7	42.5%	-0.4
12456	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	12.4	12.2	0.2	1.7	42.5%	-0.9
12457	AT4G39610.1 | expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617 | chr4:18393564-18394739 REVERSE | Aliases: F23K16.240, F23K16_240	2.4	2.5	-0.1	-1.7	42.5%	-1.1
12458	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	4.9	5.8	-0.9	-1.7	42.5%	-0.1
12459	AT1G79420.1 | expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620) | chr1:29876351-29879208 FORWARD | Aliases: T8K14.16, T8K14_16	2.5	2.7	-0.2	-1.7	42.5%	-0.6
12460	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	7.5	-1.0	-1.7	42.6%	-0.0
12461	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	4.6	3.8	0.8	1.7	42.6%	0.4
12462	AT5G01840.1 | ovate family protein, 59% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	4.9	4.7	0.2	1.7	42.6%	-0.7
12463	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	2.5	-0.1	-1.7	42.6%	-1.2
12464	AT5G65700.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:26298986-26302473 FORWARD | Aliases: MPA24.5, MPA24_5	5.5	4.7	0.8	1.7	42.6%	0.2
12465	AT3G54000.3 | expressed protein | chr3:20007585-20009601 FORWARD | Aliases: F5K20.300	3.4	3.8	-0.3	-1.7	42.6%	-0.2
12466	AT2G29880.1 | expressed protein | chr2:12749613-12750622 FORWARD | Aliases: T27A16.36	3.1	3.4	-0.3	-1.7	42.6%	-0.6
12467	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	11.8	11.1	0.7	1.7	42.6%	-0.3
12468	AT2G46150.1 | expressed protein, and genefinder | chr2:18968476-18969449 FORWARD | Aliases: T3F17.20	3.1	3.3	-0.2	-1.7	42.6%	-0.9
12469	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	2.5	-0.2	-1.7	42.6%	-1.0
12470	AT5G14850.2 | mannosyltransferase, putative, similar to PIGB from Homo sapiens (gi:1552169), Mus musculus (gi:7634741)	5.0	5.3	-0.4	-1.7	42.6%	-0.4
12471	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 impotin 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	5.0	5.6	-0.6	-1.7	42.6%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
12472	AT1G49930.1 | expressed protein | chr1:18488600-18489307 FORWARD | Aliases: F2J10.20, F2J10_20	4.1	4.8	-0.7	-1.7	42.6%	0.0
12473	AT3G44940.1 | expressed protein | chr3:16424319-16426226 REVERSE | Aliases: F14D17.10	2.9	2.7	0.2	1.7	42.6%	-0.8
12474	AT5G47000.1 | peroxidase, putative | chr5:19086171-19087560 REVERSE | Aliases: MQD22.14, MQD22_14	2.2	2.4	-0.2	-1.7	42.7%	-0.9
12475	AT5G28800.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:10822884-10823642 FORWARD | Aliases: T32B20.90, T32B20_90	3.3	3.5	-0.2	-1.7	42.7%	-0.8
12476	ATCG00130.1 | Symbol: ATPF | ATPase F subunit. | chrC:11529-12798 REVERSE | Aliases: ATPF	8.5	7.0	1.5	1.7	42.7%	0.0
12477	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	2.8	-0.3	-1.7	42.7%	-0.7
12478	AT1G07510.1 | Symbol: FTSH10 |	8.7	9.2	-0.5	-1.7	42.7%	-0.2
12479	AT4G15460.1 | glycine-rich protein | chr4:8841418-8841864 REVERSE | Aliases: DL3770C, FCAALL.299	3.8	4.3	-0.5	-1.7	42.7%	-0.1
12480	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	2.2	2.3	-0.1	-1.7	42.7%	-1.3
12481	AT4G32000.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:15474089-15476661 REVERSE | Aliases: F10N7.190, F10N7_190	4.1	4.6	-0.5	-1.7	42.7%	-0.0
12482	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	2.9	-0.2	-1.7	42.7%	-0.7
12483	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	5.9	0.5	1.7	42.7%	-0.1
12484	AT2G03180.1 | hypothetical protein | chr2:962761-963123 FORWARD | Aliases: T18E12.15, T18E12_15	2.4	2.5	-0.1	-1.7	42.8%	-1.0
12485	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	7.0	1.4	1.7	42.8%	0.2
12486	AT4G02140.1 | expressed protein | chr4:949617-950270 REVERSE | Aliases: T10M13.15, T10M13_15	2.9	2.7	0.1	1.7	42.8%	-0.9
12487	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	4.9	5.3	-0.4	-1.7	42.8%	-0.4
12488	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 S. cerevisiae Rer2 (SP:P35196)	5.6	6.1	-0.5	-1.7	42.8%	-0.3
12489	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	5.6	5.3	0.3	1.7	42.8%	-0.2
12490	AT2G35230.2 | VQ motif-containing protein, contains PF05678: VQ motif | chr2:14849397-14851510 FORWARD | Aliases: T4C15.10, T4C15_10	2.5	2.7	-0.2	-1.7	42.8%	-0.7
12491	AT3G19260.1 | Symbol: LAG1 HOMOLOG 2 |	6.7	7.7	-1.0	-1.7	42.9%	0.1
12492	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	2.9	-0.2	-1.7	42.9%	-0.7
12493	AT2G25190.1 | expressed protein | chr2:10741025-10742778 FORWARD | Aliases: F13D4.5	5.5	6.0	-0.5	-1.7	42.9%	-0.1
12494	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	5.6	6.0	-0.5	-1.7	42.9%	-0.3
12495	AT3G49420.1 | Got1-like family protein, contains Pfam profile: PF04178 Got1-like family | chr3:18340372-18342416 FORWARD | Aliases: T9C5.20	5.5	4.6	0.9	1.7	42.9%	0.5
12496	AT5G01430.1 | Got1-like family protein, contains Pfam profile: PF04178 Got1-like family | chr5:176446-178598 REVERSE | Aliases: T10O8.140	5.5	4.6	0.9	1.7	42.9%	0.5

Rank	Description	Sync	Root	M	t	adj.q	B
12497	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) (Arabidopsis thaliana); similar to calcineurin B-like protein 1 (GI:3309082) (Arabidopsis thaliana)	7.0	7.5	-0.5	-1.7	42.9%	-0.3
12498	AT3G08770.1 | Symbol: LTP6 | lipid transfer protein 6 (LTP6), identical to GI:8571927	3.4	3.6	-0.2	-1.7	42.9%	-0.6
12499	AT2G41640.1 | expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563) | chr2:17367574-17369613 FORWARD | Aliases: T32G6.16, T32G6_16	6.4	5.8	0.6	1.7	42.9%	0.1
12500	AT1G79280.1 | expressed protein, weak similarity to Nucleoprotein TPR (Swiss-Prot:P12270) (Homo sapiens) | chr1:29824069-29837702 REVERSE | Aliases: YUP8H12R.12, YUP8H12R_12	7.5	6.9	0.6	1.7	42.9%	-0.2
12501	AT5G48130.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr5:19533517-19535676 FORWARD | Aliases: MIF21.2, MIF21_2	2.9	3.1	-0.2	-1.7	42.9%	-0.7
12502	AT2G30270.1 | expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567) | chr2:12914918-12916195 REVERSE | Aliases: T9D9.8, T9D9_8	4.9	4.6	0.4	1.7	43.0%	-0.1
12503	AT3G63500.2 | expressed protein | chr3:23456858-23461145 REVERSE | Aliases: MAA21.130	6.5	7.5	-1.0	-1.7	43.0%	-0.1
12504	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	4.1	0.2	1.7	43.0%	-0.5
12505	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	3.8	4.2	-0.4	-1.7	43.0%	-0.2
12506	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	5.2	4.8	0.4	1.7	43.0%	-0.1
12507	AT2G02690.1 | expressed protein | chr2:749935-751899 FORWARD | Aliases: T20F6.17	3.1	3.6	-0.5	-1.7	43.0%	-0.0
12508	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	3.8	-0.4	-1.7	43.0%	-0.2
12509	AT3G42990.1 | hypothetical protein | chr3:15041342-15042140 FORWARD | Aliases: F18P9.150	2.1	2.2	-0.2	-1.7	43.0%	-0.9
12510	AT5G64550.1 | loricrin-related, contains weak similarity to Loricrin (Swiss-Prot:P23490) (Homo sapiens) | chr5:25818754-25822206 REVERSE | Aliases: MUB3.7, MUB3_7	5.3	5.6	-0.3	-1.7	43.0%	-0.3
12511	AT5G55400.1 | fimbrin-like protein, putative, similar to fimbrin-like protein (ATFIM1) (Arabidopsis thaliana) GI:2905893; contains Pfam profile PF00307: Calponin homology (CH) domain	8.8	7.7	1.1	1.7	43.0%	-0.0
12512	AT4G01290.1 | expressed protein | chr4:538097-543869 REVERSE | Aliases: F2N1.34, F2N1_34	6.4	7.2	-0.8	-1.7	43.1%	-0.1
12513	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	3.1	-0.2	-1.7	43.1%	-0.6
12514	AT5G34830.1 | expressed protein, ; expression supported by MPSS | chr5:12998875-12999727 FORWARD | Aliases: T3J11.1	2.6	2.9	-0.3	-1.7	43.1%	-0.5
12515	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	5.3	5.6	-0.3	-1.7	43.1%	-0.2
12516	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	3.4	-0.3	-1.7	43.1%	-0.8
12517	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	3.9	0.4	1.7	43.1%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
12518	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	2.4	2.6	-0.2	-1.7	43.1%	-1.1
12519	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	8.0	7.6	0.4	1.7	43.1%	-0.3
12520	AT1G36550.1 | hypothetical protein, weak similarity to gag-pol polyprotein (Zea mays) GI:22296822 | chr1:13796743-13798497 FORWARD | Aliases: F28J9.18, F28J9_18	2.8	3.0	-0.2	-1.7	43.1%	-0.5
12521	AT1G30790.1 | F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	3.1	3.3	-0.2	-1.7	43.1%	-0.7
12522	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	3.9	4.8	-0.9	-1.7	43.1%	-0.1
12523	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	2.9	3.1	-0.2	-1.7	43.2%	-0.8
12524	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	7.0	7.7	-0.7	-1.7	43.2%	-0.1
12525	AT3G45690.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr3:16787253-16789135 FORWARD | Aliases: T6D9.20	2.4	2.7	-0.2	-1.7	43.2%	-0.6
12526	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	3.6	-0.2	-1.7	43.2%	-0.7
12527	AT5G50375.1 | Symbol: CPI1 | cyclopropyl isomerase (CPI1) | chr5:20528893-20531468 FORWARD | Aliases: CYCLOEUCALENOL CYCLOISOMERASE, CYCLOPROPYL ISOMERASE	5.4	5.0	0.4	1.7	43.2%	-0.3
12528	AT1G04150.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr1:1081207-1084245 REVERSE | Aliases: F20D22.8, F20D22_8	3.5	3.8	-0.3	-1.7	43.2%	-0.3
12529	AT4G35890.1 | La domain-containing protein, contains Pfam PF05383: La domain | chr4:16997142-17000836 FORWARD | Aliases: T19K4.20	7.0	7.3	-0.3	-1.7	43.2%	-0.4
12530	AT5G35735.1 | auxin-responsive family protein, similar to auxin-induced protein AIR12 GI:11357190 (Arabidopsis thaliana) | chr5:13917982-13920227 REVERSE | Aliases: None	6.4	5.7	0.7	1.7	43.2%	-0.1
12531	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	8.7	-0.7	-1.7	43.2%	-0.2
12532	AT2G38820.2 | expressed protein, contains Pfam profile PF04720: Protein of unknown function (DUF506) | chr2:16228914-16230740 FORWARD | Aliases: F13I13.5, F13I13_5	5.3	5.6	-0.3	-1.7	43.2%	-0.4
12533	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	3.0	3.4	-0.3	-1.7	43.2%	-0.4
12534	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)	5.3	5.6	-0.3	-1.7	43.2%	-0.4
12535	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	5.0	5.4	-0.4	-1.7	43.3%	-0.1
12536	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	3.2	3.4	-0.2	-1.7	43.3%	-0.7
12537	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	6.6	6.3	0.3	1.7	43.3%	-0.3
12538	AT2G23110.1 | expressed protein | chr2:9847606-9848126 FORWARD | Aliases: F21P24.17, F21P24_17	2.7	2.9	-0.2	-1.7	43.3%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
12539	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	4.8	5.1	-0.4	-1.7	43.4%	-0.1
12540	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	5.4	5.0	0.4	1.7	43.4%	0.1
12541	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	8.5	8.2	0.3	1.7	43.4%	-0.5
12542	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	4.4	4.8	-0.4	-1.7	43.4%	-0.4
12543	AT5G39040.1 | Symbol: ATTAP2 |	6.1	5.9	0.3	1.7	43.4%	-0.4
12544	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	6.3	6.6	-0.3	-1.7	43.4%	-0.5
12545	AT1G20560.1 | 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 adenosine monophosphate binding protein 1 AMPBP1 (AMPBP1) GI:20799710 | chr1:7119666-7121804 REVERSE | Aliases: F5M15.12, F5M15_12	8.2	8.7	-0.5	-1.7	43.4%	-0.5
12546	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	7.6	7.2	0.4	1.7	43.4%	0.0
12547	AT2G19700.1 | expressed protein | chr2:8512053-8512721 REVERSE | Aliases: F6F22.27, F6F22_27	2.2	2.4	-0.2	-1.7	43.4%	-1.0
12548	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	5.7	5.0	0.7	1.7	43.4%	0.2
12549	AT1G50040.1 | expressed protein | chr1:18545798-18547616 FORWARD | Aliases: F2J10.8, F2J10_8	4.4	4.1	0.3	1.7	43.4%	-0.1
12550	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	6.1	-0.4	-1.7	43.4%	-0.2
12551	AT3G56690.1 | Symbol: CIP111 |	5.1	4.6	0.4	1.7	43.4%	-0.1
12552	AT4G23210.2 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr4:12148786-12151429 REVERSE | Aliases: F21P8.100, F21P8_100	2.8	3.0	-0.2	-1.7	43.4%	-0.6
12553	AT4G17460.1 | Symbol: HAT1 | homeobox-leucine zipper protein 1 (HAT1) / HD-ZIP protein 1, identical to Homeobox-leucine zipper protein HAT1 (SP:P46600) (Arabidopsis thaliana) | chr4:9739692-9741158 FORWARD | Aliases: DL4765W, FCAALL.65	5.6	4.9	0.7	1.7	43.4%	-0.1
12554	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	2.8	-0.1	-1.7	43.4%	-1.2
12555	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	2.9	3.2	-0.3	-1.7	43.4%	-0.4
12556	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	10.1	0.5	1.7	43.5%	-0.3
12557	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	6.5	6.1	0.3	1.7	43.5%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
12558	AT1G56570.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:21199469-21201386 FORWARD | Aliases: F25P12.98, F25P12_98	3.5	3.9	-0.4	-1.7	43.5%	-0.4
12559	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	5.1	5.5	-0.5	-1.7	43.5%	-0.3
12560	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	3.4	3.7	-0.3	-1.7	43.5%	-0.5
12561	AT2G04600.1 | expressed protein | chr2:1608073-1609755 REVERSE | Aliases: F7D11.4, F7D11_4	3.1	3.3	-0.2	-1.7	43.6%	-0.8
12562	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	2.8	3.1	-0.3	-1.7	43.6%	-0.4
12563	AT2G42920.1 | pentatricopeptide (PPR) repeat-containing protein, and genefinder | chr2:17865775-17867461 FORWARD | Aliases: F23E6.4	4.0	4.5	-0.5	-1.7	43.6%	-0.2
12564	AT1G07795.1 | expressed protein | chr1:2414283-2414964 FORWARD | Aliases: None	4.5	5.0	-0.5	-1.7	43.6%	-0.1
12565	AT5G03460.1 | expressed protein | chr5:864280-865672 FORWARD | Aliases: F12E4.230, F12E4_230	7.8	8.3	-0.5	-1.7	43.6%	-0.1
12566	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	6.8	0.3	1.7	43.6%	-0.4
12567	AT4G30570.1 | GDP-mannose pyrophosphorylase, putative, similar to GDP-mannose pyrophosphorylase (Arabidopsis thaliana) GI:3598958; contains Pfam profile PF00483: Nucleotidyl transferase | chr4:14930683-14931957 REVERSE | Aliases: F17I23.90, F17I23_90	4.2	4.5	-0.3	-1.7	43.6%	-0.5
12568	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	2.6	-0.2	-1.7	43.7%	-0.8
12569	AT3G46770.1 | transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain | chr3:17235049-17236301 FORWARD | Aliases: T6H20.200	3.0	3.4	-0.3	-1.7	43.7%	-0.3
12570	ATCG00050.1 | Symbol: RPS16 | Homologous to the bacterial ribosomal protein S16 | chrC:5084-6188 REVERSE | Aliases: RPS16	5.7	4.4	1.3	1.7	43.7%	0.1
12571	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	5.6	5.0	0.6	1.7	43.7%	-0.1
12572	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	5.9	6.2	-0.4	-1.7	43.7%	-0.2
12573	AT3G17130.1 | invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	3.4	3.8	-0.3	-1.7	43.7%	-0.2
12574	AT4G21300.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr4:11336489-11339062 FORWARD | Aliases: T6K22.30, T6K22_30	3.4	3.2	0.2	1.7	43.7%	-0.6
12575	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	4.1	-0.3	-1.7	43.7%	-0.5
12576	AT3G11590.1 | expressed protein | chr3:3660383-3663740 FORWARD | Aliases: F24K9.26	7.0	6.5	0.4	1.7	43.7%	-0.3
12577	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	6.1	5.4	0.7	1.7	43.7%	-0.4
12578	AT3G55950.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069; similar to cytokinin-regulated kinase 1 (Nicotiana tabacum) gi:10998537:gb:AAG25966	6.2	6.6	-0.4	-1.7	43.8%	-0.4
12579	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	3.9	-0.3	-1.7	43.8%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
12580	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	2.3	-0.1	-1.7	43.8%	-1.1
12581	AT1G17455.1 | expressed protein | chr1:5997173-5998468 FORWARD | Aliases: None	5.8	5.3	0.5	1.7	43.8%	-0.3
12582	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	2.7	3.0	-0.2	-1.7	43.8%	-0.7
12583	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	6.9	6.2	0.7	1.7	43.8%	-0.1
12584	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	4.3	0.3	1.7	43.8%	-0.3
12585	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	3.5	-0.3	-1.7	43.8%	-0.3
12586	AT3G42540.1 | expressed protein | chr3:14656093-14657428 FORWARD | Aliases: T32A11.110	3.3	3.7	-0.3	-1.7	43.8%	-0.5
12587	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	3.9	3.5	0.3	1.7	43.8%	-0.5
12588	NA	5.9	6.5	-0.6	-1.7	43.9%	-0.5
12589	AT2G16010.1 | hypothetical protein | chr2:6972692-6973081 FORWARD | Aliases: F7H1.3, F7H1_3	3.0	3.3	-0.3	-1.7	43.9%	-0.7
12590	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	2.4	2.5	-0.1	-1.7	43.9%	-1.0
12591	AT3G48350.1 | cysteine proteinase, putative, similar to cysteine endopeptidase precursor (Ricinus communis) GI:2944446; contains Pfam profile PF00112: Papain family cysteine protease	3.0	3.4	-0.3	-1.7	43.9%	-0.3
12592	AT2G25070.1 | protein phosphatase 2C, putative / PP2C, putative | chr2:10670319-10673043 REVERSE | Aliases: F13D4.1	9.7	10.0	-0.3	-1.7	43.9%	-0.7
12593	AT4G13235.1 | Encodes a defensin-like (DEFL) family protein. | chr4:7677520-7678243 REVERSE | Aliases: None	7.3	7.6	-0.2	-1.7	43.9%	-0.6
12594	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	2.6	-0.2	-1.7	43.9%	-0.8
12595	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	4.1	3.7	0.3	1.7	43.9%	-0.3
12596	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	2.1	2.3	-0.2	-1.7	43.9%	-1.0
12597	AT3G42725.1 | expressed protein | chr3:14853888-14854695 REVERSE | Aliases: None	2.6	2.8	-0.2	-1.7	43.9%	-1.1
12598	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	5.0	-0.2	-1.7	43.9%	-0.4
12599	AT3G23650.1 | protein kinase-related, contains similarity to protein kinases | chr3:8510696-8511203 REVERSE | Aliases: MDB19.15	3.1	3.4	-0.2	-1.7	43.9%	-0.5
12600	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	3.1	2.9	0.2	1.7	43.9%	-0.8
12601	AT3G43270.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr3:15233113-15236448 REVERSE | Aliases: F7K15.120	4.8	4.5	0.3	1.7	44.0%	-0.3

Rank	Description	Sync	Root	M	t	adj.q	B
12602	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	3.7	3.9	-0.2	-1.7	44.0%	-0.7
12603	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	2.6	2.8	-0.2	-1.7	44.0%	-0.7
12604	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	4.0	4.5	-0.5	-1.7	44.0%	-0.0
12605	AT5G27330.1 | expressed protein | chr5:9632706-9634886 REVERSE | Aliases: F21A20.40, F21A20_40	6.6	5.5	1.1	1.7	44.1%	0.2
12606	AT1G23890.2 | NHL repeat-containing protein, contains Pfam profile PF01436: NHL repeat	5.8	5.1	0.7	1.7	44.1%	-0.1
12607	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	3.3	-0.2	-1.7	44.1%	-0.9
12608	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	3.5	3.7	-0.2	-1.7	44.1%	-0.8
12609	AT5G05900.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:1774514-1776382 FORWARD | Aliases: K18J17.5, K18J17_5	3.3	3.6	-0.3	-1.7	44.1%	-0.3
12610	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	5.6	6.2	-0.6	-1.7	44.1%	-0.1
12611	AT1G18990.1 | expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593 | chr1:6558669-6560480 REVERSE | Aliases: F14D16.14, F14D16_14	2.7	2.9	-0.2	-1.7	44.2%	-0.8
12612	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	5.5	6.2	-0.7	-1.7	44.2%	-0.1
12613	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	2.0	0.1	1.7	44.2%	-1.0
12614	AT3G49280.1 | hypothetical protein | chr3:18281010-18281919 FORWARD | Aliases: F2K15.140	2.7	3.0	-0.3	-1.7	44.2%	-0.4
12615	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	5.8	0.4	1.7	44.2%	-0.5
12616	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	7.9	6.6	1.3	1.7	44.2%	-0.1
12617	AT1G02060.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:360918-363094 REVERSE | Aliases: T7I23.14, T7I23_14	2.9	2.8	0.2	1.7	44.2%	-0.9
12618	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)	4.7	4.3	0.4	1.7	44.2%	-0.1
12619	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	5.0	5.4	-0.4	-1.7	44.2%	-0.0
12620	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	2.9	3.2	-0.3	-1.7	44.2%	-0.6
12621	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	3.5	-0.3	-1.7	44.2%	-0.6

Rank	Description	Sync	Root	M	t	adj.q	B
12622	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	4.1	-0.4	-1.7	44.2%	-0.4
12623	AT5G27230.1 | expressed protein, ; expression supported by MPSS | chr5:9584258-9587841 FORWARD | Aliases: T21B4.140, T21B4_140	2.4	2.3	0.1	1.7	44.2%	-1.0
12624	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	4.4	4.9	-0.5	-1.7	44.2%	0.1
12625	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	12.5	12.0	0.5	1.7	44.3%	-0.9
12626	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	2.3	2.5	-0.1	-1.7	44.3%	-1.1
12627	AT1G18180.1 | expressed protein | chr1:6255896-6257590 FORWARD | Aliases: T10F20.18	6.1	5.6	0.5	1.7	44.3%	-0.2
12628	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	6.5	6.9	-0.5	-1.7	44.4%	0.1
12629	AT5G53020.1 | expressed protein | chr5:21517125-21519627 FORWARD | Aliases: MNB8.8, MNB8_8	4.4	4.1	0.3	1.7	44.4%	-0.3
12630	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	4.2	4.6	-0.4	-1.7	44.4%	-0.6
12631	AT5G24980.1 | expressed protein | chr5:8609084-8609531 FORWARD | Aliases: F6A4.190, F6A4_190	8.8	7.8	0.9	1.7	44.4%	0.1
12632	AT2G34585.1 | expressed protein | chr2:14575126-14575716 REVERSE | Aliases: None	9.1	9.4	-0.4	-1.7	44.4%	-0.9
12633	AT1G22370.2 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, glycosyltransferase family | chr1:7898105-7899868 REVERSE | Aliases: T16E15.2, T16E15_2	3.5	3.9	-0.5	-1.7	44.4%	-0.2
12634	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	6.7	7.4	-0.7	-1.7	44.4%	0.1
12635	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	2.9	-0.3	-1.7	44.5%	-0.8
12636	AT4G14605.1 | mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF | chr4:8378476-8380635 FORWARD | Aliases: None	3.5	3.3	0.2	1.7	44.5%	-0.6
12637	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	3.8	4.1	-0.2	-1.7	44.5%	-0.6
12638	AT4G25540.1 | Symbol: MSH3 | DNA mismatch repair protein MSH3 (MSH3), identical to SP:O65607 DNA mismatch repair protein MSH3 (AtMsh3) {Arabidopsis thaliana}	4.6	4.3	0.3	1.7	44.5%	-0.3
12639	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 profilePF01019: Gamma-glutamyltranspeptidase	2.7	3.0	-0.2	-1.7	44.5%	-0.7
12640	AT1G80550.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:30289838-30291596 REVERSE | Aliases: T21F11.12, T21F11_12	3.7	3.4	0.3	1.7	44.5%	-0.3
12641	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	2.6	2.8	-0.2	-1.7	44.6%	-0.6
12642	AT3G52720.2 | carbonic anhydrase family protein, low similarity to storage protein (dioscorin) (Dioscorea cayenensis) GI:433463; contains Pfam profile PF00194: Eukaryotic-type carbonic anhydrase | chr3:19550256-19552262 REVERSE | Aliases: F3C22.120	3.0	3.2	-0.3	-1.7	44.6%	-0.4
12643	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	8.7	9.6	-0.8	-1.7	44.6%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
12644	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	2.6	-0.2	-1.7	44.6%	-0.8
12645	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	3.1	2.9	0.2	1.7	44.6%	-0.5
12646	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	4.4	4.7	-0.4	-1.7	44.6%	-0.2
12647	AT2G21195.2 | expressed protein | chr2:9090271-9090990 FORWARD | Aliases: None	5.2	4.5	0.7	1.7	44.6%	0.1
12648	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	7.3	6.7	0.6	1.7	44.6%	-0.2
12649	AT1G17620.1 | expressed protein | chr1:6062227-6063284 FORWARD | Aliases: F11A6.25, F1L3.32, F1L3_32	6.0	5.4	0.6	1.7	44.7%	0.0
12650	AT3G27570.1 | expressed protein | chr3:10215233-10217973 REVERSE | Aliases: MMJ24.12	8.5	7.8	0.7	1.7	44.7%	-0.3
12651	AT1G01225.1 | NC domain-containing protein-related, contains weak hit to Pfam profile PF04970: NC domain | chr1:95987-97407 FORWARD | Aliases: None	3.4	3.1	0.2	1.7	44.7%	-0.4
12652	AT1G16380.1 | Symbol: ATCHX1 |	2.8	3.0	-0.2	-1.7	44.7%	-0.8
12653	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	3.6	3.8	-0.2	-1.7	44.7%	-0.7
12654	AT1G32730.1 | expressed protein | chr1:11840890-11843237 FORWARD | Aliases: F6N18.11, F6N18_11	3.8	3.4	0.4	1.7	44.7%	-0.3
12655	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	5.3	4.9	0.4	1.7	44.7%	-0.5
12656	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	3.6	3.3	0.3	1.7	44.7%	-0.4
12657	AT3G59170.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.6	-0.1	-1.7	44.8%	-1.1
12658	AT5G20760.1 | hypothetical protein | chr5:7032529-7033191 FORWARD | Aliases: T1M15.160, T1M15_160	3.2	3.4	-0.2	-1.7	44.8%	-0.6
12659	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	4.0	5.1	-1.1	-1.7	44.8%	-0.2
12660	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	3.7	4.1	-0.3	-1.7	44.8%	-0.5
12661	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	4.5	4.2	0.3	1.7	44.8%	-0.3
12662	AT1G53450.2 | expressed protein | chr1:19954674-19957776 REVERSE | Aliases: T3F20.23, T3F20_23	5.0	4.5	0.5	1.7	44.8%	-0.3
12663	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	2.8	0.2	1.7	44.9%	-0.7
12664	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	3.5	3.9	-0.4	-1.7	44.9%	-0.4
12665	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	5.0	5.5	-0.5	-1.7	44.9%	-0.2

Rank	Description	Sync	Root	M	t	adj.q	B
12666	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	6.1	5.6	0.5	1.7	44.9%	0.1
12667	AT2G24530.1 | expressed protein, ; expression supported by MPSS | chr2:10430142-10430900 FORWARD | Aliases: F25P17.17, F25P17_17	3.7	4.0	-0.3	-1.7	44.9%	-0.4
12668	AT1G78470.1 | hypothetical protein | chr1:29526663-29527889 FORWARD | Aliases: F3F9.2	2.8	3.1	-0.3	-1.7	44.9%	-0.5
12669	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	2.3	-0.1	-1.7	44.9%	-1.4
12670	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	0.1	1.7	44.9%	-1.6
12671	AT5G48670.1 | MADS-box family protein, contains similarity to MADS-box DNA-binding protein | chr5:19756051-19757016 REVERSE | Aliases: K15N18.16, K15N18_16	4.6	4.2	0.4	1.7	44.9%	-0.1
12672	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	2.6	-0.3	-1.7	45.0%	-0.7
12673	AT1G49890.1 | expressed protein, contains Pfam domain, PF04484: Family of unknown function (DUF566) | chr1:18473743-18477491 FORWARD | Aliases: F10F5.10, F10F5_10	3.3	3.1	0.3	1.7	45.0%	-0.5
12674	AT5G14080.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:4543137-4545258 REVERSE | Aliases: MUA22.8, MUA22_8	5.3	4.9	0.4	1.7	45.0%	-0.4
12675	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	8.3	7.4	0.9	1.7	45.0%	0.1
12676	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	2.2	2.4	-0.2	-1.7	45.0%	-0.9
12677	AT1G76185.1 | expressed protein | chr1:28595219-28596412 FORWARD | Aliases: None	4.9	5.5	-0.5	-1.7	45.0%	0.1
12678	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	5.7	5.3	0.4	1.7	45.0%	-0.1
12679	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	2.6	-0.1	-1.7	45.0%	-1.1
12680	AT1G54410.1 | dehydrin family protein, contains Pfam domain, PF00257: Dehydrin	13.4	13.7	-0.3	-1.7	45.1%	-0.9
12681	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	6.7	6.1	0.7	1.7	45.1%	-0.4
12682	AT3G18310.1 | expressed protein | chr3:6284362-6287150 REVERSE | Aliases: MYF24.3	5.1	4.9	0.2	1.7	45.1%	-0.6
12683	AT3G21680.1 | expressed protein | chr3:7633501-7633860 REVERSE | Aliases: MIL23.24	2.5	2.7	-0.2	-1.7	45.1%	-1.0
12684	AT4G39190.1 | expressed protein, ; expression supported by MPSS | chr4:18252026-18252859 REVERSE | Aliases: T22F8.90, T22F8_90	4.9	4.4	0.5	1.7	45.1%	-0.3
12685	AT3G01090.2 | Symbol: AKIN10 |	5.4	5.9	-0.5	-1.7	45.2%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
12686	AT2G07180.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr2:2980896-2983448 REVERSE | Aliases: T25N22.14, T25N22_14	6.2	6.4	-0.3	-1.7	45.2%	-0.3
12687	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	4.9	4.7	0.3	1.7	45.2%	-0.4
12688	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	3.2	3.5	-0.3	-1.7	45.2%	-0.5
12689	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	6.0	5.7	0.4	1.7	45.2%	-0.1
12690	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	7.4	-0.4	-1.7	45.2%	-0.2
12691	AT3G10140.1 | recA family protein, contains Pfam profile: PF00154 recA bacterial DNA recombination protein | chr3:3134910-3137422 FORWARD | Aliases: T22K18.3	4.6	4.3	0.3	1.7	45.2%	-0.3
12692	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	2.6	-0.2	-1.7	45.2%	-0.8
12693	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	4.7	-0.5	-1.7	45.2%	-0.4
12694	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	2.6	2.7	-0.1	-1.7	45.2%	-1.3
12695	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	3.1	-0.3	-1.7	45.2%	-0.5
12696	AT3G52270.1 | expressed protein | chr3:19398158-19399865 REVERSE | Aliases: T25B15.40	3.0	2.8	0.2	1.7	45.2%	-0.7
12697	AT2G30780.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:13123551-13125136 FORWARD | Aliases: T11J7.17, T11J7_17	3.7	3.9	-0.3	-1.7	45.2%	-0.6
12698	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	4.2	-0.2	-1.7	45.2%	-0.9
12699	AT3G43320.1 | expressed protein | chr3:15286449-15287981 REVERSE | Aliases: T5C2.20	3.2	3.4	-0.2	-1.7	45.2%	-0.7
12700	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	3.1	3.5	-0.3	-1.7	45.2%	-0.5
12701	AT1G05670.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, similar to UDP-glucose:salicylic acid glucosyltransferase (Nicotiana tabacum) GI:7385017; contains Pfam profiles PF00201: UDP-glucoronosyl and UDP-glucosyl transferase, PF01535: PPR repeat | chr1:1698573-1702719 REVERSE | Aliases: F3F20.12, F3F20_12	2.7	3.0	-0.3	-1.7	45.2%	-0.6
12702	AT2G30590.1 | Symbol: WRKY21 |	4.0	3.6	0.4	1.7	45.2%	-0.2
12703	AT1G10490.1 | expressed protein, contains Pfam profile PF05127: Putative ATPase (DUF699) | chr1:3453230-3460621 FORWARD | Aliases: T10O24.10, T10O24_10	3.7	3.5	0.3	1.7	45.3%	-0.5
12704	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	9.5	0.6	1.7	45.3%	-0.4
12705	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	9.5	0.6	1.7	45.3%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
12706	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	3.6	0.3	1.7	45.3%	-0.2
12707	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	3.2	3.6	-0.4	-1.7	45.3%	-0.1
12708	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	3.6	-0.2	-1.7	45.3%	-0.7
12709	AT5G39640.1 | hypothetical protein, contains Pfam profile PF04396: Protein of unknown function, DUF537	3.1	3.5	-0.4	-1.7	45.3%	-0.1
12710	AT4G05230.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr4:2687001-2687621 FORWARD | Aliases: C17L7.150, C17L7_150	3.3	3.7	-0.4	-1.7	45.3%	-0.2
12711	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	2.5	0.2	1.7	45.3%	-0.7
12712	AT5G42390.1 | metalloendopeptidase, identical to chloroplast processing enzyme metalloendopeptidase (Arabidopsis thaliana) gi:2827039:gb:AAC39482 | chr5:16962479-16970328 FORWARD | Aliases: MDH9.8, MDH9_8	6.7	5.9	0.8	1.7	45.4%	-0.1
12713	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	6.4	5.9	0.6	1.7	45.4%	-0.2
12714	AT1G20650.1 | protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain | chr1:7158234-7162548 REVERSE | Aliases: F5M15.3	6.5	6.8	-0.3	-1.7	45.4%	-0.2
12715	AT1G48920.1 | nucleolin, putative, similar to nuM1 protein GI:1279562 from (Medicago sativa) | chr1:18101776-18105291 FORWARD | Aliases: F27K7.6, F27K7_6	9.4	8.9	0.5	1.7	45.4%	-0.1
12716	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	3.5	0.3	1.7	45.4%	-0.3
12717	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	2.9	-0.2	-1.7	45.4%	-0.4
12718	AT3G18800.1 | expressed protein | chr3:6479694-6480384 FORWARD | Aliases: MVE11.18	3.5	3.2	0.3	1.7	45.4%	-0.3
12719	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	7.9	7.1	0.8	1.6	45.4%	-0.1
12720	AT1G50760.1 | expressed protein | chr1:18818615-18818928 REVERSE | Aliases: F8A12.1, F8A12_1	4.4	4.7	-0.3	-1.6	45.4%	-0.6
12721	AT1G06200.1 | expressed protein | chr1:1894336-1896934 REVERSE | Aliases: F9P14.6, F9P14_6	8.2	7.3	0.9	1.6	45.4%	0.0
12722	AT2G46880.2 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	2.8	3.1	-0.3	-1.6	45.4%	-0.7
12723	AT2G27870.1 | expressed protein | chr2:11874328-11875272 REVERSE | Aliases: T1E2.21	2.5	2.7	-0.3	-1.6	45.5%	-0.6
12724	AT1G06540.1 | expressed protein | chr1:2002876-2003392 REVERSE | Aliases: F12K11.13, F12K11_13	2.5	2.8	-0.3	-1.6	45.5%	-0.4
12725	ATCG00700.1 | Symbol: PSBN | PSII low MW protein | chrC:74249-74380 REVERSE | Aliases: PSBN	3.5	3.0	0.5	1.6	45.5%	-0.2
12726	AT4G34610.1 | homeodomain-containing protein, similaritry to homeotic protein BEL1, Arabidopsis thaliana, PIR2:A57632 | chr4:16530551-16532503 REVERSE | Aliases: T4L20.190, T4L20_190	5.0	4.7	0.3	1.6	45.5%	-0.3
12727	AT1G07180.1 | Symbol: ATNDI1 |	3.3	3.0	0.4	1.6	45.5%	-0.3
12728	AT1G09360.1 | invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	2.6	2.9	-0.3	-1.6	45.5%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
12729	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	4.8	5.5	-0.7	-1.6	45.5%	-0.1
12730	AT2G20310.1 | expressed protein | chr2:8768409-8770233 REVERSE | Aliases: F11A3.14, F11A3_14	3.7	3.5	0.3	1.6	45.5%	-0.7
12731	AT1G17850.1 | expressed protein | chr1:6146305-6148813 REVERSE | Aliases: F2H15.8, F2H15_8	3.2	3.0	0.2	1.6	45.5%	-0.6
12732	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	2.3	2.4	-0.2	-1.6	45.5%	-1.2
12733	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	2.9	3.2	-0.3	-1.6	45.5%	-0.4
12734	AT5G11370.1 | expressed protein, various predicted proteins, Arabidopsis thaliana | chr5:3627850-3629718 FORWARD | Aliases: F2I11.260, F2I11_260	2.8	3.0	-0.2	-1.6	45.5%	-0.7
12735	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	7.2	6.4	0.8	1.6	45.5%	-0.2
12736	AT4G11930.1 | hypothetical protein | chr4:7164898-7165716 FORWARD | Aliases: T26M18.140, T26M18_140	3.5	3.8	-0.3	-1.6	45.5%	-0.8
12737	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	7.4	6.5	0.9	1.6	45.5%	-0.2
12738	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	5.1	4.7	0.3	1.6	45.5%	-0.3
12739	AT5G03210.1 | expressed protein | chr5:762786-763320 REVERSE | Aliases: F15A17.240, F15A17_240	4.4	3.7	0.7	1.6	45.5%	-0.4
12740	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	4.5	3.7	0.8	1.6	45.5%	-0.3
12741	AT2G21480.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:9209833-9212448 REVERSE | Aliases: F3K23.24, F3K23_24	3.2	3.3	-0.2	-1.6	45.5%	-0.8
12742	AT1G34480.1 | DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain | chr1:12607254-12609062 FORWARD | Aliases: F12K21.20, F12K21_20	2.3	2.4	-0.1	-1.6	45.6%	-1.2
12743	AT3G12440.1 | extensin family protein, contains similarity to Swiss-Prot:Q38913 extensin 1 precursor (AtExt1) (AtExt4) (Arabidopsis thaliana) | chr3:3951206-3952267 REVERSE | Aliases: T2E22.24	2.8	3.0	-0.2	-1.6	45.6%	-1.0
12744	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	3.2	0.1	1.6	45.6%	-1.1
12745	AT3G42110.1 | expressed protein | chr3:14293271-14295692 REVERSE | Aliases: F4M19.70	2.4	2.6	-0.2	-1.6	45.6%	-0.8
12746	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	3.3	-0.3	-1.6	45.6%	-0.7
12747	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	2.6	-0.2	-1.6	45.6%	-0.9
12748	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	4.1	3.7	0.4	1.6	45.7%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
12749	AT3G50050.1 | aspartyl protease family protein, contains Pfam PF00026: Eukaryotic aspartyl protease | chr3:18564967-18568191 REVERSE | Aliases: F3A4.130	3.7	3.5	0.3	1.6	45.7%	-0.5
12750	AT2G02440.1 | expressed protein | chr2:638011-639304 FORWARD | Aliases: T16F16.23, T16F16_23	4.1	4.4	-0.3	-1.6	45.7%	-0.4
12751	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	3.2	3.5	-0.3	-1.6	45.7%	-0.5
12752	AT2G45580.1 | Symbol: CYP76C3 | cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome p450 | chr2:18789400-18791417 REVERSE | Aliases: F17K2.11	4.5	4.2	0.3	1.6	45.7%	-0.3
12753	AT1G17910.1 | wall-associated kinase, putative, contains similarity to wall-associated kinase 4 GI:3355308 from (Arabidopsis thaliana)	3.0	3.2	-0.2	-1.6	45.8%	-0.7
12754	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	7.0	8.0	-1.0	-1.6	45.8%	-0.3
12755	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	7.0	8.0	-1.0	-1.6	45.8%	-0.3
12756	AT5G05430.1 | expressed protein | chr5:1605276-1606704 REVERSE | Aliases: K18I23.24, K18I23_24	2.7	2.9	-0.2	-1.6	45.8%	-0.8
12757	AT5G17830.1 | expressed protein, contains Pfam domain, PF04515: Protein of unknown function, DUF580 | chr5:5893384-5895369 FORWARD | Aliases: MVA3.19, MVA3_19	2.3	2.5	-0.1	-1.6	45.8%	-0.9
12758	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	12.8	12.2	0.7	1.6	45.8%	-0.7
12759	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	8.8	8.3	0.5	1.6	45.8%	-0.4
12760	AT4G13270.1 | expressed protein | chr4:7731276-7733162 FORWARD | Aliases: T9E8.10, T9E8_10	4.9	5.3	-0.4	-1.6	45.8%	-0.3
12761	AT1G78815.1 | expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640) | chr1:29636636-29637638 REVERSE | Aliases: None	4.9	4.5	0.3	1.6	45.8%	-0.4
12762	AT1G62420.1 | expressed protein, contains Pfam profile PF04720: Protein of unknown function (DUF506) | chr1:23104084-23108269 REVERSE | Aliases: F24O1.44, F24O1_44	5.2	5.9	-0.7	-1.6	45.8%	0.0
12763	AT5G59105.1 | Encodes a defensin-like (DEFL) family protein. | chr5:23879685-23880279 REVERSE | Aliases: None	3.2	3.4	-0.3	-1.6	45.8%	-0.6
12764	AT3G60790.1 | F-box protein-related, contains weak hit to Pfam PF00646: F-box domain | chr3:22475598-22477923 FORWARD | Aliases: T4C21.200	3.0	3.3	-0.2	-1.6	45.8%	-0.8
12765	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	3.2	3.0	0.2	1.6	45.8%	-0.4
12766	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	9.0	9.4	-0.3	-1.6	45.9%	-0.5
12767	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	5.7	6.3	-0.5	-1.6	45.9%	-0.3
12768	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	9.5	10.1	-0.5	-1.6	45.9%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
12769	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	6.0	0.7	1.6	45.9%	0.1
12770	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	2.7	0.1	1.6	45.9%	-1.1
12771	AT5G35760.1 | expressed protein, ; expression supported by MPSS | chr5:13951338-13952012 FORWARD | Aliases: MXH1.19, MXH1_19	2.2	2.3	-0.1	-1.6	45.9%	-1.2
12772	AT4G22510.1 | expressed protein | chr4:11855059-11857083 REVERSE | Aliases: F7K2.90, F7K2_90	3.7	3.9	-0.2	-1.6	46.0%	-0.7
12773	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	9.0	9.5	-0.5	-1.6	46.0%	-0.3
12774	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	6.7	7.4	-0.8	-1.6	46.0%	-0.1
12775	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	7.7	7.0	0.7	1.6	46.0%	-0.2
12776	AT4G31260.1 | expressed protein | chr4:15182599-15182790 REVERSE | Aliases: F8F16.80, F8F16_80	2.9	3.0	-0.1	-1.6	46.0%	-1.3
12777	AT1G31680.1 | copper amine oxidase family protein, contains similarity to amine oxidase (copper-containing) precursor (Pisum sativum) SWISS-PROT:Q43077 | chr1:11343961-11344746 FORWARD | Aliases: F27M3.12, F27M3_12	2.8	3.1	-0.3	-1.6	46.0%	-0.7
12778	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	2.6	2.7	-0.2	-1.6	46.0%	-1.1
12779	AT2G42580.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain | chr2:17735793-17738796 FORWARD | Aliases: F14N22.15, F14N22_15	5.4	5.9	-0.5	-1.6	46.0%	-0.4
12780	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	6.0	-0.8	-1.6	46.0%	0.2
12781	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	2.7	2.8	-0.2	-1.6	46.0%	-0.9
12782	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	5.7	6.1	-0.4	-1.6	46.0%	0.0
12783	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 scienitific 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	3.2	3.0	0.2	1.6	46.0%	-0.5
12784	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	3.7	3.4	0.3	1.6	46.0%	-0.6
12785	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	2.7	-0.2	-1.6	46.0%	-0.8
12786	AT1G03000.1 | Symbol: PEX6 | AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family ('A'TPases 'A'ssociated with diverse cellular 'A'ctivities) | chr1:687908-692476 REVERSE | Aliases: F10O3.18, F10O3_18, PEROXIN6	5.6	5.9	-0.4	-1.6	46.1%	-0.3
12787	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	3.9	-0.2	-1.6	46.1%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
12788	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	4.8	-0.2	-1.6	46.1%	-0.5
12789	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	7.2	7.7	-0.4	-1.6	46.1%	-0.3
12790	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	2.5	2.3	0.2	1.6	46.1%	-0.8
12791	AT3G44960.1 | expressed protein, ; expression supported by MPSS | chr3:16438780-16440136 FORWARD | Aliases: F14D17.30	2.2	2.3	-0.1	-1.6	46.1%	-1.4
12792	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	9.7	8.9	0.8	1.6	46.1%	-0.1
12793	AT5G22530.1 | expressed protein | chr5:7480530-7481197 FORWARD | Aliases: MQJ16.7, MQJ16_7	3.0	2.8	0.2	1.6	46.1%	-0.6
12794	AT5G09390.2 | similar to SMC2orf [Podocoryne carnea] (GB:CAA08790.1) | chr5:2913535-2915924 FORWARD | Aliases: T5E8.190, T5E8_190	7.7	7.4	0.3	1.6	46.1%	-0.3
12795	AT3G29260.1 | short-chain dehydrogenase/reductase (SDR) family protein, similar to 3-beta-hydroxysteroiddehydrogenase GI:15983819 from (Digitalis lanata) | chr3:11217189-11218103 REVERSE | Aliases: MXO21.13	4.0	4.4	-0.4	-1.6	46.1%	-0.3
12796	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)	7.3	6.2	1.1	1.6	46.1%	-0.0
12797	AT1G11800.1 | endonuclease/exonuclease/phosphatase family protein, contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family | chr1:3985224-3987289 REVERSE | Aliases: F25C20.3, F25C20_3	6.0	5.6	0.4	1.6	46.1%	-0.1
12798	AT2G03630.1 | hypothetical protein | chr2:1103202-1103960 FORWARD | Aliases: F19B11.8, F19B11_8	2.2	2.4	-0.2	-1.6	46.1%	-1.0
12799	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	3.5	-0.3	-1.6	46.1%	-0.6
12800	AT5G26130.1 | pathogenesis-related protein, putative, similar to PR-1a protein (Nicotiana tabacum) GI:19944; contains Pfam profile PF00188: SCP-like extracellular protein | chr5:9128113-9128607 REVERSE | Aliases: T1N24.14, T1N24_14	3.5	3.7	-0.2	-1.6	46.1%	-0.8
12801	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	7.3	6.3	1.0	1.6	46.1%	-0.1
12802	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	5.6	6.4	-0.8	-1.6	46.1%	-0.0
12803	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	2.5	-0.2	-1.6	46.1%	-1.0
12804	AT5G63480.1 | expressed protein | chr5:25434491-25436095 FORWARD | Aliases: MLE2.11, MLE2_11	6.0	5.4	0.6	1.6	46.2%	-0.0
12805	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	2.9	3.2	-0.3	-1.6	46.2%	-0.6
12806	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	3.4	3.6	-0.2	-1.6	46.2%	-0.6
12807	AT5G26720.1 | expressed protein | chr5:9304028-9304746 FORWARD | Aliases: None	5.8	6.3	-0.4	-1.6	46.2%	-0.4
12808	AT1G43940.1 | hypothetical protein | chr1:16668858-16670257 FORWARD | Aliases: F9C16.10, F9C16_10	2.3	2.4	-0.1	-1.6	46.2%	-1.1
12809	AT3G13510.1 | expressed protein, Pfam profile PF03080: Arabidopsis proteins of unknown function | chr3:4403516-4406098 FORWARD | Aliases: MRP15.17	3.6	3.2	0.4	1.6	46.3%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
12810	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	4.8	5.3	-0.5	-1.6	46.3%	-0.2
12811	AT2G20370.1 | Symbol: MUR3 | exostosin family protein, contains Pfam profile: PF03016	5.6	5.4	0.3	1.6	46.3%	-0.5
12812	AT1G11760.1 | expressed protein, weak similarity to Pfam PF01648: 4'-phosphopantetheinyl transferase superfamily | chr1:3970545-3973295 REVERSE | Aliases: F25C20.9, F25C20_9	3.2	3.0	0.2	1.6	46.3%	-0.7
12813	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	2.8	2.7	0.2	1.6	46.3%	-0.9
12814	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	8.9	9.4	-0.5	-1.6	46.3%	-0.5
12815	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	2.9	-0.3	-1.6	46.3%	-0.6
12816	AT1G23580.1 | expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220 | chr1:8357435-8358695 REVERSE | Aliases: F28C11.28	3.4	3.7	-0.3	-1.6	46.4%	-0.8
12817	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	3.0	-0.2	-1.6	46.4%	-1.0
12818	AT5G49150.1 | Symbol: GEX2 | hypothetical protein | chr5:19942160-19945753 FORWARD | Aliases: GENAMETE EXPRESSED2, K21P3.2, K21P3_2	2.7	3.0	-0.2	-1.6	46.4%	-0.9
12819	AT5G35250.1 | expressed protein, includes At2g05890, At4g07450, At3g30630, At3g43100, At2g09960, At3g30550, At1g39430, At2g10460, At4g03640, At5g35250	3.4	3.9	-0.5	-1.6	46.4%	-0.5
12820	AT4G35740.2 | DNA helicase (RECQl3), 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	6.1	5.5	0.7	1.6	46.4%	-0.0
12821	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	5.3	-0.3	-1.6	46.4%	-0.3
12822	AT5G22570.1 | Symbol: WRKY38 |	2.4	2.3	0.2	1.6	46.4%	-1.1
12823	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	4.9	0.5	1.6	46.4%	-0.2
12824	AT5G02940.1 | expressed protein | chr5:684536-689696 REVERSE | Aliases: F9G14.250, F9G14_250	2.9	2.7	0.2	1.6	46.4%	-0.8
12825	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	3.1	3.3	-0.2	-1.6	46.4%	-0.7
12826	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	5.6	5.0	0.5	1.6	46.4%	-0.2
12827	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	2.6	-0.1	-1.6	46.5%	-1.2
12828	AT3G01700.1 | Symbol: AGP11 | arabinogalactan-protein (AGP11), identical to gi:10880499:gb:AAG24279 | chr3:258886-259638 FORWARD | Aliases: F4P13.24, F4P13_24	2.3	2.5	-0.2	-1.6	46.5%	-1.1
12829	AT3G19220.1 | expressed protein | chr3:6659170-6660858 FORWARD | Aliases: MVI11.22	3.9	3.7	0.2	1.6	46.5%	-0.7
12830	AT5G16100.1 | expressed protein | chr5:5258554-5259722 REVERSE | Aliases: T21H19.20, T21H19_20	2.1	2.2	-0.1	-1.6	46.5%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
12831	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	3.4	3.0	0.4	1.6	46.5%	-0.2
12832	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 (Petunia x hybrida) (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	3.4	-0.4	-1.6	46.5%	-0.3
12833	AT2G47490.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr2:19494316-19496689 FORWARD | Aliases: T30B22.21	5.7	6.4	-0.6	-1.6	46.5%	-0.1
12834	AT1G17930.1 | expressed protein, similar to hypothetical protein GI:4559351 from (Arabidopsis thaliana) | chr1:6166213-6168832 REVERSE | Aliases: F2H15.15, F2H15_15	5.4	4.9	0.6	1.6	46.6%	0.0
12835	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	2.3	2.7	-0.3	-1.6	46.6%	-0.4
12836	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	8.6	0.3	1.6	46.6%	-0.6
12837	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	3.0	-0.2	-1.6	46.6%	-0.7
12838	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, T27I1.16, T27I1_16	4.6	5.1	-0.5	-1.6	46.6%	-0.2
12839	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	2.6	-0.2	-1.6	46.6%	-1.2
12840	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	2.7	3.0	-0.2	-1.6	46.6%	-0.5
12841	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	3.1	3.3	-0.2	-1.6	46.6%	-0.9
12842	AT3G56160.1 | expressed protein | chr3:20848423-20852520 REVERSE | Aliases: F18O21.120	3.6	3.4	0.2	1.6	46.6%	-0.9
12843	AT5G41800.1 | amino acid transporter family protein, similar to amino acid permease 1 (Nicotiana sylvestris) GI:976402; belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II | chr5:16751059-16753219 FORWARD | Aliases: K16L22.8, K16L22_8	6.0	5.7	0.3	1.6	46.6%	-0.1
12844	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	6.7	7.2	-0.4	-1.6	46.7%	-0.3
12845	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	7.8	8.3	-0.4	-1.6	46.7%	-0.1
12846	AT4G26750.1 | hydroxyproline-rich glycoprotein family protein | chr4:13475700-13478503 REVERSE | Aliases: F10M23.90, F10M23_90	5.6	5.3	0.2	1.6	46.7%	-0.8
12847	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	9.3	0.4	1.6	46.7%	-0.5
12848	AT3G30160.1 | expressed protein, similar to hypothetical protein GB:CAB55689 GI:5881771 from (Arabidopsis thaliana) | chr3:11787469-11787856 REVERSE | Aliases: T20F20.6	4.2	4.5	-0.3	-1.6	46.7%	-0.3
12849	AT3G01250.1 | expressed protein | chr3:79312-80112 FORWARD | Aliases: T4P13.6, T4P13_6	2.6	2.7	-0.2	-1.6	46.7%	-1.2
12850	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	2.9	3.1	-0.2	-1.6	46.7%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
12851	AT2G39130.1 | amino acid transporter family protein, belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II	3.3	3.6	-0.3	-1.6	46.7%	-0.5
12852	AT5G30500.1 | galactinol synthase, putative, similar to galactinol synthase, isoform GolS-1 GI:5608497 from (Ajuga reptans) | chr5:11632575-11634156 FORWARD | Aliases: None	2.6	2.5	0.2	1.6	46.8%	-0.9
12853	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	2.7	-0.2	-1.6	46.8%	-1.2
12854	AT5G54890.1 | expressed protein | chr5:22310572-22312370 FORWARD | Aliases: MBG8.16, MBG8_16	5.1	4.8	0.3	1.6	46.8%	-0.5
12855	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	2.7	2.9	-0.2	-1.6	46.8%	-0.8
12856	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	5.3	5.9	-0.6	-1.6	46.8%	-0.2
12857	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	4.5	4.0	0.4	1.6	46.8%	-0.5
12858	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	8.1	7.3	0.8	1.6	46.8%	-0.3
12859	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) (Mus musculus) | chr3:10052849-10054915 REVERSE | Aliases: K17E12.4	5.5	4.9	0.7	1.6	46.8%	0.0
12860	AT5G12230.1 | expressed protein | chr5:3953149-3956186 REVERSE | Aliases: MXC9.19, MXC9_19	6.6	5.5	1.1	1.6	46.8%	-0.2
12861	AT4G04490.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr4:2231955-2234636 REVERSE | Aliases: T26N6.10, T26N6_10	2.6	2.7	-0.2	-1.6	46.8%	-1.1
12862	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	4.1	3.8	0.3	1.6	46.8%	-0.6
12863	AT1G64910.1 | glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	3.3	3.4	-0.1	-1.6	46.8%	-1.1
12864	AT2G32380.1 | expressed protein | chr2:13753688-13754868 REVERSE | Aliases: T32F6.10, T32F6_10	3.9	4.3	-0.4	-1.6	46.8%	-0.3
12865	AT5G18475.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:6129257-6131017 REVERSE | Aliases: None	5.0	4.6	0.5	1.6	46.9%	-0.3
12866	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	2.3	2.4	-0.1	-1.6	46.9%	-1.2
12867	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	7.5	7.0	0.5	1.6	46.9%	-0.2
12868	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	2.7	3.1	-0.4	-1.6	46.9%	-0.2
12869	AT3G24070.1 | zinc knuckle (CCHC-type) family protein, contains Pfam profile: PF00098 zinc knuckle | chr3:8693092-8694716 FORWARD | Aliases: F14O13.27	4.5	4.9	-0.4	-1.6	46.9%	-0.3
12870	AT2G04360.1 | expressed protein | chr2:1519394-1521053 REVERSE | Aliases: T23O15.18	5.3	4.8	0.5	1.6	46.9%	-0.2
12871	AT4G16250.1 | Symbol: PHYD | phytochrome D (PHYD), nearly identical to SP:P42497 Phytochrome D {Arabidopsis thaliana}	4.0	4.2	-0.2	-1.6	46.9%	-0.5
12872	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	2.8	-0.2	-1.6	46.9%	-0.8
12873	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	2.6	-0.2	-1.6	46.9%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
12874	AT2G11490.1 | hypothetical protein | chr2:4611375-4612042 FORWARD | Aliases: F14P14.18, F14P14_18	2.3	2.6	-0.3	-1.6	46.9%	-0.6
12875	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	6.3	-0.3	-1.6	46.9%	-0.2
12876	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	2.7	-0.2	-1.6	46.9%	-0.8
12877	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	3.6	-0.3	-1.6	46.9%	-0.6
12878	AT3G26310.1 | Symbol: CYP71B35 | cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450 | chr3:9642326-9644016 REVERSE | Aliases: F20C19.3	3.4	3.8	-0.3	-1.6	46.9%	-0.4
12879	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	10.8	10.1	0.7	1.6	46.9%	-0.4
12880	AT5G64450.1 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537 | chr5:25789175-25789987 FORWARD | Aliases: T12B11.4, T12B11_4	4.2	4.7	-0.4	-1.6	46.9%	-0.0
12881	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	3.4	3.7	-0.3	-1.6	47.0%	-0.4
12882	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	3.5	3.3	0.2	1.6	47.0%	-0.9
12883	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	11.4	10.5	1.0	1.6	47.0%	0.1
12884	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	11.4	10.5	1.0	1.6	47.0%	0.1
12885	AT5G13880.1 | expressed protein | chr5:4477356-4478111 REVERSE | Aliases: MAC12.16, MAC12_16	3.9	3.6	0.2	1.6	47.0%	-0.5
12886	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	2.3	-0.1	-1.6	47.0%	-1.1
12887	AT4G10560.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	2.9	-0.2	-1.6	47.1%	-0.9
12888	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	5.2	0.3	1.6	47.1%	-0.1
12889	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)	7.1	6.9	0.3	1.6	47.1%	-0.3
12890	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	2.9	-0.1	-1.6	47.1%	-1.2
12891	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	2.7	2.9	-0.2	-1.6	47.1%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
12892	AT1G01840.1 | expressed protein | chr1:303537-304358 FORWARD | Aliases: T1N6.26, T1N6_26	4.7	4.2	0.4	1.6	47.1%	-0.3
12893	AT2G17550.1 | expressed protein | chr2:7641365-7644693 REVERSE | Aliases: MJB20.11, MJB20_11	4.5	4.7	-0.2	-1.6	47.1%	-0.7
12894	AT2G42400.1 | expressed protein | chr2:17661310-17663908 REVERSE | Aliases: MHK10.12, MHK10_12	3.1	3.4	-0.3	-1.6	47.1%	-0.5
12895	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	3.0	-0.1	-1.6	47.1%	-0.9
12896	AT5G61160.1 | Symbol: AACT1 | 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 | chr5:24625950-24627530 FORWARD | Aliases: AACT1, MAF19.17, MAF19_17	2.5	2.7	-0.2	-1.6	47.1%	-0.8
12897	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	3.2	-0.3	-1.6	47.1%	-0.8
12898	AT2G22480.1 | phosphofructokinase family protein, similar to phosphofructokinase (Amycolatopsis methanolica) GI:17432243; contains Pfam profile PF00365: Phosphofructokinase | chr2:9552656-9555643 FORWARD | Aliases: F14M13.12, F14M13_12	9.1	9.7	-0.6	-1.6	47.2%	-0.2
12899	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	8.0	6.6	1.3	1.6	47.2%	0.0
12900	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	2.8	-0.2	-1.6	47.2%	-1.0
12901	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	3.2	3.3	-0.2	-1.6	47.2%	-1.1
12902	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	5.5	5.9	-0.5	-1.6	47.2%	-0.2
12903	AT5G66290.1 | expressed protein | chr5:26495003-26496667 REVERSE | Aliases: K1L20.7, K1L20_7	4.8	5.2	-0.4	-1.6	47.3%	-0.3
12904	AT3G45730.1 | expressed protein | chr3:16800965-16801567 FORWARD | Aliases: T6D9.60	2.7	2.5	0.2	1.6	47.3%	-0.8
12905	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	11.3	10.8	0.5	1.6	47.3%	-0.7
12906	AT1G43920.1 | expressed protein | chr1:16662523-16663065 FORWARD | Aliases: F9C16.8, F9C16_8	4.0	4.4	-0.4	-1.6	47.3%	-0.2
12907	AT3G24270.1 | expressed protein | chr3:8796548-8797038 REVERSE | Aliases: K7M2.3	3.1	3.6	-0.5	-1.6	47.3%	-0.2
12908	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	3.4	-0.2	-1.6	47.3%	-0.9
12909	AT5G62500.1 | Symbol: ATEB1B |	4.8	5.4	-0.6	-1.6	47.3%	0.0
12910	AT3G46380.1 | expressed protein | chr3:17070203-17070881 REVERSE | Aliases: F18L15.100	5.1	5.9	-0.9	-1.6	47.3%	0.0
12911	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	4.4	-0.2	-1.6	47.3%	-0.8
12912	AT1G78600.1 | zinc finger (B-box type) family protein, similar to zinc finger protein GI:3618316 from (Oryza sativa) | chr1:29572104-29573752 FORWARD | Aliases: T30F21.7, T30F21_7	5.8	6.0	-0.2	-1.6	47.3%	-0.6
12913	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	2.7	-0.1	-1.6	47.4%	-1.1
12914	ATCG00560.1 | Symbol: PSBL | PSII L protein | chrC:63804-63920 REVERSE | Aliases: PSBL	7.6	6.4	1.1	1.6	47.4%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
12915	AT2G15640.1 | F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	3.0	3.2	-0.2	-1.6	47.4%	-0.9
12916	AT5G07620.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:2407402-2409067 REVERSE | Aliases: MBK20.5, MBK20_5	2.4	2.6	-0.2	-1.6	47.4%	-1.0
12917	AT3G48100.1 | Symbol: ARR5 | two-component responsive regulator / response regulator 5 (ARR5) / response reactor 2 (RR2), identical to responce 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	3.8	3.5	0.3	1.6	47.4%	-0.3
12918	AT3G05390.1 | expressed protein, ; expression supported by MPSS | chr3:1546591-1547982 REVERSE | Aliases: F22F7.17, F22F7_17	4.8	4.4	0.4	1.6	47.4%	-0.2
12919	AT3G06130.1 | heavy-metal-associated domain-containing protein, contains Pfam heavy metal associated domain PF00403 | chr3:1852899-1855035 REVERSE | Aliases: F28L1.7, F28L1_7	5.7	6.2	-0.5	-1.6	47.4%	-0.2
12920	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	2.5	2.7	-0.3	-1.6	47.4%	-0.9
12921	AT2G27380.1 | Symbol: ATEPR1 |	2.5	2.8	-0.2	-1.6	47.5%	-0.8
12922	AT3G49300.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr3:18287802-18288590 REVERSE | Aliases: F2K15.160	3.8	4.1	-0.3	-1.6	47.5%	-0.6
12923	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	4.1	3.7	0.4	1.6	47.5%	-0.2
12924	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	3.2	-0.2	-1.6	47.5%	-0.7
12925	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	3.2	-0.2	-1.6	47.5%	-0.7
12926	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	8.3	7.9	0.4	1.6	47.5%	-0.2
12927	AT2G41810.1 | expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642 | chr2:17446452-17448428 REVERSE | Aliases: T11A7.9, T11A7_9	3.0	3.3	-0.3	-1.6	47.5%	-0.5
12928	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	3.2	-0.2	-1.6	47.5%	-0.7
12929	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	3.5	-0.2	-1.6	47.5%	-0.5
12930	AT4G23320.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr4:12189192-12191636 REVERSE | Aliases: F16G20.20	2.8	3.1	-0.2	-1.6	47.5%	-0.8
12931	AT1G33710.1 | expressed protein, ; expression supported by MPSS | chr1:12219637-12220269 FORWARD | Aliases: F14M2.21, F14M2_21	2.2	2.3	-0.1	-1.6	47.6%	-1.2
12932	AT3G45820.1 | expressed protein | chr3:16851015-16851968 REVERSE | Aliases: F16L2.30	2.2	2.4	-0.2	-1.6	47.6%	-1.1
12933	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	4.9	4.6	0.3	1.6	47.6%	-0.3
12934	AT1G78810.2 | expressed protein | chr1:29633206-29635446 REVERSE | Aliases: F9K20.15, F9K20_15	7.5	7.0	0.5	1.6	47.6%	-0.1
12935	AT4G39680.1 | SAP domain-containing protein, contains Pfam domain PF02037: SAP domain | chr4:18414300-18417524 REVERSE | Aliases: T19P19.70, T19P19_70	4.0	4.8	-0.8	-1.6	47.6%	-0.1
12936	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	8.9	8.4	0.5	1.6	47.6%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
12937	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	4.3	4.7	-0.4	-1.6	47.6%	-0.4
12938	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	3.6	4.1	-0.5	-1.6	47.6%	-0.2
12939	AT5G22600.1 | expressed protein, ; expression supported by MPSS | chr5:7510026-7511635 FORWARD | Aliases: MDJ22.2, MDJ22_2	3.0	3.2	-0.2	-1.6	47.6%	-1.1
12940	AT5G25060.1 | RNA recognition motif (RRM)-containing protein, KIAA0332 - Homo sapiens, EMBL:AB002330 | chr5:8634077-8640220 REVERSE | Aliases: T11H3.70, T11H3_70	7.0	7.7	-0.7	-1.6	47.6%	-0.2
12941	AT1G39350.1 | expressed protein | chr1:14610274-14611094 REVERSE | Aliases: F12G6.5	3.3	3.6	-0.2	-1.6	47.7%	-0.9
12942	AT3G57280.1 | expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136) | chr3:21204820-21206695 FORWARD | Aliases: F28O9.130	9.9	9.6	0.3	1.6	47.7%	-0.4
12943	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	3.9	-0.4	-1.6	47.7%	-0.2
12944	AT2G46680.2 | Symbol: ATHB 7 |	6.7	7.7	-1.0	-1.6	47.7%	-0.0
12945	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	6.3	6.8	-0.5	-1.6	47.7%	-0.4
12946	AT1G28760.1 | expressed protein, ; expression supported by MPSS | chr1:10103144-10104574 FORWARD | Aliases: F1K23.6, F1K23_6	4.5	4.2	0.4	1.6	47.7%	-0.1
12947	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	3.2	-0.3	-1.6	47.7%	-0.7
12948	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	2.5	-0.1	-1.6	47.7%	-1.4
12949	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	3.0	3.3	-0.3	-1.6	47.7%	-0.6
12950	AT1G09220.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:2977794-2978970 REVERSE | Aliases: T12M4.7, T12M4_7	3.1	3.0	0.2	1.6	47.7%	-0.9
12951	AT3G58760.1 | ankyrin protein kinase, putative, similar to ankyrin-kinase (Medicago truncatula) gi:18700701:gb:AAL78674 | chr3:21739691-21742904 FORWARD | Aliases: T20N10.110	4.3	4.7	-0.4	-1.6	47.8%	-0.4
12952	AT3G27410.1 | expressed protein | chr3:10146481-10146879 REVERSE | Aliases: K1G2.12	2.2	2.3	-0.2	-1.6	47.8%	-1.0
12953	AT5G19500.1 | tryptophan/tyrosine permease family protein, contains Pfam profile PF03222: Tryptophan/tyrosine permease family | chr5:6578954-6581947 FORWARD | Aliases: T20D1.20, T20D1_20	3.9	3.6	0.3	1.6	47.8%	-0.4
12954	AT4G26920.1 | expressed protein | chr4:13525037-13527178 FORWARD | Aliases: F10M23.260, F10M23_260	4.2	4.4	-0.2	-1.6	47.8%	-0.9
12955	ATMG00650.1 | Symbol: NAD4L | Encodes NADH dehydrogenase subunit 4L. | chrM:188929-189231 REVERSE | Aliases: NAD4L	4.3	5.3	-1.0	-1.6	47.8%	-0.2
12956	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	3.0	3.3	-0.3	-1.6	47.8%	-0.8
12957	AT2G35080.1 | expressed protein, ; expression supported by MPSS | chr2:14796324-14798527 REVERSE | Aliases: T4C15.25, T4C15_25	3.9	4.2	-0.4	-1.6	47.8%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
12958	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	10.9	11.8	-0.8	-1.6	47.8%	-0.4
12959	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	3.0	2.8	0.2	1.6	47.8%	-0.7
12960	AT1G35513.1 | isochorismate synthase-related / isochirismate mutase-related, similar to SP:Q9S7H8 Isochorismate synthase 1, chloroplast precursor (EC 5.4.99.6) (IcsI) (Isochorismate mutase) (Salicylic acid induction deficient 2) (Sid2) (Enhanced disease susceptibility 16) (Eds16) {Arabidopsis thaliana} | chr1:13076823-13077491 FORWARD | Aliases: F15O4.44	4.3	4.0	0.3	1.6	47.8%	-0.7
12961	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	8.9	8.3	0.6	1.6	47.9%	-0.2
12962	AT1G09100.1 | 26S protease regulatory subunit 6A, putative, identical to SP:O04019 from (Arabidopsis thaliana)	7.3	6.7	0.6	1.6	47.9%	-0.2
12963	AT5G27860.1 | expressed protein | chr5:9874838-9876467 REVERSE | Aliases: F14I23.20, F14I23_20	2.7	3.3	-0.6	-1.6	47.9%	-0.1
12964	AT1G51270.1 | vesicle-associated membrane protein, putative / VAMP, putative, similar to VAP27 GI:6688926 (Nicotiana plumbaginifolia) | chr1:19011656-19013247 FORWARD | Aliases: F11M15.13, F11M15_13	3.2	3.5	-0.2	-1.6	47.9%	-0.5
12965	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	3.5	3.7	-0.3	-1.6	47.9%	-0.7
12966	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	2.1	2.2	-0.1	-1.6	47.9%	-1.3
12967	AT5G07460.1 | Symbol: PMSR2 | peptide methionine sulfoxide reductase, putative, similar to peptide methionine sulfoxide reductase (msr) (Arabidopsis thaliana) GI:4884033; contains Pfam profile PF01625: Peptide methionine sulfoxide reductase | chr5:2360635-2362014 REVERSE | Aliases: PEPTIDEMETHIONINE SULFOXIDE REDUCTASE 2, T2I1.170, T2I1_170	7.3	6.5	0.9	1.6	47.9%	0.0
12968	AT5G03090.1 | expressed protein | chr5:725280-725961 FORWARD | Aliases: F15A17.120, F15A17_120	3.7	3.9	-0.2	-1.6	48.0%	-0.8
12969	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	3.0	0.2	1.6	48.0%	-0.9
12970	AT5G06960.2 | Symbol: OBF5 | bZIP family transcription factor (OBF5), identical to bZIP family transcription factor (OBF5) GI:414615 from (Arabidopsis thaliana) | chr5:2154823-2157647 FORWARD | Aliases: MOJ9.13, MOJ9_13, OBF5, OCS ELEMENT BINDING FACTOR 5, TGA5	5.8	6.2	-0.4	-1.6	48.0%	-0.0
12971	AT4G18500.1 | expressed protein | chr4:10209159-10209422 REVERSE | Aliases: F28J12.160, F28J12_160	3.3	3.6	-0.3	-1.6	48.0%	-0.7
12972	AT5G01200.1 | myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA binding domain | chr5:77115-78542 FORWARD | Aliases: F7J8.180, F7J8_180	3.7	4.0	-0.2	-1.6	48.0%	-0.5
12973	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	4.5	4.1	0.5	1.6	48.0%	-0.3
12974	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	2.5	-0.1	-1.6	48.0%	-1.2
12975	AT1G67635.1 | expressed protein | chr1:25353483-25353815 FORWARD | Aliases: F12A21.23, F12A21_23	2.5	2.7	-0.2	-1.6	48.0%	-0.9
12976	AT4G12770.1 | auxilin-related, low similarity to SP:Q27974 Auxilin {Bos taurus} | chr4:7506378-7511563 REVERSE | Aliases: T20K18.120, T20K18_120	3.8	4.3	-0.5	-1.6	48.0%	0.1
12977	AT5G55670.1 | RNA recognition motif (RRM)-containing protein | chr5:22561166-22564027 REVERSE | Aliases: MDF20.11, MDF20_11	5.6	5.9	-0.3	-1.6	48.1%	-0.3
12978	AT1G59780.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.1	3.3	-0.2	-1.6	48.1%	-0.6
12979	AT1G58265.1 | cytochrome P450-related | chr1:21614574-21615053 FORWARD | Aliases: None	2.3	2.5	-0.2	-1.6	48.1%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
12980	NA	10.9	11.2	-0.4	-1.6	48.1%	-1.2
12981	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	1.8	2.2	-0.3	-1.6	48.1%	-0.5
12982	AT3G33520.1 | Symbol: ATARP6 |	6.4	7.0	-0.6	-1.6	48.1%	-0.1
12983	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	2.8	3.0	-0.2	-1.6	48.1%	-0.7
12984	AT5G25210.1 | expressed protein | chr5:8723961-8725774 FORWARD | Aliases: F21J6.105, F21J6_105	3.1	3.3	-0.2	-1.6	48.1%	-0.7
12985	AT1G33000.1 | hypothetical protein | chr1:11957948-11958142 FORWARD | Aliases: F9L11.26, F9L11_26	2.6	2.8	-0.3	-1.6	48.1%	-0.9
12986	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	4.3	4.8	-0.5	-1.6	48.1%	0.0
12987	AT3G23605.1 | UBX domain-containing protein, contains Pfam profile PF00789: UBX domain	6.2	5.8	0.5	1.6	48.1%	-0.2
12988	AT3G14510.1 | geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltranstransferase, putative, similar to gi:9294375; similar to geranylgeranyl pyrophosphate synthetase GB:P34802 (Arabidopsis thaliana) | chr3:4867385-4868421 REVERSE | Aliases: MOA2.15	3.6	3.9	-0.3	-1.6	48.2%	-0.6
12989	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	4.1	4.5	-0.5	-1.6	48.2%	-0.3
12990	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	2.4	-0.1	-1.6	48.2%	-1.1
12991	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	6.0	6.4	-0.4	-1.6	48.2%	-0.2
12992	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	5.7	6.2	-0.4	-1.6	48.2%	-0.0
12993	AT2G20720.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam TIGR00756: pentatricopeptide repeat domain | chr2:8934903-8937193 REVERSE | Aliases: F5H14.31, F5H14_31	4.7	4.1	0.6	1.6	48.2%	-0.1
12994	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	4.3	-0.3	-1.6	48.2%	-0.3
12995	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	2.5	-0.2	-1.6	48.2%	-1.4
12996	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	10.1	1.0	1.6	48.2%	-0.6
12997	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	3.6	4.1	-0.5	-1.6	48.2%	-0.4
12998	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	2.7	-0.2	-1.6	48.2%	-0.9
12999	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	3.1	-0.2	-1.6	48.2%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
13000	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	2.2	-0.1	-1.6	48.2%	-1.3
13001	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	2.7	-0.3	-1.6	48.2%	-0.4
13002	AT4G37880.1 | expressed protein | chr4:17809697-17811574 FORWARD | Aliases: T28I19.160, T28I19_160	5.8	6.4	-0.6	-1.6	48.2%	-0.5
13003	AT4G17840.1 | expressed protein | chr4:9918067-9920488 REVERSE | Aliases: T6K21.20, T6K21_20	6.7	6.2	0.5	1.6	48.3%	-0.0
13004	AT2G16020.1 | hypothetical protein, and genefinder | chr2:6980438-6980668 FORWARD | Aliases: F7H1.4, F7H1_4	3.4	3.6	-0.2	-1.6	48.3%	-1.0
13005	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	6.1	6.5	-0.4	-1.6	48.3%	-0.5
13006	AT3G19020.1 | 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	2.2	2.3	-0.1	-1.6	48.3%	-1.4
13007	AT3G11020.1 | Symbol: DREB2B |	4.7	4.5	0.2	1.6	48.3%	-0.7
13008	AT2G39570.1 | ACT domain-containing protein, contains Pfam ACT domain PF01842 | chr2:16514974-16517276 FORWARD | Aliases: F12L6.23, F12L6_23	6.3	6.8	-0.6	-1.6	48.3%	-0.2
13009	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	3.0	-0.2	-1.6	48.3%	-0.9
13010	AT4G02910.1 | expressed protein | chr4:1288486-1289615 REVERSE | Aliases: T4I9.21	3.4	3.9	-0.5	-1.6	48.3%	-0.3
13011	AT5G56330.1 | carbonic anhydrase family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; contains Pfam profile PF00194: Eukaryotic-type carbonic anhydrase	2.3	2.4	-0.1	-1.6	48.3%	-1.0
13012	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	3.3	0.5	1.6	48.3%	-0.4
13013	AT3G43900.1 | hypothetical protein, predicted protein, Arabidopsis thaliana | chr3:15757827-15758081 FORWARD | Aliases: T15B3.40	3.2	3.6	-0.4	-1.6	48.3%	-0.3
13014	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	3.3	3.5	-0.3	-1.6	48.3%	-0.4
13015	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	4.7	5.1	-0.4	-1.6	48.3%	-0.5
13016	AT5G49390.1 | expressed protein | chr5:20045228-20047286 FORWARD | Aliases: K7J8.6, K7J8_6	3.5	3.3	0.2	1.6	48.4%	-0.5
13017	AT4G17200.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.7	2.9	-0.2	-1.6	48.4%	-0.9
13018	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	6.0	6.4	-0.4	-1.6	48.4%	-0.4
13019	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	5.4	5.8	-0.4	-1.6	48.4%	-0.2
13020	AT5G62990.1 | Symbol: EMB1692 | expressed protein | chr5:25295054-25296538 FORWARD | Aliases: EMB1692, EMBRYO DEFECTIVE 1692, MJH22.4, MJH22_4	3.3	3.1	0.3	1.6	48.4%	-0.9
13021	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	2.6	0.2	1.6	48.4%	-0.6
13022	AT3G47810.3 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	11.7	11.1	0.5	1.6	48.4%	-0.7

Rank	Description	Sync	Root	M	t	adj.q	B
13023	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	5.6	5.1	0.6	1.6	48.4%	-0.2
13024	AT5G43000.1 | expressed protein | chr5:17263582-17264430 REVERSE | Aliases: MBD2.20, MBD2_20	2.7	2.9	-0.2	-1.6	48.4%	-0.7
13025	AT5G35160.1 | endomembrane protein 70, putative, p76, Homo sapiens, EMBL:HSU81006 | chr5:13432184-13434151 FORWARD | Aliases: T25C13.40, T25C13_40	6.6	7.1	-0.5	-1.6	48.4%	-0.3
13026	AT1G04670.1 | expressed protein, ; expression supported by MPSS | chr1:1301984-1302531 FORWARD | Aliases: T1G11.23, T1G11_23	3.1	3.2	-0.1	-1.6	48.4%	-1.4
13027	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	6.4	6.1	0.4	1.6	48.4%	-0.2
13028	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	4.0	-0.2	-1.6	48.4%	-0.8
13029	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	5.3	0.6	1.6	48.4%	-0.3
13030	AT3G19120.1 | expressed protein | chr3:6609418-6611065 REVERSE | Aliases: MVI11.2	4.2	3.8	0.4	1.6	48.4%	-0.3
13031	AT3G45380.1 | hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287 | chr3:16655506-16658157 REVERSE | Aliases: F18N11.140	3.1	3.3	-0.2	-1.6	48.4%	-1.3
13032	AT5G54870.1 | expressed protein, strong similarity to unknown protein (pir::T04825) | chr5:22306361-22309025 FORWARD | Aliases: MBG8.14, MBG8_14	9.2	9.7	-0.6	-1.6	48.4%	-0.5
13033	AT4G11720.1 | expressed protein | chr4:7063285-7066778 FORWARD | Aliases: T5C23.150, T5C23_150	2.7	2.5	0.2	1.6	48.4%	-0.8
13034	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	3.2	3.5	-0.3	-1.6	48.4%	-0.6
13035	AT1G51260.1 | Symbol: LPAT3 | acyl-CoA:1-acylglycerol-3-phosphate acyltransferase, putative, similar to acyl-CoA:1-acylglycerol-3-phosphate acyltransferase GI:4583544 from (Brassica napus) | chr1:19007044-19009309 REVERSE | Aliases: F11M15.12, F11M15_12	3.3	3.7	-0.4	-1.6	48.5%	-0.4
13036	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	4.8	5.1	-0.3	-1.6	48.5%	-0.5
13037	AT1G67020.1 | hypothetical protein | chr1:25014671-25016650 REVERSE | Aliases: F1O19.7, F1O19_7	3.4	3.2	0.2	1.6	48.5%	-0.7
13038	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	2.1	2.2	-0.1	-1.6	48.5%	-1.3
13039	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	7.0	6.3	0.6	1.6	48.5%	-0.3
13040	AT3G28590.1 | expressed protein | chr3:10719557-10719919 FORWARD | Aliases: MZN14.7	6.2	6.6	-0.4	-1.6	48.5%	-0.4
13041	AT3G55590.1 | GDP-mannose pyrophosphorylase, putative, strong similarity to GDP-mannose pyrophosphorylase from Arabidopsis thaliana (GI:3598958), Pichia angusta (GI:7331158); contains Pfam profile PF00483 Nucleotidyl transferase | chr3:20628458-20629860 FORWARD | Aliases: F1I16.2	3.1	3.4	-0.3	-1.6	48.5%	-0.6
13042	AT5G01020.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:5916-8443 REVERSE | Aliases: F7J8.5, F7J8_5	7.4	6.9	0.6	1.6	48.5%	-0.4
13043	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	6.4	7.0	-0.6	-1.6	48.6%	-0.1
13044	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	6.8	6.5	0.3	1.6	48.6%	-0.3
13045	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	5.2	4.8	0.3	1.6	48.6%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
13046	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	3.9	3.6	0.4	1.6	48.6%	-0.4
13047	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	3.3	3.7	-0.4	-1.6	48.6%	-0.5
13048	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	12.0	11.7	0.3	1.6	48.6%	-0.8
13049	AT4G02720.1 | expressed protein, temporary automated functional assignment | chr4:1204303-1205866 REVERSE | Aliases: T5J8.1	8.6	8.0	0.6	1.6	48.7%	-0.2
13050	AT1G79540.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:29925227-29927569 REVERSE | Aliases: T8K14.4, T8K14_4	3.8	3.5	0.3	1.6	48.7%	-0.4
13051	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	2.7	-0.2	-1.6	48.7%	-1.0
13052	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	3.2	3.5	-0.3	-1.6	48.7%	-0.9
13053	AT1G73970.1 | expressed protein | chr1:27820475-27823735 FORWARD | Aliases: F2P9.16, F2P9_16	6.1	5.8	0.3	1.6	48.7%	-0.2
13054	AT5G04540.1 | expressed protein | chr5:1296443-1302429 REVERSE | Aliases: T32M21.150, T32M21_150	6.8	7.3	-0.5	-1.6	48.7%	-0.2
13055	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	2.8	-0.2	-1.6	48.8%	-0.9
13056	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	11.2	10.8	0.4	1.6	48.8%	-0.7
13057	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	2.2	-0.1	-1.6	48.9%	-1.5
13058	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	2.6	2.7	-0.2	-1.6	48.9%	-1.0
13059	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	2.7	2.9	-0.3	-1.6	48.9%	-0.8
13060	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	2.7	2.9	-0.3	-1.6	48.9%	-0.8
13061	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	5.5	5.2	0.3	1.6	48.9%	-0.4
13062	AT4G03480.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023 | chr4:1546022-1548869 REVERSE | Aliases: F9H3.11, F9H3_11	2.6	2.9	-0.3	-1.6	48.9%	-0.8
13063	AT5G28940.1 | hypothetical protein | chr5:10985292-10987604 REVERSE | Aliases: F3F24.40, F3F24_40	2.3	2.5	-0.2	-1.6	48.9%	-1.0
13064	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	3.7	4.0	-0.3	-1.6	49.0%	-0.7
13065	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	5.0	4.7	0.3	1.6	49.0%	-0.3
13066	AT2G05530.1 | glycine-rich protein | chr2:2029709-2030541 FORWARD | Aliases: T20G20.12, T20G20_12	5.4	4.9	0.5	1.6	49.0%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
13067	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)	9.6	10.1	-0.6	-1.6	49.0%	-0.5
13068	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	4.1	-0.3	-1.6	49.0%	-0.4
13069	AT4G15545.1 | expressed protein | chr4:8875918-8877755 FORWARD | Aliases: None	8.6	7.6	1.0	1.6	49.0%	-0.1
13070	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	5.6	6.0	-0.4	-1.6	49.0%	-0.5
13071	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	2.4	-0.2	-1.6	49.0%	-1.1
13072	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	2.9	0.2	1.6	49.0%	-0.7
13073	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	5.2	0.3	1.6	49.0%	-0.7
13074	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	5.1	4.7	0.3	1.6	49.0%	-0.3
13075	AT5G64180.1 | expressed protein | chr5:25694306-25695518 FORWARD | Aliases: MSJ1.2, MSJ1_2	5.3	5.7	-0.4	-1.6	49.0%	-0.4
13076	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	4.1	-0.3	-1.6	49.0%	-0.5
13077	AT2G19600.1 | Symbol: ATKEA4 |	4.5	4.2	0.3	1.6	49.1%	-0.6
13078	AT5G10020.1 | leucine-rich repeat transmembrane protein kinase, putative, receptor-like protein kinase ERECTA, Arabidopsis thaliana, EMBL:AC004484 | chr5:3133262-3137243 FORWARD | Aliases: T31P16.10, T31P16_10	3.2	3.6	-0.3	-1.6	49.1%	-0.3
13079	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	3.0	-0.2	-1.6	49.1%	-0.7
13080	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	8.2	7.6	0.7	1.6	49.1%	-0.3
13081	AT3G45320.1 | hypothetical protein | chr3:16642631-16643131 FORWARD | Aliases: F18N11.80	2.3	2.4	-0.2	-1.6	49.2%	-1.1
13082	AT5G53710.1 | expressed protein | chr5:21822485-21823020 REVERSE | Aliases: MGN6.6, MGN6_6	4.0	4.4	-0.4	-1.6	49.2%	-0.2
13083	AT5G48080.1 | expressed protein, ; expression supported by MPSS | chr5:19501391-19502198 FORWARD | Aliases: MDN11.16, MDN11_16	4.4	4.9	-0.5	-1.6	49.3%	-0.4
13084	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	5.9	5.5	0.4	1.6	49.3%	-0.1
13085	AT3G15030.2 | Symbol: TCP4 | TCP family transcription factor, putative, similar to TCP3 GB:AAC24010 (Arabidopsis thaliana) | chr3:5062026-5064045 FORWARD | Aliases: K15M2.17	4.1	3.8	0.3	1.6	49.3%	-0.4
13086	AT2G04063.1 | glycine-rich protein | chr2:1349755-1350174 REVERSE | Aliases: F3L12.1, F3L12_1	4.6	5.1	-0.5	-1.6	49.3%	-0.4
13087	AT2G23180.1 | Symbol: CYP96A1 | cytochrome P450, putative | chr2:9881987-9883674 FORWARD | Aliases: T20D16.19, T20D16_19	2.9	3.1	-0.2	-1.6	49.3%	-0.8
13088	AT3G03800.1 | Symbol: SYP131 |	3.3	3.5	-0.2	-1.6	49.3%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
13089	AT1G74800.1 | galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase | chr1:28105629-28108773 REVERSE | Aliases: F25A4.23, F25A4_23	4.6	4.2	0.4	1.6	49.4%	-0.2
13090	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	3.6	3.3	0.3	1.6	49.4%	-0.5
13091	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	4.0	-0.4	-1.6	49.4%	-0.6
13092	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 OSJNBb0103I08.15 [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	4.5	4.1	0.4	1.6	49.4%	-0.2
13093	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	3.6	-0.2	-1.6	49.4%	-0.8
13094	AT1G66110.1 | expressed protein, contains Pfam profile PF04510: Family of unknown function (DUF577) | chr1:24612757-24613895 REVERSE | Aliases: F15E12.15, F15E12_15	3.7	4.0	-0.3	-1.6	49.4%	-0.5
13095	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	5.3	4.8	0.5	1.6	49.5%	-0.4
13096	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	5.1	4.5	0.6	1.6	49.5%	0.1
13097	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	2.4	2.5	-0.2	-1.6	49.5%	-1.0
13098	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	5.7	5.3	0.4	1.6	49.5%	-0.2
13099	AT5G66670.1 | hypothetical protein, contains Pfam:PF05055: Protein of unknown function (DUF677) | chr5:26628700-26629926 REVERSE | Aliases: MSN2.5, MSN2_5	3.2	3.6	-0.4	-1.6	49.5%	-0.6
13100	AT4G14810.1 | expressed protein | chr4:8504140-8504504 FORWARD | Aliases: DL3445W, FCAALL.327	3.9	4.2	-0.3	-1.6	49.5%	-0.6
13101	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	3.5	4.1	-0.6	-1.6	49.5%	-0.1
13102	AT5G17960.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.9	3.1	-0.3	-1.6	49.5%	-0.6
13103	AT2G44930.1 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function | chr2:18536598-18538827 REVERSE | Aliases: T13E15.6	3.3	3.6	-0.3	-1.6	49.5%	-0.7
13104	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	2.6	-0.2	-1.6	49.6%	-1.4
13105	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	8.0	7.3	0.7	1.6	49.6%	-0.2
13106	AT3G53080.1 | galactose-binding lectin family protein, contains Pfam domain PF02140: Galactose binding lectin domain | chr3:19688974-19689717 FORWARD | Aliases: T4D2.10	2.3	2.4	-0.2	-1.6	49.7%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
13107	AT1G35720.1 | Symbol: ANNAT1 |	11.1	10.0	1.1	1.6	49.7%	0.1
13108	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	7.1	6.5	0.6	1.6	49.8%	-0.2
13109	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	3.2	3.4	-0.3	-1.6	49.8%	-0.6
13110	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	5.8	5.4	0.4	1.6	49.8%	-0.3
13111	AT1G02490.1 | hypothetical protein | chr1:516618-516734 FORWARD | Aliases: T14P4.35, T14P4_35	2.7	2.9	-0.2	-1.6	49.8%	-0.7
13112	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	3.3	0.2	1.6	49.8%	-0.5
13113	AT4G03570.1 | expressed protein | chr4:1590411-1594103 REVERSE | Aliases: T5L23.6, T5L23_6	3.4	3.6	-0.3	-1.6	49.9%	-0.8
13114	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	5.2	5.4	-0.2	-1.6	49.9%	-0.6
13115	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	3.9	-0.3	-1.6	49.9%	-0.9
13116	AT1G57590.1 | similar to pectinacetylesterase, putative [Arabidopsis thaliana] (TAIR:At5g26670.1); similar to putative pectinacetylesterase precursor [Oryza sativa (japonica cultivar-group)] (GB:NP_918013.1); contains InterPro domain Pectinacetylesterase (InterPro:IPR004963) | chr1:21331025-21333427 REVERSE | Aliases: T8L23.6, T8L23_6	3.9	3.6	0.3	1.6	49.9%	-0.4
13117	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	6.8	7.3	-0.4	-1.6	49.9%	-0.1
13118	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	5.6	-0.2	-1.6	50.0%	-0.7
13119	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	2.9	-0.2	-1.6	50.0%	-0.9
13120	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	4.3	4.7	-0.4	-1.6	50.0%	-0.2
13121	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	2.5	-0.2	-1.6	50.0%	-0.9
13122	AT4G32030.2 | expressed protein | chr4:15490778-15493342 FORWARD | Aliases: F10N7.160, F10N7_160	3.1	3.5	-0.4	-1.6	50.0%	-0.5
13123	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	3.9	3.6	0.3	1.6	50.0%	-0.5
13124	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	9.1	9.9	-0.8	-1.6	50.0%	-0.2
13125	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	4.0	4.3	-0.3	-1.6	50.0%	-0.8
13126	AT1G06830.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	3.6	3.2	0.4	1.6	50.1%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
13127	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	7.4	7.7	-0.4	-1.6	50.1%	-0.4
13128	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	6.5	6.0	0.5	1.6	50.1%	0.0
13129	AT5G05230.1 | expressed protein | chr5:1551389-1553806 FORWARD | Aliases: K18I23.3, K18I23_3	3.5	3.2	0.3	1.6	50.1%	-0.5
13130	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	6.3	6.0	0.3	1.6	50.1%	-0.3
13131	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	7.2	6.8	0.5	1.6	50.2%	-0.2
13132	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	5.0	4.5	0.5	1.6	50.2%	-0.3
13133	AT2G46510.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.9	3.6	0.3	1.6	50.2%	-0.6
13134	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	3.7	3.9	-0.3	-1.6	50.2%	-0.5
13135	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	3.3	3.5	-0.3	-1.6	50.2%	-0.5
13136	AT2G04039.2 | expressed protein | chr2:1333268-1334563 FORWARD | Aliases: F3L12.11, F3L12_11	3.0	2.8	0.2	1.6	50.2%	-0.8
13137	AT2G13550.1 | expressed protein | chr2:5655624-5656879 REVERSE | Aliases: T10F5.9, T10F5_9	3.0	3.3	-0.3	-1.6	50.2%	-0.8
13138	AT5G24130.1 | expressed protein | chr5:8162222-8164069 FORWARD | Aliases: MLE8.5, MLE8_5	3.1	3.4	-0.3	-1.6	50.2%	-0.6
13139	AT4G11490.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr4:6978843-6981543 FORWARD | Aliases: F25E4.110, F25E4_110	2.3	2.4	-0.1	-1.6	50.2%	-1.3
13140	AT3G57750.2 | similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:At3g57700.1); similar to OSJNBa0083N12.1 [Oryza sativa (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	6.1	-0.3	-1.6	50.2%	-0.4
13141	AT3G42240.1 | expressed protein | chr3:14408316-14409279 REVERSE | Aliases: F26B15.40	3.3	3.7	-0.4	-1.6	50.2%	-0.4
13142	AT4G31100.1 | wall-associated kinase, putative	3.6	3.3	0.3	1.6	50.2%	-0.8
13143	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	3.9	3.7	0.2	1.6	50.2%	-0.8
13144	NA	11.5	10.8	0.7	1.6	50.3%	-0.6
13145	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	4.8	0.3	1.6	50.3%	-0.4
13146	AT1G69580.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr1:26175802-26177275 FORWARD | Aliases: F24J1.30, F24J1_30	4.7	5.5	-0.7	-1.6	50.3%	-0.1
13147	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	3.6	0.2	1.6	50.3%	-0.9
13148	AT5G11080.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr5:3517450-3519450 REVERSE | Aliases: T5K6.70, T5K6_70	3.2	3.5	-0.3	-1.6	50.3%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
13149	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	5.9	6.3	-0.4	-1.6	50.3%	-0.4
13150	AT5G47490.1 | expressed protein | chr5:19281902-19288027 FORWARD | Aliases: MNJ7.8, MNJ7_8	2.9	2.6	0.2	1.6	50.4%	-0.6
13151	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	4.0	-0.5	-1.6	50.4%	-0.3
13152	AT4G19095.1 | expressed protein | chr4:10452903-10453532 REVERSE | Aliases: None	3.1	3.3	-0.3	-1.6	50.4%	-0.6
13153	AT3G59010.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr3:21813782-21816191 REVERSE | Aliases: F17J16.60	4.2	3.8	0.4	1.6	50.4%	-0.4
13154	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	2.8	0.2	1.6	50.4%	-1.1
13155	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	3.5	-0.4	-1.6	50.4%	-0.4
13156	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	4.5	4.8	-0.3	-1.6	50.4%	-0.5
13157	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	5.3	5.0	0.3	1.6	50.4%	-0.2
13158	AT1G76240.1 | expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function | chr1:28607707-28608822 REVERSE | Aliases: T23E18.17, T23E18_17	2.9	3.1	-0.2	-1.6	50.5%	-0.5
13159	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	3.9	-0.3	-1.6	50.5%	-0.3
13160	AT3G62360.1 | expressed protein | chr3:23083761-23091518 REVERSE | Aliases: T12C14.60	8.0	7.4	0.5	1.6	50.5%	-0.3
13161	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	5.6	5.0	0.6	1.6	50.5%	-0.1
13162	AT2G25780.1 | hypothetical protein | chr2:11002247-11003001 FORWARD | Aliases: F17H15.19, F17H15_19	3.1	3.3	-0.2	-1.6	50.5%	-1.2
13163	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	3.4	3.7	-0.3	-1.6	50.6%	-0.7
13164	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	6.2	5.8	0.4	1.6	50.6%	-0.3
13165	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	5.5	6.0	-0.5	-1.6	50.6%	-0.2
13166	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	3.5	3.8	-0.3	-1.6	50.6%	-0.6
13167	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	2.8	-0.2	-1.6	50.6%	-0.9
13168	AT3G22940.1 | F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain | chr3:8131475-8132713 FORWARD | Aliases: F5N5.12	3.8	4.0	-0.3	-1.6	50.6%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
13169	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	4.9	4.4	0.5	1.6	50.6%	-0.1
13170	AT2G31110.1 | expressed protein | chr2:13265406-13266629 REVERSE | Aliases: T16B12.8, T16B12_8	7.0	6.6	0.3	1.6	50.6%	-0.5
13171	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	7.6	6.9	0.7	1.6	50.6%	-0.2
13172	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	7.7	8.0	-0.3	-1.6	50.6%	-0.4
13173	AT4G14960.2 | Symbol: TUA6 | tubulin alpha-6 chain (TUA6), nearly identical to SP:P29511 Tubulin alpha-6 chain {Arabidopsis thaliana}	6.1	3.7	2.4	1.6	50.7%	-0.2
13174	AT4G33660.1 | expressed protein | chr4:16167292-16167954 REVERSE | Aliases: T16L1.2	5.7	5.4	0.3	1.6	50.7%	-0.5
13175	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	3.2	-0.2	-1.6	50.7%	-0.8
13176	AT4G31740.1 | expressed protein, weak similarity to r-sly1 (Rattus norvegicus) GI:1144569 | chr4:15363784-15364355 FORWARD | Aliases: F28M20.70, F28M20_70	2.4	2.6	-0.2	-1.6	50.7%	-0.8
13177	AT1G76910.1 | expressed protein | chr1:28892112-28892998 FORWARD | Aliases: F22K20.20, F22K20_20	3.2	3.5	-0.3	-1.6	50.7%	-0.3
13178	AT5G64510.1 | expressed protein | chr5:25801630-25803533 FORWARD | Aliases: MUB3.3, MUB3_3	5.3	4.7	0.5	1.6	50.7%	-0.1
13179	AT2G33880.1 | Symbol: WOX9 | homeobox-leucine zipper family protein | chr2:14348509-14350835 REVERSE | Aliases: HB 3, STIMPY, STIP, T1B8.31, T1B8_31	3.4	3.8	-0.4	-1.6	50.8%	-0.5
13180	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	3.2	0.2	1.6	50.8%	-0.7
13181	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	2.2	-0.1	-1.6	50.8%	-1.4
13182	AT4G17870.1 | expressed protein | chr4:9928691-9929531 FORWARD | Aliases: T6K21.50, T6K21_50	7.3	7.9	-0.6	-1.6	50.8%	-0.2
13183	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	2.8	-0.2	-1.6	50.8%	-0.9
13184	AT1G28120.1 | expressed protein | chr1:9812952-9815528 REVERSE | Aliases: F13K9.21, F13K9_21	8.2	8.5	-0.3	-1.6	50.9%	-0.6
13185	AT1G74480.1 | RWP-RK domain-containing protein, contains Pfam profile: PF02042 RWP-RK domain | chr1:27996693-27997839 REVERSE | Aliases: F1M20.16, F1M20_16	2.7	2.9	-0.2	-1.6	50.9%	-1.1
13186	AT3G25420.1 | Symbol: SCPL21 |	3.2	3.6	-0.4	-1.6	50.9%	-0.4
13187	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	3.3	-0.3	-1.5	50.9%	-0.4
13188	AT1G01230.1 | ORMDL family protein, contains Pfam domain PF04061: ORMDL family	8.6	8.1	0.5	1.5	50.9%	-0.5
13189	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	6.3	6.8	-0.4	-1.5	50.9%	-0.3
13190	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	7.5	0.7	1.5	50.9%	-0.0
13191	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	4.5	4.1	0.4	1.5	50.9%	-0.3

Rank	Description	Sync	Root	M	t	adj.q	B
13192	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	3.1	-0.2	-1.5	50.9%	-0.8
13193	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	5.6	5.1	0.5	1.5	51.0%	-0.1
13194	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	3.0	3.3	-0.3	-1.5	51.0%	-0.4
13195	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	4.4	4.9	-0.5	-1.5	51.0%	-0.3
13196	AT5G15120.1 | expressed protein | chr5:4898740-4900575 FORWARD | Aliases: F2G14.1	7.6	7.2	0.4	1.5	51.0%	-0.4
13197	AT3G47610.1 | expressed protein | chr3:17560106-17562405 FORWARD | Aliases: F1P2.160	6.9	7.4	-0.6	-1.5	51.0%	-0.1
13198	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	2.7	2.9	-0.2	-1.5	51.0%	-1.2
13199	ATMG00680.1 | Symbol: ORF122C | hypothetical protein | chrM:201729-202097 FORWARD | Aliases: ORF122C	2.6	2.9	-0.3	-1.5	51.0%	-0.7
13200	AT2G44570.1 | glycosyl hydrolase family 9 protein | chr2:18401318-18403344 REVERSE | Aliases: F16B22.6	2.8	3.0	-0.2	-1.5	51.1%	-0.7
13201	AT3G02000.1 | Symbol: ROXY1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase) | chr3:332282-332992 REVERSE | Aliases: F1C9.22	4.5	4.8	-0.4	-1.5	51.1%	-0.4
13202	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	3.1	-0.3	-1.5	51.1%	-0.7
13203	AT1G36020.1 | hypothetical protein | chr1:13435131-13435552 REVERSE | Aliases: T22A15.6, T22A15_6	3.4	3.8	-0.4	-1.5	51.1%	-0.7
13204	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	9.0	9.7	-0.7	-1.5	51.2%	-0.4
13205	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	8.2	7.0	1.1	1.5	51.2%	-0.1
13206	AT3G57720.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr3:21398699-21400703 FORWARD | Aliases: F15B8.90	3.0	3.2	-0.2	-1.5	51.2%	-0.9
13207	AT5G20620.1 | Symbol: UBQ4 | polyubiquitin (UBQ4), identical to GI:17677 | chr5:6973073-6974945 REVERSE | Aliases: T1M15.20, T1M15_20	8.2	7.6	0.7	1.5	51.2%	-0.1
13208	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	3.2	-0.2	-1.5	51.2%	-0.8
13209	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	3.2	-0.2	-1.5	51.2%	-0.8
13210	AT4G30993.2 | expressed protein | chr4:15098073-15100564 FORWARD | Aliases: None	4.3	4.0	0.3	1.5	51.2%	-0.5
13211	AT5G40750.1 | expressed protein | chr5:16325584-16327047 FORWARD | Aliases: MNF13.30, MNF13_30	2.2	2.3	-0.1	-1.5	51.2%	-1.5
13212	AT1G29090.1 | peptidase C1A papain family protein, contains similarity to cysteine protease SPCP1 GI:13491750 from (Ipomoea batatas); contains Pfam profile PF00112: Papain family cysteine protease | chr1:10162969-10164438 REVERSE | Aliases: F28N24.20, F28N24_20	3.3	3.6	-0.3	-1.5	51.2%	-0.6
13213	AT1G05540.1 | expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295) | chr1:1639285-1640810 FORWARD | Aliases: T25N20.19	4.3	4.7	-0.4	-1.5	51.2%	-0.4
13214	AT3G44370.1 | expressed protein, weak similarity to AtOXA1 (Arabidopsis thaliana) GI:6624207 | chr3:16044274-16046134 REVERSE | Aliases: T22K7.50	3.1	3.3	-0.2	-1.5	51.2%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
13215	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	4.5	4.8	-0.4	-1.5	51.3%	-0.3
13216	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	5.7	-0.3	-1.5	51.3%	-0.4
13217	AT5G58380.1 | Symbol: CIPK10 |	8.6	9.3	-0.7	-1.5	51.3%	-0.4
13218	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	4.5	3.9	0.6	1.5	51.3%	-0.3
13219	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	7.7	8.4	-0.7	-1.5	51.4%	-0.4
13220	AT3G60560.1 | hypothetical protein, 04.05.01.01 | chr3:22393433-22393753 FORWARD | Aliases: T8B10.220	2.2	2.3	-0.1	-1.5	51.4%	-1.5
13221	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	3.9	-0.2	-1.5	51.4%	-0.8
13222	AT5G59050.2 | expressed protein | chr5:23856383-23859903 REVERSE | Aliases: K18B18.4, K18B18_4	4.0	4.3	-0.3	-1.5	51.4%	-0.7
13223	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	8.2	7.8	0.4	1.5	51.4%	-0.4
13224	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	4.1	0.6	1.5	51.4%	-0.3
13225	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	3.9	3.6	0.3	1.5	51.4%	-0.4
13226	AT3G23630.1 | Symbol: ATIPT7 |	3.4	3.2	0.3	1.5	51.4%	-0.8
13227	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	2.8	-0.2	-1.5	51.4%	-0.9
13228	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	2.6	2.8	-0.2	-1.5	51.4%	-0.9
13229	AT2G22710.1 | myb family protein | chr2:9658799-9661612 FORWARD | Aliases: T9I22.15, T9I22_15	3.9	4.4	-0.4	-1.5	51.4%	-0.2
13230	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	6.7	7.4	-0.7	-1.5	51.4%	-0.2
13231	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	4.7	5.2	-0.5	-1.5	51.4%	-0.2
13232	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	3.3	-0.3	-1.5	51.5%	-0.8
13233	AT3G09520.1 | exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit; | chr3:2923749-2925635 FORWARD | Aliases: F11F8.10	3.0	3.2	-0.3	-1.5	51.5%	-0.5
13234	AT5G13460.1 | calmodulin-binding family protein, low similarity to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif | chr5:4315870-4318363 FORWARD | Aliases: T22N19.110, T22N19_110	5.3	4.9	0.3	1.5	51.5%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
13235	AT4G22370.1 | expressed protein | chr4:11810859-11811575 REVERSE | Aliases: T10I14.210, T10I14_210	3.1	3.2	-0.2	-1.5	51.5%	-1.1
13236	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)	2.5	2.4	0.1	1.5	51.5%	-1.2
13237	AT1G03530.1 | expressed protein, similar to hypothetical protein GB:O14360 | chr1:880497-883391 REVERSE | Aliases: F21B7.15	4.7	4.1	0.6	1.5	51.5%	-0.1
13238	AT5G60840.1 | expressed protein, predicted protein, Drosophila melanogaster | chr5:24490560-24491717 REVERSE | Aliases: MAE1.8, MAE1_8	4.8	4.3	0.5	1.5	51.6%	-0.0
13239	AT5G61920.1 | expressed protein | chr5:24882056-24882854 FORWARD | Aliases: K22G18.4, K22G18_4	2.9	2.7	0.2	1.5	51.6%	-0.8
13240	AT5G42810.1 | Symbol: ATIPK1 |	7.3	6.3	1.0	1.5	51.7%	-0.1
13241	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	5.8	6.3	-0.5	-1.5	51.7%	-0.2
13242	AT2G28870.1 | expressed protein | chr2:12401333-12401992 REVERSE | Aliases: F8N16.16, F8N16_16	2.8	3.0	-0.2	-1.5	51.7%	-0.9
13243	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	3.1	-0.2	-1.5	51.7%	-0.9
13244	AT1G73050.1 | (R)-mandelonitrile lyase, putative / (R)-oxynitrilase, putative, similar to mandelonitrile lyase from Prunus serotina (SP:P52706, SP:52707); contains Pfam protile PF00732 GMC oxidoreductase | chr1:27480226-27482195 REVERSE | Aliases: F3N23.25, F3N23_25	2.5	2.7	-0.1	-1.5	51.7%	-1.1
13245	AT1G04650.1 | expressed protein | chr1:1294892-1298902 REVERSE | Aliases: T1G11.9, T1G11_9	3.0	2.8	0.2	1.5	51.7%	-0.9
13246	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	4.1	3.4	0.7	1.5	51.7%	-0.2
13247	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	4.1	3.4	0.7	1.5	51.7%	-0.2
13248	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	3.3	-0.2	-1.5	51.7%	-0.8
13249	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	6.7	6.0	0.7	1.5	51.7%	-0.5
13250	AT4G13070.1 | group II intron splicing factor CRS1-related, contains weak similarity to CRS1 (Zea mays) gi:9837550:gb:AAG00595	4.5	4.1	0.4	1.5	51.7%	-0.5
13251	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	11.0	9.9	1.2	1.5	51.7%	-0.0
13252	AT3G32960.1 | hypothetical protein | chr3:13503390-13504128 FORWARD | Aliases: T13O13.4	2.3	2.4	-0.1	-1.5	51.7%	-1.2
13253	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	3.7	4.0	-0.3	-1.5	51.7%	-0.4
13254	AT1G09575.1 | expressed protein, contains Pfam domain, PF04678: Protein of unknown function, DUF607 | chr1:3101673-3102927 REVERSE | Aliases: None	3.8	3.5	0.3	1.5	51.8%	-0.3
13255	AT1G67970.1 | Symbol: AT HSFA8 | 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: HSFA8, T23K23.18, T23K23_18	5.0	5.4	-0.4	-1.5	51.8%	-0.4
13256	AT1G65295.1 | expressed protein | chr1:24255174-24255966 FORWARD | Aliases: None	6.3	5.8	0.5	1.5	51.8%	-0.1

Rank	Description	Sync	Root	M	t	adj.q	B
13257	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	2.7	-0.2	-1.5	51.8%	-1.1
13258	AT1G68300.1 | universal stress protein (USP) family protein, similar to ER6 protein (Lycopersicon esculentum) GI:5669654; contains Pfam profile PF00582: universal stress protein family | chr1:25602007-25603007 REVERSE | Aliases: T22E19.7, T22E19_7	10.4	9.9	0.6	1.5	51.9%	-0.4
13259	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	2.7	-0.1	-1.5	51.9%	-1.2
13260	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)	5.2	4.7	0.5	1.5	51.9%	-0.3
13261	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	4.6	5.2	-0.6	-1.5	51.9%	-0.1
13262	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	5.2	5.6	-0.4	-1.5	51.9%	-0.5
13263	AT5G51350.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:20885086-20887847 REVERSE | Aliases: MFG13.5, MFG13_5	5.6	5.9	-0.3	-1.5	51.9%	-0.4
13264	AT2G05760.1 | xanthine/uracil permease family protein, contains Pfam profile: PF00860 permease family | chr2:2180916-2183901 FORWARD | Aliases: T25M19.4, T25M19_4	3.1	2.9	0.2	1.5	51.9%	-1.0
13265	AT1G80840.1 | Symbol: WRKY40 |	7.1	6.5	0.6	1.5	52.0%	-0.1
13266	AT2G23160.1 | F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	3.1	3.3	-0.2	-1.5	52.0%	-0.9
13267	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	7.1	7.7	-0.6	-1.5	52.0%	-0.3
13268	AT3G42070.1 | expressed protein | chr3:14268855-14270078 FORWARD | Aliases: F4M19.30	2.6	2.8	-0.2	-1.5	52.0%	-0.9
13269	AT3G23850.1 | hypothetical protein | chr3:8615571-8616540 FORWARD | Aliases: F14O13.31	3.1	3.3	-0.2	-1.5	52.0%	-0.8
13270	AT5G47870.1 | expressed protein | chr5:19401600-19403095 REVERSE | Aliases: MCA23.21, MCA23_21	7.9	8.1	-0.2	-1.5	52.0%	-0.5
13271	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	2.6	-0.2	-1.5	52.0%	-1.1
13272	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	2.4	2.5	-0.1	-1.5	52.1%	-1.2
13273	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	4.7	-0.4	-1.5	52.1%	-0.3
13274	AT3G06290.1 | SAC3/GANP family protein, contains Pfam profile: PF03399 SAC3/GANP family | chr3:1899048-1907303 REVERSE | Aliases: F28L1.23, F28L1_23	3.1	3.4	-0.3	-1.5	52.1%	-0.7
13275	AT3G63110.1 | Symbol: ATIPT3 |	6.1	5.5	0.6	1.5	52.1%	-0.3
13276	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	3.5	-0.3	-1.5	52.1%	-0.5
13277	AT1G66470.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.7	2.9	-0.2	-1.5	52.1%	-0.8
13278	AT4G04480.1 | expressed protein | chr4:2229647-2230843 FORWARD | Aliases: T26N6.8, T26N6_8	3.0	3.3	-0.3	-1.5	52.1%	-0.7
13279	AT1G30860.1 | expressed protein | chr1:10986677-10989227 REVERSE | Aliases: T17H7.18	4.7	5.1	-0.4	-1.5	52.2%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
13280	AT2G40720.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:16994347-16996929 FORWARD | Aliases: T7D17.10, T7D17_10	3.4	3.2	0.3	1.5	52.2%	-0.7
13281	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	7.1	7.4	-0.4	-1.5	52.2%	-0.7
13282	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	5.9	6.4	-0.5	-1.5	52.2%	-0.3
13283	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	2.5	-0.1	-1.5	52.2%	-1.5
13284	AT5G51620.2 | expressed protein | chr5:20984324-20985253 FORWARD | Aliases: K17N15.17, K17N15_17	8.8	8.2	0.6	1.5	52.2%	-0.4
13285	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	4.1	-0.2	-1.5	52.2%	-1.1
13286	AT5G44770.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.3	3.6	-0.3	-1.5	52.2%	-0.6
13287	AT2G36590.1 | Symbol: ProT3 | proline transporter, putative, strong similarity to proline transporter 1 GI:1769901 from (Arabidopsis thaliana); contains Pfam profile PF01490: Transmembrane amino acid transporter protein | chr2:15349758-15352416 REVERSE | Aliases: ATPROT3, F1O11.22, F1O11_22, PROLINE TRANSPORTER 3	2.7	2.9	-0.2	-1.5	52.2%	-0.9
13288	AT4G33230.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr4:16026595-16028758 REVERSE | Aliases: F4I10.160, F4I10_160	3.2	3.4	-0.2	-1.5	52.2%	-0.9
13289	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	4.6	-0.5	-1.5	52.2%	-0.4
13290	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	7.8	8.1	-0.3	-1.5	52.3%	-0.6
13291	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	2.5	-0.1	-1.5	52.3%	-1.3
13292	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	3.2	3.5	-0.3	-1.5	52.3%	-0.5
13293	AT4G39890.1 | Ras-related GTP-binding family protein, contains Pfam profile: PF00071 Ras family | chr4:18505963-18507578 FORWARD | Aliases: T5J17.60, T5J17_60	3.4	3.6	-0.2	-1.5	52.3%	-0.7
13294	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	3.3	3.1	0.2	1.5	52.3%	-0.6
13295	AT4G23150.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr4:12125742-12128343 FORWARD | Aliases: F21P8.40, F21P8_40	2.2	2.3	-0.1	-1.5	52.3%	-1.6
13296	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	5.3	5.6	-0.3	-1.5	52.4%	-0.4
13297	AT5G11970.1 | expressed protein | chr5:3863072-3863756 REVERSE | Aliases: F14F18.140, F14F18_140	6.5	7.2	-0.7	-1.5	52.4%	-0.1
13298	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	4.4	4.0	0.4	1.5	52.4%	-0.5
13299	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	3.7	4.1	-0.4	-1.5	52.4%	-0.5
13300	AT1G80610.1 | expressed protein | chr1:30305625-30308925 REVERSE | Aliases: T21F11.6, T21F11_6	2.5	3.6	-1.1	-1.5	52.4%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
13301	AT5G16180.1 | hypothetical protein, contains Pfam domain, PF04581: Protein of unknown function (DUF578) | chr5:5279887-5282901 FORWARD | Aliases: T21H19.100, T21H19_100	4.5	4.9	-0.4	-1.5	52.4%	-0.5
13302	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	7.9	7.1	0.8	1.5	52.4%	-0.4
13303	AT1G23570.1 | expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220 | chr1:8355070-8356353 REVERSE | Aliases: F28C11.33	2.6	2.8	-0.2	-1.5	52.4%	-1.1
13304	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	4.5	4.9	-0.4	-1.5	52.4%	-0.4
13305	AT1G73350.1 | expressed protein | chr1:27579344-27580787 REVERSE | Aliases: T9L24.52, T9L24_52	4.0	4.2	-0.3	-1.5	52.4%	-0.6
13306	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	5.3	5.9	-0.6	-1.5	52.4%	-0.3
13307	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	3.8	-0.3	-1.5	52.5%	-0.8
13308	AT3G28870.1 | expressed protein | chr3:10891592-10893076 FORWARD | Aliases: MLD15.4	2.4	2.5	-0.1	-1.5	52.5%	-1.4
13309	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	4.0	4.3	-0.3	-1.5	52.5%	-0.5
13310	AT5G46570.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:18911629-18914633 FORWARD | Aliases: F10E10.4, F10E10_4	5.6	5.1	0.5	1.5	52.5%	-0.1
13311	AT4G23300.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr4:12181979-12184714 FORWARD | Aliases: F21P8.190, F21P8_190	2.8	3.0	-0.2	-1.5	52.5%	-1.1
13312	AT1G12430.1 | Symbol: PAK | armadillo/beta-catenin repeat family protein / kinesin motor family protein | chr1:4233871-4238757 REVERSE | Aliases: None	4.1	4.6	-0.5	-1.5	52.5%	-0.2
13313	AT3G32140.1 | hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287 | chr3:13141934-13142722 REVERSE | Aliases: F1M23.25	2.9	3.0	-0.1	-1.5	52.5%	-1.0
13314	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	4.2	3.8	0.4	1.5	52.5%	-0.2
13315	AT1G61120.1 | terpene synthase/cyclase family protein, similar to S-linalool synthase GI:1491939 from (Clarkia breweri)(PMID: 8768373)	2.6	2.9	-0.2	-1.5	52.5%	-1.2
13316	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	2.4	-0.2	-1.5	52.5%	-1.1
13317	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: F17I14.170, F17I14_170, SCPL19, SINAPOYLGLUCOSE ACCUMULATOR 2	3.2	3.1	0.2	1.5	52.5%	-0.9
13318	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	3.3	-0.3	-1.5	52.5%	-0.8
13319	AT1G05960.1 | expressed protein, similar to hypothetical protein GB:AAF80120 GI:8810459 from (Arabidopsis thaliana) | chr1:1807972-1815463 REVERSE | Aliases: T21E18.21, T21E18_21	6.2	5.8	0.4	1.5	52.5%	-0.3
13320	AT1G78710.1 | expressed protein, similar to hypothetical protein GI:3201617 from (Arabidopsis thaliana); expression supported by MPSS | chr1:29607601-29609450 FORWARD | Aliases: F9K20.25, F9K20_25	3.5	3.9	-0.3	-1.5	52.5%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
13321	AT2G43510.1 | Symbol: ATTI1 | Encodes a defensin-like (DEFL) family protein. | chr2:18074251-18074877 FORWARD | Aliases: T1O24.25, TRYPSIN INHIBITOR	4.2	3.9	0.3	1.5	52.5%	-0.4
13322	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	3.6	4.0	-0.4	-1.5	52.5%	-0.4
13323	AT3G15230.1 | expressed protein | chr3:5133761-5134028 FORWARD | Aliases: K7L4.3	2.6	2.8	-0.2	-1.5	52.5%	-1.0
13324	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	4.7	0.2	1.5	52.5%	-0.6
13325	AT5G54680.1 | basic helix-loop-helix (bHLH) family protein, similar to unknown protein (pir :B71406) | chr5:22234286-22236830 FORWARD | Aliases: K5F14.2, K5F14_2	9.3	9.6	-0.3	-1.5	52.6%	-0.6
13326	AT5G60080.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:24210407-24212135 REVERSE | Aliases: MGO3.6, MGO3_6	3.0	3.5	-0.5	-1.5	52.6%	-0.5
13327	AT4G12540.1 | expressed protein | chr4:7429873-7431599 REVERSE | Aliases: T1P17.130, T1P17_130	3.2	3.6	-0.3	-1.5	52.6%	-0.5
13328	AT5G28550.1 | hypothetical protein | chr5:10557726-10559783 REVERSE | Aliases: T10I18.10, T10I18_10	2.9	3.2	-0.3	-1.5	52.7%	-0.6
13329	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	3.6	-0.3	-1.5	52.7%	-0.8
13330	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	2.3	-0.1	-1.5	52.7%	-1.2
13331	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	3.8	4.4	-0.6	-1.5	52.7%	-0.1
13332	AT3G55610.1 | delta 1-pyrroline-5-carboxylate synthetase B / P5CS B (P5CS2), identical to SP:P54888 | chr3:20635001-20640072 REVERSE | Aliases: F1I16.20	3.8	4.4	-0.6	-1.5	52.7%	-0.1
13333	AT3G13960.1 | Symbol: AtGRF5 |	2.1	2.2	-0.1	-1.5	52.8%	-1.5
13334	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	5.6	5.9	-0.3	-1.5	52.8%	-0.7
13335	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	2.2	2.4	-0.2	-1.5	52.8%	-0.9
13336	AT1G02570.1 | expressed protein | chr1:541380-543983 FORWARD | Aliases: T14P4.23, T14P4_23	3.9	4.2	-0.3	-1.5	52.8%	-0.6
13337	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	3.0	-0.3	-1.5	52.8%	-0.8
13338	AT2G26790.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:11432348-11434747 REVERSE | Aliases: F12C20.17, F12C20_17	2.5	2.4	0.2	1.5	52.8%	-1.3
13339	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	8.9	7.6	1.3	1.5	52.8%	-0.7
13340	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	3.3	-0.3	-1.5	52.8%	-0.8
13341	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	7.2	6.7	0.5	1.5	52.8%	-0.2
13342	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)	4.1	4.6	-0.5	-1.5	52.9%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
13343	AT5G01660.1 | kelch repeat-containing protein, similar to SP:P57790 Kelch-like ECH-associated protein 1 (Cytosolic inhibitor of Nrf2) {Rattus norvegicus}; contains Pfam profile PF01344: Kelch motif | chr5:244501-248142 REVERSE | Aliases: F7A7.180, F7A7_180	5.2	4.8	0.4	1.5	52.9%	-0.4
13344	AT3G02860.2 | expressed protein | chr3:625187-627374 REVERSE | Aliases: F13E7.20, F13E7_20	5.8	5.5	0.3	1.5	52.9%	-0.5
13345	NA	2.6	2.8	-0.2	-1.5	52.9%	-1.2
13346	AT4G35420.1 | dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family, similar to dihydroflavonol 4-reductase (Rosa hybrid cultivar, GI:1332411), CPRD14 protein (Vigna unguiculata, GI:1854445) | chr4:16833950-16835624 REVERSE | Aliases: F15J1.1	3.1	3.3	-0.3	-1.5	52.9%	-0.6
13347	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	4.3	4.0	0.3	1.5	52.9%	-0.5
13348	AT3G11960.2 | cleavage and polyadenylation specificity factor (CPSF) A subunit C-terminal domain-containing protein, similar to Splicing factor 3B subunit 3 (Spliceosome associatedprotein 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	4.8	-0.3	-1.5	52.9%	-0.6
13349	AT3G03170.1 | expressed protein | chr3:731898-732882 FORWARD | Aliases: T17B22.14, T17B22_14	5.1	4.8	0.3	1.5	52.9%	-0.4
13350	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	-1.5	52.9%	-1.7
13351	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	4.1	4.6	-0.5	-1.5	52.9%	-0.5
13352	AT2G37550.2 | Symbol: ASP1 | similar to ARF GAP-like zinc finger-containing protein ZIGA2 (ZIGA2) [Arabidopsis thaliana] (TAIR:At3g53710.1); similar to CG4237-PA [Drosophila melanogaster] (GB:NP_524040.2); contains InterPro domain Human Rev interacting-like protein (hRIP) (InterPro:IPR001164)	5.9	5.6	0.4	1.5	52.9%	-0.5
13353	AT1G16940.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.3	3.5	-0.3	-1.5	53.0%	-0.8
13354	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	4.4	3.9	0.6	1.5	53.0%	0.1
13355	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	4.4	3.9	0.6	1.5	53.0%	0.1
13356	AT5G28190.1 | hypothetical protein | chr5:10167854-10170700 REVERSE | Aliases: F26C17.6, F26C17_6	3.5	3.7	-0.3	-1.5	53.0%	-0.8
13357	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	4.6	5.1	-0.5	-1.5	53.0%	-0.3
13358	ATCG00630.1 | Symbol: PSAJ | PSI J protein | chrC:66929-67063 FORWARD | Aliases: PSAJ	5.0	3.8	1.2	1.5	53.0%	-0.2
13359	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	2.4	2.6	-0.1	-1.5	53.0%	-1.1
13360	AT5G37610.1 | expressed protein | chr5:14955351-14955842 FORWARD | Aliases: K12B20.7, K12B20_7	2.8	3.0	-0.2	-1.5	53.0%	-0.8
13361	AT5G59400.2 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:23974971-23976858 FORWARD | Aliases: F2O15.8, F2O15_8	4.6	4.9	-0.3	-1.5	53.0%	-0.4
13362	AT5G19270.1 | hypothetical protein | chr5:6485619-6487011 REVERSE | Aliases: T24G5.2	4.2	4.5	-0.3	-1.5	53.1%	-0.5
13363	AT1G13940.1 | expressed protein | chr1:4762700-4766746 REVERSE | Aliases: F16A14.15	4.7	4.5	0.3	1.5	53.1%	-0.5
13364	AT2G15500.1 | hypothetical protein | chr2:6770789-6771833 FORWARD | Aliases: F9O13.5	3.5	3.8	-0.3	-1.5	53.1%	-0.7
13365	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	4.6	4.3	0.3	1.5	53.2%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
13366	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	7.0	-0.4	-1.5	53.2%	-0.4
13367	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	2.3	0.1	1.5	53.3%	-1.5
13368	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	3.5	3.3	0.2	1.5	53.3%	-0.8
13369	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	2.8	-0.2	-1.5	53.3%	-1.1
13370	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	3.4	3.2	0.2	1.5	53.3%	-0.8
13371	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	9.8	0.5	1.5	53.3%	-0.5
13372	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	8.1	9.0	-0.8	-1.5	53.3%	-0.2
13373	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	2.9	3.1	-0.2	-1.5	53.3%	-0.8
13374	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	2.6	-0.2	-1.5	53.3%	-1.0
13375	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	5.1	5.4	-0.3	-1.5	53.3%	-0.3
13376	AT1G65740.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.2	3.4	-0.2	-1.5	53.5%	-1.2
13377	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	2.5	-0.1	-1.5	53.5%	-1.1
13378	AT4G39910.1 | Symbol: ATUBP3 |	5.7	6.3	-0.6	-1.5	53.5%	-0.4
13379	AT5G49180.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:19957904-19960233 REVERSE | Aliases: K21P3.5, K21P3_5	2.5	2.6	-0.2	-1.5	53.5%	-1.1
13380	AT1G52470.1 | expressed protein | chr1:19558382-19559026 FORWARD | Aliases: F6D8.31, F6D8_31	3.4	3.7	-0.3	-1.5	53.5%	-0.7
13381	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	2.4	2.5	-0.1	-1.5	53.5%	-1.6
13382	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	5.4	5.8	-0.4	-1.5	53.5%	-0.3
13383	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	3.7	-0.3	-1.5	53.5%	-0.8
13384	AT1G60060.1 | expressed protein | chr1:22142849-22145455 FORWARD | Aliases: T2K10.11, T2K10_11	2.5	2.3	0.2	1.5	53.5%	-1.2
13385	AT2G13070.1 | hypothetical protein | chr2:5384509-5385228 FORWARD | Aliases: T17A11.6, T17A11_6	3.0	3.2	-0.2	-1.5	53.5%	-0.9
13386	AT5G11270.1 | Symbol: OCP3 | expressed protein | chr5:3595286-3597084 REVERSE | Aliases: F2I11.160, F2I11_160, OVEREXPRESSOR OF CATIONIC PEROXIDASE 3	4.4	4.0	0.3	1.5	53.6%	-0.6
13387	AT1G68190.1 | zinc finger (B-box type) family protein | chr1:25562911-25564875 FORWARD | Aliases: T22E19.18, T22E19_18	2.4	2.6	-0.2	-1.5	53.6%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
13388	AT1G78360.1 | Symbol: ATGSTU21 | glutathione S-transferase, putative, similar to glutathione transferase GI:2853219 from (Carica papaya) | chr1:29486963-29487859 REVERSE | Aliases: F3F9.24, F3F9_24	2.7	2.9	-0.2	-1.5	53.6%	-0.8
13389	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	2.3	-0.1	-1.5	53.6%	-1.2
13390	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	3.4	3.1	0.3	1.5	53.6%	-0.4
13391	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	2.8	3.0	-0.2	-1.5	53.6%	-0.9
13392	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	3.6	-0.2	-1.5	53.6%	-0.7
13393	AT4G16670.1 | expressed protein | chr4:9385241-9387776 FORWARD | Aliases: DL4360W, FCAALL.2	4.1	3.9	0.3	1.5	53.7%	-0.7
13394	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	4.8	5.2	-0.5	-1.5	53.7%	-0.2
13395	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	3.9	4.2	-0.4	-1.5	53.7%	-0.6
13396	AT1G35030.1 | hypothetical protein | chr1:12808224-12809459 FORWARD | Aliases: F11O6.5, F11O6_5	2.9	3.2	-0.2	-1.5	53.7%	-0.7
13397	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	4.8	5.2	-0.4	-1.5	53.7%	-0.5
13398	AT3G14640.1 | Symbol: CYP72A10 | cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus) | chr3:4919863-4921794 FORWARD | Aliases: MIE1.14	2.8	3.0	-0.2	-1.5	53.8%	-0.9
13399	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	8.6	7.7	1.0	1.5	53.8%	-0.3
13400	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	4.7	4.0	0.6	1.5	53.8%	-0.4
13401	AT1G34280.1 | expressed protein | chr1:12495120-12495359 REVERSE | Aliases: F23M19.16, F23M19_16	5.6	5.9	-0.3	-1.5	53.8%	-0.8
13402	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	5.4	5.0	0.4	1.5	53.8%	-0.2
13403	AT2G07040.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:2916535-2918939 FORWARD | Aliases: T4E14.15, T4E14_15	3.1	3.3	-0.2	-1.5	53.8%	-0.9
13404	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	2.6	-0.2	-1.5	53.8%	-1.1
13405	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	2.4	-0.2	-1.5	53.8%	-1.4
13406	AT5G34850.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	8.0	9.0	-1.0	-1.5	53.9%	-0.3
13407	AT3G24710.1 | expressed protein | chr3:9023967-9024374 REVERSE | Aliases: MSD24.9	3.3	3.6	-0.3	-1.5	53.9%	-0.6
13408	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	7.7	7.3	0.4	1.5	53.9%	-0.7

Rank	Description	Sync	Root	M	t	adj.q	B
13409	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	5.2	5.6	-0.4	-1.5	53.9%	-0.3
13410	AT1G31960.1 | hypothetical protein | chr1:11479113-11479634 REVERSE | Aliases: F5M6.4	3.2	3.5	-0.2	-1.5	53.9%	-0.7
13411	AT1G72110.1 | expressed protein | chr1:27132726-27135060 REVERSE | Aliases: F28P5.3, F28P5_3	2.8	3.0	-0.2	-1.5	53.9%	-0.9
13412	AT3G46150.1 | expressed protein | chr3:16960516-16961130 REVERSE | Aliases: F12M12.120	3.4	3.6	-0.2	-1.5	53.9%	-1.1
13413	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	3.2	-0.2	-1.5	53.9%	-0.9
13414	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	2.8	2.6	0.2	1.5	53.9%	-1.0
13415	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	2.3	-0.1	-1.5	53.9%	-1.3
13416	AT5G19630.1 | expressed protein | chr5:6627978-6629997 REVERSE | Aliases: T29J13.50, T29J13_50	7.1	6.4	0.7	1.5	53.9%	-0.0
13417	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	3.4	3.6	-0.2	-1.5	54.0%	-0.9
13418	AT3G59300.1 | expressed protein, hypothetical protein T2J13.20 - Arabidopsis thaliana, PIR:T46116 | chr3:21929432-21933683 FORWARD | Aliases: F25L23.160	3.9	4.3	-0.4	-1.5	54.0%	-0.3
13419	AT1G50140.1 | AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family | chr1:18573449-18579492 REVERSE | Aliases: F2J10.1, F2J10_1	6.3	6.7	-0.4	-1.5	54.0%	-0.4
13420	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	3.9	3.5	0.4	1.5	54.0%	-0.8
13421	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	3.3	3.1	0.2	1.5	54.0%	-1.1
13422	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	4.8	-0.3	-1.5	54.1%	-0.4
13423	AT4G05240.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr4:2688198-2689016 FORWARD | Aliases: C17L7.160, C17L7_160	2.2	2.3	-0.1	-1.5	54.1%	-1.6
13424	AT5G14990.1 | expressed protein | chr5:4850767-4853006 FORWARD | Aliases: F2G14.110, F2G14_110	2.6	2.7	-0.1	-1.5	54.1%	-1.2
13425	AT4G13195.1 | expressed protein | chr4:7662367-7663173 REVERSE | Aliases: None	3.0	2.8	0.3	1.5	54.1%	-0.8
13426	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	5.0	-0.7	-1.5	54.1%	-0.4
13427	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	3.3	3.9	-0.5	-1.5	54.2%	0.2
13428	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	10.3	9.8	0.5	1.5	54.2%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
13429	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	6.7	7.1	-0.4	-1.5	54.2%	-0.4
13430	AT1G54240.1 | expressed protein | chr1:20256755-20258240 FORWARD | Aliases: F20D21.6, F20D21_6	2.5	2.6	-0.2	-1.5	54.2%	-1.0
13431	AT1G34160.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:12441371-12443234 FORWARD | Aliases: F12G12.2, F12G12_2	5.2	4.8	0.5	1.5	54.2%	-0.3
13432	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	3.2	0.2	1.5	54.2%	-0.6
13433	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	3.1	-0.1	-1.5	54.2%	-1.0
13434	AT5G46560.1 | expressed protein | chr5:18905288-18907689 FORWARD | Aliases: F10E10.3, F10E10_3	3.6	4.0	-0.3	-1.5	54.2%	-0.4
13435	AT1G63190.1 | expressed protein | chr1:23435500-23436667 FORWARD | Aliases: F16M19.9, F16M19_9	2.1	2.2	-0.1	-1.5	54.2%	-1.6
13436	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	3.4	-0.2	-1.5	54.2%	-1.2
13437	AT4G24300.1 | hypothetical protein, hypothetical protein - Arabidopsis thaliana, PIR2:T05128 | chr4:12598990-12600223 REVERSE | Aliases: T22A6.130, T22A6_130	3.6	4.0	-0.4	-1.5	54.2%	-0.8
13438	AT4G23760.1 | expressed protein | chr4:12379384-12383044 FORWARD | Aliases: F9D16.230, F9D16_230	3.6	3.2	0.4	1.5	54.2%	-0.3
13439	AT1G54610.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr1:20397429-20400853 REVERSE | Aliases: T22H22.5, T22H22_5	7.8	7.6	0.3	1.5	54.2%	-0.7
13440	AT1G50800.1 | expressed protein | chr1:18830577-18832006 REVERSE | Aliases: F8A12.5, F8A12_5	2.6	2.8	-0.2	-1.5	54.2%	-1.3
13441	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	2.5	0.2	1.5	54.3%	-1.1
13442	AT1G35410.1 | expressed protein | chr1:13024139-13024919 FORWARD | Aliases: F12A4.5, F12A4_5	3.4	3.7	-0.3	-1.5	54.3%	-0.6
13443	AT2G13730.1 | hypothetical protein | chr2:5732639-5733085 REVERSE | Aliases: F13J11.8, F13J11_8	2.4	2.5	-0.1	-1.5	54.3%	-1.4
13444	AT3G09280.1 | expressed protein, ; expression supported by MPSS | chr3:2850926-2851264 REVERSE | Aliases: F3L24.15	3.2	3.5	-0.3	-1.5	54.3%	-0.8
13445	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	2.2	-0.1	-1.5	54.3%	-1.4
13446	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	3.8	3.4	0.5	1.5	54.3%	-0.3
13447	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	2.3	-0.1	-1.5	54.3%	-1.3
13448	AT4G16000.1 | expressed protein | chr4:9063857-9064493 REVERSE | Aliases: DL4040C, FCAALL.25	3.2	3.4	-0.2	-1.5	54.3%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
13449	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	8.9	9.5	-0.6	-1.5	54.4%	-0.5
13450	AT4G15730.1 | expressed protein | chr4:8951111-8957630 REVERSE | Aliases: DL3905C, FCAALL.370	3.3	3.1	0.2	1.5	54.4%	-0.9
13451	AT5G18810.1 | Symbol: SCL28 | SC35-like splicing factor, 28 kD (SCL28), nearly identical to SC35-like splicing factor SCL28, 28 kD (Arabidopsis thaliana) 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	3.0	3.3	-0.3	-1.5	54.4%	-0.7
13452	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	2.4	-0.2	-1.5	54.4%	-1.2
13453	AT2G26135.1 | zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile PF01485:IBR domain | chr2:11137197-11138592 FORWARD | Aliases: None	3.2	3.4	-0.2	-1.5	54.4%	-0.9
13454	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	7.1	7.6	-0.5	-1.5	54.4%	-0.4
13455	AT3G06360.1 | Symbol: AGP27 | arabinogalactan-protein (AGP27)	2.7	2.5	0.2	1.5	54.4%	-0.8
13456	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	3.9	0.2	1.5	54.4%	-0.7
13457	AT2G37570.2 | Symbol: SLT1 | expressed protein | chr2:15767955-15770461 REVERSE | Aliases: F13M22.7, F13M22_7, SLT1 PROTEIN, SODIUM AND LITHIUM TOLERANT 1	6.0	6.5	-0.5	-1.5	54.4%	-0.3
13458	AT3G14520.1 | terpene synthase/cyclase family protein, similar to terpene synthase GB:CAA72074 from (Arabidopsis thaliana) | chr3:4875755-4878340 REVERSE | Aliases: MIE1.2	3.1	3.2	-0.2	-1.5	54.4%	-1.2
13459	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	3.4	3.6	-0.2	-1.5	54.4%	-0.7
13460	AT1G29240.1 | expressed protein, contains Pfam profile: PF05097 protein of unknown function (DUF688) | chr1:10216785-10219816 REVERSE | Aliases: F28N24.8, F28N24_8	4.5	4.8	-0.3	-1.5	54.4%	-0.6
13461	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	2.9	-0.2	-1.5	54.5%	-1.0
13462	AT2G27160.1 | expressed protein | chr2:11614723-11615281 REVERSE | Aliases: F20F1.3, F20F1_3	2.5	2.6	-0.2	-1.5	54.5%	-1.1
13463	AT5G66660.1 | hypothetical protein | chr5:26626534-26627730 REVERSE | Aliases: MSN2.4, MSN2_4	2.8	3.1	-0.2	-1.5	54.5%	-0.9
13464	AT5G23760.1 | heavy-metal-associated domain-containing protein, Pfam profile PF00403: Heavy-metal-associated domain | chr5:8013090-8014231 REVERSE | Aliases: MRO11.20, MRO11_20	9.6	9.2	0.4	1.5	54.5%	-0.5
13465	AT5G49945.1 | expressed protein, strong similarity to unknown protein (pir::T09896) | chr5:20334631-20337381 FORWARD | Aliases: None	6.8	6.3	0.4	1.5	54.5%	-0.4
13466	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	2.4	2.5	-0.1	-1.5	54.5%	-1.4
13467	AT2G42780.1 | expressed protein | chr2:17807590-17809893 FORWARD | Aliases: F7D19.22, F7D19_22	7.8	8.0	-0.3	-1.5	54.6%	-0.5
13468	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	2.9	-0.2	-1.5	54.6%	-1.0
13469	AT4G34820.1 | expressed protein | chr4:16599610-16602044 REVERSE | Aliases: F11I11.60, F11I11_60	4.0	3.6	0.4	1.5	54.6%	-0.1
13470	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	2.3	2.1	0.2	1.5	54.6%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
13471	AT4G16430.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	8.2	8.7	-0.5	-1.5	54.6%	-0.5
13472	AT3G50900.1 | expressed protein | chr3:18929000-18929599 FORWARD | Aliases: F18B3.180	4.4	5.0	-0.6	-1.5	54.7%	-0.2
13473	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	3.2	2.9	0.3	1.5	54.7%	-0.7
13474	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	2.8	2.7	0.1	1.5	54.7%	-1.1
13475	AT4G15980.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr4:9057478-9059995 REVERSE | Aliases: DL4030C, FCAALL.248	2.1	2.2	-0.1	-1.5	54.7%	-1.3
13476	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	8.3	8.7	-0.4	-1.5	54.7%	-0.4
13477	AT1G78750.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.1	3.3	-0.2	-1.5	54.7%	-1.0
13478	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	6.2	5.3	0.9	1.5	54.7%	-0.3
13479	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	4.6	5.2	-0.5	-1.5	54.7%	-0.2
13480	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	7.0	6.7	0.3	1.5	54.8%	-0.4
13481	AT3G22104.1 | phototropic-responsive NPH3 protein-related, contains BTB/POZ domain, INTERPRO:IPR000210	5.2	5.7	-0.6	-1.5	54.8%	-0.3
13482	AT1G70090.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8 | chr1:26404453-26406060 FORWARD | Aliases: F20P5.18, F20P5_18	4.9	4.6	0.3	1.5	54.8%	-0.4
13483	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	3.8	4.1	-0.3	-1.5	54.8%	-0.4
13484	AT1G10000.1 | expressed protein | chr1:3263879-3264790 REVERSE | Aliases: T27I1.2, T27I1_2	3.2	3.5	-0.3	-1.5	54.9%	-0.7
13485	AT4G15955.1 | epoxide hydrolase-related, similar to epoxide hydrolase GI:1109600 from (Arabidopsis thaliana) | chr4:9043727-9045613 REVERSE | Aliases: None	2.4	2.5	-0.2	-1.5	54.9%	-0.9
13486	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	3.1	-0.3	-1.5	54.9%	-0.6
13487	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	6.2	5.8	0.4	1.5	54.9%	-0.4
13488	AT3G11730.1 | Symbol: ATFP8 | 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: ATFP8, F26K24.2	8.6	8.3	0.3	1.5	54.9%	-0.3
13489	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	3.4	-0.2	-1.5	54.9%	-1.0
13490	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	4.0	-0.4	-1.5	54.9%	-0.5
13491	AT1G57790.1 | F-box family protein, contains Pfam PF00646: F-box domain | chr1:21408073-21409621 REVERSE | Aliases: F12K22.16, F12K22_16	3.0	2.8	0.2	1.5	54.9%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
13492	AT3G59680.2 | similar to unknown [Zea mays] (GB:AAV64233.1) | chr3:22055134-22057017 FORWARD | Aliases: T16L24.230	3.6	3.9	-0.3	-1.5	54.9%	-0.8
13493	AT1G56280.2 | Symbol: ATDI19 |	9.5	10.0	-0.5	-1.5	54.9%	-0.7
13494	AT2G02515.1 | expressed protein | chr2:675255-675655 FORWARD | Aliases: None	3.6	4.0	-0.3	-1.5	55.0%	-0.6
13495	AT5G44620.1 | Symbol: CYP706A3 | cytochrome P450 family protein, similar to cytocrhome P450 monooxygenase (GI:14334057) (Gossypium arboreum) | chr5:18015006-18016785 REVERSE | Aliases: K15C23.6, K15C23_6	3.2	3.3	-0.2	-1.5	55.0%	-1.3
13496	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	5.8	5.5	0.3	1.5	55.0%	-0.3
13497	AT1G16910.1 | expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640) | chr1:5785366-5785860 FORWARD | Aliases: F17F16.11	2.8	3.0	-0.2	-1.5	55.0%	-0.9
13498	AT1G32090.1 | 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 | chr1:11540151-11544059 REVERSE | Aliases: F3C3.11, F3C3_11	3.3	3.5	-0.3	-1.5	55.0%	-0.8
13499	AT1G18510.1 | expressed protein | chr1:6373288-6374083 FORWARD | Aliases: F15H18.2, F15H18_2	3.2	3.4	-0.2	-1.5	55.0%	-1.0
13500	AT5G38630.1 | Symbol: ACYB 1 |	8.5	8.9	-0.4	-1.5	55.0%	-0.6
13501	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	3.2	-0.3	-1.5	55.0%	-0.8
13502	AT2G13760.1 | hypothetical protein | chr2:5742037-5742726 REVERSE | Aliases: F13J11.11, F13J11_11	2.4	2.6	-0.2	-1.5	55.0%	-1.1
13503	AT3G55070.1 | expressed protein | chr3:20419263-20422117 FORWARD | Aliases: T15C9.70	5.8	6.4	-0.6	-1.5	55.1%	-0.3
13504	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	2.9	3.1	-0.2	-1.5	55.1%	-0.8
13505	AT1G75030.1 | Symbol: ATLP 3 |	4.5	4.9	-0.4	-1.5	55.1%	-0.1
13506	NA	6.8	7.4	-0.6	-1.5	55.1%	-0.3
13507	AT5G09470.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr5:2949242-2950514 REVERSE | Aliases: T5E8.270, T5E8_270	3.2	3.6	-0.4	-1.5	55.1%	-0.2
13508	AT1G61750.1 | expressed protein, contains Pfam profile: PF01657 domain of unknown function | chr1:22808660-22809983 REVERSE | Aliases: T13M11.11, T13M11_11	2.4	2.6	-0.2	-1.5	55.1%	-1.1
13509	AT4G35170.1 | hypothetical protein, predicted protein, Arabidopsis thaliana | chr4:16736844-16737335 FORWARD | Aliases: T12J5.40, T12J5_40	2.3	2.5	-0.2	-1.5	55.1%	-0.9
13510	AT1G21830.1 | expressed protein, EST gb:T21171 comes from this gene | chr1:7661149-7662595 REVERSE | Aliases: AT1G21820, T26F17.4	3.5	3.3	0.2	1.5	55.1%	-0.8
13511	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	5.0	-0.4	-1.5	55.2%	-0.6
13512	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	3.9	3.6	0.3	1.5	55.2%	-0.7
13513	AT1G04810.1 | 26S proteasome regulatory subunit, putative, contains similarity to 26S proteasome regulatory subunit S1 SP:O88761, GI:3288594 from (Rattus norvegicus) | chr1:1350179-1355441 FORWARD | Aliases: F13M7.20, F13M7_20	6.9	6.4	0.5	1.5	55.2%	-0.4
13514	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	2.8	3.0	-0.3	-1.5	55.2%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
13515	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	3.7	3.5	0.2	1.5	55.3%	-0.7
13516	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	5.4	-0.4	-1.5	55.3%	-0.3
13517	AT3G52470.1 | harpin-induced family protein / HIN1 family protein / harpin-responsive family protein, similar to harpin-induced protein hin1 (GI:1619321) (Nicotiana tabacum)	6.0	7.2	-1.2	-1.5	55.3%	-0.3
13518	AT5G27490.1 | integral membrane Yip1 family protein, contains Pfam domain, PF04893: Yip1 domain | chr5:9702838-9704678 REVERSE | Aliases: F21A20.200, F21A20_200	5.0	4.6	0.4	1.5	55.3%	-0.2
13519	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	4.4	-0.2	-1.5	55.4%	-1.1
13520	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	5.0	4.5	0.5	1.5	55.4%	-0.5
13521	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	2.6	-0.2	-1.5	55.4%	-1.1
13522	AT5G19980.1 | integral membrane family protein, contains Pfam profile: PF00892 Integral membrane protein; similar to LPG2 protein (GI:9998817)	4.1	4.6	-0.4	-1.5	55.4%	-0.5
13523	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	3.6	-0.2	-1.5	55.4%	-1.0
13524	AT1G35614.1 | expressed protein | chr1:13148570-13149537 FORWARD | Aliases: F15O4.23	3.2	3.4	-0.2	-1.5	55.4%	-1.2
13525	AT3G52310.1 | ABC transporter family protein, contains Pfam profile: PF00005 ABC transporter | chr3:19410356-19413931 FORWARD | Aliases: T25B15.80	2.9	3.2	-0.3	-1.5	55.4%	-0.6
13526	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	5.8	6.8	-0.9	-1.5	55.4%	-0.4
13527	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	3.8	-0.2	-1.5	55.4%	-0.9
13528	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 ammonialyase 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	2.4	-0.1	-1.5	55.4%	-1.3
13529	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	3.5	3.7	-0.2	-1.5	55.4%	-0.7
13530	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	3.2	-0.2	-1.5	55.5%	-1.0
13531	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	4.9	4.4	0.5	1.5	55.5%	-0.3
13532	AT5G59030.1 | Symbol: COPT1 | copper transporter 1 (COPT1), nearly identical to SP:Q39065 Copper transporter 1 (COPT1) {Arabidopsis thaliana}	4.3	3.9	0.4	1.5	55.5%	-0.3

Rank	Description	Sync	Root	M	t	adj.q	B
13533	AT2G32000.2 | similar to DNA topoisomerase III alpha, putative [Arabidopsis thaliana] (TAIR:At5g63920.1); similar to topoisomerase (DNA) III beta [Mus musculus] (GB:NP_035754.1); similar to TOP3B [Homo sapiens] (GB:CAG30482.1); similar to Topoisomerase (DNA) III beta [Homo sapiens] (GB:AAH02432.1); similar to PREDICTED: similar to topoisomerase III beta [Rattus norvegicus] (GB:XP_213564.3); similar to MGC53016 protein [Xenopus laevis] (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	5.1	-0.4	-1.5	55.5%	-0.4
13534	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	9.7	9.4	0.3	1.5	55.5%	-0.8
13535	AT5G65300.1 | expressed protein | chr5:26112373-26112997 REVERSE | Aliases: MNA5.2, MNA5_2	5.5	5.9	-0.4	-1.5	55.6%	-0.3
13536	AT5G42920.2 | expressed protein | chr5:17223379-17226751 REVERSE | Aliases: MBD2.12, MBD2_12	7.6	7.2	0.4	1.5	55.6%	-0.5
13537	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	2.6	-0.1	-1.5	55.6%	-1.1
13538	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	3.5	-0.3	-1.5	55.6%	-1.0
13539	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	2.1	-0.1	-1.5	55.7%	-1.6
13540	AT2G31700.1 | hypothetical protein | chr2:13487587-13488645 FORWARD | Aliases: T9H9.22, T9H9_22	2.7	2.9	-0.2	-1.5	55.7%	-0.9
13541	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	7.9	8.5	-0.6	-1.5	55.7%	-0.3
13542	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	3.2	-0.2	-1.5	55.8%	-0.8
13543	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	-1.5	55.8%	-1.7
13544	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	3.0	0.1	1.5	55.8%	-1.1
13545	AT1G65720.1 | expressed protein | chr1:24443922-24444736 REVERSE | Aliases: F1E22.9, F1E22_9	8.9	8.2	0.7	1.5	55.8%	-0.1
13546	AT3G30210.1 | Symbol: MYB121 |	5.8	5.5	0.3	1.5	55.8%	-0.6
13547	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	2.7	-0.2	-1.5	55.8%	-0.9
13548	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	2.8	3.0	-0.2	-1.5	55.8%	-1.2
13549	AT1G61840.1 | DC1 domain-containing protein, similar to hypothetical protein GI:3184279 from (Arabidopsis thaliana); contains Pfam profile PF03107: DC1 domain	3.2	3.4	-0.2	-1.5	55.8%	-1.0
13550	AT3G32910.1 | expressed protein, similar to At2g15200, At2g04970, At1g32830, At2g14140, At4g03990 | chr3:13467801-13469328 FORWARD | Aliases: T7B9.16	2.0	2.1	-0.1	-1.5	55.8%	-1.8
13551	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	7.0	7.5	-0.5	-1.5	55.8%	-0.4
13552	AT2G32740.1 | exostosin family protein, contains Pfam profile: PF03016 Exostosin family | chr2:13893903-13895309 FORWARD | Aliases: F24L7.12, F24L7_12	2.9	3.0	-0.2	-1.5	55.9%	-1.3
13553	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	3.8	4.4	-0.5	-1.5	55.9%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
13554	AT3G59630.1 | diphthamide synthesis DPH2 family protein, contains InterPro accession IPR002728: Diphthamide synthesis DPH2 protein | chr3:22036051-22038845 REVERSE | Aliases: T16L24.180	4.6	4.3	0.2	1.5	55.9%	-0.6
13555	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	2.5	-0.1	-1.5	56.0%	-1.5
13556	AT1G47790.1 | F-box family protein, contains Pfam:PF00646 F-box domain	2.8	3.2	-0.4	-1.5	56.0%	-0.7
13557	AT4G29560.1 | expressed protein | chr4:14503879-14506020 REVERSE | Aliases: T16L4.70, T16L4_70	3.8	4.1	-0.3	-1.5	56.0%	-0.6
13558	AT4G32230.1 | expressed protein | chr4:15565301-15566977 REVERSE | Aliases: F10M6.130, F10M6_130	2.6	2.7	-0.2	-1.5	56.0%	-1.0
13559	AT4G20740.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:11126162-11128345 FORWARD | Aliases: F21C20.90, F21C20_90	3.8	3.6	0.2	1.5	56.0%	-0.7
13560	AT4G36110.1 | auxin-responsive protein, putative, similar to auxin-induced protein TGSAUR22 (GP:10185820) {Tulipa gesnerian); auxin-induced protein 15A (PIR2:JQ1096) (Glycine max) | chr4:17089952-17090828 FORWARD | Aliases: T19K4.240, T19K4_240	2.8	2.6	0.2	1.5	56.0%	-1.0
13561	AT1G09780.1 | 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 | chr1:3165372-3167871 REVERSE | Aliases: F21M12.16, F21M12_16	11.3	11.8	-0.6	-1.5	56.0%	-0.9
13562	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	4.6	5.0	-0.4	-1.5	56.0%	-0.3
13563	AT2G27950.1 | expressed protein | chr2:11906340-11910248 REVERSE | Aliases: T1E2.13, T1E2_13	2.6	2.8	-0.1	-1.5	56.1%	-1.0
13564	AT1G16730.1 | expressed protein | chr1:5726610-5727305 REVERSE | Aliases: F19K19.18	3.2	3.0	0.2	1.5	56.1%	-0.8
13565	AT2G32560.1 | F-box family protein, contains Pfam PF00646: F-box domain; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250 | chr2:13831871-13834063 FORWARD | Aliases: AT2G32570, T26B15.12, T26B15_12	3.0	3.2	-0.1	-1.5	56.1%	-1.4
13566	AT3G26350.1 | expressed protein, ; expression supported by MPSS | chr3:9654897-9655967 REVERSE | Aliases: F20C19.7	2.7	2.9	-0.2	-1.5	56.1%	-0.7
13567	AT2G05540.1 | glycine-rich protein | chr2:2033181-2034214 FORWARD | Aliases: T20G20.11, T20G20_11	4.2	4.4	-0.3	-1.5	56.2%	-0.8
13568	AT3G12580.1 | Symbol: HSP70 | heat shock protein 70, putative / HSP70, putative, strong similarity to heat shock protein GI:425194 (Spinacia oleracea) | chr3:3991268-3993798 REVERSE | Aliases: HSP70, T2E22.11	10.2	9.8	0.4	1.5	56.2%	-0.5
13569	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	2.4	2.6	-0.2	-1.5	56.2%	-1.1
13570	AT5G33380.1 | hypothetical protein | chr5:12625040-12625592 FORWARD | Aliases: F19N2.100, F19N2_100	3.1	3.4	-0.3	-1.5	56.2%	-0.7
13571	AT1G12240.1 | Symbol: ATBETAFRUCT4 | beta-fructosidase (BFRUCT4) / beta-fructofuranosidase / invertase, vacuolar, identical to beta-fructosidase GI:1871503 from (Arabidopsis thaliana); 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	5.0	5.4	-0.5	-1.5	56.2%	-0.4
13572	AT1G01450.1 | protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr1:164105-165517 REVERSE | Aliases: F22L4.1, F22L4_1	2.4	2.6	-0.2	-1.5	56.2%	-1.3
13573	AT1G31520.1 | hypothetical protein | chr1:11278964-11279620 REVERSE | Aliases: F27M3.25, F27M3_25	2.7	3.0	-0.3	-1.5	56.2%	-0.6
13574	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	6.0	6.4	-0.4	-1.5	56.2%	-0.3

Rank	Description	Sync	Root	M	t	adj.q	B
13575	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	2.2	-0.1	-1.5	56.2%	-1.5
13576	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	5.1	6.0	-0.9	-1.5	56.3%	-0.1
13577	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	5.1	6.0	-0.9	-1.5	56.3%	-0.1
13578	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	3.3	3.5	-0.2	-1.5	56.3%	-1.0
13579	AT1G23590.1 | expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220 | chr1:8359120-8360634 REVERSE | Aliases: F28C11.29	3.1	3.3	-0.2	-1.5	56.3%	-1.2
13580	AT5G53800.1 | expressed protein | chr5:21865361-21867337 FORWARD | Aliases: MGN6.19, MGN6_19	9.6	8.8	0.8	1.5	56.3%	-0.3
13581	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	5.1	5.4	-0.3	-1.5	56.3%	-0.6
13582	AT5G46120.1 | hypothetical protein | chr5:18719851-18720102 REVERSE | Aliases: MCL19.18, MCL19_18	2.4	2.6	-0.2	-1.5	56.4%	-1.6
13583	AT4G27460.1 | CBS domain-containing protein | chr4:13732916-13734310 FORWARD | Aliases: F27G19.60, F27G19_60	3.5	3.2	0.3	1.5	56.4%	-0.5
13584	AT3G52100.1 | PHD finger family protein, contains Pfam profile PF00628: PHD-finger | chr3:19330321-19333751 FORWARD | Aliases: F4F15.210	6.0	5.1	0.9	1.5	56.4%	0.3
13585	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	3.7	3.9	-0.2	-1.5	56.4%	-0.7
13586	AT1G54650.1 | expressed protein, similar to Actin-binding protein ABP140 (Swiss-Prot:Q08641) (Saccharomyces cerevisiae) | chr1:20409265-20411353 REVERSE | Aliases: T22H22.9, T22H22_9	5.2	4.9	0.3	1.5	56.4%	-0.6
13587	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	4.7	4.2	0.5	1.5	56.4%	-0.3
13588	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	5.7	0.3	1.5	56.4%	-0.4
13589	AT3G43420.1 | expressed protein | chr3:15356303-15356667 FORWARD | Aliases: T5C2.120	2.5	2.7	-0.2	-1.5	56.5%	-1.0
13590	AT5G35520.1 | kinetochore protein-related, contains Pfam PF05859: Mis12 protein | chr5:13718626-13720719 FORWARD | Aliases: MOK9.12, MOK9_12	4.1	4.3	-0.2	-1.5	56.5%	-0.8
13591	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	8.5	7.9	0.6	1.5	56.5%	-0.4
13592	AT1G05340.1 | expressed protein | chr1:1558849-1559757 REVERSE | Aliases: YUP8H12.4, YUP8H12_4	4.6	5.4	-0.8	-1.5	56.5%	-0.3
13593	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	3.5	-0.2	-1.5	56.5%	-1.0
13594	AT1G32760.1 | glutaredoxin family protein, contains Pfam profile PF00462: Glutaredoxin	5.1	4.9	0.3	1.5	56.5%	-0.7

Rank	Description	Sync	Root	M	t	adj.q	B
13595	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	4.3	-0.3	-1.5	56.5%	-0.4
13596	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	4.0	3.7	0.3	1.5	56.6%	-0.5
13597	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	7.1	6.6	0.5	1.5	56.6%	-0.4
13598	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	7.8	7.5	0.4	1.5	56.6%	-0.5
13599	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	2.8	2.6	0.2	1.5	56.6%	-1.1
13600	AT1G05380.1 | PHD finger transcription factor, putative | chr1:1578784-1582613 FORWARD | Aliases: T25N20.3, T25N20_3	5.3	4.9	0.4	1.5	56.6%	-0.5
13601	AT3G62580.1 | expressed protein | chr3:23157804-23159326 FORWARD | Aliases: T12C14.280	8.2	9.4	-1.2	-1.5	56.6%	-0.1
13602	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	2.6	-0.1	-1.5	56.7%	-1.2
13603	AT2G36040.1 | expressed protein, ; expression supported by MPSS | chr2:15137725-15137907 REVERSE | Aliases: F11F19.5, F11F19_5	2.8	3.0	-0.2	-1.5	56.7%	-1.1
13604	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: F20O9.120, F20O9_120	6.6	5.4	1.2	1.5	56.7%	-0.3
13605	AT2G40270.2 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr2:16829012-16831539 REVERSE | Aliases: T7M7.19	5.5	5.8	-0.3	-1.5	56.7%	-0.7
13606	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)	7.5	6.7	0.9	1.5	56.7%	-0.2
13607	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	3.9	-0.2	-1.5	56.7%	-1.0
13608	AT5G04280.1 | glycine-rich RNA-binding protein	5.4	4.8	0.6	1.5	56.7%	-0.3
13609	AT3G18540.1 | expressed protein | chr3:6375815-6377473 FORWARD | Aliases: K24M9.3	3.3	3.8	-0.4	-1.5	56.7%	-0.2
13610	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	5.8	5.5	0.3	1.5	56.7%	-0.8
13611	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	8.2	7.7	0.5	1.5	56.7%	-0.6
13612	AT5G24090.1 | acidic endochitinase (CHIB1), identical to SP:P19172 Acidic endochitinase precursor (EC 3.2.1.14) {Arabidopsis thaliana}	7.3	7.6	-0.3	-1.5	56.7%	-0.6
13613	AT4G21880.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:11605117-11611220 FORWARD | Aliases: T8O5.90, T8O5_90	3.4	3.1	0.3	1.5	56.7%	-0.3
13614	AT2G24320.1 | expressed protein | chr2:10352739-10353909 REVERSE | Aliases: T28I24.5, T28I24_5	2.7	2.9	-0.2	-1.5	56.8%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
13615	AT1G56310.1 | 3'-5' exonuclease domain-containing protein, contains Pfam profile PF01612: 3'-5' exonuclease | chr1:21086528-21088965 FORWARD | Aliases: F14G9.8, F14G9_8	4.3	4.0	0.4	1.5	56.8%	-0.5
13616	AT1G32050.1 | secretory carrier membrane protein (SCAMP) family protein, contains Pfam domain, PF04144: SCAMP family | chr1:11528461-11531261 FORWARD | Aliases: T12O21.5, T12O21_5	7.4	8.1	-0.7	-1.5	56.8%	-0.4
13617	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	3.4	3.1	0.3	1.5	56.8%	-0.6
13618	NA	4.4	4.7	-0.3	-1.5	56.8%	-1.0
13619	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	3.4	-0.1	-1.5	56.8%	-1.1
13620	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	3.5	3.2	0.3	1.5	56.8%	-0.8
13621	AT5G57080.1 | expressed protein | chr5:23116185-23116594 FORWARD | Aliases: MUL3.2, MUL3_2	3.7	3.4	0.3	1.5	56.9%	-0.5
13622	AT5G14270.1 | DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487 | chr5:4604735-4608908 FORWARD | Aliases: F18O22.60, F18O22_60	7.2	6.8	0.4	1.5	56.9%	-0.3
13623	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	5.0	5.3	-0.3	-1.5	56.9%	-0.5
13624	AT3G03970.3 | expressed protein | chr3:1028004-1030612 REVERSE | Aliases: T11I18.8, T11I18_8	4.4	4.7	-0.3	-1.5	56.9%	-0.5
13625	AT3G16960.1 | expressed protein | chr3:5791818-5792270 REVERSE | Aliases: K14A17.5	2.7	2.8	-0.2	-1.5	56.9%	-1.0
13626	AT2G10950.1 | BSD domain-containing protein, contains Pfam profile PF03909: BSD domain	7.1	7.4	-0.3	-1.5	56.9%	-0.8
13627	AT2G32600.1 | hydroxyproline-rich glycoprotein family protein, similar to SWISS-PROT:Q15428 | chr2:13840622-13842736 REVERSE | Aliases: T26B15.16, T26B15_16	4.1	3.5	0.5	1.5	56.9%	-0.6
13628	AT2G15600.1 | hypothetical protein | chr2:6812268-6812540 REVERSE | Aliases: F9O13.15	2.9	3.1	-0.2	-1.5	56.9%	-1.3
13629	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	6.9	6.5	0.5	1.5	57.0%	-0.6
13630	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	6.6	6.3	0.3	1.5	57.0%	-0.5
13631	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	3.1	3.3	-0.2	-1.5	57.0%	-1.0
13632	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	6.8	6.3	0.4	1.5	57.1%	-0.4
13633	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	2.4	-0.1	-1.5	57.1%	-1.5
13634	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	6.5	6.8	-0.4	-1.4	57.1%	-0.7
13635	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	4.3	4.7	-0.3	-1.4	57.2%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
13636	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	3.7	0.2	1.4	57.2%	-0.7
13637	AT4G01420.1 | Symbol: CBL5 | calcineurin B-like protein 5 (CBL5), identical to calcineurin B-like protein 5 (GI:9965366) (Arabidopsis thaliana); similar to N. crassa 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	2.1	-0.1	-1.4	57.2%	-1.6
13638	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	3.6	3.3	0.3	1.4	57.2%	-0.5
13639	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	4.0	3.7	0.3	1.4	57.2%	-0.6
13640	AT5G48940.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:19856936-19861033 FORWARD | Aliases: K19E20.5, K19E20_5	3.4	3.8	-0.4	-1.4	57.2%	-0.9
13641	AT2G28030.1 | aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease | chr2:11941285-11942463 REVERSE | Aliases: T1E2.2	2.5	2.6	-0.1	-1.4	57.2%	-1.5
13642	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	10.2	0.6	1.4	57.3%	-0.5
13643	AT4G00790.1 | expressed protein | chr4:338630-340602 REVERSE | Aliases: A_TM018A10.24, A_TM018A10_24, T18A10.5, T18A10_5	2.5	2.7	-0.2	-1.4	57.3%	-1.1
13644	ATMG01240.1 | Symbol: ORF100C | hypothetical protein | chrM:309338-309640 REVERSE | Aliases: ORF100C	2.3	2.7	-0.4	-1.4	57.3%	-0.4
13645	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	2.8	-0.2	-1.4	57.3%	-1.1
13646	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	7.8	8.3	-0.5	-1.4	57.3%	-0.5
13647	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	7.2	7.7	-0.5	-1.4	57.4%	-0.5
13648	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	9.4	9.7	-0.3	-1.4	57.4%	-0.5
13649	AT5G45830.1 | expressed protein, low similarity to tumor-related protein (Nicotiana glauca x Nicotiana langsdorffii) GI:688423	3.0	3.2	-0.2	-1.4	57.5%	-1.1
13650	AT1G71910.1 | expressed protein | chr1:27068594-27069609 FORWARD | Aliases: F17M19.6, F17M19_6	4.4	4.8	-0.4	-1.4	57.5%	-0.5
13651	AT1G04930.1 | hydroxyproline-rich glycoprotein family protein, Common family member: At2g32840 (Arabidopsis thaliana) | chr1:1396292-1399052 REVERSE | Aliases: F13M7.8, F13M7_8	4.4	4.6	-0.2	-1.4	57.5%	-0.8
13652	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	5.6	-0.3	-1.4	57.5%	-0.3
13653	AT4G01140.1 | expressed protein | chr4:490749-492199 REVERSE | Aliases: F2N1.38, F2N1_38	2.8	3.1	-0.3	-1.4	57.5%	-0.6
13654	AT1G33400.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain | chr1:12104764-12109500 REVERSE | Aliases: F10C21.7, F10C21_7	5.4	5.8	-0.4	-1.4	57.6%	-0.5
13655	AT1G28220.1 | Symbol: ATPUP3 |	4.3	4.6	-0.3	-1.4	57.6%	-0.6
13656	AT1G25250.1 | zinc finger (C2H2 type) family protein, contains zinc finger, C2H2 type, domain, PROSITE:PS00028	2.5	2.6	-0.1	-1.4	57.6%	-1.4
13657	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	3.9	4.2	-0.2	-1.4	57.6%	-0.7

Rank	Description	Sync	Root	M	t	adj.q	B
13658	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	4.6	4.3	0.3	1.4	57.6%	-0.6
13659	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	3.2	3.5	-0.3	-1.4	57.6%	-0.9
13660	AT2G27420.1 | cysteine proteinase, putative, contains similarity to cysteine protease SPCP1 GI:13491750 from (Ipomoea batatas)	2.9	3.1	-0.2	-1.4	57.6%	-1.0
13661	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	2.8	-0.2	-1.4	57.7%	-1.0
13662	AT2G21660.2 | Symbol: ATGRP7 |	11.3	10.4	0.9	1.4	57.7%	-0.3
13663	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	2.9	2.8	0.1	1.4	57.7%	-1.1
13664	AT5G09780.1 | transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain | chr5:3036957-3038485 REVERSE | Aliases: F17I14.30, F17I14_30	3.0	3.4	-0.4	-1.4	57.7%	-0.6
13665	AT1G32260.1 | expressed protein, identical to hypothetical protein GB:AAF81322 GI:8920600 from (Arabidopsis thaliana) | chr1:11640562-11641764 REVERSE | Aliases: F27G20.13	5.0	4.8	0.2	1.4	57.7%	-0.6
13666	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	3.7	-0.3	-1.4	57.7%	-0.8
13667	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	10.9	-0.3	-1.4	57.7%	-1.1
13668	AT3G42590.1 | hypothetical protein, similar to At2g16170, At2g06640, At2g12110, At2g12100, At2g05460 | chr3:14707244-14707936 FORWARD | Aliases: T12K4.40	3.1	3.3	-0.2	-1.4	57.7%	-1.3
13669	AT2G04370.1 | hypothetical protein | chr2:1523760-1524118 REVERSE | Aliases: T23O15.2	2.5	2.6	-0.1	-1.4	57.7%	-1.6
13670	AT3G28260.1 | hypothetical protein | chr3:10535777-10537381 FORWARD | Aliases: MZF16.21	2.5	2.6	-0.1	-1.4	57.7%	-1.4
13671	AT5G22370.1 | Symbol: EMB1705 | ATP-binding family protein, contains Pfam domain, PF03029: Conserved hypothetical ATP binding protein	3.3	3.0	0.3	1.4	57.7%	-0.9
13672	AT1G25520.1 | expressed protein, contains Pfam profile PF01169: Uncharacterized protein family UPF0016	7.9	8.1	-0.2	-1.4	57.8%	-0.9
13673	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	2.3	0.1	1.4	57.8%	-1.4
13674	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	5.0	4.7	0.3	1.4	57.8%	-0.4
13675	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	3.4	-0.2	-1.4	57.8%	-1.0
13676	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	3.8	-0.3	-1.4	57.8%	-0.9
13677	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	2.5	-0.1	-1.4	57.8%	-1.3
13678	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	6.4	6.1	0.3	1.4	57.8%	-0.4
13679	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	3.5	3.7	-0.2	-1.4	57.8%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
13680	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	4.5	4.8	-0.4	-1.4	57.8%	-0.6
13681	AT1G09600.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr1:3108619-3111320 FORWARD | Aliases: F14J9.26, F14J9_26	4.7	4.4	0.3	1.4	57.8%	-0.6
13682	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	2.9	-0.2	-1.4	57.8%	-1.1
13683	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) {Rattus norvegicus}; contains Pfam profile PF02020: eIF4-gamma/eIF5/eIF2-epsilon | chr2:14753386-14755860 FORWARD | Aliases: F19I3.20, F19I3_20	5.7	6.1	-0.4	-1.4	57.8%	-0.8
13684	AT4G15010.3 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr4:8572901-8575179 REVERSE | Aliases: DL3547C, FCAALL.86	5.5	5.2	0.3	1.4	57.9%	-0.8
13685	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	6.1	-0.4	-1.4	57.9%	-0.5
13686	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	4.0	4.2	-0.2	-1.4	57.9%	-0.7
13687	AT2G34690.1 | Symbol: ACD11 | expressed protein | chr2:14637430-14639029 FORWARD | Aliases: ACCELERATED CELL DEATH 11, T29F13.10, T29F13_10	10.1	9.8	0.2	1.4	57.9%	-0.7
13688	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	4.0	3.8	0.2	1.4	57.9%	-1.1
13689	AT3G53970.2 | proteasome inhibitor-related, similar to proteasome inhibitor PI31 subunit (hPI31) SP:Q92530 from (Homo sapiens)	6.4	7.2	-0.7	-1.4	57.9%	-0.4
13690	AT5G35640.1 | hypothetical protein, contains Pfam profile PF04396: Protein of unknown function, DUF537	3.0	3.3	-0.2	-1.4	57.9%	-0.9
13691	AT3G08800.1 | expressed protein | chr3:2671154-2675202 FORWARD | Aliases: F17O14.27	3.9	4.3	-0.3	-1.4	58.0%	-0.6
13692	AT4G15020.1 | expressed protein, contains Pfam profile PF04937: Protein of unknown function (DUF 659) | chr4:8575647-8578682 FORWARD | Aliases: DL3551W, FCAALL.174	3.0	3.3	-0.3	-1.4	58.0%	-0.8
13693	AT1G62310.1 | transcription factor jumonji (jmjC) domain-containing protein, similar to nuclear protein 5qNCA (Homo sapiens) GI:13161188; contains Pfam profile PF02373: jmjC domain | chr1:23039704-23042966 REVERSE | Aliases: F24O1.3, F24O1_3	4.5	4.3	0.3	1.4	58.0%	-0.4
13694	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	4.2	3.9	0.3	1.4	58.0%	-0.6
13695	AT5G04270.1 | zinc finger (DHHC type) family protein, low similarity to Golgi-specific DHHC zinc figer protein (Mus musculus) GI:21728103; contains Pfam profile PF01529: DHHC zinc finger domain | chr5:1182719-1184719 REVERSE | Aliases: T19N18.6	4.2	4.4	-0.2	-1.4	58.0%	-0.8
13696	AT1G05800.1 | lipase class 3 family protein, similar to DEFECTIVE IN ANTHER DEHISCENCE1 (Arabidopsis thaliana) GI:16215706; contains Pfam profile PF01764: Lipase | chr1:1741203-1742618 FORWARD | Aliases: T20M3.6	2.8	2.9	-0.2	-1.4	58.0%	-1.1
13697	AT3G55790.1 | expressed protein, predicted protein, Arabidopsis thaliana; expression supported by MPSS	2.5	2.6	-0.1	-1.4	58.0%	-1.2
13698	AT4G25410.1 | basix helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.2	2.3	-0.1	-1.4	58.0%	-1.3
13699	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	3.1	-0.2	-1.4	58.0%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
13700	AT1G13470.1 | expressed protein | chr1:4620242-4621539 REVERSE | Aliases: T6J4.20, T6J4_20	4.2	4.6	-0.4	-1.4	58.0%	-0.5
13701	AT5G57310.1 | expressed protein | chr5:23228256-23228846 FORWARD | Aliases: MJB24.12, MJB24_12	3.2	3.5	-0.2	-1.4	58.0%	-0.9
13702	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	2.7	-0.2	-1.4	58.0%	-0.9
13703	AT1G10910.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:3639908-3643974 FORWARD | Aliases: T19D16.17, T19D16_17	4.5	4.2	0.3	1.4	58.1%	-0.4
13704	AT3G59070.1 | auxin-responsive protein, putative, similar to auxin-induced protein AIR12 (GI:11357190) (Arabidopsis thaliana) | chr3:21843341-21845491 REVERSE | Aliases: F17J16.120	2.4	2.6	-0.2	-1.4	58.1%	-1.3
13705	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	6.3	0.4	1.4	58.1%	-0.7
13706	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	2.9	-0.1	-1.4	58.1%	-1.3
13707	AT4G14950.3 | expressed protein | chr4:8545168-8548050 FORWARD | Aliases: DL3515W, FCAALL.221	4.4	4.7	-0.4	-1.4	58.1%	-0.4
13708	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	2.2	-0.1	-1.4	58.1%	-1.7
13709	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	4.0	-0.2	-1.4	58.1%	-0.7
13710	AT4G00050.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.0	2.8	0.2	1.4	58.1%	-0.8
13711	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	3.1	-0.1	-1.4	58.1%	-1.0
13712	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	3.3	3.0	0.3	1.4	58.2%	-0.5
13713	AT1G54070.1 | dormancy/auxin associated protein-related | chr1:20186307-20186910 FORWARD | Aliases: F15I1.15, F15I1_15	3.0	3.2	-0.1	-1.4	58.2%	-1.3
13714	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)	3.9	4.2	-0.3	-1.4	58.2%	-0.7
13715	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	4.1	-0.2	-1.4	58.2%	-1.2
13716	AT4G11950.1 | hypothetical protein | chr4:7173270-7174253 REVERSE | Aliases: F16J13.20, F16J13_20	4.5	4.9	-0.4	-1.4	58.2%	-0.5
13717	AT1G48120.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	3.7	3.5	0.2	1.4	58.2%	-0.9
13718	AT5G57790.2 | expressed protein | chr5:23429319-23430850 REVERSE | Aliases: MTI20.2, MTI20_2	3.6	3.2	0.3	1.4	58.2%	-0.5
13719	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	7.4	7.0	0.5	1.4	58.3%	-0.2
13720	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	2.5	2.7	-0.2	-1.4	58.4%	-1.1
13721	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	2.6	2.7	-0.2	-1.4	58.4%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
13722	AT1G58120.1 | expressed protein | chr1:21524066-21526122 FORWARD | Aliases: T15M6.13	3.3	3.5	-0.3	-1.4	58.4%	-0.7
13723	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	2.4	-0.1	-1.4	58.4%	-1.5
13724	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	4.3	5.2	-0.9	-1.4	58.4%	-0.3
13725	AT3G21170.1 | F-box family protein, contains Pfam profile: PF00646 F-box domain | chr3:7419982-7421166 FORWARD | Aliases: MXL8.1	3.9	4.4	-0.5	-1.4	58.4%	-0.5
13726	AT5G05210.1 | nucleolar matrix protein-related, contains Pfam domain, PF04935: Surfeit locus protein 6	8.8	8.2	0.6	1.4	58.4%	-0.4
13727	AT5G05450.1 | DEAD/DEAH box helicase, putative (RH18) | chr5:1612050-1615337 FORWARD | Aliases: K18I23.26, K18I23_26	6.8	6.0	0.8	1.4	58.4%	-0.2
13728	AT1G11950.1 | transcription factor jumonji (jmjC) domain-containing protein, contains Pfam domain, PF02373: jmjC domain; non-consensus TG acceptor splice site at exon boundary 79262 | chr1:4034585-4038308 REVERSE | Aliases: F12F1.18, F12F1_18	4.3	4.0	0.2	1.4	58.5%	-0.8
13729	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	3.9	3.6	0.3	1.4	58.5%	-0.6
13730	AT1G27570.1 | phosphatidylinositol 3- and 4-kinase family protein, contains Pfam profile PF00454: Phosphatidylinositol 3- and 4-kinase	2.6	2.8	-0.2	-1.4	58.5%	-1.1
13731	AT3G04990.1 | hypothetical protein | chr3:1384002-1384685 REVERSE | Aliases: T9J14.6, T9J14_6	2.7	2.8	-0.1	-1.4	58.5%	-1.6
13732	AT5G03190.1 | expressed protein | chr5:757845-760381 FORWARD | Aliases: F15A17.220, F15A17_220	4.9	4.5	0.5	1.4	58.5%	-0.8
13733	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	10.7	-0.5	-1.4	58.5%	-0.8
13734	AT4G26550.1 | expressed protein, probable membrane protein YBL102w, yeast, PIR2:S45393	4.6	4.1	0.4	1.4	58.5%	-0.6
13735	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	2.2	-0.1	-1.4	58.5%	-1.3
13736	AT5G47120.1 | Symbol: ATBI 1 |	9.6	10.4	-0.7	-1.4	58.5%	-0.7
13737	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	3.7	-0.5	-1.4	58.5%	-0.5
13738	AT1G61170.1 | expressed protein | chr1:22553303-22554340 FORWARD | Aliases: F11P17.11, F11P17_11	3.9	3.6	0.3	1.4	58.5%	-0.7
13739	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	3.2	-0.2	-1.4	58.6%	-1.1
13740	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	3.2	-0.2	-1.4	58.6%	-1.0
13741	AT4G03160.1 | hypothetical protein | chr4:1397979-1398685 FORWARD | Aliases: F4C21.8, F4C21_8	2.3	2.4	-0.1	-1.4	58.6%	-1.7
13742	AT3G32160.1 | expressed protein | chr3:13149153-13149666 FORWARD | Aliases: F1M23.1	2.7	2.8	-0.2	-1.4	58.6%	-1.0
13743	AT1G72380.1 | expressed protein | chr1:27248832-27250525 FORWARD | Aliases: T10D10.15, T10D10_15	3.6	3.9	-0.3	-1.4	58.7%	-0.8
13744	AT2G38160.1 | expressed protein | chr2:15993864-15995600 REVERSE | Aliases: F16M14.9, F16M14_9	2.2	2.4	-0.1	-1.4	58.7%	-1.2
13745	AT5G47310.1 | expressed protein | chr5:19218088-19220148 FORWARD | Aliases: MQL5.17, MQL5_17	7.1	6.5	0.6	1.4	58.7%	-0.6

Rank	Description	Sync	Root	M	t	adj.q	B
13746	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	5.0	4.6	0.4	1.4	58.7%	-0.5
13747	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	2.4	2.6	-0.1	-1.4	58.7%	-1.6
13748	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	7.2	6.5	0.7	1.4	58.7%	-0.1
13749	ATCG00740.1 | Symbol: RPOA | RNA polymerase alpha subunit | chrC:77901-78890 REVERSE | Aliases: RPOA	9.8	9.0	0.8	1.4	58.7%	-0.3
13750	AT5G04490.1 | phosphatidate cytidylyltransferase family protein, contains Pfam profile: PF01148 phosphatidate cytidylyltransferase | chr5:1279761-1281670 FORWARD | Aliases: T32M21.90, T32M21_90	5.0	5.3	-0.4	-1.4	58.7%	-0.3
13751	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	6.3	-0.3	-1.4	58.7%	-0.7
13752	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	3.5	3.1	0.4	1.4	58.7%	-0.7
13753	AT1G10730.1 | clathrin adaptor complexes medium subunit family protein, contains Pfam profile: PF00928 adaptor complexes medium subunit family	4.1	4.4	-0.2	-1.4	58.7%	-0.8
13754	AT3G13000.2 | expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547 | chr3:4157975-4161948 REVERSE | Aliases: MGH6.15, MGH6_15	3.0	3.2	-0.2	-1.4	58.7%	-0.9
13755	AT4G21105.1 | expressed protein | chr4:11265662-11266982 FORWARD | Aliases: None	9.4	9.0	0.4	1.4	58.7%	-0.8
13756	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	2.5	2.6	-0.2	-1.4	58.7%	-1.1
13757	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: K20I9.7	7.2	7.9	-0.8	-1.4	58.7%	-0.3
13758	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	2.9	3.1	-0.3	-1.4	58.7%	-0.9
13759	AT4G09690.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	2.8	-0.2	-1.4	58.7%	-1.1
13760	AT4G07380.1 | expressed protein | chr4:4192426-4193013 REVERSE | Aliases: F28D6.12, F28D6_12	2.8	3.0	-0.2	-1.4	58.7%	-1.0
13761	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	-1.4	58.8%	-1.4
13762	AT1G79640.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:29971806-29975983 REVERSE | Aliases: F20B17.7, F20B17_7	2.6	2.5	0.1	1.4	58.8%	-1.2
13763	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	5.7	6.1	-0.4	-1.4	58.8%	-0.5
13764	AT5G15460.2 | expressed protein | chr5:5018774-5020656 REVERSE | Aliases: T20K14.70, T20K14_70	9.2	8.5	0.7	1.4	58.8%	-0.8
13765	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	10.2	9.9	0.3	1.4	58.8%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
13766	AT5G20370.1 | serine-rich protein-related, contains some similarity to serine-rich proteins | chr5:6886933-6887460 REVERSE | Aliases: F5O24.260, F5O24_260	3.8	4.0	-0.3	-1.4	58.9%	-0.9
13767	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	4.3	4.1	0.2	1.4	58.9%	-0.9
13768	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	7.8	7.5	0.4	1.4	58.9%	-0.3
13769	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	4.2	3.5	0.7	1.4	58.9%	-0.0
13770	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	3.8	-0.2	-1.4	58.9%	-1.1
13771	AT3G07760.2 | expressed protein | chr3:2476450-2478204 FORWARD | Aliases: MLP3.21	7.0	7.5	-0.5	-1.4	58.9%	-0.6
13772	AT1G02670.1 | DNA repair protein, putative, 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 | chr1:576046-580299 FORWARD | Aliases: T14P4.5, T14P4_5	3.7	3.3	0.3	1.4	58.9%	-0.9
13773	AT5G38390.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.2	3.5	-0.3	-1.4	58.9%	-0.8
13774	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	5.1	5.8	-0.7	-1.4	58.9%	-0.3
13775	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	2.1	0.1	1.4	58.9%	-1.6
13776	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	2.6	0.2	1.4	58.9%	-1.0
13777	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	2.5	2.7	-0.1	-1.4	58.9%	-1.5
13778	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,	4.1	3.6	0.4	1.4	59.0%	-0.4
13779	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	5.8	5.6	0.2	1.4	59.0%	-0.8
13780	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	4.3	4.0	0.3	1.4	59.0%	-0.4
13781	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	4.2	4.6	-0.3	-1.4	59.0%	-0.6
13782	AT5G50190.1 | expressed protein, similar to unknown protein (pir::T08985) | chr5:20450451-20452387 REVERSE | Aliases: K6A12.5, K6A12_5	2.8	3.0	-0.2	-1.4	59.0%	-1.1
13783	AT5G13500.3 | expressed protein, predicted protein At2g25260 - Arabidopsis thaliana, EMBL:AC007070 | chr5:4338234-4340998 FORWARD | Aliases: T6I14.30, T6I14_30	5.7	6.0	-0.3	-1.4	59.1%	-0.7
13784	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	5.4	5.1	0.2	1.4	59.1%	-0.7
13785	AT5G39410.1 | expressed protein | chr5:15785072-15787638 REVERSE | Aliases: MUL8.9, MUL8_9	8.2	7.4	0.8	1.4	59.1%	-0.4

Rank	Description	Sync	Root	M	t	adj.q	B
13786	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	3.5	3.3	0.2	1.4	59.2%	-1.0
13787	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	3.0	-0.1	-1.4	59.2%	-1.2
13788	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	1.9	-0.1	-1.4	59.2%	-1.6
13789	AT3G20490.1 | expressed protein | chr3:7153600-7156542 REVERSE | Aliases: K10D20.3	4.0	3.8	0.2	1.4	59.2%	-0.9
13790	AT5G08550.1 | expressed protein | chr5:2765982-2770283 REVERSE | Aliases: MAH20.11, MAH20_11	3.6	3.3	0.3	1.4	59.2%	-0.8
13791	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	6.2	-0.4	-1.4	59.2%	-0.6
13792	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	3.0	3.1	-0.2	-1.4	59.3%	-1.0
13793	AT5G19910.1 | SOH1 family protein, contains Pfam profile: PF05669 SOH1	3.9	3.6	0.2	1.4	59.3%	-0.8
13794	AT2G16400.1 | homeodomain-containing protein | chr2:7108412-7110973 REVERSE | Aliases: F16F14.10, F16F14_10	7.3	7.6	-0.3	-1.4	59.3%	-0.7
13795	AT2G38490.1 | Symbol: CIPK22 |	3.2	3.4	-0.2	-1.4	59.3%	-0.6
13796	AT5G01180.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr5:61016-63847 REVERSE | Aliases: F7J8.160, F7J8_160	2.8	2.7	0.2	1.4	59.3%	-1.0
13797	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	2.7	-0.2	-1.4	59.4%	-1.2
13798	AT2G33490.1 | hydroxyproline-rich glycoprotein family protein, Common family member:At3g26910 (Arabidopsis thaliana) | chr2:14190628-14194945 FORWARD | Aliases: F4P9.26, F4P9_26	3.9	4.2	-0.3	-1.4	59.4%	-0.7
13799	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	2.6	-0.2	-1.4	59.4%	-1.1
13800	ATMG01400.1 | Symbol: ORF105B | hypothetical protein | chrM:363725-364042 FORWARD | Aliases: ORF105B	2.8	3.3	-0.4	-1.4	59.4%	-0.5
13801	AT2G06230.1 | expressed protein | chr2:2440434-2440730 REVERSE | Aliases: F18P14.2, F18P14_2	2.7	2.9	-0.2	-1.4	59.4%	-1.2
13802	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	3.8	3.5	0.3	1.4	59.5%	-0.6
13803	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	5.3	5.9	-0.7	-1.4	59.5%	-0.7
13804	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	3.4	-0.3	-1.4	59.5%	-0.9
13805	AT5G10830.1 | embryo-abundant protein-related, similar to embryo-abundant protein (Picea glauca) GI:1350531 | chr5:3423687-3425468 FORWARD | Aliases: T30N20.100, T30N20_100	7.0	7.4	-0.4	-1.4	59.5%	-0.6
13806	AT3G42800.1 | expressed protein, hypothetical proteins - Arabidopsis thaliana; expression supported by MPSS | chr3:14916825-14917850 FORWARD | Aliases: T21C14.20	3.1	3.3	-0.2	-1.4	59.5%	-1.1
13807	AT5G51290.1 | ceramide kinase-related, contains weak similarity to ceramide kinases (GI:21624342) (Mus musculus) | chr5:20861226-20865559 REVERSE | Aliases: MWD22.24, MWD22_24	2.9	3.1	-0.2	-1.4	59.5%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
13808	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	11.2	10.7	0.5	1.4	59.5%	-0.8
13809	AT5G14410.1 | expressed protein | chr5:4646790-4647447 REVERSE | Aliases: F18O22.200, F18O22_200	2.8	3.0	-0.2	-1.4	59.5%	-0.9
13810	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	5.1	5.5	-0.4	-1.4	59.5%	-0.7
13811	AT4G24520.1 | Symbol: ATR1 | NADPH-cytochrome p450 reductase, putative / NADPH-ferrihemoprotein reductase, putative, similar to NADPH-ferrihemoprotein reductase NADPH-cytochrome P450 oxydoreductase 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	5.9	6.4	-0.5	-1.4	59.5%	-0.3
13812	AT1G01180.1 | expressed protein | chr1:75633-77446 FORWARD | Aliases: F6F3.5	3.0	3.3	-0.3	-1.4	59.6%	-0.7
13813	AT4G04610.1 | Symbol: APR1 | 5'-adenylylsulfate reductase (APR1) / PAPS reductase homolog (PRH19), identical to 5'-adenylylsulfate reductase (Arabidopsis thaliana) 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	8.7	8.1	0.6	1.4	59.6%	-0.5
13814	AT1G60420.1 | DC1 domain-containing protein, contains Pfam domain PF03107: DC1 domain | chr1:22265573-22268324 FORWARD | Aliases: T13D8.29, T13D8_29	9.3	9.8	-0.5	-1.4	59.6%	-0.7
13815	AT5G66300.1 | Symbol: ANAC105 | no apical meristem (NAM) family protein, similar to NAC2 (GI:6456751)	2.9	3.2	-0.2	-1.4	59.6%	-0.9
13816	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	4.0	-0.4	-1.4	59.7%	-0.7
13817	AT3G58860.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.2	3.4	-0.1	-1.4	59.7%	-1.2
13818	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	2.6	-0.1	-1.4	59.7%	-1.4
13819	AT4G08730.1 | expressed protein | chr4:5577387-5578776 REVERSE | Aliases: T32A17.40, T32A17_40	3.6	3.9	-0.3	-1.4	59.7%	-0.7
13820	AT5G20510.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr5:6939594-6942895 REVERSE | Aliases: F7C8.100, F7C8_100	5.7	5.4	0.3	1.4	59.7%	-0.7
13821	AT2G31570.1 | Symbol: ATGPX2 |	10.6	11.1	-0.5	-1.4	59.8%	-0.9
13822	AT4G26640.2 | Symbol: WRKY20 |	6.4	6.8	-0.4	-1.4	59.8%	-0.4
13823	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	2.6	-0.2	-1.4	59.8%	-1.0
13824	AT1G80770.1 | Symbol: PDE318 |	5.5	5.3	0.3	1.4	59.8%	-0.8
13825	AT3G16040.1 | expressed protein | chr3:5443097-5443957 FORWARD | Aliases: MSL1.7	2.9	2.8	0.2	1.4	59.8%	-1.4
13826	AT2G24800.1 | peroxidase, putative, similar to peroxidase (Spinacia oleracea) gi:1781338:emb:CAA71496 | chr2:10578334-10579649 REVERSE | Aliases: F27C12.28, F27C12_28	2.4	2.6	-0.2	-1.4	59.8%	-1.2
13827	AT3G54980.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:20381211-20384046 FORWARD | Aliases: T15C9.5	4.9	4.6	0.3	1.4	59.8%	-0.4
13828	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	3.3	-0.2	-1.4	59.9%	-1.1
13829	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	8.0	7.3	0.7	1.4	59.9%	-0.6
13830	AT2G34270.1 | hypothetical protein, and genscan | chr2:14475831-14476955 REVERSE | Aliases: F13P17.11, F13P17_11	3.3	3.5	-0.2	-1.4	59.9%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
13831	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	2.7	-0.2	-1.4	59.9%	-1.1
13832	AT1G49490.1 | leucine-rich repeat family protein / extensin family protein, contains similarity to disease resistance protein GI: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	2.7	2.8	-0.1	-1.4	59.9%	-1.5
13833	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	2.3	-0.1	-1.4	59.9%	-1.5
13834	AT5G54610.1 | ankyrin repeat family protein, contains Pfam domain, PF00023: Ankyrin repeat | chr5:22202005-22203733 REVERSE | Aliases: MRB17.11, MRB17_11	2.4	2.6	-0.2	-1.4	59.9%	-1.3
13835	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	8.5	9.0	-0.5	-1.4	59.9%	-0.5
13836	AT1G23210.1 | glycosyl hydrolase family 9 protein, similar to endo-1,4-beta-glucanase GB:CAA67157 GI:2440035 from (Arabidopsis thaliana) | chr1:8240163-8242118 FORWARD | Aliases: F26F24.6, F26F24_6	2.3	2.4	-0.1	-1.4	59.9%	-1.5
13837	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	9.9	10.2	-0.3	-1.4	59.9%	-0.6
13838	AT3G56400.1 | Symbol: WRKY70 |	4.4	4.8	-0.3	-1.4	59.9%	-0.3
13839	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	4.5	5.0	-0.5	-1.4	59.9%	-0.3
13840	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	3.1	-0.3	-1.4	60.0%	-0.9
13841	AT2G30050.1 | transducin family protein / WD-40 repeat family protein, similar to SEC13-related protein (SP:P55735) (Homo sapiens) | chr2:12831528-12833761 FORWARD | Aliases: T27E13.21, T27E13_21	6.2	5.3	0.9	1.4	60.0%	-0.2
13842	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	10.3	10.6	-0.3	-1.4	60.0%	-0.9
13843	AT1G63400.1 | pentatricopeptide (PPR) repeat-containing protein, contains multiple PPR-repeats Pfam profile: PF01535 | chr1:23510985-23512718 FORWARD | Aliases: F2K11.22, F2K11_22	3.1	2.9	0.2	1.4	60.0%	-1.0
13844	AT2G47390.1 | expressed protein | chr2:19448742-19453435 REVERSE | Aliases: T8I13.23	8.3	9.0	-0.7	-1.4	60.0%	-0.4
13845	AT1G12790.1 | expressed protein | chr1:4359149-4361267 REVERSE | Aliases: F13K23.4, F13K23_4	2.8	2.6	0.2	1.4	60.0%	-1.1
13846	NA	3.2	3.4	-0.2	-1.4	60.0%	-1.0
13847	AT2G14830.1 | expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292	2.3	2.4	-0.1	-1.4	60.0%	-1.5
13848	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	10.0	-0.8	-1.4	60.0%	-0.9
13849	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	8.0	7.2	0.8	1.4	60.0%	-0.4
13850	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	4.0	-0.3	-1.4	60.0%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
13851	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	6.3	5.8	0.5	1.4	60.0%	-0.5
13852	AT5G20330.1 | Symbol: BETAG4 |	2.5	2.7	-0.1	-1.4	60.0%	-1.1
13853	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	8.8	8.4	0.4	1.4	60.0%	-0.6
13854	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	6.9	6.4	0.5	1.4	60.0%	-0.2
13855	AT1G26860.1 | expressed protein | chr1:9304969-9305787 REVERSE | Aliases: T2P11.5, T2P11_5	2.7	2.8	-0.1	-1.4	60.1%	-1.4
13856	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	2.4	-0.1	-1.4	60.1%	-1.3
13857	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	4.6	4.2	0.4	1.4	60.1%	-0.6
13858	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	5.2	-0.3	-1.4	60.1%	-0.6
13859	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	4.5	-0.3	-1.4	60.1%	-0.8
13860	AT4G21600.1 | bifunctional nuclease, putative, similar to bifunctional nuclease (Zinnia elegans) gi:4099833:gb:AAD00694 | chr4:11485131-11487428 FORWARD | Aliases: F17L22.60	7.9	7.3	0.6	1.4	60.1%	-0.5
13861	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	3.9	3.5	0.4	1.4	60.1%	-0.3
13862	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	7.3	7.6	-0.3	-1.4	60.1%	-0.6
13863	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	5.2	4.8	0.4	1.4	60.1%	-0.5
13864	AT2G29920.1 | expressed protein | chr2:12761571-12762461 FORWARD | Aliases: F6K5.5, F6K5_5	3.4	3.7	-0.3	-1.4	60.1%	-0.8
13865	AT1G09930.1 | Symbol: ATOPT2 |	3.0	3.2	-0.2	-1.4	60.1%	-1.0
13866	AT5G20400.1 | oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to naringenin,2-oxoglutarate 3-dioxygenase (flavonone-3-hydroxylase) (SP:Q06942)(Malus domestica); contains PF031712OG-Fe(II) oxygenase superfamily domain | chr5:6894856-6896351 FORWARD | Aliases: F5O24.290, F5O24_290	7.8	7.5	0.3	1.4	60.2%	-0.7
13867	AT2G01440.1 | ATP-dependent DNA helicase, putative | chr2:194093-199055 REVERSE | Aliases: F2I9.6, F2I9_6	2.9	2.7	0.2	1.4	60.2%	-0.9
13868	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	4.6	-0.3	-1.4	60.2%	-0.5
13869	AT1G51660.1 | Symbol: ATMKK4 |	4.1	4.3	-0.2	-1.4	60.2%	-0.8
13870	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	4.2	4.8	-0.6	-1.4	60.2%	-0.4
13871	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	3.2	0.2	1.4	60.2%	-1.0
13872	AT5G18990.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:6340078-6341616 FORWARD | Aliases: T16G12.30, T16G12_30	2.3	2.5	-0.1	-1.4	60.3%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
13873	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	2.6	-0.2	-1.4	60.3%	-1.3
13874	AT2G04040.1 | MATE efflux family protein, contains Pfam profile: PF01554 uncharacterized membrane protein family | chr2:1334515-1336485 REVERSE | Aliases: F3L12.13, F3L12_13	3.9	4.1	-0.2	-1.4	60.3%	-0.9
13875	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	6.4	6.7	-0.4	-1.4	60.3%	-0.4
13876	AT5G51740.1 | peptidase M48 family protein, contains Pfam domain, PF01435: Peptidase family M48 | chr5:21034253-21036447 FORWARD | Aliases: MIO24.13, MIO24_13	6.6	6.0	0.6	1.4	60.4%	-0.6
13877	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	4.8	4.5	0.3	1.4	60.4%	-0.7
13878	AT3G11060.1 | expressed protein | chr3:3466309-3466950 REVERSE | Aliases: F11B9.2	3.2	3.3	-0.2	-1.4	60.4%	-1.0
13879	AT1G19300.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 Glycosyl transferase family 8 | chr1:6671128-6672644 REVERSE | Aliases: F18O14.2, F18O14_2	3.3	3.5	-0.3	-1.4	60.4%	-0.9
13880	AT5G39785.2 | expressed protein | chr5:15946416-15949504 FORWARD | Aliases: AT5G39780	4.2	4.5	-0.3	-1.4	60.4%	-0.9
13881	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	2.5	-0.1	-1.4	60.4%	-1.5
13882	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	2.5	2.7	-0.2	-1.4	60.4%	-1.2
13883	AT3G30510.1 | hypothetical protein | chr3:12123056-12123207 FORWARD | Aliases: MSJ3.14	2.9	3.0	-0.2	-1.4	60.4%	-1.3
13884	AT4G01960.1 | expressed protein | chr4:851210-853078 REVERSE | Aliases: T7B11.22, T7B11_22	7.2	7.6	-0.4	-1.4	60.4%	-0.5
13885	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	2.5	2.7	-0.1	-1.4	60.4%	-1.1
13886	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	4.8	4.4	0.4	1.4	60.4%	-0.3
13887	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	5.5	5.3	0.3	1.4	60.4%	-0.8
13888	AT2G24140.1 | expressed protein, contains Pfam PF04576: Protein of unknown function, DUF593 | chr2:10269634-10271113 REVERSE | Aliases: F27D4.5, F27D4_5	3.8	4.1	-0.3	-1.4	60.4%	-1.2
13889	AT4G38630.1 | Symbol: AT MCB1 | 26S proteasome regulatory subunit S5A (RPN10), identical to multiubiquitin chain binding protein (MBP1) SP:P55034, GI:1165206	8.0	8.5	-0.5	-1.4	60.4%	-0.9
13890	AT4G30500.1 | expressed protein, contains Pfam PF05620: Protein of unknown function (DUF788) | chr4:14903496-14904923 FORWARD | Aliases: F17I23.160, F17I23_160	5.5	5.2	0.3	1.4	60.5%	-0.7
13891	AT3G30360.1 | hypothetical protein | chr3:11967002-11967542 FORWARD | Aliases: T6J22.15	3.2	3.4	-0.1	-1.4	60.5%	-1.3
13892	AT3G13222.1 | Symbol: GIP1 | expressed protein | chr3:4251021-4254244 REVERSE | Aliases: GBF INTERACTING PROTEIN 1, MJG19.5	4.1	3.8	0.3	1.4	60.5%	-0.5
13893	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	7.2	0.6	1.4	60.5%	-0.5
13894	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	3.5	3.8	-0.2	-1.4	60.5%	-0.7

Rank	Description	Sync	Root	M	t	adj.q	B
13895	AT1G13040.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:4447645-4449198 FORWARD | Aliases: F3F19.6, F3F19_6	2.2	2.4	-0.1	-1.4	60.5%	-1.6
13896	AT5G64200.2 | Symbol: ATSC35 |	5.6	5.0	0.6	1.4	60.6%	-0.5
13897	AT1G30260.1 | Symbol: AGL79 | expressed protein | chr1:10651035-10651712 FORWARD | Aliases: F12P21.9, F12P21_9	2.6	2.8	-0.2	-1.4	60.6%	-1.0
13898	AT2G41570.1 | expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277 | chr2:17344815-17346071 FORWARD | Aliases: T32G6.9, T32G6_9	2.8	2.9	-0.2	-1.4	60.6%	-1.3
13899	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	3.2	-0.2	-1.4	60.6%	-1.1
13900	AT4G36620.1 | zinc finger (GATA type) family protein | chr4:17268912-17269668 REVERSE | Aliases: AP22.1, AP22_1	2.9	3.1	-0.2	-1.4	60.6%	-1.0
13901	AT1G59790.1 | cullin-related, low similarity to Hs-CUL-1 (Homo sapiens) GI:1381142 | chr1:22005169-22007050 FORWARD | Aliases: F23H11.11, F23H11_11	3.3	3.5	-0.2	-1.4	60.6%	-1.1
13902	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	2.6	2.8	-0.1	-1.4	60.6%	-1.4
13903	AT3G23680.1 | F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain | chr3:8526373-8527180 REVERSE | Aliases: MYM9.1	2.9	3.1	-0.2	-1.4	60.7%	-1.1
13904	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	3.4	0.2	1.4	60.7%	-0.9
13905	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	6.8	6.5	0.2	1.4	60.7%	-0.7
13906	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	6.3	-0.4	-1.4	60.7%	-0.6
13907	AT3G47840.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:17662897-17665017 FORWARD | Aliases: T23J7.170	3.6	3.3	0.3	1.4	60.7%	-0.7
13908	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	3.0	3.2	-0.2	-1.4	60.7%	-1.0
13909	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	3.8	3.2	0.5	1.4	60.7%	-0.1
13910	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	5.4	5.8	-0.4	-1.4	60.7%	-0.5
13911	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	7.5	7.9	-0.4	-1.4	60.7%	-0.4
13912	AT2G24255.1 | expressed protein | chr2:10323133-10324143 REVERSE | Aliases: None	3.3	3.5	-0.2	-1.4	60.8%	-1.2
13913	AT2G29510.1 | expressed protein | chr2:12641601-12645095 FORWARD | Aliases: F16P2.11, F16P2_11	5.7	6.2	-0.5	-1.4	60.8%	-0.4
13914	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	3.2	-0.3	-1.4	60.8%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
13915	AT3G31410.1 | expressed protein, similar to hypothetical protein GB:CAB77996 GI:7267513 from (Arabidopsis thaliana) | chr3:12782958-12786060 REVERSE | Aliases: T22B15.43	2.6	2.7	-0.1	-1.4	60.8%	-1.7
13916	AT1G08070.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:2514189-2516602 REVERSE | Aliases: T6D22.15, T6D22_15	4.1	3.8	0.3	1.4	60.8%	-0.7
13917	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	11.2	10.7	0.5	1.4	60.8%	-1.2
13918	AT1G80290.1 | glycosyltransferase family protein 47, similar to exostosin, Homo sapiens (SP:O43909), (SP:Q16394) | chr1:30193213-30194618 FORWARD | Aliases: F5I6.4, F5I6_4	5.0	5.4	-0.4	-1.4	60.8%	-0.6
13919	AT3G22190.1 | calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif | chr3:7831668-7833519 REVERSE | Aliases: MKA23.10	4.1	3.9	0.2	1.4	60.8%	-0.8
13920	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	2.6	-0.2	-1.4	60.8%	-1.2
13921	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	4.0	3.8	0.2	1.4	60.8%	-0.9
13922	AT3G52970.1 | Symbol: CYP76G1 | cytochrome P450 family protein, cytochrome P450 76A2, eggplant, PIR:S38534 | chr3:19652284-19654254 REVERSE | Aliases: F8J2.140	2.1	2.2	-0.1	-1.4	60.9%	-1.7
13923	AT2G20150.1 | expressed protein, and genefinder | chr2:8705280-8705561 FORWARD | Aliases: T2G17.5, T2G17_5	4.2	4.5	-0.3	-1.4	60.9%	-0.8
13924	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	7.8	7.4	0.5	1.4	60.9%	-0.3
13925	AT1G31040.1 | zinc-binding protein-related, simialr to zinc-binding protein (Pisum sativum) GI:16117799 | chr1:11069774-11070085 REVERSE | Aliases: F17F8.4	3.5	3.7	-0.3	-1.4	60.9%	-0.9
13926	AT1G59540.1 | Symbol: ZCF125 |	3.0	2.8	0.2	1.4	60.9%	-0.9
13927	AT2G20142.1 | expressed protein | chr2:8702451-8703727 FORWARD | Aliases: None	2.6	2.8	-0.2	-1.4	61.0%	-1.0
13928	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	2.8	-0.2	-1.4	61.0%	-1.0
13929	AT2G03050.1 | mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF | chr2:899689-900945 REVERSE | Aliases: T17M13.22, T17M13_22	4.1	3.7	0.4	1.4	61.0%	-0.4
13930	AT3G12680.1 | Symbol: HUA1 | floral homeotic protein (HUA1), identical to floral homeotic protein HUA1 (Arabidopsis thaliana) gi:16797661:gb:AAK01470	5.8	5.6	0.2	1.4	61.0%	-0.9
13931	AT4G28703.1 | expressed protein | chr4:14166275-14166928 FORWARD | Aliases: None	3.5	3.9	-0.4	-1.4	61.0%	-0.7
13932	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	4.0	-0.3	-1.4	61.0%	-0.7
13933	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	3.1	3.5	-0.3	-1.4	61.0%	-0.8
13934	AT2G16360.1 | 40S ribosomal protein S25 (RPS25A) | chr2:7083795-7084448 REVERSE | Aliases: F16F14.14, F16F14_14	4.3	4.0	0.3	1.4	61.1%	-0.7
13935	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	6.8	7.5	-0.7	-1.4	61.1%	-0.5
13936	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	3.1	0.2	1.4	61.1%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
13937	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	2.4	-0.1	-1.4	61.1%	-1.5
13938	AT4G03170.1 | hypothetical protein | chr4:1400832-1401584 FORWARD | Aliases: F4C21.9, F4C21_9	2.7	2.9	-0.2	-1.4	61.1%	-1.2
13939	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	4.0	0.3	1.4	61.1%	-0.5
13940	AT1G64800.1 | expressed protein, ; expression supported by MPSS | chr1:24088749-24089096 FORWARD | Aliases: F13O11.33, F13O11_33	3.2	3.4	-0.3	-1.4	61.1%	-0.8
13941	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	3.6	3.3	0.3	1.4	61.1%	-0.7
13942	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	4.0	4.4	-0.4	-1.4	61.1%	-0.6
13943	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	3.4	3.6	-0.2	-1.4	61.1%	-1.2
13944	AT1G09610.1 | expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579) | chr1:3111791-3112639 FORWARD | Aliases: F14J9.29, F14J9_29	2.5	2.6	-0.2	-1.4	61.1%	-1.1
13945	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)	2.8	2.6	0.2	1.4	61.1%	-0.9
13946	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	2.5	0.1	1.4	61.1%	-1.2
13947	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	3.8	3.3	0.4	1.4	61.2%	-0.6
13948	AT1G06140.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:1864795-1866471 FORWARD | Aliases: T21E18.19, T21E18_19	3.3	3.6	-0.3	-1.4	61.2%	-0.8
13949	AT2G33760.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:14282876-14284627 FORWARD | Aliases: T1B8.7, T1B8_7	3.8	4.1	-0.3	-1.4	61.2%	-0.6
13950	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	4.3	4.1	0.2	1.4	61.2%	-0.8
13951	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	4.1	3.8	0.3	1.4	61.2%	-0.6
13952	AT5G22760.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr5:7571638-7577869 FORWARD | Aliases: MDJ22.18, MDJ22_18	4.5	4.9	-0.4	-1.4	61.2%	-0.8
13953	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	2.4	-0.1	-1.4	61.2%	-1.6
13954	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	2.7	3.0	-0.2	-1.4	61.2%	-1.0
13955	AT3G12130.1 | KH domain-containing protein / zinc finger (CCCH type) family protein | chr3:3864158-3866596 REVERSE | Aliases: T21B14.5	5.5	5.2	0.3	1.4	61.2%	-0.6
13956	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	2.8	0.2	1.4	61.3%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
13957	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	2.7	2.9	-0.2	-1.4	61.3%	-1.2
13958	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	3.6	3.3	0.2	1.4	61.3%	-0.8
13959	AT1G62670.1 | pentatricopeptide (PPR) repeat-containing protein, contains multiple PPR repeats Pfam Profile: PF01535 | chr1:23208438-23210330 REVERSE | Aliases: F23N19.4, F23N19_4	3.4	3.0	0.3	1.4	61.4%	-0.9
13960	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	3.2	3.0	0.2	1.4	61.4%	-1.0
13961	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	2.9	3.0	-0.2	-1.4	61.4%	-1.2
13962	AT2G16620.1 | protein kinase-related, contains similarity to protein kinases | chr2:7212473-7213000 REVERSE | Aliases: T24I21.3, T24I21_3	2.8	2.9	-0.1	-1.4	61.4%	-1.7
13963	AT1G19870.1 | calmodulin-binding family protein, contains Pfam profile: PF00612 IQ calmodulin-binding motif | chr1:6895017-6898600 REVERSE | Aliases: F6F9.8, F6F9_8	4.3	5.5	-1.1	-1.4	61.4%	-0.3
13964	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	7.9	8.7	-0.8	-1.4	61.4%	-0.3
13965	AT3G58300.1 | hypothetical protein | chr3:21593741-21594367 REVERSE | Aliases: F9D24.210	3.0	3.2	-0.2	-1.4	61.4%	-1.0
13966	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)	3.3	3.5	-0.2	-1.4	61.5%	-0.9
13967	AT3G42190.1 | expressed protein | chr3:14375912-14382054 FORWARD | Aliases: F26B15.2	2.8	3.0	-0.2	-1.4	61.5%	-1.0
13968	AT5G26790.1 | expressed protein | chr5:9423095-9423614 FORWARD | Aliases: F2P16.50, F2P16_50	5.0	4.5	0.5	1.4	61.5%	-0.4
13969	AT3G05820.1 | 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 | chr3:1732997-1735632 REVERSE | Aliases: F10A16.11, F10A16_11	3.0	2.9	0.1	1.4	61.5%	-1.3
13970	NA	2.8	2.6	0.2	1.4	61.5%	-1.1
13971	AT4G14510.1 | expressed protein, contains Pfam domain, PF04581: Protein of unknown function (DUF578) | chr4:8337272-8341155 REVERSE | Aliases: DL3295C, FCAALL.243	4.3	4.1	0.3	1.4	61.5%	-0.9
13972	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	2.7	-0.2	-1.4	61.5%	-1.0
13973	AT3G08930.2 | LMBR1 integral membrane family protein, contains 5 transmembrane domains; contains Pfam PF04791: LMBR1-like conserved region; similar to unknown protein GB:BAA83351 (Oryza sativa) | chr3:2713410-2717318 FORWARD | Aliases: T16O11.13	7.2	7.7	-0.5	-1.4	61.5%	-0.5
13974	AT3G46650.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:17197346-17198797 REVERSE | Aliases: F12A12.170	3.7	4.0	-0.4	-1.4	61.5%	-0.7
13975	AT1G44960.1 | expressed protein | chr1:17001989-17004169 FORWARD | Aliases: T12C22.23, T12C22_23	5.0	4.5	0.5	1.4	61.5%	-0.4
13976	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	5.4	5.7	-0.3	-1.4	61.5%	-0.3
13977	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	3.2	3.4	-0.2	-1.4	61.5%	-1.5
13978	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	9.0	8.4	0.6	1.4	61.5%	-0.3

Rank	Description	Sync	Root	M	t	adj.q	B
13979	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	6.2	7.2	-1.0	-1.4	61.5%	-0.3
13980	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	3.7	-0.3	-1.4	61.5%	-0.8
13981	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	2.8	-0.1	-1.4	61.6%	-1.4
13982	AT3G45420.1 | lectin protein kinase family protein, contains Serine/Threonine protein kinases active-site signature, Prosite:PS00108 | chr3:16668248-16670251 REVERSE | Aliases: F18N11.180	2.9	3.1	-0.2	-1.4	61.6%	-1.1
13983	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	4.0	3.7	0.2	1.4	61.6%	-0.6
13984	AT1G74600.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:28028814-28031501 REVERSE | Aliases: F1M20.28, F1M20_28	4.5	4.3	0.2	1.4	61.6%	-0.8
13985	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	2.4	2.2	0.2	1.4	61.6%	-0.9
13986	AT4G39140.4 | expressed protein | chr4:18229325-18232034 REVERSE | Aliases: T22F8.40, T22F8_40	4.8	5.2	-0.4	-1.4	61.6%	-0.4
13987	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	9.6	9.9	-0.3	-1.4	61.6%	-0.9
13988	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	4.0	4.8	-0.8	-1.4	61.6%	-0.1
13989	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	2.7	2.9	-0.2	-1.4	61.6%	-1.0
13990	AT4G00950.1 | expressed protein | chr4:405673-407142 REVERSE | Aliases: A_TM018A10.2, A_TM018A10_2, T18A10.4, T18A10_4	3.3	3.6	-0.2	-1.4	61.6%	-1.1
13991	AT2G40400.2 | expressed protein, similar to GI:7572912 (At3g56140)(Arabidopsis thaliana) | chr2:16876412-16880336 FORWARD | Aliases: T3G21.17, T3G21_17	5.2	4.7	0.5	1.4	61.6%	-0.5
13992	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	4.0	4.3	-0.3	-1.4	61.6%	-0.8
13993	AT1G64740.1 | Symbol: TUA1 | tubulin alpha-1 chain (TUA1), nearly identical to SP:P11139 Tubulin alpha-1 chain {Arabidopsis thaliana}	4.4	4.1	0.3	1.4	61.6%	-0.6
13994	AT5G42620.1 | expressed protein | chr5:17083586-17088569 FORWARD | Aliases: MFO20.3, MFO20_3	3.1	3.3	-0.2	-1.4	61.6%	-1.2
13995	AT4G23970.1 | expressed protein | chr4:12445388-12445690 REVERSE | Aliases: T32A16.140, T32A16_140	2.6	2.8	-0.2	-1.4	61.6%	-1.0
13996	AT2G28580.1 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g44930.1); similar to OSJNBa0070O11.12 [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	3.5	-0.3	-1.4	61.6%	-0.9
13997	AT3G21220.1 | Symbol: ATMKK5 |	4.3	4.6	-0.2	-1.4	61.7%	-0.9
13998	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)	4.9	4.5	0.4	1.4	61.7%	-0.3

Rank	Description	Sync	Root	M	t	adj.q	B
13999	AT2G13900.1 | DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain | chr2:5840126-5842291 FORWARD | Aliases: F17L24.4, F17L24_4	2.7	2.8	-0.2	-1.4	61.7%	-1.1
14000	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	2.9	3.1	-0.3	-1.4	61.7%	-0.9
14001	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	7.2	6.7	0.5	1.4	61.7%	-0.5
14002	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	5.7	-0.3	-1.4	61.7%	-0.8
14003	AT2G30925.1 | hypothetical protein | chr2:13168892-13169020 FORWARD | Aliases: None	2.1	2.2	-0.1	-1.4	61.7%	-1.9
14004	AT5G25750.1 | hypothetical protein | chr5:8950887-8951146 FORWARD | Aliases: T14C9.190, T14C9_190	3.5	3.7	-0.2	-1.4	61.7%	-1.0
14005	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	3.0	-0.2	-1.4	61.7%	-1.0
14006	AT3G24630.1 | expressed protein | chr3:8988405-8990744 FORWARD | Aliases: MSD24.1	3.2	3.4	-0.2	-1.4	61.8%	-0.9
14007	AT1G37020.1 | Ulp1 protease family protein | chr1:14049176-14052183 FORWARD | Aliases: T32E20.20, T32E20_20	2.8	2.9	-0.1	-1.4	61.8%	-1.5
14008	NA	5.5	4.0	1.5	1.4	61.8%	-0.5
14009	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	2.4	2.6	-0.2	-1.4	61.8%	-0.9
14010	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	7.6	8.0	-0.4	-1.4	61.8%	-0.4
14011	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	2.1	-0.1	-1.4	61.8%	-1.8
14012	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	2.7	0.2	1.4	61.8%	-1.0
14013	AT3G05080.1 | expressed protein | chr3:1417913-1418286 FORWARD | Aliases: T12H1.4, T12H1_4	3.2	3.5	-0.3	-1.4	61.8%	-0.5
14014	AT2G20290.1 | Symbol: XIG | myosin, putative, similar to myosin (GI:499047) (Arabidopsis thaliana) | chr2:8750356-8758959 REVERSE | Aliases: ATXIG, F11A3.16, F11A3_16	4.0	3.7	0.3	1.4	61.8%	-0.6
14015	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	3.3	3.6	-0.3	-1.4	61.8%	-0.5
14016	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	4.3	4.0	0.2	1.4	61.9%	-0.9
14017	AT2G37380.1 | expressed protein | chr2:15693852-15694919 FORWARD | Aliases: F3G5.17, F3G5_17	5.4	5.0	0.4	1.4	61.9%	-0.5
14018	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	2.1	2.3	-0.1	-1.4	61.9%	-1.5
14019	AT3G52780.2 | purple acid phosphatase (PAP20), identical to purple acid phosphatase GI:20257491 from (Arabidopsis thaliana) | chr3:19572305-19575173 REVERSE | Aliases: F3C22.180	2.6	2.7	-0.1	-1.4	61.9%	-1.2
14020	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	4.4	-0.3	-1.4	61.9%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
14021	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	7.3	7.9	-0.6	-1.4	61.9%	-0.6
14022	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	2.1	0.1	1.4	61.9%	-1.5
14023	AT1G42710.1 | hypothetical protein | chr1:16080032-16081007 REVERSE | Aliases: F8D11.16	2.9	3.1	-0.2	-1.4	61.9%	-1.3
14024	AT4G28670.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr4:14151393-14153941 FORWARD | Aliases: T5F17.120, T5F17_120	2.6	2.8	-0.2	-1.4	62.0%	-1.1
14025	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	6.3	6.6	-0.3	-1.4	62.0%	-0.7
14026	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	12.1	-0.2	-1.4	62.0%	-1.3
14027	AT2G15740.1 | zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type | chr2:6863828-6864817 REVERSE | Aliases: F9O13.29	2.7	2.9	-0.2	-1.4	62.0%	-1.1
14028	AT1G11270.3 | F-box family protein, contains F-box domain Pfam:PF00646	3.1	3.3	-0.1	-1.4	62.0%	-1.2
14029	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	9.7	10.2	-0.5	-1.4	62.0%	-0.6
14030	AT1G33270.2 | patatin-related, contains Patatin domain PF01734	6.9	6.3	0.6	1.4	62.0%	-0.3
14031	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	3.2	3.3	-0.1	-1.4	62.1%	-1.2
14032	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	2.9	3.1	-0.1	-1.4	62.1%	-1.2
14033	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	3.2	-0.2	-1.4	62.1%	-1.0
14034	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	4.1	4.4	-0.3	-1.4	62.1%	-0.7
14035	AT3G26600.1 | armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat | chr3:9770981-9773272 FORWARD | Aliases: MFE16.13	5.6	5.4	0.3	1.4	62.1%	-0.6
14036	AT3G14860.2 | NHL repeat-containing protein, contains Pfam profile PF01436: NHL repeat	5.4	5.0	0.4	1.4	62.1%	-0.7
14037	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	3.3	-0.2	-1.4	62.1%	-0.9
14038	AT5G42230.1 | Symbol: SCPL41 |	2.9	3.1	-0.2	-1.4	62.1%	-1.1
14039	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	2.4	-0.1	-1.4	62.1%	-1.6
14040	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	2.9	3.2	-0.2	-1.4	62.1%	-1.0
14041	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	2.7	-0.1	-1.4	62.2%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
14042	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	4.1	3.9	0.2	1.4	62.2%	-0.8
14043	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	10.2	9.6	0.6	1.4	62.2%	-0.5
14044	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	9.6	10.0	-0.4	-1.4	62.2%	-0.9
14045	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	3.6	3.4	0.2	1.4	62.3%	-0.7
14046	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	2.6	0.1	1.4	62.3%	-1.2
14047	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)	2.0	2.2	-0.2	-1.4	62.3%	-1.5
14048	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	5.6	0.9	1.4	62.3%	-0.5
14049	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	3.0	-0.2	-1.4	62.3%	-1.2
14050	AT5G52620.1 | F-box family protein, contains Pfam profile: PF00646 F-box domain | chr5:21365780-21366907 REVERSE | Aliases: F6N7.11, F6N7_11	2.4	2.5	-0.1	-1.4	62.3%	-1.5
14051	AT5G39980.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:16018264-16020300 REVERSE | Aliases: MYH19.18, MYH19_18	3.5	3.4	0.2	1.4	62.3%	-1.0
14052	AT2G40316.1 | expressed protein | chr2:16843264-16846540 FORWARD | Aliases: AT2G40313, T7M7.21, T7M7_21	4.5	4.3	0.2	1.4	62.3%	-0.9
14053	AT3G28150.1 | expressed protein | chr3:10473135-10474991 REVERSE | Aliases: MMG15.18	3.7	3.5	0.2	1.4	62.3%	-0.9
14054	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	2.9	3.2	-0.3	-1.4	62.4%	-0.9
14055	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	2.4	-0.1	-1.4	62.4%	-1.4
14056	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	7.7	8.3	-0.7	-1.4	62.4%	-0.6
14057	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	3.0	-0.2	-1.4	62.4%	-0.9
14058	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	7.2	6.9	0.3	1.4	62.5%	-0.7
14059	AT1G35150.1 | hypothetical protein | chr1:12864136-12866216 REVERSE | Aliases: T32G9.31, T32G9_31	2.5	2.7	-0.1	-1.4	62.5%	-1.6
14060	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	3.4	3.6	-0.3	-1.4	62.5%	-1.1
14061	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	3.6	-0.4	-1.4	62.5%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
14062	AT2G40580.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:16950942-16952081 FORWARD | Aliases: T2P4.7, T2P4_7	3.0	3.3	-0.3	-1.4	62.5%	-0.9
14063	AT1G53060.1 | legume lectin family protein | chr1:19779720-19780448 FORWARD | Aliases: F8L10.8, F8L10_8	3.0	2.8	0.2	1.4	62.5%	-1.0
14064	AT5G19810.1 | proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr5:6693054-6693803 FORWARD | Aliases: T29J13.230, T29J13_230	3.3	3.5	-0.3	-1.4	62.5%	-0.9
14065	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	9.4	0.7	1.4	62.5%	-0.8
14066	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	2.6	-0.1	-1.4	62.5%	-1.7
14067	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	7.4	6.7	0.8	1.4	62.5%	-0.1
14068	AT1G69870.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr1:26319690-26323883 FORWARD | Aliases: T17F3.10, T17F3_10	2.7	2.5	0.2	1.4	62.5%	-1.1
14069	AT1G09820.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:3190290-3192416 REVERSE | Aliases: F21M12.21, F21M12_21	4.2	3.9	0.3	1.4	62.6%	-0.6
14070	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	3.3	0.2	1.4	62.6%	-0.7
14071	AT2G16730.1 | Symbol: BGAL13 |	2.0	2.1	-0.1	-1.4	62.6%	-1.8
14072	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	3.0	0.1	1.4	62.6%	-1.4
14073	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	6.1	7.1	-1.0	-1.4	62.6%	-0.2
14074	AT2G38690.1 | expressed protein | chr2:16183554-16184741 REVERSE | Aliases: T6A23.11, T6A23_11	2.5	2.6	-0.1	-1.4	62.6%	-1.2
14075	AT4G07480.1 | hypothetical protein | chr4:4268922-4270170 FORWARD | Aliases: T3E15.12, T3E15_12	2.9	3.0	-0.2	-1.4	62.6%	-1.0
14076	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	3.6	4.0	-0.3	-1.4	62.6%	-0.8
14077	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	2.6	-0.1	-1.4	62.6%	-1.5
14078	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	3.5	-0.3	-1.4	62.6%	-0.7
14079	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	5.3	5.5	-0.2	-1.4	62.6%	-0.8
14080	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	3.6	-0.3	-1.4	62.6%	-0.8
14081	AT1G26710.1 | expressed protein | chr1:9232315-9233131 REVERSE | Aliases: T24P13.9, T24P13_9	2.3	2.4	-0.1	-1.4	62.7%	-1.5
14082	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	3.8	-0.3	-1.4	62.7%	-0.8
14083	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	2.9	3.1	-0.2	-1.4	62.7%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
14084	AT5G27170.1 | expressed protein | chr5:9566010-9566415 FORWARD | Aliases: T21B4.80, T21B4_80	2.1	2.0	0.1	1.4	62.7%	-1.9
14085	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	2.6	-0.2	-1.4	62.7%	-1.1
14086	AT1G17300.1 | expressed protein | chr1:5926987-5927433 FORWARD | Aliases: T13M22.4, T13M22_4	3.0	3.2	-0.2	-1.4	62.7%	-1.2
14087	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	3.1	2.9	0.2	1.4	62.8%	-1.0
14088	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	3.5	-0.2	-1.4	62.8%	-1.0
14089	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	2.9	2.7	0.2	1.4	62.8%	-1.0
14090	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	7.1	6.7	0.4	1.4	62.8%	-0.6
14091	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	7.3	7.6	-0.3	-1.4	62.8%	-0.7
14092	NA	8.2	6.8	1.4	1.4	62.9%	-0.4
14093	AT4G13260.1 | flavin-containing monooxygenase / FMO (YUCCA2), identical to gi:16555354	4.8	4.5	0.2	1.4	62.9%	-0.6
14094	AT4G22753.1 | Symbol: SMO1 3 |	2.4	2.2	0.2	1.4	62.9%	-1.1
14095	AT5G06500.1 | MADS-box family protein, contains similarity to MADS-box transcription factor | chr5:1982445-1983173 FORWARD | Aliases: F15M7.3, F15M7_3	3.2	3.4	-0.2	-1.4	62.9%	-1.2
14096	AT1G10210.2 | Symbol: ATMPK1 |	2.9	3.1	-0.2	-1.4	62.9%	-1.0
14097	AT3G13880.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:4572187-4574433 FORWARD | Aliases: MCP4.10	2.9	2.8	0.1	1.4	63.0%	-1.2
14098	AT2G36900.1 | Symbol: MEMB11 |	8.1	7.9	0.2	1.4	63.0%	-1.0
14099	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	3.0	3.1	-0.2	-1.4	63.0%	-1.2
14100	AT3G51490.1 | sugar transporter family protein, similar to D-xylose proton-symporter (Lactobacillus brevis) GI:2895856; contains Pfam profile PF00083: major facilitator superfamily protein | chr3:19115997-19118541 REVERSE | Aliases: F26O13.130	3.2	3.4	-0.2	-1.4	63.0%	-0.9
14101	AT3G54520.1 | expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At3g54530.1) | chr3:20194538-20196178 REVERSE | Aliases: T14E10.90	2.5	2.7	-0.2	-1.4	63.1%	-1.5
14102	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	2.1	2.2	-0.1	-1.4	63.1%	-1.8
14103	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	4.5	4.8	-0.3	-1.4	63.1%	-0.6
14104	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	4.4	0.2	1.4	63.1%	-0.7
14105	AT4G12590.1 | expressed protein, contains Pfam PF05863: Eukaryotic protein of unknown function (DUF850) | chr4:7451001-7453085 REVERSE | Aliases: T1P17.180, T1P17_180	8.9	7.5	1.4	1.4	63.1%	-0.3

Rank	Description	Sync	Root	M	t	adj.q	B
14106	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)	3.7	3.5	0.2	1.4	63.2%	-1.0
14107	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	7.7	8.0	-0.3	-1.4	63.2%	-0.6
14108	AT4G20130.1 | ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase-related, contains weak similarity to Swiss-Prot:P94026 ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N- methyltransferase, chloroplast precursor (Ribulose- bisphosphate-carboxylase)-lysine N-methyltransferase, RuBisCO methyltransferase, RuBisco LSMT, rbcMT) (Nicotiana tabacum) | chr4:10878916-10881939 FORWARD | Aliases: F1C12.4	3.2	3.1	0.1	1.4	63.2%	-1.5
14109	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	6.2	6.0	0.2	1.4	63.2%	-0.8
14110	AT3G05680.1 | Symbol: EMB2016 | expressed protein | chr3:1660558-1671052 REVERSE | Aliases: EMB2016, EMBRYO DEFECTIVE 2016, F18C1.5, F18C1_5	3.5	3.8	-0.3	-1.4	63.2%	-0.6
14111	AT5G05870.1 | Symbol: UGT76C1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:1767640-1769263 FORWARD | Aliases: K18J17.2, K18J17_2, UGT76C1	5.8	5.6	0.2	1.4	63.3%	-1.0
14112	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	2.2	2.4	-0.2	-1.4	63.3%	-1.2
14113	AT1G43320.1 | hypothetical protein | chr1:16359202-16359558 FORWARD | Aliases: F1I21.16, F1I21_16	3.0	3.1	-0.1	-1.4	63.3%	-1.2
14114	AT5G11400.1 | protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr5:3636615-3638060 REVERSE | Aliases: F2I11.290, F2I11_290	2.3	2.4	-0.1	-1.4	63.3%	-1.2
14115	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	3.2	-0.2	-1.4	63.3%	-0.9
14116	AT4G10970.3 | expressed protein | chr4:6719203-6722198 REVERSE | Aliases: F25I24.180, F25I24_180	7.4	7.6	-0.3	-1.4	63.3%	-0.6
14117	AT1G48000.1 | Symbol: MYB112 |	3.4	3.6	-0.2	-1.4	63.3%	-1.0
14118	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	9.9	9.5	0.4	1.4	63.3%	-0.8
14119	AT2G23840.1 | HNH endonuclease domain-containing protein, contains Pfam profile PF01844: HNH endonuclease | chr2:10160877-10162680 REVERSE | Aliases: T29E15.4, T29E15_4	3.0	3.2	-0.2	-1.4	63.3%	-1.0
14120	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	5.1	5.5	-0.4	-1.4	63.4%	-0.7
14121	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	4.1	0.3	1.4	63.4%	-0.6
14122	AT1G05920.1 | expressed protein, contains Pfam profile PF03754: Domain of unknown function (DUF313) | chr1:1797043-1797990 FORWARD | Aliases: T20M3.20, T20M3_20	2.7	2.9	-0.2	-1.4	63.4%	-1.0
14123	AT3G20700.1 | F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain | chr3:7233531-7234511 REVERSE | Aliases: F3H11.9	3.9	4.4	-0.4	-1.4	63.4%	-0.7
14124	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	2.5	-0.1	-1.4	63.4%	-1.7
14125	AT1G70770.1 | expressed protein | chr1:26691892-26694939 REVERSE | Aliases: F5A18.5, F5A18_5	8.4	7.9	0.5	1.4	63.4%	-0.5
14126	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	5.3	5.7	-0.4	-1.4	63.5%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
14127	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	2.6	0.2	1.4	63.5%	-1.2
14128	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	3.1	-0.2	-1.4	63.5%	-0.7
14129	AT5G22730.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.9	3.7	0.2	1.4	63.5%	-1.2
14130	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	3.4	-0.2	-1.4	63.5%	-1.1
14131	AT2G18070.1 | expressed protein | chr2:7859611-7860748 FORWARD | Aliases: T27K22.6, T27K22_6	2.4	2.6	-0.2	-1.4	63.6%	-1.3
14132	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	4.0	4.6	-0.6	-1.4	63.6%	-0.4
14133	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	2.9	-0.2	-1.4	63.7%	-1.4
14134	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	3.1	-0.1	-1.4	63.7%	-1.4
14135	AT5G50770.1 | short-chain dehydrogenase/reductase (SDR) family protein, similar to sterol-binding dehydrogenase steroleosin GI:15824408 from (Sesamum indicum)	3.1	3.3	-0.2	-1.4	63.7%	-1.0
14136	AT2G46220.1 | expressed protein | chr2:18986544-18987843 FORWARD | Aliases: T3F17.13	6.8	6.2	0.6	1.4	63.7%	-0.3
14137	AT1G03710.1 | expressed protein | chr1:923487-924657 FORWARD | Aliases: F21B7.31	3.1	2.8	0.3	1.4	63.7%	-0.7
14138	AT3G43170.1 | expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295) | chr3:15183136-15183742 REVERSE | Aliases: F7K15.20	2.3	2.4	-0.1	-1.3	63.7%	-1.5
14139	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	4.9	4.5	0.4	1.3	63.7%	-0.7
14140	AT1G12140.1 | flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenase (Cavia porcellus) GI:191259; contains Pfam profile PF00743: Flavin-binding monooxygenase-like | chr1:4121367-4123540 FORWARD | Aliases: T28K15.12, T28K15_12	7.4	8.1	-0.7	-1.3	63.7%	-0.7
14141	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	3.2	-0.2	-1.3	63.7%	-0.9
14142	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	3.5	3.2	0.3	1.3	63.7%	-0.5
14143	AT2G25250.1 | expressed protein | chr2:10760927-10761791 FORWARD | Aliases: T22F11.16, T22F11_16	4.8	5.4	-0.5	-1.3	63.8%	-0.3
14144	AT4G32160.1 | phox (PX) domain-containing protein, contains Pfam profile PF00787: PX domain | chr4:15528811-15533106 FORWARD | Aliases: F10N7.30, F10N7_30	4.4	4.8	-0.3	-1.3	63.8%	-0.5
14145	AT1G49800.1 | expressed protein | chr1:18442033-18442607 REVERSE | Aliases: F10F5.5, F10F5_5	3.4	3.6	-0.2	-1.3	63.8%	-0.8
14146	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	3.7	3.9	-0.2	-1.3	63.8%	-0.9
14147	AT2G18540.1 | cupin family protein, contains Pfam profile PF00190: Cupin | chr2:8049464-8052090 REVERSE | Aliases: F24H14.11, F24H14_11	3.6	3.8	-0.2	-1.3	63.8%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
14148	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	5.5	5.1	0.4	1.3	63.8%	-0.4
14149	AT5G21070.1 | expressed protein | chr5:7156175-7157768 FORWARD | Aliases: T10F18.100, T10F18_100	4.5	4.1	0.4	1.3	63.8%	-0.8
14150	AT2G36940.1 | expressed protein | chr2:15518865-15519066 REVERSE | Aliases: T1J8.12, T1J8_12	3.0	3.2	-0.2	-1.3	63.8%	-1.1
14151	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	2.6	-0.1	-1.3	63.8%	-1.7
14152	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	3.1	3.3	-0.2	-1.3	63.8%	-1.0
14153	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	4.6	4.9	-0.4	-1.3	63.8%	-0.5
14154	AT5G46300.1 | expressed protein | chr5:18800837-18802013 FORWARD | Aliases: MPL12.8, MPL12_8	2.4	2.5	-0.1	-1.3	63.8%	-1.6
14155	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	-1.3	63.8%	-1.7
14156	AT4G16180.1 | expressed protein | chr4:9168338-9170449 REVERSE | Aliases: DL4130C, FCAALL.295	2.9	3.2	-0.2	-1.3	63.9%	-0.9
14157	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	2.9	-0.2	-1.3	63.9%	-1.3
14158	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	2.7	-0.2	-1.3	63.9%	-1.1
14159	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	3.2	2.9	0.4	1.3	63.9%	-0.7
14160	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	3.2	-0.2	-1.3	63.9%	-1.0
14161	AT5G14720.1 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr5:4747934-4753595 REVERSE | Aliases: T9L3.20, T9L3_20	2.7	2.8	-0.1	-1.3	64.0%	-1.2
14162	AT3G62330.1 | zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle | chr3:23074304-23076394 REVERSE | Aliases: T12C14.30	4.5	4.8	-0.3	-1.3	64.0%	-0.6
14163	AT3G15420.1 | expressed protein | chr3:5207711-5208296 REVERSE | Aliases: MJK13.8	4.2	4.6	-0.4	-1.3	64.0%	-0.4
14164	AT1G03880.1 | Symbol: CRU2 | 12S seed storage protein (CRB), identical to 12S seed storage protein, gi:808937 (SP:P15456) (Plant Mol Biol 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	2.6	-0.1	-1.3	64.0%	-1.3
14165	AT5G60290.1 | expressed protein | chr5:24280090-24281069 FORWARD | Aliases: F15L12.16, F15L12_16	3.8	4.1	-0.3	-1.3	64.1%	-0.8
14166	AT3G44780.1 | expressed protein | chr3:16332611-16333591 REVERSE | Aliases: T32N15.5	2.7	2.9	-0.2	-1.3	64.1%	-1.2
14167	AT3G61130.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8 | chr3:22632967-22636691 FORWARD | Aliases: T20K12.30	5.0	4.7	0.3	1.3	64.1%	-0.8
14168	AT3G62370.1 | expressed protein | chr3:23091734-23094240 FORWARD | Aliases: T12C14.70	7.2	6.8	0.4	1.3	64.1%	-0.5
14169	AT1G08410.1 | GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function | chr1:2646186-2649376 FORWARD | Aliases: T27G7.9, T27G7_9	3.5	4.0	-0.5	-1.3	64.1%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
14170	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	3.4	3.6	-0.2	-1.3	64.1%	-1.0
14171	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	3.0	3.2	-0.2	-1.3	64.1%	-0.7
14172	AT4G21720.1 | expressed protein | chr4:11542573-11544286 FORWARD | Aliases: F17L22.180, F17L22_180	4.3	4.0	0.3	1.3	64.1%	-0.8
14173	AT4G15150.1 | glycine-rich protein | chr4:8641673-8642279 REVERSE | Aliases: DL3620C, FCAALL.210	4.1	4.4	-0.3	-1.3	64.1%	-0.7
14174	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	7.1	8.6	-1.6	-1.3	64.1%	-0.5
14175	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	7.1	8.6	-1.6	-1.3	64.1%	-0.5
14176	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	3.5	-0.2	-1.3	64.2%	-1.0
14177	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	10.0	9.0	1.0	1.3	64.2%	-0.4
14178	AT1G78280.1 | transcription factor jumonji (jmjC) domain-containing protein, contains Pfam PF00646: F-box domain; contains Pfam PF02373: jmjC domain; similar to apoptotic cell clearance receptor PtdSerR (GI:11037740) (Mus musculus) | chr1:29457448-29462548 FORWARD | Aliases: F3F9.18, F3F9_18	4.7	5.0	-0.3	-1.3	64.2%	-0.7
14179	AT3G44330.1 | expressed protein | chr3:16017685-16021952 FORWARD | Aliases: T22K7.10	6.0	5.4	0.6	1.3	64.2%	-0.5
14180	AT5G12100.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:3911364-3914076 FORWARD | Aliases: MXC9.6, MXC9_6	4.3	4.5	-0.2	-1.3	64.3%	-1.0
14181	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) GI:1172219	2.6	2.5	0.1	1.3	64.3%	-1.4
14182	AT4G31520.1 | SDA1 family protein, contains Pfam profile PF05285: SDA1	3.1	2.9	0.2	1.3	64.3%	-1.2
14183	AT5G14090.1 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g27025.1) | chr5:4547214-4549419 FORWARD | Aliases: MUA22.9, MUA22_9	2.6	2.8	-0.2	-1.3	64.3%	-1.2
14184	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	3.8	4.2	-0.4	-1.3	64.3%	-0.6
14185	AT5G63290.1 | coproporphyrinogen oxidase-related, low similarity to coproporphyrinogen III oxidase from Geobacillus stearothermophilus (GI:2104798); contains Pfam profile PF04055: radical SAM domain protein	4.4	4.1	0.3	1.3	64.4%	-0.4
14186	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	3.0	3.2	-0.2	-1.3	64.4%	-1.2
14187	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	3.1	-0.2	-1.3	64.4%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
14188	AT1G55030.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.7	2.9	-0.2	-1.3	64.4%	-1.1
14189	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	4.0	4.4	-0.4	-1.3	64.5%	-0.7
14190	AT1G18980.1 | germin-like protein, putative, similar to germin-like protein subfamily T member 1 (SP:P92995); contains PS00725 germin family signature	8.5	7.8	0.7	1.3	64.5%	-0.1
14191	AT1G28650.1 | lipase, putative, strong similarity to lipase (Arabidopsis thaliana) GI:1145627 | chr1:10069533-10071068 REVERSE | Aliases: F1K23.27, F1K23_27	2.3	2.4	-0.1	-1.3	64.5%	-1.4
14192	AT1G23320.1 | alliinase family protein, contains Pfam profiles: PF04864 allinase C-terminal domain, PF04863 alliinase EGF-like domain | chr1:8273412-8275339 REVERSE | Aliases: F26F24.17, F26F24_17	2.8	2.9	-0.1	-1.3	64.5%	-1.4
14193	AT2G34800.1 | hypothetical protein | chr2:14689442-14689594 REVERSE | Aliases: F19I3.3, F19I3_3	2.4	2.5	-0.1	-1.3	64.5%	-1.9
14194	AT2G07680.1 | Symbol: ATMRP11 | ABC transporter family protein | chr2:3515959-3522488 FORWARD | Aliases: T5E7.1	4.8	4.3	0.5	1.3	64.6%	-0.4
14195	AT4G11050.1 | endo-1,4-beta-glucanase, putative / cellulase, putative, similar to endo-beta-1,4-glucanase GI:4972236 from (Fragaria x ananassa) | chr4:6747463-6751307 REVERSE | Aliases: T22B4.30, T22B4_30	3.0	3.1	-0.2	-1.3	64.6%	-1.3
14196	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	2.5	2.6	-0.1	-1.3	64.6%	-1.4
14197	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:BAB84324.1); 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)	8.0	8.6	-0.6	-1.3	64.6%	-0.5
14198	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	9.6	8.7	0.9	1.3	64.6%	-0.4
14199	AT1G15660.1 | expressed protein, similar to CENPCA protein (GI:11863170) {Zea mays} | chr1:5381165-5385249 FORWARD | Aliases: T16N11.16, T16N11_16	6.5	6.1	0.4	1.3	64.6%	-0.3
14200	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	4.2	4.5	-0.3	-1.3	64.6%	-0.7
14201	AT5G55820.1 | expressed protein | chr5:22603513-22611261 FORWARD | Aliases: MDF20.26, MDF20_26	3.0	2.9	0.2	1.3	64.6%	-1.0
14202	AT3G20220.1 | auxin-responsive protein, putative, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana) | chr3:7055066-7055422 FORWARD | Aliases: MAL21.24	2.8	3.0	-0.3	-1.3	64.6%	-1.0
14203	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	3.5	0.5	1.3	64.6%	-0.3
14204	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	3.5	0.5	1.3	64.6%	-0.3
14205	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	2.5	-0.1	-1.3	64.6%	-1.6
14206	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	9.3	8.4	0.9	1.3	64.7%	-0.3

Rank	Description	Sync	Root	M	t	adj.q	B
14207	AT5G04400.1 | Symbol: ANAC077 | no apical meristem (NAM) family protein, ontains Pfam PF02365: No apical meristem (NAM) protein | chr5:1241556-1243359 FORWARD | Aliases: ANAC077, T19N18.130, T19N18_130	3.0	3.2	-0.2	-1.3	64.7%	-1.1
14208	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	4.3	4.0	0.3	1.3	64.7%	-0.8
14209	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	4.0	4.4	-0.4	-1.3	64.8%	-0.9
14210	AT5G42110.1 | expressed protein | chr5:16849284-16849454 REVERSE | Aliases: MJC20.22, MJC20_22	4.7	4.6	0.2	1.3	64.8%	-1.1
14211	AT2G24850.1 | Symbol: TAT3 | aminotransferase, putative, similar to nicotianamine aminotransferase from Hordeum vulgare (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	2.6	2.8	-0.2	-1.3	64.8%	-1.2
14212	AT3G55680.1 | invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	3.2	3.5	-0.3	-1.3	64.8%	-0.7
14213	AT1G49270.1 | protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain | chr1:18231002-18233895 REVERSE | Aliases: F13F21.28, F13F21_28	2.5	2.7	-0.1	-1.3	64.8%	-1.3
14214	AT3G25850.1 | DC1 domain-containing protein, similar to unknown protein GB:AAC79144 from (Arabidopsis thaliana) | chr3:9459415-9460191 REVERSE | Aliases: K9I22.1	2.1	2.3	-0.1	-1.3	64.8%	-1.7
14215	AT5G57730.1 | hypothetical protein | chr5:23410608-23410736 REVERSE | Aliases: MRI1.9, MRI1_9	2.5	2.6	-0.1	-1.3	64.8%	-1.7
14216	AT1G42393.1 | expressed protein | chr1:15864058-15864714 REVERSE | Aliases: None	2.4	2.5	-0.1	-1.3	64.9%	-1.5
14217	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	2.3	0.1	1.3	64.9%	-1.4
14218	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	3.4	-0.2	-1.3	64.9%	-0.9
14219	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	2.2	2.3	-0.1	-1.3	64.9%	-1.4
14220	AT3G04740.1 | Symbol: SWP | expressed protein (SWP1) | chr3:1293813-1300720 FORWARD | Aliases: F7O18.23, F7O18_23, STRUWWELPETER	5.1	5.5	-0.4	-1.3	64.9%	-0.7
14221	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	7.0	7.3	-0.2	-1.3	64.9%	-0.9
14222	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	4.9	4.5	0.3	1.3	64.9%	-0.6
14223	AT5G28810.1 | hypothetical protein | chr5:10824437-10826579 FORWARD | Aliases: T32B20.100, T32B20_100	2.9	3.1	-0.2	-1.3	64.9%	-1.4
14224	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	2.8	-0.1	-1.3	65.0%	-1.2
14225	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	10.3	9.9	0.4	1.3	65.0%	-0.9
14226	AT1G50350.1 | expressed protein | chr1:18652424-18652895 FORWARD | Aliases: F14I3.23, F14I3_23	2.7	2.8	-0.1	-1.3	65.0%	-1.3
14227	AT1G22760.1 | Symbol: PAB3 | polyadenylate-binding protein 3 (PABP3) | chr1:8055315-8059004 FORWARD | Aliases: POLY(A) BINDING PROTEIN 3, T22J18.7, T22J18_7	3.2	3.3	-0.2	-1.3	65.0%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
14228	AT1G76420.1 | Symbol: CUC3 | no apical meristem (NAM) family protein, N-term similar to N-term of NAM GB:CAA63101 (Petunia x hybrida) (apical meristem formation), CUC2 GB:BAA19529 (Arabidopsis thaliana), GRAB2 protein GB:CAA09372 (Triticum sp.)	2.1	2.0	0.1	1.3	65.0%	-1.8
14229	AT5G44530.1 | subtilase family protein, contains Pfam profiles: PF00082 subtilase family | chr5:17955158-17958420 FORWARD | Aliases: MFC16.21, MFC16_21	5.4	5.8	-0.3	-1.3	65.1%	-0.8
14230	AT5G20540.1 | expressed protein | chr5:6947845-6952040 FORWARD | Aliases: F7C8.130, F7C8_130	4.0	3.9	0.2	1.3	65.1%	-1.0
14231	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	5.7	6.4	-0.7	-1.3	65.1%	-0.5
14232	AT2G48010.1 | Symbol: RKF3 | serine/threonine protein kinase (RFK3), identical to receptor-like serine/threonine kinase (Arabidopsis thaliana) gi:2465927:gb:AAC50045	7.5	7.8	-0.3	-1.3	65.1%	-0.9
14233	AT3G28420.1 | expressed protein | chr3:10655707-10656561 REVERSE | Aliases: MFJ20.12	2.8	3.0	-0.2	-1.3	65.1%	-1.4
14234	AT5G52870.1 | expressed protein, similar to unknown protein (gb:AAF24565.1) | chr5:21445190-21446671 REVERSE | Aliases: MXC20.9, MXC20_9	2.7	2.8	-0.2	-1.3	65.1%	-1.2
14235	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	5.8	0.2	1.3	65.1%	-0.7
14236	AT2G12320.1 | hypothetical protein | chr2:4942708-4943368 FORWARD | Aliases: T10J7.30, T10J7_30	2.9	3.1	-0.2	-1.3	65.1%	-1.3
14237	AT3G42340.1 | hypothetical protein, various predicted Helicases, Arabidopsis thaliana | chr3:14498624-14499605 FORWARD | Aliases: T14K23.50	2.6	2.7	-0.1	-1.3	65.1%	-1.5
14238	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	3.1	0.2	1.3	65.1%	-0.8
14239	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	2.4	2.2	0.2	1.3	65.2%	-1.4
14240	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	2.6	2.8	-0.1	-1.3	65.2%	-1.3
14241	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	2.3	2.2	0.1	1.3	65.2%	-1.5
14242	AT1G11860.2 | aminomethyltransferase, putative, similar to aminomethyltransferase, mitochondrial precursor SP:O49849 from (Flaveria anomala) | chr1:4001294-4003441 FORWARD | Aliases: F12F1.30, F12F1_30	9.6	9.9	-0.3	-1.3	65.2%	-0.8
14243	AT4G10010.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr4:6263594-6266242 REVERSE | Aliases: T5L19.140, T5L19_140	3.0	3.1	-0.2	-1.3	65.3%	-1.2
14244	AT3G09530.1 | exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit; | chr3:2926308-2928221 FORWARD | Aliases: F11F8.11	2.9	3.1	-0.2	-1.3	65.3%	-1.0
14245	AT1G18740.1 | expressed protein | chr1:6463985-6466445 FORWARD | Aliases: F6A14.15, F6A14_15	4.1	4.4	-0.3	-1.3	65.3%	-0.5
14246	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	3.5	-0.2	-1.3	65.3%	-1.2
14247	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	3.7	-0.3	-1.3	65.3%	-0.9
14248	AT1G23860.2 | Symbol: SRZ 21 |	6.0	6.5	-0.5	-1.3	65.4%	-0.4
14249	AT3G27473.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.3	2.4	-0.1	-1.3	65.4%	-1.7
14250	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	3.8	4.1	-0.3	-1.3	65.4%	-0.7

Rank	Description	Sync	Root	M	t	adj.q	B
14251	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	8.0	8.4	-0.4	-1.3	65.4%	-0.7
14252	AT4G31280.1 | expressed protein | chr4:15185807-15186011 REVERSE | Aliases: F8F16.100, F8F16_100	3.3	3.5	-0.2	-1.3	65.4%	-1.0
14253	NA	9.9	9.0	0.8	1.3	65.5%	-1.1
14254	AT5G47350.1 | palmitoyl protein thioesterase family protein | chr5:19229916-19231680 FORWARD | Aliases: MQL5.21, MQL5_21	3.2	3.4	-0.2	-1.3	65.5%	-1.1
14255	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	2.5	-0.1	-1.3	65.5%	-1.4
14256	AT5G53100.1 | oxidoreductase, putative, similar to forever young oxidoreductase (FEY3) GI:12004621 from (Arabidopsis thaliana)	3.6	3.7	-0.2	-1.3	65.5%	-1.0
14257	AT3G13062.3 | expressed protein, weak similarity to SP:Q9UKL6 Phosphatidylcholine transfer protein (PC-TP) {Homo sapiens} | chr3:4184576-4187091 FORWARD | Aliases: None	4.8	5.0	-0.2	-1.3	65.5%	-1.0
14258	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	6.6	6.3	0.2	1.3	65.5%	-1.0
14259	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	9.4	10.1	-0.7	-1.3	65.5%	-0.9
14260	AT1G19410.1 | expressed protein | chr1:6714483-6716430 REVERSE | Aliases: F18O14.17, F18O14_17	3.1	3.3	-0.2	-1.3	65.5%	-1.1
14261	AT1G55360.1 | expressed protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function | chr1:20669888-20672392 REVERSE | Aliases: F7A10.1, F7A10_1	4.9	4.3	0.6	1.3	65.5%	-0.4
14262	AT5G59580.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:24023305-24024915 REVERSE | Aliases: F2O15.16, F2O15_16	2.7	2.8	-0.1	-1.3	65.5%	-1.4
14263	AT3G03880.1 | expressed protein | chr3:997806-999268 FORWARD | Aliases: F20H23.7, F20H23_7	5.3	5.5	-0.2	-1.3	65.5%	-1.1
14264	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	6.1	6.5	-0.3	-1.3	65.5%	-0.4
14265	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	6.7	6.9	-0.2	-1.3	65.5%	-0.9
14266	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	6.9	7.2	-0.3	-1.3	65.5%	-0.5
14267	AT2G44040.1 | dihydrodipicolinate reductase family protein, weak similarity to SP:Q52419 Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR) {Pseudomonas syringae} ; contains Pfam profiles PF01113: Dihydrodipicolinate reductase N-terminus, PF05173: Dihydrodipicolinate reductase C-terminus | chr2:18228845-18231107 REVERSE | Aliases: F6E13.17	3.7	3.0	0.7	1.3	65.6%	0.1
14268	AT3G59890.2 | dihydrodipicolinate reductase family protein, weak similarity to SP:Q52419 Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR) {Pseudomonas syringae}; contains Pfam profiles PF01113: Dihydrodipicolinate reductase N-terminus, PF05173: Dihydrodipicolinate reductase C-terminus | chr3:22135175-22137461 REVERSE | Aliases: F24G16.160	3.7	3.0	0.7	1.3	65.6%	0.1
14269	AT1G68220.1 | expressed protein | chr1:25573894-25575375 FORWARD | Aliases: T22E19.15, T22E19_15	9.2	9.5	-0.3	-1.3	65.6%	-1.0
14270	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	2.8	-0.2	-1.3	65.6%	-1.0
14271	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	10.6	10.3	0.3	1.3	65.6%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
14272	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	5.8	6.3	-0.5	-1.3	65.6%	-0.4
14273	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	5.4	5.8	-0.4	-1.3	65.6%	-0.7
14274	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	3.5	3.7	-0.2	-1.3	65.6%	-1.0
14275	AT4G24900.1 | expressed protein | chr4:12814858-12817609 FORWARD | Aliases: F13M23.40, F13M23_40	3.4	3.6	-0.2	-1.3	65.6%	-0.9
14276	AT2G17410.1 | ARID/BRIGHT DNA-binding domain-containing protein, contains Pfam profile PF01388: ARID/BRIGHT DNA binding domain	4.8	4.7	0.2	1.3	65.6%	-1.0
14277	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	5.8	5.2	0.6	1.3	65.6%	-0.7
14278	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	5.2	-0.3	-1.3	65.6%	-0.8
14279	AT4G22430.1 | hypothetical protein | chr4:11827786-11828917 FORWARD | Aliases: F7K2.10, F7K2_10	2.7	2.9	-0.1	-1.3	65.6%	-1.2
14280	AT5G61360.1 | expressed protein | chr5:24688240-24689464 FORWARD | Aliases: MFB13.14, MFB13_14	3.3	3.1	0.2	1.3	65.7%	-0.9
14281	AT3G04080.1 | Symbol: ATAPY1 |	6.2	5.7	0.4	1.3	65.7%	-0.4
14282	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	4.1	4.4	-0.3	-1.3	65.7%	-0.9
14283	AT5G38950.1 | germin-like protein-related, contains some similarity to germin-like protein GI:5869975 from (Triticum aestivum)	2.5	2.7	-0.2	-1.3	65.7%	-1.4
14284	AT2G30280.1 | expressed protein | chr2:12916670-12919417 REVERSE | Aliases: T9D9.9, T9D9_9	5.4	4.8	0.6	1.3	65.7%	-0.5
14285	AT3G04090.1 | major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230 | chr3:1072099-1074102 REVERSE | Aliases: T6K12.29, T6K12_29	8.4	8.8	-0.5	-1.3	65.7%	-0.9
14286	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	2.1	-0.1	-1.3	65.7%	-1.6
14287	AT5G37110.1 | hypothetical protein | chr5:14686824-14692143 FORWARD | Aliases: MJG14.16, MJG14_16	2.5	2.6	-0.1	-1.3	65.7%	-1.8
14288	AT5G60030.1 | expressed protein | chr5:24189308-24190201 REVERSE | Aliases: MGO3.1	7.4	6.2	1.2	1.3	65.7%	-0.4
14289	AT5G35510.1 | expressed protein | chr5:13717060-13717266 FORWARD | Aliases: MOK9.11, MOK9_11	2.4	2.6	-0.1	-1.3	65.8%	-1.7
14290	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	2.5	2.7	-0.2	-1.3	65.8%	-1.2
14291	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	3.2	3.3	-0.2	-1.3	65.8%	-1.1
14292	AT2G13510.1 | hypothetical protein, low similarity to zinc finger protein (Arabidopsis thaliana) GI:976277 | chr2:5637083-5638189 REVERSE | Aliases: T10F5.5, T10F5_5	3.3	3.7	-0.3	-1.3	65.8%	-0.7
14293	AT3G12630.1 | zinc finger (AN1-like) family protein, contains Pfam domain, PF01428: AN1-like Zinc finger | chr3:4012615-4013590 FORWARD | Aliases: T2E22.6	9.1	9.5	-0.4	-1.3	65.8%	-0.6

Rank	Description	Sync	Root	M	t	adj.q	B
14294	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	2.5	2.8	-0.2	-1.3	65.8%	-1.2
14295	AT4G11440.1 | mitochondrial substrate carrier family protein | chr4:6955845-6958548 FORWARD | Aliases: F25E4.60, F25E4_60	2.9	2.8	0.1	1.3	65.8%	-1.4
14296	AT4G26290.1 | expressed protein | chr4:13307604-13307831 REVERSE | Aliases: T25K17.100, T25K17_100	2.6	2.8	-0.1	-1.3	65.8%	-1.3
14297	AT1G78740.1 | similar to F-box family protein [Arabidopsis thaliana] (TAIR:At1g69630.1) | chr1:29615387-29616385 REVERSE | Aliases: F9K20.22, F9K20_22	3.9	4.2	-0.3	-1.3	65.8%	-0.7
14298	AT2G40050.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	2.8	-0.2	-1.3	65.8%	-1.4
14299	AT1G01390.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr1:148120-149806 REVERSE | Aliases: F6F3.19, F6F3_19	3.2	3.4	-0.1	-1.3	65.9%	-1.2
14300	AT2G05290.1 | expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277 | chr2:1924847-1926678 REVERSE | Aliases: F5G3.19, F5G3_19	2.6	2.8	-0.2	-1.3	65.9%	-1.2
14301	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	6.0	5.7	0.3	1.3	65.9%	-0.6
14302	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	7.2	7.5	-0.3	-1.3	65.9%	-0.6
14303	AT4G16590.1 | Symbol: ATCSLA01 | glucosyltransferase-related, low similarity to beta-(1-3)-glucosyl transferase (Bradyrhizobium japonicum) GI:3687658	2.4	2.5	-0.2	-1.3	65.9%	-1.4
14304	AT1G66510.3 | AAR2 protein family, contains Pfam profile PF05282: AAR2 protein	2.7	2.6	0.1	1.3	65.9%	-1.3
14305	AT3G06720.2 | Symbol: AT IMP |	4.4	4.7	-0.3	-1.3	66.0%	-0.6
14306	AT3G19300.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:6690124-6693290 REVERSE | Aliases: MLD14.2	4.7	4.2	0.5	1.3	66.0%	-0.5
14307	AT3G45880.1 | expressed protein | chr3:16879974-16882529 REVERSE | Aliases: F16L2.90	3.0	2.8	0.2	1.3	66.0%	-1.2
14308	AT3G03230.1 | esterase/lipase/thioesterase family protein, contains Interpro entry IPR000379 | chr3:744396-746016 REVERSE | Aliases: T17B22.8, T17B22_8	3.5	3.7	-0.2	-1.3	66.1%	-1.1
14309	AT5G61740.1 | Symbol: ATATH14 | ABC transporter family protein, ABC family transporter, Entamoeba histolytica, TREMBL:EH058 | chr5:24825710-24829823 FORWARD | Aliases: MAC9.5, MAC9_5	2.3	2.5	-0.1	-1.3	66.1%	-1.4
14310	AT5G01500.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr5:198948-201551 FORWARD | Aliases: F7A7.20, F7A7_20	6.4	5.8	0.6	1.3	66.1%	-0.7
14311	AT3G18295.1 | expressed protein | chr3:6281210-6282087 FORWARD | Aliases: MIE15.10	3.4	3.2	0.1	1.3	66.2%	-1.1
14312	AT1G47280.1 | expressed protein | chr1:17334499-17336846 REVERSE | Aliases: T3F24.20, T3F24_20	3.2	3.4	-0.2	-1.3	66.2%	-1.0
14313	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	8.4	8.7	-0.3	-1.3	66.2%	-0.7
14314	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	5.4	5.7	-0.3	-1.3	66.2%	-0.9
14315	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	2.4	2.7	-0.3	-1.3	66.2%	-1.1
14316	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	3.2	-0.2	-1.3	66.2%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
14317	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	2.0	2.0	-0.1	-1.3	66.2%	-1.8
14318	AT4G01610.2 | cathepsin B-like cysteine protease, putative, similar to cathepsin B-like cysteine proteinase GI:609175 from (Nicotiana rustica); contains an unusually short, 5nt exon | chr4:694695-697126 FORWARD | Aliases: T15B16.17, T15B16_17	8.9	9.8	-0.9	-1.3	66.2%	-0.5
14319	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	4.8	-0.4	-1.3	66.2%	-0.8
14320	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	2.6	-0.1	-1.3	66.3%	-1.4
14321	AT5G39520.1 | expressed protein, predicted protein, Synechocystis sp., PIR:S77152 | chr5:15840681-15842720 REVERSE | Aliases: MUL8.22, MUL8_22	3.1	2.9	0.1	1.3	66.3%	-1.2
14322	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	4.0	0.5	1.3	66.3%	-0.6
14323	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	2.9	3.1	-0.2	-1.3	66.3%	-1.2
14324	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	5.8	-0.4	-1.3	66.3%	-0.8
14325	AT2G34340.1 | expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584 | chr2:14495865-14496681 REVERSE | Aliases: F13P17.18, F13P17_18	3.8	4.1	-0.3	-1.3	66.3%	-0.6
14326	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	3.0	0.2	1.3	66.3%	-1.2
14327	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	3.5	-0.2	-1.3	66.3%	-1.0
14328	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	2.9	-0.2	-1.3	66.3%	-0.9
14329	AT4G39930.1 | expressed protein | chr4:18518337-18518977 REVERSE | Aliases: T5J17.100, T5J17_100	2.4	2.6	-0.2	-1.3	66.3%	-1.3
14330	AT3G27380.1 | Symbol: SDH2 1 |	8.6	8.1	0.5	1.3	66.3%	-0.9
14331	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	8.0	8.4	-0.4	-1.3	66.3%	-0.5
14332	AT2G39910.1 | expressed protein | chr2:16667674-16670122 FORWARD | Aliases: T28M21.7, T28M21_7	3.2	3.0	0.1	1.3	66.4%	-1.4
14333	AT3G05240.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:1493690-1495387 REVERSE | Aliases: T12H1.21, T12H1_21	3.9	3.7	0.2	1.3	66.4%	-0.7
14334	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	3.0	-0.2	-1.3	66.4%	-1.1
14335	AT1G25380.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr1:8903522-8905989 FORWARD | Aliases: F4F7.45	7.9	8.2	-0.3	-1.3	66.4%	-0.9
14336	ATMG00690.1 | Symbol: ORF240A | hypothetical protein | chrM:203588-204310 REVERSE | Aliases: ORF240A	6.8	5.6	1.2	1.3	66.4%	-0.2
14337	AT1G22970.1 | expressed protein | chr1:8130705-8132197 REVERSE | Aliases: F19G10.8, F19G10_8	5.3	5.6	-0.3	-1.3	66.4%	-0.7

Rank	Description	Sync	Root	M	t	adj.q	B
14338	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	2.9	-0.1	-1.3	66.4%	-1.4
14339	AT3G19780.1 | expressed protein | chr3:6870205-6874856 FORWARD | Aliases: MMB12.5	2.9	3.1	-0.1	-1.3	66.5%	-1.7
14340	AT2G45470.1 | Symbol: FLA8 | fasciclin-like arabinogalactan-protein (FLA8) | chr2:18749614-18751185 REVERSE | Aliases: F4L23.2	4.8	5.5	-0.7	-1.3	66.5%	-0.4
14341	AT1G74380.1 | galactosyl transferase GMA12/MNN10 family protein, very low similarity to alpha-1,2-galactosyltransferase, Schizosaccharomyces pombe (SP:Q09174)	6.0	6.3	-0.3	-1.3	66.5%	-0.7
14342	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	2.9	2.8	0.1	1.3	66.5%	-1.6
14343	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	6.6	6.3	0.3	1.3	66.5%	-0.5
14344	AT3G46780.1 | expressed protein | chr3:17239658-17242186 FORWARD | Aliases: T6H20.190	2.3	2.2	0.1	1.3	66.5%	-1.5
14345	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) (Arabidopsis thaliana) | chr1:19898895-19899401 REVERSE | Aliases: None	2.2	2.3	-0.1	-1.3	66.5%	-1.9
14346	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	2.7	-0.1	-1.3	66.5%	-1.5
14347	AT1G02660.1 | lipase class 3 family protein, contains Pfam profile PF01764: Lipase | chr1:571955-574981 REVERSE | Aliases: T14P4.6, T14P4_6	3.8	4.0	-0.2	-1.3	66.5%	-0.9
14348	AT1G15350.3 | expressed protein | chr1:5278286-5279860 REVERSE | Aliases: F9L1.29, F9L1_29	5.4	5.8	-0.4	-1.3	66.6%	-0.5
14349	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	3.6	-0.3	-1.3	66.6%	-0.9
14350	AT5G48200.1 | expressed protein | chr5:19562481-19564496 FORWARD | Aliases: MIF21.9, MIF21_9	3.3	3.5	-0.2	-1.3	66.6%	-0.8
14351	AT5G25430.1 | anion exchange protein family, contains similarity to SWISS-PROT:P02730 anion transport protein (Anion exchange protein 1) (Human){Homo sapiens}	2.6	2.8	-0.2	-1.3	66.6%	-1.0
14352	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	9.6	8.9	0.6	1.3	66.6%	-0.8
14353	AT5G46790.1 | expressed protein, similar to unknown protein (pir::T05073) | chr5:19001097-19001986 REVERSE | Aliases: MZA15.21, MZA15_21	4.7	4.9	-0.2	-1.3	66.6%	-0.7
14354	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	6.7	7.2	-0.4	-1.3	66.6%	-0.7
14355	AT2G33720.1 | expressed protein | chr2:14270808-14272278 FORWARD | Aliases: T1B8.29, T1B8_29	2.5	2.7	-0.2	-1.3	66.7%	-1.3
14356	AT5G62220.1 | exostosin family protein, contains Pfam profile: PF03016	5.3	5.0	0.3	1.3	66.7%	-0.7
14357	AT5G64570.1 | Symbol: XYL4 | glycosyl hydrolase family 3 protein | chr5:25827341-25830561 REVERSE | Aliases: ATBXL4, MUB3.9, MUB3_9	5.9	6.3	-0.4	-1.3	66.7%	-0.4
14358	AT3G32260.1 | hypothetical protein | chr3:13222881-13225169 FORWARD | Aliases: F6H5.17	3.0	3.2	-0.2	-1.3	66.7%	-1.2
14359	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	3.7	3.9	-0.2	-1.3	66.7%	-0.9
14360	AT2G26200.1 | expressed protein | chr2:11159804-11163544 FORWARD | Aliases: T1D16.16, T1D16_16	5.4	5.2	0.2	1.3	66.7%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
14361	AT2G20470.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr2:8833358-8836578 REVERSE | Aliases: T13C7.6, T13C7_6	2.8	2.9	-0.1	-1.3	66.8%	-1.3
14362	AT2G36750.1 | Symbol: UGT72C1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:15417541-15419117 REVERSE | Aliases: F13K3.15, F13K3_15, UGT72C1	2.7	2.9	-0.2	-1.3	66.8%	-1.1
14363	AT2G07505.1 | hypothetical protein, and genefinder | chr2:3125668-3126170 FORWARD | Aliases: F9A16.18	3.7	3.9	-0.3	-1.3	66.8%	-0.9
14364	AT1G03390.1 | transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus (gi:2239091); contains Pfam transferase family domain PF002458 | chr1:841032-842417 REVERSE | Aliases: F21B7.2, F21B7_2	3.0	3.2	-0.1	-1.3	66.8%	-1.3
14365	AT5G25530.1 | DNAJ heat shock protein, putative, simlar 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	2.7	2.8	-0.2	-1.3	66.8%	-1.3
14366	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	3.5	-0.2	-1.3	66.8%	-1.1
14367	AT2G02660.1 | expressed protein | chr2:738503-739768 FORWARD | Aliases: T8K22.4, T8K22_4	2.7	2.8	-0.1	-1.3	66.9%	-1.9
14368	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	2.6	-0.1	-1.3	66.9%	-1.6
14369	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	2.7	-0.2	-1.3	66.9%	-1.3
14370	AT1G72070.1 | DNAJ heat shock N-terminal domain-containing protein, similar to TCJ2 (Trypanosoma cruzi) GI:886414; contains Pfam profile: PF00226: DnaJ domain	2.8	2.7	0.2	1.3	67.0%	-1.1
14371	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	2.8	3.0	-0.2	-1.3	67.0%	-1.0
14372	AT5G48340.1 | expressed protein | chr5:19607765-19610115 FORWARD | Aliases: K23F3.6, K23F3_6	8.9	8.2	0.6	1.3	67.0%	-1.0
14373	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	3.5	3.7	-0.2	-1.3	67.0%	-1.1
14374	AT4G11510.1 | Symbol: RALFL28 | expressed protein, ; expression supported by MPSS | chr4:6984046-6984303 REVERSE | Aliases: F25E4.130, F25E4_130, RALF LIKE 28	3.0	3.3	-0.3	-1.3	67.0%	-0.9
14375	AT1G08810.2 | Symbol: MYB60 | myb family transcription factor (MYB60)	2.1	2.2	-0.1	-1.3	67.0%	-1.8
14376	AT4G00480.1 | Symbol: ATMYC1 |	2.6	2.8	-0.2	-1.3	67.0%	-1.3
14377	AT5G41250.1 | exostosin family protein, contains Pfam profile: PF03016	2.2	2.3	-0.1	-1.3	67.0%	-1.7
14378	AT5G22810.1 | GDSL-motif lipase, putative, similar to EXL3 (GP:15054386) (Arabidopsis thaliana) | chr5:7621571-7623370 FORWARD | Aliases: MRN17.4, MRN17_4	2.6	2.7	-0.2	-1.3	67.1%	-1.3
14379	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	3.1	3.3	-0.2	-1.3	67.1%	-1.0
14380	AT3G09030.1 | potassium channel tetramerisation domain-containing protein, contains Pfam profile PF02214: K+ channel tetramerisation domain | chr3:2754787-2756511 FORWARD | Aliases: T16O11.1	4.9	5.1	-0.2	-1.3	67.1%	-1.1
14381	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	2.3	2.4	-0.1	-1.3	67.2%	-1.7
14382	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	2.8	-0.1	-1.3	67.2%	-1.5
14383	AT5G20120.1 | expressed protein | chr5:6795891-6797155 FORWARD | Aliases: F5O24.10, F5O24_10	5.4	5.7	-0.3	-1.3	67.2%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
14384	AT4G38110.1 | similar to PREDICTED: similar to MGC53988 protein [Gallus gallus] (GB:XP_415906.1) | chr4:17888521-17892120 REVERSE | Aliases: F20D10.230, F20D10_230	2.7	2.8	-0.2	-1.3	67.2%	-1.1
14385	AT5G51320.1 | expressed protein, contains Pfam profile PF03778: Protein of unknown function (DUF321) | chr5:20873295-20874090 REVERSE | Aliases: MFG13.2, MFG13_2	2.5	2.7	-0.1	-1.3	67.2%	-1.6
14386	AT2G16500.1 | Symbol: ADC1 | arginine decarboxylase 1 (SPE1) (ARGDC), identical to SP:Q9SI64 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	8.4	8.0	0.4	1.3	67.2%	-0.5
14387	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	2.2	2.4	-0.1	-1.3	67.2%	-1.5
14388	AT3G05140.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:1435704-1438347 REVERSE | Aliases: T12H1.10, T12H1_10	2.4	2.5	-0.1	-1.3	67.2%	-1.3
14389	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	5.4	5.8	-0.5	-1.3	67.2%	-0.6
14390	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	2.4	0.1	1.3	67.2%	-1.4
14391	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	2.8	-0.1	-1.3	67.3%	-1.2
14392	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	5.1	5.4	-0.3	-1.3	67.3%	-0.7
14393	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	2.9	-0.2	-1.3	67.4%	-1.1
14394	AT4G01460.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.0	3.2	-0.2	-1.3	67.4%	-1.3
14395	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	3.2	-0.1	-1.3	67.4%	-1.3
14396	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	4.9	0.3	1.3	67.4%	-0.8
14397	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	8.5	7.9	0.6	1.3	67.4%	-0.4
14398	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	9.0	0.4	1.3	67.4%	-0.8
14399	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	7.0	6.0	1.0	1.3	67.4%	0.0
14400	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	7.0	6.0	1.0	1.3	67.4%	0.0
14401	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	2.6	2.9	-0.2	-1.3	67.4%	-1.2
14402	AT3G05790.1 | Lon protease, putative, similar to Lon protease homolog 2 SP:P93655 | chr3:1720160-1725188 REVERSE | Aliases: F10A16.8, F10A16_8	2.6	2.4	0.2	1.3	67.4%	-0.9
14403	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	3.2	3.6	-0.3	-1.3	67.4%	-0.6
14404	AT3G15510.1 | Symbol: ATNAC2 |	3.9	4.2	-0.3	-1.3	67.5%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
14405	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	4.2	4.4	-0.2	-1.3	67.5%	-1.1
14406	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	3.4	3.2	0.2	1.3	67.5%	-0.8
14407	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	9.0	9.3	-0.3	-1.3	67.5%	-1.0
14408	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	2.3	-0.1	-1.3	67.5%	-1.3
14409	AT2G39160.1 | expressed protein | chr2:16340568-16341251 REVERSE | Aliases: T16B24.20, T16B24_20	4.0	4.3	-0.3	-1.3	67.5%	-1.0
14410	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	2.9	2.7	0.2	1.3	67.5%	-1.2
14411	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	3.5	-0.4	-1.3	67.5%	-0.7
14412	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	3.5	3.1	0.3	1.3	67.5%	-0.7
14413	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	2.7	2.8	-0.2	-1.3	67.5%	-1.2
14414	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	2.9	-0.2	-1.3	67.5%	-1.3
14415	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	8.6	9.3	-0.7	-1.3	67.6%	-0.4
14416	AT5G03905.1 | hesB-like domain-containing protein, low similarity to HesB (Cyanothece sp. PCC 8801) GI:2183309; contains Pfam profile PF01521: HesB-like domain | chr5:1052579-1054231 FORWARD | Aliases: None	6.2	6.4	-0.2	-1.3	67.6%	-0.8
14417	AT5G15400.1 | U-box domain-containing protein, contains Pfam profile PF04564: U-box domain | chr5:4997716-5003143 REVERSE | Aliases: T20K14.10, T20K14_10	6.8	7.1	-0.4	-1.3	67.6%	-0.7
14418	AT1G15590.1 | hypothetical protein | chr1:5367369-5368418 FORWARD | Aliases: T16N11.26, T16N11_26	2.6	2.8	-0.2	-1.3	67.6%	-1.2
14419	AT1G29490.1 | auxin-responsive family protein, similar to auxin-induced protein X10A (SP:P33080) (Glycine max)	2.4	2.3	0.1	1.3	67.6%	-1.7
14420	AT2G12520.1 | expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At4g04070.1) | chr2:5111500-5112898 REVERSE | Aliases: T27D6.9, T27D6_9	3.2	3.4	-0.2	-1.3	67.6%	-1.2
14421	AT5G55040.1 | DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487 | chr5:22347146-22347986 REVERSE | Aliases: K13P22.4, K13P22_4	3.1	3.3	-0.2	-1.3	67.7%	-1.3
14422	AT3G30250.1 | expressed protein | chr3:11893238-11893911 REVERSE | Aliases: MIL15.16	2.5	2.7	-0.2	-1.3	67.7%	-1.1
14423	AT4G40020.1 | expressed protein | chr4:18553447-18555294 REVERSE | Aliases: T5J17.190, T5J17_190	2.5	2.6	-0.1	-1.3	67.7%	-1.4
14424	AT1G62520.1 | expressed protein | chr1:23148077-23149174 FORWARD | Aliases: T3P18.8, T3P18_8	4.9	5.1	-0.2	-1.3	67.7%	-1.1
14425	AT5G51800.1 | expressed protein | chr5:21065417-21069238 FORWARD | Aliases: MIO24.6, MIO24_6	2.7	2.8	-0.1	-1.3	67.7%	-1.6
14426	AT1G10920.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.6	2.7	-0.2	-1.3	67.7%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
14427	AT1G12450.1 | expressed protein | chr1:4244308-4245990 FORWARD | Aliases: F5O11.19, F5O11_19	4.1	4.3	-0.3	-1.3	67.8%	-0.9
14428	AT4G24330.1 | expressed protein, hypothetical protein - Caenorhabditis elegans,PID:e1350884 | chr4:12603531-12606338 REVERSE | Aliases: T22A6.160, T22A6_160	10.1	9.8	0.3	1.3	67.8%	-1.2
14429	AT3G19420.1 | expressed protein | chr3:6731463-6735629 FORWARD | Aliases: MLD14.22	7.0	7.3	-0.3	-1.3	67.8%	-0.7
14430	AT5G17150.1 | expressed protein | chr5:5638872-5639594 REVERSE | Aliases: F2K13.300, F2K13_300	2.7	2.6	0.1	1.3	67.8%	-1.6
14431	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	8.4	7.3	1.1	1.3	67.8%	-0.3
14432	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	3.6	-0.1	-1.3	67.8%	-1.2
14433	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	3.6	-0.2	-1.3	67.9%	-1.1
14434	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	4.8	-0.2	-1.3	67.9%	-1.0
14435	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	3.0	-0.2	-1.3	68.0%	-1.2
14436	AT3G11460.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:3608256-3610127 FORWARD | Aliases: F24K9.13	4.0	3.8	0.1	1.3	68.0%	-1.3
14437	AT4G31760.1 | peroxidase, putative, similar to peroxidase (Spinacia oleracea) gi:1781338:emb:CAA71496 | chr4:15368266-15369730 REVERSE | Aliases: F28M20.50, F28M20_50	3.6	3.9	-0.2	-1.3	68.0%	-0.9
14438	AT1G73500.1 | Symbol: ATMKK9 |	6.8	7.1	-0.3	-1.3	68.0%	-0.6
14439	AT1G10330.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:3388749-3390152 FORWARD | Aliases: F14N23.21, F14N23_21	4.2	3.9	0.3	1.3	68.0%	-0.5
14440	AT4G07430.1 | expressed protein, similar to At2g10840, At5g35280, At2g10500, At2g05860, At4g07310, At1g39270 | chr4:4222504-4223524 REVERSE | Aliases: F28D6.17, F28D6_17	2.1	2.2	-0.1	-1.3	68.0%	-1.6
14441	AT4G07350.1 | hypothetical protein | chr4:4172606-4175224 REVERSE | Aliases: F28D6.10, F28D6_10	2.9	3.1	-0.2	-1.3	68.0%	-1.1
14442	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	2.5	0.2	1.3	68.0%	-1.4
14443	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	3.3	3.5	-0.2	-1.3	68.1%	-1.3
14444	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	2.4	-0.1	-1.3	68.1%	-1.8
14445	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	2.8	3.0	-0.2	-1.3	68.1%	-1.2
14446	AT3G25910.1 | expressed protein | chr3:9490486-9492729 FORWARD | Aliases: MPE11.8	8.4	7.9	0.5	1.3	68.1%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
14447	AT4G26650.2 | similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At5g55550.3); similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At5g55550.2); similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At5g55550.1); similar to putative RNA-binding protein [Oryza sativa (japonica cultivar-group)] (GB:AAP54226.1); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)	6.5	6.3	0.3	1.3	68.1%	-0.7
14448	AT2G15860.1 | expressed protein, and genefinder | chr2:6912470-6916477 REVERSE | Aliases: F19G14.14, F19G14_14	5.9	5.5	0.4	1.3	68.1%	-0.8
14449	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	6.8	7.2	-0.4	-1.3	68.1%	-0.7
14450	AT5G27520.1 | mitochondrial substrate carrier family protein | chr5:9714385-9716308 REVERSE | Aliases: F21A20.230, F21A20_230	6.5	6.3	0.3	1.3	68.1%	-0.7
14451	AT3G05610.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr3:1625678-1628179 REVERSE | Aliases: F18C1.12, F18C1_12	2.5	2.6	-0.1	-1.3	68.1%	-1.3
14452	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	2.7	-0.2	-1.3	68.1%	-1.2
14453	AT2G45980.1 | expressed protein | chr2:18924425-18926182 REVERSE | Aliases: F4I18.37, F4I18_37	7.8	8.3	-0.5	-1.3	68.1%	-0.4
14454	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	2.6	2.6	-0.1	-1.3	68.1%	-1.8
14455	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	3.1	-0.2	-1.3	68.2%	-1.1
14456	AT1G30135.1 | expressed protein | chr1:10596476-10597222 FORWARD | Aliases: None	2.6	2.4	0.1	1.3	68.2%	-1.5
14457	AT3G62490.1 | expressed protein, hypothetical proteins - Arabidopsis thaliana | chr3:23123476-23125975 REVERSE | Aliases: T12C14.190	2.4	2.4	-0.1	-1.3	68.2%	-1.9
14458	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	5.8	5.3	0.5	1.3	68.2%	-0.6
14459	AT3G12520.1 | Symbol: SULTR4;2 | sulfate transporter family protein, similar to sulfate transporter (Arabidopsis thaliana) GI:3777483; contains Pfam profiles PF00916: Sulfate transporter family, PF01740: STAS domain | chr3:3967823-3971925 REVERSE | Aliases: SULFATE TRANSPORTER, T2E22.36	6.1	5.7	0.3	1.3	68.2%	-0.9
14460	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	5.1	5.3	-0.2	-1.3	68.2%	-0.8
14461	AT1G03990.1 | alcohol oxidase-related, low similarity to long chain fatty alcohol oxidase from Candida cloacae (GI:6983581), Candida tropicalis (GI:6983594); Location of EST 248L9T7, gb:AA713296 | chr1:1024846-1027615 FORWARD | Aliases: F21M11.7, F21M11_7	3.3	3.6	-0.3	-1.3	68.2%	-0.8
14462	AT4G14200.1 | expressed protein | chr4:8185365-8188719 REVERSE | Aliases: DL3140C, FCAALL.116	3.1	2.9	0.2	1.3	68.2%	-0.9
14463	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	4.4	4.1	0.3	1.3	68.2%	-0.4
14464	AT1G73960.2 | similar to TATA box binding protein (TBP)-associated factor 150kDa [Danio rerio] (GB:AAT68099.1)	6.7	7.5	-0.8	-1.3	68.2%	-0.3
14465	AT3G15605.1 | expressed protein | chr3:5287970-5290948 FORWARD | Aliases: MQD17.8	3.2	3.4	-0.2	-1.3	68.2%	-0.9
14466	AT3G29190.1 | terpene synthase/cyclase family protein, contains Pfam profile: PF01397 terpene synthase family | chr3:11160610-11163800 REVERSE | Aliases: MXO21.3	3.9	4.2	-0.3	-1.3	68.2%	-0.8
14467	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	2.8	-0.2	-1.3	68.2%	-1.3
14468	AT3G62500.1 | expressed protein, hypothetical proteins - Arabidopsis thaliana; expression supported by MPSS | chr3:23131399-23133198 FORWARD | Aliases: T12C14.200	3.6	3.8	-0.2	-1.3	68.2%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
14469	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	5.3	4.7	0.6	1.3	68.2%	-0.7
14470	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	7.6	6.7	0.9	1.3	68.3%	-0.2
14471	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	3.4	0.2	1.3	68.3%	-1.2
14472	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)	5.4	5.9	-0.4	-1.3	68.4%	-0.5
14473	AT4G01530.1 | hypothetical protein | chr4:663408-665102 FORWARD | Aliases: F11O4.8, F11O4_8	2.6	2.8	-0.1	-1.3	68.5%	-1.3
14474	AT4G32695.1 | expressed protein, hypothetical protein yjbI, Bacillus subtilis, PIR2:A69844 | chr4:15768353-15769772 FORWARD | Aliases: None	2.5	2.7	-0.1	-1.3	68.5%	-1.4
14475	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	3.6	-0.3	-1.3	68.5%	-0.8
14476	AT5G05130.1 | 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) | chr5:1512121-1515080 FORWARD | Aliases: MUG13.1, MUG13_1	3.9	4.1	-0.2	-1.3	68.5%	-1.0
14477	AT4G15360.1 | Symbol: CYP705A3 | cytochrome P450 family protein | chr4:8770223-8771899 FORWARD | Aliases: DL3725W, FCAALL.277	2.8	3.0	-0.2	-1.3	68.5%	-1.3
14478	AT5G38300.1 | expressed protein, predicted protein, rice | chr5:15323162-15324238 FORWARD | Aliases: MSI17.3, MSI17_3	5.8	6.1	-0.3	-1.3	68.5%	-0.7
14479	AT3G63460.2 | Symbol: EMB2221 | WD-40 repeat family protein, hypothetical protein contains similarity to ec31p (Oryza sativa) 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	4.4	-0.3	-1.3	68.5%	-1.0
14480	AT3G44800.1 | meprin and TRAF homology domain-containing protein / MATH domain-containing protein | chr3:16354320-16357014 FORWARD | Aliases: T32N15.3	2.3	2.4	-0.1	-1.3	68.5%	-1.7
14481	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	4.4	4.7	-0.3	-1.3	68.6%	-0.9
14482	ATCG01010.1 | Symbol: NDHF | Chloroplast encoded NADH dehydrogenase unit. | chrC:110398-112638 REVERSE | Aliases: NDHF	3.0	3.7	-0.7	-1.3	68.6%	-0.5
14483	AT2G22340.1 | expressed protein | chr2:9499959-9501035 REVERSE | Aliases: F14M13.26, F14M13_26	2.8	3.1	-0.2	-1.3	68.7%	-1.2
14484	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	2.5	0.2	1.3	68.7%	-1.2
14485	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	10.0	9.6	0.4	1.3	68.7%	-0.9
14486	AT3G13780.1 | expressed protein | chr3:4525079-4526221 FORWARD | Aliases: MMM17.21	6.5	7.5	-1.0	-1.3	68.7%	-0.6
14487	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	2.6	2.9	-0.2	-1.3	68.8%	-1.2
14488	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	4.9	4.7	0.3	1.3	68.8%	-0.6

Rank	Description	Sync	Root	M	t	adj.q	B
14489	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	3.2	-0.2	-1.3	68.8%	-1.2
14490	AT4G22580.1 | exostosin family protein, contains Pfam profile: PF03016	2.9	2.7	0.2	1.3	68.8%	-1.4
14491	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	9.7	9.2	0.5	1.3	68.9%	-1.1
14492	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	3.8	4.0	-0.2	-1.3	68.9%	-1.1
14493	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	3.2	-0.1	-1.3	68.9%	-1.6
14494	AT4G10020.1 | short-chain dehydrogenase/reductase (SDR) family protein, similar to sterol-binding dehydrogenase steroleosin GI:15824408 from (Sesamum indicum)	2.6	2.8	-0.2	-1.3	68.9%	-1.1
14495	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	2.8	3.0	-0.2	-1.3	68.9%	-1.1
14496	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	3.3	3.5	-0.2	-1.3	68.9%	-1.0
14497	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	2.6	2.7	-0.1	-1.3	69.0%	-1.3
14498	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	2.9	-0.1	-1.3	69.0%	-1.2
14499	AT2G17470.1 | expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	3.2	3.4	-0.2	-1.3	69.0%	-1.2
14500	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	3.6	3.8	-0.2	-1.3	69.0%	-1.0
14501	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	3.9	3.6	0.3	1.3	69.1%	-0.6
14502	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	3.3	-0.2	-1.3	69.1%	-1.1
14503	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	4.6	4.8	-0.2	-1.3	69.1%	-1.0
14504	AT3G47440.1 | major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230 | chr3:17493010-17494364 FORWARD | Aliases: T21L8.190	3.4	3.7	-0.2	-1.3	69.1%	-1.0
14505	AT5G64610.1 | histone acetyltransferase, putative, similar to histone acetyltransferase (Homo sapiens) gi:8317213:gb:AAF72665 | chr5:25845386-25847750 REVERSE | Aliases: MUB3.13, MUB3_13	5.8	6.1	-0.3	-1.3	69.2%	-0.8
14506	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	2.3	2.5	-0.1	-1.3	69.2%	-1.4
14507	AT4G29030.1 | glycine-rich protein, glycine-rich protein - Onobrychis viciifolia,PID:g2565429 | chr4:14307255-14307979 FORWARD | Aliases: F19B15.60, F19B15_60	4.8	5.1	-0.3	-1.3	69.3%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
14508	AT4G27730.1 | Symbol: ATOPT6 |	3.6	3.3	0.2	1.3	69.3%	-0.8
14509	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) GI:13183564, GI:13183566 | chr4:14796770-14800927 FORWARD | Aliases: ARABIDOPSIS P450 REDUCTASE 2, F9N11.60, F9N11_60	5.3	5.8	-0.5	-1.3	69.3%	-0.7
14510	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	3.1	-0.2	-1.3	69.3%	-1.2
14511	AT5G13350.1 | auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter | chr5:4279887-4282290 FORWARD | Aliases: T22N19.4	2.8	2.9	-0.2	-1.3	69.3%	-1.3
14512	AT5G25100.1 | endomembrane protein 70, putative, TM4 family; | chr5:8648106-8651115 REVERSE | Aliases: T11H3.110, T11H3_110	7.2	6.9	0.4	1.3	69.3%	-1.0
14513	AT5G28310.1 | oxidoreductase-related, low similarity to glyoxylate reductase from Thermococcus litoralis (gi:13515409)	2.9	3.2	-0.2	-1.3	69.4%	-1.1
14514	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	8.1	7.7	0.4	1.3	69.4%	-1.2
14515	AT4G10925.2 | F-box family protein, contains Pfam PF00646: F-box domain | chr4:6702766-6704618 REVERSE | Aliases: None	5.8	6.1	-0.3	-1.3	69.4%	-0.8
14516	AT3G24190.1 | ABC1 family protein, contains Pfam domain, PF03109: ABC1 family | chr3:8743297-8747861 FORWARD | Aliases: MUJ8.9	6.8	7.1	-0.3	-1.3	69.4%	-0.7
14517	AT5G19670.1 | exostosin family protein, contains Pfam domain, PF03016: Exostosin family | chr5:6646721-6649500 FORWARD | Aliases: T29J13.90, T29J13_90	3.9	4.1	-0.2	-1.3	69.4%	-1.0
14518	AT5G29020.1 | expressed protein | chr5:11041955-11046506 FORWARD | Aliases: F3F24.120, F3F24_120	3.3	3.5	-0.2	-1.3	69.4%	-1.0
14519	AT2G34555.1 | Symbol: ATGA2OX3 | gibberellin 2-oxidase / GA2-oxidase (GA2OX3), identical to ga2ox3 (GI:4678370) | chr2:14564067-14565776 FORWARD | Aliases: ATGA2OX3	2.7	2.9	-0.2	-1.3	69.5%	-1.2
14520	AT3G30810.1 | expressed protein | chr3:12495302-12498859 FORWARD | Aliases: K11J14.2	3.9	4.2	-0.3	-1.3	69.5%	-0.8
14521	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	3.2	2.9	0.3	1.3	69.6%	-0.9
14522	AT1G63540.1 | hydroxyproline-rich glycoprotein family protein | chr1:23571158-23573158 FORWARD | Aliases: F2K11.10, F2K11_10	2.6	2.8	-0.2	-1.3	69.6%	-1.2
14523	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	2.7	2.8	-0.1	-1.3	69.6%	-1.4
14524	AT2G17020.1 | F-box family protein (FBL10), contains similarity to F-box protein Partner of Paired GI:10441427 from (Drosophila melanogaster) | chr2:7403419-7405920 REVERSE | Aliases: F6P23.18, F6P23_18	3.2	3.5	-0.3	-1.3	69.7%	-0.8
14525	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	2.9	0.3	1.3	69.7%	-0.9
14526	AT4G36540.2 | basic helix-loop-helix (bHLH) family protein, contains Pfam domain, PF00010: Helix-loop-helix DNA-binding domain	5.2	4.9	0.2	1.3	69.7%	-0.7
14527	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	3.6	3.8	-0.2	-1.3	69.7%	-0.9
14528	AT4G13690.1 | expressed protein | chr4:7953658-7955090 REVERSE | Aliases: F18A5.80, F18A5_80	4.0	3.6	0.4	1.3	69.7%	-0.6
14529	AT2G26430.1 | Symbol: RCY1 | ania-6a type cyclin (RCY1), nearly identical to ania-6a type cyclin (Arabidopsis thaliana) GI:13924511 | chr2:11250297-11253107 REVERSE | Aliases: ARGININE RICH CYCLIN 1, ATRCY1, T9J22.10, T9J22_10	6.6	6.3	0.2	1.3	69.8%	-0.9
14530	AT2G26210.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr2:11164230-11166369 FORWARD | Aliases: T1D16.15, T1D16_15	4.8	4.4	0.3	1.3	69.8%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
14531	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	8.1	7.8	0.3	1.3	69.9%	-0.9
14532	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	4.5	-0.3	-1.3	69.9%	-0.9
14533	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	2.4	2.6	-0.1	-1.3	69.9%	-1.6
14534	AT4G22790.1 | MATE efflux family protein, contains Pfam profile PF01554: Uncharacterized membrane protein family | chr4:11975042-11976759 REVERSE | Aliases: T12H17.180, T12H17_180	4.9	4.5	0.4	1.3	69.9%	-0.5
14535	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	8.9	7.8	1.1	1.3	70.0%	-0.2
14536	AT1G73655.1 | 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 PF00254: peptidyl-prolyl cis-trans isomerase, FKBP-type | chr1:27694020-27695475 REVERSE | Aliases: None	7.3	7.0	0.3	1.3	70.0%	-0.9
14537	AT4G26170.1 | expressed protein | chr4:13258130-13259391 FORWARD | Aliases: T25K17.5	3.1	2.9	0.2	1.3	70.0%	-1.4
14538	AT5G40070.1 | hypothetical protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana) | chr5:16056407-16056975 FORWARD | Aliases: MUD12.50, MUD12_50	2.2	2.4	-0.1	-1.3	70.1%	-1.8
14539	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	3.1	-0.2	-1.3	70.1%	-1.1
14540	AT5G40560.1 | DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana) | chr5:16261771-16263747 FORWARD | Aliases: MNF13.8, MNF13_8	2.6	2.8	-0.1	-1.3	70.1%	-1.6
14541	AT2G28010.1 | aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease | chr2:11937656-11938846 REVERSE | Aliases: T1E2.7, T1E2_7	2.4	2.6	-0.2	-1.3	70.1%	-1.1
14542	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	3.2	2.7	0.5	1.3	70.1%	-0.8
14543	AT3G11800.1 | expressed protein | chr3:3726114-3727734 FORWARD | Aliases: F26K24.9	8.0	8.6	-0.6	-1.3	70.1%	-0.8
14544	AT1G50280.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr1:18627366-18630063 REVERSE | Aliases: F14I3.11, F14I3_11	2.6	2.5	0.1	1.3	70.1%	-1.5
14545	AT3G10010.1 | HhH-GPD base excision DNA repair family protein, similar to DEMETER protein (Arabidopsis thaliana) GI:21743571; contains Pfam profile PF00730: HhH-GPD superfamily base excision DNA repair protein | chr3:3081819-3088200 REVERSE | Aliases: T22K18.18	2.8	3.0	-0.2	-1.3	70.2%	-1.0
14546	AT1G11290.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:3791454-3793883 REVERSE | Aliases: T28P6.20, T28P6_20	3.6	3.5	0.2	1.3	70.2%	-1.0
14547	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	5.0	4.6	0.3	1.3	70.2%	-0.6
14548	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	3.1	-0.1	-1.3	70.2%	-1.3
14549	AT3G13680.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.9	3.5	0.4	1.3	70.2%	-0.8
14550	AT3G15910.1 | expressed protein | chr3:5382067-5383075 FORWARD | Aliases: MVC8.3	3.3	3.6	-0.2	-1.3	70.2%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
14551	AT2G21650.1 | myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA-binding domain | chr2:9266663-9267736 FORWARD | Aliases: F2G1.8, F2G1_8	2.9	2.8	0.2	1.3	70.2%	-1.1
14552	AT1G65420.1 | expressed protein, contains Pfam profile PF04483: Protein of unknown function (DUF565) | chr1:24301148-24302233 REVERSE | Aliases: T8F5.20, T8F5_20	5.3	5.1	0.2	1.3	70.2%	-0.9
14553	AT4G26440.1 | Symbol: WRKY34 |	2.2	2.3	-0.1	-1.3	70.3%	-1.4
14554	AT3G43330.1 | hypothetical protein, putative proteins - Arabidopsis thaliana | chr3:15290335-15292896 FORWARD | Aliases: T5C2.30	2.3	2.4	-0.2	-1.3	70.3%	-1.1
14555	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	4.1	4.5	-0.4	-1.3	70.3%	-0.5
14556	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	3.5	0.2	1.3	70.3%	-1.2
14557	AT2G14540.1 | serpin family protein / serine protease inhibitor family protein, similar to phloem serpin-1 (Cucurbita maxima) GI:9937311; contains Pfam profile PF00079: Serpin (serine protease inhibitor) | chr2:6204745-6206488 REVERSE | Aliases: T13P21.8, T13P21_8	2.3	2.5	-0.2	-1.3	70.3%	-1.3
14558	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	2.8	2.9	-0.1	-1.3	70.3%	-1.4
14559	AT1G46696.1 | expressed protein, slight similarity to maebl (GI:20087019)(Plasmodium falciparum). | chr1:17264300-17266623 REVERSE | Aliases: F2G19.33, F2G19_33	2.2	2.1	0.1	1.3	70.3%	-1.7
14560	AT3G56260.1 | expressed protein | chr3:20878950-20880003 REVERSE | Aliases: F18O21.220	3.2	3.4	-0.2	-1.3	70.4%	-1.1
14561	AT5G24316.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr5:8278780-8279967 REVERSE | Aliases: None	3.0	3.2	-0.2	-1.3	70.4%	-1.1
14562	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	6.2	5.9	0.3	1.3	70.4%	-0.8
14563	AT5G59170.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr5:23899214-23900348 FORWARD | Aliases: MNC17.8, MNC17_8	3.1	3.3	-0.2	-1.3	70.4%	-1.1
14564	AT3G55820.1 | expressed protein | chr3:20725020-20725634 FORWARD | Aliases: F1I16.230	3.2	3.0	0.2	1.3	70.4%	-1.1
14565	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	3.4	3.6	-0.3	-1.3	70.5%	-0.9
14566	AT3G17010.1 | transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain. Activated by AGAMOUS ina 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	4.1	3.9	0.3	1.3	70.5%	-1.2
14567	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	2.3	2.4	-0.1	-1.3	70.5%	-1.7
14568	AT5G17950.1 | hypothetical protein | chr5:5944555-5944961 REVERSE | Aliases: MCM23.2, MCM23_2	2.8	3.1	-0.3	-1.3	70.6%	-1.0
14569	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	6.3	6.9	-0.6	-1.3	70.6%	-0.6
14570	AT4G35180.1 | amino acid transporter family protein, similar to amino acid permease 1 GI:976402 from (Nicotiana sylvestris); contains Pfam profile PF01490: Transmembrane amino acid transporter protein | chr4:16738344-16740371 REVERSE | Aliases: T12J5.50, T12J5_50	3.6	3.4	0.2	1.3	70.7%	-1.3
14571	AT3G63290.2 | expressed protein | chr3:23392659-23394513 FORWARD | Aliases: MAA21.8	3.6	3.4	0.2	1.3	70.7%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
14572	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	2.9	-0.2	-1.3	70.8%	-1.1
14573	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	4.1	-0.3	-1.3	70.8%	-0.9
14574	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	3.6	3.8	-0.2	-1.3	70.8%	-0.9
14575	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	4.0	3.7	0.3	1.3	70.9%	-0.5
14576	AT2G16820.1 | hypothetical protein | chr2:7297186-7298034 REVERSE | Aliases: T24I21.23, T24I21_23	2.9	3.0	-0.1	-1.3	70.9%	-1.6
14577	AT3G22700.1 | F-box family protein, contains Pfam:PF00646 F-box domain	2.8	2.6	0.2	1.3	70.9%	-1.6
14578	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	3.1	0.2	1.3	71.0%	-1.2
14579	AT5G63450.1 | Symbol: CYP94B1 | cytochrome P450, putative | chr5:25426121-25427799 REVERSE | Aliases: MLE2.8, MLE2_8	3.8	3.6	0.2	1.3	71.0%	-1.3
14580	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	4.5	4.9	-0.4	-1.3	71.0%	-0.7
14581	AT2G20440.1 | RabGAP/TBC domain-containing protein, similar to SP:P09379 GTPase-activating protein GYP7 (Fragment) {Yarrowia lipolytica}; contains Pfam profile PF00566: TBC domain | chr2:8817857-8820604 REVERSE | Aliases: T13C7.3, T13C7_3	4.5	4.1	0.4	1.3	71.0%	-0.4
14582	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	6.0	5.7	0.2	1.3	71.0%	-0.8
14583	AT5G61840.1 | exostosin family protein, contains Pfam profile: PF03016	6.5	6.1	0.4	1.3	71.0%	-0.5
14584	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	3.3	3.2	0.2	1.3	71.0%	-1.2
14585	AT4G09630.1 | expressed protein, contains Pfam profile: PF04765 protein of unknown function (DUF616) | chr4:6083710-6088131 FORWARD | Aliases: T25P22.70, T25P22_70	4.7	4.4	0.3	1.3	71.1%	-0.6
14586	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	6.0	6.6	-0.6	-1.3	71.1%	-0.7
14587	AT3G24640.1 | expressed protein | chr3:8992296-8992768 FORWARD | Aliases: MSD24.4	2.2	2.3	-0.1	-1.3	71.1%	-1.6
14588	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	-0.1	-1.3	71.1%	-1.9
14589	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 HOMEOBOX PROTEIN	3.1	3.3	-0.2	-1.3	71.1%	-1.0
14590	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	2.9	2.7	0.2	1.3	71.1%	-0.9
14591	AT1G47770.1 | expressed protein | chr1:17592706-17593701 FORWARD | Aliases: T2E6.25, T2E6_25	2.3	2.4	-0.1	-1.3	71.1%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
14592	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	3.5	-0.2	-1.3	71.1%	-1.1
14593	AT3G26800.1 | expressed protein | chr3:9863410-9864015 FORWARD | Aliases: MDJ14.10	4.7	4.3	0.5	1.3	71.1%	-0.3
14594	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	2.2	-0.1	-1.3	71.1%	-2.0
14595	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	2.6	-0.1	-1.3	71.1%	-1.3
14596	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	3.1	-0.2	-1.3	71.1%	-1.5
14597	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	2.4	-0.1	-1.3	71.2%	-1.7
14598	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	2.9	2.7	0.2	1.3	71.2%	-1.0
14599	AT2G26810.1 | expressed protein, and genefinder | chr2:11440811-11443156 REVERSE | Aliases: F12C20.15, F12C20_15	5.5	5.1	0.4	1.3	71.2%	-0.5
14600	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	3.0	-0.1	-1.2	71.2%	-1.5
14601	AT4G07940.1 | hypothetical protein | chr4:4792670-4794106 FORWARD | Aliases: F1K3.1, F1K3_1	4.7	4.5	0.2	1.2	71.2%	-1.0
14602	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	6.7	7.1	-0.4	-1.2	71.2%	-0.6
14603	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	8.6	8.3	0.3	1.2	71.2%	-0.8
14604	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	2.6	-0.1	-1.2	71.2%	-1.5
14605	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	2.1	-0.1	-1.2	71.2%	-1.8
14606	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	4.4	-0.3	-1.2	71.2%	-0.8
14607	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	6.5	6.2	0.3	1.2	71.3%	-0.6
14608	AT5G67280.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:26859496-26862416 REVERSE | Aliases: K3G17.4, K3G17_4	5.7	5.5	0.2	1.2	71.3%	-1.0
14609	AT2G13950.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.3	3.5	-0.3	-1.2	71.3%	-0.9
14610	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	3.9	4.3	-0.4	-1.2	71.3%	-0.6
14611	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	3.0	-0.2	-1.2	71.3%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
14612	ATMG00660.1 | Symbol: ORF149 |	9.0	10.2	-1.2	-1.2	71.3%	-0.7
14613	AT1G37000.1 | expressed protein | chr1:14038479-14039586 FORWARD | Aliases: T32E20.25, T32E20_25	2.5	2.7	-0.2	-1.2	71.4%	-1.4
14614	AT3G29610.1 | hypothetical protein | chr3:11412081-11412569 FORWARD | Aliases: MTO24.8	2.6	2.7	-0.1	-1.2	71.4%	-1.4
14615	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	9.7	0.9	1.2	71.4%	-0.4
14616	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	4.4	-0.3	-1.2	71.4%	-0.9
14617	AT1G65000.1 | expressed protein | chr1:24150707-24152352 FORWARD | Aliases: F13O11.34, F13O11_34	6.1	5.9	0.3	1.2	71.4%	-0.6
14618	AT5G49400.1 | zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle | chr5:20047956-20049392 FORWARD | Aliases: K7J8.7, K7J8_7	6.3	5.8	0.5	1.2	71.4%	-0.8
14619	AT4G08310.1 | expressed protein, glutamic acid-rich protein precursor - Plasmodium falciparum, PIR2:A54514 | chr4:5248861-5252145 REVERSE | Aliases: T12G13.150, T12G13_150	7.9	7.4	0.5	1.2	71.4%	-0.6
14620	AT5G20640.1 | expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567) | chr5:6984381-6985207 FORWARD | Aliases: T1M15.40, T1M15_40	5.7	5.4	0.3	1.2	71.5%	-0.8
14621	AT3G01170.1 | expressed protein | chr3:57675-58914 FORWARD | Aliases: T4P13.14, T4P13_14	5.2	5.3	-0.2	-1.2	71.5%	-1.1
14622	AT2G15360.1 | expressed protein | chr2:6701869-6702247 REVERSE | Aliases: F26H6.12, F26H6_12	2.6	2.7	-0.1	-1.2	71.6%	-1.7
14623	AT1G32780.1 | alcohol dehydrogenase, putative, similar to alcohol dehydrogenase GB:CAA37333 GI:297178 from (Solanum tuberosum); contains Pfam zinc-binding dehydrogenase domain PF00107 | chr1:11869809-11872774 REVERSE | Aliases: F6N18.16, F6N18_16	2.5	2.7	-0.1	-1.2	71.6%	-1.2
14624	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	3.4	3.2	0.2	1.2	71.7%	-0.9
14625	AT3G02500.1 | expressed protein | chr3:519371-521754 FORWARD | Aliases: F16B3.13, F16B3_13	3.0	2.8	0.2	1.2	71.7%	-1.2
14626	AT3G12060.1 | expressed protein, similar to hypothetical protein GB:CAB82953 GI:7340710 from (Arabidopsis thaliana) | chr3:3843148-3845156 FORWARD | Aliases: MEC18.19	2.9	3.0	-0.2	-1.2	71.7%	-1.4
14627	AT5G01460.1 | LMBR1 integral membrane family protein, contains Pfam PF04791: LMBR1-like conserved region | chr5:186693-190456 FORWARD | Aliases: T10O8.170, T10O8_170	3.7	3.9	-0.2	-1.2	71.7%	-0.9
14628	AT2G16810.1 | F-box family protein (FBX8), contains F-box domain PF:00646 | chr2:7294494-7296027 REVERSE | Aliases: T24I21.22, T24I21_22	2.2	2.3	-0.1	-1.2	71.7%	-1.8
14629	AT1G07150.1 | Symbol: MAPKKK13 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719	4.5	4.8	-0.3	-1.2	71.8%	-0.7
14630	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	2.3	2.4	-0.1	-1.2	71.8%	-1.2
14631	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	3.7	3.9	-0.2	-1.2	71.8%	-0.9
14632	AT4G08330.1 | expressed protein | chr4:5254654-5256701 REVERSE | Aliases: T28D5.20, T28D5_20	4.4	4.7	-0.2	-1.2	71.8%	-0.8
14633	AT5G18150.1 | expressed protein, similar to unknown protein (emb:CAB87627.1) | chr5:6000016-6000333 REVERSE | Aliases: MRG7.11, MRG7_11	7.7	8.0	-0.2	-1.2	71.8%	-0.8
14634	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	3.3	3.4	-0.2	-1.2	71.9%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
14635	AT5G66560.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr5:26581465-26584079 FORWARD | Aliases: K1F13.23, K1F13_23	3.4	3.2	0.2	1.2	71.9%	-0.9
14636	AT4G38120.1 | expressed protein | chr4:17894166-17896101 REVERSE | Aliases: F20D10.240, F20D10_240	2.3	2.4	-0.1	-1.2	72.0%	-1.5
14637	AT5G36250.1 | protein phosphatase 2C, putative / PP2C, putative | chr5:14299333-14301811 FORWARD | Aliases: T30G6.11, T30G6_11	4.3	4.7	-0.3	-1.2	72.0%	-0.7
14638	AT1G31270.1 | hypothetical protein | chr1:11178330-11178639 FORWARD | Aliases: T19E23.20	2.7	2.8	-0.1	-1.2	72.0%	-1.5
14639	AT2G19360.1 | hypothetical protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function | chr2:8385746-8390456 FORWARD | Aliases: F27F23.16, F27F23_16	2.6	2.8	-0.1	-1.2	72.0%	-1.3
14640	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	2.7	-0.2	-1.2	72.1%	-1.2
14641	AT1G02640.1 | Symbol: BXL2 | glycosyl hydrolase family 3 protein, similar to beta-xylosidase GB:Z84377 GI:2102655 from (Aspergillus niger) | chr1:564205-567769 FORWARD | Aliases: ATBXL2, BETA XYLOSIDASE 2, T14P4.8, T14P4_8	5.3	5.9	-0.6	-1.2	72.1%	-0.6
14642	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	3.1	-0.2	-1.2	72.1%	-1.1
14643	AT3G42140.1 | expressed protein | chr3:14313046-14314004 REVERSE | Aliases: T27B3.10	3.0	3.2	-0.2	-1.2	72.1%	-1.3
14644	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	8.0	-0.3	-1.2	72.1%	-0.8
14645	AT1G66900.1 | expressed protein | chr1:24962997-24965279 FORWARD | Aliases: T4O24.3, T4O24_3	4.6	4.3	0.3	1.2	72.1%	-0.7
14646	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	3.0	2.8	0.2	1.2	72.1%	-1.2
14647	AT4G22340.3 | similar to phosphatidate cytidylyltransferase / 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 cytidylyltransferase (InterPro:IPR000374) | chr4:11799971-11802840 REVERSE | Aliases: T10I14.170, T10I14_170	6.2	5.8	0.3	1.2	72.2%	-0.7
14648	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	9.1	8.0	1.1	1.2	72.2%	-0.5
14649	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	2.8	-0.1	-1.2	72.2%	-1.4
14650	AT1G49975.1 | expressed protein | chr1:18508484-18509265 FORWARD | Aliases: None	2.3	2.1	0.1	1.2	72.2%	-1.7
14651	AT3G29130.1 | expressed protein, ; expression supported by MPSS | chr3:11103783-11105084 REVERSE | Aliases: MXE2.11	5.2	4.9	0.3	1.2	72.2%	-0.7
14652	AT3G58590.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:21677059-21679464 FORWARD | Aliases: F14P22.180	3.4	3.2	0.2	1.2	72.3%	-1.0
14653	AT4G24980.1 | nodulin MtN21 family protein, similar to MtN21 (Medicago truncatula) GI:2598575 | chr4:12847528-12848386 REVERSE | Aliases: F13M23.120, F13M23_120	3.0	3.2	-0.2	-1.2	72.3%	-1.3
14654	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	3.0	-0.2	-1.2	72.3%	-1.2
14655	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	2.6	2.8	-0.2	-1.2	72.3%	-1.1
14656	AT3G47295.1 | expressed protein | chr3:17438935-17439496 FORWARD | Aliases: None	2.4	2.6	-0.1	-1.2	72.4%	-1.4
14657	AT4G24460.1 | expressed protein | chr4:12642898-12645438 FORWARD | Aliases: T22A6.290, T22A6_290	4.6	4.9	-0.3	-1.2	72.4%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
14658	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	5.6	0.4	1.2	72.4%	-0.7
14659	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	7.5	6.2	1.3	1.2	72.4%	-0.3
14660	AT1G53070.1 | legume lectin family protein, contains Pfam domain, PF00139: Legume lectins beta domain | chr1:19782039-19783041 FORWARD | Aliases: F8L10.7, F8L10_7	3.1	3.3	-0.1	-1.2	72.4%	-1.1
14661	AT2G17820.1 | Symbol: ATHK1 | histidine kinase 1, 99% identical to GP:4586626	4.3	4.8	-0.4	-1.2	72.5%	-0.6
14662	AT2G23040.1 | expressed protein, ; expression supported by MPSS | chr2:9814973-9816289 REVERSE | Aliases: F21P24.10, F21P24_10	2.9	2.7	0.2	1.2	72.5%	-1.1
14663	AT4G28310.1 | expressed protein | chr4:14017414-14018554 FORWARD | Aliases: F26K10.190, F26K10_190	5.2	4.7	0.5	1.2	72.5%	-0.2
14664	AT3G15550.1 | expressed protein, ; expression supported by MPSS | chr3:5267358-5268228 FORWARD | Aliases: MJK13.21	3.2	3.3	-0.1	-1.2	72.5%	-1.7
14665	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	5.8	6.1	-0.3	-1.2	72.5%	-0.8
14666	AT2G04500.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.5	2.7	-0.2	-1.2	72.5%	-1.2
14667	ATMG00010.1 | Symbol: ORF153A | hypothetical protein | chrM:273-734 REVERSE | Aliases: ORF153A	3.3	4.0	-0.7	-1.2	72.5%	-0.5
14668	AT3G19140.1 | expressed protein | chr3:6614916-6615341 REVERSE | Aliases: MVI11.4	2.3	2.4	-0.1	-1.2	72.5%	-1.8
14669	AT4G10420.1 | expressed protein | chr4:6453414-6454205 REVERSE | Aliases: F7L13.3	2.8	3.0	-0.2	-1.2	72.5%	-1.3
14670	AT1G59530.1 | bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor | chr1:21871927-21872373 FORWARD | Aliases: T30E16.6, T30E16_6	2.4	2.4	0.1	1.2	72.5%	-1.7
14671	AT1G79890.1 | helicase-related, similar to CHL1 potential helicase protein (GI:2632247) (Homo sapiens); similar to helicase GB:AAB06962 (Homo sapiens)	3.7	3.5	0.1	1.2	72.5%	-1.3
14672	AT1G67800.3 | copine-related, low similarity to SP:Q99829 Copine I {Homo sapiens} | chr1:25424443-25427386 REVERSE | Aliases: F12A21.7, F12A21_7	5.5	5.7	-0.2	-1.2	72.5%	-0.9
14673	AT5G21050.1 | expressed protein | chr5:7147892-7148959 FORWARD | Aliases: T10F18.80, T10F18_80	3.8	4.1	-0.2	-1.2	72.5%	-1.2
14674	AT1G52580.1 | rhomboid family protein, contains PFAM domain PF01694, Rhomboid family | chr1:19591306-19592721 FORWARD | Aliases: F6D8.20, F6D8_20	3.8	4.0	-0.2	-1.2	72.5%	-1.2
14675	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	4.8	4.6	0.2	1.2	72.5%	-1.0
14676	AT4G37980.2 | Symbol: ELI3 1 |	2.5	2.7	-0.2	-1.2	72.6%	-1.2
14677	AT3G19570.2 | expressed protein, contains Pfam domain, PF04484: Family of unknown function (DUF566) | chr3:6797491-6801738 FORWARD | Aliases: MMB12.3	2.9	2.8	0.2	1.2	72.6%	-1.2
14678	AT4G30590.1 | plastocyanin-like domain-containing protein | chr4:14935629-14936568 REVERSE | Aliases: F17I23.70, F17I23_70	3.6	3.8	-0.2	-1.2	72.6%	-1.0
14679	AT1G05400.1 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537 | chr1:1584341-1585243 FORWARD | Aliases: T25N20.5, T25N20_5	3.9	3.5	0.3	1.2	72.6%	-0.9
14680	AT2G30930.1 | expressed protein | chr2:13169517-13170473 FORWARD | Aliases: F7F1.14, F7F1_14	8.8	8.4	0.4	1.2	72.7%	-0.4
14681	AT1G29790.1 | expressed protein | chr1:10429961-10432018 FORWARD | Aliases: F1N18.26, F1N18_26	7.3	7.0	0.3	1.2	72.7%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
14682	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	2.4	-0.2	-1.2	72.7%	-1.6
14683	AT4G29160.2 | SNF7 family protein, contains Pfam domain, PF03357: SNF7 family | chr4:14380810-14382672 FORWARD | Aliases: F19B15.190, F19B15_190	8.9	8.7	0.2	1.2	72.8%	-1.0
14684	AT1G10930.1 | Symbol: ATSGS1 |	3.2	3.0	0.2	1.2	72.8%	-0.7
14685	AT1G09190.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:2966122-2971459 REVERSE | Aliases: T12M4.11, T12M4_11	3.7	3.5	0.3	1.2	72.8%	-0.8
14686	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	6.9	7.2	-0.3	-1.2	72.9%	-0.8
14687	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	2.2	0.1	1.2	72.9%	-1.8
14688	AT2G25610.1 | H+-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	7.7	7.0	0.7	1.2	72.9%	-0.6
14689	AT5G05220.1 | expressed protein | chr5:1550268-1550929 FORWARD | Aliases: K18I23.2, K18I23_2	3.6	3.5	0.1	1.2	72.9%	-1.5
14690	AT3G12180.1 | cornichon family protein, contains Pfam profile: PF03311 cornichon protein | chr3:3883369-3884812 FORWARD | Aliases: F28J15.3	6.2	5.7	0.5	1.2	72.9%	-0.8
14691	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	2.8	2.9	-0.2	-1.2	72.9%	-1.3
14692	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	2.5	-0.1	-1.2	72.9%	-1.7
14693	AT4G11460.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr4:6964463-6967088 FORWARD | Aliases: F25E4.80, F25E4_80	2.3	2.2	0.1	1.2	73.0%	-1.6
14694	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	8.0	8.3	-0.3	-1.2	73.0%	-0.8
14695	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	3.5	3.2	0.3	1.2	73.0%	-0.8
14696	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:	8.2	8.4	-0.2	-1.2	73.1%	-1.1
14697	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	2.9	-0.1	-1.2	73.1%	-1.3
14698	AT3G44950.1 | glycine-rich protein | chr3:16432030-16432271 FORWARD | Aliases: F14D17.20	7.0	6.6	0.4	1.2	73.1%	-0.6
14699	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	2.8	-0.2	-1.2	73.2%	-1.4
14700	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	3.5	3.4	0.2	1.2	73.2%	-1.1
14701	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) (Arabidopsis thaliana) | chr2:187797-190368 REVERSE | Aliases: F2I9.5, F2I9_5	2.7	2.8	-0.1	-1.2	73.2%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
14702	AT3G57440.1 | expressed protein | chr3:21269657-21271493 FORWARD | Aliases: T8H10.40	3.3	3.5	-0.2	-1.2	73.2%	-1.1
14703	AT5G25880.1 | malate oxidoreductase, putative, similar to NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (SP:P12628) {Phaseolus vulgaris}	3.9	4.1	-0.3	-1.2	73.2%	-0.8
14704	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	7.3	6.8	0.5	1.2	73.2%	-0.7
14705	AT2G38510.1 | MATE efflux protein-related, contains Pfam profile PF01554: Uncharacterized membrane protein family | chr2:16131063-16132523 FORWARD | Aliases: T6A23.29, T6A23_29	2.5	2.4	0.2	1.2	73.3%	-1.5
14706	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	5.5	5.8	-0.3	-1.2	73.3%	-0.8
14707	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	3.2	3.3	-0.1	-1.2	73.3%	-1.3
14708	AT2G15340.1 | glycine-rich protein | chr2:6684369-6684901 FORWARD | Aliases: F26H6.14, F26H6_14	2.9	3.1	-0.2	-1.2	73.3%	-1.3
14709	AT3G21380.1 | 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)	2.9	3.1	-0.2	-1.2	73.3%	-1.4
14710	AT1G71760.1 | expressed protein | chr1:26993076-26994161 FORWARD | Aliases: F14O23.14, F14O23_14	3.3	3.0	0.3	1.2	73.3%	-0.8
14711	AT4G39430.1 | expressed protein, ; expression supported by MPSS | chr4:18343008-18345021 FORWARD | Aliases: F23K16.60, F23K16_60	3.9	4.1	-0.2	-1.2	73.3%	-0.9
14712	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	2.7	-0.2	-1.2	73.3%	-1.4
14713	AT2G39750.1 | dehydration-responsive family protein, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase | chr2:16585902-16589482 REVERSE | Aliases: T5I7.5, T5I7_5	7.9	7.7	0.2	1.2	73.3%	-0.8
14714	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	7.1	6.7	0.5	1.2	73.3%	-0.7
14715	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	2.6	0.2	1.2	73.3%	-1.4
14716	AT4G16444.1 | expressed protein | chr4:9274467-9276349 REVERSE | Aliases: None	6.9	6.7	0.2	1.2	73.3%	-1.0
14717	AT5G59500.1 | expressed protein | chr5:24003155-24004607 FORWARD | Aliases: F2O15.18, F2O15_18	4.9	4.6	0.3	1.2	73.4%	-0.6
14718	AT3G17750.1 | protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain | chr3:6073814-6078728 FORWARD | Aliases: MIG5.5	4.1	4.3	-0.2	-1.2	73.4%	-0.9
14719	AT5G15725.1 | expressed protein | chr5:5127407-5128340 FORWARD | Aliases: None	2.8	2.9	-0.1	-1.2	73.4%	-1.4
14720	AT1G54820.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:20451032-20454528 FORWARD | Aliases: T22H22.21, T22H22_21	2.3	2.4	-0.1	-1.2	73.4%	-1.8
14721	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	6.9	6.3	0.7	1.2	73.4%	-0.5
14722	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	7.6	7.1	0.5	1.2	73.5%	-0.6
14723	AT3G16580.1 | F-box family protein, contains F-box domain Pfam:PF00646	4.3	4.4	-0.2	-1.2	73.5%	-1.4
14724	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	4.1	4.6	-0.5	-1.2	73.5%	-0.6

Rank	Description	Sync	Root	M	t	adj.q	B
14725	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	2.7	2.8	-0.1	-1.2	73.5%	-1.5
14726	AT3G17150.1 | 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 | chr3:5847297-5849550 FORWARD | Aliases: K14A17.27	2.8	3.0	-0.2	-1.2	73.5%	-1.1
14727	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	2.9	-0.1	-1.2	73.7%	-1.3
14728	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	3.1	-0.2	-1.2	73.7%	-1.1
14729	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	3.1	-0.2	-1.2	73.7%	-1.3
14730	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	2.7	2.9	-0.2	-1.2	73.7%	-1.2
14731	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	5.2	4.9	0.2	1.2	73.7%	-0.8
14732	AT2G16450.1 | F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	3.2	3.0	0.1	1.2	73.7%	-1.4
14733	AT3G14490.1 | terpene synthase/cyclase family protein, contains Pfam profile: PF01397 terpene synthase family | chr3:4863638-4865956 REVERSE | Aliases: MOA2.12	2.5	2.6	-0.1	-1.2	73.8%	-1.5
14734	AT1G72260.1 | Symbol: THI2.1 |	3.6	3.8	-0.2	-1.2	73.8%	-1.2
14735	AT1G18440.1 | peptidyl-tRNA hydrolase family protein, contains Pfam profile PF01195: peptidyl-tRNA hydrolase | chr1:6345969-6347903 FORWARD | Aliases: F15H18.24, F15H18_24	5.5	5.1	0.4	1.2	73.8%	-0.6
14736	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	7.4	7.0	0.4	1.2	73.8%	-0.8
14737	AT5G17030.1 | UDP-glucoronosyl/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	3.5	-0.2	-1.2	73.8%	-1.3
14738	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	3.7	-0.2	-1.2	73.8%	-1.5
14739	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	4.5	-0.3	-1.2	73.8%	-0.9
14740	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	3.3	3.1	0.2	1.2	73.8%	-1.0
14741	AT5G52580.1 | expressed protein | chr5:21355278-21357204 FORWARD | Aliases: F6N7.6, F6N7_6	2.9	3.1	-0.2	-1.2	73.9%	-1.0
14742	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	3.5	3.2	0.3	1.2	73.9%	-0.7
14743	AT3G07560.1 | glycine-rich protein | chr3:2411327-2413420 REVERSE | Aliases: F21O3.27	8.3	8.6	-0.4	-1.2	73.9%	-0.8
14744	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)	2.9	3.1	-0.2	-1.2	73.9%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
14745	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	5.9	5.4	0.5	1.2	73.9%	-0.2
14746	AT2G45900.1 | expressed protein | chr2:18893142-18895747 REVERSE | Aliases: F4I18.12	2.3	2.4	-0.1	-1.2	73.9%	-1.9
14747	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	3.2	0.2	1.2	73.9%	-1.0
14748	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	11.6	11.1	0.5	1.2	73.9%	-0.8
14749	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	6.4	6.1	0.3	1.2	73.9%	-0.7
14750	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	2.8	-0.2	-1.2	73.9%	-1.2
14751	AT1G23230.1 | expressed protein | chr1:8244470-8251730 FORWARD | Aliases: F26F24.8, F26F24_8	5.7	5.3	0.4	1.2	73.9%	-0.6
14752	AT3G60760.1 | expressed protein | chr3:22469591-22470177 REVERSE | Aliases: T4C21.170	2.9	3.1	-0.2	-1.2	74.0%	-1.3
14753	AT5G49480.1 | Symbol: ATCP1 | sodium-inducible calcium-binding protein (ACP1) / sodium-responsive calcium-binding protein (ACP1), identical to NaCl-inducible Ca2+-binding protein GI:2352828 from (Arabidopsis thaliana) | chr5:20087969-20088864 FORWARD | Aliases: ACP1, K6M13.2, K6M13_2	8.0	8.3	-0.3	-1.2	74.0%	-0.6
14754	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	4.1	0.3	1.2	74.0%	-0.8
14755	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	2.5	-0.1	-1.2	74.0%	-1.3
14756	AT5G24210.1 | lipase class 3 family protein, contains Pfam profile PF01764: Lipase | chr5:8217341-8219622 FORWARD | Aliases: MOP9.2, MOP9_2	3.3	3.4	-0.2	-1.2	74.0%	-1.2
14757	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	2.5	-0.1	-1.2	74.0%	-1.6
14758	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	7.4	7.0	0.5	1.2	74.0%	-0.7
14759	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	3.3	3.5	-0.3	-1.2	74.0%	-0.9
14760	AT1G19390.1 | wall-associated kinase, putative, similar to GB:CAB42872 from (Arabidopsis thaliana) (Plant Mol. Biol. 39 (6), 1189-1196 (1999))	3.0	3.3	-0.3	-1.2	74.0%	-0.8
14761	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	4.4	-0.4	-1.2	74.1%	-0.6
14762	AT2G04675.1 | expressed protein | chr2:1637481-1638644 REVERSE | Aliases: None	2.7	2.9	-0.2	-1.2	74.1%	-0.8
14763	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	3.4	-0.2	-1.2	74.1%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
14764	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	6.1	6.3	-0.3	-1.2	74.2%	-0.9
14765	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	2.6	-0.2	-1.2	74.2%	-1.5
14766	AT4G15490.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl 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	3.6	0.1	1.2	74.2%	-1.3
14767	AT1G11060.1 | expressed protein | chr1:3684568-3689844 FORWARD | Aliases: T19D16.5, T19D16_5	3.3	3.5	-0.2	-1.2	74.2%	-1.3
14768	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	2.7	2.8	-0.1	-1.2	74.2%	-1.5
14769	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	5.4	5.8	-0.4	-1.2	74.2%	-0.8
14770	AT5G43480.1 | expressed protein | chr5:17484626-17484871 REVERSE | Aliases: MWF20.20, MWF20_20	3.9	4.0	-0.1	-1.2	74.2%	-1.8
14771	AT3G61730.1 | expressed protein | chr3:22859402-22861450 REVERSE | Aliases: F21F14.11	2.4	2.6	-0.1	-1.2	74.2%	-1.3
14772	AT5G36000.1 | expressed protein, strong similarity to unknown protein (emb:CAB71103.1)	2.4	2.6	-0.1	-1.2	74.2%	-1.3
14773	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	9.3	8.7	0.5	1.2	74.2%	-0.7
14774	AT4G03830.1 | myosin heavy chain-related | chr4:1790438-1792456 FORWARD | Aliases: T7M24.5, T7M24_5	2.5	2.4	0.1	1.2	74.2%	-1.5
14775	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	3.5	3.6	-0.1	-1.2	74.2%	-1.5
14776	AT1G61710.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	2.7	-0.1	-1.2	74.3%	-1.5
14777	AT2G47010.2 | expressed protein | chr2:19324195-19326467 FORWARD | Aliases: F14M4.16	3.2	3.1	0.1	1.2	74.3%	-1.6
14778	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	4.0	0.3	1.2	74.3%	-1.0
14779	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	9.5	0.5	1.2	74.3%	-0.9
14780	AT1G42250.1 | replication protein-related, weak similarity to Replication Protein A 70	2.7	2.9	-0.3	-1.2	74.3%	-1.4
14781	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	4.5	4.0	0.5	1.2	74.3%	-0.9
14782	AT1G22610.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr1:7994280-7997574 FORWARD | Aliases: F12K8.4, F12K8_4	7.9	7.7	0.2	1.2	74.3%	-1.0
14783	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	3.4	3.6	-0.2	-1.2	74.4%	-1.0
14784	AT3G12840.1 | expressed protein | chr3:4085812-4086090 REVERSE | Aliases: MBK21.20	2.6	2.8	-0.2	-1.2	74.5%	-1.4
14785	AT3G27785.1 | Symbol: MYB118 |	3.3	3.4	-0.1	-1.2	74.5%	-1.7
14786	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	3.4	-0.1	-1.2	74.5%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
14787	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	2.6	2.7	-0.1	-1.2	74.5%	-1.4
14788	AT2G38780.1 | expressed protein, similar to hypothetical protein [Lotus corniculatus var. japonicus] (GB:BAC41325.1) | chr2:16217935-16221707 FORWARD | Aliases: T6A23.2, T6A23_2	5.8	5.5	0.3	1.2	74.5%	-0.9
14789	NA	2.4	2.4	-0.1	-1.2	74.5%	-2.1
14790	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	5.8	5.5	0.3	1.2	74.5%	-0.6
14791	AT5G15560.1 | hypothetical protein | chr5:5064054-5064892 FORWARD | Aliases: T20K14.170, T20K14_170	2.9	3.0	-0.1	-1.2	74.5%	-1.2
14792	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	2.7	2.8	-0.1	-1.2	74.5%	-1.6
14793	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	3.9	-0.2	-1.2	74.5%	-1.0
14794	AT1G30890.1 | integral membrane HRF1 family protein, contains Pfam domain PF03878: Hrf1 family	6.9	6.6	0.3	1.2	74.6%	-0.7
14795	AT3G15480.1 | expressed protein | chr3:5226255-5227794 REVERSE | Aliases: MJK13.14	7.9	7.4	0.4	1.2	74.6%	-0.8
14796	AT5G35280.1 | expressed protein, similar to At2g10840, At2g10500, At2g05860, At4g07310, At4g07430, At1g39270 | chr5:13526852-13527760 FORWARD | Aliases: T26D22.1, T26D22_1	2.7	2.9	-0.1	-1.2	74.7%	-1.9
14797	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	3.4	3.9	-0.5	-1.2	74.7%	-0.9
14798	AT2G46480.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8; | chr2:19083477-19085458 REVERSE | Aliases: F13A10.1	2.4	2.3	0.1	1.2	74.8%	-1.5
14799	AT4G24680.1 | expressed protein | chr4:12733435-12739747 FORWARD | Aliases: F22K18.120, F22K18_120	6.7	7.0	-0.3	-1.2	74.8%	-0.9
14800	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	2.8	3.0	-0.2	-1.2	74.8%	-1.2
14801	AT5G65580.1 | expressed protein | chr5:26224880-26225188 FORWARD | Aliases: K21L13.9, K21L13_9	2.5	2.6	-0.1	-1.2	74.8%	-1.8
14802	AT5G28780.1 | hypothetical protein, various predicted proteins, Arabidopsis thaliana | chr5:10812911-10814177 REVERSE | Aliases: T32B20.70, T32B20_70	2.2	2.3	-0.1	-1.2	74.9%	-1.8
14803	AT2G35290.1 | expressed protein | chr2:14868491-14869108 REVERSE | Aliases: T4C15.4, T4C15_4	5.4	4.8	0.6	1.2	74.9%	-0.5
14804	AT3G48960.1 | 60S ribosomal protein L13 (RPL13C), 60S ribosomal protein L13 (BBC1), Arabidopsis thaliana, gb:X75162 | chr3:18161429-18162397 REVERSE | Aliases: T2J13.200	2.8	2.6	0.1	1.2	74.9%	-1.3
14805	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 ATFP7 (GI:4097555); contains heavy-metal-associated domain PF00403 | chr1:26806817-26807954 REVERSE | Aliases: F23N20.4, F23N20_4	2.4	2.5	-0.1	-1.2	74.9%	-1.4
14806	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	4.0	4.3	-0.3	-1.2	74.9%	-0.8
14807	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	11.6	11.8	-0.2	-1.2	74.9%	-1.4
14808	AT5G53640.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.1	3.3	-0.3	-1.2	74.9%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
14809	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	7.6	7.1	0.5	1.2	74.9%	-0.7
14810	AT3G26410.1 | expressed protein | chr3:9670653-9672565 REVERSE | Aliases: F20C19.14	4.2	4.0	0.2	1.2	74.9%	-1.0
14811	AT3G25750.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.3	2.4	-0.1	-1.2	74.9%	-1.8
14812	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	2.7	-0.1	-1.2	75.0%	-1.6
14813	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	2.6	2.8	-0.1	-1.2	75.0%	-1.5
14814	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	2.7	2.9	-0.2	-1.2	75.0%	-1.2
14815	AT5G27240.1 | DNAJ heat shock N-terminal domain-containing protein | chr5:9597555-9600869 FORWARD | Aliases: T21B4.150, T21B4_150	3.2	3.1	0.1	1.2	75.0%	-1.4
14816	AT3G24850.1 | hypothetical protein, contains Pfam profile PF03754: Domain of unknown function (DUF313)	3.4	3.7	-0.3	-1.2	75.0%	-1.1
14817	AT5G50565.1 | expressed protein | chr5:20598068-20599052 FORWARD | Aliases: MFB16.4	5.7	6.2	-0.5	-1.2	75.0%	-0.3
14818	AT5G50665.1 | expressed protein | chr5:20631410-20632394 FORWARD | Aliases: None	5.7	6.2	-0.5	-1.2	75.0%	-0.3
14819	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	2.5	2.4	0.1	1.2	75.0%	-1.5
14820	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 pI (InterPro:IPR005795); contains InterPro domain Expansin/Lol pI (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	3.4	3.6	-0.2	-1.2	75.0%	-0.9
14821	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	2.8	-0.2	-1.2	75.0%	-1.2
14822	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	2.4	-0.1	-1.2	75.0%	-1.8
14823	AT5G08440.1 | expressed protein | chr5:2720670-2727166 FORWARD | Aliases: F8L15.170, F8L15_170	3.0	3.1	-0.1	-1.2	75.0%	-1.6
14824	AT2G36570.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:15342575-15345006 FORWARD | Aliases: F1O11.20, F1O11_20	3.8	4.0	-0.2	-1.2	75.0%	-1.3
14825	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	4.5	4.8	-0.3	-1.2	75.0%	-0.8
14826	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	2.9	-0.2	-1.2	75.0%	-1.2
14827	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	3.4	-0.2	-1.2	75.1%	-1.5
14828	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	5.8	-0.4	-1.2	75.1%	-0.9
14829	AT5G28440.1 | expressed protein | chr5:10367675-10369018 REVERSE | Aliases: F21B23.100, F21B23_100	2.9	3.1	-0.2	-1.2	75.1%	-1.0
14830	AT4G13650.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:7938963-7942894 REVERSE | Aliases: F18A5.40, F18A5_40	2.6	2.5	0.1	1.2	75.1%	-1.6
14831	AT3G52850.1 | Symbol: ATELP1 |	9.6	9.1	0.5	1.2	75.1%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
14832	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	2.5	-0.1	-1.2	75.1%	-1.3
14833	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	2.9	-0.2	-1.2	75.1%	-1.2
14834	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	2.5	-0.2	-1.2	75.1%	-1.3
14835	AT4G14000.1 | expressed protein | chr4:8090812-8092662 FORWARD | Aliases: DL3040W, FCAALL.136	6.2	5.8	0.5	1.2	75.1%	-0.8
14836	AT3G22220.2 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g15020.1); similar to transposase-like protein [Musa acuminata] (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)	5.2	5.7	-0.5	-1.2	75.1%	-0.9
14837	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	3.9	-0.2	-1.2	75.2%	-1.1
14838	AT5G51610.1 | ribosomal protein L11 family protein | chr5:20982803-20984031 FORWARD | Aliases: K17N15.16, K17N15_16	2.5	2.6	-0.1	-1.2	75.2%	-1.4
14839	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	4.4	4.8	-0.4	-1.2	75.2%	-0.4
14840	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) (Spinacia oleracea) SWISS-PROT:P05414 | chr3:4690457-4692997 REVERSE | Aliases: MAG2.11	4.4	4.8	-0.4	-1.2	75.2%	-0.4
14841	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	2.9	-0.2	-1.2	75.2%	-1.6
14842	AT3G61920.1 | expressed protein, hypothetical protein F1N19.27 - Arabidopsis thaliana, EMBL:AC009519 | chr3:22943471-22944336 REVERSE | Aliases: F21F14.90	4.1	4.3	-0.2	-1.2	75.2%	-1.3
14843	AT4G35690.1 | hypothetical protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function | chr4:16921891-16922745 FORWARD | Aliases: F8D20.200, F8D20_200	3.8	4.0	-0.2	-1.2	75.2%	-1.2
14844	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	2.9	-0.2	-1.2	75.3%	-1.3
14845	AT1G18870.1 | isochorismate synthase, putative / isochorismate mutase, putative, similar to GI:17223087 | chr1:6515657-6519273 FORWARD | Aliases: F6A14.3, F6A14_3	2.9	2.8	0.1	1.2	75.3%	-1.4
14846	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	7.9	-0.5	-1.2	75.3%	-0.7
14847	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	3.9	-0.1	-1.2	75.3%	-1.4
14848	AT2G17600.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.9	3.1	-0.2	-1.2	75.3%	-1.4
14849	AT4G05340.1 | hypothetical protein | chr4:2725687-2726062 FORWARD | Aliases: C6L9.20, C6L9_20	2.5	2.7	-0.1	-1.2	75.3%	-1.5
14850	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	7.4	7.0	0.4	1.2	75.3%	-0.9
14851	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	6.2	5.9	0.3	1.2	75.3%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
14852	AT1G52100.1 | jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) 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	4.1	-0.3	-1.2	75.3%	-1.0
14853	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	3.0	3.2	-0.2	-1.2	75.4%	-1.2
14854	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	8.9	8.7	0.2	1.2	75.4%	-1.4
14855	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	2.7	2.9	-0.2	-1.2	75.4%	-1.1
14856	AT1G79510.2 | expressed protein | chr1:29912906-29914881 REVERSE | Aliases: T8K14.7, T8K14_7	3.6	4.0	-0.3	-1.2	75.4%	-0.8
14857	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	3.4	3.6	-0.2	-1.2	75.4%	-1.0
14858	AT2G28640.1 | exocyst subunit EXO70 family protein, contains HEAT repeat and Pfam domain PF03081:exocyst subunit EXO70	3.3	3.2	0.1	1.2	75.4%	-1.6
14859	ATCG00170.1 | Symbol: RPOC2 | RNA polymerase beta' subunit-2 | chrC:15938-20068 REVERSE | Aliases: RPOC2	8.5	7.5	1.0	1.2	75.5%	-0.7
14860	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	5.1	5.3	-0.2	-1.2	75.5%	-0.8
14861	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	2.3	2.4	-0.1	-1.2	75.5%	-1.7
14862	AT3G48910.1 | expressed protein | chr3:18146073-18147324 FORWARD | Aliases: T2J13.250	2.9	3.1	-0.2	-1.2	75.5%	-1.1
14863	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	6.4	6.9	-0.5	-1.2	75.6%	-0.6
14864	AT1G07860.1 | expressed protein | chr1:2428908-2429428 REVERSE | Aliases: F24B9.36, F24B9_36	2.4	2.6	-0.2	-1.2	75.6%	-1.4
14865	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	4.8	0.2	1.2	75.6%	-1.1
14866	AT1G48030.2 | dihydrolipoamide dehydrogenase 1, mitochondrial / lipoamide dehydrogenase 1 (MTLPD1), identical to GB:AAF34795 (gi:12704696) from (Arabidopsis thaliana)	10.6	10.1	0.5	1.2	75.6%	-0.8
14867	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	4.7	4.5	0.3	1.2	75.6%	-0.6
14868	AT3G09430.1 | expressed protein | chr3:2901286-2902300 FORWARD | Aliases: F3L24.32	2.7	2.8	-0.1	-1.2	75.7%	-1.5
14869	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	3.6	3.5	0.1	1.2	75.7%	-1.2
14870	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	2.4	2.5	-0.2	-1.2	75.7%	-1.6
14871	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	2.4	2.5	-0.1	-1.2	75.7%	-1.6

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14872	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	6.3	6.6	-0.3	-1.2	75.7%	-1.1
14873	AT4G38860.1 | auxin-responsive protein, putative, auxin-induced protein 10A, Glycine max., PIR2:JQ1099	2.5	2.6	-0.1	-1.2	75.7%	-1.8
14874	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	6.1	-0.3	-1.2	75.7%	-0.6
14875	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	-1.2	75.8%	-1.7
14876	AT5G36290.2 | expressed protein, contains Pfam profile PF01169: Uncharacterized protein family UPF0016	8.1	7.5	0.6	1.2	75.9%	-0.8
14877	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	3.5	3.7	-0.2	-1.2	75.9%	-1.0
14878	AT3G28170.1 | hypothetical protein | chr3:10499598-10501597 FORWARD | Aliases: MIG10.7	3.9	4.2	-0.3	-1.2	75.9%	-1.2
14879	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	2.7	2.9	-0.2	-1.2	75.9%	-1.2
14880	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	2.6	0.1	1.2	75.9%	-1.4
14881	AT3G24490.1 | expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189 | chr3:8911029-8912182 FORWARD | Aliases: MOB24.1	7.1	6.7	0.3	1.2	75.9%	-0.8
14882	AT4G28400.1 | protein phosphatase 2C, putative / PP2C, putative, protein phosphatase 2C-fission yeast, PIR2:S54297 | chr4:14048360-14050341 FORWARD | Aliases: F20O9.80, F20O9_80	7.7	8.2	-0.5	-1.2	75.9%	-0.6
14883	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	4.6	4.9	-0.3	-1.2	76.0%	-0.8
14884	AT5G18710.1 | expressed protein, predicted proteins - Arabidopsis thaliana | chr5:6241632-6243481 FORWARD | Aliases: T1A4.90, T1A4_90	3.5	3.7	-0.2	-1.2	76.0%	-1.1
14885	NA	2.3	2.2	0.1	1.2	76.0%	-2.3
14886	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	7.4	6.9	0.5	1.2	76.1%	-0.7
14887	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	2.8	0.1	1.2	76.1%	-1.7
14888	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	6.5	-0.5	-1.2	76.1%	-0.9
14889	AT1G57680.2 | expressed protein | chr1:21366153-21368351 REVERSE | Aliases: T8L23.15, T8L23_15	5.9	6.5	-0.6	-1.2	76.1%	-0.6
14890	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	7.0	6.7	0.3	1.2	76.1%	-0.7
14891	AT5G27020.1 | expressed protein | chr5:9508190-9508684 FORWARD | Aliases: F2P16.13, F2P16_13	3.0	3.2	-0.2	-1.2	76.1%	-1.3
14892	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	3.9	3.7	0.2	1.2	76.1%	-1.1
14893	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	2.7	-0.1	-1.2	76.1%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
14894	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	5.2	4.9	0.2	1.2	76.1%	-1.0
14895	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	2.6	2.8	-0.2	-1.2	76.1%	-0.8
14896	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	10.0	9.8	0.2	1.2	76.1%	-1.2
14897	AT4G30340.1 | diacylglycerol kinase family protein, contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain | chr4:14838315-14841073 REVERSE | Aliases: F17I23.320, F17I23_320	2.4	2.5	-0.1	-1.2	76.2%	-1.6
14898	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	2.8	3.1	-0.3	-1.2	76.2%	-1.1
14899	AT3G42380.1 | hypothetical protein | chr3:14514596-14514903 FORWARD | Aliases: T14K23.90	2.5	2.4	0.1	1.2	76.2%	-1.6
14900	AT2G01700.1 | hypothetical protein | chr2:314843-315157 REVERSE | Aliases: T8O11.13, T8O11_13	2.1	2.2	-0.1	-1.2	76.2%	-1.9
14901	NA	3.0	3.0	-0.1	-1.2	76.2%	-2.0
14902	AT3G20850.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr3:7304163-7304567 FORWARD | Aliases: MOE17.16	2.5	2.6	-0.1	-1.2	76.2%	-1.4
14903	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	2.5	-0.1	-1.2	76.3%	-1.7
14904	AT1G12190.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.8	-0.2	-1.2	76.3%	-1.5
14905	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	2.9	-0.1	-1.2	76.3%	-1.6
14906	AT1G41870.1 | hypothetical protein | chr1:15649932-15651492 FORWARD | Aliases: F5A13.13, F5A13_13	2.3	2.2	0.1	1.2	76.4%	-1.8
14907	AT1G63060.1 | expressed protein | chr1:23387708-23388703 FORWARD | Aliases: F16M19.2, F16M19_2	3.5	3.7	-0.2	-1.2	76.4%	-1.2
14908	AT5G09630.1 | expressed protein | chr5:2985871-2987653 REVERSE | Aliases: F17I14.180, F17I14_180	4.6	4.8	-0.2	-1.2	76.4%	-1.1
14909	AT2G31590.1 | expressed protein | chr2:13453906-13455210 REVERSE | Aliases: T9H9.11, T9H9_11	4.7	4.9	-0.2	-1.2	76.4%	-1.0
14910	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)	4.0	4.3	-0.3	-1.2	76.4%	-1.1
14911	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	2.5	0.2	1.2	76.4%	-1.2
14912	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	3.9	4.1	-0.3	-1.2	76.4%	-1.0
14913	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	3.8	3.5	0.2	1.2	76.4%	-0.8
14914	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	5.4	-0.3	-1.2	76.4%	-1.0
14915	AT2G34580.1 | expressed protein | chr2:14572932-14574719 REVERSE | Aliases: T31E10.8, T31E10_8	3.2	3.3	-0.1	-1.2	76.5%	-1.4
14916	AT3G63180.1 | expressed protein | chr3:23347293-23351211 REVERSE | Aliases: F16M2.30	4.7	4.4	0.2	1.2	76.5%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
14917	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	2.8	-0.2	-1.2	76.5%	-1.2
14918	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	2.7	-0.1	-1.2	76.6%	-1.6
14919	AT3G14480.1 | glycine/proline-rich protein, contains 1 predicted transmembrane domain;	2.4	2.6	-0.2	-1.2	76.6%	-1.4
14920	AT3G51960.2 | bZIP family transcription factor, contains Pfam profile: PF00170 bZIP transcription factor | chr3:19293579-19295124 REVERSE | Aliases: F4F15.70	3.3	3.5	-0.1	-1.2	76.6%	-1.3
14921	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	8.8	9.1	-0.3	-1.2	76.6%	-0.9
14922	AT5G63740.1 | zinc finger protein-related | chr5:25528002-25528682 REVERSE | Aliases: MBK5.22, MBK5_22	2.6	2.7	-0.1	-1.2	76.6%	-1.6
14923	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	2.6	-0.1	-1.2	76.7%	-1.4
14924	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	4.9	-0.3	-1.2	76.7%	-1.0
14925	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	5.7	-1.0	-1.2	76.7%	-0.5
14926	AT3G50080.1 | Symbol: VFB2 | F-box family protein (FBL16), contains similarity to SKP1 interacting partner 2 GI:10716949 from (Arabidopsis thaliana); contains Pfam profile: PF00646 F-box domain | chr3:18583719-18585497 FORWARD | Aliases: F3A4.160, VFB2, VIER F BOX PROTEINE 2	6.4	6.8	-0.3	-1.2	76.8%	-0.6
14927	AT1G72790.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr1:27398409-27400461 FORWARD | Aliases: F28P22.2, F28P22_2	3.2	3.0	0.2	1.2	76.8%	-0.7
14928	ATCG01050.1 | Symbol: NDHD | Represents a plastid-encoded subunit of a NAD(P)H dehydrogenase complex.	4.7	5.6	-0.9	-1.2	76.8%	-0.6
14929	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	2.7	2.6	0.1	1.2	76.8%	-1.8
14930	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	6.0	5.4	0.6	1.2	76.8%	-0.8
14931	AT2G07110.1 | hypothetical protein | chr2:2952607-2953205 REVERSE | Aliases: T25N22.7, T25N22_7	3.0	3.1	-0.2	-1.2	76.8%	-1.2
14932	AT3G09070.1 | glycine-rich protein, similar to hypothetical protein GB:AAD32765 (Arabidopsis thaliana)	4.6	4.8	-0.2	-1.2	76.8%	-1.1
14933	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	5.6	6.5	-0.9	-1.2	76.8%	-0.6
14934	AT3G22870.1 | F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	3.0	3.2	-0.2	-1.2	76.8%	-0.9
14935	AT1G03905.1 | ABC transporter family protein, similar to NBD-like protein GB:AAD20643 | chr1:993477-995593 FORWARD | Aliases: None	6.8	7.2	-0.4	-1.2	76.8%	-0.6
14936	AT2G38590.1 | F-box family protein, contains Pfam profile: PF00646 F-box domain | chr2:16149975-16151262 FORWARD | Aliases: T6A23.21, T6A23_21	3.1	3.2	-0.2	-1.2	76.8%	-1.7
14937	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	2.8	-0.1	-1.2	76.9%	-1.6
14938	AT1G18480.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	6.8	6.4	0.4	1.2	76.9%	-0.8
14939	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	6.0	6.3	-0.3	-1.2	76.9%	-0.6

Rank	Description	Sync	Root	M	t	adj.q	B
14940	AT5G62880.1 | Symbol: ARAC10 |	4.9	4.6	0.3	1.2	76.9%	-0.7
14941	NA	8.9	9.4	-0.5	-1.2	76.9%	-0.8
14942	AT3G42980.1 | hypothetical protein | chr3:15038577-15040097 FORWARD | Aliases: F18P9.140	2.8	3.0	-0.2	-1.2	76.9%	-1.4
14943	AT4G26380.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.6	3.8	-0.3	-1.2	77.0%	-0.7
14944	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	2.8	-0.1	-1.2	77.0%	-1.5
14945	AT1G22890.1 | expressed protein | chr1:8102807-8103521 FORWARD | Aliases: F19G10.22, F19G10_22	2.9	3.0	-0.1	-1.2	77.0%	-1.8
14946	AT3G09640.2 | Symbol: APX2 | similar to L-ascorbate peroxidase 1, cytosolic (APX1) [Arabidopsis thaliana] (TAIR:At1g07890.2); similar to L-ascorbate peroxidase 1, cytosolic (APX1) [Arabidopsis thaliana] (TAIR:At1g07890.3); similar to L-ascorbate peroxidase 1, cytosolic (APX1) [Arabidopsis thaliana] (TAIR:At1g07890.1); similar to cytosolic ascorbate peroxidase [Fragaria x ananassa] (GB:AAB94574.1); similar to cytosolic ascorbate peroxidase [Vigna unguiculata] (GB:AAB03844.1); similar to cytosolic ascorbate peroxidase 2 [Glycine max] (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	3.1	3.0	0.1	1.2	77.0%	-1.3
14947	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	5.4	4.9	0.5	1.2	77.1%	-0.6
14948	AT5G17650.1 | glycine/proline-rich protein, glycine/proline-rich protein GPRP - Arabidopsis thaliana, EMBL:X84315 | chr5:5816700-5818349 REVERSE | Aliases: K10A8.130, K10A8_130	5.5	5.7	-0.2	-1.2	77.1%	-0.8
14949	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	3.0	-0.1	-1.2	77.1%	-1.4
14950	AT5G35260.1 | replication protein-related, weak similarity to Replication Protein A 70	3.2	3.4	-0.2	-1.2	77.1%	-1.7
14951	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	2.4	-0.1	-1.2	77.1%	-1.6
14952	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	0.1	1.2	77.2%	-1.9
14953	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	2.6	-0.1	-1.2	77.2%	-1.5
14954	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	3.1	3.2	-0.2	-1.2	77.2%	-1.3
14955	AT4G13330.1 | expressed protein | chr4:7754244-7755951 REVERSE | Aliases: T9E8.70, T9E8_70	4.0	4.2	-0.2	-1.2	77.2%	-1.2
14956	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	3.0	3.2	-0.2	-1.2	77.2%	-1.0
14957	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	7.1	7.4	-0.3	-1.2	77.3%	-0.7
14958	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	6.7	-0.2	-1.2	77.3%	-0.9
14959	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	5.1	5.8	-0.6	-1.2	77.3%	-0.7
14960	AT2G34120.1 | hypothetical protein | chr2:14412418-14412630 FORWARD | Aliases: T14G11.24, T14G11_24	2.8	2.9	-0.1	-1.2	77.3%	-1.7
14961	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	5.5	5.2	0.3	1.2	77.4%	-0.7

Rank	Description	Sync	Root	M	t	adj.q	B
14962	AT4G16515.1 | expressed protein | chr4:9305278-9305786 REVERSE | Aliases: None	4.1	4.5	-0.3	-1.2	77.4%	-0.9
14963	AT2G34040.2 | apoptosis inhibitory 5 (API5) family protein, contains Pfam domain PF05918 Apoptosis inhibitory protein 5 (API5)	6.8	6.4	0.4	1.2	77.4%	-0.8
14964	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	9.0	8.4	0.6	1.2	77.4%	-0.7
14965	AT1G76350.1 | RWP-RK domain-containing protein, similar to nodule inception protein (Lotus japonicus) GI:6448579; contains Pfam profile: PF02042 RWP-RK domain	4.7	4.4	0.3	1.2	77.4%	-0.9
14966	AT1G29980.2 | expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642 | chr1:10503264-10504827 REVERSE | Aliases: T1P2.9, T1P2_9	5.9	5.4	0.6	1.2	77.4%	-0.4
14967	AT3G50180.1 | expressed protein | chr3:18615926-18618145 REVERSE | Aliases: F11C1.20	2.5	2.7	-0.2	-1.2	77.5%	-1.5
14968	AT4G36105.1 | expressed protein | chr4:17083888-17085122 FORWARD | Aliases: None	2.8	2.9	-0.2	-1.2	77.5%	-1.1
14969	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	2.6	2.7	-0.1	-1.2	77.5%	-1.4
14970	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	2.9	-0.2	-1.2	77.6%	-1.3
14971	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	8.8	8.4	0.3	1.2	77.6%	-0.9
14972	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	4.3	4.1	0.1	1.2	77.6%	-1.5
14973	AT1G68875.1 | expressed protein | chr1:25895749-25896461 FORWARD | Aliases: None	2.8	2.9	-0.1	-1.2	77.6%	-1.3
14974	AT5G61050.1 | histone deacetylase-related / HD-related	2.6	2.7	-0.2	-1.2	77.6%	-1.3
14975	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	2.4	-0.1	-1.2	77.6%	-1.8
14976	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	2.7	2.9	-0.2	-1.2	77.6%	-1.3
14977	AT4G22310.1 | expressed protein, contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041) | chr4:11791357-11792848 FORWARD | Aliases: T10I14.140, T10I14_140	10.5	9.9	0.6	1.2	77.7%	-1.0
14978	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	2.7	-0.1	-1.2	77.8%	-1.6
14979	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	6.2	5.9	0.3	1.2	77.8%	-0.9
14980	AT5G24610.1 | expressed protein, similar to unknown protein (emb:CAB62459.1) | chr5:8428081-8429255 FORWARD | Aliases: K18P6.15, K18P6_15	7.0	6.4	0.6	1.2	77.8%	-0.6
14981	AT5G63900.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr5:25585924-25587597 FORWARD | Aliases: MGI19.10, MGI19_10	3.3	3.4	-0.1	-1.2	77.8%	-1.5
14982	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	3.1	3.2	-0.1	-1.2	77.8%	-1.6
14983	AT3G19050.1 | kinesin motor protein-related, contains Pfam profile: PF00225 Kinesin motor domain; contains non-consensus splice site (GC) at intron 12	2.6	2.7	-0.1	-1.2	77.8%	-1.6
14984	AT1G71200.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.1	3.3	-0.2	-1.2	77.8%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
14985	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	3.5	0.3	1.2	77.8%	-0.7
14986	AT3G43290.1 | hypothetical protein, glyceraldehyde-3-phosphate dehydrogenase, Equus caballus, EMBL:AF097179 | chr3:15241556-15242103 FORWARD | Aliases: F7K15.140	3.3	3.6	-0.2	-1.2	77.8%	-0.9
14987	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	2.6	2.8	-0.1	-1.2	77.8%	-1.5
14988	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	2.6	0.2	1.2	77.9%	-1.4
14989	AT5G22970.1 | expressed protein | chr5:7686276-7686782 REVERSE | Aliases: MRN17.20, MRN17_20	2.3	2.4	-0.1	-1.2	77.9%	-1.7
14990	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	4.0	3.9	0.2	1.2	77.9%	-1.1
14991	AT5G16510.2 | reversibly glycosylated polypeptide, putative, similar to reversibly glycosylatable polypeptide (RGP1) (Pisum sativum) GI:2130521; contains Pfam profile PF03214: Reversibly glycosylated polypeptide | chr5:5392642-5394567 FORWARD | Aliases: MQK4.26, MQK4_26	7.5	7.0	0.4	1.2	77.9%	-0.6
14992	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	5.2	5.5	-0.3	-1.2	77.9%	-0.9
14993	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	5.0	5.3	-0.3	-1.2	77.9%	-0.8
14994	AT5G49260.1 | hypothetical protein | chr5:19984025-19984753 FORWARD | Aliases: K21P3.14, K21P3_14	2.2	2.3	-0.1	-1.2	78.0%	-1.8
14995	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	6.3	5.9	0.4	1.2	78.0%	-0.6
14996	AT4G14980.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.8	4.2	-0.4	-1.2	78.0%	-0.8
14997	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	2.7	-0.1	-1.2	78.0%	-1.7
14998	AT5G54440.1 | expressed protein | chr5:22117162-22125059 FORWARD | Aliases: F24B18.6, F24B18_6	7.3	7.1	0.2	1.2	78.0%	-1.2
14999	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	7.7	7.0	0.7	1.2	78.0%	-0.8
15000	AT4G10730.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:6609420-6614877 REVERSE | Aliases: T12H20.4, T12H20_4	3.1	3.3	-0.2	-1.2	78.0%	-1.1
15001	AT5G52900.1 | expressed protein | chr5:21469668-21471034 REVERSE | Aliases: MXC20.13, MXC20_13	2.7	2.6	0.1	1.2	78.0%	-1.3
15002	AT5G52890.1 | AT hook motif-containing protein, contains Pfam profile PF02178: AT hook motif | chr5:21462061-21464440 REVERSE | Aliases: MXC20.12, MXC20_12	2.4	2.5	-0.1	-1.2	78.0%	-1.5
15003	AT2G36300.1 | integral membrane Yip1 family protein, contains Pfam domain, PF04893: Yip1 domain | chr2:15220139-15221351 REVERSE | Aliases: F2H17.9, F2H17_9	7.2	6.9	0.3	1.2	78.0%	-0.7
15004	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	6.6	0.3	1.2	78.0%	-0.8
15005	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	5.0	5.2	-0.3	-1.2	78.0%	-1.0
15006	AT5G59200.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:23906019-23907791 REVERSE | Aliases: MNC17.11, MNC17_11	2.9	3.1	-0.2	-1.2	78.1%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
15007	AT5G38580.1 | hypothetical protein | chr5:15468394-15469072 REVERSE | Aliases: MBB18.13, MBB18_13	2.6	2.7	-0.1	-1.2	78.1%	-1.6
15008	AT3G21440.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr3:7551188-7553585 REVERSE | Aliases: MHC9.12	3.7	3.8	-0.2	-1.2	78.1%	-1.2
15009	AT5G13130.1 | expressed protein, low similarity to microrchidia (Mus musculus) GI:5410255 | chr5:4166758-4170327 FORWARD | Aliases: T19L5.90, T19L5_90	2.4	2.6	-0.1	-1.2	78.1%	-1.8
15010	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	3.0	-0.1	-1.2	78.1%	-1.6
15011	AT1G54860.1 | expressed protein | chr1:20461088-20462232 REVERSE | Aliases: F14C21.37, F14C21_37	3.3	3.4	-0.1	-1.2	78.2%	-1.5
15012	AT5G67040.1 | expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295) | chr5:26775122-26775701 REVERSE | Aliases: K8A10.11, K8A10_11	3.1	3.3	-0.2	-1.2	78.2%	-1.4
15013	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	3.3	3.2	0.1	1.2	78.2%	-1.3
15014	AT5G63020.1 | 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	-1.2	78.2%	-1.2
15015	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	2.6	-0.1	-1.2	78.2%	-1.6
15016	AT3G01200.1 | expressed protein, contains Pfam domain PF03618: Domain of unknown function (DUF299) | chr3:69518-71369 REVERSE | Aliases: T4P13.11, T4P13_11	6.7	7.0	-0.3	-1.2	78.2%	-1.1
15017	AT1G55760.1 | BTB/POZ domain-containing protein, Interpro IPR000210/ PS50097: BTBB/POZ domain; similar to POZ 56 protein (GI:17483747) (Mus musculus) | chr1:20850592-20852720 REVERSE | Aliases: F20N2.15	2.8	2.6	0.2	1.2	78.2%	-1.3
15018	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	6.3	6.1	0.3	1.2	78.2%	-0.9
15019	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	5.4	5.7	-0.2	-1.2	78.2%	-0.9
15020	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	2.9	-0.1	-1.2	78.2%	-1.4
15021	AT2G15440.1 | expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579) | chr2:6750695-6751912 REVERSE | Aliases: F26H6.4, F26H6_4	5.1	5.3	-0.2	-1.2	78.3%	-1.0
15022	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	3.1	3.3	-0.2	-1.2	78.3%	-1.1
15023	AT3G57450.1 | expressed protein | chr3:21272911-21273599 FORWARD | Aliases: T8H10.50	10.9	10.5	0.3	1.2	78.3%	-1.1
15024	AT1G71420.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:26921484-26923721 REVERSE | Aliases: F3I17.26, F3I17_26	3.9	3.5	0.4	1.2	78.3%	-0.7
15025	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	8.0	8.6	-0.6	-1.2	78.3%	-0.5
15026	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	3.7	3.9	-0.2	-1.2	78.3%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
15027	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	2.4	2.5	-0.1	-1.2	78.3%	-1.7
15028	AT5G37240.1 | expressed protein | chr5:14754975-14760710 REVERSE | Aliases: MNJ8.30, MNJ8_30	2.9	3.1	-0.2	-1.2	78.4%	-1.1
15029	AT5G55790.1 | expressed protein, ; expression supported by MPSS | chr5:22597986-22598561 REVERSE | Aliases: MDF20.23, MDF20_23	3.2	2.9	0.3	1.2	78.4%	-1.1
15030	AT4G37840.1 | hexokinase, putative, similar to hexokinase 1 (Spinacia oleracea) Swiss-Prot:Q9SEK3 | chr4:17790141-17792192 REVERSE | Aliases: T28I19.120, T28I19_120	2.6	2.8	-0.2	-1.2	78.4%	-1.3
15031	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	5.9	6.4	-0.6	-1.2	78.4%	-0.9
15032	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	8.5	7.8	0.8	1.2	78.4%	-0.3
15033	AT4G15890.1 | expressed protein | chr4:9017468-9022997 FORWARD | Aliases: DL3985W, FCAALL.407	5.4	5.1	0.4	1.2	78.4%	-0.6
15034	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	2.8	3.0	-0.2	-1.2	78.5%	-1.2
15035	AT1G80330.1 | gibberellin 3-beta-dioxygenase, putative / gibberellin 3 beta-hydroxylase, putative, similar to gibberellin 3 beta-hydroxylase GA4H GB:AAC83647 (Arabidopsis thaliana), GA4 (GI:2160454)	3.6	3.8	-0.2	-1.2	78.5%	-1.0
15036	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	3.0	-0.1	-1.2	78.5%	-1.3
15037	AT5G51360.1 | hypothetical protein | chr5:20889144-20889503 FORWARD | Aliases: MFG13.7, MFG13_7	2.4	2.6	-0.2	-1.2	78.5%	-1.4
15038	AT5G15360.1 | expressed protein | chr5:4987440-4989185 REVERSE | Aliases: F8M21.250, F8M21_250	2.5	2.6	-0.1	-1.2	78.5%	-1.4
15039	AT1G22630.1 | expressed protein, contains Pfam PF00684 : DnaJ central domain (4 repeats) | chr1:8003304-8004286 FORWARD | Aliases: F12K8.2	2.8	3.0	-0.1	-1.2	78.5%	-1.3
15040	AT2G45160.1 | scarecrow transcription factor family protein | chr2:18624937-18627225 REVERSE | Aliases: T14P1.3	5.1	4.9	0.2	1.2	78.5%	-1.1
15041	AT1G15000.1 | Symbol: SCPL50 |	6.1	6.3	-0.2	-1.2	78.5%	-0.9
15042	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	3.6	3.9	-0.3	-1.2	78.6%	-1.3
15043	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	5.7	6.1	-0.4	-1.2	78.6%	-0.9
15044	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	5.7	6.0	-0.3	-1.2	78.6%	-1.1
15045	AT3G46710.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.2	3.5	-0.2	-1.2	78.6%	-0.9
15046	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	2.4	-0.1	-1.2	78.6%	-1.5
15047	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	7.3	-0.3	-1.2	78.6%	-1.0
15048	AT1G51100.1 | expressed protein | chr1:18937976-18938812 FORWARD | Aliases: F23H24.6, F23H24_6	2.7	2.5	0.1	1.2	78.7%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
15049	AT3G21520.1 | expressed protein, contains Pfam profile PF05078: Protein of unknown function (DUF679) | chr3:7581965-7582799 FORWARD | Aliases: MIL23.9	4.1	3.8	0.2	1.2	78.7%	-0.8
15050	AT3G12030.1 | expressed protein, similar to membrane protein GB:BAA86974 GI:6467175 from (Homo sapiens) | chr3:3834367-3835081 REVERSE | Aliases: MEC18.16	4.3	3.9	0.4	1.2	78.7%	-1.0
15051	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	5.0	4.7	0.3	1.2	78.8%	-0.7
15052	AT1G32520.1 | expressed protein, similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_475242.1) | chr1:11758198-11759260 REVERSE | Aliases: F5D14.31, F5D14_31	4.2	4.0	0.2	1.2	78.8%	-1.2
15053	AT3G56550.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:20963875-20965620 REVERSE | Aliases: T5P19.200	2.7	2.8	-0.1	-1.2	78.8%	-1.6
15054	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	3.7	3.8	-0.1	-1.2	78.8%	-1.4
15055	AT5G64700.1 | nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula); contains Pfam profile PF00892: Integral membrane protein	3.3	3.5	-0.2	-1.2	78.8%	-1.1
15056	AT3G63480.2 | kinesin heavy chain, putative, kinesin heavy chain, Syncephalastrum racemosum, SWISSPROT:KINH_SYNRA | chr3:23450847-23454981 REVERSE | Aliases: MAA21.110	3.8	4.0	-0.2	-1.2	78.9%	-0.9
15057	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	3.3	3.5	-0.2	-1.2	78.9%	-1.3
15058	AT1G11710.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:3948714-3951359 FORWARD | Aliases: F25C20.14, F25C20_14	3.9	3.6	0.2	1.2	78.9%	-0.9
15059	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	3.0	0.2	1.2	79.0%	-1.2
15060	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	4.1	4.5	-0.3	-1.2	79.0%	-0.7
15061	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	3.2	-0.2	-1.2	79.0%	-1.4
15062	AT4G28706.3 | pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase | chr4:14167761-14170748 FORWARD | Aliases: None	5.9	6.1	-0.2	-1.2	79.1%	-1.1
15063	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	6.9	7.2	-0.3	-1.2	79.1%	-1.0
15064	AT5G07710.1 | exonuclease family protein, contains exonuclease domain, Pfam:PF00929 | chr5:2453136-2455547 FORWARD | Aliases: MBK20.17, MBK20_17	5.3	5.1	0.2	1.2	79.1%	-0.9
15065	AT3G28770.1 | expressed protein | chr3:10797953-10804474 FORWARD | Aliases: T19N8.6	3.2	3.3	-0.1	-1.2	79.2%	-1.5
15066	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	4.4	4.1	0.3	1.2	79.2%	-0.6
15067	AT3G16260.1 | metallo-beta-lactamase family protein | chr3:5509418-5513210 FORWARD | Aliases: MYA6.7	6.2	5.8	0.4	1.2	79.2%	-0.6
15068	AT5G59360.1 | expressed protein, predicted protein, Arabidopsis thaliana; expression supported by MPSS	3.3	3.7	-0.4	-1.2	79.2%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
15069	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	6.3	6.7	-0.4	-1.2	79.2%	-0.9
15070	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	6.3	6.7	-0.4	-1.1	79.3%	-0.9
15071	AT5G52230.1 | Symbol: MBD13 | expressed protein | chr5:21225116-21229035 REVERSE | Aliases: F17P19.13, F17P19_13	2.5	2.4	0.1	1.1	79.3%	-1.4
15072	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	2.8	-0.2	-1.1	79.3%	-1.6
15073	AT4G25140.1 | glycine-rich protein / oleosin | chr4:12900440-12901587 FORWARD | Aliases: F24A6.9	2.5	2.4	0.1	1.1	79.3%	-1.7
15074	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	5.9	5.4	0.5	1.1	79.3%	-0.8
15075	AT3G22810.1 | expressed protein, ; expression supported by MPSS | chr3:8068602-8071566 FORWARD | Aliases: MWI23.18	3.4	3.6	-0.2	-1.1	79.4%	-1.1
15076	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)	3.0	3.3	-0.3	-1.1	79.4%	-0.9
15077	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	3.6	3.4	0.2	1.1	79.4%	-0.9
15078	AT4G11660.1 | Symbol: AT HSFB2B | 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: HSFB2B, T5C23.90, T5C23_90	4.5	4.7	-0.2	-1.1	79.4%	-1.1
15079	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	2.4	-0.1	-1.1	79.4%	-1.8
15080	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	3.6	3.8	-0.3	-1.1	79.4%	-1.0
15081	AT1G62880.1 | cornichon family protein, contains Pfam profile: PF03311 cornichon protein | chr1:23295594-23297217 FORWARD | Aliases: F16P17.3, F16P17_3	3.6	3.8	-0.2	-1.1	79.4%	-1.1
15082	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	4.8	-0.4	-1.1	79.4%	-0.7
15083	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	2.5	2.7	-0.2	-1.1	79.4%	-1.4
15084	AT5G07730.1 | expressed protein | chr5:2457348-2458431 REVERSE | Aliases: MBK20.19, MBK20_19	4.5	4.8	-0.2	-1.1	79.4%	-0.9
15085	AT3G49230.1 | expressed protein | chr3:18265414-18266103 FORWARD | Aliases: F2K15.90	3.6	3.8	-0.2	-1.1	79.4%	-1.1
15086	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	7.9	8.4	-0.5	-1.1	79.4%	-0.8
15087	AT4G38040.1 | exostosin family protein, contains Pfam profile: PF03016 Exostosin family | chr4:17867432-17869296 FORWARD | Aliases: F20D10.160, F20D10_160	6.3	5.9	0.4	1.1	79.5%	-0.5
15088	AT1G51320.1 | F-box family protein (FBX11), contains F-box domain PF:00646 | chr1:19029310-19030437 FORWARD | Aliases: F11M15.18, F11M15_18	2.7	2.9	-0.2	-1.1	79.5%	-1.5
15089	AT4G03820.2 | expressed protein | chr4:1771885-1774420 REVERSE | Aliases: T7M24.8, T7M24_8	2.9	3.0	-0.1	-1.1	79.5%	-1.4
15090	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	4.4	4.6	-0.2	-1.1	79.5%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
15091	AT1G53310.3 | Symbol: ATPPC1 |	9.2	10.1	-1.0	-1.1	79.5%	-0.9
15092	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	3.1	-0.1	-1.1	79.6%	-1.6
15093	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	8.5	9.1	-0.6	-1.1	79.6%	-0.7
15094	AT3G11560.3 | expressed protein | chr3:3639447-3646054 FORWARD | Aliases: F24K9.23	6.1	5.8	0.3	1.1	79.6%	-0.8
15095	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	9.4	-0.6	-1.1	79.6%	-0.7
15096	AT1G73870.1 | zinc finger (B-box type) family protein | chr1:27782839-27784337 FORWARD | Aliases: F2P9.26, F2P9_26	4.2	4.6	-0.4	-1.1	79.6%	-0.8
15097	AT5G11430.1 | transcription elongation factor-related, contains weak similarity to transcription elongation factors | chr5:3648476-3652405 FORWARD | Aliases: F15N18.20, F15N18_20	5.0	5.2	-0.3	-1.1	79.7%	-0.7
15098	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	5.7	6.0	-0.3	-1.1	79.7%	-0.5
15099	AT5G22555.1 | expressed protein | chr5:7489425-7490463 FORWARD | Aliases: None	3.1	3.2	-0.1	-1.1	79.7%	-1.3
15100	AT2G23940.1 | expressed protein, contains 2 transmembrane domains; contains Pfam profile PF05620: Protein of unknown function (DUF788)	6.3	5.9	0.3	1.1	79.7%	-1.1
15101	AT2G38000.1 | chaperone protein dnaJ-related, weak similarity to Chaperone protein dnaJ (Swiss-Prot:Q9ZFC5) (Methylovorus sp.)	5.6	5.2	0.3	1.1	79.7%	-0.9
15102	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	5.8	5.6	0.2	1.1	79.7%	-0.9
15103	AT3G45530.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.0	3.3	-0.3	-1.1	79.8%	-1.1
15104	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	6.0	6.3	-0.3	-1.1	79.8%	-0.8
15105	AT2G24460.1 | expressed protein | chr2:10401409-10402470 FORWARD | Aliases: T28I24.19, T28I24_19	2.2	2.3	-0.1	-1.1	79.8%	-1.8
15106	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	4.2	0.2	1.1	79.8%	-1.0
15107	AT2G35260.1 | expressed protein | chr2:14856615-14859048 FORWARD | Aliases: T4C15.7, T4C15_7	3.3	3.2	0.1	1.1	79.8%	-1.3
15108	AT2G10370.1 | hypothetical protein, includes At2g10370, At5g36050, At1g35090, At1g44860, At4g19300, At1g42400, At3g43040, At3g42500 | chr2:4003719-4004733 FORWARD | Aliases: F12P23.12, F12P23_12	2.3	2.4	-0.1	-1.1	79.8%	-2.0
15109	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	5.5	5.3	0.2	1.1	79.8%	-1.2
15110	AT5G54420.1 | expressed protein | chr5:22113030-22113305 FORWARD | Aliases: F24B18.4, F24B18_4	2.7	2.8	-0.1	-1.1	79.8%	-1.6
15111	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	2.8	-0.1	-1.1	79.9%	-1.5
15112	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	3.9	-0.2	-1.1	79.9%	-1.2
15113	AT3G49480.1 | expressed protein, several hypothetical proteins - Arabidopsis thaliana | chr3:18353529-18354458 REVERSE | Aliases: T9C5.80	3.4	3.6	-0.2	-1.1	79.9%	-1.3
15114	AT3G27660.1 | glycine-rich protein / oleosin, identical to oleosin isoform GB:S71286 from (Arabidopsis thaliana); identical to cDNA oleosin (isoform Atol2) GI:987013 | chr3:10244995-10246260 FORWARD | Aliases: MGF10.3	4.9	5.2	-0.3	-1.1	79.9%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
15115	AT5G67060.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.0	3.1	-0.1	-1.1	79.9%	-1.5
15116	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	3.7	3.9	-0.2	-1.1	79.9%	-1.0
15117	AT1G57943.1 | Symbol: ATPUP17 | purine permease-related, low similarity to purine permease (Arabidopsis thaliana) GI:7620007; contains Pfam profile PF03151: Domain of unknown function, DUF250 | chr1:21441267-21442554 REVERSE | Aliases: F13D13.4, F13D13_4	4.5	4.8	-0.3	-1.1	79.9%	-0.9
15118	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	3.7	4.0	-0.3	-1.1	79.9%	-0.9
15119	AT5G07910.1 | leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560 | chr5:2521570-2524202 REVERSE | Aliases: F13G24.110	3.8	4.1	-0.3	-1.1	79.9%	-1.0
15120	AT2G27270.1 | expressed protein | chr2:11679349-11680286 FORWARD | Aliases: F12K2.15, F12K2_15	2.8	3.0	-0.2	-1.1	79.9%	-1.3
15121	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	2.6	-0.1	-1.1	79.9%	-1.6
15122	AT3G26580.1 | expressed protein | chr3:9760124-9761781 FORWARD | Aliases: MFE16.11	8.8	8.4	0.4	1.1	80.0%	-0.7
15123	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	2.5	-0.1	-1.1	80.0%	-1.8
15124	AT1G44740.1 | expressed protein, ; expression supported by MPSS | chr1:16889844-16891595 FORWARD | Aliases: T12C22.1, T12C22_1	2.9	3.1	-0.2	-1.1	80.0%	-1.1
15125	AT5G17050.1 | UDP-glucoronosyl/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	9.1	8.5	0.6	1.1	80.0%	-0.7
15126	AT4G00650.1 | Symbol: FRI | FRIGIDA protein, identical to Swiss-Prot:Q9FDW0 FRIGIDA protein (Arabidopsis thaliana) | chr4:269026-271503 FORWARD | Aliases: F6N23.25, F6N23_25, FLA, FLOWERING LOCUS A, FRIGIDA	4.0	4.2	-0.2	-1.1	80.1%	-1.1
15127	AT1G42440.1 | expressed protein, contains Pfam domain, PF04950: Protein of unknown function (DUF663) | chr1:15897725-15902495 REVERSE | Aliases: F7F22.4, F7F22_4	6.0	6.2	-0.2	-1.1	80.1%	-0.9
15128	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	5.6	5.9	-0.3	-1.1	80.1%	-0.9
15129	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	3.1	-0.1	-1.1	80.2%	-1.5
15130	AT1G61667.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr1:22771328-22772160 FORWARD | Aliases: None	5.5	5.1	0.5	1.1	80.2%	-0.4
15131	AT5G22390.1 | expressed protein | chr5:7418119-7419252 REVERSE | Aliases: MWD9.19, MWD9_19	2.8	2.7	0.1	1.1	80.2%	-1.4
15132	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	3.7	-0.2	-1.1	80.2%	-1.2
15133	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	1.9	0.1	1.1	80.2%	-1.9
15134	AT1G26900.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:9319743-9321461 REVERSE | Aliases: T2P11.9, T2P11_9	4.3	3.9	0.5	1.1	80.3%	-0.7
15135	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	6.2	5.8	0.4	1.1	80.3%	-0.6

Rank	Description	Sync	Root	M	t	adj.q	B
15136	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	5.7	0.2	1.1	80.3%	-1.1
15137	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	2.5	-0.1	-1.1	80.3%	-1.5
15138	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	2.7	-0.1	-1.1	80.4%	-1.4
15139	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	7.1	0.5	1.1	80.4%	-0.7
15140	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	3.3	-0.1	-1.1	80.4%	-1.7
15141	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	3.4	3.6	-0.2	-1.1	80.4%	-1.3
15142	AT5G03130.1 | hypothetical protein | chr5:736149-736559 FORWARD | Aliases: F15A17.160, F15A17_160	2.8	3.0	-0.2	-1.1	80.4%	-1.4
15143	AT2G37780.1 | DC1 domain-containing protein, contains Pfam PF03107: DC1 domain	2.4	2.5	-0.1	-1.1	80.4%	-1.5
15144	AT3G07820.1 | polygalacturonase 3 (PGA3) / pectinase, identical to polygalacturonase (Arabidopsis thaliana) GI:3152948	2.4	2.5	-0.1	-1.1	80.5%	-1.7
15145	AT1G76620.1 | expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547 | chr1:28761453-28764191 FORWARD | Aliases: F14G6.22, F14G6_22	2.4	2.5	-0.1	-1.1	80.5%	-1.5
15146	AT3G61800.1 | expressed protein | chr3:22885530-22887821 REVERSE | Aliases: F21F14.3	5.1	5.3	-0.2	-1.1	80.6%	-1.0
15147	AT5G27650.1 | PWWP domain-containing protein, hypothetical protein F22F7.12 - Arabidopsis thaliana, EMBL:AC009606 | chr5:9785410-9789235 FORWARD | Aliases: T1G16.4	4.5	4.3	0.2	1.1	80.6%	-1.2
15148	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	2.8	0.2	1.1	80.6%	-1.4
15149	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	7.8	7.5	0.4	1.1	80.6%	-1.0
15150	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)	3.1	2.9	0.2	1.1	80.6%	-0.9
15151	AT2G31050.1 | plastocyanin-like domain-containing protein, contains plastocyanin-like domain Pfam:PF02298 | chr2:13219227-13219829 FORWARD | Aliases: T16B12.14	2.6	2.8	-0.2	-1.1	80.6%	-1.5
15152	AT2G42180.1 | expressed protein | chr2:17587995-17589034 REVERSE | Aliases: T24P15.9, T24P15_9	2.7	2.9	-0.2	-1.1	80.6%	-1.5
15153	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	5.9	5.6	0.3	1.1	80.7%	-0.8
15154	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	2.8	-0.1	-1.1	80.7%	-1.7
15155	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	3.7	4.0	-0.3	-1.1	80.7%	-0.6
15156	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	0.1	1.1	80.8%	-2.3
15157	AT1G06270.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:1918087-1919746 REVERSE | Aliases: F9P14.13, F9P14_13	4.9	4.7	0.2	1.1	80.8%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
15158	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	3.1	-0.1	-1.1	80.8%	-1.5
15159	AT1G21170.1 | expressed protein | chr1:7413039-7419400 FORWARD | Aliases: T22I11.1	3.1	3.3	-0.2	-1.1	80.8%	-1.4
15160	AT4G37590.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr4:17662836-17666056 REVERSE | Aliases: F19F18.80, F19F18_80	5.5	5.8	-0.3	-1.1	80.8%	-1.0
15161	AT1G55870.1 | CAF1 family ribonuclease, contains Pfam domain, PF04857: CAF1 family ribonuclease | chr1:20899271-20902087 FORWARD | Aliases: F14J16.11, F14J16_11	3.8	3.6	0.2	1.1	80.8%	-1.0
15162	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	2.6	-0.1	-1.1	80.8%	-1.5
15163	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	4.8	0.3	1.1	80.8%	-0.8
15164	AT4G12920.1 | aspartyl protease family protein, low similarity to CND41, chloroplast nucleoid DNA binding protein (Nicotiana tabacum) GI:2541876; contains Pfam profile PF00026: Eukaryotic aspartyl protease | chr4:7568283-7569452 FORWARD | Aliases: F25G13.10, F25G13_10	2.7	2.9	-0.1	-1.1	80.8%	-1.3
15165	AT4G29550.1 | expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626) | chr4:14502218-14503853 FORWARD | Aliases: T16L4.60, T16L4_60	2.8	2.9	-0.2	-1.1	80.8%	-1.4
15166	AT3G05940.1 | expressed protein, contains Pfam profile PF03619: Domain of unknown function | chr3:1777370-1779654 REVERSE | Aliases: F2O10.10	5.1	4.8	0.3	1.1	80.8%	-0.7
15167	AT1G51210.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr1:18991477-18992778 FORWARD | Aliases: F11M15.8, F11M15_8	5.5	5.8	-0.3	-1.1	80.9%	-0.9
15168	AT5G26640.1 | expressed protein | chr5:9347844-9348177 REVERSE | Aliases: None	3.1	3.3	-0.2	-1.1	80.9%	-1.3
15169	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	5.3	6.0	-0.6	-1.1	80.9%	-0.7
15170	AT1G33500.1 | hypothetical protein | chr1:12152754-12154665 FORWARD | Aliases: F10C21.15, F10C21_15	2.9	2.7	0.2	1.1	80.9%	-1.7
15171	ATCG00680.1 | Symbol: PSBB | encodes for CP47, subunit of the photosystem II reaction center.	7.6	6.8	0.7	1.1	80.9%	-0.8
15172	AT5G45120.1 | aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease | chr5:18258230-18259705 FORWARD | Aliases: K17O22.14, K17O22_14	3.2	3.3	-0.2	-1.1	80.9%	-1.3
15173	AT1G20940.1 | F-box family protein, contains Pfam:PF00646 F-box domain	3.2	3.5	-0.3	-1.1	80.9%	-0.9
15174	AT2G37210.1 | expressed protein, contains Pfam profile PF03641: decarboxylase family protein | chr2:15631070-15634019 REVERSE | Aliases: T2N18.3, T2N18_3	3.8	4.1	-0.2	-1.1	80.9%	-1.0
15175	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	8.3	8.5	-0.3	-1.1	80.9%	-0.8
15176	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	8.0	7.6	0.3	1.1	80.9%	-0.9
15177	AT5G58660.1 | oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to ACC oxidase, Lycopersicon esculentum (SP:P05116), gibberellin 3B-hydroxylase, Latuca sativa (gi:4164145); contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily	4.4	4.6	-0.3	-1.1	80.9%	-0.8
15178	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	2.6	-0.2	-1.1	80.9%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
15179	AT1G14530.2 | tobamovirus multiplication protein 3, putative / TOM3, putative (THH1), identical to THH1 (GI:15706301) (Arabidopsis thaliana); supporting cDNA gi:15706300:dbj:AB057678.1: | chr1:4971199-4973717 REVERSE | Aliases: F14L17.31, F14L17_31, THH1, TOM THREE HOMOLOG	5.0	5.2	-0.2	-1.1	80.9%	-0.8
15180	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	5.1	4.8	0.2	1.1	81.0%	-1.0
15181	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	4.8	5.4	-0.6	-1.1	81.0%	-0.4
15182	AT4G19620.1 | expressed protein | chr4:10682443-10682854 REVERSE | Aliases: F24J7.170, F24J7_170	3.0	2.9	0.1	1.1	81.0%	-1.2
15183	AT3G17900.1 | expressed protein | chr3:6128539-6133389 FORWARD | Aliases: MEB5.12	4.6	4.8	-0.2	-1.1	81.0%	-1.0
15184	AT5G50440.1 | Symbol: MEMB12 |	5.9	6.2	-0.3	-1.1	81.0%	-1.2
15185	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	6.0	6.3	-0.2	-1.1	81.0%	-1.2
15186	AT1G14660.1 | Symbol: ATNHX8 |	2.7	2.8	-0.2	-1.1	81.0%	-1.5
15187	AT5G28950.1 | hypothetical protein | chr5:10992509-10993439 FORWARD | Aliases: F3F24.50, F3F24_50	3.0	3.2	-0.2	-1.1	81.0%	-1.3
15188	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	2.6	2.8	-0.1	-1.1	81.1%	-1.4
15189	AT3G42630.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:14733254-14734843 FORWARD | Aliases: T12K4.80	5.3	5.5	-0.3	-1.1	81.1%	-0.9
15190	ATMG00580.1 | Symbol: NAD4 | NADH dehydrogenase subunit 4 | chrM:161693-169674 FORWARD | Aliases: NAD4	6.7	7.3	-0.6	-1.1	81.2%	-0.3
15191	AT5G24830.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:8530981-8534210 FORWARD | Aliases: F6A4.40, F6A4_40	4.1	3.9	0.2	1.1	81.2%	-1.1
15192	AT2G48090.1 | expressed protein, weak similarity to protein kinase | chr2:19676180-19676834 REVERSE | Aliases: T9J23.24	2.7	2.9	-0.2	-1.1	81.2%	-1.3
15193	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	2.4	-0.1	-1.1	81.2%	-2.0
15194	AT3G25670.1 | leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; + | chr3:9345769-9347538 REVERSE | Aliases: T5M7.12	3.5	3.7	-0.2	-1.1	81.2%	-1.2
15195	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	5.9	-0.3	-1.1	81.2%	-1.2
15196	AT5G04330.1 | cytochrome P450, putative / ferulate-5-hydroxylase, putative, Similar to	3.8	4.0	-0.2	-1.1	81.2%	-0.8
15197	AT3G45910.1 | expressed protein | chr3:16887323-16888060 REVERSE | Aliases: F16L2.120	2.2	2.3	-0.1	-1.1	81.3%	-1.5
15198	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	2.9	3.0	-0.2	-1.1	81.3%	-1.2
15199	AT1G07025.1 | mitochondrial substrate carrier family protein, contains similarity to mitochondrial carrier proteins | chr1:2157657-2158157 REVERSE | Aliases: None	2.6	2.8	-0.2	-1.1	81.3%	-1.3
15200	AT2G06120.1 | expressed protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287	4.8	5.0	-0.2	-1.1	81.3%	-1.2
15201	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	3.8	-0.2	-1.1	81.3%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
15202	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	8.7	8.3	0.5	1.1	81.3%	-0.7
15203	AT2G38570.1 | expressed protein, ; expression supported by MPSS | chr2:16143932-16145495 REVERSE | Aliases: T6A23.23, T6A23_23	3.9	3.7	0.2	1.1	81.4%	-1.1
15204	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	5.2	-0.4	-1.1	81.4%	-0.8
15205	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	2.7	2.6	0.2	1.1	81.5%	-1.2
15206	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	2.8	-0.2	-1.1	81.5%	-1.6
15207	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	5.7	5.3	0.4	1.1	81.5%	-0.8
15208	AT3G62430.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.5	3.4	0.1	1.1	81.5%	-1.4
15209	AT2G21740.1 | expressed protein | chr2:9289066-9289443 REVERSE | Aliases: F7D8.6, F7D8_6	2.4	2.3	0.1	1.1	81.5%	-1.4
15210	AT4G27000.1 | RNA-binding protein 45 (RBP45), putative, DNA binding protein ACBF - Nicotiana tabacum, PID:g1899188 | chr4:13554632-13557860 REVERSE | Aliases: ATRBP45C, F10M23.340, F10M23_340	7.4	7.9	-0.5	-1.1	81.5%	-0.6
15211	AT1G12460.1 | leucine-rich repeat transmembrane protein kinase, putative | chr1:4247247-4250628 FORWARD | Aliases: F5O11.21, F5O11_21	4.5	4.2	0.2	1.1	81.5%	-0.9
15212	AT5G52550.1 | expressed protein | chr5:21344938-21347362 REVERSE | Aliases: F6N7.3, F6N7_3	5.8	6.1	-0.2	-1.1	81.6%	-0.9
15213	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	-1.1	81.6%	-1.7
15214	NA	2.5	2.6	-0.1	-1.1	81.6%	-1.7
15215	AT4G24150.1 | Symbol: AtGRF8 |	2.7	2.6	0.1	1.1	81.6%	-1.5
15216	AT1G50500.1 | membrane trafficking VPS53 family protein, contains Pfam domain PF04100: Vps53-like, N-terminal | chr1:18711655-18719645 REVERSE | Aliases: F11F12.15	4.6	4.3	0.3	1.1	81.6%	-1.2
15217	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	9.3	0.4	1.1	81.6%	-0.8
15218	AT3G59460.1 | hypothetical protein, putative proteins - Arabidopsis thaliana | chr3:21988490-21989300 FORWARD | Aliases: T16L24.10	4.0	4.3	-0.3	-1.1	81.7%	-0.9
15219	AT1G16980.1 | Symbol: ATTPS2 |	2.6	2.7	-0.1	-1.1	81.7%	-1.6
15220	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	3.3	-0.3	-1.1	81.7%	-1.3
15221	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	3.1	3.2	-0.2	-1.1	81.7%	-1.3
15222	AT5G06900.1 | Symbol: CYP93D1 | cytochrome P450 family protein | chr5:2136161-2137926 REVERSE | Aliases: MOJ9.6, MOJ9_6	3.0	3.2	-0.1	-1.1	81.7%	-1.5
15223	AT1G21510.1 | expressed protein | chr1:7531523-7532494 REVERSE | Aliases: F24J8.12, F24J8_12	3.0	3.1	-0.2	-1.1	81.8%	-1.4
15224	AT4G10140.1 | expressed protein | chr4:6322453-6324660 FORWARD | Aliases: F28M11.60, F28M11_60	6.7	6.3	0.4	1.1	81.8%	-0.7
15225	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	8.6	9.2	-0.6	-1.1	81.8%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
15226	AT3G60620.1 | phosphatidate cytidylyltransferase family protein, contains Pfam profile: PF01148 phosphatidate cytidylyltransferase | chr3:22417381-22419572 FORWARD | Aliases: T4C21.30	3.6	3.4	0.1	1.1	81.8%	-1.2
15227	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	-0.1	-1.1	81.9%	-1.6
15228	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	2.4	-0.1	-1.1	81.9%	-1.8
15229	AT1G65630.1 | DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana) | chr1:24410205-24412731 REVERSE | Aliases: F1E22.1	2.4	2.5	-0.1	-1.1	81.9%	-2.0
15230	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	5.6	5.4	0.2	1.1	82.0%	-1.0
15231	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	7.0	7.4	-0.4	-1.1	82.0%	-1.0
15232	AT1G44810.1 | expressed protein, contains Pfam profile: PF04504 protein of unknown function, DUF573 | chr1:16925983-16927261 FORWARD | Aliases: T12C22.8, T12C22_8	6.0	6.2	-0.2	-1.1	82.0%	-1.1
15233	AT3G42160.1 | pectinesterase-related, contains weak similarity to Swiss-Prot:Q96575 pectinesterase 2 precursor	2.5	2.6	-0.1	-1.1	82.0%	-1.5
15234	AT1G21770.1 | expressed protein | chr1:7651635-7652275 REVERSE | Aliases: F8K7.21, F8K7_21	9.8	9.5	0.4	1.1	82.0%	-1.1
15235	AT3G06230.1 | Symbol: ATMKK8 |	2.3	2.2	0.1	1.1	82.0%	-1.6
15236	AT1G04600.1 | Symbol: XIA | myosin, putative, similar to myosin (GI:499047) (Arabidopsis thaliana) | chr1:1262122-1272375 FORWARD | Aliases: ATXIA, T1G11.15, T1G11_15	3.1	2.9	0.1	1.1	82.0%	-1.4
15237	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	7.8	8.1	-0.3	-1.1	82.0%	-0.8
15238	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	3.3	-0.2	-1.1	82.0%	-1.3
15239	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	8.1	7.9	0.2	1.1	82.0%	-0.9
15240	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	7.9	7.1	0.8	1.1	82.1%	-0.8
15241	AT1G06810.1 | expressed protein, contains Pfam PF04396: Protein of unknown function, DUF537 | chr1:2091920-2092527 REVERSE | Aliases: F4H5.25, F4H5_25	4.0	4.2	-0.2	-1.1	82.1%	-1.3
15242	AT2G03580.1 | F-box family protein-related, supported by tandem duplication of	3.3	3.5	-0.2	-1.1	82.1%	-1.4
15243	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	5.8	6.3	-0.5	-1.1	82.1%	-0.6
15244	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	3.2	3.3	-0.1	-1.1	82.2%	-1.7
15245	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	5.1	4.9	0.2	1.1	82.2%	-1.1
15246	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	7.0	-0.4	-1.1	82.3%	-0.7

Rank	Description	Sync	Root	M	t	adj.q	B
15247	AT2G44880.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:18512314-18513981 FORWARD | Aliases: T13E15.11	2.6	2.7	-0.1	-1.1	82.3%	-1.6
15248	AT1G04470.1 | expressed protein, EST gb:ATTS5672 comes from this gene | chr1:1211072-1214590 REVERSE | Aliases: F19P19.7, F19P19_7	2.2	2.3	-0.1	-1.1	82.3%	-1.6
15249	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	3.5	3.7	-0.2	-1.1	82.3%	-0.9
15250	AT2G33410.1 | heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative | chr2:14162963-14164838 FORWARD | Aliases: F4P9.18, F4P9_18	7.3	6.8	0.5	1.1	82.3%	-0.6
15251	AT1G77780.1 | glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase precursor GI:4097946 from (Oryza sativa) | chr1:29253194-29254422 REVERSE | Aliases: T32E8.11, T32E8_11	2.0	2.1	-0.1	-1.1	82.3%	-1.8
15252	AT4G17690.1 | peroxidase, putative, similar to peroxidase (Spinacia oleracea) gi:1781336:emb:CAA71495 | chr4:9846140-9847120 FORWARD | Aliases: DL4880W, FCAALL.96	3.0	3.2	-0.2	-1.1	82.3%	-1.3
15253	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	3.2	3.4	-0.2	-1.1	82.3%	-1.2
15254	AT2G02020.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr2:479100-481184 FORWARD | Aliases: F14H20.9, F14H20_9	5.0	4.7	0.3	1.1	82.3%	-0.7
15255	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)	4.5	4.2	0.3	1.1	82.3%	-0.8
15256	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	4.6	4.4	0.2	1.1	82.3%	-1.0
15257	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	2.9	3.1	-0.2	-1.1	82.3%	-1.1
15258	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	2.6	2.8	-0.2	-1.1	82.4%	-1.2
15259	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	2.2	2.3	-0.1	-1.1	82.4%	-1.9
15260	AT1G65760.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.8	3.0	-0.2	-1.1	82.4%	-1.5
15261	AT3G10590.1 | myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA binding domain | chr3:3310429-3311316 REVERSE | Aliases: F13M14.12	2.6	2.7	-0.1	-1.1	82.4%	-1.7
15262	AT1G67910.1 | expressed protein | chr1:25474972-25476008 REVERSE | Aliases: T23K23.24, T23K23_24	4.6	4.9	-0.3	-1.1	82.5%	-0.8
15263	AT3G44440.1 | expressed protein | chr3:16081969-16082243 FORWARD | Aliases: F14L2.2	4.7	5.2	-0.5	-1.1	82.5%	-0.9
15264	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	4.1	0.2	1.1	82.5%	-1.2
15265	AT5G44010.1 | expressed protein | chr5:17724192-17726426 REVERSE | Aliases: MRH10.12, MRH10_12	2.5	2.4	0.1	1.1	82.5%	-1.8
15266	AT2G05430.1 | expressed protein | chr2:1985993-1987263 FORWARD | Aliases: F16J10.2, F16J10_2	2.7	2.8	-0.1	-1.1	82.5%	-1.7
15267	AT5G44930.2 | exostosin family protein, contains Pfam profile: PF03016 Exostosin family | chr5:18157457-18159371 REVERSE | Aliases: K21C13.11, K21C13_11	3.2	3.3	-0.2	-1.1	82.5%	-1.4
15268	AT3G15440.1 | expressed protein | chr3:5211930-5212361 REVERSE | Aliases: MJK13.10	3.0	3.1	-0.1	-1.1	82.5%	-1.5
15269	AT2G24840.1 | MADS-box family protein | chr2:10588161-10588955 FORWARD | Aliases: F27C12.24, F27C12_24	3.5	3.7	-0.2	-1.1	82.5%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
15270	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	7.6	7.8	-0.2	-1.1	82.5%	-1.1
15271	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	2.5	-0.1	-1.1	82.5%	-1.9
15272	AT5G09350.1 | phosphatidylinositol 4-kinase, putative, strong similarity to gi:4467359	5.1	5.9	-0.8	-1.1	82.5%	-0.6
15273	AT5G64070.1 | phosphatidylinositol 4-kinase (PI4K), nearly identical to gi:4467359 | chr5:25654202-25661672 REVERSE | Aliases: MHJ24.5, MHJ24_5	5.1	5.9	-0.8	-1.1	82.5%	-0.6
15274	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	2.6	2.5	0.1	1.1	82.5%	-1.7
15275	AT5G45360.1 | F-box family protein, similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250	7.7	8.1	-0.4	-1.1	82.5%	-0.9
15276	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	2.9	0.1	1.1	82.6%	-1.3
15277	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	5.6	5.2	0.4	1.1	82.6%	-0.7
15278	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	4.5	4.3	0.3	1.1	82.6%	-1.1
15279	AT3G24510.1 | Encodes a defensin-like (DEFL) family protein. | chr3:8931984-8932715 FORWARD | Aliases: MOB24.6	2.3	2.4	-0.1	-1.1	82.6%	-1.9
15280	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	3.9	4.1	-0.2	-1.1	82.6%	-1.1
15281	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	6.1	5.7	0.4	1.1	82.7%	-0.5
15282	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 peroxismal 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	5.9	0.3	1.1	82.7%	-1.0
15283	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	4.0	3.8	0.2	1.1	82.7%	-1.1
15284	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	3.6	0.1	1.1	82.7%	-1.5
15285	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	3.9	0.2	1.1	82.7%	-1.3
15286	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	3.8	4.1	-0.2	-1.1	82.7%	-1.1
15287	AT1G15490.1 | hydrolase, alpha/beta fold family protein, Contains PF 00561 alpha/beta hydrolase fold | chr1:5320610-5323890 REVERSE | Aliases: F9L1.44, F9L1_44	4.1	4.3	-0.3	-1.1	82.7%	-1.1
15288	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	3.7	3.4	0.3	1.1	82.8%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
15289	AT5G40200.1 | DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana) | chr5:16087558-16090542 FORWARD | Aliases: MSN9.100, MSN9_100	6.1	5.7	0.4	1.1	82.8%	-0.8
15290	AT5G35270.1 | 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); | chr5:13524678-13525611 FORWARD | Aliases: T25C13.150, T25C13_150	3.3	3.6	-0.3	-1.1	82.8%	-0.9
15291	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	3.8	-0.2	-1.1	82.8%	-1.4
15292	AT1G15050.1 | Symbol: IAA34 | auxin-responsive AUX/IAA family protein, similar to auxin-responsive protein IAA12 (Indoleacetic acid-induced protein 12)(Arabidopsis thaliana); contains Pfam profile: PF02309: AUX/IAA family	4.5	4.8	-0.3	-1.1	82.8%	-1.1
15293	AT3G24260.1 | hypothetical protein | chr3:8793844-8794968 REVERSE | Aliases: K7M2.2	2.9	3.1	-0.1	-1.1	82.9%	-1.4
15294	AT5G56880.1 | expressed protein | chr5:23026324-23026935 REVERSE | Aliases: MPI10.4, MPI10_4	4.1	4.4	-0.3	-1.1	82.9%	-0.9
15295	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	3.6	3.4	0.2	1.1	82.9%	-0.9
15296	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	2.6	-0.1	-1.1	83.0%	-1.6
15297	AT5G52360.1 | actin-depolymerizing factor, putative, strong similarity to pollen specific actin-depolymerizing factor 2 (Nicotiana tabacum) GI:22857914; contains Pfam profile PF00241: Cofilin/tropomyosin-type actin-binding protein	3.2	3.0	0.1	1.1	83.0%	-1.7
15298	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	4.5	3.8	0.7	1.1	83.0%	-0.8
15299	AT2G14020.1 | expressed protein | chr2:5900869-5901354 REVERSE | Aliases: F9B22.13, F9B22_13	3.6	3.9	-0.2	-1.1	83.0%	-1.1
15300	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	3.0	-0.1	-1.1	83.0%	-1.4
15301	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	3.9	3.7	0.2	1.1	83.0%	-1.2
15302	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	3.4	3.6	-0.2	-1.1	83.0%	-1.1
15303	AT5G26620.1 | expressed protein | chr5:9366700-9366966 REVERSE | Aliases: None	2.5	2.4	0.1	1.1	83.0%	-1.8
15304	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	1.1	83.0%	-1.6
15305	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	3.6	-0.1	-1.1	83.0%	-1.4
15306	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	6.2	6.4	-0.2	-1.1	83.1%	-1.2
15307	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	2.9	-0.1	-1.1	83.1%	-1.3
15308	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	3.7	3.4	0.2	1.1	83.1%	-1.1
15309	AT4G30860.1 | SET domain-containing protein, low similarity to IL-5 promoter REII-region-binding protein (Homo sapiens) GI:12642795; contains Pfam profile PF00856: SET domain	4.3	4.0	0.3	1.1	83.1%	-0.5

Rank	Description	Sync	Root	M	t	adj.q	B
15310	AT3G49950.1 | scarecrow transcription factor family protein, lateral suppressor protein - Lycopersicon esculentum, EMBL:AF098674 | chr3:18533555-18534787 FORWARD | Aliases: F3A4.30	3.1	3.2	-0.1	-1.1	83.2%	-1.7
15311	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	3.4	-0.3	-1.1	83.2%	-0.6
15312	AT4G15060.1 | F-box protein-related, contains weak similarity to F-box domain Pfam:PF00646 | chr4:8599031-8601757 FORWARD | Aliases: DL3575W, FCAALL.180	2.6	2.8	-0.1	-1.1	83.2%	-1.6
15313	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	2.5	2.6	-0.1	-1.1	83.2%	-1.6
15314	AT1G10780.1 | F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250 | chr1:3592747-3595078 REVERSE | Aliases: T16B5.8	3.6	3.4	0.1	1.1	83.2%	-1.2
15315	AT5G57000.2 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g72690.1) | chr5:23080941-23082506 REVERSE | Aliases: MHM17.12, MHM17_12	5.5	5.8	-0.3	-1.1	83.2%	-0.8
15316	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	2.4	0.1	1.1	83.2%	-1.7
15317	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	3.0	-0.1	-1.1	83.2%	-1.6
15318	AT2G41250.1 | 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 | chr2:17207737-17209696 REVERSE | Aliases: F13H10.20, F13H10_20	4.7	5.0	-0.3	-1.1	83.2%	-0.8
15319	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	3.9	4.1	-0.2	-1.1	83.3%	-0.8
15320	AT4G04500.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr4:2238409-2240863 FORWARD | Aliases: T26N6.11, T26N6_11	2.7	2.8	-0.1	-1.1	83.3%	-1.4
15321	AT4G26130.1 | expressed protein | chr4:13240015-13241292 REVERSE | Aliases: F20B18.240, F20B18_240	2.8	2.9	-0.1	-1.1	83.3%	-1.8
15322	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	3.6	0.2	1.1	83.3%	-1.0
15323	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	2.8	-0.2	-1.1	83.3%	-1.3
15324	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	3.2	3.0	0.1	1.1	83.4%	-1.2
15325	AT1G28010.1 | multidrug resistance P-glycoprotein, putative, similar to mdr-like P-glycoprotein GI:3849833 from (Arabidopsis thaliana)	2.6	2.7	-0.1	-1.1	83.4%	-1.5
15326	AT5G13140.1 | expressed protein | chr5:4170563-4171797 REVERSE | Aliases: T19L5.100, T19L5_100	2.3	2.4	-0.1	-1.1	83.4%	-1.7
15327	AT1G14470.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:4954075-4955697 FORWARD | Aliases: F14L17.25, F14L17_25	2.9	3.0	-0.1	-1.1	83.4%	-1.5
15328	AT1G71691.2 | GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382 from (Arabidopsis thaliana);	2.5	2.7	-0.2	-1.1	83.4%	-1.6
15329	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	2.7	-0.1	-1.1	83.4%	-1.6
15330	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	2.6	2.7	-0.1	-1.1	83.5%	-1.8
15331	AT2G38750.1 | Symbol: ANNAT4 |	3.5	3.6	-0.2	-1.1	83.5%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
15332	AT2G31340.1 | Symbol: EMB1381 | expressed protein | chr2:13368583-13372277 FORWARD | Aliases: EMB1381, EMBRYO DEFECTIVE 1381, T28P16.17, T28P16_17	3.9	3.7	0.1	1.1	83.5%	-1.3
15333	AT5G35480.1 | expressed protein | chr5:13706434-13706788 REVERSE | Aliases: MOK9.7, MOK9_7	3.3	3.5	-0.2	-1.1	83.5%	-1.5
15334	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	2.9	-0.2	-1.1	83.5%	-1.3
15335	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	2.6	2.7	-0.1	-1.1	83.5%	-1.5
15336	AT1G64830.1 | aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease | chr1:24094934-24096229 REVERSE | Aliases: F13O11.13, F13O11_13	2.7	2.8	-0.1	-1.1	83.5%	-1.4
15337	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	-1.1	83.6%	-2.1
15338	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	9.4	-0.2	-1.1	83.6%	-1.0
15339	AT2G41330.1 | glutaredoxin family protein, contains Pfam profile PF00462: Glutaredoxin	3.5	3.7	-0.3	-1.1	83.6%	-0.8
15340	AT1G14800.1 | expressed protein | chr1:5099567-5102553 FORWARD | Aliases: F10B6.21, F10B6_21	3.1	3.5	-0.3	-1.1	83.6%	-0.8
15341	AT1G61290.1 | Symbol: SYP124 |	3.7	3.8	-0.1	-1.1	83.6%	-1.5
15342	AT3G55470.1 | C2 domain-containing protein, similar to phloem protein GI:4164539 from (Cucurbita maxima) | chr3:20575222-20577665 FORWARD | Aliases: T22E16.130	4.9	5.2	-0.3	-1.1	83.6%	-0.9
15343	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	3.3	3.4	-0.1	-1.1	83.6%	-1.9
15344	AT1G32870.1 | Symbol: ANAC013 | no apical meristem (NAM) family protein, similar to to NAC2 (GI:645671) (Arabidopsis thaliana); contains Pfam PF02365: No apical meristem (NAM) protein | chr1:11911701-11913927 FORWARD | Aliases: ANAC013, F9L11.7, F9L11_7	4.5	4.3	0.2	1.1	83.6%	-1.2
15345	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	6.8	6.2	0.6	1.1	83.6%	-0.6
15346	AT5G56770.1 | expressed protein | chr5:22980220-22981215 REVERSE | Aliases: MIK19.24, MIK19_24	2.7	2.8	-0.2	-1.1	83.7%	-1.4
15347	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	3.5	-0.2	-1.1	83.7%	-1.4
15348	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	8.3	0.2	1.1	83.7%	-1.0
15349	AT5G60620.1 | phospholipid/glycerol acyltransferase family protein, contains Pfam PF01553: Acyltransferase | chr5:24384442-24387015 FORWARD | Aliases: MUP24.4, MUP24_4	9.2	9.6	-0.5	-1.1	83.7%	-0.9
15350	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	2.5	2.4	0.1	1.1	83.8%	-1.5
15351	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) (GI:559920) from (Nicotiana tabacum), which, due to scienitific 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	3.4	3.3	0.2	1.1	83.8%	-1.4
15352	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	4.9	5.1	-0.3	-1.1	83.8%	-0.6
15353	AT3G24080.1 | KRR1 family protein, contains Pfam PF05178: Krr1 family | chr3:8694969-8697131 REVERSE | Aliases: F14O13.28	9.3	8.8	0.5	1.1	83.8%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
15354	AT5G01220.1 | Symbol: SQD2 | UDP-sulfoquinovose:DAG sulfoquinovosyltransferase / sulfolipid synthase (SQD2), identical to GI:20302857	3.7	3.9	-0.2	-1.1	83.8%	-1.3
15355	AT5G56860.1 | zinc finger (GATA type) family protein, similar to unknown protein (pir :T04270)	2.8	3.0	-0.2	-1.1	83.8%	-1.4
15356	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	3.1	-0.2	-1.1	83.8%	-1.2
15357	AT3G09560.2 | lipin family protein, contains Pfam profile: PF04571 lipin, N-terminal conserved region | chr3:2934622-2939461 REVERSE | Aliases: F11F8.14	3.3	3.1	0.2	1.1	83.8%	-1.2
15358	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	2.3	-0.1	-1.1	83.8%	-1.9
15359	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	2.5	-0.1	-1.1	83.8%	-1.9
15360	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	2.8	3.1	-0.2	-1.1	83.9%	-1.3
15361	AT3G42330.1 | hypothetical protein | chr3:14495405-14496319 FORWARD | Aliases: T14K23.40	3.8	4.1	-0.3	-1.1	83.9%	-0.8
15362	AT5G63910.1 | expressed protein | chr5:25589116-25591313 REVERSE | Aliases: MGI19.4, MGI19_4	6.0	6.2	-0.2	-1.1	84.0%	-0.9
15363	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	3.5	3.7	-0.2	-1.1	84.0%	-0.8
15364	AT3G43110.1 | expressed protein | chr3:15102698-15103396 REVERSE | Aliases: F7M19.120	3.0	3.2	-0.2	-1.1	84.0%	-1.0
15365	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	7.2	6.8	0.3	1.1	84.0%	-0.8
15366	AT1G59560.1 | Symbol: ZCF61 | expressed protein, contains similarity to apoptosis inhibitors | chr1:21885264-21887443 FORWARD | Aliases: T30E16.12, T30E16_12, ZCF61	5.1	4.9	0.2	1.1	84.0%	-0.9
15367	ATCG00220.1 | Symbol: PSBM | PSII low MW protein | chrC:28707-28811 REVERSE | Aliases: PSBM	10.5	9.8	0.6	1.1	84.0%	-1.3
15368	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	3.9	-0.2	-1.1	84.0%	-0.9
15369	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	3.0	-0.1	-1.1	84.0%	-1.3
15370	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	4.4	4.2	0.2	1.1	84.0%	-1.1
15371	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	3.2	3.0	0.2	1.1	84.0%	-1.0
15372	AT2G14140.1 | hypothetical protein, similar to At2g04970, At2g15200, At1g32830, At3g30450, At4g03990, At5g34895, At3g47270, At2g02200 | chr2:5974260-5978569 FORWARD | Aliases: T22C12.7, T22C12_7	1.9	2.1	-0.2	-1.1	84.0%	-2.2
15373	AT5G36280.1 | expressed protein | chr5:14316465-14316692 REVERSE | Aliases: T30G6.15, T30G6_15	2.9	3.1	-0.2	-1.1	84.1%	-1.5
15374	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	3.6	-0.1	-1.1	84.1%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
15375	AT4G22600.1 | expressed protein | chr4:11900222-11901043 REVERSE | Aliases: F7K2.180, F7K2_180	3.2	3.3	-0.2	-1.1	84.1%	-1.3
15376	AT5G53960.1 | expressed protein | chr5:21924951-21925678 FORWARD | Aliases: K19P17.13, K19P17_13	2.1	2.2	-0.1	-1.1	84.1%	-2.1
15377	AT2G04790.3 | expressed protein | chr2:1679525-1680540 FORWARD | Aliases: F28I8.17, F28I8_17	3.0	2.8	0.1	1.1	84.1%	-1.2
15378	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	9.7	9.5	0.2	1.1	84.1%	-1.1
15379	AT2G04380.1 | expressed protein | chr2:1525639-1526764 FORWARD | Aliases: T1O3.21, T1O3_21	2.9	3.0	-0.1	-1.1	84.1%	-1.6
15380	NA	12.3	12.2	0.1	1.1	84.1%	-1.8
15381	AT3G01310.2 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g15070.1); similar to mKIAA0433 protein [Mus musculus] (GB:BAC97950.1); similar to hypothetical protein LOC227399 [Mus musculus] (GB:NP_776121.2); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD53244.1); similar to P0413G02.23 [Oryza sativa (japonica cultivar-group)] (GB:NP_916369.1); similar to PREDICTED: similar to KIAA0433 [Canis familiaris] (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	5.4	5.7	-0.3	-1.1	84.1%	-0.9
15382	AT2G42380.2 | bZIP transcription factor family protein	2.1	2.1	0.1	1.1	84.2%	-1.8
15383	AT4G24840.1 | expressed protein | chr4:12796257-12800948 REVERSE | Aliases: F6I7.50, F6I7_50	6.7	6.4	0.3	1.1	84.2%	-0.8
15384	AT3G11390.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.2	2.4	-0.1	-1.1	84.2%	-1.7
15385	AT1G73030.1 | SNF7 family protein, contains Pfam domain, PF03357: SNF7 family | chr1:27477487-27478783 FORWARD | Aliases: F3N23.23, F3N23_23	8.6	8.2	0.4	1.1	84.2%	-0.7
15386	AT5G58410.1 | expressed protein, contains similarity to hypothetical proteins | chr5:23626889-23634612 FORWARD | Aliases: MCK7.28, MCK7_28	6.3	6.5	-0.2	-1.1	84.2%	-0.9
15387	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	2.5	-0.1	-1.1	84.2%	-1.6
15388	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	8.4	7.7	0.8	1.1	84.2%	-0.7
15389	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	11.1	10.7	0.4	1.1	84.3%	-1.1
15390	AT5G26840.1 | expressed protein | chr5:9442291-9442608 REVERSE | Aliases: F2P16.100, F2P16_100	4.5	4.8	-0.3	-1.1	84.4%	-1.2
15391	AT5G45780.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:18584173-18586852 REVERSE | Aliases: MRA19.22, MRA19_22	3.4	3.2	0.2	1.1	84.4%	-1.4
15392	AT1G15840.1 | expressed protein | chr1:5451427-5452369 FORWARD | Aliases: F7H2.17, F7H2_17	7.0	7.4	-0.4	-1.1	84.5%	-0.8
15393	AT1G76800.1 | nodulin, putative, similar to nodulin 21 (N-21) (Glycine max) SWISS-PROT:P16313 | chr1:28834202-28835171 FORWARD | Aliases: F28O16.17, F28O16_17	5.7	5.4	0.3	1.1	84.5%	-1.1
15394	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	1.1	84.5%	-1.9
15395	AT3G20730.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:7247101-7249151 FORWARD | Aliases: MOE17.3	3.4	3.2	0.2	1.1	84.5%	-0.8
15396	AT1G05500.1 | C2 domain-containing protein, similar to Ca2+-dependent lipid-binding protein (CLB1) GI:2789434 from (Lycopersicon esculentum) | chr1:1625097-1628939 FORWARD | Aliases: T25N20.15	6.0	6.3	-0.3	-1.1	84.5%	-1.0
15397	AT4G14530.1 | expressed protein | chr4:8343472-8343879 REVERSE | Aliases: DL3305C, FCAALL.249	3.8	3.9	-0.2	-1.1	84.5%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
15398	AT5G42600.1 | pentacyclic triterpene synthase, putative, similar to pentacyclic triterpene synthase (gi:6650207) (PMID: 11247608) | chr5:17070794-17075373 FORWARD | Aliases: MFO20.1, MFO20_1	4.1	4.4	-0.3	-1.1	84.5%	-0.8
15399	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	3.7	4.3	-0.7	-1.1	84.5%	-0.8
15400	AT1G02960.3 | expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g02965.1) | chr1:666872-669805 REVERSE | Aliases: F22D16.4, F22D16_4	6.4	6.1	0.3	1.1	84.5%	-0.8
15401	AT1G20730.1 | expressed protein, contains TIGRFAM TIGR01640 : F-box protein interaction domain	2.7	2.9	-0.2	-1.1	84.5%	-1.2
15402	AT2G17740.1 | DC1 domain-containing protein | chr2:7714164-7714910 REVERSE | Aliases: T17A5.16, T17A5_16	2.8	2.9	-0.2	-1.1	84.5%	-1.3
15403	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	5.0	4.8	0.3	1.1	84.6%	-0.9
15404	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	4.0	-0.2	-1.1	84.6%	-1.3
15405	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	3.7	0.1	1.1	84.6%	-1.6
15406	AT1G20400.1 | myosin heavy chain-related | chr1:7072182-7075828 REVERSE | Aliases: F5M15.25, F5M15_25	2.8	2.9	-0.1	-1.1	84.6%	-1.3
15407	AT2G13600.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:5678575-5680668 FORWARD | Aliases: T10F5.14, T10F5_14	4.1	4.0	0.2	1.1	84.7%	-1.3
15408	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	-0.1	-1.1	84.7%	-1.9
15409	AT5G18390.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:6090956-6092547 FORWARD | Aliases: F20L16.110, F20L16_110	4.4	4.6	-0.2	-1.1	84.7%	-1.2
15410	AT1G17080.1 | expressed protein | chr1:5839679-5841559 REVERSE | Aliases: F20D23.22, F20D23_22	9.1	9.5	-0.4	-1.1	84.7%	-0.9
15411	AT5G54160.1 | Symbol: ATOMT1 |	12.6	12.3	0.3	1.1	84.7%	-1.4
15412	AT5G53520.1 | Symbol: ATOPT8 |	2.6	2.7	-0.1	-1.1	84.8%	-1.7
15413	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)	7.3	6.6	0.7	1.1	84.8%	-0.7
15414	AT2G32630.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:13851911-13853785 FORWARD | Aliases: T26B15.19, T26B15_19	3.2	3.0	0.2	1.1	84.9%	-1.3
15415	AT1G63200.1 | hypothetical protein | chr1:23437295-23438265 REVERSE | Aliases: F16M19.10, F16M19_10	2.5	2.6	-0.1	-1.1	84.9%	-1.8
15416	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	2.7	-0.1	-1.1	84.9%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
15417	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}	2.2	2.3	-0.1	-1.1	84.9%	-1.9
15418	AT5G56250.2 | expressed protein | chr5:22785803-22790118 REVERSE | Aliases: K24C1.6, K24C1_6	3.5	3.4	0.1	1.1	85.0%	-1.6
15419	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	4.7	-0.2	-1.1	85.0%	-1.3
15420	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	3.0	-0.2	-1.1	85.0%	-1.3
15421	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	5.3	5.0	0.3	1.1	85.0%	-0.7
15422	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	4.9	5.5	-0.6	-1.1	85.0%	-1.0
15423	AT3G60850.1 | expressed protein | chr3:22492869-22495077 FORWARD | Aliases: T4C21.260	4.8	5.0	-0.2	-1.1	85.0%	-0.9
15424	AT3G52140.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain | chr3:19343907-19352635 FORWARD | Aliases: F4F15.250	6.0	6.3	-0.3	-1.1	85.1%	-0.9
15425	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	5.5	5.6	-0.2	-1.1	85.1%	-1.3
15426	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	8.0	7.8	0.2	1.1	85.1%	-1.1
15427	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	2.0	2.1	-0.1	-1.1	85.1%	-2.0
15428	AT4G19910.1 | Toll-Interleukin-Resistance (TIR) domain-containing protein, contains Pfam profile PF01582: TIR domain | chr4:10795879-10796697 REVERSE | Aliases: None	2.4	2.6	-0.1	-1.1	85.2%	-1.6
15429	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	3.5	3.4	0.2	1.1	85.2%	-1.1
15430	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	6.5	6.8	-0.3	-1.1	85.2%	-1.2
15431	AT5G01590.1 | expressed protein | chr5:224173-226923 FORWARD | Aliases: F7A7.110, F7A7_110	3.6	3.4	0.2	1.1	85.2%	-1.1
15432	AT4G05310.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr4:2714763-2716010 FORWARD | Aliases: C17L7.230, C17L7_230	3.1	3.3	-0.2	-1.1	85.2%	-1.2
15433	AT5G23150.1 | Symbol: HUA2 | PWWP domain-containing protein, identical to cDNA putative transcription factor (HUA2) GI:4868119; contains Pfam profile	3.8	3.7	0.2	1.1	85.2%	-1.2
15434	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	7.2	7.5	-0.3	-1.1	85.2%	-1.0
15435	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	6.5	-0.2	-1.1	85.2%	-1.5
15436	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	3.9	0.3	1.1	85.2%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
15437	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 simlar 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	6.7	7.0	-0.3	-1.1	85.2%	-0.9
15438	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	2.9	-0.1	-1.1	85.2%	-1.7
15439	AT1G03560.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:890164-892410 REVERSE | Aliases: F21B7.18	4.4	4.7	-0.3	-1.1	85.2%	-1.1
15440	AT3G50580.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr3:18779612-18780500 REVERSE | Aliases: T20E23.180	3.7	4.0	-0.3	-1.1	85.2%	-1.1
15441	AT3G63070.1 | PWWP domain-containing protein, putative transcription factor HUA2, Arabidopsis thaliana, EMBL:AF116556 | chr3:23313340-23320633 FORWARD | Aliases: T20O10.170	4.5	4.8	-0.4	-1.1	85.3%	-0.9
15442	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	5.3	5.7	-0.3	-1.1	85.3%	-1.0
15443	AT3G43970.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr3:15788395-15788935 REVERSE | Aliases: T15B3.110	4.2	4.4	-0.2	-1.1	85.3%	-1.4
15444	AT5G39870.1 | expressed protein | chr5:15985850-15987239 REVERSE | Aliases: MYH19.6, MYH19_6	2.4	2.5	-0.1	-1.1	85.3%	-1.6
15445	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	5.6	-0.3	-1.1	85.3%	-0.9
15446	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	5.7	5.1	0.6	1.1	85.3%	-0.7
15447	AT1G10400.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr1:3414853-3416285 REVERSE | Aliases: F14N23.30, F14N23_30	4.6	4.9	-0.3	-1.1	85.3%	-1.0
15448	AT3G21000.1 | expressed protein, ; expression supported by MPSS | chr3:7363927-7365144 FORWARD | Aliases: MSA6.5	3.3	3.5	-0.2	-1.1	85.3%	-1.6
15449	AT2G24810.1 | pathogenesis-related thaumatin family protein, similar to thaumatin-like protein (Arabidopsis thaliana) GI:2435406; contains Pfam profile PF00314: Thaumatin family | chr2:10580941-10581778 FORWARD | Aliases: F27C12.27, F27C12_27	2.5	2.7	-0.1	-1.1	85.3%	-1.5
15450	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	4.1	4.4	-0.3	-1.1	85.3%	-0.9
15451	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	-1.1	85.3%	-1.7
15452	AT1G54720.1 | early-responsive to dehydration protein-related / ERD protein-related, similar to ERD6 protein (Arabidopsis thaliana) GI:3123712	2.1	2.2	-0.1	-1.1	85.4%	-1.9
15453	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	3.4	-0.2	-1.1	85.4%	-1.3
15454	AT3G42700.1 | hypothetical protein | chr3:14783620-14784282 FORWARD | Aliases: T12K4.150	3.1	3.2	-0.1	-1.1	85.4%	-1.4
15455	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	5.6	5.9	-0.3	-1.1	85.5%	-1.0
15456	AT5G37960.1 | oxidoreductase-related | chr5:15138668-15139066 FORWARD | Aliases: K18L3.120, K18L3_120	2.4	2.5	-0.1	-1.1	85.5%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
15457	AT3G10770.2 | expressed protein | chr3:3372275-3374276 REVERSE | Aliases: T7M13.15	10.1	9.8	0.3	1.1	85.5%	-1.0
15458	AT3G62590.1 | lipase class 3 family protein, contains Pfam profile PF01764: Lipase | chr3:23158896-23161328 REVERSE | Aliases: F26K9.20	5.5	5.1	0.3	1.1	85.5%	-0.9
15459	AT3G54200.1 | expressed protein, hin1 protein, Nicotiana tabacum, PIR:T03265 | chr3:20076643-20077538 FORWARD | Aliases: F24B22.160	5.5	5.8	-0.2	-1.1	85.5%	-1.1
15460	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	5.2	0.3	1.1	85.5%	-0.9
15461	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	2.3	-0.1	-1.1	85.5%	-2.1
15462	AT4G13840.1 | transferase family protein, low similarity to acetyl-CoA:benzylalcohol acetyltranferase (Clarkia concinna) GI:6166328; contains Pfam profile PF02458: Transferase family	4.3	4.5	-0.2	-1.1	85.5%	-1.3
15463	AT3G09570.1 | expressed protein | chr3:2940451-2942114 FORWARD | Aliases: F11F8.41	7.5	7.8	-0.3	-1.1	85.5%	-0.9
15464	AT2G32360.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr2:13744096-13744623 REVERSE | Aliases: T32F6.12, T32F6_12	3.4	3.6	-0.2	-1.1	85.5%	-1.2
15465	AT4G24950.1 | expressed protein | chr4:12826292-12826765 FORWARD | Aliases: F13M23.90, F13M23_90	3.1	3.2	-0.2	-1.1	85.5%	-1.4
15466	AT1G49150.1 | expressed protein | chr1:18182245-18182691 FORWARD | Aliases: F27J15.8, F27J15_8	2.8	2.9	-0.1	-1.1	85.5%	-1.5
15467	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	4.9	5.3	-0.4	-1.1	85.5%	-0.8
15468	AT3G13670.1 | protein kinase family protein, contains Pfam domains, PF00069: Protein kinase domain | chr3:4469229-4473696 FORWARD | Aliases: MMM17.17	6.5	7.1	-0.6	-1.1	85.6%	-0.9
15469	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	3.0	-0.2	-1.1	85.6%	-0.9
15470	AT5G04830.2 | expressed protein | chr5:1402087-1403962 REVERSE | Aliases: MUK11.15, MUK11_15	7.5	7.9	-0.4	-1.1	85.6%	-0.8
15471	AT3G29220.1 | hypothetical protein | chr3:11186915-11187508 FORWARD | Aliases: MXO21.7	2.5	2.6	-0.1	-1.1	85.6%	-1.8
15472	AT1G02180.1 | ferredoxin-related, similar to Ferredoxin. (SP:O78510) (Cryptomonas phi) {Guillardia theta} | chr1:413522-414645 REVERSE | Aliases: T6A9.14	4.4	4.2	0.2	1.1	85.6%	-0.8
15473	AT2G48050.1 | expressed protein, ; expression supported by MPSS | chr2:19660284-19664981 REVERSE | Aliases: T9J23.20	2.5	2.6	-0.1	-1.1	85.6%	-1.6
15474	AT4G18080.1 | expressed protein | chr4:10033222-10033947 REVERSE | Aliases: F15J5.50, F15J5_50	3.3	3.5	-0.2	-1.1	85.6%	-1.4
15475	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	3.3	-0.2	-1.1	85.6%	-1.3
15476	AT3G01240.1 | expressed protein | chr3:78383-79044 REVERSE | Aliases: T4P13.7, T4P13_7	2.2	2.3	-0.1	-1.1	85.7%	-1.7
15477	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	3.1	-0.1	-1.1	85.7%	-1.2
15478	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	3.2	-0.2	-1.1	85.7%	-1.0
15479	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	3.3	3.2	0.1	1.1	85.7%	-1.3
15480	AT2G14260.2 | Symbol: PIP | proline iminopeptidase, identical to GP:1710151:U72711 | chr2:6048353-6050769 REVERSE | Aliases: None	8.1	8.3	-0.2	-1.1	85.7%	-1.1
15481	AT1G10570.2 | Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to EST gb:N96456	5.5	5.8	-0.3	-1.1	85.7%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
15482	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' adenylating 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	3.5	-0.2	-1.1	85.7%	-1.4
15483	AT5G25120.1 | Symbol: CYP71B11 | cytochrome P450 family protein, CYTOCHROME P450 71B1 - Thlaspi arvense, EMBL:L24438 | chr5:8662854-8664435 FORWARD | Aliases: T11H3.130, T11H3_130	5.6	5.8	-0.2	-1.1	85.7%	-1.4
15484	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	2.5	0.1	1.1	85.7%	-1.5
15485	AT4G02195.1 | Symbol: SYP42 | syntaxin 42 (SYP42) / TLG2b, identical to SP:Q9SWH4 Syntaxin 42 (AtSYP42) (AtTLG2b) {Arabidopsis thaliana} | chr4:970009-972304 REVERSE | Aliases: ATSYP42, ATTLG2B, SYNTAXIN OF PLANTS 41, TLG2B	6.8	7.1	-0.2	-1.1	85.7%	-1.3
15486	AT3G17950.2 | expressed protein | chr3:6146247-6147324 FORWARD | Aliases: MEB5.1	3.0	3.2	-0.2	-1.1	85.8%	-1.0
15487	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	6.3	5.9	0.4	1.1	85.8%	-0.5
15488	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	2.7	0.1	1.1	85.8%	-1.4
15489	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	2.8	-0.1	-1.1	85.8%	-1.6
15490	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	3.0	-0.2	-1.1	85.8%	-1.4
15491	AT5G15060.1 | expressed protein | chr5:4874988-4875759 REVERSE | Aliases: F2G14.180, F2G14_180	3.3	3.4	-0.1	-1.1	85.8%	-1.4
15492	AT3G59640.1 | glycine-rich protein | chr3:22039758-22041422 FORWARD | Aliases: T16L24.190	5.9	6.0	-0.1	-1.1	85.8%	-1.3
15493	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	6.0	0.5	1.1	85.9%	-0.8
15494	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	6.3	6.0	0.2	1.1	85.9%	-1.0
15495	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	6.7	-0.4	-1.1	85.9%	-1.0
15496	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	8.0	7.7	0.4	1.1	85.9%	-1.0
15497	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	-1.1	85.9%	-2.0
15498	AT5G22900.1 | Symbol: ATCHX3 |	2.3	2.3	0.1	1.1	85.9%	-1.7
15499	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	2.7	2.9	-0.1	-1.1	85.9%	-1.7
15500	AT3G14595.1 | expressed protein | chr3:4908957-4910483 FORWARD | Aliases: None	10.4	10.2	0.2	1.1	86.0%	-1.3
15501	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	4.4	4.2	0.2	1.1	86.0%	-1.0
15502	AT2G26160.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.4	0.1	1.1	86.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
15503	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	2.3	-0.1	-1.1	86.0%	-2.1
15504	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	3.2	3.1	0.1	1.1	86.0%	-1.4
15505	AT5G24460.1 | expressed protein | chr5:8354702-8355877 FORWARD | Aliases: T31K7.4, T31K7_4	7.6	7.3	0.3	1.1	86.0%	-0.8
15506	AT3G16670.1 | expressed protein | chr3:5681425-5682337 FORWARD | Aliases: MGL6.14	4.1	4.5	-0.4	-1.1	86.0%	-0.8
15507	AT2G18010.1 | auxin-responsive family protein, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesnerian) ;similar to indole-3-acetic acid induced protein ARG7 (SP:P32295) (Phaseolus aureus)	2.6	2.8	-0.1	-1.1	86.1%	-1.5
15508	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	3.4	3.7	-0.3	-1.1	86.1%	-0.9
15509	AT4G17990.1 | expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626) | chr4:9984524-9988265 REVERSE | Aliases: T6K21.170, T6K21_170	3.2	3.5	-0.3	-1.1	86.1%	-1.1
15510	AT1G18190.1 | expressed protein, similar to golgin-84 {Homo sapiens} (GI:4191344) | chr1:6257844-6261443 REVERSE | Aliases: T10F20.19	4.8	5.1	-0.3	-1.1	86.2%	-0.6
15511	AT2G01210.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:119440-121843 REVERSE | Aliases: F10A8.9, F10A8_9	3.9	4.1	-0.2	-1.1	86.2%	-0.8
15512	AT5G60880.2 | expressed protein | chr5:24505515-24507004 REVERSE | Aliases: MAE1.13, MAE1_13	3.8	4.2	-0.4	-1.1	86.3%	-0.9
15513	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	5.1	4.9	0.3	1.1	86.3%	-0.9
15514	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	3.5	-0.2	-1.1	86.3%	-1.5
15515	AT3G14580.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:4903019-4904236 FORWARD | Aliases: MIE1.8	3.5	3.7	-0.2	-1.1	86.3%	-1.5
15516	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	6.4	6.5	-0.2	-1.1	86.3%	-1.3
15517	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	2.7	-0.1	-1.1	86.3%	-1.4
15518	AT2G15750.1 | expressed protein | chr2:6870004-6871198 FORWARD | Aliases: F9O13.30	3.2	3.4	-0.1	-1.1	86.3%	-1.6
15519	AT4G16745.1 | exostosin family protein, contains Pfam PF03016: Exostosin family | chr4:9411914-9414133 FORWARD | Aliases: None	3.4	3.1	0.3	1.1	86.3%	-0.8
15520	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	6.5	5.5	1.0	1.1	86.4%	-0.6
15521	AT5G47400.1 | expressed protein | chr5:19246389-19248749 FORWARD | Aliases: MQL5.26, MQL5_26	2.8	3.0	-0.2	-1.1	86.4%	-1.2
15522	AT3G62320.1 | expressed protein | chr3:23072780-23073373 REVERSE | Aliases: T12C14.20	2.7	2.8	-0.1	-1.1	86.4%	-1.4
15523	AT5G63220.1 | expressed protein, contains Pfam PF04190: Protein of unknown function (DUF410) | chr5:25370285-25372707 REVERSE | Aliases: MDC12.19, MDC12_19	2.8	2.7	0.1	1.1	86.4%	-1.7
15524	AT1G34590.1 | expressed protein | chr1:12665145-12667796 FORWARD | Aliases: F12K21.7, F12K21_7	2.6	2.7	-0.1	-1.1	86.4%	-1.5
15525	AT4G11780.1 | expressed protein | chr4:7085964-7088206 FORWARD | Aliases: T5C23.210, T5C23_210	2.5	2.7	-0.1	-1.1	86.4%	-1.7
15526	AT3G55690.1 | expressed protein, predicted proteins, Arabidopsis thaliana | chr3:20677951-20679484 FORWARD | Aliases: F1I16.100	2.7	2.5	0.2	1.1	86.4%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
15527	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	4.1	-0.1	-1.1	86.4%	-1.5
15528	AT2G42960.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:17875674-17877707 REVERSE | Aliases: F7D19.4, F7D19_4	3.1	3.3	-0.1	-1.1	86.4%	-1.3
15529	AT3G61210.1 | embryo-abundant protein-related, similar to embryo-abundant protein (Picea glauca) GI:1350531 | chr3:22669653-22670845 REVERSE | Aliases: T20K12.110	2.3	2.4	-0.1	-1.1	86.4%	-1.8
15530	AT1G50460.1 | hexokinase, putative, similar to hexokinase 1 (Spinacia oleracea) Swiss-Prot:Q9SEK3 | chr1:18697352-18701327 FORWARD | Aliases: F11F12.18, F11F12_18	5.4	5.6	-0.3	-1.1	86.5%	-1.2
15531	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	3.5	-0.2	-1.1	86.5%	-1.2
15532	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	6.8	6.5	0.3	1.1	86.5%	-0.9
15533	AT3G10240.1 | F-box protein-related, contains weak Pfam:PF00646 F-box domain | chr3:3166703-3167872 FORWARD | Aliases: F14P13.16	2.9	3.0	-0.1	-1.1	86.5%	-1.5
15534	AT5G50010.1 | expressed protein | chr5:20365841-20367936 FORWARD | Aliases: K9P8.17	3.9	4.2	-0.3	-1.1	86.5%	-0.8
15535	AT3G50640.1 | expressed protein | chr3:18815008-18815644 REVERSE | Aliases: T3A5.20	3.2	3.3	-0.1	-1.1	86.5%	-1.4
15536	AT4G36210.2 | expressed protein, contains Pfam PF05277: Protein of unknown function (DUF726) | chr4:17130249-17134305 FORWARD | Aliases: F23E13.100, F23E13_100	7.2	7.0	0.2	1.1	86.6%	-1.1
15537	AT2G43630.1 | expressed protein | chr2:18102854-18104565 FORWARD | Aliases: F18O19.26	8.6	8.3	0.3	1.1	86.6%	-1.2
15538	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	5.7	5.9	-0.2	-1.1	86.6%	-1.3
15539	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	2.8	2.8	0.1	1.1	86.6%	-1.7
15540	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	2.6	-0.1	-1.1	86.6%	-1.8
15541	AT4G05250.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr4:2691458-2692414 FORWARD | Aliases: C17L7.170, C17L7_170	2.5	2.6	-0.1	-1.1	86.6%	-1.8
15542	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	4.2	4.4	-0.2	-1.1	86.6%	-0.9
15543	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	6.6	6.8	-0.2	-1.1	86.6%	-1.0
15544	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	4.4	4.8	-0.4	-1.1	86.7%	-0.9
15545	AT3G20300.1 | expressed protein | chr3:7079623-7081925 REVERSE | Aliases: MQC12.4	4.0	3.8	0.2	1.1	86.7%	-1.3
15546	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	2.9	0.2	1.1	86.7%	-0.9
15547	AT2G14390.1 | expressed protein | chr2:6117994-6119000 FORWARD | Aliases: T1O16.2, T1O16_2	2.2	2.3	-0.1	-1.1	86.7%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
15548	AT3G63370.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:23413055-23416966 FORWARD | Aliases: MAA21.7	2.6	2.7	-0.1	-1.1	86.7%	-1.6
15549	AT4G00310.2 | expressed protein | chr4:133662-135469 FORWARD | Aliases: A_IG005I10.17, A_IG005I10_17, F5I10.17, F5I10_17	2.8	2.9	-0.1	-1.1	86.7%	-1.5
15550	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	7.2	7.8	-0.6	-1.1	86.8%	-0.5
15551	AT5G14210.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:4578380-4581376 REVERSE | Aliases: MUA22.21, MUA22_21	4.2	4.4	-0.3	-1.1	86.8%	-0.8
15552	AT1G68570.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr1:25750400-25753938 FORWARD | Aliases: F24J5.19, F24J5_19	3.2	3.4	-0.2	-1.1	86.8%	-1.1
15553	ATCG00510.1 | Symbol: PSAI | PSI I protein | chrC:59247-59360 FORWARD | Aliases: PSAI	8.4	7.1	1.3	1.1	86.9%	-0.8
15554	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	4.4	4.6	-0.2	-1.1	86.9%	-1.0
15555	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	3.8	-0.2	-1.1	86.9%	-1.5
15556	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	3.3	3.5	-0.2	-1.1	86.9%	-0.7
15557	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	3.1	-0.2	-1.1	86.9%	-1.3
15558	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	3.7	3.8	-0.2	-1.1	86.9%	-1.4
15559	AT5G16430.1 | hypothetical protein | chr5:5370353-5370610 FORWARD | Aliases: MQK4.16, MQK4_16	3.0	3.1	-0.1	-1.1	86.9%	-1.7
15560	AT5G57880.1 | expressed protein, ; expression supported by MPSS | chr5:23461203-23463665 FORWARD | Aliases: MTI20.12	3.2	3.0	0.2	1.1	87.0%	-1.0
15561	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	2.7	0.1	1.1	87.0%	-1.4
15562	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	4.2	-0.2	-1.1	87.0%	-1.2
15563	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	2.1	2.2	-0.1	-1.1	87.0%	-2.0
15564	AT2G46980.2 | expressed protein | chr2:19308936-19311240 REVERSE | Aliases: F14M4.19	2.1	2.2	-0.1	-1.1	87.0%	-1.9
15565	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	2.7	-0.1	-1.1	87.1%	-1.7
15566	AT4G24650.1 | Symbol: ATIPT4 |	2.4	2.6	-0.1	-1.1	87.1%	-1.7
15567	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	3.1	-0.1	-1.1	87.1%	-1.3
15568	AT4G14790.1 | Symbol: ATSUV3 |	3.3	3.4	-0.1	-1.1	87.1%	-1.5
15569	AT5G16590.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:5431684-5434113 FORWARD | Aliases: MTG13.3, MTG13_3	3.5	3.6	-0.2	-1.1	87.1%	-1.3
15570	AT2G07320.1 | SWIM zinc finger family protein, contains Pfam profile PF04434: SWIM zinc finger	2.9	3.1	-0.2	-1.1	87.1%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
15571	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	3.2	3.0	0.2	1.1	87.1%	-1.3
15572	AT2G29040.1 | exostosin family protein, contains Pfam profile: PF03016	2.4	2.5	-0.1	-1.1	87.2%	-2.0
15573	AT4G23440.1 | expressed protein | chr4:12237775-12240818 FORWARD | Aliases: F16G20.140, F16G20_140	3.7	3.8	-0.2	-1.1	87.2%	-1.2
15574	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	6.6	7.0	-0.4	-1.1	87.2%	-0.8
15575	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	2.3	0.1	1.1	87.2%	-1.7
15576	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	9.2	-0.3	-1.1	87.3%	-1.3
15577	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	0.1	1.1	87.3%	-1.6
15578	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	2.8	2.6	0.2	1.1	87.4%	-1.0
15579	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	4.1	-0.3	-1.1	87.4%	-1.0
15580	AT1G26920.1 | expressed protein, Location of EST 228A16T7A, gb:N65686 | chr1:9329499-9330385 FORWARD | Aliases: T2P11.11, T2P11_11	4.8	4.6	0.2	1.1	87.4%	-1.0
15581	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	5.7	0.4	1.1	87.4%	-0.9
15582	AT4G25990.2 | Symbol: CIL | expressed protein	2.6	2.7	-0.1	-1.1	87.4%	-1.7
15583	AT5G25415.1 | expressed protein, several hypothetical proteins - Arabidopsis thaliana | chr5:8834209-8837179 FORWARD | Aliases: None	2.8	3.0	-0.2	-1.1	87.4%	-1.1
15584	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	3.1	-0.1	-1.1	87.4%	-1.4
15585	AT5G14380.1 | hydroxyproline-rich glycoprotein family protein, identical to gi:4775268:emb:CAB42531 | chr5:4635800-4636679 REVERSE | Aliases: F18O22.170, F18O22_170	3.4	3.2	0.2	1.1	87.4%	-1.2
15586	AT2G22530.1 | phosphatidylinositolglycan-related, similar to Pig-o (Mus musculus) GI:8099973 | chr2:9580309-9584521 REVERSE | Aliases: F14M13.7, F14M13_7	4.1	4.3	-0.2	-1.1	87.5%	-1.1
15587	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	2.2	2.1	0.1	1.1	87.5%	-2.2
15588	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	8.1	7.8	0.3	1.1	87.5%	-1.1
15589	AT5G58670.1 | Symbol: ATPLC1 |	5.7	5.5	0.2	1.1	87.5%	-1.0
15590	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	4.1	3.8	0.3	1.1	87.5%	-0.8
15591	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	5.1	5.3	-0.2	-1.1	87.6%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
15592	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	3.2	3.4	-0.2	-1.1	87.7%	-1.4
15593	AT2G25280.1 | expressed protein | chr2:10769101-10771819 REVERSE | Aliases: T22F11.13, T22F11_13	8.0	7.5	0.5	1.1	87.7%	-0.9
15594	AT2G20070.1 | expressed protein, weak similarity to SP:O61705 Neurotoxin BmK-X precursor (BmK10) (Alpha-neurotoxin TX9) {Mesobuthus martensii}	3.2	3.5	-0.2	-1.1	87.7%	-1.3
15595	AT5G15160.1 | bHLH family protein | chr5:4921269-4922638 REVERSE | Aliases: F8M21.50, F8M21_50	2.1	2.1	-0.1	-1.1	87.7%	-2.1
15596	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	3.2	3.3	-0.1	-1.1	87.7%	-1.5
15597	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	5.4	5.6	-0.2	-1.1	87.7%	-1.1
15598	AT3G52220.1 | expressed protein | chr3:19380340-19382033 REVERSE | Aliases: T25B15.5	10.6	10.3	0.3	1.0	87.8%	-1.1
15599	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	2.9	3.0	-0.1	-1.0	87.8%	-1.7
15600	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	2.5	2.6	-0.1	-1.0	87.8%	-1.7
15601	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	2.9	-0.1	-1.0	87.8%	-1.5
15602	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	3.1	3.3	-0.2	-1.0	87.8%	-1.4
15603	AT4G13060.1 | F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain | chr4:7619932-7620939 REVERSE | Aliases: F25G13.150, F25G13_150	2.9	3.0	-0.1	-1.0	87.8%	-1.4
15604	AT1G42190.1 | expressed protein | chr1:15763523-15763717 FORWARD | Aliases: F19C17.40, F19C17_40	2.9	3.0	-0.1	-1.0	87.8%	-1.7
15605	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	6.1	6.6	-0.5	-1.0	87.8%	-0.8
15606	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	2.8	-0.1	-1.0	87.9%	-1.7
15607	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	4.5	4.1	0.3	1.0	87.9%	-0.7
15608	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	3.0	3.2	-0.2	-1.0	87.9%	-1.3
15609	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	2.4	2.5	-0.1	-1.0	87.9%	-1.7
15610	ATCG00065.1 | Symbol: RPS12A |	5.2	4.1	1.0	1.0	87.9%	-0.6
15611	AT2G22270.1 | expressed protein | chr2:9470774-9472547 FORWARD | Aliases: T26C19.7, T26C19_7	3.8	4.1	-0.2	-1.0	88.0%	-1.0
15612	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	6.1	6.4	-0.2	-1.0	88.0%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
15613	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	6.6	7.2	-0.6	-1.0	88.0%	-0.7
15614	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	4.8	4.6	0.2	1.0	88.0%	-1.1
15615	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	5.8	5.6	0.2	1.0	88.0%	-0.8
15616	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	2.6	-0.1	-1.0	88.0%	-1.8
15617	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	5.8	5.5	0.3	1.0	88.0%	-1.1
15618	AT1G77980.1 | MADS-box family protein, MADS-box protein AGL66 | chr1:29320106-29321961 REVERSE | Aliases: F28K19.20, F28K19_20	3.7	3.8	-0.2	-1.0	88.0%	-1.4
15619	AT1G76200.1 | expressed protein | chr1:28598144-28599636 FORWARD | Aliases: T23E18.30, T23E18_30	13.1	13.2	-0.1	-1.0	88.1%	-1.9
15620	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	3.5	3.4	0.1	1.0	88.1%	-1.4
15621	AT3G48250.1 | pentatricopeptide (PPR) repeat-containing protein, vacontains Pfam profile PF01535: PPR repeat | chr3:17881049-17882914 REVERSE | Aliases: T29H11.230	3.1	3.0	0.2	1.0	88.1%	-1.4
15622	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	5.2	-0.2	-1.0	88.1%	-1.0
15623	AT5G58020.1 | expressed protein, contains PF04641: Protein of unknown function, DUF602	9.6	9.2	0.4	1.0	88.2%	-0.9
15624	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	3.6	-0.2	-1.0	88.2%	-1.3
15625	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	5.6	5.3	0.3	1.0	88.2%	-0.8
15626	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	3.7	3.0	0.7	1.0	88.2%	-1.2
15627	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	3.3	-0.2	-1.0	88.2%	-1.3
15628	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	2.3	-0.1	-1.0	88.3%	-1.8
15629	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	3.8	-0.2	-1.0	88.3%	-1.4
15630	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	4.6	4.3	0.2	1.0	88.3%	-0.9
15631	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	4.2	3.9	0.3	1.0	88.3%	-1.1
15632	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	5.8	5.6	0.2	1.0	88.3%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
15633	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	7.1	6.7	0.5	1.0	88.4%	-0.9
15634	AT3G16020.1 | hypothetical protein | chr3:5438293-5438657 FORWARD | Aliases: MSL1.23	2.5	2.6	-0.1	-1.0	88.4%	-1.9
15635	AT3G21760.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:7667034-7668731 FORWARD | Aliases: MSD21.9	3.9	4.1	-0.2	-1.0	88.4%	-1.2
15636	AT3G09360.1 | transcription factor IIB (TFIIB) family protein, contains Pfam domain, PF00382: Transcription factor TFIIB repeat | chr3:2873802-2878438 FORWARD | Aliases: F3L24.23	6.6	5.6	1.0	1.0	88.4%	-0.8
15637	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	4.4	4.7	-0.2	-1.0	88.4%	-1.3
15638	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	3.6	0.3	1.0	88.5%	-0.8
15639	AT1G01360.1 | expressed protein, similar to hypothetical protein GB:CAB45785 GI:5262156 from (Arabidopsis thaliana) | chr1:142024-143177 FORWARD | Aliases: F6F3.16, F6F3_16	7.4	7.9	-0.5	-1.0	88.5%	-0.8
15640	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	2.3	2.4	-0.1	-1.0	88.5%	-1.7
15641	AT3G47100.1 | expressed protein | chr3:17356555-17357091 FORWARD | Aliases: F13I12.150	2.7	2.8	-0.1	-1.0	88.5%	-1.4
15642	AT3G25680.1 | expressed protein | chr3:9350863-9353664 FORWARD | Aliases: T5M7.13	3.2	3.4	-0.1	-1.0	88.5%	-1.3
15643	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	3.0	-0.1	-1.0	88.6%	-1.5
15644	AT2G13150.1 | expressed protein, contains a bZIP transcription factor basic domain signature (PDOC00036) | chr2:5444138-5445541 FORWARD | Aliases: T17A11.14, T17A11_14	2.4	2.5	-0.1	-1.0	88.6%	-2.0
15645	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	2.6	-0.1	-1.0	88.6%	-1.7
15646	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	10.2	9.8	0.4	1.0	88.6%	-1.2
15647	AT1G19620.1 | expressed protein | chr1:6784011-6785066 FORWARD | Aliases: F14P1.5	3.1	3.4	-0.3	-1.0	88.7%	-1.0
15648	AT1G68250.1 | expressed protein | chr1:25583036-25583857 REVERSE | Aliases: T22E19.12, T22E19_12	2.5	2.7	-0.2	-1.0	88.7%	-1.5
15649	AT4G09490.1 | RNase H domain-containing protein, contains Pfam profile PF00075: RNase H | chr4:6015559-6016572 REVERSE | Aliases: T15G18.90, T15G18_90	3.8	3.5	0.3	1.0	88.7%	-0.7
15650	AT1G10140.1 | expressed protein, similar to EST gb:AA598098 | chr1:3322804-3323550 REVERSE | Aliases: F14N23.2, F14N23_2	6.0	6.2	-0.1	-1.0	88.7%	-1.3
15651	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	7.4	0.1	1.0	88.7%	-1.3
15652	AT2G40810.2 | WD-40 repeat protein family, similar to Gsa12p(GI:18307769)(Pichia pastoris); contains 3 Pfam PF00400: WD domain, G-beta repeats	5.2	5.5	-0.3	-1.0	88.8%	-0.9
15653	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	8.4	0.2	1.0	88.8%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
15654	AT2G02520.1 | expressed protein | chr2:676770-678144 REVERSE | Aliases: T8K22.18, T8K22_18	2.2	2.3	-0.1	-1.0	88.8%	-1.8
15655	AT2G41010.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr2:17120944-17121882 REVERSE | Aliases: T3K9.22, T3K9_22	6.5	6.2	0.3	1.0	88.9%	-0.7
15656	AT3G50350.1 | expressed protein | chr3:18683888-18684688 FORWARD | Aliases: F11C1.190	6.6	6.3	0.4	1.0	88.9%	-0.6
15657	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	6.4	6.2	0.2	1.0	88.9%	-0.8
15658	AT1G79580.3 | Symbol: ANAC033 | no apical meristem (NAM) family protein, similar to OsNAC7 protein (GI:6730944) (Oryza sativa); contains weak hit to Pfam PF02365 : No apical meristem (NAM) protein	2.0	2.1	-0.1	-1.0	88.9%	-2.0
15659	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	10.2	10.5	-0.3	-1.0	89.0%	-1.5
15660	AT4G02570.3 | Symbol: ATCUL1 |	7.1	7.6	-0.5	-1.0	89.0%	-0.9
15661	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	9.0	-0.3	-1.0	89.0%	-1.0
15662	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	-0.1	-1.0	89.0%	-1.7
15663	AT2G31150.1 | expressed protein | chr2:13279452-13281655 FORWARD | Aliases: T16B12.4, T16B12_4	4.2	4.7	-0.4	-1.0	89.1%	-0.7
15664	AT1G64450.1 | proline-rich family protein, contains proline rich extensins, INTERPRO:IPR0002965 | chr1:23945261-23946509 REVERSE | Aliases: F15H21.17	4.6	4.4	0.2	1.0	89.1%	-1.0
15665	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	4.2	-0.3	-1.0	89.1%	-1.3
15666	AT5G25400.1 | phosphate translocator-related, low siimilarity 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	3.0	3.2	-0.2	-1.0	89.1%	-1.4
15667	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	2.8	3.0	-0.2	-1.0	89.1%	-1.4
15668	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	2.8	2.9	-0.1	-1.0	89.1%	-1.6
15669	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	3.4	3.3	0.1	1.0	89.1%	-1.5
15670	AT3G04160.1 | expressed protein, ; expression supported by MPSS | chr3:1091654-1094303 REVERSE | Aliases: T6K12.22, T6K12_22	2.9	3.1	-0.1	-1.0	89.1%	-1.5
15671	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	2.5	-0.1	-1.0	89.1%	-1.6
15672	AT1G41810.1 | expressed protein | chr1:15582258-15582998 REVERSE | Aliases: T4I21.3, T4I21_3	2.5	2.6	-0.1	-1.0	89.1%	-1.4
15673	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	2.7	-0.2	-1.0	89.1%	-1.3
15674	AT1G24060.1 | expressed protein | chr1:8509365-8510051 REVERSE | Aliases: T23E23.21, T23E23_21	2.6	2.7	-0.1	-1.0	89.2%	-1.7
15675	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	2.7	-0.1	-1.0	89.2%	-1.5
15676	AT3G45140.1 | Symbol: LOX2 | lipoxygenase (LOX2), identical to SP:P38418 | chr3:16536395-16540337 FORWARD | Aliases: ATLOX2, LIPOXYGENASE 2, T14D3.80	3.0	2.8	0.1	1.0	89.2%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
15677	AT3G16700.1 | fumarylacetoacetate hydrolase family protein, contains Pfam domain, PF01557: fumarylacetoacetate hydrolase family protein | chr3:5687790-5689722 FORWARD | Aliases: MGL6.17	3.9	3.7	0.2	1.0	89.2%	-1.1
15678	AT1G48910.1 | flavin-containing monooxygenase family protein / FMO family protein, similar to flavin monoxygenase-like protein floozy (Petunia x hybrida) GI:15010541 | chr1:18095349-18097442 FORWARD | Aliases: F27K7.7, F27K7_7	2.9	3.1	-0.3	-1.0	89.2%	-1.0
15679	AT1G30800.1 | expressed protein, ; expression supported by MPSS | chr1:10936977-10937696 FORWARD | Aliases: T17H7.8, T17H7_8	2.4	2.5	-0.1	-1.0	89.2%	-1.8
15680	AT3G28100.1 | nodulin MtN21 family protein, similar to MtN21 (Medicago truncatula) GI:2598575 | chr3:10457372-10462202 FORWARD | Aliases: MMG15.28	2.3	2.4	-0.1	-1.0	89.2%	-1.8
15681	AT1G01530.1 | MADS-box protein (AGL28), similar to MADS-box transcription factor GI:6580943 from (Picea abies); 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	-0.1	-1.0	89.3%	-2.0
15682	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	-1.0	89.4%	-1.7
15683	AT1G01130.1 | expressed protein, ; expression supported by MPSS | chr1:61963-63811 REVERSE | Aliases: F6F3.33	4.1	3.8	0.3	1.0	89.4%	-0.8
15684	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, SPOROCYTELESS	2.9	3.1	-0.2	-1.0	89.4%	-1.2
15685	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	2.8	-0.1	-1.0	89.5%	-1.4
15686	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	10.1	10.6	-0.5	-1.0	89.5%	-1.3
15687	AT4G37170.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:17498574-17500649 REVERSE | Aliases: AP22.43, AP22_43	4.7	4.4	0.3	1.0	89.5%	-1.1
15688	AT1G32650.1 | hypothetical protein | chr1:11810537-11810611 REVERSE | Aliases: F6N18.22, F6N18_22	2.4	2.4	0.1	1.0	89.5%	-2.0
15689	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	3.9	3.7	0.2	1.0	89.5%	-0.8
15690	AT3G19890.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.7	-0.1	-1.0	89.5%	-1.9
15691	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	2.4	-0.1	-1.0	89.6%	-2.3
15692	AT2G33390.1 | expressed protein | chr2:14158655-14159820 FORWARD | Aliases: F4P9.16, F4P9_16	7.4	7.9	-0.5	-1.0	89.6%	-0.9
15693	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	4.3	0.2	1.0	89.6%	-1.2
15694	AT4G27280.1 | calcium-binding EF hand family protein, similar to EF-hand Ca2+-binding protein CCD1 (Triticum aestivum) GI:9255753; contains INTERPRO:IPR002048 calcium-binding EF-hand domain | chr4:13663582-13664246 REVERSE | Aliases: M4I22.90, M4I22_90	8.2	7.9	0.3	1.0	89.6%	-1.2
15695	AT5G53840.1 | F-box family protein (FBL13), contains F-box domain PF:00646 | chr5:21876374-21877898 REVERSE | Aliases: K6O8.1, K6O8_1	2.9	3.0	-0.1	-1.0	89.6%	-1.6
15696	AT2G28840.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr2:12385436-12387819 FORWARD | Aliases: F8N16.13, F8N16_13	9.4	9.7	-0.3	-1.0	89.6%	-1.1
15697	AT5G08080.2 | Symbol: SYP132 |	8.5	8.7	-0.2	-1.0	89.6%	-1.2
15698	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 HOMEOBOX 6	3.1	3.2	-0.1	-1.0	89.6%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
15699	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	2.9	-0.2	-1.0	89.6%	-1.2
15700	AT5G11960.1 | expressed protein | chr5:3858580-3861516 REVERSE | Aliases: F14F18.130, F14F18_130	5.7	4.9	0.7	1.0	89.6%	-0.6
15701	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	3.4	3.6	-0.1	-1.0	89.6%	-1.4
15702	AT1G64050.1 | expressed protein | chr1:23766030-23769696 FORWARD | Aliases: F22C12.19, F22C12_19	3.1	3.4	-0.3	-1.0	89.6%	-1.2
15703	AT3G24550.1 | protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain | chr3:8960265-8963575 FORWARD | Aliases: MOB24.11	7.4	7.8	-0.4	-1.0	89.6%	-1.1
15704	ATMG01410.1 | Symbol: ORF204 |	2.9	3.0	-0.1	-1.0	89.6%	-1.6
15705	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	5.8	5.6	0.2	1.0	89.7%	-1.1
15706	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	4.5	4.2	0.3	1.0	89.8%	-0.9
15707	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	3.1	-0.1	-1.0	89.8%	-1.4
15708	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	2.6	2.7	-0.1	-1.0	89.8%	-1.8
15709	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	3.0	-0.1	-1.0	89.8%	-1.7
15710	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	-0.1	-1.0	89.8%	-2.0
15711	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	8.2	0.3	1.0	89.8%	-0.9
15712	AT5G38440.1 | self-incompatibility protein-related, low similarity to self-incompatibility (Papaver nudicaule) GI:3097262, S3 self-incompatibility protein (Papaver rhoeas) GI:1107841	4.2	4.3	-0.1	-1.0	89.8%	-1.5
15713	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	4.0	-0.2	-1.0	89.8%	-1.6
15714	AT2G36630.1 | expressed protein, contains Pfam profile: PF01925 domain of unknown function DUF81 | chr2:15359570-15362213 REVERSE | Aliases: F13K3.3, F13K3_3	4.7	4.8	-0.2	-1.0	89.8%	-1.2
15715	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	8.6	8.8	-0.2	-1.0	89.9%	-1.5
15716	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	3.1	-0.1	-1.0	89.9%	-1.8
15717	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);	3.3	3.4	-0.2	-1.0	89.9%	-1.2
15718	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}	5.8	5.4	0.4	1.0	89.9%	-0.8
15719	AT5G18880.1 | expressed protein, ; expression supported by MPSS | chr5:6300537-6301424 REVERSE | Aliases: F17K4.130, F17K4_130	2.9	3.1	-0.2	-1.0	89.9%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
15720	AT3G03305.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	6.2	6.5	-0.2	-1.0	89.9%	-1.0
15721	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	4.1	4.4	-0.3	-1.0	89.9%	-1.0
15722	AT4G39450.1 | expressed protein | chr4:18347587-18355050 FORWARD | Aliases: F23K16.80, F23K16_80	5.6	5.9	-0.3	-1.0	89.9%	-1.0
15723	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	2.9	-0.1	-1.0	90.0%	-1.5
15724	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	2.7	2.8	-0.1	-1.0	90.0%	-1.5
15725	AT1G12530.1 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g56420.1) | chr1:4268990-4270772 REVERSE | Aliases: F5O11.27, F5O11_27	6.7	7.1	-0.4	-1.0	90.0%	-0.7
15726	AT1G07190.1 | hypothetical protein | chr1:2208012-2208176 FORWARD | Aliases: F10K1.10, F10K1_10	2.4	2.5	-0.1	-1.0	90.0%	-2.2
15727	AT1G20310.1 | expressed protein | chr1:7032280-7033198 FORWARD | Aliases: F14O10.9, F14O10_9	2.4	2.6	-0.1	-1.0	90.1%	-1.6
15728	AT1G50470.1 | hypothetical protein | chr1:18703668-18704112 REVERSE | Aliases: F11F12.24, F11F12_24	4.2	4.5	-0.3	-1.0	90.1%	-1.0
15729	AT1G28375.1 | expressed protein | chr1:9961041-9961646 FORWARD | Aliases: None	2.7	2.9	-0.1	-1.0	90.1%	-1.6
15730	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	2.8	2.7	0.1	1.0	90.1%	-1.4
15731	AT2G19290.1 | expressed protein | chr2:8373001-8374104 REVERSE | Aliases: F27F23.9, F27F23_9	2.4	2.5	-0.1	-1.0	90.1%	-1.9
15732	AT2G01810.1 | PHD finger family protein, contains Pfam profile: PF00628: PHD-finger | chr2:347536-349951 FORWARD | Aliases: T8O11.2, T8O11_2	3.8	3.5	0.2	1.0	90.1%	-1.1
15733	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	2.3	2.4	-0.1	-1.0	90.1%	-1.7
15734	AT2G20980.1 | expressed protein | chr2:9018735-9020937 REVERSE | Aliases: F26H11.26, F26H11_26	4.4	4.2	0.2	1.0	90.2%	-1.0
15735	AT1G73160.1 | glycosyl transferase family 1 protein, contains Pfam profile: PF00534 Glycosyl transferases group 1 | chr1:27510195-27511655 FORWARD | Aliases: T18K17.18, T18K17_18	3.6	3.8	-0.2	-1.0	90.2%	-1.2
15736	AT1G79400.1 | Symbol: ATCHX2 |	3.6	3.7	-0.2	-1.0	90.2%	-1.1
15737	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	5.7	5.4	0.2	1.0	90.3%	-1.1
15738	AT1G78800.1 | glycosyl transferase family 1 protein, contains similarity to glycosyltransferase GI:871530 from (Saccharomyces cerevisiae), Alg2 mannosyltransferase (gi:3868942) from Rhizomucor pusillus; contains Pfam profile: PF00534 Glycosyl transferases group 1 | chr1:29630552-29632862 REVERSE | Aliases: F9K20.16, F9K20_16	4.3	4.2	0.2	1.0	90.3%	-1.2
15739	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	3.2	-0.2	-1.0	90.3%	-1.5
15740	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	6.6	6.4	0.2	1.0	90.3%	-1.1
15741	AT3G13800.1 | metallo-beta-lactamase family protein, similar to Metal Dependent Hydrolase GB:AAD18619 from (Chlamydophila pneumoniae)	4.8	5.0	-0.2	-1.0	90.4%	-1.1
15742	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	2.7	0.1	1.0	90.4%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
15743	AT3G04410.1 | hypothetical protein | chr3:1168843-1169211 FORWARD | Aliases: T27C4.5, T27C4_5	2.2	2.3	-0.1	-1.0	90.4%	-2.3
15744	AT5G15330.1 | SPX (SYG1/Pho81/XPR1) domain-containing protein, similar to PHO1 protein (Arabidopsis thaliana) GI:20069032; contains Pfam profile PF03105: SPX domain | chr5:4980491-4982234 FORWARD | Aliases: F8M21.220, F8M21_220	3.5	3.6	-0.1	-1.0	90.4%	-1.3
15745	AT4G04690.1 | F-box family protein (FBX15), contains F-box domain PF:00646 | chr4:2373997-2375133 REVERSE | Aliases: T19J18.6, T19J18_6	3.2	3.4	-0.2	-1.0	90.4%	-1.3
15746	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	3.5	-0.1	-1.0	90.5%	-1.8
15747	AT5G67210.1 | expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579) | chr5:26836245-26837198 FORWARD | Aliases: K21H1.17, K21H1_17	5.9	6.1	-0.2	-1.0	90.5%	-1.3
15748	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	2.9	2.8	0.1	1.0	90.5%	-1.5
15749	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	2.3	-0.1	-1.0	90.6%	-2.2
15750	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	6.9	0.4	1.0	90.6%	-0.7
15751	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	3.2	3.0	0.2	1.0	90.6%	-1.2
15752	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	2.1	2.1	-0.1	-1.0	90.6%	-2.3
15753	AT1G10430.1 | Symbol: PP2A 2 |	5.6	5.8	-0.2	-1.0	90.6%	-0.8
15754	AT5G18750.1 | DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226 DnaJ domain | chr5:6255179-6257934 FORWARD | Aliases: F17K4.2	5.1	4.9	0.2	1.0	90.6%	-0.8
15755	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	3.7	-0.3	-1.0	90.7%	-1.2
15756	AT3G24780.1 | expressed protein | chr3:9049453-9051600 FORWARD | Aliases: K7P8.7	2.8	3.0	-0.2	-1.0	90.7%	-1.6
15757	AT1G36756.1 | expressed protein | chr1:13918543-13919028 FORWARD | Aliases: T32O22.6, T32O22_6	2.1	2.3	-0.1	-1.0	90.7%	-1.9
15758	AT1G61660.2 | basic helix-loop-helix (bHLH) family protein, contains Pfam domain, PF00010: Helix-loop-helix DNA-binding domain	5.1	5.5	-0.4	-1.0	90.7%	-1.0
15759	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	3.0	3.1	-0.1	-1.0	90.8%	-2.1
15760	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	5.3	4.9	0.4	1.0	90.8%	-1.0
15761	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	3.7	-0.1	-1.0	90.8%	-1.3
15762	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)	5.7	5.5	0.2	1.0	90.8%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
15763	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 scienitific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.	4.3	4.0	0.3	1.0	90.9%	-0.9
15764	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	2.7	-0.2	-1.0	90.9%	-1.6
15765	AT2G28310.2 | expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707) | chr2:12092516-12095126 FORWARD | Aliases: T1B3.17	6.1	6.4	-0.3	-1.0	90.9%	-1.1
15766	AT1G03260.1 | expressed protein | chr1:795532-798463 REVERSE | Aliases: F15K9.14, F15K9_14	5.1	5.3	-0.2	-1.0	90.9%	-1.0
15767	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	6.6	-0.5	-1.0	90.9%	-0.7
15768	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	4.4	4.2	0.2	1.0	90.9%	-0.9
15769	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	4.4	0.3	1.0	90.9%	-1.0
15770	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	9.1	9.3	-0.2	-1.0	90.9%	-1.4
15771	AT1G56530.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; | chr1:21182902-21184553 FORWARD | Aliases: F25P12.22, F25P12_22	3.8	4.0	-0.3	-1.0	90.9%	-1.6
15772	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	2.8	-0.2	-1.0	90.9%	-1.5
15773	AT1G10020.1 | expressed protein | chr1:3269606-3271989 REVERSE | Aliases: T27I1.4, T27I1_4	4.2	4.4	-0.2	-1.0	90.9%	-1.1
15774	AT2G23920.1 | hypothetical protein | chr2:10188078-10188291 FORWARD | Aliases: T29E15.12, T29E15_12	2.8	2.9	-0.2	-1.0	90.9%	-1.8
15775	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); simlar to DMR protein GI:18028289 (Homo sapiens); | chr3:19803509-19807731 FORWARD | Aliases: F4P12.90	5.8	6.2	-0.4	-1.0	90.9%	-1.0
15776	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	3.1	3.2	-0.2	-1.0	91.0%	-1.3
15777	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 - Mus musculus, SWISSPROT:Q61548 | chr1:707726-709860 FORWARD | Aliases: F10O3.13, F10O3_13	2.7	2.8	-0.1	-1.0	91.0%	-1.6
15778	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	3.3	3.5	-0.2	-1.0	91.0%	-1.2
15779	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	2.6	-0.1	-1.0	91.0%	-1.6
15780	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	2.5	-0.1	-1.0	91.1%	-1.5
15781	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	10.2	-0.7	-1.0	91.1%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
15782	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	10.2	-0.7	-1.0	91.1%	-0.9
15783	AT3G28270.2 | expressed protein, similar to At14a protein (GI:11994571 and GI:11994573) (Arabidopsis thaliana)	2.7	2.8	-0.1	-1.0	91.2%	-1.6
15784	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	11.0	0.4	1.0	91.2%	-1.2
15785	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	3.6	3.4	0.2	1.0	91.2%	-1.1
15786	AT1G10200.1 | transcription factor LIM, putative, strong similarity to transcription factor Ntlim1 (Nicotiana tabacum) GI:5689136, LIM domain protein WLIM-1 (Helianthus annuus) GI:5070280; contains Pfam profile PF00412: LIM domain	6.8	6.4	0.5	1.0	91.2%	-1.1
15787	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	4.9	4.6	0.3	1.0	91.2%	-1.1
15788	AT2G15520.1 | zinc finger protein, putative, strong similarity to zinc finger protein (Arabidopsis thaliana) GI:976277	3.8	4.0	-0.2	-1.0	91.3%	-1.1
15789	AT5G56920.1 | expressed protein | chr5:23042122-23043141 FORWARD | Aliases: MHM17.3, MHM17_3	3.6	3.7	-0.1	-1.0	91.3%	-1.7
15790	AT2G20170.1 | hypothetical protein, and grail contains Pfam profile PF03080: Arabidopsis proteins of unknown function	3.2	3.4	-0.2	-1.0	91.3%	-1.4
15791	AT4G17930.1 | hypothetical protein | chr4:9964631-9964852 FORWARD | Aliases: T6K21.110, T6K21_110	2.5	2.6	-0.1	-1.0	91.3%	-1.7
15792	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	3.5	3.8	-0.3	-1.0	91.4%	-0.9
15793	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	9.3	9.6	-0.3	-1.0	91.4%	-1.1
15794	AT2G21930.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.0	3.2	-0.2	-1.0	91.4%	-1.3
15795	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	3.1	-0.1	-1.0	91.4%	-1.3
15796	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	3.1	-0.1	-1.0	91.4%	-1.3
15797	AT4G14840.1 | expressed protein | chr4:8511492-8513722 REVERSE | Aliases: DL3460C, FCAALL.333	2.6	2.7	-0.1	-1.0	91.5%	-1.7
15798	AT4G37850.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.6	2.7	-0.1	-1.0	91.5%	-1.8
15799	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	9.6	8.9	0.7	1.0	91.5%	-0.7
15800	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	2.4	-0.1	-1.0	91.5%	-1.8
15801	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	4.0	3.8	0.2	1.0	91.5%	-0.9
15802	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	4.5	4.7	-0.3	-1.0	91.6%	-1.2
15803	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	2.3	-0.1	-1.0	91.6%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
15804	AT2G27285.1 | expressed protein, weak similarity to maebl (GI:20087019) (Plasmodium falciparum), chimeric erythrocyte-binding protein MAEBL (GI:22086284) (Plasmodium falciparum) | chr2:11683038-11685178 REVERSE | Aliases: None	9.0	8.6	0.4	1.0	91.6%	-1.0
15805	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	2.8	-0.1	-1.0	91.7%	-1.5
15806	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	7.1	0.4	1.0	91.7%	-1.0
15807	AT5G48280.1 | hypothetical protein | chr5:19584290-19584914 REVERSE | Aliases: MIF21.17, MIF21_17	3.1	3.2	-0.2	-1.0	91.7%	-1.8
15808	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	3.7	3.9	-0.2	-1.0	91.7%	-1.1
15809	AT5G02000.1 | hypothetical protein | chr5:380152-380592 REVERSE | Aliases: T7H20.50, T7H20_50	3.2	3.3	-0.2	-1.0	91.7%	-1.1
15810	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	5.7	5.3	0.4	1.0	91.7%	-0.8
15811	AT3G58630.1 | expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189 | chr3:21694545-21696918 REVERSE | Aliases: F14P22.220	3.1	3.2	-0.1	-1.0	91.7%	-1.6
15812	AT1G38950.1 | hypothetical protein | chr1:14590293-14590860 FORWARD | Aliases: F12G6.9	3.0	3.2	-0.2	-1.0	91.8%	-1.3
15813	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	2.3	0.1	1.0	91.8%	-1.8
15814	AT1G19670.1 | Symbol: ATCLH1 |	2.5	2.4	0.1	1.0	91.8%	-1.6
15815	AT1G49290.1 | expressed protein, ; expression supported by MPSS | chr1:18236276-18237292 REVERSE | Aliases: F13F21.27, F13F21_27	3.1	3.2	-0.2	-1.0	91.8%	-1.4
15816	AT4G01560.1 | brix domain-containing protein, contains Pfam domain, PF04427: Brix domain | chr4:677054-679229 REVERSE | Aliases: F11O4.6, F11O4_6	5.0	4.7	0.3	1.0	91.8%	-1.2
15817	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	6.7	6.4	0.2	1.0	91.9%	-1.1
15818	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	2.3	-0.1	-1.0	91.9%	-2.0
15819	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	5.1	5.5	-0.3	-1.0	91.9%	-0.6
15820	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	3.1	-0.2	-1.0	91.9%	-1.5
15821	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	2.8	2.7	0.1	1.0	91.9%	-1.4
15822	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	2.3	-0.1	-1.0	91.9%	-1.8
15823	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	8.4	0.4	1.0	92.0%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
15824	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)(Clarkia breweri) | chr4:17215131-17216478 REVERSE | Aliases: AP22.82, AP22_82	3.5	3.6	-0.1	-1.0	92.0%	-1.4
15825	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	2.5	-0.1	-1.0	92.0%	-1.8
15826	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	5.4	5.6	-0.2	-1.0	92.1%	-1.0
15827	AT3G31915.1 | expressed protein, contains similarity to hypothetical proteins | chr3:12912330-12914770 FORWARD | Aliases: T1O13.15	2.8	2.9	-0.1	-1.0	92.1%	-1.7
15828	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	9.0	8.6	0.4	1.0	92.1%	-0.9
15829	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	2.8	3.0	-0.2	-1.0	92.1%	-1.4
15830	AT5G42050.1 | expressed protein, similar to gda-1 (Pisum sativum) GI:2765418 | chr5:16832717-16834521 FORWARD | Aliases: MJC20.15, MJC20_15	7.4	7.9	-0.5	-1.0	92.1%	-0.9
15831	AT2G28400.1 | expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584 | chr2:12155381-12156129 REVERSE | Aliases: T1B3.8, T1B3_8	3.9	3.7	0.3	1.0	92.2%	-0.7
15832	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	5.1	4.6	0.4	1.0	92.2%	-0.8
15833	AT3G43240.1 | ARID/BRIGHT DNA-binding domain-containing protein, contains Pfam profile PF01388: ARID/BRIGHT DNA binding domain	6.2	6.5	-0.3	-1.0	92.2%	-1.0
15834	AT2G11360.1 | hypothetical protein | chr2:4537975-4538585 REVERSE | Aliases: F3K12.12, F3K12_12	2.4	2.6	-0.1	-1.0	92.2%	-1.7
15835	AT5G55900.1 | sucrase-related, similar to sucrase (Solanum tuberosum) GI:1200257 | chr5:22654757-22656987 FORWARD | Aliases: MYN21.1, MYN21_1	5.4	5.6	-0.2	-1.0	92.2%	-1.0
15836	AT5G18610.1 | protein kinase family protein, contains eukaryotic protein kinase domain, PROSITE:PS00107 | chr5:6192738-6195373 FORWARD | Aliases: T28N17.90, T28N17_90	2.7	2.8	-0.1	-1.0	92.2%	-1.5
15837	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	2.7	-0.1	-1.0	92.2%	-1.5
15838	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	6.5	6.8	-0.2	-1.0	92.2%	-1.1
15839	AT5G34450.1 | replication protein-related, weak similarity to Replication Protein A 70	2.8	3.0	-0.1	-1.0	92.2%	-1.5
15840	AT5G66370.1 | expressed protein, similar to unknown protein (emb CAB62624.1) | chr5:26529426-26530050 REVERSE | Aliases: K1F13.2, K1F13_2	2.2	2.3	-0.1	-1.0	92.3%	-2.1
15841	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	4.5	4.3	0.2	1.0	92.3%	-1.3
15842	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	3.1	-0.2	-1.0	92.3%	-1.5
15843	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	3.8	-0.3	-1.0	92.3%	-1.1
15844	AT4G36350.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	3.5	3.6	-0.1	-1.0	92.3%	-1.5
15845	AT4G28085.2 | expressed protein | chr4:13959976-13960578 FORWARD | Aliases: None	3.1	3.3	-0.2	-1.0	92.3%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
15846	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	2.9	-0.1	-1.0	92.3%	-1.8
15847	AT3G12220.1 | Symbol: SCPL16 |	2.6	2.7	-0.1	-1.0	92.3%	-1.5
15848	AT4G09300.1 | expressed protein | chr4:5898795-5901011 FORWARD | Aliases: T30A10.60, T30A10_60	3.2	3.3	-0.1	-1.0	92.4%	-1.6
15849	AT4G26800.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:13489846-13492060 FORWARD | Aliases: F10M23.140, F10M23_140	2.7	2.8	-0.1	-1.0	92.4%	-1.8
15850	AT5G02170.1 | amino acid transporter family protein, belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II	3.1	3.3	-0.2	-1.0	92.4%	-1.3
15851	AT5G47430.1 | expressed protein | chr5:19252858-19258448 REVERSE | Aliases: MQL5.29, MQL5_29	3.1	3.0	0.1	1.0	92.5%	-1.4
15852	AT3G49510.1 | F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	2.8	2.9	-0.1	-1.0	92.5%	-1.6
15853	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	4.0	3.8	0.2	1.0	92.5%	-1.1
15854	AT3G46910.1 | expressed protein | chr3:17289621-17290637 FORWARD | Aliases: T6H20.60	2.3	2.4	-0.1	-1.0	92.5%	-1.8
15855	AT3G29970.1 | germination protein-related, similar to HvB12D (Hordeum vulgare subsp. vulgare) gi:471319:emb:CAA54065 | chr3:11747709-11749049 FORWARD | Aliases: K17E7.15	4.6	3.7	0.9	1.0	92.5%	-1.2
15856	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	2.6	-0.1	-1.0	92.6%	-1.7
15857	AT4G31530.1 | expressed protein | chr4:15282245-15284222 FORWARD | Aliases: F3L17.100, F3L17_100	5.5	5.3	0.2	1.0	92.6%	-1.1
15858	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	4.4	-0.2	-1.0	92.6%	-1.1
15859	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	2.7	0.1	1.0	92.6%	-1.5
15860	AT3G54130.1 | josephin family protein, contains Pfam domain PF02099: Josephin | chr3:20053683-20055504 REVERSE | Aliases: F24B22.90	4.6	4.5	0.1	1.0	92.6%	-1.2
15861	AT5G66520.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr5:26569105-26570967 FORWARD | Aliases: K1F13.18, K1F13_18	2.8	2.7	0.1	1.0	92.6%	-1.5
15862	AT5G20940.1 | glycosyl hydrolase family 3 protein, beta-glucosidase, common nasturtium, PIR:T10521 | chr5:7103929-7106703 REVERSE | Aliases: F22D1.110, F22D1_110	3.7	3.6	0.2	1.0	92.7%	-1.3
15863	AT5G55300.1 | DNA topoisomerase I, identical to Swiss-Prot:P30181 DNA topoisomerase I (Arabidopsis thaliana) | chr5:22441812-22446664 REVERSE | Aliases: MTE17.1, MTE17_1	6.4	6.2	0.2	1.0	92.7%	-1.2
15864	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	6.9	7.2	-0.3	-1.0	92.7%	-0.9
15865	AT4G34340.1 | expressed protein | chr4:16426643-16428014 REVERSE | Aliases: F10M10.110, F10M10_110	4.6	4.2	0.3	1.0	92.7%	-0.8
15866	AT3G56050.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr3:20808934-20811869 REVERSE | Aliases: F18O21.10	5.2	4.9	0.3	1.0	92.7%	-1.0
15867	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	2.9	-0.1	-1.0	92.8%	-1.7
15868	AT4G14590.1 | Symbol: EMB2739 | expressed protein | chr4:8374387-8375958 FORWARD | Aliases: DL3335W, EMB2739, EMBRYO DEFECTIVE 2739, FCAALL.260	4.2	4.0	0.1	1.0	92.8%	-1.4
15869	AT4G11330.1 | Symbol: ATMPK5 |	4.6	4.9	-0.3	-1.0	92.8%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
15870	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	2.1	-0.1	-1.0	92.9%	-2.2
15871	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	12.2	11.8	0.4	1.0	92.9%	-1.3
15872	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	2.4	-0.1	-1.0	92.9%	-1.9
15873	AT4G33170.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:15995704-15998676 REVERSE | Aliases: F4I10.100, F4I10_100	3.1	3.2	-0.1	-1.0	92.9%	-1.6
15874	AT3G02125.1 | expressed protein | chr3:378212-379389 FORWARD | Aliases: None	2.3	2.4	-0.1	-1.0	92.9%	-1.7
15875	AT3G54270.1 | sucrose-phosphatase 3 (SPP3), nearly identical to sucrose-phosphatase (SPP3) (Arabidopsis thaliana) GI:16904077 | chr3:20098060-20100713 REVERSE | Aliases: F24B22.230	3.4	3.5	-0.2	-1.0	92.9%	-1.3
15876	AT4G29130.1 | Symbol: ATHXK1 |	7.9	7.0	0.9	1.0	92.9%	-0.7
15877	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	7.7	-0.5	-1.0	92.9%	-1.1
15878	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 (GI:19481678)(shrimp white spot syndrome virus); similar to nuclear protein Np95 (GI:17939938) (Mus musculus) | chr1:29849548-29858307 REVERSE | Aliases: EMB1135, EMBRYO DEFECTIVE 1135, YUP8H12R.3, YUP8H12R_3	7.8	8.1	-0.3	-1.0	92.9%	-1.0
15879	AT4G39110.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:18222477-18225113 REVERSE | Aliases: T22F8.10, T22F8_10	2.6	2.7	-0.1	-1.0	92.9%	-1.6
15880	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	2.9	2.8	0.1	1.0	93.0%	-1.4
15881	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	2.6	0.1	1.0	93.1%	-1.7
15882	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	8.6	8.1	0.4	1.0	93.1%	-0.9
15883	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	3.2	-0.1	-1.0	93.1%	-1.5
15884	AT2G16250.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:7046764-7050015 REVERSE | Aliases: F16F14.25, F16F14_25	3.7	3.8	-0.1	-1.0	93.1%	-1.2
15885	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	3.5	0.2	1.0	93.1%	-1.1
15886	AT2G20580.1 | 26S proteasome regulatory subunit S2 (RPN1), contains an APC-complex (cyclosome) and proteasome component repeat (PS50248) | chr2:8866091-8871946 FORWARD | Aliases: F23N11.10, F23N11_10	8.0	8.4	-0.4	-1.0	93.2%	-0.8
15887	AT3G43160.1 | expressed protein, merozoite surface protein 2 (MSP-2), EMBL:PFU72951, Plasmodium falciparum | chr3:15177549-15179213 FORWARD | Aliases: F7K15.10	5.4	4.9	0.5	1.0	93.2%	-0.3
15888	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	4.4	4.7	-0.2	-1.0	93.2%	-1.0
15889	AT4G23660.2 | Symbol: ATPPT1 |	4.3	4.1	0.2	1.0	93.3%	-0.8
15890	AT1G79770.1 | expressed protein | chr1:30019254-30019971 FORWARD | Aliases: F20B17.20, F20B17_20	2.8	3.0	-0.2	-1.0	93.4%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
15891	AT1G06590.1 | expressed protein | chr1:2016307-2024643 REVERSE | Aliases: F12K11.7, F12K11_7	3.8	3.6	0.2	1.0	93.4%	-1.3
15892	AT1G04030.1 | expressed protein | chr1:1040517-1042891 FORWARD | Aliases: F21M11.3, F21M11_3	3.2	3.3	-0.1	-1.0	93.4%	-1.3
15893	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	3.7	4.0	-0.3	-1.0	93.4%	-1.0
15894	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	3.7	-0.2	-1.0	93.4%	-1.1
15895	AT1G17900.1 | expressed protein | chr1:6157361-6158123 REVERSE | Aliases: F2H15.23, F2H15_23	3.0	3.1	-0.1	-1.0	93.4%	-2.1
15896	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	4.2	4.1	0.1	1.0	93.5%	-1.4
15897	AT5G01110.1 | pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587; contains Pfam profile PF01535: PPR repeat | chr5:41770-44374 REVERSE | Aliases: F7J8.90, F7J8_90	3.9	3.7	0.2	1.0	93.5%	-0.8
15898	AT5G28860.1 | expressed protein | chr5:10883456-10884287 REVERSE | Aliases: F7P1.40, F7P1_40	2.3	2.4	-0.1	-1.0	93.5%	-1.8
15899	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	-1.0	93.5%	-2.0
15900	AT3G28020.1 | expressed protein | chr3:10419143-10420386 REVERSE | Aliases: MMG15.6	3.8	4.0	-0.2	-1.0	93.5%	-1.2
15901	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	8.5	-0.5	-1.0	93.5%	-1.0
15902	AT2G14810.1 | expressed protein | chr2:6364547-6365552 REVERSE | Aliases: F26C24.5, F26C24_5	2.6	2.7	-0.1	-1.0	93.5%	-1.8
15903	AT3G62950.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	2.2	2.3	-0.1	-1.0	93.5%	-1.7
15904	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	2.3	-0.1	-1.0	93.5%	-2.1
15905	AT5G52140.1 | zinc finger protein-related | chr5:21201748-21204098 REVERSE | Aliases: F17P19.3, F17P19_3	2.3	2.4	-0.1	-1.0	93.6%	-1.6
15906	AT5G22820.1 | expressed protein | chr5:7624026-7626978 REVERSE | Aliases: MRN17.5, MRN17_5	3.1	2.9	0.1	1.0	93.6%	-1.5
15907	AT3G12830.1 | auxin-responsive family protein, similar to auxin-induced protein (SP:P33082) (Glycine max) | chr3:4078658-4079615 REVERSE | Aliases: MBK21.19	4.2	4.5	-0.3	-1.0	93.6%	-1.0
15908	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	3.6	3.8	-0.2	-1.0	93.6%	-1.3
15909	AT2G12190.1 | cytochrome P450, putative | chr2:4898724-4900427 REVERSE | Aliases: F23M2.31, F23M2_31	2.7	2.5	0.2	1.0	93.6%	-1.7
15910	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	3.1	-0.2	-1.0	93.6%	-1.6
15911	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	-1.0	93.6%	-1.7
15912	AT1G68600.1 | expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	3.3	3.1	0.1	1.0	93.6%	-1.4
15913	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	3.5	3.3	0.2	1.0	93.6%	-1.5
15914	AT2G39190.2 | Symbol: ATATH8 |	2.8	2.7	0.2	1.0	93.6%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
15915	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	3.2	-0.2	-1.0	93.7%	-1.5
15916	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	2.7	2.8	-0.1	-1.0	93.7%	-1.4
15917	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	11.1	10.7	0.4	1.0	93.7%	-1.3
15918	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	4.0	3.7	0.2	1.0	93.7%	-0.8
15919	AT1G08560.1 | Symbol: SYP111 |	7.2	7.0	0.3	1.0	93.7%	-1.0
15920	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	2.3	2.4	-0.1	-1.0	93.7%	-1.8
15921	AT2G39560.1 | expressed protein | chr2:16511924-16513086 REVERSE | Aliases: F12L6.22, F12L6_22	3.1	3.0	0.1	1.0	93.8%	-1.9
15922	AT1G26090.1 | expressed protein | chr1:9020367-9022977 FORWARD | Aliases: F14G11.6	5.7	5.5	0.2	1.0	93.8%	-1.0
15923	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	2.7	2.8	-0.2	-1.0	93.8%	-1.4
15924	AT5G62030.1 | diphthamide synthesis DPH2 family protein, contains InterPro accession IPR002728: Diphthamide synthesis DPH2 protein | chr5:24935705-24938102 FORWARD | Aliases: MTG10.5, MTG10_5	3.8	4.0	-0.2	-1.0	93.8%	-1.1
15925	AT3G42430.1 | expressed protein, various predicted proteins, Arabidopsis thaliana | chr3:14554366-14555496 FORWARD | Aliases: T14K23.140	2.5	2.5	-0.1	-1.0	93.8%	-2.1
15926	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	2.7	-0.1	-1.0	93.8%	-1.8
15927	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	2.5	-0.1	-1.0	93.8%	-1.8
15928	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	2.9	-0.1	-1.0	93.8%	-1.4
15929	AT3G30150.1 | expressed protein | chr3:11784635-11785591 REVERSE | Aliases: T20F20.5	2.8	2.9	-0.1	-1.0	93.9%	-1.6
15930	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	3.0	-0.1	-1.0	94.0%	-1.5
15931	AT3G01530.1 | myb family transcription factor (MYB57), contains PFAM profile: myb DNA binding domain PF00249 | chr3:210126-211811 REVERSE | Aliases: F4P13.8, F4P13_8	2.7	2.8	-0.1	-1.0	94.0%	-1.5
15932	AT4G20000.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr4:10838320-10839152 FORWARD | Aliases: F18F4.100, F18F4_100	2.7	2.8	-0.1	-1.0	94.1%	-1.4
15933	AT5G66620.1 | LIM domain-containing protein, contains Pfam profile PF00412: LIM domain	4.0	4.1	-0.1	-1.0	94.1%	-1.5
15934	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	4.9	-0.4	-1.0	94.2%	-1.0
15935	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	-1.0	94.2%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
15936	AT1G62490.1 | mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF | chr1:23134070-23135198 REVERSE | Aliases: T3P18.5, T3P18_5	2.5	2.6	-0.1	-1.0	94.2%	-1.8
15937	AT2G20040.1 | protein kinase, putative, similar to protein kinase (Homo sapiens) gi:1052737:emb:CAA59733 | chr2:8656515-8658454 REVERSE | Aliases: T2G17.16, T2G17_16	5.9	6.2	-0.3	-1.0	94.2%	-0.7
15938	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	3.5	-0.1	-1.0	94.2%	-1.4
15939	AT2G32170.1 | expressed protein, ;supported by cDNA GI:20259498 | chr2:13673533-13678181 FORWARD | Aliases: F22D22.8, F22D22_8	7.8	7.3	0.5	1.0	94.2%	-0.7
15940	AT5G58450.1 | expressed protein, predicted proteins from D.melanogaster, C.elegans and S.pombe	7.3	7.8	-0.5	-1.0	94.2%	-0.6
15941	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	-1.0	94.2%	-1.8
15942	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	4.4	0.3	1.0	94.2%	-0.9
15943	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	4.3	4.4	-0.1	-1.0	94.2%	-1.4
15944	AT5G42490.1 | kinesin motor family protein, contains Pfam domain, PF00225: Kinesin motor domain | chr5:17005837-17009850 REVERSE | Aliases: MDH9.19, MDH9_19	2.7	2.8	-0.1	-1.0	94.3%	-1.8
15945	AT1G67000.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	3.1	2.9	0.2	1.0	94.3%	-1.4
15946	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 ENDOTRANSGLUCOSYLASE/HYDROLASE 3	2.8	2.9	-0.1	-1.0	94.3%	-2.0
15947	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	4.0	4.4	-0.4	-1.0	94.3%	-0.5
15948	AT5G11640.1 | expressed protein, predicted proteins, Drosophila melanogaster and Homo sapiens | chr5:3742009-3743980 FORWARD | Aliases: T22P22.30, T22P22_30	6.4	6.2	0.2	1.0	94.3%	-1.2
15949	AT2G43790.1 | Symbol: ATMPK6 |	4.4	3.9	0.5	1.0	94.3%	-1.1
15950	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	3.2	-0.2	-1.0	94.3%	-1.4
15951	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	2.3	-0.1	-1.0	94.3%	-1.7
15952	AT3G52080.1 | similar to cation/hydrogen exchanger, putative (CHX15) [Arabidopsis thaliana] (TAIR:At2g13620.1); similar to Na+/H+ 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	2.8	-0.1	-1.0	94.4%	-1.5
15953	AT3G09085.1 | expressed protein | chr3:2782156-2782688 FORWARD | Aliases: None	7.3	7.7	-0.4	-1.0	94.4%	-0.8
15954	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	3.2	3.1	0.1	1.0	94.4%	-1.4
15955	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	8.9	9.1	-0.2	-1.0	94.4%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
15956	AT3G15160.1 | expressed protein | chr3:5104374-5108457 FORWARD | Aliases: F4B12.7	5.2	5.0	0.2	1.0	94.5%	-1.1
15957	AT5G16280.1 | expressed protein | chr5:5323178-5331348 REVERSE | Aliases: T21H19.200, T21H19_200	4.3	4.5	-0.2	-1.0	94.5%	-1.1
15958	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	2.7	0.1	1.0	94.5%	-1.4
15959	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	4.2	-0.2	-1.0	94.5%	-1.4
15960	AT1G69610.1 | expressed protein | chr1:26190617-26193152 FORWARD | Aliases: F24J1.24	3.2	3.1	0.2	1.0	94.5%	-1.4
15961	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	3.7	-0.2	-1.0	94.5%	-1.4
15962	AT4G35860.1 | Symbol: ATGB2 | Ras-related GTP-binding protein, putative, similar to Rab2-like GTP-binding protein GI:1765896 from (Arabidopsis thaliana) | chr4:16986843-16989041 REVERSE | Aliases: F4B14.130, F4B14_130, GTP BINDING 2, GTP BINDING PROTEIN ATGB2	7.4	7.7	-0.4	-1.0	94.6%	-1.0
15963	AT3G60470.1 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function | chr3:22355788-22357859 FORWARD | Aliases: T8B10.130	2.9	2.7	0.1	1.0	94.6%	-1.3
15964	AT1G53980.1 | polyubiquitin-related, contains similarity to polyubiquitin GI:166336 from (Aglaothamnion neglectum) | chr1:20153002-20153277 REVERSE | Aliases: T18A20.18	3.4	3.2	0.2	1.0	94.6%	-1.5
15965	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	2.9	-0.1	-1.0	94.6%	-1.8
15966	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	3.9	0.2	1.0	94.6%	-1.1
15967	AT5G51130.1 | expressed protein, contains similarity to unknown protein (pir::T26512) | chr5:20799122-20801127 FORWARD | Aliases: MWD22.7, MWD22_7	5.4	5.1	0.2	1.0	94.6%	-1.1
15968	AT3G25200.1 | hypothetical protein | chr3:9178169-9179505 FORWARD | Aliases: MJL12.15	2.2	2.3	-0.1	-1.0	94.6%	-1.9
15969	AT1G17830.1 | expressed protein | chr1:6135796-6138425 REVERSE | Aliases: F2H15.6, F2H15_6	2.9	3.1	-0.2	-1.0	94.6%	-1.2
15970	AT5G14150.1 | expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642 | chr5:4565174-4566907 REVERSE | Aliases: MUA22.15, MUA22_15	3.2	3.3	-0.1	-1.0	94.6%	-1.6
15971	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	2.4	2.5	-0.1	-1.0	94.7%	-1.5
15972	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	8.4	7.9	0.5	1.0	94.7%	-1.1
15973	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	2.6	2.7	-0.1	-1.0	94.7%	-1.5
15974	AT2G36430.1 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function | chr2:15297283-15298842 FORWARD | Aliases: F1O11.6, F1O11_6	4.3	4.5	-0.2	-1.0	94.7%	-1.3
15975	AT4G29990.1 | light repressible receptor protein kinase, identical to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376	3.9	4.2	-0.3	-1.0	94.7%	-1.1
15976	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	4.1	3.8	0.2	1.0	94.7%	-1.3
15977	AT5G63690.1 | expressed protein | chr5:25510090-25510509 REVERSE | Aliases: MBK5.17, MBK5_17	5.2	4.8	0.4	1.0	94.7%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
15978	AT1G52530.1 | similar to LIG1 [Physarum polycephalum] (GB:AAF65575.1); contains InterPro domain Hus1-like protein (InterPro:IPR007150)	3.6	3.4	0.2	1.0	94.7%	-1.2
15979	AT5G04670.1 | expressed protein, BRL protein, Homo sapiens, EMBL:AF005067 | chr5:1337840-1340885 REVERSE | Aliases: T1E3.30, T1E3_30	5.1	4.9	0.2	1.0	94.7%	-0.9
15980	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	4.2	-0.2	-1.0	94.7%	-1.2
15981	AT1G75860.1 | expressed protein | chr1:28487916-28489039 REVERSE | Aliases: T4O12.10, T4O12_10	7.3	7.8	-0.5	-1.0	94.7%	-1.0
15982	AT4G33220.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr4:16022443-16026364 FORWARD | Aliases: F4I10.150, F4I10_150	2.3	2.4	-0.1	-1.0	94.8%	-1.8
15983	AT1G54700.1 | hypothetical protein | chr1:20419565-20419936 FORWARD | Aliases: T22H22.13, T22H22_13	2.9	3.0	-0.1	-1.0	94.8%	-1.9
15984	AT5G06560.1 | expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593 | chr5:2003305-2006189 REVERSE | Aliases: F15M7.9, F15M7_9	6.3	5.8	0.4	1.0	94.8%	-1.1
15985	AT1G08250.1 | prephenate dehydratase family protein, contains similarity to prephenate dehydratase GI:1008717 from (Amycolatopsis methanolica)	6.3	6.4	-0.2	-1.0	94.9%	-1.0
15986	AT4G24290.2 | expressed protein | chr4:12594349-12598038 FORWARD | Aliases: T22A6.120, T22A6_120	3.2	3.1	0.1	1.0	94.9%	-1.5
15987	AT5G16810.1 | expressed protein | chr5:5526767-5529921 REVERSE | Aliases: F5E19.150, F5E19_150	5.2	4.9	0.3	1.0	94.9%	-0.5
15988	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	8.4	7.8	0.6	1.0	94.9%	-0.8
15989	AT3G29600.1 | hypothetical protein | chr3:11409888-11410546 REVERSE | Aliases: MTO24.7	2.3	2.4	-0.1	-1.0	94.9%	-2.2
15990	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	5.8	-0.3	-1.0	94.9%	-0.9
15991	AT3G53040.1 | late embryogenesis abundant protein, putative / LEA protein, putative, similar to LEA protein in group 3 (Arabidopsis thaliana) GI:1526424; contains Pfam profile PF02987: Late embryogenesis abundant protein | chr3:19675652-19677465 REVERSE | Aliases: F8J2.210	3.4	3.5	-0.2	-1.0	94.9%	-1.4
15992	AT1G26110.1 | expressed protein | chr1:9024332-9027745 REVERSE | Aliases: F14G11.8, F14G11_8	8.3	8.8	-0.5	-1.0	95.0%	-0.8
15993	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	2.8	-0.1	-1.0	95.0%	-1.7
15994	AT1G05680.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr1:1703091-1704688 REVERSE | Aliases: F3F20.13, F3F20_13	3.0	3.1	-0.1	-1.0	95.0%	-1.5
15995	AT5G48010.1 | Encodes an oxidosqualene cyclase involved in the	3.1	3.3	-0.2	-1.0	95.0%	-1.3
15996	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	2.8	2.9	-0.2	-1.0	95.1%	-1.6
15997	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	7.3	7.7	-0.4	-1.0	95.1%	-1.0
15998	AT2G01770.1 | integral membrane family protein, contains integral membrane protein domain, Pfam:PF01988 | chr2:334774-336424 REVERSE | Aliases: T8O11.6, T8O11_6	2.5	2.6	-0.1	-1.0	95.1%	-1.5
15999	AT3G49810.1 | U-box domain-containing protein, contains Pfam profile PF04564: U-box domain | chr3:18485522-18487819 REVERSE | Aliases: T16K5.160	3.4	3.2	0.1	1.0	95.2%	-1.6
16000	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	2.9	3.1	-0.1	-1.0	95.2%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
16001	AT3G25090.1 | F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain | chr3:9140046-9141101 REVERSE | Aliases: MJL12.3	3.2	3.5	-0.3	-1.0	95.2%	-1.1
16002	AT2G28170.1 | Symbol: ATCHX7 |	2.6	2.7	-0.1	-1.0	95.2%	-1.9
16003	AT5G64590.1 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537 | chr5:25839558-25840427 REVERSE | Aliases: MUB3.11, MUB3_11	3.3	3.5	-0.2	-1.0	95.2%	-1.4
16004	AT2G01820.1 | Symbol: CYCJ18 |	5.7	6.1	-0.4	-1.0	95.2%	-0.9
16005	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	3.2	3.4	-0.2	-1.0	95.2%	-1.1
16006	AT3G46790.1 | Symbol: CRR2 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:17242758-17244933 REVERSE | Aliases: CHLORORESPIRATORY REDUCTION 2, T6H20.180	6.6	6.4	0.3	1.0	95.3%	-1.4
16007	AT5G02410.1 | DIE2/ALG10 family, contains Pfam PF04922: DIE2/ALG10 family | chr5:517210-519754 REVERSE | Aliases: T1E22.170, T1E22_170	3.7	3.9	-0.2	-1.0	95.3%	-1.0
16008	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	2.1	0.1	1.0	95.3%	-1.9
16009	AT5G23630.1 | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase familiy 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	6.7	6.9	-0.3	-1.0	95.3%	-1.1
16010	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	7.2	7.4	-0.2	-1.0	95.4%	-1.0
16011	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	4.3	4.0	0.3	1.0	95.4%	-1.0
16012	AT1G07720.1 | beta-ketoacyl-CoA synthase family protein, similar to GB:AAC99312 from (Arabidopsis thaliana) (Plant J. (1999) In press)	2.1	2.2	-0.1	-1.0	95.5%	-2.0
16013	AT3G45090.2 | 2-phosphoglycerate kinase-related, contains weak similarity to 2-phosphoglycerate kinase (GI:467751) (Methanothermus fervidus) | chr3:16501585-16505696 REVERSE | Aliases: T14D3.30	4.0	4.4	-0.4	-1.0	95.5%	-0.8
16014	AT2G18930.1 | hypothetical protein | chr2:8205860-8206154 FORWARD | Aliases: F19F24.13, F19F24_13	2.9	3.0	-0.1	-1.0	95.5%	-1.8
16015	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)	2.4	2.6	-0.1	-1.0	95.5%	-1.6
16016	AT3G06240.1 | F-box family protein, contains F-box domain Pfam:PF00646	6.7	7.1	-0.3	-1.0	95.6%	-1.0
16017	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	2.6	0.1	1.0	95.6%	-1.5
16018	AT1G34245.1 | expressed protein | chr1:12472846-12473731 FORWARD | Aliases: None	2.4	2.5	-0.1	-1.0	95.6%	-1.9
16019	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	2.9	0.1	1.0	95.6%	-1.3
16020	AT1G06180.1 | Symbol: ATMYB13 | myb family transcription factor, identical to	2.7	2.9	-0.2	-1.0	95.6%	-1.3
16021	AT2G19830.1 | SNF7 family protein, contains Pfam domain, PF03357: SNF7 family | chr2:8564931-8566800 REVERSE | Aliases: F6F22.14, F6F22_14	7.5	7.7	-0.2	-1.0	95.7%	-1.1
16022	AT3G30370.1 | expressed protein | chr3:11967659-11968198 REVERSE | Aliases: T6J22.16	2.4	2.5	-0.1	-1.0	95.7%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
16023	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	3.1	3.0	0.2	1.0	95.7%	-1.1
16024	AT5G15530.1 | Symbol: BCCP2 | biotin carboxyl carrier protein 2 (BCCP2), identical to biotin carboxyl carrier protein isoform 2 (Arabidopsis thaliana) gi:8886869:gb:AAF80592	4.9	4.6	0.3	1.0	95.7%	-0.9
16025	AT3G17630.1 | Symbol: ATCHX19 | cation/hydrogen exchanger, putative (CHX19), similar to putative Na+/H+-exchanging protein GB:CAA23036 from (Arabidopsis thaliana); monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563	3.8	4.1	-0.2	-1.0	95.7%	-1.2
16026	AT1G58390.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.1	3.2	-0.1	-1.0	95.7%	-1.7
16027	AT4G35070.1 | expressed protein | chr4:16694175-16695699 FORWARD | Aliases: T12J5.5	3.2	3.0	0.2	1.0	95.8%	-1.4
16028	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	3.9	3.8	0.1	1.0	95.8%	-1.4
16029	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	5.9	0.2	1.0	95.8%	-1.0
16030	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	4.8	-0.2	-1.0	95.8%	-1.1
16031	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	2.6	2.8	-0.1	-1.0	95.9%	-1.5
16032	AT3G08750.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.9	3.1	-0.2	-1.0	95.9%	-1.5
16033	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	3.6	3.5	0.1	1.0	95.9%	-1.3
16034	AT4G30720.1 | expressed protein, hypothetical protein - Synechocystis sp. (strain PCC 6803),PIR2:S76076 | chr4:14971859-14976174 REVERSE | Aliases: T10C21.70, T10C21_70	4.0	3.8	0.1	1.0	95.9%	-1.3
16035	AT2G40530.1 | expressed protein | chr2:16934580-16935274 FORWARD | Aliases: T2P4.12, T2P4_12	2.8	2.9	-0.1	-1.0	95.9%	-1.8
16036	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	2.5	2.6	-0.1	-1.0	96.0%	-1.7
16037	AT1G41750.1 | expressed protein | chr1:15524452-15524877 REVERSE | Aliases: F9M8.6	3.2	3.4	-0.2	-1.0	96.0%	-1.1
16038	AT3G49130.1 | expressed protein | chr3:18221438-18222693 FORWARD | Aliases: F2K15.1	3.5	3.8	-0.3	-1.0	96.0%	-1.1
16039	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	4.6	0.1	1.0	96.0%	-1.3
16040	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	3.8	4.1	-0.3	-1.0	96.0%	-1.1
16041	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	7.2	6.8	0.4	1.0	96.1%	-1.1
16042	AT2G40475.1 | expressed protein | chr2:16913989-16915206 REVERSE | Aliases: None	3.8	4.0	-0.2	-1.0	96.1%	-1.2
16043	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	4.2	4.6	-0.4	-1.0	96.1%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
16044	AT2G38830.1 | tumor susceptibility protein-related, contains weak similarity to Swiss-Prot:Q99816 tumor susceptibility gene 101 protein (Homo sapiens)	3.0	3.2	-0.1	-1.0	96.1%	-1.6
16045	AT2G27520.1 | F-box family protein, contains Pfam profile: PF00646 F-box domain | chr2:11769139-11770182 FORWARD | Aliases: F10A12.29	3.1	3.3	-0.2	-1.0	96.1%	-1.3
16046	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	6.5	7.1	-0.5	-1.0	96.2%	-0.8
16047	AT3G23930.1 | expressed protein | chr3:8646904-8647915 FORWARD | Aliases: F14O13.11	3.4	3.5	-0.1	-1.0	96.2%	-1.6
16048	AT1G68320.1 | Symbol: MYB62 | myb family transcription factor (MYB62), similar to myb-related transcription factor (cpm7) GI:1002799 from (Craterostigma plantagineum); contains PFAM profile: myb DNA binding domain PF00249	3.3	3.2	0.1	1.0	96.2%	-1.4
16049	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	3.2	-0.2	-1.0	96.2%	-1.2
16050	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	6.1	6.5	-0.4	-1.0	96.2%	-1.0
16051	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	3.4	-0.1	-1.0	96.2%	-1.4
16052	AT1G03540.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:883782-885611 FORWARD | Aliases: F21B7.16	3.8	4.0	-0.2	-1.0	96.2%	-1.3
16053	AT5G25410.1 | expressed protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function | chr5:8831673-8833512 FORWARD | Aliases: F18G18.150, F18G18_150	3.4	3.6	-0.1	-1.0	96.2%	-1.6
16054	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	10.0	-0.3	-1.0	96.2%	-1.4
16055	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	4.7	4.9	-0.2	-1.0	96.2%	-1.1
16056	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	3.2	-0.1	-1.0	96.2%	-1.5
16057	AT5G26150.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:9137464-9140102 REVERSE | Aliases: T1N24.15, T1N24_15	2.1	2.2	-0.1	-1.0	96.2%	-2.1
16058	AT4G13960.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.6	3.8	-0.2	-1.0	96.3%	-1.3
16059	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	9.7	9.2	0.5	1.0	96.3%	-0.8
16060	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	4.6	4.4	0.1	1.0	96.3%	-1.2
16061	AT3G30560.1 | hypothetical protein | chr3:12154428-12160021 FORWARD | Aliases: MQP15.20	2.7	2.9	-0.2	-1.0	96.3%	-1.4
16062	AT5G36210.1 | expressed protein | chr5:14265143-14270460 REVERSE | Aliases: MAB16.20	7.7	7.4	0.3	1.0	96.3%	-0.9
16063	AT5G52180.1 | expressed protein | chr5:21217281-21218835 REVERSE | Aliases: F17P19.8, F17P19_8	6.4	6.6	-0.2	-1.0	96.3%	-1.2
16064	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	7.0	7.2	-0.2	-1.0	96.3%	-0.8
16065	AT1G41820.1 | expressed protein | chr1:15584864-15587584 REVERSE | Aliases: T4I21.4, T4I21_4	2.6	2.7	-0.2	-1.0	96.4%	-1.5
16066	AT4G23090.1 | expressed protein | chr4:12100566-12101491 REVERSE | Aliases: F7H19.280, F7H19_280	3.1	3.3	-0.2	-1.0	96.4%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
16067	AT5G10870.1 | Symbol: ATCM2 | chorismate mutase, cytosolic (CM2), identical to gi:5732016 | chr5:3430547-3432463 REVERSE | Aliases: None	4.8	5.0	-0.2	-1.0	96.4%	-1.0
16068	AT1G55280.1 | expressed protein | chr1:20626627-20628297 REVERSE | Aliases: F7A10.4, F7A10_4	3.2	3.4	-0.2	-1.0	96.4%	-1.1
16069	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	3.1	-0.1	-1.0	96.4%	-1.6
16070	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	3.3	-0.1	-1.0	96.4%	-1.3
16071	AT2G17960.1 | hypothetical protein | chr2:7819462-7820211 REVERSE | Aliases: T27K22.17, T27K22_17	3.0	3.2	-0.2	-1.0	96.4%	-1.4
16072	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	8.5	8.9	-0.4	-1.0	96.4%	-1.0
16073	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	2.9	-0.1	-1.0	96.5%	-1.8
16074	AT1G65070.1 | DNA mismatch repair MutS family protein, contains Pfam profile PF00488: MutS domain V | chr1:24176795-24179907 REVERSE | Aliases: F16G16.7, F16G16_7	4.3	4.0	0.3	1.0	96.5%	-0.9
16075	AT2G46300.1 | expressed protein | chr2:19015364-19016631 FORWARD | Aliases: T3F17.5	3.7	3.9	-0.2	-1.0	96.5%	-1.2
16076	AT4G12230.1 | esterase/lipase/thioesterase family protein, low similarity to 2-hydroxy-6-ketonona-2,4-dienedoic acid hydrolase; OhpC (Rhodococcus sp.) GI:8926386; contains Interpro entry IPR000379 | chr4:7284513-7287536 FORWARD | Aliases: T4C9.70, T4C9_70	4.5	4.9	-0.4	-1.0	96.5%	-1.2
16077	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	3.6	3.7	-0.1	-1.0	96.5%	-1.7
16078	AT3G60340.2 | palmitoyl protein thioesterase family protein, palmitoyl-protein thioesterase precursor, Mus musculus, EMBL:AF071025 | chr3:22315148-22317899 FORWARD | Aliases: T8B10.2	9.1	8.8	0.4	1.0	96.6%	-1.0
16079	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	7.2	8.0	-0.8	-1.0	96.6%	-0.7
16080	AT1G70270.1 | expressed protein | chr1:26468063-26468523 FORWARD | Aliases: F17O7.20, F17O7_20	2.8	2.9	-0.1	-1.0	96.6%	-1.7
16081	AT3G28750.1 | expressed protein | chr3:10792828-10794081 REVERSE | Aliases: T19N8.4	2.7	2.8	-0.1	-1.0	96.6%	-1.4
16082	AT5G46320.1 | hypothetical protein | chr5:18805473-18806115 REVERSE | Aliases: MPL12.11, MPL12_11	3.9	4.0	-0.2	-1.0	96.6%	-1.3
16083	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	8.5	-0.2	-1.0	96.6%	-1.4
16084	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	8.6	8.2	0.4	1.0	96.6%	-1.3
16085	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	5.0	5.2	-0.2	-1.0	96.6%	-1.1
16086	AT3G02555.1 | expressed protein | chr3:539712-541510 REVERSE | Aliases: None	4.4	4.3	0.2	1.0	96.7%	-1.2
16087	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	3.1	-0.1	-1.0	96.7%	-1.9
16088	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	3.9	-0.2	-1.0	96.7%	-1.6
16089	AT5G52690.1 | heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain	2.6	2.7	-0.1	-1.0	96.7%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
16090	AT5G28680.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:10719441-10722017 REVERSE | Aliases: F4I4.60, F4I4_60	3.4	3.5	-0.1	-1.0	96.8%	-1.5
16091	AT3G14240.1 | subtilase family protein, contains similarity to SBT1 GI:1771160 from (Lycopersicon esculentum) | chr3:4741480-4744124 REVERSE | Aliases: MLN21.2	6.8	6.3	0.5	1.0	96.8%	-1.0
16092	AT3G28155.1 | expressed protein, weak similarity to microtubule organization 1 protein (Arabidopsis thaliana) GI:14317953 | chr3:10486538-10487228 REVERSE | Aliases: MMG15.26	2.9	3.1	-0.1	-1.0	96.8%	-1.6
16093	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	5.3	-0.4	-1.0	96.8%	-1.1
16094	AT2G27990.1 | homeodomain-containing protein | chr2:11928510-11931775 REVERSE | Aliases: T1E2.9, T1E2_9	2.7	2.9	-0.2	-1.0	96.9%	-1.4
16095	AT5G59760.1 | expressed protein | chr5:24092854-24093519 REVERSE | Aliases: MTH12.3, MTH12_3	2.8	2.9	-0.1	-1.0	96.9%	-1.9
16096	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	3.6	3.5	0.2	1.0	96.9%	-1.3
16097	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 Rattus norvegicus, LACS 4 (SP:O60488) from Homo sapiens; contains Pfam HMM hit: AMP-binding enzymes PF00501	11.2	11.0	0.3	1.0	96.9%	-1.6
16098	AT2G44760.1 | expressed protein | chr2:18459844-18461882 REVERSE | Aliases: F16B22.25	5.9	6.1	-0.2	-1.0	97.0%	-1.3
16099	AT2G27200.1 | GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function | chr2:11632527-11635149 FORWARD | Aliases: T22O13.3, T22O13_3	5.0	4.7	0.2	0.9	97.0%	-1.2
16100	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	4.6	4.9	-0.3	-0.9	97.0%	-0.9
16101	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	3.7	3.8	-0.1	-0.9	97.0%	-1.3
16102	AT3G22650.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.8	-0.2	-0.9	97.1%	-1.6
16103	AT3G20690.1 | F-box protein-related, ontains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain; contains weak hit to Pfam PF00646: F-box domain	3.2	3.4	-0.2	-0.9	97.1%	-1.5
16104	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	-0.9	97.2%	-1.8
16105	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	8.4	-0.4	-0.9	97.2%	-1.1
16106	AT2G29210.1 | splicing factor PWI domain-containing protein, contains Pfam profile PF01480: PWI domain	8.9	8.1	0.8	0.9	97.3%	-0.8
16107	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	5.8	6.0	-0.2	-0.9	97.3%	-1.3
16108	AT5G61605.1 | expressed protein | chr5:24785608-24786192 REVERSE | Aliases: None	3.2	3.3	-0.2	-0.9	97.3%	-1.7
16109	AT4G35110.2 | expressed protein | chr4:16712467-16714958 REVERSE | Aliases: T12J5.14	3.5	3.7	-0.1	-0.9	97.3%	-1.4
16110	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	6.9	7.6	-0.7	-0.9	97.3%	-0.7
16111	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	3.1	-0.1	-0.9	97.3%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
16112	AT3G50650.1 | scarecrow-like transcription factor 7 (SCL7) | chr3:18817239-18819191 REVERSE | Aliases: T3A5.30	4.4	4.2	0.1	0.9	97.3%	-1.2
16113	AT3G57860.1 | expressed protein | chr3:21437291-21439827 FORWARD | Aliases: T10K17.70	3.4	3.5	-0.1	-0.9	97.4%	-1.6
16114	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	2.8	3.0	-0.2	-0.9	97.4%	-1.1
16115	AT5G03270.1 | expressed protein, contains Pfam profile PF03641: decarboxylase family protein | chr5:781869-783996 FORWARD | Aliases: F15A17.300, F15A17_300	3.4	3.5	-0.1	-0.9	97.4%	-1.6
16116	AT5G07570.1 | glycine/proline-rich protein, contains similarity to flagelliform silk protein (Nephila clavipes) gi:7106224:gb:AAF36090	2.3	2.4	-0.1	-0.9	97.4%	-1.8
16117	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	7.7	7.0	0.7	0.9	97.5%	-0.7
16118	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	8.2	8.5	-0.3	-0.9	97.5%	-1.0
16119	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	10.0	10.1	-0.2	-0.9	97.5%	-1.6
16120	AT5G33200.1 | hypothetical protein, predicted replication A1 proteins - Arabidopsis thaliana | chr5:12468882-12471971 REVERSE | Aliases: T29A4.10, T29A4_10	2.5	2.7	-0.1	-0.9	97.5%	-1.8
16121	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/PfpI family; TIGRFAM TIGR01383: DJ-1 family protein | chr1:19867968-19871057 REVERSE | Aliases: F12M16.18, F12M16_18	10.3	10.4	-0.2	-0.9	97.5%	-1.4
16122	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)	3.5	3.3	0.2	0.9	97.6%	-1.1
16123	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	4.3	4.4	-0.1	-0.9	97.6%	-1.2
16124	AT3G07000.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	4.4	4.2	0.2	0.9	97.6%	-1.1
16125	AT5G15270.2 | KH domain-containing protein, various predicted proteins, Arabidopsis thaliana and Oryza sativa | chr5:4958340-4961066 FORWARD | Aliases: F8M21.160, F8M21_160	5.5	5.7	-0.2	-0.9	97.6%	-1.0
16126	AT5G53900.2 | expressed protein, similar to unknown protein (gb:AAF34833.1) | chr5:21898368-21900478 REVERSE | Aliases: K19P17.6, K19P17_6	4.1	4.3	-0.2	-0.9	97.6%	-1.5
16127	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	5.4	5.7	-0.2	-0.9	97.6%	-0.9
16128	AT5G51910.2 | TCP family transcription factor, putative, similar to PCF2 ((GI:2580440) Oryza sativa) | chr5:21111811-21113058 REVERSE | Aliases: MJM18.6, MJM18_6	4.0	3.8	0.2	0.9	97.6%	-1.2
16129	AT4G10955.1 | lipase class 3 family protein, contains Pfam profile PF01764: Lipase | chr4:6713553-6718551 REVERSE | Aliases: None	4.7	4.9	-0.2	-0.9	97.6%	-1.3
16130	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	4.9	-0.2	-0.9	97.6%	-1.3
16131	AT2G32890.1 | expressed protein | chr2:13960135-13960368 REVERSE | Aliases: T21L14.17, T21L14_17	4.2	4.4	-0.2	-0.9	97.6%	-1.3
16132	AT2G03320.1 | hypothetical protein | chr2:1007379-1007942 FORWARD | Aliases: T4M8.25, T4M8_25	2.6	2.5	0.1	0.9	97.6%	-1.9
16133	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	7.5	7.2	0.3	0.9	97.6%	-1.3
16134	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	3.7	0.1	0.9	97.7%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
16135	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	2.9	-0.1	-0.9	97.7%	-1.6
16136	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	2.2	-0.1	-0.9	97.7%	-1.6
16137	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	3.1	-0.1	-0.9	97.7%	-1.7
16138	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	5.4	0.4	0.9	97.7%	-0.9
16139	AT3G12460.1 | expressed protein | chr3:3954702-3955430 REVERSE | Aliases: T2E22.22	2.1	2.2	-0.1	-0.9	97.7%	-2.0
16140	AT5G44990.1 | expressed protein | chr5:18180597-18181995 FORWARD | Aliases: K21C13.18, K21C13_18	2.3	2.5	-0.1	-0.9	97.7%	-1.6
16141	AT2G16690.1 | expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277 | chr2:7243960-7244682 REVERSE | Aliases: T24I21.10, T24I21_10	4.4	4.2	0.2	0.9	97.7%	-1.3
16142	AT3G24770.1 | Symbol: CLE41 | CLE41, putative, CLAVATA/ESR-Related 41 (CLE41)	3.0	3.1	-0.1	-0.9	97.8%	-1.5
16143	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	2.9	-0.1	-0.9	97.8%	-1.6
16144	AT3G04490.1 | exportin-related, weak similarity to Exportin 4 (Exp4) (Swiss-Prot:Q9ESJ0) (Mus musculus) and (Swiss-Prot:Q9C0E2) (Homo sapiens)	5.5	5.1	0.4	0.9	97.8%	-0.6
16145	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	4.5	4.4	0.1	0.9	97.8%	-1.4
16146	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	5.9	5.3	0.7	0.9	97.8%	-0.7
16147	AT4G28980.2 | Symbol: CAK1AT |	5.0	5.1	-0.1	-0.9	97.9%	-1.6
16148	AT5G09930.1 | Symbol: ATGCN2 |	2.8	2.7	0.1	0.9	97.9%	-1.7
16149	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	3.5	-0.1	-0.9	97.9%	-1.4
16150	AT4G02160.1 | hypothetical protein | chr4:955101-955652 REVERSE | Aliases: T10M13.23, T10M13_23	3.4	3.6	-0.2	-0.9	97.9%	-1.2
16151	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	4.4	4.8	-0.3	-0.9	98.0%	-0.9
16152	AT1G10150.1 | Symbol: ATPP2 A10 | expressed protein, similar to ESTs gb:T20511, gb:T45308, gb:H36493, and gb:AA651176	7.5	7.6	-0.1	-0.9	98.0%	-1.3
16153	AT3G31910.1 | expressed protein | chr3:12910356-12912093 REVERSE | Aliases: T1O13.14	3.0	3.2	-0.1	-0.9	98.1%	-1.6
16154	AT5G49130.1 | MATE efflux family protein, contains Pfam profile PF01554: MatE Uncharacterized membrane protein family | chr5:19933130-19934751 FORWARD | Aliases: K20J1.11, K20J1_11	2.9	3.1	-0.1	-0.9	98.1%	-1.6
16155	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	3.8	4.0	-0.2	-0.9	98.1%	-1.3
16156	AT4G23840.1 | leucine-rich repeat family protein | chr4:12400355-12403413 FORWARD | Aliases: AT4G23830, T32A16.10, T32A16_10	3.9	4.1	-0.1	-0.9	98.1%	-1.6
16157	AT3G62130.1 | epimerase-related, contains weak similarity to isopenicillin N epimerase (Swiss-Prot:P18549) (Streptomyces clavuligerus)	5.1	5.3	-0.2	-0.9	98.1%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
16158	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	9.0	8.6	0.4	0.9	98.1%	-0.9
16159	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	6.0	5.5	0.5	0.9	98.2%	-0.8
16160	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	3.7	3.4	0.2	0.9	98.2%	-1.2
16161	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	2.7	-0.1	-0.9	98.2%	-2.0
16162	AT1G64960.1 | expressed protein | chr1:24133581-24137712 FORWARD | Aliases: F13O11.26, F13O11_26	5.4	5.5	-0.1	-0.9	98.3%	-1.5
16163	AT3G60570.1 | Symbol: ATEXPB5 | beta-expansin, putative (EXPB5), conatins 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	3.4	-0.2	-0.9	98.3%	-1.1
16164	AT5G11610.2 | exostosin family protein, contains Pfam domain, PF03016: Exostosin family | chr5:3735351-3738218 REVERSE | Aliases: T22P22.3	2.6	2.7	-0.1	-0.9	98.3%	-1.8
16165	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	11.0	10.7	0.3	0.9	98.3%	-1.5
16166	AT4G26680.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:13454859-13456424 FORWARD | Aliases: F10M23.20, F10M23_20	3.8	4.1	-0.2	-0.9	98.4%	-1.1
16167	AT2G34870.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr2:14717856-14718532 FORWARD | Aliases: F19I3.10, F19I3_10	2.3	2.2	0.1	0.9	98.4%	-1.9
16168	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	2.7	2.8	-0.1	-0.9	98.4%	-1.8
16169	AT2G04900.1 | expressed protein | chr2:1722478-1723828 FORWARD | Aliases: F1O13.3	9.7	9.5	0.2	0.9	98.4%	-1.4
16170	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	5.5	-0.2	-0.9	98.5%	-1.3
16171	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	4.0	-0.2	-0.9	98.5%	-1.2
16172	AT3G30820.1 | hypothetical protein | chr3:12532322-12533714 FORWARD | Aliases: K11J14.16	2.2	2.3	-0.1	-0.9	98.5%	-1.6
16173	AT3G27770.1 | expressed protein | chr3:10286072-10288979 REVERSE | Aliases: MGF10.17	9.7	10.1	-0.4	-0.9	98.5%	-1.1
16174	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	3.1	-0.1	-0.9	98.5%	-2.0
16175	AT1G52640.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:19612525-19614096 REVERSE | Aliases: F6D8.14, F6D8_14	2.8	2.9	-0.1	-0.9	98.5%	-1.4
16176	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	7.2	6.9	0.3	0.9	98.5%	-1.0
16177	AT3G07710.1 | expressed protein | chr3:2464342-2464779 REVERSE | Aliases: MLP3.16	2.6	2.6	-0.1	-0.9	98.5%	-2.1
16178	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	7.3	7.0	0.3	0.9	98.5%	-0.9
16179	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	5.5	5.3	0.2	0.9	98.5%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
16180	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	6.7	6.4	0.3	0.9	98.5%	-1.1
16181	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	3.9	4.4	-0.5	-0.9	98.6%	-0.2
16182	AT3G09040.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:2761200-2764286 REVERSE | Aliases: MZB10.7	2.7	2.6	0.1	0.9	98.6%	-1.8
16183	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	5.5	5.7	-0.2	-0.9	98.6%	-1.0
16184	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	3.2	3.0	0.2	0.9	98.6%	-1.4
16185	AT1G56580.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr1:21201924-21202621 REVERSE | Aliases: F25P12.97, F25P12_97	10.4	10.2	0.3	0.9	98.6%	-1.4
16186	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	5.5	5.0	0.5	0.9	98.6%	-0.7
16187	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	4.4	4.7	-0.3	-0.9	98.7%	-1.1
16188	AT5G23180.1 | hypothetical protein | chr5:7801477-7801893 FORWARD | Aliases: MKD15.4, MKD15_4	2.5	2.6	-0.1	-0.9	98.7%	-1.8
16189	AT2G04000.1 | expressed protein | chr2:1267759-1268334 REVERSE | Aliases: F3C11.11, F3C11_11	2.8	2.7	0.1	0.9	98.8%	-1.4
16190	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	2.3	-0.1	-0.9	98.8%	-2.4
16191	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	5.5	-0.4	-0.9	98.8%	-1.3
16192	AT2G45460.1 | forkhead-associated domain-containing protein / FHA domain-containing protein | chr2:18743913-18748764 REVERSE | Aliases: F4L23.3	4.9	4.7	0.3	0.9	98.8%	-0.9
16193	AT4G18570.1 | proline-rich family protein, common family members: At3g25690, At4g04980, At5g61090 (Arabidopsis thaliana) | chr4:10231229-10234704 FORWARD | Aliases: F28J12.8	3.8	3.6	0.1	0.9	98.8%	-1.3
16194	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	2.5	-0.1	-0.9	98.8%	-1.8
16195	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	2.5	-0.1	-0.9	98.8%	-1.8
16196	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	5.1	5.2	-0.2	-0.9	98.9%	-1.3
16197	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	2.2	-0.1	-0.9	98.9%	-1.9
16198	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	3.0	3.0	0.1	0.9	98.9%	-2.0
16199	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	-0.9	98.9%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
16200	AT5G15420.1 | expressed protein | chr5:5007829-5008967 REVERSE | Aliases: T20K14.30, T20K14_30	2.2	2.3	-0.1	-0.9	98.9%	-1.9
16201	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	3.4	-0.2	-0.9	99.0%	-1.4
16202	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	2.9	-0.2	-0.9	99.0%	-1.5
16203	AT3G48720.1 | transferase family protein, similar to hypersensitivity-related hsr201 protein - Nicotiana tabacum,PIR2:T03274; contains Pfam transferase family domain PF00248 | chr3:18057308-18060437 FORWARD | Aliases: T8P19.230	3.2	3.1	0.1	0.9	99.0%	-1.4
16204	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	2.6	2.7	-0.1	-0.9	99.0%	-1.8
16205	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	9.6	9.8	-0.2	-0.9	99.0%	-1.7
16206	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	2.4	-0.1	-0.9	99.0%	-2.0
16207	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	4.3	4.0	0.2	0.9	99.0%	-1.3
16208	AT5G23380.1 | expressed protein | chr5:7866745-7870135 FORWARD | Aliases: T32G24.1, T32G24_1	3.8	3.7	0.1	0.9	99.1%	-1.4
16209	AT4G35990.1 | expressed protein | chr4:17036349-17036826 FORWARD | Aliases: T19K4.120, T19K4_120	3.1	3.2	-0.1	-0.9	99.1%	-1.5
16210	AT5G11410.1 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr5:3638432-3639884 REVERSE | Aliases: F15N18.1	2.3	2.2	0.1	0.9	99.2%	-2.0
16211	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	3.0	-0.2	-0.9	99.2%	-1.2
16212	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	0.1	0.9	99.2%	-1.6
16213	AT3G62400.2 | expressed protein, cytochrome c oxidase subunit 5c - Oryza sativa, EMBL:AB027123	11.3	11.1	0.2	0.9	99.2%	-1.7
16214	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	4.2	0.2	0.9	99.2%	-1.4
16215	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	2.5	-0.1	-0.9	99.2%	-1.6
16216	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	0.9	99.2%	-1.4
16217	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	4.6	4.8	-0.2	-0.9	99.2%	-1.1
16218	AT4G22560.1 | expressed protein | chr4:11880189-11880983 FORWARD | Aliases: F7K2.140, F7K2_140	4.9	4.6	0.3	0.9	99.3%	-0.9
16219	AT3G07010.1 | pectate lyase family protein, similar to pectate lyase GP:14531296 from (Fragaria x ananassa) | chr3:2212734-2216489 REVERSE | Aliases: F17A9.16	4.0	3.8	0.3	0.9	99.3%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
16220	AT3G22070.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr3:7775336-7776116 REVERSE | Aliases: MZN24.27	2.9	2.8	0.1	0.9	99.3%	-1.4
16221	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.	6.2	6.7	-0.5	-0.9	99.3%	-1.0
16222	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	7.1	-0.2	-0.9	99.3%	-1.0
16223	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	7.3	-0.4	-0.9	99.3%	-1.0
16224	AT1G73650.3 | expressed protein | chr1:27691784-27693968 REVERSE | Aliases: F25P22.7, F25P22_7	7.0	7.6	-0.6	-0.9	99.3%	-0.8
16225	AT5G12000.1 | similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At4g31230.1); similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At1g16760.1); similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At1g78940.1); similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At2g24370.1); similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At5g26150.1); similar to putative serine threonine kinase [Oryza sativa (japonica cultivar-group)] (GB:XP_468172.1); similar to serine threonine kinase [Zea mays] (GB:AAL59227.1); similar to serine threonine kinase 1 [Zea mays] (GB:AAK73111.1); similar to serine threonine kinase 1-like [Oryza sativa (japonica cultivar-group)] (GB:BAD53152.1); similar to putative serine threonine kinase [Oryza sativa (japonica 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	2.7	-0.1	-0.9	99.3%	-1.8
16226	AT1G69890.1 | expressed protein, contains Pfam profile: PF04601 protein of unknown function (DUF569 | chr1:26326774-26328267 REVERSE | Aliases: T17F3.8, T17F3_8	3.4	3.2	0.2	0.9	99.3%	-1.1
16227	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	2.3	-0.1	-0.9	99.4%	-2.1
16228	AT2G05270.1 | expressed protein | chr2:1920699-1921113 REVERSE | Aliases: F5G3.17, F5G3_17	2.9	3.1	-0.2	-0.9	99.4%	-1.7
16229	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	3.3	3.5	-0.2	-0.9	99.4%	-1.5
16230	AT5G39880.1 | expressed protein | chr5:15988115-15989465 FORWARD | Aliases: MYH19.7, MYH19_7	2.5	2.6	-0.1	-0.9	99.4%	-1.9
16231	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	7.1	7.3	-0.3	-0.9	99.4%	-1.0
16232	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	3.1	3.1	0.1	0.9	99.4%	-1.7
16233	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)	4.6	4.5	0.1	0.9	99.4%	-1.3
16234	AT1G69350.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535: PPR repeat | chr1:26073545-26075908 FORWARD | Aliases: F10D13.4, F10D13_4	2.9	2.7	0.1	0.9	99.4%	-1.5
16235	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	7.1	6.9	0.2	0.9	99.5%	-1.3
16236	AT5G17270.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain | chr5:5679997-5685599 FORWARD | Aliases: MKP11.12, MKP11_12	4.7	4.4	0.3	0.9	99.5%	-0.9
16237	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	2.9	3.1	-0.1	-0.9	99.5%	-1.5
16238	AT1G34640.1 | expressed protein | chr1:12687208-12688488 REVERSE | Aliases: F12K21.2	4.0	3.8	0.1	0.9	99.6%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
16239	AT4G17480.1 | palmitoyl protein thioesterase family protein | chr4:9745018-9746978 REVERSE | Aliases: DL4775C, FCAALL.380	3.7	3.8	-0.2	-0.9	99.6%	-1.2
16240	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	3.4	-0.1	-0.9	99.7%	-1.6
16241	NA	2.7	2.8	-0.1	-0.9	99.7%	-1.6
16242	AT2G45810.1 | DEAD/DEAH box helicase, putative	4.2	3.8	0.4	0.9	99.7%	-1.1
16243	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	-0.1	-0.9	99.7%	-2.2
16244	AT1G19080.1 | Symbol: TTN10 | expressed protein | chr1:6584257-6586426 FORWARD | Aliases: F14D16.33, TITAN 10	7.3	7.5	-0.3	-0.9	99.7%	-1.0
16245	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	3.5	3.6	-0.1	-0.9	99.7%	-1.7
16246	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	3.1	-0.1	-0.9	99.7%	-2.1
16247	AT5G32600.1 | expressed protein | chr5:12266929-12268873 REVERSE | Aliases: F3D18.1	2.8	3.0	-0.2	-0.9	99.7%	-1.3
16248	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	4.9	4.5	0.4	0.9	99.7%	-1.0
16249	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	4.8	4.5	0.2	0.9	99.7%	-1.3
16250	AT5G65570.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr5:26221194-26223410 FORWARD | Aliases: K21L13.8, K21L13_8	3.1	3.0	0.1	0.9	99.7%	-1.7
16251	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	-0.9	99.8%	-1.9
16252	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	3.1	3.2	-0.1	-0.9	99.8%	-1.5
16253	AT2G30940.2 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:13175610-13177264 FORWARD | Aliases: F7F1.15, F7F1_15	3.4	3.6	-0.2	-0.9	99.8%	-1.2
16254	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	2.8	-0.1	-0.9	99.8%	-1.4
16255	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	2.5	-0.2	-0.9	99.8%	-1.9
16256	AT3G61840.1 | expressed protein | chr3:22903456-22904244 FORWARD | Aliases: F21F14.10	2.5	2.6	-0.1	-0.9	99.8%	-2.0
16257	AT5G08090.1 | hypothetical protein | chr5:2591712-2592900 FORWARD | Aliases: T22D6.30, T22D6_30	3.5	3.7	-0.2	-0.9	99.8%	-1.3
16258	AT1G67780.1 | hypothetical protein | chr1:25416479-25419193 FORWARD | Aliases: F12A21.9, F12A21_9	2.7	2.7	-0.1	-0.9	99.8%	-2.2
16259	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	4.5	4.8	-0.2	-0.9	99.8%	-1.1
16260	AT4G09850.1 | expressed protein, ; expression supported by MPSS | chr4:6192509-6193127 FORWARD | Aliases: F17A8.200, F17A8_200	2.5	2.7	-0.2	-0.9	99.8%	-1.8
16261	AT2G32340.1 | TraB family protein, contains Pfam domain PF01963: TraB family | chr2:13739324-13741611 FORWARD | Aliases: T32F6.14, T32F6_14	5.3	5.6	-0.3	-0.9	99.8%	-1.1
16262	AT2G22890.1 | expressed protein, ; expression supported by MPSS | chr2:9749580-9750419 REVERSE | Aliases: T20K9.10, T20K9_10	3.5	3.3	0.2	0.9	99.8%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
16263	AT4G07460.1 | hypothetical protein | chr4:4257794-4259250 FORWARD | Aliases: F28D6.2, F28D6_2	2.3	2.4	-0.1	-0.9	99.9%	-2.0
16264	AT1G02910.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain | chr1:655577-658148 REVERSE | Aliases: F22D16.9, F22D16_9	5.3	5.5	-0.2	-0.9	99.9%	-1.1
16265	AT4G26480.1 | KH domain-containing protein, qkI-7, Mus musculus | chr4:13372893-13378398 REVERSE | Aliases: M3E9.90, M3E9_90	6.2	6.8	-0.6	-0.9	99.9%	-0.7
16266	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	2.3	2.2	0.1	0.9	99.9%	-2.2
16267	AT1G77910.1 | expressed protein, contains similarity to NADH dehydrogenase subunit 1 | chr1:29301032-29301301 FORWARD | Aliases: F28K19.12, F28K19_12	2.3	2.4	-0.1	-0.9	99.9%	-2.1
16268	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	8.8	0.2	0.9	99.9%	-1.7
16269	AT3G24790.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:9052989-9054538 FORWARD | Aliases: K7P8.12	2.7	2.8	-0.1	-0.9	99.9%	-1.9
16270	AT2G20250.1 | expressed protein | chr2:8741130-8743497 REVERSE | Aliases: F11A3.20, F11A3_20	2.2	2.3	-0.1	-0.9	99.9%	-2.0
16271	AT2G14250.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr2:6044056-6045463 FORWARD | Aliases: T1O16.16, T1O16_16	3.2	3.4	-0.2	-0.9	99.9%	-0.8
16272	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	2.4	0.1	0.9	99.9%	-1.6
16273	AT1G21020.1 | expressed protein, similar to At3g26530, At1g08760, At1g08740, At2g29240, At1g35650 | chr1:7353529-7356589 FORWARD | Aliases: T22I11.15, T22I11_15	2.5	2.4	0.1	0.9	99.9%	-1.6
16274	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	2.4	0.1	0.9	99.9%	-1.6
16275	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	2.4	0.1	0.9	99.9%	-1.6
16276	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	2.4	0.1	0.9	99.9%	-1.6
16277	AT1G75870.1 | expressed protein | chr1:28490193-28490775 FORWARD | Aliases: T4O12.11, T4O12_11	2.7	2.8	-0.1	-0.9	99.9%	-1.9
16278	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	5.0	4.8	0.2	0.9	100.0%	-1.3
16279	AT5G48150.2 | Symbol: PAT1 | phytochrome A signal transduction 1 (PAT1) | chr5:19539485-19541834 REVERSE | Aliases: MIF21.4, MIF21_4, PHYTOCHROME A SIGNAL TRANSDUCTION 1	6.5	6.8	-0.4	-0.9	100.0%	-0.9
16280	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	2.9	3.0	-0.1	-0.9	100.0%	-1.8
16281	AT2G21110.1 | disease resistance-responsive family protein, similar to disease resistance response protein 206-d (Pisum sativum) gi:508844:gb:AAB18669	3.1	3.2	-0.1	-0.9	100.0%	-1.6
16282	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	2.0	2.1	-0.1	-0.9	100.0%	-2.2
16283	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	3.8	-0.2	-0.9	100.0%	-1.5
16284	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	3.0	-0.1	-0.9	100.0%	-1.5
16285	AT2G47290.1 | hypothetical protein | chr2:19425803-19426470 FORWARD | Aliases: T8I13.13	3.1	3.2	-0.2	-0.9	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
16286	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	3.8	4.1	-0.3	-0.9	100.0%	-1.1
16287	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	6.8	6.6	0.2	0.9	100.0%	-1.4
16288	AT5G16110.1 | expressed protein, hypothetical protein T26J14.6 - Arabidopsis thaliana, EMBL:AC011915 | chr5:5260607-5262843 REVERSE | Aliases: T21H19.30, T21H19_30	5.2	5.5	-0.4	-0.9	100.0%	-1.0
16289	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	5.3	5.0	0.3	0.9	100.0%	-1.0
16290	AT3G26550.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	2.8	-0.2	-0.9	100.0%	-1.7
16291	AT1G48095.1 | expressed protein | chr1:17763811-17765667 FORWARD | Aliases: F21D18.19, F21D18_19	2.6	2.8	-0.1	-0.9	100.0%	-1.4
16292	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	-0.9	100.0%	-1.8
16293	AT1G49810.1 | Symbol: ATNHD2 |	4.2	4.4	-0.2	-0.9	100.0%	-1.3
16294	AT3G60780.1 | expressed protein | chr3:22473632-22474760 FORWARD | Aliases: T4C21.190	2.6	2.7	-0.1	-0.9	100.0%	-1.5
16295	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	3.0	-0.1	-0.9	100.0%	-1.5
16296	AT5G40460.1 | expressed protein | chr5:16219475-16220160 FORWARD | Aliases: K21I16.3, K21I16_3	3.5	3.7	-0.3	-0.9	100.0%	-1.0
16297	AT1G30250.1 | expressed protein | chr1:10646971-10647495 REVERSE | Aliases: F12P21.5, F12P21_5	3.5	3.7	-0.2	-0.9	100.0%	-1.1
16298	AT3G52760.1 | integral membrane Yip1 family protein, contains Pfam domain, PF04893: Yip1 domain | chr3:19564657-19565790 REVERSE | Aliases: F3C22.160	5.9	6.0	-0.1	-0.9	100.0%	-1.3
16299	AT1G35730.1 | pumilio/Puf RNA-binding domain-containing protein | chr1:13228536-13231008 REVERSE | Aliases: F14D7.3, F14D7_3	2.5	2.6	-0.1	-0.9	100.0%	-1.7
16300	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	2.5	2.7	-0.1	-0.9	100.0%	-1.7
16301	AT3G44820.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr3:16372851-16375396 REVERSE | Aliases: F28D10.10	3.2	3.1	0.1	0.9	100.0%	-1.8
16302	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	2.7	2.9	-0.1	-0.9	100.0%	-1.5
16303	AT3G27130.1 | expressed protein | chr3:10003896-10005518 REVERSE | Aliases: MOJ10.23	3.1	3.2	-0.1	-0.9	100.0%	-1.7
16304	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	-0.1	-0.9	100.0%	-1.8
16305	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	3.6	-0.1	-0.9	100.0%	-1.2
16306	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	3.1	-0.1	-0.9	100.0%	-1.4
16307	AT5G60440.1 | MADS-box protein (AGL62), contains Pfal profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain) | chr5:24323555-24324746 FORWARD | Aliases: MUF9.24, MUF9_24	3.0	3.1	-0.1	-0.9	100.0%	-1.6
16308	AT5G51090.1 | expressed protein | chr5:20789463-20790420 REVERSE | Aliases: MWD22.3, MWD22_3	2.3	2.4	-0.1	-0.9	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
16309	AT1G29860.1 | Symbol: WRKY71 |	3.2	3.3	-0.1	-0.9	100.0%	-1.3
16310	AT1G60500.1 | dynamin family protein, similar to RBTMx2 (Oncorhynchus mykiss) 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	2.8	-0.1	-0.9	100.0%	-1.9
16311	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	3.7	3.9	-0.2	-0.9	100.0%	-1.6
16312	AT5G39400.1 | pollen specific phosphatase, putative / phosphatase and tensin, putative (PTEN1), identical to phosphatase and tensin homolog (Arabidopsis thaliana) GI:21535746	2.4	2.5	-0.1	-0.9	100.0%	-2.0
16313	AT2G24762.1 | expressed protein | chr2:10566463-10567213 FORWARD | Aliases: None	4.6	4.8	-0.2	-0.9	100.0%	-1.1
16314	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	5.7	5.4	0.3	0.9	100.0%	-0.6
16315	AT3G13710.1 | prenylated rab acceptor (PRA1) family protein, weak similarity to prenylated Rab acceptor (Mus musculus) GI:7716652; contains Pfam profile PF03208: Prenylated rab acceptor (PRA1) | chr3:4490635-4493838 REVERSE | Aliases: MMM17.13	5.7	5.4	0.3	0.9	100.0%	-0.6
16316	AT3G02910.1 | expressed protein, contains Pfam domain PF03674: Uncharacterised protein family (UPF0131) | chr3:649821-650928 FORWARD | Aliases: F13E7.14, F13E7_14	8.8	9.4	-0.6	-0.9	100.0%	-0.9
16317	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	4.9	5.1	-0.2	-0.9	100.0%	-1.2
16318	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	10.6	10.7	-0.2	-0.9	100.0%	-1.1
16319	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	3.2	-0.1	-0.9	100.0%	-1.5
16320	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	3.8	-0.2	-0.9	100.0%	-1.1
16321	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	3.1	3.3	-0.1	-0.9	100.0%	-1.7
16322	AT4G17410.1 | expressed protein | chr4:9717226-9721937 FORWARD | Aliases: DL4740W, FCAALL.426	2.8	2.7	0.1	0.9	100.0%	-1.5
16323	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	3.7	0.2	0.9	100.0%	-1.1
16324	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	4.6	4.4	0.2	0.9	100.0%	-1.2
16325	AT3G32090.1 | transcription factor-related, contains weak similarity to WIZZ (Nicotiana tabacum) gi:6472585:dbj:BAA87058 | chr3:13082669-13083634 FORWARD | Aliases: F1M23.9	3.3	3.4	-0.1	-0.9	100.0%	-1.5
16326	AT3G18570.1 | glycine-rich protein / oleosin, contains similarity to Pfam profile: PF01277 Oleosin | chr3:6395866-6396612 REVERSE | Aliases: K24M9.6	2.7	2.9	-0.1	-0.9	100.0%	-1.6
16327	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	3.2	-0.1	-0.9	100.0%	-1.3
16328	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	3.2	3.4	-0.2	-0.9	100.0%	-1.5
16329	AT1G19710.1 | glycosyl transferase family 1 protein, contains Pfam profile: PF00534 glycosyl transferases group 1 | chr1:6814828-6816707 FORWARD | Aliases: F14P1.19, F14P1_19	6.5	6.3	0.2	0.9	100.0%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
16330	AT1G10880.1 | expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266 | chr1:3624035-3627082 REVERSE | Aliases: T19D16.28, T19D16_28	2.7	2.8	-0.1	-0.9	100.0%	-1.7
16331	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	3.2	3.4	-0.2	-0.9	100.0%	-1.0
16332	AT1G21010.1 | expressed protein | chr1:7346145-7346957 FORWARD | Aliases: F9H16.19, F9H16_19	4.0	4.1	-0.1	-0.9	100.0%	-1.5
16333	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	2.7	2.8	-0.1	-0.9	100.0%	-1.5
16334	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	3.6	0.2	0.9	100.0%	-0.9
16335	AT1G07290.1 | nucleotide-sugar transporter family protein, similar to SP:Q941R4 GDP-mannose transporter {Arabidopsis thaliana}	4.0	4.2	-0.2	-0.9	100.0%	-1.2
16336	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	5.5	5.7	-0.2	-0.9	100.0%	-1.2
16337	AT1G27200.1 | expressed protein, contains Pfam PF01697: Domain of unknown function | chr1:9449536-9451737 REVERSE | Aliases: T7N9.26, T7N9_26	3.4	3.5	-0.1	-0.9	100.0%	-1.6
16338	AT5G39430.1 | expressed protein | chr5:15792530-15794827 REVERSE | Aliases: MUL8.11, MUL8_11	2.7	2.8	-0.1	-0.9	100.0%	-1.8
16339	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	2.4	0.1	0.9	100.0%	-1.7
16340	AT1G53420.1 | serine/threonine protein kinase-related, contains 1 predicted transmembrane domain; low similarity to receptor-like serine/threonine kinase (Arabidopsis thaliana) GI:2465923 | chr1:19930294-19935162 REVERSE | Aliases: F12M16.30	2.3	2.2	0.1	0.9	100.0%	-2.2
16341	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	7.7	7.3	0.4	0.9	100.0%	-1.1
16342	AT2G15420.1 | myosin heavy chain-related | chr2:6731030-6735265 REVERSE | Aliases: F26H6.6, F26H6_6	2.9	3.0	-0.1	-0.9	100.0%	-1.5
16343	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	8.1	8.4	-0.3	-0.9	100.0%	-1.3
16344	AT5G39930.1 | expressed protein, ; expression supported by MPSS | chr5:16002477-16004468 REVERSE | Aliases: MYH19.90, MYH19_90	2.6	2.7	-0.1	-0.9	100.0%	-1.8
16345	AT4G04630.1 | expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584 | chr4:2331675-2332798 REVERSE | Aliases: F4H6.15, F4H6_15	3.0	3.2	-0.1	-0.9	100.0%	-1.6
16346	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	6.4	5.8	0.6	0.9	100.0%	-0.5
16347	AT5G06540.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:1999182-2001050 REVERSE | Aliases: F15M7.7, F15M7_7	3.2	3.0	0.2	0.9	100.0%	-1.5
16348	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	6.1	0.2	0.9	100.0%	-1.1
16349	AT5G63960.1 | DNA-directed DNA polymerase delta catalytic subunit, putative (POLD1), similar to DNA polymerase delta (Glycine max) GI:2895198, OsPol delta large subunit (Oryza sativa (japonica cultivar-group) GI:9188570; contains Pfam profiles: PF03175 DNA polymerase type B, organellar and viral, PF00136 DNA polymerase family B, PF03104 DNA polymerase family B, exonuclease domain	4.4	4.2	0.2	0.9	100.0%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
16350	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	-0.1	-0.9	100.0%	-1.8
16351	AT3G04480.1 | endoribonuclease L-PSP family protein, contains Pfam domain PF01902: Domain of unknown function | chr3:1193636-1197403 REVERSE | Aliases: T27C4.13, T27C4_13	5.3	5.5	-0.2	-0.9	100.0%	-1.1
16352	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	5.8	0.3	0.9	100.0%	-1.2
16353	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 (kdotransferase) | chr5:995159-997847 FORWARD | Aliases: F17C15.190, F17C15_190	4.9	4.7	0.2	0.9	100.0%	-1.2
16354	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	3.1	3.3	-0.2	-0.9	100.0%	-1.5
16355	AT1G30515.1 | expressed protein | chr1:10809271-10809897 REVERSE | Aliases: None	3.0	3.1	-0.1	-0.9	100.0%	-1.4
16356	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	5.9	-0.2	-0.9	100.0%	-1.2
16357	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	2.9	0.2	0.9	100.0%	-1.4
16358	AT4G17940.1 | expressed protein | chr4:9965754-9966978 FORWARD | Aliases: T6K21.120, T6K21_120	9.1	8.7	0.3	0.9	100.0%	-1.5
16359	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	2.8	-0.1	-0.9	100.0%	-1.6
16360	AT5G12280.1 | expressed protein | chr5:3972015-3973637 REVERSE | Aliases: None	3.0	3.1	-0.1	-0.9	100.0%	-1.6
16361	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	3.3	-0.1	-0.9	100.0%	-1.3
16362	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	3.8	3.9	-0.2	-0.9	100.0%	-1.3
16363	AT5G59080.1 | expressed protein | chr5:23864634-23865721 REVERSE | Aliases: K18B18.8, K18B18_8	3.3	3.4	-0.1	-0.9	100.0%	-1.7
16364	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	6.4	6.6	-0.3	-0.9	100.0%	-1.0
16365	AT1G09620.1 | similar to leucyl-tRNA synthetase, putative / leucine--tRNA ligase, putative [Arabidopsis thaliana] (TAIR:At4g04350.1); similar to leucyl tRNA synthetase [Homo sapiens] (GB:BAA95667.1); similar to SYLC_HUMAN Leucyl-tRNA synthetase, cytoplasmic (Leucine--tRNA ligase) (LeuRS) (GB:Q9P2J5); similar to KIAA1352 protein [Homo sapiens] (GB:BAA92590.1); similar to MGC82093 protein [Xenopus laevis] (GB:AAH79713.1); similar to PREDICTED: similar to Leucyl-tRNA synthetase, cytoplasmic (Leucine--tRNA ligase) (LeuRS) [Canis familiaris] (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	5.6	5.3	0.3	0.9	100.0%	-1.1
16366	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	-0.9	100.0%	-1.7
16367	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	5.7	5.5	0.2	0.9	100.0%	-1.2
16368	AT3G22231.1 | Symbol: PCC1 | expressed protein | chr3:7845879-7846612 REVERSE | Aliases: PATHOGEN AND CIRCADIAN CONTROLLED 1	3.0	3.2	-0.1	-0.9	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
16369	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	12.1	12.4	-0.2	-0.9	100.0%	-1.6
16370	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	7.9	8.4	-0.5	-0.9	100.0%	-0.9
16371	AT5G38400.1 | expressed protein | chr5:15393076-15393531 FORWARD | Aliases: MXI10.12, MXI10_12	3.8	3.9	-0.1	-0.9	100.0%	-1.3
16372	AT4G24890.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	2.3	2.3	0.1	0.9	100.0%	-1.9
16373	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	3.3	3.6	-0.3	-0.9	100.0%	-1.0
16374	AT5G20310.1 | expressed protein | chr5:6857555-6859003 FORWARD | Aliases: F5O24.200, F5O24_200	3.0	3.2	-0.2	-0.9	100.0%	-1.4
16375	AT3G27420.1 | expressed protein | chr3:10149824-10151538 FORWARD | Aliases: K1G2.14	4.2	4.5	-0.3	-0.9	100.0%	-1.0
16376	AT2G02470.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr2:652579-654914 FORWARD | Aliases: T16F16.26, T16F16_26	7.1	7.5	-0.4	-0.9	100.0%	-1.0
16377	AT5G10860.1 | CBS domain-containing protein, contains Pfam profile PF00571: CBS domain	9.2	9.8	-0.7	-0.9	100.0%	-0.7
16378	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	5.9	6.1	-0.2	-0.9	100.0%	-0.9
16379	AT2G33270.1 | thioredoxin family protein, contains Pfam profile: PF00085 Thioredoxin | chr2:14110758-14112281 FORWARD | Aliases: F4P9.4, F4P9_4	2.9	3.1	-0.2	-0.9	100.0%	-1.3
16380	AT2G32190.1 | expressed protein | chr2:13681594-13682362 FORWARD | Aliases: F22D22.6, F22D22_6	2.1	2.0	0.1	0.9	100.0%	-2.4
16381	AT4G01026.1 | expressed protein | chr4:447090-448510 FORWARD | Aliases: None	5.2	5.0	0.2	0.9	100.0%	-1.0
16382	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	3.2	-0.1	-0.9	100.0%	-1.9
16383	AT2G28370.1 | expressed protein, contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana) | chr2:12138651-12140776 FORWARD | Aliases: T1B3.11, T1B3_11	5.2	5.7	-0.5	-0.9	100.0%	-0.9
16384	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	-0.9	100.0%	-1.6
16385	AT2G22760.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.4	2.5	-0.1	-0.9	100.0%	-1.7
16386	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	4.2	4.0	0.2	0.9	100.0%	-1.2
16387	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	6.4	6.7	-0.3	-0.9	100.0%	-1.2
16388	AT1G22490.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.3	3.1	0.1	0.9	100.0%	-1.5
16389	AT5G27810.1 | expressed protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana) | chr5:9855831-9856190 FORWARD | Aliases: T1G16.140, T1G16_140	2.6	2.7	-0.1	-0.9	100.0%	-1.9
16390	AT4G39440.1 | expressed protein, ; expression supported by MPSS | chr4:18345679-18347221 FORWARD | Aliases: F23K16.70, F23K16_70	3.2	3.3	-0.1	-0.9	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
16391	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	2.8	0.1	0.9	100.0%	-1.7
16392	AT3G32150.1 | hypothetical protein | chr3:13147340-13148538 FORWARD | Aliases: F1M23.27	2.4	2.4	-0.1	-0.9	100.0%	-2.0
16393	AT3G32130.1 | hypothetical protein | chr3:13131192-13131878 FORWARD | Aliases: F1M23.22	2.4	2.4	-0.1	-0.9	100.0%	-2.2
16394	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	5.8	6.0	-0.1	-0.9	100.0%	-1.3
16395	AT3G57510.1 | Symbol: ADPG1 | endo-polygalacturonase (ADPG1), identical to endo-polygalacturonase (Arabidopsis thaliana) GI:2597824 | chr3:21294315-21296918 REVERSE | Aliases: T8H10.110	3.4	3.5	-0.1	-0.9	100.0%	-1.5
16396	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	2.6	-0.1	-0.9	100.0%	-2.1
16397	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	2.6	-0.0	-0.9	100.0%	-2.5
16398	AT3G04880.1 | Symbol: DRT102 |	6.4	6.2	0.2	0.9	100.0%	-1.1
16399	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	2.9	-0.1	-0.9	100.0%	-1.8
16400	AT2G07280.1 | expressed protein | chr2:3026395-3029071 FORWARD | Aliases: T13E11.5, T13E11_5	2.2	2.3	-0.1	-0.9	100.0%	-2.3
16401	AT3G50540.1 | hypothetical protein | chr3:18768730-18769121 FORWARD | Aliases: T20E23.140	5.7	6.0	-0.3	-0.9	100.0%	-1.1
16402	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	5.6	5.5	0.2	0.9	100.0%	-1.5
16403	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	2.7	-0.1	-0.9	100.0%	-1.8
16404	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	2.9	-0.1	-0.9	100.0%	-1.5
16405	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	-0.9	100.0%	-1.7
16406	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	2.2	0.1	0.9	100.0%	-1.9
16407	AT1G54420.1 | expressed protein | chr1:20315286-20316085 FORWARD | Aliases: F20D21.41, F20D21_41	2.3	2.4	-0.1	-0.9	100.0%	-1.7
16408	AT2G16460.2 | expressed protein | chr2:7140559-7142734 REVERSE | Aliases: F16F14.4, F16F14_4	5.7	5.6	0.1	0.9	100.0%	-1.4
16409	AT4G01370.1 | Symbol: ATMPK4 |	9.3	9.0	0.3	0.9	100.0%	-1.0
16410	AT1G31770.1 | ABC transporter family protein, contains Pfam profile: PF00005: ABC transporter | chr1:11374874-11377775 REVERSE | Aliases: F5M6.22	6.4	6.1	0.4	0.9	100.0%	-0.9
16411	AT3G09790.1 | Symbol: UBQ8 | polyubiquitin (UBQ8), identical to polyubiquitin (ubq8) GI:870793, GB:L05917 (Arabidopsis thaliana) (Genetics 139 (2), 921-939 (1995)) | chr3:3003867-3006197 REVERSE | Aliases: F11F8.38	2.7	2.8	-0.1	-0.9	100.0%	-1.7
16412	AT4G31340.2 | similar to DNA repair ATPase-related [Arabidopsis thaliana] (TAIR:At2g24420.2); similar to DNA repair ATPase-related [Arabidopsis thaliana] (TAIR:At2g24420.1); similar to unknown [Oryza sativa (japonica cultivar-group)] (GB:AAO72581.1) | chr4:15205486-15209607 FORWARD | Aliases: F8F16.160, F8F16_160	7.4	6.9	0.5	0.9	100.0%	-1.1
16413	AT3G17360.1 | kinesin motor protein-related, similar to KLP2 protein GB:CAA63826 from (Xenopus laevis)	2.3	2.3	-0.1	-0.9	100.0%	-2.3

Rank	Description	Sync	Root	M	t	adj.q	B
16414	AT5G15150.1 | Symbol: ATHB 3 |	2.4	2.4	-0.1	-0.9	100.0%	-2.2
16415	AT1G62070.1 | expressed protein | chr1:22947259-22947954 FORWARD | Aliases: F19K23.2, F19K23_2	3.3	3.4	-0.1	-0.9	100.0%	-1.5
16416	AT3G20920.2 | similar to translocation protein sec62, putative [Plasmodium berghei] (GB:CAH98034.1); contains InterPro domain Translocation protein Sec62 (InterPro:IPR004728)	8.2	7.9	0.3	0.9	100.0%	-1.2
16417	AT3G43770.1 | expressed protein | chr3:15661574-15661987 REVERSE | Aliases: T28A8.60	2.8	2.9	-0.1	-0.9	100.0%	-1.8
16418	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	3.8	3.7	0.1	0.9	100.0%	-1.5
16419	AT3G46670.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:17203574-17205382 REVERSE | Aliases: F12A12.190	3.3	3.4	-0.2	-0.9	100.0%	-1.5
16420	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	3.2	0.1	0.9	100.0%	-1.4
16421	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	9.3	8.9	0.3	0.9	100.0%	-1.2
16422	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	5.9	5.7	0.2	0.9	100.0%	-1.2
16423	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	3.5	3.7	-0.2	-0.9	100.0%	-1.3
16424	AT2G11830.1 | expressed protein | chr2:4778947-4780327 REVERSE | Aliases: F7E22.2, F7E22_2	3.4	3.6	-0.1	-0.9	100.0%	-1.6
16425	AT3G18100.2 | Symbol: MYB4R1 |	3.4	3.7	-0.3	-0.9	100.0%	-1.5
16426	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	2.7	2.9	-0.2	-0.9	100.0%	-1.6
16427	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	4.9	4.7	0.2	0.9	100.0%	-1.2
16428	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	3.5	-0.1	-0.9	100.0%	-1.5
16429	AT3G27880.1 | expressed protein | chr3:10339449-10340673 FORWARD | Aliases: K16N12.10	5.2	5.4	-0.3	-0.9	100.0%	-1.0
16430	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	5.8	5.6	0.2	0.9	100.0%	-1.3
16431	AT1G20670.1 | DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487 | chr1:7164527-7167923 REVERSE | Aliases: F2D10.15, F2D10_15	3.7	3.9	-0.2	-0.9	100.0%	-1.1
16432	AT5G62860.1 | F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain | chr5:25249858-25251793 FORWARD | Aliases: MQB2.19, MQB2_19	3.3	3.2	0.1	0.9	100.0%	-1.3
16433	AT5G18850.1 | expressed protein | chr5:6286862-6287592 FORWARD | Aliases: F17K4.100, F17K4_100	6.6	6.7	-0.2	-0.9	100.0%	-1.2
16434	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	6.1	5.5	0.6	0.9	100.0%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
16435	AT5G35490.1 | expressed protein (MRU1), contains Pfam domain, PF04827: Protein of unknown function (DUF635) | chr5:13707047-13707778 FORWARD | Aliases: MOK9.8, MOK9_8	3.3	3.5	-0.2	-0.9	100.0%	-1.3
16436	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	2.7	-0.1	-0.9	100.0%	-1.7
16437	AT2G41430.4 | Symbol: ERD15 | dehydration-induced protein (ERD15), identical to dehydration-induced protein ERD15 GI:710626 from (Arabidopsis thaliana) | chr2:17276388-17277620 FORWARD | Aliases: CID1, DEHYDRATION INDUCED PROTEIN, EARLY RESPONSIVE TO DEHYDRATION 15, LIGHT STRESS REGULATED 1, LSR1, T26J13.2	11.3	11.5	-0.2	-0.9	100.0%	-1.1
16438	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	3.5	3.4	0.1	0.9	100.0%	-1.4
16439	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	3.2	-0.1	-0.9	100.0%	-1.4
16440	AT3G52690.1 | hypothetical protein, predicted proteins, Arabidopsis thaliana | chr3:19541714-19542789 FORWARD | Aliases: F3C22.90	3.6	3.7	-0.1	-0.9	100.0%	-1.6
16441	AT1G16680.1 | DNAJ heat shock N-terminal domain-containing protein / S-locus protein, putative, similar to S-locus protein 5 GI:6069485 from (Brassica rapa); contains Pfam profile PF00226 DnaJ domain | chr1:5702806-5705831 FORWARD | Aliases: F19K19.3, F19K19_3	5.7	5.5	0.2	0.9	100.0%	-1.0
16442	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	0.1	0.9	100.0%	-2.2
16443	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	5.8	6.1	-0.3	-0.9	100.0%	-1.1
16444	AT3G21800.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:7680113-7681692 REVERSE | Aliases: MSD21.16	4.1	4.3	-0.1	-0.9	100.0%	-1.5
16445	AT3G08600.1 | expressed protein | chr3:2612400-2613829 FORWARD | Aliases: F17O14.7	4.7	4.9	-0.2	-0.9	100.0%	-1.0
16446	AT5G27890.1 | expressed protein | chr5:9903644-9905918 FORWARD | Aliases: F14I23.50, F14I23_50	4.0	3.8	0.2	0.9	100.0%	-1.1
16447	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	6.2	5.9	0.3	0.9	100.0%	-1.1
16448	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	7.6	7.9	-0.4	-0.9	100.0%	-1.2
16449	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	6.7	6.9	-0.2	-0.9	100.0%	-1.3
16450	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	3.8	3.6	0.2	0.9	100.0%	-1.4
16451	AT3G58330.1 | expressed protein | chr3:21598339-21598979 REVERSE | Aliases: F9D24.240	3.3	3.4	-0.1	-0.9	100.0%	-1.6
16452	AT4G25510.1 | hypothetical protein | chr4:13027453-13028046 REVERSE | Aliases: T30C3.8	2.5	2.5	-0.1	-0.9	100.0%	-2.1
16453	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	3.5	0.1	0.9	100.0%	-1.2
16454	AT2G23260.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:9907009-9908519 REVERSE | Aliases: T20D16.11, T20D16_11	2.9	3.0	-0.1	-0.9	100.0%	-1.6
16455	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, HOMEOBOX PROTEIN SHOOTMERISTEMLESS, SHL, SHOOT MERISTEMLESS, SHOOTLESS, SHOOTMERISTEMLESS, STM, WALDMEISTER, WAM, WAM1	2.6	2.7	-0.1	-0.9	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
16456	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	2.9	-0.1	-0.9	100.0%	-1.5
16457	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	2.9	-0.1	-0.9	100.0%	-1.5
16458	AT2G33130.1 | Symbol: RALFL18 | rapid alkalinization factor (RALF) family protein | chr2:14053598-14053909 REVERSE | Aliases: F25I18.13, F25I18_13, RALF LIKE 18	3.1	3.2	-0.1	-0.9	100.0%	-1.8
16459	AT2G20660.1 | Symbol: RALFL14 | rapid alkalinization 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	2.8	-0.1	-0.9	100.0%	-1.8
16460	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	4.2	4.1	0.2	0.9	100.0%	-1.2
16461	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	3.5	3.3	0.2	0.9	100.0%	-1.4
16462	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	6.4	6.7	-0.2	-0.9	100.0%	-1.3
16463	AT5G15010.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:4857262-4858962 FORWARD | Aliases: F2G14.130, F2G14_130	3.5	3.3	0.2	0.9	100.0%	-1.6
16464	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	2.6	2.5	0.1	0.9	100.0%	-2.0
16465	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	8.2	7.8	0.4	0.9	100.0%	-1.0
16466	AT2G41440.1 | expressed protein | chr2:17278281-17284775 FORWARD | Aliases: T26J13.3, T26J13_3	2.8	2.9	-0.1	-0.9	100.0%	-1.7
16467	AT3G22690.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:8020764-8024541 REVERSE | Aliases: MWI23.6	3.2	3.1	0.1	0.9	100.0%	-1.4
16468	AT5G62120.1 | Symbol: ARR23 | hypothetical protein | chr5:24964181-24965451 REVERSE | Aliases: ARABIDOPSIS RESPONSE REGULATOR 23, MTG10.15, MTG10_15	2.4	2.5	-0.1	-0.9	100.0%	-1.9
16469	AT2G44850.1 | expressed protein | chr2:18505747-18507898 FORWARD | Aliases: T13E15.14	3.8	3.6	0.2	0.9	100.0%	-1.3
16470	AT2G20595.1 | expressed protein | chr2:8878632-8879142 REVERSE | Aliases: None	3.5	3.6	-0.1	-0.9	100.0%	-1.4
16471	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	4.3	4.5	-0.2	-0.9	100.0%	-1.2
16472	AT3G28830.1 | expressed protein | chr3:10832470-10834521 FORWARD | Aliases: T19N8.13	2.8	3.0	-0.2	-0.9	100.0%	-1.5
16473	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	3.1	3.3	-0.2	-0.9	100.0%	-1.4
16474	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	2.9	3.1	-0.2	-0.9	100.0%	-1.4
16475	AT1G33350.1 | pentatricopeptide (PPR) repeat-containing protein, contains multiple Pfam domains: PF01535: PPR repeat | chr1:12089383-12091667 REVERSE | Aliases: F10C21.4	3.7	3.6	0.2	0.9	100.0%	-1.4
16476	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	4.6	-0.2	-0.9	100.0%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
16477	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	3.1	3.2	-0.1	-0.9	100.0%	-1.5
16478	AT2G44560.1 | glycosyl hydrolase family 9 protein | chr2:18398990-18400730 REVERSE | Aliases: F16B22.5	3.2	3.3	-0.1	-0.9	100.0%	-1.6
16479	AT5G63680.1 | pyruvate kinase, putative, similar to pyruvate kinase, cytosolic isozyme (Glycine max) SWISS-PROT:Q42806	6.6	5.9	0.7	0.9	100.0%	-1.1
16480	AT5G28150.1 | expressed protein | chr5:10135475-10136981 FORWARD | Aliases: T24G3.80, T24G3_80	6.9	7.0	-0.2	-0.9	100.0%	-1.3
16481	AT1G35490.1 | bZIP family transcription factor	2.2	2.3	-0.1	-0.9	100.0%	-2.1
16482	AT1G56180.1 | expressed protein | chr1:21029569-21031729 REVERSE | Aliases: F14G9.20	4.3	4.1	0.3	0.9	100.0%	-1.0
16483	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	2.2	-0.1	-0.9	100.0%	-1.8
16484	AT1G53490.1 | bZIP protein | chr1:19969496-19970382 FORWARD | Aliases: F22G10.16	3.6	3.8	-0.1	-0.9	100.0%	-1.3
16485	AT4G24510.1 | Symbol: CER2 | eceriferum protein (CER2), identical to (CER2) (Arabidopsis thaliana) GI:1213594; contains Pfam profile PF02458: Transferase family | chr4:12660759-12662666 FORWARD | Aliases: ECERIFERUM 2, F22K18.290, F22K18_290, VC 2, VC2	2.3	2.4	-0.1	-0.9	100.0%	-2.0
16486	AT1G56060.1 | expressed protein | chr1:20970193-20970809 REVERSE | Aliases: T6H22.17, T6H22_17	5.0	5.2	-0.2	-0.9	100.0%	-1.3
16487	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	6.1	5.6	0.5	0.9	100.0%	-0.8
16488	AT2G21240.2 | expressed protein | chr2:9108397-9110127 REVERSE | Aliases: F7O24.4, F7O24_4	7.6	7.8	-0.2	-0.9	100.0%	-1.1
16489	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	7.3	7.1	0.2	0.9	100.0%	-1.2
16490	AT1G54060.1 | expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189 | chr1:20184347-20185992 FORWARD | Aliases: F15I1.14, F15I1_14	6.8	7.1	-0.3	-0.9	100.0%	-1.1
16491	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 scienitific 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	2.7	0.1	0.9	100.0%	-1.6
16492	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	6.2	-0.2	-0.9	100.0%	-1.3
16493	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	5.6	6.1	-0.5	-0.9	100.0%	-1.1
16494	AT3G11330.1 | leucine-rich repeat family protein | chr3:3551980-3554769 REVERSE | Aliases: F11B9.22	5.5	5.7	-0.2	-0.9	100.0%	-1.0
16495	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	2.9	2.8	0.1	0.9	100.0%	-1.6
16496	AT4G29750.1 | expressed protein, contains Pfam domain, PF04581: Protein of unknown function (DUF578) | chr4:14569734-14572810 FORWARD | Aliases: T16L4.260, T16L4_260	5.2	5.0	0.2	0.9	100.0%	-1.0
16497	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	6.3	0.3	0.9	100.0%	-1.2
16498	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	5.3	5.0	0.3	0.9	100.0%	-0.8

Rank	Description	Sync	Root	M	t	adj.q	B
16499	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	2.9	0.1	0.9	100.0%	-1.4
16500	AT5G14790.1 | expressed protein | chr5:4782949-4785808 FORWARD | Aliases: T9L3.90, T9L3_90	4.2	4.0	0.2	0.9	100.0%	-1.6
16501	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	-0.9	100.0%	-1.7
16502	AT1G33820.1 | hypothetical protein | chr1:12278418-12279431 REVERSE | Aliases: F14M2.4, F14M2_4	2.5	2.6	-0.1	-0.9	100.0%	-2.2
16503	AT1G64690.1 | expressed protein | chr1:24041732-24042742 FORWARD | Aliases: F13O11.1, F13O11_1	5.0	4.8	0.2	0.9	100.0%	-0.9
16504	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	3.2	3.3	-0.1	-0.9	100.0%	-1.6
16505	AT1G19360.1 | expressed protein | chr1:6690447-6692461 REVERSE | Aliases: F18O14.8, F18O14_8	7.6	8.1	-0.5	-0.9	100.0%	-0.9
16506	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	2.7	-0.1	-0.9	100.0%	-1.6
16507	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	3.1	3.2	-0.1	-0.9	100.0%	-1.8
16508	AT5G38500.1 | hypothetical protein, contains Pfam profile PF03754: Domain of unknown function (DUF313)	2.3	2.4	-0.1	-0.9	100.0%	-2.0
16509	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	2.4	-0.1	-0.9	100.0%	-1.9
16510	AT4G02210.1 | expressed protein | chr4:973924-976129 REVERSE | Aliases: T2H3.2	4.6	4.7	-0.1	-0.9	100.0%	-1.5
16511	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	2.6	0.1	0.9	100.0%	-1.8
16512	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 ISOFOM 3	7.0	6.8	0.2	0.9	100.0%	-1.3
16513	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	10.3	10.7	-0.4	-0.9	100.0%	-1.0
16514	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	3.9	4.1	-0.2	-0.9	100.0%	-1.3
16515	AT3G05410.1 | expressed protein | chr3:1554779-1555405 FORWARD | Aliases: F22F7.15, F22F7_15	3.1	2.9	0.1	0.9	100.0%	-1.4
16516	AT5G07160.1 | bZIP family transcription factor, contains Pfam profile: PF00170 bZIP transcription factor | chr5:2220213-2220710 REVERSE | Aliases: T28J14.100, T28J14_100	2.5	2.6	-0.1	-0.9	100.0%	-1.8
16517	AT2G34820.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.2	2.2	0.1	0.9	100.0%	-2.0
16518	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	8.1	-0.3	-0.9	100.0%	-1.2
16519	AT5G49690.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:20206881-20208616 REVERSE | Aliases: K2I5.5, K2I5_5	3.5	3.6	-0.1	-0.9	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
16520	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	2.4	-0.1	-0.9	100.0%	-2.3
16521	AT4G09960.2 | Symbol: STK | MADS-box protein (AGL11) | chr4:6236482-6240770 REVERSE | Aliases: AGL11, SEEDSTICK, T5L19.90, T5L19_90	2.8	2.9	-0.1	-0.9	100.0%	-2.1
16522	AT1G73150.1 | DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487 | chr1:27507773-27509773 REVERSE | Aliases: F3N23.35, F3N23_35	3.4	3.5	-0.1	-0.9	100.0%	-1.5
16523	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	4.5	0.3	0.9	100.0%	-1.1
16524	AT3G11540.2 | Symbol: SPY | gibberellin signal transduction protein (SPINDLY), identical to spindly GB:AAC49446 (GI:1589778) (Arabidopsis thaliana); contains Pfam profile PF00515 TPR Domain	4.5	4.3	0.2	0.9	100.0%	-1.1
16525	AT5G58130.1 | RNA recognition motif (RRM)-containing protein | chr5:23538276-23541022 REVERSE | Aliases: K21L19.13, K21L19_13	7.0	6.8	0.2	0.9	100.0%	-1.3
16526	AT1G03920.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr1:1001320-1004382 FORWARD | Aliases: F21M11.15, F21M11_15	8.7	8.3	0.4	0.9	100.0%	-1.2
16527	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	2.4	-0.1	-0.9	100.0%	-1.8
16528	AT5G43740.2 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.1	2.9	0.2	0.9	100.0%	-1.5
16529	AT3G04750.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:1301397-1303382 REVERSE | Aliases: F7O18.24, F7O18_24	4.2	4.0	0.2	0.9	100.0%	-1.5
16530	AT4G23240.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr4:12160512-12161964 REVERSE | Aliases: F21P8.130, F21P8_130	3.3	3.1	0.2	0.9	100.0%	-1.4
16531	AT5G66340.1 | hypothetical protein | chr5:26519728-26520379 FORWARD | Aliases: K1L20.12, K1L20_12	4.3	4.5	-0.2	-0.9	100.0%	-1.4
16532	AT5G26110.1 | expressed protein | chr5:9117910-9119809 REVERSE | Aliases: T1N24.12, T1N24_12	5.4	5.8	-0.3	-0.9	100.0%	-0.8
16533	AT2G43970.2 | La domain-containing protein, contains Pfam profile PF05383: La domain | chr2:18212311-18215294 REVERSE | Aliases: F6E13.10	11.4	11.2	0.2	0.9	100.0%	-1.5
16534	AT3G63020.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr3:23305400-23306014 FORWARD | Aliases: T20O10.120	2.5	2.4	0.1	0.9	100.0%	-1.8
16535	AT4G31090.1 | expressed protein | chr4:15122235-15123492 FORWARD | Aliases: F6E21.10, F6E21_10	4.4	4.8	-0.4	-0.9	100.0%	-1.0
16536	AT4G29940.1 | Symbol: PRHA | pathogenesis-related homeodomain protein (PRHA), identical to Pathogenesis-related homeodomain protein (PRHA) (SP:P48785) (Arabidopsis thaliana)	5.5	5.1	0.4	0.9	100.0%	-1.3
16537	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	2.7	2.8	-0.1	-0.9	100.0%	-1.8
16538	AT1G31300.2 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g19645.2); similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g19645.1); similar to unknown protein [Oryza sativa (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	5.7	6.0	-0.2	-0.9	100.0%	-1.2
16539	AT1G11960.1 | early-responsive to dehydration protein-related / ERD protein-related, low similarity to ERD4 protein (Arabidopsis thaliana) GI:15375406	4.7	4.9	-0.2	-0.9	100.0%	-1.2
16540	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	0.9	100.0%	-1.6
16541	AT2G43760.1 | molybdopterin biosynthesis MoaE family protein, contains Pfam profile: PF02391 molybdopterin converting factor, subunit 2 | chr2:18140026-18141047 FORWARD | Aliases: F18O19.13	7.8	8.0	-0.3	-0.9	100.0%	-1.0
16542	AT3G11160.1 | expressed protein | chr3:3496073-3497169 REVERSE | Aliases: F11B9.9	3.5	3.3	0.2	0.9	100.0%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
16543	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	-0.1	-0.9	100.0%	-1.8
16544	AT5G45630.1 | expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584 | chr5:18523036-18523550 REVERSE | Aliases: MRA19.3, MRA19_3	2.6	2.7	-0.1	-0.9	100.0%	-1.9
16545	AT2G28085.1 | auxin-responsive family protein, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana) | chr2:11975197-11975697 REVERSE | Aliases: None	2.7	2.8	-0.1	-0.9	100.0%	-1.9
16546	AT1G18610.1 | kelch repeat-containing protein, contains Pfam profile PF01344: Kelch motif | chr1:6405771-6408823 FORWARD | Aliases: F25I16.5, F25I16_5	3.1	3.2	-0.1	-0.9	100.0%	-2.0
16547	AT5G11120.1 | hypothetical protein | chr5:3542321-3542991 FORWARD | Aliases: T5K6.11	2.3	2.4	-0.1	-0.9	100.0%	-2.0
16548	AT5G08600.1 | U3 ribonucleoprotein (Utp) family protein, contains Pfam profile: PF04615 Utp14 protein | chr5:2786299-2789737 FORWARD | Aliases: MAH20.16, MAH20_16	3.2	3.1	0.1	0.9	100.0%	-1.7
16549	AT4G00530.1 | expressed protein | chr4:233030-233553 REVERSE | Aliases: F6N23.20, F6N23_20	3.8	3.6	0.1	0.9	100.0%	-1.2
16550	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	3.4	-0.2	-0.9	100.0%	-1.4
16551	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	2.3	2.4	-0.1	-0.9	100.0%	-2.0
16552	AT4G22620.1 | auxin-responsive family protein, auxin-induced protein 10A, Glycine max., PIR2:JQ1099 | chr4:11907642-11908124 FORWARD | Aliases: T12H17.10	4.6	4.4	0.2	0.9	100.0%	-1.2
16553	AT4G39010.1 | glycosyl hydrolase family 9 protein, endo-1,4-beta-glucanase precursor - Fragariax ananassa, PID:g3549291 | chr4:18175896-18179177 REVERSE | Aliases: F19H22.110, F19H22_110	2.7	2.8	-0.1	-0.9	100.0%	-1.6
16554	AT5G21110.1 | expressed protein, predicted protein - Arabidopsis thaliana, EMBL:AL163852 | chr5:7178618-7179089 FORWARD | Aliases: T10F18.140, T10F18_140	2.9	3.1	-0.1	-0.9	100.0%	-1.6
16555	AT5G07200.1 | Symbol: YAP169 |	2.4	2.5	-0.1	-0.9	100.0%	-1.9
16556	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	4.3	-0.2	-0.9	100.0%	-1.3
16557	AT4G37950.1 | expressed protein | chr4:17844424-17849266 FORWARD | Aliases: F20D10.70, F20D10_70	2.5	2.6	-0.1	-0.9	100.0%	-2.2
16558	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	3.4	-0.2	-0.9	100.0%	-1.4
16559	AT1G75800.1 | pathogenesis-related thaumatin family protein, similar to receptor serine/threonine kinase PR5K (Arabidopsis thaliana) GI:1235680; contains Pfam profile: PF00314 Thaumatin family | chr1:28462443-28464515 FORWARD | Aliases: T4O12.3, T4O12_3	5.8	6.1	-0.3	-0.9	100.0%	-1.3
16560	AT4G13210.1 | pectate lyase family protein, similar to pectate lyase GP:14531296 from (Fragaria x ananassa) | chr4:7670036-7673131 FORWARD | Aliases: F17N18.100, F17N18_100	2.5	2.6	-0.1	-0.9	100.0%	-1.9
16561	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	7.8	7.5	0.3	0.9	100.0%	-1.0
16562	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	-0.1	-0.9	100.0%	-2.2

Rank	Description	Sync	Root	M	t	adj.q	B
16563	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	4.6	4.1	0.5	0.9	100.0%	-0.8
16564	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	2.7	0.1	0.9	100.0%	-1.6
16565	AT5G57600.1 | expressed protein | chr5:23338972-23339913 REVERSE | Aliases: MUA2.18, MUA2_18	3.6	3.7	-0.1	-0.9	100.0%	-1.7
16566	AT5G45850.1 | expressed protein, contains Pfam profile: PF05097 protein of unknown function (DUF688) | chr5:18617328-18618797 REVERSE | Aliases: K15I22.5, K15I22_5	2.0	2.0	-0.1	-0.9	100.0%	-2.4
16567	AT3G45110.1 | hypothetical protein | chr3:16519155-16519517 FORWARD | Aliases: T14D3.50	2.8	2.9	-0.1	-0.9	100.0%	-1.8
16568	AT3G16830.1 | WD-40 repeat family protein, contains 10 WD-40 repeats (PF00400) (1 weak) | chr3:5731540-5737778 FORWARD | Aliases: K20I9.6	5.4	5.7	-0.3	-0.9	100.0%	-1.4
16569	AT3G60220.1 | Symbol: ATL4 | zinc finger (C3HC4-type RING finger) family protein (ATL4), contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	2.8	2.9	-0.1	-0.9	100.0%	-1.7
16570	AT5G08490.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:2745209-2747758 REVERSE | Aliases: F8L15.18	2.9	3.1	-0.2	-0.9	100.0%	-1.5
16571	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	3.4	3.6	-0.2	-0.9	100.0%	-1.1
16572	AT1G43760.1 | expressed protein | chr1:16531320-16533505 REVERSE | Aliases: F2J6.14	3.0	3.1	-0.1	-0.9	100.0%	-1.6
16573	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	-0.1	-0.9	100.0%	-1.8
16574	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}	3.0	3.1	-0.2	-0.9	100.0%	-1.4
16575	AT2G19270.1 | expressed protein | chr2:8367271-8369006 REVERSE | Aliases: F27F23.7, F27F23_7	8.3	8.5	-0.2	-0.9	100.0%	-1.8
16576	AT1G01770.1 | expressed protein | chr1:278615-282891 FORWARD | Aliases: T1N6.18, T1N6_18	5.7	5.4	0.3	0.9	100.0%	-1.0
16577	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	2.3	0.1	0.9	100.0%	-2.0
16578	AT5G17660.1 | expressed protein, contains Pfam profile PF02390: Putative methyltransferase | chr5:5818550-5820866 REVERSE | Aliases: MVA3.1, MVA3_1	3.2	3.1	0.1	0.9	100.0%	-1.3
16579	AT4G18980.1 | expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584 | chr4:10398929-10399523 FORWARD | Aliases: F13C5.150, F13C5_150	2.4	2.5	-0.1	-0.9	100.0%	-2.0
16580	AT2G43270.1 | F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	3.7	3.9	-0.2	-0.9	100.0%	-1.4
16581	AT1G26310.1 | Symbol: CAL | MADS-box protein, putative, strong similarity to DNA-binding protein (Brassica rapa subsp. pekinensis) GI:6469345, SP:Q41276 Floral homeotic protein APETALA1 (MADS C) {Sinapis alba}; contains InterPro accession IPR002100: Transcription factor, MADS-box | chr1:9100145-9103590 REVERSE | Aliases: AGL10, CAL1, CAULIFLOWER, F28B23.25, F28B23_25, MADS3	2.3	2.3	-0.1	-0.9	100.0%	-1.8
16582	AT5G57720.1 | transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain | chr5:23407153-23408752 REVERSE | Aliases: MRI1.8, MRI1_8	2.6	2.7	-0.1	-0.9	100.0%	-1.6
16583	AT4G13280.1 | terpene synthase/cyclase family protein, predicted protein, Arabidopsis thaliana	3.1	2.9	0.1	0.9	100.0%	-1.4
16584	AT2G25800.1 | expressed protein | chr2:11012980-11016817 REVERSE | Aliases: F17H15.17, F17H15_17	4.8	5.1	-0.2	-0.9	100.0%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
16585	AT1G21810.1 | expressed protein | chr1:7656567-7658623 REVERSE | Aliases: T26F17.2	2.7	2.8	-0.1	-0.9	100.0%	-2.0
16586	AT3G03410.1 | calmodulin-related protein, putative, similar to calmodulin-related protein 2, touch-induced SP:P25070 from (Arabidopsis thaliana) | chr3:811331-811726 REVERSE | Aliases: T21P5.17, T21P5_17	2.8	3.0	-0.1	-0.9	100.0%	-1.5
16587	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)	2.5	2.6	-0.1	-0.9	100.0%	-1.9
16588	AT5G17620.1 | expressed protein | chr5:5805762-5808563 REVERSE | Aliases: K10A8.100, K10A8_100	5.8	5.5	0.3	0.9	100.0%	-1.1
16589	AT5G56070.1 | expressed protein | chr5:22725905-22726430 FORWARD | Aliases: MDA7.12, MDA7_12	2.1	2.2	-0.1	-0.9	100.0%	-2.2
16590	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	4.2	4.0	0.2	0.9	100.0%	-1.1
16591	AT1G36030.1 | F-box family protein, similar to hypothetical protein GB:AAC61810 | chr1:13437798-13438040 FORWARD | Aliases: T22A15.5, T22A15_5	2.5	2.5	-0.1	-0.9	100.0%	-2.2
16592	AT2G48160.1 | PWWP domain-containing protein | chr2:19696484-19703891 REVERSE | Aliases: F11L15.11, F11L15_11	3.4	3.5	-0.1	-0.9	100.0%	-1.4
16593	AT4G13710.1 | pectate lyase family protein | chr4:7962428-7966440 FORWARD | Aliases: F18A5.100, F18A5_100	3.6	3.5	0.2	0.9	100.0%	-1.1
16594	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}	4.7	4.5	0.2	0.9	100.0%	-1.1
16595	AT5G51340.1 | expressed protein | chr5:20880169-20884596 FORWARD | Aliases: MFG13.4, MFG13_4	5.0	4.7	0.3	0.9	100.0%	-1.0
16596	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	3.7	3.4	0.3	0.9	100.0%	-1.0
16597	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	2.3	2.3	-0.1	-0.9	100.0%	-1.9
16598	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	2.5	-0.1	-0.9	100.0%	-1.9
16599	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	5.8	6.2	-0.4	-0.9	100.0%	-1.2
16600	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	2.4	-0.1	-0.9	100.0%	-2.3
16601	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	3.0	-0.2	-0.9	100.0%	-1.3
16602	AT3G10750.1 | hypothetical protein | chr3:3366932-3368274 FORWARD | Aliases: T7M13.17	3.1	3.2	-0.1	-0.9	100.0%	-1.6
16603	AT5G61710.1 | expressed protein | chr5:24817271-24817738 FORWARD | Aliases: MAC9.2, MAC9_2	2.9	3.0	-0.1	-0.9	100.0%	-1.4
16604	AT5G27800.1 | expressed protein, predicted protein, Arabidopsis thaliana; expression supported by MPSS	2.4	2.5	-0.1	-0.9	100.0%	-1.7
16605	AT5G62090.2 | expressed protein | chr5:24952189-24956335 REVERSE | Aliases: MTG10.12, MTG10_12	3.5	3.4	0.2	0.8	100.0%	-1.4
16606	AT4G11220.1 | reticulon family protein (RTNLB2), similar to SP:Q64548 Reticulon 1 (Neuroendocrine-specific protein) {Rattus norvegicus}; contains Pfam profile PF02453: Reticulon | chr4:6837946-6839791 REVERSE | Aliases: F8L21.10, F8L21_10	8.8	9.1	-0.3	-0.8	100.0%	-1.3
16607	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	2.4	-0.1	-0.8	100.0%	-1.9
16608	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 (Arabidopsis thaliana) | chr1:22230550-22231593 REVERSE | Aliases: ANAC023, T13D8.17, T13D8_17	3.2	3.3	-0.1	-0.8	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
16609	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	3.1	-0.1	-0.8	100.0%	-1.7
16610	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	3.5	-0.1	-0.8	100.0%	-1.5
16611	AT4G17470.1 | palmitoyl protein thioesterase family protein | chr4:9742771-9744859 REVERSE | Aliases: DL4770C, FCAALL.11	2.9	3.0	-0.1	-0.8	100.0%	-1.6
16612	AT5G42280.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.0	3.1	-0.1	-0.8	100.0%	-1.9
16613	AT1G18530.1 | calmodulin, putative, similar to calmodulin GI:1565285 from (Toxoplasma gondii) | chr1:6376776-6377249 FORWARD | Aliases: F25I16.13, F25I16_13	2.5	2.4	0.1	0.8	100.0%	-2.0
16614	AT1G57760.1 | expressed protein | chr1:21393747-21398199 FORWARD | Aliases: T8L23.22, T8L23_22	4.6	4.5	0.1	0.8	100.0%	-1.3
16615	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	2.5	0.1	0.8	100.0%	-1.9
16616	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	3.8	-0.2	-0.8	100.0%	-1.1
16617	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	3.5	0.1	0.8	100.0%	-1.4
16618	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	2.6	2.5	0.1	0.8	100.0%	-1.9
16619	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: F10O3.12, F10O3_12	4.7	5.0	-0.2	-0.8	100.0%	-1.2
16620	AT3G03340.1 | LUC7 N_terminus domain-containing protein, contains Pfam domain PF03194: LUC7 N_terminus	7.1	7.3	-0.2	-0.8	100.0%	-1.6
16621	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	7.4	7.0	0.4	0.8	100.0%	-0.9
16622	AT5G28890.1 | expressed protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana) | chr5:10904106-10904804 REVERSE | Aliases: F7P1.70, F7P1_70	2.8	2.9	-0.1	-0.8	100.0%	-1.9
16623	AT5G27510.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	3.1	3.3	-0.2	-0.8	100.0%	-1.3
16624	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	5.4	-0.2	-0.8	100.0%	-1.4
16625	AT2G29060.1 | scarecrow transcription factor family protein | chr2:12489068-12494060 FORWARD | Aliases: T9I4.14, T9I4_14	3.9	3.8	0.1	0.8	100.0%	-1.7
16626	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	2.5	-0.1	-0.8	100.0%	-1.7
16627	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	3.0	3.1	-0.1	-0.8	100.0%	-1.7
16628	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	2.7	-0.1	-0.8	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
16629	AT1G26500.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:9158367-9159884 FORWARD | Aliases: T1K7.14, T1K7_14	4.5	4.8	-0.3	-0.8	100.0%	-1.0
16630	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	2.3	2.4	-0.1	-0.8	100.0%	-2.2
16631	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	7.6	8.2	-0.6	-0.8	100.0%	-0.9
16632	AT1G62350.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:23060318-23061600 FORWARD | Aliases: F24O1.37, F24O1_37	3.8	3.9	-0.2	-0.8	100.0%	-1.3
16633	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	8.0	0.2	0.8	100.0%	-1.2
16634	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	7.5	7.1	0.5	0.8	100.0%	-0.6
16635	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	7.5	7.1	0.5	0.8	100.0%	-0.6
16636	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	3.0	3.1	-0.1	-0.8	100.0%	-1.5
16637	AT5G04520.1 | expressed protein, ; expression supported by MPSS | chr5:1290013-1291064 REVERSE | Aliases: T32M21.120, T32M21_120	5.5	5.3	0.2	0.8	100.0%	-1.3
16638	AT4G16040.1 | hypothetical protein | chr4:9087194-9087466 REVERSE | Aliases: DL4060C, FCAALL.265	2.1	2.2	-0.1	-0.8	100.0%	-2.4
16639	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	2.3	-0.1	-0.8	100.0%	-2.2
16640	AT4G23950.1 | expressed protein, ; expression supported by MPSS | chr4:12442563-12444340 FORWARD | Aliases: T32A16.120, T32A16_120	4.5	4.3	0.2	0.8	100.0%	-1.3
16641	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	4.4	4.2	0.3	0.8	100.0%	-1.0
16642	AT2G22650.1 | FAD-dependent oxidoreductase family protein | chr2:9631702-9634041 REVERSE | Aliases: T9I22.9, T9I22_9	5.7	5.5	0.2	0.8	100.0%	-1.3
16643	AT2G10460.1 | expressed protein, includes At2g05890, At4g07450, At3g30630, At3g43100, At2g09960, At3g30550, At1g39430, At2g10460, At4g03640, At5g35250	2.7	2.6	0.1	0.8	100.0%	-1.3
16644	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 scienitific 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	6.3	5.8	0.5	0.8	100.0%	-0.9
16645	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	2.3	2.4	-0.1	-0.8	100.0%	-2.0
16646	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	3.6	3.9	-0.3	-0.8	100.0%	-1.3
16647	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	3.0	-0.1	-0.8	100.0%	-1.2
16648	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	3.7	3.6	0.1	0.8	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
16649	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	3.8	4.0	-0.3	-0.8	100.0%	-1.2
16650	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	3.0	3.1	-0.1	-0.8	100.0%	-1.7
16651	AT4G38880.1 | Symbol: ATASE3 |	3.0	3.1	-0.1	-0.8	100.0%	-1.8
16652	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	-0.8	100.0%	-1.8
16653	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	6.1	6.3	-0.2	-0.8	100.0%	-1.1
16654	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	5.1	5.0	0.1	0.8	100.0%	-1.3
16655	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	2.7	-0.1	-0.8	100.0%	-2.0
16656	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	3.6	-0.2	-0.8	100.0%	-1.2
16657	AT3G29380.1 | transcription factor IIB (TFIIB) family protein, contains Pfam profile: PF00382 transcription factor TFIIB repeat | chr3:11283644-11284761 REVERSE | Aliases: MUO10.22	2.7	2.8	-0.1	-0.8	100.0%	-1.5
16658	ATMG00670.1 | Symbol: ORF275 |	3.8	4.2	-0.4	-0.8	100.0%	-0.9
16659	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	-0.8	100.0%	-2.0
16660	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	3.8	4.1	-0.2	-0.8	100.0%	-1.2
16661	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	6.0	6.2	-0.2	-0.8	100.0%	-1.4
16662	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	3.1	-0.2	-0.8	100.0%	-1.6
16663	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	3.2	-0.1	-0.8	100.0%	-1.5
16664	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	8.5	8.0	0.4	0.8	100.0%	-1.2
16665	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	2.6	-0.1	-0.8	100.0%	-1.7
16666	AT2G21900.1 | Symbol: WRKY59 |	2.2	2.1	0.1	0.8	100.0%	-1.7
16667	AT3G48480.1 | expressed protein | chr3:17968311-17970047 REVERSE | Aliases: T29H11.250	3.7	3.8	-0.1	-0.8	100.0%	-1.4
16668	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	2.2	-0.1	-0.8	100.0%	-2.0
16669	AT1G59510.1 | Symbol: CF9 | expressed protein	3.6	3.8	-0.2	-0.8	100.0%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
16670	AT4G38560.1 | expressed protein | chr4:18029269-18031185 FORWARD | Aliases: F20M13.120, F20M13_120	2.8	2.9	-0.1	-0.8	100.0%	-1.6
16671	NA	7.9	8.2	-0.3	-0.8	100.0%	-1.3
16672	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	2.3	2.4	-0.1	-0.8	100.0%	-2.1
16673	AT2G36700.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr2:15391785-15393500 REVERSE | Aliases: F13K3.10, F13K3_10	3.2	3.3	-0.1	-0.8	100.0%	-1.4
16674	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	6.5	6.3	0.2	0.8	100.0%	-1.0
16675	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	4.9	-0.2	-0.8	100.0%	-1.3
16676	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 Mg2+ transporter protein | chr3:6820936-6823312 FORWARD | Aliases: MMB12.11	9.9	9.7	0.2	0.8	100.0%	-1.2
16677	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	6.2	6.7	-0.5	-0.8	100.0%	-0.9
16678	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	2.9	-0.1	-0.8	100.0%	-1.5
16679	AT3G42770.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.5	3.6	-0.2	-0.8	100.0%	-1.4
16680	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	4.7	4.6	0.1	0.8	100.0%	-1.4
16681	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	2.7	2.8	-0.1	-0.8	100.0%	-1.8
16682	AT2G15020.1 | expressed protein, and genefinder | chr2:6498516-6500434 REVERSE | Aliases: T15J14.6, T15J14_6	3.0	3.1	-0.1	-0.8	100.0%	-1.6
16683	AT1G01410.1 | hypothetical protein | chr1:153113-154198 FORWARD | Aliases: F6F3.21, F6F3_21	2.8	2.9	-0.1	-0.8	100.0%	-1.8
16684	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	8.2	7.7	0.6	0.8	100.0%	-1.0
16685	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	3.0	-0.1	-0.8	100.0%	-1.6
16686	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	2.8	-0.1	-0.8	100.0%	-2.1
16687	AT3G51690.1 | expressed protein, low similarity to SP:P07271 DNA repair and recombination protein PIF1, mitochondrial precursor {Saccharomyces cerevisiae} | chr3:19187416-19189086 REVERSE | Aliases: T18N14.70	2.1	2.1	0.1	0.8	100.0%	-2.3
16688	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	3.1	-0.1	-0.8	100.0%	-1.5
16689	AT4G38980.1 | expressed protein | chr4:18166703-18168170 REVERSE | Aliases: F19H22.80, F19H22_80	5.7	5.9	-0.1	-0.8	100.0%	-1.5
16690	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	9.7	0.3	0.8	100.0%	-1.2
16691	AT3G05110.1 | expressed protein | chr3:1426303-1427725 REVERSE | Aliases: T12H1.7, T12H1_7	2.8	2.8	-0.1	-0.8	100.0%	-2.2

Rank	Description	Sync	Root	M	t	adj.q	B
16692	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	3.1	0.1	0.8	100.0%	-1.5
16693	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	3.1	2.9	0.2	0.8	100.0%	-1.3
16694	AT4G19320.1 | expressed protein, simlar to At5g28170, At1g35110, At1g44880, At3g42530, At5g36020, At4g03970, At3g43010, At2g10350 | chr4:10549359-10552983 REVERSE | Aliases: T5K18.100, T5K18_100	2.1	2.2	-0.1	-0.8	100.0%	-2.1
16695	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	2.2	-0.1	-0.8	100.0%	-2.1
16696	AT3G30845.1 | hypothetical protein | chr3:12626916-12627233 REVERSE | Aliases: MJI6.6	2.9	3.0	-0.1	-0.8	100.0%	-2.0
16697	AT1G48180.1 | expressed protein, ; expression supported by MPSS | chr1:17796118-17797386 REVERSE | Aliases: F21D18.8, F21D18_8	3.1	3.2	-0.1	-0.8	100.0%	-1.6
16698	AT5G57140.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 Calcineurin-like phosphoesterase	3.5	3.4	0.1	0.8	100.0%	-1.5
16699	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	2.7	-0.1	-0.8	100.0%	-1.8
16700	AT1G55630.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:20795344-20797226 REVERSE | Aliases: F20N2.6	4.3	4.1	0.2	0.8	100.0%	-1.0
16701	AT4G18860.1 | expressed protein, ; expression supported by MPSS | chr4:10344698-10345599 FORWARD | Aliases: F13C5.30, F13C5_30	2.3	2.4	-0.1	-0.8	100.0%	-2.1
16702	AT4G11570.2 | haloacid dehalogenase-like hydrolase family protein, similar to genetic modifier (Zea mays) GI:10444400; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase | chr4:7004329-7006075 FORWARD | Aliases: F25E4.190, F25E4_190	7.3	7.5	-0.3	-0.8	100.0%	-1.2
16703	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	4.7	0.1	0.8	100.0%	-1.4
16704	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	9.6	0.2	0.8	100.0%	-1.4
16705	AT3G16550.1 | DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana) | chr3:5629926-5632423 REVERSE | Aliases: MDC8.18	2.9	3.0	-0.1	-0.8	100.0%	-1.7
16706	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	3.6	-0.1	-0.8	100.0%	-1.5
16707	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	3.5	3.4	0.1	0.8	100.0%	-1.7
16708	AT1G16720.1 | expressed protein | chr1:5723081-5726471 FORWARD | Aliases: F19K19.14	8.1	7.9	0.2	0.8	100.0%	-1.2
16709	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	5.4	5.5	-0.1	-0.8	100.0%	-1.7
16710	AT4G03600.1 | expressed protein | chr4:1603700-1604506 REVERSE | Aliases: T5L23.9, T5L23_9	4.6	4.7	-0.1	-0.8	100.0%	-1.6
16711	AT5G63730.1 | IBR domain-containing protein, contains similarity to Swiss-Prot:Q94981 ariadne-1 protein (Ari-1) (Drosophila melanogaster) and Pfam:PF01485 IBR domain | chr5:25525326-25526932 REVERSE | Aliases: MBK5.21, MBK5_21	3.1	3.2	-0.1	-0.8	100.0%	-1.6
16712	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	3.5	-0.1	-0.8	100.0%	-1.7
16713	AT5G04750.1 | F1F0-ATPase inhibitor protein, putative, similar to F1F0-ATPase inhibitor protein (Oryza sativa (japonica cultivar-group)) gi:5106371:dbj:BAA81661 | chr5:1372148-1374006 FORWARD | Aliases: MUK11.3	11.2	11.3	-0.1	-0.8	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
16714	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	6.0	-0.1	-0.8	100.0%	-1.6
16715	AT3G27370.1 | expressed protein | chr3:10131661-10131993 REVERSE | Aliases: K1G2.16	3.0	3.1	-0.1	-0.8	100.0%	-1.5
16716	AT5G20935.1 | expressed protein | chr5:7103473-7104023 FORWARD | Aliases: None	2.4	2.5	-0.1	-0.8	100.0%	-2.0
16717	AT1G52140.1 | expressed protein | chr1:19411033-19411923 REVERSE | Aliases: F5F19.20, F5F19_20	3.6	3.4	0.2	0.8	100.0%	-1.5
16718	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	2.1	-0.1	-0.8	100.0%	-2.2
16719	ATCG00330.1 | Symbol: RPS14 | 30S chloroplast ribosomal protein S14 | chrC:36938-37240 REVERSE | Aliases: RIBOSOMAL PROTEIN S14, RPS14	3.4	3.7	-0.3	-0.8	100.0%	-1.8
16720	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	8.3	8.6	-0.3	-0.8	100.0%	-1.1
16721	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	7.5	7.9	-0.4	-0.8	100.0%	-1.1
16722	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	-0.8	100.0%	-1.7
16723	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	2.7	0.1	0.8	100.0%	-1.6
16724	AT2G40070.1 | expressed protein | chr2:16735272-16738664 REVERSE | Aliases: T28M21.23, T28M21_23	4.4	4.2	0.2	0.8	100.0%	-1.0
16725	AT2G19660.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.3	2.4	-0.1	-0.8	100.0%	-2.2
16726	AT2G02700.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.0	3.2	-0.1	-0.8	100.0%	-1.5
16727	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	3.0	-0.1	-0.8	100.0%	-1.6
16728	AT2G18220.1 | expressed protein, contains Pfam domain PF03715: Uncharacterised protein family (UPF0120) | chr2:7935336-7938933 FORWARD | Aliases: T30D6.27, T30D6_27	5.5	5.0	0.5	0.8	100.0%	-0.9
16729	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	2.3	2.2	0.1	0.8	100.0%	-2.3
16730	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	5.7	5.5	0.2	0.8	100.0%	-1.2
16731	AT3G28330.1 | F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain | chr3:10587803-10588949 REVERSE | Aliases: MZF16.14	3.0	3.1	-0.1	-0.8	100.0%	-1.4
16732	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)	3.8	4.0	-0.2	-0.8	100.0%	-1.3
16733	AT2G37670.1 | WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); similiar to rab11 binding protein (GI:4512103) (Bos taurus) | chr2:15804462-15807614 REVERSE | Aliases: F13M22.17, F13M22_17	4.4	4.2	0.2	0.8	100.0%	-1.2
16734	AT5G52975.1 | expressed protein | chr5:21498683-21499261 FORWARD | Aliases: None	3.1	3.2	-0.1	-0.8	100.0%	-1.5
16735	AT4G18530.1 | expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707) | chr4:10217123-10220511 FORWARD | Aliases: F28J12.190, F28J12_190	3.8	3.9	-0.1	-0.8	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
16736	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	-0.1	-0.8	100.0%	-2.3
16737	AT3G02700.1 | NC domain-containing protein, contains Pfam domain, PF04970: NC domain | chr3:581548-582952 REVERSE | Aliases: F16B3.33, F16B3_33	6.9	6.7	0.3	0.8	100.0%	-1.4
16738	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	6.3	6.1	0.1	0.8	100.0%	-1.4
16739	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	5.7	5.9	-0.2	-0.8	100.0%	-1.2
16740	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	7.2	7.0	0.3	0.8	100.0%	-1.1
16741	AT4G27750.1 | expressed protein | chr4:13841694-13843639 FORWARD | Aliases: T29A15.240, T29A15_240	9.9	9.6	0.3	0.8	100.0%	-1.1
16742	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	5.9	5.7	0.2	0.8	100.0%	-1.2
16743	AT5G60400.3 | expressed protein | chr5:24308366-24309158 REVERSE | Aliases: MUF9.14, MUF9_14	6.3	6.7	-0.4	-0.8	100.0%	-0.9
16744	AT3G25870.1 | expressed protein | chr3:9464553-9465520 REVERSE | Aliases: MPE11.2	3.9	3.6	0.2	0.8	100.0%	-1.1
16745	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	4.1	3.9	0.2	0.8	100.0%	-1.2
16746	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	2.1	-0.1	-0.8	100.0%	-2.1
16747	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	0.8	100.0%	-2.4
16748	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	8.1	8.3	-0.3	-0.8	100.0%	-1.2
16749	AT1G15060.1 | expressed protein | chr1:5183623-5186936 REVERSE | Aliases: F9L1.1	3.6	3.5	0.1	0.8	100.0%	-1.5
16750	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	3.3	-0.1	-0.8	100.0%	-1.6
16751	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	2.4	2.5	-0.1	-0.8	100.0%	-1.9
16752	AT2G02750.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:771154-773539 REVERSE | Aliases: T20F6.11, T20F6_11	2.9	3.0	-0.1	-0.8	100.0%	-1.8
16753	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	2.5	0.1	0.8	100.0%	-1.9
16754	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	4.5	4.7	-0.1	-0.8	100.0%	-1.5
16755	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	3.9	3.8	0.2	0.8	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
16756	AT4G35725.1 | expressed protein | chr4:16929950-16930565 REVERSE | Aliases: None	2.6	2.7	-0.1	-0.8	100.0%	-1.7
16757	AT5G61910.3 | expressed protein | chr5:24877104-24881330 REVERSE | Aliases: K22G18.3, K22G18_3	2.4	2.5	-0.1	-0.8	100.0%	-2.0
16758	AT3G11350.1 | expressed protein | chr3:3558501-3560084 FORWARD | Aliases: F11B9.27	3.7	4.0	-0.2	-0.8	100.0%	-1.1
16759	AT4G20510.1 | expressed protein | chr4:11041668-11044810 FORWARD | Aliases: F9F13.160, F9F13_160	1.9	2.0	-0.1	-0.8	100.0%	-1.4
16760	AT1G44980.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr1:17006696-17008363 REVERSE | Aliases: F27F5.7, F27F5_7	2.6	2.7	-0.1	-0.8	100.0%	-1.7
16761	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	2.5	2.6	-0.1	-0.8	100.0%	-1.7
16762	AT3G45540.1 | zinc finger (C3HC4-type RING finger) family protein, contains a Prosite:PS00518 Zinc finger, C3HC4 type (RING finger), signature	2.8	2.7	0.1	0.8	100.0%	-1.5
16763	AT3G52640.3 | expressed protein, similar to hypothetical protein DDB0187645 [Dictyostelium discoideum] (GB:EAL63547.1)	5.7	5.6	0.2	0.8	100.0%	-1.3
16764	AT3G13175.1 | expressed protein | chr3:4235133-4235731 REVERSE | Aliases: None	3.8	3.9	-0.2	-0.8	100.0%	-1.3
16765	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	-0.1	-0.8	100.0%	-1.9
16766	AT1G17730.1 | SNF7 family protein, contains Pfam domain, PF03357: SNF7 family | chr1:6099097-6100308 FORWARD | Aliases: F11A6.7, F11A6_7	5.8	6.0	-0.2	-0.8	100.0%	-0.8
16767	AT4G33370.1 | DEAD-box protein abstrakt, putative, RNA helicase DBP2 - Saccharomyces cerevisiae, PID:g5272 | chr4:16069672-16071408 REVERSE | Aliases: F17M5.130, F17M5_130	3.6	3.8	-0.1	-0.8	100.0%	-1.4
16768	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	3.5	-0.1	-0.8	100.0%	-1.5
16769	AT5G49380.1 | expressed protein, contains Pfam domain, PF04802: Protein of unknown function (DUF625) | chr5:20042791-20044304 FORWARD | Aliases: K7J8.5, K7J8_5	3.0	3.2	-0.1	-0.8	100.0%	-1.6
16770	AT2G36730.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:15412147-15413652 REVERSE | Aliases: F13K3.13, F13K3_13	5.7	5.5	0.2	0.8	100.0%	-1.4
16771	AT1G24764.1 | Symbol: ATMAP70 2 | Member of the MAP70 protein family.	4.5	4.3	0.2	0.8	100.0%	-1.2
16772	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	3.8	3.6	0.2	0.8	100.0%	-1.2
16773	AT5G34460.1 | replication protein-related, weak similarity to Replication Protein A 70	2.7	2.7	-0.1	-0.8	100.0%	-2.2
16774	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	6.3	5.9	0.3	0.8	100.0%	-1.0
16775	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	5.8	5.5	0.2	0.8	100.0%	-1.0
16776	AT5G03930.1 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g03920.1) | chr5:1059503-1060153 FORWARD | Aliases: F8F6.140, F8F6_140	2.5	2.6	-0.1	-0.8	100.0%	-1.8
16777	AT1G15900.1 | expressed protein | chr1:5464350-5464691 FORWARD | Aliases: F7H2.24, F7H2_24	3.0	3.1	-0.1	-0.8	100.0%	-1.8
16778	AT2G26060.2 | Symbol: EMB1345 | similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At4g32990.1); similar to GA11817-PA [Drosophila pseudoobscura] (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	7.6	-0.2	-0.8	100.0%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
16779	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	2.6	-0.1	-0.8	100.0%	-2.0
16780	AT4G22760.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:11958488-11962881 FORWARD | Aliases: T12H17.150, T12H17_150	3.2	3.4	-0.1	-0.8	100.0%	-1.5
16781	AT5G41860.1 | expressed protein | chr5:16775179-16775757 FORWARD | Aliases: K16L22.15, K16L22_15	2.5	2.6	-0.1	-0.8	100.0%	-2.0
16782	AT1G77860.1 | Symbol: KOM | rhomboid family protein, contains PFAM domain PF01694, Rhomboid family | chr1:29287572-29289352 REVERSE | Aliases: F28K19.7, F28K19_7, KOMPEITO	3.5	3.6	-0.2	-0.8	100.0%	-1.5
16783	AT5G38960.1 | germin-like protein, putative, similar to germin-like protein subfamily 1 member 8 (SP:Q9LEA7); contains PS00725 germin family signature	2.2	2.3	-0.1	-0.8	100.0%	-2.1
16784	AT5G36650.1 | hypothetical protein | chr5:14397498-14397974 REVERSE | Aliases: F24C7.1, F24C7_1	3.3	3.0	0.3	0.8	100.0%	-0.5
16785	AT3G13420.1 | expressed protein | chr3:4364534-4366798 FORWARD | Aliases: MRP15.5	3.2	3.4	-0.2	-0.8	100.0%	-1.3
16786	AT3G43500.1 | expressed protein | chr3:15411245-15411706 REVERSE | Aliases: T18D12.70	2.2	2.3	-0.1	-0.8	100.0%	-1.8
16787	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	4.5	4.4	0.2	0.8	100.0%	-1.2
16788	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	-0.8	100.0%	-1.9
16789	AT3G07090.1 | expressed protein | chr3:2243060-2244826 REVERSE | Aliases: T1B9.26	8.5	8.0	0.6	0.8	100.0%	-1.0
16790	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	3.2	3.4	-0.2	-0.8	100.0%	-1.1
16791	AT2G27410.1 | expressed protein, contains Pfam profile PF03754: Domain of unknown function (DUF313) | chr2:11731724-11732763 REVERSE | Aliases: F12K2.1, F12K2_1	2.7	2.8	-0.1	-0.8	100.0%	-1.7
16792	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)	2.7	2.8	-0.1	-0.8	100.0%	-1.7
16793	AT2G14450.1 | expressed protein, includes At5g34960, At2g14450, At1g35920 | chr2:6156679-6159199 FORWARD | Aliases: T13P21.17, T13P21_17	2.5	2.6	-0.1	-0.8	100.0%	-2.1
16794	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)	6.6	6.8	-0.2	-0.8	100.0%	-1.3
16795	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	2.7	-0.1	-0.8	100.0%	-1.7
16796	AT1G50230.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:18610731-18612759 FORWARD | Aliases: F14I3.15, F14I3_15	3.3	3.5	-0.1	-0.8	100.0%	-1.5
16797	AT1G53110.1 | expressed protein | chr1:19793857-19796157 FORWARD | Aliases: F8L10.22	3.6	3.8	-0.2	-0.8	100.0%	-1.1
16798	AT3G15150.1 | expressed protein | chr3:5101992-5104147 REVERSE | Aliases: F4B12.6	3.0	2.9	0.1	0.8	100.0%	-1.5
16799	AT2G34315.1 | disease resistance protein-related, similar to SP:P54120 AIG1 protein {Arabidopsis thaliana} | chr2:14487333-14490135 REVERSE | Aliases: None	2.5	2.6	-0.1	-0.8	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
16800	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	-0.8	100.0%	-1.8
16801	AT5G66940.1 | Dof-type zinc finger domain-containing protein | chr5:26745215-26745892 REVERSE | Aliases: K8A10.1, K8A10_1	3.6	3.8	-0.1	-0.8	100.0%	-1.6
16802	AT3G13890.1 | Symbol: MYB26 | myb family transcription factor (MYB26), similar to myb-related transcription factor GI:1167486 from (Lycopersicon esculentum); contains myb DNA binding domain: PF0049	2.2	2.3	-0.1	-0.8	100.0%	-1.9
16803	AT2G17140.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:7469893-7473439 FORWARD | Aliases: F6P23.26, F6P23_26	3.2	3.3	-0.1	-0.8	100.0%	-1.6
16804	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	3.5	-0.1	-0.8	100.0%	-1.5
16805	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	2.8	2.7	0.1	0.8	100.0%	-1.8
16806	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	3.7	-0.1	-0.8	100.0%	-1.5
16807	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	4.3	0.1	0.8	100.0%	-1.4
16808	AT5G35090.1 | expressed protein | chr5:13375644-13376318 FORWARD | Aliases: F7N22.40, F7N22_40	2.2	2.2	-0.0	-0.8	100.0%	-2.3
16809	AT4G38760.1 | expressed protein, KIAA0169 gene, Homo sapiens, D79991 | chr4:18091796-18095595 REVERSE | Aliases: T9A14.40, T9A14_40	2.6	2.5	0.1	0.8	100.0%	-1.8
16810	AT2G24340.1 | expressed protein | chr2:10362510-10366626 REVERSE | Aliases: T28I24.7, T28I24_7	2.6	2.7	-0.1	-0.8	100.0%	-1.8
16811	AT3G42850.1 | galactokinase, putative, contains some similarity to galactokinase (Pasteurella multocida) SWISS-PROT:P57899 | chr3:14951102-14956279 REVERSE | Aliases: F18P9.10	4.0	4.1	-0.1	-0.8	100.0%	-1.6
16812	AT5G58050.1 | glycerophosphoryl diester phosphodiesterase family protein, contains Pfam PF03009 : Glycerophosphoryl diester phosphodiesterase family; similar to Glycerophosphoryl diester phosphodiesterase precursor	2.3	2.3	-0.1	-0.8	100.0%	-1.9
16813	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	3.2	0.2	0.8	100.0%	-1.5
16814	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	6.2	6.7	-0.5	-0.8	100.0%	-0.8
16815	AT3G62960.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	3.2	3.1	0.1	0.8	100.0%	-1.6
16816	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	3.0	3.1	-0.1	-0.8	100.0%	-1.6
16817	AT5G15860.2 | expressed protein | chr5:5178508-5181293 REVERSE | Aliases: F14F8.240, F14F8_240	6.8	7.2	-0.4	-0.8	100.0%	-0.8
16818	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	4.1	-0.2	-0.8	100.0%	-1.3
16819	AT5G03590.1 | GDSL-motif lipase/hydrolase protein-related | chr5:908562-910148 FORWARD | Aliases: F17C15.10, F17C15_10	2.3	2.4	-0.1	-0.8	100.0%	-2.1
16820	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	3.2	-0.1	-0.8	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
16821	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) {Deinococcus proteolyticus}; contains Pfam profile PF00226: DnaJ domain | chr5:7826737-7828727 REVERSE | Aliases: MKD15.10, MKD15_10	5.0	4.7	0.3	0.8	100.0%	-1.1
16822	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	5.2	4.8	0.3	0.8	100.0%	-0.9
16823	AT3G28560.1 | expressed protein, similar to mitochondrial protein-like protein (GI:11559424) (Cucumis sativus)	2.4	2.5	-0.1	-0.8	100.0%	-2.3
16824	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	3.2	-0.1	-0.8	100.0%	-1.4
16825	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	2.6	0.1	0.8	100.0%	-2.0
16826	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	2.9	-0.1	-0.8	100.0%	-1.6
16827	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	3.3	0.1	0.8	100.0%	-1.7
16828	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	9.2	9.5	-0.3	-0.8	100.0%	-1.2
16829	AT4G14350.2 | protein kinase family protein, contains similarity to Swiss-Prot:O13310 serine/threonine-protein kinase orb6 (Schizosaccharomyces pombe)	4.9	5.2	-0.3	-0.8	100.0%	-1.0
16830	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	4.2	3.9	0.3	0.8	100.0%	-1.1
16831	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	3.8	4.1	-0.2	-0.8	100.0%	-1.0
16832	AT5G48420.1 | expressed protein | chr5:19643588-19644016 REVERSE | Aliases: MJE7.5, MJE7_5	3.1	3.2	-0.1	-0.8	100.0%	-1.8
16833	AT4G21323.1 | subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa) | chr4:11342504-11345642 FORWARD | Aliases: None	2.7	2.8	-0.1	-0.8	100.0%	-1.8
16834	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	2.7	-0.1	-0.8	100.0%	-1.7
16835	AT2G01960.1 | expressed protein | chr2:450378-452416 FORWARD | Aliases: F14H20.3, F14H20_3	2.4	2.6	-0.1	-0.8	100.0%	-1.4
16836	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	2.8	2.9	-0.2	-0.8	100.0%	-1.6
16837	AT2G29860.1 | kelch repeat-containing F-box family protein, contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	2.6	2.7	-0.1	-0.8	100.0%	-2.0
16838	AT3G56650.1 | thylakoid lumenal 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	0.8	100.0%	-1.4
16839	AT1G15030.1 | expressed protein | chr1:5177524-5180339 FORWARD | Aliases: T15D22.8, T15D22_8	3.0	3.1	-0.1	-0.8	100.0%	-1.6
16840	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	3.9	-0.2	-0.8	100.0%	-1.7
16841	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	4.5	4.3	0.2	0.8	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
16842	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	2.5	2.7	-0.1	-0.8	100.0%	-1.6
16843	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	4.0	-0.2	-0.8	100.0%	-1.4
16844	AT1G27610.1 | expressed protein, identical to hypothetical protein GB:AAF24964 GI:6693038 from (Arabidopsis thaliana) | chr1:9607098-9607564 REVERSE | Aliases: T22C5.5	2.6	2.7	-0.1	-0.8	100.0%	-1.6
16845	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	2.4	2.5	-0.1	-0.8	100.0%	-2.1
16846	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	-0.8	100.0%	-1.6
16847	AT3G12910.1 | expressed protein | chr3:4110046-4110655 FORWARD | Aliases: MGH6.1, MGH6.22, MGH6_1, MJM20.5	2.2	2.2	-0.0	-0.8	100.0%	-2.4
16848	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	2.4	2.5	-0.1	-0.8	100.0%	-2.2
16849	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	2.5	2.4	0.1	0.8	100.0%	-1.8
16850	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	3.7	3.9	-0.2	-0.8	100.0%	-1.3
16851	AT3G31940.1 | hypothetical protein | chr3:12943265-12944247 FORWARD | Aliases: F8N14.6	2.2	2.1	0.1	0.8	100.0%	-2.1
16852	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	5.1	5.0	0.1	0.8	100.0%	-1.4
16853	AT4G04510.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr4:2242120-2244654 FORWARD | Aliases: F4H6.1	3.2	3.4	-0.1	-0.8	100.0%	-1.5
16854	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	-0.8	100.0%	-2.0
16855	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	2.7	0.1	0.8	100.0%	-1.8
16856	AT1G49220.1 | zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	2.7	2.8	-0.1	-0.8	100.0%	-1.9
16857	ATMG00130.1 | Symbol: ORF121A | hypothetical protein | chrM:34190-34555 FORWARD | Aliases: ORF121A	2.2	2.2	-0.1	-0.8	100.0%	-2.1
16858	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	2.4	-0.1	-0.8	100.0%	-1.8
16859	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	8.3	7.6	0.7	0.8	100.0%	-0.8
16860	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	4.1	-0.2	-0.8	100.0%	-0.9
16861	AT1G37010.1 | hypothetical protein | chr1:14043359-14043668 FORWARD | Aliases: T32E20.23, T32E20_23	2.6	2.7	-0.1	-0.8	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
16862	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	2.3	2.2	0.1	0.8	100.0%	-1.6
16863	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	7.4	6.8	0.6	0.8	100.0%	-0.9
16864	AT3G42440.1 | hypothetical protein, several hypothetical proteins - Arabidopsis thaliana | chr3:14588317-14588810 FORWARD | Aliases: T32A11.10	2.6	2.7	-0.1	-0.8	100.0%	-1.6
16865	AT2G25530.1 | AFG1-like ATPase family protein, contains Pfam profile: PF03969 AFG1-like ATPase	7.2	7.5	-0.3	-0.8	100.0%	-1.0
16866	AT3G32280.1 | hypothetical protein | chr3:13237545-13243867 FORWARD | Aliases: F6H5.21	2.7	2.6	0.1	0.8	100.0%	-2.1
16867	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	2.9	-0.1	-0.8	100.0%	-1.7
16868	AT5G48210.1 | expressed protein | chr5:19565640-19566367 FORWARD | Aliases: MIF21.10, MIF21_10	2.7	2.8	-0.1	-0.8	100.0%	-2.1
16869	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	3.6	3.8	-0.2	-0.8	100.0%	-1.5
16870	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	4.0	-0.2	-0.8	100.0%	-1.2
16871	AT4G23910.1 | expressed protein, various predicted proteins, Arabidopsis thaliana | chr4:12426718-12429297 FORWARD | Aliases: T32A16.80, T32A16_80	5.4	5.6	-0.2	-0.8	100.0%	-1.1
16872	AT1G15180.1 | MATE efflux family protein, contains Pfam profile PF01554: Uncharacterized membrane protein family | chr1:5224385-5226697 FORWARD | Aliases: F9L1.12, F9L1_12	2.4	2.5	-0.1	-0.8	100.0%	-1.9
16873	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	4.2	3.9	0.2	0.8	100.0%	-1.1
16874	AT5G43900.1 | Symbol: MYA2 | myosin heavy chain (MYA2), nearly identical to PIR:S51824 myosin heavy chain MYA2 (Arabidopsis thaliana)	5.1	4.8	0.3	0.8	100.0%	-1.1
16875	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	3.2	3.4	-0.2	-0.8	100.0%	-1.5
16876	AT3G20980.1 | expressed protein | chr3:7355969-7357972 FORWARD | Aliases: MSA6.3	2.9	3.0	-0.1	-0.8	100.0%	-1.7
16877	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	-0.8	100.0%	-2.0
16878	AT3G33064.1 | hypothetical protein | chr3:13623922-13624638 FORWARD | Aliases: T25F15.11	2.4	2.3	0.1	0.8	100.0%	-1.6
16879	AT5G47750.1 | protein kinase, putative, similar to protein kinase G11A (Oryza sativa) SWISS-PROT:P47997 | chr5:19356929-19359582 REVERSE | Aliases: MCA23.7, MCA23_7	5.3	5.5	-0.1	-0.8	100.0%	-1.4
16880	AT4G14500.1 | expressed protein, weak similarity to SP:Q9UKL6 Phosphatidylcholine transfer protein (PC-TP) {Homo sapiens} | chr4:8334172-8337269 FORWARD | Aliases: DL3290W, FCAALL.198	8.4	8.5	-0.1	-0.8	100.0%	-1.5
16881	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	8.0	8.3	-0.2	-0.8	100.0%	-1.1
16882	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	3.0	-0.1	-0.8	100.0%	-1.3
16883	AT5G06190.1 | expressed protein | chr5:1876035-1876638 REVERSE | Aliases: MBL20.7, MBL20_7	5.9	5.5	0.4	0.8	100.0%	-1.0
16884	AT5G02680.1 | expressed protein | chr5:605710-606763 FORWARD | Aliases: F9G14.1	3.8	4.0	-0.2	-0.8	100.0%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
16885	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	8.0	7.7	0.3	0.8	100.0%	-1.0
16886	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	3.5	3.6	-0.2	-0.8	100.0%	-1.4
16887	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	3.4	-0.2	-0.8	100.0%	-1.7
16888	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	-0.1	-0.8	100.0%	-2.3
16889	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	11.0	11.2	-0.2	-0.8	100.0%	-1.6
16890	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	3.2	3.3	-0.1	-0.8	100.0%	-1.6
16891	AT3G24120.2 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr3:8705643-8708322 REVERSE | Aliases: MUJ8.2	6.3	6.1	0.2	0.8	100.0%	-1.3
16892	AT1G74055.1 | expressed protein | chr1:27852891-27853473 FORWARD | Aliases: None	4.2	4.3	-0.2	-0.8	100.0%	-1.3
16893	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	2.5	2.4	0.1	0.8	100.0%	-2.0
16894	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	2.3	2.3	0.1	0.8	100.0%	-2.0
16895	AT3G42790.1 | PHD finger family protein, contains PHD-finger domain, INTERPRO:IPR001965 | chr3:14888946-14890755 REVERSE | Aliases: T21C14.10	8.7	8.5	0.2	0.8	100.0%	-1.5
16896	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	7.0	6.5	0.4	0.8	100.0%	-0.9
16897	AT1G62910.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:23302722-23306827 FORWARD | Aliases: F16P17.6, F16P17_6	2.7	2.8	-0.1	-0.8	100.0%	-2.0
16898	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	8.1	7.7	0.4	0.8	100.0%	-0.8
16899	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	3.8	3.6	0.2	0.8	100.0%	-1.2
16900	AT1G32570.1 | hypothetical protein | chr1:11777281-11777537 FORWARD | Aliases: T9G5.6, T9G5_6	4.4	4.7	-0.2	-0.8	100.0%	-1.1
16901	AT1G70520.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr1:26588441-26591082 REVERSE | Aliases: F24J13.9, F24J13_9	5.2	5.4	-0.1	-0.8	100.0%	-1.3
16902	AT3G07400.1 | lipase class 3 family protein, contains Pfam profile PF01764: Lipase | chr3:2367308-2372721 FORWARD | Aliases: F21O3.11	6.6	6.5	0.2	0.8	100.0%	-1.3
16903	AT4G04890.1 | Symbol: PDF2 | homeobox-leucine zipper protein protodermal factor 2 (PDF2), identical to GP:14276060: protodermal factor2 (GI:14276060)	4.3	4.5	-0.2	-0.8	100.0%	-1.3
16904	AT3G28980.1 | expressed protein | chr3:10994427-10996239 REVERSE | Aliases: K5K13.11	3.3	3.4	-0.1	-0.8	100.0%	-1.8
16905	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	6.4	6.0	0.4	0.8	100.0%	-0.9
16906	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	6.4	6.0	0.4	0.8	100.0%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
16907	AT5G11680.1 | expressed protein, predicted proteins, Arabidopsis thaliana | chr5:3758859-3760848 FORWARD | Aliases: T22P22.70, T22P22_70	9.3	9.4	-0.1	-0.8	100.0%	-1.3
16908	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	2.4	2.5	-0.1	-0.8	100.0%	-1.4
16909	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	2.6	-0.1	-0.8	100.0%	-1.8
16910	AT5G47260.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.9	3.0	-0.1	-0.8	100.0%	-1.6
16911	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	5.2	5.5	-0.4	-0.8	100.0%	-0.9
16912	AT4G03370.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr4:1478077-1478964 REVERSE | Aliases: F4C21.32, F4C21_32	2.6	2.7	-0.1	-0.8	100.0%	-1.7
16913	AT4G20400.2 | similar to transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein [Arabidopsis thaliana] (TAIR:At2g34880.1); similar to transcription factor jumonji (jmj) 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, jmjC (InterPro:IPR003347) | chr4:11009704-11013871 FORWARD | Aliases: F9F13.50, F9F13_50	4.5	4.6	-0.1	-0.8	100.0%	-1.8
16914	AT5G58390.1 | peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi:5381253:dbj:BAA82306 | chr5:23616793-23618551 REVERSE | Aliases: MCK7.26, MCK7_26	2.2	2.3	-0.1	-0.8	100.0%	-2.1
16915	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	3.5	0.1	0.8	100.0%	-1.6
16916	AT3G29660.1 | hypothetical protein | chr3:11525003-11526500 FORWARD | Aliases: MOD1.2	3.1	3.2	-0.1	-0.8	100.0%	-1.8
16917	AT5G16420.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:5368037-5369644 FORWARD | Aliases: MQK4.15, MQK4_15	4.7	4.6	0.2	0.8	100.0%	-1.2
16918	AT5G42090.1 | expressed protein | chr5:16843926-16845682 FORWARD | Aliases: MJC20.20, MJC20_20	6.7	7.0	-0.3	-0.8	100.0%	-1.1
16919	AT3G44070.1 | expressed protein, ; expression supported by MPSS | chr3:15839164-15840075 REVERSE | Aliases: F26G5.20	3.0	3.1	-0.1	-0.8	100.0%	-1.6
16920	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 - Arabidopsis thaliana, PIR:S59548	2.6	2.7	-0.1	-0.8	100.0%	-1.7
16921	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	3.4	3.5	-0.2	-0.8	100.0%	-1.2
16922	AT2G36050.1 | ovate protein-related, contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568 | chr2:15142651-15143828 REVERSE | Aliases: F11F19.32, F11F19_32	3.1	3.3	-0.2	-0.8	100.0%	-1.4
16923	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	2.9	2.8	0.1	0.8	100.0%	-1.6
16924	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	2.5	0.1	0.8	100.0%	-2.0
16925	AT2G40680.1 | hypothetical protein | chr2:16979907-16980797 FORWARD | Aliases: T7D17.14, T7D17_14	2.5	2.7	-0.2	-0.8	100.0%	-1.2
16926	AT1G08470.1 | strictosidine synthase family protein, similar to strictosidine synthase (Rauvolfia serpentina)(SP:P15324) | chr1:2682130-2684103 REVERSE | Aliases: T27G7.16, T27G7_16	7.4	7.5	-0.2	-0.8	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
16927	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	3.7	-0.1	-0.8	100.0%	-1.5
16928	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	4.2	0.1	0.8	100.0%	-1.4
16929	AT3G52700.1 | expressed protein, teichoic acid biosynthesis gene TagB, Staphylococcus aureus, EMBL:SAU91741 | chr3:19543394-19544071 REVERSE | Aliases: F3C22.100	2.4	2.5	-0.1	-0.8	100.0%	-1.9
16930	AT4G13980.1 | Symbol: AT HSFA5 | heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain | chr4:8076975-8079284 REVERSE | Aliases: DL3030C, FCAALL.27, HSFA5	3.5	3.4	0.1	0.8	100.0%	-1.8
16931	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	2.6	-0.1	-0.8	100.0%	-1.9
16932	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)	6.0	6.3	-0.3	-0.8	100.0%	-1.7
16933	AT3G22990.1 | expressed protein | chr3:8163965-8166352 FORWARD | Aliases: MXC7.2	6.7	6.3	0.4	0.8	100.0%	-1.0
16934	AT2G26520.1 | expressed protein | chr2:11287103-11288018 FORWARD | Aliases: T9J22.19, T9J22_19	3.1	3.0	0.1	0.8	100.0%	-1.7
16935	AT2G44970.1 | lipase-related, contains weak similarity to lipase (Pseudomonas aeruginosa) gi:3550950:gb:AAC34733. | chr2:18555898-18559130 REVERSE | Aliases: T14P1.23, T14P1_23	8.6	8.4	0.2	0.8	100.0%	-1.2
16936	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	3.7	0.1	0.8	100.0%	-1.6
16937	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	4.7	0.2	0.8	100.0%	-1.4
16938	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	2.9	3.0	-0.1	-0.8	100.0%	-2.0
16939	AT5G61660.1 | glycine-rich protein | chr5:24796441-24797156 REVERSE | Aliases: K11J9.19, K11J9_19	6.1	6.3	-0.2	-0.8	100.0%	-1.1
16940	AT4G24570.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr4:12686469-12687660 FORWARD | Aliases: F22K18.230, F22K18_230	6.9	6.6	0.2	0.8	100.0%	-1.1
16941	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	0.1	0.8	100.0%	-1.9
16942	AT1G62920.1 | expressed protein, ; expression supported by MPSS | chr1:23307978-23310039 FORWARD | Aliases: F16P17.25, F16P17_25	3.0	3.1	-0.1	-0.8	100.0%	-1.5
16943	AT4G18090.1 | expressed protein | chr4:10034023-10034859 REVERSE | Aliases: F15J5.60, F15J5_60	2.9	3.0	-0.1	-0.8	100.0%	-1.9
16944	AT1G64100.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:23795248-23797304 FORWARD | Aliases: F22C12.14	3.5	3.7	-0.2	-0.8	100.0%	-1.7
16945	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	4.5	4.7	-0.2	-0.8	100.0%	-1.1
16946	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	4.1	4.2	-0.1	-0.8	100.0%	-1.4
16947	AT3G29020.1 | Symbol: MYB110 |	3.1	3.0	0.1	0.8	100.0%	-1.6
16948	AT1G20680.1 | expressed protein, contains Pfam profile PF05742: Protein of unknown function (DUF833) | chr1:7168301-7173330 FORWARD | Aliases: F2D10.17, F2D10_17	2.9	3.0	-0.1	-0.8	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
16949	AT4G04650.1 | expressed protein | chr4:2353987-2355211 REVERSE | Aliases: T19J18.5, T19J18_5	3.3	3.5	-0.2	-0.8	100.0%	-1.4
16950	AT5G59330.1 | expressed protein | chr5:23948640-23948903 FORWARD | Aliases: MNC17.24, MNC17_24	3.0	3.1	-0.1	-0.8	100.0%	-1.6
16951	AT5G45760.2 | transducin family protein / WD-40 repeat family protein | chr5:18578338-18580422 FORWARD | Aliases: MRA19.19, MRA19_19	6.1	5.9	0.2	0.8	100.0%	-1.0
16952	AT2G17220.2 | protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) Swiss-Prot:Q06548 | chr2:7494757-7497258 REVERSE | Aliases: T23A1.8, T23A1_8	7.1	7.5	-0.3	-0.8	100.0%	-1.0
16953	AT2G03510.1 | band 7 family protein, contains Pfam profile PF01145: SPFH domain / Band 7 family | chr2:1066639-1069096 FORWARD | Aliases: T4M8.5, T4M8_5	8.6	8.2	0.4	0.8	100.0%	-1.1
16954	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	4.7	4.9	-0.2	-0.8	100.0%	-1.2
16955	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	3.3	3.4	-0.1	-0.8	100.0%	-1.6
16956	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	7.3	6.9	0.4	0.8	100.0%	-1.0
16957	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	2.3	2.4	-0.1	-0.8	100.0%	-2.1
16958	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	10.0	10.2	-0.2	-0.8	100.0%	-1.8
16959	AT3G11100.1 | expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189 | chr3:3476220-3477411 REVERSE | Aliases: F11B9.6	3.5	3.6	-0.1	-0.8	100.0%	-1.5
16960	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	5.7	5.8	-0.2	-0.8	100.0%	-1.2
16961	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	4.7	4.8	-0.1	-0.8	100.0%	-1.4
16962	AT4G02700.1 | Symbol: AST77 | sulfate transporter, identical to sulfate transporter (Arabidopsis thaliana) GI:2130944	2.5	2.6	-0.1	-0.8	100.0%	-1.9
16963	AT1G26780.1 | Symbol: MYB117 |	2.6	2.7	-0.1	-0.8	100.0%	-1.6
16964	AT1G69470.1 | expressed protein | chr1:26117238-26117660 FORWARD | Aliases: F10D13.12, F10D13_12	3.0	3.1	-0.1	-0.8	100.0%	-1.5
16965	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	3.5	-0.2	-0.8	100.0%	-1.2
16966	AT5G17730.1 | AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 | chr5:5852500-5854001 REVERSE | Aliases: MVA3.80, MVA3_80	2.3	2.2	0.1	0.8	100.0%	-2.2
16967	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	4.8	4.6	0.1	0.8	100.0%	-1.7
16968	AT3G25720.1 | expressed protein | chr3:9381471-9382642 FORWARD | Aliases: K13N2.4	3.2	3.4	-0.2	-0.8	100.0%	-1.2
16969	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	4.0	4.3	-0.2	-0.8	100.0%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
16970	AT3G51150.1 | kinesin motor family protein, contains Pfam domain, PF00225: Kinesin motor domain | chr3:19011835-19017748 FORWARD | Aliases: F24M12.190	2.9	2.8	0.1	0.8	100.0%	-1.8
16971	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	3.6	3.4	0.2	0.8	100.0%	-1.3
16972	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	3.6	-0.1	-0.8	100.0%	-1.7
16973	AT1G80630.1 | leucine-rich repeat family protein | chr1:30313588-30315548 REVERSE | Aliases: T21F11.4, T21F11_4	4.7	4.8	-0.2	-0.8	100.0%	-1.2
16974	AT1G01160.1 | Symbol: GIF2 | SSXT protein-related / transcription co-activator-related, similar to SYT/SSX4 fusion protein (GI:11127695) (Homo sapiens); 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	4.3	4.0	0.3	0.8	100.0%	-1.1
16975	AT3G16870.1 | zinc finger (GATA type) family protein, contains Pfam profile:PF00320 GATA:GATA zinc finger | chr3:5763592-5764660 REVERSE | Aliases: MUH15.3	4.4	4.5	-0.2	-0.8	100.0%	-1.2
16976	AT1G67360.2 | rubber elongation factor (REF) family protein, contains Pfam profile: PF05755 rubber elongation factor protein (REF) | chr1:25240474-25241757 REVERSE | Aliases: F1N21.18	7.4	7.2	0.2	0.8	100.0%	-1.2
16977	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	3.3	3.5	-0.2	-0.8	100.0%	-1.2
16978	AT5G52800.2 | expressed protein, similar to hypothetical protein [Homo sapiens] (GB:CAI46079.1) | chr5:21413170-21415862 FORWARD | Aliases: MXC20.1, MXC20_1	3.1	3.0	0.1	0.8	100.0%	-1.3
16979	AT1G23330.1 | expressed protein | chr1:8279700-8281880 REVERSE | Aliases: F26F24.20, F26F24_20	4.9	4.6	0.3	0.8	100.0%	-1.2
16980	AT5G23870.3 | pectinacetylesterase family protein, contains Pfam profile: PF03283 pectinacetylesterase	3.3	3.4	-0.1	-0.8	100.0%	-1.5
16981	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	2.4	2.4	0.1	0.8	100.0%	-2.1
16982	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	4.9	0.1	0.8	100.0%	-1.4
16983	AT5G51880.1 | expressed protein | chr5:21106659-21108167 FORWARD | Aliases: MJM18.3, MJM18_3	8.0	7.8	0.2	0.8	100.0%	-1.4
16984	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	6.2	6.3	-0.1	-0.8	100.0%	-1.4
16985	AT4G36250.1 | Symbol: ALDH3F1 | aldehyde dehydrogenase family protein, contais aldehyde dehydrogenase (NADP) family protein domain, Pfam:PF00171 | chr4:17150941-17153581 FORWARD | Aliases: F23E13.140, F23E13_140	2.5	2.6	-0.1	-0.8	100.0%	-1.8
16986	AT1G33410.1 | expressed protein | chr1:12109600-12118808 REVERSE | Aliases: F10C21.8, F10C21_8	6.0	6.1	-0.1	-0.8	100.0%	-1.2
16987	AT1G14760.1 | expressed protein | chr1:5084683-5085208 REVERSE | Aliases: F10B6.16, F10B6_16	2.7	2.8	-0.1	-0.8	100.0%	-1.7
16988	AT2G21780.1 | expressed protein | chr2:9298116-9298749 FORWARD | Aliases: F7D8.10, F7D8_10	3.0	2.9	0.1	0.8	100.0%	-1.6
16989	AT1G66100.1 | thionin, putative, similar to thionin (Arabidopsis thaliana) GI:1181533 | chr1:24609334-24610200 REVERSE | Aliases: F15E12.20, F15E12_20	2.5	2.6	-0.1	-0.8	100.0%	-1.7
16990	AT2G16190.1 | expressed protein | chr2:7027576-7028683 REVERSE | Aliases: F7H1.21, F7H1_21	2.9	2.8	0.1	0.8	100.0%	-1.8
16991	AT3G14920.1 | expressed protein | chr3:5018282-5020280 FORWARD | Aliases: K15M2.6	8.2	7.8	0.3	0.8	100.0%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
16992	AT5G48100.1 | laccase family protein / diphenol oxidase family protein, similar to laccase (Pinus taeda)(GI:13661197)	2.4	2.5	-0.1	-0.8	100.0%	-2.0
16993	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	3.1	-0.1	-0.8	100.0%	-1.5
16994	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	3.1	0.1	0.8	100.0%	-1.7
16995	AT5G49360.1 | Symbol: BXL1 | glycosyl hydrolase family 3 protein | chr5:20029105-20033968 REVERSE | Aliases: ATBXL1, BETA XYLOSIDASE 1, K7J8.3, K7J8_3	3.6	3.4	0.1	0.8	100.0%	-1.4
16996	AT5G48120.1 | expressed protein, low similarity to MMS19 (Mus musculus) GI:14029390 | chr5:19525177-19532000 REVERSE | Aliases: MDN11.21, MDN11_21	4.6	4.7	-0.1	-0.8	100.0%	-1.3
16997	AT5G41140.1 | expressed protein | chr5:16485675-16489774 FORWARD | Aliases: MEE6.21, MEE6_21	3.4	3.8	-0.4	-0.8	100.0%	-1.0
16998	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	2.4	2.5	-0.1	-0.8	100.0%	-2.1
16999	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	3.0	3.2	-0.2	-0.8	100.0%	-1.4
17000	AT2G45590.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:18793732-18796062 FORWARD | Aliases: F17K2.12	6.4	6.8	-0.4	-0.8	100.0%	-1.1
17001	AT5G57100.1 | transporter-related, low similarity to GDP-fucose transporter (Caenorhabditis elegans) GI:13940504, phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275 | chr5:23123528-23125824 REVERSE | Aliases: MUL3.4, MUL3_4	6.4	6.2	0.2	0.8	100.0%	-1.0
17002	AT5G63905.1 | expressed protein | chr5:25588084-25588812 REVERSE | Aliases: None	5.2	5.4	-0.3	-0.8	100.0%	-1.0
17003	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	3.4	-0.1	-0.8	100.0%	-1.7
17004	AT2G03310.1 | expressed protein | chr2:1006253-1007180 REVERSE | Aliases: T4M8.26, T4M8_26	4.8	4.7	0.2	0.8	100.0%	-1.2
17005	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	3.2	-0.1	-0.8	100.0%	-1.9
17006	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	6.5	6.3	0.3	0.8	100.0%	-1.4
17007	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	3.4	-0.2	-0.8	100.0%	-1.4
17008	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	2.7	2.6	0.1	0.8	100.0%	-1.7
17009	AT1G50620.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr1:18752205-18755006 FORWARD | Aliases: F17J6.14, F17J6_14	3.0	3.0	0.1	0.8	100.0%	-1.8
17010	AT4G39820.1 | expressed protein | chr4:18476001-18477937 REVERSE | Aliases: T5J17.8	5.7	5.9	-0.3	-0.8	100.0%	-1.2
17011	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	4.0	4.2	-0.2	-0.8	100.0%	-1.4
17012	AT4G01390.1 | meprin and TRAF homology domain-containing protein / MATH domain-containing protein, weak similarity to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain | chr4:570242-571483 REVERSE | Aliases: F2N1.33, F2N1_33	3.7	3.8	-0.2	-0.8	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
17013	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	9.5	9.3	0.2	0.8	100.0%	-1.7
17014	AT1G20290.1 | expressed protein | chr1:7025538-7029688 REVERSE | Aliases: F14O10.11, F14O10_11	2.5	2.5	-0.1	-0.8	100.0%	-2.2
17015	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	3.4	-0.1	-0.8	100.0%	-1.7
17016	AT3G14310.1 | Symbol: ATPME3 |	9.4	8.9	0.5	0.8	100.0%	-1.1
17017	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	2.3	-0.1	-0.8	100.0%	-2.0
17018	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	-0.8	100.0%	-1.8
17019	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	5.6	5.5	0.1	0.8	100.0%	-1.6
17020	AT2G29080.1 | Symbol: FTSH3 | encodes an FtsH protease that is localized to the mitochondrion	7.7	8.0	-0.3	-0.8	100.0%	-1.2
17021	AT3G61120.1 | Symbol: AGL13 | MADS-box protein (AGL13) | chr3:22629234-22631466 REVERSE | Aliases: AGAMOUS LIKE 13, MADS BOX PROTEIN AGL13, T20K12.20	2.0	2.1	-0.1	-0.8	100.0%	-2.4
17022	AT1G47470.1 | hypothetical protein | chr1:17417051-17417521 REVERSE | Aliases: F16N3.31, F16N3_31	2.4	2.5	-0.1	-0.8	100.0%	-2.2
17023	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	6.4	6.2	0.1	0.8	100.0%	-1.5
17024	AT2G06040.1 | expressed protein | chr2:2354031-2355495 REVERSE | Aliases: F5K7.20, F5K7_20	2.9	2.8	0.1	0.8	100.0%	-1.6
17025	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	5.3	5.6	-0.3	-0.8	100.0%	-1.1
17026	AT1G20520.1 | expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function | chr1:7106912-7107607 REVERSE | Aliases: F5M15.16, F5M15_16	3.2	3.3	-0.1	-0.8	100.0%	-1.6
17027	AT5G65540.1 | expressed protein | chr5:26212915-26215913 FORWARD | Aliases: K21L13.5, K21L13_5	4.7	4.9	-0.2	-0.8	100.0%	-1.2
17028	AT3G52870.1 | calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif | chr3:19604151-19606797 REVERSE | Aliases: F8J2.40	6.7	6.9	-0.2	-0.8	100.0%	-1.2
17029	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	4.7	4.6	0.1	0.8	100.0%	-1.5
17030	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	2.5	2.4	0.1	0.8	100.0%	-1.6
17031	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	5.2	5.3	-0.2	-0.8	100.0%	-1.3
17032	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	3.8	3.7	0.1	0.8	100.0%	-1.6
17033	AT2G22950.1 | calcium-transporting ATPase, plasma membrane-type, putative / Ca2+-ATPase, putative (ACA7), identical to SP:O64806 Potential calcium-transporting ATPase 7, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 7) {Arabidopsis thaliana}; strong similarity to SP:O81108 Calcium-transporting ATPase 2, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-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	3.2	3.4	-0.1	-0.8	100.0%	-1.6
17034	AT2G14290.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.9	3.7	0.2	0.8	100.0%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
17035	AT2G17870.1 | cold-shock DNA-binding family protein, contains Pfam domains, PF00313: 'Cold-shock' DNA-binding domain and PF00098: Zinc knuckle	9.7	9.9	-0.2	-0.8	100.0%	-1.4
17036	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	0.8	100.0%	-1.9
17037	AT3G12420.1 | expressed protein | chr3:3947927-3948889 REVERSE | Aliases: T2E22.26	2.1	2.2	-0.1	-0.8	100.0%	-2.0
17038	AT3G48200.1 | expressed protein | chr3:17843758-17848499 REVERSE | Aliases: T24C20.80	3.2	3.1	0.1	0.8	100.0%	-1.9
17039	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	5.6	5.3	0.2	0.8	100.0%	-0.9
17040	AT5G23000.1 | myb family transcription factor (MYB37), contains PFAM profile: myb DNA binding domain PF00249; | chr5:7696237-7697930 FORWARD | Aliases: T20O7.2, T20O7_2	2.8	2.7	0.1	0.8	100.0%	-1.5
17041	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	2.7	2.7	-0.1	-0.8	100.0%	-1.7
17042	AT1G73830.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.1	3.3	-0.1	-0.8	100.0%	-1.7
17043	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	8.6	8.9	-0.3	-0.8	100.0%	-1.1
17044	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	3.2	3.3	-0.1	-0.8	100.0%	-1.6
17045	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	4.5	4.7	-0.2	-0.8	100.0%	-1.3
17046	AT5G26760.2 | expressed protein | chr5:9403683-9407304 REVERSE | Aliases: F2P16.20, F2P16_20	5.0	4.8	0.2	0.8	100.0%	-1.0
17047	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	4.9	4.6	0.3	0.8	100.0%	-0.9
17048	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	5.1	5.0	0.1	0.8	100.0%	-1.5
17049	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	2.8	-0.1	-0.8	100.0%	-1.9
17050	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	5.5	0.2	0.8	100.0%	-1.3
17051	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	7.2	6.8	0.4	0.8	100.0%	-1.0
17052	AT4G10260.1 | pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase | chr4:6371482-6372766 REVERSE | Aliases: T9A4.3	3.1	3.2	-0.1	-0.8	100.0%	-1.6
17053	AT5G10310.1 | expressed protein | chr5:3241519-3242128 REVERSE | Aliases: F18D22.80, F18D22_80	2.2	2.3	-0.1	-0.8	100.0%	-2.2
17054	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	2.6	-0.1	-0.8	100.0%	-1.9
17055	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	2.8	2.7	0.1	0.8	100.0%	-1.5
17056	AT2G41760.1 | expressed protein | chr2:17429848-17432066 FORWARD | Aliases: T11A7.14, T11A7_14	6.2	6.0	0.3	0.8	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
17057	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	-0.8	100.0%	-2.4
17058	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	4.5	4.7	-0.2	-0.8	100.0%	-1.2
17059	AT2G11370.1 | hypothetical protein | chr2:4538787-4539393 FORWARD | Aliases: F3K12.11, F3K12_11	2.3	2.4	-0.1	-0.8	100.0%	-2.1
17060	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	3.1	3.1	0.1	0.8	100.0%	-1.7
17061	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	-0.1	-0.8	100.0%	-2.0
17062	AT4G11560.1 | bromo-adjacent homology (BAH) domain-containing protein, contains Pfam profile PF01426: BAH domain | chr4:6999890-7003487 REVERSE | Aliases: F25E4.180, F25E4_180	7.2	7.4	-0.3	-0.8	100.0%	-1.1
17063	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	3.3	-0.1	-0.8	100.0%	-1.4
17064	AT5G28140.1 | hypothetical protein | chr5:10115253-10116616 REVERSE | Aliases: T24G3.70, T24G3_70	2.7	2.8	-0.1	-0.8	100.0%	-1.7
17065	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)	9.6	9.3	0.3	0.8	100.0%	-1.3
17066	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	5.6	-0.2	-0.8	100.0%	-1.5
17067	AT1G67460.1 | expressed protein, contains Pfam domain PF03193: Protein of unknown function, DUF258 | chr1:25273289-25275280 REVERSE | Aliases: T1F15.7, T1F15_7	4.5	4.3	0.2	0.8	100.0%	-1.3
17068	AT3G31310.1 | hypothetical protein | chr3:12679707-12681196 FORWARD | Aliases: T22B15.2	2.1	2.1	-0.1	-0.8	100.0%	-2.1
17069	AT2G28650.1 | exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit | chr2:12296229-12298122 REVERSE | Aliases: T8O18.6, T8O18_6	5.5	5.7	-0.2	-0.8	100.0%	-1.4
17070	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	2.8	-0.1	-0.8	100.0%	-1.9
17071	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	6.6	6.3	0.3	0.8	100.0%	-0.9
17072	AT1G54955.1 | expressed protein | chr1:20497787-20498401 FORWARD | Aliases: F14C21.48, F14C21_48	2.8	3.0	-0.1	-0.8	100.0%	-1.5
17073	AT4G11610.1 | Symbol: NTRB | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr4:7013723-7018043 REVERSE | Aliases: ATNTRB, T5C23.40, T5C23_40	3.5	3.6	-0.1	-0.8	100.0%	-1.3
17074	AT3G26990.1 | expressed protein, contains Pfam domain, PF04818: Protein of unknown function, DUF618 | chr3:9949502-9953278 REVERSE | Aliases: MOJ10.6	2.4	2.5	-0.1	-0.8	100.0%	-1.8
17075	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	3.9	3.8	0.1	0.8	100.0%	-1.3
17076	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	2.8	2.9	-0.1	-0.8	100.0%	-1.6
17077	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	4.8	5.1	-0.3	-0.8	100.0%	-1.3
17078	AT4G10845.1 | expressed protein | chr4:6662524-6664138 FORWARD | Aliases: None	4.2	4.1	0.1	0.8	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
17079	AT5G40155.1 | Encodes a defensin-like (DEFL) family protein. | chr5:16079119-16079965 FORWARD | Aliases: None	2.9	2.8	0.1	0.8	100.0%	-1.8
17080	AT5G26180.2 | NOL1/NOP2/sun family protein, similar to NOL1R (Homo sapiens) GI:16226071; contains Pfam profile PF01189: NOL1/NOP2/sun family | chr5:9149230-9153505 FORWARD | Aliases: T19G15.30, T19G15_30	5.0	4.8	0.2	0.8	100.0%	-1.1
17081	AT5G44250.1 | expressed protein, contains Pfam PF05705: Eukaryotic protein of unknown function (DUF829) | chr5:17840972-17842943 REVERSE | Aliases: MLN1.18, MLN1_18	6.5	6.1	0.4	0.8	100.0%	-1.1
17082	AT2G33255.1 | haloacid dehalogenase-like hydrolase family protein, contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	6.5	6.2	0.3	0.8	100.0%	-1.1
17083	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	4.9	4.7	0.2	0.8	100.0%	-1.7
17084	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	5.0	4.9	0.1	0.8	100.0%	-1.4
17085	AT3G18360.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr3:6300833-6301690 REVERSE | Aliases: MYF24.8	2.5	2.6	-0.1	-0.8	100.0%	-1.8
17086	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	2.5	2.4	0.1	0.8	100.0%	-1.6
17087	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	3.6	-0.1	-0.8	100.0%	-1.6
17088	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	9.4	9.7	-0.3	-0.8	100.0%	-1.3
17089	AT2G04580.1 | hypothetical protein | chr2:1599679-1600830 REVERSE | Aliases: T1O3.1, T1O3_1	2.6	2.7	-0.1	-0.8	100.0%	-2.0
17090	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	7.6	7.3	0.3	0.8	100.0%	-1.1
17091	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	3.0	3.1	-0.1	-0.8	100.0%	-1.5
17092	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	5.2	5.3	-0.2	-0.8	100.0%	-1.4
17093	AT3G58770.1 | expressed protein, ; expression supported by MPSS | chr3:21743497-21746160 FORWARD | Aliases: T20N10.120	2.8	2.7	0.1	0.8	100.0%	-1.8
17094	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	2.6	-0.1	-0.8	100.0%	-1.8
17095	AT5G51180.2 | expressed protein | chr5:20814243-20817440 FORWARD | Aliases: MWD22.12, MWD22_12	6.2	6.0	0.2	0.8	100.0%	-1.2
17096	AT3G53030.1 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr3:19673262-19675481 FORWARD | Aliases: F8J2.200	5.5	5.7	-0.2	-0.8	100.0%	-1.3
17097	AT2G20050.1 | protein phosphatase 2C, putative / PP2C, putative, contains PF00481: Protein phosphatase 2C domain; | chr2:8659554-8661274 REVERSE | Aliases: T2G17.15, T2G17_15	3.4	3.6	-0.2	-0.8	100.0%	-1.3
17098	AT1G75560.1 | zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle | chr1:28374802-28376902 REVERSE | Aliases: F10A5.22, F10A5_22	3.9	3.3	0.6	0.8	100.0%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
17099	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	3.7	-0.1	-0.8	100.0%	-1.6
17100	NA	2.7	2.7	0.1	0.8	100.0%	-2.2
17101	AT1G56590.1 | clathrin adaptor complexes medium subunit family protein, contains Pfam profile: PF00928 adaptor complexes medium subunit family	4.8	4.5	0.2	0.8	100.0%	-1.3
17102	AT1G54520.1 | expressed protein | chr1:20367115-20369706 FORWARD | Aliases: F20D21.34, F20D21_34	8.0	8.3	-0.3	-0.8	100.0%	-1.1
17103	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	2.7	-0.1	-0.8	100.0%	-1.7
17104	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	5.5	0.2	0.8	100.0%	-1.4
17105	AT1G52540.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr1:19573727-19575873 REVERSE | Aliases: F6D8.24, F6D8_24	4.9	5.1	-0.2	-0.8	100.0%	-1.4
17106	AT4G02010.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:881185-885399 FORWARD | Aliases: T10M13.2, T10M13_2	5.7	5.5	0.2	0.8	100.0%	-1.0
17107	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	4.9	0.2	0.8	100.0%	-1.2
17108	AT5G03350.1 | legume lectin family protein, contains Pfam domain, PF00139: Legume lectins beta domain | chr5:815673-816657 REVERSE | Aliases: F12E4.80, F12E4_80	3.3	3.1	0.2	0.8	100.0%	-1.3
17109	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	6.3	0.2	0.8	100.0%	-1.2
17110	AT2G18610.1 | expressed protein | chr2:8083430-8084396 REVERSE | Aliases: F24H14.4, F24H14_4	3.3	3.4	-0.1	-0.8	100.0%	-1.6
17111	AT3G28280.1 | expressed protein | chr3:10541883-10542808 REVERSE | Aliases: MZF16.6	2.5	2.4	0.1	0.8	100.0%	-2.0
17112	AT1G59830.2 | Symbol: PP2A 1 |	7.0	6.8	0.2	0.8	100.0%	-1.2
17113	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	-0.1	-0.8	100.0%	-1.9
17114	AT2G15010.1 | thionin, putative, similar to thionin (Arabidopsis thaliana) gi:1181533:gb:AAC41679 | chr2:6491461-6492234 FORWARD | Aliases: T15J14.5, T15J14_5	2.9	3.0	-0.1	-0.8	100.0%	-1.7
17115	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	3.4	3.5	-0.2	-0.8	100.0%	-1.4
17116	AT5G37060.1 | Symbol: ATCHX24 | cation/hydrogen exchanger, putative (CHX24), similar to Na+/H+-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	3.4	3.5	-0.1	-0.8	100.0%	-1.8
17117	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	6.8	6.4	0.4	0.8	100.0%	-1.0
17118	ATCG00140.1 | Symbol: ATPH | ATPase III subunit | chrC:13262-13507 REVERSE | Aliases: ATPH	9.0	8.7	0.3	0.8	100.0%	-1.1
17119	AT3G47950.1 | Symbol: AHA4 | 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 | chr3:17703687-17709837 FORWARD | Aliases: T17F15.180	3.9	4.0	-0.1	-0.8	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
17120	AT5G13400.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr5:4295757-4299108 REVERSE | Aliases: T22N19.50, T22N19_50	2.9	3.0	-0.1	-0.8	100.0%	-1.7
17121	AT2G25440.1 | leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to NL0E (Lycopersicon esculentum) gi:4235643:gb:AAD13303 | chr2:10833814-10836481 FORWARD | Aliases: F13B15.10, F13B15_10	2.9	3.0	-0.1	-0.8	100.0%	-2.1
17122	NA	6.2	6.5	-0.3	-0.8	100.0%	-1.3
17123	AT2G06820.1 | expressed protein, low similarity to zinc finger protein (Arabidopsis thaliana) GI:976277 | chr2:2726653-2727481 REVERSE | Aliases: T9F8.1, T9F8_1	2.1	2.2	-0.1	-0.8	100.0%	-2.3
17124	AT4G08250.1 | scarecrow transcription factor family protein, SCARECROW - Arabidopsis thaliana, PID:g1497987 | chr4:5196784-5198235 FORWARD | Aliases: T12G13.90, T12G13_90	3.1	3.2	-0.1	-0.8	100.0%	-1.9
17125	AT5G23770.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr5:8014516-8016274 REVERSE | Aliases: MRO11.19, MRO11_19	3.3	3.4	-0.1	-0.8	100.0%	-1.9
17126	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	6.8	6.3	0.5	0.8	100.0%	-0.9
17127	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	7.6	7.9	-0.2	-0.8	100.0%	-0.9
17128	AT3G20870.1 | metal transporter family protein, contains ZIP Zinc transporter domain, Pfam:PF02535 | chr3:7309359-7312708 REVERSE | Aliases: MOE17.18	8.8	9.1	-0.3	-0.8	100.0%	-1.1
17129	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	8.9	7.9	1.0	0.8	100.0%	-1.4
17130	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	2.7	2.8	-0.1	-0.8	100.0%	-1.8
17131	NA	2.4	2.4	-0.1	-0.8	100.0%	-2.4
17132	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	-0.1	-0.8	100.0%	-2.0
17133	AT1G53080.1 | legume lectin family protein | chr1:19785036-19785887 FORWARD | Aliases: F8L10.6, F8L10_6	2.8	2.7	0.1	0.8	100.0%	-2.1
17134	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	4.3	4.5	-0.2	-0.8	100.0%	-1.4
17135	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 (Oryza longistaminata) (Science 270 (5243), 1804-1806 (1995)) | chr1:12201943-12203388 FORWARD | Aliases: F14M2.19, F14M2_19	2.6	2.7	-0.1	-0.8	100.0%	-1.8
17136	AT1G13410.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:4601636-4603171 FORWARD | Aliases: T6J4.15, T6J4_15	3.2	3.3	-0.1	-0.8	100.0%	-1.7
17137	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	4.4	4.3	0.2	0.7	100.0%	-1.4
17138	AT1G74120.1 | mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF | chr1:27875584-27876921 REVERSE | Aliases: F9E11.3, F9E11_3	3.8	3.9	-0.1	-0.7	100.0%	-1.4
17139	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%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
17140	AT5G46100.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:18711543-18712961 REVERSE | Aliases: MCL19.15, MCL19_15	3.2	3.4	-0.1	-0.7	100.0%	-1.5
17141	AT5G62170.1 | expressed protein, various predicted proteins, Arabidopsis thaliana | chr5:24990209-24992764 REVERSE | Aliases: MTG10.21, MTG10_21	3.2	3.3	-0.1	-0.7	100.0%	-1.8
17142	AT1G71810.1 | ABC1 family protein, contains Pfam domain, PF03109: ABC1 family | chr1:27006076-27011838 REVERSE | Aliases: F14O23.19, F14O23_19	4.6	4.8	-0.1	-0.7	100.0%	-1.4
17143	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	5.2	5.4	-0.3	-0.7	100.0%	-1.3
17144	AT1G36970.1 | expressed protein | chr1:14018826-14020797 REVERSE | Aliases: T32E20.31, T32E20_31	3.2	3.3	-0.1	-0.7	100.0%	-1.5
17145	AT2G31850.1 | expressed protein | chr2:13547276-13547617 FORWARD | Aliases: F20M17.11, F20M17_11	3.1	3.2	-0.1	-0.7	100.0%	-1.7
17146	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	2.8	2.8	-0.1	-0.7	100.0%	-1.7
17147	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	2.7	2.8	-0.1	-0.7	100.0%	-2.0
17148	AT4G25920.1 | expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295) | chr4:13165484-13166881 FORWARD | Aliases: F20B18.30, F20B18_30	2.4	2.3	0.1	0.7	100.0%	-1.7
17149	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	2.7	-0.1	-0.7	100.0%	-1.6
17150	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) GI:31415724 | chr5:7061105-7069221 REVERSE | Aliases: F22D1.10, F22D1_10	4.6	4.4	0.2	0.7	100.0%	-1.3
17151	AT4G30150.1 | expressed protein | chr4:14742458-14749993 FORWARD | Aliases: F6G3.180, F6G3_180	5.7	5.5	0.1	0.7	100.0%	-1.3
17152	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	6.8	7.1	-0.3	-0.7	100.0%	-1.3
17153	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	-0.1	-0.7	100.0%	-2.1
17154	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	0.7	100.0%	-1.6
17155	AT2G27610.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:11791004-11793610 REVERSE | Aliases: F15K20.29, F15K20_29	2.9	2.8	0.1	0.7	100.0%	-1.8
17156	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	4.6	4.5	0.1	0.7	100.0%	-1.4
17157	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	-0.1	-0.7	100.0%	-2.3
17158	AT1G60460.3 | expressed protein | chr1:22279149-22282450 FORWARD | Aliases: F8A5.1, F8A5_1	2.5	2.6	-0.1	-0.7	100.0%	-1.9
17159	AT3G48185.1 | expressed protein | chr3:17803996-17804528 REVERSE | Aliases: None	6.4	6.1	0.3	0.7	100.0%	-1.1
17160	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	3.1	-0.1	-0.7	100.0%	-1.7
17161	AT3G42400.1 | hypothetical protein, various predicted proteins, Arabadopsis thaliana | chr3:14531604-14533752 FORWARD | Aliases: T14K23.110	2.7	2.8	-0.1	-0.7	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
17162	AT4G19440.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:10600801-10604531 REVERSE | Aliases: T5K18.220, T5K18_220	3.1	3.2	-0.1	-0.7	100.0%	-1.7
17163	AT2G39590.1 | 40S ribosomal protein S15A (RPS15aC) | chr2:16524666-16525343 REVERSE | Aliases: F12L6.25, F12L6_25	3.1	3.0	0.1	0.7	100.0%	-1.9
17164	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	5.4	5.1	0.3	0.7	100.0%	-1.3
17165	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	2.9	-0.1	-0.7	100.0%	-2.0
17166	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	2.6	2.7	-0.1	-0.7	100.0%	-1.4
17167	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	2.2	-0.1	-0.7	100.0%	-2.0
17168	AT5G46730.1 | glycine-rich protein | chr5:18981239-18982295 FORWARD | Aliases: MZA15.15, MZA15_15	10.3	9.9	0.3	0.7	100.0%	-1.3
17169	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	-0.7	100.0%	-1.8
17170	AT1G08020.1 | expressed protein | chr1:2489773-2490304 REVERSE | Aliases: T6D22.10, T6D22_10	3.5	3.6	-0.1	-0.7	100.0%	-1.4
17171	AT3G04020.1 | expressed protein | chr3:1041078-1042525 FORWARD | Aliases: T11I18.13, T11I18_13	3.4	3.3	0.1	0.7	100.0%	-1.8
17172	AT1G21950.1 | expressed protein | chr1:7723428-7723852 REVERSE | Aliases: T26F17.18, T26F17_18	3.0	3.1	-0.1	-0.7	100.0%	-1.8
17173	AT5G33340.1 | aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease | chr5:12611697-12613182 FORWARD | Aliases: F19N2.60, F19N2_60	2.5	2.6	-0.1	-0.7	100.0%	-1.8
17174	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	5.3	5.2	0.1	0.7	100.0%	-1.6
17175	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	7.9	-0.2	-0.7	100.0%	-1.4
17176	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	9.8	9.7	0.1	0.7	100.0%	-1.5
17177	AT5G37520.1 | expressed protein, predicted proteins, Arabidopsis thaliana | chr5:14919900-14921441 FORWARD | Aliases: MPA22.6, MPA22_6	3.3	3.5	-0.1	-0.7	100.0%	-1.5
17178	AT3G21570.1 | expressed protein | chr3:7600303-7600713 REVERSE | Aliases: MIL23.14	2.7	2.8	-0.1	-0.7	100.0%	-1.8
17179	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	2.5	-0.1	-0.7	100.0%	-1.8
17180	AT5G13420.1 | transaldolase, putative, similar to transaldolase (Solanum tuberosum) gi:2078350:gb:AAB54016 | chr5:4301795-4304315 REVERSE | Aliases: T22N19.70, T22N19_70	10.9	11.1	-0.3	-0.7	100.0%	-1.8
17181	AT4G00350.1 | MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) 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	2.5	2.4	0.1	0.7	100.0%	-1.7
17182	AT1G22770.1 | Symbol: GI | gigantea protein (GI), identical to gigantea protein SP:Q9SQI2 from (Arabidopsis thaliana)	7.1	7.4	-0.2	-0.7	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
17183	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 (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563 | chr5:24977333-24978489 FORWARD | Aliases: MTG10.20, MTG10_20	4.8	4.9	-0.1	-0.7	100.0%	-1.6
17184	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%	-1.9
17185	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	2.7	-0.1	-0.7	100.0%	-1.9
17186	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:BAB72550.1); contains InterPro domain ABC1 protein (InterPro:IPR004147) | chr4:15233080-15237115 FORWARD | Aliases: F3L17.6	5.2	5.0	0.2	0.7	100.0%	-1.1
17187	AT1G03950.1 | SNF7 family protein, contains Pfam domain, PF03357: SNF7 family | chr1:1011235-1013359 REVERSE | Aliases: F21M11.12, F21M11_12	5.3	5.0	0.3	0.7	100.0%	-0.9
17188	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	3.1	0.2	0.7	100.0%	-1.3
17189	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	7.5	7.8	-0.3	-0.7	100.0%	-1.1
17190	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	-0.1	-0.7	100.0%	-1.7
17191	AT1G52770.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr1:19659507-19661402 FORWARD | Aliases: F14G24.4, F14G24_4	2.9	2.8	0.1	0.7	100.0%	-1.8
17192	AT5G38320.1 | expressed protein, ; expression supported by MPSS | chr5:15333390-15334028 REVERSE | Aliases: MSI17.5, MSI17_5	2.5	2.6	-0.1	-0.7	100.0%	-1.9
17193	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	-0.7	100.0%	-2.1
17194	AT3G22250.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:7867813-7870060 FORWARD | Aliases: MMP21.3	3.6	3.8	-0.2	-0.7	100.0%	-1.4
17195	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	3.4	3.6	-0.1	-0.7	100.0%	-1.5
17196	AT1G36100.1 | myosin heavy chain-related, similar to hypothetical protein GI:4263830 from (Arabidopsis thaliana) (similar to MYOSIN HEAVY CHAIN (Encephalitozoon cuniculi) GI:19074177) (similar to MYOSIN HEAVY CHAIN (Encephalitozoon cuniculi) GI:19074177)	2.6	2.7	-0.1	-0.7	100.0%	-2.0
17197	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	3.3	-0.1	-0.7	100.0%	-1.4
17198	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	2.5	-0.1	-0.7	100.0%	-2.2
17199	AT2G10465.1 | replication protein-related, weak similarity to Replication Protein A 70	2.6	2.7	-0.1	-0.7	100.0%	-2.2
17200	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	2.9	-0.1	-0.7	100.0%	-1.6
17201	AT1G74900.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat | chr1:28137594-28139042 FORWARD | Aliases: F25A4.13, F25A4_13	5.0	5.2	-0.2	-0.7	100.0%	-1.4
17202	AT4G34840.1 | nucleosidase-related, contains weak similarity to MTA/SAH nucleosidase (Swiss-Prot:O51931) (Buchnera aphidicola)	4.5	4.3	0.1	0.7	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
17203	AT1G45145.1 | Symbol: ATTRX5 |	12.1	11.9	0.2	0.7	100.0%	-1.8
17204	AT5G40420.1 | Symbol: OLEO2 | glycine-rich protein / oleosin | chr5:16190621-16192011 REVERSE | Aliases: OLEOSIN TYPE 2, PA23	2.9	3.1	-0.1	-0.7	100.0%	-1.4
17205	AT4G02920.2 | expressed protein | chr4:1292640-1294861 FORWARD | Aliases: T4I9.20	5.8	6.0	-0.2	-0.7	100.0%	-1.4
17206	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	2.7	-0.1	-0.7	100.0%	-2.0
17207	AT1G47660.1 | expressed protein | chr1:17536381-17537991 REVERSE | Aliases: F16N3.35, F16N3_35	2.2	2.3	-0.1	-0.7	100.0%	-1.9
17208	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	3.2	-0.1	-0.7	100.0%	-1.9
17209	AT5G01780.1 | oxidoreductase, 2OG-Fe(II) oxygenase family protein, low similarity to alkB protein - Escherichia coli, PIR:BVECKB, alkB (Caulobacter crescentus)(GI:2055386); contains Pfam domain PF03171 2OG-Fe(II) oxygenase superfamily | chr5:302362-304169 REVERSE | Aliases: T20L15.50, T20L15_50	5.9	6.2	-0.3	-0.7	100.0%	-1.0
17210	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	2.3	2.3	-0.0	-0.7	100.0%	-2.4
17211	AT2G46360.1 | expressed protein | chr2:19035561-19036088 FORWARD | Aliases: F11C10.5	2.3	2.3	0.1	0.7	100.0%	-2.3
17212	AT3G13130.1 | expressed protein | chr3:4223015-4223620 FORWARD | Aliases: MJG19.8	3.3	3.4	-0.1	-0.7	100.0%	-1.7
17213	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	2.9	-0.1	-0.7	100.0%	-1.6
17214	AT1G37130.1 | Symbol: NIA2 | nitrate reductase 2 (NR2), identical to SP:P11035 Nitrate reductase 2 (formerly EC 1.6.6.1) (NR2) {Arabidopsis thaliana}	10.4	10.7	-0.3	-0.7	100.0%	-1.3
17215	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	3.6	3.5	0.1	0.7	100.0%	-1.3
17216	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	2.9	2.8	0.1	0.7	100.0%	-1.9
17217	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:BAB93003.1); similar to NADPH:protochlorophyllide oxidoreductase [Daucus carota] (GB:AAF20949.1); contains InterPro domain Light-dependent protochlorophyllide reductase (InterPro:IPR005979)	4.0	3.9	0.1	0.7	100.0%	-1.3
17218	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	-0.1	-0.7	100.0%	-1.7
17219	AT2G09840.1 | expressed protein | chr2:3712042-3712533 REVERSE | Aliases: T14C8.6, T14C8_6	2.3	2.4	-0.1	-0.7	100.0%	-2.2
17220	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	2.4	2.5	-0.1	-0.7	100.0%	-2.0
17221	AT2G29050.1 | rhomboid family protein, contains PFAM domain PF01694, Rhomboid family | chr2:12485223-12487449 FORWARD | Aliases: T9I4.13, T9I4_13	4.1	3.9	0.2	0.7	100.0%	-1.0
17222	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	3.7	-0.2	-0.7	100.0%	-1.7
17223	AT3G54810.2 | zinc finger (GATA type) family protein, GATA transcription factor 3, Arabidopsis thaliana, Y13650 | chr3:20307246-20309669 FORWARD | Aliases: T5N23.3	4.6	4.4	0.2	0.7	100.0%	-1.0
17224	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	2.2	-0.1	-0.7	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
17225	AT3G42860.1 | zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle | chr3:14957176-14959155 REVERSE | Aliases: F18P9.20	3.7	3.6	0.1	0.7	100.0%	-1.9
17226	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	3.2	-0.1	-0.7	100.0%	-1.2
17227	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	2.3	2.3	0.1	0.7	100.0%	-1.9
17228	AT1G29110.1 | cysteine proteinase, putative, contains similarity to cysteine protease SPCP1 GI:13491750 from (Ipomoea batatas)	4.1	4.3	-0.2	-0.7	100.0%	-1.2
17229	AT5G49440.1 | expressed protein | chr5:20065465-20066823 FORWARD | Aliases: K7J8.12, K7J8_12	3.0	2.9	0.2	0.7	100.0%	-1.3
17230	AT5G41660.1 | expressed protein, similar to unknown protein (emb:CAB86921.1) | chr5:16674244-16674876 FORWARD | Aliases: MBK23.19, MBK23_19	2.5	2.5	-0.1	-0.7	100.0%	-1.9
17231	AT1G74220.1 | expressed protein, similar to GB:AAD20071 from (Arabidopsis thaliana) | chr1:27916760-27917795 REVERSE | Aliases: F1O17.11, F1O17_11	2.7	2.7	-0.1	-0.7	100.0%	-2.0
17232	AT2G32210.1 | expressed protein | chr2:13685063-13685907 FORWARD | Aliases: F22D22.4, F22D22_4	2.5	2.4	0.1	0.7	100.0%	-2.2
17233	AT4G09880.1 | hypothetical protein, F21E10.5 Arabidopsis thaliana BAC F21E10, PID:g3047086 | chr4:6214621-6215335 FORWARD | Aliases: T5L19.10, T5L19_10	3.4	3.5	-0.1	-0.7	100.0%	-1.8
17234	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	2.7	-0.1	-0.7	100.0%	-2.2
17235	AT2G18500.1 | ovate family protein, 69% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	4.9	4.8	0.2	0.7	100.0%	-1.2
17236	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	3.1	3.0	0.1	0.7	100.0%	-1.7
17237	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	2.4	-0.1	-0.7	100.0%	-1.8
17238	AT1G43570.1 | expressed protein | chr1:16404310-16405356 REVERSE | Aliases: T10P12.5, T10P12_5	3.5	3.7	-0.2	-0.7	100.0%	-1.4
17239	AT5G13010.1 | Symbol: EMB3011 | RNA helicase, putative, similar to DEAH-box RNA helicase (Chlamydomonas reinhardtii) 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	8.5	8.8	-0.3	-0.7	100.0%	-1.5
17240	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	2.3	2.3	0.1	0.7	100.0%	-2.1
17241	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	0.1	0.7	100.0%	-1.8
17242	AT4G08270.1 | hypothetical protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana) | chr4:5218102-5218401 FORWARD | Aliases: T12G13.110, T12G13_110	3.1	3.2	-0.1	-0.7	100.0%	-1.6
17243	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	6.6	6.7	-0.2	-0.7	100.0%	-1.6
17244	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	-0.7	100.0%	-2.2
17245	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	2.9	-0.1	-0.7	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
17246	AT1G22040.1 | kelch repeat-containing F-box family protein, contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	4.8	5.0	-0.2	-0.7	100.0%	-1.2
17247	AT3G20740.1 | Symbol: FIE | fertilization-independent endosperm protein (FIE), contains 6 WD-40 repeats (PF00400); identical to fertilization-independent endosperm protein (GI:4567095) (Arabidopsis thaliana) | chr3:7248815-7252458 REVERSE | Aliases: FERTILIZATION INDEPENDENT ENDOSPERM, FERTILIZATION INDEPENDENT ENDOSPERM 1, FIE1, FIS3, MOE17.5	5.2	5.1	0.1	0.7	100.0%	-1.6
17248	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	2.5	-0.1	-0.7	100.0%	-1.9
17249	AT4G37130.1 | hydroxyproline-rich glycoprotein family protein | chr4:17489461-17492004 FORWARD | Aliases: AP22.15, AP22_15	6.7	6.5	0.1	0.7	100.0%	-1.5
17250	AT4G27930.1 | expressed protein | chr4:13902641-13902984 REVERSE | Aliases: T13J8.40, T13J8_40	2.4	2.5	-0.1	-0.7	100.0%	-1.9
17251	AT2G28630.1 | beta-ketoacyl-CoA synthase family protein | chr2:12282396-12284322 REVERSE | Aliases: T8O18.8, T8O18_8	2.6	2.7	-0.1	-0.7	100.0%	-1.9
17252	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	3.4	-0.1	-0.7	100.0%	-1.3
17253	AT3G30220.1 | expressed protein | chr3:11880345-11880937 REVERSE | Aliases: MIL15.3	2.0	2.1	-0.0	-0.7	100.0%	-2.4
17254	AT1G47810.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.4	-0.1	-0.7	100.0%	-2.1
17255	AT3G27980.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr3:10395141-10397098 FORWARD | Aliases: K24A2.9	2.0	2.1	-0.0	-0.7	100.0%	-2.5
17256	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	2.5	2.5	-0.1	-0.7	100.0%	-2.0
17257	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	3.6	-0.2	-0.7	100.0%	-1.6
17258	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	2.4	-0.1	-0.7	100.0%	-2.3
17259	AT5G52320.1 | Symbol: CYP96A4 | cytochrome P450, putative | chr5:21262204-21263908 REVERSE | Aliases: K24M7.5, K24M7_5	2.5	2.6	-0.1	-0.7	100.0%	-2.0
17260	AT4G19480.1 | expressed protein | chr4:10614791-10615327 REVERSE | Aliases: F24J7.40, F24J7_40	2.8	3.0	-0.1	-0.7	100.0%	-1.6
17261	AT3G17330.1 | expressed protein, contains Pfam profile PF04146: YT521-B-like family | chr3:5916946-5920194 REVERSE | Aliases: MGD8.17	4.4	4.3	0.1	0.7	100.0%	-1.9
17262	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	-0.7	100.0%	-1.8
17263	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	3.3	3.4	-0.2	-0.7	100.0%	-1.5
17264	AT1G22550.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr1:7966522-7968630 REVERSE | Aliases: F12K8.11, F12K8_11	6.6	6.4	0.2	0.7	100.0%	-0.9
17265	AT1G20130.1 | family II extracellular lipase, putative, contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase; similar to EXL3 (PMID:11431566)	3.2	3.3	-0.1	-0.7	100.0%	-1.8
17266	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	5.4	6.4	-1.0	-0.7	100.0%	-1.1
17267	AT4G26040.1 | hypothetical protein | chr4:13206844-13207212 FORWARD | Aliases: F20B18.150, F20B18_150	2.9	3.0	-0.1	-0.7	100.0%	-1.8
17268	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	2.9	0.1	0.7	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
17269	AT1G11380.1 | expressed protein, contains Pfam profile PF04749: Protein of unknown function, DUF614 | chr1:3832623-3834189 FORWARD | Aliases: T23J18.4, T23J18_4	5.1	5.4	-0.3	-0.7	100.0%	-1.1
17270	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	2.5	-0.1	-0.7	100.0%	-2.0
17271	AT1G21790.1 | expressed protein | chr1:7654173-7655872 FORWARD | Aliases: F8K7.23, F8K7_23	3.9	3.7	0.2	0.7	100.0%	-1.5
17272	AT2G17350.1 | expressed protein | chr2:7552620-7553456 REVERSE | Aliases: F5J6.11, F5J6_11	8.2	8.0	0.2	0.7	100.0%	-1.2
17273	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	2.6	-0.1	-0.7	100.0%	-2.1
17274	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	3.9	3.7	0.2	0.7	100.0%	-1.1
17275	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	0.7	100.0%	-1.8
17276	AT4G31070.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr4:15118702-15120543 REVERSE | Aliases: F6I18.20, F6I18_20	3.0	2.9	0.0	0.7	100.0%	-2.3
17277	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	4.4	4.5	-0.1	-0.7	100.0%	-1.6
17278	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	3.8	0.2	0.7	100.0%	-1.4
17279	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	-0.1	-0.7	100.0%	-1.9
17280	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	3.2	-0.1	-0.7	100.0%	-1.8
17281	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	3.0	3.2	-0.2	-0.7	100.0%	-1.5
17282	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	4.2	0.1	0.7	100.0%	-1.8
17283	AT1G02470.1 | expressed protein, contains non-consensus splice sites; | chr1:511765-513611 REVERSE | Aliases: T6A9.26	3.3	3.5	-0.2	-0.7	100.0%	-1.1
17284	AT1G59710.1 | expressed protein, contains Pfam profile: PF04601 protein of unknown function (DUF569 | chr1:21942032-21943849 FORWARD | Aliases: F23H11.2, F23H11_2	4.4	4.5	-0.1	-0.7	100.0%	-1.5
17285	AT1G07330.1 | expressed protein | chr1:2251130-2253584 FORWARD | Aliases: F22G5.33, F22G5_33	3.1	3.1	-0.1	-0.7	100.0%	-1.8
17286	AT2G19180.1 | expressed protein | chr2:8331798-8333040 FORWARD | Aliases: T20K24.20, T20K24_20	2.6	2.5	0.1	0.7	100.0%	-1.7
17287	AT2G47280.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr2:19423918-19425322 FORWARD | Aliases: T8I13.12	3.1	3.2	-0.1	-0.7	100.0%	-1.6
17288	AT3G29075.1 | glycine-rich protein | chr3:11052726-11053931 REVERSE | Aliases: MRI12.9	9.8	9.5	0.3	0.7	100.0%	-1.3
17289	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	2.4	-0.1	-0.7	100.0%	-1.7
17290	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	3.0	2.9	0.1	0.7	100.0%	-1.4
17291	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	0.7	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
17292	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	4.1	0.1	0.7	100.0%	-1.4
17293	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	6.9	6.7	0.2	0.7	100.0%	-1.5
17294	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	3.8	3.6	0.1	0.7	100.0%	-1.4
17295	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	5.6	5.8	-0.2	-0.7	100.0%	-1.1
17296	AT2G26700.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr2:11375691-11378092 FORWARD | Aliases: F18A8.7, F18A8_7	2.6	2.7	-0.1	-0.7	100.0%	-1.6
17297	AT5G38910.1 | germin-like protein, putative, similar to SP:Q9LEA7; contains PS00725 germin family signature | chr5:15596041-15596814 FORWARD | Aliases: K15E6.90, K15E6_90	2.4	2.4	-0.1	-0.7	100.0%	-2.1
17298	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	-0.7	100.0%	-2.1
17299	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	8.4	8.2	0.2	0.7	100.0%	-1.4
17300	AT5G14560.1 | expressed protein | chr5:4693967-4694089 FORWARD | Aliases: T15N1.50, T15N1_50	3.1	3.2	-0.1	-0.7	100.0%	-2.1
17301	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	3.6	0.1	0.7	100.0%	-1.5
17302	AT4G38440.1 | expressed protein | chr4:17989061-17994717 FORWARD | Aliases: F22I13.210, F22I13_210	3.4	3.3	0.1	0.7	100.0%	-1.6
17303	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	7.8	8.0	-0.2	-0.7	100.0%	-1.6
17304	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	3.9	-0.1	-0.7	100.0%	-1.5
17305	AT3G59800.1 | expressed protein | chr3:22105454-22107151 REVERSE | Aliases: F24G16.70	6.7	6.2	0.5	0.7	100.0%	-1.0
17306	AT3G26010.1 | F-box family protein, contains Pfam:PF00646 F-box domain	3.4	3.5	-0.1	-0.7	100.0%	-1.6
17307	AT1G69480.1 | 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	3.0	2.9	0.1	0.7	100.0%	-1.6
17308	AT1G53970.1 | hypothetical protein | chr1:20152087-20152566 FORWARD | Aliases: T18A20.21	1.9	1.9	-0.0	-0.7	100.0%	-2.4
17309	AT1G47310.1 | expressed protein | chr1:17345354-17347242 FORWARD | Aliases: T3F24.7, T3F24_7	8.3	8.5	-0.2	-0.7	100.0%	-1.0
17310	AT3G50250.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr3:18641014-18641460 REVERSE | Aliases: F11C1.90	8.2	8.5	-0.3	-0.7	100.0%	-0.9
17311	AT2G15550.1 | expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277 | chr2:6790268-6792262 REVERSE | Aliases: F9O13.10	4.2	4.3	-0.2	-0.7	100.0%	-1.1
17312	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	2.7	2.7	-0.1	-0.7	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
17313	AT5G38140.1 | histone-like transcription factor (CBF/NF-Y) family protein, similar to CCAAT-binding transcription factor subunit AAB-1 (GI:2583171) (Neurospora crassa); contains a CBF/NF-Y subunit signature (PDOC00578) presernt in members of histone-like transcription factor family; contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone	3.8	4.0	-0.2	-0.7	100.0%	-1.2
17314	AT3G33080.1 | expressed protein, similar to protein prospero GI:1346808 (Drosophila melanogaster) | chr3:13827628-13828157 REVERSE | Aliases: None	1.8	1.8	-0.1	-0.7	100.0%	-2.2
17315	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) {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	6.3	5.7	0.5	0.7	100.0%	-0.9
17316	AT2G30420.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr2:12968014-12968992 REVERSE | Aliases: T9D9.23, T9D9_23	2.8	2.9	-0.1	-0.7	100.0%	-1.4
17317	AT1G80040.2 | expressed protein | chr1:30114040-30116163 REVERSE | Aliases: F18B13.13, F18B13_13	8.5	8.4	0.2	0.7	100.0%	-1.6
17318	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	7.8	8.3	-0.5	-0.7	100.0%	-1.0
17319	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	4.8	4.5	0.3	0.7	100.0%	-1.2
17320	AT2G25625.2 | expressed protein | chr2:10913538-10914357 FORWARD | Aliases: None	3.5	3.4	0.1	0.7	100.0%	-1.7
17321	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	5.3	5.6	-0.3	-0.7	100.0%	-0.9
17322	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	5.3	5.1	0.1	0.7	100.0%	-1.4
17323	AT5G02070.1 | protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr5:405892-408217 REVERSE | Aliases: T7H20.120, T7H20_120	2.7	2.8	-0.1	-0.7	100.0%	-2.2
17324	AT2G30810.1 | gibberellin-regulated family protein, similar to GASA5 (Arabidopsis thaliana) GI:1289320; contains Pfam profile PF02704: Gibberellin regulated protein | chr2:13134904-13135732 REVERSE | Aliases: F7F1.2, F7F1_2	2.5	2.5	-0.1	-0.7	100.0%	-2.1
17325	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	3.0	3.1	-0.1	-0.7	100.0%	-1.6
17326	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	4.3	-0.2	-0.7	100.0%	-1.5
17327	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	2.5	2.6	-0.1	-0.7	100.0%	-1.9
17328	ATCG00520.1 | Symbol: YCF4 | hypothetical protein | chrC:59772-60326 FORWARD | Aliases: YCF4	6.6	7.4	-0.7	-0.7	100.0%	-0.9
17329	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	2.3	2.4	-0.1	-0.7	100.0%	-2.4
17330	AT3G33073.1 | expressed protein | chr3:13652020-13652925 REVERSE | Aliases: T25F15.5	3.6	3.7	-0.2	-0.7	100.0%	-1.3
17331	AT5G47340.1 | palmitoyl protein thioesterase family protein | chr5:19226734-19228361 FORWARD | Aliases: MQL5.20, MQL5_20	2.6	2.7	-0.1	-0.7	100.0%	-1.9
17332	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	3.4	3.5	-0.2	-0.7	100.0%	-1.4
17333	AT1G02320.1 | expressed protein | chr1:461828-461974 FORWARD | Aliases: T6A9.30	2.5	2.5	-0.1	-0.7	100.0%	-2.0
17334	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	3.4	3.5	-0.1	-0.7	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
17335	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	8.5	8.9	-0.4	-0.7	100.0%	-0.8
17336	AT4G11640.1 | serine racemase, putative, similar to serine racemase (Mus musculus) GI:6448865; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme | chr4:7021764-7023246 FORWARD | Aliases: T5C23.70, T5C23_70	4.8	4.9	-0.1	-0.7	100.0%	-1.4
17337	AT5G42220.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr5:16889582-16894894 FORWARD | Aliases: K5J14.2, K5J14_2	7.2	7.4	-0.2	-0.7	100.0%	-1.3
17338	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	3.5	-0.1	-0.7	100.0%	-1.8
17339	AT2G14910.2 | expressed protein | chr2:6413558-6416234 REVERSE | Aliases: T26I20.7, T26I20_7	9.0	8.6	0.4	0.7	100.0%	-1.0
17340	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	0.7	100.0%	-1.5
17341	AT4G33870.1 | peroxidase, putative, similar to peroxidase (Spinacia oleracea) gi:1781334:emb:CAA71494 | chr4:16234675-16236497 REVERSE | Aliases: F17I5.60, F17I5_60	3.1	3.0	0.1	0.7	100.0%	-1.6
17342	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	3.8	3.9	-0.1	-0.7	100.0%	-1.5
17343	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	3.6	3.5	0.1	0.7	100.0%	-1.4
17344	AT4G11000.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr4:6731016-6732460 FORWARD | Aliases: T22B4.2	2.9	3.0	-0.1	-0.7	100.0%	-1.5
17345	AT4G38270.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8 | chr4:17938366-17941547 FORWARD | Aliases: F22I13.40, F22I13_40	6.7	6.8	-0.2	-0.7	100.0%	-1.3
17346	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	9.4	9.2	0.2	0.7	100.0%	-1.1
17347	AT2G22940.1 | expressed protein, ; expression supported by MPSS | chr2:9768735-9770542 REVERSE | Aliases: T20K9.15, T20K9_15	2.3	2.4	-0.1	-0.7	100.0%	-2.2
17348	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	9.2	9.5	-0.3	-0.7	100.0%	-1.3
17349	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	4.1	4.0	0.2	0.7	100.0%	-1.3
17350	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	3.3	3.2	0.1	0.7	100.0%	-1.5
17351	AT4G24820.2 | 26S proteasome regulatory subunit, putative (RPN7), contains similarity to ubiquitin activating enzyme GI:3647283 from (Lycopersicon esculentum)	8.8	8.1	0.7	0.7	100.0%	-0.8
17352	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	2.7	0.1	0.7	100.0%	-2.1
17353	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	6.7	6.5	0.2	0.7	100.0%	-1.3
17354	AT5G09340.1 | ubiquitin, putative, similar to ubiquitin SP:P42740 from (Aglaothamnion neglectum) | chr5:2896676-2896915 REVERSE | Aliases: T5E8.140, T5E8_140	2.6	2.7	-0.1	-0.7	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
17355	ATCG01070.1 | Symbol: NDHE | NADH dehydrogenase ND4L | chrC:117804-118109 REVERSE | Aliases: NDHE	4.9	4.3	0.6	0.7	100.0%	-0.8
17356	AT1G66720.1 | 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) | chr1:24884843-24886143 FORWARD | Aliases: F4N21.15, F4N21_15	3.3	3.5	-0.1	-0.7	100.0%	-1.6
17357	AT5G08200.1 | peptidoglycan-binding LysM domain-containing protein, contains Pfam profile PF01476: LysM domain	3.8	3.6	0.2	0.7	100.0%	-1.4
17358	AT5G25920.1 | expressed protein | chr5:9044209-9046000 REVERSE | Aliases: T1N24.2, T1N24_2	2.8	2.9	-0.1	-0.7	100.0%	-1.8
17359	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	3.9	3.8	0.2	0.7	100.0%	-1.2
17360	AT3G19680.1 | expressed protein | chr3:6840287-6842326 FORWARD | Aliases: MMB12.17	6.4	6.3	0.1	0.7	100.0%	-1.3
17361	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	6.5	6.7	-0.2	-0.7	100.0%	-1.4
17362	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	2.8	-0.1	-0.7	100.0%	-1.7
17363	AT5G13030.1 | expressed protein, contains Pfam profile PF02696: Uncharacterized ACR, YdiU/UPF0061 family | chr5:4133219-4136921 FORWARD | Aliases: AT5G13040, T19L5.1	6.3	6.2	0.1	0.7	100.0%	-1.7
17364	AT5G11360.1 | expressed protein | chr5:3625575-3626701 REVERSE | Aliases: F2I11.250, F2I11_250	3.6	3.8	-0.2	-0.7	100.0%	-1.1
17365	AT4G20200.1 | terpene synthase/cyclase family protein, 5-epi-aristolochene synthase, Nicotiana tabacum, PATX:G505588 | chr4:10908682-10911161 REVERSE | Aliases: F1C12.120, F1C12_120	2.5	2.5	0.1	0.7	100.0%	-1.8
17366	AT1G42550.1 | expressed protein | chr1:15979855-15982392 FORWARD | Aliases: T8D8.2, T8D8_2	4.8	4.3	0.5	0.7	100.0%	-1.1
17367	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	2.9	2.9	-0.1	-0.7	100.0%	-2.0
17368	AT3G29265.1 | hypothetical protein | chr3:11232949-11233659 FORWARD | Aliases: MMF24.1	2.2	2.2	-0.1	-0.7	100.0%	-2.2
17369	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	3.3	-0.1	-0.7	100.0%	-1.4
17370	AT2G17310.1 | Symbol: SON1 | F-box family protein, contains F-box domain Pfam:PF00646	3.2	3.3	-0.1	-0.7	100.0%	-1.5
17371	AT3G57980.1 | DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487 | chr3:21477896-21480125 REVERSE | Aliases: T10K17.190	3.3	3.4	-0.1	-0.7	100.0%	-1.9
17372	AT3G60900.1 | Symbol: FLA10 | fasciclin-like arabinogalactan-protein (FLA10) | chr3:22510335-22512214 REVERSE | Aliases: T4C21.310	2.2	2.1	0.1	0.7	100.0%	-2.2
17373	AT4G27510.1 | expressed protein | chr4:13745615-13749037 REVERSE | Aliases: F27G19.110, F27G19_110	4.1	3.9	0.2	0.7	100.0%	-1.3
17374	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	5.0	5.3	-0.2	-0.7	100.0%	-1.0
17375	AT5G53670.1 | hypothetical protein, similar to unknown protein (pir :T17429) | chr5:21814223-21814957 FORWARD | Aliases: MGN6.1, MGN6_1	2.9	2.9	-0.1	-0.7	100.0%	-1.8
17376	AT1G72060.1 | expressed protein | chr1:27122109-27122673 FORWARD | Aliases: F28P5.12, F28P5_12	3.4	3.6	-0.1	-0.7	100.0%	-1.6
17377	AT4G27110.1 | phytochelatin synthetase-related, contains Pfam PF04833: Phytochelatin synthetase-like conserved region | chr4:13599242-13601527 REVERSE | Aliases: T24A18.60, T24A18_60	2.9	3.0	-0.1	-0.7	100.0%	-1.7
17378	AT1G04490.1 | expressed protein | chr1:1218004-1219913 REVERSE | Aliases: F19P19.4, F19P19_4	3.7	3.8	-0.1	-0.7	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
17379	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	7.9	8.2	-0.4	-0.7	100.0%	-1.1
17380	AT3G55920.1 | peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, similar to cyclophilin (Arabidopsis thaliana) gi:2443755:gb:AAB71401	7.2	7.4	-0.2	-0.7	100.0%	-1.3
17381	AT2G02730.2 | expressed protein | chr2:764546-767429 REVERSE | Aliases: T20F6.13, T20F6_13	4.3	4.2	0.1	0.7	100.0%	-1.7
17382	AT5G61120.1 | expressed protein | chr5:24599529-24601312 REVERSE | Aliases: MAF19.12, MAF19_12	2.5	2.6	-0.1	-0.7	100.0%	-1.5
17383	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	2.5	-0.1	-0.7	100.0%	-1.9
17384	AT1G68930.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:25921977-25924208 FORWARD | Aliases: T6L1.11, T6L1_11	2.5	2.6	-0.1	-0.7	100.0%	-2.0
17385	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	6.7	7.2	-0.5	-0.7	100.0%	-1.1
17386	AT5G38040.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:15202307-15203738 FORWARD | Aliases: F16F17.40, F16F17_40	3.8	3.7	0.2	0.7	100.0%	-1.6
17387	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	8.6	8.4	0.2	0.7	100.0%	-1.2
17388	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	-0.7	100.0%	-2.0
17389	AT2G41930.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:17508708-17509762 FORWARD | Aliases: T6D20.17, T6D20_17	3.6	3.8	-0.1	-0.7	100.0%	-1.5
17390	AT1G18370.1 | Symbol: HIK | kinesin motor family protein (NACK1), similar to kinesin heavy chain isolog GB:AAB63609 GI:2262101 from (Arabidopsis thaliana) | chr1:6319643-6323813 REVERSE | Aliases: F15H18.12, F15H18_12, HINKEL	3.6	3.8	-0.1	-0.7	100.0%	-1.3
17391	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	3.1	3.2	-0.1	-0.7	100.0%	-1.5
17392	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	6.0	6.1	-0.1	-0.7	100.0%	-1.5
17393	AT5G27550.1 | kinesin motor protein-related, kinesin-like heavy chain - Arabidopsis thaliana, EMBL:AF080249 | chr5:9728450-9730308 REVERSE | Aliases: F21A20.1	4.0	3.8	0.2	0.7	100.0%	-1.3
17394	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	2.6	2.5	0.1	0.7	100.0%	-1.8
17395	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	2.6	-0.1	-0.7	100.0%	-1.9
17396	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	2.4	-0.1	-0.7	100.0%	-2.0
17397	ATMG00710.1 | Symbol: ORF120 |	3.3	3.4	-0.1	-0.7	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
17398	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	0.1	0.7	100.0%	-1.9
17399	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	4.1	4.2	-0.1	-0.7	100.0%	-1.5
17400	AT1G79570.1 | protein kinase family protein, low similarity to EDR1 (Arabidopsis thaliana) GI:11127925	4.1	4.2	-0.1	-0.7	100.0%	-1.5
17401	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	3.6	3.7	-0.1	-0.7	100.0%	-1.3
17402	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	9.9	10.2	-0.4	-0.7	100.0%	-1.2
17403	AT4G36440.1 | expressed protein | chr4:17206861-17210010 REVERSE | Aliases: AP22.38, AP22_38	6.4	6.5	-0.1	-0.7	100.0%	-1.5
17404	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	2.3	2.3	-0.0	-0.7	100.0%	-2.4
17405	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	8.8	8.6	0.1	0.7	100.0%	-1.4
17406	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	2.6	2.5	0.1	0.7	100.0%	-1.9
17407	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	4.9	5.1	-0.2	-0.7	100.0%	-1.1
17408	AT3G22950.1 | Symbol: ATARFC1 | Gene encoding ADP-ribosylation factor and similar to ADP-ribosylation factor GB:P91924 (Dugesia japonica), 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.	8.5	8.2	0.2	0.7	100.0%	-1.2
17409	AT2G45840.1 | expressed protein | chr2:18876335-18878561 FORWARD | Aliases: F4I18.18	2.8	2.9	-0.1	-0.7	100.0%	-1.6
17410	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	3.2	3.3	-0.1	-0.7	100.0%	-1.8
17411	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	0.7	100.0%	-1.9
17412	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	4.0	3.8	0.2	0.7	100.0%	-1.1
17413	AT5G61570.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:24775573-24777878 FORWARD | Aliases: K11J9.21, K11J9_21	2.5	2.5	-0.1	-0.7	100.0%	-1.8
17414	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	2.3	2.3	-0.1	-0.7	100.0%	-2.1
17415	AT2G26690.1 | nitrate transporter (NTP2), identical to nitrate transporter (ntp2) (Arabidopsis thaliana) GI:4490321 | chr2:11354225-11358071 REVERSE | Aliases: F18A8.6, F18A8_6	3.3	3.2	0.1	0.7	100.0%	-1.6
17416	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	6.3	6.1	0.1	0.7	100.0%	-1.4
17417	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	3.1	-0.1	-0.7	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
17418	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	5.2	5.4	-0.1	-0.7	100.0%	-1.3
17419	AT2G16880.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:7319228-7321615 REVERSE | Aliases: F12A24.6, F12A24_6	3.7	3.7	0.1	0.7	100.0%	-1.8
17420	AT4G14750.1 | calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif | chr4:8470376-8472182 FORWARD | Aliases: DL3415W, FCAALL.303	2.9	3.0	-0.1	-0.7	100.0%	-1.6
17421	AT4G14230.1 | CBS domain-containing protein-related, contains Pfam profile PF01595: Domain of unknown function	6.5	6.6	-0.1	-0.7	100.0%	-1.2
17422	AT5G50270.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.1	3.3	-0.2	-0.7	100.0%	-1.4
17423	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	3.6	3.5	0.1	0.7	100.0%	-1.4
17424	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	3.1	-0.1	-0.7	100.0%	-1.8
17425	AT2G36030.1 | expressed protein | chr2:15134638-15134850 REVERSE | Aliases: F11F19.6, F11F19_6	3.6	3.7	-0.1	-0.7	100.0%	-1.7
17426	AT1G10890.1 | F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	2.9	3.0	-0.1	-0.7	100.0%	-1.8
17427	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	5.2	5.4	-0.2	-0.7	100.0%	-1.0
17428	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 domian PF04280: Mitochondrial import inner membrane, translocase subunit TIM44 | chr2:8843099-8845679 REVERSE | Aliases: T13C7.10, T13C7_10	2.2	2.3	-0.1	-0.7	100.0%	-2.1
17429	AT4G34650.1 | Symbol: SQS2 | farnesyl-diphosphate farnesyltransferase 2 / squalene synthase 2 (SQS2), nearly identical to GI:2228795; synonomous with farnesyl-diphosphate farnesyltransferase, FPP:FPP farnesyltransferase, and squalene synthetase | chr4:16542382-16544552 FORWARD | Aliases: SQUALENE SYNTHASE 2, T4L20.230, T4L20_230	3.2	3.3	-0.1	-0.7	100.0%	-1.6
17430	AT4G01400.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:573098-577243 REVERSE | Aliases: F3D13.1, F3D13_1	6.5	6.8	-0.2	-0.7	100.0%	-1.2
17431	AT4G19490.2 | expressed protein | chr4:10615807-10623532 FORWARD | Aliases: F24J7.50, F24J7_50	3.5	3.3	0.1	0.7	100.0%	-1.3
17432	AT2G15610.1 | expressed protein | chr2:6813115-6814534 FORWARD | Aliases: F9O13.16	2.3	2.4	-0.1	-0.7	100.0%	-1.9
17433	AT2G27980.1 | expressed protein | chr2:11920706-11926818 REVERSE | Aliases: T1E2.10, T1E2_10	3.3	3.4	-0.1	-0.7	100.0%	-1.6
17434	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	3.2	0.1	0.7	100.0%	-1.9
17435	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	2.4	2.5	-0.1	-0.7	100.0%	-1.8
17436	AT2G21490.1 | dehydrin family protein, contains Pfam domain, PF00257: Dehydrin	2.8	2.9	-0.1	-0.7	100.0%	-1.7
17437	AT3G51400.1 | expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function | chr3:19088829-19089934 REVERSE | Aliases: F26O13.40	2.5	2.5	-0.1	-0.7	100.0%	-1.8
17438	AT5G26230.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:9173520-9174545 REVERSE | Aliases: F9D12.20	3.7	3.8	-0.1	-0.7	100.0%	-1.4
17439	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	2.9	0.1	0.7	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
17440	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	2.9	0.1	0.7	100.0%	-1.8
17441	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 GI:9294423 from (Arabidopsis thaliana) | chr1:5453240-5454083 REVERSE | Aliases: F7H2.18, F7H2_18	2.9	2.9	-0.0	-0.7	100.0%	-2.4
17442	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	2.2	-0.0	-0.7	100.0%	-2.4
17443	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)	5.9	5.6	0.2	0.7	100.0%	-1.0
17444	AT2G34210.1 | KOW domain-containing transcription factor family protein | chr2:14453017-14457601 FORWARD | Aliases: F13P17.5, F13P17_5	2.7	2.8	-0.1	-0.7	100.0%	-1.9
17445	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)	10.0	10.1	-0.1	-0.7	100.0%	-1.7
17446	AT4G19220.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr4:10505277-10508132 REVERSE | Aliases: T18B16.190, T18B16_190	3.3	3.4	-0.2	-0.7	100.0%	-1.4
17447	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	3.4	3.2	0.2	0.7	100.0%	-1.4
17448	AT2G33260.1 | tryptophan/tyrosine permease family protein, contains Pfam profile PF03222: Tryptophan/tyrosine permease family | chr2:14107917-14109329 REVERSE | Aliases: F4P9.3, F4P9_3	3.0	3.1	-0.1	-0.7	100.0%	-1.4
17449	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	7.9	7.5	0.4	0.7	100.0%	-1.3
17450	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	3.7	3.6	0.1	0.7	100.0%	-1.3
17451	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	2.8	3.0	-0.1	-0.7	100.0%	-1.4
17452	AT4G10930.1 | expressed protein | chr4:6705143-6708842 REVERSE | Aliases: F25I24.140, F25I24_140	5.1	4.9	0.2	0.7	100.0%	-1.5
17453	AT1G10710.1 | expressed protein | chr1:3558424-3560408 FORWARD | Aliases: T16B5.15	2.7	2.6	0.1	0.7	100.0%	-1.8
17454	ATCG00530.1 | Symbol: YCF10 | hypothetical protein | chrC:60741-61430 FORWARD | Aliases: YCF10	5.4	5.9	-0.6	-0.7	100.0%	-1.1
17455	AT2G41080.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:17139931-17141671 FORWARD | Aliases: T3K9.15, T3K9_15	3.6	3.5	0.1	0.7	100.0%	-1.5
17456	AT1G21140.1 | nodulin, putative, similar to nodulin 21 (N-21) (Glycine max) SWISS-PROT:P16313 | chr1:7404372-7405270 FORWARD | Aliases: T22I11.3, T22I11_3	8.3	8.1	0.2	0.7	100.0%	-1.3
17457	AT5G37680.1 | Symbol: ATARLA1A | ADP-ribosylation factor, putative, ADP-ribosylation factor, Leishmania major, EMBL:LMFP1421 and ADP-ribosylation factor-like protein 1 (ARL1) (SP:P40616) Homo sapiens; contains PF00025: ADP-ribosylation factor family | chr5:14986826-14988458 REVERSE | Aliases: ATARLA1A, K12B20.130, K12B20_130	5.8	5.7	0.1	0.7	100.0%	-1.3
17458	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	4.1	4.3	-0.1	-0.7	100.0%	-1.5
17459	AT1G05370.1 | expressed protein | chr1:1569191-1572279 REVERSE | Aliases: YUP8H12.1	2.7	2.8	-0.1	-0.7	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
17460	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	4.8	5.0	-0.2	-0.7	100.0%	-1.0
17461	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	4.6	4.8	-0.1	-0.7	100.0%	-1.3
17462	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%	-1.9
17463	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	3.7	-0.1	-0.7	100.0%	-1.7
17464	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	2.9	2.8	0.1	0.7	100.0%	-1.7
17465	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	6.5	6.1	0.4	0.7	100.0%	-1.2
17466	AT5G33240.1 | expressed protein | chr5:12507395-12508221 REVERSE | Aliases: T29A4.50, T29A4_50	2.5	2.4	0.1	0.7	100.0%	-2.3
17467	AT2G03880.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:1181534-1183700 FORWARD | Aliases: T18C20.8, T18C20_8	2.5	2.4	0.1	0.7	100.0%	-2.1
17468	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	0.1	0.7	100.0%	-2.0
17469	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	5.1	5.3	-0.2	-0.7	100.0%	-1.3
17470	AT4G11890.3 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:7148242-7149915 FORWARD | Aliases: T26M18.100, T26M18_100	3.3	3.4	-0.1	-0.7	100.0%	-1.7
17471	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	5.8	-0.1	-0.7	100.0%	-1.4
17472	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	2.8	2.7	0.1	0.7	100.0%	-1.8
17473	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	4.3	-0.2	-0.7	100.0%	-1.2
17474	AT4G39380.1 | expressed protein | chr4:18309148-18312718 REVERSE | Aliases: F23K16.10, F23K16_10	3.2	3.1	0.1	0.7	100.0%	-1.7
17475	AT1G50750.1 | expressed protein | chr1:18812852-18815958 REVERSE | Aliases: F4M15.2, F4M15_2	3.3	3.4	-0.1	-0.7	100.0%	-1.7
17476	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	-0.7	100.0%	-1.8
17477	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	0.1	0.7	100.0%	-2.0
17478	AT2G32460.1 | myb family transcription factor (MYB101), identical to putative transcription factor MYB101 GI:18087348 from (Arabidopsis thaliana) | chr2:13789285-13791548 REVERSE | Aliases: T32F6.1	2.5	2.4	0.1	0.7	100.0%	-2.1
17479	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	2.3	-0.1	-0.7	100.0%	-2.0
17480	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:At3g62740.1); 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	2.5	0.1	0.7	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
17481	AT5G63720.1 | hypothetical protein | chr5:25523575-25525243 FORWARD | Aliases: MBK5.20, MBK5_20	3.1	3.2	-0.1	-0.7	100.0%	-1.8
17482	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	7.0	7.7	-0.7	-0.7	100.0%	-1.0
17483	AT5G52430.1 | hydroxyproline-rich glycoprotein family protein, Common family member At4g25620 (Arabidopsis thaliana) | chr5:21298999-21302431 REVERSE | Aliases: K24M7.18, K24M7_18	4.2	4.3	-0.1	-0.7	100.0%	-1.4
17484	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	4.5	-0.1	-0.7	100.0%	-1.6
17485	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	6.3	6.0	0.2	0.7	100.0%	-1.1
17486	AT3G44140.1 | expressed protein | chr3:15896064-15896367 REVERSE | Aliases: F26G5.90	8.8	8.9	-0.2	-0.7	100.0%	-1.2
17487	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	8.3	8.6	-0.3	-0.7	100.0%	-1.5
17488	AT1G28260.2 | expressed protein | chr1:9875587-9879254 REVERSE | Aliases: F3H9.9, F3H9_9	4.4	4.3	0.1	0.7	100.0%	-1.3
17489	AT5G39940.1 | expressed protein | chr5:16004781-16007929 FORWARD | Aliases: MYH19.13, MYH19_13	4.1	4.0	0.1	0.7	100.0%	-1.5
17490	AT4G26590.1 | Symbol: ATOPT5 |	4.5	4.7	-0.2	-0.7	100.0%	-1.5
17491	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	-0.7	100.0%	-1.4
17492	AT5G42570.1 | expressed protein, low similarity to SP:P51572 B-cell receptor-associated protein 31 (6C6-AG tumor-associated antigen) (DXS1357E) {Homo sapiens}	5.7	5.5	0.2	0.7	100.0%	-1.2
17493	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	4.3	-0.1	-0.7	100.0%	-1.5
17494	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	9.1	9.4	-0.3	-0.7	100.0%	-1.4
17495	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	8.5	-0.2	-0.7	100.0%	-1.3
17496	AT3G42320.1 | expressed protein, various predicted Helicases, Arabidopsis thaliana | chr3:14489392-14493635 REVERSE | Aliases: T14K23.30	2.4	2.3	0.1	0.7	100.0%	-2.1
17497	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	9.2	9.4	-0.3	-0.7	100.0%	-1.0
17498	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	3.2	0.1	0.7	100.0%	-1.7
17499	AT5G63050.1 | Symbol: EMB2759 | expressed protein | chr5:25309661-25312221 FORWARD | Aliases: EMB2759, EMBRYO DEFECTIVE 2759, MDC12.1, MDC12_1	4.2	4.0	0.2	0.7	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
17500	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	3.0	-0.1	-0.7	100.0%	-1.7
17501	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	3.2	0.1	0.7	100.0%	-1.7
17502	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	5.9	6.0	-0.2	-0.7	100.0%	-1.3
17503	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	4.8	4.7	0.1	0.7	100.0%	-1.5
17504	AT3G46660.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:17200249-17202152 REVERSE | Aliases: F12A12.180	2.6	2.7	-0.1	-0.7	100.0%	-1.9
17505	AT2G05090.1 | hypothetical protein, includes At5g37080, At5g37170, At2g05090 | chr2:1818139-1820698 REVERSE | Aliases: F1O13.22, F1O13_22	2.5	2.6	-0.1	-0.7	100.0%	-2.3
17506	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	2.1	-0.0	-0.7	100.0%	-2.5
17507	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	4.2	4.4	-0.3	-0.7	100.0%	-1.1
17508	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	2.5	-0.1	-0.7	100.0%	-2.1
17509	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	3.2	-0.1	-0.7	100.0%	-1.7
17510	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	2.9	-0.1	-0.7	100.0%	-2.3
17511	AT1G53345.1 | expressed protein | chr1:19906163-19907549 FORWARD | Aliases: None	3.5	3.6	-0.1	-0.7	100.0%	-1.5
17512	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	6.0	6.2	-0.2	-0.7	100.0%	-1.3
17513	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	2.5	-0.1	-0.7	100.0%	-2.0
17514	AT3G27750.1 | expressed protein | chr3:10286057-10286728 FORWARD | Aliases: None	2.4	2.5	-0.1	-0.7	100.0%	-1.7
17515	AT2G14850.1 | expressed protein | chr2:6392954-6394652 FORWARD | Aliases: F26C24.1	4.8	4.9	-0.1	-0.7	100.0%	-1.5
17516	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	2.7	-0.1	-0.7	100.0%	-1.8
17517	AT5G17330.1 | Symbol: GAD | glutamate decarboxylase 1 (GAD 1), sp:Q42521 | chr5:5711070-5715077 FORWARD | Aliases: GAD1, GLUTAMATE DECARBOXYLASE, MKP11.30, MKP11_30	8.7	9.2	-0.5	-0.7	100.0%	-1.4
17518	AT1G35617.1 | expressed protein | chr1:13153561-13153926 FORWARD | Aliases: F15O4.21	4.0	4.1	-0.2	-0.7	100.0%	-1.4
17519	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	6.9	7.0	-0.1	-0.7	100.0%	-1.3
17520	AT5G58560.1 | phosphatidate cytidylyltransferase family protein, contains Pfam profile: PF01148 phosphatidate cytidylyltransferase | chr5:23687641-23690513 FORWARD | Aliases: MZN1.8, MZN1_8	6.3	6.1	0.2	0.7	100.0%	-1.3
17521	AT3G01840.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:296589-298641 REVERSE | Aliases: F28J7.37, F28J7_37	2.8	3.0	-0.1	-0.7	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
17522	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	3.0	-0.1	-0.7	100.0%	-2.0
17523	AT5G19590.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr5:6611616-6612105 REVERSE | Aliases: T29J13.10, T29J13_10	7.8	7.4	0.4	0.7	100.0%	-1.0
17524	AT4G19450.1 | nodulin-related, weak similarity to nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366 | chr4:10606464-10609346 FORWARD | Aliases: T5K18.230, T5K18_230	5.7	5.8	-0.1	-0.7	100.0%	-1.5
17525	AT2G41830.1 | cyclin-related, contains Pfam profile PF02984: Cyclin, C-terminal domain	3.1	3.0	0.1	0.7	100.0%	-1.7
17526	AT5G22680.1 | expressed protein | chr5:7540044-7540751 REVERSE | Aliases: MDJ22.10, MDJ22_10	3.0	3.1	-0.1	-0.7	100.0%	-1.4
17527	ATCG00690.1 | Symbol: PSBT | photosystem II protein T. Encodes the chlorophyll a apoprotein CP47. | chrC:74082-74183 FORWARD | Aliases: PSBT	4.6	5.8	-1.2	-0.7	100.0%	-0.9
17528	AT5G24340.1 | 3'-5' exonuclease domain-containing protein, contains Pfam profile PF01612: 3'-5' exonuclease | chr5:8297308-8300377 FORWARD | Aliases: K16H17.2, K16H17_2	3.4	3.5	-0.1	-0.7	100.0%	-1.7
17529	AT1G73400.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:27602073-27603473 FORWARD | Aliases: T9L24.39, T9L24_39	3.5	3.6	-0.1	-0.7	100.0%	-1.5
17530	AT4G24550.2 | clathrin adaptor complexes medium subunit family protein, contains Pfam profile: PF00928 adaptor complexes medium subunit family	9.4	9.6	-0.2	-0.7	100.0%	-1.7
17531	AT1G22010.1 | hypothetical protein | chr1:7749560-7750051 FORWARD | Aliases: F2E2.5, F2E2_5	2.9	2.8	0.1	0.7	100.0%	-1.8
17532	AT1G67540.1 | expressed protein, ; expression supported by MPSS | chr1:25315159-25315857 REVERSE | Aliases: F12B7.9, F12B7_9	3.2	3.3	-0.1	-0.7	100.0%	-1.8
17533	AT1G64130.1 | expressed protein, similar to hypothetical protein GB:AAF24579 GI:6692114 from (Arabidopsis thaliana) | chr1:23806222-23807196 FORWARD | Aliases: F22C12.11, F22C12_11	2.9	2.9	-0.1	-0.7	100.0%	-2.3
17534	AT1G68120.1 | expressed protein | chr1:25529959-25531197 REVERSE | Aliases: T23K23.3, T23K23_3	4.1	3.9	0.2	0.7	100.0%	-1.3
17535	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	2.3	2.4	-0.1	-0.7	100.0%	-1.8
17536	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	2.5	2.6	-0.1	-0.7	100.0%	-1.9
17537	AT2G05950.1 | hypothetical protein | chr2:2297813-2298718 FORWARD | Aliases: T6P5.15, T6P5_15	2.7	2.8	-0.1	-0.7	100.0%	-1.9
17538	AT2G19330.1 | leucine-rich repeat family protein, contains leucine rich repeats, Pfam:PF00560 | chr2:8380029-8381535 FORWARD | Aliases: F27F23.13, F27F23_13	2.1	2.1	0.0	0.7	100.0%	-2.3
17539	AT1G68500.1 | expressed protein | chr1:25705666-25706174 FORWARD | Aliases: T26J14.7, T26J14_7	8.6	8.4	0.3	0.7	100.0%	-1.2
17540	AT1G09410.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:3035445-3037562 FORWARD | Aliases: F14J9.7, F14J9_7	2.6	2.7	-0.1	-0.7	100.0%	-1.8
17541	AT5G20520.1 | Symbol: WAV2 | expressed protein | chr5:6943156-6946451 REVERSE | Aliases: F7C8.110, F7C8_110	6.3	6.5	-0.2	-0.7	100.0%	-1.3
17542	AT5G23710.1 | expressed protein | chr5:7996531-7997223 REVERSE | Aliases: MQM1.2, MQM1_2	5.7	5.6	0.2	0.7	100.0%	-1.1
17543	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	3.5	-0.1	-0.7	100.0%	-1.6
17544	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	3.2	3.3	-0.1	-0.7	100.0%	-1.7
17545	AT1G69980.1 | expressed protein | chr1:26360043-26361330 REVERSE | Aliases: F20P5.28, F20P5_28	5.3	5.1	0.2	0.7	100.0%	-0.9

Rank	Description	Sync	Root	M	t	adj.q	B
17546	AT4G11700.1 | expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626) | chr4:7058080-7058631 REVERSE | Aliases: T5C23.130, T5C23_130	2.4	2.5	-0.1	-0.7	100.0%	-2.0
17547	NA	2.3	2.4	-0.0	-0.7	100.0%	-2.6
17548	AT5G54850.1 | expressed protein | chr5:22297809-22298589 REVERSE | Aliases: MBG8.11, MBG8_11	4.4	4.5	-0.1	-0.7	100.0%	-1.5
17549	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	3.7	3.5	0.1	0.7	100.0%	-1.8
17550	AT5G49220.1 | expressed protein | chr5:19973663-19976059 FORWARD | Aliases: K21P3.10, K21P3_10	3.7	3.8	-0.1	-0.7	100.0%	-1.6
17551	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	3.5	3.7	-0.2	-0.7	100.0%	-1.5
17552	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	3.2	-0.1	-0.7	100.0%	-1.6
17553	AT2G37700.1 | CER1 protein, putative, similar to CER1 GI:1199467 and maize gl1 homolog (glossy1 locus) GI: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	4.1	-0.3	-0.7	100.0%	-0.8
17554	AT4G16050.1 | expressed protein | chr4:9092238-9094369 FORWARD | Aliases: DL4065W, FCAALL.267	2.8	2.8	-0.1	-0.7	100.0%	-2.3
17555	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	3.2	3.2	-0.1	-0.7	100.0%	-1.9
17556	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	3.0	-0.1	-0.7	100.0%	-1.5
17557	AT2G38950.1 | 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 | chr2:16267931-16272297 FORWARD | Aliases: T7F6.12, T7F6_12	5.7	5.6	0.2	0.7	100.0%	-1.3
17558	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	3.0	2.9	0.1	0.7	100.0%	-1.6
17559	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	5.3	5.6	-0.3	-0.7	100.0%	-1.1
17560	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	9.1	9.2	-0.1	-0.7	100.0%	-1.7
17561	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	6.0	6.6	-0.5	-0.7	100.0%	-1.3
17562	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	4.0	-0.1	-0.7	100.0%	-1.9
17563	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:At5g58140.4); similar to protein kinase family protein / non phototropic hypocotyl 1-like protein (NPL1) [Arabidopsis thaliana] (TAIR:At5g58140.3); 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	3.6	3.6	-0.1	-0.7	100.0%	-1.9
17564	AT3G56820.1 | expressed protein | chr3:21050790-21052724 REVERSE | Aliases: T8M16.150	7.0	7.1	-0.1	-0.7	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
17565	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)	6.9	7.1	-0.1	-0.7	100.0%	-1.4
17566	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	2.2	2.2	-0.0	-0.7	100.0%	-2.3
17567	AT5G46770.1 | expressed protein | chr5:18994635-18995387 FORWARD | Aliases: MZA15.19, MZA15_19	3.0	3.0	0.1	0.7	100.0%	-2.3
17568	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)	5.4	5.2	0.2	0.7	100.0%	-1.2
17569	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	4.3	4.2	0.2	0.7	100.0%	-1.1
17570	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	4.6	4.8	-0.1	-0.7	100.0%	-1.2
17571	AT3G45750.1 | expressed protein | chr3:16804596-16808918 REVERSE | Aliases: T6D9.80	3.6	3.7	-0.1	-0.7	100.0%	-1.6
17572	AT1G73200.1 | expressed protein | chr1:27527115-27530234 REVERSE | Aliases: T18K17.13, T18K17_13	4.5	4.4	0.1	0.7	100.0%	-1.5
17573	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	4.4	4.3	0.2	0.7	100.0%	-1.4
17574	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	3.3	3.3	0.1	0.7	100.0%	-1.5
17575	AT5G28410.1 | hypothetical protein, DYNAMIN-LIKE PROTEIN- Arabidopsis thaliana, EMBL:L36939 | chr5:10358377-10359442 FORWARD | Aliases: F21B23.2, F21B23_2	2.5	2.5	-0.1	-0.7	100.0%	-2.3
17576	AT5G47330.1 | palmitoyl protein thioesterase family protein | chr5:19224333-19226049 FORWARD | Aliases: MQL5.19, MQL5_19	3.3	3.4	-0.1	-0.7	100.0%	-1.8
17577	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	5.1	0.1	0.7	100.0%	-1.4
17578	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	6.0	5.8	0.3	0.7	100.0%	-1.1
17579	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	-0.7	100.0%	-1.7
17580	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	7.7	7.4	0.3	0.7	100.0%	-1.4
17581	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	6.8	7.1	-0.3	-0.7	100.0%	-1.2
17582	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	8.2	7.8	0.3	0.7	100.0%	-1.0
17583	AT4G03090.1 | expressed protein | chr4:1366495-1371155 REVERSE | Aliases: T4I9.3, T4I9_3	3.9	3.8	0.1	0.7	100.0%	-1.6
17584	AT1G62720.1 | pentatricopeptide (PPR) repeat-containing protein, contains multiple PPR repeats Pfam Profile: PF01535 | chr1:23231416-23233114 FORWARD | Aliases: F23N19.8, F23N19_8	5.4	5.3	0.2	0.7	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
17585	AT1G48060.1 | F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	2.1	2.2	-0.1	-0.7	100.0%	-2.4
17586	AT5G26890.1 | hypothetical protein | chr5:9460468-9460719 FORWARD | Aliases: F2P16.150, F2P16_150	3.0	3.2	-0.2	-0.7	100.0%	-1.3
17587	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	2.8	2.9	-0.1	-0.7	100.0%	-1.8
17588	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	7.6	7.4	0.2	0.7	100.0%	-1.2
17589	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	4.8	4.7	0.1	0.7	100.0%	-1.3
17590	AT5G63460.2 | SAP domain-containing protein, contains Pfam domain PF02037: SAP domain | chr5:25430599-25432716 REVERSE | Aliases: MLE2.9, MLE2_9	4.4	4.2	0.2	0.7	100.0%	-0.9
17591	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	2.4	2.5	-0.1	-0.7	100.0%	-2.3
17592	AT2G27750.1 | nucleolar matrix protein-related, contains Pfam domain, PF04935: Surfeit locus protein 6	2.9	3.0	-0.1	-0.7	100.0%	-1.9
17593	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	-0.1	-0.7	100.0%	-1.7
17594	AT5G16640.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:5460979-5462548 FORWARD | Aliases: MTG13.9, MTG13_9	3.8	3.9	-0.1	-0.7	100.0%	-1.8
17595	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	3.2	3.3	-0.1	-0.7	100.0%	-1.8
17596	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) {Homo sapiens} | chr5:9789902-9792427 REVERSE | Aliases: T1G16.1	4.6	4.4	0.2	0.7	100.0%	-1.3
17597	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	2.5	-0.0	-0.7	100.0%	-2.4
17598	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	3.2	3.0	0.1	0.7	100.0%	-1.3
17599	AT4G33380.1 | expressed protein | chr4:16071895-16074876 FORWARD | Aliases: F17M5.140, F17M5_140	7.9	8.0	-0.2	-0.7	100.0%	-1.3
17600	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	2.6	-0.1	-0.7	100.0%	-2.1
17601	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	3.3	-0.1	-0.7	100.0%	-1.7
17602	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	6.9	7.1	-0.2	-0.7	100.0%	-1.3
17603	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	2.7	2.7	-0.1	-0.7	100.0%	-2.1
17604	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	3.0	0.1	0.7	100.0%	-1.8
17605	AT5G08010.1 | expressed protein, condensin subunit SMC4, Drosophila melanogaster, EMBL:AF186472 | chr5:2569607-2571735 FORWARD | Aliases: F13G24.210, F13G24_210	6.8	6.6	0.1	0.7	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
17606	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	3.5	-0.1	-0.7	100.0%	-1.1
17607	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	4.4	4.7	-0.2	-0.7	100.0%	-1.5
17608	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	-0.1	-0.7	100.0%	-2.0
17609	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	8.2	8.0	0.2	0.7	100.0%	-1.4
17610	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	3.1	-0.2	-0.7	100.0%	-1.5
17611	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	4.0	4.2	-0.2	-0.7	100.0%	-1.2
17612	AT3G18630.1 | uracil DNA glycosylase family protein, contains Pfam profile: PF03167 uracil DNA glycosylase superfamily	2.9	2.9	0.1	0.7	100.0%	-1.7
17613	AT3G18790.1 | expressed protein | chr3:6477705-6479554 FORWARD | Aliases: MVE11.17	6.1	6.3	-0.2	-0.7	100.0%	-1.2
17614	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	9.3	9.1	0.3	0.7	100.0%	-1.4
17615	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	3.4	3.6	-0.1	-0.7	100.0%	-1.2
17616	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	6.4	6.7	-0.3	-0.7	100.0%	-1.3
17617	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	-0.1	-0.7	100.0%	-1.7
17618	AT4G30090.1 | Symbol: EMB1353 | expressed protein | chr4:14708723-14711618 REVERSE | Aliases: EMB1353, EMBRYO DEFECTIVE 1353, F6G3.120, F6G3_120	3.0	3.1	-0.1	-0.7	100.0%	-1.8
17619	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	7.3	7.0	0.2	0.7	100.0%	-1.3
17620	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	3.5	0.1	0.7	100.0%	-1.9
17621	AT5G09980.1 | expressed protein | chr5:3122757-3123909 FORWARD | Aliases: MYH9.20, MYH9_20	3.9	3.7	0.2	0.7	100.0%	-1.6
17622	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	3.7	3.8	-0.1	-0.7	100.0%	-2.0
17623	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	2.6	-0.1	-0.7	100.0%	-2.0
17624	AT2G43370.1 | U1 small nuclear ribonucleoprotein 70 kDa, putative | chr2:18020454-18022531 FORWARD | Aliases: T1O24.11	4.8	4.9	-0.1	-0.7	100.0%	-1.1
17625	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	7.7	7.5	0.1	0.7	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
17626	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	2.8	-0.1	-0.7	100.0%	-1.9
17627	AT2G38640.1 | expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567) | chr2:16164682-16165632 REVERSE | Aliases: T6A23.16, T6A23_16	4.9	5.1	-0.2	-0.7	100.0%	-1.0
17628	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	4.1	4.3	-0.2	-0.7	100.0%	-1.5
17629	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	5.7	5.9	-0.2	-0.7	100.0%	-1.4
17630	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	2.6	2.6	0.1	0.7	100.0%	-1.7
17631	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	6.7	6.9	-0.1	-0.7	100.0%	-1.5
17632	AT3G63400.2 | peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, similar to cyclophylin (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	3.6	0.1	0.7	100.0%	-1.6
17633	AT2G37920.1 | Symbol: EMB1513 | expressed protein | chr2:15876187-15877149 REVERSE | Aliases: EMB1513, EMBRYO DEFECTIVE 1513, T8P21.17, T8P21_17	4.8	4.7	0.1	0.7	100.0%	-1.6
17634	AT3G53840.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:19956549-19958697 FORWARD | Aliases: F5K20.140	4.1	4.0	0.1	0.7	100.0%	-1.5
17635	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	4.0	4.1	-0.1	-0.7	100.0%	-1.3
17636	AT5G50390.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr5:20538015-20540206 REVERSE | Aliases: MXI22.11, MXI22_11	4.4	4.6	-0.1	-0.7	100.0%	-1.5
17637	AT3G25210.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 domain of unknown function | chr3:9181625-9183076 FORWARD | Aliases: MJL12.16	4.5	4.6	-0.1	-0.7	100.0%	-1.7
17638	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	3.2	3.1	0.1	0.7	100.0%	-1.6
17639	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	2.6	-0.1	-0.7	100.0%	-1.7
17640	AT2G31120.1 | expressed protein | chr2:13268210-13269148 REVERSE | Aliases: T16B12.7, T16B12_7	3.2	3.3	-0.1	-0.7	100.0%	-1.3
17641	AT2G02980.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:868358-870384 FORWARD | Aliases: T17M13.15, T17M13_15	2.8	2.8	0.1	0.7	100.0%	-2.0
17642	AT4G39840.1 | expressed protein | chr4:18484895-18486808 FORWARD | Aliases: T5J17.10, T5J17_10	4.6	4.5	0.1	0.7	100.0%	-1.7
17643	AT3G19900.1 | expressed protein | chr3:6922574-6925029 REVERSE | Aliases: MPN9.15	5.5	5.6	-0.2	-0.7	100.0%	-1.2
17644	AT1G78895.1 | expressed protein | chr1:29663009-29664869 REVERSE | Aliases: None	5.7	5.4	0.3	0.7	100.0%	-1.0
17645	AT2G42670.1 | expressed protein | chr2:17778901-17781481 REVERSE | Aliases: F14N22.6, F14N22_6	4.4	4.2	0.1	0.7	100.0%	-1.4
17646	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	3.0	-0.1	-0.7	100.0%	-2.1
17647	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	2.6	-0.1	-0.7	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
17648	AT3G59530.2 | strictosidine synthase family protein, similar to strictosidine synthase (Rauvolfia serpentina)(SP:P15324) | chr3:22004259-22006238 FORWARD | Aliases: T16L24.80	4.6	4.4	0.1	0.7	100.0%	-1.6
17649	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	7.0	6.8	0.2	0.7	100.0%	-1.5
17650	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	2.8	2.9	-0.1	-0.7	100.0%	-1.7
17651	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	5.4	5.2	0.1	0.7	100.0%	-1.5
17652	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	-0.6	100.0%	-2.3
17653	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	2.5	-0.1	-0.6	100.0%	-2.1
17654	AT2G16835.1 | water channel protein, putative, similar to MipC (Mesembryanthemum crystallinum) gi:1657948:gb:AAB18227 | chr2:7302933-7303400 FORWARD | Aliases: F12A24.1	3.1	3.2	-0.1	-0.6	100.0%	-2.1
17655	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	2.9	2.9	-0.1	-0.6	100.0%	-2.1
17656	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)	8.9	8.6	0.2	0.6	100.0%	-1.2
17657	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	6.7	6.9	-0.2	-0.6	100.0%	-1.0
17658	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	3.2	3.3	-0.1	-0.6	100.0%	-1.7
17659	AT2G40630.1 | expressed protein | chr2:16965224-16968222 FORWARD | Aliases: T2P4.2, T2P4_2	3.4	3.3	0.1	0.6	100.0%	-1.7
17660	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	3.3	0.1	0.6	100.0%	-1.6
17661	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	5.9	5.8	0.1	0.6	100.0%	-1.5
17662	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	3.1	-0.1	-0.6	100.0%	-1.7
17663	AT4G07510.1 | hypothetical protein | chr4:4312209-4313619 FORWARD | Aliases: T3E15.7, T3E15_7	2.9	3.0	-0.1	-0.6	100.0%	-1.9
17664	AT1G54450.1 | calcium-binding EF-hand family protein, contains Pfam profile: PF00036 EF hand | chr1:20340222-20343202 REVERSE | Aliases: F20D21.27, F20D21_27	4.2	4.3	-0.1	-0.6	100.0%	-1.8
17665	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	7.9	7.5	0.3	0.6	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
17666	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	2.8	-0.1	-0.6	100.0%	-1.9
17667	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	5.6	5.5	0.1	0.6	100.0%	-1.4
17668	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	4.9	4.8	0.1	0.6	100.0%	-1.2
17669	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	2.3	2.3	-0.1	-0.6	100.0%	-2.3
17670	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	2.7	-0.1	-0.6	100.0%	-2.0
17671	AT4G31960.1 | expressed protein | chr4:15459113-15459774 REVERSE | Aliases: F11C18.11	2.3	2.3	-0.0	-0.6	100.0%	-2.2
17672	AT5G39350.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:15768157-15770190 FORWARD | Aliases: MUL8.30, MUL8_30	4.8	4.6	0.1	0.6	100.0%	-1.2
17673	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	2.9	-0.1	-0.6	100.0%	-1.7
17674	AT1G76630.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile: PF00515 TPR Domain (5 copies) | chr1:28764593-28769680 FORWARD | Aliases: F14G6.23	2.8	2.9	-0.1	-0.6	100.0%	-1.7
17675	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	7.5	7.2	0.3	0.6	100.0%	-1.0
17676	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	2.5	-0.1	-0.6	100.0%	-2.0
17677	AT3G58280.1 | expressed protein | chr3:21589594-21590261 REVERSE | Aliases: F9D24.190	2.7	2.7	-0.1	-0.6	100.0%	-1.9
17678	AT5G67600.1 | expressed protein | chr5:26976797-26977535 REVERSE | Aliases: K9I9.17, K9I9_17	9.9	10.2	-0.2	-0.6	100.0%	-1.3
17679	AT5G40320.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.2	3.3	-0.1	-0.6	100.0%	-1.5
17680	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	4.2	0.1	0.6	100.0%	-1.8
17681	AT3G18524.1 | Symbol: MSH2 | DNA mismatch repair protein MSH2 (MSH2), identical to SP:O24617 DNA mismatch repair protein MSH2 (AtMsh2) {Arabidopsis thaliana}	4.1	3.9	0.1	0.6	100.0%	-1.2
17682	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	3.1	3.2	-0.1	-0.6	100.0%	-1.7
17683	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	2.8	-0.1	-0.6	100.0%	-1.4
17684	AT3G26400.1 | Symbol: EIF4B1 |	5.9	6.0	-0.1	-0.6	100.0%	-1.1
17685	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	4.1	3.9	0.1	0.6	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
17686	AT3G27700.2 | RNA recognition motif (RRM)-containing protein, contains Pfam profile: PF00076 RNA recognition motif | chr3:10258354-10263211 REVERSE | Aliases: MGF10.11	4.3	4.4	-0.1	-0.6	100.0%	-1.5
17687	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	2.8	2.9	-0.1	-0.6	100.0%	-1.8
17688	AT2G21080.1 | expressed protein | chr2:9050780-9052421 FORWARD | Aliases: F26H11.16, F26H11_16	4.3	4.4	-0.1	-0.6	100.0%	-1.6
17689	AT1G19290.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:6666717-6668954 FORWARD | Aliases: T29M8.15	3.0	2.9	0.1	0.6	100.0%	-2.1
17690	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	7.1	6.7	0.5	0.6	100.0%	-0.9
17691	AT3G53360.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:19795480-19797786 FORWARD | Aliases: F4P12.60	3.0	2.9	0.1	0.6	100.0%	-2.0
17692	AT5G55010.1 | hypothetical protein | chr5:22339126-22339455 FORWARD | Aliases: K13P22.1, K13P22_1	2.2	2.3	-0.1	-0.6	100.0%	-2.2
17693	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	2.8	2.9	-0.1	-0.6	100.0%	-1.9
17694	AT5G28090.1 | hypothetical protein | chr5:10101046-10102278 FORWARD | Aliases: T24G3.20, T24G3_20	2.7	2.8	-0.1	-0.6	100.0%	-1.8
17695	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	7.1	6.8	0.3	0.6	100.0%	-1.2
17696	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	3.8	0.1	0.6	100.0%	-1.9
17697	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	3.3	3.5	-0.1	-0.6	100.0%	-1.3
17698	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	4.8	4.5	0.3	0.6	100.0%	-1.2
17699	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	2.6	-0.1	-0.6	100.0%	-2.0
17700	AT1G32080.1 | membrane protein, putative, contains 12 transmembrane domains; similar to yohK (GI:405873) (Escherichia coli) | chr1:11537328-11539780 REVERSE | Aliases: F3C3.12	3.2	3.4	-0.1	-0.6	100.0%	-1.5
17701	AT3G44980.1 | expressed protein | chr3:16452008-16453083 FORWARD | Aliases: F14D17.50	3.2	3.3	-0.1	-0.6	100.0%	-1.9
17702	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	3.3	-0.1	-0.6	100.0%	-1.6
17703	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	-0.1	-0.6	100.0%	-2.1
17704	AT3G24220.1 | Symbol: nced6 | 9-cis-epoxycarotenoid dioxygenase, putative / neoxanthin cleavage enzyme, putative / carotenoid cleavage dioxygenase, putative, similar to GB:CAB10168 from (Lycopersicon esculentum) (J. Exp. Bot. 47, 2111-2112 (1997)); similar to 9-cis-epoxycarotenoid dioxygenase (Phaseolus vulgaris)(GI:6715257) | chr3:8761441-8763179 FORWARD | Aliases: ATNCED6, MUJ8.12	2.8	2.9	-0.1	-0.6	100.0%	-1.9
17705	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	9.6	9.2	0.4	0.6	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
17706	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	5.7	5.4	0.3	0.6	100.0%	-1.0
17707	AT1G49820.1 | 5-methylthioribose kinase family, contains TIGRfam TIGR01767: 5-methylthioribose kinase profile | chr1:18446600-18448766 FORWARD | Aliases: F10F5.1, F10F5_1	9.7	9.3	0.3	0.6	100.0%	-1.5
17708	AT5G46190.1 | KH domain-containing protein, strong similarity to unknown protein (pir::T04533)	4.2	4.1	0.1	0.6	100.0%	-1.3
17709	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	4.1	4.3	-0.2	-0.6	100.0%	-1.3
17710	AT5G38880.1 | expressed protein | chr5:15580536-15586424 REVERSE | Aliases: K15E6.9, K15E6_9	3.9	4.1	-0.2	-0.6	100.0%	-1.3
17711	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	2.8	-0.0	-0.6	100.0%	-2.2
17712	AT2G32850.2 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:13942263-13945054 REVERSE | Aliases: T21L14.21, T21L14_21	5.8	5.9	-0.2	-0.6	100.0%	-1.7
17713	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	0.6	100.0%	-2.3
17714	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	3.5	0.1	0.6	100.0%	-1.7
17715	AT3G43660.1 | nodulin, putative, similar to nodulin 21 (N-21) (Glycine max) SWISS-PROT:P16313 | chr3:15576320-15576916 FORWARD | Aliases: F23N14.40	4.6	4.8	-0.2	-0.6	100.0%	-1.2
17716	AT1G53930.1 | ubiquitin family protein, contains Pfam profile: PF00240 ubiquitin family | chr1:20144079-20144555 REVERSE | Aliases: T18A20.19	2.5	2.6	-0.1	-0.6	100.0%	-1.7
17717	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%	-2.5
17718	AT3G48140.1 | senescence-associated protein, putative, similar to B12D protein (Ipomoea batatas) GB:AAD22104 | chr3:17789385-17790534 FORWARD | Aliases: T24C20.20	12.2	12.1	0.1	0.6	100.0%	-2.0
17719	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	6.8	6.4	0.3	0.6	100.0%	-0.9
17720	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	0.6	100.0%	-2.1
17721	AT3G50220.1 | expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579) | chr3:18628406-18629711 REVERSE | Aliases: F11C1.60	3.1	3.2	-0.1	-0.6	100.0%	-1.4
17722	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	2.3	2.4	-0.1	-0.6	100.0%	-2.1
17723	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	2.9	-0.1	-0.6	100.0%	-1.9
17724	AT1G49260.1 | expressed protein | chr1:18229996-18230445 FORWARD | Aliases: F13F21.29, F13F21_29	3.6	3.5	0.1	0.6	100.0%	-1.8
17725	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}	5.0	4.9	0.1	0.6	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
17726	AT2G15800.1 | expressed protein, and genefinder | chr2:6887907-6889823 FORWARD | Aliases: F19G14.20, F19G14_20	3.0	3.1	-0.1	-0.6	100.0%	-1.8
17727	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	6.3	-0.1	-0.6	100.0%	-1.5
17728	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	3.1	3.2	-0.1	-0.6	100.0%	-1.6
17729	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	9.3	9.4	-0.1	-0.6	100.0%	-1.6
17730	AT4G04540.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr4:2259578-2262136 FORWARD | Aliases: F4H6.4	2.7	2.5	0.1	0.6	100.0%	-1.4
17731	AT4G04570.1 | protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain | chr4:2289957-2292753 FORWARD | Aliases: F4H6.9, F4H6_9	2.7	2.5	0.1	0.6	100.0%	-1.4
17732	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	3.5	3.5	-0.1	-0.6	100.0%	-1.7
17733	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	4.4	0.2	0.6	100.0%	-1.1
17734	AT3G58600.1 | expressed protein, hypothetical protein F21M11.17 - Arabidopsis thaliana, EMBL:AC003027 | chr3:21679173-21682140 REVERSE | Aliases: F14P22.190	8.6	8.9	-0.3	-0.6	100.0%	-1.5
17735	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	2.6	2.7	-0.1	-0.6	100.0%	-1.8
17736	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	-0.6	100.0%	-2.1
17737	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	7.1	7.2	-0.1	-0.6	100.0%	-1.5
17738	AT4G20290.1 | expressed protein | chr4:10955169-10955594 REVERSE | Aliases: F1C12.200, F1C12_200	2.8	2.9	-0.1	-0.6	100.0%	-1.7
17739	AT5G26100.1 | hypothetical protein | chr5:9117293-9117820 REVERSE | Aliases: T1N24.107, T1N24_107	2.8	2.9	-0.1	-0.6	100.0%	-1.9
17740	AT4G34180.1 | cyclase family protein, contains Pfam profile: PF04199 putative cyclase | chr4:16369361-16371434 REVERSE | Aliases: F10M10.6	8.6	8.3	0.3	0.6	100.0%	-1.0
17741	AT5G60090.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:24213308-24214951 REVERSE | Aliases: MGO3.7, MGO3_7	3.1	3.2	-0.1	-0.6	100.0%	-1.6
17742	AT1G12210.1 | Symbol: RFL1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.0	3.2	-0.1	-0.6	100.0%	-1.7
17743	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	0.6	100.0%	-1.8
17744	AT1G19030.1 | expressed protein | chr1:6571175-6572928 FORWARD | Aliases: F14D16.18, F14D16_18	2.1	2.1	0.0	0.6	100.0%	-2.3
17745	AT5G65180.2 | expressed protein, contains Pfam domain, PF04818: Protein of unknown function, DUF618 | chr5:26062602-26065257 FORWARD | Aliases: MQN23.12, MQN23_12	4.4	4.6	-0.2	-0.6	100.0%	-1.4
17746	AT5G03920.1 | expressed protein | chr5:1058145-1058762 FORWARD | Aliases: F8F6.130, F8F6_130	2.7	2.8	-0.1	-0.6	100.0%	-2.2
17747	AT3G24000.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:8672781-8674682 FORWARD | Aliases: F14O13.19	3.6	3.7	-0.1	-0.6	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
17748	AT1G18880.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr1:6520744-6523359 FORWARD | Aliases: F6A14.2, F6A14_2	10.7	10.4	0.3	0.6	100.0%	-1.3
17749	AT5G12390.1 | expressed protein | chr5:4010444-4012040 REVERSE | Aliases: None	9.2	9.3	-0.2	-0.6	100.0%	-1.5
17750	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	8.3	8.1	0.2	0.6	100.0%	-1.1
17751	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	3.4	3.5	-0.1	-0.6	100.0%	-1.6
17752	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	3.1	-0.1	-0.6	100.0%	-1.8
17753	AT2G06000.2 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:2327391-2329662 REVERSE | Aliases: T6P5.20, T6P5_20	4.8	4.7	0.1	0.6	100.0%	-1.4
17754	AT4G35940.1 | expressed protein | chr4:17021675-17023767 FORWARD | Aliases: T19K4.70	6.0	6.1	-0.2	-0.6	100.0%	-1.3
17755	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	8.4	8.5	-0.1	-0.6	100.0%	-1.7
17756	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	3.9	4.1	-0.2	-0.6	100.0%	-0.9
17757	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	3.9	4.1	-0.2	-0.6	100.0%	-0.9
17758	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	10.0	10.2	-0.2	-0.6	100.0%	-1.4
17759	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	5.0	0.1	0.6	100.0%	-1.2
17760	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	5.3	5.6	-0.4	-0.6	100.0%	-0.9
17761	AT2G18870.1 | expressed protein, contains 1 transmembrane domain; tandem duplication of fibronectin type III domain protein (GI:3004551) (TIGR_Ath1:At2g18880) (Arabidopsis thaliana) | chr2:8174553-8175750 FORWARD | Aliases: F19F24.7, F19F24_7	3.9	4.2	-0.3	-0.6	100.0%	-0.6
17762	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	3.3	3.4	-0.1	-0.6	100.0%	-1.6
17763	AT1G79170.1 | hypothetical protein | chr1:29787166-29787515 FORWARD | Aliases: YUP8H12R.22, YUP8H12R_22	5.1	5.3	-0.2	-0.6	100.0%	-1.4
17764	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	3.3	-0.1	-0.6	100.0%	-1.6
17765	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	5.5	5.4	0.1	0.6	100.0%	-1.6
17766	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	4.4	4.6	-0.1	-0.6	100.0%	-1.5
17767	AT2G20830.2 | expressed protein, weak similarity to formiminotransferase cyclodeaminase (GI:3980064) (Gallus gallus) | chr2:8975451-8977687 REVERSE | Aliases: F5H14.20, F5H14_20	7.2	7.4	-0.2	-0.6	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
17768	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	5.4	5.7	-0.3	-0.6	100.0%	-1.2
17769	AT1G76280.2 | similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At2g18940.1); similar to P0529E05.10 [Oryza sativa (japonica cultivar-group)] (GB:NP_915531.1); contains InterPro domain PPR repeat (InterPro:IPR002885) | chr1:28623258-28627625 REVERSE | Aliases: F15M4.22	3.6	3.5	0.1	0.6	100.0%	-1.8
17770	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	4.6	0.1	0.6	100.0%	-1.5
17771	AT1G63710.1 | Symbol: CYP86A7 | cytochrome P450, putative, similar to cytochrome P450 GB:O23066 (Arabidopsis thaliana) | chr1:23635841-23637605 REVERSE | Aliases: F24D7.10, F24D7_10	2.5	2.5	0.1	0.6	100.0%	-2.0
17772	AT1G73220.1 | sugar transporter family protein, contains Pfam profile: PF00083 sugar (and other) transporter | chr1:27541937-27544352 FORWARD | Aliases: T18K17.11, T18K17_11	3.2	3.3	-0.1	-0.6	100.0%	-1.6
17773	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	11.4	11.3	0.1	0.6	100.0%	-1.6
17774	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	2.0	-0.1	-0.6	100.0%	-2.6
17775	AT2G07190.1 | hypothetical protein | chr2:2987364-2988942 FORWARD | Aliases: T25N22.15, T25N22_15	3.4	3.5	-0.1	-0.6	100.0%	-1.9
17776	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	4.2	4.3	-0.1	-0.6	100.0%	-1.6
17777	AT2G37000.1 | TCP family transcription factor, putative, similar to TFPD (GI:6681577) (Arabidopsis thaliana) | chr2:15547469-15548227 FORWARD | Aliases: T1J8.18, T1J8_18	2.4	2.4	-0.1	-0.6	100.0%	-2.0
17778	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	3.0	0.1	0.6	100.0%	-1.7
17779	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	3.5	3.6	-0.1	-0.6	100.0%	-1.8
17780	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	3.8	3.7	0.2	0.6	100.0%	-1.4
17781	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	4.0	4.2	-0.2	-0.6	100.0%	-1.4
17782	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	4.5	4.6	-0.1	-0.6	100.0%	-1.4
17783	AT1G63670.1 | expressed protein | chr1:23611085-23613666 REVERSE | Aliases: F24D7.14, F24D7_14	3.2	3.1	0.1	0.6	100.0%	-1.6
17784	AT5G36150.1 | Symbol: ATPEN3 |	2.5	2.6	-0.1	-0.6	100.0%	-2.1
17785	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	8.3	8.1	0.2	0.6	100.0%	-1.1
17786	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	-0.0	-0.6	100.0%	-2.4
17787	AT4G22150.1 | Symbol: pux3 | UBX domain-containing protein, similar to XY40 protein (Rattus norvegicus) GI:2547025; contains Pfam profile PF00789: UBX domain	8.8	8.9	-0.2	-0.6	100.0%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
17788	AT3G52620.1 | expressed protein, phosphate actyltransferase, Staphylococcus aureus, EMBL:SAU271496 | chr3:19524091-19524534 FORWARD | Aliases: F3C22.20	3.2	3.1	0.1	0.6	100.0%	-1.6
17789	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	2.9	-0.1	-0.6	100.0%	-1.7
17790	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}	3.6	3.6	-0.1	-0.6	100.0%	-2.0
17791	AT3G26960.1 | expressed protein | chr3:9945905-9946816 REVERSE | Aliases: MOJ10.4	3.2	3.1	0.1	0.6	100.0%	-1.9
17792	AT2G25230.1 | Symbol: MYB100 |	2.6	2.6	0.0	0.6	100.0%	-2.4
17793	AT1G31640.1 | MADS-box protein-related, contains INTERPRO:IPR02100 MADS-box domain ;similar to MADS box transcription factor GI:3688589 from (Triticum aestivum) | chr1:11322673-11324157 REVERSE | Aliases: F27M3.16, F27M3_16	2.6	2.7	-0.1	-0.6	100.0%	-2.1
17794	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%	-2.4
17795	AT3G12350.1 | F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250 | chr3:3931571-3933363 FORWARD | Aliases: T2E22.32	6.1	6.2	-0.1	-0.6	100.0%	-1.5
17796	AT3G56990.1 | glycine-rich protein, conserved hypothetical protein SPCC330.09 - Schizosaccharomyces pombe, PIR:T41319 | chr3:21099242-21103036 REVERSE | Aliases: F24I3.70	4.5	4.4	0.1	0.6	100.0%	-1.5
17797	AT4G22860.1 | expressed protein | chr4:11997491-12001636 FORWARD | Aliases: F7H19.40, F7H19_40	4.1	4.2	-0.1	-0.6	100.0%	-1.3
17798	AT5G14860.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:4805890-4807762 FORWARD | Aliases: T9L3.160, T9L3_160	4.1	4.3	-0.2	-0.6	100.0%	-1.4
17799	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	-0.6	100.0%	-1.8
17800	AT5G17460.1 | expressed protein | chr5:5757100-5759721 REVERSE | Aliases: K3M16.30, K3M16_30	3.1	3.0	0.1	0.6	100.0%	-1.7
17801	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	0.6	100.0%	-2.5
17802	AT4G12880.1 | plastocyanin-like domain-containing protein | chr4:7544379-7545301 REVERSE | Aliases: T20K18.230, T20K18_230	6.7	7.1	-0.4	-0.6	100.0%	-1.2
17803	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	4.8	-0.1	-0.6	100.0%	-1.7
17804	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	4.4	4.3	0.1	0.6	100.0%	-1.6
17805	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	9.0	9.1	-0.1	-0.6	100.0%	-1.4
17806	AT2G16510.1 | Symbol: AVA P1 |	9.2	8.9	0.3	0.6	100.0%	-1.2
17807	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	5.6	-0.2	-0.6	100.0%	-1.7
17808	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	2.7	2.8	-0.1	-0.6	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
17809	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	2.2	2.2	-0.1	-0.6	100.0%	-2.2
17810	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	3.3	3.6	-0.3	-0.6	100.0%	-1.3
17811	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	3.1	3.0	0.1	0.6	100.0%	-1.6
17812	AT1G20800.1 | F-box family protein, contains Pfam:PF00646 F-box domain	3.1	3.2	-0.1	-0.6	100.0%	-1.6
17813	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	7.4	7.7	-0.3	-0.6	100.0%	-1.2
17814	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	4.7	4.8	-0.1	-0.6	100.0%	-1.2
17815	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	3.8	3.9	-0.1	-0.6	100.0%	-1.6
17816	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	6.3	-0.5	-0.6	100.0%	-1.2
17817	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	3.3	-0.1	-0.6	100.0%	-1.6
17818	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	3.4	3.3	0.1	0.6	100.0%	-1.7
17819	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%	-2.1
17820	AT3G02810.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:608467-610992 REVERSE | Aliases: F13E7.25, F13E7_25	2.4	2.5	-0.1	-0.6	100.0%	-2.0
17821	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	3.6	0.1	0.6	100.0%	-1.5
17822	AT2G22880.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr2:9748199-9748543 REVERSE | Aliases: T20K9.9, T20K9_9	3.8	3.7	0.2	0.6	100.0%	-1.2
17823	AT3G58450.2 | universal stress protein (USP) family protein, contains Pfam PF00582: universal stress protein family | chr3:21632979-21634131 FORWARD | Aliases: F14P22.40	3.3	3.3	-0.1	-0.6	100.0%	-1.7
17824	AT1G19520.1 | expressed protein | chr1:6759956-6761224 FORWARD | Aliases: F18O14.40	4.4	4.5	-0.2	-0.6	100.0%	-1.5
17825	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	3.2	3.3	-0.1	-0.6	100.0%	-1.6
17826	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	2.9	-0.1	-0.6	100.0%	-2.0
17827	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	2.2	2.2	0.1	0.6	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
17828	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	3.1	3.2	-0.1	-0.6	100.0%	-1.7
17829	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	-0.6	100.0%	-1.8
17830	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	3.9	-0.1	-0.6	100.0%	-1.4
17831	AT5G66090.1 | expressed protein | chr5:26442962-26444394 FORWARD | Aliases: K2A18.17, K2A18_17	4.1	4.0	0.1	0.6	100.0%	-1.3
17832	AT2G21655.1 | expressed protein, contains Pfam PF05617: Arabidopsis thaliana protein of unknown function (DUF784) | chr2:9270617-9271178 FORWARD | Aliases: None	2.6	2.7	-0.1	-0.6	100.0%	-1.8
17833	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	4.9	4.7	0.2	0.6	100.0%	-1.3
17834	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	5.5	5.6	-0.1	-0.6	100.0%	-1.3
17835	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	3.8	3.6	0.2	0.6	100.0%	-1.0
17836	AT2G24000.1 | Symbol: SCPL22 |	2.8	2.8	0.1	0.6	100.0%	-1.9
17837	AT3G19650.1 | cyclin-related, contains weak similarity to Cylicin I (Multiple-band polypeptide I) (Swiss-Prot:P35662) (Bos taurus) | chr3:6823526-6825267 FORWARD | Aliases: MMB12.12	6.3	6.1	0.2	0.6	100.0%	-1.3
17838	AT3G05730.1 | Encodes a defensin-like (DEFL) family protein. | chr3:1695982-1696714 FORWARD | Aliases: F18C1.19	3.4	3.5	-0.1	-0.6	100.0%	-1.6
17839	AT4G22920.1 | expressed protein | chr4:12016536-12018503 REVERSE | Aliases: F7H19.100, F7H19_100	6.0	5.9	0.1	0.6	100.0%	-1.5
17840	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	2.9	-0.1	-0.6	100.0%	-1.9
17841	AT1G31360.1 | DNA helicase, putative (RECQl2), nearly identical to DNA Helicase (Arabidopsis thaliana) GI:11121445 | chr1:11232314-11237511 FORWARD | Aliases: T19E23.16, T19E23_16	3.6	3.4	0.2	0.6	100.0%	-1.7
17842	AT4G17980.1 | Symbol: ANAC071 | no apical meristem (NAM) family protein, NAM (GI:6066595) (Petunia x hybrida)	3.7	3.6	0.1	0.6	100.0%	-1.7
17843	AT3G32190.1 | expressed protein | chr3:13166991-13168270 REVERSE | Aliases: F6H5.102	2.9	2.8	0.1	0.6	100.0%	-1.7
17844	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	4.1	0.2	0.6	100.0%	-1.3
17845	AT1G55660.1 | F-box family protein, contains F-box domain Pfam:PF00646	4.2	4.1	0.1	0.6	100.0%	-1.3
17846	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	2.5	-0.1	-0.6	100.0%	-2.3
17847	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	3.3	-0.1	-0.6	100.0%	-2.1
17848	AT4G34250.1 | fatty acid elongase, putative, similar to fatty acid elongase 1 (Fae1), Arabidopsis thaliana, U29142 (GI:881615)	2.8	2.9	-0.1	-0.6	100.0%	-1.9
17849	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	10.5	10.7	-0.2	-0.6	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
17850	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	2.4	0.1	0.6	100.0%	-2.2
17851	AT1G05040.1 | expressed protein | chr1:1447757-1448447 REVERSE | Aliases: T7A14.9, T7A14_9	2.3	2.3	0.0	0.6	100.0%	-2.2
17852	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	3.9	4.1	-0.1	-0.6	100.0%	-1.9
17853	AT2G06200.1 | Symbol: AtGRF6 |	2.3	2.3	-0.0	-0.6	100.0%	-2.3
17854	AT3G09780.1 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr3:3000764-3003170 REVERSE | Aliases: F11F8.37	4.2	4.1	0.2	0.6	100.0%	-1.1
17855	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	3.6	3.6	0.1	0.6	100.0%	-1.9
17856	AT1G54920.2 | expressed protein | chr1:20474487-20478819 FORWARD | Aliases: F14C21.46, F14C21_46	3.0	3.1	-0.1	-0.6	100.0%	-1.6
17857	AT1G70720.1 | invertase/pectin methylesterase inhibitor family protein, low similarity to pectinesterase from Lycopersicon esculentum SP:Q43143, Arabidopsis thaliana SP:Q42534, Phaseolus vulgaris SP:Q43111; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor | chr1:26670070-26670866 FORWARD | Aliases: F5A18.10, F5A18_10	2.3	2.3	-0.1	-0.6	100.0%	-2.1
17858	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	-0.1	-0.6	100.0%	-2.1
17859	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	2.8	-0.1	-0.6	100.0%	-1.7
17860	AT4G29980.1 | expressed protein | chr4:14664960-14665589 REVERSE | Aliases: F6G3.10, F6G3_10	3.6	3.7	-0.2	-0.6	100.0%	-1.3
17861	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	2.9	-0.1	-0.6	100.0%	-2.0
17862	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	2.8	-0.1	-0.6	100.0%	-1.9
17863	AT3G28140.2 | calmodulin-binding protein | chr3:10471683-10472625 FORWARD | Aliases: MMG15.17	3.4	3.5	-0.1	-0.6	100.0%	-1.8
17864	AT5G04240.1 | Symbol: ELF6 | similar to zinc finger (C2H2 type) family protein / transcription factor jumonji (jmj) 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, jmjC (InterPro:IPR003347) | chr5:1169545-1174858 FORWARD | Aliases: EARLY FLOWERING 6, F21E1.160, F21E1_160	6.3	6.2	0.1	0.6	100.0%	-1.5
17865	AT3G06840.1 | expressed protein | chr3:2156868-2157856 FORWARD | Aliases: F3E22.2	2.5	2.4	0.1	0.6	100.0%	-1.9
17866	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	2.7	0.1	0.6	100.0%	-2.0
17867	AT4G27850.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr4:13870388-13873515 FORWARD | Aliases: T27E11.90, T27E11_90	3.2	3.1	0.1	0.6	100.0%	-1.8
17868	AT5G59350.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:23958008-23959433 FORWARD | Aliases: F2O15.1, F2O15_1	3.4	3.4	-0.1	-0.6	100.0%	-1.5
17869	AT1G04920.1 | sucrose-phosphate synthase, putative, similar to GB:Y11795 from (Craterostigma plantagineum) | chr1:1391501-1395863 REVERSE | Aliases: F13M7.9, F13M7_9	3.2	3.4	-0.2	-0.6	100.0%	-1.4
17870	AT4G24500.2 | hydroxyproline-rich glycoprotein family protein | chr4:12658742-12660615 FORWARD | Aliases: F22K18.300, F22K18_300	3.7	3.8	-0.1	-0.6	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
17871	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	2.8	2.8	-0.1	-0.6	100.0%	-2.0
17872	AT3G10210.1 | expressed protein, similar to putative protein GB:CAA20045 (Arabidopsis thaliana) | chr3:3160244-3161599 REVERSE | Aliases: F14P13.19	4.8	4.9	-0.1	-0.6	100.0%	-1.3
17873	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	2.2	0.1	0.6	100.0%	-2.2
17874	AT1G04800.1 | glycine-rich protein | chr1:1348451-1349285 REVERSE | Aliases: F13M7.21, F13M7_21	6.4	6.7	-0.2	-0.6	100.0%	-1.3
17875	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	-0.6	100.0%	-2.4
17876	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	2.5	2.6	-0.1	-0.6	100.0%	-2.1
17877	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	6.5	0.2	0.6	100.0%	-1.5
17878	AT1G52970.1 | expressed protein | chr1:19740302-19740751 REVERSE | Aliases: F14G24.24, F14G24_24	2.7	2.8	-0.1	-0.6	100.0%	-1.9
17879	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	7.0	7.4	-0.4	-0.6	100.0%	-1.1
17880	NA	2.3	2.3	-0.0	-0.6	100.0%	-2.5
17881	AT5G23940.1 | Symbol: EMB3009 | transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus (gi:2239091); contains Pfam transferase family domain PF002458 | chr5:8076332-8079796 REVERSE | Aliases: EMB3009, EMBRYO DEFECTIVE 3009, MRO11.2, MRO11_2	2.6	2.7	-0.1	-0.6	100.0%	-2.0
17882	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	0.1	0.6	100.0%	-1.9
17883	AT5G06660.1 | expressed protein, contains PF05809: Eukaryotic protein of unknown function (DUF841) | chr5:2046811-2047795 FORWARD | Aliases: F15M7.19, F15M7_19	5.3	5.4	-0.1	-0.6	100.0%	-1.6
17884	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	0.1	0.6	100.0%	-2.1
17885	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	2.7	-0.0	-0.6	100.0%	-2.3
17886	AT5G64060.1 | Symbol: ANAC103 | no apical meristem (NAM) family protein, similar to NAC1 (GI:7716952)	3.1	3.0	0.1	0.6	100.0%	-1.6
17887	AT2G03160.1 | Symbol: ASK19 | E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At19), putative, E3 ubiquitin ligase; similar to Skp1 GI:4959710 from (Medicago sativa) | chr2:959642-960244 FORWARD | Aliases: ARABIDOPSIS SKP1 LIKE 19, ASK19, T18E12.17, T18E12_17	2.8	2.9	-0.1	-0.6	100.0%	-1.7
17888	AT2G19650.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.9	2.9	-0.1	-0.6	100.0%	-1.9
17889	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	3.0	-0.1	-0.6	100.0%	-1.7
17890	AT2G39230.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:16388725-16391328 FORWARD | Aliases: T16B24.13, T16B24_13	3.1	3.0	0.1	0.6	100.0%	-1.8
17891	AT1G48780.1 | expressed protein | chr1:18045657-18046412 FORWARD | Aliases: F11I4.5, F11I4_5	2.5	2.6	-0.1	-0.6	100.0%	-1.5
17892	AT1G76230.1 | expressed protein | chr1:28604701-28605274 REVERSE | Aliases: T23E18.16, T23E18_16	3.1	3.2	-0.1	-0.6	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
17893	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	3.5	3.6	-0.1	-0.6	100.0%	-2.0
17894	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	2.9	-0.1	-0.6	100.0%	-1.7
17895	AT4G05470.1 | F-box family protein (FBL21), contains similarity to N7 protein GI:3273101 from (Medicago truncatula) | chr4:2763253-2767954 REVERSE | Aliases: None	2.5	2.6	-0.1	-0.6	100.0%	-2.3
17896	AT2G30630.2 | expressed protein, similar to H1-1flk (Arabidopsis thaliana) GI:388260 | chr2:13053755-13056296 REVERSE | Aliases: T11J7.2, T11J7_2	2.4	2.5	-0.0	-0.6	100.0%	-2.4
17897	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.	2.9	2.8	0.0	0.6	100.0%	-2.2
17898	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	9.5	9.3	0.2	0.6	100.0%	-1.1
17899	AT5G04630.1 | Symbol: CYP77A9 | cytochrome P450, putative, cytochrome P450 77A3p, Glycine max, PIR:T05948 | chr5:1330579-1332108 FORWARD | Aliases: T1E3.4	4.0	4.1	-0.1	-0.6	100.0%	-1.8
17900	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	5.8	6.0	-0.2	-0.6	100.0%	-1.1
17901	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	3.0	3.1	-0.1	-0.6	100.0%	-1.7
17902	AT5G06820.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:2112995-2116664 FORWARD | Aliases: MPH15.19, MPH15_19	2.9	2.8	0.1	0.6	100.0%	-1.8
17903	AT3G03510.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr3:836046-837714 FORWARD | Aliases: T21P5.7, T21P5_7	4.2	4.3	-0.2	-0.6	100.0%	-1.5
17904	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	5.6	5.9	-0.2	-0.6	100.0%	-1.1
17905	AT5G12130.1 | Symbol: PDE149 |	5.7	5.8	-0.1	-0.6	100.0%	-1.5
17906	AT5G51490.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:20930779-20932832 REVERSE | Aliases: K17N15.4, K17N15_4	2.9	2.9	0.1	0.6	100.0%	-1.7
17907	AT5G17290.1 | autophagy protein Apg5 family, contains Pfam profile: PF04106 autophagy protein Apg5 | chr5:5686947-5689878 REVERSE | Aliases: MKP11.20, MKP11_20	6.5	6.7	-0.2	-0.6	100.0%	-1.2
17908	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	-0.6	100.0%	-1.7
17909	AT4G38710.1 | glycine-rich protein, cylicin II - bovine, PIR2:I46014 | chr4:18077784-18080077 REVERSE | Aliases: T9A14.5	7.7	7.3	0.4	0.6	100.0%	-1.0
17910	AT1G13680.1 | expressed protein | chr1:4690694-4692838 FORWARD | Aliases: F21F23.12, F21F23_12	2.2	2.2	-0.1	-0.6	100.0%	-2.5
17911	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	2.7	0.1	0.6	100.0%	-1.6
17912	AT4G38160.2 | Symbol: PDE191 |	2.8	2.8	-0.1	-0.6	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
17913	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	3.0	3.0	-0.1	-0.6	100.0%	-1.9
17914	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	3.7	3.8	-0.1	-0.6	100.0%	-1.7
17915	AT4G31950.1 | Symbol: CYP82C3 | cytochrome P450 family protein, cytochrome P450 monooxygenase, Pisum sativum, PATCHX:G894153 | chr4:15455169-15457127 FORWARD | Aliases: F11C18.9	2.4	2.5	-0.1	-0.6	100.0%	-2.5
17916	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	0.6	100.0%	-2.0
17917	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	5.8	5.6	0.1	0.6	100.0%	-1.5
17918	AT2G01510.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:230751-232505 REVERSE | Aliases: F2I9.13, F2I9_13	3.3	3.4	-0.1	-0.6	100.0%	-1.6
17919	AT5G05490.2 | Symbol: SYN1.1 |	2.2	2.2	0.0	0.6	100.0%	-2.5
17920	AT4G32860.1 | expressed protein | chr4:15856615-15857363 REVERSE | Aliases: T16I18.70, T16I18_70	2.3	2.3	0.1	0.6	100.0%	-2.0
17921	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	5.5	5.7	-0.1	-0.6	100.0%	-1.4
17922	AT2G31035.1 | expressed protein | chr2:13215744-13215995 FORWARD | Aliases: F7F1.25, F7F1_25	2.6	2.6	0.1	0.6	100.0%	-2.4
17923	AT2G15260.1 | zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	2.9	2.8	0.1	0.6	100.0%	-1.9
17924	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	0.1	0.6	100.0%	-1.8
17925	AT1G35190.1 | oxidoreductase, 2OG-Fe(II) oxygenase family protein, low similarity to hyoscyamine 6-dioxygenase hydroxylase from Hyoscyamus niger (GB:P24397)(SP:P24397), Atropa belladona (gi:4996123); contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily	7.8	8.0	-0.2	-0.6	100.0%	-1.3
17926	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	6.1	5.9	0.2	0.6	100.0%	-1.4
17927	AT4G36770.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr4:17329833-17331630 REVERSE | Aliases: AP22.28, AP22_28	3.1	3.2	-0.1	-0.6	100.0%	-2.0
17928	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	4.7	4.5	0.2	0.6	100.0%	-1.5
17929	AT1G35660.1 | expressed protein | chr1:13192721-13197262 FORWARD | Aliases: F15O4.11	2.5	2.4	0.0	0.6	100.0%	-2.3
17930	AT2G26470.1 | expressed protein, contains PF02586: Uncharacterized ACR, COG2135; weak similarity to NF-M protein (GI:205688) (Rattus norvegicus) | chr2:11266231-11269563 REVERSE | Aliases: T9J22.14, T9J22_14	3.2	3.1	0.1	0.6	100.0%	-1.8
17931	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)	6.5	6.7	-0.2	-0.6	100.0%	-0.9
17932	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	3.2	3.3	-0.1	-0.6	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
17933	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	4.6	4.7	-0.1	-0.6	100.0%	-1.6
17934	AT1G14280.1 | Symbol: PKS2 | phytochrome kinase, putative, contains similarity to Swiss-Prot:Q9SWI1 phytochrome kinase substrate 1 (Arabidopsis thaliana) | chr1:4877622-4879144 FORWARD | Aliases: F14L17.4, F14L17_4, PHYTOCHROME KINASE SUBSTRATE 2	2.3	2.4	-0.1	-0.6	100.0%	-2.3
17935	AT5G16460.1 | expressed protein, similar to unknown protein (pir::T02326) | chr5:5377088-5378536 REVERSE | Aliases: MQK4.19, MQK4_19	2.2	2.3	-0.1	-0.6	100.0%	-2.2
17936	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	3.1	-0.1	-0.6	100.0%	-1.9
17937	AT3G42080.1 | hypothetical protein, hypothetical proteins - Arabidopsis thaliana | chr3:14271580-14272153 FORWARD | Aliases: F4M19.40	2.6	2.5	0.0	0.6	100.0%	-2.4
17938	AT2G18830.1 | hypothetical protein | chr2:8163286-8163483 REVERSE | Aliases: MSF3.21, MSF3_21	2.8	2.9	-0.1	-0.6	100.0%	-2.0
17939	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	4.4	-0.2	-0.6	100.0%	-1.3
17940	AT3G55640.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr3:20650818-20653638 FORWARD | Aliases: F1I16.50	3.7	3.6	0.1	0.6	100.0%	-1.8
17941	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	3.5	3.6	-0.1	-0.6	100.0%	-1.8
17942	AT5G32470.1 | expressed protein | chr5:12102558-12105829 REVERSE | Aliases: F18O9.80, F18O9_80	6.2	6.4	-0.2	-0.6	100.0%	-1.2
17943	AT5G61720.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:24818780-24820395 FORWARD | Aliases: MAC9.3, MAC9_3	2.3	2.4	-0.1	-0.6	100.0%	-2.3
17944	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	6.5	6.6	-0.1	-0.6	100.0%	-1.9
17945	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	3.0	3.1	-0.1	-0.6	100.0%	-1.8
17946	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	2.7	2.8	-0.1	-0.6	100.0%	-1.8
17947	AT5G54400.1 | expressed protein | chr5:22107906-22109352 FORWARD | Aliases: F24B18.2, F24B18_2	4.3	4.4	-0.1	-0.6	100.0%	-1.3
17948	AT5G44860.1 | expressed protein, strong similarity to unknown protein (gb AAC79135.1) | chr5:18127685-18129014 REVERSE | Aliases: K21C13.3, K21C13_3	6.4	6.2	0.2	0.6	100.0%	-1.4
17949	AT4G34730.1 | ribosome-binding factor A family protein, contains PFam PF02033: Ribosome-binding factor A | chr4:16569401-16573685 REVERSE | Aliases: T4L20.310, T4L20_310	4.0	3.9	0.1	0.6	100.0%	-1.5
17950	AT3G01300.1 | protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) Swiss-Prot:Q06548 | chr3:90605-93592 REVERSE | Aliases: T22N4.7, T22N4_7	2.6	2.4	0.2	0.6	100.0%	-1.5
17951	AT5G15080.1 | protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) Swiss-Prot:Q06548 | chr5:4886131-4888791 FORWARD | Aliases: F2G14.200, F2G14_200	2.6	2.4	0.2	0.6	100.0%	-1.5
17952	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	5.2	5.3	-0.1	-0.6	100.0%	-1.3
17953	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	5.1	5.0	0.1	0.6	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
17954	AT1G50530.1 | expressed protein | chr1:18724880-18725397 REVERSE | Aliases: F11F12.27	2.4	2.5	-0.1	-0.6	100.0%	-2.3
17955	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	4.2	-0.1	-0.6	100.0%	-1.3
17956	AT1G54390.4 | PHD finger protein-related, contains low similarity to PHD-finger domain proteins | chr1:20308290-20310657 REVERSE | Aliases: F20D21.22, F20D21_22	3.9	4.1	-0.2	-0.6	100.0%	-1.6
17957	AT5G08310.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:2670135-2675255 REVERSE | Aliases: F8L15.40, F8L15_40	3.9	4.0	-0.2	-0.6	100.0%	-1.4
17958	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	2.2	2.3	-0.1	-0.6	100.0%	-2.1
17959	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	4.5	4.4	0.1	0.6	100.0%	-1.5
17960	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	2.9	3.0	-0.1	-0.6	100.0%	-1.6
17961	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	2.5	2.5	-0.1	-0.6	100.0%	-2.2
17962	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	8.3	7.6	0.7	0.6	100.0%	-0.8
17963	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	8.3	7.6	0.7	0.6	100.0%	-0.8
17964	AT1G72410.1 | COP1-interacting protein-related, similar to COP1-Interacting ProteinI 7 (CIP7) (Arabidopsis thaliana) GI:3327870 | chr1:27255358-27259908 REVERSE | Aliases: T10D10.12, T10D10_12	3.5	3.5	0.0	0.6	100.0%	-2.1
17965	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	-0.1	-0.6	100.0%	-2.0
17966	AT1G27990.1 | expressed protein | chr1:9752786-9753906 REVERSE | Aliases: F13K9.9, F13K9_9	3.5	3.6	-0.1	-0.6	100.0%	-1.4
17967	AT4G24410.1 | expressed protein | chr4:12623540-12624049 REVERSE | Aliases: T22A6.240, T22A6_240	2.2	2.3	-0.0	-0.6	100.0%	-2.5
17968	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	5.4	5.3	0.1	0.6	100.0%	-1.2
17969	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	4.4	4.2	0.1	0.6	100.0%	-1.4
17970	AT3G13140.1 | hydroxyproline-rich glycoprotein family protein | chr3:4226661-4227384 REVERSE | Aliases: MJG19.9	2.7	2.7	-0.1	-0.6	100.0%	-2.0
17971	AT5G35830.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr5:14017543-14018646 REVERSE | Aliases: MIK22.14, MIK22_14	2.4	2.5	-0.1	-0.6	100.0%	-2.0
17972	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	3.4	3.4	-0.1	-0.6	100.0%	-1.7
17973	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	-0.1	-0.6	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
17974	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	3.1	3.0	0.1	0.6	100.0%	-1.4
17975	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	-0.6	100.0%	-2.6
17976	AT1G14685.3 | expressed protein | chr1:5042583-5044289 FORWARD | Aliases: F10B6.5, F10B6_5	6.6	6.5	0.1	0.6	100.0%	-1.4
17977	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	5.6	5.4	0.2	0.6	100.0%	-0.9
17978	AT2G29560.1 | enolase, putative, similar to enolase (Spinacia oleracea) gi:8919731:emb:CAB96173 | chr2:12653666-12656983 FORWARD | Aliases: F16P2.6, F16P2_6	7.8	7.6	0.2	0.6	100.0%	-1.5
17979	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))	2.8	2.8	-0.1	-0.6	100.0%	-2.0
17980	AT3G32180.1 | expressed protein | chr3:13166126-13166495 REVERSE | Aliases: F6H5.2	2.8	2.9	-0.1	-0.6	100.0%	-1.9
17981	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	3.1	0.1	0.6	100.0%	-1.9
17982	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	2.9	0.1	0.6	100.0%	-2.1
17983	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	2.9	-0.1	-0.6	100.0%	-1.9
17984	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	3.6	-0.1	-0.6	100.0%	-1.8
17985	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)	6.6	6.4	0.2	0.6	100.0%	-1.1
17986	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	2.8	-0.1	-0.6	100.0%	-1.9
17987	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	7.7	7.9	-0.2	-0.6	100.0%	-1.2
17988	AT2G22520.1 | hypothetical protein, and grail	2.9	3.0	-0.1	-0.6	100.0%	-1.7
17989	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	4.9	4.9	-0.1	-0.6	100.0%	-1.6
17990	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	5.5	5.6	-0.1	-0.6	100.0%	-1.3
17991	AT2G27060.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:11558405-11561853 FORWARD | Aliases: T20P8.11, T20P8_11	5.4	5.3	0.1	0.6	100.0%	-1.4
17992	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	3.2	3.3	-0.1	-0.6	100.0%	-1.7
17993	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	7.8	7.4	0.4	0.6	100.0%	-0.8
17994	AT2G35750.1 | expressed protein | chr2:15036908-15037369 REVERSE | Aliases: T20F21.6, T20F21_6	4.2	4.4	-0.2	-0.6	100.0%	-1.1
17995	AT2G45150.3 | phosphatidate cytidylyltransferase family protein, contains Pfam profile: PF01148 phosphatidate cytidylyltransferase | chr2:18620495-18622792 FORWARD | Aliases: T14P1.4	2.9	2.8	0.1	0.6	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
17996	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	6.4	6.3	0.1	0.6	100.0%	-1.7
17997	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	-0.6	100.0%	-1.9
17998	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	3.2	-0.1	-0.6	100.0%	-1.8
17999	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	0.1	0.6	100.0%	-1.9
18000	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	8.8	8.9	-0.1	-0.6	100.0%	-1.2
18001	AT3G54190.1 | expressed protein, GTP-binding regulatory protein beta chain, Dictyostelium discoideum, PIR:A47370 | chr3:20072506-20075132 REVERSE | Aliases: F24B22.150	4.6	4.7	-0.2	-0.6	100.0%	-1.5
18002	AT5G50880.1 | expressed protein | chr5:20718592-20718870 REVERSE | Aliases: K3K7.2, K3K7_2	2.9	2.9	-0.1	-0.6	100.0%	-2.3
18003	AT1G14110.1 | xyloglucan fucosyltransferase family protein, contains Pfam profile: PF03254 xyloglucan fucosyltransferase | chr1:4827958-4831912 FORWARD | Aliases: F7A19.19, F7A19_19	2.5	2.5	-0.0	-0.6	100.0%	-2.4
18004	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	5.7	5.8	-0.2	-0.6	100.0%	-1.1
18005	AT4G03930.1 | pectin methylesterase, putative, similar to pectin methylesterase GI:1617588 from (Lycopersicon esculentum) | chr4:1870420-1872528 FORWARD | Aliases: T24M8.6, T24M8_6	2.8	3.0	-0.1	-0.6	100.0%	-1.4
18006	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	0.1	0.6	100.0%	-2.0
18007	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	6.1	5.9	0.1	0.6	100.0%	-1.3
18008	AT4G09860.1 | expressed protein | chr4:6194706-6195298 REVERSE | Aliases: F17A8.210, F17A8_210	2.2	2.2	0.0	0.6	100.0%	-2.6
18009	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	8.8	9.0	-0.2	-0.6	100.0%	-1.6
18010	AT1G70920.1 | homeobox-leucine zipper protein, putative / HD-ZIP transcription factor, putative, similar to homeodomain leucine zipper protein GI:5006851 from (Oryza sativa) | chr1:26739702-26742241 FORWARD | Aliases: F15H11.30	4.3	4.4	-0.1	-0.6	100.0%	-1.8
18011	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	9.3	9.1	0.3	0.6	100.0%	-1.1
18012	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	3.6	-0.1	-0.6	100.0%	-1.3
18013	AT4G26190.1 | expressed protein | chr4:13262245-13266969 REVERSE | Aliases: T25K17.7	6.0	5.9	0.1	0.6	100.0%	-1.7
18014	AT2G35470.1 | expressed protein | chr2:14916005-14916881 REVERSE | Aliases: T32F12.15, T32F12_15	4.7	4.5	0.1	0.6	100.0%	-1.4
18015	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	2.3	-0.1	-0.6	100.0%	-2.5

Rank	Description	Sync	Root	M	t	adj.q	B
18016	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	-0.6	100.0%	-1.9
18017	AT1G58250.1 | Symbol: SAB | SABRE, putative, similar to SABRE (GI:719291) (Arabidopsis thaliana) | chr1:21590707-21605286 REVERSE | Aliases: F16M22.5, F16M22_5, SABRE	7.2	7.4	-0.2	-0.6	100.0%	-1.2
18018	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	5.5	5.7	-0.1	-0.6	100.0%	-1.3
18019	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	4.3	4.4	-0.1	-0.6	100.0%	-1.6
18020	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	3.7	3.6	0.1	0.6	100.0%	-1.7
18021	AT3G04690.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:1273392-1275944 REVERSE | Aliases: F7O18.16, F7O18_16	2.5	2.5	-0.1	-0.6	100.0%	-2.0
18022	AT3G17450.1 | hAT dimerisation domain-containing protein, contains Pfam profile PF04937: Protein of unknown function (DUF 659)	6.2	6.4	-0.2	-0.6	100.0%	-1.3
18023	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	7.0	7.2	-0.1	-0.6	100.0%	-1.6
18024	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	3.0	-0.1	-0.6	100.0%	-1.5
18025	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	2.5	2.6	-0.0	-0.6	100.0%	-2.3
18026	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	3.7	3.9	-0.1	-0.6	100.0%	-1.7
18027	AT5G33280.1 | chloride channel-like (CLC) protein, putative, similar to CLC-c, At5g49890 (Arabidopsis thaliana) and chloride channel protein ClC-1 - Nicotiana tabacum, PIR:T02939 | chr5:12566510-12569737 FORWARD | Aliases: F19N2.1	4.5	4.7	-0.1	-0.6	100.0%	-1.2
18028	AT3G55670.1 | hypothetical protein, various predicted proteins, Arabidopsis thaliana | chr3:20668992-20670482 REVERSE | Aliases: F1I16.80	3.2	3.2	-0.1	-0.6	100.0%	-2.2
18029	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	4.8	0.1	0.6	100.0%	-1.1
18030	AT5G19070.1 | expressed protein | chr5:6375247-6377662 FORWARD | Aliases: T16G12.110, T16G12_110	5.6	5.3	0.4	0.6	100.0%	-1.2
18031	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	2.5	2.6	-0.1	-0.6	100.0%	-2.2
18032	AT1G53760.1 | expressed protein | chr1:20072827-20074586 REVERSE | Aliases: T18A20.23, T18A20_23	3.8	4.0	-0.2	-0.6	100.0%	-1.4
18033	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	3.6	-0.1	-0.6	100.0%	-1.3
18034	AT3G28840.1 | expressed protein | chr3:10839655-10841183 FORWARD | Aliases: T19N8.14	2.7	2.8	-0.1	-0.6	100.0%	-1.6
18035	NA	2.2	2.2	-0.0	-0.6	100.0%	-2.2
18036	AT4G07740.1 | expressed protein | chr4:4539635-4540679 FORWARD | Aliases: T6L9.5, T6L9_5	2.4	2.5	-0.1	-0.6	100.0%	-1.7
18037	AT1G71490.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:26936567-26939487 REVERSE | Aliases: F26A9.13	3.3	3.4	-0.1	-0.6	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
18038	AT2G35360.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr2:14896128-14897922 REVERSE | Aliases: T32F12.26, T32F12_26	4.3	4.2	0.1	0.6	100.0%	-1.6
18039	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	2.2	2.2	0.0	0.6	100.0%	-2.6
18040	AT1G04645.1 | self-incompatibility protein-related, similar to S3 self-incompatibility protein (Papaver rhoeas) GI:1107841 | chr1:1293769-1294262 REVERSE | Aliases: None	2.7	2.8	-0.1	-0.6	100.0%	-2.1
18041	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	3.9	-0.1	-0.6	100.0%	-1.9
18042	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	4.7	4.9	-0.2	-0.6	100.0%	-1.2
18043	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)	3.6	3.4	0.1	0.6	100.0%	-1.5
18044	AT2G45680.1 | TCP family transcription factor, putative, similar to PCF2 (GI:2580440) (Oryza sativa) | chr2:18827320-18828963 REVERSE | Aliases: F17K2.21	3.3	3.2	0.1	0.6	100.0%	-1.6
18045	AT3G60940.1 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537; expression supported by MPSS | chr3:22532590-22534004 REVERSE | Aliases: T27I15.30	2.5	2.4	0.1	0.6	100.0%	-1.9
18046	AT1G78110.1 | expressed protein | chr1:29396730-29398079 FORWARD | Aliases: T11I11.5, T11I11_5	7.1	7.4	-0.3	-0.6	100.0%	-1.1
18047	AT5G64490.1 | expressed protein | chr5:25796536-25797534 REVERSE | Aliases: T12B11.8, T12B11_8	2.3	2.4	-0.1	-0.6	100.0%	-2.0
18048	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	2.6	-0.1	-0.6	100.0%	-2.0
18049	AT2G14120.2 | dynamin-like protein 2b (ADL2b), identical to dynamin like protein 2b (ADL2b) (Arabidopsis thaliana) GI:19032339	7.8	7.6	0.2	0.6	100.0%	-1.4
18050	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	3.2	3.3	-0.1	-0.6	100.0%	-2.1
18051	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	3.4	3.5	-0.1	-0.6	100.0%	-1.7
18052	AT1G76310.1 | Symbol: CYCB2;4 | cyclin, putative, similar to B-like cyclin GI: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	0.6	100.0%	-2.1
18053	AT1G44130.1 | nucellin protein, putative, similar to nucellin GI:2290202 from (Hordeum vulgare) | chr1:16789948-16791758 REVERSE | Aliases: T7O23.17, T7O23_17	2.8	2.9	-0.1	-0.6	100.0%	-2.0
18054	AT5G28560.1 | expressed protein | chr5:10566850-10567134 FORWARD | Aliases: T10I18.20, T10I18_20	3.2	3.3	-0.1	-0.6	100.0%	-1.9
18055	AT2G19390.1 | expressed protein | chr2:8396882-8404944 REVERSE | Aliases: F27F23.19, F27F23_19	3.9	4.3	-0.4	-0.6	100.0%	-1.1
18056	AT5G15710.1 | F-box family protein, unusual floral organs protein UFO - Arabidopsis thaliana, PIR:S57710 | chr5:5122495-5124374 FORWARD | Aliases: F14F8.90, F14F8_90	4.7	4.8	-0.1	-0.6	100.0%	-1.4
18057	AT1G06770.2 | zinc finger (C3HC4-type RING finger) family protein | chr1:2078910-2081938 REVERSE | Aliases: F4H5.14, F4H5_14	4.2	4.1	0.1	0.6	100.0%	-1.6
18058	AT5G67050.1 | lipase class 3 family protein, similar to lipase precursor (Rhizopus arrhizus) GI:6942320; contains Pfam profile PF01764: Lipase	3.1	3.0	0.1	0.6	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
18059	AT4G22030.1 | F-box family protein, PF0064: F-box domain; similar to F-box protein family, AtFBX7 (GI:20197899) (Arabidopsis thaliana)	3.2	3.3	-0.1	-0.6	100.0%	-1.8
18060	AT5G16500.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:5386678-5389168 REVERSE | Aliases: MQK4.24, MQK4_24	2.6	2.7	-0.0	-0.6	100.0%	-2.2
18061	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)	7.4	7.6	-0.2	-0.6	100.0%	-1.1
18062	AT5G53330.1 | expressed protein | chr5:21656443-21658189 FORWARD | Aliases: K19E1.13, K19E1_13	7.1	6.9	0.1	0.6	100.0%	-1.4
18063	AT4G00770.1 | expressed protein | chr4:331157-333477 FORWARD | Aliases: A_TM018A10.11, A_TM018A10_11, T18A10.2, T18A10_2	2.8	2.9	-0.1	-0.6	100.0%	-1.7
18064	AT5G07560.1 | Symbol: GRP20 | glycine-rich protein (GRP20), oleosin; glycine-rich protein 20 (GRP20); similar to - Brassica napus, PIR:S50195	2.2	2.2	-0.1	-0.6	100.0%	-1.9
18065	AT5G50500.1 | expressed protein | chr5:20579376-20579783 REVERSE | Aliases: MBA10.5, MBA10_5	2.4	2.4	-0.1	-0.6	100.0%	-2.1
18066	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	9.9	10.1	-0.2	-0.6	100.0%	-1.3
18067	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)	3.0	3.1	-0.1	-0.6	100.0%	-1.7
18068	AT2G46190.1 | hypothetical protein | chr2:18978872-18979877 FORWARD | Aliases: T3F17.16	2.4	2.4	0.0	0.6	100.0%	-2.5
18069	AT2G47660.1 | expressed protein | chr2:19550022-19550230 FORWARD | Aliases: F17A22.5	3.0	3.1	-0.1	-0.6	100.0%	-2.0
18070	AT2G25565.1 | expressed protein | chr2:10891140-10892373 REVERSE | Aliases: F3N11.20	3.0	3.0	-0.1	-0.6	100.0%	-1.8
18071	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	7.6	7.4	0.2	0.6	100.0%	-1.1
18072	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	6.5	6.4	0.1	0.6	100.0%	-1.2
18073	AT2G07630.1 | expressed protein | chr2:3208707-3210806 REVERSE | Aliases: F9A16.16, F9A16_16	2.0	2.1	-0.0	-0.6	100.0%	-2.8
18074	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	3.9	-0.1	-0.6	100.0%	-1.6
18075	ATCG00430.1 | Symbol: PSBG | photosystem II G protein	3.6	3.4	0.2	0.6	100.0%	-1.3
18076	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	3.8	0.1	0.6	100.0%	-1.7
18077	AT3G18700.1 | expressed protein | chr3:6431728-6432911 REVERSE | Aliases: MVE11.6	2.4	2.4	-0.1	-0.6	100.0%	-2.1
18078	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	6.5	6.3	0.2	0.6	100.0%	-1.3
18079	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	2.7	2.8	-0.1	-0.6	100.0%	-1.8
18080	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.	3.2	3.2	-0.1	-0.6	100.0%	-1.5
18081	AT3G27800.1 | expressed protein | chr3:10303165-10303438 REVERSE | Aliases: MGF10.20	2.7	2.6	0.1	0.6	100.0%	-2.1
18082	AT5G20600.1 | expressed protein | chr5:6966206-6968035 REVERSE | Aliases: F7C8.190, F7C8_190	6.2	6.1	0.2	0.6	100.0%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
18083	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	2.7	2.8	-0.1	-0.6	100.0%	-2.0
18084	AT3G42060.1 | myosin heavy chain-related | chr3:14262586-14265255 REVERSE | Aliases: F4M19.20	2.7	2.7	-0.1	-0.6	100.0%	-2.0
18085	AT2G24310.1 | expressed protein | chr2:10351438-10352590 FORWARD | Aliases: T28I24.4, T28I24_4	2.4	2.4	-0.1	-0.6	100.0%	-2.1
18086	AT2G32980.1 | expressed protein | chr2:14004459-14006905 REVERSE | Aliases: T21L14.8, T21L14_8	7.0	6.7	0.3	0.6	100.0%	-1.2
18087	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%	-1.7
18088	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	5.4	5.7	-0.3	-0.6	100.0%	-1.3
18089	AT2G27220.1 | homeodomain-containing protein | chr2:11644384-11646615 REVERSE | Aliases: T22O13.1, T22O13_1	3.9	3.8	0.1	0.6	100.0%	-1.9
18090	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	0.1	0.6	100.0%	-2.2
18091	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	0.1	0.6	100.0%	-2.2
18092	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	6.9	6.6	0.3	0.6	100.0%	-1.0
18093	AT3G50960.1 | expressed protein | chr3:18948325-18951365 REVERSE | Aliases: F18B3.240	7.0	6.8	0.2	0.6	100.0%	-1.3
18094	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	7.3	7.2	0.1	0.6	100.0%	-1.5
18095	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	2.7	2.7	0.1	0.6	100.0%	-2.2
18096	AT5G46310.1 | WRKY family transcription factor, identical to WRKY transcription factor 8 GI:15384212 from (Arabidopsis thaliana) | chr5:18802899-18804183 FORWARD | Aliases: MPL12.9, MPL12_9	3.9	4.1	-0.1	-0.6	100.0%	-1.6
18097	AT4G03040.1 | expressed protein | chr4:1341083-1343140 FORWARD | Aliases: T4I9.8, T4I9_8	2.8	2.8	0.1	0.6	100.0%	-2.2
18098	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	4.6	-0.1	-0.6	100.0%	-1.6
18099	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	3.0	2.9	0.1	0.6	100.0%	-1.7
18100	AT3G24750.1 | expressed protein | chr3:9036275-9037731 FORWARD | Aliases: K7P8.4	2.2	2.3	-0.0	-0.6	100.0%	-2.4
18101	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	3.5	3.6	-0.1	-0.6	100.0%	-1.4
18102	AT3G60650.1 | expressed protein | chr3:22430926-22431249 FORWARD | Aliases: T4C21.60	2.5	2.5	-0.1	-0.6	100.0%	-2.6
18103	AT2G30760.1 | expressed protein | chr2:13112847-13115298 REVERSE | Aliases: T11J7.15, T11J7_15	2.3	2.4	-0.0	-0.6	100.0%	-2.1
18104	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	4.8	5.0	-0.1	-0.6	100.0%	-1.5
18105	AT2G18200.1 | expressed protein | chr2:7931349-7931741 REVERSE | Aliases: F8D23.12	2.7	2.7	-0.1	-0.6	100.0%	-2.0
18106	AT3G10410.1 | Symbol: SCPL49 |	10.4	10.1	0.3	0.6	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
18107	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	3.4	-0.1	-0.6	100.0%	-1.4
18108	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)	3.1	3.2	-0.1	-0.6	100.0%	-2.0
18109	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	2.4	2.4	-0.0	-0.6	100.0%	-2.4
18110	AT5G42450.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:16994871-16996244 FORWARD | Aliases: MDH9.15, MDH9_15	3.5	3.4	0.1	0.6	100.0%	-1.5
18111	AT1G68765.1 | Symbol: IDA | expressed protein	3.9	4.0	-0.1	-0.6	100.0%	-1.9
18112	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	7.3	7.1	0.1	0.6	100.0%	-1.4
18113	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	7.0	6.8	0.2	0.6	100.0%	-1.6
18114	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	3.0	-0.1	-0.6	100.0%	-1.8
18115	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	3.8	3.9	-0.1	-0.6	100.0%	-1.7
18116	AT1G21440.1 | mutase family protein, similar to carboxyvinyl-carboxyphosphonate phosphorylmutase GB:O49290 from (Arabidopsis thaliana); similar to carboxyphosphonoenolpyruvate mutase (GI:47149) (Streptomyces hygroscopicus); contains Prosite PS00161: Isocitrate lyase signature | chr1:7502159-7504140 REVERSE | Aliases: F24J8.7, F24J8_7	10.1	9.9	0.3	0.6	100.0%	-1.7
18117	AT5G52290.1 | expressed protein | chr5:21247579-21253780 REVERSE | Aliases: K24M7.2, K24M7_2	2.2	2.2	0.0	0.6	100.0%	-2.6
18118	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	3.7	-0.1	-0.6	100.0%	-1.3
18119	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	3.1	0.1	0.6	100.0%	-1.7
18120	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	0.6	100.0%	-1.6
18121	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	3.7	3.9	-0.1	-0.6	100.0%	-1.5
18122	AT3G11290.1 | expressed protein | chr3:3535616-3537849 REVERSE | Aliases: F11B9.20	4.0	4.1	-0.1	-0.6	100.0%	-1.9
18123	AT2G04220.1 | expressed protein | chr2:1445398-1446321 FORWARD | Aliases: T23O15.16	2.4	2.4	-0.0	-0.6	100.0%	-2.2
18124	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	9.0	8.8	0.2	0.6	100.0%	-1.6
18125	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%	-1.6
18126	AT5G64970.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr5:25975251-25977870 REVERSE | Aliases: MXK3.20, MXK3_20	4.2	4.1	0.1	0.6	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
18127	AT1G17210.1 | expressed protein, distantly related to dentin phosphoryn (Homo sapiens) (GI:4322670) | chr1:5880123-5884749 REVERSE | Aliases: F20D23.9, F20D23_9	7.9	7.7	0.2	0.6	100.0%	-1.4
18128	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	4.1	3.8	0.2	0.6	100.0%	-1.4
18129	AT3G20720.1 | expressed protein | chr3:7239914-7247011 FORWARD | Aliases: MOE17.2	5.7	5.5	0.2	0.6	100.0%	-1.3
18130	AT5G55610.2 | expressed protein | chr5:22543043-22545274 FORWARD | Aliases: MDF20.5, MDF20_5	7.1	6.9	0.2	0.6	100.0%	-1.4
18131	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	3.1	-0.1	-0.6	100.0%	-1.7
18132	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	6.7	6.4	0.3	0.6	100.0%	-1.0
18133	AT2G30480.2 | expressed protein | chr2:12995344-12999804 REVERSE | Aliases: T6B20.25, T6B20_25	3.2	3.3	-0.1	-0.6	100.0%	-1.8
18134	AT1G51000.1 | expressed protein, ; expression supported by MPSS | chr1:18913592-18913950 FORWARD | Aliases: F8A12.22, F8A12_22	2.6	2.6	-0.0	-0.6	100.0%	-2.6
18135	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	2.8	-0.1	-0.6	100.0%	-2.2
18136	AT5G15940.1 | short-chain dehydrogenase/reductase (SDR) family protein, similar to forever young oxidoreductase GI:18138083 from (Lycopersicon esculentum) | chr5:5202858-5204878 FORWARD | Aliases: F1N13.80, F1N13_80	2.8	2.7	0.1	0.6	100.0%	-2.1
18137	AT1G79090.2 | expressed protein, 11408 (cDNA not full-length)	3.7	3.9	-0.2	-0.6	100.0%	-1.6
18138	AT1G75770.1 | expressed protein | chr1:28453651-28454769 FORWARD | Aliases: F10A5.4, F10A5_4	2.8	2.8	0.1	0.6	100.0%	-1.9
18139	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	2.6	2.5	0.0	0.6	100.0%	-2.0
18140	AT1G12845.1 | expressed protein | chr1:4378937-4379514 REVERSE | Aliases: None	3.2	3.4	-0.2	-0.6	100.0%	-1.6
18141	AT4G19000.1 | IWS1 C-terminus family protein, contains Pfam profile PF05909: IWS1 C-terminus | chr4:10405514-10407350 FORWARD | Aliases: F13C5.170, F13C5_170	2.6	2.7	-0.0	-0.6	100.0%	-2.2
18142	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).	2.9	2.9	-0.1	-0.6	100.0%	-2.1
18143	AT5G40360.1 | Symbol: MYB115 |	3.0	3.0	-0.1	-0.6	100.0%	-2.0
18144	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	3.6	0.1	0.6	100.0%	-1.4
18145	AT5G51560.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:20962913-20966080 FORWARD | Aliases: K17N15.11, K17N15_11	3.0	3.1	-0.1	-0.6	100.0%	-1.9
18146	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	4.8	5.0	-0.2	-0.6	100.0%	-1.4
18147	AT2G37520.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr2:15751847-15756866 REVERSE | Aliases: F13M22.2, F13M22_2	3.4	3.3	0.1	0.6	100.0%	-1.8
18148	AT3G49150.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.5	-0.1	-0.6	100.0%	-1.9
18149	AT3G62350.1 | expressed protein | chr3:23082055-23082741 REVERSE | Aliases: T12C14.50	2.8	2.9	-0.1	-0.6	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
18150	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	5.0	5.2	-0.1	-0.6	100.0%	-1.3
18151	AT1G69430.1 | expressed protein | chr1:26101688-26102740 FORWARD | Aliases: F10D13.10, F10D13_10	3.9	4.0	-0.1	-0.6	100.0%	-1.6
18152	AT3G26050.1 | expressed protein | chr3:9523019-9525789 FORWARD | Aliases: MPE11.22	3.2	3.3	-0.1	-0.6	100.0%	-1.6
18153	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	3.5	3.6	-0.1	-0.6	100.0%	-1.7
18154	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	4.4	4.8	-0.3	-0.6	100.0%	-1.2
18155	AT5G66050.2 | expressed protein | chr5:26429324-26431754 REVERSE | Aliases: K2A18.12, K2A18_12	4.5	4.3	0.2	0.6	100.0%	-1.1
18156	AT4G03740.1 | expressed protein | chr4:1661990-1663513 REVERSE | Aliases: T5L23.25, T5L23_25	2.3	2.3	-0.1	-0.6	100.0%	-2.3
18157	AT2G45880.1 | glycosyl hydrolase family 14 protein, similar to beta-amylase GI:13560977 from (Castanea crenata) | chr2:18885593-18889649 REVERSE | Aliases: F4I18.14	3.9	3.8	0.1	0.6	100.0%	-1.7
18158	AT2G46910.1 | plastid-lipid associated protein PAP / fibrillin family protein, contains Pfam profile PF04755: PAP_fibrillin | chr2:19279350-19281071 FORWARD | Aliases: F14M4.46	4.6	4.7	-0.1	-0.6	100.0%	-1.4
18159	AT4G26950.1 | expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584 | chr4:13533570-13534101 REVERSE | Aliases: F10M23.290, F10M23_290	2.8	2.7	0.1	0.6	100.0%	-2.0
18160	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	2.9	2.7	0.1	0.6	100.0%	-1.2
18161	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	7.5	7.2	0.3	0.6	100.0%	-1.2
18162	AT5G37570.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:14941724-14943376 REVERSE | Aliases: K12B20.3, K12B20_3	3.3	3.2	0.1	0.6	100.0%	-1.7
18163	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	3.4	0.1	0.6	100.0%	-1.6
18164	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	5.6	5.9	-0.3	-0.6	100.0%	-1.4
18165	AT1G67230.1 | expressed protein | chr1:25154914-25159942 REVERSE | Aliases: F1N21.5	6.7	6.8	-0.1	-0.6	100.0%	-1.6
18166	AT1G35230.1 | Symbol: AGP5 | arabinogalactan-protein (AGP5), identical to gi_3883128_gb_AAC77827 | chr1:12917127-12917741 FORWARD | Aliases: ARABINOGALACTAN PROTEIN 5, T9I1.2, T9I1_2	3.2	3.1	0.1	0.5	100.0%	-1.6
18167	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	2.6	2.6	-0.1	-0.5	100.0%	-2.0
18168	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	3.1	3.0	0.1	0.5	100.0%	-1.9
18169	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	2.3	2.4	-0.0	-0.5	100.0%	-2.2
18170	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	2.5	-0.1	-0.5	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
18171	AT1G19370.1 | expressed protein | chr1:6692755-6694925 REVERSE | Aliases: F18O14.9, F18O14_9	5.8	5.7	0.1	0.5	100.0%	-1.4
18172	AT5G09940.1 | expressed protein | chr5:3101193-3101834 FORWARD | Aliases: MYH9.15, MYH9_15	2.9	3.0	-0.1	-0.5	100.0%	-1.9
18173	AT4G23220.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr4:12153967-12156948 REVERSE | Aliases: F21P8.110, F21P8_110	2.4	2.4	0.1	0.5	100.0%	-2.2
18174	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	4.3	4.2	0.2	0.5	100.0%	-1.4
18175	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	3.4	3.3	0.1	0.5	100.0%	-1.6
18176	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	2.7	-0.1	-0.5	100.0%	-2.1
18177	AT1G05440.1 | expressed protein, contains domain THR_RICH (PS50325) | chr1:1596006-1597847 REVERSE | Aliases: T25N20.9, T25N20_9	2.7	2.8	-0.1	-0.5	100.0%	-2.0
18178	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	2.3	0.0	0.5	100.0%	-2.2
18179	AT3G15220.1 | protein kinase, putative, similar to serine/threonine protein kinase 24 (Homo sapiens) SWISS-PROT:Q9Y6E | chr3:5126605-5132313 REVERSE | Aliases: K7L4.2	5.1	5.2	-0.2	-0.5	100.0%	-1.3
18180	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	3.4	0.1	0.5	100.0%	-1.5
18181	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	3.9	3.8	0.1	0.5	100.0%	-1.4
18182	AT4G23080.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr4:12096797-12098899 FORWARD | Aliases: F7H19.270, F7H19_270	2.4	2.4	-0.0	-0.5	100.0%	-2.4
18183	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	-0.1	-0.5	100.0%	-2.0
18184	AT5G32610.1 | hypothetical protein, predicted proteins, Arabidopsis thaliana and Borrelia burgdorferi | chr5:12273907-12276326 REVERSE | Aliases: F15I15.20, F15I15_20	2.3	2.4	-0.1	-0.5	100.0%	-2.3
18185	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	4.7	4.7	0.1	0.5	100.0%	-1.9
18186	AT5G08130.1 | Symbol: BIM1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	5.8	6.1	-0.2	-0.5	100.0%	-1.3
18187	AT1G28250.1 | expressed protein | chr1:9874234-9875560 FORWARD | Aliases: F3H9.10, F3H9_10	3.4	3.3	0.1	0.5	100.0%	-1.7
18188	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	9.2	9.4	-0.3	-0.5	100.0%	-1.3
18189	AT5G24480.1 | expressed protein, similar to unknown protein (gb:AAD32930.1) | chr5:8363834-8365039 REVERSE | Aliases: T31K7.6, T31K7_6	3.7	3.9	-0.1	-0.5	100.0%	-1.5
18190	AT3G32080.1 | expressed protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287	3.9	3.8	0.1	0.5	100.0%	-1.9
18191	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	-0.1	-0.5	100.0%	-2.0
18192	AT1G50270.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:18625712-18627502 FORWARD | Aliases: F14I3.12, F14I3_12	4.2	4.3	-0.1	-0.5	100.0%	-1.5
18193	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	4.7	4.6	0.1	0.5	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
18194	AT1G51430.1 | expressed protein | chr1:19071909-19073444 FORWARD | Aliases: F5D21.20, F5D21_20	4.6	4.4	0.1	0.5	100.0%	-1.3
18195	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.	3.6	3.7	-0.1	-0.5	100.0%	-1.5
18196	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	3.0	0.1	0.5	100.0%	-2.0
18197	AT3G25490.1 | wall-associated kinase, putative, similar to wall-associated kinase 4 GB:CAA08793 from (Arabidopsis thaliana) | chr3:9242962-9244722 FORWARD | Aliases: MWL2.11	2.5	2.5	0.0	0.5	100.0%	-2.4
18198	ATCG01060.1 | Symbol: PSAC | Encodes the PsaC subunit of photosystem I. | chrC:117318-117563 REVERSE | Aliases: PSAC	4.6	5.2	-0.5	-0.5	100.0%	-1.1
18199	AT5G37880.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:15101690-15102218 REVERSE | Aliases: K18L3.7, K18L3_7	3.3	3.4	-0.1	-0.5	100.0%	-2.1
18200	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	2.7	0.0	0.5	100.0%	-2.1
18201	AT5G28520.1 | 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	-0.1	-0.5	100.0%	-1.5
18202	AT3G56720.1 | expressed protein | chr3:21022032-21024398 FORWARD | Aliases: T8M16.50	8.1	8.3	-0.2	-0.5	100.0%	-1.5
18203	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	6.5	6.7	-0.1	-0.5	100.0%	-1.5
18204	AT3G55450.1 | protein kinase, putative, similar to protein kinase APK1B (Arabidopsis thaliana) SWISS-PROT:P46573 | chr3:20568986-20571189 FORWARD | Aliases: T22E16.110	7.4	7.7	-0.3	-0.5	100.0%	-1.3
18205	AT1G18400.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.7	3.8	-0.1	-0.5	100.0%	-1.5
18206	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	6.6	6.4	0.2	0.5	100.0%	-1.5
18207	AT2G47970.2 | NPL4 family protein, contains Pfam domain, PF05021: NPL4 family | chr2:19636544-19638208 FORWARD | Aliases: T9J23.1	7.3	7.2	0.1	0.5	100.0%	-1.5
18208	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	3.8	3.7	0.1	0.5	100.0%	-1.7
18209	AT5G13620.1 | expressed protein, ; expression supported by MPSS | chr5:4385388-4386376 REVERSE | Aliases: T6I14.11	2.4	2.4	-0.1	-0.5	100.0%	-2.0
18210	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	0.5	100.0%	-1.7
18211	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	7.5	-0.4	-0.5	100.0%	-1.2
18212	AT5G37090.1 | replication protein-related, weak similarity to Replication Protein A 70	2.6	2.6	-0.1	-0.5	100.0%	-2.1
18213	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	3.7	3.6	0.1	0.5	100.0%	-1.6
18214	AT2G43350.1 | Symbol: ATGPX3 |	6.5	6.3	0.2	0.5	100.0%	-1.5
18215	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	7.4	7.1	0.3	0.5	100.0%	-1.3
18216	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	6.8	6.6	0.1	0.5	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
18217	AT1G32770.1 | Symbol: ANAC012 | no apical meristem (NAM) family protein, similar to OsNAC7 protein GB:BAA89801 GI:6730944 from (Oryza sativa)	2.3	2.4	-0.1	-0.5	100.0%	-2.1
18218	AT3G32050.1 | expressed protein | chr3:13071339-13072295 REVERSE | Aliases: F1M23.5	3.4	3.6	-0.1	-0.5	100.0%	-1.5
18219	AT3G42090.1 | hypothetical protein | chr3:14285208-14285685 FORWARD | Aliases: F4M19.50	2.3	2.3	-0.0	-0.5	100.0%	-2.9
18220	AT2G20970.1 | expressed protein | chr2:9016948-9018148 FORWARD | Aliases: F26H11.27, F26H11_27	2.6	2.6	-0.1	-0.5	100.0%	-2.0
18221	AT3G08670.1 | expressed protein | chr3:2633743-2636542 FORWARD | Aliases: F17O14.14	2.5	2.4	0.1	0.5	100.0%	-2.1
18222	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	5.9	-0.1	-0.5	100.0%	-2.0
18223	AT2G19930.1 | RNA-dependent RNA polymerase family protein, contains Pfam domain, PF05183: RNA dependent RNA polymerase	5.4	5.6	-0.2	-0.5	100.0%	-1.1
18224	AT3G28620.1 | zinc finger (C3HC4-type RING finger) family protein, low similarity to RING-H2 finger protein RHA2b (Arabidopsis thaliana) GI:3790571; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger) | chr3:10729063-10729698 FORWARD | Aliases: MZN14.9	2.8	2.7	0.1	0.5	100.0%	-2.0
18225	NA	2.7	2.8	-0.0	-0.5	100.0%	-2.3
18226	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	5.3	5.4	-0.1	-0.5	100.0%	-1.6
18227	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	-0.5	100.0%	-2.1
18228	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	3.3	-0.1	-0.5	100.0%	-1.9
18229	AT3G58230.1 | hypothetical protein | chr3:21577837-21578373 REVERSE | Aliases: F9D24.140	2.8	2.8	-0.1	-0.5	100.0%	-1.9
18230	AT3G42250.1 | hypothetical protein | chr3:14414669-14414971 FORWARD | Aliases: F26B15.50	3.1	3.2	-0.1	-0.5	100.0%	-2.2
18231	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	4.1	-0.1	-0.5	100.0%	-1.8
18232	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	3.6	3.5	0.1	0.5	100.0%	-1.4
18233	AT2G44360.1 | expressed protein | chr2:18327499-18328766 REVERSE | Aliases: F4I1.17	7.2	7.1	0.1	0.5	100.0%	-1.4
18234	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	4.8	4.7	0.1	0.5	100.0%	-1.5
18235	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	6.0	6.1	-0.1	-0.5	100.0%	-1.3
18236	AT1G74630.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:28034182-28036113 FORWARD | Aliases: F1M20.31, F1M20_31	2.9	3.0	-0.1	-0.5	100.0%	-1.7
18237	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	4.3	-0.1	-0.5	100.0%	-1.5
18238	AT2G19420.1 | expressed protein | chr2:8418783-8420965 FORWARD | Aliases: F27F23.26	2.6	2.7	-0.0	-0.5	100.0%	-2.4
18239	AT4G24600.1 | hypothetical protein | chr4:12699996-12700488 FORWARD | Aliases: F22K18.200, F22K18_200	3.0	2.9	0.1	0.5	100.0%	-1.9
18240	AT1G17640.1 | RNA recognition motif (RRM)-containing protein, similar to GB:L02953 from (Xenopus laevis) (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	4.3	0.1	0.5	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
18241	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	5.1	5.0	0.1	0.5	100.0%	-1.8
18242	AT3G06220.1 | transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain | chr3:1883678-1884726 REVERSE | Aliases: F28L1.16, F28L1_16	2.6	2.5	0.1	0.5	100.0%	-2.0
18243	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	0.5	100.0%	-2.0
18244	AT1G58470.1 | Symbol: ATRBP1 |	3.3	3.2	0.1	0.5	100.0%	-1.9
18245	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	5.4	5.6	-0.2	-0.5	100.0%	-1.3
18246	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	4.9	0.1	0.5	100.0%	-1.4
18247	AT3G30840.1 | expressed protein | chr3:12590931-12591505 REVERSE | Aliases: MJI6.20	2.7	2.8	-0.1	-0.5	100.0%	-2.0
18248	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	3.5	-0.1	-0.5	100.0%	-1.8
18249	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	3.6	3.7	-0.1	-0.5	100.0%	-1.4
18250	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-Ip60) (Homo sapiens) | chr5:25850486-25853610 FORWARD | Aliases: FASCIATA 2, MUB3, MUB3.15, MUB3_15, NFB01, NFB1	3.2	3.3	-0.1	-0.5	100.0%	-1.3
18251	AT1G39430.1 | expressed protein, includes At2g05890, At4g07450, At3g30630, At3g43100, At2g09960, At3g30550, At1g39430, At2g10460, At4g03640, At5g35250	4.0	4.2	-0.2	-0.5	100.0%	-1.3
18252	AT5G04030.1 | expressed protein | chr5:1088461-1088691 REVERSE | Aliases: F8F6.240, F8F6_240	2.8	2.8	-0.1	-0.5	100.0%	-1.9
18253	AT4G22940.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:12021774-12023478 REVERSE | Aliases: F7H19.120, F7H19_120	2.4	2.5	-0.0	-0.5	100.0%	-2.0
18254	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	6.5	6.2	0.4	0.5	100.0%	-1.1
18255	AT2G21230.2 | bZIP family transcription factor, contains a bZIP transcription factor basic domain signature (PDOC00036) | chr2:9101413-9103407 REVERSE | Aliases: F7O24.5, F7O24_5	5.1	5.0	0.1	0.5	100.0%	-1.2
18256	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	2.6	-0.1	-0.5	100.0%	-2.2
18257	AT1G21590.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr1:7566221-7569890 REVERSE | Aliases: F24J8.18, F24J8_18	3.8	3.9	-0.1	-0.5	100.0%	-1.5
18258	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	3.3	-0.1	-0.5	100.0%	-1.5
18259	AT1G26290.1 | expressed protein | chr1:9098038-9098542 FORWARD | Aliases: F28B23.5, F28B23_5	3.3	3.2	0.1	0.5	100.0%	-1.6
18260	AT1G55600.1 | Symbol: WRKY10 |	2.9	3.0	-0.1	-0.5	100.0%	-1.8
18261	AT5G12930.1 | expressed protein | chr5:4082893-4085300 REVERSE | Aliases: T24H18.90, T24H18_90	2.7	2.8	-0.0	-0.5	100.0%	-2.0
18262	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	2.9	2.9	-0.1	-0.5	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
18263	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)	2.9	3.1	-0.1	-0.5	100.0%	-1.6
18264	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	3.9	4.0	-0.1	-0.5	100.0%	-1.3
18265	AT1G32680.1 | hypothetical protein | chr1:11818014-11818259 FORWARD | Aliases: F6N18.21, F6N18_21	3.1	3.2	-0.1	-0.5	100.0%	-1.8
18266	AT1G55220.1 | expressed protein | chr1:20604550-20605103 REVERSE | Aliases: F7A10.6, F7A10_6	2.3	2.3	-0.1	-0.5	100.0%	-2.1
18267	AT4G11550.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.2	3.3	-0.1	-0.5	100.0%	-1.9
18268	AT4G37990.1 | Symbol: ELI3 2 |	3.2	3.3	-0.1	-0.5	100.0%	-1.5
18269	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	3.0	-0.1	-0.5	100.0%	-1.8
18270	AT5G64480.1 | expressed protein | chr5:25795412-25796145 FORWARD | Aliases: T12B11.7, T12B11_7	5.3	5.2	0.1	0.5	100.0%	-1.8
18271	AT3G26040.1 | transferase family protein, similar to deacetylvindoline 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	2.7	-0.1	-0.5	100.0%	-1.9
18272	AT4G19430.1 | expressed protein | chr4:10598456-10599155 REVERSE | Aliases: T5K18.210, T5K18_210	2.7	2.7	-0.1	-0.5	100.0%	-2.1
18273	AT1G31200.1 | Symbol: ATPP2 A9 | expressed protein | chr1:11146904-11147659 REVERSE | Aliases: ATPP2 A9, F28K20.16, F28K20_16	3.3	3.4	-0.1	-0.5	100.0%	-1.5
18274	AT2G31210.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain; PMID: 12679534	2.6	2.6	0.1	0.5	100.0%	-2.1
18275	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	6.2	6.4	-0.1	-0.5	100.0%	-1.2
18276	AT5G52850.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr5:21432161-21434842 REVERSE | Aliases: MXC20.7, MXC20_7	3.7	3.6	0.1	0.5	100.0%	-1.9
18277	AT1G09390.1 | GDSL-motif lipase/hydrolase family protein, Similar to 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	5.5	5.4	0.1	0.5	100.0%	-1.4
18278	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	2.7	2.8	-0.1	-0.5	100.0%	-1.7
18279	AT5G65820.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:26357102-26359015 REVERSE | Aliases: K22J17.3, K22J17_3	2.8	2.7	0.1	0.5	100.0%	-2.1
18280	AT2G18380.1 | zinc finger (GATA type) family protein | chr2:7989950-7991096 REVERSE | Aliases: T30D6.11, T30D6_11	3.1	3.2	-0.1	-0.5	100.0%	-2.0
18281	AT4G04970.1 | Symbol: ATGSL1 |	3.5	3.6	-0.1	-0.5	100.0%	-1.5
18282	AT4G10000.2 | expressed protein | chr4:6260320-6263178 REVERSE | Aliases: T5L19.130, T5L19_130	3.5	3.4	0.1	0.5	100.0%	-1.6
18283	AT5G58550.1 | tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain | chr5:23682538-23685700 REVERSE | Aliases: MZN1.1	3.4	3.4	0.1	0.5	100.0%	-1.9
18284	AT5G47510.1 | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, similar to phosphatidylinositol transfer-like protein IV (GI:14486707) (Lotus japonicus), SEC14 cytosolic factor (Phosphatidylinositol/phosphatidylcholine transfer protein) (PI/PCTP) (SP:P24859) (Kluyveromyces lactis) and to SEC14 cytosolic factor (SP:P53989) (Candida glabrata)	3.2	3.1	0.1	0.5	100.0%	-2.2
18285	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	8.1	8.3	-0.2	-0.5	100.0%	-1.2
18286	AT2G17080.1 | hypothetical protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function | chr2:7440408-7441199 REVERSE | Aliases: F6P23.10, F6P23_10	2.8	2.9	-0.1	-0.5	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
18287	AT3G50430.1 | expressed protein | chr3:18724678-18728654 FORWARD | Aliases: T20E23.30	4.5	4.6	-0.1	-0.5	100.0%	-1.3
18288	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%	-2.1
18289	AT5G50830.2 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g22795.1); similar to Hypothetical protein C33G8.2 [Caenorhabditis elegans] (GB:AAC25848.1)	3.4	3.5	-0.1	-0.5	100.0%	-1.5
18290	AT1G55820.1 | hydroxyproline-rich glycoprotein family protein | chr1:20868063-20871084 FORWARD | Aliases: F20N2.19	2.8	2.7	0.0	0.5	100.0%	-2.4
18291	AT2G43990.1 | expressed protein | chr2:18219000-18220998 FORWARD | Aliases: F6E13.12	3.7	3.6	0.1	0.5	100.0%	-1.9
18292	AT2G32910.1 | expressed protein | chr2:13966127-13969195 FORWARD | Aliases: T21L14.15, T21L14_15	6.7	6.9	-0.2	-0.5	100.0%	-1.4
18293	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	4.7	4.5	0.3	0.5	100.0%	-1.5
18294	AT1G66310.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.6	0.1	0.5	100.0%	-2.1
18295	AT5G49540.1 | expressed protein, contains Pfam profile PF05646: Protein of unknown function (DUF786) | chr5:20121810-20123334 REVERSE | Aliases: K6M13.9, K6M13_9	9.9	9.8	0.1	0.5	100.0%	-1.5
18296	AT3G43280.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr3:15240766-15241239 REVERSE | Aliases: F7K15.130	2.4	2.4	-0.1	-0.5	100.0%	-2.0
18297	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	7.1	7.3	-0.2	-0.5	100.0%	-1.3
18298	AT5G07420.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:2349456-2351509 FORWARD | Aliases: T2I1.130, T2I1_130	2.4	2.4	-0.0	-0.5	100.0%	-2.2
18299	AT5G23480.1 | expressed protein | chr5:7918338-7919276 FORWARD | Aliases: K19M13.11, K19M13_11	2.9	3.0	-0.1	-0.5	100.0%	-1.9
18300	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	4.0	-0.1	-0.5	100.0%	-1.5
18301	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	-0.1	-0.5	100.0%	-1.8
18302	AT4G17170.1 | Symbol: AT RAB2 | Rab2-like GTP-binding protein (RAB2), identical to Rab2-like protein (At-RAB2) GI:1765896 from (Arabidopsis thaliana)	7.2	7.4	-0.2	-0.5	100.0%	-1.4
18303	AT1G24110.1 | peroxidase, putative, similar to peroxidase ATP26a, GB:CAA72487 | chr1:8527827-8528807 FORWARD | Aliases: F3I6.3, F3I6_3	3.6	3.7	-0.1	-0.5	100.0%	-1.7
18304	AT5G59900.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:24141209-24143932 REVERSE | Aliases: MMN10.14, MMN10_14	3.3	3.3	0.1	0.5	100.0%	-1.9
18305	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	2.4	2.5	-0.0	-0.5	100.0%	-2.3
18306	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	3.1	3.1	0.1	0.5	100.0%	-1.7
18307	AT3G12590.1 | expressed protein | chr3:3995729-4003664 REVERSE | Aliases: T2E22.10	2.4	2.4	0.1	0.5	100.0%	-2.0
18308	AT2G04330.1 | hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287 | chr2:1510447-1513139 REVERSE | Aliases: T23O15.4	2.4	2.5	-0.0	-0.5	100.0%	-2.5
18309	AT2G25890.1 | glycine-rich protein / oleosin | chr2:11044458-11045204 FORWARD | Aliases: F17H15.8, F17H15_8	2.2	2.2	-0.0	-0.5	100.0%	-2.3
18310	AT5G40760.1 | Symbol: G6PD6 | Encodes a cytosolic glucose-6-phosphate dehydrogenase that is insensitive to reduction by DTT and whose mRNA is expressed ubiquitously.	9.3	9.1	0.3	0.5	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
18311	AT2G43450.1 | expressed protein, ; expression supported by MPSS | chr2:18050311-18051302 REVERSE | Aliases: T1O24.19	2.3	2.4	-0.1	-0.5	100.0%	-2.3
18312	AT2G19630.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.7	2.8	-0.1	-0.5	100.0%	-2.1
18313	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	7.1	7.4	-0.3	-0.5	100.0%	-1.1
18314	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	3.5	3.6	-0.1	-0.5	100.0%	-1.4
18315	AT4G17585.1 | hypothetical protein | chr4:9792536-9793272 REVERSE | Aliases: FCAALL.48	2.4	2.5	-0.0	-0.5	100.0%	-2.2
18316	AT1G11850.2 | expressed protein | chr1:3999201-3999875 FORWARD | Aliases: F12F1.31, F12F1_31	4.1	4.2	-0.1	-0.5	100.0%	-1.8
18317	AT1G54990.1 | expressed protein | chr1:20515186-20517348 FORWARD | Aliases: F14C21.51, F14C21_51	7.5	7.4	0.1	0.5	100.0%	-1.3
18318	AT2G18210.1 | expressed protein | chr2:7932280-7932948 REVERSE | Aliases: F8D23.2	3.0	3.1	-0.1	-0.5	100.0%	-1.6
18319	AT5G57760.1 | expressed protein | chr5:23417951-23418480 FORWARD | Aliases: MRI1.12, MRI1_12	2.6	2.6	-0.1	-0.5	100.0%	-2.0
18320	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	3.2	3.1	0.1	0.5	100.0%	-1.4
18321	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	4.6	4.7	-0.1	-0.5	100.0%	-1.4
18322	AT5G40440.1 | Symbol: ATMKK3 |	4.6	4.7	-0.1	-0.5	100.0%	-2.1
18323	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	-0.5	100.0%	-2.0
18324	AT1G11560.1 | OST3/OST6 family protein, contains Pfam profile PF04756: OST3 / OST6 family | chr1:3881788-3882819 FORWARD | Aliases: T23J18.22, T23J18_22	2.9	3.0	-0.1	-0.5	100.0%	-1.8
18325	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	2.9	-0.1	-0.5	100.0%	-1.7
18326	AT3G21310.1 | expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266 | chr3:7497296-7499158 FORWARD | Aliases: MXL8.19	3.2	3.2	-0.0	-0.5	100.0%	-2.3
18327	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	3.3	-0.1	-0.5	100.0%	-1.9
18328	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	-0.5	100.0%	-1.8
18329	AT5G56520.1 | expressed protein | chr5:22902397-22903141 FORWARD | Aliases: MKN22.3, MKN22_3	4.7	4.6	0.1	0.5	100.0%	-1.3
18330	AT1G51960.1 | calmodulin-binding family protein, contains IQ calmodulin-binding motif, Pfam:PF00612 | chr1:19314024-19315352 FORWARD | Aliases: T14L22.17	2.6	2.5	0.1	0.5	100.0%	-2.1
18331	AT2G30560.1 | glycine-rich protein | chr2:13024424-13025934 FORWARD | Aliases: T6B20.9, T6B20_9	6.2	6.4	-0.2	-0.5	100.0%	-1.1
18332	AT5G06920.1 | expressed protein | chr5:2142859-2143920 FORWARD | Aliases: MOJ9.9, MOJ9_9	3.4	3.5	-0.1	-0.5	100.0%	-1.8
18333	AT4G21820.1 | calmodulin-binding family protein, contains IQ calmodulin-binding motif, Pfam:PF00612 | chr4:11577536-11584065 FORWARD | Aliases: T8O5.30, T8O5_30	2.7	2.7	0.0	0.5	100.0%	-2.2
18334	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	3.1	3.2	-0.1	-0.5	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
18335	AT4G34630.1 | expressed protein | chr4:16536870-16537751 REVERSE | Aliases: T4L20.210, T4L20_210	6.1	6.2	-0.1	-0.5	100.0%	-1.5
18336	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	2.6	2.6	-0.1	-0.5	100.0%	-2.2
18337	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	3.1	-0.1	-0.5	100.0%	-1.9
18338	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	3.5	0.1	0.5	100.0%	-1.5
18339	AT3G17710.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.7	3.8	-0.1	-0.5	100.0%	-1.6
18340	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	8.4	8.1	0.2	0.5	100.0%	-1.5
18341	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	3.4	-0.1	-0.5	100.0%	-2.0
18342	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	4.0	4.2	-0.2	-0.5	100.0%	-1.4
18343	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	4.0	4.2	-0.2	-0.5	100.0%	-1.4
18344	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	2.9	2.9	0.1	0.5	100.0%	-1.7
18345	AT5G25290.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.6	-0.1	-0.5	100.0%	-2.2
18346	AT1G28460.1 | MADS-box family protein, contains similarity to MADS-box transcription factor GI:6580947 from (Picea abies) | chr1:10006216-10006764 FORWARD | Aliases: F3M18.10, F3M18_10	2.9	3.0	-0.1	-0.5	100.0%	-1.5
18347	AT1G64550.1 | Symbol: ATGCN3 |	6.2	5.8	0.3	0.5	100.0%	-1.0
18348	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	2.5	0.2	0.5	100.0%	-1.8
18349	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	6.0	5.9	0.2	0.5	100.0%	-1.5
18350	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	3.9	3.9	0.1	0.5	100.0%	-1.4
18351	AT1G22290.1 | 14-3-3 protein GF14, putative (GRF10), similar to 14-3-3 protein GF14 epsilon GI:5802798 from (Arabidopsis thaliana) | chr1:7876955-7877904 REVERSE | Aliases: T16E15.9, T16E15_9	2.3	2.4	-0.0	-0.5	100.0%	-2.2
18352	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	-0.0	-0.5	100.0%	-2.2
18353	AT3G13330.1 | expressed protein | chr3:4319654-4330068 REVERSE | Aliases: MDC11.16	8.0	7.8	0.2	0.5	100.0%	-1.2
18354	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	-0.1	-0.5	100.0%	-2.2

Rank	Description	Sync	Root	M	t	adj.q	B
18355	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	2.7	-0.1	-0.5	100.0%	-2.0
18356	AT5G09970.1 | Symbol: CYP78A7 | cytochrome P450 family protein | chr5:3111946-3114240 FORWARD | Aliases: MYH9.18, MYH9_18	2.3	2.4	-0.0	-0.5	100.0%	-2.1
18357	AT3G42130.1 | glycine-rich protein | chr3:14309227-14309869 REVERSE | Aliases: F4M19.90	6.7	6.4	0.2	0.5	100.0%	-0.9
18358	AT5G61520.1 | hexose transporter, putative, similar to	4.8	4.9	-0.2	-0.5	100.0%	-1.4
18359	AT5G22980.1 | Symbol: SCPL47 |	4.3	4.4	-0.1	-0.5	100.0%	-1.5
18360	AT1G33430.1 | galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase | chr1:12124343-12126449 REVERSE | Aliases: F10C21.10, F10C21_10	3.4	3.5	-0.1	-0.5	100.0%	-1.7
18361	AT5G58400.1 | peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi:5381253:dbj:BAA82306 | chr5:23622428-23624244 REVERSE | Aliases: MCK7.27, MCK7_27	2.1	2.2	-0.0	-0.5	100.0%	-2.2
18362	AT2G24370.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:10377059-10380143 REVERSE | Aliases: T28I24.10, T28I24_10	2.9	2.9	-0.1	-0.5	100.0%	-1.9
18363	AT3G55630.3 | Symbol: ATDFD | dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS4), nearly identical to folylpolyglutamate-dihydrofolate synthetase (Arabidopsis thaliana) GI:17976761	4.4	4.3	0.1	0.5	100.0%	-1.7
18364	AT5G54410.1 | hypothetical protein | chr5:22111473-22112132 REVERSE | Aliases: F24B18.3, F24B18_3	2.6	2.6	-0.1	-0.5	100.0%	-2.1
18365	AT2G23230.1 | terpene synthase/cyclase family protein | chr2:9899796-9902480 FORWARD | Aliases: T20D16.14, T20D16_14	3.0	3.0	-0.1	-0.5	100.0%	-1.6
18366	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	8.2	-0.4	-0.5	100.0%	-1.0
18367	AT5G43160.1 | expressed protein, contains Pfam profile: PF04484 family of unknown function (DUF566) | chr5:17345679-17347923 FORWARD | Aliases: MMG4.20, MMG4_20	3.4	3.5	-0.1	-0.5	100.0%	-1.7
18368	AT3G29150.1 | expressed protein | chr3:11108985-11115588 REVERSE | Aliases: MXE2.13	3.0	3.1	-0.1	-0.5	100.0%	-1.7
18369	AT4G10130.1 | DNAJ heat shock N-terminal domain-containing protein, low similarity to SP:Q9QYI7 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	4.8	-0.1	-0.5	100.0%	-1.9
18370	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	2.4	-0.0	-0.5	100.0%	-2.4
18371	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	2.5	-0.1	-0.5	100.0%	-2.0
18372	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	3.1	3.0	0.1	0.5	100.0%	-2.1
18373	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	7.0	7.1	-0.1	-0.5	100.0%	-1.4
18374	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	0.5	100.0%	-1.6
18375	AT3G31930.1 | expressed protein | chr3:12930821-12931699 FORWARD | Aliases: T1O13.1	2.6	2.7	-0.1	-0.5	100.0%	-2.2
18376	AT2G24010.1 | Symbol: SCPL23 |	2.5	2.5	0.0	0.5	100.0%	-2.3

Rank	Description	Sync	Root	M	t	adj.q	B
18377	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	2.6	-0.1	-0.5	100.0%	-2.2
18378	AT1G26390.1 | 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 | chr1:9130004-9131766 REVERSE | Aliases: T1K7.23, T1K7_23	2.8	2.7	0.1	0.5	100.0%	-1.8
18379	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	5.6	5.5	0.1	0.5	100.0%	-1.4
18380	AT4G38990.1 | glycosyl hydrolase family 9 protein, endo-1,4-beta-glucanase precursor - Fragariax ananassa, PID:g3549291 A short intron was annotated between exons 4 and 5 to circumvent a frameshift.	3.0	3.1	-0.1	-0.5	100.0%	-1.9
18381	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	3.8	3.7	0.1	0.5	100.0%	-1.4
18382	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	0.1	0.5	100.0%	-2.1
18383	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	5.4	5.2	0.2	0.5	100.0%	-1.2
18384	AT4G08210.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr4:5183810-5185870 REVERSE | Aliases: T12G13.50, T12G13_50	2.9	2.9	0.1	0.5	100.0%	-1.9
18385	AT1G07140.1 | Symbol: SIRANBP | Ran-binding protein 1a (RanBP1a), identical to Ran-binding protein (atranbp1a) GI:2058282 from (Arabidopsis thaliana)	11.5	11.4	0.2	0.5	100.0%	-1.8
18386	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	7.4	7.8	-0.4	-0.5	100.0%	-1.0
18387	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	4.0	4.0	0.1	0.5	100.0%	-1.8
18388	AT4G32680.1 | expressed protein | chr4:15763242-15765119 REVERSE | Aliases: F4D11.120, F4D11_120	4.5	4.7	-0.1	-0.5	100.0%	-1.6
18389	AT1G25330.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.2	2.2	0.0	0.5	100.0%	-2.5
18390	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	3.1	3.2	-0.1	-0.5	100.0%	-1.8
18391	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	4.5	0.1	0.5	100.0%	-1.4
18392	AT2G06630.1 | hypothetical protein, similar to At2g12120, At1g45090, At2g05470, At5g28482 | chr2:2645685-2646380 REVERSE | Aliases: T14A4.21, T14A4_21	2.9	3.0	-0.1	-0.5	100.0%	-2.5
18393	AT2G36440.1 | expressed protein | chr2:15299727-15299951 FORWARD | Aliases: F1O11.7, F1O11_7	2.8	2.9	-0.1	-0.5	100.0%	-2.1
18394	AT4G17770.1 | Symbol: ATTPS5 |	8.2	8.3	-0.1	-0.5	100.0%	-1.6
18395	AT5G53140.1 | protein phosphatase 2C, putative / PP2C, putative | chr5:21565701-21569696 FORWARD | Aliases: MFH8.8, MFH8_8	4.8	4.4	0.4	0.5	100.0%	-1.3
18396	AT2G18920.1 | hypothetical protein | chr2:8204835-8205242 REVERSE | Aliases: F19F24.12, F19F24_12	3.0	3.0	-0.1	-0.5	100.0%	-1.9
18397	AT4G38500.1 | expressed protein, contains Pfam profile: PF04765 protein of unknown function (DUF616) | chr4:18007750-18011343 FORWARD | Aliases: F20M13.60, F20M13_60	6.4	6.2	0.2	0.5	100.0%	-1.2
18398	AT5G18520.1 | expressed protein | chr5:6145029-6146532 FORWARD | Aliases: T28N17.5	6.2	6.0	0.3	0.5	100.0%	-1.2
18399	AT3G55060.1 | expressed protein, contains weak similarity to intracellular protein transport protein USO1 (Swiss-Prot:P25386) (Saccharomyces cerevisiae); expression supported by MPSS	3.8	3.9	-0.1	-0.5	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
18400	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	6.3	6.5	-0.3	-0.5	100.0%	-1.1
18401	AT5G16940.1 | expressed protein, contains Pfam profile PF04828: Protein of unknown function (DUF636) | chr5:5571554-5572393 REVERSE | Aliases: F2K13.90, F2K13_90	5.2	5.4	-0.2	-0.5	100.0%	-1.3
18402	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	7.7	7.4	0.3	0.5	100.0%	-1.1
18403	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	3.2	3.3	-0.1	-0.5	100.0%	-1.6
18404	AT2G46640.1 | expressed protein, and genefinder; expression supported by MPSS	2.9	3.0	-0.0	-0.5	100.0%	-2.2
18405	AT1G53770.1 | expressed protein | chr1:20074982-20077391 REVERSE | Aliases: T18A20.22, T18A20_22	5.1	5.2	-0.1	-0.5	100.0%	-1.6
18406	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	7.1	7.2	-0.1	-0.5	100.0%	-1.5
18407	AT5G58610.1 | PHD finger transcription factor, putative | chr5:23703997-23708279 REVERSE | Aliases: MZN1.7, MZN1_7	3.6	3.5	0.1	0.5	100.0%	-1.9
18408	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%	-2.5
18409	AT3G07530.1 | expressed protein, ; expression supported by MPSS | chr3:2400799-2404286 FORWARD | Aliases: F21O3.24	4.6	4.4	0.1	0.5	100.0%	-1.5
18410	AT1G75300.1 | isoflavone reductase, putative, identical to SP:P52577 Isoflavone reductase homolog P3 (EC 1.3.1.-) {Arabidopsis thaliana}; contains Pfam profile PF02716: Isoflavone reductase | chr1:28259156-28260701 FORWARD | Aliases: F22H5.16, F22H5_16	3.4	3.4	-0.1	-0.5	100.0%	-1.7
18411	ATCG00590.1 | Symbol: ORF31 | hypothetical protein | chrC:65712-65807 FORWARD | Aliases: ORF31	4.7	4.2	0.5	0.5	100.0%	-1.1
18412	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	2.7	2.7	0.1	0.5	100.0%	-1.9
18413	AT2G23250.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains similarity to glucosyltransferases | chr2:9904889-9906205 REVERSE | Aliases: T20D16.12, T20D16_12	2.3	2.3	-0.0	-0.5	100.0%	-2.3
18414	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	-0.1	-0.5	100.0%	-2.1
18415	AT2G21910.1 | Symbol: CYP96A5 | cytochrome P450, putative | chr2:9348578-9350110 FORWARD | Aliases: F7D8.23, F7D8_23	2.7	2.8	-0.1	-0.5	100.0%	-1.8
18416	AT5G44980.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.7	-0.0	-0.5	100.0%	-2.3
18417	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	-0.5	100.0%	-1.9
18418	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 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) | chr1:10310231-10313741 REVERSE | Aliases: F15D2.5, F15D2_5	10.1	10.0	0.1	0.5	100.0%	-1.6
18419	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	5.3	5.5	-0.3	-0.5	100.0%	-0.9
18420	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	5.3	5.5	-0.3	-0.5	100.0%	-0.9
18421	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	0.5	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
18422	AT5G58850.1 | Symbol: MYB119 |	2.9	2.9	-0.1	-0.5	100.0%	-1.8
18423	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	3.7	3.8	-0.1	-0.5	100.0%	-1.5
18424	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%	-1.9
18425	AT5G52860.1 | ABC transporter family protein | chr5:21437002-21438793 REVERSE | Aliases: MXC20.8, MXC20_8	2.7	2.7	-0.1	-0.5	100.0%	-1.8
18426	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	7.0	7.2	-0.2	-0.5	100.0%	-1.3
18427	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	2.9	-0.1	-0.5	100.0%	-1.8
18428	AT4G16320.1 | expressed protein, ; expression supported by MPSS | chr4:9223705-9225726 FORWARD | Aliases: DL4190W, FCAALL.344	3.4	3.5	-0.1	-0.5	100.0%	-1.6
18429	AT5G37050.1 | expressed protein, hypothetical protein T28J14.60 - Arabidopsis thaliana, PIR:T48483 | chr5:14657740-14658651 REVERSE | Aliases: MJG14.3	2.3	2.4	-0.0	-0.5	100.0%	-2.3
18430	AT1G61760.1 | harpin-induced protein-related / HIN1-related / harpin-responsive protein-related, similar to hin1 (Nicotiana tabacum) GI:1619321 | chr1:22811105-22811779 REVERSE | Aliases: T13M11.12, T13M11_12	2.2	2.2	-0.0	-0.5	100.0%	-2.1
18431	AT5G61480.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:24741767-24745068 REVERSE | Aliases: MCI2.4, MCI2_4	5.5	5.4	0.1	0.5	100.0%	-1.7
18432	AT3G04270.1 | expressed protein | chr3:1127911-1128087 REVERSE | Aliases: T6K12.11, T6K12_11	3.3	3.4	-0.1	-0.5	100.0%	-1.9
18433	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	2.8	0.1	0.5	100.0%	-2.0
18434	AT2G33680.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:14256684-14258867 FORWARD | Aliases: T1B8.1, T1B8_1	3.7	3.6	0.1	0.5	100.0%	-1.6
18435	AT1G21130.2 | O-methyltransferase, putative, similar to GI:2781394 | chr1:7399051-7400593 REVERSE | Aliases: T22I11.4, T22I11_4	3.8	3.9	-0.1	-0.5	100.0%	-1.8
18436	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	3.7	-0.1	-0.5	100.0%	-1.8
18437	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	5.2	5.0	0.2	0.5	100.0%	-1.2
18438	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	2.6	-0.1	-0.5	100.0%	-2.3
18439	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	2.8	0.1	0.5	100.0%	-1.9
18440	AT3G55160.1 | expressed protein | chr3:20456389-20463377 REVERSE | Aliases: T26I12.40	3.4	3.3	0.1	0.5	100.0%	-1.7
18441	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 (rhm2 gene) GI:31559258 | chr1:19970612-19973425 REVERSE | Aliases: F22G10.13, MUCILAGE MODIFIED 4, RHAMNOSE BIOSYNTHESIS 2, RHM2	6.0	5.9	0.2	0.5	100.0%	-1.2
18442	AT5G12240.1 | expressed protein | chr5:3959121-3960778 REVERSE | Aliases: MXC9.20, MXC9_20	3.5	3.5	0.1	0.5	100.0%	-1.7
18443	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	3.1	3.2	-0.1	-0.5	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
18444	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	0.5	100.0%	-2.7
18445	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	3.3	-0.1	-0.5	100.0%	-1.8
18446	AT2G21920.1 | expressed protein | chr2:9350490-9354239 REVERSE | Aliases: F7D8.24, F7D8_24	3.2	3.2	-0.1	-0.5	100.0%	-1.9
18447	AT3G51760.1 | expressed protein | chr3:19209125-19210477 REVERSE | Aliases: ATEM1.1	3.2	3.3	-0.1	-0.5	100.0%	-1.6
18448	AT1G35570.1 | hypothetical protein | chr1:13119597-13120417 REVERSE | Aliases: F15O4.34	3.4	3.4	-0.0	-0.5	100.0%	-2.0
18449	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	2.6	-0.1	-0.5	100.0%	-1.8
18450	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	-0.0	-0.5	100.0%	-2.3
18451	AT5G42030.1 | expressed protein, similar to unknown protein (emb:CAB66408.1) | chr5:16828623-16830333 REVERSE | Aliases: MJC20.13, MJC20_13	4.9	5.0	-0.1	-0.5	100.0%	-1.2
18452	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	3.0	3.1	-0.1	-0.5	100.0%	-2.1
18453	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	3.3	-0.1	-0.5	100.0%	-1.5
18454	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	2.6	2.7	-0.1	-0.5	100.0%	-1.8
18455	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	12.4	12.5	-0.1	-0.5	100.0%	-2.0
18456	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	6.0	6.1	-0.1	-0.5	100.0%	-1.6
18457	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	2.7	0.1	0.5	100.0%	-2.0
18458	AT3G10960.1 | xanthine/uracil permease family protein, contains Pfam profile: PF00860 permease family | chr3:3424818-3427002 REVERSE | Aliases: F9F8.22	4.5	4.4	0.1	0.5	100.0%	-1.6
18459	AT5G06040.1 | self-incompatibility protein-related | chr5:1815129-1816038 FORWARD | Aliases: K18J17.24, K18J17_24	2.7	2.7	0.0	0.5	100.0%	-2.4
18460	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	0.1	0.5	100.0%	-1.5
18461	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)	3.7	3.8	-0.1	-0.5	100.0%	-1.6
18462	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	5.7	5.9	-0.1	-0.5	100.0%	-1.5
18463	AT4G00232.1 | expressed protein | chr4:100257-100721 REVERSE | Aliases: None	4.0	4.2	-0.1	-0.5	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
18464	AT5G49170.1 | expressed protein, similar to unknown protein (gb:AAF63814.1) | chr5:19955802-19956797 REVERSE | Aliases: K21P3.4, K21P3_4	2.6	2.6	-0.0	-0.5	100.0%	-2.0
18465	AT2G17920.1 | expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277 | chr2:7789794-7791369 FORWARD | Aliases: T13L16.6, T13L16_6	2.5	2.6	-0.0	-0.5	100.0%	-2.1
18466	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	4.1	4.0	0.1	0.5	100.0%	-1.6
18467	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.	5.0	5.2	-0.2	-0.5	100.0%	-1.3
18468	AT1G31750.1 | proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965 | chr1:11370640-11372058 REVERSE | Aliases: F5M6.24	4.4	4.3	0.2	0.5	100.0%	-1.0
18469	AT1G10530.1 | expressed protein | chr1:3471457-3472673 REVERSE | Aliases: T10O24.15, T10O24_15	3.3	3.2	0.1	0.5	100.0%	-1.5
18470	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	2.8	2.8	-0.1	-0.5	100.0%	-2.1
18471	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	2.8	2.8	-0.1	-0.5	100.0%	-2.1
18472	AT2G16630.1 | proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr2:7216321-7218104 FORWARD | Aliases: T24I21.4, T24I21_4	3.0	3.1	-0.1	-0.5	100.0%	-1.9
18473	AT4G10410.1 | expressed protein | chr4:6448979-6449994 REVERSE | Aliases: F7L13.2	2.8	2.9	-0.1	-0.5	100.0%	-1.7
18474	AT1G43870.1 | hypothetical protein, similar to fructose binding protein FrcB (GI:11066207)(Sinorhizobium meliloti) | chr1:16629534-16630535 FORWARD | Aliases: F28H19.12, F28H19_12	2.4	2.5	-0.0	-0.5	100.0%	-2.2
18475	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	-0.1	-0.5	100.0%	-2.1
18476	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	2.9	-0.1	-0.5	100.0%	-2.0
18477	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	10.5	-0.1	-0.5	100.0%	-1.5
18478	AT3G17365.1 | expressed protein, low similarity to PIR:I46078 endothelin converting enzyme from Bos primigenius taurus	6.1	6.0	0.1	0.5	100.0%	-1.7
18479	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	4.9	5.1	-0.2	-0.5	100.0%	-1.1
18480	AT1G70985.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr1:26768334-26768947 REVERSE | Aliases: None	3.3	3.4	-0.1	-0.5	100.0%	-1.7
18481	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	3.4	0.1	0.5	100.0%	-1.8
18482	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	4.6	0.1	0.5	100.0%	-1.5
18483	ATMG01350.1 | Symbol: ORF145C | hypothetical protein | chrM:346757-347194 FORWARD | Aliases: ORF145C	2.9	2.8	0.1	0.5	100.0%	-1.7
18484	AT4G36370.1 | expressed protein | chr4:17187253-17187945 FORWARD | Aliases: F23E13.210, F23E13_210	3.2	3.3	-0.1	-0.5	100.0%	-1.8
18485	AT2G38130.2 | Symbol: ATMAK3 |	7.3	7.4	-0.1	-0.5	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
18486	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	3.4	-0.1	-0.5	100.0%	-1.8
18487	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	10.0	10.3	-0.3	-0.5	100.0%	-1.1
18488	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	5.2	5.1	0.1	0.5	100.0%	-1.5
18489	AT4G12300.1 | Symbol: CYP706A4 | cytochrome P450 family protein, flavonoid 3',5'-hydroxylase - Campanula medium, PID:d1003951	5.2	5.1	0.2	0.5	100.0%	-1.2
18490	AT2G18260.1 | Symbol: SYP112 |	3.4	3.5	-0.1	-0.5	100.0%	-2.0
18491	AT1G75840.1 | Symbol: ATROP4 |	6.2	6.1	0.1	0.5	100.0%	-1.3
18492	AT2G04800.2 | expressed protein | chr2:1687193-1687686 REVERSE | Aliases: F28I8.16, F28I8_16	7.2	7.3	-0.2	-0.5	100.0%	-1.1
18493	AT4G35510.1 | expressed protein | chr4:16860457-16862377 REVERSE | Aliases: F8D20.20, F8D20_20	6.2	6.1	0.2	0.5	100.0%	-1.1
18494	AT2G39300.1 | expressed protein, ; expression supported by MPSS | chr2:16417187-16419947 REVERSE | Aliases: T16B24.6, T16B24_6	4.5	4.4	0.1	0.5	100.0%	-1.6
18495	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	5.9	5.6	0.2	0.5	100.0%	-1.2
18496	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	4.6	4.5	0.1	0.5	100.0%	-1.3
18497	AT3G01220.1 | homeobox-leucine zipper protein, putative / HD-ZIP transcription factor, putative, similar to homeobox-leucine zipper protein, HAT7 (GB:Q00466) (Arabidopsis thaliana) | chr3:73488-75545 FORWARD | Aliases: T4P13.9, T4P13_9	4.0	4.1	-0.1	-0.5	100.0%	-1.6
18498	AT2G25970.1 | KH domain-containing protein | chr2:11078729-11082747 REVERSE | Aliases: F17H15.1, F17H15_1	6.4	6.6	-0.2	-0.5	100.0%	-1.2
18499	AT2G42340.1 | expressed protein | chr2:17642385-17644700 REVERSE | Aliases: MHK10.6, MHK10_6	2.8	2.9	-0.1	-0.5	100.0%	-1.9
18500	AT4G18850.1 | hypothetical protein | chr4:10342074-10342253 REVERSE | Aliases: F13C5.20, F13C5_20	2.4	2.4	-0.0	-0.5	100.0%	-2.4
18501	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	5.1	5.2	-0.1	-0.5	100.0%	-1.3
18502	AT2G28790.1 | osmotin-like protein, putative, similar to SP:Q41350 Osmotin-like protein precursor {Lycopersicon esculentum}; contains Pfam profile PF00314: Thaumatin family | chr2:12361507-12362508 REVERSE | Aliases: F8N16.8, F8N16_8	4.6	4.4	0.2	0.5	100.0%	-1.1
18503	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	6.8	6.7	0.2	0.5	100.0%	-1.3
18504	AT4G05080.1 | F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	2.4	2.4	-0.0	-0.5	100.0%	-2.2
18505	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	4.5	4.4	0.1	0.5	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
18506	AT5G65610.1 | expressed protein, ; expression supported by MPSS | chr5:26236484-26238254 FORWARD | Aliases: K21L13.12, K21L13_12	3.7	3.8	-0.1	-0.5	100.0%	-1.4
18507	AT4G25660.1 | expressed protein | chr4:13083416-13085194 FORWARD | Aliases: L73G19.40, L73G19_40	7.7	7.9	-0.2	-0.5	100.0%	-1.7
18508	AT5G13240.1 | expressed protein, prdeicted proteins, Schizosaccharomyces pombe	6.3	6.4	-0.2	-0.5	100.0%	-1.4
18509	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	-0.5	100.0%	-2.2
18510	AT3G23840.1 | transferase family protein, low similarity to hypersensitivity-related gene (Nicotiana tabacum) GI:1171577, acetyl-CoA:benzylalcohol acetyltranferase (Clarkia concinna) GI:6166330; contains Pfam profile PF02458: Transferase family | chr3:8611133-8612697 FORWARD | Aliases: F14O13.22	4.8	5.0	-0.2	-0.5	100.0%	-1.1
18511	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	7.0	7.2	-0.3	-0.5	100.0%	-1.1
18512	AT2G10870.1 | expressed protein | chr2:4290762-4291013 FORWARD | Aliases: F16G22.7, F16G22_7	3.8	3.9	-0.1	-0.5	100.0%	-1.7
18513	AT3G54940.3 | cysteine proteinase, putative, contains similarity to cysteine proteinase GI:479060 from (Glycine max) | chr3:20365330-20367245 FORWARD | Aliases: F28P10.80	3.5	3.7	-0.2	-0.5	100.0%	-1.0
18514	AT4G30310.3 | ribitol kinase, putative, similar to ribitol kinase (Klebsiella pneumoniae) gi:2905643:gb:AAC26495 | chr4:14832322-14835098 FORWARD | Aliases: F17I23.350, F17I23_350	6.7	6.8	-0.1	-0.5	100.0%	-1.5
18515	AT5G24110.1 | Symbol: WRKY30 |	2.8	2.8	0.0	0.5	100.0%	-2.3
18516	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	3.3	3.2	0.1	0.5	100.0%	-1.8
18517	AT1G21520.1 | expressed protein | chr1:7534522-7534722 REVERSE | Aliases: F24J8.16, F24J8_16	2.3	2.3	-0.0	-0.5	100.0%	-2.1
18518	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	4.5	4.6	-0.1	-0.5	100.0%	-1.7
18519	AT1G69160.1 | expressed protein | chr1:26003877-26005251 FORWARD | Aliases: F4N2.12, F4N2_12	2.7	2.7	0.0	0.5	100.0%	-2.1
18520	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	2.5	-0.1	-0.5	100.0%	-1.8
18521	AT5G39260.1 | Symbol: ATEXPA21 | expansin, putative (EXP21), similar to alpha-expansin GI:6573157 from (Regnellidium diphyllum); 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	-0.1	-0.5	100.0%	-1.6
18522	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	4.0	4.1	-0.1	-0.5	100.0%	-1.8
18523	AT4G31800.2 | Symbol: WRKY18 |	5.2	5.3	-0.2	-0.5	100.0%	-1.2
18524	AT5G12970.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr5:4102138-4105330 FORWARD | Aliases: T24H18.140, T24H18_140	4.0	4.2	-0.2	-0.5	100.0%	-1.0
18525	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	3.4	3.4	-0.1	-0.5	100.0%	-1.9
18526	AT1G31080.1 | F-box family protein, contains Pfam profile: PF00646 F-box domain | chr1:11091813-11092880 FORWARD | Aliases: F28K20.2, F28K20_2	2.7	2.8	-0.1	-0.5	100.0%	-2.0
18527	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	-0.1	-0.5	100.0%	-2.2
18528	AT1G70040.1 | hypothetical protein | chr1:26384896-26385571 FORWARD | Aliases: F20P5.22, F20P5_22	2.6	2.7	-0.1	-0.5	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
18529	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	-0.1	-0.5	100.0%	-1.8
18530	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	2.4	-0.1	-0.5	100.0%	-2.2
18531	AT4G27890.1 | nuclear movement family protein, contains Pfam profile: PF03593 nuclear movement protein	3.0	3.1	-0.1	-0.5	100.0%	-1.9
18532	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	-0.5	100.0%	-1.8
18533	AT5G14770.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:4772884-4775700 REVERSE | Aliases: T9L3.70, T9L3_70	3.0	2.9	0.1	0.5	100.0%	-1.9
18534	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	-0.5	100.0%	-1.8
18535	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	3.9	0.1	0.5	100.0%	-1.7
18536	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	4.2	4.4	-0.2	-0.5	100.0%	-1.5
18537	AT4G23230.1 | protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain | chr4:12157579-12160280 REVERSE | Aliases: F21P8.120, F21P8_120	2.5	2.4	0.1	0.5	100.0%	-2.1
18538	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	8.5	8.1	0.3	0.5	100.0%	-1.0
18539	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	8.1	8.0	0.1	0.5	100.0%	-1.9
18540	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	-0.5	100.0%	-2.0
18541	AT5G24000.1 | expressed protein, contains Pfam profile PF05684: Protein of unknown function (DUF819) | chr5:8110316-8112695 REVERSE | Aliases: MZF18.12, MZF18_12	4.1	4.2	-0.1	-0.5	100.0%	-1.6
18542	AT1G12960.1 | 60S ribosomal protein L27A (RPL27aA), similar to GB:BAA96068 from (Panax ginseng) | chr1:4422705-4423153 REVERSE | Aliases: F13K23.22, F13K23_22	4.2	4.3	-0.1	-0.5	100.0%	-1.7
18543	AT4G39420.1 | expressed protein, ; expression supported by MPSS | chr4:18339725-18342147 FORWARD | Aliases: F23K16.50, F23K16_50	2.9	2.9	0.0	0.5	100.0%	-2.1
18544	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	5.5	5.6	-0.1	-0.5	100.0%	-1.3
18545	AT3G52105.1 | expressed protein | chr3:19334310-19334805 FORWARD | Aliases: None	5.1	5.4	-0.3	-0.5	100.0%	-0.7
18546	AT1G04500.1 | zinc finger CONSTANS-related, similar to Zinc finger protein constans-like 15 (SP:Q9FHH8) {Arabidopsis thaliana}	2.1	2.2	-0.0	-0.5	100.0%	-2.5
18547	AT3G42780.1 | hypothetical protein, hypothetical protein MZB10.16 - Arabidopsis thaliana, EMBL:AC009326 | chr3:14882201-14882731 FORWARD | Aliases: T21C14.1	2.9	3.0	-0.1	-0.5	100.0%	-1.8
18548	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	5.8	5.9	-0.1	-0.5	100.0%	-1.3
18549	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	2.9	2.9	-0.1	-0.5	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
18550	AT5G66770.1 | scarecrow transcription factor family protein | chr5:26677826-26680120 FORWARD | Aliases: MUD21.1, MUD21_1	2.7	2.6	0.1	0.5	100.0%	-1.7
18551	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	-0.5	100.0%	-2.2
18552	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	4.3	4.4	-0.1	-0.5	100.0%	-1.5
18553	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	-0.0	-0.5	100.0%	-2.2
18554	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	3.0	-0.1	-0.5	100.0%	-2.0
18555	AT5G27050.1 | MADS-box family protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana) | chr5:9520279-9520641 FORWARD | Aliases: F15P11.2, F15P11_2	3.8	3.9	-0.1	-0.5	100.0%	-1.9
18556	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	2.9	2.9	-0.1	-0.5	100.0%	-2.0
18557	AT1G72390.1 | expressed protein | chr1:27250615-27255238 FORWARD | Aliases: T10D10.14, T10D10_14	4.4	4.4	-0.1	-0.5	100.0%	-1.4
18558	AT3G43840.1 | expressed protein | chr3:15711339-15711842 FORWARD | Aliases: T28A8.130	2.2	2.3	-0.0	-0.5	100.0%	-2.5
18559	AT4G14300.1 | heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative | chr4:8231013-8232987 FORWARD | Aliases: DL3190W, FCAALL.156	6.9	7.0	-0.1	-0.5	100.0%	-1.5
18560	AT5G57460.1 | expressed protein | chr5:23292395-23294707 FORWARD | Aliases: MUA2.4, MUA2_4	4.2	4.1	0.1	0.5	100.0%	-1.5
18561	AT4G22756.1 | Symbol: SMO1 2 |	6.3	6.1	0.3	0.5	100.0%	-1.4
18562	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	3.3	-0.1	-0.5	100.0%	-1.8
18563	AT2G37110.1 | expressed protein, contains Pfam profile PF04749: Protein of unknown function, DUF614 | chr2:15599636-15601072 FORWARD | Aliases: T2N18.13, T2N18_13	8.8	9.0	-0.1	-0.5	100.0%	-1.6
18564	AT3G04700.1 | expressed protein | chr3:1276674-1277830 FORWARD | Aliases: F7O18.17, F7O18_17	3.0	3.1	-0.1	-0.5	100.0%	-2.2
18565	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	6.7	6.6	0.1	0.5	100.0%	-1.5
18566	AT2G21070.2 | expressed protein, similar to hypothetical protein DDB0203108 [Dictyostelium discoideum] (GB:EAL69882.1)	3.4	3.4	0.1	0.5	100.0%	-1.8
18567	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)	6.5	6.8	-0.3	-0.5	100.0%	-1.3
18568	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	3.1	0.1	0.5	100.0%	-1.8
18569	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	2.9	3.0	-0.1	-0.5	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
18570	AT3G06520.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr3:2020290-2021961 FORWARD | Aliases: F5E6.15, F5E6_15	4.0	3.9	0.1	0.5	100.0%	-1.4
18571	AT2G38770.1 | expressed protein | chr2:16210041-16217416 REVERSE | Aliases: T6A23.3, T6A23_3	3.5	3.6	-0.1	-0.5	100.0%	-1.7
18572	AT3G08820.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:2677124-2679185 REVERSE | Aliases: T16O11.25	5.0	4.8	0.2	0.5	100.0%	-1.2
18573	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	8.1	7.8	0.2	0.5	100.0%	-1.2
18574	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	2.8	-0.1	-0.5	100.0%	-2.0
18575	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	3.0	-0.1	-0.5	100.0%	-1.7
18576	AT3G29160.3 | Symbol: AKIN11 |	6.3	6.4	-0.1	-0.5	100.0%	-1.4
18577	AT5G67310.1 | Symbol: CYP81G1 | cytochrome P450 family protein | chr5:26871249-26874167 REVERSE | Aliases: K8K14.3, K8K14_3	3.7	3.6	0.1	0.5	100.0%	-1.6
18578	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	3.1	3.1	0.0	0.5	100.0%	-2.3
18579	AT5G12260.1 | expressed protein | chr5:3966366-3968879 FORWARD | Aliases: MXC9.22, MXC9_22	6.2	6.3	-0.1	-0.5	100.0%	-1.8
18580	AT2G45650.1 | Symbol: AGL6 | MADS-box protein (AGL6) | chr2:18811424-18813596 FORWARD | Aliases: F17K2.18	2.4	2.5	-0.0	-0.5	100.0%	-2.3
18581	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	4.8	4.7	0.1	0.5	100.0%	-1.5
18582	AT4G37120.1 | Symbol: SMP2 | expressed protein | chr4:17486641-17489282 FORWARD | Aliases: AP22.39, AP22_39	9.2	9.1	0.1	0.5	100.0%	-1.8
18583	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	8.9	8.5	0.4	0.5	100.0%	-1.5
18584	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	3.7	-0.1	-0.5	100.0%	-1.7
18585	AT1G21540.1 | AMP-binding protein, putative, strong similarity to AMP-binding protein GI:1903034 from (Brassica napus); 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	4.0	4.1	-0.1	-0.5	100.0%	-1.8
18586	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	8.3	8.6	-0.2	-0.5	100.0%	-1.4
18587	AT1G07135.1 | glycine-rich protein | chr1:2189927-2190623 REVERSE | Aliases: None	7.4	7.7	-0.3	-0.5	100.0%	-0.7
18588	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	3.9	-0.1	-0.5	100.0%	-1.6
18589	AT4G28760.2 | expressed protein, predicted protein. Arabidopsis thaliana | chr4:14207467-14212050 FORWARD | Aliases: F16A16.130, F16A16_130	4.0	3.9	0.1	0.5	100.0%	-1.5
18590	AT2G14730.1 | expressed protein | chr2:6312631-6314391 FORWARD | Aliases: T6B13.5	3.0	3.1	-0.1	-0.5	100.0%	-1.8
18591	AT2G38220.1 | expressed protein | chr2:16015190-16017136 FORWARD | Aliases: F16M14.15, F16M14_15	2.9	2.8	0.1	0.5	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
18592	AT3G52540.1 | ovate family protein, 52% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	2.9	2.8	0.1	0.5	100.0%	-1.9
18593	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	2.6	0.1	0.5	100.0%	-2.1
18594	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	4.2	4.1	0.1	0.5	100.0%	-1.6
18595	AT5G17690.1 | Symbol: TFL2 | like heterochromatin protein (LHP1), identical to like heterochromatin protein LHP1 (Arabidopsis thaliana) GI: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	4.0	4.1	-0.1	-0.5	100.0%	-1.8
18596	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	3.0	3.1	-0.1	-0.5	100.0%	-2.2
18597	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	9.4	9.5	-0.2	-0.5	100.0%	-1.7
18598	AT1G47765.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.8	2.9	-0.1	-0.5	100.0%	-2.1
18599	AT4G17050.1 | expressed protein | chr4:9589601-9592606 FORWARD | Aliases: DL4555W, FCAALL.343	5.4	5.0	0.4	0.5	100.0%	-0.9
18600	AT5G11550.1 | expressed protein | chr5:3708010-3709247 REVERSE | Aliases: F15N18.140, F15N18_140	3.6	3.7	-0.1	-0.5	100.0%	-1.4
18601	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	3.1	3.0	0.1	0.5	100.0%	-1.7
18602	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	5.3	5.4	-0.1	-0.5	100.0%	-1.5
18603	AT3G06000.1 | leucine-rich repeat family protein, contains Pfam doamin 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	3.2	-0.1	-0.5	100.0%	-2.2
18604	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	2.7	2.8	-0.0	-0.5	100.0%	-2.3
18605	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	-0.5	100.0%	-2.3
18606	AT4G05060.1 | vesicle-associated membrane family protein / VAMP family protein, similar to VAP27 GI:6688926 (Nicotiana plumbaginifolia) | chr4:2590063-2592161 REVERSE | Aliases: C17L7.8	4.5	4.6	-0.1	-0.5	100.0%	-1.7
18607	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	0.5	100.0%	-1.9
18608	AT1G77340.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:29073237-29074722 REVERSE | Aliases: F2P24.5, F2P24_5	2.8	2.9	-0.1	-0.5	100.0%	-2.1
18609	AT1G03055.2 | expressed protein | chr1:710063-711803 REVERSE | Aliases: None	2.8	2.9	-0.1	-0.5	100.0%	-1.9
18610	AT5G19490.1 | repressor protein-related, similar to repressor protein (Oryza sativa) GI:18481624 | chr5:6576771-6577843 REVERSE | Aliases: T20D1.10, T20D1_10	4.0	3.9	0.1	0.5	100.0%	-1.6
18611	AT3G48740.1 | nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula) | chr3:18063492-18065738 REVERSE | Aliases: T21J18.1	7.1	6.8	0.2	0.5	100.0%	-0.6
18612	AT4G15040.1 | subtilase family protein, contains similarity to prepro-cucumisin GI:807698 from (Cucumis melo) | chr4:8581368-8584117 REVERSE | Aliases: DL3561C, FCAALL.176	2.3	2.4	-0.0	-0.5	100.0%	-2.3

Rank	Description	Sync	Root	M	t	adj.q	B
18613	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	-0.5	100.0%	-1.9
18614	AT2G46375.1 | expressed protein | chr2:19044937-19045452 FORWARD | Aliases: None	3.4	3.4	-0.1	-0.5	100.0%	-1.9
18615	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	3.2	0.1	0.5	100.0%	-1.6
18616	AT1G31690.1 | copper amine oxidase, putative, similar to copper amine oxidase (Lens culinaris) gi:15451834:gb:AAB34918	2.5	2.5	-0.1	-0.5	100.0%	-1.9
18617	AT1G79970.2 | expressed protein | chr1:30087004-30088642 FORWARD | Aliases: F18B13.5, F18B13_5	4.4	4.6	-0.2	-0.5	100.0%	-1.4
18618	AT3G28630.2 | expressed protein, contains Pfam profile: PF04601 protein of unknown function (DUF569 | chr3:10730405-10732086 FORWARD | Aliases: MZN14.10	2.4	2.4	-0.0	-0.5	100.0%	-2.2
18619	AT4G13450.2 | expressed protein | chr4:7815035-7816000 REVERSE | Aliases: T9E8.190, T9E8_190	2.2	2.2	-0.0	-0.5	100.0%	-2.1
18620	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	7.7	7.6	0.1	0.5	100.0%	-1.4
18621	AT1G50150.1 | hypothetical protein, similar to hypothetical protein GB:AAD50048 GI:5734783 from (Arabidopsis thaliana)	3.1	3.2	-0.2	-0.5	100.0%	-1.5
18622	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	5.7	5.6	0.1	0.5	100.0%	-1.4
18623	AT2G31460.1 | hypothetical protein, contains Pfam profile PF03754: Domain of unknown function (DUF313)	3.1	3.2	-0.1	-0.5	100.0%	-2.1
18624	AT3G59290.1 | epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain;	6.0	6.2	-0.2	-0.5	100.0%	-1.4
18625	AT1G62260.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:23001491-23003461 REVERSE | Aliases: F19K23.18, F19K23_18	3.0	3.0	-0.1	-0.5	100.0%	-1.9
18626	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	-0.5	100.0%	-2.5
18627	AT5G56570.1 | expressed protein, similar to unknown protein (pir :T06019) | chr5:22919962-22921630 FORWARD | Aliases: MIK19.1, MIK19_1	2.4	2.4	0.0	0.5	100.0%	-2.4
18628	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	0.5	100.0%	-2.4
18629	AT3G05675.2 | expressed protein | chr3:1658277-1660312 REVERSE | Aliases: None	4.1	4.2	-0.1	-0.5	100.0%	-1.7
18630	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	4.6	-0.1	-0.5	100.0%	-1.6
18631	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	5.2	-0.1	-0.5	100.0%	-1.6
18632	AT3G15570.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr3:5270171-5271860 REVERSE | Aliases: MQD17.2	3.2	3.1	0.1	0.5	100.0%	-1.8
18633	AT4G16460.1 | expressed protein | chr4:9285651-9286168 FORWARD | Aliases: DL4255W, FCAALL.371	2.7	2.8	-0.1	-0.5	100.0%	-2.2
18634	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	4.0	-0.1	-0.5	100.0%	-1.3
18635	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	2.6	-0.0	-0.5	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
18636	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	0.0	0.5	100.0%	-2.3
18637	AT2G47920.1 | kinase interacting family protein, similar to kinase interacting protein 1 (GI:13936326) (Petunia integrifolia) | chr2:19622847-19623974 FORWARD | Aliases: F17A22.31, F17A22_31	2.2	2.2	-0.0	-0.5	100.0%	-2.4
18638	AT2G46200.2 | expressed protein, low similarity to ES18 (Mus musculus) GI:4416181 | chr2:18981737-18983923 REVERSE | Aliases: T3F17.15	3.9	3.9	0.1	0.5	100.0%	-1.5
18639	AT3G47330.1 | expressed protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287	2.9	2.9	-0.0	-0.5	100.0%	-2.3
18640	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	3.7	0.1	0.5	100.0%	-1.5
18641	AT1G15010.1 | expressed protein | chr1:5171202-5171737 FORWARD | Aliases: T15D22.5, T15D22_5	2.8	2.9	-0.1	-0.5	100.0%	-1.6
18642	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	9.6	9.8	-0.2	-0.5	100.0%	-1.0
18643	AT5G22710.1 | expressed protein | chr5:7547800-7549372 REVERSE | Aliases: MDJ22.13, MDJ22_13	3.7	3.8	-0.1	-0.5	100.0%	-1.3
18644	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	4.2	-0.1	-0.5	100.0%	-1.9
18645	AT2G26880.1 | MADS-box family protein | chr2:11466984-11468177 REVERSE | Aliases: F12C20.8, F12C20_8	2.6	2.6	-0.0	-0.5	100.0%	-2.1
18646	AT2G33240.1 | Symbol: XID | myosin, putative, similar to myosin (GI:433663) (Arabidopsis thaliana); myosin my5A (SP:Q02440) {Gallus gallus} | chr2:14094019-14103991 REVERSE | Aliases: ATXID, F25I18.2, F25I18_2	2.4	2.3	0.0	0.5	100.0%	-2.1
18647	AT3G16610.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:5656377-5658341 REVERSE | Aliases: MGL6.8	3.0	3.0	0.1	0.5	100.0%	-1.8
18648	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	9.7	9.5	0.2	0.5	100.0%	-1.5
18649	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	-0.1	-0.5	100.0%	-1.9
18650	AT5G12180.1 | Symbol: CPK17 | calcium-dependent protein kinase, putative / CDPK, putative | chr5:3937025-3939597 FORWARD | Aliases: MXC9.14, MXC9_14	2.9	3.0	-0.1	-0.5	100.0%	-2.0
18651	AT3G10650.1 | expressed protein | chr3:3325175-3330897 REVERSE | Aliases: F13M14.6	3.4	3.5	-0.1	-0.5	100.0%	-1.5
18652	AT1G08135.1 | cation/hydrogen exchanger (CHX6b), Note: CHX6a and CHX6b were originally 1 gene but were split pased on alignments with other family members; may be a pseudogene and requires futher investigation; monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563 | chr1:2548816-2551470 REVERSE | Aliases: None	3.4	3.4	-0.1	-0.5	100.0%	-1.9
18653	AT1G36940.1 | expressed protein | chr1:14006344-14007352 FORWARD | Aliases: T32E20.35, T32E20_35	3.1	3.0	0.0	0.5	100.0%	-2.0
18654	AT1G77405.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:29092039-29093415 FORWARD | Aliases: F2P24.16, F2P24_16	5.3	5.2	0.1	0.5	100.0%	-1.6
18655	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	2.8	2.8	-0.0	-0.5	100.0%	-2.2
18656	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:AAP53220.1); contains InterPro domain Glycoside hydrolase, family 10 (InterPro:IPR001000) | chr2:6290586-6293137 REVERSE | Aliases: T6B13.7, T6B13_7	2.9	2.9	-0.1	-0.5	100.0%	-1.8
18657	AT4G21240.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.5	-0.0	-0.5	100.0%	-2.3
18658	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	-0.1	-0.5	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
18659	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	5.1	5.3	-0.2	-0.5	100.0%	-1.2
18660	AT3G45300.1 | Symbol: IVD | isovaleryl-CoA-dehydrogenase (IVD), identical to isovaleryl-CoA-dehydrogenase precursor (Arabidopsis thaliana) GI:5596622	8.2	8.4	-0.2	-0.5	100.0%	-1.1
18661	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	4.6	4.6	-0.1	-0.5	100.0%	-1.6
18662	AT4G17240.1 | expressed protein | chr4:9666700-9668386 REVERSE | Aliases: DL4655C, FCAALL.387	2.9	2.9	-0.0	-0.5	100.0%	-2.3
18663	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) (Homo sapiens); similar to rab11 binding protein GI:4512103 from (Bos taurus) | chr1:18075993-18078125 REVERSE | Aliases: T24P22.7	3.8	3.7	0.1	0.5	100.0%	-1.5
18664	AT4G09140.1 | Symbol: ATMLH1 |	4.0	4.0	0.1	0.5	100.0%	-1.8
18665	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	3.6	3.7	-0.1	-0.5	100.0%	-1.7
18666	AT3G12203.1 | Symbol: SCPL17 |	3.1	3.1	0.1	0.5	100.0%	-1.8
18667	AT3G28890.1 | 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	2.7	2.8	-0.0	-0.5	100.0%	-2.2
18668	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	-0.5	100.0%	-2.4
18669	AT4G12890.1 | 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) | chr4:7546375-7547569 FORWARD | Aliases: T20K18.240, T20K18_240	2.9	2.9	0.1	0.5	100.0%	-1.8
18670	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	5.4	5.3	0.1	0.5	100.0%	-1.5
18671	AT5G28270.1 | hypothetical protein, similar to At2g12100, At2g05450, At1g45090, At2g16180, At2g06750 | chr5:10258094-10260475 REVERSE | Aliases: T8M17.40, T8M17_40	2.4	2.5	-0.0	-0.5	100.0%	-2.3
18672	AT3G32100.1 | hypothetical protein | chr3:13100684-13101017 FORWARD | Aliases: F1M23.29	2.4	2.5	-0.0	-0.5	100.0%	-2.6
18673	AT3G50860.1 | clathrin adaptor complex small chain family protein, contains Pfam profile: PF01217 clathrin adaptor complex small chain	3.7	3.5	0.2	0.5	100.0%	-1.4
18674	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	-0.5	100.0%	-2.1
18675	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	5.4	5.5	-0.1	-0.5	100.0%	-1.8
18676	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	5.1	5.1	-0.1	-0.5	100.0%	-1.4
18677	AT1G69640.1 | acid phosphatase, putative, similar to GI:5360721 from (Lupinus albus) | chr1:26197322-26199319 REVERSE | Aliases: F24J1.22	3.7	3.6	0.1	0.5	100.0%	-1.8
18678	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	-0.1	-0.5	100.0%	-2.2
18679	AT3G29370.1 | expressed protein | chr3:11279826-11280345 FORWARD | Aliases: MUO10.6	2.9	3.0	-0.1	-0.5	100.0%	-2.0
18680	AT3G06350.1 | Symbol: EMB3004 | dehydroquinate dehydratase, putative / shikimate dehydrogenase, putative, similar to dehydroquinate dehydratase/shikimate dehydrogenase (Nicotiana tabacum)(GI:535771), dehydroquinate dehydratase/shikimate:NADP oxidoreductase (Lycopersicon esculentum)(GI:3169883) | chr3:1924368-1927759 REVERSE | Aliases: EMB3004, EMBRYO DEFECTIVE 3004, F24P17.18, F24P17_18	9.8	9.7	0.1	0.5	100.0%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
18681	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	-0.5	100.0%	-1.8
18682	AT3G44900.1 | Symbol: ATCHX4 |	2.0	2.1	-0.0	-0.5	100.0%	-2.5
18683	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	3.2	-0.1	-0.5	100.0%	-1.9
18684	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	2.9	0.0	0.5	100.0%	-2.1
18685	AT3G56250.1 | expressed protein | chr3:20877099-20878819 FORWARD | Aliases: F18O21.210	3.1	3.0	0.1	0.5	100.0%	-1.7
18686	AT5G35540.1 | hypothetical protein | chr5:13739367-13740223 FORWARD | Aliases: MOK9.17, MOK9_17	2.8	2.9	-0.0	-0.5	100.0%	-2.0
18687	AT3G14030.1 | expressed protein | chr3:4646279-4647131 REVERSE | Aliases: MDC16.17	2.6	2.5	0.0	0.5	100.0%	-2.0
18688	AT1G22730.1 | MA3 domain-containing protein, contains Pfam profile PF02847: MA3 domain; low similarity to programmed cell death 4 protein (Gallus gallus) GI:12958564 | chr1:8046142-8049028 FORWARD | Aliases: T22J18.10, T22J18_10	5.0	5.1	-0.1	-0.5	100.0%	-1.4
18689	AT3G26490.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr3:9705379-9707398 FORWARD | Aliases: F20C19.23	3.2	3.2	0.1	0.5	100.0%	-1.9
18690	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	3.8	-0.1	-0.5	100.0%	-1.7
18691	AT1G67270.1 | expressed protein | chr1:25187032-25189456 REVERSE | Aliases: F1N21.9	3.9	3.9	-0.1	-0.5	100.0%	-2.2
18692	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	6.3	6.7	-0.4	-0.5	100.0%	-0.9
18693	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	9.0	9.1	-0.1	-0.5	100.0%	-1.4
18694	AT3G61590.1 | F-box family protein, contains weak hit to Pfam PF00646: F-box domain; stamina pistilloidia (Stp) - Pisum sativum, EMBL:AF004843	4.7	4.8	-0.1	-0.5	100.0%	-1.5
18695	AT1G34070.1 | expressed protein | chr1:12402261-12403187 FORWARD | Aliases: F12G12.10, F12G12_10	3.1	3.1	-0.1	-0.5	100.0%	-1.6
18696	AT1G17630.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:6064518-6066713 FORWARD | Aliases: F11A6.24	3.5	3.4	0.1	0.5	100.0%	-1.6
18697	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	5.1	5.3	-0.2	-0.5	100.0%	-1.3
18698	AT2G20760.1 | expressed protein | chr2:8949844-8952304 REVERSE | Aliases: F5H14.27, F5H14_27	7.1	7.0	0.2	0.5	100.0%	-1.1
18699	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%	-1.9
18700	AT5G23640.1 | expressed protein | chr5:7968262-7968505 REVERSE | Aliases: MQM1.10, MQM1_10	3.0	3.1	-0.0	-0.5	100.0%	-2.4
18701	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	2.9	2.9	-0.1	-0.4	100.0%	-1.9
18702	AT5G09330.1 | Symbol: ANAC082 | no apical meristem (NAM) family protein, similar to NAC1 (GI:7716952)	7.4	7.5	-0.1	-0.4	100.0%	-1.5
18703	AT1G18350.1 | Symbol: ATMKK7 |	2.6	2.5	0.0	0.4	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
18704	AT4G27980.1 | expressed protein | chr4:13921683-13923576 FORWARD | Aliases: T13J8.90, T13J8_90	3.0	3.0	0.1	0.4	100.0%	-1.6
18705	AT4G27580.1 | expressed protein | chr4:13765667-13766603 REVERSE | Aliases: T29A15.70, T29A15_70	3.0	3.0	0.1	0.4	100.0%	-1.9
18706	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	2.6	0.1	0.4	100.0%	-1.9
18707	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	2.6	2.7	-0.1	-0.4	100.0%	-2.0
18708	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	3.7	3.6	0.1	0.4	100.0%	-1.8
18709	AT5G23780.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr5:8017195-8019029 REVERSE | Aliases: MRO11.18, MRO11_18	3.0	3.0	0.1	0.4	100.0%	-2.1
18710	AT3G17100.2 | expressed protein | chr3:5831279-5832425 FORWARD | Aliases: K14A17.17	5.5	5.4	0.1	0.4	100.0%	-1.6
18711	AT5G38460.1 | ALG6, ALG8 glycosyltransferase family protein, similar to SP:Q9Y672 Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase (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	3.2	3.1	0.1	0.4	100.0%	-1.6
18712	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	2.3	0.0	0.4	100.0%	-2.4
18713	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	2.2	2.2	0.0	0.4	100.0%	-2.2
18714	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	2.7	-0.0	-0.4	100.0%	-2.2
18715	AT5G02580.2 | expressed protein | chr5:579850-580785 FORWARD | Aliases: T22P11.170, T22P11_170	3.5	3.5	0.1	0.4	100.0%	-1.8
18716	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	-0.4	100.0%	-2.0
18717	AT5G05950.1 | expressed protein | chr5:1788768-1789439 FORWARD | Aliases: K18J17.12, K18J17_12	4.6	4.5	0.1	0.4	100.0%	-1.5
18718	AT1G42580.1 | hypothetical protein, contains similarity to hypothetical proteins | chr1:15994136-15994615 REVERSE | Aliases: F8D11.4, F8D11_4	3.0	3.1	-0.1	-0.4	100.0%	-2.1
18719	AT4G18920.1 | expressed protein | chr4:10368766-10370223 FORWARD | Aliases: F13C5.90, F13C5_90	3.6	3.5	0.1	0.4	100.0%	-1.6
18720	AT3G02680.1 | expressed protein | chr3:578335-578920 FORWARD | Aliases: F16B3.31, F16B3_31	3.6	3.5	0.1	0.4	100.0%	-1.5
18721	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	2.6	2.6	0.0	0.4	100.0%	-2.1
18722	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	3.1	-0.1	-0.4	100.0%	-2.0
18723	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	-0.4	100.0%	-1.9
18724	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	3.3	-0.0	-0.4	100.0%	-1.9
18725	AT1G70950.1 | expressed protein | chr1:26756351-26759011 FORWARD | Aliases: F15H11.15, F15H11_15	3.9	4.0	-0.1	-0.4	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
18726	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	2.9	-0.1	-0.4	100.0%	-1.9
18727	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: ATKT2, ATKT2P, ATKUP2, KUP2, POTASSIUM TRANSPORTER 2, SHY3, T2P4.11, T2P4_11, TRK2	5.1	5.0	0.1	0.4	100.0%	-1.6
18728	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	3.2	3.2	0.0	0.4	100.0%	-2.0
18729	AT3G20510.1 | expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136) | chr3:7160683-7161997 FORWARD | Aliases: K10D20.5	9.2	9.2	-0.1	-0.4	100.0%	-1.7
18730	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	5.0	0.1	0.4	100.0%	-1.9
18731	AT5G64800.1 | Symbol: CLE21 | CLE21, putative, CLAVATA3/ESR-Related 21 (CLE21) | chr5:25923309-25923629 FORWARD | Aliases: CLAVATA3/ESR RELATED 21, MXK3.2, MXK3_2	2.7	2.8	-0.1	-0.4	100.0%	-2.0
18732	AT1G48820.1 | terpene synthase/cyclase family protein, similar to terpene cyclase GI:9293912 from (Arabidopsis thaliana) | chr1:18058897-18063035 FORWARD | Aliases: F11I4.2, F11I4_2	2.4	2.4	-0.0	-0.4	100.0%	-2.2
18733	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	3.2	-0.1	-0.4	100.0%	-1.6
18734	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	5.2	5.2	-0.1	-0.4	100.0%	-1.4
18735	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	0.4	100.0%	-2.1
18736	AT5G49590.1 | hypothetical protein, similar to unknown protein (pir::T02348) | chr5:20145962-20146780 FORWARD | Aliases: K6M13.15, K6M13_15	3.0	3.0	-0.0	-0.4	100.0%	-2.5
18737	AT1G17330.1 | metal-dependent phosphohydrolase HD domain-containing protein-related | chr1:5929959-5931588 FORWARD | Aliases: T13M22.1	2.5	2.5	-0.0	-0.4	100.0%	-2.1
18738	AT1G43680.1 | expressed protein | chr1:16474645-16475706 FORWARD | Aliases: F2J6.3, F2J6_3	2.2	2.3	-0.0	-0.4	100.0%	-2.4
18739	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	2.2	2.2	-0.0	-0.4	100.0%	-2.2
18740	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	2.7	2.8	-0.0	-0.4	100.0%	-2.1
18741	AT3G30310.1 | hypothetical protein | chr3:11931181-11931706 FORWARD | Aliases: T6J22.6	2.3	2.3	-0.0	-0.4	100.0%	-2.4
18742	AT5G37300.1 | expressed protein | chr5:14784729-14787479 FORWARD | Aliases: MNJ8.9, MNJ8_9	3.2	3.3	-0.0	-0.4	100.0%	-2.3
18743	AT1G13540.1 | expressed protein | chr1:4635471-4636705 REVERSE | Aliases: F13B4.29, F13B4_29	2.8	2.8	-0.0	-0.4	100.0%	-2.2
18744	AT5G30520.1 | hypothetical protein | chr5:11653422-11653868 REVERSE | Aliases: None	3.0	3.0	-0.1	-0.4	100.0%	-1.9
18745	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	0.0	0.4	100.0%	-2.1
18746	AT1G23420.1 | Symbol: INO | inner no outer protein (INO), identical to INNER NO OUTER (INO) (Arabidopsis thaliana) GI:6684816	3.1	3.2	-0.1	-0.4	100.0%	-1.7
18747	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	8.3	8.2	0.1	0.4	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
18748	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	3.1	3.2	-0.0	-0.4	100.0%	-2.0
18749	AT2G13270.1 | expressed protein | chr2:5499735-5500937 FORWARD | Aliases: F15O11.9, F15O11_9	2.1	2.2	-0.0	-0.4	100.0%	-2.4
18750	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	5.7	5.8	-0.1	-0.4	100.0%	-1.4
18751	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	3.0	3.1	-0.1	-0.4	100.0%	-1.9
18752	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	3.7	3.8	-0.0	-0.4	100.0%	-1.9
18753	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	6.2	6.0	0.2	0.4	100.0%	-1.6
18754	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	4.9	5.0	-0.1	-0.4	100.0%	-1.5
18755	AT3G07080.1 | membrane protein, contains Pfam profile: PF00892 Integral membrane protein | chr3:2241042-2243047 FORWARD | Aliases: T1B9.27	4.9	5.0	-0.1	-0.4	100.0%	-1.6
18756	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	6.4	6.4	0.1	0.4	100.0%	-1.6
18757	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	4.5	4.6	-0.1	-0.4	100.0%	-1.4
18758	ATCG00190.1 | Symbol: RPOB | Chloroplast DNA-dependent RNA polymerase B subunit. | chrC:23111-26329 REVERSE | Aliases: RPOB	4.1	4.2	-0.1	-0.4	100.0%	-1.5
18759	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	0.1	0.4	100.0%	-1.7
18760	AT3G18215.1 | expressed protein, contains Pfam profile PF04654: Protein of unknown function, DUF599 | chr3:6240890-6242577 FORWARD | Aliases: None	7.8	8.0	-0.2	-0.4	100.0%	-1.4
18761	AT4G38750.1 | expressed protein | chr4:18084902-18090840 REVERSE | Aliases: T9A14.30, T9A14_30	6.8	6.7	0.1	0.4	100.0%	-1.9
18762	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	3.7	0.1	0.4	100.0%	-1.8
18763	AT5G03060.1 | expressed protein, ; expression supported by MPSS | chr5:716721-717677 REVERSE | Aliases: F15A17.90, F15A17_90	2.7	2.7	-0.0	-0.4	100.0%	-2.2
18764	AT3G10460.1 | self-incompatibility protein-related, similar to self-incompatibility (Papaver nudicaule) GI:3097262 | chr3:3255805-3256444 FORWARD | Aliases: F13M14.26	3.4	3.5	-0.1	-0.4	100.0%	-1.7
18765	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	-0.0	-0.4	100.0%	-2.2
18766	AT2G27280.1 | expressed protein | chr2:11680904-11682691 REVERSE | Aliases: F12K2.14, F12K2_14	3.2	3.3	-0.1	-0.4	100.0%	-1.8
18767	AT5G10500.1 | kinase interacting family protein, similar to kinase interacting protein 1 (GI:13936326) (Petunia integrifolia) | chr5:3305332-3308110 FORWARD | Aliases: F12B17.150, F12B17_150	2.5	2.5	-0.1	-0.4	100.0%	-2.2
18768	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	4.4	4.5	-0.1	-0.4	100.0%	-1.6
18769	AT1G76010.1 | expressed protein | chr1:28531744-28534427 REVERSE | Aliases: T4O12.22, T4O12_22	6.7	6.9	-0.2	-0.4	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
18770	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	3.1	-0.1	-0.4	100.0%	-1.8
18771	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	8.7	8.6	0.1	0.4	100.0%	-1.2
18772	AT1G18690.1 | galactosyl transferase GMA12/MNN10 family protein, very low similarity to alpha-1,2-galactosyltransferase, Schizosaccharomyces pombe (SP:Q09174)	4.6	4.5	0.1	0.4	100.0%	-1.2
18773	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	7.4	7.2	0.1	0.4	100.0%	-1.4
18774	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%	-1.3
18775	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	5.8	5.9	-0.1	-0.4	100.0%	-1.2
18776	AT5G19250.1 | expressed protein | chr5:6471951-6472947 FORWARD | Aliases: T24G5.150, T24G5_150	5.1	5.2	-0.1	-0.4	100.0%	-1.6
18777	AT3G06120.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.7	2.6	0.1	0.4	100.0%	-1.7
18778	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 (Gossypium hirsutum) | chr4:17775468-17777391 REVERSE | Aliases: T28I19.80, T28I19_80	2.5	2.5	-0.0	-0.4	100.0%	-2.0
18779	AT1G05550.1 | expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295) | chr1:1641228-1643747 REVERSE | Aliases: T25N20.20	3.7	3.8	-0.1	-0.4	100.0%	-1.8
18780	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	3.2	3.1	0.1	0.4	100.0%	-1.8
18781	AT3G44230.1 | hypothetical protein | chr3:15943121-15943735 FORWARD | Aliases: T10D17.20	2.7	2.7	-0.1	-0.4	100.0%	-2.0
18782	NA	12.4	12.5	-0.1	-0.4	100.0%	-2.2
18783	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	6.5	6.4	0.1	0.4	100.0%	-1.4
18784	AT2G12610.1 | expressed protein, ; expression supported by MPSS | chr2:5148919-5150611 FORWARD | Aliases: T4E5.7, T4E5_7	2.1	2.2	-0.0	-0.4	100.0%	-2.5
18785	AT3G42390.1 | hypothetical protein | chr3:14529007-14529453 REVERSE | Aliases: T14K23.100	3.3	3.4	-0.1	-0.4	100.0%	-1.8
18786	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	-0.4	100.0%	-2.2
18787	AT1G30570.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:10828915-10831464 FORWARD | Aliases: T5I8.2, T5I8_2	3.9	3.8	0.1	0.4	100.0%	-1.7
18788	AT1G52160.1 | metallo-beta-lactamase family protein | chr1:19424442-19428108 REVERSE | Aliases: F9I5.1, F9I5_1	6.5	6.4	0.1	0.4	100.0%	-1.8
18789	AT1G67980.2 | Symbol: CCoAMT |	3.6	3.7	-0.1	-0.4	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
18790	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	3.1	0.1	0.4	100.0%	-1.9
18791	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	0.4	100.0%	-2.4
18792	AT3G60590.3 | expressed protein | chr3:22409203-22410728 FORWARD | Aliases: T4C21.1	4.4	4.3	0.1	0.4	100.0%	-1.6
18793	AT3G28430.1 | expressed protein, non-consensus GC donor splice site at exon 16	3.3	3.3	0.1	0.4	100.0%	-1.8
18794	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	3.7	-0.1	-0.4	100.0%	-1.8
18795	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	2.5	2.5	0.0	0.4	100.0%	-2.2
18796	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	8.4	8.5	-0.1	-0.4	100.0%	-1.3
18797	AT4G22120.1 | 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 | chr4:11715836-11719557 REVERSE | Aliases: F1N20.220, F1N20_220	7.7	7.5	0.2	0.4	100.0%	-1.4
18798	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	6.8	6.8	-0.1	-0.4	100.0%	-1.7
18799	AT5G48710.1 | ubiquitin-related, similar to SP:O13351 Ubiquitin-like protein smt3/pmt3 {Schizosaccharomyces pombe} | chr5:19772291-19772798 REVERSE | Aliases: K24G6.4, K24G6_4	4.1	4.2	-0.1	-0.4	100.0%	-1.6
18800	AT2G44810.1 | Symbol: DAD1 | defective in anther dehiscence1 (DAD1), identical to DEFECTIVE IN ANTHER DEHISCENCE1 (Arabidopsis thaliana) GI:16215706; contains Pfam profile PF01764: Lipase | chr2:18486128-18487268 FORWARD | Aliases: DEFECTIVE ANTHER DEHISCENCE 1, F16B22.45	2.8	2.8	-0.1	-0.4	100.0%	-1.6
18801	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	2.6	2.7	-0.0	-0.4	100.0%	-2.2
18802	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	2.9	-0.0	-0.4	100.0%	-2.0
18803	AT3G43150.1 | hypothetical protein | chr3:15154683-15155333 FORWARD | Aliases: T6L19.10	2.3	2.4	-0.0	-0.4	100.0%	-2.0
18804	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	5.3	5.4	-0.2	-0.4	100.0%	-1.4
18805	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	2.8	2.8	-0.0	-0.4	100.0%	-2.4
18806	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	4.0	4.1	-0.1	-0.4	100.0%	-1.7
18807	AT1G10420.1 | expressed protein | chr1:3426978-3427458 REVERSE | Aliases: T10O24.3, T10O24_3	3.0	3.1	-0.0	-0.4	100.0%	-1.9
18808	AT1G15080.1 | Symbol: ATPAP2 |	4.2	4.3	-0.1	-0.4	100.0%	-1.7
18809	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	2.8	2.8	0.0	0.4	100.0%	-2.3
18810	AT1G19650.1 | SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative, similar to SP:P24859 from (Kluyveromyces lactissimilar to phosphatidylinositol transfer-like protein IV (GI:14486707) (Lotus japonicus); contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus	3.6	3.7	-0.1	-0.4	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
18811	AT2G14630.1 | hypothetical protein, contains Pfam profile PF03004: Plant transposase (Ptta/En/Spm family) | chr2:6259574-6260493 REVERSE | Aliases: T6B13.13, T6B13_13	2.4	2.4	-0.0	-0.4	100.0%	-2.5
18812	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	-0.1	-0.4	100.0%	-1.8
18813	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	7.0	6.9	0.1	0.4	100.0%	-1.3
18814	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	3.6	3.6	-0.1	-0.4	100.0%	-1.7
18815	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	-0.4	100.0%	-2.5
18816	AT1G60560.2 | SWIM zinc finger family protein, contains Pfam domain PF04434: SWIM zinc finger | chr1:22312214-22315015 REVERSE | Aliases: F8A5.10, F8A5_10	4.1	4.0	0.2	0.4	100.0%	-1.2
18817	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	-0.0	-0.4	100.0%	-2.4
18818	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%	-1.8
18819	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)	7.9	8.4	-0.4	-0.4	100.0%	-0.9
18820	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	6.9	6.7	0.2	0.4	100.0%	-1.3
18821	AT3G60110.1 | DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487 | chr3:22208802-22212426 FORWARD | Aliases: T2O9.90	4.2	4.3	-0.1	-0.4	100.0%	-1.7
18822	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	3.0	-0.0	-0.4	100.0%	-1.9
18823	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	0.1	0.4	100.0%	-1.7
18824	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	5.3	5.2	0.1	0.4	100.0%	-1.6
18825	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	6.3	6.4	-0.1	-0.4	100.0%	-1.3
18826	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	3.0	3.1	-0.1	-0.4	100.0%	-1.9
18827	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	3.4	3.4	-0.1	-0.4	100.0%	-1.7
18828	AT2G13660.1 | expressed protein | chr2:5699179-5700098 REVERSE | Aliases: T10F5.25	2.7	2.6	0.0	0.4	100.0%	-2.2
18829	AT5G59305.1 | expressed protein | chr5:23940428-23941128 FORWARD | Aliases: None	2.7	2.8	-0.1	-0.4	100.0%	-2.1
18830	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	6.2	6.3	-0.1	-0.4	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
18831	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	3.2	3.3	-0.1	-0.4	100.0%	-1.7
18832	AT3G18640.1 | zinc finger protein-related, contains similarity to zinc finger proteins (CCCH type) | chr3:6413623-6415835 REVERSE | Aliases: K24M9.13	4.2	4.3	-0.1	-0.4	100.0%	-1.2
18833	AT2G41200.1 | expressed protein | chr2:17178704-17180208 FORWARD | Aliases: T3K9.3, T3K9_3	3.7	3.7	0.1	0.4	100.0%	-1.4
18834	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	2.6	2.6	-0.0	-0.4	100.0%	-2.1
18835	AT1G35500.1 | expressed protein | chr1:13066065-13066574 FORWARD | Aliases: F12A4.10, F12A4_10	3.3	3.4	-0.1	-0.4	100.0%	-1.7
18836	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	6.1	6.0	0.1	0.4	100.0%	-1.5
18837	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)	2.7	2.8	-0.1	-0.4	100.0%	-1.2
18838	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	9.1	8.8	0.3	0.4	100.0%	-1.2
18839	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	3.8	3.9	-0.1	-0.4	100.0%	-1.3
18840	AT4G24000.1 | Symbol: ATCSLG2 | cellulose synthase family protein, similar to cellulose synthase from Gossypium hirsutum (gi:1706956), cellulose synthase-5 from Zea mays (gi:9622882) | chr4:12462040-12465634 FORWARD | Aliases: CSLG2, T32A16.170, T32A16_170	2.4	2.3	0.0	0.4	100.0%	-2.1
18841	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	2.6	-0.1	-0.4	100.0%	-2.1
18842	AT3G10020.1 | expressed protein | chr3:3091048-3091771 REVERSE | Aliases: T22K18.16	8.5	8.6	-0.1	-0.4	100.0%	-1.6
18843	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	3.4	3.4	0.0	0.4	100.0%	-2.1
18844	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	6.6	6.8	-0.2	-0.4	100.0%	-1.1
18845	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	3.3	3.4	-0.1	-0.4	100.0%	-1.3
18846	NA	10.5	10.2	0.2	0.4	100.0%	-1.4
18847	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	9.3	-0.2	-0.4	100.0%	-1.2
18848	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	8.0	7.7	0.2	0.4	100.0%	-1.2
18849	AT3G14395.1 | expressed protein | chr3:4810930-4811486 FORWARD | Aliases: None	3.3	3.3	0.0	0.4	100.0%	-2.1
18850	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 Mus musculus (SP:Q10470), Rattus norvegicus (SP:Q02527), Homo sapiens (SP:Q09327); contains Pfam profile PF04724 :Glycosyltransferase family 17 | chr1:4433638-4436068 FORWARD | Aliases: F3F19.2, F3F19_2	3.1	3.0	0.1	0.4	100.0%	-1.8
18851	AT3G54500.2 | expressed protein | chr3:20186382-20189958 REVERSE | Aliases: T14E10.70	4.5	4.4	0.1	0.4	100.0%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
18852	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	6.4	-0.1	-0.4	100.0%	-1.4
18853	AT3G54540.1 | Symbol: ATGCN4 |	8.7	8.8	-0.1	-0.4	100.0%	-1.5
18854	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	-0.1	-0.4	100.0%	-2.1
18855	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	5.0	5.1	-0.1	-0.4	100.0%	-1.5
18856	AT5G02630.1 | expressed protein | chr5:591769-593185 FORWARD | Aliases: T22P11.220, T22P11_220	4.2	4.1	0.1	0.4	100.0%	-1.6
18857	AT4G12380.1 | expressed protein | chr4:7333508-7334466 REVERSE | Aliases: T1P17.1	2.8	2.9	-0.1	-0.4	100.0%	-1.8
18858	AT3G62710.1 | glycosyl hydrolase family 3 protein, exhydrolase II - Zea mays, EMBL:AF064707 | chr3:23208634-23211611 REVERSE | Aliases: F26K9.140	2.6	2.6	-0.0	-0.4	100.0%	-2.0
18859	AT2G15670.1 | hypothetical protein | chr2:6835215-6836703 FORWARD | Aliases: F9O13.22	2.5	2.6	-0.1	-0.4	100.0%	-2.2
18860	AT2G32310.1 | expressed protein | chr2:13731746-13733451 FORWARD | Aliases: T32F6.17, T32F6_17	2.8	2.8	0.1	0.4	100.0%	-2.0
18861	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	2.7	2.7	0.0	0.4	100.0%	-2.0
18862	AT3G29796.1 | hypothetical protein | chr3:11711040-11715507 FORWARD | Aliases: K17E7.8	2.9	3.0	-0.1	-0.4	100.0%	-1.7
18863	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	6.3	6.4	-0.2	-0.4	100.0%	-1.4
18864	AT1G52620.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:19607479-19609955 FORWARD | Aliases: F6D8.16, F6D8_16	3.0	3.0	0.1	0.4	100.0%	-1.8
18865	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	8.7	8.5	0.1	0.4	100.0%	-1.3
18866	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)-tetraphosphatase (InterPro:IPR006186) | chr5:23896563-23898855 FORWARD | Aliases: MNC17.9, MNC17_9, PPO	9.3	9.2	0.2	0.4	100.0%	-1.6
18867	AT2G34410.3 | similar to O-acetyltransferase-related [Arabidopsis thaliana] (TAIR:At5g46340.1); similar to acetyltransferase-related [Arabidopsis thaliana] (TAIR:At1g29890.1); similar to OSJNBb0035I14.15 [Oryza sativa (japonica cultivar-group)] (GB:NP_917822.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_475947.1) | chr2:14525485-14530648 FORWARD | Aliases: F13P17.23	3.6	3.5	0.1	0.4	100.0%	-1.5
18868	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	5.8	0.1	0.4	100.0%	-1.4
18869	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	3.9	3.9	0.1	0.4	100.0%	-1.8
18870	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	-0.1	-0.4	100.0%	-1.9
18871	AT5G37840.1 | expressed protein, predicted proteins, Arabidopsis thaliana | chr5:15079238-15080557 REVERSE | Aliases: K22F20.80, K22F20_80	2.9	2.8	0.1	0.4	100.0%	-1.9
18872	AT5G64420.1 | DNA polymerase V family, contains Pfam domain PF04931: DNA polymerase V | chr5:25773558-25778567 FORWARD | Aliases: MSJ1.26, MSJ1_26	5.9	5.8	0.1	0.4	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
18873	AT3G57830.1 | leucine-rich repeat transmembrane protein kinase, putative, several receptor-like protein kinases | chr3:21430494-21433523 FORWARD | Aliases: T10K17.40	2.6	2.6	-0.0	-0.4	100.0%	-2.1
18874	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	2.4	2.4	0.0	0.4	100.0%	-2.6
18875	AT5G55660.1 | expressed protein, similar to unknown protein (pir::T08929) | chr5:22556601-22560700 FORWARD | Aliases: MDF20.10, MDF20_10	5.9	5.7	0.2	0.4	100.0%	-1.2
18876	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 eculentum, PIR:T07182 | chr3:20958086-20958710 REVERSE | Aliases: T5P19.170	2.4	2.4	-0.0	-0.4	100.0%	-2.4
18877	AT5G48350.1 | expressed protein | chr5:19610792-19611391 FORWARD | Aliases: K23F3.7, K23F3_7	2.5	2.4	0.1	0.4	100.0%	-2.2
18878	AT1G04660.1 | glycine-rich protein | chr1:1300485-1301772 REVERSE | Aliases: T1G11.8, T1G11_8	6.5	6.6	-0.1	-0.4	100.0%	-1.7
18879	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	6.2	0.1	0.4	100.0%	-1.6
18880	AT5G03120.1 | expressed protein | chr5:733978-734942 FORWARD | Aliases: F15A17.150, F15A17_150	3.4	3.4	0.1	0.4	100.0%	-1.8
18881	AT1G32460.1 | expressed protein | chr1:11738190-11739306 FORWARD | Aliases: F5D14.24, F5D14_24	10.8	10.9	-0.1	-0.4	100.0%	-1.7
18882	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	-0.4	100.0%	-2.3
18883	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	3.5	3.4	0.0	0.4	100.0%	-2.0
18884	AT3G48640.1 | expressed protein | chr3:18032635-18033309 REVERSE | Aliases: T8P19.150	3.0	3.1	-0.1	-0.4	100.0%	-2.1
18885	AT2G02590.1 | expressed protein | chr2:704936-706667 FORWARD | Aliases: T8K22.11, T8K22_11	4.4	4.3	0.1	0.4	100.0%	-1.8
18886	AT1G61090.1 | expressed protein | chr1:22503196-22506141 REVERSE | Aliases: T7P1.22	2.7	2.7	-0.0	-0.4	100.0%	-2.1
18887	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	6.5	0.2	0.4	100.0%	-1.1
18888	AT3G10830.1 | hypothetical protein | chr3:3390255-3390698 FORWARD | Aliases: T7M13.9	2.2	2.2	-0.0	-0.4	100.0%	-2.4
18889	AT1G16950.1 | expressed protein | chr1:5796002-5796552 FORWARD | Aliases: F17F16.23	2.4	2.5	-0.0	-0.4	100.0%	-2.2
18890	AT5G07960.1 | expressed protein, contains Pfam PF03669: Uncharacterised protein family (UPF0139) | chr5:2542247-2543460 FORWARD | Aliases: F13G24.160	6.6	6.5	0.1	0.4	100.0%	-1.6
18891	AT2G41990.1 | expressed protein | chr2:17534335-17536015 FORWARD | Aliases: T6D20.12, T6D20_12	2.4	2.3	0.0	0.4	100.0%	-2.1
18892	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	9.1	9.3	-0.2	-0.4	100.0%	-1.2
18893	AT2G12480.2 | Symbol: SCPL43 |	3.6	3.7	-0.1	-0.4	100.0%	-1.8
18894	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	3.2	0.1	0.4	100.0%	-1.8
18895	AT2G38370.1 | expressed protein | chr2:16079148-16081269 REVERSE | Aliases: T19C21.14, T19C21_14	7.3	7.5	-0.2	-0.4	100.0%	-1.5
18896	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	2.2	-0.0	-0.4	100.0%	-2.5

Rank	Description	Sync	Root	M	t	adj.q	B
18897	AT4G38840.1 | auxin-responsive protein, putative, auxin-inducible SAUR gene, Raphanus sativus,AB000708	2.8	2.8	0.1	0.4	100.0%	-1.7
18898	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	0.4	100.0%	-2.4
18899	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	-0.4	100.0%	-2.3
18900	AT4G11790.1 | Ran-binding protein 1 domain-containing protein / RanBP1 domain-containing protein, contains Pfam profile PF00638: RanBP1 domain	4.3	4.4	-0.1	-0.4	100.0%	-1.6
18901	AT3G42920.1 | expressed protein, predicted proteins, Arabidopsis thaliana | chr3:14997907-14998416 REVERSE | Aliases: F18P9.80	3.4	3.5	-0.1	-0.4	100.0%	-1.8
18902	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	3.2	3.1	0.1	0.4	100.0%	-1.7
18903	AT2G13430.1 | expressed protein | chr2:5597134-5598504 FORWARD | Aliases: T26C18.2, T26C18_2	2.6	2.6	-0.0	-0.4	100.0%	-2.1
18904	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	3.1	3.1	0.1	0.4	100.0%	-1.8
18905	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	-0.4	100.0%	-2.3
18906	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	6.8	6.9	-0.1	-0.4	100.0%	-1.3
18907	AT4G17483.1 | palmitoyl protein thioesterase family protein | chr4:9747356-9748904 REVERSE | Aliases: FCAALL.16	4.5	4.4	0.1	0.4	100.0%	-1.6
18908	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	3.0	3.1	-0.1	-0.4	100.0%	-1.8
18909	AT1G20220.1 | expressed protein | chr1:7004889-7007640 REVERSE | Aliases: T20H2.2, T20H2_2	6.1	6.0	0.1	0.4	100.0%	-1.4
18910	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	2.8	2.9	-0.1	-0.4	100.0%	-1.9
18911	AT1G12050.1 | fumarylacetoacetase, putative, similar to fumarylacetoacetase (Fumarylacetoacetate hydrolase, Beta-diketonase, FAA)(Rattus norvegicus) SWISS-PROT:P25093	7.4	7.3	0.1	0.4	100.0%	-1.4
18912	AT5G17180.1 | expressed protein | chr5:5651438-5651809 FORWARD | Aliases: MKP11.3, MKP11_3	3.3	3.4	-0.1	-0.4	100.0%	-1.9
18913	AT3G54290.1 | expressed protein, contains Pfam PF03794: Domain of Unknown function | chr3:20115377-20117022 REVERSE | Aliases: F24B22.250	7.6	7.5	0.1	0.4	100.0%	-1.7
18914	AT4G05630.1 | expressed protein | chr4:2988445-2988819 REVERSE | Aliases: F21I2.20, F21I2_20	2.8	2.9	-0.1	-0.4	100.0%	-1.9
18915	AT1G66120.1 | acyl-activating enzyme 11 (AAE11), similar to AMP-binding protein GI:1903034 from (Brassica napus); contains Pfam AMP-binding domain PF00501; identical to cDNA acyl-activating enzyme 11 (At1g66120) GI:29893230, acyl-activating enzyme 11 (Arabidopsis thaliana) GI:29893231 | chr1:24616284-24618468 FORWARD | Aliases: F15E12.22, F15E12_22	3.6	3.7	-0.1	-0.4	100.0%	-1.4
18916	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%	-1.5
18917	AT4G22330.1 | Symbol: ATCES1 |	5.3	5.2	0.2	0.4	100.0%	-1.4
18918	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	0.4	100.0%	-2.2
18919	AT3G60450.1 | expressed protein | chr3:22351940-22353285 FORWARD | Aliases: T8B10.110	9.8	9.6	0.2	0.4	100.0%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
18920	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	4.9	0.2	0.4	100.0%	-1.3
18921	AT1G02540.1 | expressed protein | chr1:534827-535699 REVERSE | Aliases: T14P4.13, T14P4_13	2.6	2.7	-0.0	-0.4	100.0%	-2.1
18922	AT1G09240.1 | nicotianamine synthase, putative, similar to nicotianamine synthase (Lycopersicon esculentum)(GI:4753801), nicotianamine synthase 2 (Hordeum vulgare)(GI:4894912) | chr1:2984883-2986132 FORWARD | Aliases: T12M4.5, T12M4_5	3.2	3.2	-0.1	-0.4	100.0%	-1.8
18923	AT3G50420.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:18721852-18724630 REVERSE | Aliases: T20E23.20	2.8	2.8	-0.1	-0.4	100.0%	-1.8
18924	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	6.7	0.1	0.4	100.0%	-1.3
18925	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	8.1	8.0	0.1	0.4	100.0%	-1.6
18926	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	3.1	3.0	0.1	0.4	100.0%	-1.5
18927	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	-0.0	-0.4	100.0%	-2.5
18928	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	4.2	0.1	0.4	100.0%	-1.6
18929	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	3.3	3.2	0.0	0.4	100.0%	-1.8
18930	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	3.7	0.1	0.4	100.0%	-1.6
18931	AT5G20860.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:7076892-7079079 REVERSE | Aliases: F22D1.30, F22D1_30	2.8	2.9	-0.0	-0.4	100.0%	-2.1
18932	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	3.0	3.1	-0.0	-0.4	100.0%	-2.0
18933	AT5G16850.1 | Symbol: ATTERT |	2.5	2.6	-0.0	-0.4	100.0%	-2.2
18934	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	9.8	9.7	0.1	0.4	100.0%	-1.8
18935	AT5G23890.1 | expressed protein, weak similarity to SP:P12957 Caldesmon (CDM) {Gallus gallus} | chr5:8058694-8063204 FORWARD | Aliases: MRO11.7, MRO11_7	6.6	6.7	-0.1	-0.4	100.0%	-1.7
18936	AT5G66740.1 | hypothetical protein, contains Pfam profile PF04788: Protein of unknown function (DUF620) | chr5:26664956-26665784 FORWARD | Aliases: MSN2.13, MSN2_13	3.0	3.0	-0.0	-0.4	100.0%	-2.2
18937	AT4G14720.1 | expressed protein | chr4:8431968-8435070 REVERSE | Aliases: DL3400C, FCAALL.297	5.8	6.0	-0.2	-0.4	100.0%	-1.3
18938	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	3.0	0.0	0.4	100.0%	-1.9
18939	AT1G06750.1 | expressed protein | chr1:2074029-2076349 FORWARD | Aliases: F4H5.16, F4H5_16	2.6	2.5	0.0	0.4	100.0%	-2.3
18940	AT5G11950.2 | expressed protein, contains Pfam profile PF03641: decarboxylase family protein | chr5:3854917-3856977 FORWARD | Aliases: F14F18.120, F14F18_120	7.6	7.5	0.1	0.4	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
18941	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	-0.1	-0.4	100.0%	-1.7
18942	AT4G25680.1 | expressed protein | chr4:13088249-13090170 FORWARD | Aliases: L73G19.60, L73G19_60	6.7	7.0	-0.2	-0.4	100.0%	-1.3
18943	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	3.0	2.9	0.0	0.4	100.0%	-2.0
18944	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	2.7	2.8	-0.0	-0.4	100.0%	-1.9
18945	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	0.4	100.0%	-1.3
18946	NA	2.2	2.2	-0.0	-0.4	100.0%	-2.4
18947	AT3G59130.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.9	2.9	-0.0	-0.4	100.0%	-2.1
18948	AT5G06830.1 | expressed protein, contains Pfam profile: PF05600 protein of unknown function (DUF773) | chr5:2116784-2119630 REVERSE | Aliases: MPH15.20, MPH15_20	4.9	4.9	0.1	0.4	100.0%	-1.7
18949	AT4G01130.1 | acetylesterase, putative, similar to lanatoside 15'-O-acetylesterase (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	-0.4	100.0%	-2.4
18950	AT1G37080.1 | expressed protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana) | chr1:14113899-14114696 REVERSE | Aliases: F28L22.13, F28L22_13	2.8	2.7	0.0	0.4	100.0%	-2.2
18951	AT5G55650.1 | hypothetical protein | chr5:22553586-22554050 FORWARD | Aliases: MDF20.9, MDF20_9	3.8	3.9	-0.1	-0.4	100.0%	-1.8
18952	AT4G32880.1 | Symbol: ATHB 8 |	6.0	6.1	-0.1	-0.4	100.0%	-1.3
18953	AT4G00231.1 | ataxin-related, contains weak similarity to Ataxin-10 (Spinocerebellar ataxia type 10 protein) (Brain protein E46 homolog) (Swiss-Prot:Q9UBB4) (Homo sapiens) | chr4:97499-99353 FORWARD | Aliases: None	4.6	4.5	0.1	0.4	100.0%	-1.5
18954	AT2G18270.1 | expressed protein | chr2:7953240-7953488 REVERSE | Aliases: T30D6.22, T30D6_22	3.2	3.2	-0.1	-0.4	100.0%	-2.0
18955	AT1G16760.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:5734227-5737300 FORWARD | Aliases: F19K19.25	2.3	2.2	0.0	0.4	100.0%	-2.5
18956	AT5G48370.1 | thioesterase family protein, similar to SP:Q9R0X4 48 kDa acyl-CoA thioester hydrolase, mitochondrial precursor (EC 3.1.2.-) {Mus musculus}; contains Pfam profile PF03061: thioesterase family protein | chr5:19615754-19617810 REVERSE | Aliases: K23F3.9, K23F3_9	6.6	6.4	0.2	0.4	100.0%	-1.2
18957	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	10.8	0.1	0.4	100.0%	-1.6
18958	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	2.8	-0.1	-0.4	100.0%	-1.8
18959	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	3.1	-0.1	-0.4	100.0%	-1.9
18960	AT3G56590.1 | hydroxyproline-rich glycoprotein family protein | chr3:20975888-20978654 FORWARD | Aliases: None	4.8	4.8	0.1	0.4	100.0%	-1.4
18961	AT4G28950.1 | Symbol: ARAC7 | Rac-like GTP-binding protein (ARAC7), identical to rac GTP binding protein Arac7 GI:3702962 from (Arabidopsis thaliana)	3.6	3.7	-0.1	-0.4	100.0%	-1.9
18962	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	4.1	4.1	-0.1	-0.4	100.0%	-1.4
18963	AT1G29060.1 | expressed protein | chr1:10147679-10149667 FORWARD | Aliases: F28N24.23, F28N24_23	5.3	5.2	0.1	0.4	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
18964	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	2.3	-0.0	-0.4	100.0%	-2.5
18965	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	-0.0	-0.4	100.0%	-2.3
18966	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	3.8	3.9	-0.1	-0.4	100.0%	-1.7
18967	AT4G20080.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr4:10865305-10867629 FORWARD | Aliases: F18F4.180, F18F4_180	2.6	2.7	-0.1	-0.4	100.0%	-2.0
18968	AT4G14430.1 | enoyl-CoA hydratase/isomerase family protein, low siimilarity 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	7.2	7.2	0.1	0.4	100.0%	-1.6
18969	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	-0.4	100.0%	-1.8
18970	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	3.8	3.9	-0.1	-0.4	100.0%	-1.5
18971	AT4G05370.1 | expressed protein | chr4:2736132-2736581 FORWARD | Aliases: C6L9.50, C6L9_50	2.3	2.2	0.0	0.4	100.0%	-2.3
18972	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	5.8	5.8	0.1	0.4	100.0%	-1.6
18973	AT2G19510.1 | LOB domain family protein / lateral organ boundaries domain family protein (LBD8), identical to SP:Q9ZUP0: Putative LOB domain protein 8 {Arabidopsis thaliana}; similar to lateral organ boundaries (LOB) domain-containing proteins from Arabidopsis thaliana; identical to ASYMMETRIC LEAVES2-like protein 34 (Arabidopsis thaliana) GI:19919039 | chr2:8460312-8460758 FORWARD | Aliases: F3P11.11, F3P11_11	2.7	2.7	-0.0	-0.4	100.0%	-2.2
18974	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	8.8	-0.1	-0.4	100.0%	-1.5
18975	AT3G20190.1 | leucine-rich repeat transmembrane protein kinase, putative, similar to receptor kinase GB:AAA33715 (Petunia integrifolia) | chr3:7044950-7047396 FORWARD | Aliases: MAL21.23	3.2	3.1	0.0	0.4	100.0%	-2.0
18976	AT2G26120.1 | glycine-rich protein | chr2:11130508-11130895 FORWARD | Aliases: T19L18.7, T19L18_7	4.8	4.9	-0.1	-0.4	100.0%	-1.2
18977	AT3G46070.1 | zinc finger (C2H2 type) family protein, contains zinc finger, C2H2 type, domain, PROSITE:PS00028	3.2	3.2	-0.1	-0.4	100.0%	-1.8
18978	AT3G42120.1 | expressed protein | chr3:14306707-14307936 FORWARD | Aliases: F4M19.80	2.5	2.4	0.0	0.4	100.0%	-2.5
18979	AT1G61920.1 | expressed protein | chr1:22892122-22892433 FORWARD | Aliases: F8K4.11, F8K4_11	7.1	7.3	-0.1	-0.4	100.0%	-1.4
18980	AT1G71940.1 | expressed protein | chr1:27082242-27083892 FORWARD | Aliases: F17M19.9, F17M19_9	6.0	6.1	-0.1	-0.4	100.0%	-1.4
18981	AT1G48310.1 | SNF2 domain-containing protein / helicase domain-containing protein, contains similarity to DNA-dependent ATPase A GI:6651385 from (Bos taurus)}; contains PFam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 | chr1:17851314-17857475 REVERSE | Aliases: F11A17.14, F11A17_14	4.6	4.5	0.1	0.4	100.0%	-1.4
18982	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	0.1	0.4	100.0%	-2.0
18983	AT5G51580.1 | expressed protein | chr5:20969668-20970619 REVERSE | Aliases: K17N15.13, K17N15_13	2.8	2.8	-0.0	-0.4	100.0%	-2.3
18984	AT3G43670.1 | copper amine oxidase, putative, similar to copper amine oxidase (Cicer arietinum) gi:3819099:emb:CAA08855 | chr3:15578087-15580889 FORWARD | Aliases: F23N14.50	6.8	6.6	0.2	0.4	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
18985	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 scienitific 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	4.6	0.1	0.4	100.0%	-1.8
18986	AT2G43180.4 | expressed protein | chr2:17960020-17962875 REVERSE | Aliases: F14B2.12	3.5	3.6	-0.1	-0.4	100.0%	-1.3
18987	AT5G58190.2 | expressed protein, contains Pfam profile PF04146: YT521-B-like family | chr5:23563599-23566775 FORWARD | Aliases: MCK7.6, MCK7_6	5.9	5.8	0.1	0.4	100.0%	-1.3
18988	AT5G43720.1 | expressed protein | chr5:17574393-17576581 REVERSE | Aliases: MQD19.5, MQD19_5	4.8	4.7	0.1	0.4	100.0%	-1.6
18989	AT4G37240.1 | expressed protein | chr4:17524455-17525153 FORWARD | Aliases: AP22.53, AP22_53	4.6	4.7	-0.1	-0.4	100.0%	-1.2
18990	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	3.4	-0.1	-0.4	100.0%	-1.7
18991	AT4G00440.1 | expressed protein | chr4:193879-198579 FORWARD | Aliases: A_IG005I10.23, A_IG005I10_23, F5I10.23, F5I10_23	4.2	4.3	-0.1	-0.4	100.0%	-1.7
18992	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	3.2	3.2	-0.0	-0.4	100.0%	-2.0
18993	AT4G14640.1 | Symbol: CAM8 | calmodulin-8 (CAM8), identical to calmodulin 8 GI:5825600 from (Arabidopsis thaliana) | chr4:8397764-8400069 FORWARD | Aliases: CALMODULIN 8, DL3360W, FCAALL.157	2.5	2.5	-0.0	-0.4	100.0%	-2.6
18994	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	-0.0	-0.4	100.0%	-2.3
18995	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	2.9	3.0	-0.1	-0.4	100.0%	-1.7
18996	AT3G60800.1 | zinc finger (DHHC type) family protein, contains DHHC zinc finger domain PF01529	6.5	6.7	-0.2	-0.4	100.0%	-1.3
18997	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	3.9	-0.1	-0.4	100.0%	-1.0
18998	AT1G04120.1 | Symbol: ATMRP5 |	9.7	9.6	0.1	0.4	100.0%	-1.4
18999	AT5G03345.1 | expressed protein | chr5:814122-815618 FORWARD | Aliases: None	10.4	10.4	-0.1	-0.4	100.0%	-1.9
19000	AT4G35870.1 | expressed protein | chr4:16990176-16992891 FORWARD | Aliases: F4B14.140, F4B14_140	4.4	4.5	-0.1	-0.4	100.0%	-1.2
19001	AT1G72450.1 | expressed protein | chr1:27277727-27279950 REVERSE | Aliases: T10D10.8, T10D10_8	6.3	6.4	-0.1	-0.4	100.0%	-1.5
19002	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	7.2	7.4	-0.2	-0.4	100.0%	-1.2
19003	AT3G60630.1 | scarecrow transcription factor family protein, scarecrow-like 6, Arabidopsis thaliana, EMBL:AF036303 | chr3:22421340-22423583 REVERSE | Aliases: T4C21.40	5.1	5.2	-0.1	-0.4	100.0%	-1.2
19004	AT5G13190.1 | expressed protein | chr5:4204820-4206408 REVERSE | Aliases: T19L5.5	9.1	9.1	-0.1	-0.4	100.0%	-1.4
19005	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	2.6	2.5	0.0	0.4	100.0%	-2.1
19006	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	-0.4	100.0%	-2.2
19007	AT5G36080.1 | hypothetical protein | chr5:14201653-14202507 FORWARD | Aliases: MAB16.2, MAB16_2	2.5	2.6	-0.0	-0.4	100.0%	-2.4

Rank	Description	Sync	Root	M	t	adj.q	B
19008	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	3.3	-0.1	-0.4	100.0%	-1.5
19009	AT2G47570.1 | 60S ribosomal protein L18 (RPL18A) | chr2:19522968-19523787 REVERSE | Aliases: T30B22.13	2.9	2.9	0.1	0.4	100.0%	-1.7
19010	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	3.0	3.1	-0.1	-0.4	100.0%	-1.8
19011	AT1G33070.1 | hypothetical protein | chr1:11982869-11985279 FORWARD | Aliases: T9L6.11, T9L6_11	2.3	2.2	0.0	0.4	100.0%	-2.3
19012	AT4G12750.1 | expressed protein | chr4:7497811-7503640 REVERSE | Aliases: T20K18.100, T20K18_100	4.6	4.7	-0.1	-0.4	100.0%	-1.5
19013	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	6.1	6.0	0.1	0.4	100.0%	-1.3
19014	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	3.3	3.3	0.1	0.4	100.0%	-1.6
19015	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	-0.4	100.0%	-1.5
19016	AT3G42600.1 | hypothetical protein | chr3:14708749-14709408 FORWARD | Aliases: T12K4.50	2.7	2.8	-0.0	-0.4	100.0%	-2.6
19017	AT4G25870.1 | expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266 | chr4:13149700-13152286 REVERSE | Aliases: F14M19.150, F14M19_150	7.3	7.4	-0.0	-0.4	100.0%	-1.9
19018	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	2.6	-0.0	-0.4	100.0%	-2.1
19019	AT4G21950.1 | expressed protein | chr4:11644230-11644617 FORWARD | Aliases: F1N20.4	2.9	2.9	-0.0	-0.4	100.0%	-2.1
19020	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	0.4	100.0%	-2.0
19021	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	8.8	8.7	0.1	0.4	100.0%	-1.4
19022	AT1G36240.1 | 60S ribosomal protein L30 (RPL30A), similar to GI:6984132 from (Euphorbia esula)	2.9	2.8	0.1	0.4	100.0%	-1.8
19023	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	2.7	2.7	0.0	0.4	100.0%	-2.1
19024	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	6.4	0.2	0.4	100.0%	-1.6
19025	AT3G45830.1 | expressed protein | chr3:16852262-16856526 FORWARD | Aliases: F16L2.40	6.4	6.5	-0.1	-0.4	100.0%	-1.7
19026	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	5.0	4.8	0.2	0.4	100.0%	-1.2
19027	AT1G32800.1 | PHD finger protein-related, contains low similarity to PHD-finger domain proteins | chr1:11881790-11883073 FORWARD | Aliases: F9L11.28	4.4	4.3	0.1	0.4	100.0%	-1.4
19028	AT2G47880.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	2.7	2.8	-0.1	-0.4	100.0%	-1.7
19029	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	5.3	5.4	-0.1	-0.4	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
19030	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	3.5	3.4	0.1	0.4	100.0%	-1.6
19031	AT3G18350.1 | expressed protein, contains Pfam profile: PF04842 plant protein of unknown function (DUF639) | chr3:6296856-6300679 FORWARD | Aliases: MYF24.7	5.5	5.6	-0.1	-0.4	100.0%	-1.3
19032	AT1G28280.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr1:9886064-9887465 REVERSE | Aliases: F3H9.7, F3H9_7	4.8	4.8	-0.1	-0.4	100.0%	-1.5
19033	AT2G33870.1 | Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303742 from (Pisum sativum)	2.3	2.3	0.0	0.4	100.0%	-2.4
19034	AT2G12170.1 | expressed protein | chr2:4897274-4898273 REVERSE | Aliases: F23M2.37	3.1	3.0	0.1	0.4	100.0%	-2.0
19035	AT3G23410.1 | alcohol oxidase-related, similar to long chain fatty alcohol oxidase from Candida cloacae (GI:6983581), Candida tropicalis (GI:6983594) | chr3:8382818-8386155 FORWARD | Aliases: MLM24.14	6.3	6.5	-0.1	-0.4	100.0%	-1.3
19036	AT5G02440.1 | expressed protein | chr5:531064-532723 FORWARD | Aliases: T22P11.30, T22P11_30	3.3	3.4	-0.1	-0.4	100.0%	-1.7
19037	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	-0.4	100.0%	-2.1
19038	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	3.9	-0.0	-0.4	100.0%	-2.0
19039	AT3G12200.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	7.4	7.5	-0.1	-0.4	100.0%	-1.3
19040	AT5G42700.1 | transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain | chr5:17139399-17141581 FORWARD | Aliases: MJB21.7, MJB21_7	2.5	2.5	-0.0	-0.4	100.0%	-2.1
19041	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	6.9	-0.1	-0.4	100.0%	-1.6
19042	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	2.9	0.1	0.4	100.0%	-2.2
19043	AT1G73510.1 | expressed protein | chr1:27646312-27646779 REVERSE | Aliases: T9L24.31, T9L24_31	2.5	2.4	0.0	0.4	100.0%	-2.2
19044	AT4G31400.1 | expressed protein | chr4:15237417-15239062 FORWARD | Aliases: F3L17.7	3.5	3.4	0.1	0.4	100.0%	-1.5
19045	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	6.2	6.1	0.1	0.4	100.0%	-1.2
19046	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	3.2	3.1	0.1	0.4	100.0%	-1.6
19047	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	-0.4	100.0%	-2.3
19048	AT5G58570.1 | expressed protein | chr5:23689929-23690513 REVERSE | Aliases: MZN1.2, MZN1_2	2.5	2.4	0.0	0.4	100.0%	-2.2
19049	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	8.1	7.9	0.2	0.4	100.0%	-1.2
19050	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	2.6	2.6	-0.0	-0.4	100.0%	-2.0
19051	AT3G14610.1 | Symbol: CYP72A7 | cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus) | chr3:4912473-4914659 FORWARD | Aliases: MIE1.11	7.8	7.7	0.1	0.4	100.0%	-1.4
19052	AT5G11220.1 | expressed protein | chr5:3577058-3577979 FORWARD | Aliases: F2I11.110, F2I11_110	2.3	2.3	-0.0	-0.4	100.0%	-2.6

Rank	Description	Sync	Root	M	t	adj.q	B
19053	AT3G58210.1 | 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 | chr3:21573419-21575044 REVERSE | Aliases: F9D24.120	2.6	2.6	0.0	0.4	100.0%	-2.5
19054	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	2.9	0.1	0.4	100.0%	-1.9
19055	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	2.7	-0.0	-0.4	100.0%	-2.3
19056	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	4.5	4.4	0.1	0.4	100.0%	-1.6
19057	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	4.3	4.2	0.1	0.4	100.0%	-1.3
19058	AT5G28420.1 | hypothetical protein, predicted proteins - Arabidopsis thaliana | chr5:10364838-10365293 FORWARD | Aliases: F21B23.80, F21B23_80	2.6	2.7	-0.1	-0.4	100.0%	-1.8
19059	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	3.3	3.3	-0.1	-0.4	100.0%	-1.7
19060	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	5.3	-0.1	-0.4	100.0%	-1.4
19061	AT2G28240.1 | hydroxyproline-rich glycoprotein family protein | chr2:12046289-12049220 FORWARD | Aliases: T3B23.9, T3B23_9	4.6	4.5	0.2	0.4	100.0%	-1.6
19062	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	2.7	-0.0	-0.4	100.0%	-2.3
19063	AT2G13360.2 | Symbol: AGT | serine-glyoxylate aminotransferase-related, similar to serine-glyoxylate aminotransferase	3.4	3.5	-0.1	-0.4	100.0%	-1.5
19064	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	4.2	4.1	0.1	0.4	100.0%	-1.7
19065	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	4.6	4.7	-0.1	-0.4	100.0%	-1.6
19066	AT2G24280.1 | serine carboxypeptidase S28 family protein, contains Pfam profile: PF05577 Serine carboxypeptidase S28 | chr2:10340364-10344161 FORWARD | Aliases: F27D4.19, F27D4_19	3.8	3.7	0.1	0.4	100.0%	-1.4
19067	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	3.4	3.4	-0.1	-0.4	100.0%	-1.8
19068	AT1G18830.1 | transducin family protein / WD-40 repeat family protein, similar to Sec31p (GI:13928450)	2.6	2.7	-0.0	-0.4	100.0%	-2.0
19069	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	2.5	2.5	0.0	0.4	100.0%	-2.0
19070	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	-0.4	100.0%	-2.4
19071	AT4G27030.1 | expressed protein | chr4:13571957-13572928 FORWARD | Aliases: F10M23.370, F10M23_370	4.8	5.0	-0.1	-0.4	100.0%	-1.6
19072	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	5.5	5.4	0.1	0.4	100.0%	-1.6
19073	AT3G01780.1 | expressed protein, est hit, | chr3:279067-283554 FORWARD | Aliases: F28J7.11, F28J7_11	8.6	8.7	-0.1	-0.4	100.0%	-1.3
19074	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-sulfhydryl 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	7.4	7.2	0.2	0.4	100.0%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
19075	AT5G41950.1 | expressed protein | chr5:16802942-16806741 FORWARD | Aliases: MJC20.5, MJC20_5	5.4	5.3	0.1	0.4	100.0%	-1.5
19076	AT5G59060.1 | expressed protein, ; expression supported by MPSS | chr5:23861620-23861952 REVERSE | Aliases: K18B18.6, K18B18_6	3.0	3.1	-0.0	-0.4	100.0%	-2.1
19077	AT2G44730.1 | expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189 | chr2:18444408-18445640 REVERSE | Aliases: F16B22.22	6.1	6.3	-0.2	-0.4	100.0%	-1.2
19078	AT3G07950.1 | rhomboid protein-related, contains 6 transmembrane domains; similar to phosphatidyl inositol glycan class T (GI:14456615) (Homo sapiens)	4.5	4.3	0.2	0.4	100.0%	-1.5
19079	AT4G27990.1 | YGGT family protein, contains Pfam profile PF02325: YGGT family (unknown function) | chr4:13923779-13924698 REVERSE | Aliases: T13J8.100, T13J8_100	5.3	5.2	0.1	0.4	100.0%	-1.2
19080	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	0.0	0.4	100.0%	-1.9
19081	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	2.7	0.1	0.4	100.0%	-2.0
19082	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	2.3	2.3	0.0	0.4	100.0%	-2.3
19083	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	3.0	2.9	0.1	0.4	100.0%	-2.0
19084	AT4G30990.1 | expressed protein, ; expression supported by MPSS | chr4:15084691-15095956 FORWARD | Aliases: F6I18.5	2.8	2.8	0.0	0.4	100.0%	-2.2
19085	AT2G32750.1 | exostosin family protein, contains Pfam profile: PF03016 exostosin family | chr2:13896718-13898247 FORWARD | Aliases: F24L7.11, F24L7_11	2.5	2.5	-0.0	-0.4	100.0%	-2.1
19086	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	5.0	0.1	0.4	100.0%	-1.4
19087	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	3.8	3.8	-0.1	-0.4	100.0%	-1.7
19088	AT3G19550.1 | expressed protein | chr3:6787247-6788296 REVERSE | Aliases: T31J18.5	2.7	2.7	-0.0	-0.4	100.0%	-2.3
19089	AT1G23000.1 | heavy-metal-associated domain-containing protein, similar to farnesylated protein ATFP3 (GI:4097547); contains PF00403 Heavy-metal-associated domain | chr1:8143393-8145059 FORWARD | Aliases: F19G10.6, F19G10_6	2.7	2.7	-0.0	-0.4	100.0%	-2.1
19090	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	3.2	3.1	0.1	0.4	100.0%	-1.9
19091	AT5G37640.1 | Symbol: UBQ9 | polyubiquitin (UBQ9), identical to polyubiquitin (ubq9) gene sequence GI:304120 from (Arabidopsis thaliana) | chr5:14970012-14970980 REVERSE | Aliases: K12B20.90, K12B20_90	3.4	3.3	0.0	0.4	100.0%	-2.1
19092	AT5G49640.1 | expressed protein | chr5:20168389-20169068 FORWARD | Aliases: MNI5.2, MNI5_2	2.5	2.6	-0.0	-0.4	100.0%	-2.5
19093	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	3.2	3.1	0.0	0.4	100.0%	-2.2
19094	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	-0.4	100.0%	-2.4
19095	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	3.7	3.8	-0.1	-0.4	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
19096	AT1G22050.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr1:7771659-7773640 FORWARD | Aliases: F2E2.12, F2E2_12	8.3	8.2	0.1	0.4	100.0%	-1.5
19097	AT3G49740.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:18458773-18461079 FORWARD | Aliases: T16K5.90	4.0	4.0	0.1	0.4	100.0%	-1.7
19098	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	2.2	2.2	-0.0	-0.4	100.0%	-2.3
19099	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	3.5	0.1	0.4	100.0%	-1.6
19100	AT4G01100.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr4:477155-479935 FORWARD | Aliases: F2N1.16, F2N1_16	5.8	6.0	-0.2	-0.4	100.0%	-1.5
19101	AT4G31010.2 | expressed protein | chr4:15106650-15108967 FORWARD | Aliases: F6I18.80, F6I18_80	3.6	3.7	-0.1	-0.4	100.0%	-1.5
19102	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	2.9	2.9	-0.1	-0.4	100.0%	-1.8
19103	AT4G12650.1 | endomembrane protein 70, putative, TM4 family; | chr4:7467975-7469787 REVERSE | Aliases: T1P17.240, T1P17_240	7.2	7.0	0.2	0.4	100.0%	-1.5
19104	AT5G22860.2 | serine carboxypeptidase S28 family protein, contains Pfam profile: PF05577 serine carboxypeptidase S28 | chr5:7639855-7642987 REVERSE | Aliases: MRN17.9, MRN17_9	3.9	3.8	0.1	0.4	100.0%	-1.6
19105	AT3G25060.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:9128523-9130328 FORWARD | Aliases: K3G3.8	2.9	2.9	0.1	0.4	100.0%	-1.9
19106	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	5.9	6.1	-0.2	-0.4	100.0%	-1.2
19107	AT1G27510.1 | expressed protein | chr1:9554932-9558280 REVERSE | Aliases: T17H3.1	3.9	3.8	0.1	0.4	100.0%	-1.5
19108	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	2.2	0.0	0.4	100.0%	-2.4
19109	AT1G48940.1 | plastocyanin-like domain-containing protein | chr1:18109476-18110090 REVERSE | Aliases: F27K7.4	2.4	2.5	-0.0	-0.4	100.0%	-2.2
19110	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	2.5	-0.0	-0.4	100.0%	-2.1
19111	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	2.1	2.2	-0.0	-0.4	100.0%	-2.2
19112	AT1G29570.1 | zinc finger protein-related, contains similarity to zinc finger proteins (CCCH type) | chr1:10335896-10337840 FORWARD | Aliases: F15D2.36, F15D2_36	2.8	2.8	0.0	0.4	100.0%	-2.2
19113	AT1G49870.1 | expressed protein, ; expression supported by MPSS | chr1:18464013-18467225 FORWARD | Aliases: F10F5.13, F10F5_13	3.9	3.8	0.1	0.4	100.0%	-1.5
19114	AT2G44820.2 | expressed protein | chr2:18491426-18492885 FORWARD | Aliases: F16B22.34, F16B22_34	8.7	8.4	0.2	0.4	100.0%	-1.6
19115	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	-0.0	-0.4	100.0%	-2.4
19116	AT4G18420.1 | hypothetical protein | chr4:10174422-10174971 REVERSE | Aliases: F28J12.80, F28J12_80	3.9	4.0	-0.1	-0.4	100.0%	-1.1
19117	AT1G78410.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr1:29507475-29508134 FORWARD | Aliases: F3F9.8, F3F9_8	2.8	2.8	-0.0	-0.4	100.0%	-2.3
19118	AT1G58260.1 | Symbol: CYP79C2 | cytochrome P450 family protein, similar to cytochrome P450 GI:984542 from (Sorghum bicolor) | chr1:21609417-21611660 FORWARD | Aliases: CYP79C3P, F19C14.12, F19C14_12	3.7	3.6	0.2	0.4	100.0%	-0.6

Rank	Description	Sync	Root	M	t	adj.q	B
19119	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	4.9	5.0	-0.1	-0.4	100.0%	-1.3
19120	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	0.4	100.0%	-2.5
19121	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	3.9	3.9	0.1	0.4	100.0%	-1.5
19122	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	-0.1	-0.4	100.0%	-1.8
19123	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	-0.1	-0.4	100.0%	-2.2
19124	AT2G42370.1 | expressed protein | chr2:17650412-17652611 FORWARD | Aliases: MHK10.9, MHK10_9	3.9	3.7	0.1	0.4	100.0%	-1.5
19125	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	7.6	7.7	-0.1	-0.4	100.0%	-1.4
19126	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	3.8	-0.1	-0.4	100.0%	-1.6
19127	AT3G02330.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:473888-476599 REVERSE | Aliases: F11A12.2, F11A12_2	3.3	3.2	0.1	0.4	100.0%	-1.8
19128	AT2G15930.1 | expressed protein, and grail | chr2:6948672-6949060 REVERSE | Aliases: F19G14.7, F19G14_7	4.3	4.4	-0.1	-0.4	100.0%	-1.4
19129	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	3.1	-0.0	-0.4	100.0%	-2.2
19130	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	10.7	10.8	-0.1	-0.4	100.0%	-1.7
19131	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	9.6	0.1	0.4	100.0%	-1.8
19132	AT1G53950.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr1:20150116-20151656 REVERSE | Aliases: T18A20.25	2.3	2.3	-0.0	-0.4	100.0%	-2.3
19133	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	4.9	5.1	-0.1	-0.4	100.0%	-1.3
19134	AT2G31250.1 | glutamyl-tRNA reductase, putative, similar to HEMA2 (SP:P49294), HEMA1 (SP:P42804) | chr2:13326698-13328603 REVERSE | Aliases: F16D14.9, F16D14_9	4.3	4.2	0.1	0.4	100.0%	-1.5
19135	AT2G27375.1 | hypothetical protein | chr2:11717752-11718402 FORWARD | Aliases: None	2.2	2.3	-0.0	-0.4	100.0%	-2.2
19136	AT5G03450.1 | zinc finger (C3HC4-type RING finger) family protein | chr5:858768-862296 REVERSE | Aliases: F12E4.210, F12E4_210	3.7	3.7	-0.0	-0.4	100.0%	-2.1
19137	AT1G72270.1 | expressed protein | chr1:27203395-27214784 REVERSE | Aliases: T9N14.23, T9N14_23	3.0	3.0	0.0	0.4	100.0%	-1.8
19138	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	4.5	4.4	0.1	0.4	100.0%	-1.1
19139	AT5G44050.1 | MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family | chr5:17739711-17743606 FORWARD | Aliases: MRH10.16, MRH10_16	3.4	3.4	-0.1	-0.4	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
19140	AT3G42350.1 | hypothetical protein | chr3:14500913-14503573 REVERSE | Aliases: T14K23.60	2.7	2.8	-0.0	-0.4	100.0%	-2.5
19141	AT4G08130.1 | hypothetical protein | chr4:5093870-5095313 FORWARD | Aliases: F9M13.12, F9M13_12	2.1	2.2	-0.0	-0.4	100.0%	-2.5
19142	AT5G47710.1 | C2 domain-containing protein, contains similarity to CLB1 (Lycopersicon esculentum) GI:2789434; contains Pfam profile PF00168: C2 domain	4.9	5.0	-0.1	-0.4	100.0%	-1.5
19143	AT4G26340.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.5	-0.0	-0.4	100.0%	-2.3
19144	AT5G04480.1 | expressed protein | chr5:1271516-1277986 REVERSE | Aliases: T32M21.80, T32M21_80	3.8	3.9	-0.1	-0.4	100.0%	-1.5
19145	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	7.9	7.7	0.2	0.4	100.0%	-1.3
19146	AT2G29190.1 | pumilio/Puf RNA-binding domain-containing protein | chr2:12550889-12555567 REVERSE | Aliases: F16P2.43, F16P2_43	3.3	3.3	-0.0	-0.4	100.0%	-2.1
19147	AT3G54060.2 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g37960.1) | chr3:20029639-20031904 REVERSE | Aliases: F24B22.20	2.3	2.2	0.0	0.4	100.0%	-2.4
19148	AT2G40740.1 | Symbol: WRKY55 |	3.6	3.7	-0.1	-0.4	100.0%	-1.9
19149	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	2.6	2.7	-0.1	-0.4	100.0%	-1.8
19150	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	2.8	-0.1	-0.4	100.0%	-1.8
19151	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	7.5	7.6	-0.2	-0.4	100.0%	-1.2
19152	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	4.6	-0.1	-0.4	100.0%	-1.6
19153	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	2.2	-0.0	-0.4	100.0%	-2.4
19154	AT5G20430.1 | mob1/phocein family protein, contains Pfam profile: PF03637 mob1/phocein family | chr5:6904707-6905393 FORWARD | Aliases: F7C8.20, F7C8_20	2.8	2.7	0.1	0.4	100.0%	-1.7
19155	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	2.8	2.7	0.1	0.4	100.0%	-1.7
19156	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	8.4	8.6	-0.1	-0.4	100.0%	-1.4
19157	AT1G27930.1 | expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579) | chr1:9731252-9732706 REVERSE | Aliases: F13K9.4, F13K9_4	7.1	7.0	0.1	0.4	100.0%	-1.5
19158	AT5G05520.1 | outer membrane OMP85 family protein, contains Pfam profile PF01103: outer membrane protein, OMP85 family	6.8	6.8	-0.1	-0.4	100.0%	-1.5
19159	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	-0.0	-0.4	100.0%	-2.0
19160	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	2.3	2.4	-0.0	-0.4	100.0%	-2.5

Rank	Description	Sync	Root	M	t	adj.q	B
19161	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	6.6	6.7	-0.1	-0.4	100.0%	-1.5
19162	AT5G38980.1 | expressed protein | chr5:15624001-15624579 FORWARD | Aliases: K15E6.160, K15E6_160	2.9	3.0	-0.0	-0.4	100.0%	-1.9
19163	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	2.6	2.7	-0.0	-0.4	100.0%	-2.0
19164	ATMG01130.1 | Symbol: ORF106F | hypothetical protein | chrM:289197-289517 REVERSE | Aliases: ORF106F	3.6	3.7	-0.1	-0.4	100.0%	-1.6
19165	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	3.4	-0.1	-0.4	100.0%	-1.8
19166	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	0.0	0.4	100.0%	-2.2
19167	AT5G22430.1 | expressed protein | chr5:7433794-7434938 FORWARD | Aliases: MWD9.23, MWD9_23	2.2	2.2	-0.0	-0.4	100.0%	-2.4
19168	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	6.7	6.5	0.2	0.4	100.0%	-1.3
19169	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	7.5	7.6	-0.2	-0.4	100.0%	-1.5
19170	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	-0.4	100.0%	-1.9
19171	AT2G38610.2 | KH domain-containing protein | chr2:16154191-16156841 REVERSE | Aliases: T6A23.19, T6A23_19	4.2	4.3	-0.1	-0.4	100.0%	-1.5
19172	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	3.1	0.1	0.4	100.0%	-1.7
19173	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	0.4	100.0%	-2.3
19174	AT3G24250.1 | glycine-rich protein | chr3:8786771-8787188 FORWARD | Aliases: K13K6.2	5.7	5.8	-0.1	-0.4	100.0%	-1.6
19175	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	6.4	6.6	-0.2	-0.4	100.0%	-1.0
19176	AT1G51805.1 | 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 | chr1:19224646-19229358 REVERSE | Aliases: F19C24.2, F19C24_2	2.6	2.7	-0.0	-0.4	100.0%	-2.5
19177	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	3.9	3.8	0.1	0.4	100.0%	-1.8
19178	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%	-2.3
19179	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	0.1	0.4	100.0%	-1.8
19180	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	7.1	7.0	0.1	0.4	100.0%	-1.6
19181	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	2.7	-0.0	-0.4	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
19182	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	9.3	9.2	0.1	0.4	100.0%	-1.7
19183	AT5G09760.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:3032376-3034544 FORWARD | Aliases: F17I14.50, F17I14_50	9.0	9.1	-0.1	-0.4	100.0%	-1.5
19184	AT5G28790.1 | hypothetical protein | chr5:10820177-10820529 FORWARD | Aliases: T32B20.80, T32B20_80	2.3	2.3	-0.0	-0.4	100.0%	-2.3
19185	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	2.7	2.6	0.0	0.4	100.0%	-2.2
19186	AT4G11860.1 | expressed protein, contains Pfam domain PF04424: Protein of unknown function (DUF544) | chr4:7134078-7138497 REVERSE | Aliases: T26M18.70, T26M18_70	7.0	6.9	0.1	0.4	100.0%	-1.2
19187	AT3G02420.1 | expressed protein | chr3:495892-498841 REVERSE | Aliases: F16B3.5, F16B3_5	7.4	7.6	-0.2	-0.4	100.0%	-1.0
19188	AT5G59130.1 | subtilase family protein, contains similarity to prepro-cucumisin GI:807698 from (Cucumis melo) | chr5:23887418-23890917 REVERSE | Aliases: MNC17.3, MNC17_3	2.3	2.3	0.0	0.4	100.0%	-2.4
19189	AT1G68810.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	5.1	5.0	0.1	0.4	100.0%	-1.2
19190	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	-0.4	100.0%	-2.1
19191	AT2G39660.1 | protein kinase, putative, similar to protein kinase gi:166809:gb:AAA18853 | chr2:16538803-16540700 FORWARD | Aliases: F12L6.32, F12L6_32	7.1	7.3	-0.2	-0.4	100.0%	-1.4
19192	AT3G19160.1 | Symbol: ATIPT8 |	3.0	3.0	-0.0	-0.4	100.0%	-2.2
19193	AT1G05520.1 | transport protein, putative, similar to Swiss-Prot:Q15436 protein transport protein Sec23A (Homo sapiens) | chr1:1630899-1635710 REVERSE | Aliases: T25N20.17	4.1	4.0	0.2	0.4	100.0%	-1.6
19194	AT3G06750.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr3:2129629-2130321 REVERSE | Aliases: F3E22.11	5.6	5.7	-0.1	-0.4	100.0%	-1.4
19195	AT1G77655.1 | expressed protein | chr1:29187502-29188066 REVERSE | Aliases: None	3.9	3.9	-0.0	-0.4	100.0%	-2.0
19196	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	4.0	4.1	-0.1	-0.4	100.0%	-1.7
19197	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	2.7	-0.0	-0.4	100.0%	-1.9
19198	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	4.5	4.5	0.1	0.4	100.0%	-1.7
19199	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	0.0	0.4	100.0%	-1.9
19200	AT5G27440.1 | expressed protein | chr5:9689501-9690314 REVERSE | Aliases: F21A20.150, F21A20_150	3.6	3.5	0.1	0.4	100.0%	-2.0
19201	AT2G37290.1 | RabGAP/TBC domain-containing protein, low similarity to Rab6 GTPase activating protein, GAPCenA (Homo sapiens) GI:12188746; contains Pfam profile PF00566: TBC domain | chr2:15664014-15668414 REVERSE | Aliases: F3G5.8, F3G5_8	2.6	2.5	0.0	0.3	100.0%	-2.1
19202	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	3.0	3.0	-0.0	-0.3	100.0%	-2.0
19203	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	2.4	0.0	0.3	100.0%	-2.2

Rank	Description	Sync	Root	M	t	adj.q	B
19204	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	-0.3	100.0%	-2.0
19205	AT5G17570.1 | tatD-related deoxyribonuclease family protein, contains Pfam profile PF01026: TatD related DNase	4.5	4.4	0.1	0.3	100.0%	-1.4
19206	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	7.6	7.4	0.2	0.3	100.0%	-1.3
19207	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	3.7	3.6	0.1	0.3	100.0%	-1.5
19208	AT1G31790.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:11394132-11395999 REVERSE | Aliases: F5M6.20, F5M6_20	3.6	3.5	0.1	0.3	100.0%	-1.7
19209	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	7.6	7.4	0.2	0.3	100.0%	-1.4
19210	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	2.4	2.4	-0.0	-0.3	100.0%	-2.3
19211	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	5.7	5.8	-0.1	-0.3	100.0%	-1.4
19212	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	0.3	100.0%	-1.9
19213	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	2.9	2.8	0.0	0.3	100.0%	-1.9
19214	AT4G39530.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:18374730-18377234 REVERSE | Aliases: F23K16.160, F23K16_160	3.0	2.9	0.0	0.3	100.0%	-1.8
19215	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	2.3	2.3	0.0	0.3	100.0%	-2.2
19216	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%	-2.6
19217	AT3G47510.1 | expressed protein | chr3:17522084-17522600 FORWARD | Aliases: F1P2.60	8.4	8.4	0.1	0.3	100.0%	-1.8
19218	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%	-1.8
19219	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%	-1.7
19220	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	7.3	7.1	0.2	0.3	100.0%	-1.3
19221	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	4.9	4.8	0.1	0.3	100.0%	-1.5
19222	AT3G24150.1 | expressed protein | chr3:8724168-8725919 REVERSE | Aliases: MUJ8.5	4.4	4.4	0.1	0.3	100.0%	-1.7
19223	AT3G61040.2 | Symbol: CYP76C7 | cytochrome P450 family protein, similar to cytochrome P450 monooxygenase - Arabidopsis thaliana, EMBL:D78600 | chr3:22605384-22607100 REVERSE | Aliases: T27I15.130	3.3	3.3	-0.1	-0.3	100.0%	-1.8
19224	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	4.5	4.3	0.2	0.3	100.0%	-1.1

Rank	Description	Sync	Root	M	t	adj.q	B
19225	AT3G11200.2 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr3:3508048-3510558 REVERSE | Aliases: F11B9.12	6.9	6.8	0.1	0.3	100.0%	-1.4
19226	ATCG00360.1 | Symbol: YCF3 | hypothetical protein | chrC:42584-43751 REVERSE | Aliases: YCF3	7.1	6.8	0.3	0.3	100.0%	-0.9
19227	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	4.5	4.6	-0.1	-0.3	100.0%	-1.3
19228	AT2G19350.1 | expressed protein | chr2:8383284-8384425 FORWARD | Aliases: F27F23.15, F27F23_15	6.7	6.8	-0.1	-0.3	100.0%	-1.5
19229	AT1G47740.2 | expressed protein | chr1:17570148-17572599 FORWARD | Aliases: T2E6.19, T2E6_19	6.6	6.4	0.1	0.3	100.0%	-1.5
19230	AT3G17140.1 | invertase inhibitor-related, weak similarity to tomato invertase inhibitor (Lycopersicon esculentum) GI:3582002 | chr3:5846008-5846595 REVERSE | Aliases: K14A17.21	3.5	3.5	-0.1	-0.3	100.0%	-1.6
19231	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	2.9	-0.0	-0.3	100.0%	-2.2
19232	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	3.7	3.8	-0.1	-0.3	100.0%	-1.6
19233	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	7.1	-0.1	-0.3	100.0%	-1.5
19234	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	2.8	2.9	-0.1	-0.3	100.0%	-2.1
19235	AT1G65090.1 | similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At5g36100.1); similar to glutamic acid-rich protein cNBL1700 [Trichinella spiralis] (GB:AAM19760.1)	3.5	3.6	-0.1	-0.3	100.0%	-1.7
19236	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	3.8	3.8	-0.1	-0.3	100.0%	-1.7
19237	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	4.3	4.4	-0.1	-0.3	100.0%	-1.7
19238	AT2G45450.1 | expressed protein | chr2:18740351-18741056 REVERSE | Aliases: F4L23.4	3.5	3.4	0.1	0.3	100.0%	-1.6
19239	AT3G29570.1 | expressed protein | chr3:11366285-11367268 REVERSE | Aliases: MWE13.1	2.7	2.7	-0.0	-0.3	100.0%	-2.2
19240	AT5G23970.1 | transferase family protein, similar to acetyl CoA: benzylalcohol acetyltransferase; BEAT (Clarkia breweri)(GI:3170250)(PMID:9628024), deacetylvindoline 4-O-acetyltransferase (Catharanthus roseus)(GI:4091808)(PMID:9681034) | chr5:8096293-8097657 FORWARD | Aliases: MZF18.15, MZF18_15	2.7	2.7	0.0	0.3	100.0%	-2.1
19241	AT3G43590.1 | zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle | chr3:15520609-15523562 FORWARD | Aliases: F22J12.30	6.7	6.9	-0.2	-0.3	100.0%	-1.0
19242	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	0.0	0.3	100.0%	-2.1
19243	AT4G30900.1 | expressed protein | chr4:15039514-15042352 FORWARD | Aliases: F6I18.190, F6I18_190	7.5	7.6	-0.1	-0.3	100.0%	-1.5
19244	AT2G45140.1 | vesicle-associated membrane protein, putative / VAMP, putative, similar to VAP27 GI:6688926 (Nicotiana plumbaginifolia) | chr2:18617881-18620365 FORWARD | Aliases: T14P1.5	7.7	7.6	0.1	0.3	100.0%	-1.5
19245	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	3.7	3.7	0.0	0.3	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
19246	AT2G20700.1 | expressed protein | chr2:8932029-8932813 REVERSE | Aliases: F5H14.33, F5H14_33	4.0	3.9	0.1	0.3	100.0%	-1.6
19247	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	-0.3	100.0%	-2.3
19248	AT3G26930.1 | hypothetical protein | chr3:9927168-9928588 FORWARD | Aliases: MQP17.1	3.2	3.1	0.1	0.3	100.0%	-1.8
19249	AT4G00160.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.4	-0.0	-0.3	100.0%	-2.4
19250	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%	-2.4
19251	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	7.0	7.1	-0.1	-0.3	100.0%	-1.6
19252	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	0.0	0.3	100.0%	-2.5
19253	AT5G60240.1 | expressed protein | chr5:24268608-24268854 FORWARD | Aliases: F15L12.5, F15L12_5	3.2	3.2	-0.1	-0.3	100.0%	-1.8
19254	AT4G34400.1 | transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain | chr4:16445327-16447600 FORWARD | Aliases: F10M10.170, F10M10_170	3.0	3.1	-0.1	-0.3	100.0%	-1.8
19255	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	-0.3	100.0%	-2.2
19256	ATCG00270.1 | Symbol: PSBD | PSII D2 protein | chrC:32711-33772 FORWARD | Aliases: PSBD	4.6	4.4	0.1	0.3	100.0%	-1.3
19257	AT3G08560.1 | Symbol: VHA E2 |	3.4	3.5	-0.1	-0.3	100.0%	-1.6
19258	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	6.5	-0.0	-0.3	100.0%	-1.9
19259	AT2G36980.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:15538240-15540117 FORWARD | Aliases: T1J8.16, T1J8_16	3.2	3.1	0.1	0.3	100.0%	-1.7
19260	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	2.8	2.8	-0.0	-0.3	100.0%	-1.9
19261	AT5G35450.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.5	3.6	-0.1	-0.3	100.0%	-1.6
19262	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	5.3	-0.1	-0.3	100.0%	-1.6
19263	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	3.2	3.3	-0.1	-0.3	100.0%	-1.8
19264	AT2G43910.1 | thiol methyltransferase, putative, similar to thiol methyltransferase 1 GI:14583119 from (Brassica oleracea) | chr2:18191557-18194101 REVERSE | Aliases: F6E13.4	8.1	8.3	-0.3	-0.3	100.0%	-1.2
19265	AT2G43920.1 | thiol methyltransferase, putative, similar to thiol methyltransferase 1 GI:14583119 from (Brassica oleracea) | chr2:18196128-18198324 REVERSE | Aliases: F6E13.5	8.1	8.3	-0.3	-0.3	100.0%	-1.2
19266	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	0.1	0.3	100.0%	-1.7
19267	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	4.3	4.1	0.1	0.3	100.0%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
19268	AT4G29420.1 | F-box family protein, contains F-box Pfam:PF00646 ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250 | chr4:14470465-14472238 REVERSE | Aliases: F17A13.240, F17A13_240	2.5	2.4	0.0	0.3	100.0%	-2.5
19269	AT4G29640.1 | cytidine deaminase, putative / cytidine aminohydrolase, putative, identical to cytidine deaminase 5 (CDA5) (Arabidopsis thaliana) GI:3818578, cytidine deaminase homolog DesG (Arabidopsis thaliana) GI:4836449; similar to cytidine deaminase (CDD) (Arabidopsis thaliana) GI:3046700; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding | chr4:14525836-14526876 FORWARD | Aliases: T16L4.150, T16L4_150	3.4	3.5	-0.1	-0.3	100.0%	-1.4
19270	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	2.7	2.8	-0.0	-0.3	100.0%	-2.1
19271	AT5G11280.1 | expressed protein | chr5:3597258-3598515 FORWARD | Aliases: F2I11.170, F2I11_170	5.9	5.7	0.2	0.3	100.0%	-1.3
19272	AT1G75730.1 | expressed protein | chr1:28439367-28443328 REVERSE | Aliases: F10A5.7, F10A5_7	2.8	2.9	-0.0	-0.3	100.0%	-1.9
19273	AT2G38420.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:16098183-16099628 FORWARD | Aliases: T19C21.9, T19C21_9	4.4	4.4	0.1	0.3	100.0%	-1.7
19274	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	-0.3	100.0%	-2.1
19275	AT4G10330.1 | glycine-rich protein | chr4:6406537-6407773 FORWARD | Aliases: F24G24.130, F24G24_130	7.9	7.9	0.1	0.3	100.0%	-1.7
19276	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	4.5	4.3	0.1	0.3	100.0%	-1.4
19277	AT1G31814.1 | Symbol: FRL2 | expressed protein | chr1:11412589-11414414 REVERSE | Aliases: F5M6.26, F5M6_26, FRIGIDA LIKE 2	3.3	3.3	0.0	0.3	100.0%	-1.8
19278	AT3G21660.1 | UBX domain-containing protein, contains Pfam profile: PF00789 UBX domain	3.2	3.3	-0.1	-0.3	100.0%	-2.0
19279	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	-0.1	-0.3	100.0%	-1.7
19280	AT3G26540.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat | chr3:9745779-9747881 REVERSE | Aliases: MFE16.1	2.5	2.5	0.0	0.3	100.0%	-2.3
19281	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	7.7	7.6	0.1	0.3	100.0%	-1.4
19282	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	-0.0	-0.3	100.0%	-2.1
19283	AT1G64900.1 | Symbol: CYP89A2 | cytochrome P450, putative, similar to cytochrome p450 GI:438240 from (Solanum melongena) | chr1:24116878-24118647 FORWARD | Aliases: CYP89, CYP89A2, CYTOCHROME P450 89A2, F13O11.20, F13O11_20	3.0	2.9	0.0	0.3	100.0%	-2.1
19284	AT5G28600.1 | hypothetical protein | chr5:10597813-10603454 FORWARD | Aliases: T10I18.60, T10I18_60	3.2	3.2	-0.1	-0.3	100.0%	-1.8
19285	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	-0.1	-0.3	100.0%	-1.9
19286	AT3G31320.1 | hypothetical protein | chr3:12697106-12698481 FORWARD | Aliases: T22B15.7	3.1	3.1	0.0	0.3	100.0%	-1.9
19287	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	2.8	2.8	-0.0	-0.3	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
19288	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	5.3	5.6	-0.2	-0.3	100.0%	-1.3
19289	AT2G46180.1 | intracellular protein transport protein USO1-related, similar to Intracellular protein transport protein USO1 (Swiss-Prot:P25386) (Saccharomyces cerevisiae) | chr2:18974432-18978423 REVERSE | Aliases: T3F17.17	8.3	8.2	0.1	0.3	100.0%	-1.4
19290	AT1G60180.1 | expressed protein, similar to hypothetical protein GI:6017113 from (Arabidopsis thaliana) | chr1:22199190-22200350 REVERSE | Aliases: T13D8.7, T13D8_7	2.8	2.7	0.0	0.3	100.0%	-2.0
19291	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	4.2	0.1	0.3	100.0%	-1.5
19292	AT1G25375.1 | metallo-beta-lactamase family protein | chr1:8900189-8903244 REVERSE | Aliases: None	6.5	6.4	0.1	0.3	100.0%	-1.8
19293	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	0.0	0.3	100.0%	-1.8
19294	AT1G45150.1 | expressed protein | chr1:17079888-17084886 REVERSE | Aliases: F27F5.22, F27F5_22	6.8	6.7	0.1	0.3	100.0%	-1.4
19295	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	2.2	2.2	0.0	0.3	100.0%	-2.4
19296	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	4.5	0.1	0.3	100.0%	-1.2
19297	AT1G06980.1 | expressed protein, similar to hypothetical protein GI:2347189 from (Arabidopsis thaliana) | chr1:2143030-2143820 REVERSE | Aliases: F10K1.30, F10K1_30	3.1	3.1	-0.0	-0.3	100.0%	-2.2
19298	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	3.1	3.2	-0.0	-0.3	100.0%	-1.8
19299	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	0.0	0.3	100.0%	-1.9
19300	AT5G62330.1 | expressed protein | chr5:25048827-25049430 FORWARD | Aliases: MMI9.16, MMI9_16	2.7	2.7	-0.0	-0.3	100.0%	-1.8
19301	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	-0.0	-0.3	100.0%	-2.0
19302	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	9.1	8.9	0.2	0.3	100.0%	-1.5
19303	AT1G24020.1 | Bet v I allergen family protein, similar to major pollen allergen Bet v 1 GB:CAA96544 GI:1321726 from (Betula pendula); contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family | chr1:8500466-8501504 REVERSE | Aliases: T23E23.28, T23E23_28	3.9	4.0	-0.1	-0.3	100.0%	-1.6
19304	AT4G18395.1 | expressed protein | chr4:10169455-10169941 FORWARD | Aliases: None	3.3	3.3	-0.0	-0.3	100.0%	-2.1
19305	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	2.2	-0.0	-0.3	100.0%	-2.4
19306	AT5G27270.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:9605653-9609790 FORWARD | Aliases: F21A20.6	4.7	4.6	0.1	0.3	100.0%	-1.6
19307	AT5G64960.1 | Symbol: CDKC;2 |	6.1	6.0	0.1	0.3	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
19308	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	2.2	2.3	-0.0	-0.3	100.0%	-2.2
19309	AT3G25840.1 | protein kinase family protein, contains Pfam profile: PF00069 eukaryotic protein kinase domain | chr3:9453926-9458791 REVERSE | Aliases: K9I22.6	6.4	6.5	-0.1	-0.3	100.0%	-1.5
19310	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	4.4	4.3	0.1	0.3	100.0%	-1.7
19311	AT2G20300.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:8763006-8767303 REVERSE | Aliases: F11A3.15, F11A3_15	4.3	4.3	-0.1	-0.3	100.0%	-1.6
19312	AT1G48730.1 | expressed protein | chr1:18024005-18025945 REVERSE | Aliases: F11I4.10, F11I4_10	2.9	2.9	0.0	0.3	100.0%	-1.9
19313	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	-0.3	100.0%	-2.2
19314	AT5G50860.1 | protein kinase family protein, contains PF00069: Protein kinase domain | chr5:20710689-20714265 REVERSE | Aliases: K16E14.1	4.2	4.1	0.1	0.3	100.0%	-1.7
19315	AT1G40230.1 | expressed protein | chr1:15417336-15418247 FORWARD | Aliases: F9D18.23, F9D18_23	2.2	2.2	-0.0	-0.3	100.0%	-2.3
19316	AT1G73130.1 | expressed protein | chr1:27502696-27505557 FORWARD | Aliases: T18K17.21, T18K17_21	5.1	5.2	-0.1	-0.3	100.0%	-1.5
19317	AT3G26950.1 | expressed protein | chr3:9942375-9944648 REVERSE | Aliases: MOJ10.3	8.4	8.5	-0.1	-0.3	100.0%	-1.6
19318	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	2.3	2.4	-0.0	-0.3	100.0%	-2.3
19319	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	2.0	2.0	-0.0	-0.3	100.0%	-2.9
19320	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	2.0	2.0	-0.0	-0.3	100.0%	-2.9
19321	AT4G28170.1 | expressed protein | chr4:13981641-13982048 FORWARD | Aliases: F26K10.50, F26K10_50	3.1	3.1	-0.0	-0.3	100.0%	-2.3
19322	AT5G37730.1 | expressed protein | chr5:15003263-15004147 REVERSE | Aliases: K12B20.20, K12B20_20	2.2	2.2	-0.0	-0.3	100.0%	-2.6
19323	AT4G22800.1 | hypothetical protein | chr4:11978016-11983082 REVERSE | Aliases: T12H17.190, T12H17_190	2.5	2.5	-0.0	-0.3	100.0%	-2.6
19324	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%	-1.9
19325	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	7.0	6.9	0.2	0.3	100.0%	-1.0
19326	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	-0.0	-0.3	100.0%	-2.4
19327	AT1G56270.1 | expressed protein | chr1:21074813-21075301 REVERSE | Aliases: F14G9.12, F14G9_12	2.9	3.0	-0.1	-0.3	100.0%	-1.7
19328	AT3G53320.1 | expressed protein | chr3:19780154-19783347 REVERSE | Aliases: F4P12.20	5.1	5.1	-0.1	-0.3	100.0%	-1.8
19329	AT2G27180.1 | expressed protein | chr2:11627311-11628252 FORWARD | Aliases: T22O13.5, T22O13_5	3.7	3.6	0.1	0.3	100.0%	-1.6
19330	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%	-2.1
19331	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%	-2.2

Rank	Description	Sync	Root	M	t	adj.q	B
19332	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	7.7	0.1	0.3	100.0%	-1.5
19333	AT3G48700.1 | expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873 | chr3:18049633-18050861 REVERSE | Aliases: T8P19.210	3.0	3.1	-0.1	-0.3	100.0%	-1.7
19334	AT2G21630.1 | transport protein, putative, similar to Swiss-Prot:Q15436 protein transport protein Sec23A (Homo sapiens) | chr2:9257403-9260995 FORWARD | Aliases: F2G1.10, F2G1_10	3.6	3.6	0.0	0.3	100.0%	-1.8
19335	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	0.3	100.0%	-1.8
19336	AT3G44080.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.4	0.0	0.3	100.0%	-2.5
19337	AT1G59930.1 | expressed protein | chr1:22064748-22065146 REVERSE | Aliases: F23H11.24, F23H11_24	2.4	2.5	-0.1	-0.3	100.0%	-1.7
19338	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	-0.3	100.0%	-2.7
19339	AT2G29140.1 | pumilio/Puf RNA-binding domain-containing protein | chr2:12538469-12542334 FORWARD | Aliases: F16P2.48, F16P2_48	4.0	3.8	0.1	0.3	100.0%	-0.9
19340	AT2G29200.1 | pumilio/Puf RNA-binding domain-containing protein, similar to BPM (Hordeum vulgare) GI:20513851 | chr2:12556361-12560262 REVERSE | Aliases: F16P2.42, F16P2_42	4.0	3.8	0.1	0.3	100.0%	-0.9
19341	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	5.4	5.5	-0.1	-0.3	100.0%	-1.5
19342	AT1G03020.1 | glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	2.7	2.8	-0.0	-0.3	100.0%	-2.0
19343	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	2.8	2.8	0.0	0.3	100.0%	-2.1
19344	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	2.3	-0.0	-0.3	100.0%	-2.2
19345	AT1G23270.1 | expressed protein | chr1:8259591-8260133 REVERSE | Aliases: F26F24.11, F26F24_11	2.5	2.5	-0.1	-0.3	100.0%	-1.9
19346	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	-0.3	100.0%	-1.9
19347	AT5G59810.1 | subtilase family protein, subtilisin-like protease AIR3, Arabidopsis thaliana, EMBL:AF098632 | chr5:24114041-24117783 REVERSE | Aliases: MMN10.6, MMN10_6	2.8	2.9	-0.0	-0.3	100.0%	-2.0
19348	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	-0.3	100.0%	-1.5
19349	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	-0.3	100.0%	-1.5
19350	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	9.6	9.5	0.1	0.3	100.0%	-1.7
19351	NA	2.8	2.8	-0.0	-0.3	100.0%	-2.3
19352	AT2G41820.1 | leucine-rich repeat transmembrane protein kinase, putative | chr2:17453822-17457149 FORWARD | Aliases: T11A7.8, T11A7_8	5.4	5.5	-0.0	-0.3	100.0%	-1.6
19353	AT4G35930.1 | expressed protein | chr4:17018978-17021063 FORWARD | Aliases: T19K4.60	2.5	2.5	-0.0	-0.3	100.0%	-2.1
19354	AT2G40980.1 | expressed protein | chr2:17109168-17111880 FORWARD | Aliases: T3K9.25, T3K9_25	3.2	3.2	0.1	0.3	100.0%	-2.0
19355	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	-0.0	-0.3	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
19356	AT2G25670.2 | expressed protein | chr2:10935742-10938135 REVERSE | Aliases: F3N11.12, F3N11_12	10.2	10.1	0.1	0.3	100.0%	-1.8
19357	AT4G00910.1 | expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	3.1	3.2	-0.0	-0.3	100.0%	-1.7
19358	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	3.4	3.4	-0.1	-0.3	100.0%	-1.7
19359	AT5G37080.1 | hypothetical protein, includes At5g37080, At5g37170, At2g05090 | chr5:14676363-14679638 FORWARD | Aliases: MJG14.6, MJG14_6	2.9	3.0	-0.1	-0.3	100.0%	-2.0
19360	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	4.2	4.3	-0.1	-0.3	100.0%	-1.4
19361	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	2.2	2.3	-0.0	-0.3	100.0%	-2.6
19362	AT1G69523.1 | UbiE/COQ5 methyltransferase family protein, low similarity to SP:Q05197 Phosphatidylethanolamine N-methyltransferase (EC 2.1.1.17) (Rhodopseudomonas sphaeroides) {Rhodobacter sphaeroides}; contains Pfam profile PF01209: methlytransferase, UbiE/COQ5 family | chr1:26133214-26134912 FORWARD | Aliases: None	3.3	3.2	0.1	0.3	100.0%	-1.7
19363	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	8.4	8.6	-0.2	-0.3	100.0%	-1.4
19364	AT3G47230.1 | expressed protein | chr3:17403084-17404684 REVERSE | Aliases: F13I12.280	2.6	2.6	-0.0	-0.3	100.0%	-2.2
19365	AT5G54010.1 | glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	3.7	3.7	-0.1	-0.3	100.0%	-1.7
19366	AT5G39210.1 | expressed protein | chr5:15720421-15721328 FORWARD | Aliases: K3K3.10, K3K3_10	2.7	2.7	-0.0	-0.3	100.0%	-2.1
19367	AT2G47310.1 | flowering time control protein-related / FCA gamma-related | chr2:19430754-19434347 FORWARD | Aliases: T8I13.15	3.3	3.3	-0.0	-0.3	100.0%	-2.1
19368	AT5G24860.1 | Symbol: FPF1 | expressed protein | chr5:8541781-8542452 FORWARD | Aliases: F6A4.70, F6A4_70, FLOWERING PROMOTING FACTOR 1, FPF	3.1	3.1	0.0	0.3	100.0%	-2.0
19369	AT4G13000.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr4:7598090-7599254 REVERSE | Aliases: F25G13.90, F25G13_90	3.5	3.5	-0.0	-0.3	100.0%	-2.2
19370	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	7.5	7.5	-0.1	-0.3	100.0%	-1.3
19371	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	3.0	3.0	-0.0	-0.3	100.0%	-2.0
19372	AT2G37880.1 | expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617 | chr2:15867711-15868696 FORWARD | Aliases: T8P21.21, T8P21_21	3.6	3.5	0.1	0.3	100.0%	-1.7
19373	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	6.2	6.1	0.1	0.3	100.0%	-1.4
19374	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	3.5	3.6	-0.0	-0.3	100.0%	-2.1
19375	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	3.0	2.9	0.0	0.3	100.0%	-2.2
19376	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	-0.3	100.0%	-1.9
19377	AT3G13280.1 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537; expression supported by MPSS | chr3:4295334-4297007 REVERSE | Aliases: MDC11.11	3.5	3.5	0.0	0.3	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
19378	AT3G18810.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr3:6480707-6483599 REVERSE | Aliases: MVE11.19	2.6	2.5	0.0	0.3	100.0%	-2.3
19379	AT2G01300.1 | expressed protein | chr2:151062-151728 REVERSE | Aliases: F10A8.18, F10A8_18	2.7	2.6	0.0	0.3	100.0%	-2.0
19380	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	3.7	-0.1	-0.3	100.0%	-1.3
19381	AT3G26630.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat | chr3:9792608-9794222 REVERSE | Aliases: MLJ15.2	3.6	3.5	0.0	0.3	100.0%	-1.8
19382	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	2.4	2.5	-0.0	-0.3	100.0%	-2.3
19383	AT1G67865.1 | expressed protein | chr1:25449952-25450400 REVERSE | Aliases: None	3.8	3.8	-0.1	-0.3	100.0%	-1.7
19384	AT5G18090.1 | transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain | chr5:5985390-5987163 FORWARD | Aliases: MRG7.5, MRG7_5	3.4	3.4	-0.0	-0.3	100.0%	-1.9
19385	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	3.2	3.2	0.1	0.3	100.0%	-2.1
19386	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	-0.3	100.0%	-2.2
19387	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	6.9	7.0	-0.1	-0.3	100.0%	-1.2
19388	AT2G26050.1 | expressed protein | chr2:11105730-11106458 REVERSE | Aliases: T19L18.14, T19L18_14	2.6	2.7	-0.0	-0.3	100.0%	-2.0
19389	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	3.3	3.4	-0.1	-0.3	100.0%	-1.5
19390	AT1G40390.1 | expressed protein | chr1:15435017-15437115 REVERSE | Aliases: F9D18.22, F9D18_22	2.7	2.8	-0.0	-0.3	100.0%	-2.1
19391	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	2.7	2.7	-0.0	-0.3	100.0%	-2.2
19392	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	3.8	3.7	0.1	0.3	100.0%	-1.7
19393	AT4G13320.1 | expressed protein | chr4:7753307-7754082 FORWARD | Aliases: T9E8.60, T9E8_60	2.7	2.6	0.1	0.3	100.0%	-2.0
19394	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	-0.0	-0.3	100.0%	-2.9
19395	AT4G26020.1 | expressed protein, weak similarity to cardiac muscle factor 1 (Gallus gallus) GI:14422164 | chr4:13202022-13204037 REVERSE | Aliases: F20B18.130, F20B18_130	2.6	2.6	0.0	0.3	100.0%	-2.4
19396	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	-0.3	100.0%	-1.8
19397	AT2G18190.1 | AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 | chr2:7921387-7922954 REVERSE | Aliases: F8D23.3, F8D23_3	3.5	3.5	0.1	0.3	100.0%	-1.6
19398	AT1G30020.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr1:10515858-10516331 REVERSE | Aliases: T1P2.11, T1P2_11	2.6	2.7	-0.0	-0.3	100.0%	-2.2
19399	AT2G47300.1 | expressed protein | chr2:19427076-19428593 FORWARD | Aliases: T8I13.14	2.1	2.1	0.0	0.3	100.0%	-2.6
19400	AT3G26870.1 | self-incompatibility protein-related, low similarity to self-incompatibility (Papaver nudicaule) GI:3097262 | chr3:9904525-9904917 REVERSE | Aliases: MDJ14.21	2.3	2.4	-0.0	-0.3	100.0%	-2.3

Rank	Description	Sync	Root	M	t	adj.q	B
19401	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	6.8	7.0	-0.1	-0.3	100.0%	-1.4
19402	AT1G32000.1 | expressed protein | chr1:11508265-11508889 REVERSE | Aliases: T12O21.10, T12O21_10	2.0	2.0	-0.0	-0.3	100.0%	-2.7
19403	AT2G23960.1 | defense-related protein, putative, similar to defense-related protein (Brassica carinata) GI:14009290 | chr2:10203139-10204690 FORWARD | Aliases: T29E15.16, T29E15_16	3.0	3.0	0.1	0.3	100.0%	-1.5
19404	AT2G43060.1 | expressed protein, similar to cDNA bHLH transcription factor (bHLH zeta gene) GI:32563005 | chr2:17916262-17917159 FORWARD | Aliases: MFL8.8	5.9	6.0	-0.1	-0.3	100.0%	-1.3
19405	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	3.4	3.4	0.1	0.3	100.0%	-1.6
19406	AT2G19000.1 | expressed protein | chr2:8248186-8248866 FORWARD | Aliases: T20K24.1, T20K24_1	2.7	2.7	-0.0	-0.3	100.0%	-2.3
19407	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%	-2.1
19408	AT2G37260.1 | Symbol: TTG2 | WRKY family transcription factor (TTG2), contains Pfam profile: PF03106 WRKY DNA -binding domain	2.6	2.6	-0.0	-0.3	100.0%	-2.1
19409	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%	-2.3
19410	AT5G51900.1 | cytochrome P450 family, similar to cytochrome P450 86A1 (SP:P48422) (Arabidopsis thaliana) | chr5:21110907-21111680 REVERSE | Aliases: MJM18.5, MJM18_5	2.4	2.5	-0.0	-0.3	100.0%	-2.5
19411	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	-0.3	100.0%	-2.0
19412	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	4.1	0.1	0.3	100.0%	-1.5
19413	AT5G03630.1 | monodehydroascorbate reductase, putative, monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182 | chr5:922165-924676 REVERSE | Aliases: F17C15.50, F17C15_50	8.8	9.1	-0.3	-0.3	100.0%	-1.2
19414	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	3.9	4.0	-0.1	-0.3	100.0%	-1.5
19415	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	2.4	2.5	-0.1	-0.3	100.0%	-1.9
19416	AT3G63100.1 | glycine-rich protein | chr3:23326462-23327144 REVERSE | Aliases: T20O10.200	4.2	4.2	-0.0	-0.3	100.0%	-1.8
19417	AT5G46540.1 | ABC transporter family protein, contains Pfam profile: PF00005 ABC transporter; similar to multidrug-resistant protein CjMDR1 GI:14715462 from (Coptis japonica)	3.1	3.2	-0.0	-0.3	100.0%	-1.7
19418	AT2G30900.1 | expressed protein | chr2:13157561-13159494 FORWARD | Aliases: F7F1.11, F7F1_11	3.6	3.7	-0.1	-0.3	100.0%	-1.2
19419	AT3G20530.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:7166066-7167930 FORWARD | Aliases: K10D20.14	3.0	3.1	-0.0	-0.3	100.0%	-2.1
19420	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	2.5	2.5	-0.0	-0.3	100.0%	-2.6
19421	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	2.6	2.6	0.0	0.3	100.0%	-2.0
19422	AT2G03130.1 | ribosomal protein L12 family protein | chr2:940741-941073 FORWARD | Aliases: T18E12.20, T18E12_20	5.1	5.2	-0.1	-0.3	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
19423	AT4G03580.1 | expressed protein | chr4:1596983-1599089 FORWARD | Aliases: T5L23.7, T5L23_7	2.5	2.5	-0.0	-0.3	100.0%	-2.6
19424	AT2G26780.1 | expressed protein, contains Pfam profile TBP (TATA-binding protein) -interacting protein 120 (TIP120); contains TIGRFAM profile TIGR01612: reticulocyte binding protein	6.6	6.5	0.1	0.3	100.0%	-1.4
19425	ATCG00490.1 | Symbol: RBCL | large subunit of RUBISCO. | chrC:54958-56397 FORWARD | Aliases: RBCL	9.8	9.6	0.2	0.3	100.0%	-1.7
19426	AT1G03420.1 | expressed protein, similar to gb:T45484, emb:Z30724, and emb:Z30531 | chr1:846790-847682 FORWARD | Aliases: F21B7.4, F21B7_4	5.2	5.2	0.1	0.3	100.0%	-1.6
19427	AT2G40650.1 | pre-mRNA splicing factor PRP38 family protein, contains Pfam profile PF03371: PRP38 family | chr2:16970397-16972830 REVERSE | Aliases: T7D17.17, T7D17_17	7.7	7.5	0.2	0.3	100.0%	-1.1
19428	AT5G06970.1 | expressed protein | chr5:2158229-2166399 REVERSE | Aliases: MOJ9.14, MOJ9_14	6.6	6.7	-0.1	-0.3	100.0%	-1.7
19429	AT5G50420.1 | expressed protein, strong similarity to unknown protein (gb:AAD50008.1) | chr5:20547433-20550082 REVERSE | Aliases: MXI22.14, MXI22_14	4.8	4.7	0.1	0.3	100.0%	-1.6
19430	AT5G60970.1 | TCP family transcription factor, putative, putative basic helix-loop-helix DNA binding protein TCP2, Arabidopsis thaliana, EMBL:AF072691	2.1	2.1	-0.0	-0.3	100.0%	-2.7
19431	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	3.2	3.2	-0.1	-0.3	100.0%	-2.0
19432	AT4G04330.1 | expressed protein | chr4:2116551-2118592 REVERSE | Aliases: T19B17.5, T19B17_5	2.9	2.8	0.0	0.3	100.0%	-2.0
19433	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	4.9	4.8	0.0	0.3	100.0%	-1.8
19434	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	3.1	3.0	0.1	0.3	100.0%	-1.7
19435	AT1G69560.1 | Symbol: MYB105 |	2.4	2.4	0.0	0.3	100.0%	-2.2
19436	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	2.5	2.5	-0.0	-0.3	100.0%	-2.3
19437	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	4.9	4.8	0.1	0.3	100.0%	-1.2
19438	AT1G24350.1 | expressed protein, contains Pfam domain, PF02681: Uncharacterized BCR, COG1963 | chr1:8638509-8640476 REVERSE | Aliases: F3I6.29, F3I6_29	5.3	5.2	0.1	0.3	100.0%	-1.8
19439	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	8.2	8.3	-0.1	-0.3	100.0%	-1.5
19440	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	-0.0	-0.3	100.0%	-2.2
19441	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	-0.0	-0.3	100.0%	-2.3
19442	AT2G17540.2 | expressed protein | chr2:7637502-7638980 REVERSE | Aliases: MJB20.10, MJB20_10	4.2	4.2	0.1	0.3	100.0%	-1.7
19443	AT4G25030.2 | expressed protein | chr4:12864838-12866837 FORWARD | Aliases: F13M23.170, F13M23_170	9.4	9.3	0.1	0.3	100.0%	-1.6
19444	AT1G76850.1 | expressed protein | chr1:28852845-28859393 FORWARD | Aliases: F7O12.2, F7O12_2	4.4	4.5	-0.1	-0.3	100.0%	-1.4
19445	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	4.1	4.2	-0.1	-0.3	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
19446	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	4.2	4.1	0.1	0.3	100.0%	-1.5
19447	AT5G58630.1 | expressed protein | chr5:23712906-23714678 REVERSE | Aliases: MZN1.24, MZN1_24	2.9	2.9	-0.0	-0.3	100.0%	-2.0
19448	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	8.0	8.2	-0.2	-0.3	100.0%	-1.4
19449	AT5G47440.1 | expressed protein, strong similarity to unknown protein (pir::G71442) | chr5:19260797-19262431 REVERSE | Aliases: MNJ7.2, MNJ7_2	3.0	3.0	-0.0	-0.3	100.0%	-2.1
19450	AT3G42480.1 | expressed protein | chr3:14639205-14639621 REVERSE | Aliases: T32A11.50	2.6	2.7	-0.0	-0.3	100.0%	-2.3
19451	AT5G42520.1 | expressed protein | chr5:17017511-17019835 FORWARD | Aliases: MDH9.22, MDH9_22	9.0	9.0	-0.1	-0.3	100.0%	-1.6
19452	AT4G15280.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr4:8719182-8720618 FORWARD | Aliases: DL3685W, FCAALL.255	3.8	3.8	0.0	0.3	100.0%	-2.0
19453	AT2G01970.1 | endomembrane protein 70, putative | chr2:451870-454884 REVERSE | Aliases: F14H20.4, F14H20_4	5.6	5.3	0.3	0.3	100.0%	-1.1
19454	AT1G56080.1 | expressed protein | chr1:20977826-20979956 REVERSE | Aliases: T6H22.12, T6H22_12	4.2	4.3	-0.1	-0.3	100.0%	-1.4
19455	AT2G47800.1 | Symbol: ATMRP4 |	4.4	4.5	-0.1	-0.3	100.0%	-1.8
19456	AT1G67860.1 | expressed protein | chr1:25448468-25448926 REVERSE | Aliases: T23K23.29, T23K23_29	2.9	2.8	0.1	0.3	100.0%	-2.0
19457	AT1G19060.1 | expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626) | chr1:6582057-6583592 REVERSE | Aliases: F14D16.21, F14D16_21	2.8	2.8	-0.0	-0.3	100.0%	-1.9
19458	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	2.6	2.7	-0.0	-0.3	100.0%	-2.1
19459	AT1G30660.1 | toprim domain-containing protein, contains Pfam profile PF01751: Toprim domain | chr1:10876835-10878999 FORWARD | Aliases: T5I8.11, T5I8_11	4.6	4.4	0.1	0.3	100.0%	-1.2
19460	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	4.4	4.3	0.1	0.3	100.0%	-1.2
19461	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	8.2	0.0	0.3	100.0%	-1.7
19462	AT3G44580.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr3:16171499-16171990 REVERSE | Aliases: F14L2.130	2.8	2.8	-0.0	-0.3	100.0%	-2.2
19463	AT4G13985.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.4	-0.0	-0.3	100.0%	-2.3
19464	AT5G28170.1 | expressed protein, similar to At1g35110, At1g44880, At3g42530, At4g19320, At5g36020, At4g03970, At3g43010, At2g10350 | chr5:10152151-10154738 FORWARD | Aliases: F26C17.3	2.8	2.8	0.0	0.3	100.0%	-1.8
19465	AT1G77250.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr1:29025201-29028349 REVERSE | Aliases: T14N5.11, T14N5_11	5.7	5.6	0.1	0.3	100.0%	-1.4
19466	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	3.2	3.2	-0.1	-0.3	100.0%	-1.7
19467	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	2.2	-0.0	-0.3	100.0%	-2.8
19468	AT5G52200.1 | expressed protein | chr5:21219865-21221976 REVERSE | Aliases: F17P19.10, F17P19_10	8.2	8.1	0.1	0.3	100.0%	-1.5
19469	AT1G11390.1 | ABC1 family protein, contains Pfam domain, PF03109: ABC1 family | chr1:3834459-3837498 REVERSE | Aliases: T23J18.5, T23J18_5	4.8	4.8	0.0	0.3	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
19470	AT1G78920.1 | Symbol: AVP2 | vacuolar-type H+-translocating inorganic pyrophosphatase (AVPL1), identical to vacuolar-type H+-translocating inorganic pyrophosphatase GI:6901676 from (Arabidopsis thaliana) | chr1:29676386-29681874 FORWARD | Aliases: F9K20.2, F9K20_2, VACUOLAR TYPE H+ TRANSLOCATING INORGANIC PYROPHOSPHATASE	8.5	8.6	-0.1	-0.3	100.0%	-1.6
19471	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	4.9	4.7	0.2	0.3	100.0%	-1.1
19472	ATMG00050.1 | Symbol: ORF131 |	3.2	3.2	-0.1	-0.3	100.0%	-1.2
19473	AT2G07728.1 | expressed protein, ; expression supported by MPSS | chr2:3453683-3456124 FORWARD | Aliases: T5E7.16, T5E7_16	2.2	2.2	-0.0	-0.3	100.0%	-2.1
19474	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	5.8	5.7	0.1	0.3	100.0%	-1.7
19475	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	2.8	2.8	-0.0	-0.3	100.0%	-2.1
19476	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	2.1	-0.0	-0.3	100.0%	-2.4
19477	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	5.0	-0.1	-0.3	100.0%	-1.5
19478	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	2.8	-0.0	-0.3	100.0%	-2.1
19479	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	-0.3	100.0%	-1.8
19480	AT5G11810.1 | expressed protein | chr5:3808721-3810749 FORWARD | Aliases: F14F18.1	7.6	7.7	-0.1	-0.3	100.0%	-1.6
19481	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	-0.0	-0.3	100.0%	-1.7
19482	AT1G20080.1 | C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain | chr1:6962227-6964903 FORWARD | Aliases: T20H2.13, T20H2_13	3.4	3.4	0.0	0.3	100.0%	-2.0
19483	AT3G09380.1 | expressed protein, contains Pfam profile PF01883: Domain of unknown function | chr3:2885271-2886122 REVERSE | Aliases: F3L24.26	3.3	3.3	0.0	0.3	100.0%	-2.1
19484	AT3G52770.1 | expressed protein, emm32, Streptococcus pyogenes, EMBL:SPEMM32G | chr3:19568699-19569985 REVERSE | Aliases: F3C22.170	2.7	2.6	0.0	0.3	100.0%	-2.7
19485	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%	-2.1
19486	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	3.0	-0.0	-0.3	100.0%	-2.0
19487	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	4.2	4.3	-0.0	-0.3	100.0%	-1.7
19488	AT1G77220.1 | expressed protein, contains Pfam profile PF03619: Domain of unknown function | chr1:29017665-29020697 FORWARD | Aliases: T14N5.8, T14N5_8	5.0	4.9	0.1	0.3	100.0%	-1.5
19489	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	6.2	6.1	0.1	0.3	100.0%	-1.6
19490	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	-0.3	100.0%	-2.0
19491	AT4G03680.1 | expressed protein | chr4:1628883-1629934 FORWARD | Aliases: T5L23.18, T5L23_18	2.8	2.8	-0.0	-0.3	100.0%	-2.3

Rank	Description	Sync	Root	M	t	adj.q	B
19492	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	-0.0	-0.3	100.0%	-2.5
19493	AT3G59190.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.8	2.8	-0.0	-0.3	100.0%	-2.1
19494	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	-0.0	-0.3	100.0%	-1.7
19495	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	2.6	2.6	-0.0	-0.3	100.0%	-1.8
19496	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	9.6	-0.3	-0.3	100.0%	-0.9
19497	AT3G59910.1 | expressed protein | chr3:22141460-22144533 REVERSE | Aliases: F24G16.180	4.0	4.0	-0.1	-0.3	100.0%	-1.9
19498	AT5G41320.1 | expressed protein | chr5:16551670-16553217 FORWARD | Aliases: MYC6.3, MYC6_3	2.7	2.6	0.0	0.3	100.0%	-2.0
19499	AT5G51510.1 | expressed protein | chr5:20938659-20940204 FORWARD | Aliases: K17N15.6, K17N15_6	8.0	7.9	0.1	0.3	100.0%	-1.5
19500	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	4.9	4.9	0.1	0.3	100.0%	-1.7
19501	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	4.0	3.9	0.1	0.3	100.0%	-1.6
19502	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	2.5	2.5	-0.0	-0.3	100.0%	-2.5
19503	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	3.7	0.1	0.3	100.0%	-1.8
19504	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	3.2	0.0	0.3	100.0%	-2.3
19505	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	2.9	2.8	0.1	0.3	100.0%	-1.8
19506	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	7.4	7.3	0.1	0.3	100.0%	-1.5
19507	AT1G68290.1 | bifunctional nuclease, putative, similar to bifunctional nuclease (Zinnia elegans) gi:4099833:gb:AAD00694 | chr1:25600334-25602101 FORWARD | Aliases: T22E19.8, T22E19_8	2.6	2.7	-0.1	-0.3	100.0%	-1.8
19508	AT5G58784.1 | dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative, similar to GI:796076 | chr5:23757176-23758220 REVERSE | Aliases: None	2.3	2.4	-0.0	-0.3	100.0%	-2.2
19509	AT1G07850.1 | fringe-related protein, + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.	2.5	2.6	-0.0	-0.3	100.0%	-2.2
19510	AT1G29680.1 | expressed protein | chr1:10377503-10378947 REVERSE | Aliases: F15D2.23, F15D2_23	3.1	3.0	0.1	0.3	100.0%	-2.0
19511	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%	-2.3
19512	AT1G76870.1 | expressed protein | chr1:28862144-28863301 FORWARD | Aliases: F7O12.4, F7O12_4	3.2	3.2	0.0	0.3	100.0%	-2.2
19513	AT4G17710.1 | homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, similar to HD-Zip homeo domain OCL4 protein (GI:8920425) (Zea mays); contains Pfam PF00046: Homeobox domain and Pfam PF01852: START domain | chr4:9856309-9859301 REVERSE | Aliases: DL4890C, FCAALL.102	3.4	3.5	-0.1	-0.3	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
19514	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	3.3	3.3	-0.1	-0.3	100.0%	-1.9
19515	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	2.5	2.4	0.0	0.3	100.0%	-2.0
19516	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	-0.3	100.0%	-2.2
19517	AT5G44230.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:17831563-17833536 FORWARD | Aliases: MLN1.16, MLN1_16	2.6	2.5	0.0	0.3	100.0%	-2.1
19518	AT1G72760.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:27389083-27391936 REVERSE | Aliases: F28P22.5, F28P22_5	2.9	3.0	-0.0	-0.3	100.0%	-1.9
19519	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	-0.3	100.0%	-2.0
19520	AT1G66550.1 | Symbol: WRKY67 |	2.3	2.3	0.0	0.3	100.0%	-2.7
19521	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	-0.0	-0.3	100.0%	-2.5
19522	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	-0.0	-0.3	100.0%	-2.5
19523	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	-0.0	-0.3	100.0%	-2.5
19524	AT5G33230.1 | hypothetical protein | chr5:12493907-12494364 FORWARD | Aliases: T29A4.40, T29A4_40	2.6	2.7	-0.0	-0.3	100.0%	-2.5
19525	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	-0.0	-0.3	100.0%	-2.5
19526	AT5G44415.1 | hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287 | chr5:17911173-17913602 FORWARD | Aliases: None	2.6	2.7	-0.0	-0.3	100.0%	-2.5
19527	AT4G10640.1 | calmodulin-binding family protein, contains IQ calmodulin-binding motif, Pfam:PF00612 | chr4:6571895-6574423 FORWARD | Aliases: T4F9.100, T4F9_100	4.1	4.1	0.1	0.3	100.0%	-1.3
19528	AT3G19610.1 | hypothetical protein | chr3:6812499-6814582 REVERSE | Aliases: MMB12.8	2.3	2.3	0.0	0.3	100.0%	-2.5
19529	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	2.5	2.5	0.0	0.3	100.0%	-2.4
19530	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	-0.3	100.0%	-2.3
19531	NA	3.1	3.1	-0.0	-0.3	100.0%	-2.0
19532	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	0.3	100.0%	-2.2
19533	AT1G67960.1 | expressed protein, AT-AC non-consensus splice sites at intron 6 | chr1:25484315-25487925 REVERSE | Aliases: T23K23.19, T23K23_19	5.5	5.4	0.1	0.3	100.0%	-1.5
19534	AT5G37310.1 | endomembrane protein 70, putative, multispanning membrane protein, Homo sapiens, EMBL:HSU94831 | chr5:14790059-14793436 REVERSE | Aliases: MNJ8.100, MNJ8_100	4.5	4.6	-0.1	-0.3	100.0%	-1.4
19535	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	3.7	3.6	0.1	0.3	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
19536	AT5G38370.1 | hypothetical protein | chr5:15357623-15357925 REVERSE | Aliases: MXI10.4, MXI10_4	2.6	2.6	-0.0	-0.3	100.0%	-2.3
19537	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%	-2.3
19538	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	3.0	3.0	0.0	0.3	100.0%	-1.8
19539	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	0.3	100.0%	-2.3
19540	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	6.1	6.0	0.1	0.3	100.0%	-1.3
19541	AT1G80130.1 | expressed protein | chr1:30145855-30147538 REVERSE | Aliases: F18B13.21, F18B13_21	3.8	3.9	-0.0	-0.3	100.0%	-2.0
19542	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	3.0	-0.0	-0.3	100.0%	-1.7
19543	AT4G18840.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:10338730-10340367 REVERSE | Aliases: F13C5.10, F13C5_10	4.3	4.3	0.1	0.3	100.0%	-1.6
19544	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	6.3	6.2	0.1	0.3	100.0%	-1.8
19545	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%	-2.3
19546	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	12.3	0.1	0.3	100.0%	-2.0
19547	AT2G47220.1 | 3' exoribonuclease family domain 1 protein-related, similar to polynucleotide phosphorylase (Pisum sativum) GI:2286200, polyribonucleotide phophorylase (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	-0.3	100.0%	-1.9
19548	AT4G36510.1 | hypothetical protein | chr4:17228780-17229454 FORWARD | Aliases: AP22.52, AP22_52	4.2	4.2	-0.0	-0.3	100.0%	-1.8
19549	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	0.0	0.3	100.0%	-2.5
19550	AT5G66800.1 | expressed protein | chr5:26688649-26689740 FORWARD | Aliases: MUD21.4, MUD21_4	3.8	3.7	0.1	0.3	100.0%	-1.4
19551	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	-0.3	100.0%	-2.0
19552	AT3G58010.1 | expressed protein | chr3:21486790-21488475 REVERSE | Aliases: T10K17.220	6.6	6.6	0.1	0.3	100.0%	-1.3
19553	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%	-2.0
19554	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	2.8	2.7	0.0	0.3	100.0%	-1.9
19555	AT1G02710.1 | glycine-rich protein | chr1:589706-589996 REVERSE | Aliases: T14P4.26, T14P4_26	6.2	6.3	-0.1	-0.3	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
19556	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	2.7	2.7	-0.0	-0.3	100.0%	-2.2
19557	AT5G62910.1 | expressed protein, predicted proteins, Arabidopsis thaliana | chr5:25267960-25269430 FORWARD | Aliases: MQB2.23, MQB2_23	5.5	5.5	0.1	0.3	100.0%	-1.6
19558	AT5G46230.1 | expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538 | chr5:18759667-18760272 REVERSE | Aliases: MPL12.1, MPL12_1	5.1	5.0	0.1	0.3	100.0%	-1.4
19559	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	0.0	0.3	100.0%	-2.0
19560	AT4G13150.1 | expressed protein | chr4:7651532-7652585 REVERSE | Aliases: F17N18.40, F17N18_40	3.0	3.1	-0.0	-0.3	100.0%	-2.5
19561	AT1G50080.1 | hypothetical protein | chr1:18557669-18557944 REVERSE | Aliases: F2J10.18, F2J10_18	2.7	2.7	-0.0	-0.3	100.0%	-2.1
19562	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	7.9	8.2	-0.3	-0.3	100.0%	-1.1
19563	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)	5.8	5.9	-0.1	-0.3	100.0%	-1.2
19564	AT3G54630.1 | expressed protein, weak similarity to retinoblastoma-associated protein HEC (Homo sapiens) GI:2501873 | chr3:20232075-20234006 REVERSE | Aliases: T14E10.200	5.6	5.5	0.1	0.3	100.0%	-1.3
19565	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	2.8	2.8	-0.0	-0.3	100.0%	-2.1
19566	AT3G10120.1 | expressed protein | chr3:3130077-3130896 FORWARD | Aliases: T22K18.5	3.9	4.0	-0.1	-0.3	100.0%	-1.8
19567	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	2.4	-0.0	-0.3	100.0%	-2.2
19568	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.	3.1	3.2	-0.1	-0.3	100.0%	-1.8
19569	AT1G16840.4 | expressed protein | chr1:5762706-5764027 REVERSE | Aliases: F17F16.27	7.3	7.2	0.1	0.3	100.0%	-1.3
19570	AT3G43700.1 | Symbol: ATBPM6 |	3.7	3.6	0.1	0.3	100.0%	-1.7
19571	AT2G41590.1 | expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277 | chr2:17350438-17352083 FORWARD | Aliases: T32G6.11, T32G6_11	2.5	2.5	-0.0	-0.3	100.0%	-2.1
19572	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	2.7	2.8	-0.1	-0.3	100.0%	-1.9
19573	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	2.5	2.6	-0.0	-0.3	100.0%	-2.1
19574	AT3G57140.2 | patatin-related, contains Patatin domain PF01734	2.6	2.7	-0.0	-0.3	100.0%	-2.1
19575	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	8.8	8.6	0.2	0.3	100.0%	-1.2
19576	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	4.0	-0.1	-0.3	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
19577	AT4G21640.1 | subtilase family protein, similar to subtilase SP1 (Oryza sativa) GI:9957714 | chr4:11496846-11500630 REVERSE | Aliases: F17L22.100, F17L22_100	1.8	1.8	-0.0	-0.3	100.0%	-1.8
19578	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	3.3	0.1	0.3	100.0%	-1.8
19579	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	2.6	2.6	-0.0	-0.3	100.0%	-2.1
19580	AT2G19860.1 | Symbol: ATHXK2 |	5.6	5.5	0.1	0.3	100.0%	-1.7
19581	AT2G34190.1 | xanthine/uracil permease family protein, contains Pfam profile: PF00860 permease family | chr2:14443888-14446595 FORWARD | Aliases: F13P17.3, F13P17_3	5.6	5.6	0.1	0.3	100.0%	-1.5
19582	AT5G05790.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr5:1740573-1742029 REVERSE | Aliases: MJJ3.20, MJJ3_20	8.7	8.7	-0.1	-0.3	100.0%	-1.6
19583	AT5G27730.1 | expressed protein | chr5:9820253-9823090 FORWARD | Aliases: T1G16.60, T1G16_60	4.3	4.3	0.1	0.3	100.0%	-1.8
19584	AT3G50120.1 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function; expression supported by MPSS | chr3:18596140-18598229 REVERSE | Aliases: F3A4.200	2.5	2.6	-0.0	-0.3	100.0%	-2.3
19585	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	4.6	4.7	-0.1	-0.3	100.0%	-1.3
19586	AT5G64190.1 | expressed protein | chr5:25696658-25698379 FORWARD | Aliases: MSJ1.3, MSJ1_3	2.6	2.6	-0.0	-0.3	100.0%	-2.1
19587	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	5.4	5.4	0.1	0.3	100.0%	-1.9
19588	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	4.0	3.9	0.0	0.3	100.0%	-1.8
19589	AT1G01500.1 | expressed protein, identical to cDNA unknown protein GI:1922247 embY10087.1 | chr1:185133-186923 FORWARD | Aliases: F22L4.17, F22L4_17	6.6	6.6	0.0	0.3	100.0%	-1.7
19590	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	3.1	3.1	-0.0	-0.3	100.0%	-1.5
19591	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	3.1	3.1	-0.0	-0.3	100.0%	-1.5
19592	AT5G17580.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr5:5795304-5797180 FORWARD | Aliases: K10A8.60, K10A8_60	3.8	3.9	-0.1	-0.3	100.0%	-1.3
19593	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	3.0	-0.0	-0.3	100.0%	-2.5
19594	AT3G01960.1 | expressed protein | chr3:324588-325094 REVERSE | Aliases: F28J7.29, F28J7_29	2.3	2.2	0.0	0.3	100.0%	-2.4
19595	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	3.9	4.0	-0.0	-0.3	100.0%	-1.7
19596	AT3G16710.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:5690245-5691549 FORWARD | Aliases: MGL6.18	2.8	2.9	-0.0	-0.3	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
19597	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	6.1	6.1	0.1	0.3	100.0%	-1.4
19598	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	5.2	5.3	-0.1	-0.3	100.0%	-1.4
19599	AT4G00660.2 | DEAD/DEAH box helicase, putative, similar to ATP-dependent RNA helicases	4.8	4.6	0.2	0.3	100.0%	-1.4
19600	AT1G17690.1 | expressed protein | chr1:6082748-6088333 REVERSE | Aliases: F11A6.3, F11A6_3	6.0	5.9	0.0	0.3	100.0%	-1.7
19601	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	-0.3	100.0%	-1.8
19602	AT1G05270.1 | TraB family protein, contains Pfam domain PF01963: TraB family | chr1:1531640-1534389 REVERSE | Aliases: YUP8H12.12, YUP8H12_12	4.1	4.2	-0.1	-0.3	100.0%	-1.4
19603	AT4G21020.1 | late embryogenesis abundant domain-containing protein / LEA domain-containing protein, low similarity to SP:P23283 Desiccation-related protein {Craterostigma plantagineum}; contains Pfam profile PF02987: Late embryogenesis abundant protein | chr4:11228198-11229588 FORWARD | Aliases: T13K14.180, T13K14_180	2.9	2.9	0.0	0.3	100.0%	-2.1
19604	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 homeodomain-containing transcription factor FWA (FWA)GI:13506819 | chr4:13038369-13042452 FORWARD | Aliases: FWA, M7J2.100, M7J2_100	2.5	2.5	-0.0	-0.3	100.0%	-2.2
19605	AT1G13900.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	7.1	7.1	0.1	0.3	100.0%	-1.7
19606	AT5G54540.1 | expressed protein | chr5:22173738-22175280 FORWARD | Aliases: MRB17.4, MRB17_4	9.2	9.3	-0.1	-0.3	100.0%	-1.3
19607	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	3.2	-0.0	-0.3	100.0%	-2.1
19608	AT1G35890.1 | expressed protein | chr1:13342512-13343165 FORWARD | Aliases: F10O5.6, F10O5_6	2.8	2.8	-0.0	-0.3	100.0%	-2.1
19609	AT2G46400.1 | Symbol: WRKY46 |	4.2	4.1	0.1	0.3	100.0%	-1.4
19610	AT3G13370.1 | hypothetical protein | chr3:4341671-4342237 FORWARD | Aliases: MDC11.21	2.8	2.8	-0.0	-0.3	100.0%	-2.3
19611	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	7.5	7.4	0.1	0.3	100.0%	-1.4
19612	AT3G44570.1 | hypothetical protein | chr3:16169891-16170822 FORWARD | Aliases: F14L2.120	2.1	2.1	0.0	0.3	100.0%	-2.6
19613	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	3.3	3.4	-0.1	-0.3	100.0%	-1.8
19614	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	2.6	2.6	0.0	0.3	100.0%	-2.1
19615	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	6.0	6.0	0.1	0.3	100.0%	-1.4
19616	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	3.0	-0.0	-0.3	100.0%	-2.2
19617	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)	3.6	3.7	-0.1	-0.3	100.0%	-1.7
19618	AT5G09570.1 | expressed protein, contains Pfam domain, PF04933: Protein of unknown function (DUF657) | chr5:2970670-2972182 FORWARD | Aliases: F17I14.240, F17I14_240	5.1	5.2	-0.1	-0.3	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
19619	AT2G30120.1 | expressed protein | chr2:12867618-12868987 REVERSE | Aliases: T27E13.14, T27E13_14	2.8	2.7	0.0	0.3	100.0%	-2.3
19620	AT2G35780.1 | Symbol: SCPL26 |	7.6	7.6	-0.0	-0.3	100.0%	-1.5
19621	AT1G24706.1 | expressed protein | chr1:8741926-8755544 FORWARD | Aliases: F5A9.21, F5A9_21	4.7	4.8	-0.1	-0.3	100.0%	-1.5
19622	NA	2.8	2.8	-0.0	-0.3	100.0%	-2.3
19623	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	4.3	4.3	0.0	0.3	100.0%	-1.6
19624	AT4G39260.4 | Symbol: ATGRP8 |	10.8	11.0	-0.2	-0.3	100.0%	-1.0
19625	AT1G74540.1 | Symbol: CYP98A8 | cytochrome P450, putative, similar to cytochrome P450 GB:O48922 (Glycine max); contains Pfam profile: PF00067 cytochrome P450	2.7	2.7	0.0	0.3	100.0%	-2.2
19626	AT3G24230.1 | pectate lyase family protein, similar to pectate lyase GP:14531296 from (Fragaria x ananassa) | chr3:8774623-8777414 FORWARD | Aliases: MUJ8.14	2.3	2.4	-0.0	-0.3	100.0%	-2.2
19627	AT5G49110.1 | expressed protein, ; expression supported by MPSS | chr5:19917429-19923151 FORWARD | Aliases: K20J1.8, K20J1_8	3.7	3.7	-0.0	-0.3	100.0%	-2.0
19628	AT5G47500.1 | pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase | chr5:19288186-19290101 REVERSE | Aliases: MNJ7.9, MNJ7_9	3.1	3.2	-0.0	-0.3	100.0%	-2.0
19629	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	6.0	6.1	-0.1	-0.3	100.0%	-1.6
19630	AT3G49020.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.8	2.8	-0.0	-0.3	100.0%	-2.1
19631	AT3G13540.1 | Symbol: ATMYB5 |	3.3	3.3	0.0	0.3	100.0%	-1.8
19632	AT5G15470.1 | glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8 | chr5:5021013-5024745 REVERSE | Aliases: T20K14.80, T20K14_80	3.2	3.2	-0.1	-0.3	100.0%	-1.5
19633	AT1G13740.1 | expressed protein | chr1:4713671-4715404 FORWARD | Aliases: F21F23.17, F21F23_17	7.2	7.1	0.1	0.3	100.0%	-1.3
19634	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%	-1.6
19635	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	5.2	5.3	-0.1	-0.3	100.0%	-1.4
19636	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	4.6	4.6	-0.0	-0.3	100.0%	-1.4
19637	AT1G09450.1 | haspin-related, similar to haspin (GI:9229937) {Mus musculus} and haploid germ cell-specific nuclear protein kinase (GI:13561418) {Mus musculus}	2.9	2.8	0.0	0.3	100.0%	-1.9
19638	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	6.5	6.4	0.1	0.3	100.0%	-1.6
19639	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	3.1	3.0	0.1	0.3	100.0%	-1.6
19640	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	0.3	100.0%	-2.1
19641	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%	-2.3

Rank	Description	Sync	Root	M	t	adj.q	B
19642	AT5G02770.1 | expressed protein | chr5:627117-629253 REVERSE | Aliases: F9G14.80, F9G14_80	4.1	4.0	0.1	0.3	100.0%	-1.5
19643	AT1G68380.1 | expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266 | chr1:25639501-25641125 REVERSE | Aliases: T2E12.7	2.1	2.1	-0.0	-0.3	100.0%	-2.5
19644	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	4.3	4.4	-0.1	-0.3	100.0%	-1.6
19645	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	-0.3	100.0%	-2.6
19646	AT4G34850.1 | chalcone and stilbene synthase family protein, similar to chalcone synthase homolog PrChS1, Pinus radiata, gb:U90341; similar to anther-specific protein (Nicotiana sylvestris)(GI:2326774), YY2 protein (Oryza sativa)(GI:2645170) | chr4:16608318-16610253 FORWARD | Aliases: F11I11.90, F11I11_90	3.8	3.8	-0.1	-0.3	100.0%	-1.6
19647	AT5G49250.1 | expressed protein | chr5:19982569-19983171 FORWARD | Aliases: K21P3.13, K21P3_13	2.7	2.8	-0.0	-0.3	100.0%	-1.8
19648	AT5G21010.1 | Symbol: ATBPM5 |	5.0	5.1	-0.0	-0.3	100.0%	-1.7
19649	AT3G23720.1 | expressed protein | chr3:8537372-8537617 FORWARD | Aliases: MYM9.7	2.9	2.8	0.0	0.3	100.0%	-2.8
19650	AT4G11940.1 | hypothetical protein, predicted proteins Arabidopsis thaliana | chr4:7168167-7168961 FORWARD | Aliases: F16J13.10, F16J13_10	2.6	2.6	-0.0	-0.3	100.0%	-2.0
19651	AT3G29640.1 | hypothetical protein, contains similarity to hypothetical proteins | chr3:11490525-11491040 FORWARD | Aliases: T13J10.7	2.4	2.5	-0.0	-0.3	100.0%	-2.0
19652	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	0.3	100.0%	-2.1
19653	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	0.0	0.3	100.0%	-2.2
19654	AT5G55380.1 | membrane bound O-acyl transferase (MBOAT) family protein / wax synthase-related,	4.5	4.6	-0.1	-0.3	100.0%	-1.3
19655	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	3.3	3.3	-0.1	-0.3	100.0%	-1.7
19656	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	0.3	100.0%	-2.3
19657	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	-0.3	100.0%	-1.9
19658	AT2G01100.3 | expressed protein | chr2:81455-83217 FORWARD | Aliases: F23H14.7, F23H14_7	8.8	8.9	-0.1	-0.3	100.0%	-1.8
19659	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)	3.7	3.7	-0.0	-0.3	100.0%	-1.7
19660	AT5G32440.1 | expressed protein | chr5:12094126-12095787 FORWARD | Aliases: F18O9.50, F18O9_50	7.8	7.9	-0.1	-0.3	100.0%	-1.4
19661	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	4.5	4.4	0.1	0.3	100.0%	-1.4
19662	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	-0.0	-0.3	100.0%	-1.8
19663	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	2.8	-0.0	-0.3	100.0%	-2.3

Rank	Description	Sync	Root	M	t	adj.q	B
19664	AT2G43070.1 | protease-associated (PA) domain-containing protein, contains protease associated (PA) domain, Pfam:PF02225 | chr2:17918015-17921928 REVERSE | Aliases: None	5.1	4.9	0.2	0.3	100.0%	-1.2
19665	AT1G20410.1 | expressed protein | chr1:7078889-7082537 REVERSE | Aliases: F5M15.23, F5M15_23	3.6	3.6	-0.1	-0.3	100.0%	-1.6
19666	NA	2.3	2.3	-0.0	-0.3	100.0%	-2.9
19667	AT5G41920.1 | scarecrow transcription factor family protein | chr5:16796977-16798427 FORWARD | Aliases: MJC20.2, MJC20_2	5.3	5.3	0.0	0.3	100.0%	-1.8
19668	AT4G36780.1 | brassinosteroid signalling positive regulator-related, contains similarity to BZR1 protein (Arabidopsis thaliana) gi:20270971:gb:AAM18490 | chr4:17332523-17334347 REVERSE | Aliases: AP22.34, AP22_34	3.2	3.2	-0.0	-0.3	100.0%	-2.0
19669	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	-0.3	100.0%	-2.1
19670	AT5G40630.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr5:16288368-16289698 REVERSE | Aliases: MNF13.18, MNF13_18	4.2	4.2	0.0	0.3	100.0%	-1.5
19671	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	11.4	11.4	-0.1	-0.3	100.0%	-1.7
19672	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	0.3	100.0%	-1.7
19673	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	2.9	-0.0	-0.3	100.0%	-1.9
19674	AT4G08602.1 | expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g43205.1) | chr4:5489256-5489971 REVERSE | Aliases: None	2.6	2.6	-0.0	-0.3	100.0%	-1.7
19675	AT1G78620.2 | integral membrane family protein, contains Pfam domain PF01940: Integral membrane protein | chr1:29577764-29580687 REVERSE | Aliases: T30F21.5, T30F21_5	6.6	6.5	0.1	0.3	100.0%	-1.6
19676	AT3G13520.1 | Symbol: AGP12 | arabinogalactan-protein (AGP12), identical to gi:10880501:gb:AAG24280 | chr3:4408932-4409447 FORWARD | Aliases: ARABINOGALACTAN PROTEIN 12, MRP15.18	12.0	12.1	-0.0	-0.3	100.0%	-2.2
19677	AT4G33480.1 | expressed protein | chr4:16105614-16108649 REVERSE | Aliases: F17M5.240, F17M5_240	3.0	3.0	0.0	0.3	100.0%	-2.1
19678	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	8.8	9.0	-0.2	-0.3	100.0%	-1.5
19679	AT3G55730.1 | Symbol: MYB109 |	5.0	4.9	0.1	0.3	100.0%	-1.6
19680	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	2.2	2.2	-0.0	-0.3	100.0%	-2.5
19681	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	3.5	-0.1	-0.3	100.0%	-1.9
19682	AT4G09150.1 | T-complex protein 11, contains Pfam PF05794: T-complex protein 11 | chr4:5828622-5833657 FORWARD | Aliases: F23J3.180, F23J3_180	5.7	5.8	-0.1	-0.3	100.0%	-1.4
19683	AT1G54180.1 | expressed protein | chr1:20231364-20232186 FORWARD | Aliases: F15I1.28, F15I1_28	2.9	3.0	-0.0	-0.3	100.0%	-2.1
19684	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	0.3	100.0%	-2.2
19685	AT5G49800.1 | expressed protein | chr5:20251868-20253410 REVERSE | Aliases: K21G20.1, K21G20_1	3.4	3.4	-0.0	-0.3	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
19686	AT3G43880.1 | hypothetical protein, p97 homologous protein, Canis familiaris, EMBL:CFA388531 | chr3:15749160-15749603 REVERSE | Aliases: T15B3.20	2.9	2.9	-0.0	-0.3	100.0%	-1.9
19687	AT5G18930.1 | adenosylmethionine decarboxylase family protein, contains Pfam profile: PF01536 adenosylmethionine decarboxylase	2.9	2.9	-0.0	-0.3	100.0%	-2.3
19688	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%	-1.4
19689	AT1G01110.1 | expressed protein, contains Prosite PS00165: Serine/threonine dehydratases pyridoxal-phosphate attachment site | chr1:52869-54685 FORWARD | Aliases: T25K16.10, T25K16_10	3.0	3.0	-0.0	-0.3	100.0%	-2.0
19690	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	-0.0	-0.3	100.0%	-2.7
19691	AT2G43320.1 | expressed protein | chr2:18003727-18007004 REVERSE | Aliases: F14B2.22	3.6	3.5	0.0	0.3	100.0%	-1.9
19692	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	2.7	2.7	0.0	0.3	100.0%	-2.2
19693	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	3.8	3.8	0.1	0.3	100.0%	-1.8
19694	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	3.3	3.3	-0.0	-0.3	100.0%	-1.7
19695	AT5G47200.1 | Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303750 from (Pisum sativum)	9.8	9.7	0.1	0.3	100.0%	-1.4
19696	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	6.8	7.0	-0.1	-0.3	100.0%	-1.3
19697	AT1G32375.1 | F-box family protein, contains F-box domain Pfam:PF00646	4.1	4.0	0.1	0.3	100.0%	-1.6
19698	AT1G43770.1 | PHD finger family protein, contains Pfam domain, PF00628: PHD-finger | chr1:16550949-16552991 FORWARD | Aliases: F28H19.3, F28H19_3	4.4	4.4	-0.1	-0.3	100.0%	-1.5
19699	AT1G53230.1 | Symbol: TCP3 | TCP family transcription factor 3 (TCP3), identical to transcription factor 3 (TCP3) (Arabidopsis thaliana) (GI:3243274); similar to flower development protein cycloidea (cyc3) GI:6358611 from (Misopates orontium) | chr1:19853456-19855393 REVERSE | Aliases: F12M16.13, F12M16_13, TCP3	2.8	2.8	0.0	0.3	100.0%	-1.8
19700	AT1G23670.2 | expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220 | chr1:8373275-8375857 REVERSE | Aliases: F28C11.25	2.4	2.4	-0.0	-0.3	100.0%	-2.4
19701	AT4G01210.1 | glycosyltransferase family protein 1, contains Pfam profile: PF00534 Glycosyl transferases group 1 | chr4:507738-512782 REVERSE | Aliases: F2N1.24, F2N1_24	7.9	7.8	0.1	0.3	100.0%	-1.6
19702	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	5.2	5.3	-0.1	-0.3	100.0%	-1.4
19703	AT1G69680.1 | expressed protein, similar to MOG1 isoform A (GI:9864064) (Homo sapiens)	5.3	5.3	0.1	0.3	100.0%	-1.3
19704	AT1G25360.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:8894415-8896787 FORWARD | Aliases: F4F7.25, F4F7_25	4.3	4.4	-0.1	-0.3	100.0%	-1.6
19705	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%	-2.6
19706	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	3.6	3.7	-0.0	-0.3	100.0%	-1.8
19707	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	-0.0	-0.3	100.0%	-2.3

Rank	Description	Sync	Root	M	t	adj.q	B
19708	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	2.4	2.4	-0.0	-0.3	100.0%	-2.3
19709	AT3G01430.1 | expressed protein | chr3:165415-166254 REVERSE | Aliases: T13O15.7, T13O15_7	5.4	5.4	0.1	0.3	100.0%	-1.4
19710	AT4G12220.1 | expressed protein | chr4:7283242-7283733 REVERSE | Aliases: T4C9.60, T4C9_60	2.3	2.3	-0.0	-0.3	100.0%	-2.4
19711	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	2.5	2.5	-0.0	-0.3	100.0%	-2.1
19712	AT3G05760.1 | expressed protein | chr3:1707909-1710529 FORWARD | Aliases: F10A16.5, F10A16_5	9.5	9.6	-0.1	-0.3	100.0%	-1.8
19713	AT2G35540.1 | DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226: DnaJ domain	5.4	5.4	-0.0	-0.3	100.0%	-2.0
19714	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	2.7	2.7	-0.0	-0.3	100.0%	-2.2
19715	AT3G47140.1 | F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain | chr3:17368011-17368786 FORWARD | Aliases: F13I12.190	2.5	2.6	-0.0	-0.3	100.0%	-2.2
19716	AT2G36920.1 | expressed protein | chr2:15515877-15516926 FORWARD | Aliases: T1J8.10, T1J8_10	3.1	3.1	-0.0	-0.3	100.0%	-2.0
19717	AT1G23600.1 | expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220; expression supported by MPSS | chr1:8361187-8362347 REVERSE | Aliases: F28C11.31	2.7	2.7	0.0	0.3	100.0%	-1.9
19718	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	3.7	3.6	0.1	0.3	100.0%	-1.5
19719	AT2G39280.1 | RabGAP/TBC domain-containing protein, contains Pfam profile PF00566: TBC domain | chr2:16408837-16413728 REVERSE | Aliases: T16B24.8, T16B24_8	2.6	2.6	0.0	0.3	100.0%	-2.1
19720	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	3.2	3.2	-0.0	-0.3	100.0%	-1.8
19721	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	3.1	-0.0	-0.3	100.0%	-1.8
19722	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	0.3	100.0%	-1.7
19723	AT4G17760.2 | similar to Rad1-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_550603.1) | chr4:9871803-9873411 FORWARD | Aliases: DL4915W, FCAALL.108	3.3	3.4	-0.0	-0.3	100.0%	-1.7
19724	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	2.1	0.0	0.3	100.0%	-2.7
19725	AT2G07020.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:2908470-2911195 REVERSE | Aliases: T4E14.13, T4E14_13	4.7	4.6	0.0	0.3	100.0%	-1.8
19726	AT2G19550.1 | esterase/lipase/thioesterase family protein, low similarity to cinnamoyl ester hydrolase CinI (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	3.6	3.7	-0.1	-0.3	100.0%	-1.6
19727	AT4G03380.1 | expressed protein | chr4:1485048-1490227 REVERSE | Aliases: F4C21.34, F4C21_34	3.2	3.2	-0.0	-0.3	100.0%	-2.1
19728	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)	6.9	6.6	0.3	0.3	100.0%	-1.1
19729	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	3.7	3.7	0.0	0.3	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
19730	AT5G46630.2 | clathrin adaptor complexes medium subunit family protein, contains Pfam profile: PF00928 adaptor complexes medium subunit family	8.7	8.6	0.1	0.3	100.0%	-1.6
19731	AT3G17440.2 | Symbol: NPSN13 |	5.3	5.2	0.1	0.3	100.0%	-1.5
19732	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	-0.3	100.0%	-2.3
19733	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	4.6	4.5	0.1	0.3	100.0%	-1.4
19734	AT5G41850.1 | expressed protein | chr5:16773926-16775019 REVERSE | Aliases: K16L22.14, K16L22_14	4.0	4.0	-0.0	-0.3	100.0%	-1.7
19735	AT3G13630.1 | expressed protein | chr3:4456961-4458141 FORWARD | Aliases: MMM17.2	2.8	2.8	-0.0	-0.3	100.0%	-2.1
19736	AT5G16550.1 | expressed protein | chr5:5405468-5406887 FORWARD | Aliases: MQK4.30, MQK4_30	6.0	5.9	0.1	0.3	100.0%	-1.4
19737	AT4G25770.1 | expressed protein | chr4:13117548-13120123 REVERSE | Aliases: F14M19.50, F14M19_50	4.0	3.9	0.1	0.3	100.0%	-1.3
19738	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	0.0	0.3	100.0%	-1.9
19739	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	8.4	8.4	-0.1	-0.3	100.0%	-1.5
19740	AT3G54360.1 | expressed protein, DNA-binding Mel-18 protein, Homo sapiens, PIR:JN0717 | chr3:20139283-20142832 REVERSE | Aliases: T12E18.50	7.9	8.0	-0.1	-0.3	100.0%	-1.5
19741	AT1G77850.1 | Symbol: ARF17 | transcriptional factor B3 family protein, similar to auxin response factor 10 GI:6165644 from (Arabidopsis thaliana); contains Pfam profile PF02362: B3 DNA binding domain | chr1:29277207-29280313 FORWARD | Aliases: ARF17, AUXIN RESPONSE FACTOR 17, F28K19.6, F28K19_6	3.3	3.4	-0.1	-0.3	100.0%	-1.5
19742	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	8.5	-0.1	-0.3	100.0%	-1.5
19743	AT3G19920.1 | expressed protein | chr3:6929717-6931812 REVERSE | Aliases: MPN9.17	3.3	3.4	-0.0	-0.3	100.0%	-2.1
19744	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	3.1	3.2	-0.0	-0.3	100.0%	-1.7
19745	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	2.7	-0.0	-0.3	100.0%	-1.9
19746	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	2.9	2.9	0.0	0.3	100.0%	-1.9
19747	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	5.2	5.3	-0.1	-0.3	100.0%	-1.2
19748	AT5G65170.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr5:26058400-26059532 FORWARD | Aliases: MQN23.11, MQN23_11	3.0	2.9	0.0	0.3	100.0%	-2.1
19749	AT3G19880.1 | F-box family protein, contains Pfam profile: PF00646 F-box domain | chr3:6911441-6912610 REVERSE | Aliases: MPN9.12	2.8	2.8	-0.0	-0.3	100.0%	-2.1
19750	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	6.6	6.6	-0.1	-0.3	100.0%	-1.3
19751	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	3.7	3.7	-0.1	-0.3	100.0%	-1.6
19752	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%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
19753	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	2.4	-0.0	-0.3	100.0%	-2.4
19754	AT4G16470.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:9287884-9289485 REVERSE | Aliases: DL4260C, FCAALL.374	4.3	4.4	-0.1	-0.3	100.0%	-1.5
19755	AT1G65210.1 | hypothetical protein | chr1:24228475-24229478 FORWARD | Aliases: T23K8.12, T23K8_12	2.3	2.3	0.0	0.3	100.0%	-2.5
19756	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	3.4	-0.0	-0.3	100.0%	-1.8
19757	AT5G12160.1 | expressed protein, similar to unknown protein (pir::T09909) | chr5:3931650-3932090 FORWARD | Aliases: MXC9.12, MXC9_12	3.5	3.5	0.0	0.3	100.0%	-1.8
19758	AT3G45460.1 | expressed protein | chr3:16689750-16691028 REVERSE | Aliases: F9K21.40	2.7	2.8	-0.0	-0.3	100.0%	-2.1
19759	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	0.0	0.3	100.0%	-2.0
19760	AT1G22110.1 | expressed protein | chr1:7801405-7802462 REVERSE | Aliases: F2E2.18, F2E2_18	3.6	3.7	-0.0	-0.3	100.0%	-1.7
19761	AT3G10150.1 | calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	2.9	2.8	0.0	0.3	100.0%	-1.8
19762	AT1G56700.1 | pyrrolidone-carboxylate peptidase family protein, similar to Pyrrolidone-carboxylate peptidase (5-oxoprolyl- peptidase) (Pyroglutamyl-peptidase I) (PGP-I) (Pyrase). (Swiss-Prot:O73944) (Pyrococcus furiosus); similar to Pyrrolidone-carboxylate peptidase (5-oxoprolyl- peptidase) (Pyroglutamyl-peptidase I) (PGP-I). (Swiss-Prot:O07883) (Thermococcus litoralis); contains Pfam PF01470: pyrrolidone-carboxylate peptidase	11.7	11.6	0.1	0.3	100.0%	-1.8
19763	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	5.7	5.7	0.1	0.3	100.0%	-1.6
19764	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	6.1	6.1	0.0	0.3	100.0%	-1.7
19765	AT1G64150.1 | expressed protein, contains Pfam profile PF01169: Uncharacterized protein family UPF0016	4.6	4.5	0.1	0.3	100.0%	-1.4
19766	AT1G31370.1 | expressed protein, ; expression supported by MPSS | chr1:11238279-11239344 REVERSE | Aliases: T8E3.14	2.2	2.2	-0.0	-0.3	100.0%	-2.6
19767	AT2G24780.1 | expressed protein | chr2:10572701-10573025 REVERSE | Aliases: F27A10.9, F27A10_9	2.3	2.3	-0.0	-0.3	100.0%	-2.2
19768	AT1G06340.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr1:1933296-1934013 REVERSE | Aliases: T2D23.4, T2D23_4	2.7	2.7	-0.0	-0.3	100.0%	-2.2
19769	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	4.1	4.1	-0.0	-0.3	100.0%	-1.6
19770	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	5.4	5.3	0.1	0.3	100.0%	-1.4
19771	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	-0.0	-0.2	100.0%	-2.4
19772	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	-0.2	100.0%	-2.3
19773	AT1G70760.1 | inorganic carbon transport protein-related, contains weak similarity to Swiss-Prot:P27372 inorganic carbon transport protein (Synechocystis sp.)	2.0	2.0	-0.0	-0.2	100.0%	-2.8
19774	AT1G50180.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	4.5	4.5	-0.0	-0.2	100.0%	-2.2

Rank	Description	Sync	Root	M	t	adj.q	B
19775	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}	4.9	5.0	-0.1	-0.2	100.0%	-1.5
19776	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%	-2.2
19777	AT1G76780.1 | expressed protein, ; expression supported by MPSS | chr1:28821535-28827150 FORWARD | Aliases: F28O16.15, F28O16_15	3.5	3.5	0.0	0.2	100.0%	-1.9
19778	AT5G60140.1 | transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain | chr5:24231303-24232581 REVERSE | Aliases: MGO3.2, MGO3_2	2.8	2.7	0.0	0.2	100.0%	-2.0
19779	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	6.3	6.3	0.1	0.2	100.0%	-1.5
19780	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	3.3	3.2	0.0	0.2	100.0%	-1.8
19781	AT2G05030.1 | hypothetical protein | chr2:1781883-1782500 FORWARD | Aliases: F1O13.16, F1O13_16	2.2	2.2	-0.0	-0.2	100.0%	-2.5
19782	AT2G18770.1 | expressed protein | chr2:8141726-8143642 FORWARD | Aliases: MSF3.15, MSF3_15	5.6	5.7	-0.1	-0.2	100.0%	-1.4
19783	AT2G45770.1 | Symbol: CPFTSY |	4.8	4.7	0.0	0.2	100.0%	-1.5
19784	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	2.8	2.8	0.0	0.2	100.0%	-2.0
19785	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	11.0	11.1	-0.1	-0.2	100.0%	-1.8
19786	AT3G11870.1 | protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr3:3747004-3749099 REVERSE | Aliases: F26K24.16	2.7	2.6	0.0	0.2	100.0%	-2.0
19787	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	3.5	3.5	0.0	0.2	100.0%	-1.7
19788	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	6.7	6.7	-0.0	-0.2	100.0%	-1.7
19789	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	3.1	3.1	0.0	0.2	100.0%	-2.0
19790	AT3G14670.1 | expressed protein | chr3:4927854-4928875 FORWARD | Aliases: MIE1.17	2.8	2.8	0.0	0.2	100.0%	-2.2
19791	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	4.2	4.3	-0.0	-0.2	100.0%	-1.7
19792	AT1G02940.1 | Symbol: ATGSTF5 | glutathione S-transferase, putative, similar to glutathione S-transferase GI:860955 from (Hyoscyamus muticus)	2.3	2.3	-0.0	-0.2	100.0%	-2.6
19793	AT1G34400.1 | expressed protein | chr1:12565970-12566593 REVERSE | Aliases: F7P12.11, F7P12_11	4.4	4.5	-0.1	-0.2	100.0%	-1.3
19794	AT3G18250.1 | expressed protein, ; expression supported by MPSS | chr3:6258183-6258413 REVERSE | Aliases: MIE15.4	4.6	4.6	0.0	0.2	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
19795	AT1G33420.1 | PHD finger family protein, contains Pfam profile: PF00628: PHD-finger | chr1:12120866-12123556 REVERSE | Aliases: F10C21.9, F10C21_9	5.8	5.8	0.0	0.2	100.0%	-1.7
19796	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	4.0	-0.1	-0.2	100.0%	-1.7
19797	AT3G49710.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:18448830-18450995 FORWARD | Aliases: T16K5.60	5.5	5.4	0.1	0.2	100.0%	-1.4
19798	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	8.5	8.6	-0.1	-0.2	100.0%	-1.4
19799	AT1G22080.1 | expressed protein | chr1:7792473-7794580 REVERSE | Aliases: F2E2.15, F2E2_15	3.2	3.1	0.0	0.2	100.0%	-2.0
19800	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	9.5	9.5	0.1	0.2	100.0%	-1.9
19801	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	8.9	-0.1	-0.2	100.0%	-1.6
19802	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	0.0	0.2	100.0%	-2.1
19803	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	0.0	0.2	100.0%	-2.1
19804	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%	-1.8
19805	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	5.0	5.1	-0.1	-0.2	100.0%	-1.6
19806	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	3.0	3.1	-0.0	-0.2	100.0%	-2.0
19807	AT5G52130.1 | expressed protein | chr5:21199694-21201101 REVERSE | Aliases: F17P19.2, F17P19_2	2.4	2.3	0.0	0.2	100.0%	-2.3
19808	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	4.5	4.4	0.1	0.2	100.0%	-1.5
19809	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	-0.0	-0.2	100.0%	-2.2
19810	AT1G17665.1 | expressed protein | chr1:6072591-6074477 REVERSE | Aliases: None	3.2	3.2	0.0	0.2	100.0%	-1.9
19811	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	9.9	9.9	-0.0	-0.2	100.0%	-1.7
19812	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	-0.2	100.0%	-1.9
19813	AT1G32290.1 | expressed protein | chr1:11650202-11650547 REVERSE | Aliases: F27G20.4	8.6	8.7	-0.1	-0.2	100.0%	-1.8
19814	AT3G52920.2 | expressed protein, weak similarity to enterophilin-2L (Cavia porcellus) GI:12718845; contains Pfam profile PF04949: Family of unknown function (DUF662) | chr3:19635358-19637236 FORWARD | Aliases: F8J2.90	7.8	7.6	0.2	0.2	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
19815	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	3.5	3.5	0.0	0.2	100.0%	-1.9
19816	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	4.0	4.0	0.0	0.2	100.0%	-1.8
19817	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	2.3	2.4	-0.0	-0.2	100.0%	-2.2
19818	AT5G55470.1 | Symbol: ATNHX3 |	4.2	4.2	-0.0	-0.2	100.0%	-1.8
19819	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	-0.2	100.0%	-1.8
19820	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	8.5	0.1	0.2	100.0%	-1.7
19821	AT2G04410.1 | expressed protein | chr2:1533838-1535165 REVERSE | Aliases: T1O3.18, T1O3_18	7.6	7.6	-0.1	-0.2	100.0%	-1.4
19822	AT2G40800.1 | expressed protein | chr2:17031469-17034051 REVERSE | Aliases: T7D17.2, T7D17_2	4.2	4.2	0.0	0.2	100.0%	-1.8
19823	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%	-2.5
19824	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	6.4	6.4	0.0	0.2	100.0%	-1.9
19825	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	2.7	-0.0	-0.2	100.0%	-2.2
19826	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	8.1	8.2	-0.1	-0.2	100.0%	-1.2
19827	AT5G52030.2 | TraB protein-related | chr5:21145355-21147316 FORWARD | Aliases: MSG15.11, MSG15_11	5.6	5.6	-0.1	-0.2	100.0%	-1.6
19828	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	-0.0	-0.2	100.0%	-2.1
19829	AT4G09500.2 | glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	4.1	4.1	0.1	0.2	100.0%	-1.6
19830	AT1G70750.1 | expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593; supporting cDNA gi:4101563:gb:AF004556.1:AF004556	6.0	6.1	-0.1	-0.2	100.0%	-1.2
19831	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	5.0	4.9	0.0	0.2	100.0%	-1.6
19832	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	0.2	100.0%	-2.4
19833	AT1G23050.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr1:8168432-8169256 FORWARD | Aliases: F19G10.1	3.5	3.6	-0.0	-0.2	100.0%	-1.8
19834	AT5G26731.1 | expressed protein | chr5:9295577-9296383 FORWARD | Aliases: None	7.0	7.1	-0.1	-0.2	100.0%	-1.5
19835	AT1G63130.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:23416395-23418814 FORWARD | Aliases: F16M19.5, F16M19_5	6.7	6.7	0.1	0.2	100.0%	-1.0
19836	AT3G47000.1 | glycosyl hydrolase family 3 protein, beta-D-glucan exohydrolase, Nicotiana tabacum, TREMBL:AB017502_1 | chr3:17324631-17327547 REVERSE | Aliases: F13I12.50	9.3	9.2	0.1	0.2	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
19837	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%	-2.6
19838	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	-0.0	-0.2	100.0%	-1.8
19839	AT3G01570.1 | glycine-rich protein / oleosin, similar to oleosin GB:AAB58402 (Sesamum indicum)	2.5	2.5	0.0	0.2	100.0%	-2.3
19840	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	4.3	4.3	0.0	0.2	100.0%	-1.8
19841	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	2.6	0.0	0.2	100.0%	-2.1
19842	AT1G36380.1 | expressed protein, similar to vanilloid receptor-like protein GB:AAD26363 from (Homo sapiens) | chr1:13702026-13702844 FORWARD | Aliases: F7F23.10, F7F23_10	6.9	6.8	0.1	0.2	100.0%	-1.6
19843	AT1G15830.1 | expressed protein | chr1:5448721-5450172 FORWARD | Aliases: F7H2.23, F7H2_23	5.8	5.8	-0.1	-0.2	100.0%	-1.4
19844	AT5G50335.1 | expressed protein | chr5:20506320-20506953 REVERSE | Aliases: None	2.6	2.6	0.0	0.2	100.0%	-2.5
19845	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	2.8	-0.0	-0.2	100.0%	-2.3
19846	AT3G22860.1 | Symbol: TIF3C2 |	2.9	2.9	-0.0	-0.2	100.0%	-2.0
19847	AT1G36510.1 | hypothetical protein | chr1:13763138-13765477 FORWARD | Aliases: F28J9.5, F28J9_5	4.0	4.0	-0.0	-0.2	100.0%	-1.9
19848	AT2G06530.1 | SNF7 family protein, contains Pfam domain, PF03357: SNF7 family | chr2:2588542-2590442 REVERSE | Aliases: T12H3.8, T12H3_8	9.3	9.3	0.1	0.2	100.0%	-1.5
19849	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	0.2	100.0%	-2.0
19850	AT2G22070.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:9390682-9393144 FORWARD | Aliases: T16B14.8, T16B14_8	2.9	3.0	-0.0	-0.2	100.0%	-2.3
19851	AT3G53680.1 | PHD finger transcription factor, putative, predicted proteins, Arabidopsis thaliana | chr3:19903841-19908390 REVERSE | Aliases: F4P12.380	4.2	4.2	-0.0	-0.2	100.0%	-1.8
19852	AT1G36670.1 | expressed protein | chr1:13865447-13866548 REVERSE | Aliases: T15P17.10, T15P17_10	3.2	3.3	-0.0	-0.2	100.0%	-2.2
19853	AT2G03060.1 | MADS-box family protein | chr2:901613-903568 FORWARD | Aliases: T17M13.23, T17M13_23	2.8	2.8	0.0	0.2	100.0%	-2.2
19854	AT3G09060.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:2766372-2768435 REVERSE | Aliases: MZB10.9	3.5	3.5	-0.0	-0.2	100.0%	-2.0
19855	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	-0.2	100.0%	-2.0
19856	AT1G22380.1 | similar to UDP-glucose glucosyltransferase, putative [Arabidopsis thaliana] (TAIR:At1g78270.1); similar to UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22340.1); similar to UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22360.1); similar to UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22400.1); similar to UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22370.2); similar to glycosyltransferase NTGT5a [Nicotiana tabacum] (GB:BAD93689.1); contains InterPro domain UDP-glucoronosyl/UDP-glucosyl transferase (InterPro:IPR002213) | chr1:7900376-7902321 REVERSE | Aliases: F12K8.28	3.0	2.9	0.0	0.2	100.0%	-1.9
19857	NA	2.6	2.6	-0.0	-0.2	100.0%	-2.6

Rank	Description	Sync	Root	M	t	adj.q	B
19858	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	0.2	100.0%	-2.4
19859	AT3G42500.1 | expressed protein, includes At2g10370, At5g36050, At1g35090, At1g44860, At4g19300, At1g42400, At3g43040, At3g42500 | chr3:14642275-14642911 REVERSE | Aliases: T32A11.70	2.4	2.4	0.0	0.2	100.0%	-2.6
19860	AT4G24540.1 | Symbol: AGL24 | MADS-box family protein	3.0	3.0	-0.0	-0.2	100.0%	-2.0
19861	AT4G01250.1 | Symbol: WRKY22 |	3.9	3.8	0.1	0.2	100.0%	-1.5
19862	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	2.8	2.8	0.0	0.2	100.0%	-2.2
19863	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	6.6	6.6	-0.0	-0.2	100.0%	-1.5
19864	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	3.2	-0.0	-0.2	100.0%	-2.1
19865	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	5.8	5.9	-0.1	-0.2	100.0%	-1.3
19866	AT3G28320.1 | expressed protein, similar to At14a (GI:11994571 and GI:11994573) (Arabidopsis thaliana)	4.3	4.3	-0.0	-0.2	100.0%	-1.6
19867	AT3G24500.1 | ethylene-responsive transcriptional coactivator, putative, similar to ethylene-responsive transcriptional coactivator (Lycopersicon esculentum) gi:5669634:gb:AAD46402 | chr3:8918686-8919315 FORWARD | Aliases: MOB24.13	6.9	7.0	-0.0	-0.2	100.0%	-1.4
19868	AT3G25280.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr3:9207420-9209273 FORWARD | Aliases: MJL12.24	3.5	3.6	-0.0	-0.2	100.0%	-1.8
19869	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%	-1.8
19870	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	5.0	4.9	0.1	0.2	100.0%	-1.6
19871	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	2.8	2.8	0.0	0.2	100.0%	-2.1
19872	AT3G02885.1 | Symbol: GASA5 | gibberellin-regulated protein 5 (GASA5) / gibberellin-responsive protein 5, identical to GASA5 (Arabidopsis thaliana) GI:1289320 | chr3:638111-639059 REVERSE | Aliases: GASA5	4.3	4.4	-0.0	-0.2	100.0%	-1.4
19873	AT3G19850.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr3:6898187-6901248 REVERSE | Aliases: MPN9.9	2.2	2.3	-0.0	-0.2	100.0%	-2.6
19874	AT5G61230.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr5:24644413-24646174 FORWARD | Aliases: MAF19.22, MAF19_22	8.1	8.1	-0.1	-0.2	100.0%	-1.4
19875	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	0.0	0.2	100.0%	-2.4
19876	AT2G03280.2 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g14020.1); similar to putative auxin-independent growth promoter [Oryza sativa (japonica cultivar-group)] (GB:BAD69015.1); contains InterPro domain Hypothetical plant protein (InterPro:IPR004348)	5.8	5.7	0.0	0.2	100.0%	-1.7
19877	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	3.2	3.3	-0.0	-0.2	100.0%	-1.9
19878	AT3G53110.1 | Symbol: LOS4 | DEAD/DEAH box helicase, putative, RNA helicase, Mus musculus, PIR:I49731	9.2	9.1	0.0	0.2	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
19879	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	5.6	5.6	-0.0	-0.2	100.0%	-1.7
19880	AT5G44570.1 | expressed protein | chr5:17981666-17982841 FORWARD | Aliases: K15C23.1, K15C23_1	2.4	2.3	0.0	0.2	100.0%	-2.3
19881	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)(Arabidopsis thaliana) | chr1:6781474-6782030 REVERSE | Aliases: F14P1.6, F14P1_6, LCR78, Low molecular weight cysteine rich 78, PDF1.4	3.2	3.2	-0.0	-0.2	100.0%	-1.8
19882	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	1.9	0.0	0.2	100.0%	-2.7
19883	AT4G23780.1 | expressed protein | chr4:12386363-12386809 REVERSE | Aliases: F9D16.250, F9D16_250	2.8	2.8	-0.0	-0.2	100.0%	-2.3
19884	AT1G47680.1 | hypothetical protein | chr1:17543215-17543529 FORWARD | Aliases: F16N3.39, F16N3_39	3.3	3.3	-0.0	-0.2	100.0%	-2.0
19885	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	3.7	3.8	-0.1	-0.2	100.0%	-1.5
19886	AT1G65640.1 | DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana) | chr1:24414514-24417190 REVERSE | Aliases: F1E22.2	2.4	2.4	0.0	0.2	100.0%	-2.2
19887	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	5.3	5.3	-0.0	-0.2	100.0%	-1.5
19888	AT3G12960.1 | expressed protein, similar to seed maturation protein PM28 GB:AAD30427 from (Glycine max) | chr3:4136553-4136834 FORWARD | Aliases: MGH6.8	2.9	2.9	0.0	0.2	100.0%	-2.1
19889	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	5.8	5.8	0.1	0.2	100.0%	-1.4
19890	AT5G58100.1 | expressed protein | chr5:23524928-23532246 FORWARD | Aliases: K21L19.10, K21L19_10	5.8	5.7	0.0	0.2	100.0%	-1.5
19891	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	-0.0	-0.2	100.0%	-1.8
19892	AT1G56620.1 | pectinesterase inhibitor domain-containing protein | chr1:21223483-21224022 FORWARD | Aliases: F25P12.14, F25P12_14	2.5	2.5	-0.0	-0.2	100.0%	-2.3
19893	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	6.4	-0.1	-0.2	100.0%	-1.4
19894	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	0.2	100.0%	-2.5
19895	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	5.3	5.3	-0.1	-0.2	100.0%	-1.5
19896	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) (4CL 1) (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	9.9	9.8	0.2	0.2	100.0%	-1.5
19897	AT2G05210.1 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g06310.1) | chr2:1891769-1894359 FORWARD | Aliases: F5G3.11, F5G3_11	3.5	3.6	-0.1	-0.2	100.0%	-1.4
19898	AT4G23930.2 | expressed protein, hin1 protein homolog, Oryza sativa, PIR:T02662 | chr4:12435956-12436722 REVERSE | Aliases: T32A16.100, T32A16_100	4.0	4.0	0.0	0.2	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
19899	AT5G57780.1 | expressed protein, similar to unknown protein (emb CAB79759.1) | chr5:23422550-23423535 REVERSE | Aliases: MTI20.1, MTI20_1	2.1	2.1	-0.0	-0.2	100.0%	-2.2
19900	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	2.0	0.0	0.2	100.0%	-2.5
19901	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	7.5	7.4	0.1	0.2	100.0%	-1.2
19902	AT3G49770.1 | expressed protein | chr3:18471875-18472861 REVERSE | Aliases: T16K5.120	3.4	3.5	-0.0	-0.2	100.0%	-1.8
19903	AT3G07060.1 | Symbol: EMB1974 | expressed protein, ; expression supported by MPSS | chr3:2233000-2236919 FORWARD | Aliases: EMB1974, EMBRYO DEFECTIVE 1974, F17A9.23	3.7	3.7	-0.0	-0.2	100.0%	-1.8
19904	AT1G51900.1 | hypothetical protein | chr1:19283553-19286564 REVERSE | Aliases: T14L22.11, T14L22_11	2.3	2.3	-0.0	-0.2	100.0%	-2.6
19905	AT1G27595.1 | expressed protein, similar to Symplekin (SP:Q92797) {Homo sapiens} | chr1:9595480-9603242 FORWARD | Aliases: T22C5.3	3.2	3.2	0.0	0.2	100.0%	-2.0
19906	AT3G20180.1 | hypothetical protein | chr3:7043391-7043847 REVERSE | Aliases: MAL21.22	2.7	2.7	0.0	0.2	100.0%	-2.0
19907	AT4G07500.1 | expressed protein | chr4:4300046-4301481 REVERSE | Aliases: T3E15.18, T3E15_18	2.4	2.4	0.0	0.2	100.0%	-2.0
19908	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	2.5	0.0	0.2	100.0%	-2.4
19909	AT2G46850.1 | expressed protein | chr2:19258135-19260437 FORWARD | Aliases: F19D11.13	2.7	2.8	-0.0	-0.2	100.0%	-1.8
19910	AT2G19400.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr2:8406239-8409682 REVERSE | Aliases: F27F23.20, F27F23_20	3.6	3.6	-0.0	-0.2	100.0%	-1.8
19911	AT3G26750.1 | expressed protein | chr3:9841247-9843316 REVERSE | Aliases: MDJ14.3	3.8	3.8	0.0	0.2	100.0%	-1.7
19912	AT4G21500.1 | expressed protein, ; expression supported by MPSS | chr4:11441077-11441724 REVERSE | Aliases: F18E5.120, F18E5_120	3.0	3.1	-0.0	-0.2	100.0%	-1.8
19913	AT1G17840.1 | ABC transporter family protein, similar to ABC transporter GI:10280532 from (Homo sapiens) | chr1:6142603-6146514 FORWARD | Aliases: F2H15.7, F2H15_7	2.7	2.8	-0.0	-0.2	100.0%	-2.1
19914	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	0.1	0.2	100.0%	-1.9
19915	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	4.0	3.9	0.1	0.2	100.0%	-1.6
19916	AT3G60310.1 | expressed protein | chr3:22298660-22301354 FORWARD | Aliases: F27H5.100	3.6	3.7	-0.0	-0.2	100.0%	-1.7
19917	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	10.4	10.5	-0.1	-0.2	100.0%	-1.6
19918	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	-0.0	-0.2	100.0%	-1.8
19919	AT3G20760.1 | expressed protein | chr3:7257193-7258897 REVERSE | Aliases: MOE17.7	3.6	3.6	-0.0	-0.2	100.0%	-2.1
19920	AT1G13630.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat | chr1:4670305-4672823 REVERSE | Aliases: F21F23.6, F21F23_6	2.4	2.4	0.0	0.2	100.0%	-2.4
19921	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	4.9	4.7	0.2	0.2	100.0%	-1.2

Rank	Description	Sync	Root	M	t	adj.q	B
19922	AT4G15260.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr4:8713689-8715339 FORWARD | Aliases: DL3675W, FCAALL.250	4.8	4.7	0.1	0.2	100.0%	-1.3
19923	AT1G69860.1 | proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family | chr1:26313291-26315837 FORWARD | Aliases: T17F3.11, T17F3_11	2.5	2.5	-0.0	-0.2	100.0%	-1.9
19924	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	4.3	4.3	-0.0	-0.2	100.0%	-1.5
19925	AT5G45820.1 | Symbol: CIPK20 |	2.9	2.8	0.0	0.2	100.0%	-1.9
19926	AT3G57700.1 | protein kinase, putative, contains protein kinase domain, Pfam:PF00069 | chr3:21395894-21396916 FORWARD | Aliases: F15B8.110	2.8	2.8	-0.0	-0.2	100.0%	-2.3
19927	AT3G01330.1 | Symbol: DEL3 | transcription factor, putative / E2F-like repressor E2L2 (E2L2), identical to E2F-like repressor E2L2 (Arabidopsis thaliana) GI:20502506	3.9	3.9	0.0	0.2	100.0%	-1.7
19928	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	2.9	2.9	-0.0	-0.2	100.0%	-2.3
19929	AT1G36050.1 | expressed protein | chr1:13451416-13454454 FORWARD | Aliases: F5J5.4, F5J5_4	8.6	8.5	0.1	0.2	100.0%	-1.7
19930	AT1G15190.1 | expressed protein | chr1:5227270-5228016 FORWARD | Aliases: F9L1.13, F9L1_13	2.7	2.6	0.0	0.2	100.0%	-2.2
19931	AT3G07660.1 | expressed protein | chr3:2444784-2450567 REVERSE | Aliases: MLP3.11	3.1	3.0	0.0	0.2	100.0%	-1.9
19932	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	2.7	2.6	0.0	0.2	100.0%	-1.9
19933	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	-0.2	100.0%	-1.9
19934	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	2.6	0.0	0.2	100.0%	-2.3
19935	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	3.5	3.5	0.0	0.2	100.0%	-1.7
19936	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%	-2.4
19937	AT3G28970.1 | expressed protein, contains Pfam domain PF03556: Domain of unknown function (DUF298) | chr3:10989024-10991122 REVERSE | Aliases: K5K13.10	8.3	8.3	0.0	0.2	100.0%	-1.9
19938	AT3G48770.1 | expressed protein | chr3:18090246-18097802 REVERSE | Aliases: T21J18.40	2.9	2.9	-0.0	-0.2	100.0%	-2.0
19939	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	2.8	2.8	-0.0	-0.2	100.0%	-2.1
19940	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	-0.2	100.0%	-2.4
19941	AT5G58150.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:23547307-23550066 REVERSE | Aliases: MCK7.2, MCK7_2	5.7	5.7	-0.0	-0.2	100.0%	-1.9
19942	AT2G32160.2 | expressed protein | chr2:13669296-13673346 FORWARD | Aliases: F22D22.9, F22D22_9	2.8	2.8	-0.0	-0.2	100.0%	-2.1
19943	AT1G48130.1 | Symbol: ATPER1 |	2.4	2.4	-0.0	-0.2	100.0%	-2.0
19944	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	5.0	4.9	0.0	0.2	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
19945	AT4G25120.1 | UvrD/REP helicase family protein, contains Pfam PF00580: UvrD/REP helicase | chr4:12890704-12898511 FORWARD | Aliases: F24A6.8	3.0	3.0	0.0	0.2	100.0%	-1.9
19946	AT1G70550.2 | expressed protein, similar to hypothetical protein GB:AAD31338 (Arabidopsis thaliana) and to putative putative carboxyl-terminal peptidase GB:AAC16072 (Arabidopsis thaliana) contains Pfam profile PF03080: Arabidopsis proteins of unknown function | chr1:26600815-26603882 FORWARD | Aliases: F24J13.12, F24J13_12	4.5	4.5	0.1	0.2	100.0%	-1.2
19947	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 (GIi:2739002) (Glycine max) | chr5:8694633-8696224 REVERSE | Aliases: F21J6.102, F21J6_102	3.0	2.9	0.0	0.2	100.0%	-2.2
19948	AT3G43680.1 | hypothetical protein | chr3:15587444-15589257 FORWARD | Aliases: F23N14.60	3.4	3.4	-0.0	-0.2	100.0%	-1.6
19949	AT1G74400.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 domain of unknown function | chr1:27967614-27969002 FORWARD | Aliases: F1M20.8, F1M20_8	3.5	3.5	-0.0	-0.2	100.0%	-1.9
19950	AT2G04830.1 | F-box family protein, similar to F-box protein family, AtFBX7 (GI:20197899) (Arabidopsis thaliana); confirmed by FLcDNA GI:16604421; contains uncharacterized Arabidoppsis domain shared by 33 Arabidopsis proteins | chr2:1695352-1695853 FORWARD | Aliases: F28I8.13, F28I8_13	2.7	2.7	0.0	0.2	100.0%	-2.4
19951	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	9.6	9.6	-0.0	-0.2	100.0%	-1.7
19952	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	4.4	4.4	0.1	0.2	100.0%	-1.7
19953	AT1G17000.1 | Symbol: ATTPS3 |	2.4	2.4	-0.0	-0.2	100.0%	-2.4
19954	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	-0.2	100.0%	-2.3
19955	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 (GI:21591637) (Arabidopsis thaliana); similar to suppressor of forked protein; Su(f) protein (Drosophila virilis) GI:4092534 | chr1:6110100-6116610 REVERSE | Aliases: F11A6.10, F11A6_10	6.1	6.1	-0.1	-0.2	100.0%	-1.5
19956	AT5G54470.1 | zinc finger (B-box type) family protein, similar to unknown protein (pir::T05755) | chr5:22131660-22132683 REVERSE | Aliases: F24B18.9, F24B18_9	3.8	3.8	-0.0	-0.2	100.0%	-1.8
19957	AT3G28230.1 | hypothetical protein | chr3:10530551-10531436 FORWARD | Aliases: MZF16.2	2.8	2.8	0.0	0.2	100.0%	-2.4
19958	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	-0.0	-0.2	100.0%	-2.1
19959	AT4G05260.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr4:2693678-2694457 FORWARD | Aliases: C17L7.180, C17L7_180	2.8	2.8	0.0	0.2	100.0%	-1.9
19960	AT2G39180.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr2:16351245-16353686 REVERSE | Aliases: T16B24.18, T16B24_18	4.1	4.0	0.0	0.2	100.0%	-1.7
19961	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	3.0	0.0	0.2	100.0%	-1.9
19962	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) (4CL 2) (4-coumaroyl-CoA synthase 2) {Arabidopsis thaliana} | chr3:7454282-7457385 REVERSE | Aliases: COUMARATE:COA LIGASE, AT4CL2, MXL8.10	11.2	11.1	0.1	0.2	100.0%	-1.9
19963	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	4.5	4.5	0.1	0.2	100.0%	-1.6
19964	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	-0.2	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
19965	NA	2.3	2.3	0.0	0.2	100.0%	-2.7
19966	AT4G10910.1 | expressed protein | chr4:6696708-6697451 FORWARD | Aliases: F25I24.120, F25I24_120	3.4	3.4	0.0	0.2	100.0%	-2.1
19967	AT5G24500.1 | expressed protein | chr5:8367071-8368739 REVERSE | Aliases: K18P6.2, K18P6_2	6.6	6.6	0.1	0.2	100.0%	-1.3
19968	AT2G46840.1 | expressed protein, ; expression supported by MPSS | chr2:19256260-19256978 REVERSE | Aliases: F19D11.12	2.5	2.5	-0.0	-0.2	100.0%	-2.0
19969	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	0.2	100.0%	-1.8
19970	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	0.0	0.2	100.0%	-2.0
19971	AT3G58870.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr3:21776856-21778275 REVERSE | Aliases: T20N10.220	2.6	2.6	-0.0	-0.2	100.0%	-2.1
19972	AT1G33230.1 | expressed protein | chr1:12046621-12050026 FORWARD | Aliases: T9L6.9, T9L6_9	7.5	7.5	0.1	0.2	100.0%	-1.3
19973	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	3.3	3.3	-0.1	-0.2	100.0%	-1.4
19974	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	6.7	6.7	0.1	0.2	100.0%	-1.5
19975	AT5G13390.1 | Symbol: NEF1 | expressed protein | chr5:4292804-4296575 FORWARD | Aliases: NO EXINE FORMATION 1, T22N19.40, T22N19_40	5.9	5.8	0.1	0.2	100.0%	-1.3
19976	AT2G16520.1 | expressed protein | chr2:7169004-7169466 REVERSE | Aliases: F1P15.10, F1P15_10	2.7	2.6	0.0	0.2	100.0%	-2.4
19977	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	7.9	8.1	-0.2	-0.2	100.0%	-1.1
19978	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	8.0	0.1	0.2	100.0%	-1.5
19979	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	0.0	0.2	100.0%	-2.4
19980	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	4.6	4.8	-0.1	-0.2	100.0%	-1.3
19981	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	0.1	0.2	100.0%	-1.5
19982	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	7.1	7.0	0.1	0.2	100.0%	-1.5
19983	AT1G55370.2 | expressed protein | chr1:20678449-20680014 FORWARD | Aliases: T18I3.2	4.1	4.0	0.0	0.2	100.0%	-2.0
19984	AT5G01010.1 | expressed protein | chr5:1279-4993 REVERSE | Aliases: TOPTELOMERE.1, TOPTELOMERE_1	3.6	3.5	0.0	0.2	100.0%	-1.7
19985	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	4.5	4.4	0.1	0.2	100.0%	-1.3
19986	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	6.6	6.5	0.1	0.2	100.0%	-1.6
19987	AT2G18340.1 | 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 | chr2:7976482-7978107 FORWARD | Aliases: T30D6.15, T30D6_15	2.9	2.9	-0.0	-0.2	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
19988	AT5G56310.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:22819542-22821140 FORWARD | Aliases: MCD7.3, MCD7_3	3.4	3.5	-0.0	-0.2	100.0%	-2.2
19989	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	5.3	5.3	0.0	0.2	100.0%	-1.5
19990	AT1G32810.1 | expressed protein | chr1:11883495-11885823 FORWARD | Aliases: F9L11.1, F9L11_1	7.8	7.8	0.1	0.2	100.0%	-1.6
19991	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	-0.2	100.0%	-1.6
19992	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)	2.6	2.6	0.0	0.2	100.0%	-2.2
19993	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	-0.1	-0.2	100.0%	-1.6
19994	AT1G07090.1 | expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640) | chr1:2173951-2174893 REVERSE | Aliases: F10K1.20, F10K1_20	4.7	4.8	-0.0	-0.2	100.0%	-1.8
19995	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	3.9	0.0	0.2	100.0%	-2.1
19996	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	3.4	3.4	-0.0	-0.2	100.0%	-2.0
19997	AT3G43950.1 | expressed protein | chr3:15777348-15778001 FORWARD | Aliases: T15B3.90	2.9	2.8	0.0	0.2	100.0%	-2.2
19998	AT5G65590.1 | Dof-type zinc finger domain-containing protein | chr5:26228972-26230362 REVERSE | Aliases: K21L13.10, K21L13_10	2.4	2.4	-0.0	-0.2	100.0%	-2.1
19999	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	6.2	6.1	0.1	0.2	100.0%	-1.3
20000	AT4G23110.1 | expressed protein | chr4:12110955-12111401 FORWARD | Aliases: F7H19.300, F7H19_300	2.2	2.2	0.0	0.2	100.0%	-2.8
20001	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	2.7	2.7	0.0	0.2	100.0%	-1.9
20002	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	2.7	2.7	-0.0	-0.2	100.0%	-2.2
20003	AT1G54840.2 | expressed protein | chr1:20456117-20457916 REVERSE | Aliases: T22H22.23, T22H22_23	3.9	3.9	0.0	0.2	100.0%	-1.9
20004	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%	-2.1
20005	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	3.0	0.0	0.2	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
20006	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	9.7	9.6	0.0	0.2	100.0%	-1.6
20007	AT1G18485.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:6363165-6366226 FORWARD | Aliases: None	3.6	3.6	-0.0	-0.2	100.0%	-1.6
20008	AT2G26140.1 | Symbol: FTSH4 | encodes an FtsH protease that is localized to the mitochondrion	6.8	6.7	0.1	0.2	100.0%	-1.3
20009	AT2G14700.1 | expressed protein | chr2:6299548-6302808 FORWARD | Aliases: T6B13.6, T6B13_6	3.9	4.0	-0.0	-0.2	100.0%	-1.7
20010	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	4.7	4.8	-0.0	-0.2	100.0%	-1.5
20011	AT1G51340.2 | MATE efflux family protein, contains Pfam profile PF01554: MatE | chr1:19035665-19038647 FORWARD | Aliases: F11M15.20, F11M15_20	2.2	2.2	-0.0	-0.2	100.0%	-2.3
20012	AT3G03670.1 | peroxidase, putative, similar to peroxidase GB:CAA66966 (Arabidopsis thaliana) | chr3:901862-903384 REVERSE | Aliases: T12J13.5, T12J13_5	3.2	3.2	-0.0	-0.2	100.0%	-1.8
20013	AT2G32350.1 | ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain | chr2:13742056-13742865 FORWARD | Aliases: T32F6.13, T32F6_13	2.8	2.7	0.0	0.2	100.0%	-2.4
20014	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	2.6	2.6	-0.0	-0.2	100.0%	-1.9
20015	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	3.2	3.2	0.0	0.2	100.0%	-1.8
20016	AT2G38250.1 | DNA-binding protein-related, contains similarity to DNA-binding protein GI:170271 from (Nicotiana tabacum) | chr2:16025462-16026578 FORWARD | Aliases: F16M14.18, F16M14_18	4.7	4.6	0.1	0.2	100.0%	-1.4
20017	AT1G35880.1 | expressed protein | chr1:13341063-13342440 REVERSE | Aliases: F10O5.5, F10O5_5	2.2	2.2	0.0	0.2	100.0%	-2.5
20018	AT3G04960.1 | expressed protein, low similarity to SP:P32380 NUF1 protein (Spindle poly body spacer protein SPC110) {Saccharomyces cerevisiae}	3.5	3.4	0.0	0.2	100.0%	-1.6
20019	AT4G30040.1 | aspartyl protease family, contains Pfam domain, PF00026: eukaryotic aspartyl protease | chr4:14685608-14686891 FORWARD | Aliases: F6G3.70, F6G3_70	2.7	2.7	-0.0	-0.2	100.0%	-2.1
20020	AT2G19320.1 | expressed protein | chr2:8377946-8378179 REVERSE | Aliases: F27F23.12, F27F23_12	2.7	2.7	-0.0	-0.2	100.0%	-2.2
20021	AT5G07510.2 | Symbol: GRP14 | similar to glycine-rich protein (GRP18) [Arabidopsis thaliana] (TAIR:At5g07520.1); similar to pollen coat oleosin-glycine rich protein [Sisymbrium irio] (GB:AAR15428.1); similar to pollen coat oleosin-glycine rich protein [Capsella rubella] (GB:AAR15467.1); contains InterPro domain Eggshell protein (InterPro:IPR002952); contains InterPro domain Oleosin (InterPro:IPR000136)	3.2	3.2	-0.0	-0.2	100.0%	-1.7
20022	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%	-2.5
20023	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	5.2	5.1	0.1	0.2	100.0%	-1.4
20024	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	4.3	4.3	0.0	0.2	100.0%	-1.6
20025	AT1G04310.1 | Symbol: ERS2 | ethylene receptor-related, similar to ethylene receptor CS-ETR2 (Cucumis sativus) GI:6136818; contains Pfam profiles PF01590: GAF domain, PF00512: His Kinase A (phosphoacceptor) domain	4.2	4.2	0.0	0.2	100.0%	-1.7
20026	AT1G68330.1 | expressed protein | chr1:25614586-25615865 FORWARD | Aliases: T22E19.4, T22E19_4	2.4	2.4	-0.0	-0.2	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
20027	AT3G13770.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:4519654-4521540 FORWARD | Aliases: MMM17.3	2.9	2.8	0.0	0.2	100.0%	-2.0
20028	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	7.6	7.6	-0.1	-0.2	100.0%	-1.2
20029	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	-0.0	-0.2	100.0%	-2.4
20030	AT3G28710.1 | H+-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	7.9	7.7	0.1	0.2	100.0%	-1.0
20031	AT3G28715.1 | H+-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	7.9	7.7	0.1	0.2	100.0%	-1.0
20032	AT1G68020.2 | Symbol: ATTPS6 |	4.0	4.0	-0.0	-0.2	100.0%	-1.8
20033	AT5G24690.1 | expressed protein | chr5:8455460-8458741 REVERSE | Aliases: MXC17.8, MXC17_8	4.3	4.3	-0.0	-0.2	100.0%	-1.6
20034	AT2G19340.2 | membrane protein, putative, contains 3 transmembrane domains; | chr2:8382199-8383021 REVERSE | Aliases: F27F23.14, F27F23_14	4.1	4.1	0.0	0.2	100.0%	-2.0
20035	AT1G54020.2 | myrosinase-associated protein, putative, strong similarity to myrosinase-associated proteins GI:1769968, GI:1769970, GI:1216389,GI:1216391 from (Brassica napus); contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family | chr1:20165340-20167406 REVERSE | Aliases: F15I1.10, F15I1_10	2.1	2.2	-0.0	-0.2	100.0%	-2.4
20036	AT3G03130.1 | expressed protein, ; expression supported by MPSS | chr3:721446-723571 REVERSE | Aliases: T17B22.18, T17B22_18	4.5	4.4	0.1	0.2	100.0%	-1.6
20037	AT3G61950.2 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.4	2.4	0.0	0.2	100.0%	-2.2
20038	AT1G29195.1 | expressed protein | chr1:10202522-10203382 REVERSE | Aliases: None	2.8	2.8	0.0	0.2	100.0%	-2.0
20039	AT1G63940.4 | monodehydroascorbate reductase, putative, similar to monodehydroascorbate reductase GB:AAD28178 (Brassica juncea) | chr1:23733769-23737555 FORWARD | Aliases: T12P18.4, T12P18_4	9.8	9.9	-0.1	-0.2	100.0%	-1.5
20040	AT4G36515.1 | expressed protein | chr4:17229557-17230299 REVERSE | Aliases: None	9.3	9.2	0.1	0.2	100.0%	-1.0
20041	ATCG01110.1 | Symbol: NDHH | plastid NAD(P)H dehydrogenase subunit H 49KDa protein | chrC:122011-123192 REVERSE | Aliases: NDHH	3.3	3.4	-0.1	-0.2	100.0%	-1.8
20042	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	-0.2	100.0%	-2.0
20043	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	0.0	0.2	100.0%	-1.9
20044	AT5G18600.1 | glutaredoxin family protein, contains glutaredoxin domain, INTERPRO:IPR002109 | chr5:6183265-6183956 REVERSE | Aliases: T28N17.80, T28N17_80	4.0	4.0	0.0	0.2	100.0%	-1.8
20045	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	4.8	4.9	-0.1	-0.2	100.0%	-1.4
20046	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%	-2.1
20047	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	-0.0	-0.2	100.0%	-1.8
20048	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%	-2.2

Rank	Description	Sync	Root	M	t	adj.q	B
20049	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	9.9	-0.1	-0.2	100.0%	-1.7
20050	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	7.1	7.0	0.1	0.2	100.0%	-1.3
20051	AT1G69630.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.9	2.9	-0.0	-0.2	100.0%	-2.1
20052	AT1G61240.2 | expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707) | chr1:22585176-22588868 FORWARD | Aliases: F11P17.21, F11P17_21	3.8	3.9	-0.0	-0.2	100.0%	-1.5
20053	NA	2.4	2.4	0.0	0.2	100.0%	-2.7
20054	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	2.9	2.9	0.0	0.2	100.0%	-1.8
20055	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	0.0	0.2	100.0%	-2.1
20056	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	4.1	4.0	0.1	0.2	100.0%	-1.5
20057	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	6.1	6.2	-0.1	-0.2	100.0%	-1.5
20058	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	0.2	100.0%	-2.8
20059	AT1G65490.1 | expressed protein | chr1:24358434-24358975 FORWARD | Aliases: F5I14.26	2.3	2.3	-0.0	-0.2	100.0%	-2.1
20060	AT3G11640.1 | expressed protein | chr3:3674505-3675204 FORWARD | Aliases: T19F11.4	3.9	3.8	0.1	0.2	100.0%	-1.6
20061	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	2.5	0.0	0.2	100.0%	-2.3
20062	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	5.8	5.7	0.1	0.2	100.0%	-1.4
20063	AT3G09130.1 | hypothetical protein | chr3:2799317-2800510 FORWARD | Aliases: MZB10.16	2.4	2.4	-0.0	-0.2	100.0%	-2.1
20064	AT5G55680.1 | glycine-rich protein | chr5:22564961-22565587 REVERSE | Aliases: MDF20.12, MDF20_12	5.3	5.3	0.1	0.2	100.0%	-1.6
20065	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	-0.2	100.0%	-2.3
20066	AT5G11730.1 | expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266 | chr5:3780312-3782714 FORWARD | Aliases: T22P22.120, T22P22_120	5.2	5.2	-0.0	-0.2	100.0%	-1.5
20067	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	2.9	2.9	-0.0	-0.2	100.0%	-2.2
20068	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	2.5	2.5	-0.0	-0.2	100.0%	-2.0
20069	AT1G60780.1 | clathrin adaptor complexes medium subunit family protein, contains Pfam profile: PF00928 adaptor complexes medium subunit family	7.9	8.0	-0.1	-0.2	100.0%	-1.5
20070	AT5G42950.1 | GYF domain-containing protein, contains Pfam profile: PF02213 GYF domain	6.7	6.6	0.1	0.2	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
20071	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	3.7	0.0	0.2	100.0%	-2.0
20072	AT2G29250.1 | 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 | chr2:12585986-12587857 REVERSE | Aliases: F16P2.37, F16P2_37	2.5	2.5	-0.0	-0.2	100.0%	-2.3
20073	AT2G40435.1 | expressed protein | chr2:16893902-16895716 FORWARD | Aliases: T2P4.23	2.3	2.3	-0.0	-0.2	100.0%	-2.7
20074	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	7.8	0.1	0.2	100.0%	-1.5
20075	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	5.3	5.4	-0.1	-0.2	100.0%	-1.3
20076	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	2.2	2.2	-0.0	-0.2	100.0%	-2.4
20077	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	6.7	6.6	0.1	0.2	100.0%	-1.5
20078	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	0.0	0.2	100.0%	-2.0
20079	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	-0.2	100.0%	-1.6
20080	AT5G43860.1 | Symbol: ATCLH2 |	3.4	3.3	0.0	0.2	100.0%	-1.7
20081	AT3G17620.1 | F-box family protein, contains Pfam profile: PF00646 F-box domain | chr3:6026452-6027700 REVERSE | Aliases: MKP6.18	3.4	3.4	0.0	0.2	100.0%	-2.1
20082	AT2G44195.1 | hypothetical protein | chr2:18281882-18282713 FORWARD | Aliases: F4I1.13	2.8	2.8	-0.0	-0.2	100.0%	-2.3
20083	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	3.5	3.4	0.0	0.2	100.0%	-1.6
20084	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	11.4	11.3	0.1	0.2	100.0%	-1.7
20085	AT3G20280.2 | PHD finger family protein, contains Pfam profile: PF00628 PHD-finger | chr3:7071199-7074647 FORWARD | Aliases: MQC12.7	2.4	2.4	-0.0	-0.2	100.0%	-2.4
20086	AT1G24140.1 | matrixin family protein, similar to matrix metalloproteinase (Cucumis sativus) GI:7159629; contains InterPro accession IPR001818: Matrixin | chr1:8536034-8537376 REVERSE | Aliases: F3I6.6, F3I6_6	3.1	3.2	-0.0	-0.2	100.0%	-1.9
20087	AT1G16030.1 | Symbol: HSP70B |	5.7	5.6	0.1	0.2	100.0%	-1.5
20088	AT1G30780.1 | F-box family protein | chr1:10923901-10926543 REVERSE | Aliases: T17H7.3, T17H7_3	3.3	3.3	0.0	0.2	100.0%	-2.2
20089	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	2.7	0.0	0.2	100.0%	-2.0
20090	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	3.2	-0.0	-0.2	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
20091	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	5.2	0.0	0.2	100.0%	-1.9
20092	AT2G21680.1 | 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 | chr2:9274810-9276099 FORWARD | Aliases: F2G1.5, F2G1_5	3.6	3.6	-0.0	-0.2	100.0%	-1.7
20093	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	-0.2	100.0%	-1.7
20094	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	5.1	5.0	0.1	0.2	100.0%	-1.3
20095	AT3G51720.1 | expressed protein, contains Pfam PF05701: Plant protein of unknown function (DUF827) | chr3:19196030-19197613 FORWARD | Aliases: T18N14.100	7.4	7.3	0.1	0.2	100.0%	-1.2
20096	AT4G09290.1 | expressed protein | chr4:5893341-5894966 REVERSE | Aliases: T30A10.50, T30A10_50	2.8	2.7	0.0	0.2	100.0%	-2.4
20097	AT5G01750.2 | expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567) | chr5:289762-291323 FORWARD | Aliases: T20L15.20, T20L15_20	8.6	8.7	-0.1	-0.2	100.0%	-1.4
20098	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	4.2	-0.1	-0.2	100.0%	-1.7
20099	AT4G31420.2 | zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type | chr4:15245822-15247930 REVERSE | Aliases: F3L17.9	8.4	8.4	0.0	0.2	100.0%	-1.6
20100	AT3G06190.2 | Symbol: ATBPM2 |	4.2	4.2	0.0	0.2	100.0%	-1.7
20101	AT5G02900.1 | Symbol: CYP96A13 | cytochrome P450, putative, cytochrome P450 homolog, Arabidopsis thaliana, PIR:T09367	3.0	3.0	-0.0	-0.2	100.0%	-2.0
20102	AT2G22320.1 | hypothetical protein | chr2:9487185-9487520 FORWARD | Aliases: T26C19.2, T26C19_2	2.4	2.4	0.0	0.2	100.0%	-2.7
20103	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	-0.0	-0.2	100.0%	-2.2
20104	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)	5.9	6.0	-0.0	-0.2	100.0%	-1.5
20105	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	4.4	4.4	-0.1	-0.2	100.0%	-1.5
20106	AT3G47850.1 | expressed protein | chr3:17665064-17666984 REVERSE | Aliases: T23J7.180	5.7	5.7	-0.0	-0.2	100.0%	-1.4
20107	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	0.0	0.2	100.0%	-2.1
20108	AT2G25990.1 | hypothetical protein | chr2:11087664-11087784 FORWARD | Aliases: T19L18.20, T19L18_20	3.4	3.4	0.0	0.2	100.0%	-2.1
20109	AT5G64340.1 | expressed protein | chr5:25747561-25750539 REVERSE | Aliases: MSJ1.18, MSJ1_18	4.0	4.0	0.0	0.2	100.0%	-1.5
20110	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	6.3	6.4	-0.1	-0.2	100.0%	-0.9
20111	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%	-2.2
20112	AT1G66520.1 | Symbol: PDE194 |	3.4	3.3	0.0	0.2	100.0%	-1.5
20113	ATMG00140.1 | Symbol: ORF167 |	2.4	2.4	-0.0	-0.2	100.0%	-2.4

Rank	Description	Sync	Root	M	t	adj.q	B
20114	AT2G44080.1 | expressed protein | chr2:18244261-18245249 FORWARD | Aliases: F6E13.21	9.1	9.2	-0.0	-0.2	100.0%	-1.9
20115	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	7.6	7.6	-0.0	-0.2	100.0%	-1.5
20116	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	3.2	0.0	0.2	100.0%	-2.1
20117	NA	10.5	10.4	0.1	0.2	100.0%	-1.6
20118	AT4G00300.1 | fringe-related protein, + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.	7.0	7.2	-0.1	-0.2	100.0%	-1.3
20119	AT5G28920.1 | expressed protein | chr5:10940039-10943382 REVERSE | Aliases: F7P1.1	4.5	4.5	0.0	0.2	100.0%	-1.3
20120	AT1G47980.1 | expressed protein | chr1:17695503-17697530 REVERSE | Aliases: T2J15.11, T2J15_11	3.7	3.8	-0.0	-0.2	100.0%	-1.4
20121	AT1G62540.1 | flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenase GB:AAA21178 GI:349534 from Oryctolagus cuniculus (SP:P32417), SP:P97501 from Mus musculus; contains Pfam profile PF00743 Flavin-binding monooxygenase-like | chr1:23155459-23159382 FORWARD | Aliases: T3P18.10, T3P18_10	2.8	2.8	-0.0	-0.2	100.0%	-1.9
20122	AT3G15760.1 | expressed protein | chr3:5337560-5338470 FORWARD | Aliases: MSJ11.16	2.9	3.0	-0.0	-0.2	100.0%	-1.7
20123	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%	-2.1
20124	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	4.5	4.4	0.0	0.2	100.0%	-1.5
20125	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	3.1	3.1	-0.0	-0.2	100.0%	-2.1
20126	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	-0.2	100.0%	-2.6
20127	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	6.3	6.4	-0.0	-0.2	100.0%	-1.5
20128	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	8.2	8.1	0.1	0.2	100.0%	-1.8
20129	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	4.9	4.9	-0.1	-0.2	100.0%	-1.6
20130	AT5G60790.1 | Symbol: ATGCN1 |	6.1	6.2	-0.1	-0.2	100.0%	-1.5
20131	AT3G24760.1 | F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250 | chr3:9040095-9041841 FORWARD | Aliases: K7P8.5	6.9	6.8	0.0	0.2	100.0%	-1.6
20132	AT1G13890.1 | Symbol: SNAP30 |	2.7	2.7	0.0	0.2	100.0%	-2.2
20133	AT2G46080.1 | expressed protein | chr2:18955190-18957178 REVERSE | Aliases: T3F17.27	7.5	7.4	0.0	0.2	100.0%	-1.5
20134	AT3G51700.1 | expressed protein | chr3:19190245-19192168 REVERSE | Aliases: T18N14.80	2.8	2.8	-0.0	-0.2	100.0%	-2.3
20135	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}	5.4	5.4	-0.1	-0.2	100.0%	-1.2

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20136	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	0.2	100.0%	-2.1
20137	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%	-2.5
20138	AT4G00150.1 | scarecrow-like transcription factor 6 (SCL6) | chr4:57199-59286 REVERSE | Aliases: F6N15.20, F6N15_20	4.6	4.6	-0.0	-0.2	100.0%	-1.8
20139	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	2.2	0.0	0.2	100.0%	-2.7
20140	AT1G43660.1 | hypothetical protein | chr1:16452800-16453084 FORWARD | Aliases: F2J6.16, F2J6_16	2.6	2.6	-0.0	-0.2	100.0%	-2.7
20141	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	3.1	3.1	-0.0	-0.2	100.0%	-2.0
20142	AT5G17510.1 | expressed protein | chr5:5769975-5772397 REVERSE | Aliases: K3M16.80, K3M16_80	2.9	3.0	-0.0	-0.2	100.0%	-1.7
20143	AT4G15180.1 | SET domain-containing protein, contains Pfam profile PF00856: SET domain	3.9	4.0	-0.1	-0.2	100.0%	-1.1
20144	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	-0.2	100.0%	-1.8
20145	AT5G64300.1 | Symbol: ATGCH | similar to riboflavin biosynthesis protein, putative [Arabidopsis thaliana] (TAIR:At2g22450.1); similar to GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phosphate synthase [Lycopersicon esculentum] (GB:CAA05308.1); similar to putative riboflavin biosynthesis protein ribA [Oryza sativa (japonica 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	-0.1	-0.2	100.0%	-1.6
20146	AT4G00955.1 | expressed protein | chr4:412118-413278 FORWARD | Aliases: None	4.0	4.1	-0.0	-0.2	100.0%	-1.2
20147	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	3.4	0.0	0.2	100.0%	-1.9
20148	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	-0.0	-0.2	100.0%	-2.1
20149	AT1G53600.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:20004931-20009463 FORWARD | Aliases: F22G10.27	5.4	5.4	-0.0	-0.2	100.0%	-1.6
20150	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	3.0	3.0	0.0	0.2	100.0%	-2.0
20151	AT4G25430.1 | hypothetical protein | chr4:12998600-13000221 FORWARD | Aliases: T30C3.7	2.4	2.4	-0.0	-0.2	100.0%	-2.2
20152	AT5G29090.1 | expressed protein | chr5:11149626-11150544 FORWARD | Aliases: F23C8.60, F23C8_60	3.6	3.6	-0.0	-0.2	100.0%	-1.9
20153	AT5G42820.2 | U2 snRNP auxiliary factor small subunit, putative, strong similarity to U2 snRNP auxiliary factor, small subunit (Oryza sativa) GI:3850816 | chr5:17186511-17188897 REVERSE | Aliases: MJB21.20, MJB21_20	7.0	7.0	-0.0	-0.2	100.0%	-1.5
20154	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%	-1.5
20155	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	4.7	4.7	-0.0	-0.2	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
20156	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	5.4	5.3	0.1	0.2	100.0%	-1.4
20157	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))	2.2	2.2	-0.0	-0.2	100.0%	-2.5
20158	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	3.2	3.2	0.0	0.2	100.0%	-1.9
20159	AT4G24350.1 | phosphorylase family protein, contains Pfam PF01048: Phosphorylase family | chr4:12609538-12611477 FORWARD | Aliases: T22A6.180, T22A6_180	2.4	2.4	0.0	0.2	100.0%	-2.2
20160	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	3.9	-0.0	-0.2	100.0%	-1.4
20161	AT3G22770.1 | F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain | chr3:8047691-8048674 REVERSE | Aliases: MWI23.14	3.8	3.9	-0.0	-0.2	100.0%	-2.0
20162	AT1G78290.2 | serine/threonine protein kinase, putative, similar to serine-threonine protein kinase (Triticum aestivum) gi:2055374:gb:AAB58348	5.1	5.1	0.0	0.2	100.0%	-1.6
20163	AT2G18320.1 | hypothetical protein | chr2:7963302-7964613 FORWARD | Aliases: T30D6.17, T30D6_17	3.3	3.3	-0.0	-0.2	100.0%	-1.9
20164	AT1G62210.1 | expressed protein | chr1:22989667-22990526 FORWARD | Aliases: F19K23.14, F19K23_14	3.3	3.3	-0.0	-0.2	100.0%	-1.4
20165	AT1G13760.1 | expressed protein | chr1:4720178-4720507 REVERSE | Aliases: F21F23.20, F21F23_20	2.3	2.3	-0.0	-0.2	100.0%	-2.2
20166	AT4G28080.1 | expressed protein | chr4:13948609-13957424 REVERSE | Aliases: T13J8.190, T13J8_190	3.9	3.9	0.0	0.2	100.0%	-1.9
20167	AT5G07840.1 | ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023 | chr5:2506657-2508374 REVERSE | Aliases: F13G24.40	6.8	6.8	-0.0	-0.2	100.0%	-1.8
20168	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	-0.2	100.0%	-2.1
20169	AT2G35600.1 | expressed protein | chr2:14948171-14952407 REVERSE | Aliases: T32F12.2, T32F12_2	2.8	2.8	0.0	0.2	100.0%	-2.2
20170	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	3.7	3.7	0.0	0.2	100.0%	-1.5
20171	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	4.2	4.2	-0.0	-0.2	100.0%	-1.6
20172	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	2.4	-0.0	-0.2	100.0%	-2.3
20173	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	0.2	100.0%	-1.6
20174	AT5G59070.1 | glycosyl transferase family 1 protein, contains Pfam profile: PF00534 Glycosyl transferases group 1 | chr5:23862424-23864619 FORWARD | Aliases: K18B18.2, K18B18_2	2.8	2.7	0.0	0.2	100.0%	-1.9
20175	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	8.4	8.4	0.0	0.2	100.0%	-1.7
20176	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 (GI:20197985) (Arabidopsis thaliana)	2.8	2.9	-0.0	-0.2	100.0%	-2.6
20177	AT3G42970.1 | hypothetical protein | chr3:15035795-15036132 FORWARD | Aliases: F18P9.130	2.9	3.0	-0.0	-0.2	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
20178	AT3G23350.1 | expressed protein, ; expression supported by MPSS | chr3:8354111-8355208 FORWARD | Aliases: MLM24.8	2.0	2.0	0.0	0.2	100.0%	-2.6
20179	AT3G14710.1 | F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250 | chr3:4941552-4943062 FORWARD | Aliases: MIE1.21	2.7	2.6	0.0	0.2	100.0%	-2.2
20180	AT1G10870.1 | ARF GTPase-activating domain-containing protein | chr1:3616610-3623757 REVERSE | Aliases: T19D16.20, T19D16_20	6.0	6.0	0.0	0.2	100.0%	-1.1
20181	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	2.2	2.2	0.0	0.2	100.0%	-2.3
20182	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	5.7	5.7	0.1	0.2	100.0%	-1.0
20183	AT5G53750.1 | similar to CBS domain-containing protein [Arabidopsis thaliana] (TAIR:At4g27460.1); similar to OSJNBb0017I01.11 [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	5.7	5.7	0.0	0.2	100.0%	-1.5
20184	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	5.2	5.3	-0.0	-0.2	100.0%	-1.4
20185	AT1G55560.1 | Symbol: SKS14 | multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)(Brassica napus); contains Pfam profile: PF00394 Multicopper oxidase | chr1:20757989-20760320 REVERSE | Aliases: SKS14, T5A14.2, T5A14_2	2.2	2.2	-0.0	-0.2	100.0%	-2.7
20186	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	2.3	2.4	-0.0	-0.2	100.0%	-2.6
20187	AT1G01460.1 | Type I phosphatidylinositol-4-phosphate 5-kinase, subfamily A. | chr1:168723-171165 FORWARD | Aliases: F22L4.2, F22L4_2	2.6	2.6	-0.0	-0.2	100.0%	-2.2
20188	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	2.8	2.8	0.0	0.2	100.0%	-2.1
20189	AT3G30490.1 | expressed protein | chr3:12117914-12118455 REVERSE | Aliases: MSJ3.13	2.3	2.3	-0.0	-0.2	100.0%	-2.0
20190	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	2.9	2.9	-0.0	-0.2	100.0%	-2.1
20191	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	-0.0	-0.2	100.0%	-2.3
20192	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	3.1	3.1	-0.0	-0.2	100.0%	-1.6
20193	AT2G05600.1 | hypothetical protein | chr2:2072643-2073544 FORWARD | Aliases: T20G20.5, T20G20_5	2.9	2.8	0.0	0.2	100.0%	-1.9
20194	AT4G38870.1 | F-box family protein, contains Pfam profile: PF00646 F-box domain | chr4:18132577-18133857 REVERSE | Aliases: F19H22.2	2.1	2.1	-0.0	-0.2	100.0%	-2.5
20195	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%	-2.3
20196	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	8.0	-0.1	-0.2	100.0%	-1.4
20197	AT1G11170.2 | expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707) | chr1:3741129-3744675 FORWARD | Aliases: T28P6.16, T28P6_16	3.7	3.7	-0.0	-0.2	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
20198	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%	-2.2
20199	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	0.2	100.0%	-2.3
20200	AT1G24390.1 | expressed protein, similar to EST emb:Z37190 | chr1:8648190-8648984 FORWARD | Aliases: F21J9.5	3.0	3.0	-0.0	-0.2	100.0%	-2.1
20201	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	3.4	3.4	-0.0	-0.2	100.0%	-1.9
20202	AT1G11900.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:4013120-4014680 REVERSE | Aliases: F12F1.26, F12F1_26	5.1	5.1	0.0	0.2	100.0%	-1.4
20203	AT5G61670.2 | expressed protein | chr5:24800807-24803171 FORWARD | Aliases: K11J9.20, K11J9_20	8.5	8.5	-0.0	-0.2	100.0%	-1.5
20204	AT3G60060.1 | hypothetical protein, male sterility protein 2 - Brassica napus, PIR:T08096 | chr3:22193268-22194055 FORWARD | Aliases: T2O9.40	2.5	2.5	0.0	0.2	100.0%	-2.2
20205	AT1G68340.1 | expressed protein | chr1:25617860-25619066 REVERSE | Aliases: T22E19.3, T22E19_3	4.2	4.2	-0.0	-0.2	100.0%	-1.7
20206	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	2.2	0.0	0.2	100.0%	-2.4
20207	AT4G23200.1 | protein kinase family protein, contains Pfam PF00069: Protein kinase domain | chr4:12145391-12147945 REVERSE | Aliases: F21P8.90, F21P8_90	2.5	2.5	0.0	0.2	100.0%	-2.2
20208	AT3G30240.1 | hypothetical protein | chr3:11886304-11886966 FORWARD | Aliases: MIL15.14	3.0	3.0	0.0	0.2	100.0%	-2.1
20209	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	-0.0	-0.2	100.0%	-2.0
20210	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	3.3	3.3	0.0	0.2	100.0%	-1.6
20211	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	-0.2	100.0%	-2.3
20212	AT5G51400.1 | expressed protein, contains Pfam profile PF04749: Protein of unknown function, DUF614 | chr5:20895839-20897360 REVERSE | Aliases: MFG13.11, MFG13_11	7.6	7.7	-0.1	-0.2	100.0%	-1.4
20213	AT1G67600.1 | expressed protein, contains Pfam domain, PF02681: Uncharacterized BCR, COG1963 | chr1:25340090-25341325 REVERSE | Aliases: F12A21.27, F12A21_27	3.9	3.9	0.0	0.2	100.0%	-1.9
20214	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	7.2	7.1	0.1	0.2	100.0%	-1.4
20215	AT5G53740.1 | expressed protein | chr5:21828859-21832134 FORWARD | Aliases: MGN6.10, MGN6_10	2.6	2.6	-0.0	-0.2	100.0%	-2.1
20216	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	-0.0	-0.2	100.0%	-1.9
20217	AT1G17040.1 | transcription factor-related, contains Pfam profile: PF00017 Src homology domain 2; similar to transcription factor (Danio rerio) (GI:3687402) | chr1:5824844-5828226 FORWARD | Aliases: F20D23.26, F20D23_26	4.5	4.5	-0.0	-0.2	100.0%	-1.6
20218	AT4G22060.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.3	3.3	-0.0	-0.2	100.0%	-1.8
20219	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	4.9	5.0	-0.0	-0.2	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
20220	AT3G13410.1 | expressed protein | chr3:4361889-4364242 REVERSE | Aliases: MRP15.4	9.6	9.6	0.1	0.2	100.0%	-1.5
20221	AT1G28327.1 | expressed protein | chr1:9931921-9933438 FORWARD | Aliases: F3H9.2, F3H9_2	2.9	2.9	0.0	0.2	100.0%	-2.4
20222	AT1G13710.1 | Symbol: CYP78A5 | cytochrome P450 family protein, similar to cytochrome P450 78A1 (SP:P48420) GI:349717 from (Zea mays)	2.8	2.8	-0.0	-0.2	100.0%	-1.9
20223	AT1G80640.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:30316559-30319267 FORWARD | Aliases: T21F11.3, T21F11_3	4.3	4.4	-0.0	-0.2	100.0%	-1.4
20224	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	3.6	3.5	0.0	0.2	100.0%	-1.8
20225	AT1G04530.1 | expressed protein | chr1:1234198-1236033 REVERSE | Aliases: T1G11.22, T1G11_22	5.7	5.7	0.0	0.2	100.0%	-1.4
20226	AT3G03240.1 | esterase/lipase/thioesterase family protein, contains Interpro entry IPR000379 | chr3:746662-748607 REVERSE | Aliases: T17B22.7, T17B22_7	3.4	3.4	-0.0	-0.2	100.0%	-2.2
20227	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	3.4	3.3	0.0	0.2	100.0%	-2.2
20228	AT5G57800.1 | Symbol: WAX2 | CER1 protein, putative (WAX2), similar to maize glossy1 homolog GI:2213643 from (Oryza sativa); contains Pfam profile PF01598: Sterol desaturase	4.2	4.1	0.0	0.2	100.0%	-1.7
20229	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	0.2	100.0%	-2.0
20230	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	4.1	4.1	0.0	0.2	100.0%	-1.5
20231	AT2G03070.1 | expressed protein | chr2:905618-908944 FORWARD | Aliases: T17M13.24, T17M13_24	3.9	3.9	-0.0	-0.2	100.0%	-1.7
20232	AT5G64090.1 | expressed protein | chr5:25665253-25666846 FORWARD | Aliases: MHJ24.7, MHJ24_7	4.9	4.9	-0.0	-0.2	100.0%	-1.8
20233	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	4.0	4.0	-0.0	-0.2	100.0%	-1.6
20234	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	4.1	0.0	0.2	100.0%	-1.7
20235	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	3.4	0.0	0.2	100.0%	-1.6
20236	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	4.4	4.4	0.0	0.2	100.0%	-1.9
20237	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	3.4	3.5	-0.1	-0.2	100.0%	-1.2
20238	AT5G53830.1 | VQ motif-containing protein, contains PF05678: VQ motif | chr5:21874276-21875210 FORWARD | Aliases: MGN6.22, MGN6_22	2.6	2.5	0.0	0.2	100.0%	-2.3
20239	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	4.3	0.0	0.2	100.0%	-1.8
20240	AT2G24410.1 | hypothetical protein | chr2:10386239-10386487 REVERSE | Aliases: T28I24.14, T28I24_14	2.7	2.7	0.0	0.2	100.0%	-2.5
20241	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	0.2	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
20242	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	2.7	-0.0	-0.2	100.0%	-1.9
20243	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	-0.2	100.0%	-2.3
20244	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	0.0	0.2	100.0%	-1.7
20245	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	3.6	3.6	-0.0	-0.2	100.0%	-1.8
20246	AT3G27325.1 | expressed protein | chr3:10097461-10103324 FORWARD | Aliases: K17E12.15	2.4	2.4	0.0	0.2	100.0%	-2.3
20247	AT1G35900.1 | expressed protein | chr1:13348716-13349645 REVERSE | Aliases: F10O5.7, F10O5_7	3.3	3.3	0.0	0.2	100.0%	-1.5
20248	AT3G61820.1 | aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease | chr3:22890779-22892605 REVERSE | Aliases: F21F14.7	5.0	5.1	-0.1	-0.2	100.0%	-1.3
20249	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	7.4	7.5	-0.1	-0.2	100.0%	-1.4
20250	AT3G43610.1 | tubulin family protein | chr3:15528760-15534915 REVERSE | Aliases: F22J12.50	3.6	3.6	0.0	0.2	100.0%	-1.6
20251	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	0.2	100.0%	-2.1
20252	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	2.8	2.8	-0.0	-0.2	100.0%	-1.9
20253	AT5G27340.1 | hypothetical protein | chr5:9635888-9636887 FORWARD | Aliases: F21A20.50, F21A20_50	3.7	3.7	-0.0	-0.2	100.0%	-1.8
20254	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	4.7	4.6	0.0	0.2	100.0%	-1.6
20255	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%	-1.9
20256	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	2.8	0.0	0.2	100.0%	-2.0
20257	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)	7.1	7.0	0.1	0.2	100.0%	-1.2
20258	AT5G17360.1 | expressed protein | chr5:5720378-5721661 FORWARD | Aliases: MKP11.17, MKP11_17	2.9	2.9	0.0	0.2	100.0%	-2.3
20259	AT4G19740.1 | glycosyl hydrolase family 18 protein, similar to chitinase, class V GI:899342 from (Nicotiana tabacum) | chr4:10739577-10740630 REVERSE | Aliases: T16H5.100, T16H5_100	3.0	3.0	-0.0	-0.2	100.0%	-2.0
20260	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	-0.0	-0.2	100.0%	-1.8
20261	AT5G28590.1 | DNA-binding protein-related, contains similarity to DNA-binding proteins	3.3	3.3	-0.0	-0.2	100.0%	-1.6
20262	AT3G11850.2 | expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593 | chr3:3738903-3741720 REVERSE | Aliases: F26K24.14	5.0	5.1	-0.0	-0.2	100.0%	-1.5
20263	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	4.1	4.2	-0.1	-0.2	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
20264	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	5.9	6.0	-0.1	-0.2	100.0%	-1.3
20265	AT1G74230.1 | glycine-rich RNA-binding protein, similar to RNA-binding protein GB:S46286 from (Nicotiana sylvestris) | chr1:27918367-27920744 FORWARD | Aliases: F1O17.10, F1O17_10	8.9	8.9	-0.0	-0.2	100.0%	-1.7
20266	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%	-1.8
20267	AT3G22150.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr3:7812975-7815497 FORWARD | Aliases: MKA23.11	3.3	3.3	-0.0	-0.2	100.0%	-1.6
20268	AT1G46336.1 | hypothetical protein | chr1:17232851-17233093 REVERSE | Aliases: F2G19.35, F2G19_35	2.5	2.5	-0.0	-0.2	100.0%	-2.6
20269	AT5G58040.1 | fip1 motif-containing protein, contains Pfam profile PF05182: Fip1 motif	7.2	7.1	0.1	0.2	100.0%	-1.2
20270	AT2G31470.1 | F-box family protein, contains F-box domain Pfam:PF00646	3.2	3.2	-0.0	-0.2	100.0%	-2.1
20271	AT5G36190.1 | expressed protein, similar to unknown protein (gb:AAD08947.1) | chr5:14260339-14260776 REVERSE | Aliases: MAB16.14, MAB16_14	2.2	2.2	-0.0	-0.2	100.0%	-2.5
20272	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%	-1.9
20273	AT2G23050.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr2:9817737-9819740 FORWARD | Aliases: F21P24.11, F21P24_11	2.9	2.9	-0.0	-0.2	100.0%	-1.7
20274	AT2G34060.1 | peroxidase, putative, similar to peroxidase ATP20a {Arabidopsis thaliana} GP:9757794:dbj:BAB08292 | chr2:14391993-14393748 FORWARD | Aliases: T14G11.18, T14G11_18	3.2	3.3	-0.0	-0.2	100.0%	-1.8
20275	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	2.5	2.6	-0.0	-0.2	100.0%	-2.1
20276	AT5G02720.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr5:613780-614311 REVERSE | Aliases: F9G14.30, F9G14_30	2.9	2.8	0.0	0.2	100.0%	-2.1
20277	AT2G11000.1 | Symbol: ATMAK10 | similar to Unknown (protein for MGC:64157) [Danio rerio] (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	6.1	6.0	0.0	0.2	100.0%	-1.4
20278	AT3G44280.1 | expressed protein | chr3:15979580-15982083 REVERSE | Aliases: T10D17.70	6.9	6.8	0.1	0.2	100.0%	-1.3
20279	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	3.5	3.5	-0.0	-0.2	100.0%	-1.8
20280	AT3G12010.1 | expressed protein, contains Prosite PS00626: Regulator of chromosome condensation (RCC1) signature 2 | chr3:3821523-3825543 FORWARD | Aliases: MEC18.14	5.4	5.3	0.0	0.2	100.0%	-1.7
20281	AT3G10180.1 | kinesin motor protein-related, similar to centromere protein E GB:4502781 (Homo sapiens)	3.0	3.1	-0.0	-0.2	100.0%	-2.1
20282	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	3.0	2.9	0.0	0.2	100.0%	-1.9
20283	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	0.2	100.0%	-1.5
20284	AT3G14100.1 | oligouridylate-binding protein, putative, similar to GB:CAB75429 (GI:6996560) from (Nicotiana plumbaginifolia), contains Pfam profiles: PF00076 RNA recognition motif (3 copies)	8.0	7.9	0.1	0.2	100.0%	-1.4
20285	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	9.2	9.1	0.1	0.2	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
20286	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	-0.2	100.0%	-2.1
20287	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	4.3	4.2	0.0	0.2	100.0%	-1.5
20288	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	3.9	3.9	-0.0	-0.2	100.0%	-1.5
20289	AT3G12600.1 | MutT/nudix family protein, contains Pfam profile PF00293: NUDIX domain | chr3:4004590-4006205 FORWARD | Aliases: T2E22.9, T2E22_9	7.4	7.4	0.0	0.2	100.0%	-1.5
20290	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	0.2	100.0%	-2.1
20291	AT3G19200.1 | expressed protein | chr3:6649484-6650012 REVERSE | Aliases: MVI11.12	3.1	3.1	0.0	0.2	100.0%	-1.8
20292	AT1G23910.1 | hypothetical protein | chr1:8451057-8451278 REVERSE | Aliases: T23E23.8, T23E23_8	2.8	2.9	-0.0	-0.2	100.0%	-2.4
20293	AT3G30843.1 | expressed protein | chr3:12609750-12610729 REVERSE | Aliases: MJI6.4	3.2	3.2	0.0	0.2	100.0%	-1.9
20294	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	10.9	10.8	0.1	0.2	100.0%	-1.9
20295	AT4G35720.1 | expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function | chr4:16927977-16929175 FORWARD | Aliases: F8D20.230, F8D20_230	3.5	3.6	-0.0	-0.2	100.0%	-1.8
20296	AT3G17190.1 | hypothetical protein | chr3:5867398-5867954 FORWARD | Aliases: MCE21.3	2.6	2.6	-0.0	-0.2	100.0%	-2.5
20297	AT2G28090.1 | heavy-metal-associated domain-containing protein, similar to farnesylated protein ATFP3 (GI:4097547); contains Pfam profile PF00403: Heavy-metal-associated domain | chr2:11979475-11981084 REVERSE | Aliases: F24D13.12, F24D13_12	3.8	3.9	-0.0	-0.2	100.0%	-1.4
20298	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	3.6	0.0	0.2	100.0%	-1.5
20299	AT1G29950.2 | expressed protein | chr1:10491959-10494582 FORWARD | Aliases: T1P2.2	4.8	4.8	0.0	0.2	100.0%	-1.8
20300	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	0.2	100.0%	-1.5
20301	AT2G34310.3 | expressed protein | chr2:14484820-14487041 REVERSE | Aliases: F13P17.27	6.7	6.6	0.0	0.2	100.0%	-1.5
20302	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	3.8	3.7	0.0	0.2	100.0%	-1.5
20303	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	5.3	5.3	0.0	0.2	100.0%	-1.8
20304	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	4.8	-0.0	-0.2	100.0%	-1.5
20305	AT3G62440.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.5	0.0	0.2	100.0%	-2.2
20306	AT5G58820.1 | subtilase family protein, contains similarity to prepro-cucumisin GI:807698 from (Cucumis melo) | chr5:23769182-23771999 FORWARD | Aliases: K19M22.2, K19M22_2	2.6	2.6	-0.0	-0.2	100.0%	-2.7

Rank	Description	Sync	Root	M	t	adj.q	B
20307	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	-0.2	100.0%	-1.9
20308	AT1G22720.1 | wall-associated kinase, putative, contains similarity to serine/threonine kinase gb:Y12531 from Brassica oleracea | chr1:8044221-8045654 REVERSE | Aliases: T22J18.11, T22J18_11	3.0	3.1	-0.0	-0.2	100.0%	-2.1
20309	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	4.7	4.8	-0.0	-0.1	100.0%	-1.7
20310	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%	-2.2
20311	AT2G27790.1 | expressed protein | chr2:11854412-11856362 REVERSE | Aliases: F15K20.11, F15K20_11	3.4	3.4	-0.0	-0.1	100.0%	-1.9
20312	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	0.1	100.0%	-1.9
20313	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	-0.1	100.0%	-2.2
20314	AT5G52500.1 | expressed protein, strong similarity to unknown protein (emb:CAB68146.1)	2.7	2.7	-0.0	-0.1	100.0%	-2.1
20315	AT5G11040.1 | expressed protein, weak similarity to hypercellular protein (Aspergillus nidulans) GI:9309269 | chr5:3495288-3500923 FORWARD | Aliases: T5K6.30, T5K6_30	5.7	5.8	-0.0	-0.1	100.0%	-1.5
20316	AT1G13340.1 | expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292	4.4	4.4	0.0	0.1	100.0%	-1.3
20317	AT3G48810.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:18108033-18110012 FORWARD | Aliases: T21J18.80	4.3	4.2	0.0	0.1	100.0%	-1.4
20318	AT5G56270.1 | Symbol: WRKY2 | WRKY family transcription factor | chr5:22796919-22800494 FORWARD | Aliases: ATWRKY2, MXK23.1, MXK23_1	4.6	4.6	0.0	0.1	100.0%	-1.4
20319	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	-0.1	100.0%	-2.2
20320	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	2.4	2.4	-0.0	-0.1	100.0%	-2.5
20321	AT2G14330.1 | expressed protein, siimilar to At3g45350, At4g09400 | chr2:6081244-6082476 FORWARD | Aliases: T1O16.8, T1O16_8	2.4	2.4	-0.0	-0.1	100.0%	-2.5
20322	AT3G12690.3 | protein kinase, putative, similar to viroid symptom modulation protein (Lycopersicon esculentum) gi:7672777:gb:AAF66637 | chr3:4030462-4032820 REVERSE | Aliases: MBK21.5	4.0	4.0	0.0	0.1	100.0%	-1.8
20323	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	2.4	2.5	-0.0	-0.1	100.0%	-2.2
20324	AT5G57920.1 | plastocyanin-like domain-containing protein | chr5:23470825-23471623 FORWARD | Aliases: MTI20.18, MTI20_18	6.5	6.5	-0.0	-0.1	100.0%	-1.8
20325	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	-0.1	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
20326	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	3.5	0.0	0.1	100.0%	-1.8
20327	AT4G04980.1 | hydroxyproline-rich glycoprotein family protein, Common family members: At4g18570, At3g25690, At5g61090 (Arabidopsis thaliana) | chr4:2544208-2546831 REVERSE | Aliases: C17L7.1	2.7	2.7	-0.0	-0.1	100.0%	-1.9
20328	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	4.0	4.0	0.0	0.1	100.0%	-1.6
20329	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	7.8	7.7	0.1	0.1	100.0%	-1.2
20330	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	-0.0	-0.1	100.0%	-1.8
20331	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	5.2	5.2	0.0	0.1	100.0%	-1.4
20332	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	9.3	9.3	-0.1	-0.1	100.0%	-1.5
20333	AT1G79190.1 | expressed protein | chr1:29793532-29799063 FORWARD | Aliases: YUP8H12R.20, YUP8H12R_20	5.0	4.9	0.0	0.1	100.0%	-1.8
20334	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	5.5	5.6	-0.1	-0.1	100.0%	-1.4
20335	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	5.7	5.7	0.0	0.1	100.0%	-1.3
20336	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	7.9	7.9	0.1	0.1	100.0%	-1.4
20337	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	-0.1	100.0%	-2.5
20338	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	4.2	4.2	-0.0	-0.1	100.0%	-1.5
20339	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	-0.1	100.0%	-2.2
20340	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	8.5	8.6	-0.1	-0.1	100.0%	-1.1
20341	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	-0.1	100.0%	-2.7
20342	AT4G16710.2 | glycosyltransferase family protein 28, low similarity to C terminus subunit of GlcA transferase from Escherichia coli (GI:2586169); contains Pfam profile PF04101: Glycosyltransferase family 28 C-terminal domain | chr4:9398589-9399823 FORWARD | Aliases: DL4380W, FCAALL.10	8.1	8.1	-0.0	-0.1	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
20343	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	3.0	3.0	-0.0	-0.1	100.0%	-1.8
20344	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	3.0	3.0	-0.0	-0.1	100.0%	-1.8
20345	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	3.0	3.0	-0.0	-0.1	100.0%	-1.8
20346	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	2.2	0.0	0.1	100.0%	-2.4
20347	AT5G35430.1 | expressed protein | chr5:13679171-13683245 FORWARD | Aliases: AT5G35440, MOK9.1, MOK9_1	3.4	3.4	-0.0	-0.1	100.0%	-2.1
20348	AT3G32120.1 | hypothetical protein | chr3:13128179-13129029 FORWARD | Aliases: F1M23.21	2.9	2.9	0.0	0.1	100.0%	-1.7
20349	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	2.6	-0.0	-0.1	100.0%	-2.1
20350	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	3.2	3.2	0.0	0.1	100.0%	-1.5
20351	AT5G11390.1 | expressed protein | chr5:3633668-3636562 FORWARD | Aliases: F2I11.280, F2I11_280	7.7	7.7	-0.1	-0.1	100.0%	-1.1
20352	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	2.7	2.8	-0.0	-0.1	100.0%	-1.9
20353	AT2G05940.1 | protein kinase, putative, similar to auxin-regulated dual specificity cytosolic kinase (Lycopersicon esculentum) gi:14484938:gb:AAK62821	6.6	6.5	0.1	0.1	100.0%	-1.3
20354	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	-0.1	100.0%	-1.3
20355	AT5G22630.1 | prephenate dehydratase family protein, contains Pfam profile PF00800: prephenate dehydratase | chr5:7524345-7526163 FORWARD | Aliases: MDJ22.5, MDJ22_5	9.2	9.1	0.1	0.1	100.0%	-1.3
20356	AT5G40980.1 | expressed protein | chr5:16432076-16432448 REVERSE | Aliases: MEE6.5, MEE6_5	5.5	5.6	-0.0	-0.1	100.0%	-1.4
20357	AT5G47380.1 | expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547 | chr5:19238699-19241698 REVERSE | Aliases: MQL5.24, MQL5_24	2.6	2.6	-0.0	-0.1	100.0%	-2.1
20358	AT1G76090.1 | Symbol: SMT3 | S-adenosyl-methionine-sterol-C-methyltransferase, identical to S-adenosyl-methionine-sterol-C-methyltransferase GI:2246456 from (Arabidopsis thaliana) | chr1:28555303-28556675 REVERSE | Aliases: SMT3, T23E18.40, T23E18_40	5.3	5.3	-0.1	-0.1	100.0%	-1.6
20359	AT3G15310.1 | expressed protein | chr3:5152106-5153649 REVERSE | Aliases: K7L4.11	2.0	2.0	-0.0	-0.1	100.0%	-2.5
20360	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	-0.0	-0.1	100.0%	-2.0
20361	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	5.4	0.0	0.1	100.0%	-1.5
20362	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	2.9	2.8	0.0	0.1	100.0%	-1.8
20363	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 scienitific 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	5.9	6.0	-0.0	-0.1	100.0%	-1.4

Rank	Description	Sync	Root	M	t	adj.q	B
20364	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	4.4	4.4	-0.0	-0.1	100.0%	-1.2
20365	AT3G12890.1 | Symbol: ASML2 | expressed protein | chr3:4099206-4100476 FORWARD | Aliases: ACTIVATOR OF SPOMIN::LUC2, MJM20.3	2.8	2.8	0.0	0.1	100.0%	-2.3
20366	AT2G42860.1 | expressed protein | chr2:17840842-17842190 FORWARD | Aliases: F7D19.14, F7D19_14	2.7	2.6	0.0	0.1	100.0%	-2.0
20367	AT4G19100.1 | expressed protein | chr4:10453464-10454370 FORWARD | Aliases: None	4.0	4.0	0.0	0.1	100.0%	-1.8
20368	AT4G20220.1 | expressed protein | chr4:10918686-10922406 FORWARD | Aliases: F1C12.140, F1C12_140	2.6	2.6	0.0	0.1	100.0%	-2.5
20369	AT5G61110.1 | expressed protein | chr5:24598304-24599217 REVERSE | Aliases: MAF19.11, MAF19_11	2.2	2.2	-0.0	-0.1	100.0%	-2.5
20370	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	-0.0	-0.1	100.0%	-2.0
20371	AT3G46390.1 | expressed protein | chr3:17082240-17082668 REVERSE | Aliases: F18L15.110	2.3	2.3	0.0	0.1	100.0%	-2.2
20372	AT1G67570.1 | expressed protein | chr1:25328826-25331469 FORWARD | Aliases: F12B7.12, F12B7_12	4.8	4.8	0.0	0.1	100.0%	-1.6
20373	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	-0.1	100.0%	-2.1
20374	AT2G03380.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:1028289-1030358 FORWARD | Aliases: T4M8.19, T4M8_19	3.1	3.1	-0.0	-0.1	100.0%	-2.0
20375	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	6.0	5.9	0.1	0.1	100.0%	-1.3
20376	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	2.5	2.5	0.0	0.1	100.0%	-2.2
20377	AT5G39990.1 | glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/I-Branching enzyme | chr5:16021520-16023968 FORWARD | Aliases: MYH19.150, MYH19_150	4.8	4.7	0.0	0.1	100.0%	-1.5
20378	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	0.1	100.0%	-2.1
20379	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	0.1	100.0%	-2.0
20380	AT1G65900.1 | expressed protein | chr1:24519509-24522111 REVERSE | Aliases: F12P19.7, F12P19_7	3.9	3.9	-0.0	-0.1	100.0%	-1.6
20381	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	3.0	3.0	0.0	0.1	100.0%	-1.8
20382	AT4G10800.1 | expressed protein, predicted proteins, Arabidopsis thaliana | chr4:6643659-6644841 FORWARD | Aliases: F25I24.10, F25I24_10	3.9	3.9	-0.0	-0.1	100.0%	-2.0
20383	AT1G74450.1 | expressed protein | chr1:27986170-27987941 FORWARD | Aliases: F1M20.13, F1M20_13	5.1	5.2	-0.0	-0.1	100.0%	-1.4
20384	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	3.1	-0.0	-0.1	100.0%	-1.6
20385	AT3G24140.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 Helix-loop-helix DNA-binding domain	2.7	2.8	-0.0	-0.1	100.0%	-2.0
20386	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	4.8	4.9	-0.0	-0.1	100.0%	-1.2
20387	AT1G66380.1 | Symbol: MYB114 |	2.9	2.9	-0.0	-0.1	100.0%	-2.4

Rank	Description	Sync	Root	M	t	adj.q	B
20388	AT5G24570.1 | expressed protein | chr5:8405684-8406135 REVERSE | Aliases: K18P6.10, K18P6_10	4.6	4.6	-0.1	-0.1	100.0%	-1.5
20389	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	4.3	4.3	0.0	0.1	100.0%	-1.5
20390	AT3G19516.1 | expressed protein | chr3:6770167-6771084 REVERSE | Aliases: T31J18.1	2.3	2.3	0.0	0.1	100.0%	-2.3
20391	AT1G28135.1 | expressed protein | chr1:9829319-9829474 FORWARD | Aliases: F3H9.27, F3H9_27	2.5	2.5	0.0	0.1	100.0%	-2.5
20392	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%	-2.7
20393	AT1G35750.1 | pumilio/Puf RNA-binding domain-containing protein | chr1:13254610-13256782 REVERSE | Aliases: F14D7.5, F14D7_5	2.7	2.7	-0.0	-0.1	100.0%	-2.1
20394	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	6.9	-0.1	-0.1	100.0%	-1.5
20395	AT3G23295.1 | expressed protein | chr3:8327674-8327898 FORWARD | Aliases: MLM24.1	2.5	2.5	0.0	0.1	100.0%	-2.2
20396	AT1G23780.1 | F-box family protein, contains Pfam PF00646: F-box domain; similar to SP:Q9Y3I1 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%	-1.8
20397	AT4G08710.1 | hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287 | chr4:5567739-5570569 FORWARD | Aliases: T32A17.20, T32A17_20	3.6	3.6	-0.0	-0.1	100.0%	-1.9
20398	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	0.0	0.1	100.0%	-2.1
20399	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	4.1	0.0	0.1	100.0%	-1.6
20400	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	-0.1	100.0%	-1.9
20401	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	4.9	-0.0	-0.1	100.0%	-1.6
20402	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	0.1	100.0%	-2.3
20403	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	8.8	8.8	-0.0	-0.1	100.0%	-1.9
20404	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	-0.0	-0.1	100.0%	-2.7
20405	AT3G27090.1 | expressed protein, similar to gda-1 (Pisum sativum) GI:2765418 | chr3:9990780-9993063 FORWARD | Aliases: MOJ10.16	8.1	8.1	-0.1	-0.1	100.0%	-1.6
20406	AT5G48530.1 | expressed protein | chr5:19685796-19686056 REVERSE | Aliases: MJE7.17, MJE7_17	2.6	2.6	0.0	0.1	100.0%	-2.4
20407	AT1G23840.1 | expressed protein | chr1:8424286-8425365 REVERSE | Aliases: F5O8.40, F5O8_40	4.6	4.6	-0.0	-0.1	100.0%	-1.9
20408	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	3.6	0.0	0.1	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
20409	AT2G22100.1 | RNA recognition motif (RRM)-containing protein, similar to UBP1 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	5.4	-0.0	-0.1	100.0%	-1.7
20410	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	2.7	0.0	0.1	100.0%	-2.4
20411	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	2.9	2.9	-0.0	-0.1	100.0%	-2.0
20412	AT3G16270.1 | expressed protein, gene model | chr3:5513331-5516942 FORWARD | Aliases: MYA6.8	2.8	2.7	0.0	0.1	100.0%	-1.7
20413	AT5G62110.1 | expressed protein | chr5:24960130-24963307 REVERSE | Aliases: MTG10.14, MTG10_14	2.3	2.3	0.0	0.1	100.0%	-2.8
20414	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	3.7	3.7	-0.0	-0.1	100.0%	-1.7
20415	AT3G57950.1 | expressed protein, hypothetical protein T24P15.9 - Arabidopsis thaliana, PIR:T00927; expression supported by MPSS | chr3:21471400-21471945 FORWARD | Aliases: T10K17.160	2.7	2.7	-0.0	-0.1	100.0%	-2.2
20416	AT1G61610.1 | S-locus lectin protein kinase family protein, similar to KI 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	2.7	2.8	-0.0	-0.1	100.0%	-2.2
20417	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	12.7	12.6	0.0	0.1	100.0%	-2.3
20418	AT5G01400.1 | expressed protein, contains low similarity to symplekin SP:Q92797 from (Homo sapiens) | chr5:162549-171071 REVERSE | Aliases: T10O8.110, T10O8_110	5.2	5.1	0.0	0.1	100.0%	-1.4
20419	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	4.9	4.9	-0.0	-0.1	100.0%	-1.4
20420	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	2.6	-0.0	-0.1	100.0%	-2.1
20421	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	3.2	3.2	-0.0	-0.1	100.0%	-2.1
20422	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	5.0	4.9	0.0	0.1	100.0%	-1.3
20423	AT5G49000.1 | similar to kelch repeat-containing F-box family protein [Arabidopsis thaliana] (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	7.1	7.1	-0.0	-0.1	100.0%	-2.0
20424	AT4G26540.1 | protein kinase family protein, Three false introns were added with non-consensus splice sites to circumenvent frameshifts likely due to sequencing errors; this is extremely unusual and is under investigation.	2.3	2.3	-0.0	-0.1	100.0%	-2.4
20425	AT2G20540.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr2:8851241-8852845 FORWARD | Aliases: T13C7.13, T13C7_13	3.8	3.9	-0.0	-0.1	100.0%	-1.4
20426	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	3.2	3.2	-0.0	-0.1	100.0%	-2.1
20427	AT4G39410.1 | Symbol: WRKY13 |	3.5	3.6	-0.0	-0.1	100.0%	-2.0

Rank	Description	Sync	Root	M	t	adj.q	B
20428	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	6.6	6.5	0.0	0.1	100.0%	-1.4
20429	AT1G79960.1 | ovate protein-related, contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568 | chr1:30084558-30085442 REVERSE | Aliases: F18B13.4, F18B13_4	3.2	3.1	0.0	0.1	100.0%	-1.6
20430	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	4.6	4.5	0.0	0.1	100.0%	-1.1
20431	AT1G51080.1 | expressed protein | chr1:18933551-18934408 REVERSE | Aliases: F23H24.7, F23H24_7	3.9	3.9	0.0	0.1	100.0%	-1.7
20432	AT1G16190.1 | DNA repair protein RAD23, putative, similar to DNA repair by nucleotide excision (NER) RAD23 protein, isoform II GI:1914685 from (Daucus carota)	3.2	3.1	0.0	0.1	100.0%	-1.8
20433	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	2.4	0.0	0.1	100.0%	-2.4
20434	AT1G64710.1 | alcohol dehydrogenase, putative, similar to alcohol dehydrogenase GI:551257 from (Nicotiana tabacum) | chr1:24048233-24050215 FORWARD | Aliases: F13O11.3, F13O11_3	3.2	3.2	-0.0	-0.1	100.0%	-1.8
20435	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	2.3	2.3	0.0	0.1	100.0%	-2.2
20436	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	3.2	3.2	0.0	0.1	100.0%	-1.8
20437	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	5.2	5.2	0.0	0.1	100.0%	-1.6
20438	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	2.8	2.8	-0.0	-0.1	100.0%	-2.0
20439	AT1G05100.1 | Symbol: MAPKKK18 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:1469609-1470880 FORWARD | Aliases: T7A14.2, T7A14_2	4.4	4.4	-0.0	-0.1	100.0%	-1.7
20440	AT5G45790.1 | expressed protein, ; expression supported by MPSS | chr5:18589620-18590891 FORWARD | Aliases: MRA19.23, MRA19_23	3.1	3.1	-0.0	-0.1	100.0%	-1.7
20441	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	9.2	9.3	-0.0	-0.1	100.0%	-1.6
20442	AT2G24920.1 | expressed protein | chr2:10608939-10609529 FORWARD | Aliases: F27C12.16, F27C12_16	3.9	3.9	-0.0	-0.1	100.0%	-1.3
20443	NA	2.3	2.3	-0.0	-0.1	100.0%	-2.9
20444	AT2G35075.1 | expressed protein | chr2:14793761-14796102 FORWARD | Aliases: None	3.0	3.0	0.0	0.1	100.0%	-2.1
20445	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	8.3	8.3	-0.0	-0.1	100.0%	-1.3
20446	AT1G22060.1 | expressed protein | chr1:7773052-7780575 REVERSE | Aliases: F2E2.13, F2E2_13	4.2	4.2	0.0	0.1	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
20447	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	3.3	-0.0	-0.1	100.0%	-1.8
20448	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	2.7	2.7	0.0	0.1	100.0%	-2.3
20449	AT2G39620.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:16526046-16528556 REVERSE | Aliases: F12L6.28, F12L6_28	3.0	3.0	0.0	0.1	100.0%	-2.1
20450	AT1G22180.3 | SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, contains Pfam profile: PF00650 CRAL/TRIO domain; similar to polyphosphoinositide binding protein Ssh1p (GI::2739044) {Glycine max}; similar to Phosphatidylinositol Transfer Protein Sec14p (GI:2780955) (Saccharomyces cerevisiae) | chr1:7828315-7830307 REVERSE | Aliases: F16L1.9, F16L1_9	7.7	7.8	-0.1	-0.1	100.0%	-1.4
20451	AT4G01880.1 | expressed protein, contains Pfam PF05206: Protein of unknown function (DUF715) | chr4:810699-812925 REVERSE | Aliases: T7B11.14, T7B11_14	4.0	4.0	0.0	0.1	100.0%	-1.4
20452	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	-0.1	100.0%	-2.3
20453	AT2G45120.1 | zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type | chr2:18610693-18611826 FORWARD | Aliases: T14P1.7	2.5	2.5	-0.0	-0.1	100.0%	-2.2
20454	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	3.7	0.0	0.1	100.0%	-1.8
20455	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	6.5	-0.0	-0.1	100.0%	-1.6
20456	AT3G60100.1 | citrate synthase, mitochondrial, putative, strong similarity to SP:Q43175 Citrate synthase, mitochondrial precursor {Solanum tuberosum}; contains Pfam profile PF00285: Citrate synthase	3.6	3.6	-0.0	-0.1	100.0%	-1.8
20457	NA	2.2	2.2	0.0	0.1	100.0%	-2.6
20458	AT1G64950.1 | Symbol: CYP89A5 | cytochrome P450, putative, similar to cytochrome P450 89A2 (CYPLXXXIX) (SP:Q42602) (Arabidopsis thaliana);similar to cytochrome P450 (GI:438242) (Solanum melongena) | chr1:24131224-24133121 FORWARD | Aliases: F13O11.25, F13O11_25	10.1	10.1	0.0	0.1	100.0%	-2.3
20459	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	4.4	4.4	-0.0	-0.1	100.0%	-1.6
20460	AT1G54310.2 | expressed protein | chr1:20277234-20279116 FORWARD | Aliases: F20D21.13, F20D21_13	3.7	3.7	-0.0	-0.1	100.0%	-1.4
20461	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	7.8	7.7	0.1	0.1	100.0%	-1.1
20462	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	7.1	7.1	-0.0	-0.1	100.0%	-1.9
20463	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	3.5	0.0	0.1	100.0%	-2.0
20464	AT1G50910.1 | expressed protein | chr1:18870751-18873507 REVERSE | Aliases: F8A12.13, F8A12_13	2.6	2.6	-0.0	-0.1	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
20465	AT1G69310.2 | Symbol: WRKY57 |	3.1	3.1	0.0	0.1	100.0%	-2.0
20466	AT4G16790.1 | hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 | chr4:9451604-9453273 REVERSE | Aliases: DL4420C, FCAALL.137	3.9	3.9	0.0	0.1	100.0%	-1.9
20467	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	3.0	3.0	0.0	0.1	100.0%	-2.0
20468	AT2G41410.1 | calmodulin, putative, identical to SP:P30188 Calmodulin-like protein {Arabidopsis thaliana} | chr2:17268806-17269962 REVERSE | Aliases: F13H10.4, F13H10_4	7.4	7.4	0.0	0.1	100.0%	-1.6
20469	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	3.4	-0.0	-0.1	100.0%	-1.8
20470	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	-0.1	100.0%	-2.3
20471	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, Saccharomyces cerevisiae, PIR2:S48466 | chr4:10438224-10443797 REVERSE | Aliases: T18B16.1	4.8	4.8	0.0	0.1	100.0%	-1.7
20472	AT1G76510.2 | ARID/BRIGHT DNA-binding domain-containing protein, contains Pfam profile PF01388: ARID/BRIGHT DNA binding domain	6.4	6.4	-0.0	-0.1	100.0%	-1.4
20473	AT1G28550.1 | Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303742 from (Pisum sativum)	2.3	2.3	0.0	0.1	100.0%	-2.3
20474	AT1G20693.2 | Symbol: HMGB2 | similar to high mobility group protein beta2 (HMGbeta2) / HMG protein beta2 [Arabidopsis thaliana] (TAIR:At1g20696.1); similar to high mobility group protein [Solanum tuberosum] (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	6.8	6.8	-0.1	-0.1	100.0%	-1.3
20475	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%	-2.0
20476	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/PfpI (InterPro:IPR002818); contains InterPro domain DJ-1 protein (InterPro:IPR006287)	2.6	2.6	-0.0	-0.1	100.0%	-1.9
20477	AT3G61700.1 | expressed protein | chr3:22847618-22848930 FORWARD | Aliases: F15G16.90	2.4	2.4	-0.0	-0.1	100.0%	-2.3
20478	AT1G05740.1 | expressed protein, contains Pfam PF05811: Eukaryotic protein of unknown function (DUF842) | chr1:1720673-1721308 FORWARD | Aliases: F3F20.19, F3F20_19	2.9	3.0	-0.0	-0.1	100.0%	-1.7
20479	AT5G18870.1 | inosine-uridine preferring nucleoside hydrolase-related | chr5:6298388-6300291 FORWARD | Aliases: F17K4.120, F17K4_120	2.4	2.4	0.0	0.1	100.0%	-2.6
20480	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	9.2	9.1	0.0	0.1	100.0%	-1.6
20481	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	0.1	100.0%	-1.8
20482	AT4G35320.1 | expressed protein, predicted protein, Arabidopsis thaliana | chr4:16805874-16806660 REVERSE | Aliases: F23E12.120, F23E12_120	3.6	3.6	-0.0	-0.1	100.0%	-1.9
20483	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	6.3	6.4	-0.1	-0.1	100.0%	-0.9
20484	AT4G01700.1 | chitinase, putative, similar to peanut type II chitinase GI:1237025 from (Arachis hypogaea) | chr4:732010-733510 REVERSE | Aliases: T15B16.5, T15B16_5	7.6	7.7	-0.1	-0.1	100.0%	-1.0

Rank	Description	Sync	Root	M	t	adj.q	B
20485	AT2G48150.1 | Symbol: ATGPX4 |	2.4	2.4	-0.0	-0.1	100.0%	-2.2
20486	AT2G42500.2 | Symbol: PP2A 4 |	6.3	6.5	-0.1	-0.1	100.0%	-1.0
20487	AT3G58500.1 | Symbol: PP2A 3 |	6.3	6.5	-0.1	-0.1	100.0%	-1.0
20488	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	3.4	3.4	0.0	0.1	100.0%	-2.2
20489	AT4G21380.1 | Symbol: ARK3 | S-locus protein kinase, putative (ARK3), identical to PIR:T05180:T05180 S-receptor kinase ARK3 precursor - (Arabidopsis thaliana) | chr4:11388936-11393237 REVERSE | Aliases: T6K22.110, T6K22_110	3.1	3.1	0.0	0.1	100.0%	-2.1
20490	AT4G32900.2 | expressed protein | chr4:15878751-15881044 REVERSE | Aliases: F26P21.20, F26P21_20	3.4	3.3	0.0	0.1	100.0%	-1.5
20491	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	0.1	100.0%	-2.7
20492	AT3G21465.2 | similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g15640.1); similar to putative adenyl cyclase [Oryza sativa (japonica cultivar-group)] (GB:XP_479441.1) | chr3:7560726-7563433 FORWARD | Aliases: MHC9.15	3.2	3.2	0.0	0.1	100.0%	-1.5
20493	AT4G23610.1 | expressed protein | chr4:12314035-12314839 FORWARD | Aliases: F9D16.80, F9D16_80	2.4	2.3	0.0	0.1	100.0%	-2.4
20494	AT3G15860.1 | expressed protein | chr3:5361214-5361726 REVERSE | Aliases: MSJ11.26	2.2	2.2	0.0	0.1	100.0%	-2.5
20495	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	-0.0	-0.1	100.0%	-2.3
20496	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	3.3	-0.0	-0.1	100.0%	-1.9
20497	AT1G25510.1 | aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease | chr1:8959181-8960835 REVERSE | Aliases: F2J7.6, F2J7_6	3.4	3.4	-0.0	-0.1	100.0%	-1.3
20498	AT3G62230.1 | F-box family protein, contains Pfam:PF00646 F-box domain	2.7	2.7	-0.0	-0.1	100.0%	-2.1
20499	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	3.9	3.9	0.0	0.1	100.0%	-1.9
20500	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	-0.0	-0.1	100.0%	-1.6
20501	AT5G38840.1 | forkhead-associated domain-containing protein / FHA domain-containing protein, related to adaptor protein kanadaptin (Homo sapiens) gi:13562130:gb:AAK29177 | chr5:15568526-15572300 FORWARD | Aliases: K15E6.5, K15E6_5	8.3	8.2	0.1	0.1	100.0%	-1.2
20502	AT5G50350.1 | expressed protein | chr5:20515702-20518906 REVERSE | Aliases: MXI22.6, MXI22_6	5.1	5.1	0.0	0.1	100.0%	-1.5
20503	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	-0.0	-0.1	100.0%	-2.1
20504	AT5G67370.1 | expressed protein, similar to unknown protein (gb:AAC18972.1) | chr5:26894794-26896768 REVERSE | Aliases: K8K14.9, K8K14_9	7.7	7.7	-0.0	-0.1	100.0%	-1.6
20505	AT5G63820.1 | expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626) | chr5:25558802-25560119 FORWARD | Aliases: MGI19.2, MGI19_2	3.2	3.3	-0.0	-0.1	100.0%	-2.0
20506	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%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
20507	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	4.0	4.0	0.0	0.1	100.0%	-1.6
20508	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	3.0	3.0	0.0	0.1	100.0%	-1.9
20509	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	3.0	3.0	-0.0	-0.1	100.0%	-1.8
20510	AT3G12820.1 | myb family transcription factor (MYB10), similar to myb factor GI:1945279 from (Oryza sativa) | chr3:4074165-4075621 REVERSE | Aliases: MBK21.18	4.3	4.2	0.0	0.1	100.0%	-1.8
20511	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	6.1	6.1	0.0	0.1	100.0%	-1.7
20512	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	3.5	3.4	0.0	0.1	100.0%	-2.0
20513	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	6.5	6.4	0.0	0.1	100.0%	-1.6
20514	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	3.7	3.8	-0.0	-0.1	100.0%	-1.5
20515	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	0.1	100.0%	-2.2
20516	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	2.7	-0.0	-0.1	100.0%	-1.8
20517	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	3.6	-0.0	-0.1	100.0%	-1.8
20518	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	3.4	3.5	-0.0	-0.1	100.0%	-1.7
20519	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	7.0	7.1	-0.0	-0.1	100.0%	-1.7
20520	AT2G06140.1 | expressed protein | chr2:2392857-2394901 FORWARD | Aliases: F5K7.10, F5K7_10	2.7	2.7	-0.0	-0.1	100.0%	-2.2
20521	AT5G54740.1 | protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to 2S seed storage proteins from Arabidosis 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	2.4	2.4	-0.0	-0.1	100.0%	-2.3
20522	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%	-1.6
20523	AT5G17340.1 | expressed protein, weak similarity to M3.4 protein (Brassica napus) GI:4574746 | chr5:5715626-5716270 REVERSE | Aliases: MKP11.1, MKP11_1	2.5	2.4	0.0	0.1	100.0%	-2.5
20524	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	-0.1	100.0%	-2.2
20525	AT3G06930.2 | protein arginine N-methyltransferase family protein, similar to protein arginine methyltransferase (Mus musculus) GI:5257221 | chr3:2185149-2189390 REVERSE | Aliases: F17A9.8	3.8	3.8	-0.0	-0.1	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
20526	AT5G08520.1 | myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain | chr5:2755176-2758335 REVERSE | Aliases: F8L15.2	5.6	5.7	-0.0	-0.1	100.0%	-1.2
20527	AT4G31080.1 | expressed protein | chr4:15120927-15121977 FORWARD | Aliases: F6I18.10, F6I18_10	3.8	3.8	0.0	0.1	100.0%	-1.5
20528	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	2.7	2.7	-0.0	-0.1	100.0%	-2.1
20529	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	2.8	2.7	0.0	0.1	100.0%	-1.9
20530	AT2G39520.1 | expressed protein | chr2:16503891-16504699 FORWARD | Aliases: F12L6.18, F12L6_18	3.4	3.5	-0.0	-0.1	100.0%	-1.9
20531	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	2.7	2.7	0.0	0.1	100.0%	-2.0
20532	AT1G71410.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:26916421-26921337 REVERSE | Aliases: F3I17.28, F3I17_28	3.7	3.8	-0.1	-0.1	100.0%	-1.6
20533	AT3G15490.1 | expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292	2.4	2.4	-0.0	-0.1	100.0%	-2.6
20534	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 scienitific 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%	-2.8
20535	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	7.3	7.3	0.0	0.1	100.0%	-1.8
20536	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	0.0	0.1	100.0%	-2.1
20537	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	2.4	2.4	-0.0	-0.1	100.0%	-2.4
20538	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	7.1	7.1	-0.0	-0.1	100.0%	-1.1
20539	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	0.1	100.0%	-1.8
20540	AT4G32640.1 | sec23/sec24 transport protein-related | chr4:15742076-15750550 FORWARD | Aliases: F4D11.160, F4D11_160	4.6	4.7	-0.0	-0.1	100.0%	-1.3
20541	AT2G28050.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:11945342-11946730 REVERSE | Aliases: T1E2.3, T1E2_3	3.7	3.7	-0.0	-0.1	100.0%	-1.4
20542	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	3.8	3.8	0.0	0.1	100.0%	-1.7
20543	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	2.8	-0.0	-0.1	100.0%	-2.2
20544	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	4.3	4.3	-0.0	-0.1	100.0%	-1.7
20545	AT2G45780.1 | expressed protein | chr2:18861265-18862162 REVERSE | Aliases: F4I18.24	4.4	4.4	-0.0	-0.1	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
20546	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	5.8	5.8	0.0	0.1	100.0%	-1.5
20547	AT3G19750.1 | hypothetical protein | chr3:6861152-6862936 REVERSE | Aliases: MMB12.24	2.4	2.4	0.0	0.1	100.0%	-2.4
20548	AT2G42870.1 | expressed protein | chr2:17843493-17844327 REVERSE | Aliases: F7D19.13, F7D19_13	2.8	2.8	0.0	0.1	100.0%	-2.0
20549	AT3G54340.1 | Symbol: AP3 | floral homeotic protein APETALA3 (AP3) | chr3:20130152-20132101 REVERSE | Aliases: APETALA 3, FLORAL HOMEOTIC PROTEIN APETALA 3, T12E18.30	2.5	2.5	-0.0	-0.1	100.0%	-2.3
20550	AT2G47980.1 | expressed protein | chr2:19638329-19644323 FORWARD | Aliases: T9J23.3	7.3	7.3	-0.0	-0.1	100.0%	-1.7
20551	AT4G32570.1 | expressed protein | chr4:15716039-15718864 REVERSE | Aliases: F4D11.230, F4D11_230	3.7	3.7	-0.0	-0.1	100.0%	-2.0
20552	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	-0.1	100.0%	-1.9
20553	AT5G65560.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr5:26218238-26221004 REVERSE | Aliases: K21L13.7, K21L13_7	3.7	3.6	0.0	0.1	100.0%	-1.3
20554	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%	-2.5
20555	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	2.7	-0.0	-0.1	100.0%	-1.8
20556	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	-0.1	100.0%	-1.3
20557	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	9.7	9.6	0.0	0.1	100.0%	-2.0
20558	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	0.0	0.1	100.0%	-2.1
20559	AT5G55570.1 | expressed protein | chr5:22531756-22532486 REVERSE | Aliases: MDF20.1, MDF20_1	3.7	3.6	0.0	0.1	100.0%	-1.5
20560	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	-0.1	100.0%	-1.8
20561	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	6.6	6.6	-0.0	-0.1	100.0%	-1.6
20562	AT1G06230.2 | DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487 | chr1:1907247-1910847 FORWARD | Aliases: F9P14.9, F9P14_9	5.3	5.4	-0.1	-0.1	100.0%	-1.3
20563	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	-0.1	100.0%	-2.5
20564	AT5G40180.1 | hypothetical protein, predicted protein, Arabidopsis thaliana | chr5:16085151-16085434 FORWARD | Aliases: MSN9.8, MSN9_8	2.9	2.9	-0.0	-0.1	100.0%	-2.4
20565	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	-0.1	100.0%	-1.9
20566	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	4.7	4.8	-0.0	-0.1	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
20567	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	3.2	3.2	-0.0	-0.1	100.0%	-1.8
20568	AT4G08740.1 | expressed protein | chr4:5579031-5579742 FORWARD | Aliases: T32A17.50, T32A17_50	2.3	2.3	-0.0	-0.1	100.0%	-2.3
20569	AT5G29210.1 | expressed protein | chr5:11153470-11153949 REVERSE | Aliases: F23C8.80, F23C8_80	2.8	2.8	0.0	0.1	100.0%	-1.8
20570	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	4.6	-0.0	-0.1	100.0%	-1.5
20571	AT5G28720.1 | hypothetical protein | chr5:10776059-10776956 FORWARD | Aliases: T32B20.10, T32B20_10	2.7	2.7	0.0	0.1	100.0%	-2.2
20572	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	-0.1	100.0%	-1.8
20573	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	2.8	2.8	0.0	0.1	100.0%	-2.1
20574	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	2.6	0.0	0.1	100.0%	-2.2
20575	AT5G27910.1 | CCAAT-box binding transcription factor Hap5a, putative | chr5:9940740-9941303 REVERSE | Aliases: F15F15.1	2.4	2.4	0.0	0.1	100.0%	-1.9
20576	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	0.0	0.1	100.0%	-1.9
20577	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	3.8	3.8	-0.0	-0.1	100.0%	-1.6
20578	AT5G53890.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:21894087-21897687 FORWARD | Aliases: K19P17.5, K19P17_5	5.4	5.4	-0.0	-0.1	100.0%	-1.4
20579	AT1G47485.1 | expressed protein | chr1:17424888-17425506 FORWARD | Aliases: None	2.5	2.5	-0.0	-0.1	100.0%	-2.5
20580	AT3G57850.1 | hypothetical protein | chr3:21435354-21435768 FORWARD | Aliases: T10K17.60	3.1	3.1	0.0	0.1	100.0%	-2.0
20581	AT4G03200.1 | expressed protein, contains Pfam PF03190: Protein of unknown function, DUF255 | chr4:1408159-1412756 FORWARD | Aliases: F4C21.12, F4C21_12	7.6	7.6	-0.0	-0.1	100.0%	-1.5
20582	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	0.1	100.0%	-2.5
20583	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	8.8	8.9	-0.1	-0.1	100.0%	-1.8
20584	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	10.5	10.5	0.1	0.1	100.0%	-1.6
20585	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	4.1	4.2	-0.0	-0.1	100.0%	-1.2
20586	AT2G10920.1 | expressed protein | chr2:4308965-4309216 REVERSE | Aliases: F16G22.2, F16G22_2	6.7	6.7	-0.1	-0.1	100.0%	-1.1
20587	AT1G63320.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:23492549-23493195 REVERSE | Aliases: F9N12.6, F9N12_6	2.4	2.4	-0.0	-0.1	100.0%	-2.4
20588	AT5G11840.1 | expressed protein, predicted proteins in Synechococcus ,Cyanophora and other organisms | chr5:3813611-3814806 REVERSE | Aliases: F14F18.10, F14F18_10	5.4	5.4	0.0	0.1	100.0%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
20589	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	8.7	8.7	-0.0	-0.1	100.0%	-1.8
20590	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	-0.0	-0.1	100.0%	-2.2
20591	AT4G01930.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.8	3.8	0.0	0.1	100.0%	-1.7
20592	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	7.0	7.0	-0.0	-0.1	100.0%	-1.9
20593	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	2.5	2.5	-0.0	-0.1	100.0%	-2.0
20594	AT1G80960.3 | F-box protein-related, contains weak hit to Pfam PF00646: F-box domain | chr1:30420729-30423183 FORWARD | Aliases: F23A5.32, F23A5_32	6.2	6.3	-0.0	-0.1	100.0%	-1.5
20595	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	6.3	6.3	-0.0	-0.1	100.0%	-1.6
20596	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	2.8	2.8	0.0	0.1	100.0%	-1.8
20597	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	3.0	2.9	0.0	0.1	100.0%	-1.8
20598	AT5G23405.2 | high mobility group (HMG1/2) family protein, contains Pfam profile PF00505: HMG (high mobility group) box | chr5:7882851-7884363 REVERSE | Aliases: None	3.5	3.5	0.0	0.1	100.0%	-1.9
20599	AT3G57210.1 | expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626) | chr3:21184341-21184670 REVERSE | Aliases: F28O9.60	2.6	2.6	0.0	0.1	100.0%	-2.1
20600	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%	-2.0
20601	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	7.4	7.4	0.0	0.1	100.0%	-1.4
20602	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	11.0	11.1	-0.0	-0.1	100.0%	-2.0
20603	AT1G26210.1 | expressed protein, similar to hypothetical protein GI:6524175 from (Arabidopsis thaliana) | chr1:9067026-9068194 FORWARD | Aliases: F28B23.12, F28B23_12	3.0	3.0	0.0	0.1	100.0%	-2.1
20604	AT2G39170.1 | expressed protein | chr2:16341708-16343288 REVERSE | Aliases: T16B24.19, T16B24_19	6.2	6.3	-0.0	-0.1	100.0%	-1.4
20605	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	2.5	-0.0	-0.1	100.0%	-2.2
20606	AT1G43810.1 | hypothetical protein | chr1:16582887-16583240 REVERSE | Aliases: F28H19.20, F28H19_20	2.7	2.8	-0.0	-0.1	100.0%	-2.1
20607	AT2G32780.1 | ubiquitin-specific protease 1, putative (UBP1), similar to GI:11993461 | chr2:13905508-13908947 REVERSE | Aliases: F24L7.8, F24L7_8	2.4	2.4	-0.0	-0.1	100.0%	-2.4
20608	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	6.4	-0.0	-0.1	100.0%	-1.5
20609	AT4G22440.1 | expressed protein | chr4:11831036-11832280 FORWARD | Aliases: F7K2.20, F7K2_20	2.9	2.9	0.0	0.1	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
20610	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	0.1	100.0%	-2.3
20611	AT5G39030.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:15637296-15639716 FORWARD | Aliases: MXF12.40, MXF12_40	2.7	2.7	0.0	0.1	100.0%	-2.5
20612	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	5.2	5.2	0.0	0.1	100.0%	-1.3
20613	AT5G65850.1 | F-box family protein | chr5:26363543-26364721 FORWARD | Aliases: K14B20.2, K14B20_2	3.3	3.3	0.0	0.1	100.0%	-1.8
20614	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	3.2	3.2	0.0	0.1	100.0%	-2.1
20615	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	0.1	100.0%	-1.3
20616	AT4G19570.1 | 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 | chr4:10665304-10667328 FORWARD | Aliases: F24J7.130, F24J7_130	3.3	3.3	-0.0	-0.1	100.0%	-2.0
20617	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	7.7	7.7	0.0	0.1	100.0%	-1.5
20618	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	2.9	2.9	-0.0	-0.1	100.0%	-2.0
20619	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	0.1	100.0%	-1.9
20620	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	2.8	-0.0	-0.1	100.0%	-1.8
20621	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	2.6	-0.0	-0.1	100.0%	-2.2
20622	AT4G30030.1 | aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease | chr4:14682216-14683490 REVERSE | Aliases: F6G3.60, F6G3_60	2.5	2.5	-0.0	-0.1	100.0%	-2.2
20623	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	5.7	5.7	0.0	0.1	100.0%	-1.4
20624	AT5G63520.1 | expressed protein, contains InterPro domain Cyclin-like F-box (InterPro:IPR001810) | chr5:25443403-25446338 REVERSE | Aliases: MLE2.15, MLE2_15	5.8	5.7	0.0	0.1	100.0%	-1.4
20625	AT4G28910.2 | expressed protein | chr4:14264073-14266659 REVERSE | Aliases: F25O24.30, F25O24_30	7.9	7.9	0.0	0.1	100.0%	-1.1
20626	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	0.1	100.0%	-1.9
20627	AT1G16500.1 | expressed protein | chr1:5639025-5640166 FORWARD | Aliases: F3O9.30, F3O9_30	6.0	6.0	0.0	0.1	100.0%	-1.5
20628	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	3.9	4.0	-0.0	-0.1	100.0%	-2.0
20629	AT3G42300.1 | expressed protein | chr3:14465318-14466582 FORWARD | Aliases: T14K23.10	3.2	3.3	-0.0	-0.1	100.0%	-1.9
20630	AT4G10710.1 | transcriptional regulator-related, similar to chromatin-specific transcription elongation factor FACT 140 kDa subunit (GI:5499741) (Homo sapiens) | chr4:6601985-6606350 REVERSE | Aliases: T12H20.3, T12H20_3	7.4	7.3	0.0	0.1	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
20631	AT1G67770.1 | RNA-binding protein, putative, similar to terminal ear1 gb:AAC39463.1 | chr1:25411706-25413816 FORWARD | Aliases: F12A21.10, F12A21_10	3.3	3.3	0.0	0.1	100.0%	-2.2
20632	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	5.5	5.6	-0.0	-0.1	100.0%	-1.5
20633	AT1G62430.1 | Symbol: ATCDS1 |	4.5	4.5	0.0	0.1	100.0%	-1.6
20634	AT4G11200.1 | expressed protein, contains weak hit to Pfam profile PF03108: MuDR family transposase | chr4:6827754-6829492 REVERSE | Aliases: T22B4.180, T22B4_180	3.7	3.7	0.0	0.1	100.0%	-1.8
20635	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	4.3	4.3	0.0	0.1	100.0%	-1.8
20636	AT3G13270.1 | expressed protein, contains similarity to replication protein A1	2.8	2.8	0.0	0.1	100.0%	-2.1
20637	AT4G38820.1 | expressed protein | chr4:18121537-18121969 REVERSE | Aliases: T9A14.100, T9A14_100	2.7	2.7	-0.0	-0.1	100.0%	-2.2
20638	AT2G04620.1 | cation efflux family protein, potential member of the cation diffusion facilitator (CDF) family, or cation efflux (CE) family, see PMID:11500563	4.7	4.7	-0.0	-0.1	100.0%	-1.7
20639	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	10.6	10.7	-0.0	-0.1	100.0%	-1.6
20640	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	-0.0	-0.1	100.0%	-2.3
20641	AT5G03010.1 | kelch repeat-containing protein, contains Pfam PF01344: Kelch motif (1 repeat) | chr5:704682-705437 FORWARD | Aliases: F15A17.40, F15A17_40	3.4	3.4	0.0	0.1	100.0%	-1.2
20642	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%	-1.9
20643	AT3G44690.1 | expressed protein | chr3:16241672-16245202 REVERSE | Aliases: T18B22.90	2.9	2.9	-0.0	-0.1	100.0%	-2.4
20644	AT5G54150.1 | expressed protein, similar to unknown protein (pir::T05871) | chr5:21993691-21995463 REVERSE | Aliases: K18G13.2, K18G13_2	2.6	2.6	-0.0	-0.1	100.0%	-2.3
20645	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	3.1	0.0	0.1	100.0%	-2.2
20646	AT5G28130.1 | expressed protein | chr5:10114437-10114784 REVERSE | Aliases: T24G3.60, T24G3_60	2.9	2.9	0.0	0.1	100.0%	-1.9
20647	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	10.5	10.5	0.0	0.1	100.0%	-1.4
20648	AT5G01015.1 | expressed protein | chr5:5261-5890 REVERSE | Aliases: None	3.4	3.5	-0.0	-0.1	100.0%	-1.6
20649	AT3G58520.1 | expressed protein | chr3:21654333-21656463 REVERSE | Aliases: F14P22.110	3.2	3.3	-0.0	-0.1	100.0%	-2.3
20650	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	0.1	100.0%	-2.2
20651	AT5G26740.2 | expressed protein, contains Pfam profile PF03619: Domain of unknown function | chr5:9291985-9294690 FORWARD | Aliases: None	7.3	7.2	0.1	0.1	100.0%	-1.1
20652	AT5G08260.1 | Symbol: SCPL35 |	4.5	4.6	-0.0	-0.1	100.0%	-1.8
20653	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	2.8	2.8	-0.0	-0.1	100.0%	-1.9
20654	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%	-1.3

Rank	Description	Sync	Root	M	t	adj.q	B
20655	AT1G78060.1 | glycosyl hydrolase family 3 protein, similar to xylosidase GI:2102655 from (Aspergillus niger) | chr1:29354573-29357818 REVERSE | Aliases: F28K19.27, F28K19_27	7.4	7.3	0.1	0.1	100.0%	-1.2
20656	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	3.1	-0.0	-0.1	100.0%	-1.9
20657	AT2G11090.1 | expressed protein | chr2:4406516-4407042 REVERSE | Aliases: F15K19.16, F15K19_16	2.0	2.0	-0.0	-0.1	100.0%	-2.9
20658	AT5G42470.1 | expressed protein, low similarity to BRE alpha b isoform (Homo sapiens) GI:16326573 | chr5:16999544-17002112 FORWARD | Aliases: MDH9.17, MDH9_17	7.4	7.4	-0.0	-0.1	100.0%	-1.3
20659	AT2G36400.1 | Symbol: AtGRF3 |	3.7	3.7	-0.0	-0.1	100.0%	-1.8
20660	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	4.5	4.4	0.0	0.1	100.0%	-1.7
20661	AT3G30610.1 | hypothetical protein | chr3:12189170-12189508 REVERSE | Aliases: MQP15.14	3.0	3.0	-0.0	-0.1	100.0%	-1.5
20662	AT1G28080.1 | expressed protein | chr1:9789813-9791533 FORWARD | Aliases: F13K9.18, F13K9_18	3.4	3.5	-0.0	-0.1	100.0%	-1.7
20663	AT2G48110.1 | expressed protein | chr2:19680440-19686564 FORWARD | Aliases: F11L15.1, T9J23.25	2.6	2.6	-0.0	-0.1	100.0%	-2.1
20664	AT2G16340.1 | hypothetical protein | chr2:7080216-7080566 FORWARD | Aliases: F16F14.16, F16F14_16	6.4	6.5	-0.0	-0.1	100.0%	-1.5
20665	AT1G54040.2 | Symbol: ESP | kelch repeat-containing protein, contains Pfam PF01344: Kelch motif (4 repeats); similar to jsimilar to epithiospecifier (GI:16118838) (Arabidopsis thaliana) isioform contains AT-AG splice sites at intron | chr1:20174383-20177617 REVERSE | Aliases: EPITHIOSPECIFIER PROTEIN, F15I1.12, F15I1_12, TASTY	2.5	2.5	0.0	0.1	100.0%	-2.3
20666	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	2.6	0.0	0.1	100.0%	-2.3
20667	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	7.6	7.6	0.0	0.1	100.0%	-1.4
20668	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%	-1.5
20669	AT3G60430.1 | expressed protein | chr3:22347088-22348305 FORWARD | Aliases: T8B10.90	2.3	2.3	0.0	0.1	100.0%	-2.5
20670	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	3.8	3.8	-0.0	-0.1	100.0%	-1.5
20671	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	8.8	8.9	-0.1	-0.1	100.0%	-1.3
20672	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	8.3	8.3	-0.0	-0.1	100.0%	-1.6
20673	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	4.5	4.5	-0.0	-0.1	100.0%	-1.4
20674	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	5.1	5.1	-0.0	-0.1	100.0%	-1.3
20675	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%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
20676	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	7.1	7.1	0.0	0.1	100.0%	-1.5
20677	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	0.1	100.0%	-1.8
20678	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	0.1	100.0%	-2.0
20679	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	3.8	3.8	0.0	0.1	100.0%	-1.9
20680	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	3.9	0.0	0.1	100.0%	-2.2
20681	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	0.1	100.0%	-2.5
20682	AT4G17250.1 | expressed protein | chr4:9671101-9673430 FORWARD | Aliases: DL4660W, FCAALL.204	2.2	2.2	-0.0	-0.1	100.0%	-2.6
20683	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	-0.0	-0.1	100.0%	-2.1
20684	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	3.3	-0.0	-0.1	100.0%	-1.7
20685	AT3G50010.1 | DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	4.6	4.6	-0.0	-0.1	100.0%	-2.5
20686	AT1G72580.1 | hypothetical protein | chr1:27338068-27338364 REVERSE | Aliases: F28P22.23, F28P22_23	2.9	2.9	0.0	0.1	100.0%	-2.2
20687	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	5.8	5.8	0.0	0.1	100.0%	-1.5
20688	AT3G50310.1 | Symbol: MAPKKK20 | protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr3:18659133-18660503 REVERSE | Aliases: F11C1.150	3.9	3.9	0.0	0.1	100.0%	-1.6
20689	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	3.5	3.5	0.0	0.1	100.0%	-2.1
20690	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	5.6	5.5	0.0	0.1	100.0%	-1.2
20691	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	4.2	4.2	0.0	0.1	100.0%	-1.4
20692	AT4G02020.1 | Symbol: EZA1 | zeste-like protein 1 (EZA1), identical to enhancer of zeste-like protein 1(EZA1) (GI:4185507) (Arabidopsis thaliana); similar to polycomb group (Arabidopsis thaliana) GI:1903019 (curly leaf); contains Pfam profile PF00856: SET domain | chr4:886600-891955 FORWARD | Aliases: T10M13.3, T10M13_3	7.8	7.8	0.0	0.1	100.0%	-1.6
20693	NA	2.2	2.2	-0.0	-0.1	100.0%	-3.0
20694	AT1G54115.1 | cation exchanger, putative | chr1:20205786-20207720 FORWARD | Aliases: None	6.9	6.9	0.0	0.1	100.0%	-1.6
20695	AT5G52040.2 | Symbol: ATRSP41 | arginine/serine-rich splicing factor RSP41 (RSP41), nearly identical to SP:P92966 Arginine/serine-rich splicing factor RSP41 {Arabidopsis thaliana} | chr5:21147562-21150777 FORWARD | Aliases: ARGININE/SERINE RICH SPLICING FACTOR, MSG15.12, MSG15_12	6.8	6.8	-0.0	-0.1	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
20696	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%	-2.1
20697	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	5.7	5.7	-0.0	-0.1	100.0%	-1.2
20698	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	2.4	2.4	-0.0	-0.1	100.0%	-2.6
20699	AT1G62850.1 | expressed protein, similar to Immature colon carcinoma transcript 1 (Digestion substraction 1) (DS- 1) (Swiss-Prot:Q14197) (Homo sapiens) | chr1:23276139-23277071 REVERSE | Aliases: F23N19.20, F23N19_20	6.4	6.4	0.0	0.1	100.0%	-1.5
20700	AT2G27250.2 | Symbol: CLV3 | CLAVATA3, CLAVATA3/ESR-Related (CLE) family of proteins; ligand for CLV1; responsible for negative regulation of meristem cell differention and replacement | chr2:11672064-11672846 REVERSE | Aliases: CLAVATA 3, CLAVATA3, F12K2.17, F12K2_17	2.6	2.6	0.0	0.1	100.0%	-2.0
20701	AT3G06640.1 | protein kinase family protein, contains Serine/Threonine protein kinases active-site signature, PROSITE:PS00108 | chr3:2074544-2078323 REVERSE | Aliases: T8E24.12	3.9	3.9	-0.0	-0.1	100.0%	-1.7
20702	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	5.7	5.7	-0.0	-0.1	100.0%	-1.9
20703	AT3G23460.1 | cyclopropane fatty acid synthase-related, similar to cyclopropane synthase (Sterculia foetida) GI:21069167 | chr3:8412326-8414326 FORWARD | Aliases: MLM24.19	2.8	2.8	-0.0	-0.1	100.0%	-2.5
20704	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	0.1	100.0%	-2.3
20705	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	-0.0	-0.1	100.0%	-1.8
20706	AT2G17950.1 | Symbol: WUS | homeodomain transcription factor (WUSCHEL), 99.4% identical to WUSCHELL (GI:4090200) (Arabidopsis thaliana) | chr2:7815959-7817877 REVERSE | Aliases: PGA6, T27K22.18, T27K22_18, WUSCHEL	2.2	2.2	0.0	0.1	100.0%	-2.6
20707	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	0.0	0.1	100.0%	-2.1
20708	AT1G54460.1 | expressed protein | chr1:20344267-20347196 REVERSE | Aliases: F20D21.28, F20D21_28	5.1	5.1	-0.0	-0.1	100.0%	-1.3
20709	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%	-2.1
20710	AT2G24260.1 | basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	6.6	6.5	0.0	0.1	100.0%	-1.7
20711	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	3.7	3.7	0.0	0.1	100.0%	-1.4
20712	AT1G53350.1 | disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.4	2.4	-0.0	-0.1	100.0%	-2.3
20713	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%	-1.9
20714	AT2G20920.1 | expressed protein | chr2:9005767-9007013 FORWARD | Aliases: F5H14.11, F5H14_11	9.0	9.0	-0.0	-0.1	100.0%	-1.8
20715	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	3.2	3.3	-0.0	-0.1	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
20716	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	5.1	5.1	0.0	0.1	100.0%	-1.5
20717	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	4.4	4.4	-0.0	-0.1	100.0%	-1.6
20718	AT2G05850.1 | Symbol: SCPL38 |	2.3	2.3	-0.0	-0.1	100.0%	-2.4
20719	AT1G64310.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:23869716-23871374 FORWARD | Aliases: F15H21.19, F15H21_19	3.1	3.1	0.0	0.1	100.0%	-2.1
20720	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	0.1	100.0%	-2.1
20721	AT2G34400.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr2:14523317-14525265 FORWARD | Aliases: F13P17.24	4.3	4.3	-0.0	-0.1	100.0%	-1.6
20722	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	2.9	2.9	0.0	0.1	100.0%	-2.0
20723	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	4.4	4.4	-0.0	-0.1	100.0%	-1.4
20724	AT4G27840.1 | expressed protein | chr4:13865051-13866293 REVERSE | Aliases: T27E11.80, T27E11_80	3.7	3.7	-0.0	-0.1	100.0%	-1.7
20725	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	4.0	-0.0	-0.1	100.0%	-1.8
20726	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%	-2.0
20727	AT4G00416.1 | Symbol: MBD3 | methyl-CpG-binding domain-containing protein, contains Pfam profile PF01429: Methyl-CpG binding domain | chr4:179022-179513 FORWARD | Aliases: None	2.3	2.3	0.0	0.1	100.0%	-2.6
20728	AT1G02070.1 | expressed protein | chr1:370257-370967 REVERSE | Aliases: T7I23.30, T7I23_30	3.2	3.2	-0.0	-0.1	100.0%	-2.1
20729	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%	-2.6
20730	AT3G19520.1 | expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626) | chr3:6772696-6774449 FORWARD | Aliases: T31J18.2	6.9	6.9	0.0	0.1	100.0%	-1.5
20731	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	0.1	100.0%	-2.7
20732	AT3G46680.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr3:17206303-17207728 REVERSE | Aliases: F12A12.200	3.3	3.2	0.0	0.1	100.0%	-1.9
20733	AT1G13650.2 | expressed protein | chr1:4680434-4682094 REVERSE | Aliases: F21F23.9, F21F23_9	2.4	2.4	-0.0	-0.1	100.0%	-2.1
20734	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%	-2.3
20735	AT3G03740.1 | Symbol: ATBPM4 |	4.3	4.3	0.0	0.1	100.0%	-1.6
20736	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	3.0	3.1	-0.0	-0.1	100.0%	-1.6
20737	AT2G10020.1 | expressed protein, and genefinder | chr2:3804313-3804513 FORWARD | Aliases: F7B19.16, F7B19_16	6.3	6.3	-0.0	-0.1	100.0%	-1.4
20738	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	4.0	4.0	0.0	0.1	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
20739	AT4G15710.1 | hypothetical protein | chr4:8940290-8940856 FORWARD | Aliases: DL3895W, FCAALL.366	2.7	2.7	0.0	0.1	100.0%	-2.1
20740	AT2G13500.1 | hypothetical protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277 | chr2:5635018-5636181 FORWARD | Aliases: T10F5.4, T10F5_4	2.2	2.2	0.0	0.1	100.0%	-2.7
20741	AT3G06830.1 | pectinesterase family protein, contains Pfam profiles: PF01095 pectinesterase,PF04043 plant invertase/pectin methylesterase inhibitor | chr3:2153870-2156154 FORWARD | Aliases: F3E22.3	3.0	3.0	-0.0	-0.1	100.0%	-2.1
20742	AT1G16650.1 | expressed protein | chr1:5687936-5691191 FORWARD | Aliases: F19K19.6, F19K19_6	4.2	4.1	0.0	0.1	100.0%	-1.6
20743	AT1G80590.1 | Symbol: WRKY66 |	2.6	2.6	-0.0	-0.1	100.0%	-2.2
20744	AT2G20805.1 | expressed protein | chr2:8963450-8963818 FORWARD | Aliases: F5H14.4, F5H14_4	2.4	2.4	0.0	0.1	100.0%	-2.6
20745	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	2.4	2.4	-0.0	-0.1	100.0%	-2.0
20746	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	3.3	0.0	0.1	100.0%	-1.9
20747	AT2G33420.1 | expressed protein | chr2:14165781-14169603 FORWARD | Aliases: F4P9.19, F4P9_19	3.1	3.1	0.0	0.1	100.0%	-2.1
20748	AT5G52400.1 | Symbol: CYP715A1 | cytochrome P450 family protein, similar to Cytochrome P450 72A1 (SP:Q05047) (cytochrome P450 lxxii hydroxylase) (ge10h) (Catharanthus roseus) | chr5:21290175-21292735 FORWARD | Aliases: K24M7.14, K24M7_14	3.3	3.3	0.0	0.1	100.0%	-1.9
20749	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	7.0	7.0	-0.0	-0.1	100.0%	-1.3
20750	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	2.6	2.6	0.0	0.1	100.0%	-2.4
20751	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	0.1	100.0%	-1.7
20752	AT3G44850.1 | protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr3:16385602-16387916 REVERSE | Aliases: F28D10.40	5.0	5.0	0.0	0.1	100.0%	-1.4
20753	AT1G69910.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:26333777-26335929 FORWARD | Aliases: T17F3.6, T17F3_6	4.8	4.8	-0.0	-0.1	100.0%	-1.7
20754	AT3G16200.1 | expressed protein | chr3:5491412-5493635 REVERSE | Aliases: MYA6.1	5.6	5.6	0.0	0.1	100.0%	-1.2
20755	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	3.1	3.1	-0.0	-0.1	100.0%	-2.0
20756	AT5G19855.1 | expressed protein | chr5:6711974-6713582 REVERSE | Aliases: None	3.4	3.4	0.0	0.1	100.0%	-2.3
20757	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	4.0	4.0	0.0	0.1	100.0%	-1.3
20758	AT3G49270.1 | expressed protein | chr3:18278237-18279255 REVERSE | Aliases: F2K15.130	2.6	2.6	-0.0	-0.1	100.0%	-2.2
20759	AT2G25660.1 | Symbol: EMB2410 | expressed protein | chr2:10923281-10934468 REVERSE | Aliases: EMB2410, EMBRYO DEFECTIVE 2410, F3N11.11, F3N11_11	5.0	5.0	-0.0	-0.1	100.0%	-1.7
20760	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	2.6	2.6	-0.0	-0.1	100.0%	-1.9
20761	AT1G03180.2 | expressed protein | chr1:773411-775344 FORWARD | Aliases: F15K9.21, F15K9_21	3.9	3.9	0.0	0.1	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
20762	AT4G21170.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr4:11286766-11288641 REVERSE | Aliases: F7J7.110, F7J7_110	5.1	5.0	0.0	0.1	100.0%	-1.6
20763	AT1G62890.1 | expressed protein | chr1:23298642-23299229 FORWARD | Aliases: F16P17.24, F16P17_24	2.9	2.9	0.0	0.1	100.0%	-1.9
20764	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%	-2.7
20765	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	3.5	0.0	0.1	100.0%	-1.9
20766	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	0.0	0.1	100.0%	-1.9
20767	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	4.2	4.2	0.0	0.1	100.0%	-0.6
20768	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	2.7	2.7	0.0	0.1	100.0%	-2.0
20769	AT2G32900.1 | Symbol: ATZW10 |	3.9	3.9	-0.0	-0.1	100.0%	-1.6
20770	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	5.5	5.5	-0.0	-0.1	100.0%	-1.5
20771	AT5G53030.2 | expressed protein | chr5:21522300-21523846 FORWARD | Aliases: MNB8.9, MNB8_9	3.1	3.1	0.0	0.1	100.0%	-1.6
20772	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	2.9	2.9	0.0	0.1	100.0%	-2.1
20773	AT1G72820.1 | mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein | chr1:27406540-27408335 FORWARD | Aliases: F3N23.2, F3N23_2	9.1	9.1	-0.0	-0.1	100.0%	-1.6
20774	AT4G01240.1 | expressed protein | chr4:517795-521972 REVERSE | Aliases: F2N1.7, F2N1_7	2.6	2.5	0.0	0.1	100.0%	-2.4
20775	AT5G03490.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr5:871459-873046 FORWARD | Aliases: F12E4.260, F12E4_260	6.5	6.5	-0.0	-0.1	100.0%	-1.6
20776	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	2.4	-0.0	-0.1	100.0%	-2.6
20777	AT2G04340.1 | expressed protein | chr2:1513555-1515400 FORWARD | Aliases: T23O15.19	5.7	5.7	0.0	0.1	100.0%	-1.5
20778	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	0.1	100.0%	-2.5
20779	AT1G23450.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr1:8324687-8326686 FORWARD | Aliases: F28C11.30, F28C11_30	3.3	3.3	0.0	0.1	100.0%	-2.3
20780	AT4G11470.1 | protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain | chr4:6967724-6970156 FORWARD | Aliases: F25E4.90, F25E4_90	2.8	2.8	-0.0	-0.1	100.0%	-2.1
20781	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	2.9	-0.0	-0.1	100.0%	-2.0
20782	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	3.2	3.2	0.0	0.1	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
20783	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	1.9	0.0	0.1	100.0%	-2.6
20784	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	-0.1	100.0%	-2.4
20785	AT3G29140.1 | hypothetical protein | chr3:11107042-11107381 FORWARD | Aliases: MXE2.16	5.5	5.5	0.0	0.1	100.0%	-1.2
20786	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	3.3	-0.0	-0.1	100.0%	-1.8
20787	AT5G35600.1 | histone deacetylase, putative (HDA7), similar to SP:O22446 Histone deacetylase (HD) {Arabidopsis thaliana}; contains Pfam profile PF00850: Histone deacetylase family | chr5:13787351-13788942 REVERSE | Aliases: K2K18.5, K2K18_5	3.5	3.5	-0.0	-0.1	100.0%	-1.7
20788	AT3G09750.1 | expressed protein | chr3:2992187-2992574 REVERSE | Aliases: F11F8.34	2.6	2.6	-0.0	-0.1	100.0%	-2.2
20789	AT1G66210.1 | subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa) | chr1:24669292-24672446 REVERSE | Aliases: T6J19.3, T6J19_3	2.3	2.3	0.0	0.1	100.0%	-2.4
20790	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	0.1	100.0%	-1.8
20791	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	3.8	3.8	0.0	0.1	100.0%	-2.1
20792	AT3G25650.1 | Symbol: ASK15 | Skp1 family protein, similar toSkp1 (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	-0.1	100.0%	-2.0
20793	AT5G53810.1 | O-methyltransferase, putative, similar to GI:2781394 | chr5:21867405-21870237 REVERSE | Aliases: MGN6.20, MGN6_20	3.2	3.2	-0.0	-0.1	100.0%	-1.9
20794	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	-0.0	-0.1	100.0%	-2.7
20795	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	3.5	3.5	-0.0	-0.1	100.0%	-2.0
20796	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	3.3	3.3	0.0	0.1	100.0%	-1.7
20797	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	3.2	3.2	-0.0	-0.1	100.0%	-1.9
20798	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	4.4	4.4	-0.0	-0.1	100.0%	-1.7
20799	AT2G35840.2 | sucrose-phosphatase 1 (SPP1), identical to sucrose-phosphatase (SPP1) (Arabidopsis thaliana) GI:11127757	7.5	7.5	-0.0	-0.1	100.0%	-1.4
20800	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	2.7	0.0	0.1	100.0%	-2.2
20801	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	0.1	100.0%	-1.2
20802	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	0.1	100.0%	-2.2

<table>
<tr><th>Rank</th><th>Description</th><th>Sync</th><th>Root</th><th>M</th><th>t</th><th>adj.q</th><th>B</th></tr>
<tr><td>20803</td><td>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</td><td>4.6</td><td>4.7</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-1.0</td></tr>
<tr><td>20804</td><td>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</td><td>2.4</td><td>2.4</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-2.3</td></tr>
<tr><td>20805</td><td>AT5G66500.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr5:26565221-26566903 REVERSE | Aliases: K1F13.16, K1F13_16</td><td>3.2</td><td>3.1</td><td>0.0</td><td>0.1</td><td>100.0%</td><td>-2.0</td></tr>
<tr><td>20806</td><td>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</td><td>10.6</td><td>10.6</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-1.9</td></tr>
<tr><td>20807</td><td>AT1G35040.1 | hypothetical protein | chr1:12812135-12812547 FORWARD | Aliases: F11O6.10, F11O6_10</td><td>3.8</td><td>3.8</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-1.8</td></tr>
<tr><td>20808</td><td>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</td><td>3.3</td><td>3.3</td><td>0.0</td><td>0.1</td><td>100.0%</td><td>-1.9</td></tr>
<tr><td>20809</td><td>AT5G47790.1 | forkhead-associated domain-containing protein / FHA domain-containing protein | chr5:19368531-19370670 FORWARD | Aliases: MCA23.11, MCA23_11</td><td>4.9</td><td>5.0</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-1.7</td></tr>
<tr><td>20810</td><td>AT1G08480.1 | expressed protein | chr1:2684237-2685620 FORWARD | Aliases: T27G7.26</td><td>9.6</td><td>9.6</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-1.6</td></tr>
<tr><td>20811</td><td>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</td><td>3.2</td><td>3.2</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-1.8</td></tr>
<tr><td>20812</td><td>AT1G19500.1 | expressed protein | chr1:6754943-6755527 REVERSE | Aliases: F18O14.44</td><td>3.4</td><td>3.3</td><td>0.0</td><td>0.1</td><td>100.0%</td><td>-1.7</td></tr>
<tr><td>20813</td><td>NA</td><td>2.3</td><td>2.3</td><td>0.0</td><td>0.1</td><td>100.0%</td><td>-2.1</td></tr>
<tr><td>20814</td><td>AT1G11250.1 | Symbol: SYP125 |</td><td>4.0</td><td>4.0</td><td>0.0</td><td>0.1</td><td>100.0%</td><td>-1.8</td></tr>
<tr><td>20815</td><td>AT4G10440.1 | dehydration-responsive family protein, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase | chr4:6459724-6461928 REVERSE | Aliases: F7L13.20, F7L13_20</td><td>3.1</td><td>3.1</td><td>0.0</td><td>0.1</td><td>100.0%</td><td>-1.7</td></tr>
<tr><td>20816</td><td>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</td><td>2.6</td><td>2.6</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-2.3</td></tr>
<tr><td>20817</td><td>AT3G27310.1 | Symbol: PUX1 | expressed protein | chr3:10088438-10090338 REVERSE | Aliases: K17E12.13, PLANT UBX DOMAIN CONTAINING PROTEIN 1</td><td>6.8</td><td>6.8</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-1.6</td></tr>
<tr><td>20818</td><td>AT2G21990.1 | expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617 | chr2:9366436-9367744 REVERSE | Aliases: F7D8.31, F7D8_31</td><td>3.2</td><td>3.1</td><td>0.0</td><td>0.1</td><td>100.0%</td><td>-1.8</td></tr>
<tr><td>20819</td><td>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</td><td>2.6</td><td>2.6</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-2.0</td></tr>
<tr><td>20820</td><td>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</td><td>6.6</td><td>6.6</td><td>0.0</td><td>0.1</td><td>100.0%</td><td>-1.1</td></tr>
<tr><td>20821</td><td>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</td><td>4.6</td><td>4.6</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-1.5</td></tr>
<tr><td>20822</td><td>AT4G35010.1 | Symbol: BGAL11 |</td><td>2.5</td><td>2.5</td><td>0.0</td><td>0.1</td><td>100.0%</td><td>-2.2</td></tr>
<tr><td>20823</td><td>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</td><td>3.8</td><td>3.8</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-1.9</td></tr>
<tr><td>20824</td><td>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</td><td>2.4</td><td>2.5</td><td>-0.0</td><td>-0.1</td><td>100.0%</td><td>-2.3</td></tr>
</table>

Rank	Description	Sync	Root	M	t	adj.q	B
20825	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	0.0	0.1	100.0%	-2.2
20826	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	6.6	6.7	-0.0	-0.1	100.0%	-1.6
20827	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%	-2.1
20828	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	6.8	6.8	0.0	0.1	100.0%	-1.7
20829	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	2.7	-0.0	-0.1	100.0%	-2.1
20830	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%	-2.3
20831	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	5.0	5.0	-0.0	-0.1	100.0%	-1.2
20832	AT4G19650.1 | similar to mitochondrial transcription termination factor-related / mTERF-related [Arabidopsis thaliana] (TAIR:At5g45113.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:NP_912680.1); contains InterPro domain Mitochodrial transcription termination factor-related (InterPro:IPR003690) | chr4:10691684-10695176 FORWARD | Aliases: T16H5.10, T16H5_10	2.3	2.3	0.0	0.1	100.0%	-2.3
20833	AT2G40170.1 | Symbol: ATEM6 | Em-like protein GEA6 (EM6), identical toSP: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	3.5	3.6	-0.0	-0.1	100.0%	-1.8
20834	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	4.4	0.0	0.1	100.0%	-1.8
20835	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	6.2	6.2	0.0	0.1	100.0%	-1.4
20836	AT3G11880.1 | expressed protein | chr3:3751666-3754066 FORWARD | Aliases: F26K24.17	6.5	6.5	-0.0	-0.1	100.0%	-1.7
20837	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%	-2.6
20838	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	2.7	2.7	0.0	0.1	100.0%	-2.0
20839	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	3.6	0.0	0.1	100.0%	-1.7
20840	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	-0.0	-0.1	100.0%	-1.7
20841	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%	-2.1
20842	AT2G19640.2 | SET domain-containing protein, contains Pfam profile PF00856: SET domain	3.7	3.7	-0.0	-0.1	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
20843	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%	-2.2
20844	AT5G59990.1 | expressed protein, ; expression supported by MPSS | chr5:24168432-24170310 REVERSE | Aliases: MMN10.24, MMN10_24	2.6	2.6	0.0	0.1	100.0%	-2.2
20845	AT4G32980.1 | Symbol: ATH1 | homeobox protein (ATH1), identical to SWISS-PROT:P48731 homeobox protein ATH1. (Arabidopsis thaliana) | chr4:15914725-15918047 REVERSE | Aliases: ARABIDOPSIS THALIANA HOMEOBOX GENE 1, F26P21.100, F26P21_100	2.8	2.8	-0.0	-0.1	100.0%	-2.1
20846	AT1G32630.1 | expressed protein | chr1:11797344-11798537 FORWARD | Aliases: F6N18.3, F6N18_3	6.7	6.7	-0.0	-0.1	100.0%	-1.0
20847	AT3G18770.1 | expressed protein | chr3:6459890-6463058 REVERSE | Aliases: MVE11.13	3.1	3.1	0.0	0.1	100.0%	-1.8
20848	AT1G70610.1 | Symbol: ATTAP1 |	6.1	6.0	0.0	0.1	100.0%	-1.3
20849	AT1G04090.1 | expressed protein | chr1:1057150-1059418 FORWARD | Aliases: F20D22.17, F20D22_17	2.8	2.8	0.0	0.1	100.0%	-2.1
20850	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	2.8	2.8	0.0	0.1	100.0%	-2.2
20851	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%	-2.5
20852	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	6.7	6.7	-0.0	-0.1	100.0%	-1.6
20853	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	2.6	0.0	0.1	100.0%	-2.1
20854	AT5G10270.1 | Symbol: CDKC;1 |	5.7	5.7	-0.0	-0.1	100.0%	-1.5
20855	AT3G05100.1 | expressed protein | chr3:1424102-1426006 FORWARD | Aliases: T12H1.6, T12H1_6	4.1	4.1	0.0	0.1	100.0%	-1.5
20856	AT3G14910.1 | expressed protein | chr3:5015437-5017573 FORWARD | Aliases: K15M2.5	4.2	4.2	-0.0	-0.1	100.0%	-1.8
20857	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) {Homo sapiens}; contains Pfam profile PF00226 DnaJ domain	5.4	5.3	0.0	0.1	100.0%	-1.7
20858	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%	-1.8
20859	AT5G46620.1 | expressed protein, similar to unknown protein (pir::T05082) | chr5:18934886-18936647 REVERSE | Aliases: F10E10.1, F10E10_1	9.2	9.2	-0.0	-0.1	100.0%	-1.5
20860	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	2.9	2.9	-0.0	-0.1	100.0%	-2.0
20861	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	8.3	8.3	0.0	0.1	100.0%	-1.7
20862	ATCG00770.1 | Symbol: RPS8 | chloroplast 30S ribosomal protein S8 | chrC:80068-80472 REVERSE | Aliases: RPS8	5.8	5.7	0.1	0.1	100.0%	-1.2
20863	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	6.4	6.4	-0.0	-0.1	100.0%	-1.2
20864	AT5G53160.2 | expressed protein, similar to unknown protein (pir::T02893) | chr5:21577944-21579486 FORWARD | Aliases: MFH8.10, MFH8_10	6.4	6.3	0.0	0.1	100.0%	-1.5
20865	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	3.7	3.7	0.0	0.1	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
20866	AT1G29720.1 | protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719 | chr1:10393783-10395589 REVERSE | Aliases: T3M22.6, T3M22_6	2.7	2.7	0.0	0.1	100.0%	-2.2
20867	AT1G28270.1 | Symbol: RALFL4 |	2.4	2.4	-0.0	-0.1	100.0%	-2.2
20868	AT3G52110.1 | expressed protein | chr3:19334761-19336629 REVERSE | Aliases: F4F15.220	3.7	3.7	-0.0	-0.1	100.0%	-2.0
20869	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	2.4	-0.0	-0.1	100.0%	-2.6
20870	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	0.0	0.1	100.0%	-1.8
20871	AT2G40790.1 | thioredoxin family protein, contains Pfam profile: PF00085 thioredoxin | chr2:17030041-17031346 REVERSE | Aliases: T7D17.3, T7D17_3	3.9	3.9	-0.0	-0.1	100.0%	-1.7
20872	AT1G23850.1 | expressed protein | chr1:8425728-8427062 REVERSE | Aliases: T23E23.1, T23E23_1	5.7	5.7	0.0	0.1	100.0%	-1.4
20873	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	8.1	8.1	-0.0	-0.1	100.0%	-1.8
20874	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	7.0	7.0	0.0	0.1	100.0%	-1.1
20875	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	8.2	8.2	-0.0	-0.1	100.0%	-1.6
20876	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	0.0	0.1	100.0%	-2.0
20877	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	2.8	2.8	-0.0	-0.1	100.0%	-1.8
20878	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%	-1.7
20879	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	-0.1	100.0%	-2.7
20880	AT4G23890.1 | expressed protein, hypothetical protein, Synechocystis sp., PIR:S76577 | chr4:12420424-12421474 REVERSE | Aliases: T32A16.60, T32A16_60	5.2	5.2	-0.0	-0.1	100.0%	-1.2
20881	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%	-2.2
20882	AT3G13950.1 | expressed protein | chr3:4604156-4605432 FORWARD | Aliases: MDC16.7	3.0	3.0	0.0	0.1	100.0%	-1.8
20883	AT1G53720.1 | cyclophilin-RNA interacting protein, putative | chr1:20060201-20063306 FORWARD | Aliases: F22G10.24, F22G10_24	6.2	6.1	0.0	0.1	100.0%	-1.2
20884	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	-0.0	100.0%	-1.7
20885	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	3.5	3.5	0.0	0.0	100.0%	-1.7
20886	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	3.2	3.2	0.0	0.0	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
20887	AT2G37810.1 | CHP-rich zinc finger protein, putative | chr2:15852428-15853129 REVERSE | Aliases: T8P21.28, T8P21_28	2.3	2.3	-0.0	-0.0	100.0%	-2.3
20888	AT2G28180.1 | Symbol: ATCHX8 |	2.4	2.4	0.0	0.0	100.0%	-2.5
20889	AT5G03870.1 | glutaredoxin family protein, contains Pfam profile PF00462: Glutaredoxin	4.0	4.0	-0.0	-0.0	100.0%	-1.6
20890	AT1G26640.1 | aspartate/glutamate/uridylate kinase family protein, contains Pfam amino acid kinase family PF00696 | chr1:9206978-9209887 REVERSE | Aliases: T24P13.2, T24P13_2	7.8	7.8	-0.0	-0.0	100.0%	-1.4
20891	AT2G15560.1 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537 | chr2:6794951-6797183 REVERSE | Aliases: F9O13.11	2.7	2.7	0.0	0.0	100.0%	-1.3
20892	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	-0.0	100.0%	-2.6
20893	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	3.1	3.1	0.0	0.0	100.0%	-2.1
20894	AT5G13200.1 | GRAM domain-containing protein / ABA-responsive protein-related, similar to ABA-responsive protein (Hordeum vulgare) GI:4103635; contains Pfam profile PF02893: GRAM domain | chr5:4207007-4208292 FORWARD | Aliases: T19L5.4	4.5	4.5	-0.0	-0.0	100.0%	-1.6
20895	AT3G30190.1 | hypothetical protein | chr3:11823753-11824820 FORWARD | Aliases: MIL15.1	2.2	2.2	-0.0	-0.0	100.0%	-2.6
20896	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	2.2	0.0	0.0	100.0%	-2.2
20897	AT2G34110.1 | expressed protein | chr2:14409579-14410396 FORWARD | Aliases: T14G11.23, T14G11_23	3.7	3.6	0.0	0.0	100.0%	-1.9
20898	AT1G19040.1 | expressed protein | chr1:6576886-6577404 FORWARD | Aliases: F14D16.19, F14D16_19	2.2	2.2	-0.0	-0.0	100.0%	-2.3
20899	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	2.5	2.5	0.0	0.0	100.0%	-2.1
20900	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	2.7	-0.0	-0.0	100.0%	-2.1
20901	AT5G22540.1 | expressed protein, contains Pfam profile PF03140: Plant protein of unknown function | chr5:7481497-7482902 REVERSE | Aliases: MQJ16.8, MQJ16_8	3.0	3.0	0.0	0.0	100.0%	-1.8
20902	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	4.1	4.1	-0.0	-0.0	100.0%	-1.9
20903	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	5.9	5.9	0.0	0.0	100.0%	-1.2
20904	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	0.0	0.0	100.0%	-2.5
20905	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	-0.0	-0.0	100.0%	-2.2
20906	AT2G02370.1 | expressed protein | chr2:621154-623343 FORWARD | Aliases: T16F16.16, T16F16_16	6.0	6.0	0.0	0.0	100.0%	-1.2
20907	AT3G56390.1 | hypothetical protein | chr3:20918333-20918676 FORWARD | Aliases: T5P19.40	2.2	2.2	-0.0	-0.0	100.0%	-2.6
20908	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	3.1	3.1	0.0	0.0	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
20909	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	3.7	3.7	-0.0	-0.0	100.0%	-1.7
20910	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	4.0	4.0	0.0	0.0	100.0%	-1.5
20911	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	2.7	-0.0	-0.0	100.0%	-2.2
20912	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 (Arabidopsis thaliana) | chr5:5151080-5154156 REVERSE | Aliases: AGL2, F14F8.180, F14F8_180, SEPALLATA1	2.8	2.8	0.0	0.0	100.0%	-2.0
20913	AT3G06710.1 | expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g32670.1) | chr3:2118214-2120065 FORWARD | Aliases: T8E24.2	3.3	3.3	-0.0	-0.0	100.0%	-1.9
20914	AT5G17910.1 | expressed protein | chr5:5927404-5932724 FORWARD | Aliases: MPI7.8, MPI7_8	5.3	5.3	-0.0	-0.0	100.0%	-1.1
20915	AT5G64770.1 | expressed protein | chr5:25914593-25915350 REVERSE | Aliases: MVP7.10, MVP7_10	3.5	3.5	0.0	0.0	100.0%	-1.8
20916	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	4.2	4.2	0.0	0.0	100.0%	-1.3
20917	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	3.2	3.2	0.0	0.0	100.0%	-2.0
20918	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	-0.0	100.0%	-2.1
20919	AT5G40050.1 | F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.5	0.0	0.0	100.0%	-2.4
20920	AT2G15695.1 | expressed protein, contains Pfam PF05705: Eukaryotic protein of unknown function (DUF829) | chr2:6840962-6843506 REVERSE | Aliases: None	5.7	5.7	-0.0	-0.0	100.0%	-1.5
20921	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	3.4	3.4	-0.0	-0.0	100.0%	-1.8
20922	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%	-1.9
20923	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	0.0	0.0	100.0%	-2.7
20924	AT2G35950.1 | expressed protein | chr2:15111863-15113167 FORWARD | Aliases: F11F19.14, F11F19_14	2.1	2.1	0.0	0.0	100.0%	-2.6
20925	AT5G58170.1 | glycerophosphoryl diester phosphodiesterase family protein, contains Pfam PF03009 : Glycerophosphoryl diester phosphodiesterase family; similar to Glycerophosphoryl diester phosphodiesterase precursor	3.6	3.6	-0.0	-0.0	100.0%	-2.1
20926	AT2G36760.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:15420121-15421673 REVERSE | Aliases: F13K3.16, F13K3_16	2.8	2.8	-0.0	-0.0	100.0%	-2.1
20927	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	8.0	8.0	0.0	0.0	100.0%	-2.0
20928	AT5G60260.1 | expressed protein, various predicted proteins, Arabidopsis thaliana | chr5:24272660-24273511 REVERSE | Aliases: F15L12.14, F15L12_14	3.0	3.0	0.0	0.0	100.0%	-2.0
20929	AT1G75240.1 | zinc finger homeobox family protein / ZF-HD homeobox family protein | chr1:28244735-28246417 FORWARD | Aliases: F22H5.4, F22H5_4	3.6	3.6	-0.0	-0.0	100.0%	-1.6
20930	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	-0.0	100.0%	-1.8

Rank	Description	Sync	Root	M	t	adj.q	B
20931	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	3.2	3.2	-0.0	-0.0	100.0%	-1.7
20932	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	3.0	3.0	0.0	0.0	100.0%	-1.9
20933	AT1G10030.1 | integral membrane family protein, contains Pfam PF03694: Erg28 like protein | chr1:3273863-3275839 FORWARD | Aliases: T27I1.5, T27I1_5	7.9	7.9	-0.0	-0.0	100.0%	-1.5
20934	AT5G63710.1 | leucine-rich repeat transmembrane protein kinase, putative | chr5:25516640-25520024 FORWARD | Aliases: MBK5.19, MBK5_19	4.9	4.9	0.0	0.0	100.0%	-1.8
20935	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	2.2	2.2	0.0	0.0	100.0%	-2.3
20936	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	5.5	-0.0	-0.0	100.0%	-1.5
20937	AT4G01380.1 | plastocyanin-like domain-containing protein | chr4:569148-570076 REVERSE | Aliases: F2N1.2, F2N1_2	2.2	2.2	0.0	0.0	100.0%	-2.3
20938	AT1G10650.1 | expressed protein | chr1:3524019-3526336 REVERSE | Aliases: F20B24.9, F20B24_9	8.5	8.5	-0.0	-0.0	100.0%	-1.9
20939	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	3.6	3.6	-0.0	-0.0	100.0%	-1.7
20940	AT1G59720.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr1:21943533-21945449 REVERSE | Aliases: F23H11.3, F23H11_3	3.2	3.2	0.0	0.0	100.0%	-1.8
20941	AT5G15300.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr5:4968166-4970037 REVERSE | Aliases: F8M21.190, F8M21_190	3.1	3.1	-0.0	-0.0	100.0%	-1.9
20942	AT1G41860.1 | expressed protein | chr1:15642597-15643235 FORWARD | Aliases: F5A13.6, F5A13_6	2.7	2.7	0.0	0.0	100.0%	-2.4
20943	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	-0.0	100.0%	-2.0
20944	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	3.4	0.0	0.0	100.0%	-1.6
20945	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	8.9	8.9	-0.0	-0.0	100.0%	-1.5
20946	AT2G34660.1 | Symbol: ATMRP2 |	7.6	7.6	-0.0	-0.0	100.0%	-1.3
20947	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	5.8	5.8	-0.0	-0.0	100.0%	-1.5
20948	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	10.1	10.2	-0.0	-0.0	100.0%	-1.8
20949	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	-0.0	100.0%	-2.5
20950	AT2G29740.1 | UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase | chr2:12713787-12715444 FORWARD | Aliases: T27A16.16, T27A16_16	4.3	4.3	-0.0	-0.0	100.0%	-1.3
20951	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	2.9	0.0	0.0	100.0%	-1.7
20952	AT3G54250.1 | mevalonate diphosphate decarboxylase, putative, similar to mevalonate diphosphate decarboxylase (Arabidopsis thaliana) gi:2288887:emb:CAA74700 | chr3:20093286-20095710 REVERSE | Aliases: F24B22.210	4.1	4.1	-0.0	-0.0	100.0%	-1.6

Rank	Description	Sync	Root	M	t	adj.q	B
20953	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	-0.0	-0.0	100.0%	-2.4
20954	AT1G78170.1 | expressed protein | chr1:29418952-29419987 FORWARD | Aliases: T11I11.11, T11I11_11	1.9	1.9	-0.0	-0.0	100.0%	-2.7
20955	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	6.5	6.5	0.0	0.0	100.0%	-1.4
20956	AT4G19240.1 | expressed protein | chr4:10527811-10529103 REVERSE | Aliases: T5K18.20, T5K18_20	3.0	3.0	-0.0	-0.0	100.0%	-2.0
20957	AT4G15720.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr4:8949458-8951926 FORWARD | Aliases: DL3900W, FCAALL.369	3.6	3.6	-0.0	-0.0	100.0%	-1.4
20958	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	5.0	0.0	0.0	100.0%	-1.9
20959	AT4G04260.1 | bromo-adjacent homology (BAH) domain-containing protein, similar to ES43 (Hordeum vulgare) GI:1345528; contains Pfam profile PF01426: BAH domain	2.5	2.5	0.0	0.0	100.0%	-2.4
20960	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	4.1	4.1	-0.0	-0.0	100.0%	-1.4
20961	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	4.2	4.2	-0.0	-0.0	100.0%	-1.7
20962	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	0.0	100.0%	-2.3
20963	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	3.6	3.6	-0.0	-0.0	100.0%	-1.2
20964	AT1G55545.1 | nucleoporin-related, similar to nucleoporin CAN (Xenopus laevis) gi:5764080:emb:CAB53357	2.7	2.7	0.0	0.0	100.0%	-2.3
20965	AT3G15200.1 | pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat | chr3:5117496-5119067 REVERSE | Aliases: F4B12.11	3.3	3.3	-0.0	-0.0	100.0%	-2.0
20966	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	-0.0	100.0%	-1.5
20967	AT2G05910.1 | expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567) | chr2:2258297-2259378 REVERSE | Aliases: T6P5.11, T6P5_11	4.9	4.9	-0.0	-0.0	100.0%	-1.9
20968	AT5G58980.1 | ceramidase family protein, contains Pfam domain, PF04734: Neutral/alkaline nonlysosomal ceramidase | chr5:23828675-23831621 REVERSE | Aliases: K19M22.22, K19M22_22	7.0	7.0	-0.0	-0.0	100.0%	-1.3
20969	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	8.4	8.4	-0.0	-0.0	100.0%	-1.5
20970	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	-0.0	100.0%	-1.5
20971	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	0.0	100.0%	-2.2

Rank	Description	Sync	Root	M	t	adj.q	B
20972	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)	6.6	6.6	-0.0	-0.0	100.0%	-1.5
20973	AT5G48800.1 | phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000 | chr5:19803990-19806733 FORWARD | Aliases: K24G6.13, K24G6_13	4.0	4.0	0.0	0.0	100.0%	-1.6
20974	AT5G55420.1 | expressed protein | chr5:22479129-22479544 FORWARD | Aliases: MTE17.13, MTE17_13	2.7	2.7	-0.0	-0.0	100.0%	-2.2
20975	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	3.5	0.0	0.0	100.0%	-1.7
20976	AT3G06280.1 | expressed protein | chr3:1898161-1898757 REVERSE | Aliases: F28L1.22, F28L1_22	2.2	2.2	-0.0	-0.0	100.0%	-2.5
20977	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	3.4	3.4	-0.0	-0.0	100.0%	-1.6
20978	AT1G16260.1 | protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain | chr1:5559702-5562012 REVERSE | Aliases: F3O9.6, F3O9_6	2.7	2.7	-0.0	-0.0	100.0%	-2.0
20979	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	7.9	7.9	0.0	0.0	100.0%	-1.4
20980	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	3.4	3.4	0.0	0.0	100.0%	-1.7
20981	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	2.5	2.5	-0.0	-0.0	100.0%	-2.2
20982	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	6.0	6.0	-0.0	-0.0	100.0%	-1.8
20983	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	7.9	7.9	0.0	0.0	100.0%	-1.8
20984	AT5G03400.1 | expressed protein | chr5:837918-839201 REVERSE | Aliases: F12E4.140, F12E4_140	3.6	3.6	-0.0	-0.0	100.0%	-2.1
20985	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	0.0	100.0%	-2.2
20986	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%	-2.4
20987	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%	-2.2
20988	AT1G35320.1 | expressed protein | chr1:12960432-12962831 REVERSE | Aliases: T9I1.9, T9I1_9	4.6	4.6	-0.0	-0.0	100.0%	-1.3
20989	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	2.5	2.5	-0.0	-0.0	100.0%	-2.4
20990	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	-0.0	100.0%	-1.5
20991	AT2G12900.1 | expressed protein, similar to transcription factor(bZIP family) VSF-1 GI:3425907 from (Lycopersicon esculentum) | chr2:5300979-5302562 FORWARD | Aliases: T18E17.2	2.7	2.7	0.0	0.0	100.0%	-2.0
20992	AT1G76500.1 | DNA-binding family protein, contains Pfam domain, PF02178: AT hook motif	4.9	4.9	-0.0	-0.0	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
20993	AT5G35380.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr5:13610659-13613523 REVERSE | Aliases: T26D22.11, T26D22_11	2.1	2.1	-0.0	-0.0	100.0%	-2.5
20994	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	-0.0	100.0%	-2.1
20995	AT2G33670.1 | Symbol: MLO5 | seven transmembrane MLO family protein / MLO-like protein 5 (MLO5), identical to MLO-like protein 5 (AtMlo5) (Arabidopsis thaliana) SWISS-PROT:O22815; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 (Hordeum vulgare)(Barley) | chr2:14252106-14255007 FORWARD | Aliases: F4P9.44, F4P9_44	2.8	2.8	0.0	0.0	100.0%	-2.1
20996	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	7.4	7.4	0.0	0.0	100.0%	-1.3
20997	AT4G18540.1 | expressed protein, ; expression supported by MPSS | chr4:10221214-10223039 REVERSE | Aliases: F28J12.200, F28J12_200	2.9	2.9	-0.0	-0.0	100.0%	-1.9
20998	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	7.5	7.5	0.0	0.0	100.0%	-1.2
20999	AT3G49830.1 | DNA helicase-related, similar to DNA helicase GI:4521249 from (Mus musculus) | chr3:18493368-18494925 FORWARD | Aliases: T16K5.180	2.5	2.5	-0.0	-0.0	100.0%	-2.3
21000	AT4G31020.2 | expressed protein | chr4:15108107-15110153 REVERSE | Aliases: F6I18.70, F6I18_70	2.8	2.8	0.0	0.0	100.0%	-2.1
21001	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	-0.0	100.0%	-2.5
21002	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	2.3	2.3	0.0	0.0	100.0%	-2.3
21003	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	-0.0	100.0%	-2.3
21004	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	2.9	2.9	-0.0	-0.0	100.0%	-2.2
21005	AT4G30760.2 | expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537 | chr4:14982528-14983425 FORWARD | Aliases: T10C21.110, T10C21_110	9.0	9.0	-0.0	-0.0	100.0%	-2.4
21006	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	-0.0	100.0%	-1.7
21007	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	2.9	0.0	0.0	100.0%	-1.8
21008	AT1G79590.2 | Symbol: SYP52 | similar to syntaxin 51 (SYP51) [Arabidopsis thaliana] (TAIR:At1g16240.1); 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) | chr1:29951130-29953667 FORWARD | Aliases: ATSYP52, F20B17.2, F20B17_2, SYNTAXIN OF PLANTS 52	7.1	7.1	-0.0	-0.0	100.0%	-1.2
21009	AT4G31970.1 | Symbol: CYP82C2 | cytochrome P450 family protein, similar to cytochrome P450 82C1 (CYP82C1p)(GI:2739004) (Glycine max); flavonoid 3 ,5'-hydroxylase, Campanula medium, PATCHX:D1003951 | chr4:15462414-15464364 FORWARD | Aliases: F11C18.12	2.8	2.8	0.0	0.0	100.0%	-2.2
21010	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%	-1.8
21011	AT3G27670.1 | expressed protein | chr3:10246371-10254530 FORWARD | Aliases: MGF10.8	5.1	5.1	-0.0	-0.0	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
21012	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	7.8	0.0	0.0	100.0%	-1.9
21013	AT3G23660.1 | transport protein, putative, similar to Swiss-Prot:Q15436 protein transport protein Sec23A (Homo sapiens) | chr3:8513464-8517790 REVERSE | Aliases: MDB19.16	5.1	5.1	0.0	0.0	100.0%	-1.9
21014	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	2.3	2.3	0.0	0.0	100.0%	-2.6
21015	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	0.0	100.0%	-1.9
21016	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	3.5	3.5	-0.0	-0.0	100.0%	-1.9
21017	AT1G43260.1 | hypothetical protein, contains Pfam domain, PF04937: Protein of unknown function (DUF 659) | chr1:16320693-16321674 FORWARD | Aliases: F1I21.5, F1I21_5	2.4	2.4	0.0	0.0	100.0%	-2.4
21018	AT1G70150.1 | zinc finger (MYND type) family protein, contains Pfam profile PF01753: MYND finger | chr1:26420561-26422880 FORWARD | Aliases: F20P5.13, F20P5_13	4.0	4.0	-0.0	-0.0	100.0%	-1.5
21019	AT4G15800.1 | Symbol: RALFL33 | rapid alkalinization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316 | chr4:8984866-8985413 FORWARD | Aliases: DL3940C, FCAALL.206, RALF LIKE 33	7.1	7.1	-0.0	-0.0	100.0%	-1.6
21020	AT4G28810.1 | expressed protein, PMID: 12679534, putative bHLH127 transcription factor	2.4	2.4	0.0	0.0	100.0%	-2.5
21021	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%	-1.5
21022	AT3G58690.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr3:21720168-21722358 FORWARD | Aliases: T20N10.40	5.5	5.5	-0.0	-0.0	100.0%	-1.4
21023	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	2.6	2.6	0.0	0.0	100.0%	-2.2
21024	AT2G28330.1 | expressed protein | chr2:12106967-12107834 REVERSE | Aliases: T1B3.15, T1B3_15	3.7	3.7	0.0	0.0	100.0%	-1.8
21025	AT5G34930.1 | arogenate dehydrogenase, identical to arogenate dehydrogenase GI:16903098 from (Arabidopsis thaliana); contains Pfam profile: PF02153: prephenate dehydrogenase | chr5:13250604-13252797 FORWARD | Aliases: T2L5.1	5.2	5.2	-0.0	-0.0	100.0%	-1.6
21026	AT5G42320.1 | zinc carboxypeptidase family protein, contains Pfam domain, PF00246: Zinc carboxypeptidase | chr5:16935879-16938685 REVERSE | Aliases: K5J14.5, K5J14_5	6.2	6.2	-0.0	-0.0	100.0%	-1.7
21027	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	0.0	0.0	100.0%	-2.0
21028	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	0.0	100.0%	-2.4
21029	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	4.5	0.0	0.0	100.0%	-1.3
21030	AT2G40730.1 | HEAT repeat-containing protein, contains INTERPRO:IPR000357 HEAT repeat | chr2:16996914-17003295 REVERSE | Aliases: T7D17.9, T7D17_9	2.9	2.9	-0.0	-0.0	100.0%	-2.1
21031	AT5G39860.1 | bHLH protein, putative DNA-binding protein - Arabidopsis thaliana, EMBL:AC011765	2.4	2.4	-0.0	-0.0	100.0%	-2.1
21032	AT1G11470.1 | expressed protein | chr1:3859874-3860522 REVERSE | Aliases: T23J18.14, T23J18_14	3.2	3.2	-0.0	-0.0	100.0%	-1.7

Rank	Description	Sync	Root	M	t	adj.q	B
21033	AT2G43940.1 | thiol methyltransferase, putative, similar to thiol methyltransferase 2 GI:14583121 from (Brassica oleracea) | chr2:18203029-18204763 REVERSE | Aliases: F6E13.7	4.8	4.8	-0.0	-0.0	100.0%	-1.3
21034	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	3.0	-0.0	-0.0	100.0%	-1.7
21035	AT5G28070.1 | hypothetical protein | chr5:10083174-10083523 FORWARD | Aliases: T24G3.1	2.5	2.5	-0.0	-0.0	100.0%	-2.5
21036	AT2G21220.1 | auxin-responsive protein, putative, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana) | chr2:9096407-9096894 FORWARD | Aliases: F7O24.6, F7O24_6	2.4	2.4	-0.0	-0.0	100.0%	-2.3
21037	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	2.3	2.3	-0.0	-0.0	100.0%	-2.5
21038	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	0.0	0.0	100.0%	-2.0
21039	AT1G09060.3 | similar to transcription factor jumonji (jmjC) 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, jmjC (InterPro:IPR003347)	6.8	6.8	0.0	0.0	100.0%	-1.5
21040	AT2G05000.1 | hypothetical protein, and genefinder | chr2:1761801-1762375 REVERSE | Aliases: F1O13.13, F1O13_13	2.5	2.5	0.0	0.0	100.0%	-2.4
21041	AT3G28790.1 | expressed protein | chr3:10814571-10816936 REVERSE | Aliases: T19N8.9	3.0	3.0	0.0	0.0	100.0%	-2.0
21042	AT5G56090.1 | cytochrome oxidase assembly family protein, contains PF02628: Cytochrome oxidase assembly protein | chr5:22731744-22734061 FORWARD | Aliases: MDA7.15, MDA7_15	8.0	8.0	0.0	0.0	100.0%	-1.2
21043	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	9.5	9.5	-0.0	-0.0	100.0%	-1.7
21044	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	0.0	0.0	100.0%	-2.4
21045	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	2.4	2.4	0.0	0.0	100.0%	-2.3
21046	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	5.4	5.4	-0.0	-0.0	100.0%	-1.6
21047	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	9.6	9.6	0.0	0.0	100.0%	-1.5
21048	AT5G46460.1 | pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats | chr5:18857532-18859625 FORWARD | Aliases: K11I1.5, K11I1_5	3.8	3.8	-0.0	-0.0	100.0%	-1.5
21049	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%	-1.5
21050	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	-0.0	100.0%	-2.4

Rank	Description	Sync	Root	M	t	adj.q	B
21051	AT1G65020.1 | expressed protein | chr1:24158033-24160239 REVERSE | Aliases: F13O11.31	5.6	5.6	0.0	0.0	100.0%	-1.3
21052	AT5G46295.1 | expressed protein | chr5:18797023-18797429 REVERSE | Aliases: None	4.2	4.2	-0.0	-0.0	100.0%	-1.4
21053	AT4G16310.1 | amine oxidase family protein / SWIRM domain-containing protein, low similarity to polyamine oxidase isoform-1 (Homo sapiens) GI:14860862; contains Pfam profiles PF01593: amine oxidase flavin-containing, PF04433: SWIRM domain	2.7	2.7	-0.0	-0.0	100.0%	-2.2
21054	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	5.5	5.5	0.0	0.0	100.0%	-1.2
21055	AT5G35230.1 | expressed protein | chr5:13507208-13508903 REVERSE | Aliases: T25C13.110, T25C13_110	2.6	2.6	-0.0	-0.0	100.0%	-2.2
21056	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	4.2	4.2	-0.0	-0.0	100.0%	-1.3
21057	AT1G32040.1 | expressed protein | chr1:11518398-11520050 FORWARD | Aliases: T12O21.6, T12O21_6	2.6	2.6	0.0	0.0	100.0%	-2.1
21058	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	9.6	9.6	-0.0	-0.0	100.0%	-1.7
21059	AT3G11760.1 | expressed protein | chr3:3718535-3721129 FORWARD | Aliases: F26K24.5	5.4	5.4	0.0	0.0	100.0%	-1.5
21060	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	9.2	9.2	0.0	0.0	100.0%	-1.4
21061	AT1G22870.1 | protein kinase family protein, contains protein kinase domain, Pfam:PF00069 | chr1:8089490-8094162 FORWARD | Aliases: F19G10.17, F19G10_17	4.0	4.1	-0.0	-0.0	100.0%	-1.6
21062	AT1G60930.1 | DNA helicase, putative, strong similarity to DNA Helicase recQl4B (Arabidopsis thaliana) 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	2.9	2.9	0.0	0.0	100.0%	-2.0
21063	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	0.0	100.0%	-2.3
21064	AT1G79760.1 | Symbol: DTA4 | expressed protein | chr1:30016947-30018045 FORWARD | Aliases: DOWNSTREAM TARGET OF AGL15 4, F19K16.26, F19K16_26	3.9	3.9	-0.0	-0.0	100.0%	-1.6
21065	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	7.0	0.0	0.0	100.0%	-1.5
21066	AT3G19085.1 | expressed protein | chr3:6599595-6600590 FORWARD | Aliases: K13E13.22	2.3	2.3	0.0	0.0	100.0%	-2.6
21067	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	5.3	0.0	0.0	100.0%	-1.5
21068	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	3.0	3.0	-0.0	-0.0	100.0%	-1.5
21069	AT1G27100.1 | expressed protein, contains Pfam profile: PF04601 protein of unknown function (DUF569 | chr1:9407112-9411159 REVERSE | Aliases: T7N9.16, T7N9_16	5.8	5.8	0.0	0.0	100.0%	-1.6
21070	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	0.0	100.0%	-1.8
21071	AT5G54095.1 | expressed protein | chr5:21969959-21970723 REVERSE | Aliases: None	2.6	2.6	-0.0	-0.0	100.0%	-2.0
21072	AT5G58370.2 | expressed protein | chr5:23610343-23613252 FORWARD | Aliases: MCK7.24, MCK7_24	3.9	3.9	-0.0	-0.0	100.0%	-1.9

Rank	Description	Sync	Root	M	t	adj.q	B
21073	NA	3.0	3.0	-0.0	-0.0	100.0%	-2.4
21074	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	3.0	3.0	-0.0	-0.0	100.0%	-2.2
21075	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	4.0	4.0	0.0	0.0	100.0%	-2.0
21076	AT1G36230.1 | hypothetical protein | chr1:13612197-13615263 REVERSE | Aliases: F15C21.12, F15C21_12	3.4	3.4	-0.0	-0.0	100.0%	-1.9
21077	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	6.4	6.4	-0.0	-0.0	100.0%	-1.8
21078	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	3.1	3.1	0.0	0.0	100.0%	-1.8
21079	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	4.5	4.5	0.0	0.0	100.0%	-1.5
21080	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	-0.0	100.0%	-2.5
21081	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	3.3	3.3	0.0	0.0	100.0%	-1.8
21082	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: ATSYP81, F19C24.5, F19C24_5	4.0	4.1	-0.0	-0.0	100.0%	-1.5
21083	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	2.3	0.0	0.0	100.0%	-2.2
21084	AT1G05510.1 | expressed protein | chr1:1629452-1630862 FORWARD | Aliases: T25N20.16	2.7	2.7	0.0	0.0	100.0%	-2.0
21085	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	3.0	3.0	-0.0	-0.0	100.0%	-2.2
21086	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	-0.0	-0.0	100.0%	-2.6
21087	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	5.5	5.5	-0.0	-0.0	100.0%	-1.3
21088	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	0.0	100.0%	-1.9
21089	AT2G28755.1 | UDP-D-glucuronate carboxy-lyase-related, contains similarity to UDP-D-glucuronate carboxy-lyase GI:13591616 from (Pisum sativum)	2.8	2.8	-0.0	-0.0	100.0%	-2.1
21090	AT2G29420.1 | Symbol: ATGSTU7 | glutathione S-transferase, putative | chr2:12625013-12625976 REVERSE | Aliases: F16P2.20, F16P2_20, GLUTATHIONE S TRANSFERASE 25, GST25	9.0	9.0	0.0	0.0	100.0%	-1.6
21091	AT4G37190.2 | similar to misato [Mus musculus] (GB:NP_659147.1) | chr4:17507253-17510102 FORWARD | Aliases: AP22.7, AP22_7	2.9	2.9	0.0	0.0	100.0%	-1.9
21092	AT1G64360.1 | expressed protein | chr1:23891533-23892167 FORWARD | Aliases: F15H21.8, F15H21_8	2.5	2.5	0.0	0.0	100.0%	-2.4
21093	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	4.4	4.4	-0.0	-0.0	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
21094	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	6.3	6.3	-0.0	-0.0	100.0%	-2.0
21095	AT4G32620.1 | expressed protein, predicted protein T10M13.8, Arabidopsis thaliana | chr4:15731679-15737278 FORWARD | Aliases: F4D11.180, F4D11_180	5.9	5.9	0.0	0.0	100.0%	-1.6
21096	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	7.5	7.5	-0.0	-0.0	100.0%	-1.6
21097	AT1G70360.1 | F-box protein-related | chr1:26512441-26512988 FORWARD | Aliases: F17O7.10, F17O7_10	5.4	5.4	0.0	0.0	100.0%	-1.9
21098	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	2.9	2.9	0.0	0.0	100.0%	-2.0
21099	AT5G46830.1 | basic helix-loop-helix (bHLH) family protein | chr5:19019946-19021481 FORWARD | Aliases: MZA15.1	2.4	2.4	-0.0	-0.0	100.0%	-2.6
21100	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	3.3	-0.0	-0.0	100.0%	-2.1
21101	AT3G16680.1 | expressed protein, ; expression supported by MPSS | chr3:5683342-5684251 FORWARD | Aliases: MGL6.11	2.9	2.9	0.0	0.0	100.0%	-2.4
21102	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	5.8	5.8	-0.0	-0.0	100.0%	-1.6
21103	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	6.5	6.5	-0.0	-0.0	100.0%	-1.7
21104	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	6.1	6.1	0.0	0.0	100.0%	-1.7
21105	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	2.3	0.0	0.0	100.0%	-2.7
21106	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	0.0	100.0%	-2.5
21107	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	3.0	-0.0	-0.0	100.0%	-1.9
21108	AT3G20140.1 | Symbol: CYP705A23 | cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450 | chr3:7029181-7030793 FORWARD | Aliases: MAL21.2	3.0	3.0	-0.0	-0.0	100.0%	-1.7
21109	AT1G16770.1 | expressed protein | chr1:5737893-5739103 FORWARD | Aliases: F17F16.12, F17F16_12	3.4	3.4	-0.0	-0.0	100.0%	-2.0
21110	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	6.7	6.7	-0.0	-0.0	100.0%	-1.4
21111	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	8.3	8.3	0.0	0.0	100.0%	-1.6
21112	AT4G21326.1 | subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa) | chr4:11346991-11349664 FORWARD | Aliases: None	3.0	3.0	-0.0	-0.0	100.0%	-1.8
21113	AT2G45930.1 | expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295) | chr2:18908465-18909871 REVERSE | Aliases: F4I18.9	3.3	3.3	-0.0	-0.0	100.0%	-2.1

Rank	Description	Sync	Root	M	t	adj.q	B
21114	AT3G12150.1 | expressed protein | chr3:3876414-3878907 REVERSE | Aliases: T21B14.3	4.1	4.1	0.0	0.0	100.0%	-1.6
21115	AT4G18930.1 | cyclic phosphodiesterase, identical to cyclic phosphodiesterase (Arabidopsis thaliana) gi:2065013:emb:CAA72363 | chr4:10370715-10372056 FORWARD | Aliases: F13C5.100, F13C5_100	9.4	9.4	0.0	0.0	100.0%	-1.5
21116	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)	4.5	4.5	0.0	0.0	100.0%	-1.5
21117	AT3G02170.1 | expressed protein | chr3:396019-399786 REVERSE | Aliases: F1C9.4	2.2	2.2	-0.0	-0.0	100.0%	-2.7
21118	AT2G04750.1 | fimbrin-like protein, putative, similar to fimbrin-like protein (ATFIM1) (Arabidopsis thaliana) GI:2905893; contains Pfam profile PF00307: Calponin homology (CH) domain	2.4	2.4	-0.0	-0.0	100.0%	-2.5
21119	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	-0.0	100.0%	-1.5
21120	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	3.6	3.6	-0.0	-0.0	100.0%	-1.7
21121	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	3.7	3.7	0.0	0.0	100.0%	-2.0
21122	AT5G05540.1 | exonuclease family protein, contains exonuclease domain, Pfam:PF00929 | chr5:1636307-1638940 FORWARD | Aliases: MOP10.8, MOP10_8	4.5	4.5	-0.0	-0.0	100.0%	-1.4
21123	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	3.3	3.3	-0.0	-0.0	100.0%	-2.0
21124	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	3.5	3.5	-0.0	-0.0	100.0%	-1.9
21125	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	4.4	4.4	-0.0	-0.0	100.0%	-1.8
21126	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	6.0	6.0	0.0	0.0	100.0%	-1.4
21127	AT5G57220.1 | Symbol: CYP81F2 | cytochrome P450, putative, similar to	4.5	4.5	-0.0	-0.0	100.0%	-1.8
21128	AT4G17486.1 | expressed protein | chr4:9749741-9751721 REVERSE | Aliases: FCAALL.234	7.7	7.7	-0.0	-0.0	100.0%	-1.2
21129	NA	2.2	2.2	0.0	0.0	100.0%	-2.9
21130	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	2.5	-0.0	-0.0	100.0%	-2.4
21131	AT2G14590.1 | hypothetical protein | chr2:6235919-6236890 FORWARD | Aliases: T13P21.3	2.6	2.6	-0.0	-0.0	100.0%	-2.3
21132	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	-0.0	-0.0	100.0%	-2.2
21133	AT3G29170.1 | expressed protein, contains Pfam PF05915: Eukaryotic protein of unknown function (DUF872) | chr3:11137243-11139086 REVERSE | Aliases: MXE2.17	7.2	7.2	-0.0	-0.0	100.0%	-1.6
21134	AT1G06430.1 | Symbol: FTSH8 | encodes a FtsH protease that is localized to the chloroplast | chr1:1960057-1963006 REVERSE | Aliases: F12K11.22, FTSH8	5.4	5.4	0.0	0.0	100.0%	-1.5

Rank	Description	Sync	Root	M	t	adj.q	B
21135	AT2G47230.1 | agenet domain-containing protein, contains Pfam PF05641: Agenet domain | chr2:19394090-19397302 FORWARD | Aliases: T8I13.7	3.4	3.4	0.0	0.0	100.0%	-2.0
21136	AT2G10090.1 | expressed protein | chr2:3830613-3830972 REVERSE | Aliases: F7B19.23, F7B19_23	2.6	2.6	-0.0	-0.0	100.0%	-2.1
21137	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	2.7	2.7	0.0	0.0	100.0%	-2.2
21138	AT3G42680.1 | expressed protein | chr3:14773857-14774386 REVERSE | Aliases: T12K4.130	3.3	3.3	0.0	0.0	100.0%	-2.1