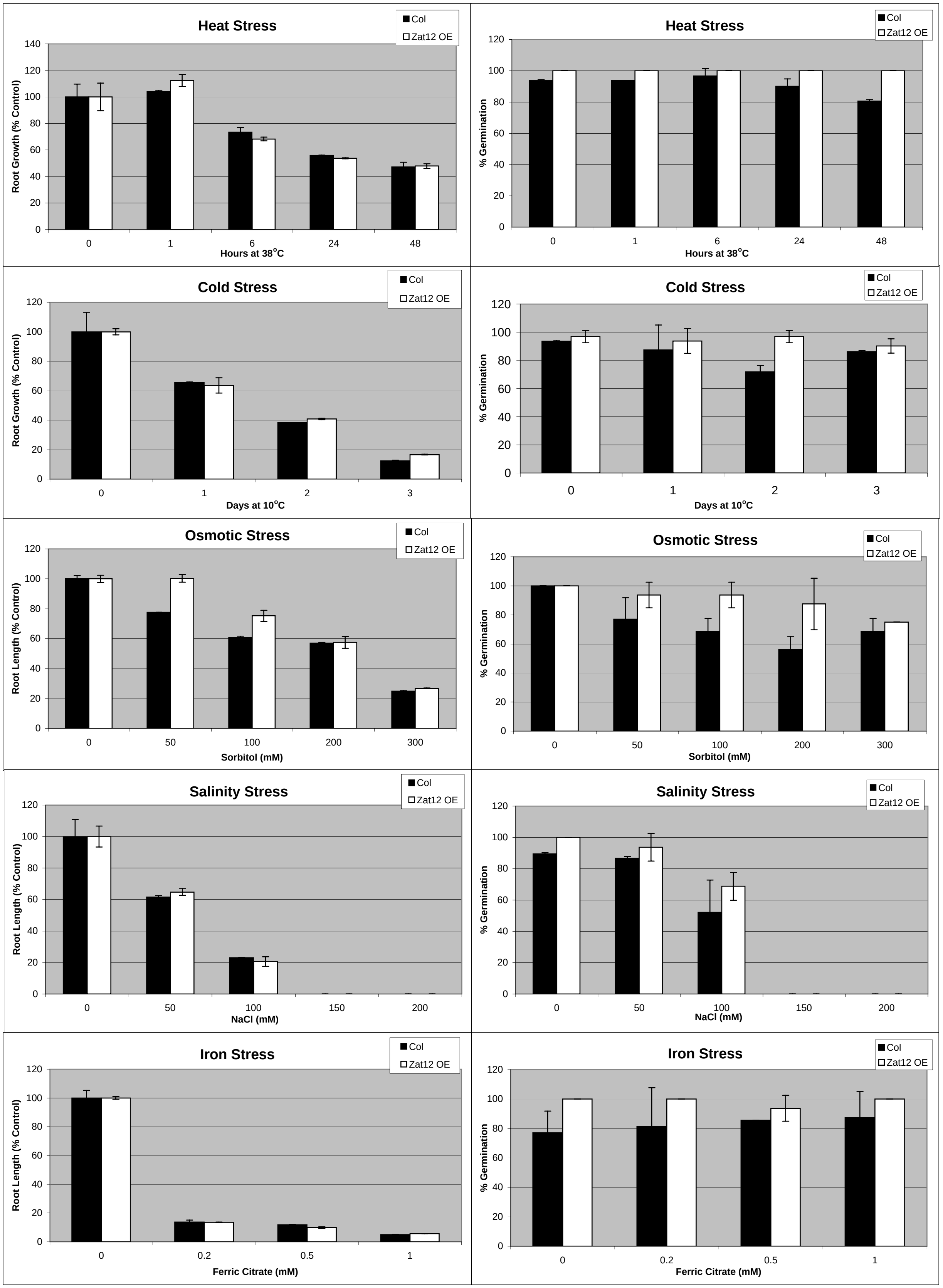
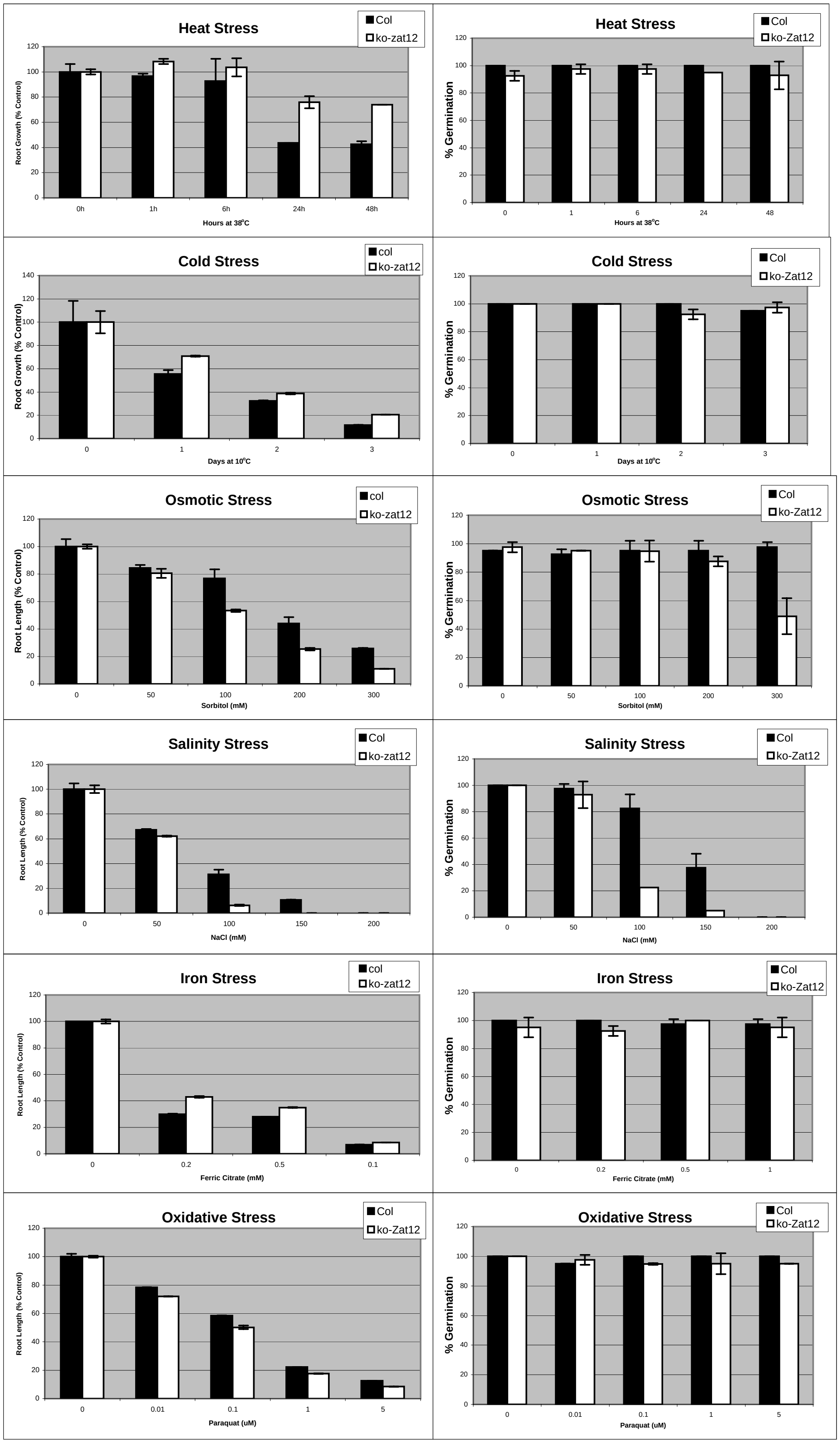


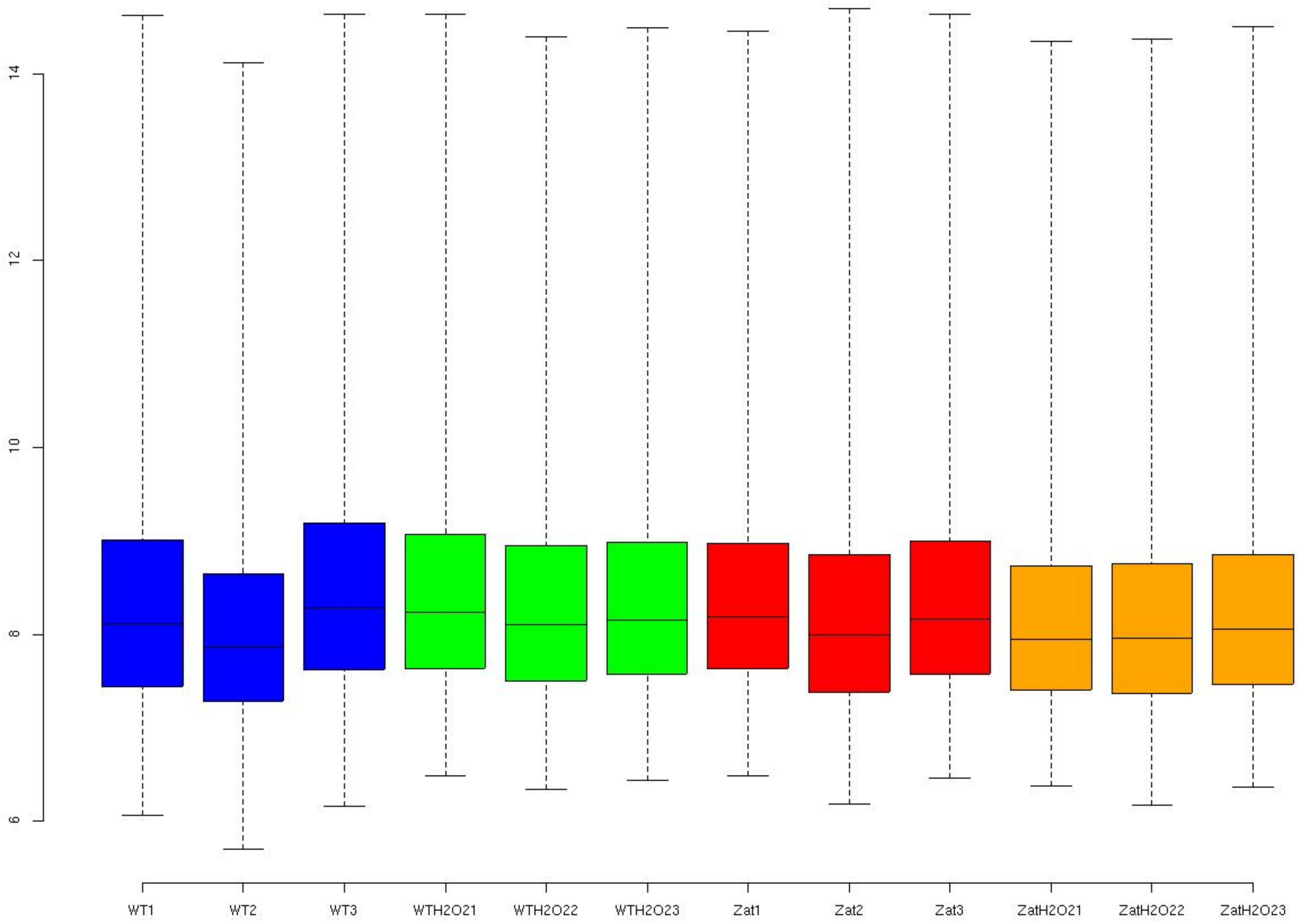
Suppl. Fig. 1. Tolerance of Zat12 over-expressing (OE) seedlings to abiotic stresses



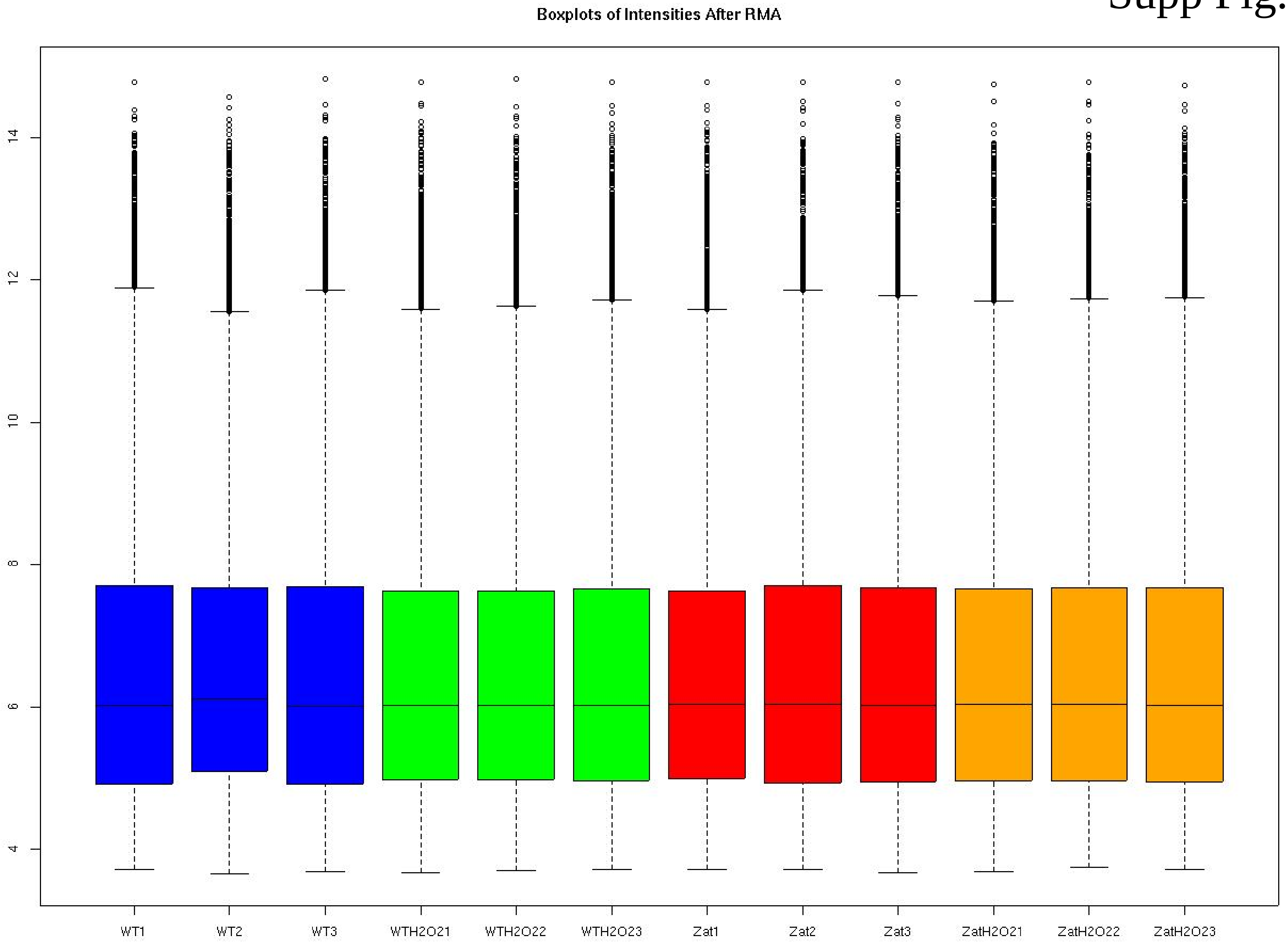
Suppl. Fig. 2. Tolerance of Zat12 knockout (KO-Zat12) seedlings to abiotic stresses

Boxplots of Intensities Before RMA

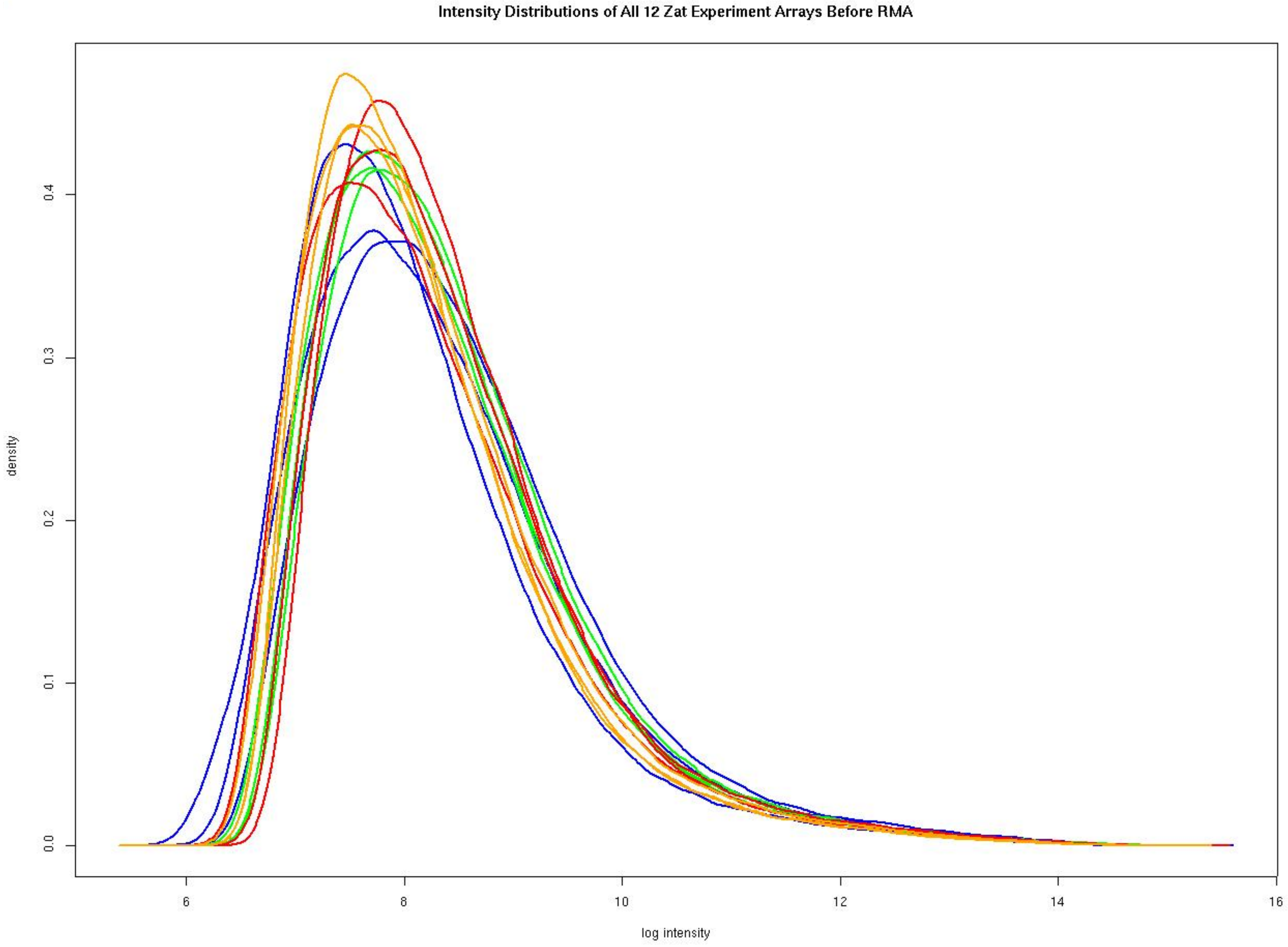
Supp Fig. 3



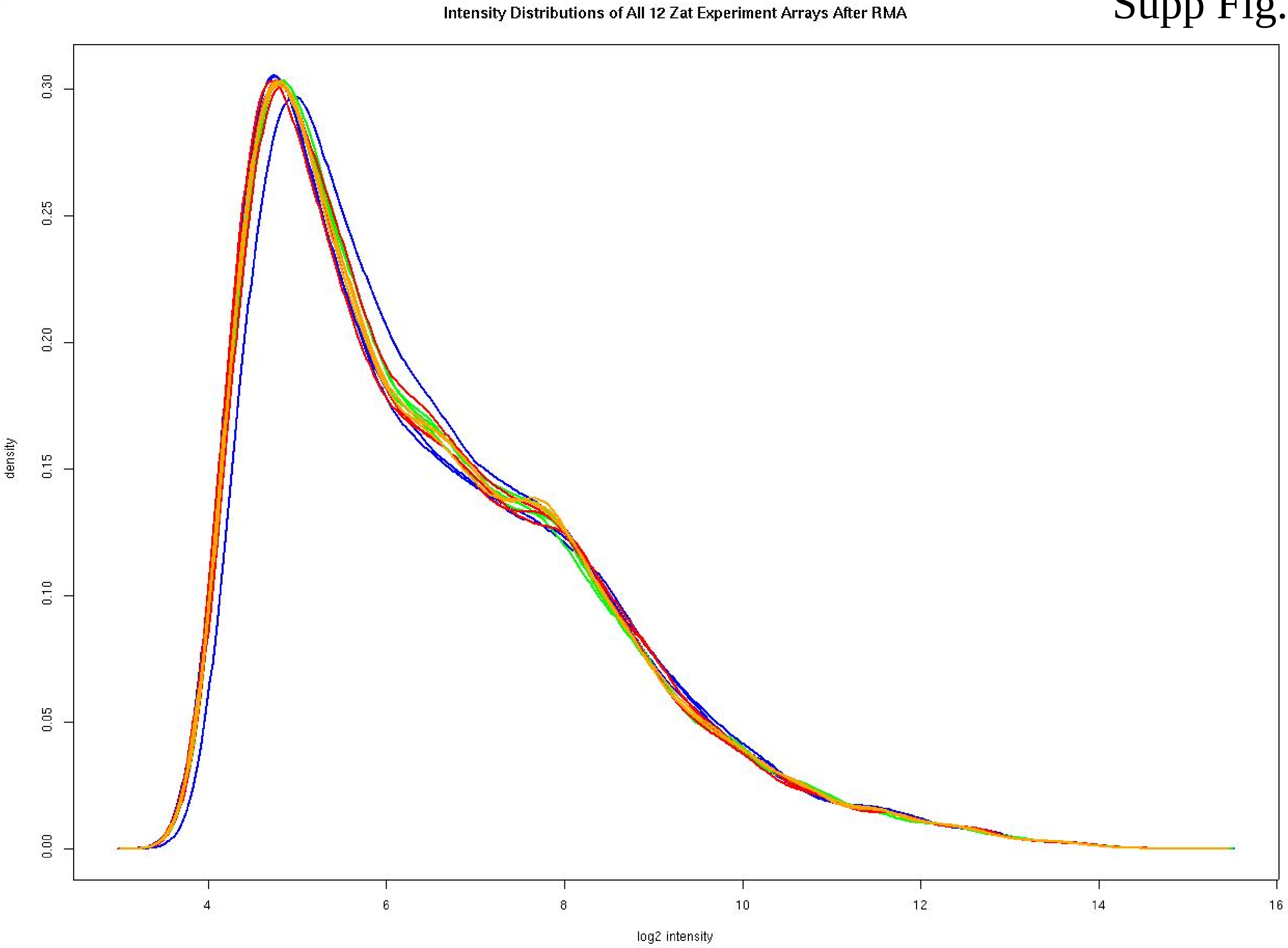
Supp Fig. 4


Boxplots of Intensities After RMA
14
12
10
8
6
4
WT1
WT2
WT3
WTH2O21
WTH2O22
WTH2O23
Zat1
Zat2
Zat3
ZatH2O21
ZatH2O22
ZatH2O23

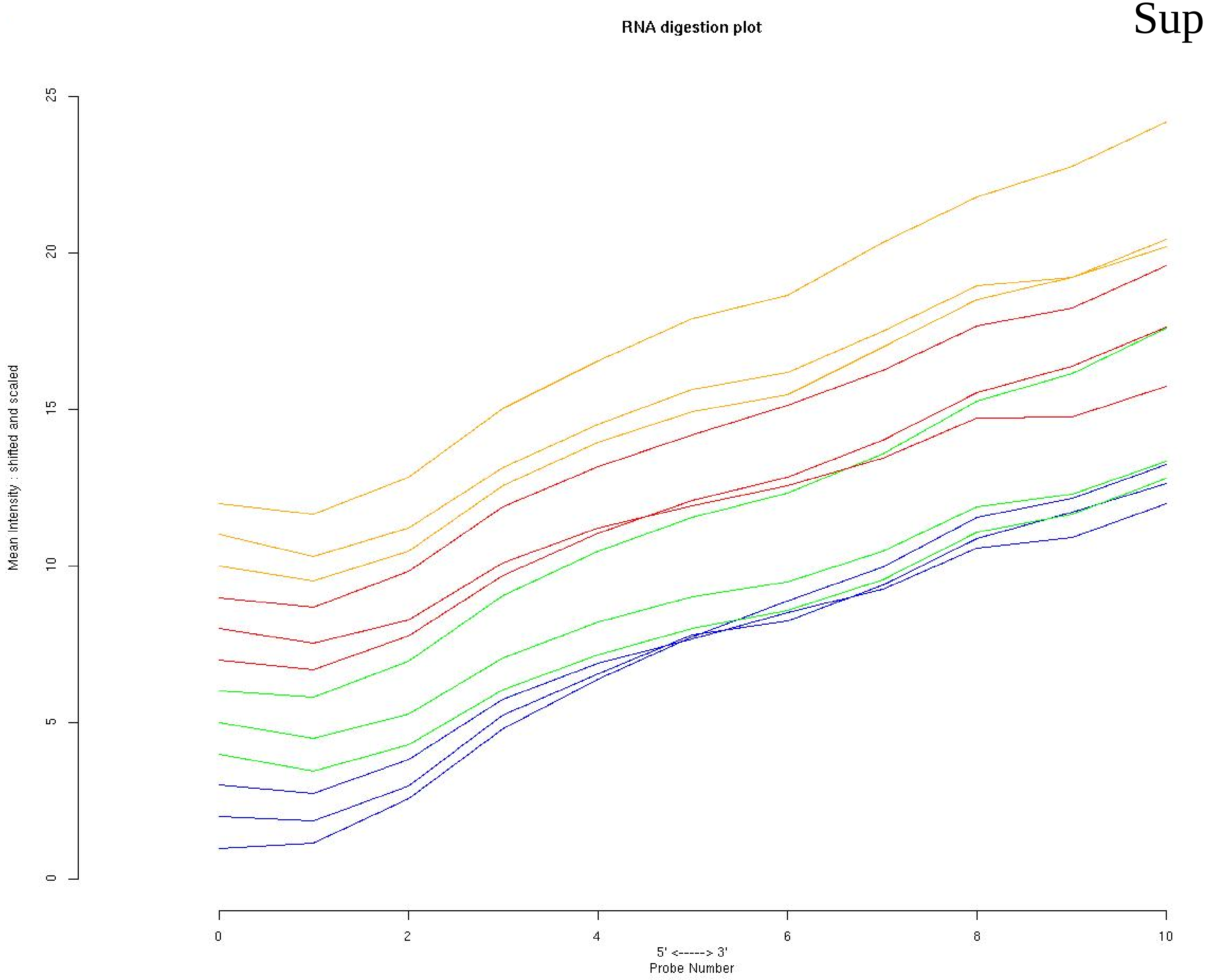
Supp Fig. 5


Intensity Distributions of All 12 Zat Experiment Arrays Before RMA
density
0.0
0.1
0.2
0.3
0.4
6
8
10
12
14
16
log intensity

Supp Fig. 6


Intensity Distributions of All 12 Zat Experiment Arrays After RMA
density
0.00
0.05
0.10
0.15
0.20
0.25
0.30
4
6
8
10
12
14
16
log2 intensity

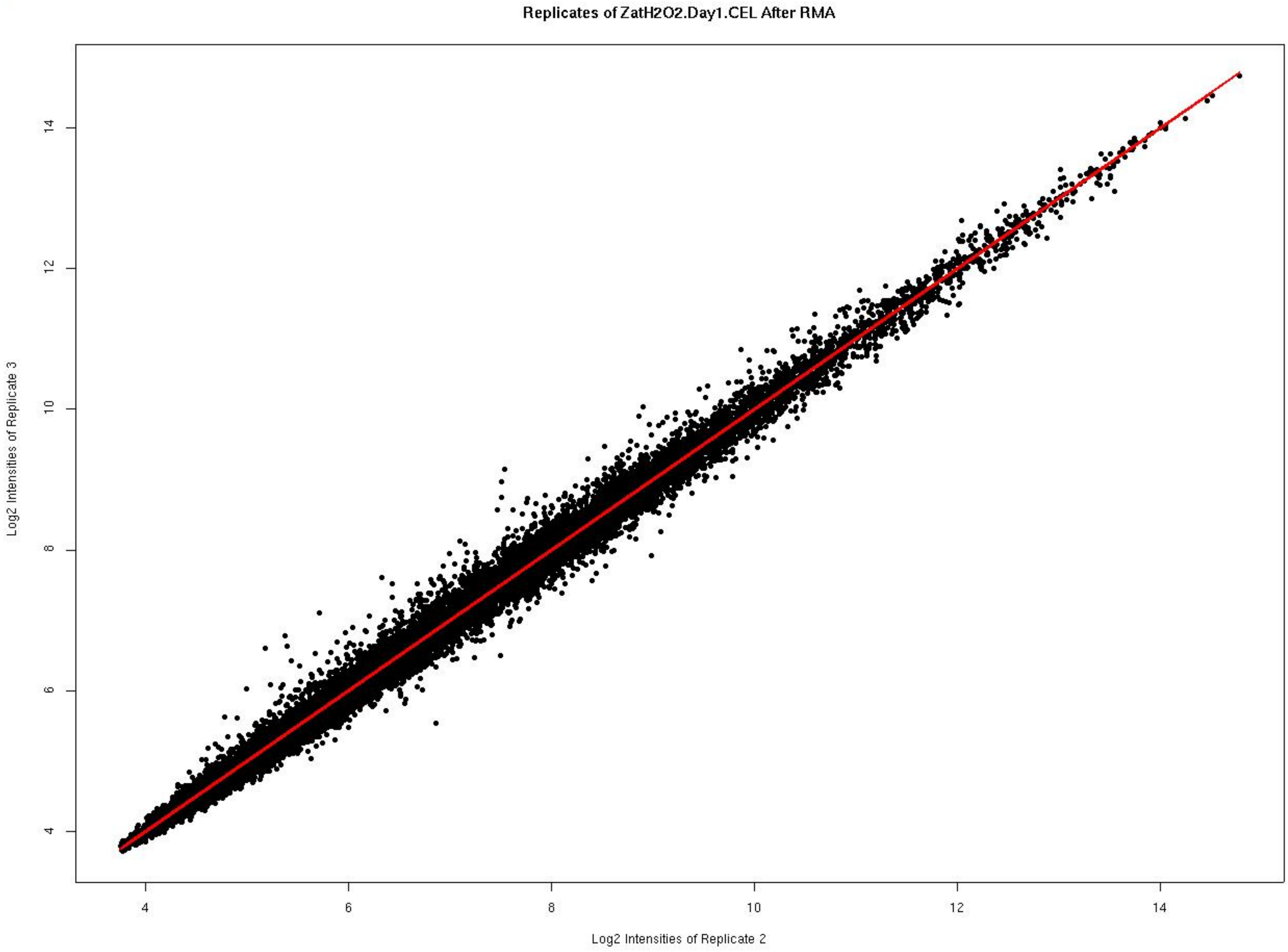
Supp Fig. 7



RNA digestion plot
Mean Intensity : shifted and scaled
0
5
10
15
20
25
0
2
4
6
8
10
5' <-----> 3'
Probe Number

One Replicate Graph

Supp Fig. 8



Pearson and Spearman Correlation Coefficients of Biological Reps

Experiment	P_R1R2	P_R1R3	P_R2R3	S_R1R2	S_R1R3	S_R2R3
WT.Day1	0.989	0.996	0.989	0.985	0.996	0.985
WTH2O2.Day1	0.995	0.996	0.998	0.995	0.996	0.997
Zat.Day1	0.996	0.997	0.996	0.995	0.996	0.996
ZatH2O2.Day1	0.996	0.996	0.996	0.995	0.995	0.996

Supp Table 1

Supp Table 2. Transcripts significantly elevated/suppressed (>2-fold) in wild type plants treated with hydrogen peroxide (20mM, 1h)

Array Element	Locus Identifier	Annotation	log2(WT+/WT)
247949_at	AT5G57220	cytochrome P450, putative similar to Cytochrome P450 (SP:O65790) [Arabidopsis thaliana]; Cytochrome P450 (GI:7415996) [Lotus japonicus]	5.321
261892_at	AT1G80840	WRKY family transcription factor similar to WRKY transcription factor GB:BAA87058 GI:6472585 from [Nicotiana tabacum]	5.31
262518_at	AT1G17170	glutathione S-transferase, putative One of three repeated putativ glutathione transferases. 72% identical to glutathione transferase	5.219
259875_s_at	AT1G76690	[AT1G76690, 12-oxophytodienoate reductase (OPR2) identical to 1 oxophytodienoate reductase OPR2 GB:AAC78441 [Arabidopsis	5.01
261450_s_at	AT1G21120	[AT1G21120, O-methyltransferase, putative similar to GI:2781394];[AT1G21110, O-methyltransferase, putative similar to	4.99
265499_at	AT2G15480	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	4.975
250296_at	AT5G12020	17.6 kDa class II heat shock protein (HSP17.6-CII) identical to 17.6 kDa class II heat shock protein SP:P29830 from [Arabidopsis thaliana]	4.89
262911_s_at	AT1G59860	17.6 kDa class I heat shock protein (HSP17.6A-CI) similar to 17.5 kDa class I heat shock protein SP:P04793 from [Glycine max]	4.729
250781_at	AT5G05410	DRE-binding protein (DREB2A) identical to DREB2A GI:3738230 from [Arabidopsis thaliana] ; supported by	4.586
261648_at	AT1G27730	zinc finger (C2H2 type) family protein (ZAT10) / salt-tolerance zinc finge protein (STZ) identical to salt-tolerance zinc finger protein GB:CAA64820	4.55
254343_at	AT4G21990	5'-adenylylsulfate reductase (APR3) / PAPS reductase homolog (PRH26 identical to 5'-adenylylsulfate reductase [Arabidopsis thaliana] GI:2738760;	4.546
253046_at	AT4G37370	cytochrome P450, putative similar to Cytochrome P450 91A1 (SP:Q9FG65)[Arabidopsis thaliana]; cytochrome P450, Glycyrrhiza	4.538
255284_at	AT4G04610	5'-adenylylsulfate reductase (APR1) / PAPS reductase homolog (PRH19 identical to 5'-adenylylsulfate reductase [Arabidopsis thaliana] GI:2738756;	4.508
263182_at	AT1G05575	expressed protein	4.461
255543_at	AT4G01870	tolB protein-related contains weak similarity to TolB protein precurso (Swiss-Prot:P44677) [Haemophilus influenzae]	4.405
245250_at	AT4G17490	ethylene-responsive element-binding protein, putative similar t SP|O80341 Ethylene responsive element binding factor 5 (AtERF5)	4.376
249719_at	AT5G35735	auxin-responsive family protein similar to auxin-induced protein AIR1 GI:11357190 [Arabidopsis thaliana]	4.364
258133_at	AT3G24500	ethylene-responsive transcriptional coactivator, putative similar to ethylen responsive transcriptional coactivator [Lycopersicon esculentum]	4.249
260248_at	AT1G74310	heat shock protein 101 (HSP101) identical to heat shock protein 101 GI:6715468 GB:AAF26423 from [Arabidopsis thaliana]	4.241
266294_at	AT2G29500	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,	4.234
256245_at	AT3G12580	heat shock protein 70, putative / HSP70, putative strong similarity to hea shock protein GI:425194 [Spinacia oleracea]	4.094
266590_at	AT2G46240	IQ domain-containing protein / BAG domain-containing protein contains Pfam profiles PF00612: IQ calmodulin-binding motif, PF02179: BAG	4.09
261449_at	AT1G21120	O-methyltransferase, putative similar to GI:2781394	4.089
248332_at	AT5G52640	heat shock protein 81-1 (HSP81-1) / heat shock protein 83 (HSP83) nearl identical to SP|P27323 Heat shock protein 81-1 (HSP81-1) (Heat shock	4.085
260978_at	AT1G53540	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-	4.078
245711_at	AT5G04340	zinc finger (C2H2 type) family protein contains Pfam domain, PF00096: Zinc finger, C2H2 type	3.957
261838_at	AT1G16030	heat shock protein 70, putative / HSP70, putative similar to heat shock protein hsp70 GI:1771478 from [Pisum sativum]	3.948
261021_at	AT1G26380	FAD-binding domain-containing protein similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE)	3.921
250182_at	AT5G14470	GHMP kinase-related contains similarity to D-glycero-D-manno-heptose phosphate kinase [Aneurinibacillus thermoaerophilus]	3.841
260602_at	AT1G55920	serine O-acetyltransferase, putative identical to GI:608677 fro [Arabidopsis thaliana]	3.82
262517_at	AT1G17180	glutathione S-transferase, putative Second of three repeated putativ glutathione transferases. 72% identical to glutathione transferase	3.796
256589_at	AT3G28730	[AT3G28730, structure-specific recognition protein 1 / high mobility group protein / HMG protein nearly identical to SP|Q05153 Structure-specific	3.756
267028_at	AT2G38470	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain;	3.724

248381_at	AT5G51830	pfkB-type carbohydrate kinase family protein contains Pfam profile PF00294 pfkB family carbohydrate kinase	3.717
254204_at	AT4G24160	hydrolase, alpha/beta fold family protein contains Pfam profile PF00561 hydrolase, alpha/beta fold family	3.71
250351_at	AT5G12030	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]	3.698
245041_at	AT2G26530	expressed protein	3.671
247351_at	AT5G63790	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; contains similarity to NAC-domain protein	3.67
248434_at	AT5G51440	23.5 kDa mitochondrial small heat shock protein (HSP23.5-M) similar to heat shock 22 kDa protein, mitochondrial precursor SP:Q96331 from	3.645
263150_at	AT1G54050	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	3.644
259479_at	AT1G19020	expressed protein	3.634
260406_at	AT1G69920	glutathione S-transferase, putative similar to glutathione transferas GB:CAA09188 [Alopecurus myosuroides]; supported by cDNA	3.632
254331_s_at	AT4G22710	[AT4G22710, cytochrome P450 family protein contains Pfam profile: PF00067 cytochrome p450];[AT4G22690, cytochrome P450 family protein	3.609
246099_at	AT5G20230	plastocyanin-like domain-containing protein	3.519
252515_at	AT3G46230	[AT3G46230, 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	3.517
257206_at	AT3G16530	legume lectin family protein contains Pfam domain, PF00139: Legume lectins beta domain	3.476
246858_at	AT5G25930	leucine-rich repeat family protein / protein kinase family protein contains similarity to Swiss-Prot:P47735 receptor-like protein kinase 5 precursor	3.452
261459_at	AT1G21100	[AT1G21100, O-methyltransferase, putative similar to GI:2781394];[AT1G21130, O-methyltransferase, putative similar to	3.438
248657_at	AT5G48570	peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative similar to rof1 [Arabidopsis thaliana] GI:1373396	3.415
259979_at	AT1G76600	expressed protein	3.359
249494_at	AT5G39050	transferase family protein similar to anthocyanin 5-aromatic acyltransferas from Gentiana triflora GI:4185599, malonyl CoA:anthocyanin 5-O-	3.357
253268_s_at	AT4G34135	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	3.356
252265_at	AT3G49620	2-oxoacid-dependent oxidase, putative (DIN11) identical to partial cds of oxoacid-dependent oxidase (din11) from GI:10834554 [Arabidopsis	3.345
263184_at	AT1G05560	UDP-glucose transferase (UGT75B2) similar to UDP-glucose:indole-3 acetate beta-D-glucosyltransferase GI:2149127 from (Arabidopsis	3.345
263231_at	AT1G05680	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	3.33
262381_at	AT1G72900	disease resistance protein (TIR-NBS class), putative domain signature TIR NBS exists, suggestive of a disease resistance protein.	3.235
259037_at	AT3G09350	armadillo/beta-catenin repeat family protein contains Pfam profile PF00514 armadillo/beta-catenin-like repeat	3.216
263931_at	AT2G36220	expressed protein	3.214
248134_at	AT5G54860	integral membrane transporter family protein contains 10 transmembrane domains; contains Pfam PF03092: BT1 family; contains TIGRFAMS	3.196
266800_at	AT2G22880	[AT2G22880, VQ motif-containing protein contains PF05678: VQ motif];[AT2G22870, expressed protein]	3.172
245252_at	AT4G17500	ethylene-responsive element-binding protein 1 (ERF1) / EREBP-2 protein identical to SP|O80337 Ethylene responsive element binding factor 1	3.169
246584_at	AT5G14730	expressed protein	3.159
263379_at	AT2G40140	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,	3.081
245038_at	AT2G26560	patatin, putative similar to patatin-like latex allergen [Hevea brasiliensis][PMID:10589016]; contains patatin domain PF01734	3.057
256576_at	AT3G28210	zinc finger (AN1-like) family protein contains Pfam profile: PF01428 AN1 like zinc finger	3
265075_at	AT1G55450	embryo-abundant protein-related similar to embryo-abundant protein GI:1350531 from [Picea glauca]	2.992
254256_at	AT4G23180	receptor-like protein kinase 4, putative (RLK4) nearly identical to recepto like protein kinase 4 [Arabidopsis thaliana] GI:13506745; contains Pfam	2.957
251745_at	AT3G55980	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,	2.955

263475_at	AT2G31945	expressed protein	2.951
266296_at	AT2G29420	glutathione S-transferase, putative	2.945
254926_at	AT4G11280	1-aminocyclopropane-1-carboxylate synthase 6 / ACC synthase 6 (ACS6 identical to GI:3746125	2.923
262119_s_at	AT1G02920	[AT1G02920, glutathione S-transferase, putative similar to glutathione S transferase GI:860955 from [Hyoscyamus muticus]; supported by cDNA	2.922
263866_at	AT2G36950	heavy-metal-associated domain-containing protein nearly identical to farnesylated protein ATFP2 [GI:4097545] Pfam profile PF00403: Heavy-	2.916
265501_at	AT2G15490	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	2.91
244940_at	ATCG00900	[ATCG00900, rps7.1 ribosomal protein S12];[ATCG00905, rps12c rps12.3];[ATCG01230, rps12b rps12.2];[ATCG00065, rps12a rps12.1]	2.906
254432_at	AT4G20830	FAD-binding domain-containing protein similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE)	2.895
244992_s_at	ATCG01240	rps7.2 ribosomal protein S7	2.873
249575_at	AT5G37670	15.7 kDa class I-related small heat shock protein-like (HSP15.7-CI) contains Pfam profile: PF00011 Hsp20/alpha crystallin family; identified in	2.85
260411_at	AT1G69890	expressed protein contains Pfam profile: PF04601 protein of unknown function (DUF569	2.844
247573_at	AT5G61160	transferase family protein similar to anthocyanin 5-aromatic acyltransferas from Gentiana triflora GI:4185599, malonyl CoA:anthocyanin 5-O-	2.829
244962_at	ATCG01050	ndhD NADH dehydrogenase ND4	2.828
264758_at	AT1G61340	F-box family protein contains Pfam PF00646: F-box domain; similar to late embryogenesis abundant protein GI:1350540 from [Picea glauca]	2.822
254120_at	AT4G24570	mitochondrial substrate carrier family protein contains Pfam profile PF00153 mitochondrial carrier protein	2.802
259445_at	AT1G02400	gibberellin 2-oxidase, putative / GA2-oxidase, putative similar to GA2ox2 [GI:4678368]; similar to dioxygenase GI:1666096 from [Marah	2.798
265200_s_at	AT2G36790	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	2.796
244965_at	ATCG00590	orf31 hypothetical protein	2.792
267083_at	AT2G41100	touch-responsive protein / calmodulin-related protein 3, touch-induced (TCH3) identical to calmodulin-related protein 3, touch-induced	2.791
259705_at	AT1G77450	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to GRAB1 protein GB:CAA09371,	2.783
250449_at	AT5G10830	embryo-abundant protein-related similar to embryo-abundant protein [Picea glauca] GI:1350531	2.77
245007_at	ATCG00350	psaA PSI P700 apoprotein A1	2.737
247047_at	AT5G66650	expressed protein contains Pfam domain, PF04678: Protein of unknown function, DUF607	2.729
257536_at	AT3G02800	tyrosine specific protein phosphatase family protein contains tyrosine specific protein phosphatases active site, PROSITE:PS00383	2.716
245731_at	AT1G73500	mitogen-activated protein kinase kinase (MAPKK), putative (MKK9) mitogen-activated protein kinase kinase (MAPKK) family, PMID:12119167	2.708
250670_at	AT5G06860	polygalacturonase inhibiting protein 1 (PGIP1) identical to polygalacturonase inhibiting protein 1 (PGIP1) [Arabidopsis thaliana]	2.708
263800_at	AT2G24600	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023	2.69
258786_at	AT3G11820	syntaxin 121 (SYP121) / syntaxin-related protein (SYR1) contains Pfam profiles: PF00804 syntaxin and PF05739: SNARE domain; identical to	2.689
246744_at	AT5G27760	hypoxia-responsive family protein contains Pfam profile: PF04588 hypoxia induced protein conserved region	2.685
255733_at	AT1G25400	expressed protein similar to unknown protein GI:6714347 from [Arabidopsis thaliana]	2.659
264746_at	AT1G62300	WRKY family transcription factor similar to putative DNA-binding protein GI:7268215 from [Arabidopsis thaliana]	2.658
253643_at	AT4G29780	expressed protein	2.643
261564_at	AT1G01720	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAC domain protein NAM	2.626
245254_at	AT4G14680	sulfate adenylyltransferase 3 / ATP-sulfurylase 3 (APS3) identical to ATP sulfurylase (APS3) [Arabidopsis thaliana] GI:1575327	2.59
248448_at	AT5G51190	AP2 domain-containing transcription factor, putative contains similarity to ethylene responsive element binding factor	2.569

250054_at	AT5G17860	cation exchanger, putative (CAX7) contains similarity to SWISS- PROT:Q9HC58 NKX3_HUMAN Sodium/potassium/calcium exchanger 3	2.567
245765_at	AT1G33600	leucine-rich repeat family protein contains leucine rich-repeat (LRR domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to	2.544
248607_at	AT5G49480	sodium-inducible calcium-binding protein (ACP1) / sodium-responsive calcium-binding protein (ACP1) identical to NaCl-inducible Ca2+-binding	2.543
249078_at	AT5G44070	phytochelatin synthase 1 (PCS1) identical to phytochelatin synthase [Arabidopsis thaliana] gi|18254401|gb|AAL66747; identical to cDNA	2.538
253414_at	AT4G33050	calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif	2.537
263935_at	AT2G35930	U-box domain-containing protein similar to immediate-early fungal elicito protein CMPG1 [Petroselinum crispum] GI:14582200; contains Pfam	2.534
246463_at	AT5G16970	NADP-dependent oxidoreductase, putative (P1) identical to probable NADP-dependent oxidoreductase P1, zeta-crystallin homolog	2.523
245003_at	ATCG00280	psbC PSII 43 KDa protein	2.515
258507_at	AT3G06500	beta-fructofuranosidase, putative / invertase, putative / saccharase putative / beta-fructosidase, putative similar to neutral invertase [Daucus	2.504
247543_at	AT5G61600	ethylene-responsive element-binding family protein contains similarity to ethylene responsive element binding factor 5 (AtERF5) (Swiss-	2.503
245193_at	AT1G67810	Fe-S metabolism associated domain-containing protein contains Pfam PF02657: Fe-S metabolism associated domain	2.501
262571_at	AT1G15430	expressed protein	2.496
251774_at	AT3G55830	[AT3G55830, glycosyltransferase family protein 47 similar to exostose related protein 2, Homo sapiens, PIR:JC5935 [SP|Q93063], EXTL2, Mus	2.492
254784_at	AT4G12720	MutT/nudix family protein similar to SP|P53370 Nucleoside diphosphate linked moiety X motif 6 {Homo sapiens}; contains Pfam profile PF00293:	2.491
254318_at	AT4G22530	embryo-abundant protein-related similar to embryo-abundant protein [Picea glauca] GI:1350531	2.48
249983_at	AT5G18470	curculin-like (mannose-binding) lectin family protein contains Pfam profile: PF01453 lectin (probable mannose binding)	2.47
253628_at	AT4G30280	[AT4G30280, xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	2.469
265221_s_at	AT2G02010	[AT2G02010, glutamate decarboxylase, putative strong similarity to glutamate decarboxylase isozyme 3 [Nicotiana tabacum]	2.463
267357_at	AT2G40000	expressed protein	2.461
261023_at	AT1G12200	flavin-containing monooxygenase family protein / FMO family protein low similarity to FMO2 from Homo sapiens [SP|Q99518]; contains Pfam	2.456
245025_at	ATCG00130	atpF ATPase I subunit	2.442
262374_s_at	AT1G72910	[AT1G72910, disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance	2.436
254605_at	AT4G18950	ankyrin protein kinase, putative similar to ankyrin-kinase [Medicago truncatula] gi|18700701|gb|AAL78674	2.432
246631_at	AT1G50740	expressed protein contains Pfam profile PF03647: Uncharacterised protein family (UPF0136)	2.419
244973_at	ATCG00690	psbT PSII T protein	2.418
260405_at	AT1G69930	glutathione S-transferase, putative similar to glutathione transferase GB:CAA09188 [Alopecurus myosuroides]	2.416
262656_at	AT1G14200	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile PF00097 zinc finger, C3HC4 type (RING finger)	2.399
253284_at	AT4G34150	C2 domain-containing protein similar to calcium-dependent protein kinase [Dunaliella tertiolecta] GI:6644464; contains Pfam profile PF00168: C2	2.398
263374_at	AT2G20560	DNAJ heat shock family protein SP|Q9UDY4 DnaJ homolog subfamily B member 4 (Heat shock 40 kDa protein 1 homolog) {Homo sapiens};	2.38
247693_at	AT5G59730	exocyst subunit EXO70 family protein leucine zipper-containing protein Lycopersicon esculentum, PIR:S21495 contains Pfam domain PF03081:	2.374
258282_at	AT3G26910	hydroxyproline-rich glycoprotein family protein common family member:At2g33490 [Arabidopsis thaliana]	2.37
253827_at	AT4G28085	expressed protein	2.356
248164_at	AT5G54490	calcium-binding EF-hand protein, putative similar to EF-hand Ca2+ binding protein CCD1 [Triticum aestivum] GI:9255753; contains	2.33
248799_at	AT5G47230	ethylene-responsive element-binding factor 5 (ERF5) identical to SP|O80341 Ethylene responsive element binding factor 5 (AtERF5)	2.327
252671_at	AT3G44190	pyridine nucleotide-disulphide oxidoreductase family protein low similarity to dihydrolipoamide dehydrogenase from Clostridium magnum	2.316

247655_at	AT5G59820	zinc finger (C2H2 type) family protein (ZAT12) identical to zinc finger protein ZAT12 [Arabidopsis thaliana] gi|1418325|emb|CAA67232	2.313
252976_s_at	AT4G38550	expressed protein	2.305
254211_at	AT4G23570	phosphatase-related low similarity to phosphoprotein phosphatase [Mu musculus] GI:567040; contains Pfam profiles PF00515: TPR Domain,	2.299
256017_at	AT1G19180	expressed protein	2.297
245662_at	AT1G28190	expressed protein	2.278
252592_at	AT3G45640	mitogen-activated protein kinase, putative / MAPK, putative (MPK3) identical to mitogen-activated protein kinase homolog	2.276
262935_at	AT1G79410	transporter-related low similarity to organic anion transporter 3 [Rattu norvegicus] GI:5545293; contains Pfam profile PF00083: major facilitator	2.268
245369_at	AT4G15975	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)	2.263
253915_at	AT4G27280	calcium-binding EF hand family protein similar to EF-hand Ca2+-binding protein CCD1 [Triticum aestivum] GI:9255753; contains	2.245
265670_s_at	AT2G32210	expressed protein	2.242
246289_at	AT3G56880	VQ motif-containing protein contains PF05678: VQ motif	2.24
245006_at	ATCG00340	psaB PSI P700 apoprotein A2	2.237
246464_at	AT5G16990	[AT5G16990, NADP-dependent oxidoreductase, putative strong similarity to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1	2.234
253664_at	AT4G30210	NADPH-cytochrome p450 reductase, putative / NADPH-ferrihemoprotei reductase, putative similar to NADPH-cytochrome P450 oxydoreductase	2.224
266737_at	AT2G47140	short-chain dehydrogenase/reductase (SDR) family protein similar to beta-hydroxysteroiddehydrogenase GI:15983819 from [Digitalis lanata]	2.219
260592_at	AT1G55850	cellulose synthase family protein similar to cellulose synthase catalyti subunit [gi:13925881] from Nicotiana alata, cellulose synthase-5	2.208
266368_at	AT2G41380	embryo-abundant protein-related similar to embryo-abundant protei [Picea glauca] GI:1350531	2.185
246293_at	AT3G56710	sigA-binding protein identical to SigA binding protein [Arabidopsis thaliana gi|6980074|gb|AAF34713; contains Pfam PF05678: VQ motif	2.184
252908_at	AT4G39670	expressed protein	2.184
260025_at	AT1G30070	SGS domain-containing protein similar to calcyclin binding protein [Mus musculus] GI:3142331; contains Pfam profile PF05002: SGS domain	2.179
266983_at	AT2G39400	hydrolase, alpha/beta fold family protein similar to monoglyceride lipas from [Homo sapiens] GI:14594904, [Mus musculus] GI:2632162; contains	2.179
256835_at	AT3G22890	sulfate adenylyltransferase 1 / ATP-sulfurylase 1 (APS1) nearly identical t ATP sulfurylase (APS1) [Arabidopsis thaliana] GI:6606509	2.176
259879_at	AT1G76650	calcium-binding EF hand family protein similar to regulator of gene silencing calmodulin-related protein GI:12963415 from [Nicotiana	2.169
264365_s_at	AT1G03220	[AT1G03220, extracellular dermal glycoprotein, putative / EDGP, putative similar to extracellular dermal glycoprotein EDGP precursor [Daucus	2.168
257918_at	AT3G23230	ethylene-responsive factor, putative similar to EREBP-4 GB:BAA0732 from [Nicotiana tabacum]	2.16
244975_at	ATCG00710	psbH PSII 10KDa phosphoprotein	2.158
245026_at	ATCG00140	atpH ATPase III subunit	2.155
249918_at	AT5G19240	expressed protein	2.154
262383_at	AT1G72940	disease resistance protein (TIR-NBS class), putative domain signature TI NBS exists, suggestive of a disease resistance protein.	2.152
246270_at	AT4G36500	expressed protein	2.151
257670_at	AT3G20340	expressed protein	2.142
266010_at	AT2G37430	zinc finger (C2H2 type) family protein (ZAT11) contains Pfam domain, PF00096: Zinc finger, C2H2 type	2.141
245024_at	ATCG00120	atpA ATPase alpha subunit	2.135
246018_at	AT5G10695	expressed protein	2.119
246777_at	AT5G27420	zinc finger (C3HC4-type RING finger) family protein similar to RING-H2 zinc finger protein ATL6 [Arabidopsis thaliana]	2.114

246034_at	AT5G08350	GRAM domain-containing protein / ABA-responsive protein-relatec contains similarity to ABA-responsive protein in barley (GI:4103635)	2.109
254549_at	AT4G19880	glutathione S-transferase-related contains weak hit to Pfam profile PF00043: Glutathione S-transferase, C-terminal domain	2.105
245277_at	AT4G15550	UDP-glucose:indole-3-acetate beta-D-glucosyltransferase (IAGLU identical to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase	2.102
244972_at	ATCG00680	psbB PSII 47KDa protein	2.068
260915_at	AT1G02660	lipase class 3 family protein contains Pfam profile PF01764: Lipase	2.068
261748_at	AT1G76070	expressed protein	2.065
255622_at	AT4G01070	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfan profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	2.061
265675_at	AT2G32120	heat shock protein 70 family protein / HSP70 family protein similar to SP|P22953 Heat shock cognate 70 kDa protein 1 (Hsc70.1) {Arabidopsis	2.061
254759_at	AT4G13180	short-chain dehydrogenase/reductase (SDR) family protein similar to shor chain type dehydrogenase/reductase SP:Q08632 [Picea abies]	2.052
262649_at	AT1G14040	EXS family protein / ERD1/XPR1/SYG1 family protein similar to PHO1 protein [Arabidopsis thaliana] GI:20069032; contains Pfam profiles	2.046
257751_at	AT3G18690	[AT3G18690, VQ motif-containing protein contains PF05678: VQ motif];[AT3G18680, aspartate/glutamate/uridylate kinase family protein	2.043
260126_at	AT1G36370	glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative	2.043
253535_at	AT4G31550	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain	2.035
264153_at	AT1G65390	disease resistance protein (TIR class), putative domain signature TIF exists, suggestive of a disease resistance protein.	2.028
248794_at	AT5G47220	ethylene-responsive element-binding factor 2 (ERF2) identical tc SP|O80338 Ethylene responsive element binding factor 2 (AtERF2)	2.015
264314_at	AT1G70420	expressed protein	2.014
250550_at	AT5G07870	transferase family protein similar to anthranilate N hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus [gi:2239091];	2.013
251884_at	AT3G54150	embryo-abundant protein-related similar to embryo-abundant proteir [Picea glauca] GI:1350531	2.012
244961_at	ATCG01040	ycf5 hypothetical protein	2.01
249459_at	AT5G39580	peroxidase, putative identical to peroxidase ATP24a [Arabidopsis thaliana gi|1890313|emb|CAA72484	2.005
252278_at	AT3G49530	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAC2 - Arabidopsis thaliana,	2.004
248719_at	AT5G47910	respiratory burst oxidase protein D (RbohD) / NADPH oxidase identical t respiratory burst oxidase protein D from Arabidopsis thaliana [gi:3242789]	2
251176_at	AT3G63380	calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+) ATPase, putative (ACA12) identical to SP|Q9LY77 Potential calcium-	2
246532_at	AT5G15870	glycosyl hydrolase family 81 protein similar to beta-glucan-elicitor recepto GI:1752734 from [Glycine max]	1.998
252474_at	AT3G46620	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)	1.996
256453_at	AT1G75270	dehydroascorbate reductase, putative similar to GI:6939839 from [Oryza sativa]	1.984
264745_at	AT1G62180	5'-adenylylsulfate reductase 2, chloroplast (APR2) (APSR) / adenosine 5 phosphosulfate 5'-adenylylsulfate (APS) sulfotransferase 2 / 3'-	1.983
264213_at	AT1G65390	disease resistance protein (TIR class), putative domain signature TIF exists, suggestive of a disease resistance protein.	1.982
255753_at	AT1G18570	myb family transcription factor (MYB51) contains PFAM profile: PF00249	1.974
253606_at	AT4G30530	defense-related protein, putative strong similarity to defense-related protei [Brassica carinata] GI:14009290; contains Pfam profile PF00117:	1.958
254158_at	AT4G24380	expressed protein contains Pfam profile: PF03959 domain of unknowr function (DUF341)	1.95
258336_at	AT3G16050	stress-responsive protein, putative similar to ethylene-inducible proteir HEVER [Hevea brasiliensis] SWISS-PROT:Q39963; contains Pfam	1.945
251061_at	AT5G01830	armadillo/beta-catenin repeat family protein / U-box domain-containinç protein contains Pfam domain, PF00514: Armadillo/beta-catenin-like	1.94
254487_at	AT4G20780	calcium-binding protein, putative similar to SP|Q09011 Calcium-binding protein CAST {Solanum tuberosum}; contains INTERPRO:IPR002048	1.936
266259_at	AT2G27830	expressed protein	1.923

245009_at	ATCG00380	rps4 ribosomal protein S4	1.918
262325_at	AT1G64160	disease resistance-responsive family protein / dirigent family protein simila to dirigent protein GB:AAF25365 GI:6694709 from [Thuja plicata]; similar	1.918
244976_at	ATCG00720	petB cytochrome B6	1.917
247708_at	AT5G59550	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)	1.916
253485_at	AT4G31800	WRKY family transcription factor	1.906
254592_at	AT4G18880	heat shock transcription factor 21 (HSF21) identical to heat shock transcription factor 21 [Arabidopsis thaliana] GI:3399765; contains Pfam	1.904
262072_at	AT1G59590	expressed protein	1.901
258436_at	AT3G16720	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)	1.894
260401_at	AT1G69840	band 7 family protein strong similarity to hypersensitive-induced response protein [Zea mays] GI:7716466; contains Pfam profile PF01145: SPFH	1.889
246612_at	AT5G35320	expressed protein	1.885
251400_at	AT3G60420	expressed protein	1.878
248686_at	AT5G48540	33 kDa secretory protein-related contains Pfam PF01657: Domain o unknown function, duplicated in 33 KDa secretory proteins	1.868
261934_at	AT1G22400	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfan profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	1.868
267300_at	AT2G30140	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfan profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	1.864
264202_at	AT1G22810	AP2 domain-containing transcription factor, putative Contains similarity tc transcription factor (TINY) isolog T02O04.22 gb|2062174 from A. thaliana	1.863
244971_at	ATCG00670	clpP ATP-dependent protease subunit	1.861
247137_at	AT5G66210	calcium-dependent protein kinase family protein / CDPK family proteir contains Pfam domains, PF00069: Protein kinase domain and PF00036:	1.858
247488_at	AT5G61820	expressed protein MtN19, Medicago truncatula, EMBL:MTY15367	1.856
249942_at	AT5G22300	nitrilase 4 (NIT4) identical to SP|P46011 Nitrilase 4 (EC 3.5.5.1) {Arabidopsis thaliana}	1.855
260243_at	AT1G63720	expressed protein similar to putative protein GB:CAA18164 [Arabidopsis thaliana]	1.847
245528_at	AT4G15530	pyruvate phosphate dikinase family protein contains Pfam profiles PF01326 pyruvate phosphate dikinase, PEP/pyruvate binding domain,	1.834
256337_at	AT1G72060	expressed protein	1.831
251937_at	AT3G53400	expressed protein	1.819
248981_at	AT5G45110	ankyrin repeat family protein / BTB/POZ domain-containing proteir contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain,	1.817
258207_at	AT3G14050	RelA/SpoT protein, putative (RSH2) nearly identical to RelA/SpoT homolo RSH2 [Arabidopsis thaliana] GI:7141306; contains Pfam profiles PF01966	1.816
266658_at	AT2G25735	expressed protein	1.815
245866_s_at	AT1G57990	[AT1G57990, purine permease-related low similarity to purine permease [Arabidopsis thaliana] GI:7620007; contains Pfam profile PF03151:	1.814
261718_at	AT1G18390	protein kinase family protein contains protein kinase domain Pfam:PF00069	1.807
265841_at	AT2G35710	glycogenin glucosyltransferase (glycogenin)-related low similarity tc glycogenin-2 from Homo sapiens [SP|O15488]	1.806
259272_at	AT3G01290	band 7 family protein similar to hypersensitive-induced response proteir [Zea mays] GI:7716470; contains Pfam profile PF01145: SPFH domain /	1.8
247279_at	AT5G64310	arabinogalactan-protein (AGP1) identical to gi:3883120 gb:AAC77823	1.791
255502_at	AT4G02410	lectin protein kinase family protein contains Pfam domains, PF00069: Protein kinase domain, PF00139: Legume lectins beta domain and	1.79
AFFX-Athal-25SrRNA_s_at			1.789
246870_at	AT5G26030	ferrochelatase I identical to Swiss-Prot:P42043 ferrochelatase I chloroplast/mitochondrial precursor (EC 4.99.1.1) (Protoheme ferro-lyase)	1.788
264299_s_at	AT1G78860	curculin-like (mannose-binding) lectin family protein low similarity to Ser/Thr protein kinase [Zea mays] GI:2598067; contains Pfam profile	1.786

251636_at	AT3G57530	calcium-dependent protein kinase, putative / CDPK, putative similar to calmodulin-domain protein kinase CDPK isoform 7 [Arabidopsis thaliana]	1.782
251144_at	AT5G01210	transferase family protein contains Pfam profile PF02458 transferase family	1.78
266841_at	AT2G26150	heat shock transcription factor family protein contains Pfam profile PF00447 HSF-type DNA-binding domain	1.772
251507_at	AT3G59080	aspartyl protease family protein contains similarity to CND41, chloroplas nucleoid DNA binding protein (GI:2541876) [Nicotiana tabacum]; contains	1.768
259312_at	AT3G05200	zinc finger (C3HC4-type RING finger) family protein (ATL6) contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)	1.755
256442_at	AT3G10930	expressed protein	1.752
258792_at	AT3G04640	glycine-rich protein predicted proteins, Arabidopsis thaliana	1.751
264655_at	AT1G09070	C2 domain-containing protein / src2-like protein, putative similar to cold regulated gene SRC2 [Glycine max] GI:2055230; contains Pfam profile	1.747
261445_at	AT1G28380	expressed protein	1.746
254200_at	AT4G24110	expressed protein	1.742
263478_at	AT2G31880	[AT2G31880, leucine-rich repeat transmembrane protein kinase, putative];[AT2G31890, expressed protein]	1.74
265199_s_at	AT2G36770	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfan profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	1.729
246305_at	AT3G51890	expressed protein protein At2g40060 - Arabidopsis thaliana EMBL:AF002109	1.727
253203_at	AT4G34710	arginine decarboxylase 2 (SPE2) identical to SP|O23141 Arginine decarboxylase 2 (EC 4.1.1.19) (ARGDC 2) (ADC 2) (ADC-N) {Arabidopsis	1.726
245048_at	ATCG00040	matK hypothetical protein	1.724
264624_at	AT1G08930	early-responsive to dehydration stress protein (ERD6) / sugar transporte family protein identical to ERD6 protein {Arabidopsis thaliana} GI:3123712	1.724
266017_at	AT2G18690	expressed protein	1.707
261526_at	AT1G14380	[AT1G14380, calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif];[AT1G14370, protein kinase	1.705
265725_at	AT2G32030	GCN5-related N-acetyltransferase (GNAT) family protein contains Pfan profile PF00583: acetyltransferase, GNAT family	1.69
244983_at	ATCG00790	rpl16 ribosomal protein L16	1.684
245051_at	AT2G23320	WRKY family transcription factor identical to WRKY DNA-binding protein 15 GI:13506742 from [Arabidopsis thaliana]	1.684
265184_at	AT1G23710	expressed protein	1.684
261719_at	AT1G18380	expressed protein	1.683
260974_at	AT1G53430	[AT1G53430, leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich Repeat and	1.679
266461_at	AT2G47730	glutathione S-transferase 6 (GST6) identical to GB:X95295. Based or identical cDNA hits, the translation is now 40 AAs longer at the N-terminal,	1.673
248964_at	AT5G45340	cytochrome P450 family protein similar to SP|Q42569|C901_ARATH Cytochrome P450 90A1 (SP:Q42569) [Arabidopsis thaliana]; contains	1.672
248162_at	AT5G54500	quinone reductase, putative similar to 1,4-benzoquinone reductase [Phanerochaete chrysosporium][GI:4454993]; contains flavodoxin domain	1.665
254408_at	AT4G21390	S-locus lectin protein kinase family protein contains Pfam profiles PF00954 S-locus glycoprotein family, PF00069 protein kinase domain,	1.664
249417_at	AT5G39670	[AT5G39670, calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain];[AT5G39680,	1.663
257654_at	AT3G13310	DNAJ heat shock N-terminal domain-containing protein similar to J11 protein [Arabidopsis thaliana] GI:9843641; contains Pfam profile: PF0022	1.66
267337_at	AT2G39980	transferase family protein contains Pfam profile PF02458 transferase family	1.657
254839_at	AT4G12400	stress-inducible protein, putative similar to sti (stress inducible protein) [Glycine max] GI:872116; contains Pfam profile PF00515 TPR Domain	1.65
251342_at	AT3G60690	auxin-responsive family protein similar to auxin-induced protein SAUR-AC (GP:546362) (PIR:T06084)[Arabidopsis thaliana] PIR:T06084	1.648
253859_at	AT4G27657	expressed protein	1.645
253332_at	AT4G33420	peroxidase, putative identical to class III peroxidase ATP32 [Arabidopsis thaliana] gi|17530547|gb|AAL40837; identical to cDNA class III peroxidase	1.639

248327_at	AT5G52750	heavy-metal-associated domain-containing protein Pfam profile PF00403 Heavy-metal-associated domain	1.63
245047_at	ATCG00020	psbA PSII 32 KDa protein	1.629
263403_at	AT2G04040	MATE efflux family protein contains Pfam profile: PF01554 uncharacterized membrane protein family	1.628
245002_at	ATCG00270	psbD PSII D2 protein	1.626
254042_at	AT4G25810	xyloglucan:xyloglucosyl transferase, putative / xyloglucai endotransglycosylase, putative / endo-xyloglucan transferase, putative	1.626
245768_at	AT1G33590	disease resistance protein-related / LRR protein-related contains leucin rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to	1.625
262505_at	AT1G21680	expressed protein similar to TolB protein precursor (SP:Q9ZDM5 {Rickettsia prowazekii}; ESTs gb|N96028, gb|F14286, gb|T20680,	1.624
260477_at	AT1G11050	protein kinase family protein contains protein kinase domain Pfam:PF00069	1.623
250826_at	AT5G05220	expressed protein	1.622
260556_at	AT2G43620	chitinase, putative similar to basic endochitinase CHB4 precursoı SP:Q06209 from [Brassica napus]	1.621
250676_at	AT5G06320	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein / NDR1/HIN1-like protein 3 similar to harpin-induced protein	1.62
260656_at	AT1G19380	expressed protein	1.617
261143_at	AT1G19770	purine permease-related low similarity to purine permease [Arabidopsi thaliana] GI:7620007; contains Pfam profile PF03151: Domain of unknowr	1.612
267623_at	AT2G39650	expressed protein contains Pfam profile PF04720: Protein of unknowr function (DUF506)	1.611
249835_s_at	AT5G23490	[AT5G23490, expressed protein];[AT5G23510, expressed protein]	1.61
253884_at	AT4G27670	25.3 kDa small heat shock protein, chloroplast precursor (HSP25.3-P identical to small heat shock protein, chloroplast precursor SP:P31170	1.606
256433_at	AT3G10985	wound-responsive protein-related similar to SP|P20144 Wound-inducec protein 1 {Solanum tuberosum}	1.603
258921_at	AT3G10500	no apical meristem (NAM) family protein similar to to NAC2 (GI:645671) [Arabidopsis thaliana]; contains Pfam PF02365: No apical meristem	1.595
245788_at	AT1G32120	expressed protein contains Pfam profile PF04819: Family of unknowr function (DUF716) (Plant viral-response family)	1.586
262503_at	AT1G21670	expressed protein similar to TolB protein precursor (SP:P50601 {Pseudomonas aeruginosa}	1.576
256044_at	AT1G07160	protein phosphatase 2C, putative / PP2C, putative similar to proteir phosphatase 2C GI:2582800 from [Medicago sativa]	1.574
264663_at	AT1G09970	leucine-rich repeat transmembrane protein kinase, putative Similar to A thaliana receptor-like protein kinase (gb|RLK5_ARATH). ESTs	1.573
258395_at	AT3G15500	no apical meristem (NAM) family protein (NAC3) identical to AtNAC3 [Arabidopsis thaliana] GI:12060424; contains Pfam PF02365: No apical	1.565
261344_at	AT1G79710	integral membrane transporter family protein similar to high affinity folic acid/methotrexate transporter 5 (GI:21898554) [Leishmania tarentolae];	1.564
248205_at	AT5G54300	expressed protein contains similarity to cotton fiber expressed protein [Gossypium hirsutum] gi|3264828|gb|AAC33276	1.558
263823_s_at	AT2G40350	AP2 domain-containing transcription factor, putative (DREB2) similar to DREB2A (GP:3738230) and DREB2B (GP:3738232) [Arabidopsis	1.558
247433_at	AT5G62540	ubiquitin-conjugating enzyme 3 (UBC3) E2; identical to gi:431261, SP:P42746	1.556
261650_at	AT1G27770	calcium-transporting ATPase 1, plasma membrane-type / Ca(2+)-ATPase isoform 1 (ACA1) / plastid envelope ATPase 1 (PEA1) identical to	1.555
246108_at	AT5G28630	glycine-rich protein	1.551
265572_at	AT2G28210	carbonic anhydrase family protein similar to storage protein (dioscorin [Dioscorea cayenensis] GI:433463; contains Pfam profile PF00194:	1.551
247811_at	AT5G58430	exocyst subunit EXO70 family protein leucine zipper-containing protein Lycopersicon esculentum, PIR:S21495; contains Pfam domain PF03081:	1.547
248330_at	AT5G52810	ornithine cyclodeaminase/mu-crystallin family protein contains Pfam PF02423: Ornithine cyclodeaminase/mu-crystallin family	1.547
259297_at	AT3G05360	disease resistance family protein / LRR family protein contains leucine rich repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to elicitor-	1.541
255811_at	AT4G10250	22.0 kDa ER small heat shock protein (HSP22.0-ER) identical to endomembrane-localized small heat shock protein GI:511795 from	1.534
248564_at	AT5G49700	DNA-binding protein-related contains Pfam domain PF03479: Domain oı unknown function (DUF296), found in AT-hook motifs Pfam:PF02178	1.53

266364_at	AT2G41230	expressed protein	1.522
247679_at	AT5G59540	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar t desacetoxyvindoline-4-hydroxylase [Catharanthus roseus] GI:2352812;	1.511
260399_at	AT1G72520	lipoxygenase, putative similar to lipoxygenase gi:1495804 [Solanu tuberosum], gi:1654140 [Lycopersicon esculentum], GB:CAB56692	1.509
244996_at	ATCG00160	rps2 ribosomal protein S2	1.508
247283_at	AT5G64250	2-nitropropane dioxygenase family / NPD family contains Pfam profil PF03060: oxidoreductase, 2-nitropropane dioxygenase (NPD) family	1.501
253911_at	AT4G27300	S-locus protein kinase, putative similar to receptor protein kinase [Ipomoe trifida] gi|836954|gb|AAC23542; contains S-locus glycoprotein family	1.501
257700_at	AT3G12740	LEM3 (ligand-effect modulator 3) family protein / CDC50 family protei Similar to GI:4585976; GI:4966357; GI:4835763; GI:9757735 from	1.501
258682_at	AT3G08720	serine/threonine protein kinase (PK19) identical to serine/threonine-protei kinase AtPK19 (Ribosomal-protein S6 kinase homolog) [Arabidopsis	1.5
261177_at	AT1G04770	male sterility MS5 family protein similar to male sterility MS5 [Arabidopsis thaliana] GI:3859112; contains Pfam profile PF00515 TPR Domain	1.496
248606_at	AT5G49450	bZIP family transcription factor similar to bZIP transcription factor GI:1769891 from [Arabidopsis thaliana]	1.493
253125_at	AT4G36040	DNAJ heat shock N-terminal domain-containing protein (J11) identical t dnaJ heat shock protein J11 [Arabidopsis thaliana] GI:9843641; contains	1.493
247272_at	AT5G64300	riboflavin biosynthesis protein, putative (RIBA) similar to SP|P47924 {Arabidopsis thaliana}, SP|P51695 Riboflavin biosynthesis protein ribA	1.491
254694_at	AT4G17900	zinc-binding family protein similar to zinc-binding protein [Pisum sativum] GI:16117799; contains Pfam profile PF04640 : Protein of unknown	1.491
258452_at	AT3G22370	alternative oxidase 1a, mitochondrial (AOX1A) identical to GB:Q3921 [SP|Q39219] from [Arabidopsis thaliana]	1.49
262899_at	AT1G59870	ABC transporter family protein similar to PDR5-like ABC transporte GI:1514643 from [Spirodela polyrhiza]	1.484
265662_at	AT2G24500	zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type	1.484
253140_at	AT4G35480	zinc finger (C3HC4-type RING finger) family protein contains Pfam domai PF00097: Zinc finger, C3HC4 type (RING finger)	1.481
247125_at	AT5G66070	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile PF00097 zinc finger, C3HC4 type (RING finger)	1.469
253281_at	AT4G34138	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfa profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	1.468
254050_s_at	AT4G25690	[AT4G25690, expressed protein];[AT4G25670, expressed protein]	1.467
255110_at	AT4G08770	peroxidase, putative identical to class III peroxidase ATP38 [Arabidopsi thaliana] gi|17530568|gb|AAL40851; similar to peroxidase C2 precursor	1.465
264756_at	AT1G61370	S-locus lectin protein kinase family protein contains Pfam domains, PF00954: S-locus glycoprotein family, PF00069: Protein kinase domain,	1.465
266101_at	AT2G37940	expressed protein	1.464
257866_at	AT3G17770	dihydroxyacetone kinase family protein contains Pfam domains, PF02733 DAK1 domain and PF02734: DAK2 domain	1.461
256046_at	AT1G07130	OB-fold nucleic acid binding domain-containing protein contains InterPr entry IPR004365: OB-fold nucleic acid binding domain	1.46
266155_at	AT1G64950	cytochrome P450, putative similar to cytochrome P450 89A2 (CYPLXXXIX) (SP:Q42602) [Arabidopsis thaliana];similar to cytochrome	1.459
267624_at	AT2G39660	protein kinase, putative similar to protein kinase gi|166809|gb|AAA18853	1.458
254241_at	AT4G23190	protein kinase family protein contains Pfam PF00069: Protein kinas domain	1.438
267293_at	AT2G23810	senescence-associated family protein similar to senescence-associate protein 5 [Hemerocallis hybrid cultivar] gi|3551954|gb|AAC34855	1.438
264400_at	AT1G61800	glucose-6-phosphate/phosphate translocator, putative similar to glucose- phosphate/phosphate-translocator precursor GI:2997591 from [Pisum	1.437
266290_at	AT2G29490	glutathione S-transferase, putative similar to glutathione S-transferase 10 1A [Arabidopsis thaliana] SWISS-PROT:P46421	1.437
250252_at	AT5G13750	transporter-related	1.435
256300_at	AT1G69490	no apical meristem (NAM) family protein similar to N-term half of NAC domain protein NAM [Arabidopsis thaliana] GI:4325282	1.432
259018_at	AT3G07390	auxin-responsive protein / auxin-induced protein (AIR12) identical (with residue gap) to auxin-induced protein AIR12 GI:11357190 [Arabidopsis	1.424
262382_at	AT1G72920	disease resistance protein (TIR-NBS class), putative domain signature TI NBS exists, suggestive of a disease resistance protein.	1.422

260387_at	AT1G74100	sulfotransferase family protein similar to SP|P52837 Flavonol 4 sulfotransferase (EC 2.8.2.-) (F4-ST) {Flaveria chloraefolia}; contains Pfam	1.419
265093_at	AT1G03905	ABC transporter family protein similar to NBD-like protein GB:AAD20643	1.419
250944_at	AT5G03380	heavy-metal-associated domain-containing protein similar to farnesylate protein ATFP2 [GI:4097545]; contains Pfam profile PF00403: Heavy-meta	1.414
260362_at	AT1G70530	protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain	1.408
256185_at	AT1G51700	Dof-type zinc finger domain-containing protein (ADOF1) identical to cDNA adof1 mRNA for dof zinc finger protein, GI:3608260; contains Pfam profile	1.407
256756_at	AT3G25610	haloacid dehalogenase-like hydrolase family protein similar to Potentia phospholipid-transporting ATPase (EC 3.6.3.1) from Mus musculus	1.406
258787_at	AT3G11840	U-box domain-containing protein low similarity to immediate-early funga elicitor protein CMPG1 [Petroselinum crispum] GI:14582200; contains	1.403
262455_at	AT1G11310	seven transmembrane MLO family protein / MLO-like protein 2 (MLO2 idenctical to membrane protein Mlo2 [Arabidopsis thaliana]	1.403
244932_at	ATCG01060	psaC PSI 9KDa protein	1.402
252928_at	AT4G38940	kelch repeat-containing F-box family protein low similarity to SKP1 interacting partner 6 [Arabidopsis thaliana] GI:10716957; contains Pfam	1.399
266536_at	AT2G16900	expressed protein	1.398
265679_at	AT2G32240	expressed protein contains Pfam profile: PF04508 viral A-type inclusion protein repeat	1.393
253637_at	AT4G30390	expressed protein	1.39
245247_at	AT4G17230	scarecrow-like transcription factor 13 (SCL13)	1.383
266821_at	AT2G44840	ethylene-responsive element-binding protein, putative	1.382
246935_at	AT5G25350	F-box family protein contains Pfam PF00646: F-box domain and Pfam PF00560: Leucine Rich Repeat (6 copies); similar to F-box protein FBL6	1.381
259749_at	AT1G71100	ribose 5-phosphate isomerase-related similar to ribose-5-phosphat isomerase GI:18654317 from [Spinacia oleracea]	1.381
252679_at	AT3G44260	CCR4-NOT transcription complex protein, putative similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like	1.377
249752_at	AT5G24660	expressed protein	1.376
253630_at	AT4G30490	AFG1-like ATPase family protein contains Pfam profile: PF03969 AFG1 like ATPase	1.375
266072_at	AT2G18700	glycosyl transferase family 20 protein / trehalose-phosphatase famil protein similar to trehalose-6-phosphate synthase SL-TPS/P [Selaginella	1.371
254293_at	AT4G23060	calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif	1.366
257216_at	AT3G14990	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein putative supporting cDNA gi|11908017|gb|AF326856.1|; contains Pfam	1.362
250829_at	AT5G04720	disease resistance protein (CC-NBS-LRR class), putative domain signatur CC-NBS-LRR exists, suggestive of a disease resistance protein.	1.355
263704_at	AT1G31130	expressed protein	1.355
267280_at	AT2G19450	diacylglycerol O-acyltransferase / acyl CoA:diacylglycerol acyltransferas (DGAT) identical to gi:5050913, gi:6625553	1.349
257805_at	AT3G18830	mannitol transporter, putative similar to mannitol transporter [Apium graveolens var. dulce] GI:12004316; contains Pfam profile PF00083:	1.346
264867_at	AT1G24150	formin homology 2 domain-containing protein / FH2 domain-containing protein contains formin homology 2 domain, Pfam:PF02181	1.344
256525_at	AT1G66180	aspartyl protease family protein contains Pfam PF00026: Eukaryotic aspartyl protease profile; similar to CND41, chloroplast nucleoid DNA	1.343
265674_at	AT2G32190	expressed protein	1.343
260314_at	AT1G63830	proline-rich family protein contains proline-rich extensin domains INTERPRO:IPR002965; contains 1 predicted transmembrane domain	1.34
267451_at	AT2G33710	AP2 domain-containing transcription factor family protein similar to RAP2.6 (GI:17065542) {Arabidopsis thaliana}	1.34
262635_at	AT1G06570	4-hydroxyphenylpyruvate dioxygenase (HPD) identical to 4 hydroxyphenylpyruvate dioxygenase (HPD) SP:P93836 [Arabidopsis	1.338
250289_at	AT5G13190	expressed protein	1.337
265943_at	AT2G19570	cytidine deaminase (CDD) / cytidine aminohydrolase identical to cytidine deaminase (CDD) [Arabidopsis thaliana] GI:3046700	1.337

255568_at	AT4G01250	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain	1.336
264460_at	AT1G10170	NF-X1 type zinc finger family protein contains Pfam PF01422: NF-X1 type zinc finger; similar to transcriptional repressor NF-X1 (SP:Q12986) [Homo	1.332
254652_at	AT4G18170	WRKY family transcription factor similar to DNA-binding protein 2 GI:4322940 from [Nicotiana tabacum]; contains Pfam profile: PF03106	1.323
255524_at	AT4G02330	pectinesterase family protein contains Pfam profile: PF0109 pectinesterase	1.323
262772_at	AT1G13210	haloacid dehalogenase-like hydrolase family protein similar to Potentia phospholipid-transporting ATPase (EC 3.6.3.1) (Chromaffin granule	1.321
258830_at	AT3G07090	expressed protein	1.318
249987_at	AT5G18490	expressed protein	1.316
250990_at	AT5G02280	[AT5G02280, synbindin, putative similar to Swiss-Prot:Q9ES56 synbindin (TRS23 homolog) [Mus musculus]];[AT5G02290, protein kinase, putative	1.314
267076_at	AT2G41090	calmodulin-like calcium-binding protein, 22 kDa (CaBP-22) identical to SP|P30187 22 kDa calmodulin-like calcium-binding protein (CABP-22)	1.309
254215_at	AT4G23700	cation/hydrogen exchanger, putative (CHX17) similar to Na+/H+ exchanging protein slr1595 - Synechocystis sp., EMBL:D90902;	1.307
262832_s_at	AT1G14870	expressed protein similar to PGPS/D12 [Petunia x hybrida] GI:4105794 contains Pfam profile PF04749: Protein of unknown function, DUF614	1.301
252422_at	AT3G47550	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)	1.297
250580_at	AT5G07440	glutamate dehydrogenase 2 (GDH2) identical to glutamate dehydrogenas 2 (GDH 2) [Arabidopsis thaliana] SWISS-PROT:Q38946	1.296
261193_at	AT1G32920	expressed protein	1.296
256526_at	AT1G66090	disease resistance protein (TIR-NBS class), putative domain signature TI NBS exists, suggestive of a disease resistance protein.	1.295
258979_at	AT3G09440	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3) identical t SP|O65719 Heat shock cognate 70 kDa protein 3 (Hsc70.3) {Arabidopsis	1.293
258100_at	AT3G23550	[AT3G23550, MATE efflux family protein similar to ripening regulate protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfa	1.292
267230_at	AT2G44080	expressed protein	1.292
261453_at	AT1G21130	O-methyltransferase, putative similar to GI:2781394	1.291
246327_at	AT1G16670	protein kinase family protein contains protein kinase domain Pfam:PF00069; similar to receptor-like serine/threonine kinase GI:246592	1.286
262085_at	AT1G56060	expressed protein	1.286
265737_at	AT2G01180	phosphatidic acid phosphatase family protein / PAP2 family protein simila to phosphatidic acid phosphatase 2a2 [Cavia porcellus] GI:3641336;	1.285
250287_at	AT5G13330	AP2 domain-containing transcription factor family protein similar to AP2 domain containing protein RAP2.6, Arabidopsis thaliana,	1.284
261899_at	AT1G80820	cinnamoyl-CoA reductase, putative identical to CCR2 (GI:12407990), similar to cinnamoyl CoA reductase from Eucalyptus gunnii [GI:2058311]	1.284
262165_at	AT1G75020	phospholipid/glycerol acyltransferase family protein contains Pfam profile PF01553 Acyltransferase	1.282
258501_at	AT3G06780	[AT3G06780, glycine-rich protein];[AT3G06790, plastid developmental protein DAG, putative similar to DAG protein, chloroplast precursor	1.281
261618_at	AT1G33110	MATE efflux family protein similar to ripening regulated protein DDTFR1 [Lycopersicon esculentum] GI:12231296; contains Pfam profile PF01554	1.281
258606_at	AT3G02840	[AT3G02840, immediate-early fungal elicitor family protein similar to immediate-early fungal elicitor protein CMPG1 (GI:14582200)	1.279
267069_at	AT2G41010	VQ motif-containing protein contains PF05678: VQ motif	1.272
261081_at	AT1G07350	transformer serine/arginine-rich ribonucleoprotein, putative similar t GB:Y09506 from [Nicotiana tabacum] (Plant Mol. Biol. 35 (3), 261-269	1.268
258683_at	AT3G08760	protein kinase family protein contains protein kinase domain Pfam:PF00069	1.267
249770_at	AT5G24110	WRKY family transcription factor	1.265
251705_at	AT3G56400	WRKY family transcription factor DNA-binding protein 4 WRKY4 - Nicotiana tabacum, EMBL:AF193771	1.261
256454_at	AT1G75280	isoflavone reductase, putative identical to SP|P52577 Isoflavone reductas homolog P3 (EC 1.3.1.-) {Arabidopsis thaliana}; contains Pfam profile	1.261
245119_at	AT2G41640	expressed protein contains Pfam domain, PF04577: Protein of unknow function (DUF563)	1.259

249237_at	AT5G42050	expressed protein similar to gda-1 [Pisum sativum] GI:2765418	1.258
258939_at	AT3G10020	expressed protein	1.257
259792_at	AT1G29690	expressed protein	1.256
255039_at	AT4G09570	calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase [Arabidopsis thaliana]	1.252
264788_at	AT2G17880	DNAJ heat shock protein, putative similar to J11 protein [Arabidopsis thaliana] GI:9843641; contains Pfam profile PF00226 DnaJ domain	1.251
266231_at	AT2G02220	leucine-rich repeat transmembrane protein kinase, putative	1.25
245017_at	ATCG00510	psaI PSI I protein	1.24
248713_at	AT5G48180	kelch repeat-containing protein contains Pfam PF01344: Kelch motif (5 repeats) ;similar to Tip elongation aberrant protein 1 (Cell polarity protein	1.24
266746_s_at	AT4G02520	[AT4G02520, glutathione S-transferase, putative];[AT2G02930, glutathione S-transferase, putative]	1.238
248563_at	AT5G49690	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	1.237
252009_at	AT3G52800	zinc finger (AN1-like) family protein contains Pfam domain, PF01428: AN1 like Zinc finger	1.235
248230_at	AT5G53830	VQ motif-containing protein contains PF05678: VQ motif	1.234
252957_at	AT4G38680	cold-shock DNA-binding family protein contains Pfam domains PF00313: 'Cold-shock' DNA-binding domain and PF00098: Zinc knuckle	1.231
265327_at	AT2G18210	expressed protein	1.229
258094_at	AT3G14690	cytochrome P450, putative similar to GB:Q05047 from [Catharanthus roseus]	1.228
254248_at	AT4G23270	protein kinase family protein contains Pfam PF00069: Protein kinase domain	1.227
252533_at	AT3G46110	expressed protein	1.226
255080_at	AT4G09030	arabinogalactan-protein (AGP10) identical to gi|10880497|gb|AAG24278 supported by Ceres cDNA 265772	1.224
264986_at	AT1G27130	glutathione S-transferase, putative similar to glutathione S-transferase GB AAF22517 GI:6652870 from [Papaver somniferum]	1.224
256999_at	AT3G14200	DNAJ heat shock N-terminal domain-containing protein low similarity to SP|O75190|DJB6_HUMAN DnaJ homolog subfamily B member 6 (Heat	1.22
248870_at	AT5G46710	zinc-binding family protein similar zinc-binding protein [Pisum sativum] GI:16117799; contains Pfam profile PF04640 : Protein of unknown	1.217
256968_at	AT3G21070	ATP-NAD kinase family protein contains Pfam domain, PF01513: ATP-NAD kinase	1.217
267381_at	AT2G26190	calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif	1.217
264107_s_at	AT2G13800	[AT2G13800, leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich Repeat and	1.212
267392_at	AT2G44490	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-	1.211
248040_at	AT5G55970	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile PF00097 zinc finger, C3HC4 type (RING finger)	1.21
245019_at	ATCG00530	ycf10 hypothetical protein	1.203
267389_at	AT2G44460	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-	1.201
266299_at	AT2G29450	glutathione S-transferase (103-1A) identical to Swiss-Prot:P46421 glutathione S-transferase 103-1A [Arabidopsis thaliana]	1.199
264841_at	AT1G03740	protein kinase family protein contains protein kinase domain Pfam:PF00069	1.197
253273_at	AT4G34180	cyclase family protein contains Pfam profile: PF04199 putative cyclase	1.196
253061_at	AT4G37610	TAZ zinc finger family protein / BTB/POZ domain-containing protein contains Pfam PF00651 : BTB/POZ domain; contains Pfam PF02135 :	1.192
253994_at	AT4G26080	protein phosphatase 2C ABI1 / PP2C ABI1 / abscisic acid-insensitive 1 (ABI1) nearly identical to SP|P49597 Protein phosphatase 2C ABI1 (EC	1.191
251722_at	AT3G56200	amino acid transporter family protein low similarity to N system amino acids transporter NAT-1 [Mus musculus] GI:7406950; belongs to	1.187
266792_at	AT2G02860	sucrose transporter / sucrose-proton symporter (SUC3) identical to sucros transporter [Arabidopsis thaliana] GI:8052190; similar to sucrose	1.187

254059_at	AT4G25200	23.6 kDa mitochondrial small heat shock protein (HSP23.6-M) contain Pfam profile PF00011: Hsp20/alpha crystallin family	1.186
260847_s_at	AT1G17290	alanine aminotransferase, putative similar to alanine aminotransferase fro Panicum miliaceum [SP|P34106], GB:AAC62456 GI:3694807 from [Zea	1.185
245015_at	ATCG00490	rbcL large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase	1.182
252421_at	AT3G47540	chitinase, putative similar to basic endochitinase CHB4 precurso SP:Q06209 from [Brassica napus]	1.177
245272_at	AT4G17250	expressed protein	1.174
257822_at	AT3G25230	peptidyl-prolyl cis-trans isomerase / FK506-binding protein (ROF1 identical to rotamase FKBP (ROF1) GB:U49453 [Arabidopsis thaliana]	1.173
247293_at	AT5G64510	expressed protein	1.171
254396_at	AT4G21680	proton-dependent oligopeptide transport (POT) family protein contain Pfam profile: PF00854 POT family	1.17
256922_at	AT3G19010	oxidoreductase, 2OG-Fe(II) oxygenase family protein contains similarity t flavonol synthase (FLS) from [Solanum tuberosum] SP|Q41452, {Petunia	1.17
255945_at	AT5G28610	expressed protein	1.169
260648_at	AT1G08050	zinc finger (C3HC4-type RING finger) family protein low similarity to SP|P79263 Inter-alpha-trypsin inhibitor heavy chain H4 precursor {Sus	1.166
262801_at	AT1G21010	expressed protein	1.166
247925_at	AT5G57560	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase endo-xyloglucan transferase (TCH4) identical to xyloglucan	1.16
255904_at	AT1G17860	trypsin and protease inhibitor family protein / Kunitz family protein simila to LeMir (miraculin homolog) GI:2654440 from [Lycopersicon esculentum],	1.16
244993_s_at	ATCG01000	[ATCG01000, ycf1.1 hypothetical protein];[ATCG01130, ycf1.2 hypothetical protein]	1.157
247691_at	AT5G59720	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];	1.147
247215_at	AT5G64905	expressed protein	1.143
260975_at	AT1G53430	[AT1G53430, leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich Repeat and	1.14
262229_at	AT1G68620	expressed protein similar to PrMC3 [Pinus radiata] GI:5487873	1.14
249339_at	AT5G41100	expressed protein	1.137
256861_at	AT3G23920	beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putativ similar to beta-amylase enzyme [Arabidopsis thaliana] GI:6065749, beta-	1.135
252483_at	AT3G46600	scarecrow transcription factor family protein scarecrow-like 11 Arabidopsis thaliana, EMBL:AF036307	1.134
244986_at	ATCG00820	rps19 ribosomal protein S19	1.133
251196_at	AT3G62950	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	1.132
258984_at	AT3G08970	DNAJ heat shock N-terminal domain-containing protein low similarity to PIR|A47079|A47079 heat shock protein dnaJ - Lactococcus lactis;	1.132
247177_at	AT5G65300	expressed protein	1.129
251028_at	AT5G02230	haloacid dehalogenase-like hydrolase family protein contains InterPr accession IPR005834: Haloacid dehalogenase-like hydrolase	1.127
251187_at	AT3G62770	transport protein-related weak similarity to Gsa12p [Pichia pastoris GI:18307769; contains 1 WD-40 repeat (PF00400); putative proteins -	1.125
264929_at	AT1G60730	aldo/keto reductase family protein contains Pfam profile PF00248 oxidoreductase, aldo/keto reductase family	1.123
256793_at	AT3G22160	VQ motif-containing protein contains PF05678: VQ motif	1.119
246944_at	AT5G25450	ubiquinol-cytochrome C reductase complex 14 kDa protein, putativ similar to SP|P48502 Ubiquinol-cytochrome C reductase complex 14 kDa	1.113
252193_at	AT3G50060	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA MYB-related protein (1107 bp)	1.113
251804_at	AT3G55430	glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative simila to beta-1,3 glucanase GI:7414433 from [Pisum sativum]; contains Pfam	1.109
265276_at	AT2G28400	expressed protein contains Pfam profile PF04520: Protein of unknow function, DUF584	1.107
252827_at	AT4G39950	cytochrome P450 79B2, putative (CYP79B2) identical to cytochrome P450 (79B2) SP:O81346 from [Arabidopsis thaliana]	1.105

260047_at	AT1G73740	glycosyl transferase family 28 protein similar to UDP-N-acetylglucosamine N-acetylmuramyl-(pentapeptide)-pyrophosphoryl-undecaprenol N-	1.105
254103_at	AT4G25030	expressed protein	1.103
257053_at	AT3G15210	ethylene-responsive element-binding factor 4 (ERF4) identical to ethylen responsive element binding factor 4 SP:O80340 from [Arabidopsis	1.101
245740_at	AT1G44100	amino acid permease 5, putative (AAP5) nearly identical to amino acid permease (AAP5) GI:608673 from [Arabidopsis thaliana]	1.1
248146_at	AT5G54940	eukaryotic translation initiation factor SUI1, putative similar to SP|P32911 Protein translation factor SUI1 {Saccharomyces cerevisiae}; contains Pfa	1.1
263221_at	AT1G30620	UDP-D-xylose 4-epimerase, putative (MUR4) similar to SP|P55180 UD glucose 4-epimerase (EC 5.1.3.2) from Bacillus subtilis, GI:3021357 UDP-	1.098
260807_at	AT1G78310	VQ motif-containing protein contains PF05678: VQ motif	1.097
266888_s_at	AT2G44750	[AT2G44750, thiamin pyrophosphokinase, putative similar to thiamin pyrophosphokinase [Mus musculus]	1.096
251624_at	AT3G57280	expressed protein contains Pfam profile PF03647: Uncharacterised protei family (UPF0136)	1.095
247284_at	AT5G64410	oligopeptide transporter OPT family protein similar to SP|P40900 Sexua differentiation process protein isp4 {Schizosaccharomyces pombe};	1.094
250339_at	AT5G11670	malate oxidoreductase, putative similar to NADP-dependent malic enzym (EC 1.1.1.40) (NADP-ME) (SP|P12628) {Phaseolus vulgaris}	1.092
245018_at	ATCG00520	ycf4 hypothetical protein	1.09
255895_at	AT1G17990	[AT1G17990, 12-oxophytodienoate reductase, putative similar to OPR1 [GI:3882355] and OPR2 [GI:3882356]];[AT1G18020, 12-oxophytodienoat	1.09
244936_at	ATCG01100	ndhA NADH dehydrogenase ND1	1.088
252652_at	AT3G44720	prephenate dehydratase family protein similar to bacterial PheA gen products	1.087
250738_at	AT5G05730	anthranilate synthase, alpha subunit, component I-1 (ASA1) identical t SP|P32068	1.082
259911_at	AT1G72680	cinnamyl-alcohol dehydrogenase, putative similar to cinnamyl-alcoho dehydrogenase GB:AAC35846 [Medicago sativa], SP|Q08350 [Picea	1.082
252131_at	AT3G50930	AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004	1.081
250818_at	AT5G04930	phospholipid-transporting ATPase 1 / aminophospholipid flippase 1 magnesium-ATPase 1 (ALA1) nearly identical to SP|P98204 Phospholipid-	1.077
260522_x_at	AT2G41730	expressed protein	1.075
264645_at	AT1G08940	phosphoglycerate/bisphosphoglycerate mutase family protein contain Pfam profile PF00300: phosphoglycerate mutase family	1.073
252939_at	AT4G39230	isoflavone reductase, putative similar to allergenic isoflavone reductase-lik protein Bet v 6.0102 [Betula pendula][GI:10764491]; contains Pfam profile	1.072
264000_at	AT2G22500	mitochondrial substrate carrier family protein contains Pfam profile PF00153 mitochondrial carrier protein	1.071
252415_at	AT3G47340	asparagine synthetase 1 [glutamine-hydrolyzing] / glutamine-dependen asparagine synthetase 1 (ASN1) identical to SP|P49078 Asparagine	1.07
257194_at	AT3G13110	serine O-acetyltransferase (SAT-1) identical to serine acetyltransferas (Sat-1) GI:1184048 [Arabidopsis thaliana]	1.066
258406_at	AT3G17611	rhomboid family protein / zinc finger protein-related contains Pfam profile PF01694: Rhomboid family, PF00641: Zn-finger in Ran binding protein	1.066
251163_at	AT3G63310	expressed protein low similarity to N-methyl-D-aspartate recepto associated protein [Drosophila melanogaster] GI:567104; contains Pfam	1.065
244935_at	ATCG01090	ndhI NADH dehydrogenase subunit	1.063
259626_at	AT1G42990	bZIP transcription factor family protein contains Pfam profile: PF00170: bZIP transcription factor	1.062
258275_at	AT3G15760	expressed protein	1.06
259982_at	AT1G76410	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)	1.059
267486_at	AT2G02800	protein kinase (APK2b) identical to protein kinase APK2b [Arabidopsi thaliana] gi|2852449|dbj|BAA24695	1.059
256697_at	AT3G20660	organic cation transporter family protein similar to organic catio transporter OCT3 [Rattus norvegicus] GI:3273722, organic cation	1.058
265067_at	AT1G03850	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	1.056
255116_at	AT4G08850	leucine-rich repeat family protein / protein kinase family protein contain Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein	1.055

260900_s_at	AT1G21400	[AT1G21400, 2-oxoisovalerate dehydrogenase, putative / 3-methyl-2 oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid	1.052
246195_at	AT4G36410	ubiquitin-conjugating enzyme 17 (UBC17) E2; identical to gi:2801446	1.051
263228_at	AT1G30700	FAD-binding domain-containing protein similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE)	1.051
257062_at	AT3G18290	zinc finger protein-related weak alignment to Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies)	1.049
259216_at	AT3G09000	proline-rich family protein	1.047
251200_at	AT3G63010	expressed protein similar to PrMC3 [Pinus radiata] GI:5487873	1.044
254665_at	AT4G18340	glycosyl hydrolase family 17 protein similar to elicitor inducible chitinase N SubE76 GI:11071974 from [Nicotiana tabacum]	1.044
267289_at	AT2G23770	protein kinase family protein / peptidoglycan-binding LysM domain containing protein contains Pfam domains, PF00069: Protein kinase	1.043
248487_at	AT5G51070	ATP-dependent Clp protease ATP-binding subunit (ClpD), (ERD1) SAG15/ERD1; identical to ERD1 protein GI:497629, SP:P42762 from	1.042
260741_at	AT1G15040	glutamine amidotransferase-related	1.042
256050_at	AT1G07000	exocyst subunit EXO70 family protein similar to leucine zipper protein GI:10177020 from [Arabidopsis thaliana] contains Pfam domain PF03081:	1.041
254688_at	AT4G13830	DNAJ heat shock N-terminal domain-containing protein (J20) identical to DnaJ-like protein [Arabidopsis thaliana] GI:6691127; similar to SP|Q05646	1.039
254532_at	AT4G19660	ankyrin repeat family protein / BTB/POZ domain-containing protein contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain,	1.037
266749_at	AT2G47060	serine/threonine protein kinase, putative similar to Pto kinase interactor 1 (Pti1)[Lycopersicon esculentum] gi|3668069|gb|AAC61805	1.037
245013_at	ATCG00470	atpE ATPase epsilon subunit	1.036
260206_at	AT1G70740	protein kinase family protein contains protein kinase domain Pfam:PF00069	1.035
264026_at	AT2G21060	cold-shock DNA-binding family protein / glycine-rich protein (GRP2) identical to Glycine-rich protein 2b (AtGRP2b) [Arabidopsis thaliana]	1.035
250025_at	AT5G18290	major intrinsic protein-related / MIP-related contains weak similarity to Pfam profile: MIP PF00230; annotated based on segmental duplication	1.032
266995_at	AT2G34500	cytochrome P450 family protein similar to Cytochrome P450 61 (C-22 sterol desaturase) (SP:P54781) {Saccharomyces cerevisiae}	1.029
249125_at	AT5G43450	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (GI:599622 and tomato ethylene synthesis regulatory protein E8 (SP|P10967)	1.027
245313_at	AT4G15420	PRLI-interacting factor K nearly identical to PRLI-interacting factor K [Arabidopsis thaliana] GI:11139266; contains Pfam profiles PF03152:	1.024
256183_at	AT1G51660	mitogen-activated protein kinase kinase (MAPKK), putative (MKK4) identical to MAP kinase kinase 4 [Arabidopsis thaliana]	1.021
249393_at	AT5G40170	disease resistance family protein contains leucine rich-repeat (LRR domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-4	1.02
259977_at	AT1G76590	zinc-binding family protein similar to zinc-binding protein [Pisum sativum] GI:16117799; contains Pfam profile PF04640 : Protein of unknown	1.02
252851_at	AT4G40080	epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related contains Pfam PF01417: ENTH domain. ENTH	1.018
244912_at	ATMG00830	ccb382 cytochrome c biogenesis orf382	1.017
258114_at	AT3G14650	[AT3G14650, cytochrome P450, putative similar to GB:Q05047 from [Catharanthus roseus]];[AT3G14660, cytochrome P450, putative similar to	1.017
264660_at	AT1G09940	glutamyl-tRNA reductase 2 / GluTR (HEMA2) identical to glutamyl-tRNA reductase 2, chloroplast [SP|P49294]	1.017
254508_at	AT4G20170	expressed protein	1.016
266834_s_at	AT2G30020	protein phosphatase 2C, putative / PP2C, putative similar to protein phosphatase 2C (GI:4587992){Arabidopsis thaliana}	1.014
264279_s_at	AT1G78820	curculin-like (mannose-binding) lectin family protein / PAN domain containing protein similar to S locus glycoprotein [Brassica rapa]	1.012
248208_at	AT5G53980	homeobox-leucine zipper family protein contains Pfam PF00046 Homeobox domain; similar to homeobox protein PpHB5 (GI:7415622)	1.011
251649_at	AT3G57330	calcium-transporting ATPase, plasma membrane-type, putative / Ca2+ ATPase, putative (ACA11) identical to SP|Q9M2L4|ACAB_ARATH	1.009
256972_at	AT3G21140	expressed protein	1.009
245008_at	ATCG00360	ycf3 hypothetical protein	1.007

254847_at	AT4G11840	[AT4G11840, phospholipase D gamma 3 / PLD gamma 3 (PLDGAMMA3) identical to phospholipase D gamma 3 sp:Q9T052 from [Arabidopsis	1.006
255926_at	AT1G22190	AP2 domain-containing transcription factor, putative similar to AP2 domair containing protein RAP2.4 GI:2281633 from [Arabidopsis thaliana]	1.006
253455_at	AT4G32020	expressed protein NuLL	1.005
255967_at	AT1G22280	protein phosphatase 2C, putative / PP2C, putative similar to proteir phosphatase type 2C GI:4336436 from [Lotus japonicus]	1.005
244998_at	ATCG00180	rpoC1 RNA polymerase beta' subunit-1	1.001
246755_at	AT5G27920	F-box family protein contains similarity to leucine-rich repeats containing F box protein FBL3 GI:5919219 from [Homo sapiens]	1.001
260995_at	AT1G12120	expressed protein contains Pfam domain PF05904: Plant protein o unknown function (DUF863)	-1.005
263333_at	AT2G03890	phosphatidylinositol 3- and 4-kinase family protein low similarity tc phosphatidylinositol 4-kinase type-II beta [Homo sapiens] GI:20159767;	-1.006
255482_at	AT4G02510	chloroplast outer membrane protein, putative similar to chloroplast proteir import component Toc159 [Pisum sativum] GI:8489806, chloroplast outer	-1.013
247252_at	AT5G64770	expressed protein	-1.014
256601_s_at	AT3G28290	[AT3G28290, integrin-related protein 14a identical to At14a proteir GI:11994573 [Arabidopsis thaliana] [Gene 230 (1), 33-40 (1999)], At14a	-1.022
260494_at	AT2G41820	leucine-rich repeat transmembrane protein kinase, putative	-1.025
257952_at	AT3G21770	peroxidase 30 (PER30) (P30) (PRXR9) identical to SP|Q9LSY7 Peroxidase 30 precursor (EC 1.11.1.7) (Atperox P30) (PRXR9) (ATP7a)	-1.026
253849_at	AT4G28080	expressed protein	-1.033
259596_at	AT1G28130	auxin-responsive GH3 family protein similar to auxin-responsive GH: product [Glycine max] GI:18591; contains Pfam profile PF03321: GH3	-1.034
259373_at	AT1G69160	expressed protein	-1.036
259783_at	AT1G29510	auxin-responsive protein, putative similar to auxin-induced protein 6E (SP:P33083) [Glycine max]	-1.039
250937_at	AT5G03230	expressed protein contains Pfam profile PF04520: Protein of unknowr function, DUF584	-1.042
245947_at	AT5G19530	spermine/spermidine synthase family protein similar to SP|P09158 Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase)	-1.043
258355_at	AT3G14330	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat	-1.043
264315_at	AT1G70370	BURP domain-containing protein / polygalacturonase, putative similar tc polygalacturonase isoenzyme 1 beta subunit [Lycopersicon esculentum]	-1.044
245688_at	AT1G28290	pollen Ole e 1 allergen and extensin family protein similar tc arabinogalactan protein [Daucus carota] GI:11322245; contains Pfam	-1.046
267481_at	AT2G02780	leucine-rich repeat transmembrane protein kinase, putative	-1.047
255587_at	AT4G01480	inorganic pyrophosphatase, putative [soluble] / pyrophosphate phosph hydrolase, putative / PPase, putative strong similarity to SP|Q43187	-1.049
258181_at	AT3G21670	nitrate transporter (NTP3) nearly identical to nitrate transporte [Arabidopsis thaliana] GI:4490323; contains Pfam profile: PF00854 POT	-1.052
263989_at	AT2G42880	mitogen-activated protein kinase, putative / MAPK, putative (MPK20) mitogen-activated protein kinase (MAPK)(AtMPK20), PMID:12119167	-1.056
252238_at	AT3G49960	peroxidase, putative identical to peroxidase ATP21a [Arabidopsis thaliana gi|1546696|emb|CAA67339	-1.058
250892_at	AT5G03760	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosy transferase GB:AAC62210 GI:3687658 from [Bradyrhizobium japonicum],	-1.062
262830_at	AT1G14700	purple acid phosphatase, putative contains Pfam profile: PF0014 calcineurin-like phosphoesterase; similar to purple acid phosphatase	-1.069
265050_at	AT1G52070	jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767; contains Pfam profile PF01419 jacalin-	-1.071
246476_at	AT5G16730	expressed protein weak similarity to microtubule binding protein D-CLIF 190 [Drosophila melanogaster] GI:2773363, SMC2-like condensin	-1.076
253736_at	AT4G28780	GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) [Arabidopsis	-1.083
261500_at	AT1G28400	expressed protein similar to E6 (GI:1000090) [Gossypium barbadense]	-1.089
252353_at	AT3G48200	expressed protein	-1.09
261594_at	AT1G33240	trihelix DNA-binding protein, putative similar to GTL1 [Arabidopsis thaliana] GI:2664198	-1.096

258003_at	AT3G29030	expansin, putative (EXP5) identical to expansin At-EXP5 GB:AAB38071 from [Arabidopsis thaliana]; alpha-expansin gene family, PMID:11641069	-1.098
248075_at	AT5G55740	pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats	-1.107
264568_at	AT1G05150	calcium-binding EF hand family protein low similarity to O-linked GlcNAc transferase [Homo sapiens] GI:2266994; contains Pfam profiles PF00036:	-1.115
265272_at	AT2G28350	auxin-responsive factor (ARF10) similar to auxin response factor 1 GI:6165644 from [Arabidopsis thaliana]; identical to cDNA auxin response	-1.116
257673_at	AT3G20370	meprin and TRAF homology domain-containing protein / MATH domain containing protein similar to ubiquitin-specific protease 12 [Arabidopsis	-1.117
249347_at	AT5G40820	[AT5G40820, FAT domain-containing protein / phosphatidylinositol 3- and 4-kinase family protein similar to Atr protein [Xenopus laevis]	-1.119
265048_at	AT1G52050	jacalin lectin family protein similar to myrosinase-binding protein homolo [Arabidopsis thaliana] GI:2997767; contains Pfam profile PF01419 jacalin-	-1.119
266322_at	AT2G46690	auxin-responsive family protein similar to indole-3-acetic acid induce protein ARG7 (SP:P32295) [Phaseolus aureus]	-1.125
252207_at	AT3G50370	expressed protein	-1.128
247882_at	AT5G57785	expressed protein	-1.135
259173_at	AT3G03640	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-	-1.141
262260_at	AT1G70830	[AT1G70830, Bet v I allergen family protein similar to Csf-2 [Cucumis sativus][GI:5762258][J Am Soc Hortic Sci 124, 136-139 (1999)] ; contains	-1.146
253004_at	AT4G38280	[AT4G38280, expressed protein unknown protein F4L23.24 Arabidopsi thaliana chromosome II BAC F4L23, PID:g2583136];[AT4G38330,	-1.147
263183_at	AT1G05570	callose synthase 1 (CALS1) / 1,3-beta-glucan synthase 1 nearly identica to callose synthase 1 catalytic subunit [Arabidopsis thaliana] GI:13649388	-1.155
250207_at	AT5G13930	chalcone synthase / naringenin-chalcone synthase identical to SP|P13114	-1.159
247191_at	AT5G65310	homeobox-leucine zipper protein 5 (HB-5) / HD-ZIP transcription factor identical to homeobox-leucine zipper protein ATHB-5 (HD-ZIP protein	-1.164
252412_at	AT3G47295	expressed protein	-1.166
265342_at	AT2G18300	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF0001 helix-loop-helix DNA-binding domain ;supported by cDNA	-1.17
245304_at	AT4G15630	integral membrane family protein contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain	-1.171
247162_at	AT5G65730	xyloglucan:xyloglucosyl transferase, putative / xylogluca endotransglycosylase, putative / endo-xyloglucan transferase, putative	-1.171
267619_at	AT2G26730	leucine-rich repeat transmembrane protein kinase, putative	-1.172
262577_at	AT1G15290	tetratricopeptide repeat (TPR)-containing protein ESTs gb|F20110 an gb|F20109 come from this gene; contains Pfam profile PF00515: TPR	-1.174
256751_at	AT3G27170	chloride channel protein (CLC-b) identical to CLC-b chloride channe protein GB:CAA96058 from [Arabidopsis thaliana] (J. Biol. Chem. 271	-1.178
261562_at	AT1G01750	actin-depolymerizing factor, putative strong similarity to SP|P30175 Actin depolymerizing factor (ADF) {Lilium longiflorum}; contains Pfam profile	-1.183
263192_at	AT1G36160	acetyl-CoA carboxylase 1 (ACC1) nearly identical to acetyl-Co carboxylase 1 (ACC1) [Arabidopsis thaliana] GI:11869927	-1.183
252911_at	AT4G39510	cytochrome P450 family protein contains Pfam PF00067: Cytochrome P450; similar to Cytochrome P450 86A2 (SP:O23066) [Arabidopsis	-1.186
260618_at	AT1G53230	TCP family transcription factor 3 (TCP3) identical to transcription factor 3 (TCP3) [Arabidopsis thaliana] (GI:3243274); similar to flower development	-1.191
251261_at	AT3G62110	glycoside hydrolase family 28 protein / polygalacturonase (pectinase family protein weak similarity to polygalacturonase [Lycopersicon	-1.192
264926_at	AT1G60660	cytochrome b5 domain-containing protein contains InterPro accessio IPR001199: Cytochrome b5	-1.195
256792_at	AT3G22150	pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats	-1.197
265102_at	AT1G30870	cationic peroxidase, putative similar to cationic peroxidase (gi|1232069) similar to EST gb|AI100412	-1.202
263296_at	AT2G38800	calmodulin-binding protein-related contains similarity to potato calmoduli binding protein PCBP GI:17933110 from [Solanum tuberosum]	-1.216
261804_at	AT1G30530	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfa profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	-1.223
254024_at	AT4G25780	pathogenesis-related protein, putative similar to gene PR-1 protein Medicago truncatula, SP|Q40374; contains Pfam profile PF00188: SCP-	-1.226
251714_at	AT3G56370	leucine-rich repeat transmembrane protein kinase, putative leucine-ric receptor-like protein kinase - Malus domestica, EMBL:AF053127	-1.228

248393_at	AT5G52060	BAG domain-containing protein contains Pfam:PF02179 BAG domain	-1.233
266131_at	AT2G45160	scarecrow transcription factor family protein	-1.243
260453_s_at	AT1G72510	expressed protein	-1.246
262871_at	AT1G65010	expressed protein similar to endosome-associated protein (GI:1016368 [Homo sapiens]; similar to Centromeric protein E (CENP-E protein) (Swiss	-1.246
249008_at	AT5G44680	methyladenine glycosylase family protein similar to SP|P05100 DNA-3 methyladenine glycosylase I (EC 3.2.2.20) (3-methyladenine-DNA	-1.252
246275_at	AT4G36540	basic helix-loop-helix (bHLH) family protein contains Pfam domain PF00010: Helix-loop-helix DNA-binding domain	-1.255
262598_at	AT1G15260	expressed protein EST gb|N65467 comes from this gene	-1.264
248427_at	AT5G51750	subtilase family protein similar to subtilisin-like protease GI:3687307 fron [Lycopersicon esculentum]	-1.268
263841_at	AT2G36870	xyloglucan:xyloglucosyl transferase, putative / xyloglucai endotransglycosylase, putative / endo-xyloglucan transferase, putative	-1.283
260693_at	AT1G32450	proton-dependent oligopeptide transport (POT) family protein contain: Pfam profile: PF00854 POT family	-1.293
262614_at	AT1G13980	pattern formation protein (EMB30) (GNOM) identical to SP|Q42510; contains Pfam profile PF01369: Sec7 domain	-1.293
252833_at	AT4G40090	arabinogalactan-protein (AGP3) InDels between the genome sequenc and the cDNA prevent identical translations from being annotated; the	-1.337
260041_at	AT1G68780	leucine-rich repeat family protein contains leucine rich-repeat (LRR domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to	-1.346
251226_at	AT3G62680	proline-rich family protein contains proline-rich region, INTERPRO:IPR000694	-1.347
258293_at	AT3G23430	phosphate transporter, putative (PHO1) identical to PHO1 proteir [Arabidopsis thaliana] GI:20069032; supporting cDNA	-1.347
259786_at	AT1G29660	GDSL-motif lipase/hydrolase family protein low similarity to family II lipase EXL1 [Arabidopsis thaliana] GI:15054382; contains InterPro Entry	-1.349
251413_at	AT3G60320	expressed protein contains Pfam profiles: PF04782: protein of unknowr function (DUF632), PF04783: protein of unknown function (DUF630)	-1.359
253495_at	AT4G31850	[AT4G31850, pentatricopeptide (PPR) repeat-containing protein contain: Pfam profile PF01535: PPR repeat];[AT4G31860, protein phosphatase 2C	-1.377
246510_at	AT5G15410	cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channe (CNGC2) identical to cyclic nucleotide-gated cation channel GI:3894399	-1.386
258060_at	AT3G26030	serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' putative similar to SWISS-PROT:Q28653 serine/threonine protein	-1.414
247871_at	AT5G57530	[AT5G57530, xyloglucan:xyloglucosyl transferase, putative / xyloglucai endotransglycosylase, putative / endo-xyloglucan transferase, putative	-1.443
250778_at	AT5G05500	pollen Ole e 1 allergen and extensin family protein contains Pfam domain PF01190: Pollen proteins Ole e I family	-1.5
258080_at	AT3G25930	universal stress protein (USP) family protein contains Pfam PF0058: universal stress protein family	-1.504
246652_at	AT5G35190	proline-rich extensin-like family protein contains proline-rich extensi domains, INTERPRO:IPR002965	-1.506
257297_at	AT3G28040	leucine-rich repeat transmembrane protein kinase, putative contains Pfan profiles: PF00560 leucine rich repeat, PF00069 eukaryotic protein kinase	-1.517
265175_at	AT1G23480	glycosyl transferase family 2 protein similar to cellulose synthase fron Agrobacterium tumefiens [gi:710492] and Agrobacterium radiobacter	-1.575
253255_at	AT4G34760	auxin-responsive family protein auxin-induced protein X15, Glycine max PIR2:JQ1097	-1.578
250059_at	AT5G17820	peroxidase 57 (PER57) (P57) (PRXR10) identical to SP|Q43729 Peroxidase 57 precursor (EC 1.11.1.7) (Atperox P57) (PRXR10) (ATP13a)	-1.591
245567_at	AT4G14630	germin-like protein (GLP9) identical to germin-like protein subfamily 1 member 8 [SP|Q9LEA7]	-1.66
259790_s_at	AT1G29430	auxin-responsive family protein similar to auxin-induced protein 10a 6E {SP:P33083} [Glycine max]	-1.724
248636_at	AT5G49080	proline-rich extensin-like family protein contains proline-rich extensi domains, INTERPRO:IPR002965	-1.742
259328_at	AT3G16440	jacalin lectin family protein contains Pfam profile: PF01419 jacalin-like lectin domain; similar to myrosinase-binding protein homolog [Arabidopsis	-1.853
255516_at	AT4G02270	pollen Ole e 1 allergen and extensin family protein contains Pfam domain PF01190: Pollen proteins Ole e I family	-1.913
246991_at	AT5G67400	peroxidase 73 (PER73) (P73) (PRXR11) identical to SP|Q43873 Peroxidase 73 precursor (EC 1.11.1.7) (Atperox P73) (PRXR11) (ATP10a)	-1.93
264567_s_at	AT1G05250	[AT1G05250, peroxidase, putative similar to peroxidase; peroxidas ATP11a [Arabidopsis thaliana] gi|1546688|emb|CAA67334];[AT1G05240,	-2.054

254044_at	AT4G25820	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase endo-xyloglucan transferase (XTR9) identical to xyloglucan	-2.104
264014_at	AT2G21210	auxin-responsive protein, putative similar to small auxin-up regulate protein SAUR (GI:3043536) [Raphanus sativus]	-2.132
253998_at	AT4G26010	peroxidase, putative peroxidase ATP13a - Arabidopsis thaliana PID:e264765; identical to cDNA class III peroxidase ATP35, GI:17530565	-2.319
252972_at	AT4G38840	auxin-responsive protein, putative auxin-inducible SAUR gene, Raphanu sativus,AB000708	-2.404
262427_s_at	AT1G47600	[AT1G47600, glycosyl hydrolase family 1 protein contains Pfam PF00232 Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-	-2.732

Supp Table 3. Transcripts significantly enhanced in Zat12 over-expressing plants more than in WT plants in response to the hydrogen peroxide (20mM, 1h)

GeneNum	Locus Identifier	Annotation	log2(Zat+/Zat)
262911_s_at	AT1G59860	17.6 kDa class I heat shock protein (HSP17.6A-CI) similar to 17.5 kDa class I heat shock protein SP:P04793 from [Glycine	5.731
266294_at	AT2G29500	17.6 kDa class I small heat shock protein (HSP17.6B-CI) contains Pfam PF00011: Hsp20/alpha crystallin family;	5.375
263150_at	AT1G54050	17.4 kDa class III heat shock protein (HSP17.4-CIII) contains Pfam profile: PF00011 Hsp20/alpha crystallin family; identified	4.8
246018_at	AT5G10695	expressed protein	3.325
246270_at	AT4G36500	expressed protein	3.291
256442_at	AT3G10930	expressed protein	3.148
249752_at	AT5G24660	expressed protein	2.862
254839_at	AT4G12400	stress-inducible protein, putative similar to sti (stress inducible protein) [Glycine max] GI:872116; contains Pfam profile	2.672

Supp Table 4. Transcripts specifically and significantly enhanced (>2-fold) in Zat12 over-expressing plants in response to hydrogen peroxide (20mM, 1h)

Array Element	Locus Identifier	Annotation	log2(Zat+/Zat)
251336_at	AT3G61190	BON1-associated protein 1 (BAP1) identical to BON1-associated protein 1 [Arabidopsis thaliana] GI:15487384; contains Pfam profile	1.732
251640_at	AT3G57450	expressed protein	1.709
251428_at	AT3G60140	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-	1.673
255787_at	AT2G33590	cinnamoyl-CoA reductase family similar to cinnamoyl-CoA reductase from Pinus taeda [GI:17978649], Eucalyptus gunnii [GI:2058311]	1.604
256518_at	AT1G66080	expressed protein	1.511
261265_at	AT1G26800	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	1.49
256522_at	AT1G66160	U-box domain-containing protein similar to immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] GI:14582200; contains	1.476
257784_at	AT3G26980	ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain	1.468
266168_at	AT2G38870	protease inhibitor, putative similar to SP|P24076 Glu S.griseus protease inhibitor (BGIA) {Momordica charantia}; contains Pfam	1.423
245777_at	AT1G73540	MutT/nudix family protein low similarity to SP|Q09790 Diadenosine 5',5'''-P1,P6-hexaphosphate hydrolase (EC 3.6.1.-) (Ap6A hydrolase)	1.417
253453_at	AT4G31860	protein phosphatase 2C, putative / PP2C, putative protein phosphatase 2C, Schizosaccharomyces pombe, PIR2:S54297	1.412
267336_at	AT2G19310	expressed protein	1.401
245757_at	AT1G35140	phosphate-responsive protein, putative similar to phi-1 (phosphate-induced gene) [Nicotiana tabacum] GI:3759184; contains Pfam profile	1.39
249984_at	AT5G18400	expressed protein contains Pfam profile PF05093: Protein of unknown function (DUF689)	1.387
245329_at	AT4G14365	zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein contains Pfam profile: PF00097 zinc finger, C3HC4	1.357
246931_at	AT5G25170	expressed protein	1.347
258915_at	AT3G10640	SNF7 family protein contains Pfam domain, PF03357: SNF7 family	1.337
259841_at	AT1G52200	expressed protein similar to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04749: Protein of unknown	1.32
253780_at	AT4G28400	protein phosphatase 2C, putative / PP2C, putative protein phosphatase 2C-fission yeast, PIR2:S54297	1.316
247509_at	AT5G62020	heat shock factor protein, putative (HSF6) / heat shock transcription factor, putative (HTSF6) identical to heat shock transcription factor 6	1.306
252037_at	AT3G51920	calmodulin-9 (CAM9) identical to calmodulin 9 GI:5825602 from [Arabidopsis thaliana]; contains Pfam profile PF00036: EF hand	1.302
254890_at	AT4G11600	glutathione peroxidase, putative	1.276

258665_at	AT3G08710	thioredoxin family protein similar to thioredoxin H-type GB:P29448 SP|P29448 [Arabidopsis thaliana], Thioredoxin H-type 2 (TRX-H2)	1.276
247240_at	AT5G64660	U-box domain-containing protein similar to immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] GI:14582200; contains	1.271
247065_s_at	AT5G66910	[AT5G66910, disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a	1.257
263320_at	AT2G47180	galactinol synthase, putative similar to galactinol synthase, isoform GolS-1 GI:5608497 from [Ajuga reptans]	1.257
245642_at	AT1G25275	expressed protein	1.251
253104_at	AT4G36010	pathogenesis-related thaumatin family protein similar to receptor serine/threonine kinase PR5K [Arabidopsis thaliana] GI:1235680;	1.25
250098_at	AT5G17350	expressed protein	1.242
254424_at	AT4G21510	F-box family protein contains Pfam PF00646: F-box domain; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250	1.24
255844_at	AT2G33580	protein kinase family protein / peptidoglycan-binding LysM domain-containing protein protein kinase [Arabidopsis thaliana] GI:2852449;	1.238
256356_s_at	AT1G66500	[AT1G66500, zinc finger (C2H2-type) family protein contains Prosite PS00028: Zinc finger, C2H2 type, domain; similar to S-locus protein 4	1.237
250549_at	AT5G07860	transferase family protein similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus	1.213
264524_at	AT1G10070	branched-chain amino acid aminotransferase 2 / branched-chain amino acid transaminase 2 (BCAT2) identical to SP|Q9M439	1.213
251237_at	AT3G62420	bZIP transcription factor family protein similar to common plant regulatory factor 6 GI:9650826 from [Petroselinum crispum]	1.21
248821_at	AT5G47070	protein kinase, putative similar to protein kinase [Lophopyrum elongatum] gi|13022177|gb|AAK11674	1.209
260746_at	AT1G78380	glutathione S-transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]	1.208
258201_at	AT3G13910	expressed protein	1.207
245251_at	AT4G17615	calcineurin B-like protein 1 (CBL1) identical to calcineurin B-like protein 1 (GI:3309082) [Arabidopsis thaliana]	1.183
257785_at	AT3G26980	ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain	1.181
262148_at	AT1G52560	26.5 kDa class I small heat shock protein-like (HSP26.5-P) contains Pfam profile: PF00011 Hsp20/alpha crystallin family; identified in	1.177
253324_at	AT4G33940	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	1.168
249188_at	AT5G42830	transferase family protein similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus	1.167
254083_at	AT4G24920	protein transport protein SEC61 gamma subunit, putative similar to Swiss-Prot:Q19967 protein transport protein SEC61 gamma subunit	1.167
260005_at	AT1G67930	[AT1G67930, Golgi transport complex protein-related similar to golgi transport complex protein (GTC90) GB:5453670 [Homo sapiens]	1.163
267493_at	AT2G30400	ovate family protein 57% similar to ovate protein (GI:23429649) [Lycopersicon esculentum]; contains TIGRFAM TIGR01568 :	1.16

264777_at	AT1G08630	L-allo-threonine aldolase-related similar to L-allo-threonine aldolase (EC 4.1.2.-) (L-allo-TA) (L-allo-threonine acetaldehyde-lyase)	1.157
246098_at	AT5G20400	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to naringenin,2-oxoglutarate 3-dioxygenase (flavonone-3-hydroxylase)	1.157
249583_at	AT5G37770	touch-responsive protein / calmodulin-related protein 2, touch-induced (TCH2) identical to calmodulin-related protein 2,touch-	1.153
262677_at	AT1G75860	expressed protein	1.148
248698_at	AT5G48380	leucine-rich repeat family protein / protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains leucine-rich	1.14
258650_at	AT3G09830	protein kinase, putative similar to protein kinase [Lophopyrum elongatum] gi|13022177|gb|AAK11674	1.134
255504_at	AT4G02200	drought-responsive family protein similar to drought-induced mRNA, Di19 [Arabidopsis thaliana] gi|469110|emb|CAA55321	1.129
248868_at	AT5G46780	VQ motif-containing protein contains PF05678: VQ motif	1.127
257407_at	AT1G27100	expressed protein contains Pfam profile: PF04601 protein of unknown function (DUF569	1.12
267537_at	AT2G41880	guanylate kinase 1 (GK-1) identical to guanylate kinase (GK-1) [Arabidopsis thaliana] gi|7861795|gb|AAF70408	1.107
248665_at	AT5G48655	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	1.104
256221_at	AT1G56300	DNAJ heat shock N-terminal domain-containing protein similar to SP|Q9QYI7 DnaJ homolog subfamily B member 8 Mus musculus;	1.099
263457_at	AT2G22300	ethylene-responsive calmodulin-binding protein, putative (SR1) identical to partial sequence of ethylene-induced calmodulin-binding	1.089
255230_at	AT4G05390	ferredoxin--NADP(+) reductase, putative / adrenodoxin reductase, putative strong similarity to SP|P41345 Ferredoxin--NADP reductase,	1.088
253161_at	AT4G35770	senescence-associated protein (SEN1) identical to senescence-associated protein GI:1046270 from [Arabidopsis thaliana]	1.088
253999_at	AT4G26200	1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative similar to ACC synthase from Malus x domestica,	1.086
258105_at	AT3G23605	UBX domain-containing protein contains Pfam profile PF00789: UBX domain	1.073
247864_s_at	AT1G25083	[AT1G25083, anthranilate synthase beta subunit, putative strong similarity to anthranilate synthase beta subunit GI:403434 from	1.071
250304_at	AT5G12110	elongation factor 1B alpha-subunit 1 (eEF1Balpha1) identical to elongation factor 1B alpha-subunit [Arabidopsis thaliana] GI:6686819	1.065
259980_at	AT1G76520	auxin efflux carrier family protein contains auxin efflux carrier domain, Pfam:PF03547	1.063
252993_at	AT4G38540	monooxygenase, putative (MO2) identical to GI:3426064	1.06
258173_at	AT3G21630	protein kinase family protein contains protein kinase domain, Pfam:PF00069	1.059
264580_at	AT1G05340	expressed protein	1.058
261225_at	AT1G20100	expressed protein	1.058

247930_at	AT5G57060	expressed protein	1.055
251597_at	AT3G57750	protein kinase, putative similar to wall-associated kinase 1 [Arabidopsis thaliana] gi|3549626|emb|CAA08794; contains protein	1.055
263472_at	AT2G31955	molybdopterin biosynthesis protein, putative / molybdenum cofactor biosynthesis enzyme, putative 3' fragment; strong similarity to	1.055
252214_at	AT3G50260	AP2 domain-containing transcription factor, putative EREBP-3 homolog, Stylosanthes hamata, EMBL:U91982	1.051
263265_at	AT2G38820	expressed protein contains Pfam profile PF04720: Protein of unknown function (DUF506)	1.048
250692_at	AT5G06560	expressed protein contains Pfam profile PF04576: Protein of unknown function, DUF593	1.044
252470_at	AT3G46930	protein kinase family protein contains protein kinase domain, Pfam:PF00069	1.043
258351_at	AT3G17700	cyclic nucleotide-binding transporter 1 / CNBT1 (CNGC20) identical to cyclic nucleotide-binding transporter 1 (CNBT1) GI:8131898 from	1.043
261901_at	AT1G80920	DNAJ heat shock N-terminal domain-containing protein similar to SP|Q05646 Chaperone protein dnaJ Erysipelothrix rhusiopathiae,	1.043
265440_at	AT2G20960	expressed protein pEARLI 4 gene product [Arabidopsis thaliana] GI:871782	1.04
267154_at	AT2G30870	[AT2G30870, glutathione S-transferase, putative supported by cDNA GI:443698 GB:D17673];[AT2G30880, pleckstrin homology (PH)	1.033
261957_at	AT1G64660	Cys/Met metabolism pyridoxal-phosphate-dependent enzyme family protein similar to SP|P13254 Methionine gamma-lyase (EC 4.4.1.11)	1.026
256633_at	AT3G28340	galactinol synthase, putative	1.026
254861_at	AT4G12040	zinc finger (AN1-like) family protein contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger	1.021
264304_at	AT1G78895	expressed protein	1.02
249895_at	AT5G22500	acyl CoA reductase, putative / male-sterility protein, putative similar to acyl CoA reductase [Simmondsia chinensis] GI:5020215; contains	1.017
248676_at	AT5G48850	male sterility MS5 family protein similar to male sterility MS5 [Arabidopsis thaliana] GI:3859112; contains Pfam profile PF00515	1.015
261506_at	AT1G71697	choline kinase, putative similar to GmCK2p choline kinase gi|1438881|gb|AAC49375	1.013
254707_at	AT4G18010	inositol polyphosphate 5-phosphatase II (IP5PII) nearly identical to inositol polyphosphate 5-phosphatase II [Arabidopsis thaliana]	1.005
246214_at	AT4G36990	heat shock factor protein 4 (HSF4) / heat shock transcription factor 4 (HSTF4) identical to heat shock transcription factor 4 (HSF4)	1.004

Supp Table 5. Transcripts significantly enahnced/suppressed (>2-fold) in Zat12 over-expressing plants in response to hydrogen peroxide (20mM, 1h)

Array Element	Locus Identifier	Annotation	log2(Zat+/Zat)
262911_s_at	AT1G59860	17.6 kDa class I heat shock protein (HSP17.6A-CI) similar to 17.5 kDa class I heat shock protein SP:P04793 from [Glycine max]	5.731
262518_at	AT1G17170	glutathione S-transferase, putative One of three repeated putative glutathione transferases. 72% identical to glutathione transferase	5.681
250296_at	AT5G12020	17.6 kDa class II heat shock protein (HSP17.6-CII) identical to 17.6 kDa class II heat shock protein SP:P29830 from [Arabidopsis	5.628
261892_at	AT1G80840	WRKY family transcription factor similar to WRKY transcription factor GB:BAA87058 GI:6472585 from [Nicotiana tabacum]	5.55
263182_at	AT1G05575	expressed protein	5.397
266294_at	AT2G29500	17.6 kDa class I small heat shock protein (HSP17.6B-CI) contains Pfam PF00011: Hsp20/alpha crystallin family; identified in Scharf, K	5.376
261648_at	AT1G27730	zinc finger (C2H2 type) family protein (ZAT10) / salt-tolerance zinc finger protein (STZ) identical to salt-tolerance zinc finger protein	5.32
247949_at	AT5G57220	cytochrome P450, putative similar to Cytochrome P450 (SP:O65790) [Arabidopsis thaliana]; Cytochrome P450	5.316
250781_at	AT5G05410	DRE-binding protein (DREB2A) identical to DREB2A GI:3738230 from [Arabidopsis thaliana] ; supported by	5.007
255284_at	AT4G04610	5'-adenylylsulfate reductase (APR1) / PAPS reductase homolog (PRH19) identical to 5'-adenylylsulfate reductase [Arabidopsis	4.888
260978_at	AT1G53540	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)	4.877
265499_at	AT2G15480	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl	4.818
263150_at	AT1G54050	17.4 kDa class III heat shock protein (HSP17.4-CIII) contains Pfam profile: PF00011 Hsp20/alpha crystallin family; identified as class	4.8
258133_at	AT3G24500	ethylene-responsive transcriptional coactivator, putative similar to ethylene-responsive transcriptional coactivator [Lycopersicon	4.774
259875_s_at	AT1G76690	[AT1G76690, 12-oxophytodienoate reductase (OPR2) identical to 12-oxophytodienoate reductase OPR2 GB:AAC78441 [Arabidopsis	4.774
248332_at	AT5G52640	heat shock protein 81-1 (HSP81-1) / heat shock protein 83 (HSP83) nearly identical to SP|P27323 Heat shock protein 81-1 (HSP81-1)	4.763
261838_at	AT1G16030	heat shock protein 70, putative / HSP70, putative similar to heat shock protein hsp70 GI:1771478 from [Pisum sativum]	4.734
261450_s_at	AT1G21120	[AT1G21120, O-methyltransferase, putative similar to GI:2781394];[AT1G21110, O-methyltransferase, putative similar to	4.692
266590_at	AT2G46240	IQ domain-containing protein / BAG domain-containing protein contains Pfam profiles PF00612: IQ calmodulin-binding motif,	4.667
253046_at	AT4G37370	cytochrome P450, putative similar to Cytochrome P450 91A1 (SP:Q9FG65)[Arabidopsis thaliana]; cytochrome P450, Glycyrrhiza	4.618
259479_at	AT1G19020	expressed protein	4.585

256245_at	AT3G12580	heat shock protein 70, putative / HSP70, putative strong similarity to heat shock protein GI:425194 [Spinacia oleracea]	4.487
262517_at	AT1G17180	glutathione S-transferase, putative Second of three repeated putative glutathione transferases. 72% identical to glutathione	4.423
260248_at	AT1G74310	heat shock protein 101 (HSP101) identical to heat shock protein 101 GI:6715468 GB:AAF26423 from [Arabidopsis thaliana]	4.388
248434_at	AT5G51440	23.5 kDa mitochondrial small heat shock protein (HSP23.5-M) similar to heat shock 22 kDa protein, mitochondrial precursor	4.371
245250_at	AT4G17490	ethylene-responsive element-binding protein, putative similar to SP|O80341 Ethylene responsive element binding factor 5 (AtERF5)	4.37
250351_at	AT5G12030	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]	4.319
248657_at	AT5G48570	peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative similar to rof1 [Arabidopsis thaliana] GI:1373396	4.303
249719_at	AT5G35735	auxin-responsive family protein similar to auxin-induced protein AIR12 GI:11357190 [Arabidopsis thaliana]	4.279
245711_at	AT5G04340	zinc finger (C2H2 type) family protein contains Pfam domain, PF00096: Zinc finger, C2H2 type	4.23
252515_at	AT3G46230	[AT3G46230, 17.4 kDa class I heat shock protein (HSP17.4-CI) identical to 17.4 kDa class I heat shock protein SP:P19036 from	4.207
259037_at	AT3G09350	armadillo/beta-catenin repeat family protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat	4.166
254343_at	AT4G21990	5'-adenylylsulfate reductase (APR3) / PAPS reductase homolog (PRH26) identical to 5'-adenylylsulfate reductase [Arabidopsis	4.114
261449_at	AT1G21120	O-methyltransferase, putative similar to GI:2781394	4.083
245041_at	AT2G26530	expressed protein	4.08
250182_at	AT5G14470	GHMP kinase-related contains similarity to D-glycero-D-manno-heptose 7-phosphate kinase [Aneurinibacillus thermoaerophilus]	4.042
255543_at	AT4G01870	tolB protein-related contains weak similarity to TolB protein precursor (Swiss-Prot:P44677) [Haemophilus influenzae]	4.029
266800_at	AT2G22880	[AT2G22880, VQ motif-containing protein contains PF05678: VQ motif];[AT2G22870, expressed protein]	3.945
256589_at	AT3G28730	[AT3G28730, structure-specific recognition protein 1 / high mobility group protein / HMG protein nearly identical to SP|Q05153	3.934
254331_s_at	AT4G22710	[AT4G22710, cytochrome P450 family protein contains Pfam profile: PF00067 cytochrome p450];[AT4G22690, cytochrome P450	3.909
260602_at	AT1G55920	serine O-acetyltransferase, putative identical to GI:608677 from [Arabidopsis thaliana]	3.905
261021_at	AT1G26380	FAD-binding domain-containing protein similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme)	3.857
254204_at	AT4G24160	hydrolase, alpha/beta fold family protein contains Pfam profile PF00561: hydrolase, alpha/beta fold family	3.797
257206_at	AT3G16530	legume lectin family protein contains Pfam domain, PF00139: Legume lectins beta domain	3.794

267028_at	AT2G38470	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain;	3.793
248381_at	AT5G51830	pfkB-type carbohydrate kinase family protein contains Pfam profile: PF00294 pfkB family carbohydrate kinase	3.704
247351_at	AT5G63790	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; contains similarity to NAC-	3.68
246858_at	AT5G25930	leucine-rich repeat family protein / protein kinase family protein contains similarity to Swiss-Prot:P47735 receptor-like protein	3.571
259979_at	AT1G76600	expressed protein	3.558
256576_at	AT3G28210	zinc finger (AN1-like) family protein contains Pfam profile: PF01428 AN1-like zinc finger	3.552
260406_at	AT1G69920	glutathione S-transferase, putative similar to glutathione transferase GB:CAA09188 [Alopecurus myosuroides]; supported by cDNA	3.53
254120_at	AT4G24570	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein	3.509
266296_at	AT2G29420	glutathione S-transferase, putative	3.497
262381_at	AT1G72900	disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance	3.488
264758_at	AT1G61340	F-box family protein contains Pfam PF00646: F-box domain; similar to late embryogenesis abundant protein GI:1350540 from [Picea	3.469
254926_at	AT4G11280	1-aminocyclopropane-1-carboxylate synthase 6 / ACC synthase 6 (ACS6) identical to GI:3746125	3.401
246744_at	AT5G27760	hypoxia-responsive family protein contains Pfam profile: PF04588 hypoxia induced protein conserved region	3.387
246018_at	AT5G10695	expressed protein	3.325
245038_at	AT2G26560	patatin, putative similar to patatin-like latex allergen [Hevea brasiliensis][PMID:10589016]; contains patatin domain PF01734	3.315
246270_at	AT4G36500	expressed protein	3.29
249575_at	AT5G37670	15.7 kDa class I-related small heat shock protein-like (HSP15.7-CI) contains Pfam profile: PF00011 Hsp20/alpha crystallin family;	3.267
263374_at	AT2G20560	DNAJ heat shock family protein SP|Q9UDY4 DnaJ homolog subfamily B member 4 (Heat shock 40 kDa protein 1 homolog)	3.254
265075_at	AT1G55450	embryo-abundant protein-related similar to embryo-abundant protein GI:1350531 from [Picea glauca]	3.227
257536_at	AT3G02800	tyrosine specific protein phosphatase family protein contains tyrosine specific protein phosphatases active site,	3.221
246584_at	AT5G14730	expressed protein	3.196
262119_s_at	AT1G02920	[AT1G02920, glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from [Hyoscyamus muticus];	3.196
245252_at	AT4G17500	ethylene-responsive element-binding protein 1 (ERF1) / EREBP-2 protein identical to SP|O80337 Ethylene responsive element	3.185

251745_at	AT3G55980	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and	3.179
256442_at	AT3G10930	expressed protein	3.148
263475_at	AT2G31945	expressed protein	3.137
260411_at	AT1G69890	expressed protein contains Pfam profile: PF04601 protein of unknown function (DUF569	3.13
262656_at	AT1G14200	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	3.125
254256_at	AT4G23180	receptor-like protein kinase 4, putative (RLK4) nearly identical to receptor-like protein kinase 4 [Arabidopsis thaliana] GI:13506745;	3.102
260025_at	AT1G30070	SGS domain-containing protein similar to calcyclin binding protein [Mus musculus] GI:3142331; contains Pfam profile PF05002: SGS	3.048
265501_at	AT2G15490	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl	3.026
253268_s_at	AT4G34135	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl	3.022
259705_at	AT1G77450	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to GRAB1 protein	3.001
262571_at	AT1G15430	expressed protein	2.999
267083_at	AT2G41100	touch-responsive protein / calmodulin-related protein 3, touch-induced (TCH3) identical to calmodulin-related protein 3, touch-	2.994
263231_at	AT1G05680	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl	2.992
253915_at	AT4G27280	calcium-binding EF hand family protein similar to EF-hand Ca2+-binding protein CCD1 [Triticum aestivum] GI:9255753; contains	2.988
266010_at	AT2G37430	zinc finger (C2H2 type) family protein (ZAT11) contains Pfam domain, PF00096: Zinc finger, C2H2 type	2.987
261459_at	AT1G21100	[AT1G21100, O-methyltransferase, putative similar to GI:2781394];[AT1G21130, O-methyltransferase, putative similar to	2.974
250449_at	AT5G10830	embryo-abundant protein-related similar to embryo-abundant protein [Picea glauca] GI:1350531	2.961
254605_at	AT4G18950	ankyrin protein kinase, putative similar to ankyrin-kinase [Medicago truncatula] gi|18700701|gb|AAL78674	2.945
263184_at	AT1G05560	UDP-glucose transferase (UGT75B2) similar to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase GI:2149127	2.884
259445_at	AT1G02400	gibberellin 2-oxidase, putative / GA2-oxidase, putative similar to GA2ox2 [GI:4678368]; similar to dioxygenase GI:1666096 from	2.879
246631_at	AT1G50740	expressed protein contains Pfam profile PF03647: Uncharacterised protein family (UPF0136)	2.878
267357_at	AT2G40000	expressed protein	2.878
253643_at	AT4G29780	expressed protein	2.867

246777_at	AT5G27420	zinc finger (C3HC4-type RING finger) family protein similar to RING- H2 zinc finger protein ATL6 [Arabidopsis thaliana]	2.865
251774_at	AT3G55830	[AT3G55830, glycosyltransferase family protein 47 similar to exostose-related protein 2, Homo sapiens, PIR:JC5935	2.865
254432_at	AT4G20830	FAD-binding domain-containing protein similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme)	2.865
249752_at	AT5G24660	expressed protein	2.862
248164_at	AT5G54490	calcium-binding EF-hand protein, putative similar to EF-hand Ca2+- binding protein CCD1 [Triticum aestivum] GI:9255753; contains	2.845
248134_at	AT5G54860	integral membrane transporter family protein contains 10 transmembrane domains; contains Pfam PF03092: BT1 family;	2.844
263379_at	AT2G40140	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and	2.834
263866_at	AT2G36950	heavy-metal-associated domain-containing protein nearly identical to farnesylated protein ATFP2 [GI:4097545] Pfam profile PF00403:	2.815
249078_at	AT5G44070	phytochelatin synthase 1 (PCS1) identical to phytochelatin synthase [Arabidopsis thaliana] gi|18254401|gb|AAL66747; identical to cDNA	2.757
250670_at	AT5G06860	polygalacturonase inhibiting protein 1 (PGIP1) identical to polygalacturonase inhibiting protein 1 (PGIP1) [Arabidopsis	2.748
263931_at	AT2G36220	expressed protein	2.724
248448_at	AT5G51190	AP2 domain-containing transcription factor, putative contains similarity to ethylene responsive element binding factor	2.717
264202_at	AT1G22810	AP2 domain-containing transcription factor, putative Contains similarity to transcription factor (TINY) isolog T02O04.22	2.69
247543_at	AT5G61600	ethylene-responsive element-binding family protein contains similarity to ethylene responsive element binding factor 5 (AtERF5)	2.685
265675_at	AT2G32120	heat shock protein 70 family protein / HSP70 family protein similar to SP|P22953 Heat shock cognate 70 kDa protein 1 (Hsc70.1)	2.674
254839_at	AT4G12400	stress-inducible protein, putative similar to sti (stress inducible protein) [Glycine max] GI:872116; contains Pfam profile PF00515	2.672
258336_at	AT3G16050	stress-responsive protein, putative similar to ethylene-inducible protein HEVER [Hevea brasiliensis] SWISS-PROT:Q39963;	2.663
253628_at	AT4G30280	[AT4G30280, xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan	2.659
252671_at	AT3G44190	pyridine nucleotide-disulphide oxidoreductase family protein low similarity to dihydrolipoamide dehydrogenase from Clostridium	2.654
254487_at	AT4G20780	calcium-binding protein, putative similar to SP|Q09011 Calcium- binding protein CAST {Solanum tuberosum}; contains	2.647
261564_at	AT1G01720	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAC domain protein	2.642
249494_at	AT5G39050	transferase family protein similar to anthocyanin 5-aromatic acyltransferase from Gentiana triflora GI:4185599, malonyl	2.628
254549_at	AT4G19880	glutathione S-transferase-related contains weak hit to Pfam profile PF00043: Glutathione S-transferase, C-terminal domain	2.621

261023_at	AT1G12200	flavin-containing monooxygenase family protein / FMO family protein low similarity to FMO2 from Homo sapiens [SP|Q99518];	2.621
252265_at	AT3G49620	2-oxoacid-dependent oxidase, putative (DIN11) identical to partial cds of 2-oxoacid-dependent oxidase (din11) from GI:10834554	2.617
245731_at	AT1G73500	mitogen-activated protein kinase kinase (MAPKK), putative (MKK9) mitogen-activated protein kinase kinase (MAPKK) family,	2.598
254211_at	AT4G23570	phosphatase-related low similarity to phosphoprotein phosphatase [Mus musculus] GI:567040; contains Pfam profiles PF00515: TPR	2.598
255733_at	AT1G25400	expressed protein similar to unknown protein GI:6714347 from [Arabidopsis thaliana]	2.581
257918_at	AT3G23230	ethylene-responsive factor, putative similar to EREBP-4 GB:BAA07323 from [Nicotiana tabacum]	2.581
266658_at	AT2G25735	expressed protein	2.577
247047_at	AT5G66650	expressed protein contains Pfam domain, PF04678: Protein of unknown function, DUF607	2.571
253414_at	AT4G33050	calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif	2.567
254784_at	AT4G12720	MutT/nudix family protein similar to SP|P53370 Nucleoside diphosphate-linked moiety X motif 6 {Homo sapiens}; contains	2.562
257670_at	AT3G20340	expressed protein	2.546
258786_at	AT3G11820	syntaxin 121 (SYP121) / syntaxin-related protein (SYR1) contains Pfam profiles: PF00804 syntaxin and PF05739: SNARE domain;	2.539
254318_at	AT4G22530	embryo-abundant protein-related similar to embryo-abundant protein [Picea glauca] GI:1350531	2.514
254592_at	AT4G18880	heat shock transcription factor 21 (HSF21) identical to heat shock transcription factor 21 [Arabidopsis thaliana] GI:3399765; contains	2.507
252474_at	AT3G46620	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)	2.505
256044_at	AT1G07160	protein phosphatase 2C, putative / PP2C, putative similar to protein phosphatase 2C GI:2582800 from [Medicago sativa]	2.495
248607_at	AT5G49480	sodium-inducible calcium-binding protein (ACP1) / sodium-responsive calcium-binding protein (ACP1) identical to NaCl-	2.492
247693_at	AT5G59730	exocyst subunit EXO70 family protein leucine zipper-containing protein, Lycopersicon esculentum, PIR:S21495 contains Pfam	2.489
266841_at	AT2G26150	heat shock transcription factor family protein contains Pfam profile: PF00447 HSF-type DNA-binding domain	2.489
265221_s_at	AT2G02010	[AT2G02010, glutamate decarboxylase, putative strong similarity to glutamate decarboxylase isozyme 3 [Nicotiana tabacum]	2.472
263935_at	AT2G35930	U-box domain-containing protein similar to immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] GI:14582200;	2.462
264314_at	AT1G70420	expressed protein	2.461
246099_at	AT5G20230	plastocyanin-like domain-containing protein	2.454

250550_at	AT5G07870	transferase family protein similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus	2.454
246612_at	AT5G35320	expressed protein	2.447
252908_at	AT4G39670	expressed protein	2.445
262374_s_at	AT1G72910	[AT1G72910, disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease	2.444
246463_at	AT5G16970	NADP-dependent oxidoreductase, putative (P1) identical to probable NADP-dependent oxidoreductase P1, zeta-crystallin	2.418
265200_s_at	AT2G36790	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl	2.414
254158_at	AT4G24380	expressed protein contains Pfam profile: PF03959 domain of unknown function (DUF341)	2.409
265670_s_at	AT2G32210	expressed protein	2.409
248799_at	AT5G47230	ethylene-responsive element-binding factor 5 (ERF5) identical to SP|O80341 Ethylene responsive element binding factor 5 (AtERF5)	2.402
254241_at	AT4G23190	protein kinase family protein contains Pfam PF00069: Protein kinase domain	2.4
247708_at	AT5G59550	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)	2.398
246464_at	AT5G16990	[AT5G16990, NADP-dependent oxidoreductase, putative strong similarity to probable NADP-dependent oxidoreductase (zeta-	2.396
253606_at	AT4G30530	defense-related protein, putative strong similarity to defense-related protein [Brassica carinata] GI:14009290; contains Pfam profile	2.395
245254_at	AT4G14680	sulfate adenylyltransferase 3 / ATP-sulfurylase 3 (APS3) identical to ATP sulfurylase (APS3) [Arabidopsis thaliana] GI:1575327	2.394
249983_at	AT5G18470	curculin-like (mannose-binding) lectin family protein contains Pfam profile: PF01453 lectin (probable mannose binding)	2.378
261748_at	AT1G76070	expressed protein	2.366
260401_at	AT1G69840	band 7 family protein strong similarity to hypersensitive-induced response protein [Zea mays] GI:7716466; contains Pfam profile	2.355
258507_at	AT3G06500	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative similar to neutral invertase	2.351
263800_at	AT2G24600	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023	2.348
253535_at	AT4G31550	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain	2.326
260126_at	AT1G36370	glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase,	2.325
259879_at	AT1G76650	calcium-binding EF hand family protein similar to regulator of gene silencing calmodulin-related protein GI:12963415 from [Nicotiana	2.322
260405_at	AT1G69930	glutathione S-transferase, putative similar to glutathione transferase GB:CAA09188 [Alopecurus myosuroides]	2.319

254408_at	AT4G21390	S-locus lectin protein kinase family protein contains Pfam profiles: PF00954 S-locus glycoprotein family, PF00069 protein kinase	2.308
248686_at	AT5G48540	33 kDa secretory protein-related contains Pfam PF01657: Domain of unknown function, duplicated in 33 KDa secretory proteins	2.305
246034_at	AT5G08350	GRAM domain-containing protein / ABA-responsive protein-related contains similarity to ABA-responsive protein in barley (GI:4103635)	2.299
266983_at	AT2G39400	hydrolase, alpha/beta fold family protein similar to monoglyceride lipase from [Homo sapiens] GI:14594904, [Mus musculus]	2.296
253827_at	AT4G28085	expressed protein	2.294
249417_at	AT5G39670	[AT5G39670, calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand	2.293
253284_at	AT4G34150	C2 domain-containing protein similar to calcium-dependent protein kinase [Dunaliella tertiolecta] GI:6644464; contains Pfam profile	2.283
252592_at	AT3G45640	mitogen-activated protein kinase, putative / MAPK, putative (MPK3) identical to mitogen-activated protein kinase homolog	2.281
266737_at	AT2G47140	short-chain dehydrogenase/reductase (SDR) family protein similar to 3-beta-hydroxysteroiddehydrogenase GI:15983819 from [Digitalis	2.277
245765_at	AT1G33600	leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains	2.275
252278_at	AT3G49530	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAC2 - Arabidopsis	2.272
253859_at	AT4G27657	expressed protein	2.257
253664_at	AT4G30210	NADPH-cytochrome p450 reductase, putative / NADPH-ferrihemoprotein reductase, putative similar to NADPH-cytochrome	2.249
258792_at	AT3G04640	glycine-rich protein predicted proteins, Arabidopsis thaliana	2.244
247573_at	AT5G61160	transferase family protein similar to anthocyanin 5-aromatic acyltransferase from Gentiana triflora GI:4185599, malonyl	2.239
255753_at	AT1G18570	myb family transcription factor (MYB51) contains PFAM profile: PF00249	2.233
266259_at	AT2G27830	expressed protein	2.225
254759_at	AT4G13180	short-chain dehydrogenase/reductase (SDR) family protein similar to short-chain type dehydrogenase/reductase SP:Q08632 [Picea	2.223
253332_at	AT4G33420	peroxidase, putative identical to class III peroxidase ATP32 [Arabidopsis thaliana] gi|17530547|gb|AAL40837; identical to cDNA	2.216
254042_at	AT4G25810	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase,	2.194
264746_at	AT1G62300	WRKY family transcription factor similar to putative DNA-binding protein GI:7268215 from [Arabidopsis thaliana]	2.191
256835_at	AT3G22890	sulfate adenylyltransferase 1 / ATP-sulfurylase 1 (APS1) nearly identical to ATP sulfurylase (APS1) [Arabidopsis thaliana]	2.188
259272_at	AT3G01290	band 7 family protein similar to hypersensitive-induced response protein [Zea mays] GI:7716470; contains Pfam profile PF01145:	2.183

260592_at	AT1G55850	cellulose synthase family protein similar to cellulose synthase catalytic subunit [gi:13925881] from Nicotiana alata, cellulose	2.18
262072_at	AT1G59590	expressed protein	2.169
258606_at	AT3G02840	[AT3G02840, immediate-early fungal elicitor family protein similar to immediate-early fungal elicitor protein CMPG1 (GI:14582200)	2.168
266368_at	AT2G41380	embryo-abundant protein-related similar to embryo-abundant protein [Picea glauca] GI:1350531	2.162
246293_at	AT3G56710	sigA-binding protein identical to SigA binding protein [Arabidopsis thaliana] gi|6980074|gb|AAF34713; contains Pfam PF05678: VQ	2.161
257751_at	AT3G18690	[AT3G18690, VQ motif-containing protein contains PF05678: VQ motif];[AT3G18680, aspartate/glutamate/uridylate kinase family	2.16
245866_s_at	AT1G57990	[AT1G57990, purine permease-related low similarity to purine permease [Arabidopsis thaliana] GI:7620007; contains Pfam profile	2.152
250676_at	AT5G06320	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein / NDR1/HIN1-like protein 3 similar to	2.143
251884_at	AT3G54150	embryo-abundant protein-related similar to embryo-abundant protein [Picea glauca] GI:1350531	2.12
256017_at	AT1G19180	expressed protein	2.116
256337_at	AT1G72060	expressed protein	2.115
264213_at	AT1G65390	disease resistance protein (TIR class), putative domain signature TIR exists, suggestive of a disease resistance protein.	2.114
256453_at	AT1G75270	dehydroascorbate reductase, putative similar to GI:6939839 from [Oryza sativa]	2.111
253485_at	AT4G31800	WRKY family transcription factor	2.108
245193_at	AT1G67810	Fe-S metabolism associated domain-containing protein contains Pfam PF02657: Fe-S metabolism associated domain	2.102
264153_at	AT1G65390	disease resistance protein (TIR class), putative domain signature TIR exists, suggestive of a disease resistance protein.	2.099
246532_at	AT5G15870	glycosyl hydrolase family 81 protein similar to beta-glucan-elicitor receptor GI:1752734 from [Glycine max]	2.089
258436_at	AT3G16720	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)	2.08
264365_s_at	AT1G03220	[AT1G03220, extracellular dermal glycoprotein, putative / EDGP, putative similar to extracellular dermal glycoprotein EDGP	2.08
248327_at	AT5G52750	heavy-metal-associated domain-containing protein Pfam profile PF00403: Heavy-metal-associated domain	2.077
247279_at	AT5G64310	arabinogalactan-protein (AGP1) identical to gi:3883120 gb:AAC77823	2.075
251636_at	AT3G57530	calcium-dependent protein kinase, putative / CDPK, putative similar to calmodulin-domain protein kinase CDPK isoform 7 [Arabidopsis	2.074
246289_at	AT3G56880	VQ motif-containing protein contains PF05678: VQ motif	2.07

247137_at	AT5G66210	calcium-dependent protein kinase family protein / CDPK family protein contains Pfam domains, PF00069: Protein kinase domain	2.07
258282_at	AT3G26910	hydroxyproline-rich glycoprotein family protein common family member:At2g33490 [Arabidopsis thaliana]	2.064
255622_at	AT4G01070	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl	2.062
263478_at	AT2G31880	[AT2G31880, leucine-rich repeat transmembrane protein kinase, putative];[AT2G31890, expressed protein]	2.06
256526_at	AT1G66090	disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance	2.041
262649_at	AT1G14040	EXS family protein / ERD1/XPR1/SYG1 family protein similar to PHO1 protein [Arabidopsis thaliana] GI:20069032; contains Pfam	2.033
248719_at	AT5G47910	respiratory burst oxidase protein D (RbohD) / NADPH oxidase identical to respiratory burst oxidase protein D from Arabidopsis	2.029
247925_at	AT5G57560	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (TCH4)	2.025
262935_at	AT1G79410	transporter-related low similarity to organic anion transporter 3 [Rattus norvegicus] GI:5545293; contains Pfam profile PF00083:	2.004
267293_at	AT2G23810	senescence-associated family protein similar to senescence-associated protein 5 [Hemerocallis hybrid cultivar]	1.977
248606_at	AT5G49450	bZIP family transcription factor similar to bZIP transcription factor GI:1769891 from [Arabidopsis thaliana]	1.96
260656_at	AT1G19380	expressed protein	1.955
255502_at	AT4G02410	lectin protein kinase family protein contains Pfam domains, PF00069: Protein kinase domain, PF00139: Legume lectins beta	1.953
262832_s_at	AT1G14870	expressed protein similar to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04749: Protein of unknown	1.948
251937_at	AT3G53400	expressed protein	1.947
249459_at	AT5G39580	peroxidase, putative identical to peroxidase ATP24a [Arabidopsis thaliana] gi|1890313|emb|CAA72484	1.939
249835_s_at	AT5G23490	[AT5G23490, expressed protein];[AT5G23510, expressed protein]	1.938
265725_at	AT2G32030	GCN5-related N-acetyltransferase (GNAT) family protein contains Pfam profile PF00583: acetyltransferase, GNAT family	1.938
258830_at	AT3G07090	expressed protein	1.922
260974_at	AT1G53430	[AT1G53430, leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich	1.916
262383_at	AT1G72940	disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance	1.911
246944_at	AT5G25450	ubiquinol-cytochrome C reductase complex 14 kDa protein, putative similar to SP|P48502 Ubiquinol-cytochrome C reductase complex	1.898
249918_at	AT5G19240	expressed protein	1.885

265184_at	AT1G23710	expressed protein	1.885
248981_at	AT5G45110	ankyrin repeat family protein / BTB/POZ domain-containing protein contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain,	1.881
264756_at	AT1G61370	S-locus lectin protein kinase family protein contains Pfam domains, PF00954: S-locus glycoprotein family, PF00069: Protein kinase	1.878
247433_at	AT5G62540	ubiquitin-conjugating enzyme 3 (UBC3) E2; identical to gi:431261, SP:P42746	1.877
265572_at	AT2G28210	carbonic anhydrase family protein similar to storage protein (dioscorin) [Dioscorea cayenensis] GI:433463; contains Pfam	1.875
245313_at	AT4G15420	PRLI-interacting factor K nearly identical to PRLI-interacting factor K [Arabidopsis thaliana] GI:11139266; contains Pfam profiles	1.862
245369_at	AT4G15975	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)	1.846
258787_at	AT3G11840	U-box domain-containing protein low similarity to immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] GI:14582200;	1.846
251176_at	AT3G63380	calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA12) identical to SP|Q9LY77 Potential	1.833
247488_at	AT5G61820	expressed protein MtN19, Medicago truncatula, EMBL:MTY15367	1.828
252976_s_at	AT4G38550	expressed protein	1.828
251507_at	AT3G59080	aspartyl protease family protein contains similarity to CND41, chloroplast nucleoid DNA binding protein (GI:2541876) [Nicotiana	1.815
267451_at	AT2G33710	AP2 domain-containing transcription factor family protein similar to RAP2.6 (GI:17065542) {Arabidopsis thaliana}	1.814
261143_at	AT1G19770	purine permease-related low similarity to purine permease [Arabidopsis thaliana] GI:7620007; contains Pfam profile PF03151:	1.809
250054_at	AT5G17860	cation exchanger, putative (CAX7) contains similarity to SWISS-PROT:Q9HC58 NKX3_HUMAN Sodium/potassium/calcium	1.803
264655_at	AT1G09070	C2 domain-containing protein / src2-like protein, putative similar to cold-regulated gene SRC2 [Glycine max] GI:2055230; contains	1.803
261718_at	AT1G18390	protein kinase family protein contains protein kinase domain, Pfam:PF00069	1.801
262801_at	AT1G21010	expressed protein	1.795
248794_at	AT5G47220	ethylene-responsive element-binding factor 2 (ERF2) identical to SP|O80338 Ethylene responsive element binding factor 2 (AtERF2)	1.793
250826_at	AT5G05220	expressed protein	1.791
248964_at	AT5G45340	cytochrome P450 family protein similar to SP|Q42569|C901_ARATH Cytochrome P450 90A1 (SP:Q42569)	1.784
265674_at	AT2G32190	expressed protein	1.784
247283_at	AT5G64250	2-nitropropane dioxygenase family / NPD family contains Pfam profile PF03060: oxidoreductase, 2-nitropropane dioxygenase	1.779

260243_at	AT1G63720	expressed protein similar to putative protein GB:CAA18164 [Arabidopsis thaliana]	1.772
265199_s_at	AT2G36770	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl	1.761
250990_at	AT5G02280	[AT5G02280, synbindin, putative similar to Swiss-Prot:Q9ES56 synbindin (TRS23 homolog) [Mus musculus]];[AT5G02290, protein	1.758
261193_at	AT1G32920	expressed protein	1.758
261650_at	AT1G27770	calcium-transporting ATPase 1, plasma membrane-type / Ca(2+)-ATPase isoform 1 (ACA1) / plastid envelope ATPase 1 (PEA1)	1.749
266017_at	AT2G18690	expressed protein	1.739
246305_at	AT3G51890	expressed protein protein At2g40060 - Arabidopsis thaliana, EMBL:AF002109	1.736
251336_at	AT3G61190	BON1-associated protein 1 (BAP1) identical to BON1-associated protein 1 [Arabidopsis thaliana] GI:15487384; contains Pfam profile	1.732
264745_at	AT1G62180	5'-adenylylsulfate reductase 2, chloroplast (APR2) (APSR) / adenosine 5'-phosphosulfate 5'-adenylylsulfate (APS)	1.728
267623_at	AT2G39650	expressed protein contains Pfam profile PF04720: Protein of unknown function (DUF506)	1.723
265841_at	AT2G35710	glycogenin glucosyltransferase (glycogenin)-related low similarity to glycogenin-2 from Homo sapiens [SP|O15488]	1.721
247811_at	AT5G58430	exocyst subunit EXO70 family protein leucine zipper-containing protein, Lycopersicon esculentum, PIR:S21495; contains Pfam	1.719
253630_at	AT4G30490	AFG1-like ATPase family protein contains Pfam profile: PF03969 AFG1-like ATPase	1.716
249942_at	AT5G22300	nitrilase 4 (NIT4) identical to SP|P46011 Nitrilase 4 (EC 3.5.5.1) {Arabidopsis thaliana}	1.713
264663_at	AT1G09970	leucine-rich repeat transmembrane protein kinase, putative Similar to A. thaliana receptor-like protein kinase (gb|RLK5_ARATH). ESTs	1.71
248146_at	AT5G54940	eukaryotic translation initiation factor SUI1, putative similar to SP|P32911 Protein translation factor SUI1 {Saccharomyces	1.708
251640_at	AT3G57450	expressed protein	1.708
248162_at	AT5G54500	quinone reductase, putative similar to 1,4-benzoquinone reductase [Phanerochaete chrysosporium][GI:4454993]; contains flavodoxin	1.703
264624_at	AT1G08930	early-responsive to dehydration stress protein (ERD6) / sugar transporter family protein identical to ERD6 protein {Arabidopsis	1.701
256922_at	AT3G19010	oxidoreductase, 2OG-Fe(II) oxygenase family protein contains similarity to flavonol synthase (FLS) from [Solanum tuberosum]	1.689
265662_at	AT2G24500	zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type	1.685
261526_at	AT1G14380	[AT1G14380, calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif];[AT1G14370, protein	1.682
259312_at	AT3G05200	zinc finger (C3HC4-type RING finger) family protein (ATL6) contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING	1.678

251428_at	AT3G60140	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-	1.673
247293_at	AT5G64510	expressed protein	1.667
260399_at	AT1G72520	lipoxygenase, putative similar to lipoxygenase gi:1495804 [Solanum tuberosum], gi:1654140 [Lycopersicon esculentum], GB:CAB56692	1.665
266101_at	AT2G37940	expressed protein	1.664
245788_at	AT1G32120	expressed protein contains Pfam profile PF04819: Family of unknown function (DUF716) (Plant viral-response family)	1.659
249770_at	AT5G24110	WRKY family transcription factor	1.646
266536_at	AT2G16900	expressed protein	1.636
259792_at	AT1G29690	expressed protein	1.626
254694_at	AT4G17900	zinc-binding family protein similar to zinc-binding protein [Pisum sativum] GI:16117799; contains Pfam profile PF04640 : Protein of	1.62
250944_at	AT5G03380	heavy-metal-associated domain-containing protein similar to farnesylated protein ATFP2 [GI:4097545]; contains Pfam profile	1.615
257654_at	AT3G13310	DNAJ heat shock N-terminal domain-containing protein similar to J11 protein [Arabidopsis thaliana] GI:9843641; contains Pfam	1.614
258921_at	AT3G10500	no apical meristem (NAM) family protein similar to to NAC2 (GI:645671) [Arabidopsis thaliana]; contains Pfam PF02365: No	1.609
255787_at	AT2G33590	cinnamoyl-CoA reductase family similar to cinnamoyl-CoA reductase from Pinus taeda [GI:17978649], Eucalyptus gunnii	1.605
265679_at	AT2G32240	expressed protein contains Pfam profile: PF04508 viral A-type inclusion protein repeat	1.605
245051_at	AT2G23320	WRKY family transcription factor identical to WRKY DNA-binding protein 15 GI:13506742 from [Arabidopsis thaliana]	1.6
261177_at	AT1G04770	male sterility MS5 family protein similar to male sterility MS5 [Arabidopsis thaliana] GI:3859112; contains Pfam profile PF00515	1.6
267076_at	AT2G41090	calmodulin-like calcium-binding protein, 22 kDa (CaBP-22) identical to SP|P30187 22 kDa calmodulin-like calcium-binding protein	1.6
247215_at	AT5G64905	expressed protein	1.597
250252_at	AT5G13750	transporter-related	1.597
258682_at	AT3G08720	serine/threonine protein kinase (PK19) identical to serine/threonine-protein kinase AtPK19 (Ribosomal-protein S6 kinase homolog)	1.597
253884_at	AT4G27670	25.3 kDa small heat shock protein, chloroplast precursor (HSP25.3-P) identical to small heat shock protein, chloroplast precursor	1.596
246108_at	AT5G28630	glycine-rich protein	1.595
257700_at	AT3G12740	LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein Similar to GI:4585976; GI:4966357; GI:4835763;	1.59

245662_at	AT1G28190	expressed protein	1.582
249987_at	AT5G18490	expressed protein	1.581
266290_at	AT2G29490	glutathione S-transferase, putative similar to glutathione S-transferase 103-1A [Arabidopsis thaliana] SWISS-PROT:P46421	1.581
258207_at	AT3G14050	RelA/SpoT protein, putative (RSH2) nearly identical to RelA/SpoT homolog RSH2 [Arabidopsis thaliana] GI:7141306; contains Pfam	1.58
256433_at	AT3G10985	wound-responsive protein-related similar to SP|P20144 Wound-induced protein 1 {Solanum tuberosum}	1.576
253273_at	AT4G34180	cyclase family protein contains Pfam profile: PF04199 putative cyclase	1.573
255568_at	AT4G01250	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain	1.571
253140_at	AT4G35480	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	1.566
265093_at	AT1G03905	ABC transporter family protein similar to NBD-like protein GB:AAD20643	1.562
255811_at	AT4G10250	22.0 kDa ER small heat shock protein (HSP22.0-ER) identical to endomembrane-localized small heat shock protein GI:511795 from	1.559
264299_s_at	AT1G78860	curculin-like (mannose-binding) lectin family protein low similarity to Ser/Thr protein kinase [Zea mays] GI:2598067; contains Pfam	1.555
254200_at	AT4G24110	expressed protein	1.546
262085_at	AT1G56060	expressed protein	1.546
261081_at	AT1G07350	transformer serine/arginine-rich ribonucleoprotein, putative similar to GB:Y09506 from [Nicotiana tabacum] (Plant Mol. Biol. 35 (3),	1.539
245277_at	AT4G15550	UDP-glucose:indole-3-acetate beta-D-glucosyltransferase (IAGLU) identical to UDP-glucose:indole-3-acetate beta-D-	1.537
251342_at	AT3G60690	auxin-responsive family protein similar to auxin-induced protein SAUR-AC1 (GP:546362) (PIR:T06084)[Arabidopsis thaliana]	1.537
266461_at	AT2G47730	glutathione S-transferase 6 (GST6) identical to GB:X95295. Based on identical cDNA hits, the translation is now 40 AAs longer at the	1.535
261618_at	AT1G33110	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam	1.531
266888_s_at	AT2G44750	[AT2G44750, thiamin pyrophosphokinase, putative similar to thiamin pyrophosphokinase [Mus musculus]	1.529
256756_at	AT3G25610	haloacid dehalogenase-like hydrolase family protein similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from Mus	1.527
260915_at	AT1G02660	lipase class 3 family protein contains Pfam profile PF01764: Lipase	1.526
262455_at	AT1G11310	seven transmembrane MLO family protein / MLO-like protein 2 (MLO2) idenctical to membrane protein Mlo2 [Arabidopsis thaliana]	1.523
266155_at	AT1G64950	cytochrome P450, putative similar to cytochrome P450 89A2 (CYPLXXXIX) (SP:Q42602) [Arabidopsis thaliana];similar to	1.519

245768_at	AT1G33590	disease resistance protein-related / LRR protein-related contains leucine rich-repeat domains Pfam:PF00560,	1.518
267389_at	AT2G44460	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-	1.517
261344_at	AT1G79710	integral membrane transporter family protein similar to high affinity folic acid/methotrexate transporter 5 (GI:21898554) [Leishmania	1.514
245528_at	AT4G15530	pyruvate phosphate dikinase family protein contains Pfam profiles: PF01326 pyruvate phosphate dikinase, PEP/pyruvate binding	1.513
256518_at	AT1G66080	expressed protein	1.512
260362_at	AT1G70530	protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain	1.511
267392_at	AT2G44490	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-	1.509
247272_at	AT5G64300	riboflavin biosynthesis protein, putative (RIBA) similar to SP|P47924 {Arabidopsis thaliana}, SP|P51695 Riboflavin	1.508
251061_at	AT5G01830	armadillo/beta-catenin repeat family protein / U-box domain- containing protein contains Pfam domain, PF00514: Armadillo/beta-	1.503
254050_s_at	AT4G25690	[AT4G25690, expressed protein];[AT4G25670, expressed protein]	1.503
252193_at	AT3G50060	myb family transcription factor contains Pfam profile: PF00249 myb- like DNA-binding domain; identical to cDNA MYB-related protein	1.499
252679_at	AT3G44260	CCR4-NOT transcription complex protein, putative similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit	1.496
264400_at	AT1G61800	glucose-6-phosphate/phosphate translocator, putative similar to glucose-6-phosphate/phosphate-translocator precursor GI:2997591	1.493
261265_at	AT1G26800	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	1.49
262772_at	AT1G13210	haloacid dehalogenase-like hydrolase family protein similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1)	1.486
256046_at	AT1G07130	OB-fold nucleic acid binding domain-containing protein contains InterPro entry IPR004365: OB-fold nucleic acid binding domain	1.485
256454_at	AT1G75280	isoflavone reductase, putative identical to SP|P52577 Isoflavone reductase homolog P3 (EC 1.3.1.-) {Arabidopsis thaliana}; contains	1.484
263823_s_at	AT2G40350	AP2 domain-containing transcription factor, putative (DREB2) similar to DREB2A (GP:3738230) and DREB2B (GP:3738232)	1.48
247679_at	AT5G59540	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to desacetoxyvindoline-4-hydroxylase [Catharanthus roseus]	1.479
255904_at	AT1G17860	trypsin and protease inhibitor family protein / Kunitz family protein similar to LeMir (miraculin homolog) GI:2654440 from	1.477
256999_at	AT3G14200	DNAJ heat shock N-terminal domain-containing protein low similarity to SP|O75190|DJB6_HUMAN DnaJ homolog subfamily B	1.477
256522_at	AT1G66160	U-box domain-containing protein similar to immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] GI:14582200;	1.476
250289_at	AT5G13190	expressed protein	1.473

266299_at	AT2G29450	glutathione S-transferase (103-1A) identical to Swiss-Prot:P46421 glutathione S-transferase 103-1A [Arabidopsis thaliana]	1.471
257784_at	AT3G26980	ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain	1.468
264986_at	AT1G27130	glutathione S-transferase, putative similar to glutathione S-transferase GB: AAF22517 GI:6652870 from [Papaver somniferum]	1.46
256050_at	AT1G07000	exocyst subunit EXO70 family protein similar to leucine zipper protein GI:10177020 from [Arabidopsis thaliana] contains Pfam	1.455
258984_at	AT3G08970	DNAJ heat shock N-terminal domain-containing protein low similarity to PIR|A47079|A47079 heat shock protein dnaJ -	1.455
261719_at	AT1G18380	expressed protein	1.455
262899_at	AT1G59870	ABC transporter family protein similar to PDR5-like ABC transporter GI:1514643 from [Spirodela polyrhiza]	1.448
257216_at	AT3G14990	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative supporting cDNA gi|11908017|gb|AF326856.1|;	1.445
258452_at	AT3G22370	alternative oxidase 1a, mitochondrial (AOX1A) identical to GB:Q39219 [SP|Q39219] from [Arabidopsis thaliana]	1.443
255039_at	AT4G09570	calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase [Arabidopsis thaliana]	1.44
264645_at	AT1G08940	phosphoglycerate/bisphosphoglycerate mutase family protein contains Pfam profile PF00300: phosphoglycerate mutase family	1.439
254396_at	AT4G21680	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family	1.438
261453_at	AT1G21130	O-methyltransferase, putative similar to GI:2781394	1.435
260522_x_at	AT2G41730	expressed protein	1.432
253061_at	AT4G37610	TAZ zinc finger family protein / BTB/POZ domain-containing protein contains Pfam PF00651 : BTB/POZ domain; contains Pfam	1.426
266168_at	AT2G38870	protease inhibitor, putative similar to SP|P24076 Glu S.griseus protease inhibitor (BGIA) {Momordica charantia}; contains Pfam	1.423
259297_at	AT3G05360	disease resistance family protein / LRR family protein contains leucine rich-repeat domains Pfam:PF00560,	1.419
245777_at	AT1G73540	MutT/nudix family protein low similarity to SP|Q09790 Diadenosine 5',5'''-P1,P6-hexaphosphate hydrolase (EC 3.6.1.-) (Ap6A	1.417
253453_at	AT4G31860	protein phosphatase 2C, putative / PP2C, putative protein phosphatase 2C, Schizosaccharomyces pombe, PIR2:S54297	1.412
255524_at	AT4G02330	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase	1.41
262325_at	AT1G64160	disease resistance-responsive family protein / dirigent family protein similar to dirigent protein GB:AAF25365 GI:6694709 from [Thuja	1.41
258395_at	AT3G15500	no apical meristem (NAM) family protein (NAC3) identical to AtNAC3 [Arabidopsis thaliana] GI:12060424; contains Pfam	1.409
258100_at	AT3G23550	[AT3G23550, MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum]	1.408

249237_at	AT5G42050	expressed protein similar to gda-1 [Pisum sativum] GI:2765418	1.406
259911_at	AT1G72680	cinnamyl-alcohol dehydrogenase, putative similar to cinnamyl-alcohol dehydrogenase GB:AAC35846 [Medicago sativa],	1.406
262382_at	AT1G72920	disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance	1.406
263221_at	AT1G30620	UDP-D-xylose 4-epimerase, putative (MUR4) similar to SP|P55180 UDP-glucose 4-epimerase (EC 5.1.3.2) from Bacillus subtilis,	1.406
258939_at	AT3G10020	expressed protein	1.404
261445_at	AT1G28380	expressed protein	1.403
260477_at	AT1G11050	protein kinase family protein contains protein kinase domain, Pfam:PF00069	1.402
264107_s_at	AT2G13800	[AT2G13800, leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich	1.401
267336_at	AT2G19310	expressed protein	1.401
252131_at	AT3G50930	AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004	1.391
245757_at	AT1G35140	phosphate-responsive protein, putative similar to phi-1 (phosphate-induced gene) [Nicotiana tabacum] GI:3759184; contains Pfam	1.39
249984_at	AT5G18400	expressed protein contains Pfam profile PF05093: Protein of unknown function (DUF689)	1.388
267280_at	AT2G19450	diacylglycerol O-acyltransferase / acyl CoA:diacylglycerol acyltransferase (DGAT) identical to gi:5050913, gi:6625553	1.381
254059_at	AT4G25200	23.6 kDa mitochondrial small heat shock protein (HSP23.6-M) contains Pfam profile PF00011: Hsp20/alpha crystallin family	1.376
261934_at	AT1G22400	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl	1.373
248205_at	AT5G54300	expressed protein contains similarity to cotton fiber expressed protein 1 [Gossypium hirsutum] gi|3264828|gb|AAC33276	1.37
256185_at	AT1G51700	Dof-type zinc finger domain-containing protein (ADOF1) identical to cDNA adof1 mRNA for dof zinc finger protein, GI:3608260;	1.368
266834_s_at	AT2G30020	protein phosphatase 2C, putative / PP2C, putative similar to protein phosphatase 2C (GI:4587992){Arabidopsis thaliana}	1.366
247691_at	AT5G59720	18.1 kDa class I heat shock protein (HSP18.1-CI) identical to 18.2 kDa class I heat shock protein (HSP 18.2)	1.364
254248_at	AT4G23270	protein kinase family protein contains Pfam PF00069: Protein kinase domain	1.363
245329_at	AT4G14365	zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein contains Pfam profile: PF00097 zinc finger, C3HC4	1.358
246327_at	AT1G16670	protein kinase family protein contains protein kinase domain, Pfam:PF00069; similar to receptor-like serine/threonine kinase	1.355
260648_at	AT1G08050	zinc finger (C3HC4-type RING finger) family protein low similarity to SP|P79263 Inter-alpha-trypsin inhibitor heavy chain H4 precursor	1.351

253637_at	AT4G30390	expressed protein	1.35
246931_at	AT5G25170	expressed protein	1.347
264929_at	AT1G60730	aldo/keto reductase family protein contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family	1.346
252928_at	AT4G38940	kelch repeat-containing F-box family protein low similarity to SKP1 interacting partner 6 [Arabidopsis thaliana] GI:10716957; contains	1.343
248330_at	AT5G52810	ornithine cyclodeaminase/mu-crystallin family protein contains Pfam PF02423: Ornithine cyclodeaminase/mu-crystallin family	1.341
258915_at	AT3G10640	SNF7 family protein contains Pfam domain, PF03357: SNF7 family	1.337
252422_at	AT3G47550	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)	1.323
246195_at	AT4G36410	ubiquitin-conjugating enzyme 17 (UBC17) E2; identical to gi:2801446	1.321
259841_at	AT1G52200	expressed protein similar to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04749: Protein of unknown	1.32
246870_at	AT5G26030	ferrochelatase I identical to Swiss-Prot:P42043 ferrochelatase I, chloroplast/mitochondrial precursor (EC 4.99.1.1) (Protoheme ferro-	1.318
253780_at	AT4G28400	protein phosphatase 2C, putative / PP2C, putative protein phosphatase 2C-fission yeast, PIR2:S54297	1.316
266231_at	AT2G02220	leucine-rich repeat transmembrane protein kinase, putative	1.316
267300_at	AT2G30140	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl	1.314
248713_at	AT5G48180	kelch repeat-containing protein contains Pfam PF01344: Kelch motif (5 repeats) ;similar to Tip elongation aberrant protein 1 (Cell	1.311
257822_at	AT3G25230	peptidyl-prolyl cis-trans isomerase / FK506-binding protein (ROF1) identical to rotamase FKBP (ROF1) GB:U49453 [Arabidopsis	1.31
251400_at	AT3G60420	expressed protein	1.307
247509_at	AT5G62020	heat shock factor protein, putative (HSF6) / heat shock transcription factor, putative (HTSF6) identical to heat shock transcription factor	1.306
252037_at	AT3G51920	calmodulin-9 (CAM9) identical to calmodulin 9 GI:5825602 from [Arabidopsis thaliana]; contains Pfam profile PF00036: EF hand	1.303
253911_at	AT4G27300	S-locus protein kinase, putative similar to receptor protein kinase [Ipomoea trifida] gi|836954|gb|AAC23542; contains S-locus	1.303
267381_at	AT2G26190	calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif	1.299
245272_at	AT4G17250	expressed protein	1.298
250287_at	AT5G13330	AP2 domain-containing transcription factor family protein similar to AP2 domain containing protein RAP2.6, Arabidopsis thaliana,	1.293
260975_at	AT1G53430	[AT1G53430, leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich	1.293

257805_at	AT3G18830	mannitol transporter, putative similar to mannitol transporter [Apium graveolens var. dulce] GI:12004316; contains Pfam profile	1.287
267624_at	AT2G39660	protein kinase, putative similar to protein kinase gi|166809|gb|AAA18853	1.282
254890_at	AT4G11600	glutathione peroxidase, putative	1.277
265737_at	AT2G01180	phosphatidic acid phosphatase family protein / PAP2 family protein similar to phosphatidic acid phosphatase 2a2 [Cavia porcellus]	1.277
258665_at	AT3G08710	thioredoxin family protein similar to thioredoxin H-type GB:P29448 SP|P29448 [Arabidopsis thaliana], Thioredoxin H-type 2 (TRX-H2)	1.276
264000_at	AT2G22500	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein	1.274
247240_at	AT5G64660	U-box domain-containing protein similar to immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] GI:14582200;	1.271
263403_at	AT2G04040	MATE efflux family protein contains Pfam profile: PF01554 uncharacterized membrane protein family	1.27
248040_at	AT5G55970	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	1.266
252483_at	AT3G46600	scarecrow transcription factor family protein scarecrow-like 11 - Arabidopsis thaliana, EMBL:AF036307	1.266
259749_at	AT1G71100	ribose 5-phosphate isomerase-related similar to ribose-5-phosphate isomerase GI:18654317 from [Spinacia oleracea]	1.263
265276_at	AT2G28400	expressed protein contains Pfam profile PF04520: Protein of unknown function, DUF584	1.262
249339_at	AT5G41100	expressed protein	1.261
254532_at	AT4G19660	ankyrin repeat family protein / BTB/POZ domain-containing protein contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain,	1.261
247065_s_at	AT5G66910	[AT5G66910, disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a	1.257
263320_at	AT2G47180	galactinol synthase, putative similar to galactinol synthase, isoform GolS-1 GI:5608497 from [Ajuga reptans]	1.257
245642_at	AT1G25275	expressed protein	1.251
250580_at	AT5G07440	glutamate dehydrogenase 2 (GDH2) identical to glutamate dehydrogenase 2 (GDH 2) [Arabidopsis thaliana] SWISS-	1.251
255895_at	AT1G17990	[AT1G17990, 12-oxophytodienoate reductase, putative similar to OPR1 [GI:3882355] and OPR2 [GI:3882356]];[AT1G18020, 12-	1.251
253104_at	AT4G36010	pathogenesis-related thaumatin family protein similar to receptor serine/threonine kinase PR5K [Arabidopsis thaliana] GI:1235680;	1.25
245119_at	AT2G41640	expressed protein contains Pfam domain, PF04577: Protein of unknown function (DUF563)	1.243
250098_at	AT5G17350	expressed protein	1.241
254424_at	AT4G21510	F-box family protein contains Pfam PF00646: F-box domain; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250	1.241

255844_at	AT2G33580	protein kinase family protein / peptidoglycan-binding LysM domain-containing protein protein kinase [Arabidopsis thaliana] GI:2852449;	1.237
256356_s_at	AT1G66500	[AT1G66500, zinc finger (C2H2-type) family protein contains Prosite PS00028: Zinc finger, C2H2 type, domain; similar to S-locus	1.237
261899_at	AT1G80820	cinnamoyl-CoA reductase, putative identical to CCR2 (GI:12407990), similar to cinnamoyl CoA reductase from	1.231
258406_at	AT3G17611	rhomboid family protein / zinc finger protein-related contains Pfam profiles PF01694: Rhomboid family, PF00641: Zn-finger in Ran	1.23
266792_at	AT2G02860	sucrose transporter / sucrose-proton symporter (SUC3) identical to sucrose transporter [Arabidopsis thaliana] GI:8052190; similar to	1.228
266746_s_at	AT4G02520	[AT4G02520, glutathione S-transferase, putative];[AT2G02930, glutathione S-transferase, putative]	1.226
250829_at	AT5G04720	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a disease resistance	1.222
253281_at	AT4G34138	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl	1.222
256861_at	AT3G23920	beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative similar to beta-amylase enzyme [Arabidopsis thaliana]	1.221
264524_at	AT1G10070	branched-chain amino acid aminotransferase 2 / branched-chain amino acid transaminase 2 (BCAT2) identical to SP|Q9M439	1.214
250549_at	AT5G07860	transferase family protein similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus	1.213
264660_at	AT1G09940	glutamyl-tRNA reductase 2 / GluTR (HEMA2) identical to glutamyl-tRNA reductase 2, chloroplast [SP|P49294]	1.211
251237_at	AT3G62420	bZIP transcription factor family protein similar to common plant regulatory factor 6 GI:9650826 from [Petroselinum crispum]	1.21
248821_at	AT5G47070	protein kinase, putative similar to protein kinase [Lophopyrum elongatum] gi|13022177|gb|AAK11674	1.208
260746_at	AT1G78380	glutathione S-transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya]	1.208
254652_at	AT4G18170	WRKY family transcription factor similar to DNA-binding protein 2 GI:4322940 from [Nicotiana tabacum]; contains Pfam profile:	1.207
258201_at	AT3G13910	expressed protein	1.207
252009_at	AT3G52800	zinc finger (AN1-like) family protein contains Pfam domain, PF01428: AN1-like Zinc finger	1.205
252851_at	AT4G40080	epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related contains Pfam PF01417: ENTH	1.204
256793_at	AT3G22160	VQ motif-containing protein contains PF05678: VQ motif	1.204
262635_at	AT1G06570	4-hydroxyphenylpyruvate dioxygenase (HPD) identical to 4-hydroxyphenylpyruvate dioxygenase (HPD) SP:P93836	1.204
258979_at	AT3G09440	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3) identical to SP|O65719 Heat shock cognate 70 kDa protein 3	1.197
250818_at	AT5G04930	phospholipid-transporting ATPase 1 / aminophospholipid flippase 1 / magnesium-ATPase 1 (ALA1) nearly identical to SP|P98204	1.187

260314_at	AT1G63830	proline-rich family protein contains proline-rich extensin domains, INTERPRO:IPR002965; contains 1 predicted transmembrane	1.186
262505_at	AT1G21680	expressed protein similar to TolB protein precursor (SP:Q9ZDM5) {Rickettsia prowazekii}; ESTs gb|N96028, gb|F14286, gb|T20680,	1.184
264460_at	AT1G10170	NF-X1 type zinc finger family protein contains Pfam PF01422: NF-X1 type zinc finger; similar to transcriptional repressor NF-X1	1.184
245251_at	AT4G17615	calcineurin B-like protein 1 (CBL1) identical to calcineurin B-like protein 1 (GI:3309082) [Arabidopsis thaliana]	1.182
252533_at	AT3G46110	expressed protein	1.182
257785_at	AT3G26980	ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain	1.18
258114_at	AT3G14650	[AT3G14650, cytochrome P450, putative similar to GB:Q05047 from [Catharanthus roseus]];[AT3G14660, cytochrome P450,	1.178
262148_at	AT1G52560	26.5 kDa class I small heat shock protein-like (HSP26.5-P) contains Pfam profile: PF00011 Hsp20/alpha crystallin family;	1.178
247125_at	AT5G66070	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	1.174
264841_at	AT1G03740	protein kinase family protein contains protein kinase domain, Pfam:PF00069	1.173
253324_at	AT4G33940	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	1.168
249188_at	AT5G42830	transferase family protein similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus	1.167
254083_at	AT4G24920	protein transport protein SEC61 gamma subunit, putative similar to Swiss-Prot:Q19967 protein transport protein SEC61 gamma	1.166
260005_at	AT1G67930	[AT1G67930, Golgi transport complex protein-related similar to golgi transport complex protein (GTC90) GB:5453670 [Homo	1.164
267493_at	AT2G30400	ovate family protein 57% similar to ovate protein (GI:23429649) [Lycopersicon esculentum]; contains TIGRFAM TIGR01568 :	1.16
264777_at	AT1G08630	L-allo-threonine aldolase-related similar to L-allo-threonine aldolase (EC 4.1.2.-) (L-allo-TA) (L-allo-threonine acetaldehyde-lyase)	1.157
246098_at	AT5G20400	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to naringenin,2-oxoglutarate 3-dioxygenase (flavonone-3-hydroxylase)	1.156
249583_at	AT5G37770	touch-responsive protein / calmodulin-related protein 2, touch-induced (TCH2) identical to calmodulin-related protein 2,touch-	1.152
266072_at	AT2G18700	glycosyl transferase family 20 protein / trehalose-phosphatase family protein similar to trehalose-6-phosphate synthase SL-TPS/P	1.151
265067_at	AT1G03850	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	1.15
262677_at	AT1G75860	expressed protein	1.148
267289_at	AT2G23770	protein kinase family protein / peptidoglycan-binding LysM domain-containing protein contains Pfam domains, PF00069: Protein	1.147
267069_at	AT2G41010	VQ motif-containing protein contains PF05678: VQ motif	1.144

248698_at	AT5G48380	leucine-rich repeat family protein / protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains leucine-	1.14
256968_at	AT3G21070	ATP-NAD kinase family protein contains Pfam domain, PF01513: ATP-NAD kinase	1.136
258650_at	AT3G09830	protein kinase, putative similar to protein kinase [Lophopyrum elongatum] gi|13022177|gb|AAK11674	1.134
251705_at	AT3G56400	WRKY family transcription factor DNA-binding protein 4 WRKY4 - Nicotiana tabacum, EMBL:AF193771	1.133
251722_at	AT3G56200	amino acid transporter family protein low similarity to N system amino acids transporter NAT-1 [Mus musculus] GI:7406950;	1.132
254103_at	AT4G25030	expressed protein	1.132
255504_at	AT4G02200	drought-responsive family protein similar to drought-induced mRNA, Di19 [Arabidopsis thaliana] gi|469110|emb|CAA55321	1.129
265327_at	AT2G18210	expressed protein	1.128
248868_at	AT5G46780	VQ motif-containing protein contains PF05678: VQ motif	1.127
245247_at	AT4G17230	scarecrow-like transcription factor 13 (SCL13)	1.126
263228_at	AT1G30700	FAD-binding domain-containing protein similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme)	1.124
267230_at	AT2G44080	expressed protein	1.123
257407_at	AT1G27100	expressed protein contains Pfam profile: PF04601 protein of unknown function (DUF569	1.12
258275_at	AT3G15760	expressed protein	1.119
259626_at	AT1G42990	bZIP transcription factor family protein contains Pfam profile: PF00170: bZIP transcription factor	1.119
262165_at	AT1G75020	phospholipid/glycerol acyltransferase family protein contains Pfam profile: PF01553 Acyltransferase	1.119
263704_at	AT1G31130	expressed protein	1.117
267486_at	AT2G02800	protein kinase (APK2b) identical to protein kinase APK2b [Arabidopsis thaliana] gi|2852449|dbj|BAA24695	1.109
267537_at	AT2G41880	guanylate kinase 1 (GK-1) identical to guanylate kinase (GK-1) [Arabidopsis thaliana] gi|7861795|gb|AAF70408	1.108
250339_at	AT5G11670	malate oxidoreductase, putative similar to NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (SP|P12628) {Phaseolus	1.107
262503_at	AT1G21670	expressed protein similar to TolB protein precursor (SP:P50601) {Pseudomonas aeruginosa}	1.105
248665_at	AT5G48655	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	1.104
258683_at	AT3G08760	protein kinase family protein contains protein kinase domain, Pfam:PF00069	1.102

252939_at	AT4G39230	isoflavone reductase, putative similar to allergenic isoflavone reductase-like protein Bet v 6.0102 [Betula pendula][GI:10764491];	1.1
256221_at	AT1G56300	DNAJ heat shock N-terminal domain-containing protein similar to SP|Q9QYI7 DnaJ homolog subfamily B member 8 Mus musculus;	1.099
264867_at	AT1G24150	formin homology 2 domain-containing protein / FH2 domain-containing protein contains formin homology 2 domain,	1.09
260387_at	AT1G74100	sulfotransferase family protein similar to SP|P52837 Flavonol 4'-sulfotransferase (EC 2.8.2.-) (F4-ST) {Flaveria chloraefolia};	1.089
253161_at	AT4G35770	senescence-associated protein (SEN1) identical to senescence-associated protein GI:1046270 from [Arabidopsis thaliana]	1.088
255230_at	AT4G05390	ferredoxin--NADP(+) reductase, putative / adrenodoxin reductase, putative strong similarity to SP|P41345 Ferredoxin--NADP	1.088
263457_at	AT2G22300	ethylene-responsive calmodulin-binding protein, putative (SR1) identical to partial sequence of ethylene-induced calmodulin-binding	1.088
253999_at	AT4G26200	1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative similar to ACC synthase from Malus x	1.085
259018_at	AT3G07390	auxin-responsive protein / auxin-induced protein (AIR12) identical (with 7 residue gap) to auxin-induced protein AIR12 GI:11357190	1.082
251624_at	AT3G57280	expressed protein contains Pfam profile PF03647: Uncharacterised protein family (UPF0136)	1.075
258105_at	AT3G23605	UBX domain-containing protein contains Pfam profile PF00789: UBX domain	1.073
266821_at	AT2G44840	ethylene-responsive element-binding protein, putative	1.072
247864_s_at	AT1G25083	[AT1G25083, anthranilate synthase beta subunit, putative strong similarity to anthranilate synthase beta subunit GI:403434 from	1.07
250304_at	AT5G12110	elongation factor 1B alpha-subunit 1 (eEF1Balpha1) identical to elongation factor 1B alpha-subunit [Arabidopsis thaliana]	1.065
251196_at	AT3G62950	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	1.063
259980_at	AT1G76520	auxin efflux carrier family protein contains auxin efflux carrier domain, Pfam:PF03547	1.063
249393_at	AT5G40170	disease resistance family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-4	1.06
252993_at	AT4G38540	monooxygenase, putative (MO2) identical to GI:3426064	1.06
258173_at	AT3G21630	protein kinase family protein contains protein kinase domain, Pfam:PF00069	1.059
261225_at	AT1G20100	expressed protein	1.058
264580_at	AT1G05340	expressed protein	1.058
263472_at	AT2G31955	molybdopterin biosynthesis protein, putative / molybdenum cofactor biosynthesis enzyme, putative 3' fragment; strong similarity to	1.056
247930_at	AT5G57060	expressed protein	1.055

251597_at	AT3G57750	protein kinase, putative similar to wall-associated kinase 1 [Arabidopsis thaliana] gi|3549626|emb|CAA08794; contains protein	1.055
255967_at	AT1G22280	protein phosphatase 2C, putative / PP2C, putative similar to protein phosphatase type 2C GI:4336436 from [Lotus japonicus]	1.052
252214_at	AT3G50260	AP2 domain-containing transcription factor, putative EREBP-3 homolog, Stylosanthes hamata, EMBL:U91982	1.051
254665_at	AT4G18340	glycosyl hydrolase family 17 protein similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from [Nicotiana tabacum]	1.048
263265_at	AT2G38820	expressed protein contains Pfam profile PF04720: Protein of unknown function (DUF506)	1.048
250692_at	AT5G06560	expressed protein contains Pfam profile PF04576: Protein of unknown function, DUF593	1.044
252470_at	AT3G46930	protein kinase family protein contains protein kinase domain, Pfam:PF00069	1.044
258351_at	AT3G17700	cyclic nucleotide-binding transporter 1 / CNBT1 (CNGC20) identical to cyclic nucleotide-binding transporter 1 (CNBT1) GI:8131898 from	1.043
261901_at	AT1G80920	DNAJ heat shock N-terminal domain-containing protein similar to SP|Q05646 Chaperone protein dnaJ Erysipelothrix rhusiopathiae,	1.043
253125_at	AT4G36040	DNAJ heat shock N-terminal domain-containing protein (J11) identical to dnaJ heat shock protein J11 [Arabidopsis thaliana]	1.042
256183_at	AT1G51660	mitogen-activated protein kinase kinase (MAPKK), putative (MKK4) identical to MAP kinase kinase 4 [Arabidopsis thaliana]	1.042
265440_at	AT2G20960	expressed protein pEARLI 4 gene product [Arabidopsis thaliana] GI:871782	1.04
251649_at	AT3G57330	calcium-transporting ATPase, plasma membrane-type, putative / Ca2+-ATPase, putative (ACA11) identical to	1.035
255110_at	AT4G08770	peroxidase, putative identical to class III peroxidase ATP38 [Arabidopsis thaliana] gi|17530568|gb|AAL40851; similar to	1.033
267154_at	AT2G30870	[AT2G30870, glutathione S-transferase, putative supported by cDNA GI:443698 GB:D17673];[AT2G30880, pleckstrin homology	1.033
256633_at	AT3G28340	galactinol synthase, putative	1.026
261957_at	AT1G64660	Cys/Met metabolism pyridoxal-phosphate-dependent enzyme family protein similar to SP|P13254 Methionine gamma-lyase (EC	1.026
254861_at	AT4G12040	zinc finger (AN1-like) family protein contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger	1.021
257866_at	AT3G17770	dihydroxyacetone kinase family protein contains Pfam domains, PF02733: DAK1 domain and PF02734: DAK2 domain	1.021
264304_at	AT1G78895	expressed protein	1.02
249895_at	AT5G22500	acyl CoA reductase, putative / male-sterility protein, putative similar to acyl CoA reductase [Simmondsia chinensis] GI:5020215;	1.018
258094_at	AT3G14690	cytochrome P450, putative similar to GB:Q05047 from [Catharanthus roseus]	1.018
248676_at	AT5G48850	male sterility MS5 family protein similar to male sterility MS5 [Arabidopsis thaliana] GI:3859112; contains Pfam profile PF00515	1.015

261506_at	AT1G71697	choline kinase, putative similar to GmCK2p choline kinase gi|1438881|gb|AAC49375	1.013
252415_at	AT3G47340	asparagine synthetase 1 [glutamine-hydrolyzing] / glutamine-dependent asparagine synthetase 1 (ASN1) identical to SP|P49078	1.012
252652_at	AT3G44720	prephenate dehydratase family protein similar to bacterial PheA gene products	1.008
251144_at	AT5G01210	transferase family protein contains Pfam profile PF02458 transferase family	1.006
254707_at	AT4G18010	inositol polyphosphate 5-phosphatase II (IP5PII) nearly identical to inositol polyphosphate 5-phosphatase II [Arabidopsis thaliana]	1.005
246214_at	AT4G36990	heat shock factor protein 4 (HSF4) / heat shock transcription factor 4 (HSTF4) identical to heat shock transcription factor 4 (HSF4)	1.004
264568_at	AT1G05150	calcium-binding EF hand family protein low similarity to O-linked GlcNAc transferase [Homo sapiens] GI:2266994; contains Pfam	-1
261594_at	AT1G33240	trihelix DNA-binding protein, putative similar to GTL1 [Arabidopsis thaliana] GI:2664198	-1.001
245947_at	AT5G19530	spermine/spermidine synthase family protein similar to SP|P09158 Spermidine synthase (EC 2.5.1.16) (Putrescine	-1.002
263333_at	AT2G03890	phosphatidylinositol 3- and 4-kinase family protein low similarity to phosphatidylinositol 4-kinase type-II beta [Homo sapiens]	-1.002
264315_at	AT1G70370	BURP domain-containing protein / polygalacturonase, putative similar to polygalacturonase isoenzyme 1 beta subunit	-1.002
264770_at	AT1G23030	armadillo/beta-catenin repeat family protein / U-box domain-containing protein contains Pfam domain, PF00514: Armadillo/beta-	-1.002
250801_at	AT5G04960	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase	-1.009
250892_at	AT5G03760	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from [Bradyrhizobium	-1.02
262045_at	AT1G80240	expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642	-1.02
267619_at	AT2G26730	leucine-rich repeat transmembrane protein kinase, putative	-1.021
262951_at	AT1G75500	nodulin MtN21 family protein similar to MtN21 GB:CAA75575 GI:2598575 from (Medicago truncatula) (Mol. Plant Microbe	-1.024
264898_at	AT1G23205	invertase/pectin methylesterase inhibitor family protein low similarity to pectinesterase from Phaseolus vulgaris SP|Q43111,	-1.035
251169_at	AT3G63210	expressed protein identical to senescence-associated protein SAG102 (GI::22331931) [Arabidopsis thaliana] (unpublished);	-1.044
258293_at	AT3G23430	phosphate transporter, putative (PHO1) identical to PHO1 protein [Arabidopsis thaliana] GI:20069032; supporting cDNA	-1.047
262871_at	AT1G65010	expressed protein similar to endosome-associated protein (GI:1016368) [Homo sapiens]; similar to Centromeric protein E	-1.052
253849_at	AT4G28080	expressed protein	-1.069
252199_at	AT3G50270	transferase family protein similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus	-1.072

246275_at	AT4G36540	basic helix-loop-helix (bHLH) family protein contains Pfam domain, PF00010: Helix-loop-helix DNA-binding domain	-1.074
251174_at	AT3G63200	patatin-related low similarity to patatin-like latex protein allergen Hev b 7 - Hevea brasiliensis, EMBL:AF113546; contains patatin	-1.074
260618_at	AT1G53230	TCP family transcription factor 3 (TCP3) identical to transcription factor 3 (TCP3) [Arabidopsis thaliana] (GI:3243274); similar to	-1.074
251413_at	AT3G60320	expressed protein contains Pfam profiles: PF04782: protein of unknown function (DUF632), PF04783: protein of unknown function	-1.079
249675_at	AT5G35940	jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767; contains Pfam profile	-1.081
263406_at	AT2G04160	subtilisin-like protease (AIR3) almost identical to subtilisin-like protease AIR3 GI:4218991 from [Arabidopsis thaliana], missing 200	-1.082
259173_at	AT3G03640	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-	-1.09
259632_at	AT1G56430	nicotianamine synthase, putative similar to nicotianamine synthase [Lycopersicon esculentum][GI:4753801], nicotianamine synthase 2	-1.093
260130_s_at	AT1G66280	[AT1G66280, glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM	-1.094
263841_at	AT2G36870	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase,	-1.094
253736_at	AT4G28780	GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384)	-1.101
262263_at	AT1G70940	auxin transport protein, putative (PIN3) similar to auxin transport protein [Arabidopsis thaliana] gi|5817301|gb|AAD52695	-1.101
263552_x_at	AT5G49080	[AT5G49080, proline-rich extensin-like family protein contains proline-rich extensin domains,	-1.101
252123_at	AT3G51240	naringenin 3-dioxygenase / flavanone 3-hydroxylase (F3H) identical to GI:3790548	-1.125
262598_at	AT1G15260	expressed protein EST gb|N65467 comes from this gene	-1.127
266131_at	AT2G45160	scarecrow transcription factor family protein	-1.127
253582_at	AT4G30670	expressed protein	-1.132
247914_at	AT5G57530	[AT5G57530, xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan	-1.137
259525_at	AT1G12560	expansin, putative (EXP7) similar to expansin GI:2828241 from [Brassica napus]; alpha-expansin gene family, PMID:11641069	-1.146
255632_at	AT4G00680	actin-depolymerizing factor, putative strong similarity to SP|P30175 Actin-depolymerizing factor (ADF) {Lilium longiflorum}; contains	-1.156
247162_at	AT5G65730	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase,	-1.158
265471_at	AT2G37130	peroxidase 21 (PER21) (P21) (PRXR5) identical to SP|Q42580 Peroxidase 21 precursor (EC 1.11.1.7) (Atperox P21) (PRXR5)	-1.171
254820_s_at	AT4G12510	[AT4G12510, protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to 14 kDa polypeptide [Catharanthus	-1.175

247645_at	AT5G60530	late embryogenesis abundant protein-related / LEA protein-related similar to late embryogenesis abundant protein [Picea glauca]	-1.184
259786_at	AT1G29660	GDSL-motif lipase/hydrolase family protein low similarity to family II lipase EXL1 [Arabidopsis thaliana] GI:15054382; contains InterPro	-1.189
260770_at	AT1G49220	[AT1G49220, zinc finger (C3HC4-type RING finger) family protein contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING	-1.193
260950_s_at	AT1G06090	[AT1G06090, fatty acid desaturase family protein similar to delta 9 acyl-lipid desaturase GB:BAA25180 GI:2970034 (ADS1) from	-1.203
261562_at	AT1G01750	actin-depolymerizing factor, putative strong similarity to SP|P30175 Actin-depolymerizing factor (ADF) {Lilium longiflorum}; contains	-1.204
250533_at	AT5G08640	flavonol synthase 1 (FLS1) identical to SP|Q96330; contains PF03171 2OG-Fe(II) oxygenase superfamily	-1.23
251843_x_at	AT3G54590	proline-rich extensin-like family protein contains proline-rich extensin domains, INTERPRO:IPR002965	-1.233
246510_at	AT5G15410	cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC2) identical to cyclic nucleotide-gated cation	-1.243
253495_at	AT4G31850	[AT4G31850, pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat];[AT4G31860, protein	-1.253
256352_at	AT1G54970	proline-rich family protein similar to proline-rich protein GI:170048 from [Glycine max]	-1.255
253667_at	AT4G30170	peroxidase, putative identical to peroxidase ATP8a [Arabidopsis thaliana] gi|1546706|emb|CAA67361	-1.256
258080_at	AT3G25930	universal stress protein (USP) family protein contains Pfam PF00582: universal stress protein family	-1.303
257297_at	AT3G28040	leucine-rich repeat transmembrane protein kinase, putative contains Pfam profiles: PF00560 leucine rich repeat, PF00069	-1.312
265050_at	AT1G52070	jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767; contains Pfam profile	-1.32
254550_at	AT4G19690	iron-responsive transporter (IRT1) identical to Fe(II) transport protein [Arabidopsis thaliana] gi|1353266|gb|AAB01678; member of	-1.396
253255_at	AT4G34760	auxin-responsive family protein auxin-induced protein X15, Glycine max, PIR2:JQ1097	-1.415
260557_at	AT2G43610	glycoside hydrolase family 19 protein similar to chitinase GI:17799 from [Brassica napus]; contains Pfam profiles PF00182: Chitinase	-1.46
256751_at	AT3G27170	chloride channel protein (CLC-b) identical to CLC-b chloride channel protein GB:CAA96058 from [Arabidopsis thaliana] (J. Biol.	-1.471
259276_at	AT3G01190	peroxidase 27 (PER27) (P27) (PRXR7) identical to SP|Q43735 Peroxidase 27 precursor (EC 1.11.1.7) (Atperox P27) (PRXR7)	-1.481
261500_at	AT1G28400	expressed protein similar to E6 (GI:1000090) [Gossypium barbadense]	-1.488
252238_at	AT3G49960	peroxidase, putative identical to peroxidase ATP21a [Arabidopsis thaliana] gi|1546696|emb|CAA67339	-1.489
249477_s_at	AT5G38940	[AT5G38940, germin-like protein, putative similar to germin-like portein GLP9 [SP|Q9LEA7]; contains PS00725 Germin family	-1.539
250207_at	AT5G13930	chalcone synthase / naringenin-chalcone synthase identical to SP|P13114	-1.571

251226_at	AT3G62680	proline-rich family protein contains proline-rich region, INTERPRO:IPR000694	-1.63
259790_s_at	AT1G29430	auxin-responsive family protein similar to auxin-induced protein 10a 6B {SP:P33083) [Glycine max]	-1.689
259328_at	AT3G16440	jacalin lectin family protein contains Pfam profile: PF01419 jacalin-like lectin domain; similar to myrosinase-binding protein homolog	-1.73
265102_at	AT1G30870	cationic peroxidase, putative similar to cationic peroxidase (gi|1232069); similar to EST gb|AI100412	-1.854
247871_at	AT5G57530	[AT5G57530, xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan	-1.862
252833_at	AT4G40090	arabinogalactan-protein (AGP3) InDels between the genome sequence and the cDNA prevent identical translations from being	-1.922
248636_at	AT5G49080	proline-rich extensin-like family protein contains proline-rich extensin domains, INTERPRO:IPR002965	-1.946
264014_at	AT2G21210	auxin-responsive protein, putative similar to small auxin-up regulated protein SAUR (GI:3043536) [Raphanus sativus]	-1.977
252972_at	AT4G38840	auxin-responsive protein, putative auxin-inducible SAUR gene, Raphanus sativus,AB000708	-2.054
255516_at	AT4G02270	pollen Ole e 1 allergen and extensin family protein contains Pfam domain, PF01190: Pollen proteins Ole e I family	-2.087
250778_at	AT5G05500	pollen Ole e 1 allergen and extensin family protein contains Pfam domain, PF01190: Pollen proteins Ole e I family	-2.141
246652_at	AT5G35190	proline-rich extensin-like family protein contains proline-rich extensin domains, INTERPRO:IPR002965	-2.185
250059_at	AT5G17820	peroxidase 57 (PER57) (P57) (PRXR10) identical to SP|Q43729 Peroxidase 57 precursor (EC 1.11.1.7) (Atperox P57) (PRXR10)	-2.243
254044_at	AT4G25820	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (XTR9)	-2.504
246991_at	AT5G67400	peroxidase 73 (PER73) (P73) (PRXR11) identical to SP|Q43873 Peroxidase 73 precursor (EC 1.11.1.7) (Atperox P73) (PRXR11)	-2.619
264567_s_at	AT1G05250	[AT1G05250, peroxidase, putative similar to peroxidase; peroxidase ATP11a [Arabidopsis thaliana]	-2.669
262427_s_at	AT1G47600	[AT1G47600, glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM	-3.136
253998_at	AT4G26010	peroxidase, putative peroxidase ATP13a - Arabidopsis thaliana, PID:e264765; identical to cDNA class III peroxidase ATP35,	-3.261