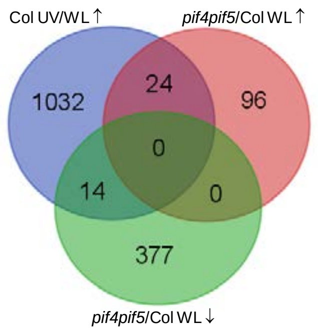
Table S3. UV-B-induced genes in Col wild type and/or genes misexpressed in *pif4-101 pif5-3* in white light grown plants (lists corresponding to Figure 2F).

Description

Col UV/WL Up and *pif45* /Col WL Up: 24 genes
Col UV/WL Up and *pif45* /Col WL Down: 14 genes
Col UV/WL Up: 1032 genes
pif45 /Col WL Up: 96 genes
pif45 /Col WL Down: 377 genes



Col UV/WL Up and *pif45* /Col WL Up			Col UV/WL			*pif45* /Col WL		
AGI	gene	description	Col_UV/WL_FC	pvalue	pvalue_with_FDR	*pif45* /Col_WL_FC	pvalue	pvalue_with_FDR
AT5G10760	*AT5G10760*	Eukaryotic aspartyl protease family protein	33.9	5.2E-03	1.9E-02	51.2	8.9E-04	1.5E-02
AT3G44450	*AT3G44450*	hypothetical protein	30.7	2.7E-21	2.6E-18	2.2	3.4E-04	7.6E-03
AT3G21080	*AT3G21080*	ABC transporter-like protein	11.0	8.1E-04	4.1E-03	11.5	5.6E-04	1.1E-02
AT1G13610	*AT1G13610*	alpha/beta-Hydrolases superfamily protein	10.7	3.4E-11	1.9E-09	2.4	2.7E-03	3.1E-02
AT5G20230	*BCB*	blue-copper-binding protein	6.4	4.8E-10	1.9E-08	3.7	4.4E-07	7.6E-05
AT1G26790	*AT1G26790*	Dof-type zinc finger DNA-binding family protein	6.4	2.2E-11	1.3E-09	2.0	1.4E-03	2.0E-02
AT5G24420	*PGL5*	6-phosphogluconolactonase 5	5.9	1.7E-10	8.1E-09	2.1	9.9E-04	1.6E-02
AT3G28220	*AT3G28220*	TRAF-like family protein	5.8	1.9E-09	6.5E-08	2.7	4.9E-05	2.0E-03
AT2G40200	*AT2G40200*	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	3.9	1.7E-06	2.2E-05	2.1	4.5E-03	4.4E-02
AT4G15680	*AT4G15680*	Thioredoxin superfamily protein	3.9	4.0E-04	2.3E-03	3.6	6.5E-04	1.2E-02
AT4G26150	*CGA1*	cytokinin-responsive gata factor 1	3.4	1.3E-10	6.1E-09	2.3	3.4E-07	6.2E-05
AT4G15660	*AT4G15660*	Thioredoxin superfamily protein	3.3	7.1E-03	2.5E-02	6.2	4.9E-05	2.0E-03
AT5G11410	*AT5G11410*	Protein kinase superfamily protein	3.3	2.0E-04	1.3E-03	2.7	1.6E-03	2.1E-02
AT3G18217	*MIR157C*		3.2	6.0E-04	3.2E-03	2.6	4.3E-03	4.2E-02
AT3G15850	*FAD5*	fatty acid desaturase 5	2.8	6.7E-09	1.9E-07	2.1	3.8E-06	3.5E-04
AT4G15670	*AT4G15670*	Thioredoxin superfamily protein	2.7	3.8E-03	1.5E-02	2.8	2.5E-03	3.0E-02
AT4G15700	*AT4G15700*	Thioredoxin superfamily protein	2.6	4.2E-03	1.6E-02	4.5	2.1E-05	1.1E-03
AT3G20440	*EMB2729*	Alpha amylase family protein	2.6	1.9E-05	1.7E-04	2.0	9.1E-04	1.5E-02
AT4G29030	*AT4G29030*	Putative membrane lipoprotein	2.5	1.5E-05	1.4E-04	2.6	8.0E-06	6.0E-04
AT1G22400	*UGT85A1*	UDP-Glycosyltransferase superfamily protein	2.5	6.1E-08	1.3E-06	2.1	1.5E-06	1.9E-04
AT2G29670	*AT2G29670*	Tetratricopeptide repeat (TPR)-like superfamily protein	2.4	1.6E-05	1.5E-04	2.1	2.3E-04	5.8E-03
AT5G33370	*AT5G33370*	GDSL-like Lipase/Acylhydrolase superfamily protein	2.3	1.5E-02	4.6E-02	3.0	1.5E-03	2.1E-02
AT5G62360	*AT5G62360*	Plant invertase/pectin methylesterase inhibitor superfamily protein	2.3	7.1E-04	3.7E-03	2.3	9.4E-04	1.5E-02
AT2G33850	*AT2G33850*	E6-like protein	2.0	5.2E-04	2.8E-03	2.0	3.9E-04	8.4E-03

Col UV/WL Up and *pif45* /Col WL Down			Col UV/WL			*pif45* /Col WL		
AGI	gene	description	Col_UV/WL_FC	pvalue	pvalue_with_FDR	*pif45* /Col_WL_FC	pvalue	pvalue_with_FDR
AT5G17780	*AT5G17780*	alpha/beta-Hydrolases superfamily protein	6.4	2.4E-14	3.3E-12	-3.3	1.5E-07	3.5E-05
AT4G13810	*RLP47*	receptor like protein 47	4.8	1.2E-06	1.7E-05	-3.1	3.2E-03	3.5E-02
AT5G44568	*AT5G44568*	transmembrane protein	4.4	2.1E-06	2.6E-05	-5.5	1.1E-04	3.3E-03
AT1G66100	*AT1G66100*	Plant thionin	4.4	2.5E-04	1.5E-03	-6.7	4.7E-05	1.9E-03
AT5G05390	*LAC12*	laccase 12	4.2	4.4E-05	3.5E-04	-4.0	1.7E-03	2.3E-02
AT1G19510	*RL5*	RAD-like 5	3.8	9.3E-05	6.7E-04	-7.2	1.5E-04	4.3E-03
AT2G36590	*ProT3*	proline transporter 3	3.4	9.9E-10	3.6E-08	-2.4	5.8E-06	4.8E-04
AT3G22235	*AT3G22235*	cysteine-rich TM module stress tolerance protein	3.2	2.6E-03	1.1E-02	-5.7	3.7E-03	3.8E-02
AT5G17700	*AT5G17700*	MATE efflux family protein	2.7	5.6E-06	6.2E-05	-2.2	1.8E-04	4.8E-03
AT1G78440	*ATGA2OX1*	gibberellin 2-beta-dioxygenase	2.5	1.4E-03	6.6E-03	-4.7	2.0E-04	5.2E-03
AT4G29110	*AT4G29110*	cotton fiber protein	2.4	2.7E-05	2.4E-04	-2.1	6.3E-04	1.2E-02
AT2G29370	*AT2G29370*	NAD(P)-binding Rossmann-fold superfamily protein	2.3	4.2E-04	2.4E-03	-2.8	7.8E-04	1.3E-02
AT1G62560	*FMO GS-OX3*	flavin-monooxygenase glucosinolate S-oxygenase 3	2.3	6.3E-04	3.3E-03	-2.3	2.9E-03	3.2E-02
AT1G18710	*MYB47*	myb domain protein 47	2.0	1.3E-03	6.2E-03	-3.7	2.2E-05	1.2E-03

Col UV/WL Up			Col UV/WL			*pif45* /Col WL		
AGI	gene	description	Col_UV/WL_FC	pvalue	pvalue_with_FDR	*pif45* /Col_WL_FC	pvalue	pvalue_with_FDR
AT2G22590	*AT2G22590*	UDP-Glycosyltransferase superfamily protein	1047.8	2.4E-24	1.3E-20	-1.1	9.0E-01	9.6E-01
AT3G22840	*ELIP1*	Chlorophyll A-B binding family protein	470.0	3.6E-16	9.4E-14	1.5	5.7E-01	7.8E-01
AT4G34550	*AT4G34550*	F-box protein	340.6	1.2E-16	3.5E-14	-1.1	9.3E-01	9.8E-01
AT4G31870	*GPX7*	glutathione peroxidase 7	221.3	1.6E-21	1.9E-18	1.4	5.2E-01	7.4E-01
AT4G15480	*UGT84A1*	UDP-Glycosyltransferase superfamily protein	164.6	2.1E-21	2.2E-18	-1.3	5.0E-01	7.4E-01
AT5G17030	*UGT78D3*	UDP-glucosyl transferase 78D3	155.4	3.1E-06	3.7E-05	1.0	1.0E+00	1.0E+00
AT5G62210	*AT5G62210*	Embryo-specific protein 3, (ATS3)	148.9	2.2E-22	3.4E-19	-1.3	5.4E-01	7.6E-01
AT1G64340	*AT1G64340*	Serine/Threonine-kinase	130.0	7.0E-06	7.4E-05	6.0	1.8E-01	4.3E-01
AT5G13930	*TT4*	Chalcone and stilbene synthase family protein	102.0	2.2E-13	2.4E-11	-1.2	6.3E-01	8.3E-01
AT5G08640	*FLS1*	flavonol synthase 1	92.8	7.6E-15	1.2E-12	-1.0	9.9E-01	1.0E+00
AT1G75040	*PR5*	pathogenesis-related protein 5	69.3	2.8E-10	1.2E-08	4.3	5.6E-02	2.2E-01
AT1G76290	*AT1G76290*	AMP-dependent synthetase and ligase family	63.9	2.8E-04	1.7E-03	1.0	1.0E+00	1.0E+00
AT5G17040	*AT5G17040*	UDP-Glycosyltransferase superfamily protein	61.6	9.6E-17	2.9E-14	-1.4	4.7E-01	7.1E-01
AT2G42540	*COR15A*	cold-regulated 15a	61.4	6.6E-06	7.1E-05	-18.1	2.5E-01	5.1E-01
AT1G69560	*MYB105*	myb domain protein 105	55.4	1.0E-04	7.2E-04	3.5	3.2E-01	5.8E-01
AT3G62610	*MYB11*	myb domain protein 11	53.3	4.8E-10	2.0E-08	-1.1	9.2E-01	9.7E-01
AT1G80340	*GA3OX2*	gibberellin 3-oxidase 2	50.4	2.7E-12	2.1E-10	2.9	5.8E-02	2.2E-01
AT1G66540	*AT1G66540*	Cytochrome P450 superfamily protein	41.8	5.5E-16	1.3E-13	2.0	4.3E-02	1.9E-01
AT3G10185	*AT3G10185*	Gibberellin-regulated family protein	41.8	8.7E-03	2.9E-02	1.0	1.0E+00	1.0E+00
AT2G16367	*AT2G16367*		41.7	3.3E-05	2.8E-04	-1.1	9.6E-01	9.9E-01
AT4G12320	*CYP706A6*	cytochrome P450, family 706, subfamily A, polypeptide 6	37.5	7.1E-13	6.6E-11	1.2	7.7E-01	9.0E-01
AT5G55570	*AT5G55570*	transmembrane protein	36.3	1.5E-10	7.0E-09	1.1	9.3E-01	9.8E-01

AT3G07620	*AT3G07620*	glycosyltransferase	34.4	1.6E-08	4.0E-07	-1.1	9.1E-01	9.7E-01
AT4G23496	*SP1L5*	SPIRAL1-like5	33.0	9.3E-11	4.7E-09	1.3	7.0E-01	8.7E-01
AT5G48880	*KAT5*	peroxisomal 3-keto-acyl-CoA thiolase 2	31.4	4.4E-20	3.0E-17	1.2	2.3E-01	4.9E-01
AT4G22090	*AT4G22090*	Pectin lyase-like superfamily protein	31.1	4.4E-05	3.5E-04	1.6	7.2E-01	8.7E-01
AT1G52770	*AT1G52770*	Phototropic-responsive NPH3 family protein	29.7	1.3E-05	1.2E-04	3.6	2.0E-01	4.5E-01
AT3G30460	*AT3G30460*	RING/U-box superfamily protein	29.6	3.4E-09	1.1E-07	1.2	8.3E-01	9.3E-01
AT2G36750	*UGT73C1*	UDP-glucosyl transferase 73C1	27.7	2.7E-11	1.6E-09	2.7	4.8E-02	2.0E-01
AT5G07990	*TT7*	Cytochrome P450 superfamily protein	26.6	5.4E-23	1.2E-19	-1.0	9.9E-01	1.0E+00
AT5G09930	*ABCF2*	ABC transporter family protein	25.9	1.5E-14	2.2E-12	1.1	8.1E-01	9.2E-01
AT2G24000	*scpl22*	serine carboxypeptidase-like 22	25.6	4.5E-03	1.7E-02	1.0	1.0E+00	1.0E+00
AT1G10370	*ERD9*	Glutathione S-transferase family protein	24.9	8.7E-25	6.3E-21	-1.4	1.6E-02	9.9E-02
AT4G18422	*AT4G18422*	transmembrane protein	23.1	2.9E-05	2.5E-04	-1.1	9.4E-01	9.8E-01
AT3G63320	*AT3G63320*	Protein phosphatase 2C family protein	23.0	7.0E-03	2.4E-02	11.0	5.4E-02	2.1E-01
AT2G15020	*AT2G15020*	hypothetical protein	22.4	9.7E-12	6.3E-10	1.8	6.7E-02	2.4E-01
AT5G17220	*GSTF12*	glutathione S-transferase phi 12	21.7	1.2E-10	5.7E-09	-1.2	6.3E-01	8.2E-01
AT1G27940	*ABCB13*	P-glycoprotein 13	21.4	3.1E-10	1.3E-08	-2.7	1.4E-01	3.7E-01
AT2G27420	*AT2G27420*	Cysteine proteinases superfamily protein	21.3	2.4E-15	4.6E-13	1.0	9.7E-01	9.9E-01
AT1G12570	*AT1G12570*	Glucose-methanol-choline (GMC) oxidoreductase family protein	21.2	1.7E-09	5.8E-08	1.1	8.8E-01	9.6E-01
AT5G05270	*CHIL*	Chalcone-flavanone isomerase family protein	20.9	1.2E-21	1.5E-18	-1.5	8.5E-03	6.7E-02
AT5G66740	*AT5G66740*	spindle assembly abnormal protein (DUF620)	20.2	5.1E-09	1.5E-07	2.3	1.3E-01	3.6E-01
AT2G47460	*MYB12*	myb domain protein 12	19.7	4.9E-22	6.6E-19	1.4	1.3E-02	8.7E-02
AT1G07330	*AT1G07330*	dentin sialophosphoprotein	19.7	2.8E-08	6.5E-07	1.7	3.8E-01	6.4E-01
AT1G65060	*4CL3*	4-coumarate:CoA ligase 3	19.6	1.8E-14	2.5E-12	1.1	7.0E-01	8.7E-01
AT4G10250	*ATHSP22.0*	HSP20-like chaperones superfamily protein	16.7	4.5E-05	3.6E-04	3.5	1.2E-01	3.4E-01
AT3G55120	*TT5*	Chalcone-flavanone isomerase family protein	15.2	7.2E-25	6.3E-21	-1.6	1.3E-05	8.4E-04
AT5G15960	*KIN1*	stress-responsive protein (KIN1) / stress-induced protein (KIN1)	14.8	5.6E-09	1.6E-07	1.0	9.5E-01	9.9E-01
AT4G04840	*MSRB6*	methionine sulfoxide reductase B6	14.3	2.0E-14	2.9E-12	1.5	3.0E-02	1.5E-01
AT5G62240	*AT5G62240*	Cell cycle regulated microtubule associated protein	14.2	1.8E-11	1.1E-09	1.3	4.7E-01	7.1E-01
AT5G51030	*AT5G51030*	NAD(P)-binding Rossmann-fold superfamily protein	14.0	1.4E-10	6.7E-09	2.4	1.6E-02	1.0E-01
AT2G03520	*UPS4*	ureide permease 4	13.3	2.5E-10	1.1E-08	-1.6	3.1E-01	5.7E-01
AT3G52740	*AT3G52740*	hypothetical protein	13.2	1.3E-20	9.9E-18	1.6	2.4E-03	2.9E-02
AT2G20825	*ULT2*	Developmental regulator, ULTRAPETALA	12.7	2.8E-06	3.4E-05	2.7	9.5E-02	3.0E-01
AT3G21560	*UGT84A2*	UDP-Glycosyltransferase superfamily protein	12.7	1.3E-23	3.6E-20	1.0	7.2E-01	8.8E-01
AT1G65490	*AT1G65490*	transmembrane protein	12.6	1.4E-14	2.1E-12	1.6	3.0E-02	1.5E-01
AT5G36910	*THI2.2*	thionin 2.2	12.1	9.4E-14	1.1E-11	-1.4	9.0E-02	2.9E-01
AT1G06000	*AT1G06000*	UDP-Glycosyltransferase superfamily protein	11.3	8.3E-20	5.4E-17	1.0	9.5E-01	9.9E-01
AT3G21150	*BBX32*	B-box 32	11.0	4.0E-12	3.0E-10	1.6	6.7E-02	2.4E-01
AT5G50800	*SWEET13*	Nodulin MtN3 family protein	10.8	8.9E-06	9.1E-05	3.0	6.0E-02	2.3E-01
AT4G27560	*AT4G27560*	UDP-Glycosyltransferase superfamily protein	10.6	4.5E-17	1.5E-14	-1.1	4.4E-01	6.9E-01
AT1G06180	*MYB13*	myb domain protein 13	10.5	1.5E-14	2.2E-12	1.5	6.0E-02	2.3E-01
AT1G65870	*AT1G65870*	Disease resistance-responsive (dirigent-like protein) family protein	10.4	4.4E-13	4.4E-11	1.5	1.0E-01	3.1E-01
AT3G62960	*AT3G62960*	Thioredoxin superfamily protein	10.2	1.3E-05	1.3E-04	-1.2	7.7E-01	9.0E-01
AT5G24150	*SQP1*	FAD/NAD(P)-binding oxidoreductase family protein	10.2	8.6E-13	7.9E-11	-1.1	7.7E-01	9.0E-01
AT1G09500	*AT1G09500*	NAD(P)-binding Rossmann-fold superfamily protein	10.1	4.9E-05	3.8E-04	1.7	4.3E-01	6.8E-01
AT4G05110	*ENT6*	equilibrative nucleoside transporter 6	10.0	1.7E-11	1.1E-09	-1.2	4.9E-01	7.2E-01
AT2G29170	*AT2G29170*	NAD(P)-binding Rossmann-fold superfamily protein	9.9	3.4E-07	5.5E-06	-1.7	3.2E-01	5.8E-01
AT1G23010	*LPR1*	Cupredoxin superfamily protein	9.8	2.7E-14	3.7E-12	-1.3	1.6E-01	4.0E-01
AT1G52990	*AT1G52990*	thioredoxin family protein	9.8	1.1E-06	1.5E-05	1.8	1.9E-01	4.5E-01
AT1G01520	*ASG4*	Homeodomain-like superfamily protein	9.5	6.8E-15	1.1E-12	1.4	7.9E-02	2.7E-01
AT1G76530	*AT1G76530*	Auxin efflux carrier family protein	9.4	5.4E-05	4.2E-04	1.3	7.2E-01	8.7E-01
AT5G04000	*AT5G04000*	hypothetical protein	9.4	1.2E-14	1.8E-12	1.4	8.3E-02	2.8E-01
AT2G25530	*AT2G25530*	AFG1-like ATPase family protein	9.4	1.4E-21	1.7E-18	1.1	5.0E-01	7.3E-01
AT3G23810	*SAHH2*	S-adenosyl-l-homocysteine (SAH) hydrolase 2	9.4	4.5E-15	7.7E-13	-1.8	8.7E-04	1.4E-02
AT5G16530	*PIN5*	Auxin efflux carrier family protein	9.2	3.8E-06	4.4E-05	3.2	1.6E-02	1.0E-01
AT3G10150	*PAP16*	purple acid phosphatase 16	9.1	2.7E-06	3.3E-05	1.4	4.9E-01	7.2E-01
AT3G57020	*AT3G57020*	Calcium-dependent phosphotriesterase superfamily protein	9.1	2.0E-16	5.7E-14	1.0	8.4E-01	9.4E-01
AT5G23730	*RUP2*	Transducin/WD40 repeat-like superfamily protein	9.0	1.3E-19	8.1E-17	1.2	1.2E-01	3.4E-01
AT5G09990	*PROPEP5*	elicitor peptide 5 precursor	9.0	5.3E-09	1.5E-07	1.1	7.0E-01	8.7E-01
AT1G06540	*AT1G06540*	hypothetical protein	9.0	1.8E-09	6.2E-08	-1.9	1.2E-01	3.4E-01
AT4G00970	*CRK41*	cysteine-rich RLK (RECEPTOR-like protein kinase) 41	8.9	8.2E-09	2.2E-07	1.3	4.2E-01	6.7E-01
AT1G02820	*LEA3*	Late embryogenesis abundant 3 (LEA3) family protein	8.7	3.5E-12	2.6E-10	1.2	4.5E-01	7.0E-01
AT3G01550	*PPT2*	phosphoenolpyruvate (pep)/phosphate translocator 2	8.6	5.3E-12	3.8E-10	1.1	5.7E-01	7.9E-01
AT4G18650	*AT4G18650*	transcription factor-like protein	8.6	2.8E-10	1.2E-08	-1.5	2.2E-01	4.8E-01
AT1G57770	*AT1G57770*	FAD/NAD(P)-binding oxidoreductase family protein	8.5	1.3E-18	6.1E-16	1.1	2.8E-01	5.5E-01
AT5G49330	*MYB111*	myb domain protein 111	8.4	5.3E-08	1.1E-06	1.4	3.7E-01	6.3E-01
AT4G26530	*FBA5*	Aldolase superfamily protein	8.4	3.1E-06	3.7E-05	-2.7	1.3E-02	8.8E-02
AT4G37760	*SQE3*	squalene epoxidase 3	7.8	3.5E-17	1.2E-14	-1.1	5.5E-01	7.7E-01
AT5G60900	*RLK1*	receptor-like protein kinase 1	7.6	6.0E-05	4.6E-04	-1.1	8.7E-01	9.5E-01
AT1G66725	*MIR163*		7.6	2.0E-15	3.8E-13	-1.1	4.8E-01	7.2E-01
AT1G56650	*PAP1*	production of anthocyanin pigment 1	7.4	5.5E-03	2.0E-02	1.6	6.0E-01	8.0E-01
AT5G17050	*UGT78D2*	UDP-glucosyl transferase 78D2	7.3	5.1E-23	1.2E-19	1.1	4.6E-01	7.1E-01
AT1G55960	*AT1G55960*	Polyketide cyclase/dehydrase and lipid transport superfamily protein	7.3	6.1E-15	1.0E-12	1.5	1.2E-02	8.1E-02
AT2G18490	*AT2G18490*	C2H2-like zinc finger protein	7.2	9.6E-04	4.7E-03	2.9	9.5E-02	3.0E-01
AT1G55320	*AAE18*	acyl-activating enzyme 18	7.2	2.6E-17	8.9E-15	1.2	1.8E-01	4.2E-01
AT2G36295	*AT2G36295*	hypothetical protein	7.1	1.9E-05	1.7E-04	1.5	4.0E-01	6.6E-01

AT3G51238	*AT3G51238*	Natural antisense transcript overlaps with AT3G51240	7.1	1.8E-06	2.3E-05	-7.4	6.5E-03	5.6E-02
AT1G28610	*AT1G28610*	GDSL-like Lipase/Acylhydrolase superfamily protein	7.1	3.5E-13	3.6E-11	-1.1	6.8E-01	8.5E-01
AT1G65560	*AT1G65560*	Zinc-binding dehydrogenase family protein	7.0	1.7E-18	7.3E-16	1.1	3.6E-01	6.2E-01
AT3G56290	*AT3G56290*	potassium transporter	6.8	1.0E-18	5.0E-16	1.4	5.7E-03	5.1E-02
AT4G13900	*RLP49*	pseudogene of receptor like protein 47	6.8	6.4E-09	1.8E-07	-1.7	1.0E-01	3.1E-01
AT3G46260	*AT3G46260*	kinase-like protein	6.7	2.0E-03	8.6E-03	2.5	1.8E-01	4.3E-01
AT1G14250	*AT1G14250*	GDA1/CD39 nucleoside phosphatase family protein	6.6	1.1E-03	5.1E-03	2.1	2.4E-01	5.1E-01
AT1G03940	*AT1G03940*	HXXXD-type acyl-transferase family protein	6.6	1.1E-03	5.3E-03	-1.6	5.6E-01	7.7E-01
AT2G36145	*AT2G36145*	hypothetical protein	6.6	2.6E-16	7.0E-14	1.4	2.3E-02	1.3E-01
AT1G78570	*RHM1*	rhamnose biosynthesis 1	6.5	1.4E-22	2.4E-19	-1.2	6.5E-02	2.4E-01
AT1G09240	*NAS3*	nicotianamine synthase 3	6.4	2.8E-05	2.4E-04	1.7	2.8E-01	5.4E-01
AT5G22020	*AT5G22020*	Calcium-dependent phosphotriesterase superfamily protein	6.3	4.6E-22	6.6E-19	-1.2	6.0E-02	2.3E-01
AT1G04880	*AT1G04880*	HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain-containing protein	6.3	5.6E-10	2.2E-08	1.4	2.0E-01	4.5E-01
AT3G61400	*AT3G61400*	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	6.3	5.3E-03	1.9E-02	-1.1	9.2E-01	9.7E-01
AT1G47370	*AT1G47370*	Toll-Interleukin-Resistance (TIR) domain family protein	6.3	4.7E-03	1.8E-02	3.2	1.0E-01	3.1E-01
AT4G13410	*ATCSLA15*	Nucleotide-diphospho-sugar transferases superfamily protein	6.3	1.5E-09	5.2E-08	1.4	2.1E-01	4.7E-01
AT1G64940	*CYP89A6*	cytochrome P450, family 87, subfamily A, polypeptide 6	6.3	6.8E-12	4.6E-10	1.1	5.9E-01	8.0E-01
AT2G40460	*AT2G40460*	Major facilitator superfamily protein	6.3	1.3E-14	1.9E-12	-1.4	3.5E-02	1.6E-01
AT2G47370	*AT2G47370*	Calcium-dependent phosphotriesterase superfamily protein	6.2	2.7E-15	5.0E-13	1.1	6.2E-01	8.2E-01
AT5G37550	*AT5G37550*	hypothetical protein	6.1	2.9E-14	3.9E-12	-1.3	1.1E-01	3.2E-01
AT2G36790	*UGT73C6*	UDP-glucosyl transferase 73C6	6.1	2.9E-10	1.3E-08	-1.5	1.3E-01	3.6E-01
AT5G56090	*COX15*	cytochrome c oxidase 15	6.1	3.1E-21	2.8E-18	-1.0	6.6E-01	8.4E-01
AT3G51750	*AT3G51750*	hypothetical protein	6.1	6.2E-12	4.3E-10	1.3	2.2E-01	4.7E-01
AT5G02270	*ABCI20*	non-intrinsic ABC protein 9	6.1	7.5E-21	6.3E-18	1.0	6.6E-01	8.4E-01
AT1G54570	*PES1*	Esterase/lipase/thioesterase family protein	6.0	6.8E-19	3.7E-16	1.1	4.3E-01	6.8E-01
AT1G03495	*AT1G03495*	HXXXD-type acyl-transferase family protein	6.0	1.3E-02	4.0E-02	-1.4	6.9E-01	8.6E-01
AT1G06690	*AT1G06690*	NAD(P)-linked oxidoreductase superfamily protein	6.0	3.5E-21	3.0E-18	-1.1	4.3E-01	6.8E-01
AT4G32770	*VTE1*	tocopherol cyclase, chloroplast / vitamin E deficient 1 (VTE1) / sucrose export defective 1 (SXD1)	5.9	9.4E-18	3.6E-15	1.1	3.6E-01	6.2E-01
AT2G39240	*AT2G39240*	RNA polymerase I specific transcription initiation factor RRN3 protein	5.9	5.2E-04	2.9E-03	2.7	6.2E-02	2.3E-01
AT5G49730	*FRO6*	ferric reduction oxidase 6	5.9	3.1E-06	3.7E-05	-2.4	2.4E-02	1.3E-01
AT1G32780	*AT1G32780*	GroES-like zinc-binding dehydrogenase family	5.9	5.3E-16	1.3E-13	1.1	3.7E-01	6.3E-01
AT5G24155	*AT5G24155*	FAD/NAD(P)-binding oxidoreductase family protein	5.8	3.5E-13	3.6E-11	-1.0	9.9E-01	1.0E+00
AT1G73650	*AT1G73650*	3-oxo-5-alpha-steroid 4-dehydrogenase (DUF1295)	5.8	1.2E-19	7.4E-17	1.2	4.9E-02	2.0E-01
AT5G24120	*SIGE*	sigma factor E	5.8	6.7E-17	2.1E-14	1.4	7.3E-03	6.0E-02
AT1G23550	*SRO2*	similar to RCD one 2	5.7	3.8E-15	6.8E-13	-1.2	1.4E-01	3.7E-01
AT3G25260	*AT3G25260*	Major facilitator superfamily protein	5.7	3.9E-03	1.5E-02	2.3	2.1E-01	4.6E-01
AT4G27030	*FADA*	fatty acid desaturase A	5.7	2.5E-13	2.7E-11	1.4	3.2E-02	1.5E-01
AT1G30530	*UGT78D1*	UDP-glucosyl transferase 78D1	5.7	2.5E-13	2.7E-11	-1.0	9.1E-01	9.7E-01
AT5G17165	*AT5G17165*	hypothetical protein	5.6	1.6E-16	4.6E-14	1.2	1.6E-01	4.0E-01
AT5G10230	*ANNAT7*	annexin 7	5.6	1.6E-08	3.9E-07	-1.3	3.1E-01	5.7E-01
AT2G29090	*CYP707A2*	cytochrome P450, family 707, subfamily A, polypeptide 2	5.6	3.4E-09	1.1E-07	1.3	2.5E-01	5.2E-01
AT2G23000	*scpl10*	serine carboxypeptidase-like 10	5.5	3.0E-10	1.3E-08	-1.1	7.4E-01	8.8E-01
AT3G44970	*AT3G44970*	Cytochrome P450 superfamily protein	5.5	4.7E-06	5.3E-05	1.8	5.9E-02	2.2E-01
AT2G32530	*CSLB03*	cellulose synthase-like B3	5.5	2.2E-12	1.7E-10	1.6	8.6E-03	6.7E-02
AT2G36970	*AT2G36970*	UDP-Glycosyltransferase superfamily protein	5.5	2.5E-09	8.2E-08	-1.3	2.5E-01	5.2E-01
AT5G44590	*AT5G44590*	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	5.4	1.0E-03	5.0E-03	-2.0	3.3E-01	5.9E-01
AT4G09750	*AT4G09750*	NAD(P)-binding Rossmann-fold superfamily protein	5.4	6.5E-24	2.3E-20	1.1	5.6E-02	2.2E-01
AT2G36885	*AT2G36885*	translation initiation factor	5.3	2.1E-11	1.3E-09	-1.0	9.7E-01	9.9E-01
AT5G36790	*AT5G36790*	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	5.3	6.3E-08	1.3E-06	1.6	1.0E-01	3.1E-01
AT1G24580	*AT1G24580*	RING/U-box superfamily protein	5.3	2.3E-08	5.5E-07	1.6	5.4E-02	2.1E-01
AT5G44110	*ABCI21*	P-loop containing nucleoside triphosphate hydrolases superfamily protein	5.3	5.3E-13	5.2E-11	1.1	3.5E-01	6.2E-01
AT5G51720	*NEET*	2 iron, 2 sulfur cluster binding protein	5.3	1.5E-09	5.4E-08	-1.5	6.6E-02	2.4E-01
AT2G16890	*AT2G16890*	UDP-Glycosyltransferase superfamily protein	5.2	1.5E-15	3.1E-13	-1.7	3.0E-04	6.9E-03
AT1G16730	*UP6*	hypothetical protein	5.2	7.2E-11	3.7E-09	-1.0	9.0E-01	9.7E-01
AT5G58120	*AT5G58120*	Disease resistance protein (TIR-NBS-LRR class)	5.2	9.8E-11	4.9E-09	1.0	8.4E-01	9.4E-01
AT3G62410	*CP12-2*	CP12 domain-containing protein 2	5.1	1.2E-13	1.4E-11	1.1	6.1E-01	8.1E-01
AT2G21970	*SEP2*	stress enhanced protein 2	5.1	2.0E-22	3.4E-19	-1.1	2.0E-01	4.5E-01
AT5G24210	*AT5G24210*	alpha/beta-Hydrolases superfamily protein	5.1	4.2E-09	1.3E-07	1.7	2.5E-02	1.3E-01
AT5G07190	*ATS3*	embryo-specific protein 3	5.0	7.8E-04	4.0E-03	-3.8	6.6E-02	2.4E-01
AT2G13680	*CALS5*	callose synthase 5	5.0	3.3E-05	2.8E-04	-1.1	8.2E-01	9.3E-01
AT1G13650	*AT1G13650*	hypothetical protein	5.0	6.6E-08	1.3E-06	1.5	1.2E-01	3.3E-01
AT3G62990	*AT3G62990*	myelin transcription factor-like protein	4.9	1.1E-06	1.6E-05	-1.5	2.3E-01	4.9E-01
AT1G78720	*AT1G78720*	SecY protein transport family protein	4.9	9.3E-07	1.3E-05	-2.0	4.5E-02	1.9E-01
AT3G12955	*AT3G12955*	SAUR-like auxin-responsive protein family	4.9	5.2E-08	1.1E-06	1.2	4.9E-01	7.3E-01
AT5G05410	*DREB2A*	DRE-binding protein 2A	4.9	8.0E-15	1.3E-12	-1.2	2.2E-01	4.7E-01
AT5G22300	*NIT4*	nitrilase 4	4.8	2.7E-08	6.2E-07	-1.2	3.7E-01	6.3E-01
AT4G27360	*AT4G27360*	Dynein light chain type 1 family protein	4.8	2.3E-06	2.9E-05	1.5	2.0E-01	4.6E-01
AT4G25640	*DTX35*	detoxifying efflux carrier 35	4.8	2.6E-20	1.9E-17	-1.3	3.2E-03	3.5E-02

AT1G02813	*AT1G02813*	pectinesterase (Protein of unknown function, DUF538)	4.8	1.4E-02	4.2E-02	-1.1	8.9E-01	9.6E-01
AT1G76570	*AT1G76570*	Chlorophyll A-B binding family protein	4.8	1.2E-14	1.8E-12	1.0	7.0E-01	8.6E-01
AT2G37040	*PAL1*	PHE ammonia lyase 1	4.8	1.7E-18	7.3E-16	-1.1	4.0E-01	6.6E-01
AT3G48350	*CEP3*	Cysteine proteinases superfamily protein	4.8	2.7E-10	1.2E-08	-1.4	7.1E-02	2.5E-01
AT5G49740	*FRO7*	ferric reduction oxidase 7	4.7	6.7E-08	1.4E-06	-1.4	2.2E-01	4.8E-01
AT2G41040	*AT2G41040*	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	4.7	2.3E-17	8.3E-15	1.1	6.0E-01	8.1E-01
AT3G46090	*ZAT7*	C2H2 and C2HC zinc fingers superfamily protein	4.7	1.1E-02	3.5E-02	3.4	5.0E-02	2.0E-01
AT5G43570	*AT5G43570*	Serine protease inhibitor, potato inhibitor I-type family protein	4.7	4.5E-06	5.1E-05	1.1	8.6E-01	9.5E-01
AT4G21200	*GA2OX8*	gibberellin 2-oxidase 8	4.7	4.9E-06	5.5E-05	-1.5	2.3E-01	5.0E-01
AT5G51950	*AT5G51950*	Glucose-methanol-choline (GMC) oxidoreductase family protein	4.7	3.4E-06	4.0E-05	1.3	4.4E-01	6.9E-01
AT3G47830	*AT3G47830*	DNA glycosylase superfamily protein	4.7	1.1E-05	1.1E-04	2.0	4.7E-02	2.0E-01
AT5G24850	*CRY3*	cryptochrome 3	4.6	1.8E-14	2.5E-12	1.0	9.4E-01	9.8E-01
AT1G12100	*AT1G12100*	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	4.6	2.8E-04	1.7E-03	2.6	2.9E-02	1.4E-01
AT2G21650	*MEE3*	Homeodomain-like superfamily protein	4.6	1.5E-02	4.6E-02	2.4	2.0E-01	4.5E-01
AT5G54060	*UF3GT*	UDP-glucose:flavonoid 3-o-glucosyltransferase	4.6	6.3E-03	2.2E-02	-1.4	6.0E-01	8.0E-01
AT4G10120	*ATSPS4F*	Sucrose-phosphate synthase family protein	4.6	9.7E-11	4.9E-09	-1.4	3.9E-02	1.7E-01
AT3G11110	*AT3G11110*	RING/U-box superfamily protein	4.5	3.0E-06	3.7E-05	1.0	9.9E-01	1.0E+00
AT5G50100	*AT5G50100*	Putative thiol-disulfide oxidoreductase DCC	4.5	8.2E-16	1.9E-13	1.2	1.2E-01	3.5E-01
AT1G19550	*AT1G19550*	Glutathione S-transferase family protein	4.5	1.9E-04	1.2E-03	1.2	7.2E-01	8.7E-01
AT1G12370	*PHR1*	photolyase 1	4.5	6.8E-14	8.4E-12	1.2	2.8E-01	5.4E-01
AT3G56260	*AT3G56260*	hypothetical protein	4.5	5.2E-08	1.1E-06	-2.3	6.0E-03	5.2E-02
AT5G13170	*SAG29*	senescence-associated gene 29	4.5	4.4E-04	2.5E-03	1.3	5.3E-01	7.6E-01
AT1G20470	*AT1G20470*	SAUR-like auxin-responsive protein family	4.5	1.7E-10	7.9E-09	1.3	2.0E-01	4.5E-01
AT4G33010	*GLDP1*	glycine decarboxylase P-protein 1	4.5	2.5E-11	1.5E-09	-1.4	2.6E-02	1.4E-01
AT3G11050	*FER2*	ferritin 2	4.5	3.5E-10	1.5E-08	1.2	2.9E-01	5.5E-01
AT2G38210	*PDX1L4*	putative PDX1-like protein 4	4.5	1.7E-11	1.0E-09	1.1	5.6E-01	7.7E-01
AT5G15970	*KIN2*	stress-responsive protein (KIN2) / stress-induced protein (KIN2) / cold-responsive protein (COR6.6) / cold-regulated protein (COR6.6)	4.4	9.2E-07	1.3E-05	-1.1	7.3E-01	8.8E-01
AT5G23000	*MYB37*	myb domain protein 37	4.4	1.2E-05	1.2E-04	-1.0	9.3E-01	9.8E-01
AT5G05580	*FAD8*	fatty acid desaturase 8	4.4	5.9E-10	2.3E-08	1.5	1.6E-02	1.0E-01
AT3G06490	*MYB108*	myb domain protein 108	4.4	6.4E-04	3.4E-03	2.4	5.2E-02	2.1E-01
AT2G36870	*XTH32*	xyloglucan endotransglucosylase/hydrolase 32	4.4	3.0E-13	3.1E-11	1.1	5.8E-01	7.9E-01
AT5G40210	*UMAMIT42*	nodulin MtN21 /EamA-like transporter family	4.3	4.7E-07	7.4E-06	1.2	4.5E-01	7.0E-01
AT3G19170	*PREP1*	presequence protease 1	4.3	1.3E-16	3.7E-14	1.3	1.5E-02	9.4E-02
AT1G42560	*MLO9*	Seven transmembrane MLO family protein	4.3	6.8E-06	7.3E-05	-1.6	1.9E-01	4.4E-01
AT4G01660	*ABC1*	ABC transporter 1	4.3	1.1E-23	3.5E-20	1.1	1.8E-01	4.2E-01
AT3G07700	*AT3G07700*	Protein kinase superfamily protein	4.3	1.2E-18	5.6E-16	1.0	8.1E-01	9.2E-01
AT4G04850	*KEA3*	K efflux antiporter 3	4.3	5.0E-14	6.4E-12	1.4	6.3E-03	5.4E-02
AT1G35140	*PHI-1*	Phosphate-responsive 1 family protein	4.2	4.2E-10	1.8E-08	1.4	3.6E-02	1.6E-01
AT3G53260	*PAL2*	phenylalanine ammonia-lyase 2	4.2	2.4E-17	8.8E-15	-1.0	7.0E-01	8.6E-01
AT2G46750	*GulLO2*	D-arabinono-1,4-lactone oxidase family protein	4.2	1.6E-05	1.5E-04	1.3	3.5E-01	6.1E-01
AT5G17010	*AT5G17010*	Major facilitator superfamily protein	4.2	1.4E-19	8.3E-17	-1.1	2.1E-01	4.7E-01
AT4G30650	*AT4G30650*	Low temperature and salt responsive protein family	4.2	1.1E-08	2.9E-07	1.3	1.7E-01	4.1E-01
AT2G35660	*CTF2A*	FAD/NAD(P)-binding oxidoreductase family protein	4.2	4.4E-16	1.1E-13	1.3	5.4E-03	4.9E-02
AT2G24540	*AFR*	Galactose oxidase/kelch repeat superfamily protein	4.1	1.2E-18	5.6E-16	1.2	3.8E-02	1.7E-01
AT1G61300	*AT1G61300*	LRR and NB-ARC domains-containing disease resistance protein	4.1	1.6E-08	4.0E-07	-1.4	1.4E-01	3.8E-01
AT3G29200	*CM1*	chorismate mutase 1	4.1	2.1E-19	1.2E-16	-1.1	4.7E-01	7.1E-01
AT1G62510	*AT1G62510*	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	4.1	7.8E-08	1.5E-06	-1.5	4.0E-02	1.8E-01
AT5G44050	*AT5G44050*	MATE efflux family protein	4.1	8.7E-11	4.5E-09	-1.2	2.4E-01	5.0E-01
AT1G47510	*5PTASE11*	inositol polyphosphate 5-phosphatase 11	4.1	8.6E-04	4.3E-03	1.1	9.1E-01	9.7E-01
AT4G17090	*CT-BMY*	chloroplast beta-amylase	4.1	5.2E-09	1.5E-07	-1.1	4.5E-01	7.0E-01
AT5G24200	*AT5G24200*	alpha/beta-Hydrolases superfamily protein	4.1	8.0E-03	2.7E-02	3.1	3.7E-02	1.7E-01
AT4G27820	*BGLU9*	beta glucosidase 9	4.1	2.3E-13	2.6E-11	1.1	3.1E-01	5.8E-01
AT4G14090	*AT4G14090*	UDP-Glycosyltransferase superfamily protein	4.1	1.3E-02	4.0E-02	-1.0	9.7E-01	9.9E-01
AT2G41660	*MIZ1*	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617)	4.1	4.3E-14	5.6E-12	1.2	1.5E-01	3.9E-01
AT1G28170	*SOT7*	sulfotransferase 7	4.1	1.0E-02	3.3E-02	-1.1	8.7E-01	9.5E-01
AT4G36530	*AT4G36530*	alpha/beta-Hydrolases superfamily protein	4.0	2.2E-15	4.1E-13	1.1	2.1E-01	4.6E-01
AT2G37970	*SOUL-1*	SOUL heme-binding family protein	4.0	3.8E-18	1.5E-15	-1.1	3.0E-01	5.6E-01
AT1G78510	*SPS1*	solanesyl diphosphate synthase 1	4.0	1.4E-18	6.4E-16	1.1	5.2E-01	7.5E-01
AT1G16720	*HCF173*	high chlorophyll fluorescence phenotype 173	4.0	8.9E-13	8.0E-11	1.4	1.1E-02	7.6E-02
AT4G17098	*AT4G17098*	Natural antisense transcript overlaps with AT4G17100	4.0	4.2E-10	1.7E-08	1.4	7.2E-02	2.5E-01
AT2G36630	*AT2G36630*	Sulfite exporter TauE/SafE family protein	4.0	3.8E-13	3.9E-11	1.2	1.1E-01	3.2E-01
AT1G70000	*AT1G70000*	myb-like transcription factor family protein	4.0	9.8E-17	2.9E-14	1.1	2.1E-01	4.6E-01
AT4G29590	*AT4G29590*	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	4.0	3.3E-18	1.3E-15	1.1	1.3E-01	3.6E-01
AT2G05440	*GRP9*	GLYCINE RICH PROTEIN 9	4.0	1.5E-06	1.9E-05	1.4	1.7E-01	4.1E-01
AT3G61220	*SDR1*	NAD(P)-binding Rossmann-fold superfamily protein	4.0	1.6E-15	3.3E-13	-1.0	6.8E-01	8.5E-01
AT1G62620	*AT1G62620*	Flavin-binding monooxygenase family protein	4.0	1.4E-04	9.3E-04	1.3	5.1E-01	7.4E-01
AT3G24190	*AT3G24190*	Protein kinase superfamily protein	4.0	3.8E-16	9.7E-14	1.2	8.6E-02	2.8E-01
AT2G01580	*AT2G01580*	transmembrane protein	4.0	5.1E-04	2.8E-03	1.4	4.2E-01	6.8E-01
AT5G60540	*PDX2*	pyridoxine biosynthesis 2	4.0	2.0E-21	2.1E-18	1.1	2.0E-01	4.6E-01
AT1G06170	*AT1G06170*	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	3.9	3.2E-05	2.7E-04	-1.3	4.7E-01	7.1E-01

AT5G43860	*CLH2*	chlorophyllase 2	3.9	1.0E-10	5.0E-09	1.5	2.1E-02	1.2E-01
AT2G42150	*AT2G42150*	DNA-binding bromodomain-containing protein	3.9	2.3E-06	2.9E-05	-1.8	7.5E-02	2.6E-01
AT1G72490	*AT1G72490*	hypothetical protein	3.9	3.7E-06	4.3E-05	-2.3	1.1E-02	7.7E-02
AT4G01883	*AT4G01883*	Polyketide cyclase / dehydrase and lipid transport protein	3.9	8.0E-12	5.4E-10	1.5	8.3E-03	6.6E-02
AT1G17100	*HBP1*	SOUL heme-binding family protein	3.9	1.6E-15	3.3E-13	-1.0	7.2E-01	8.8E-01
AT5G11260	*HY5*	Basic-leucine zipper (bZIP) transcription factor family protein	3.9	9.8E-15	1.5E-12	1.1	3.5E-01	6.2E-01
AT5G19850	*AT5G19850*	alpha/beta-Hydrolases superfamily protein	3.9	7.2E-15	1.2E-12	1.4	5.5E-03	5.0E-02
AT3G54420	*EP3*	homolog of carrot EP3-3 chitinase	3.9	8.1E-09	2.2E-07	-1.1	5.3E-01	7.5E-01
AT4G26950	*AT4G26950*	senescence regulator (Protein of unknown function, DUF584)	3.9	3.3E-03	1.3E-02	-3.0	1.1E-01	3.2E-01
AT3G44720	*ADT4*	arogenate dehydratase 4	3.9	5.3E-24	2.3E-20	1.2	2.2E-04	5.6E-03
AT5G52250	*RUP1*	Transducin/WD40 repeat-like superfamily protein	3.9	4.6E-16	1.1E-13	-1.1	3.5E-01	6.1E-01
AT4G04750	*AT4G04750*	Major facilitator superfamily protein	3.9	2.9E-10	1.2E-08	-1.5	2.0E-02	1.1E-01
AT1G20120	*AT1G20120*	GDSL-like Lipase/Acylhydrolase superfamily protein	3.9	6.0E-03	2.2E-02	1.5	4.4E-01	6.9E-01
AT2G46790	*PRR9*	pseudo-response regulator 9	3.8	2.5E-07	4.3E-06	1.5	6.2E-02	2.3E-01
AT5G53200	*TRY*	Homeodomain-like superfamily protein	3.8	2.1E-07	3.6E-06	-1.0	8.8E-01	9.6E-01
AT5G49350	*AT5G49350*	Glycine-rich protein family	3.8	8.0E-03	2.7E-02	2.4	8.9E-02	2.9E-01
AT2G45800	*PLIM2a*	GATA type zinc finger transcription factor family protein	3.8	7.9E-05	5.8E-04	-2.1	5.6E-02	2.2E-01
AT2G29270	*AT2G29270*	pseudogene of senescence-associated gene 13	3.8	3.0E-03	1.2E-02	1.9	1.6E-01	4.0E-01
AT4G27570	*AT4G27570*	UDP-Glycosyltransferase superfamily protein	3.8	3.8E-03	1.5E-02	-1.3	6.0E-01	8.0E-01
AT1G55010	*PDF1.5*	plant defensin 1.5	3.8	3.3E-03	1.3E-02	3.0	1.8E-02	1.1E-01
AT5G01410	*RSR4*	Aldolase-type TIM barrel family protein	3.8	8.5E-19	4.3E-16	-1.1	3.2E-01	5.9E-01
AT2G38465	*AT2G38465*	hypothetical protein	3.8	1.2E-10	5.8E-09	-1.0	9.9E-01	1.0E+00
AT2G14060	*AT2G14060*	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	3.8	3.2E-05	2.7E-04	1.7	6.2E-02	2.3E-01
AT4G17480	*AT4G17480*	alpha/beta-Hydrolases superfamily protein	3.8	2.2E-03	9.2E-03	2.2	7.4E-02	2.6E-01
AT3G14690	*CYP72A15*	cytochrome P450, family 72, subfamily A, polypeptide 15	3.8	1.0E-20	7.8E-18	1.0	6.8E-01	8.5E-01
AT1G03055	*D27*	beta-carotene isomerase D27-like protein	3.8	9.9E-07	1.4E-05	1.2	3.6E-01	6.2E-01
AT4G36220	*FAH1*	ferulic acid 5-hydroxylase 1	3.8	9.4E-14	1.1E-11	1.0	9.5E-01	9.8E-01
AT3G28160	*AT3G28160*	transposable_element_gene	3.8	8.6E-15	1.3E-12	1.4	7.6E-04	1.3E-02
AT1G66780	*AT1G66780*	MATE efflux family protein	3.8	2.4E-03	1.0E-02	-1.9	2.8E-01	5.4E-01
AT5G54710	*AT5G54710*	Ankyrin repeat family protein	3.8	3.5E-08	7.8E-07	-1.1	5.3E-01	7.6E-01
AT3G06220	*AT3G06220*	AP2/B3-like transcriptional factor family protein	3.7	1.1E-02	3.4E-02	2.7	5.6E-02	2.2E-01
AT5G54720	*AT5G54720*	Ankyrin repeat family protein	3.7	5.4E-06	5.9E-05	1.0	9.7E-01	9.9E-01
AT4G15810	*AT4G15810*	P-loop containing nucleoside triphosphate hydrolases superfamily protein	3.7	2.3E-12	1.8E-10	1.0	7.2E-01	8.8E-01
AT1G17600	*AT1G17600*	Disease resistance protein (TIR-NBS-LRR class)	3.7	8.9E-05	6.4E-04	1.7	1.2E-01	3.4E-01
AT3G09650	*HCF152*	Tetratricopeptide repeat (TPR)-like superfamily protein	3.7	1.2E-14	1.8E-12	1.1	1.9E-01	4.4E-01
AT4G12830	*AT4G12830*	alpha/beta-Hydrolases superfamily protein	3.7	1.1E-08	3.0E-07	-1.1	5.4E-01	7.6E-01
AT1G17050	*SPS2*	solanesyl diphosphate synthase 2	3.7	4.0E-15	7.0E-13	1.2	1.1E-01	3.3E-01
AT1G19140	*AT1G19140*	ubiquinone biosynthesis COQ9-like protein	3.7	2.5E-16	6.7E-14	1.0	7.7E-01	9.0E-01
AT4G37310	*CYP81H1*	cytochrome P450, family 81, subfamily H, polypeptide 1	3.7	1.7E-15	3.3E-13	1.1	3.8E-01	6.4E-01
AT1G06550	*AT1G06550*	ATP-dependent caseinolytic (Clp) protease/crotonase family protein	3.7	2.8E-20	1.9E-17	-1.1	1.4E-01	3.7E-01
AT3G56890	*AT3G56890*	F-box associated ubiquitination effector family protein	3.7	4.9E-06	5.5E-05	-1.7	1.3E-01	3.5E-01
AT1G79510	*AT1G79510*	hypothetical protein (DUF2358)	3.6	1.3E-11	8.4E-10	1.1	5.8E-01	7.9E-01
AT2G39560	*AT2G39560*	Putative membrane lipoprotein	3.6	4.2E-08	9.1E-07	1.7	6.9E-03	5.8E-02
AT1G64770	*PnsB2*	NDH-dependent cyclic electron flow 1	3.6	1.2E-12	1.1E-10	1.4	1.3E-02	8.9E-02
AT5G57785	*AT5G57785*	hypothetical protein	3.6	2.1E-09	7.0E-08	-1.1	5.1E-01	7.4E-01
AT1G33720	*CYP76C6*	cytochrome P450, family 76, subfamily C, polypeptide 6	3.6	1.9E-04	1.2E-03	1.6	1.6E-01	4.0E-01
AT3G21670	*AT3G21670*	Major facilitator superfamily protein	3.6	1.2E-07	2.2E-06	1.2	2.8E-01	5.5E-01
AT3G23410	*FAO3*	fatty alcohol oxidase 3	3.6	1.6E-14	2.4E-12	1.6	2.5E-05	1.2E-03
AT2G45360	*AT2G45360*	ankyrin repeat/KH domain protein (DUF1442)	3.6	3.0E-06	3.6E-05	-1.0	1.0E+00	1.0E+00
AT1G60270	*BGLU6*	beta glucosidase 6	3.6	8.3E-09	2.3E-07	-1.9	9.2E-04	1.5E-02
AT3G57190	*PrfB3*	peptide chain release factor	3.6	5.2E-14	6.5E-12	1.1	2.9E-01	5.6E-01
AT1G09340	*CRB*	chloroplast RNA binding protein	3.5	5.3E-11	2.9E-09	1.2	1.4E-01	3.8E-01
AT2G32640	*AT2G32640*	Lycopene beta/epsilon cyclase protein	3.5	9.4E-12	6.2E-10	-1.1	6.7E-01	8.5E-01
AT4G33660	*AT4G33660*	cysteine-rich TM module stress tolerance protein	3.5	9.1E-12	6.0E-10	1.3	7.5E-02	2.6E-01
AT4G25700	*BETA-OHASE*	beta-hydroxylase 1	3.5	1.9E-15	3.7E-13	1.2	7.7E-02	2.6E-01
AT4G24130	*AT4G24130*	DUF538 family protein (Protein of unknown function, DUF538)	3.5	1.1E-08	2.9E-07	1.0	9.7E-01	9.9E-01
AT3G49630	*AT3G49630*	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	3.5	7.9E-03	2.7E-02	2.2	1.0E-01	3.1E-01
AT2G26080	*GLDP2*	glycine decarboxylase P-protein 2	3.5	5.5E-13	5.5E-11	1.0	8.4E-01	9.4E-01
AT3G04420	*NAC048*	NAC domain containing protein 48	3.5	1.0E-04	7.3E-04	-1.1	7.4E-01	8.9E-01
AT5G51040	*SDHAF2*	succinate dehydrogenase assembly factor	3.5	2.6E-17	8.9E-15	-1.0	8.5E-01	9.5E-01
AT1G07150	*MAPKKK13*	mitogen-activated protein kinase kinase kinase 13	3.5	1.8E-18	7.5E-16	1.3	3.7E-04	8.0E-03
AT5G54470	*BBX29*	B-box type zinc finger family protein	3.5	2.2E-05	1.9E-04	-1.3	3.2E-01	5.8E-01
AT5G51220	*AT5G51220*	ubiquinol-cytochrome C chaperone family protein	3.5	2.3E-16	6.3E-14	1.1	3.1E-01	5.8E-01
AT2G25780	*AT2G25780*	hypothetical protein (DUF1677)	3.5	8.3E-03	2.8E-02	2.2	9.8E-02	3.0E-01
AT3G47070	*AT3G47070*	thylakoid soluble phosphoprotein	3.5	3.2E-12	2.4E-10	1.1	3.3E-01	5.9E-01
AT1G47980	*AT1G47980*	desiccation-like protein	3.5	3.5E-04	2.0E-03	-1.4	3.1E-01	5.7E-01
AT1G52342	*AT1G52342*	hypothetical protein	3.5	1.0E-11	6.7E-10	1.1	5.2E-01	7.5E-01
AT5G42270	*VAR1*	FtsH extracellular protease family	3.5	5.4E-14	6.7E-12	1.2	3.4E-02	1.6E-01
AT2G36800	*DOGT1*	don-glucosyltransferase 1	3.4	1.8E-11	1.1E-09	-1.3	5.2E-02	2.1E-01

AT2G29300	*AT2G29300*	NAD(P)-binding Rossmann-fold superfamily protein	3.4	2.0E-08	4.8E-07	1.9	5.2E-04	1.0E-02
AT2G24190	*SDR2*	NAD(P)-binding Rossmann-fold superfamily protein	3.4	4.2E-09	1.3E-07	-1.2	2.7E-01	5.3E-01
AT2G16365	*AT2G16365*	F-box family protein	3.4	7.2E-19	3.7E-16	1.0	6.9E-01	8.6E-01
AT1G24148	*AT1G24148*	hypothetical protein	3.4	5.6E-07	8.6E-06	1.2	4.6E-01	7.1E-01
AT5G54100	*AT5G54100*	SPFH/Band 7/PHB domain-containing membrane-associated protein family	3.4	9.0E-21	7.2E-18	1.1	3.1E-02	1.5E-01
AT2G37720	*TBL15*	TRICHOME BIREFRINGENCE-LIKE 15	3.4	9.9E-05	7.0E-04	1.1	8.4E-01	9.4E-01
AT4G17760	*AT4G17760*	PCNA domain-containing protein	3.4	1.8E-08	4.4E-07	1.0	9.8E-01	1.0E+00
AT5G14760	*AO*	L-aspartate oxidase	3.4	2.5E-12	2.0E-10	-1.4	9.5E-03	7.1E-02
AT3G09930	*AT3G09930*	GDSL-like Lipase/Acylhydrolase superfamily protein	3.4	6.7E-03	2.3E-02	1.1	8.8E-01	9.6E-01
AT3G01140	*MYB106*	myb domain protein 106	3.4	6.4E-07	9.6E-06	-1.2	3.5E-01	6.2E-01
AT3G48460	*AT3G48460*	GDSL-like Lipase/Acylhydrolase superfamily protein	3.4	1.4E-15	2.9E-13	-1.6	3.3E-05	1.5E-03
AT2G40080	*ELF4*	EARLY FLOWERING-like protein (DUF1313)	3.4	4.7E-13	4.7E-11	1.2	4.8E-02	2.0E-01
AT2G18120	*SRS4*	SHI-related sequence 4	3.3	7.1E-05	5.3E-04	1.5	1.8E-01	4.3E-01
AT4G27657	*AT4G27657*	hypothetical protein	3.3	4.9E-08	1.0E-06	1.2	3.4E-01	6.1E-01
AT2G40150	*TBL28*	TRICHOME BIREFRINGENCE-LIKE 28	3.3	8.5E-16	1.9E-13	1.0	9.9E-01	1.0E+00
AT5G20220	*AT5G20220*	zinc knuckle (CCHC-type) family protein	3.3	2.7E-15	5.0E-13	1.2	1.2E-01	3.3E-01
AT1G67070	*DIN9*	Mannose-6-phosphate isomerase, type I	3.3	2.9E-16	7.6E-14	-1.1	2.8E-01	5.5E-01
AT4G28660	*PSB28*	photosystem II reaction center PSB28 protein	3.3	9.7E-10	3.6E-08	1.2	1.7E-01	4.1E-01
AT3G16350	*AT3G16350*	Homeodomain-like superfamily protein	3.3	7.8E-16	1.8E-13	1.2	1.1E-01	3.2E-01
AT1G51820	*AT1G51820*	Leucine-rich repeat protein kinase family protein	3.3	7.0E-05	5.2E-04	1.0	9.4E-01	9.8E-01
AT3G23530	*AT3G23530*	Cyclopropane-fatty-acyl-phospholipid synthase	3.3	1.1E-12	9.8E-11	1.3	2.7E-02	1.4E-01
AT5G67370	*CGLD27*	DUF1230 family protein (DUF1230)	3.3	3.2E-09	1.0E-07	-1.1	6.9E-01	8.6E-01
AT1G53670	*MSRB1*	methionine sulfoxide reductase B 1	3.3	4.9E-17	1.6E-14	1.1	2.7E-01	5.3E-01
AT4G11600	*GPX6*	glutathione peroxidase 6	3.3	3.2E-14	4.3E-12	1.0	6.6E-01	8.4E-01
AT5G65730	*XTH6*	xyloglucan endotransglucosylase/hydrolase 6	3.3	1.2E-05	1.1E-04	1.2	4.9E-01	7.3E-01
AT5G24160	*SQE6*	squalene monooxygenase 6	3.3	3.8E-05	3.1E-04	1.6	8.9E-02	2.9E-01
AT5G45630	*AT5G45630*	senescence regulator (Protein of unknown function, DUF584)	3.3	1.5E-03	6.9E-03	-1.6	3.2E-01	5.8E-01
AT5G06790	*AT5G06790*	cotton fiber protein	3.3	1.3E-05	1.3E-04	1.4	1.6E-01	4.0E-01
AT1G13670	*AT1G13670*	hypothetical protein	3.3	3.5E-13	3.6E-11	1.1	3.4E-01	6.1E-01
AT1G78820	*AT1G78820*	D-mannose binding lectin protein with Apple-like carbohydrate-binding domain-containing protein	3.3	3.8E-09	1.2E-07	-1.0	8.0E-01	9.2E-01
AT5G66940	*AT5G66940*	Dof-type zinc finger DNA-binding family protein	3.3	2.0E-03	8.6E-03	2.5	1.7E-02	1.0E-01
AT2G47890	*AT2G47890*	B-box type zinc finger protein with CCT domain-containing protein	3.3	2.1E-13	2.4E-11	1.1	4.6E-01	7.0E-01
AT5G22390	*AT5G22390*	FANTASTIC four-like protein (DUF3049)	3.3	8.7E-11	4.4E-09	1.6	7.1E-04	1.3E-02
AT3G09520	*EXO70H4*	exocyst subunit exo70 family protein H4	3.3	2.1E-08	5.0E-07	-1.1	6.3E-01	8.2E-01
AT3G18950	*AT3G18950*	Transducin/WD40 repeat-like superfamily protein	3.3	6.3E-08	1.3E-06	-1.3	1.5E-01	3.9E-01
AT5G43840	*HSFA6A*	heat shock transcription factor A6A	3.3	7.1E-09	2.0E-07	1.1	4.0E-01	6.6E-01
AT5G62150	*AT5G62150*	peptidoglycan-binding LysM domain-containing protein	3.3	2.5E-06	3.1E-05	1.2	3.6E-01	6.2E-01
AT1G50020	*AT1G50020*	tubulin alpha-6 chain	3.3	2.2E-13	2.5E-11	1.1	3.0E-01	5.7E-01
AT2G30040	*MAPKKK14*	mitogen-activated protein kinase kinase kinase 14	3.3	3.0E-15	5.5E-13	1.0	8.5E-01	9.4E-01
AT3G16360	*AHP4*	HPT phosphotransmitter 4	3.3	6.1E-05	4.7E-04	-1.2	5.5E-01	7.7E-01
AT1G66330	*AT1G66330*	senescence-associated family protein	3.3	2.1E-14	3.0E-12	1.2	1.2E-01	3.3E-01
AT1G50450	*AT1G50450*	Saccharopine dehydrogenase	3.2	1.6E-13	1.9E-11	1.3	6.4E-03	5.5E-02
AT2G38230	*PDX1.1*	pyridoxine biosynthesis 1.1	3.2	2.4E-12	1.9E-10	1.1	2.9E-01	5.5E-01
AT3G18485	*ILR2*	iaa-leucine resistant 2	3.2	1.2E-05	1.1E-04	-1.2	4.2E-01	6.7E-01
AT3G15830	*AT3G15830*	phosphatidic acid phosphatase-related / PAP2-like protein	3.2	1.1E-02	3.4E-02	1.5	4.1E-01	6.6E-01
AT4G19820	*AT4G19820*	Glycosyl hydrolase family protein with chitinase insertion domain-containing protein	3.2	9.3E-09	2.5E-07	1.5	2.3E-02	1.3E-01
AT4G00050	*UNE10*	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	3.2	2.1E-17	8.0E-15	-1.5	3.3E-06	3.2E-04
AT3G46480	*AT3G46480*	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	3.2	3.5E-04	2.0E-03	1.6	1.4E-01	3.7E-01
AT3G52130	*AT3G52130*	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	3.2	7.6E-03	2.6E-02	-2.8	1.0E-01	3.1E-01
AT1G70580	*AOAT2*	alanine-2-oxoglutarate aminotransferase 2	3.2	2.7E-13	2.9E-11	1.3	9.9E-03	7.3E-02
AT3G48310	*CYP71A22*	cytochrome P450, family 71, subfamily A, polypeptide 22	3.2	9.5E-06	9.6E-05	-1.4	2.0E-01	4.6E-01
AT2G23590	*MES8*	methyl esterase 8	3.2	1.4E-07	2.5E-06	-1.3	2.1E-01	4.7E-01
AT3G55110	*ABCG18*	ABC-2 type transporter family protein	3.2	1.3E-05	1.3E-04	1.4	1.9E-01	4.4E-01
AT2G33250	*AT2G33250*	transmembrane protein	3.2	7.9E-13	7.4E-11	1.3	2.5E-02	1.3E-01
AT1G70820	*AT1G70820*	phosphoglucomutase, putative / glucose phosphomutase	3.2	2.8E-06	3.5E-05	1.9	4.2E-03	4.2E-02
AT4G08870	*ARGAH2*	Arginase/deacetylase superfamily protein	3.2	9.5E-10	3.5E-08	1.1	5.2E-01	7.5E-01
AT2G48150	*GPX4*	glutathione peroxidase 4	3.2	9.4E-03	3.1E-02	3.0	1.2E-02	8.4E-02
AT2G39730	*RCA*	rubisco activase	3.1	5.7E-10	2.2E-08	1.4	2.3E-02	1.3E-01
AT1G79600	*AT1G79600*	Protein kinase superfamily protein	3.1	3.8E-16	9.7E-14	1.2	2.0E-02	1.2E-01
AT5G46800	*BOU*	Mitochondrial substrate carrier family protein	3.1	4.6E-14	5.9E-12	1.1	4.7E-01	7.1E-01
AT5G08710	*RUG1*	Regulator of chromosome condensation (RCC1) family protein	3.1	2.3E-16	6.3E-14	1.0	8.1E-01	9.2E-01
AT3G22830	*HSFA6B*	heat shock transcription factor A6B	3.1	1.3E-07	2.4E-06	1.3	2.2E-01	4.8E-01
AT4G23170	*EP1*	receptor-like protein kinase-related family protein	3.1	7.2E-03	2.5E-02	1.7	2.1E-01	4.7E-01
AT4G16750	*AT4G16750*	Integrase-type DNA-binding superfamily protein	3.1	7.4E-09	2.1E-07	-1.3	1.6E-01	4.0E-01
AT1G06430	*FTSH8*	FTSH protease 8	3.1	5.9E-13	5.7E-11	1.1	2.4E-01	5.1E-01
AT1G65620	*AS2*	Lateral organ boundaries (LOB) domain family protein	3.1	2.0E-05	1.8E-04	1.7	3.4E-02	1.6E-01
AT3G03780	*MS2*	methionine synthase 2	3.1	9.4E-16	2.1E-13	-1.2	2.8E-02	1.4E-01
AT5G67030	*ABA1*	zeaxanthin epoxidase (ZEP) (ABA1)	3.1	2.8E-10	1.2E-08	1.1	3.0E-01	5.7E-01
AT3G21690	*AT3G21690*	MATE efflux family protein	3.1	7.9E-14	9.6E-12	-1.2	4.9E-02	2.0E-01

AT3G17609	*HYH*	HY5-homolog	3.1	2.4E-09	7.7E-08	1.2	1.2E-01	3.4E-01
AT4G35250	*HCF244*	NAD(P)-binding Rossmann-fold superfamily protein	3.1	1.2E-11	7.8E-10	1.3	1.8E-02	1.1E-01
AT1G44575	*NPQ4*	Chlorophyll A-B binding family protein	3.1	6.6E-13	6.2E-11	1.3	2.7E-02	1.4E-01
AT2G17270	*PHT3*		3.1	6.6E-13	6.2E-11	1.1	3.5E-01	6.1E-01
AT1G31800	*CYP97A3*	cytochrome P450, family 97, subfamily A, polypeptide 3	3.1	3.2E-09	1.0E-07	1.2	2.2E-01	4.8E-01
AT4G12917	*AT4G12917*		3.1	1.1E-03	5.3E-03	1.2	6.5E-01	8.3E-01
AT1G69523	*AT1G69523*	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	3.1	2.5E-08	5.9E-07	1.0	9.5E-01	9.9E-01
AT1G32220	*AT1G32220*	NAD(P)-binding Rossmann-fold superfamily protein	3.1	3.7E-12	2.8E-10	1.1	3.5E-01	6.1E-01
AT1G18060	*AT1G18060*	microbial collagenase	3.1	2.6E-12	2.1E-10	1.1	3.9E-01	6.5E-01
AT3G47430	*PEX11B*	peroxin 11B	3.1	2.7E-12	2.1E-10	1.2	5.9E-02	2.2E-01
AT1G49405	*AT1G49405*	Uncharacterized protein family (UPF0497)	3.0	1.4E-03	6.4E-03	1.7	1.1E-01	3.3E-01
AT3G49320	*AT3G49320*	Metal-dependent protein hydrolase	3.0	3.0E-08	6.8E-07	1.3	1.3E-01	3.5E-01
AT4G33666	*AT4G33666*	hypothetical protein	3.0	4.2E-09	1.3E-07	1.4	1.8E-02	1.1E-01
AT2G25450	*AT2G25450*	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	3.0	2.8E-11	1.6E-09	-1.6	1.8E-04	4.9E-03
AT3G58150	*AT3G58150*	Optic atrophy 3 protein (OPA3)	3.0	4.1E-03	1.6E-02	1.8	1.3E-01	3.6E-01
AT1G76110	*AT1G76110*	HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain-containing protein	3.0	1.1E-09	4.1E-08	1.8	1.1E-04	3.3E-03
AT2G35700	*ERF38*	ERF family protein 38	3.0	8.6E-04	4.3E-03	-1.2	6.4E-01	8.3E-01
AT5G16350	*AT5G16350*	O-acyltransferase (WSD1-like) family protein	3.0	1.3E-06	1.8E-05	-1.1	6.3E-01	8.2E-01
AT3G57520	*SIP2*	seed imbibition 2	3.0	1.8E-09	6.1E-08	-1.7	3.9E-04	8.3E-03
AT3G13061	*AT3G13061*	Natural antisense transcript overlaps with AT3G13060	3.0	1.8E-08	4.4E-07	1.2	3.6E-01	6.2E-01
AT5G59820	*RHL41*	C2H2-type zinc finger family protein	3.0	1.1E-06	1.5E-05	1.2	4.5E-01	7.0E-01
AT2G34060	*AT2G34060*	Peroxidase superfamily protein	3.0	6.2E-10	2.4E-08	1.5	4.8E-03	4.5E-02
AT1G78600	*LZF1*	light-regulated zinc finger protein 1	3.0	8.8E-13	8.0E-11	1.1	2.2E-01	4.7E-01
AT1G29700	*AT1G29700*	Metallo-hydrolase/oxidoreductase superfamily protein	3.0	6.2E-10	2.4E-08	1.5	2.9E-03	3.3E-02
AT2G27820	*PD1*	prephenate dehydratase 1	3.0	3.3E-19	1.8E-16	-1.1	4.2E-01	6.7E-01
AT2G40100	*LHCB4.3*	light harvesting complex photosystem II	3.0	6.5E-12	4.5E-10	1.0	8.1E-01	9.2E-01
AT2G21280	*SULA*	NAD(P)-binding Rossmann-fold superfamily protein	3.0	1.1E-12	1.0E-10	1.2	4.2E-02	1.8E-01
AT1G69310	*WRKY57*	WRKY DNA-binding protein 57	3.0	7.1E-15	1.2E-12	-1.2	5.0E-02	2.0E-01
AT4G37930	*SHM1*	serine transhydroxymethyltransferase 1	3.0	1.9E-10	8.7E-09	1.1	3.3E-01	6.0E-01
AT1G22690	*AT1G22690*	Gibberellin-regulated family protein	3.0	8.0E-06	8.3E-05	-1.1	6.4E-01	8.3E-01
AT5G10470	*KAC1*	kinesin like protein for actin based chloroplast movement 1	3.0	2.7E-13	2.9E-11	1.1	2.2E-01	4.8E-01
AT4G18810	*AT4G18810*	NAD(P)-binding Rossmann-fold superfamily protein	3.0	1.9E-09	6.5E-08	1.2	1.5E-01	3.8E-01
AT3G47780	*ABCA7*	ABC2 homolog 6	3.0	1.1E-14	1.7E-12	-1.2	1.0E-01	3.1E-01
AT2G38380	*AT2G38380*	Peroxidase superfamily protein	3.0	2.6E-06	3.2E-05	1.1	7.0E-01	8.7E-01
AT1G21140	*AT1G21140*	Vacuolar iron transporter (VIT) family protein	3.0	4.2E-04	2.4E-03	1.2	5.4E-01	7.6E-01
AT3G48320	*CYP71A21*	cytochrome P450, family 71, subfamily A, polypeptide 21	3.0	4.6E-07	7.2E-06	1.1	7.2E-01	8.8E-01
AT3G22370	*AOX1A*	alternative oxidase 1A	3.0	1.3E-11	8.3E-10	-1.3	3.6E-02	1.6E-01
AT3G01990	*ACR6*	ACT domain repeat 6	3.0	3.0E-08	6.8E-07	-1.1	4.5E-01	7.0E-01
AT4G15248	*BBX30*	B-box type zinc finger family protein	3.0	4.7E-05	3.7E-04	-1.4	1.6E-01	4.0E-01
AT1G66840	*PMI2*	PLASTID MOVEMENT IMPAIRED protein (DUF827)	2.9	5.1E-12	3.7E-10	1.1	2.9E-01	5.6E-01
AT2G34180	*CIPK13*	CBL-interacting protein kinase 13	2.9	1.1E-04	7.4E-04	-1.2	4.9E-01	7.2E-01
AT2G18328	*RL4*	RAD-like 4	2.9	1.1E-04	7.9E-04	1.3	3.2E-01	5.9E-01
AT1G73990	*SPPA*	signal peptide peptidase	2.9	1.5E-16	4.5E-14	1.2	2.8E-02	1.4E-01
AT2G32390	*GLR3.5*	glutamate receptor 3.5	2.9	3.3E-11	1.9E-09	1.5	2.0E-03	2.5E-02
AT5G41740	*AT5G41740*	Disease resistance protein (TIR-NBS-LRR class)	2.9	8.3E-06	8.6E-05	1.7	1.2E-02	8.1E-02
AT5G36925	*AT5G36925*	hypothetical protein	2.9	2.3E-03	9.7E-03	-1.5	2.9E-01	5.6E-01
AT1G12250	*AT1G12250*	Pentapeptide repeat-containing protein	2.9	5.5E-12	3.9E-10	1.1	2.0E-01	4.5E-01
AT2G41000	*AT2G41000*	Chaperone DnaJ-domain superfamily protein	2.9	1.2E-14	1.8E-12	1.0	8.5E-01	9.4E-01
AT3G50560	*AT3G50560*	NAD(P)-binding Rossmann-fold superfamily protein	2.9	5.6E-10	2.2E-08	-1.2	2.1E-01	4.7E-01
AT5G18670	*BMY3*	beta-amylase 3	2.9	3.1E-14	4.1E-12	-1.2	3.7E-02	1.7E-01
AT4G23450	*AIRP1*	RING/U-box superfamily protein	2.9	4.0E-08	8.7E-07	1.0	9.9E-01	1.0E+00
AT4G18220	*AT4G18220*	Drug/metabolite transporter superfamily protein	2.9	2.2E-07	3.8E-06	1.2	3.1E-01	5.8E-01
AT1G54575	*AT1G54575*	hypothetical protein	2.9	1.2E-06	1.6E-05	1.5	5.0E-02	2.0E-01
AT1G65860	*FMO GS-OX1*	flavin-monooxygenase glucosinolate S-oxygenase 1	2.9	3.4E-04	2.0E-03	-1.4	2.6E-01	5.2E-01
AT3G26570	*PHT2*		2.9	3.8E-12	2.8E-10	1.2	7.1E-02	2.5E-01
AT5G35970	*AT5G35970*	P-loop containing nucleoside triphosphate hydrolases superfamily protein	2.9	3.8E-09	1.2E-07	1.3	5.8E-02	2.2E-01
AT4G15630	*AT4G15630*	Uncharacterized protein family (UPF0497)	2.9	1.6E-07	2.9E-06	1.1	6.4E-01	8.3E-01
AT3G26320	*CYP71B36*	cytochrome P450, family 71, subfamily B, polypeptide 36	2.9	3.9E-04	2.2E-03	1.4	2.7E-01	5.3E-01
AT1G78990	*AT1G78990*	HXXXD-type acyl-transferase family protein	2.9	3.2E-03	1.3E-02	1.3	4.8E-01	7.2E-01
AT2G32500	*AT2G32500*	Stress responsive alpha-beta barrel domain protein	2.9	1.2E-09	4.3E-08	1.5	6.6E-03	5.6E-02
AT3G47580	*AT3G47580*	Leucine-rich repeat protein kinase family protein	2.9	5.3E-08	1.1E-06	-1.1	6.7E-01	8.5E-01
AT5G10250	*DOT3*	Phototropic-responsive NPH3 family protein	2.9	2.2E-04	1.4E-03	1.6	8.7E-02	2.8E-01
AT3G24170	*GR1*	glutathione-disulfide reductase	2.9	7.1E-19	3.7E-16	-1.1	3.5E-01	6.1E-01
AT5G41460	*AT5G41460*	transferring glycosyl group transferase (DUF604)	2.9	3.6E-07	5.8E-06	-1.5	4.5E-02	1.9E-01
AT3G57920	*SPL15*	squamosa promoter binding protein-like 15	2.9	1.8E-08	4.4E-07	1.4	5.2E-02	2.1E-01
AT2G19650	*AT2G19650*	Cysteine/Histidine-rich C1 domain family protein	2.9	5.6E-11	3.0E-09	-1.1	5.1E-01	7.4E-01
AT2G47200	*AT2G47200*	hypothetical protein	2.9	6.1E-03	2.2E-02	1.4	4.1E-01	6.7E-01
AT4G28740	*AT4G28740*	LOW PSII ACCUMULATION-like protein	2.9	2.5E-13	2.7E-11	1.3	1.9E-02	1.1E-01
AT2G48130	*AT2G48130*	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	2.8	6.7E-07	1.0E-05	-1.2	3.6E-01	6.2E-01
AT3G46370	*AT3G46370*	Leucine-rich repeat protein kinase family protein	2.8	4.5E-03	1.7E-02	1.7	1.7E-01	4.1E-01
AT2G04795	*AT2G04795*	hypothetical protein	2.8	2.4E-05	2.1E-04	1.2	3.4E-01	6.0E-01

AT5G38420	*RBCS2B*	Ribulose bisphosphate carboxylase (small chain) family protein	2.8	3.2E-08	7.2E-07	1.1	7.3E-01	8.8E-01
AT4G19170	*NCED4*	nine-cis-epoxycarotenoid dioxygenase 4	2.8	4.1E-05	3.4E-04	-1.2	4.8E-01	7.2E-01
AT1G21120	*IGMT2*	O-methyltransferase family protein	2.8	1.3E-05	1.2E-04	-1.1	7.1E-01	8.7E-01
AT1G55480	*ZKT*	protein containing PDZ domain, a K-box domain, and a TPR region	2.8	1.5E-10	7.3E-09	1.1	2.9E-01	5.6E-01
AT3G05936	*AT3G05936*	hypothetical protein	2.8	1.7E-06	2.2E-05	1.4	7.3E-02	2.6E-01
AT2G34460	*AT2G34460*	NAD(P)-binding Rossmann-fold superfamily protein	2.8	1.7E-12	1.5E-10	1.1	1.9E-01	4.4E-01
AT2G16895	*AT2G16895*	pseudogene of UDP-Glycosyltransferase superfamily protein	2.8	8.3E-03	2.8E-02	1.1	7.9E-01	9.1E-01
AT5G63060	*AT5G63060*	Sec14p-like phosphatidylinositol transfer family protein	2.8	1.5E-06	1.9E-05	1.9	1.7E-03	2.2E-02
AT1G14150	*PnsL2*	PsbQ-like 2	2.8	2.2E-09	7.2E-08	1.1	3.9E-01	6.5E-01
AT5G07020	*AT5G07020*	proline-rich family protein	2.8	3.3E-12	2.5E-10	1.2	4.3E-02	1.8E-01
AT1G79770	*AT1G79770*	CASP-like protein (DUF1677)	2.8	6.1E-07	9.2E-06	-1.1	6.4E-01	8.3E-01
AT3G04140	*AT3G04140*	Ankyrin repeat family protein	2.8	2.9E-12	2.3E-10	-1.1	4.8E-01	7.2E-01
AT2G38780	*AT2G38780*	cytochrome C oxidase subunit	2.8	1.4E-13	1.6E-11	1.1	2.7E-01	5.4E-01
AT5G62140	*AT5G62140*	ATP-dependent Clp protease ATP-binding subunit	2.8	1.2E-11	7.5E-10	1.1	3.0E-01	5.7E-01
AT1G35290	*AT1G35290*	Thioesterase superfamily protein	2.8	8.8E-05	6.4E-04	-1.2	3.7E-01	6.3E-01
AT5G26820	*IREG3*	iron-regulated protein 3	2.8	3.1E-11	1.8E-09	1.4	4.4E-03	4.3E-02
AT3G21510	*AHP1*	histidine-containing phosphotransmitter 1	2.8	4.8E-07	7.5E-06	1.1	6.2E-01	8.2E-01
AT5G56840	*AT5G56840*	myb-like transcription factor family protein	2.8	5.6E-03	2.0E-02	-1.6	2.7E-01	5.3E-01
AT2G31790	*AT2G31790*	UDP-Glycosyltransferase superfamily protein	2.8	4.4E-11	2.4E-09	1.1	5.7E-01	7.9E-01
AT1G52870	*AT1G52870*	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	2.8	9.4E-10	3.5E-08	1.0	7.3E-01	8.8E-01
AT1G62250	*AT1G62250*	orotidine 5'-phosphate decarboxylase	2.8	1.5E-12	1.3E-10	-1.0	6.3E-01	8.2E-01
AT5G59130	*AT5G59130*	Subtilase family protein	2.8	1.2E-12	1.1E-10	-1.2	5.4E-02	2.1E-01
AT3G48420	*AT3G48420*	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	2.8	5.3E-09	1.6E-07	1.3	4.0E-02	1.8E-01
AT5G52420	*AT5G52420*	transmembrane protein	2.8	2.3E-13	2.6E-11	1.1	2.7E-01	5.3E-01
AT3G46650	*AT3G46650*	UDP-Glycosyltransferase superfamily protein	2.8	3.6E-05	3.0E-04	1.9	7.5E-03	6.1E-02
AT5G65840	*AT5G65840*	Thioredoxin superfamily protein	2.8	5.4E-16	1.3E-13	-1.1	3.2E-01	5.9E-01
AT4G18210	*PUP10*	purine permease 10	2.8	6.9E-08	1.4E-06	1.3	1.1E-01	3.3E-01
AT1G62750	*SCO1*	Translation elongation factor EFG/EF2 protein	2.8	2.0E-11	1.2E-09	1.2	5.1E-02	2.1E-01
AT2G15080	*RLP19*	receptor like protein 19	2.8	1.8E-04	1.2E-03	1.3	3.3E-01	5.9E-01
AT1G68240	*AT1G68240*	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	2.8	1.3E-02	4.1E-02	2.4	3.9E-02	1.7E-01
AT5G38510	*AT5G38510*	Rhomboid-related intramembrane serine protease family protein	2.8	9.8E-11	4.9E-09	1.0	7.6E-01	9.0E-01
AT3G28840	*AT3G28840*	hypothetical protein (DUF1216)	2.8	1.1E-02	3.4E-02	-3.3	3.2E-02	1.5E-01
AT3G01500	*CA1*	carbonic anhydrase 1	2.8	4.8E-08	1.0E-06	1.2	2.7E-01	5.3E-01
AT3G19450	*ATCAD4*	GroES-like zinc-binding alcohol dehydrogenase family protein	2.8	5.8E-13	5.6E-11	1.1	4.0E-01	6.6E-01
AT4G35090	*CAT2*	catalase 2	2.8	2.0E-13	2.3E-11	1.0	8.3E-01	9.4E-01
AT2G30490	*C4H*	cinnamate-4-hydroxylase	2.8	8.4E-16	1.9E-13	1.0	5.2E-01	7.5E-01
AT1G01250	*AT1G01250*	Integrase-type DNA-binding superfamily protein	2.8	4.2E-03	1.6E-02	-1.0	1.0E+00	1.0E+00
AT2G47270	*UPB1*	transcription factor UPBEAT protein	2.8	1.0E-07	1.9E-06	1.1	5.6E-01	7.8E-01
AT5G08760	*AT5G08760*	transmembrane protein	2.8	4.1E-04	2.3E-03	-1.2	6.0E-01	8.0E-01
AT2G35960	*NHL12*	NDR1/HIN1-like 12	2.8	1.1E-08	2.9E-07	-1.5	1.2E-02	8.2E-02
AT4G29930	*AT4G29930*	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	2.8	8.8E-05	6.3E-04	1.6	5.4E-02	2.1E-01
AT4G34138	*UGT73B1*	UDP-glucosyl transferase 73B1	2.8	3.1E-12	2.4E-10	-1.0	8.8E-01	9.6E-01
AT1G70985	*AT1G70985*	hydroxyproline-rich glycoprotein family protein	2.7	2.7E-08	6.3E-07	-1.9	3.9E-04	8.3E-03
AT1G78140	*AT1G78140*	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	2.7	3.9E-17	1.3E-14	1.2	5.6E-03	5.0E-02
AT4G34060	*DML3*	demeter-like protein 3	2.7	2.8E-04	1.7E-03	-1.2	5.8E-01	7.9E-01
AT1G50250	*FTSH1*	FTSH protease 1	2.7	4.6E-12	3.3E-10	1.2	2.7E-02	1.4E-01
AT3G22210	*AT3G22210*	transmembrane protein	2.7	2.1E-07	3.7E-06	1.8	4.7E-04	9.5E-03
AT1G02220	*NAC003*	NAC domain containing protein 3	2.7	3.7E-08	8.2E-07	-1.1	5.2E-01	7.5E-01
AT3G23400	*FIB4*	Plastid-lipid associated protein PAP / fibrillin family protein	2.7	2.3E-15	4.4E-13	1.2	6.3E-02	2.3E-01
AT3G14770	*SWEET2*	Nodulin MtN3 family protein	2.7	1.5E-05	1.4E-04	1.4	1.3E-01	3.6E-01
AT2G31750	*UGT74D1*	UDP-glucosyl transferase 74D1	2.7	1.3E-19	8.1E-17	-1.1	2.0E-01	4.6E-01
AT4G38970	*FBA2*	fructose-bisphosphate aldolase 2	2.7	5.3E-10	2.1E-08	1.3	4.1E-02	1.8E-01
AT2G29310	*AT2G29310*	NAD(P)-binding Rossmann-fold superfamily protein	2.7	9.8E-09	2.6E-07	-1.2	1.7E-01	4.2E-01
AT3G46670	*UGT76E11*	UDP-glucosyl transferase 76E11	2.7	9.4E-07	1.3E-05	1.7	2.8E-03	3.2E-02
AT2G23840	*AT2G23840*	HNH endonuclease	2.7	2.3E-07	3.9E-06	1.2	3.0E-01	5.6E-01
AT1G72930	*TIR*	toll/interleukin-1 receptor-like protein	2.7	1.5E-04	1.0E-03	1.4	2.2E-01	4.7E-01
AT4G15720	*AT4G15720*	Tetratricopeptide repeat (TPR)-like superfamily protein	2.7	5.3E-03	2.0E-02	1.8	9.7E-02	3.0E-01
AT2G37240	*AT2G37240*	Thioredoxin superfamily protein	2.7	7.5E-10	2.8E-08	1.0	9.3E-01	9.8E-01
AT5G17170	*ENH1*	rubredoxin family protein	2.7	1.2E-11	7.7E-10	-1.0	7.4E-01	8.8E-01
AT3G27110	*AT3G27110*	Peptidase family M48 family protein	2.7	4.2E-16	1.0E-13	-1.1	3.8E-01	6.4E-01
AT2G04790	*AT2G04790*	PTB domain engulfment adapter	2.7	5.4E-09	1.6E-07	1.4	2.6E-02	1.4E-01
AT3G03630	*CS26*	cysteine synthase 26	2.7	5.9E-09	1.7E-07	1.8	5.2E-05	2.1E-03
AT3G22420	*WNK2*	with no lysine (K) kinase 2	2.7	5.4E-11	2.9E-09	1.3	1.5E-02	9.6E-02
AT5G66760	*SDH1-1*	succinate dehydrogenase 1-1	2.7	2.0E-18	8.2E-16	1.0	4.8E-01	7.2E-01
AT3G01970	*WRKY45*	WRKY DNA-binding protein 45	2.7	3.6E-07	5.8E-06	1.3	1.4E-01	3.8E-01
AT5G38410	*RBCS3B*	Ribulose bisphosphate carboxylase (small chain) family protein	2.7	1.9E-08	4.5E-07	1.4	2.8E-02	1.4E-01
AT4G23493	*AT4G23493*	hypothetical protein	2.7	3.3E-06	3.9E-05	1.1	5.5E-01	7.7E-01
AT1G34000	*OHP2*	one-helix protein 2	2.7	2.9E-12	2.3E-10	1.2	1.0E-01	3.1E-01
AT1G78476	*AT1G78476*	hypothetical protein	2.7	1.4E-03	6.4E-03	1.1	8.6E-01	9.5E-01

AT2G28105	*AT2G28105*	replication factor-A carboxy-terminal domain	2.7	3.5E-06	4.1E-05	1.6	1.5E-02	9.7E-02
AT5G44575	*AT5G44575*	hypothetical protein	2.7	5.5E-03	2.0E-02	1.6	1.8E-01	4.3E-01
AT1G08550	*NPQ1*	non-photochemical quenching 1	2.7	1.2E-11	7.8E-10	1.5	1.0E-04	3.2E-03
AT1G15980	*PnsB1*	NDH-dependent cyclic electron flow 1	2.7	7.9E-09	2.2E-07	1.1	4.8E-01	7.2E-01
AT1G23740	*AOR*	Oxidoreductase, zinc-binding dehydrogenase family protein	2.7	1.1E-10	5.2E-09	1.1	5.4E-01	7.6E-01
AT1G76080	*CDSP32*	chloroplastic drought-induced stress protein of 32	2.7	5.9E-12	4.1E-10	1.5	1.3E-04	3.9E-03
AT2G41120	*AT2G41120*	DUF309 domain protein	2.7	8.7E-07	1.3E-05	1.1	7.7E-01	9.0E-01
AT4G15563	*AT4G15563*	F-box-like protein	2.7	8.5E-08	1.7E-06	1.0	9.0E-01	9.6E-01
AT5G19855	*RbcX2*	Chaperonin-like RbcX protein	2.7	4.1E-12	3.0E-10	1.2	3.2E-02	1.5E-01
AT1G47610	*AT1G47610*	Transducin/WD40 repeat-like superfamily protein	2.7	1.0E-02	3.4E-02	1.1	8.6E-01	9.5E-01
AT1G74430	*MYB95*	myb domain protein 95	2.7	5.7E-15	9.7E-13	-1.3	1.8E-02	1.1E-01
AT1G76800	*AT1G76800*	Vacuolar iron transporter (VIT) family protein	2.7	5.8E-04	3.1E-03	1.3	3.0E-01	5.7E-01
AT2G32510	*MAPKKK17*	mitogen-activated protein kinase kinase kinase 17	2.7	1.8E-09	6.2E-08	-1.4	1.2E-02	8.0E-02
AT3G16175	*AT3G16175*	Thioesterase superfamily protein	2.7	6.9E-07	1.0E-05	1.3	8.9E-02	2.9E-01
AT3G47770	*ABCA6*	ABC2 homolog 5	2.7	9.7E-03	3.2E-02	1.1	8.6E-01	9.5E-01
AT1G71810	*AT1G71810*	Protein kinase superfamily protein	2.7	4.4E-11	2.4E-09	-1.0	6.6E-01	8.4E-01
AT5G08740	*NDC1*	NAD(P)H dehydrogenase C1	2.7	4.7E-14	6.0E-12	1.2	2.2E-02	1.2E-01
AT4G16690	*MES16*	methyl esterase 16	2.7	2.1E-07	3.7E-06	-1.1	6.4E-01	8.3E-01
AT5G64120	*AT5G64120*	Peroxidase superfamily protein	2.7	1.5E-06	2.0E-05	-1.4	5.9E-02	2.2E-01
AT1G13930	*AT1G13930*	oleosin-B3-like protein	2.7	3.9E-10	1.6E-08	1.0	7.4E-01	8.8E-01
AT3G20200	*AT3G20200*	kinase with adenine nucleotide alpha hydrolases-like domain-containing protein	2.7	3.3E-08	7.4E-07	-1.1	5.2E-01	7.5E-01
AT5G41170	*AT5G41170*	Pentatricopeptide repeat (PPR-like) superfamily protein	2.7	1.1E-06	1.5E-05	1.1	6.9E-01	8.6E-01
AT4G37610	*BT5*	BTB and TAZ domain protein 5	2.7	5.1E-10	2.1E-08	-1.3	1.5E-02	9.7E-02
AT3G21890	*BBX31*	B-box type zinc finger family protein	2.6	2.2E-06	2.8E-05	-1.2	2.3E-01	4.9E-01
AT5G35110	*AT5G35110*	hypothetical protein	2.6	7.5E-04	3.8E-03	1.4	2.1E-01	4.6E-01
AT3G55800	*SBPASE*	sedoheptulose-bisphosphatase	2.6	5.0E-10	2.0E-08	1.1	2.4E-01	5.1E-01
AT5G09230	*SRT2*	sirtuin 2	2.6	6.7E-15	1.1E-12	1.0	5.7E-01	7.9E-01
AT1G74640	*AT1G74640*	alpha/beta-Hydrolases superfamily protein	2.6	1.3E-15	2.7E-13	1.1	1.7E-01	4.1E-01
AT1G69730	*AT1G69730*	Wall-associated kinase family protein	2.6	8.1E-07	1.2E-05	-1.2	2.5E-01	5.2E-01
AT5G43260	*AT5G43260*	chaperone protein dnaJ-like protein	2.6	6.2E-13	5.9E-11	-1.0	1.0E+00	1.0E+00
AT4G37560	*AT4G37560*	Acetamidase/Formamidase family protein	2.6	7.7E-07	1.1E-05	1.6	8.1E-03	6.4E-02
AT1G55020	*LOX1*	lipoxygenase 1	2.6	2.6E-08	6.0E-07	1.0	7.9E-01	9.1E-01
AT5G02180	*AT5G02180*	Transmembrane amino acid transporter family protein	2.6	2.0E-08	4.8E-07	1.5	6.6E-03	5.6E-02
AT3G05790	*LON4*	lon protease 4	2.6	9.1E-03	3.0E-02	1.4	4.0E-01	6.6E-01
AT5G58760	*DDB2*	damaged DNA binding 2	2.6	1.3E-14	1.9E-12	1.0	8.3E-01	9.3E-01
AT4G25290	*AT4G25290*	DNA photolyase	2.6	1.8E-09	6.2E-08	1.3	5.5E-02	2.1E-01
AT5G02120	*OHP*	one helix protein	2.6	5.3E-11	2.9E-09	1.1	2.8E-01	5.5E-01
AT2G01110	*APG2*	Sec-independent periplasmic protein translocase	2.6	3.8E-13	3.8E-11	1.2	6.6E-02	2.4E-01
AT2G35130	*AT2G35130*	Tetratricopeptide repeat (TPR)-like superfamily protein	2.6	2.9E-09	9.3E-08	1.3	2.9E-02	1.4E-01
AT1G23200	*AT1G23200*	Plant invertase/pectin methylesterase inhibitor superfamily	2.6	4.2E-04	2.3E-03	-1.2	4.9E-01	7.2E-01
AT2G30950	*VAR2*	FtsH extracellular protease family	2.6	2.7E-11	1.6E-09	1.3	2.2E-02	1.2E-01
AT4G17215	*AT4G17215*	Pollen Ole e 1 allergen and extensin family protein	2.6	3.2E-06	3.9E-05	-1.0	9.0E-01	9.7E-01
AT4G09350	*NdhT*	Chaperone DnaJ-domain superfamily protein	2.6	4.0E-08	8.6E-07	1.2	1.4E-01	3.7E-01
AT4G37150	*MES9*	methyl esterase 9	2.6	2.6E-11	1.5E-09	-1.1	2.5E-01	5.1E-01
AT2G34810	*AT2G34810*	FAD-binding Berberine family protein	2.6	7.7E-07	1.1E-05	-1.8	1.4E-03	2.0E-02
AT3G10840	*AT3G10840*	alpha/beta-Hydrolases superfamily protein	2.6	1.3E-08	3.2E-07	1.2	2.8E-01	5.5E-01
AT1G22750	*AT1G22750*	transmembrane protein	2.6	1.2E-08	3.1E-07	1.2	1.2E-01	3.4E-01
AT1G65240	*AT1G65240*	Eukaryotic aspartyl protease family protein	2.6	6.6E-03	2.3E-02	1.7	1.5E-01	3.8E-01
AT1G07250	*UGT71C4*	UDP-glucosyl transferase 71C4	2.6	8.4E-16	1.9E-13	1.1	9.0E-02	2.9E-01
AT3G48480	*AT3G48480*	Cysteine proteinases superfamily protein	2.6	8.9E-07	1.3E-05	-1.5	6.6E-02	2.4E-01
AT1G53090	*SPA4*	SPA1-related 4	2.6	2.3E-13	2.6E-11	-1.1	1.6E-01	4.0E-01
AT2G21560	*AT2G21560*	nucleolar-like protein	2.6	3.8E-11	2.2E-09	-1.0	6.6E-01	8.4E-01
AT1G07128	*AT1G07128*	Natural antisense transcript overlaps with AT1G07130	2.6	1.6E-07	2.9E-06	1.1	5.2E-01	7.5E-01
AT2G22240	*MIPS2*	myo-inositol-1-phosphate synthase 2	2.6	2.0E-10	8.9E-09	-1.2	8.7E-02	2.8E-01
AT5G04830	*AT5G04830*	Nuclear transport factor 2 (NTF2) family protein	2.6	2.4E-15	4.6E-13	-1.0	7.3E-01	8.8E-01
AT3G46870	*AT3G46870*	Pentatricopeptide repeat (PPR) superfamily protein	2.5	2.4E-08	5.6E-07	1.2	2.6E-01	5.2E-01
AT1G29530	*AT1G29530*	hypothetical protein	2.5	6.1E-10	2.4E-08	1.4	4.3E-03	4.2E-02
AT1G66230	*MYB20*	myb domain protein 20	2.5	2.3E-07	4.0E-06	1.4	2.8E-02	1.4E-01
AT5G11590	*TINY2*	Integrase-type DNA-binding superfamily protein	2.5	7.4E-05	5.5E-04	1.1	8.1E-01	9.3E-01
AT4G01080	*TBL26*	TRICHOME BIREFRINGENCE-LIKE 26	2.5	1.1E-04	7.7E-04	-1.3	2.2E-01	4.8E-01
AT2G23010	*SCPL9*	serine carboxypeptidase-like 9	2.5	1.4E-06	1.9E-05	-1.6	9.0E-03	6.9E-02
AT1G80300	*NTT1*	nucleotide transporter 1	2.5	2.9E-14	3.9E-12	-1.0	7.2E-01	8.8E-01
AT2G34960	*CAT5*	cationic amino acid transporter 5	2.5	6.0E-05	4.6E-04	1.1	7.3E-01	8.8E-01
AT3G61870	*AT3G61870*	plant/protein	2.5	5.7E-11	3.1E-09	1.2	1.5E-01	3.9E-01
AT3G04210	*AT3G04210*	Disease resistance protein (TIR-NBS class)	2.5	6.6E-04	3.5E-03	-1.6	1.0E-01	3.1E-01
AT4G11570	*AT4G11570*	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	2.5	5.4E-12	3.8E-10	1.1	5.5E-01	7.7E-01
AT3G50980	*XERO1*	dehydrin xero 1	2.5	3.2E-04	1.9E-03	1.7	3.5E-02	1.6E-01
AT1G72610	*GER1*	germin-like protein 1	2.5	3.7E-07	6.0E-06	1.2	1.8E-01	4.3E-01
AT2G33855	*AT2G33855*	transmembrane protein	2.5	4.6E-10	1.9E-08	-1.1	4.3E-01	6.9E-01
AT1G51110	*AT1G51110*	Plastid-lipid associated protein PAP / fibrillin family protein	2.5	1.7E-06	2.2E-05	1.6	4.2E-03	4.2E-02
AT1G74290	*AT1G74290*	alpha/beta-Hydrolases superfamily protein	2.5	2.0E-03	8.7E-03	-1.2	5.7E-01	7.8E-01
AT3G27380	*SDH2-1*	succinate dehydrogenase 2-1	2.5	6.0E-14	7.4E-12	-1.1	2.3E-01	4.9E-01
AT2G46420	*AT2G46420*	helicase with zinc finger protein	2.5	4.1E-12	3.0E-10	-1.0	7.4E-01	8.9E-01
AT1G33110	*AT1G33110*	MATE efflux family protein	2.5	5.1E-08	1.1E-06	1.1	4.4E-01	6.9E-01

AT5G38430	*RBCS1B*	Ribulose bisphosphate carboxylase (small chain) family protein	2.5	3.0E-07	5.0E-06	1.4	3.0E-02	1.5E-01
AT3G15090	*AT3G15090*	GroES-like zinc-binding alcohol dehydrogenase family protein	2.5	1.3E-18	6.1E-16	-1.1	6.9E-02	2.5E-01
AT3G06145	*AT3G06145*	RING zinc finger protein	2.5	4.4E-07	6.9E-06	-1.1	4.7E-01	7.1E-01
AT1G65230	*AT1G65230*	transmembrane protein, putative (DUF2358)	2.5	3.3E-09	1.0E-07	1.4	1.0E-02	7.4E-02
AT4G26200	*ACS7*	1-amino-cyclopropane-1-carboxylate synthase 7	2.5	2.4E-04	1.5E-03	-1.0	8.5E-01	9.4E-01
AT2G37770	*ChlAKR*	NAD(P)-linked oxidoreductase superfamily protein	2.5	5.4E-03	2.0E-02	-1.9	1.2E-01	3.4E-01
AT4G38620	*MYB4*	myb domain protein 4	2.5	7.4E-08	1.5E-06	-1.5	5.0E-03	4.7E-02
AT1G65130	*AT1G65130*	Ubiquitin carboxyl-terminal hydrolase-related protein	2.5	3.0E-03	1.2E-02	-1.1	9.0E-01	9.6E-01
AT5G11160	*APT5*	adenine phosphoribosyltransferase 5	2.5	4.0E-06	4.6E-05	1.6	5.7E-03	5.1E-02
AT3G61880	*CYP78A9*	cytochrome p450 78a9	2.5	7.3E-04	3.8E-03	-2.0	2.9E-02	1.4E-01
AT1G32440	*PKp3*	plastidial pyruvate kinase 3	2.5	9.4E-16	2.1E-13	-1.0	4.8E-01	7.2E-01
AT4G21760	*BGLU47*	beta-glucosidase 47	2.5	1.2E-02	3.6E-02	1.4	4.0E-01	6.5E-01
AT5G45680	*FKBP13*	FK506-binding protein 13	2.5	5.5E-09	1.6E-07	1.4	3.6E-03	3.7E-02
AT2G48090	*AT2G48090*	hypothetical protein	2.5	9.3E-04	4.6E-03	1.0	9.9E-01	1.0E+00
AT4G28290	*AT4G28290*	hypothetical protein	2.5	3.8E-11	2.1E-09	-1.2	1.4E-01	3.8E-01
AT1G10960	*FD1*	ferredoxin 1	2.5	7.9E-09	2.2E-07	1.3	5.2E-02	2.1E-01
AT3G57830	*AT3G57830*	Leucine-rich repeat protein kinase family protein	2.5	1.1E-09	4.1E-08	1.1	6.4E-01	8.3E-01
AT5G64850	*AT5G64850*	sorbin/SH3 domain protein	2.5	2.2E-11	1.3E-09	1.0	6.7E-01	8.4E-01
AT1G32080	*LrgB*	membrane protein	2.5	1.0E-07	1.9E-06	-1.3	9.3E-02	2.9E-01
AT2G04530	*CPZ*	Metallo-hydrolase/oxidoreductase superfamily protein	2.5	1.5E-07	2.8E-06	1.5	7.1E-03	5.9E-02
AT3G10986	*AT3G10986*	LURP-one-like protein (DUF567)	2.5	1.7E-04	1.1E-03	1.2	3.4E-01	6.1E-01
AT2G40390	*AT2G40390*	neuronal PAS domain protein	2.5	2.8E-03	1.2E-02	1.5	1.7E-01	4.2E-01
AT4G17970	*ALMT12*	aluminum-activated, malate transporter 12	2.5	3.1E-05	2.6E-04	-1.2	4.4E-01	6.9E-01
AT4G27410	*RD26*	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	2.5	1.0E-08	2.7E-07	1.2	9.5E-02	3.0E-01
AT3G44990	*XTH31*	xyloglucan endo-transglycosylase-related 8	2.5	2.6E-10	1.2E-08	-1.2	6.5E-02	2.4E-01
AT5G18470	*AT5G18470*	Curculin-like (mannose-binding) lectin family	2.4	2.1E-05	1.9E-04	-1.2	2.8E-01	5.5E-01
AT1G51090	*AT1G51090*	Heavy metal transport/detoxification superfamily protein	2.4	2.5E-03	1.0E-02	-1.5	2.4E-01	5.0E-01
AT3G03440	*AT3G03440*	ARM repeat superfamily protein	2.4	4.3E-11	2.4E-09	-1.1	3.2E-01	5.9E-01
AT5G40500	*AT5G40500*	hypothetical protein	2.4	1.8E-08	4.4E-07	1.3	2.2E-02	1.2E-01
AT5G08650	*AT5G08650*	Small GTP-binding protein	2.4	1.9E-09	6.3E-08	1.3	4.8E-02	2.0E-01
AT1G48320	*DHNAT1*	Thioesterase superfamily protein	2.4	3.9E-10	1.6E-08	-1.0	9.5E-01	9.9E-01
AT4G28025	*AT4G28025*	hypothetical protein	2.4	3.4E-13	3.6E-11	1.0	5.5E-01	7.7E-01
AT3G19480	*AT3G19480*	D-3-phosphoglycerate dehydrogenase	2.4	7.6E-09	2.1E-07	1.5	1.7E-03	2.3E-02
AT5G13650	*SVR3*	elongation factor family protein	2.4	1.8E-10	8.5E-09	1.2	7.7E-02	2.6E-01
AT3G22060	*AT3G22060*	Receptor-like protein kinase-related family protein	2.4	2.9E-06	3.5E-05	1.0	9.6E-01	9.9E-01
AT4G04330	*RbcX1*	Chaperonin-like RbcX protein	2.4	4.3E-06	4.9E-05	1.6	9.5E-03	7.1E-02
AT1G48650	*AT1G48650*	DEA(D/H)-box RNA helicase family protein	2.4	3.2E-14	4.2E-12	1.2	4.9E-03	4.6E-02
AT3G21400	*AT3G21400*	dynein beta chain, ciliary protein	2.4	1.5E-10	7.1E-09	1.1	2.1E-01	4.6E-01
AT1G08570	*ACHT4*	atypical CYS HIS rich thioredoxin 4	2.4	6.4E-17	2.0E-14	-1.2	3.0E-03	3.3E-02
AT1G07010	*SLP1*	Calcineurin-like metallo-phosphoesterase superfamily protein	2.4	7.3E-10	2.8E-08	1.1	3.3E-01	5.9E-01
AT1G32900	*GBSS1*	UDP-Glycosyltransferase superfamily protein	2.4	1.1E-06	1.5E-05	1.1	6.0E-01	8.0E-01
AT3G10060	*AT3G10060*	FKBP-like peptidyl-prolyl cis-trans isomerase family protein	2.4	1.9E-09	6.4E-08	1.5	5.7E-04	1.1E-02
AT5G48300	*ADG1*	ADP glucose pyrophosphorylase 1	2.4	8.4E-09	2.3E-07	-1.0	8.4E-01	9.4E-01
AT4G39980	*DHS1*	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1	2.4	2.4E-13	2.6E-11	1.2	5.3E-02	2.1E-01
AT3G05360	*RLP30*	receptor like protein 30	2.4	8.3E-08	1.6E-06	1.1	5.1E-01	7.4E-01
AT1G49380	*AT1G49380*	cytochrome c biogenesis protein family	2.4	1.6E-09	5.6E-08	1.4	3.2E-03	3.5E-02
AT1G18660	*AT1G18660*	zinc finger (C3HC4-type RING finger) family protein	2.4	1.7E-15	3.3E-13	-1.0	7.7E-01	9.0E-01
AT2G13570	*NF-YB7*	nuclear factor Y, subunit B7	2.4	6.7E-03	2.3E-02	-1.7	1.4E-01	3.8E-01
AT5G05200	*AT5G05200*	Protein kinase superfamily protein	2.4	1.6E-12	1.4E-10	1.0	7.3E-01	8.8E-01
AT1G44000	*AT1G44000*	STAY-GREEN-like protein	2.4	1.8E-07	3.2E-06	1.5	4.7E-03	4.5E-02
AT2G03310	*AT2G03310*	transmembrane protein	2.4	2.1E-06	2.6E-05	1.5	2.3E-02	1.2E-01
AT1G16080	*AT1G16080*	nuclear protein	2.4	2.5E-10	1.1E-08	1.1	2.0E-01	4.6E-01
AT3G52540	*OFP18*	ovate family protein 18	2.4	3.9E-06	4.5E-05	1.1	4.5E-01	7.0E-01
AT2G35390	*AT2G35390*	Phosphoribosyltransferase family protein	2.4	5.4E-10	2.2E-08	1.0	9.7E-01	9.9E-01
AT4G24700	*AT4G24700*	hypothetical protein	2.4	2.3E-09	7.5E-08	1.2	1.8E-01	4.2E-01
AT4G26790	*AT4G26790*	GDSL-like Lipase/Acylhydrolase superfamily protein	2.4	7.4E-05	5.5E-04	-1.5	8.3E-02	2.8E-01
AT1G77090	*AT1G77090*	thylakoid lumenal protein (Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family	2.4	5.1E-11	2.8E-09	1.2	3.3E-02	1.6E-01
AT4G35783	*RTFL6*	ROTUNDIFOLIA like 6	2.4	1.1E-04	7.7E-04	-1.4	1.5E-01	3.8E-01
AT4G00370	*ANTR2*	Major facilitator superfamily protein	2.4	2.1E-12	1.7E-10	-1.0	6.0E-01	8.1E-01
AT2G04039	*AT2G04039*	DUF2996 family protein	2.4	2.4E-08	5.6E-07	1.3	4.8E-02	2.0E-01
AT4G10040	*CYTC-2*	cytochrome c-2	2.4	4.3E-15	7.4E-13	-1.1	1.4E-01	3.8E-01
AT2G36290	*AT2G36290*	alpha/beta-Hydrolases superfamily protein	2.4	5.7E-13	5.6E-11	1.0	8.8E-01	9.6E-01
AT2G36895	*AT2G36895*	D-tagatose-1,6-bisphosphate aldolase subunit	2.4	7.6E-10	2.8E-08	1.2	1.7E-01	4.2E-01
AT3G62090	*PIL2*	phytochrome interacting factor 3-like 2	2.4	2.6E-06	3.2E-05	-1.0	8.9E-01	9.6E-01
AT4G34190	*SEP1*	stress enhanced protein 1	2.4	7.0E-10	2.7E-08	1.2	7.3E-02	2.5E-01
AT4G39730	*PLAT1*	Lipase/lipooxygenase, PLAT/LH2 family protein	2.4	2.4E-09	7.8E-08	-1.4	3.2E-03	3.5E-02
AT1G45474	*Lhca5*	photosystem I light harvesting complex protein 5	2.4	6.9E-10	2.6E-08	1.2	1.1E-01	3.2E-01
AT2G04030	*CR88*	Chaperone protein htpG family protein	2.4	5.9E-10	2.3E-08	1.3	6.9E-03	5.7E-02
AT5G01260	*AT5G01260*	Carbohydrate-binding-like fold	2.4	1.5E-09	5.2E-08	1.1	4.5E-01	7.0E-01
AT4G19560	*CYCT1*		2.4	8.5E-04	4.3E-03	1.7	3.1E-02	1.5E-01
AT1G69200	*FLN2*	fructokinase-like protein	2.4	2.2E-07	3.9E-06	1.4	1.4E-02	9.0E-02
AT2G19150	*AT2G19150*	Pectin lyase-like superfamily protein	2.4	6.1E-03	2.2E-02	1.2	5.6E-01	7.8E-01
AT3G21390	*AT3G21390*	Mitochondrial substrate carrier family protein	2.4	2.2E-11	1.3E-09	1.1	3.6E-01	6.3E-01

AT3G48240	*AT3G48240*	Octicosapeptide/Phox/Bem1p family protein	2.4	1.2E-02	3.8E-02	-1.9	1.2E-01	3.4E-01
AT2G21330	*FBA1*	fructose-bisphosphate aldolase 1	2.4	3.2E-08	7.3E-07	1.2	1.8E-01	4.3E-01
AT5G62490	*HVA22B*	HVA22 homologue B	2.4	8.7E-03	2.9E-02	1.3	4.1E-01	6.7E-01
AT3G08505	*AT3G08505*	zinc finger (CCCH-type/C3HC4-type RING finger) family protein	2.4	1.7E-10	7.8E-09	-1.1	4.8E-01	7.2E-01
AT5G04140	*GLU1*	glutamate synthase 1	2.4	4.5E-07	7.1E-06	1.1	3.5E-01	6.1E-01
AT5G14700	*AT5G14700*	NAD(P)-binding Rossmann-fold superfamily protein	2.4	3.0E-07	4.9E-06	-1.3	4.7E-02	2.0E-01
AT1G24090	*AT1G24090*	RNase H family protein	2.4	1.4E-03	6.6E-03	1.7	4.1E-02	1.8E-01
AT5G55620	*AT5G55620*	hypothetical protein	2.4	9.7E-07	1.4E-05	-1.3	7.2E-02	2.5E-01
AT5G15910	*AT5G15910*	NAD(P)-binding Rossmann-fold superfamily protein	2.4	1.6E-15	3.3E-13	1.1	3.4E-01	6.0E-01
AT2G23600	*ACL*	acetone-cyanohydrin lyase	2.4	7.3E-08	1.5E-06	-1.0	8.1E-01	9.3E-01
AT5G38520	*AT5G38520*	alpha/beta-Hydrolases superfamily protein	2.4	4.4E-10	1.8E-08	1.3	2.5E-02	1.3E-01
AT2G28305	*LOG1*	Putative lysine decarboxylase family protein	2.4	1.4E-09	4.9E-08	-1.3	2.0E-02	1.1E-01
AT5G44550	*AT5G44550*	Uncharacterized protein family (UPF0497)	2.4	6.8E-05	5.1E-04	1.3	1.5E-01	3.9E-01
AT5G58260	*NdhN*	oxidoreductases, acting on NADH or NADPH, quinone or similar compound as acceptor	2.3	1.2E-08	3.2E-07	-1.1	5.0E-01	7.3E-01
AT1G08270	*AT1G08270*	vacuolar protein sorting-associated protein	2.3	9.1E-04	4.5E-03	1.3	3.4E-01	6.1E-01
AT5G13370	*AT5G13370*	Auxin-responsive GH3 family protein	2.3	5.9E-13	5.7E-11	1.1	1.7E-01	4.1E-01
AT5G08720	*AT5G08720*	polyketide cyclase/dehydrase/lipid transporter	2.3	3.6E-08	7.9E-07	1.3	1.8E-02	1.1E-01
AT5G43290	*WRKY49*	WRKY DNA-binding protein 49	2.3	4.3E-05	3.5E-04	1.4	5.9E-02	2.2E-01
AT5G20070	*NUDX19*	nudix hydrolase homolog 19	2.3	1.1E-17	4.0E-15	-1.1	8.6E-02	2.8E-01
AT1G10657	*AT1G10657*	transmembrane protein	2.3	3.3E-06	4.0E-05	-1.2	2.9E-01	5.5E-01
AT2G30420	*ETC2*	Homeodomain-like superfamily protein	2.3	1.4E-02	4.2E-02	-1.0	9.2E-01	9.7E-01
AT2G01590	*CRR3*	chlororespiratory reduction 3	2.3	2.0E-08	4.8E-07	1.5	7.1E-04	1.3E-02
AT1G55910	*ZIP11*	zinc transporter 11 precursor	2.3	9.9E-11	4.9E-09	-1.2	4.6E-02	1.9E-01
AT4G14210	*PDS3*	phytoene desaturase 3	2.3	3.9E-12	2.9E-10	1.2	3.0E-02	1.5E-01
AT1G17220	*FUG1*	Translation initiation factor 2, small GTP-binding protein	2.3	3.7E-09	1.2E-07	1.3	1.8E-02	1.1E-01
AT5G21482	*CKX7*	cytokinin oxidase 7	2.3	5.3E-07	8.2E-06	1.7	4.3E-04	9.0E-03
AT3G09160	*AT3G09160*	RNA-binding (RRM/RBD/RNP motifs) family protein	2.3	1.5E-05	1.4E-04	2.0	3.2E-04	7.2E-03
AT4G22200	*KT2/3*	potassium transport 2/3	2.3	3.1E-07	5.1E-06	-1.5	6.5E-03	5.5E-02
AT4G30470	*AT4G30470*	NAD(P)-binding Rossmann-fold superfamily protein	2.3	2.9E-10	1.3E-08	-1.6	3.6E-05	1.6E-03
AT4G06744	*AT4G06744*	Leucine-rich repeat (LRR) family protein	2.3	9.1E-09	2.4E-07	1.0	8.2E-01	9.3E-01
AT5G51010	*AT5G51010*	Rubredoxin-like superfamily protein	2.3	3.0E-12	2.3E-10	1.2	1.5E-02	9.6E-02
AT1G63580	*AT1G63580*	Receptor-like protein kinase-related family protein	2.3	1.3E-02	3.9E-02	1.4	3.5E-01	6.1E-01
AT1G16390	*OCT3*	organic cation/carnitine transporter 3	2.3	3.2E-06	3.9E-05	-1.4	2.8E-02	1.4E-01
AT5G47870	*RAD52-2*	cobalt ion-binding protein	2.3	9.0E-14	1.1E-11	1.0	8.1E-01	9.2E-01
AT2G30424	*TCL2*	Homeodomain-like superfamily protein	2.3	3.8E-07	6.1E-06	1.1	4.5E-01	7.0E-01
AT5G23120	*HCF136*	photosystem II stability/assembly factor, chloroplast (HCF136)	2.3	1.7E-09	6.0E-08	1.2	4.4E-02	1.9E-01
AT3G62930	*AT3G62930*	Thioredoxin superfamily protein	2.3	1.4E-05	1.3E-04	1.3	1.9E-01	4.5E-01
AT4G20860	*AT4G20860*	FAD-binding Berberine family protein	2.3	3.3E-08	7.4E-07	-1.1	5.8E-01	7.9E-01
AT1G14345	*AT1G14345*	NAD(P)-linked oxidoreductase superfamily protein	2.3	2.9E-09	9.1E-08	1.3	1.7E-02	1.0E-01
AT1G68010	*HPR*	hydroxypyruvate reductase	2.3	8.4E-08	1.7E-06	1.2	2.3E-01	4.9E-01
AT3G49160	*AT3G49160*	pyruvate kinase family protein	2.3	6.1E-05	4.7E-04	-1.7	1.1E-02	7.8E-02
AT3G19800	*AT3G19800*	E3 ubiquitin-protein ligase, putative (DUF177)	2.3	2.0E-09	6.8E-08	1.3	3.2E-02	1.5E-01
AT5G50240	*PIMT2*	protein-l-isoaspartate methyltransferase 2	2.3	2.6E-10	1.2E-08	-1.2	7.9E-02	2.7E-01
AT2G27290	*AT2G27290*	FAM210B-like protein, putative (DUF1279)	2.3	9.4E-10	3.5E-08	1.1	1.8E-01	4.3E-01
AT2G40340	*DREB2C*	Integrase-type DNA-binding superfamily protein	2.3	2.5E-03	1.1E-02	1.5	1.6E-01	4.0E-01
AT1G70610	*ABCB26*	transporter associated with antigen processing protein 1	2.3	3.9E-08	8.5E-07	1.1	2.8E-01	5.5E-01
AT5G18660	*PCB2*	NAD(P)-binding Rossmann-fold superfamily protein	2.3	1.5E-05	1.4E-04	1.6	6.4E-03	5.5E-02
AT1G33102	*AT1G33102*	hypothetical protein	2.3	4.3E-03	1.6E-02	1.3	3.3E-01	5.9E-01
AT1G80030	*AT1G80030*	Molecular chaperone Hsp40/DnaJ family protein	2.3	1.2E-12	1.0E-10	1.1	3.3E-01	6.0E-01
AT1G61890	*AT1G61890*	MATE efflux family protein	2.3	8.6E-11	4.4E-09	-1.5	4.5E-05	1.9E-03
AT4G34090	*AT4G34090*	cyclin delta-3	2.3	3.6E-09	1.1E-07	1.3	3.9E-02	1.7E-01
AT2G29450	*GSTU5*	glutathione S-transferase tau 5	2.3	1.3E-11	8.3E-10	1.2	8.1E-02	2.7E-01
AT5G65870	*PSK5*	phytosulfokine 5 precursor	2.3	1.2E-06	1.7E-05	-1.8	4.7E-04	9.5E-03
AT1G26500	*AT1G26500*	Pentatricopeptide repeat (PPR) superfamily protein	2.3	1.6E-03	7.2E-03	1.3	2.9E-01	5.5E-01
AT4G15765	*AT4G15765*	FAD/NAD(P)-binding oxidoreductase family protein	2.3	4.0E-06	4.6E-05	-1.2	3.5E-01	6.1E-01
AT5G08050	*AT5G08050*	wiskott-aldrich syndrome family protein, putative (DUF1118)	2.3	1.9E-09	6.4E-08	1.4	1.6E-03	2.2E-02
AT4G15440	*HPL1*	hydroperoxide lyase 1	2.3	8.9E-03	3.0E-02	-1.5	2.6E-01	5.3E-01
AT2G39470	*PnsL1*	PsbP-like protein 2	2.3	7.4E-07	1.1E-05	1.5	5.9E-03	5.2E-02
AT5G16010	*AT5G16010*	3-oxo-5-alpha-steroid 4-dehydrogenase family protein	2.3	5.5E-11	3.0E-09	1.3	5.4E-03	4.9E-02
AT1G05340	*AT1G05340*	cysteine-rich TM module stress tolerance protein	2.3	3.9E-04	2.2E-03	1.0	8.4E-01	9.4E-01
AT1G64500	*AT1G64500*	Glutaredoxin family protein	2.3	1.1E-09	4.0E-08	-1.0	9.5E-01	9.9E-01
AT3G17800	*AT3G17800*	alanine-tRNA ligase, putative (DUF760)	2.3	7.6E-12	5.2E-10	1.0	9.1E-01	9.7E-01
AT1G71140	*AT1G71140*	MATE efflux family protein	2.3	2.1E-03	8.8E-03	-1.1	6.9E-01	8.6E-01
AT5G24460	*AT5G24460*	RING-H2 zinc finger protein	2.3	6.6E-12	4.6E-10	-1.0	6.6E-01	8.4E-01
AT3G16220	*AT3G16220*	Putative eukaryotic LigT	2.3	5.4E-08	1.1E-06	1.3	4.3E-02	1.8E-01
AT3G15352	*COX17*	cytochrome c oxidase 17	2.3	6.6E-06	7.1E-05	-1.2	2.5E-01	5.1E-01
AT3G01060	*AT3G01060*	lysine-tRNA ligase	2.3	6.0E-09	1.7E-07	1.2	7.0E-02	2.5E-01
AT2G25080	*GPX1*	glutathione peroxidase 1	2.3	1.6E-06	2.1E-05	1.3	6.8E-02	2.4E-01
AT2G40330	*PYL6*	PYR1-like 6	2.3	1.9E-03	8.1E-03	2.0	6.5E-03	5.5E-02
AT4G36580	*AT4G36580*	AAA-type ATPase family protein	2.3	8.1E-06	8.4E-05	1.3	1.4E-01	3.8E-01
AT4G06746	*RAP2.9*	related to AP2 9	2.3	4.5E-03	1.7E-02	1.0	9.5E-01	9.8E-01
AT2G25620	*DBP1*	DNA-binding protein phosphatase 1	2.3	1.1E-12	9.9E-11	1.0	5.7E-01	7.9E-01
AT1G05562	*AT1G05562*	Natural antisense transcript overlaps with AT1G05560	2.3	6.0E-08	1.2E-06	1.3	2.5E-02	1.3E-01
AT5G27290	*AT5G27290*	stress regulated protein	2.3	1.4E-06	1.9E-05	1.5	6.1E-03	5.3E-02
AT4G34990	*MYB32*	myb domain protein 32	2.3	2.7E-06	3.3E-05	1.4	2.0E-02	1.1E-01

AT4G21380	*RK3*	receptor kinase 3	2.3	9.3E-03	3.1E-02	1.3	3.8E-01	6.4E-01
AT1G36160	*ACC1*	acetyl-CoA carboxylase 1	2.3	3.6E-13	3.7E-11	-1.0	8.8E-01	9.6E-01
AT4G28250	*EXPB3*	expansin B3	2.3	1.3E-06	1.8E-05	1.1	4.8E-01	7.2E-01
AT2G05510	*AT2G05510*	Glycine-rich protein family	2.3	3.3E-03	1.3E-02	-1.1	8.3E-01	9.3E-01
AT1G26761	*AT1G26761*	Arabinanase/levansucrase/invertase	2.3	9.5E-08	1.8E-06	1.5	1.0E-03	1.6E-02
AT5G17300	*RVE1*	Homeodomain-like superfamily protein	2.3	5.6E-09	1.6E-07	1.2	1.5E-01	3.9E-01
AT4G27520	*ENODL2*	early nodulin-like protein 2	2.3	6.4E-08	1.3E-06	1.5	2.4E-03	2.8E-02
AT5G47650	*NUDT2*	nudix hydrolase homolog 2	2.3	5.1E-13	5.1E-11	1.0	5.8E-01	7.9E-01
AT5G15340	*AT5G15340*	Pentatricopeptide repeat (PPR) superfamily protein	2.3	5.9E-04	3.2E-03	1.6	4.0E-02	1.8E-01
AT1G11790	*ADT1*	arogenate dehydratase 1	2.3	1.4E-08	3.4E-07	1.1	2.4E-01	5.0E-01
AT1G71480	*AT1G71480*	Nuclear transport factor 2 (NTF2) family protein	2.3	1.8E-09	6.2E-08	-1.1	3.2E-01	5.8E-01
AT5G24130	*AT5G24130*	polypyrimidine tract-binding-like protein	2.3	1.0E-04	7.1E-04	-1.2	3.4E-01	6.1E-01
AT1G32870	*NAC13*	NAC domain protein 13	2.3	6.8E-12	4.7E-10	-1.0	9.6E-01	9.9E-01
AT5G22630	*ADT5*	arogenate dehydratase 5	2.3	2.1E-09	7.1E-08	1.1	3.3E-01	5.9E-01
AT5G06220	*AT5G06220*	LETM1-like protein	2.3	2.8E-12	2.2E-10	1.2	7.0E-02	2.5E-01
AT3G01440	*PnsL3*	PsbQ-like 1	2.3	2.3E-06	2.9E-05	-1.1	4.7E-01	7.1E-01
AT1G05065	*CLE20*	CLAVATA3/ESR-RELATED 20	2.3	7.2E-04	3.7E-03	-1.6	8.6E-02	2.8E-01
AT3G14900	*EMB3120*	hypothetical protein	2.3	5.1E-04	2.8E-03	1.8	8.5E-03	6.6E-02
AT5G20140	*HBP5*	SOUL heme-binding family protein	2.3	6.4E-09	1.8E-07	1.1	2.0E-01	4.6E-01
AT4G08390	*SAPX*	stromal ascorbate peroxidase	2.3	8.5E-15	1.3E-12	1.1	3.6E-01	6.2E-01
AT1G43670	*FBP*	Inositol monophosphatase family protein	2.3	4.5E-08	9.6E-07	1.3	4.7E-02	2.0E-01
AT4G39710	*PnsL4*	FK506-binding protein 16-2	2.3	2.1E-07	3.6E-06	-1.0	9.2E-01	9.7E-01
AT1G15510	*ECB2*	Tetratricopeptide repeat (TPR)-like superfamily protein	2.3	5.1E-08	1.1E-06	1.1	6.0E-01	8.1E-01
AT3G30775	*ERD5*	Methylenetetrahydrofolate reductase family	2.3	3.1E-10	1.3E-08	-1.5	1.2E-04	3.5E-03
AT1G47760	*AGL102*	AGAMOUS-like 102	2.3	1.3E-03	6.2E-03	-1.1	6.9E-01	8.6E-01
AT4G25130	*PMSR4*	peptide met sulfoxide reductase 4	2.3	1.8E-14	2.5E-12	1.1	2.9E-01	5.6E-01
AT2G47180	*GolS1*	galactinol synthase 1	2.3	2.4E-05	2.1E-04	1.2	3.6E-01	6.2E-01
AT1G22850	*AT1G22850*	SNARE associated Golgi protein family	2.2	8.1E-12	5.4E-10	1.4	1.2E-04	3.6E-03
AT1G29640	*AT1G29640*	senescence regulator (Protein of unknown function, DUF584)	2.2	1.7E-06	2.2E-05	-1.1	7.4E-01	8.8E-01
AT1G29420	*AT1G29420*	SAUR-like auxin-responsive protein family	2.2	1.7E-02	4.9E-02	-2.6	2.0E-02	1.1E-01
AT5G14660	*PDF1B*	peptide deformylase 1B	2.2	2.9E-10	1.3E-08	1.1	5.3E-01	7.6E-01
AT1G58340	*ZF14*	MATE efflux family protein	2.2	1.5E-07	2.7E-06	1.6	1.1E-03	1.6E-02
AT1G35720	*ANNAT1*	annexin 1	2.2	9.4E-06	9.5E-05	-1.3	1.4E-01	3.8E-01
AT2G30150	*AT2G30150*	UDP-Glycosyltransferase superfamily protein	2.2	3.4E-10	1.5E-08	-1.0	6.9E-01	8.6E-01
AT4G30610	*BRS1*	alpha/beta-Hydrolases superfamily protein	2.2	4.9E-07	7.6E-06	1.1	5.6E-01	7.8E-01
AT4G24120	*YSL1*	YELLOW STRIPE like 1	2.2	1.2E-04	8.1E-04	-1.3	1.9E-01	4.4E-01
AT3G26960	*AT3G26960*	Pollen Ole e 1 allergen and extensin family protein	2.2	8.7E-03	2.9E-02	1.2	5.9E-01	8.0E-01
AT1G62630	*AT1G62630*	Disease resistance protein (CC-NBS-LRR class)	2.2	6.5E-06	7.0E-05	1.0	8.8E-01	9.5E-01
AT4G26260	*MIOX4*	myo-inositol oxygenase 4	2.2	2.5E-04	1.5E-03	-1.8	6.7E-03	5.6E-02
AT1G68870	*SOFL2*	SOB five-like 2	2.2	1.4E-04	9.4E-04	1.4	7.6E-02	2.6E-01
AT3G55630	*DFD*	DHFS-FPGS homolog D	2.2	1.3E-06	1.7E-05	1.1	5.3E-01	7.6E-01
AT3G25250	*AGC2-1*	AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein	2.2	3.3E-05	2.8E-04	1.1	6.1E-01	8.1E-01
AT4G28680	*TYRDC*	L-tyrosine decarboxylase	2.2	1.2E-02	3.7E-02	-1.3	4.4E-01	6.9E-01
AT1G71500	*AT1G71500*	Rieske (2Fe-2S) domain-containing protein	2.2	2.6E-10	1.2E-08	1.2	2.3E-02	1.3E-01
AT3G55330	*PPL1*	PsbP-like protein 1	2.2	3.1E-06	3.7E-05	1.3	1.1E-01	3.3E-01
AT2G16430	*PAP10*	purple acid phosphatase 10	2.2	2.4E-09	7.7E-08	1.2	8.7E-02	2.8E-01
AT1G05690	*BT3*	BTB and TAZ domain protein 3	2.2	1.1E-05	1.1E-04	-1.0	8.8E-01	9.6E-01
AT2G30390	*FC2*	ferrochelatase 2	2.2	1.2E-09	4.2E-08	1.2	1.5E-01	3.9E-01
AT3G54090	*FLN1*	fructokinase-like 1	2.2	2.3E-08	5.4E-07	1.6	7.7E-05	2.7E-03
AT2G29340	*AT2G29340*	NAD-dependent epimerase/dehydratase family protein	2.2	2.7E-08	6.2E-07	1.3	2.0E-02	1.2E-01
AT1G75690	*LQY1*	DnaJ/Hsp40 cysteine-rich domain superfamily protein	2.2	1.7E-09	6.0E-08	1.3	1.2E-02	8.4E-02
AT2G19800	*MIOX2*	myo-inositol oxygenase 2	2.2	9.8E-08	1.9E-06	-1.4	4.1E-03	4.1E-02
AT5G24990	*AT5G24990*	enhanced disease resistance-like protein	2.2	3.5E-06	4.1E-05	1.3	6.4E-02	2.3E-01
AT5G23170	*AT5G23170*	Protein kinase superfamily protein	2.2	1.2E-06	1.7E-05	-1.1	6.1E-01	8.1E-01
AT1G65190	*AT1G65190*	Protein kinase superfamily protein	2.2	1.4E-08	3.5E-07	1.0	9.1E-01	9.7E-01
AT5G08070	*TCP17*	TCP domain protein 17	2.2	2.0E-05	1.8E-04	1.5	2.2E-02	1.2E-01
AT5G38660	*APE1*	acclimation of photosynthesis to environment	2.2	1.4E-10	6.7E-09	1.3	1.1E-02	7.7E-02
AT3G14810	*MSL5*	mechanosensitive channel of small conductance-like 5	2.2	6.7E-07	1.0E-05	-1.1	6.5E-01	8.3E-01
AT5G43630	*TZP*	zinc knuckle (CCHC-type) family protein	2.2	4.6E-12	3.4E-10	1.0	5.8E-01	7.9E-01
AT1G70700	*TIFY7*	TIFY domain/Divergent CCT motif family protein	2.2	5.7E-10	2.2E-08	1.2	1.1E-01	3.2E-01
AT5G47250	*AT5G47250*	LRR and NB-ARC domains-containing disease resistance protein	2.2	7.2E-06	7.6E-05	1.1	7.5E-01	8.9E-01
AT2G46450	*CNGC12*	cyclic nucleotide-gated channel 12	2.2	1.9E-09	6.5E-08	1.4	2.3E-03	2.8E-02
AT3G04790	*EMB3119*	Ribose 5-phosphate isomerase, type A protein	2.2	1.0E-07	1.9E-06	1.1	4.0E-01	6.6E-01
AT3G17930	*DAC*	transmembrane protein	2.2	1.3E-10	6.2E-09	1.1	3.0E-01	5.6E-01
AT2G33530	*scpl46*	serine carboxypeptidase-like 46	2.2	5.7E-06	6.2E-05	-1.1	5.5E-01	7.7E-01
AT5G13360	*AT5G13360*	Auxin-responsive GH3 family protein	2.2	2.1E-12	1.7E-10	1.2	6.4E-02	2.3E-01
AT1G68440	*AT1G68440*	transmembrane protein	2.2	2.5E-14	3.3E-12	-1.4	1.3E-05	8.5E-04
AT2G28605	*AT2G28605*	Photosystem II reaction center PsbP family protein	2.2	7.8E-06	8.1E-05	1.5	7.2E-03	5.9E-02
AT2G26040	*PYL2*	PYR1-like 2	2.2	2.0E-03	8.6E-03	1.7	3.9E-02	1.7E-01
AT1G67360	*AT1G67360*	Rubber elongation factor protein (REF)	2.2	4.7E-11	2.6E-09	-1.1	2.4E-01	5.0E-01
AT1G07510	*ftsh10*	FTSH protease 10	2.2	7.5E-17	2.3E-14	-1.1	2.5E-01	5.2E-01
AT5G54130	*AT5G54130*	Calcium-binding endonuclease/exonuclease/phosphatase family	2.2	5.2E-09	1.5E-07	-1.2	4.6E-02	1.9E-01
AT1G07985	*AT1G07985*	Expressed protein	2.2	5.8E-06	6.4E-05	-1.5	1.3E-02	8.8E-02
AT5G54960	*PDC2*	pyruvate decarboxylase-2	2.2	5.2E-11	2.8E-09	-1.3	2.8E-03	3.2E-02

AT4G31398	*AT4G31398*	Natural antisense transcript overlaps with AT4G31400	2.2	1.5E-02	4.5E-02	1.2	6.2E-01	8.2E-01
AT4G02530	*AT4G02530*	chloroplast thylakoid lumen protein	2.2	4.0E-10	1.6E-08	1.2	3.8E-02	1.7E-01
AT5G20380	*PHT4*		2.2	1.5E-12	1.3E-10	1.2	4.2E-02	1.8E-01
AT1G61470	*AT1G61470*	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	2.2	5.2E-03	1.9E-02	2.0	1.5E-02	9.7E-02
AT5G01600	*FER1*	ferretin 1	2.2	2.5E-05	2.2E-04	-1.6	4.9E-03	4.6E-02
AT5G13630	*GUN5*	magnesium-chelatase subunit chlH, chloroplast, putative / Mg-protoporphyrin IX chelatase, putative (CHLH)	2.2	1.3E-07	2.4E-06	1.5	3.1E-03	3.4E-02
AT2G28880	*emb1997*	para-aminobenzoate (PABA) synthase family	2.2	4.0E-08	8.7E-07	1.1	5.3E-01	7.5E-01
AT3G13680	*AT3G13680*	F-box and associated interaction domains-containing protein	2.2	1.4E-02	4.2E-02	1.3	3.6E-01	6.3E-01
AT5G03210	*DIP2*	E3 ubiquitin-protein ligase	2.2	7.0E-03	2.4E-02	-1.5	2.1E-01	4.6E-01
AT4G21940	*CPK15*	calcium-dependent protein kinase 15	2.2	1.3E-05	1.3E-04	1.1	6.5E-01	8.3E-01
AT2G38060	*PHT4*		2.2	1.2E-05	1.2E-04	-1.1	6.3E-01	8.2E-01
AT3G59250	*AT3G59250*	F-box/RNI-like superfamily protein	2.2	3.0E-05	2.5E-04	1.7	2.1E-03	2.6E-02
AT1G75460	*AT1G75460*	ATP-dependent protease La (LON) domain protein	2.2	1.3E-07	2.3E-06	1.1	2.7E-01	5.4E-01
AT5G08150	*SOB5*	suppressor of phytochrome b 5	2.2	8.0E-04	4.1E-03	-1.4	1.7E-01	4.1E-01
AT1G70760	*NdhL*	inorganic carbon transport protein-like protein	2.2	3.3E-07	5.4E-06	1.4	1.3E-02	8.9E-02
AT2G29360	*AT2G29360*	NAD(P)-binding Rossmann-fold superfamily protein	2.2	6.8E-08	1.4E-06	1.2	2.1E-01	4.6E-01
AT1G16310	*AT1G16310*	Cation efflux family protein	2.2	4.5E-08	9.6E-07	1.1	3.9E-01	6.5E-01
AT1G64900	*CYP89A2*	cytochrome P450, family 89, subfamily A, polypeptide 2	2.2	4.4E-04	2.5E-03	1.1	7.0E-01	8.6E-01
AT3G04870	*ZDS*	zeta-carotene desaturase	2.2	5.7E-10	2.2E-08	1.1	3.7E-01	6.3E-01
AT4G11175	*AT4G11175*	Nucleic acid-binding, OB-fold-like protein	2.2	1.3E-06	1.8E-05	1.3	7.2E-02	2.5E-01
AT4G37000	*ACD2*	accelerated cell death 2 (ACD2)	2.2	1.7E-09	6.0E-08	-1.0	6.5E-01	8.3E-01
AT2G42770	*AT2G42770*	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	2.2	9.8E-11	4.9E-09	1.3	8.8E-03	6.8E-02
AT1G52510	*AT1G52510*	alpha/beta-Hydrolases superfamily protein	2.2	1.1E-08	2.8E-07	1.5	8.1E-04	1.4E-02
AT3G63140	*CSP41A*	chloroplast stem-loop binding protein of 41 kDa	2.2	4.5E-08	9.6E-07	1.2	1.7E-01	4.1E-01
AT1G48870	*AT1G48870*	Transducin/WD40 repeat-like superfamily protein	2.2	6.0E-05	4.6E-04	1.4	5.7E-02	2.2E-01
AT5G62200	*AT5G62200*	Embryo-specific protein 3, (ATS3)	2.2	7.1E-09	2.0E-07	-1.1	4.8E-01	7.2E-01
AT1G09850	*XBCP3*	xylem bark cysteine peptidase 3	2.2	1.1E-12	9.5E-11	-1.3	3.8E-03	3.9E-02
AT1G35515	*HOS10*	high response to osmotic stress 10	2.2	5.8E-05	4.5E-04	-1.3	1.7E-01	4.1E-01
AT4G34240	*ALDH3I1*	aldehyde dehydrogenase 3I1	2.2	7.2E-09	2.0E-07	-1.0	7.1E-01	8.7E-01
AT1G48850	*EMB1144*	chorismate synthase, putative / 5-enolpyruvylshikimate-3-phosphate phospholyase	2.2	4.2E-16	1.0E-13	-1.0	8.7E-01	9.5E-01
AT5G43750	*PnsB5*	NAD(P)H dehydrogenase 18	2.2	1.0E-07	1.9E-06	1.1	2.8E-01	5.4E-01
AT1G78290	*SNRK2-8*	Protein kinase superfamily protein	2.2	2.0E-09	6.7E-08	1.1	5.0E-01	7.3E-01
AT2G40900	*UMAMIT11*	nodulin MtN21 /EamA-like transporter family	2.2	2.5E-09	8.0E-08	-1.1	2.8E-01	5.5E-01
AT4G34730	*AT4G34730*	ribosome-binding factor A family protein	2.2	1.8E-10	8.5E-09	1.3	6.8E-03	5.7E-02
AT3G59120	*AT3G59120*	Cysteine/Histidine-rich C1 domain family protein	2.2	3.6E-04	2.1E-03	1.1	6.9E-01	8.6E-01
AT5G56850	*AT5G56850*	hypothetical protein	2.2	3.2E-07	5.3E-06	1.1	4.1E-01	6.6E-01
AT5G41050	*AT5G41050*	Pollen Ole e 1 allergen and extensin family protein	2.2	2.0E-06	2.5E-05	-1.0	7.4E-01	8.8E-01
AT5G26742	*emb1138*	DEAD box RNA helicase (RH3)	2.2	8.2E-09	2.2E-07	1.6	1.1E-04	3.3E-03
AT5G24810	*AT5G24810*	ABC1 family protein	2.2	8.2E-13	7.5E-11	-1.1	2.2E-01	4.8E-01
AT2G23670	*YCF37*	homolog of Synechocystis YCF37	2.2	5.5E-10	2.2E-08	1.3	1.6E-02	1.0E-01
AT2G34660	*ABCC2*	multidrug resistance-associated protein 2	2.2	9.8E-14	1.2E-11	-1.0	6.3E-01	8.2E-01
AT3G17130	*AT3G17130*	Plant invertase/pectin methylesterase inhibitor superfamily protein	2.2	2.7E-03	1.1E-02	-1.5	1.4E-01	3.7E-01
AT4G14010	*RALFL32*	ralf-like 32	2.1	9.4E-08	1.8E-06	-1.0	7.7E-01	9.0E-01
AT1G68660	*AT1G68660*	Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein	2.1	1.7E-11	1.1E-09	1.1	3.0E-01	5.6E-01
AT5G38980	*AT5G38980*	transmembrane protein	2.1	9.5E-07	1.3E-05	-1.6	9.9E-04	1.6E-02
AT1G74730	*AT1G74730*	transmembrane protein, putative (DUF1118)	2.1	2.5E-09	8.2E-08	1.4	7.0E-04	1.2E-02
AT5G22090	*AT5G22090*	FAF-like protein (DUF3049)	2.1	6.9E-06	7.4E-05	1.4	3.2E-02	1.5E-01
AT5G61270	*PIF7*	phytochrome-interacting factor7	2.1	5.1E-07	7.9E-06	1.4	1.1E-02	7.7E-02
AT4G34830	*MRL1*	Pentatricopeptide repeat (PPR) superfamily protein	2.1	4.1E-07	6.6E-06	1.5	4.2E-03	4.2E-02
AT2G41290	*SSL2*	strictosidine synthase-like 2	2.1	1.3E-06	1.8E-05	1.3	4.9E-02	2.0E-01
AT5G49480	*CP1*	Ca2 -binding protein 1	2.1	5.9E-11	3.1E-09	1.0	6.0E-01	8.1E-01
AT3G57010	*AT3G57010*	Calcium-dependent phosphotriesterase superfamily protein	2.1	2.0E-08	4.7E-07	-1.1	5.1E-01	7.4E-01
AT3G48030	*AT3G48030*	hypoxia-responsive family protein / zinc finger (C3HC4-type RING finger) family protein	2.1	3.7E-10	1.5E-08	1.0	6.0E-01	8.1E-01
AT3G12580	*HSP70*	heat shock protein 70	2.1	6.5E-06	7.0E-05	-1.5	1.1E-02	7.8E-02
AT1G51440	*AT1G51440*	alpha/beta-Hydrolases superfamily protein	2.1	1.4E-02	4.4E-02	1.5	2.1E-01	4.7E-01
AT3G48700	*CXE13*	carboxyesterase 13	2.1	5.2E-05	4.1E-04	1.0	9.4E-01	9.8E-01
AT5G64840	*ABCF5*	general control non-repressible 5	2.1	5.1E-08	1.1E-06	1.3	1.7E-02	1.0E-01
AT1G56510	*WRR4*	Disease resistance protein (TIR-NBS-LRR class)	2.1	6.8E-10	2.6E-08	1.1	2.3E-01	4.9E-01
AT2G21320	*BBX18*	B-box zinc finger family protein	2.1	7.5E-07	1.1E-05	1.3	4.8E-02	2.0E-01
AT2G14660	*AT2G14660*	thymocyte nuclear-like protein	2.1	5.9E-06	6.4E-05	1.1	4.2E-01	6.7E-01
AT1G33560	*ADR1*	Disease resistance protein (CC-NBS-LRR class)	2.1	7.2E-09	2.0E-07	-1.3	8.8E-03	6.7E-02
AT2G34630	*GPS1*	geranyl diphosphate synthase 1	2.1	2.2E-14	3.0E-12	1.2	2.4E-03	2.9E-02
AT5G48470	*AT5G48470*	hypothetical protein	2.1	1.6E-05	1.5E-04	1.4	4.1E-02	1.8E-01
AT2G13360	*AGT*	alanine:glyoxylate aminotransferase	2.1	5.3E-07	8.1E-06	1.2	8.7E-02	2.8E-01
AT4G32590	*AT4G32590*	2Fe-2S ferredoxin-like superfamily protein	2.1	1.2E-11	7.5E-10	1.2	1.9E-02	1.1E-01
AT3G57180	*BPG2*	P-loop containing nucleoside triphosphate hydrolases superfamily protein	2.1	5.1E-09	1.5E-07	1.2	5.5E-02	2.1E-01
AT4G36430	*AT4G36430*	Peroxidase superfamily protein	2.1	8.1E-03	2.7E-02	1.0	9.4E-01	9.8E-01
AT5G45960	*AT5G45960*	GDSL-like Lipase/Acylhydrolase superfamily protein	2.1	1.3E-04	9.1E-04	-1.2	4.2E-01	6.8E-01
AT1G24600	*AT1G24600*	hypothetical protein	2.1	6.9E-03	2.4E-02	1.7	6.1E-02	2.3E-01

AT3G49330	*AT3G49330*	Plant invertase/pectin methylesterase inhibitor superfamily protein	2.1	6.8E-04	3.5E-03	-1.5	7.5E-02	2.6E-01
AT3G09162	*AT3G09162*	hypothetical protein	2.1	7.9E-06	8.2E-05	1.6	2.9E-03	3.3E-02
AT1G70170	*MMP*	matrix metalloproteinase	2.1	2.3E-04	1.4E-03	1.2	3.8E-01	6.4E-01
AT5G58870	*ftsh9*	FTSH protease 9	2.1	5.1E-10	2.1E-08	1.1	3.9E-01	6.5E-01
AT2G16740	*UBC29*	ubiquitin-conjugating enzyme 29	2.1	9.8E-06	9.9E-05	-1.1	6.3E-01	8.2E-01
AT1G26560	*BGLU40*	beta glucosidase 40	2.1	1.2E-08	3.2E-07	-1.2	1.5E-01	3.9E-01
AT1G19700	*BEL10*	BEL1-like homeodomain 10	2.1	4.2E-14	5.5E-12	-1.1	2.9E-01	5.6E-01
AT1G27360	*SPL11*	squamosa promoter-like 11	2.1	6.4E-08	1.3E-06	1.1	2.7E-01	5.4E-01
AT3G09220	*LAC7*	laccase 7	2.1	6.8E-07	1.0E-05	-1.2	1.2E-01	3.4E-01
AT4G19460	*AT4G19460*	UDP-Glycosyltransferase superfamily protein	2.1	1.1E-04	7.6E-04	-1.1	6.2E-01	8.2E-01
AT1G79270	*ECT8*	evolutionarily conserved C-terminal region 8	2.1	8.6E-12	5.7E-10	-1.3	3.9E-03	3.9E-02
AT3G59880	*AT3G59880*	hypothetical protein	2.1	3.3E-05	2.8E-04	-1.4	3.7E-02	1.7E-01
AT3G27170	*CLC-B*	chloride channel B	2.1	1.2E-06	1.6E-05	1.0	9.2E-01	9.7E-01
AT2G43910	*HOL1*	HARMLESS TO OZONE LAYER 1	2.1	1.7E-13	1.9E-11	-1.2	1.8E-02	1.1E-01
AT3G23210	*bHLH34*	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	2.1	4.5E-08	9.6E-07	1.2	5.9E-02	2.2E-01
AT3G25410	*AT3G25410*	Sodium Bile acid symporter family	2.1	6.4E-11	3.4E-09	1.2	4.7E-02	2.0E-01
AT3G22620	*AT3G22620*	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	2.1	6.6E-06	7.1E-05	-1.8	2.5E-04	6.2E-03
AT1G27480	*AT1G27480*	alpha/beta-Hydrolases superfamily protein	2.1	7.7E-10	2.9E-08	1.0	9.9E-01	1.0E+00
AT4G19830	*AT4G19830*	FKBP-like peptidyl-prolyl cis-trans isomerase family protein	2.1	1.8E-09	6.1E-08	1.1	2.5E-01	5.1E-01
AT2G41250	*AT2G41250*	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	2.1	1.2E-11	8.0E-10	1.4	1.2E-04	3.5E-03
AT1G18810	*AT1G18810*	phytochrome kinase substrate-like protein	2.1	2.3E-06	2.9E-05	-1.1	5.7E-01	7.9E-01
AT3G06125	*AT3G06125*		2.1	1.2E-08	3.1E-07	-1.5	3.4E-04	7.5E-03
AT1G43160	*RAP2.6*	related to AP2 6	2.1	3.0E-04	1.8E-03	1.2	3.5E-01	6.1E-01
AT5G43450	*AT5G43450*	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2.1	1.5E-05	1.4E-04	1.0	9.0E-01	9.6E-01
AT3G02140	*TMAC2*	AFP2 (ABI five-binding protein 2) family protein	2.1	2.1E-10	9.4E-09	-1.1	3.7E-01	6.3E-01
AT1G73360	*HDG11*	homeodomain GLABROUS 11	2.1	4.8E-05	3.8E-04	-1.0	8.4E-01	9.4E-01
AT1G09300	*AT1G09300*	Metallopeptidase M24 family protein	2.1	5.4E-08	1.1E-06	1.3	4.4E-02	1.9E-01
AT5G62840	*AT5G62840*	Phosphoglycerate mutase family protein	2.1	1.0E-07	1.9E-06	1.3	2.3E-02	1.2E-01
AT3G18400	*NAC058*	NAC domain containing protein 58	2.1	9.1E-04	4.5E-03	1.0	9.0E-01	9.6E-01
AT3G05932	*AT3G05932*	Natural antisense transcript overlaps with AT3G05930	2.1	7.5E-08	1.5E-06	1.4	5.4E-03	4.9E-02
AT1G11330	*AT1G11330*	S-locus lectin protein kinase family protein	2.1	1.0E-06	1.4E-05	1.0	7.6E-01	9.0E-01
AT3G48520	*CYP94B3*	cytochrome P450, family 94, subfamily B, polypeptide 3	2.1	2.0E-06	2.6E-05	1.0	7.3E-01	8.8E-01
AT3G18750	*WNK6*	with no lysine (K) kinase 6	2.1	4.8E-09	1.4E-07	1.1	1.9E-01	4.4E-01
AT5G36120	*CCB3*	cofactor assembly, complex C (B6F)	2.1	2.6E-07	4.4E-06	1.3	3.3E-02	1.6E-01
AT2G23540	*AT2G23540*	GDSL-like Lipase/Acylhydrolase superfamily protein	2.1	1.1E-02	3.5E-02	1.4	2.9E-01	5.5E-01
AT1G64780	*AMT1*		2.1	8.8E-07	1.3E-05	-1.1	3.1E-01	5.7E-01
AT4G22890	*PGR5-LIKE A*	PGR5-LIKE A	2.1	2.1E-06	2.7E-05	1.3	3.4E-02	1.6E-01
AT4G08555	*AT4G08555*	hypothetical protein	2.1	1.5E-02	4.4E-02	-1.5	2.3E-01	4.9E-01
AT3G01660	*AT3G01660*	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	2.1	8.5E-07	1.2E-05	1.2	2.0E-01	4.6E-01
AT3G15360	*TRX-M4*	thioredoxin M-type 4	2.1	6.4E-10	2.5E-08	1.4	5.8E-04	1.1E-02
AT5G21430	*NdhU*	Chaperone DnaJ-domain superfamily protein	2.1	3.1E-08	7.1E-07	1.0	7.8E-01	9.0E-01
AT3G55040	*GSTL2*	glutathione transferase lambda 2	2.1	1.0E-08	2.7E-07	-1.1	2.6E-01	5.2E-01
AT5G17670	*AT5G17670*	alpha/beta-Hydrolases superfamily protein	2.1	9.5E-08	1.8E-06	1.5	7.2E-04	1.3E-02
AT3G49668	*AT3G49668*	Natural antisense transcript overlaps with AT3G49670	2.1	1.1E-02	3.4E-02	-1.0	9.6E-01	9.9E-01
AT4G21445	*AT4G21445*	receptor-interacting protein	2.1	1.0E-05	1.0E-04	1.2	1.5E-01	3.8E-01
AT5G57560	*TCH4*	Xyloglucan endotransglucosylase/hydrolase family protein	2.1	1.6E-02	4.8E-02	-2.2	1.0E-02	7.3E-02
AT5G03190	*CPUORF47*	peptide upstream protein	2.1	3.8E-13	3.9E-11	1.0	8.2E-01	9.3E-01
AT5G41080	*GDPD2*	PLC-like phosphodiesterases superfamily protein	2.1	1.7E-07	3.1E-06	-1.9	2.0E-06	2.3E-04
AT4G27290	*AT4G27290*	S-locus lectin protein kinase family protein	2.1	1.6E-04	1.0E-03	1.3	1.7E-01	4.2E-01
AT1G78995	*AT1G78995*	hypothetical protein	2.1	3.0E-07	5.0E-06	1.3	5.1E-02	2.1E-01
AT5G09660	*PMDH2*	peroxisomal NAD-malate dehydrogenase 2	2.1	3.7E-07	5.9E-06	1.1	4.6E-01	7.1E-01
AT3G52880	*MDAR1*	monodehydroascorbate reductase 1	2.1	1.6E-15	3.3E-13	-1.1	2.4E-01	5.1E-01
AT5G46490	*AT5G46490*	Disease resistance protein (TIR-NBS-LRR class)	2.1	5.3E-08	1.1E-06	1.4	2.3E-03	2.8E-02
AT2G31945	*AT2G31945*	transmembrane protein	2.1	2.2E-04	1.4E-03	-1.1	5.0E-01	7.4E-01
AT3G23580	*RNR2A*	ribonucleotide reductase 2A	2.1	4.3E-12	3.2E-10	1.2	6.0E-03	5.3E-02
AT4G03020	*AT4G03020*	transducin family protein / WD-40 repeat family protein	2.1	3.9E-15	6.9E-13	-1.1	2.0E-01	4.5E-01
AT1G43560	*ty2*	thioredoxin Y2	2.1	2.9E-07	4.9E-06	1.1	2.9E-01	5.6E-01
AT1G23880	*AT1G23880*	NHL domain-containing protein	2.1	3.5E-07	5.8E-06	-1.1	5.6E-01	7.8E-01
AT3G11090	*LBD21*	LOB domain-containing protein 21	2.1	2.3E-06	2.9E-05	1.1	3.8E-01	6.4E-01
AT1G64680	*AT1G64680*	beta-carotene isomerase D27	2.1	3.1E-09	9.8E-08	1.1	5.2E-01	7.5E-01
AT5G25890	*IAA28*	indole-3-acetic acid inducible 28	2.1	1.7E-09	5.8E-08	1.2	8.3E-02	2.8E-01
AT5G17310	*UGP2*	UDP-glucose pyrophosphorylase 2	2.1	2.2E-10	1.0E-08	-1.1	3.5E-01	6.1E-01
AT1G77330	*AT1G77330*	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2.1	1.3E-05	1.2E-04	1.0	8.4E-01	9.4E-01
AT4G01490	*AT4G01490*	transposable_element_gene	2.1	1.4E-02	4.4E-02	1.4	2.6E-01	5.2E-01
AT2G23672	*AT2G23672*	Natural antisense transcript overlaps with AT2G23670	2.1	1.9E-05	1.7E-04	1.1	3.7E-01	6.3E-01
AT3G15520	*AT3G15520*	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein	2.1	5.4E-07	8.2E-06	1.4	5.9E-03	5.2E-02
AT1G22630	*AT1G22630*	SSUH2-like protein	2.1	7.7E-10	2.9E-08	1.3	6.9E-03	5.8E-02
AT3G44020	*AT3G44020*	thylakoid lumenal P17.1 protein	2.1	4.6E-08	9.9E-07	-1.0	9.1E-01	9.7E-01

AT4G24930	*AT4G24930*	thylakoid lumenal 17.9 kDa protein, chloroplast	2.1	4.0E-08	8.7E-07	1.2	8.7E-02	2.8E-01
AT3G05935	*AT3G05935*	hypothetical protein	2.1	1.9E-11	1.2E-09	1.0	9.0E-01	9.6E-01
AT1G30680	*AT1G30680*	toprim domain-containing protein	2.1	1.1E-09	4.1E-08	1.4	1.1E-03	1.7E-02
AT3G50270	*AT3G50270*	HXXXD-type acyl-transferase family protein	2.1	1.9E-07	3.3E-06	1.9	2.9E-06	2.9E-04
AT3G03770	*AT3G03770*	Leucine-rich repeat protein kinase family protein	2.1	1.5E-04	1.0E-03	1.2	2.6E-01	5.2E-01
AT4G13550	*AT4G13550*	putative triglyceride lipase	2.1	8.6E-10	3.2E-08	1.0	7.8E-01	9.1E-01
AT4G23260	*CRK18*	cysteine-rich RLK (RECEPTOR-like protein kinase) 18	2.1	1.1E-04	7.8E-04	1.9	4.4E-04	9.1E-03
AT4G27940	*MTM1*	manganese tracking factor for mitochondrial SOD2	2.1	7.6E-08	1.5E-06	1.1	4.6E-01	7.1E-01
AT2G24120	*SCA3*	DNA/RNA polymerases superfamily protein	2.1	6.5E-09	1.9E-07	1.9	1.4E-07	3.4E-05
AT4G04020	*FIB*	fibrillin	2.1	3.9E-08	8.5E-07	-1.2	1.3E-01	3.6E-01
AT2G29290	*AT2G29290*	NAD(P)-binding Rossmann-fold superfamily protein	2.1	4.7E-05	3.7E-04	-1.0	9.2E-01	9.7E-01
AT5G34850	*PAP26*	purple acid phosphatase 26	2.1	1.5E-12	1.3E-10	-1.2	2.9E-02	1.4E-01
AT5G10730	*AT5G10730*	NAD(P)-binding Rossmann-fold superfamily protein	2.1	2.4E-12	1.9E-10	-1.1	7.2E-02	2.5E-01
AT3G14420	*GOX1*	Aldolase-type TIM barrel family protein	2.1	1.7E-06	2.3E-05	1.1	3.5E-01	6.2E-01
AT1G23390	*AT1G23390*	Kelch repeat-containing F-box family protein	2.1	1.6E-08	4.0E-07	-1.0	8.9E-01	9.6E-01
AT3G12930	*AT3G12930*	Lojap-related protein	2.1	1.5E-08	3.7E-07	1.4	1.5E-03	2.1E-02
AT1G54500	*AT1G54500*	Rubredoxin-like superfamily protein	2.1	8.5E-08	1.7E-06	1.3	3.1E-02	1.5E-01
AT5G01840	*OFP1*	ovate family protein 1	2.1	5.3E-06	5.9E-05	1.3	3.6E-02	1.6E-01
AT2G43140	*AT2G43140*	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	2.1	3.5E-03	1.4E-02	1.3	2.3E-01	5.0E-01
AT5G41590	*AT5G41590*	LURP-one-like protein (DUF567)	2.1	3.7E-03	1.4E-02	-1.1	7.3E-01	8.8E-01
AT4G37925	*NdhM*	subunit NDH-M of NAD(P)H:plastoquinone dehydrogenase complex	2.1	3.2E-07	5.3E-06	1.0	7.1E-01	8.7E-01
AT5G28750	*AT5G28750*	Bacterial sec-independent translocation protein mttA/Hcf106	2.1	4.1E-10	1.7E-08	1.2	4.8E-02	2.0E-01
AT5G49910	*cpHsc70-2*	chloroplast heat shock protein 70-2	2.1	7.2E-11	3.7E-09	1.2	4.8E-02	2.0E-01
AT1G30360	*ERD4*	Early-responsive to dehydration stress protein	2.1	3.8E-09	1.2E-07	-1.2	9.0E-02	2.9E-01
AT2G01850	*EXGT-A3*	endoxyloglucan transferase A3	2.1	6.4E-13	6.1E-11	1.1	2.1E-01	4.7E-01
AT5G57180	*CIA2*	chloroplast import apparatus 2	2.0	1.3E-08	3.4E-07	1.2	7.3E-02	2.5E-01
AT3G03990	*AT3G03990*	alpha/beta-Hydrolases superfamily protein	2.0	1.8E-14	2.5E-12	1.0	6.0E-01	8.0E-01
AT5G59720	*HSP18.2*	heat shock protein 18.2	2.0	6.7E-05	5.1E-04	-1.0	9.5E-01	9.9E-01
AT4G20360	*RABE1b*	RAB GTPase homolog E1B	2.0	3.7E-07	5.9E-06	1.4	1.1E-02	7.8E-02
AT4G17360	*AT4G17360*	Formyl transferase	2.0	5.0E-06	5.6E-05	-1.2	3.1E-01	5.7E-01
AT1G69870	*NRT1.7*	nitrate transporter 1.7	2.0	2.5E-05	2.2E-04	-1.4	4.4E-02	1.9E-01
AT2G42130	*AT2G42130*	Plastid-lipid associated protein PAP / fibrillin family protein	2.0	5.4E-10	2.1E-08	1.3	9.0E-03	6.9E-02
AT5G28500	*AT5G28500*	rubisco accumulation factor-like protein	2.0	5.2E-08	1.1E-06	1.4	9.5E-04	1.5E-02
AT1G03905	*ABCI19*	P-loop containing nucleoside triphosphate hydrolases superfamily protein	2.0	5.1E-08	1.1E-06	1.0	6.6E-01	8.4E-01
AT1G74650	*MYB31*	myb domain protein 31	2.0	8.1E-04	4.1E-03	-1.9	2.9E-03	3.3E-02
AT3G54990	*SMZ*	Integrase-type DNA-binding superfamily protein	2.0	6.4E-10	2.5E-08	-1.2	1.4E-02	9.1E-02
AT4G26860	*AT4G26860*	Putative pyridoxal phosphate-dependent enzyme, YBL036C type	2.0	1.6E-11	1.0E-09	-1.2	3.4E-02	1.6E-01
AT5G54770	*THI1*	thiazole biosynthetic enzyme, chloroplast (ARA6) (THI1) (THI4)	2.0	2.5E-06	3.2E-05	-1.1	6.9E-01	8.6E-01
AT4G21860	*MSRB2*	methionine sulfoxide reductase B 2	2.0	2.7E-13	2.9E-11	1.1	2.2E-01	4.8E-01
AT2G22360	*AT2G22360*	DNAJ heat shock family protein	2.0	3.1E-11	1.8E-09	1.3	4.1E-03	4.1E-02
AT5G02940	*AT5G02940*	ion channel POLLUX-like protein, putative	2.0	2.5E-07	4.3E-06	1.1	3.6E-01	6.2E-01
AT3G52605	*AT3G52605*	Natural antisense transcript overlaps with AT3G52610	2.0	1.1E-05	1.1E-04	1.3	4.6E-02	1.9E-01
AT1G21110	*IGMT3*	O-methyltransferase family protein	2.0	1.9E-04	1.2E-03	1.5	1.6E-02	9.9E-02
AT5G49970	*PPOX*	pyridoxin (pyrodoxamine) 5'-phosphate oxidase	2.0	1.8E-12	1.5E-10	-1.1	3.8E-01	6.4E-01
AT1G19150	*Lhca6*	PSI type II chlorophyll a/b-binding protein	2.0	8.0E-07	1.2E-05	1.4	4.8E-03	4.6E-02
AT3G53830	*AT3G53830*	Regulator of chromosome condensation (RCC1) family protein	2.0	5.9E-05	4.5E-04	1.2	1.8E-01	4.3E-01
AT3G62030	*ROC4*	rotamase CYP 4	2.0	6.9E-05	5.2E-04	1.4	4.0E-02	1.8E-01
AT3G49760	*bZIP5*	basic leucine-zipper 5	2.0	2.1E-03	8.9E-03	1.0	9.7E-01	9.9E-01
AT1G26600	*CLE9*	CLAVATA3/ESR-RELATED 9	2.0	3.6E-03	1.4E-02	1.1	6.2E-01	8.2E-01
AT4G39970	*AT4G39970*	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	2.0	2.7E-06	3.3E-05	1.1	3.1E-01	5.7E-01
AT3G27050	*AT3G27050*	plant/protein	2.0	7.6E-08	1.5E-06	1.2	5.2E-02	2.1E-01
AT3G43600	*AAO2*	aldehyde oxidase 2	2.0	2.3E-11	1.4E-09	-1.0	6.4E-01	8.3E-01
AT5G44005	*AT5G44005*	hypothetical protein	2.0	7.7E-05	5.7E-04	-1.2	2.2E-01	4.8E-01
AT5G49030	*OVA2*	tRNA synthetase class I (I, L, M and V) family	2.0	1.1E-07	2.1E-06	1.3	8.4E-03	6.6E-02
AT1G11860	*AT1G11860*	Glycine cleavage T-protein family	2.0	7.7E-08	1.5E-06	1.2	6.1E-02	2.3E-01
AT1G05540	*AT1G05540*	hypothetical protein (DUF295)	2.0	1.6E-03	7.1E-03	-1.6	4.5E-02	1.9E-01
AT1G62960	*ACS10*	ACC synthase 10	2.0	2.9E-10	1.3E-08	1.3	1.2E-03	1.8E-02
AT3G11945	*HST*	homogentisate prenyltransferase	2.0	1.1E-05	1.1E-04	1.3	9.6E-02	3.0E-01
AT5G09590	*MTHSC70-2*	mitochondrial HSO70 2	2.0	8.9E-09	2.4E-07	1.1	4.7E-01	7.1E-01
AT2G16500	*ADC1*	arginine decarboxylase 1	2.0	8.2E-09	2.2E-07	1.1	3.6E-01	6.2E-01
AT1G01790	*KEA1*	K efflux antiporter 1	2.0	9.1E-07	1.3E-05	-1.1	2.5E-01	5.2E-01
AT1G48100	*AT1G48100*	Pectin lyase-like superfamily protein	2.0	9.5E-07	1.3E-05	-1.5	4.4E-03	4.3E-02
AT4G03280	*PETC*	photosynthetic electron transfer C	2.0	8.6E-08	1.7E-06	1.4	3.5E-03	3.7E-02
AT1G45191	*BGLU1*	Glycosyl hydrolase superfamily protein	2.0	5.8E-04	3.1E-03	-1.1	6.8E-01	8.5E-01
AT5G47610	*AT5G47610*	RING/U-box superfamily protein	2.0	8.0E-07	1.2E-05	-1.2	7.5E-02	2.6E-01
AT1G28815	*AT1G28815*	hypothetical protein	2.0	6.6E-04	3.5E-03	-1.4	1.0E-01	3.1E-01
AT1G72620	*AT1G72620*	alpha/beta-Hydrolases superfamily protein	2.0	7.8E-03	2.7E-02	1.1	8.4E-01	9.4E-01
AT3G12345	*AT3G12345*	FKBP-type peptidyl-prolyl cis-trans isomerase	2.0	2.2E-08	5.1E-07	1.4	1.2E-03	1.8E-02
AT4G31390	*ACDO1*	Protein kinase superfamily protein	2.0	9.4E-08	1.8E-06	-1.1	5.0E-01	7.3E-01
AT2G30100	*AT2G30100*	pentatricopeptide (PPR) repeat-containing protein	2.0	3.0E-11	1.7E-09	1.0	7.3E-01	8.8E-01
AT3G01180	*SS2*	starch synthase 2	2.0	3.7E-11	2.1E-09	1.1	4.1E-01	6.7E-01
AT3G52370	*FLA15*	FASCICLIN-like arabinogalactan protein 15	2.0	5.6E-05	4.3E-04	-1.6	2.9E-03	3.3E-02

AT5G44490	*AT5G44490*	FBD, F-box, Skp2-like and Leucine Rich Repeat domains containing protein	2.0	6.0E-04	3.2E-03	1.2	2.8E-01	5.5E-01
AT1G43675	*AT1G43675*	transposable_element_gene	2.0	9.0E-03	3.0E-02	1.1	8.1E-01	9.2E-01
AT5G41315	*GL3*	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	2.0	1.8E-03	8.0E-03	-1.1	7.1E-01	8.7E-01
AT4G17810	*AT4G17810*	C2H2 and C2HC zinc fingers superfamily protein	2.0	3.8E-07	6.0E-06	1.6	9.1E-05	3.0E-03
AT2G17695	*AT2G17695*	outer envelope protein	2.0	7.5E-09	2.1E-07	1.1	3.1E-01	5.7E-01
AT4G27830	*BGLU10*	beta glucosidase 10	2.0	1.2E-07	2.3E-06	1.0	6.6E-01	8.4E-01
AT1G42550	*PMI1*	plastid movement impaired1	2.0	8.0E-09	2.2E-07	1.0	8.1E-01	9.3E-01
AT1G79470	*AT1G79470*	Aldolase-type TIM barrel family protein	2.0	1.4E-05	1.3E-04	1.2	1.8E-01	4.3E-01
AT5G10150	*AT5G10150*	UPSTREAM OF FLC protein (DUF966)	2.0	1.1E-06	1.6E-05	1.1	2.5E-01	5.1E-01
AT3G56160	*AT3G56160*	Sodium Bile acid symporter family	2.0	5.1E-07	7.9E-06	1.4	7.2E-03	6.0E-02
AT1G16320	*AT1G16320*	plant/protein (DUF2358)	2.0	3.8E-08	8.4E-07	1.0	7.5E-01	8.9E-01
AT1G04350	*AT1G04350*	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2.0	9.6E-08	1.8E-06	1.1	2.6E-01	5.3E-01
AT1G51805	*AT1G51805*	Leucine-rich repeat protein kinase family protein	2.0	6.0E-06	6.5E-05	-1.2	1.0E-01	3.1E-01
AT5G59050	*AT5G59050*	G patch domain protein	2.0	7.4E-06	7.8E-05	-1.3	1.0E-01	3.1E-01

***pif45* /Col WL Up**			Col UV/WL			*pif45* /Col WL		
AGI	gene	description	Col_UV/WL_FC	pvalue	pvalue_with_FDR	*pif45* /Col_WL_FC	pvalue	pvalue_with_FDR
AT4G08093	*AT4G08093*	pseudogene of dihydroorotate dehydrogenase	-1.2	6.2E-01	7.4E-01	27.6	1.4E-15	1.5E-11
AT1G33960	*AIG1*	P-loop containing nucleoside triphosphate hydrolases superfamily protein	-3.8	3.7E-01	5.2E-01	20.0	4.0E-04	8.5E-03
AT3G60170	*AT3G60170*	transposable_element_gene	-6.6	1.6E-01	2.9E-01	17.8	2.8E-05	1.4E-03
AT2G11780	*AT2G11780*	transposable_element_gene	1.4	7.5E-01	8.4E-01	12.8	5.5E-04	1.1E-02
AT4G32540	*YUC1*	Flavin-binding monooxygenase family protein	4.0	3.0E-02	7.8E-02	7.2	1.2E-03	1.8E-02
AT1G13400	*NUB*	C2H2 and C2HC zinc fingers superfamily protein	2.8	9.3E-02	1.9E-01	6.0	1.8E-03	2.4E-02
AT1G68480	*JAG*	C2H2 and C2HC zinc fingers superfamily protein	2.1	1.2E-01	2.4E-01	5.5	2.5E-04	6.1E-03
AT4G09430	*AT4G09430*	disease resistance protein (TIR-NBS-LRR class)	1.2	7.6E-01	8.5E-01	5.3	2.3E-04	5.8E-03
AT5G07040	*AT5G07040*	RING/U-box superfamily protein	-1.0	9.8E-01	9.9E-01	5.2	5.5E-03	5.0E-02
AT5G35935	*AT5G35935*	transposable_element_gene	-1.7	4.1E-02	9.9E-02	5.1	6.7E-08	2.2E-05
AT5G51800	*AT5G51800*	Protein kinase superfamily protein	2.3	9.6E-02	1.9E-01	4.9	7.0E-04	1.2E-02
AT5G61610	*AT5G61610*	Oleosin family protein	1.7	3.8E-01	5.3E-01	4.9	2.9E-03	3.2E-02
AT3G28770	*AT3G28770*	transmembrane protein, putative (DUF1216)	1.5	4.4E-01	5.9E-01	4.8	8.9E-04	1.5E-02
AT5G20240	*PI*	K-box region and MADS-box transcription factor family protein	2.1	3.0E-02	7.9E-02	4.6	1.4E-05	8.7E-04
AT4G02960	*RE2*	transposable_element_gene	1.1	7.7E-01	8.5E-01	4.4	3.8E-04	8.2E-03
AT3G10780	*AT3G10780*	emp24/gp25L/p24 family/GOLD family protein	-1.9	3.9E-01	5.4E-01	4.4	3.9E-03	4.0E-02
AT2G04135	*AT2G04135*	transposable_element_gene	-1.0	9.6E-01	9.8E-01	4.0	5.1E-03	4.7E-02
AT5G55450	*AT5G55450*	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-1.2	6.1E-01	7.4E-01	4.0	4.7E-04	9.5E-03
AT5G11412	*AT5G11412*	RNA-binding (RRM/RBD/RNP motifs) family protein	-4.1	2.9E-02	7.5E-02	4.0	7.6E-04	1.3E-02
AT4G29150	*IQD25*	IQ-domain 25	2.4	6.7E-02	1.5E-01	3.9	3.7E-03	3.8E-02
AT2G25470	*RLP21*	receptor like protein 21	2.5	4.0E-02	9.9E-02	3.8	2.3E-03	2.8E-02
AT4G23200	*CRK12*	cysteine-rich RLK (RECEPTOR-like protein kinase) 12	2.0	6.0E-02	1.3E-01	3.8	3.2E-04	7.2E-03
AT4G34950	*AT4G34950*	Major facilitator superfamily protein	-1.1	5.3E-01	6.7E-01	3.8	3.2E-08	1.4E-05
AT5G05900	*AT5G05900*	UDP-Glycosyltransferase superfamily protein	1.2	6.6E-01	7.7E-01	3.3	3.3E-03	3.6E-02
AT1G02065	*SPL8*	squamosa promoter binding protein-like 8	2.1	2.3E-02	6.4E-02	3.2	2.7E-04	6.5E-03
AT2G02010	*GAD4*	glutamate decarboxylase 4	1.2	5.4E-01	6.8E-01	3.2	4.6E-05	1.9E-03
AT1G16510	*AT1G16510*	SAUR-like auxin-responsive protein family	1.4	2.2E-01	3.7E-01	3.1	2.6E-04	6.3E-03
AT3G08770	*LTP6*	lipid transfer protein 6	1.6	3.1E-02	8.0E-02	3.1	8.7E-06	6.3E-04
AT2G35310	*AT2G35310*	Transcriptional factor B3 family protein	1.2	7.1E-01	8.1E-01	3.0	2.0E-03	2.5E-02
AT2G23050	*NPY4*	Phototropic-responsive NPH3 family protein	-1.2	5.9E-01	7.2E-01	3.0	2.3E-03	2.8E-02
AT4G22517	*AT4G22517*	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	1.9	6.7E-02	1.5E-01	2.9	3.3E-03	3.6E-02
AT5G11320	*YUC4*	Flavin-binding monooxygenase family protein	1.4	2.6E-01	4.0E-01	2.9	4.1E-04	8.6E-03
AT2G16230	*AT2G16230*	O-Glycosyl hydrolases family 17 protein	-2.2	1.0E-01	2.0E-01	2.9	5.6E-03	5.0E-02
AT4G15690	*AT4G15690*	Thioredoxin superfamily protein	1.6	1.6E-01	2.9E-01	2.9	1.5E-03	2.1E-02
AT1G62500	*AT1G62500*	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	1.2	4.7E-01	6.2E-01	2.8	2.8E-04	6.6E-03
AT1G26680	*AT1G26680*	transcriptional factor B3 family protein	-1.9	9.1E-02	1.9E-01	2.8	2.5E-03	3.0E-02
AT5G35480	*AT5G35480*	hypothetical protein	1.7	1.3E-01	2.5E-01	2.8	4.3E-03	4.2E-02
AT3G13400	*sks13*	SKU5 similar 13	1.7	2.8E-02	7.5E-02	2.7	6.4E-05	2.4E-03
AT4G23590	*AT4G23590*	Tyrosine transaminase family protein	-2.2	2.5E-02	6.8E-02	2.7	1.1E-03	1.7E-02
AT1G56150	*AT1G56150*	SAUR-like auxin-responsive protein family	1.1	8.2E-01	8.9E-01	2.7	2.1E-05	1.1E-03
AT4G34400	*AT4G34400*	AP2/B3-like transcriptional factor family protein	1.8	9.9E-02	2.0E-01	2.7	4.9E-03	4.6E-02
AT3G54160	*AT3G54160*	RNI-like superfamily protein	1.4	3.9E-01	5.4E-01	2.7	3.6E-03	3.8E-02
AT1G28360	*ERF12*	ERF domain protein 12	1.3	3.1E-01	4.6E-01	2.7	7.2E-04	1.3E-02
AT4G22485	*AT4G22485*	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	1.8	8.0E-02	1.7E-01	2.7	4.5E-03	4.4E-02
AT5G53950	*CUC2*	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	1.4	3.4E-01	4.9E-01	2.6	1.8E-03	2.3E-02
AT1G73620	*AT1G73620*	Pathogenesis-related thaumatin superfamily	-1.9	7.0E-02	1.5E-01	2.6	2.3E-03	2.8E-02
AT5G23940	*PEL3*	HXXXD-type acyl-transferase family protein	2.0	2.6E-04	1.6E-03	2.6	1.2E-06	1.6E-04
AT1G10000	*AT1G10000*	Ribonuclease H-like superfamily protein	1.6	1.4E-01	2.5E-01	2.6	4.3E-03	4.2E-02
AT3G06020	*FAF4*	FANTASTIC four-like protein (DUF3049)	1.2	4.8E-01	6.2E-01	2.6	1.4E-04	4.1E-03
AT3G14530	*AT3G14530*	Terpenoid synthases superfamily protein	-1.5	2.3E-01	3.7E-01	2.5	4.2E-03	4.2E-02
AT1G75430	*BLH11*	BEL1-like homeodomain 11	1.2	5.1E-01	6.5E-01	2.5	3.1E-03	3.4E-02
AT5G18600	*AT5G18600*	Thioredoxin superfamily protein	1.2	3.6E-01	5.2E-01	2.5	3.5E-04	7.7E-03
AT5G48940	*AT5G48940*	Leucine-rich repeat transmembrane protein kinase family protein	-1.5	2.4E-01	3.9E-01	2.5	3.1E-03	3.4E-02
AT1G64920	*AT1G64920*	UDP-Glycosyltransferase superfamily protein	-1.5	1.4E-01	2.6E-01	2.5	1.0E-04	3.2E-03
AT5G25980	*TGG2*	glucoside glucohydrolase 2	1.1	5.4E-01	6.7E-01	2.5	2.0E-05	1.1E-03

AT1G05280	*AT1G05280*	ERV-F (C)1 provirus ancestral Env polyprotein, putative (DUF604)	-1.4	3.9E-01	5.4E-01	2.5	4.5E-03	4.4E-02
AT2G14820	*NPY2*	Phototropic-responsive NPH3 family protein	1.0	8.9E-01	9.4E-01	2.5	2.2E-03	2.7E-02
AT4G23750	*CRF2*	cytokinin response factor 2	1.0	9.6E-01	9.8E-01	2.4	3.6E-07	6.4E-05
AT1G66270	*BGLU21*	Glycosyl hydrolase superfamily protein	-2.2	5.9E-03	2.1E-02	2.4	1.6E-03	2.1E-02
AT4G30130	*AT4G30130*	DUF630 family protein (DUF630 and DUF632)	1.3	3.2E-01	4.7E-01	2.4	7.0E-04	1.2E-02
AT1G78750	*AT1G78750*	F-box/RNI-like superfamily protein	1.5	5.3E-02	1.2E-01	2.4	7.1E-05	2.6E-03
AT1G60590	*AT1G60590*	Pectin lyase-like superfamily protein	4.8	2.8E-08	6.5E-07	2.4	4.0E-04	8.5E-03
AT1G74890	*ARR15*	response regulator 15	-1.0	8.9E-01	9.4E-01	2.4	2.5E-05	1.3E-03
AT1G03010	*AT1G03010*	Phototropic-responsive NPH3 family protein	1.8	3.7E-03	1.4E-02	2.4	4.1E-05	1.7E-03
AT2G36770	*AT2G36770*	UDP-Glycosyltransferase superfamily protein	1.4	2.3E-01	3.7E-01	2.4	3.4E-03	3.6E-02
AT1G53160	*SPL4*	squamosa promoter binding protein-like 4	-1.2	4.6E-01	6.1E-01	2.3	1.4E-03	2.0E-02
AT2G24700	*AT2G24700*	Transcriptional factor B3 family protein	1.0	8.3E-01	9.0E-01	2.3	2.0E-04	5.2E-03
AT2G26220	*AT2G26220*	pseudogene of Polynucleotidyl transferase%2C ribonuclease H-like superfamily protein	-1.3	2.6E-01	4.0E-01	2.3	6.0E-04	1.1E-02
AT5G52050	*AT5G52050*	MATE efflux family protein	-2.2	5.5E-03	2.0E-02	2.3	8.2E-04	1.4E-02
AT1G11070	*AT1G11070*	hydroxyproline-rich glycoprotein family protein	-1.9	3.9E-02	9.6E-02	2.3	1.5E-03	2.1E-02
AT2G04450	*NUDT6*	nudix hydrolase homolog 6	-1.6	1.7E-01	3.0E-01	2.3	4.6E-03	4.4E-02
AT5G46500	*AT5G46500*	protein VARIATION IN COMPOUND TRIGGERED ROOT growth protein	1.3	3.4E-01	4.9E-01	2.3	4.5E-04	9.2E-03
AT2G26211	*MIR825A*		-1.3	4.6E-01	6.1E-01	2.3	5.3E-03	4.9E-02
AT3G14930	*HEME1*	Uroporphyrinogen decarboxylase	1.2	2.1E-01	3.5E-01	2.2	6.7E-08	2.2E-05
AT1G68570	*AT1G68570*	Major facilitator superfamily protein	2.9	2.8E-07	4.7E-06	2.2	3.0E-05	1.4E-03
AT1G63820	*AT1G63820*	CCT motif family protein	-1.3	2.9E-01	4.4E-01	2.2	5.4E-04	1.0E-02
AT5G09220	*AAP2*	amino acid permease 2	-1.7	1.0E-03	5.0E-03	2.2	1.2E-05	7.5E-04
AT5G48820	*ICK6*	inhibitor/interactor with cyclin-dependent kinase	1.5	8.7E-02	1.8E-01	2.2	1.0E-03	1.6E-02
AT5G51910	*AT5G51910*	TCP family transcription factor	1.4	1.9E-02	5.4E-02	2.1	9.6E-06	6.7E-04
AT4G19080	*AT4G19080*	hypothetical protein (DUF594)	-1.0	8.6E-01	9.2E-01	2.1	4.0E-03	4.1E-02
AT3G49410	*AT3G49410*	Transcription factor IIIC, subunit 5	1.1	7.1E-01	8.1E-01	2.1	2.3E-03	2.8E-02
AT1G33080	*AT1G33080*	MATE efflux family protein	1.3	1.6E-01	2.9E-01	2.1	3.2E-04	7.2E-03
AT3G24240	*AT3G24240*	Leucine-rich repeat receptor-like protein kinase family protein	1.6	1.7E-02	5.1E-02	2.1	5.3E-04	1.0E-02
AT5G08030	*GDPD6*	PLC-like phosphodiesterases superfamily protein	-1.1	6.5E-01	7.7E-01	2.1	1.9E-03	2.4E-02
AT2G15880	*AT2G15880*	Leucine-rich repeat (LRR) family protein	-1.4	1.1E-02	3.4E-02	2.1	4.2E-06	3.8E-04
AT3G08920	*AT3G08920*	Rhodanese/Cell cycle control phosphatase superfamily protein	1.1	2.6E-01	4.1E-01	2.1	2.2E-09	2.0E-06
AT5G44572	*AT5G44572*	transmembrane protein	1.6	1.7E-03	7.5E-03	2.1	1.6E-05	9.3E-04
AT3G13960	*GRF5*	growth-regulating factor 5	1.0	9.1E-01	9.5E-01	2.1	4.1E-03	4.1E-02
AT2G23130	*AGP17*	arabinogalactan protein 17	1.8	5.5E-07	8.4E-06	2.1	8.8E-09	5.9E-06
AT1G35730	*PUM9*	pumilio 9	-2.0	2.0E-02	5.7E-02	2.1	5.2E-03	4.8E-02
AT5G27230	*AT5G27230*	Frigida-like protein	1.4	1.2E-01	2.3E-01	2.1	5.8E-04	1.1E-02
AT5G09445	*AT5G09445*	hypothetical protein	1.3	2.4E-01	3.8E-01	2.0	2.9E-03	3.3E-02
AT1G33930	*AT1G33930*	P-loop containing nucleoside triphosphate hydrolases superfamily protein	1.3	2.4E-01	3.8E-01	2.0	1.2E-03	1.8E-02
AT5G64490	*AT5G64490*	ARM repeat superfamily protein	-1.5	8.2E-02	1.7E-01	2.0	7.8E-04	1.3E-02
AT2G18800	*XTH21*	xyloglucan endotransglucosylase/hydrolase 21	-2.8	1.7E-05	1.6E-04	2.0	2.3E-04	5.8E-03
AT1G54000	*GLL22*	GDSL-like Lipase/Acylhydrolase superfamily protein	-2.1	6.6E-04	3.5E-03	2.0	7.4E-04	1.3E-02

***pif45* /Col WL Down**			Col UV/WL			*pif45* /Col WL		
AGI	gene	description	Col_UV/WL_FC	pvalue	pvalue_with_FDR	*pif45* /Col_WL_FC	pvalue	pvalue_with_FDR
AT3G01345	*AT3G01345*	Expressed protein	1.0	9.9E-01	1.0E+00	-292.4	1.2E-06	1.5E-04
AT3G03260	*HDG8*	homeodomain GLABROUS 8	-3.6	5.4E-03	2.0E-02	-102.8	1.7E-06	2.0E-04
AT3G30720	*QQS*	qua-quine starch	1.1	8.6E-01	9.2E-01	-52.1	2.4E-05	1.2E-03
AT1G15405	*AT1G15405*		-51.7	2.9E-05	2.5E-04	-46.6	3.3E-05	1.5E-03
AT4G13790	*AT4G13790*	SAUR-like auxin-responsive protein family	-11.9	9.7E-03	3.2E-02	-44.5	2.0E-03	2.5E-02
AT3G43400	*AT3G43400*	ELMO/CED-12 family protein	-8.8	1.4E-02	4.3E-02	-32.7	2.2E-03	2.7E-02
ATMG01380	*RRN5*		-9.7	4.0E-04	2.3E-03	-27.3	2.1E-05	1.1E-03
AT3G59060	*PIL6*	phytochrome interacting factor 3-like 6	1.1	6.2E-01	7.5E-01	-21.6	4.9E-16	1.1E-11
AT1G20520	*AT1G20520*	DUF241 domain protein, putative (DUF241)	-4.4	1.4E-03	6.5E-03	-20.5	4.9E-06	4.3E-04
AT2G22810	*ACS4*	1-aminocyclopropane-1-carboxylate synthase 4	-4.8	7.1E-04	3.7E-03	-19.5	2.2E-06	2.5E-04
AT2G46970	*PIL1*	phytochrome interacting factor 3-like 1	-2.7	2.2E-03	9.4E-03	-19.1	1.1E-08	6.8E-06
AT3G29060	*AT3G29060*	EXS (ERD1/XPR1/SYG1) family protein	-2.0	6.8E-02	1.5E-01	-17.2	1.4E-05	8.5E-04
AT2G31141	*AT2G31141*	hypothetical protein	-19.8	8.5E-05	6.1E-04	-17.0	1.2E-04	3.5E-03
AT4G10160	*AT4G10160*	RING/U-box superfamily protein	-25.9	1.4E-06	1.9E-05	-16.5	3.5E-06	3.3E-04
AT5G37300	*WSD1*	O-acyltransferase (WSD1-like) family protein	-11.7	2.9E-05	2.5E-04	-15.5	1.0E-05	6.9E-04
AT1G52830	*IAA6*	indole-3-acetic acid 6	-7.8	4.5E-06	5.2E-05	-14.9	1.4E-07	3.4E-05
AT4G32280	*IAA29*	indole-3-acetic acid inducible 29	-3.6	2.7E-05	2.4E-04	-14.6	4.0E-10	6.8E-07
AT5G04380	*AT5G04380*	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	1.3	6.0E-01	7.3E-01	-14.6	1.1E-03	1.7E-02
AT5G37940	*AT5G37940*	Zinc-binding dehydrogenase family protein	-50.3	3.1E-04	1.8E-03	-14.3	1.1E-03	1.7E-02
ATCG00700	*PSBN*	photosystem II reaction center protein N	-26.2	2.5E-04	1.5E-03	-13.9	6.5E-04	1.2E-02
AT5G37950	*AT5G37950*	UDP-Glycosyltransferase superfamily protein	-7.5	3.6E-09	1.1E-07	-13.7	5.4E-11	3.1E-07
AT5G07010	*ST2A*	sulfotransferase 2A	-7.8	2.6E-06	3.3E-05	-12.5	1.6E-07	3.7E-05
AT5G44440	*AT5G44440*	FAD-binding Berberine family protein	-11.6	1.8E-07	3.1E-06	-12.3	1.2E-07	3.0E-05
AT3G09640	*APX2*	ascorbate peroxidase 2	1.5	3.3E-01	4.8E-01	-12.1	1.8E-03	2.3E-02
AT5G57810	*TET15*	tetraspanin15	1.3	3.6E-01	5.1E-01	-10.9	2.7E-06	2.8E-04
AT3G48960	*AT3G48960*	Ribosomal protein L13e family protein	-1.1	8.3E-01	9.0E-01	-10.7	8.0E-04	1.4E-02
AT2G18010	*AT2G18010*	SAUR-like auxin-responsive protein family	-3.9	2.8E-03	1.2E-02	-10.3	3.8E-05	1.7E-03
AT4G37770	*ACS8*	1-amino-cyclopropane-1-carboxylate synthase 8	-14.6	5.2E-05	4.1E-04	-9.8	1.4E-04	3.9E-03
AT5G53870	*ENODL1*	early nodulin-like protein 1	-1.1	6.2E-01	7.4E-01	-9.7	1.4E-09	1.7E-06
AT5G18050	*SAUR22*	SAUR-like auxin-responsive protein family	-1.9	5.0E-02	1.2E-01	-9.4	6.5E-07	9.9E-05
AT3G15540	*IAA19*	indole-3-acetic acid inducible 19	-5.6	8.2E-07	1.2E-05	-9.3	1.5E-08	9.0E-06
AT3G02670	*AT3G02670*	Glycine-rich protein family	-5.8	8.4E-09	2.3E-07	-9.3	1.2E-10	3.1E-07

AT5G66260	*AT5G66260*	SAUR-like auxin-responsive protein family	-25.2	4.3E-08	9.3E-07	-8.9	1.0E-06	1.4E-04
AT5G22500	*FAR1*	fatty acid reductase 1	-5.7	1.1E-05	1.1E-04	-8.9	4.7E-07	7.9E-05
AT1G68800	*TCP12*	TCP domain protein 12	-3.5	1.5E-05	1.4E-04	-8.8	9.2E-09	6.1E-06
AT4G35720	*AT4G35720*	DUF241 domain protein, putative (DUF241)	-5.1	5.1E-06	5.7E-05	-8.7	9.4E-08	2.7E-05
AT1G54040	*ESP*	epithiospecifier protein	-1.0	9.4E-01	9.7E-01	-8.6	1.1E-05	7.5E-04
AT1G80740	*CMT1*	chromomethylase 1	-7.8	1.8E-05	1.6E-04	-8.6	8.3E-06	6.1E-04
AT5G02540	*AT5G02540*	NAD(P)-binding Rossmann-fold superfamily protein	-3.5	3.8E-04	2.2E-03	-8.1	7.8E-07	1.2E-04
AT1G29395	*COR413IM1*	COLD REGULATED 314 INNER MEMBRANE 1	-2.1	5.3E-02	1.2E-01	-8.1	1.6E-05	9.5E-04
AT5G35525	*AT5G35525*	PLAC8 family protein	-2.5	6.1E-05	4.7E-04	-7.8	1.1E-10	3.1E-07
AT4G01190	*PIPK10*	phosphatidylinositol phosphate kinase 10	-1.5	2.3E-01	3.7E-01	-7.6	1.5E-05	9.1E-04
AT5G50750	*RGP4*	reversibly glycosylated polypeptide 4	-2.6	4.7E-02	1.1E-01	-7.6	9.1E-04	1.5E-02
AT3G41768	*AT3G41768*		-6.6	5.1E-03	1.9E-02	-7.6	3.1E-03	3.4E-02
ATCG01210	*RRN16S.2*		-7.2	3.5E-03	1.4E-02	-7.6	2.8E-03	3.2E-02
AT3G52310	*ABCG27*	ABC transporter G family member 27	1.9	2.5E-02	6.8E-02	-7.4	8.0E-05	2.8E-03
AT2G47880	*AT2G47880*	Glutaredoxin family protein	1.5	3.5E-01	5.0E-01	-7.3	1.8E-03	2.4E-02
AT2G07687	*AT2G07687*	Cytochrome c oxidase, subunit III	-3.0	5.7E-02	1.3E-01	-7.2	4.7E-03	4.5E-02
AT2G01010	*AT2G01010*		-8.7	9.5E-04	4.7E-03	-7.2	1.6E-03	2.2E-02
AT2G34655	*AT2G34655*	hypothetical protein	-3.5	3.1E-02	8.0E-02	-7.1	3.8E-03	3.9E-02
AT5G18010	*SAUR19*	SAUR-like auxin-responsive protein family	-2.7	2.7E-03	1.1E-02	-7.0	3.0E-06	3.0E-04
AT2G01770	*VIT1*	vacuolar iron transporter 1	-6.2	5.4E-03	2.0E-02	-6.7	3.7E-03	3.8E-02
AT1G73700	*AT1G73700*	MATE efflux family protein	1.0	9.3E-01	9.6E-01	-6.6	4.1E-03	4.1E-02
AT3G30120	*AT3G30120*	pseudogene of mediator of RNA polymerase II transcription subunit	-1.6	1.3E-01	2.4E-01	-6.5	1.9E-05	1.0E-03
AT3G23635	*RTFL13*	ROTUNDIFOLIA like 13	-9.7	4.6E-06	5.3E-05	-6.5	2.0E-05	1.1E-03
AT1G15580	*IAA5*	indole-3-acetic acid inducible 5	-2.3	1.2E-02	3.8E-02	-6.5	1.7E-05	9.6E-04
AT5G51210	*OLEO3*	oleosin3	-5.5	7.6E-05	5.6E-04	-6.4	2.9E-05	1.4E-03
AT2G16140	*AT2G16140*	transposable_element_gene	1.3	4.4E-01	5.9E-01	-6.3	2.7E-03	3.1E-02
ATCG00210	*YCF6*	electron transporter, transferring electrons within cytochrome b6/f complex of photosystem II	-9.9	1.3E-03	5.9E-03	-6.2	4.0E-03	4.0E-02
AT5G06720	*PA2*	peroxidase 2	-4.8	2.9E-07	4.9E-06	-6.2	2.3E-08	1.2E-05
AT5G64590	*AT5G64590*	NYN domain protein	-1.9	1.1E-01	2.2E-01	-6.1	8.8E-04	1.5E-02
AT1G73120	*AT1G73120*	F-box/RNI superfamily protein	-2.9	3.1E-03	1.3E-02	-6.1	1.2E-05	7.6E-04
AT4G31380	*FLP1*	flowering-promoting factor-like protein	-2.2	1.5E-02	4.4E-02	-6.0	6.3E-06	5.1E-04
AT4G10020	*HSD5*	hydroxysteroid dehydrogenase 5	-5.5	4.3E-05	3.5E-04	-6.0	2.2E-05	1.1E-03
AT3G28857	*PRE5*	basic helix-loop-helix (bHLH) DNA-binding family protein	-5.0	6.4E-05	4.9E-04	-5.8	2.0E-05	1.1E-03
AT2G21140	*PRP2*	proline-rich protein 2	-1.7	3.2E-03	1.3E-02	-5.7	8.1E-11	3.1E-07
AT3G60700	*AT3G60700*	hypothetical protein (DUF1163)	-2.7	6.3E-04	3.3E-03	-5.6	9.9E-07	1.4E-04
AT1G60450	*GolS7*	galactinol synthase 7	-3.3	1.5E-02	4.4E-02	-5.6	1.7E-03	2.3E-02
AT4G12410	*AT4G12410*	SAUR-like auxin-responsive protein family	-2.6	6.1E-03	2.2E-02	-5.4	5.7E-05	2.2E-03
AT5G64210	*AOX2*	alternative oxidase 2	-1.6	2.7E-01	4.2E-01	-5.3	1.6E-03	2.2E-02
AT4G19970	*AT4G19970*	nucleotide-diphospho-sugar transferase family protein	-1.3	3.3E-01	4.8E-01	-5.3	4.9E-05	2.0E-03
AT5G18060	*SAUR23*	SAUR-like auxin-responsive protein family	-1.8	4.3E-02	1.0E-01	-5.2	4.4E-06	4.0E-04
AT1G28450	*AGL58*	AGAMOUS-like 58	-13.0	1.3E-04	8.7E-04	-5.1	1.4E-03	1.9E-02
AT4G25420	*GA20OX1*	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	-7.1	6.1E-08	1.2E-06	-5.0	8.7E-07	1.3E-04
AT5G44130	*FLA13*	FASCICLIN-like arabinogalactan protein 13	1.5	2.1E-02	5.9E-02	-5.0	1.5E-09	1.7E-06
AT1G34480	*AT1G34480*	Cysteine/Histidine-rich C1 domain family protein	-1.6	2.8E-01	4.3E-01	-5.0	3.2E-03	3.5E-02
AT4G16515	*RGF6*	root meristem growth factor	-3.7	1.8E-05	1.7E-04	-5.0	1.1E-06	1.4E-04
AT3G59010	*PME61*	pectin methylesterase 61	-2.2	2.5E-03	1.1E-02	-4.9	6.4E-07	9.9E-05
AT4G08109	*AT4G08109*	transposable_element_gene	-2.8	7.3E-04	3.8E-03	-4.9	9.6E-06	6.7E-04
AT4G32500	*KT5*	K transporter 5	-1.7	1.8E-01	3.1E-01	-4.9	2.7E-03	3.2E-02
AT2G36110	*AT2G36110*	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	-1.7	8.8E-02	1.8E-01	-4.9	5.8E-05	2.2E-03
AT1G51530	*AT1G51530*	RNA-binding (RRM/RBD/RNP motifs) family protein	-3.2	2.3E-03	9.8E-03	-4.9	1.6E-04	4.4E-03
AT2G01200	*IAA32*	indole-3-acetic acid inducible 32	-3.2	1.1E-03	5.3E-03	-4.8	6.7E-05	2.5E-03
AT1G18835	*MIF3*	mini zinc finger	-6.4	8.3E-05	6.0E-04	-4.8	2.6E-04	6.3E-03
AT5G67020	*AT5G67020*	hypothetical protein	-3.1	1.6E-04	1.1E-03	-4.8	3.3E-06	3.2E-04
AT1G63710	*CYP86A7*	cytochrome P450, family 86, subfamily A, polypeptide 7	-3.5	1.6E-02	4.7E-02	-4.7	4.7E-03	4.5E-02
AT5G18080	*SAUR24*	SAUR-like auxin-responsive protein family	-2.0	1.9E-02	5.5E-02	-4.7	1.5E-05	8.9E-04
AT3G48790	*AT3G48790*	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	-2.2	1.8E-04	1.2E-03	-4.7	5.2E-09	3.8E-06
AT5G61660	*AT5G61660*	glycine-rich protein	-2.6	1.2E-05	1.2E-04	-4.7	7.1E-09	4.9E-06
AT3G59440	*AT3G59440*	Calcium-binding EF-hand family protein	-4.0	1.5E-03	6.9E-03	-4.6	6.4E-04	1.2E-02
AT1G12080	*AT1G12080*	Vacuolar calcium-binding protein-like protein	-4.0	9.6E-10	3.5E-08	-4.6	1.3E-10	3.1E-07
AT2G18150	*AT2G18150*	Peroxidase superfamily protein	1.2	3.0E-01	4.5E-01	-4.6	2.9E-08	1.3E-05
AT3G13900	*AT3G13900*	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein	-6.0	4.1E-08	8.9E-07	-4.5	3.4E-07	6.2E-05
AT1G29490	*AT1G29490*	SAUR-like auxin-responsive protein family	-4.8	1.1E-04	7.9E-04	-4.5	1.4E-04	4.0E-03
AT4G34770	*AT4G34770*	SAUR-like auxin-responsive protein family	-2.2	7.9E-04	4.0E-03	-4.4	2.2E-07	4.6E-05
AT2G45610	*AT2G45610*	alpha/beta-Hydrolases superfamily protein	-2.5	3.9E-03	1.5E-02	-4.4	3.7E-05	1.6E-03
AT1G04180	*YUC9*	YUCCA 9	-5.3	3.4E-05	2.9E-04	-4.4	1.2E-04	3.7E-03
AT4G11190	*AT4G11190*	Disease resistance-responsive (dirigent-like protein) family protein	-3.3	2.0E-05	1.8E-04	-4.3	9.0E-07	1.3E-04
AT1G18400	*BEE1*	BR enhanced expression 1	-1.3	1.9E-01	3.2E-01	-4.2	3.0E-08	1.4E-05
AT1G75900	*AT1G75900*	GDSL-like Lipase/Acylhydrolase superfamily protein	-2.5	6.0E-06	6.5E-05	-4.2	2.3E-09	2.0E-06
AT4G38825	*AT4G38825*	SAUR-like auxin-responsive protein family	-1.7	1.6E-02	4.7E-02	-4.1	2.8E-07	5.4E-05
AT5G15430	*AT5G15430*	Plant calmodulin-binding protein-like protein	-4.2	7.0E-04	3.6E-03	-4.1	6.0E-04	1.1E-02
AT5G18020	*SAUR20*	SAUR-like auxin-responsive protein family	-1.0	9.2E-01	9.6E-01	-4.1	5.5E-07	9.1E-05
AT4G22710	*CYP706A2*	cytochrome P450, family 706, subfamily A, polypeptide 2	-1.8	1.2E-01	2.2E-01	-4.1	1.3E-03	1.8E-02

AT1G26890	*AT1G26890*	FBD, F-box and Leucine Rich Repeat domains containing protein	-2.7	8.0E-04	4.1E-03	-4.1	2.1E-05	1.1E-03
AT5G17860	*CAX7*	calcium exchanger 7	-1.7	1.5E-01	2.7E-01	-4.0	7.6E-04	1.3E-02
AT5G18030	*AT5G18030*	SAUR-like auxin-responsive protein family	-1.1	8.4E-01	9.0E-01	-4.0	1.5E-05	9.2E-04
AT1G69540	*AGL94*	AGAMOUS-like 94	-1.2	5.9E-01	7.2E-01	-4.0	1.7E-04	4.6E-03
AT1G73550	*AT1G73550*	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-1.7	1.1E-01	2.1E-01	-3.9	5.2E-04	1.0E-02
AT4G11170	*AT4G11170*	Disease resistance protein (TIR-NBS-LRR class)	-1.3	3.3E-01	4.8E-01	-3.9	4.4E-04	9.0E-03
AT1G01390	*AT1G01390*	UDP-Glycosyltransferase superfamily protein	-1.1	7.3E-01	8.2E-01	-3.9	9.6E-06	6.7E-04
AT3G14370	*WAG2*	Protein kinase superfamily protein	-8.5	1.1E-10	5.4E-09	-3.8	2.6E-07	5.2E-05
AT1G09350	*GolS3*	galactinol synthase 3	-3.6	3.5E-04	2.0E-03	-3.8	2.3E-04	5.7E-03
AT5G49130	*AT5G49130*	MATE efflux family protein	-1.3	4.5E-01	6.0E-01	-3.8	1.7E-03	2.2E-02
AT5G63820	*AT5G63820*	hypothetical protein (DUF626)	-4.8	7.1E-08	1.4E-06	-3.8	8.2E-07	1.2E-04
AT3G28540	*AT3G28540*	P-loop containing nucleoside triphosphate hydrolases superfamily protein	1.8	2.1E-03	9.2E-03	-3.7	7.0E-07	1.1E-04
AT4G17470	*AT4G17470*	alpha/beta-Hydrolases superfamily protein	-2.1	2.6E-03	1.1E-02	-3.7	5.5E-06	4.6E-04
AT4G04223	*AT4G04223*		-1.1	8.5E-01	9.1E-01	-3.7	2.1E-03	2.6E-02
AT5G24580	*AT5G24580*	Heavy metal transport/detoxification superfamily protein	-2.4	1.6E-03	7.3E-03	-3.7	1.6E-05	9.3E-04
AT5G13700	*PAO1*	polyamine oxidase 1	-2.7	9.7E-06	9.8E-05	-3.7	1.0E-07	2.8E-05
AT5G22580	*AT5G22580*	Stress responsive A/B Barrel Domain-containing protein	-2.7	8.1E-06	8.4E-05	-3.7	8.2E-08	2.5E-05
AT2G05950	*AT2G05950*	transposable_element_gene	-1.6	1.7E-01	3.0E-01	-3.6	2.9E-03	3.3E-02
AT5G07000	*ST2B*	sulfotransferase 2B	-1.6	3.5E-03	1.4E-02	-3.6	2.1E-09	2.0E-06
AT4G27580	*AT4G27580*	phosphatidylinositol transfer SFH5-like protein	-1.9	1.1E-01	2.1E-01	-3.6	5.2E-03	4.8E-02
AT1G78970	*LUP1*	lupeol synthase 1	-1.2	2.8E-01	4.2E-01	-3.6	1.1E-09	1.5E-06
AT1G04660	*AT1G04660*	glycine-rich protein	-2.6	3.8E-05	3.1E-04	-3.6	5.6E-07	9.1E-05
AT3G18530	*AT3G18530*	ARM repeat superfamily protein	-3.1	5.5E-03	2.0E-02	-3.6	2.2E-03	2.7E-02
AT2G14900	*AT2G14900*	Gibberellin-regulated family protein	-3.8	5.1E-10	2.1E-08	-3.6	1.0E-09	1.5E-06
AT1G75450	*CKX5*	cytokinin oxidase 5	-2.4	6.1E-04	3.2E-03	-3.6	7.2E-06	5.5E-04
AT3G48970	*AT3G48970*	Heavy metal transport/detoxification superfamily protein	-1.2	3.1E-01	4.6E-01	-3.6	9.5E-07	1.4E-04
AT2G25000	*WRKY60*	WRKY DNA-binding protein 60	-2.6	1.1E-05	1.1E-04	-3.6	7.9E-08	2.5E-05
AT5G53980	*HB52*	homeobox protein 52	-1.3	2.5E-01	4.0E-01	-3.6	1.5E-06	1.9E-04
AT5G50335	*AT5G50335*	hypothetical protein	-2.9	1.2E-03	5.7E-03	-3.6	2.0E-04	5.2E-03
AT5G03435	*AT5G03435*	Ca2 dependent plant phosphoribosyltransferase family protein	-1.5	2.1E-01	3.5E-01	-3.5	1.9E-03	2.4E-02
AT4G10150	*AT4G10150*	RING/U-box superfamily protein	-2.7	7.6E-04	3.9E-03	-3.5	5.8E-05	2.2E-03
AT1G68725	*AGP19*	arabinogalactan protein 19	1.0	8.2E-01	8.9E-01	-3.4	8.3E-08	2.5E-05
AT5G41900	*AT5G41900*	alpha/beta-Hydrolases superfamily protein	-2.4	4.5E-05	3.6E-04	-3.4	2.0E-07	4.4E-05
AT1G53690	*AT1G53690*	DNA directed RNA polymerase, 7 kDa subunit	-5.3	3.6E-08	7.9E-07	-3.4	2.6E-06	2.8E-04
AT1G63380	*AT1G63380*	NAD(P)-binding Rossmann-fold superfamily protein	-2.1	3.8E-02	9.4E-02	-3.4	2.6E-03	3.0E-02
AT3G17050	*AT3G17050*	transposable_element_gene	-1.9	3.3E-04	1.9E-03	-3.4	3.5E-08	1.4E-05
AT1G68620	*AT1G68620*	alpha/beta-Hydrolases superfamily protein	1.7	1.1E-02	3.6E-02	-3.4	8.9E-06	6.4E-04
AT3G03830	*SAUR28*	SAUR-like auxin-responsive protein family	-2.2	2.4E-03	1.0E-02	-3.4	2.3E-05	1.2E-03
AT1G74420	*FUT3*	fucosyltransferase 3	-2.7	1.3E-04	8.9E-04	-3.4	8.1E-06	6.0E-04
AT5G12940	*AT5G12940*	Leucine-rich repeat (LRR) family protein	-5.6	2.5E-08	5.9E-07	-3.4	5.9E-06	4.9E-04
AT4G10310	*HKT1*	high-affinity K transporter 1	-1.1	5.7E-01	7.0E-01	-3.4	1.1E-06	1.5E-04
AT4G38850	*SAUR15*	SAUR-like auxin-responsive protein family	-1.4	1.6E-01	2.8E-01	-3.3	4.8E-05	1.9E-03
AT3G28890	*RLP43*	receptor like protein 43	1.2	6.3E-01	7.5E-01	-3.3	4.0E-03	4.1E-02
AT2G07711	*AT2G07711*	pseudogene of NADH dehydrogenase 5B	-2.3	2.1E-02	5.9E-02	-3.3	2.7E-03	3.1E-02
AT1G67265	*RTFL21*	ROTUNDIFOLIA like 21	-5.8	9.8E-06	9.9E-05	-3.2	5.6E-04	1.1E-02
AT2G46440	*CNGC11*	cyclic nucleotide-gated channels	1.0	9.3E-01	9.6E-01	-3.2	2.4E-03	2.8E-02
AT4G25260	*AT4G25260*	Plant invertase/pectin methylesterase inhibitor superfamily protein	-2.1	7.0E-04	3.6E-03	-3.2	1.8E-06	2.2E-04
AT1G68350	*AT1G68350*	cotton fiber protein	-1.7	1.1E-02	3.4E-02	-3.2	2.5E-06	2.7E-04
AT1G18870	*ICS2*	isochorismate synthase 2	-1.6	1.1E-02	3.6E-02	-3.1	2.2E-07	4.6E-05
AT5G39860	*PRE1*	basic helix-loop-helix (bHLH) DNA-binding family protein	-1.9	4.2E-04	2.4E-03	-3.1	1.4E-07	3.4E-05
AT3G48300	*CYP71A23*	cytochrome P450, family 71, subfamily A, polypeptide 23	-4.6	4.2E-04	2.4E-03	-3.1	2.7E-03	3.1E-02
AT1G29460	*AT1G29460*	SAUR-like auxin-responsive protein family	-1.5	1.4E-01	2.6E-01	-3.1	2.2E-04	5.5E-03
AT4G01335	*AT4G01335*	TATA box-binding protein associated factor RNA polymerase I subunit B-like protein	-4.2	6.2E-06	6.7E-05	-3.1	8.8E-05	3.0E-03
AT5G33340	*CDR1*	Eukaryotic aspartyl protease family protein	-1.5	2.4E-01	3.8E-01	-3.1	4.8E-03	4.5E-02
AT3G03840	*SAUR27*	SAUR-like auxin-responsive protein family	-1.7	2.1E-02	5.8E-02	-3.1	4.6E-05	1.9E-03
AT1G17810	*BETA-TIP*	beta-tonoplast intrinsic protein	-5.5	2.2E-05	1.9E-04	-3.1	1.3E-03	1.9E-02
AT5G24770	*VSP2*	vegetative storage protein 2	1.1	6.0E-01	7.3E-01	-3.1	3.0E-04	6.9E-03
AT1G26730	*AT1G26730*	EXS (ERD1/XPR1/SYG1) family protein	-2.8	1.6E-05	1.5E-04	-3.1	4.8E-06	4.2E-04
AT3G03850	*SAUR26*	SAUR-like auxin-responsive protein family	-1.9	2.8E-03	1.2E-02	-3.1	3.9E-06	3.6E-04
AT1G16850	*AT1G16850*	transmembrane protein	1.5	8.0E-02	1.7E-01	-3.1	1.2E-04	3.7E-03
AT2G26695	*AT2G26695*	Ran BP2/NZF zinc finger-like superfamily protein	-1.5	6.4E-02	1.4E-01	-3.0	1.6E-05	9.3E-04
AT1G76610	*AT1G76610*	MIZU-KUSSEI-like protein (Protein of unknown function, DUF617)	-3.1	4.6E-03	1.7E-02	-3.0	4.7E-03	4.5E-02
AT5G10770	*AT5G10770*	Eukaryotic aspartyl protease family protein	-1.1	5.8E-01	7.1E-01	-3.0	3.1E-07	5.8E-05
AT1G01600	*CYP86A4*	cytochrome P450, family 86, subfamily A, polypeptide 4	-1.7	3.8E-03	1.5E-02	-3.0	3.2E-07	5.9E-05
AT4G18970	*AT4G18970*	GDSL-like Lipase/Acylhydrolase superfamily protein	-2.3	2.7E-06	3.3E-05	-3.0	1.5E-08	9.0E-06
AT5G03090	*AT5G03090*	Mto 1 responding down protein	1.3	2.8E-01	4.3E-01	-3.0	1.5E-03	2.1E-02
AT1G21520	*AT1G21520*	hypothetical protein	-3.6	1.4E-03	6.3E-03	-3.0	3.7E-03	3.8E-02
AT1G49900	*AT1G49900*	C2H2 type zinc finger transcription factor family	-1.2	5.1E-01	6.5E-01	-3.0	9.3E-04	1.5E-02
AT3G42800	*AT3G42800*	AF-like protein	-2.7	1.8E-04	1.2E-03	-3.0	5.4E-05	2.1E-03
AT4G14560	*IAA1*	indole-3-acetic acid inducible	-1.4	1.2E-01	2.3E-01	-3.0	7.1E-06	5.5E-04

AT3G55940	*AT3G55940*	Phosphoinositide-specific phospholipase C family protein	-1.6	1.1E-02	3.4E-02	-3.0	1.4E-06	1.8E-04
AT4G14130	*XTH15*	xyloglucan endotransglucosylase/hydrolase 15	-3.4	3.3E-07	5.4E-06	-3.0	2.1E-06	2.4E-04
AT4G21730	*AT4G21730*	pseudogene of AAA-type ATPase family protein	-3.1	4.9E-06	5.5E-05	-2.9	8.5E-06	6.2E-04
AT2G19660	*AT2G19660*	Cysteine/Histidine-rich C1 domain family protein	-4.8	1.1E-11	7.0E-10	-2.9	2.5E-08	1.3E-05
AT1G29500	*AT1G29500*	SAUR-like auxin-responsive protein family	-1.1	5.5E-01	6.8E-01	-2.9	1.3E-05	8.4E-04
AT3G51895	*SULTR3*		1.3	3.3E-01	4.8E-01	-2.9	1.6E-03	2.2E-02
AT5G46240	*KAT1*		-1.5	1.0E-02	3.3E-02	-2.9	3.1E-08	1.4E-05
AT3G25717	*RTFL16*	ROTUNDIFOLIA like 16	-1.8	7.4E-03	2.5E-02	-2.9	1.2E-05	7.7E-04
AT2G29120	*GLR2.7*	glutamate receptor 2.7	-1.2	1.7E-01	3.0E-01	-2.9	6.0E-07	9.7E-05
AT3G16470	*JR1*	Mannose-binding lectin superfamily protein	1.0	8.6E-01	9.2E-01	-2.9	1.1E-07	2.9E-05
AT1G02340	*HFR1*	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	1.2	2.6E-01	4.1E-01	-2.9	1.2E-06	1.6E-04
AT1G29450	*AT1G29450*	SAUR-like auxin-responsive protein family	-1.3	2.3E-01	3.8E-01	-2.8	1.9E-04	5.0E-03
AT4G37980	*ELI3-1*	cinnamyl alcohol dehydrogenase 7	1.3	1.8E-01	3.1E-01	-2.8	9.1E-06	6.5E-04
AT5G66640	*DAR3*	DA1-related protein 3	-2.4	1.1E-02	3.5E-02	-2.8	3.7E-03	3.8E-02
AT1G03445	*BSU1*	Serine/threonine protein phosphatase family	2.0	1.5E-03	7.0E-03	-2.8	1.4E-04	4.1E-03
AT1G43590	*AT1G43590*	transposable_element_gene	-1.4	1.5E-01	2.7E-01	-2.8	1.7E-04	4.6E-03
AT4G14819	*AT4G14819*	hypothetical protein (DUF1677)	-3.5	1.6E-04	1.1E-03	-2.8	8.8E-04	1.5E-02
AT5G67180	*TOE3*	target of early activation tagged (EAT) 3	-1.1	7.8E-01	8.6E-01	-2.8	9.1E-04	1.5E-02
AT1G73220	*OCT1*	organic cation/carnitine transporter1	-5.7	5.5E-06	6.0E-05	-2.8	1.1E-03	1.7E-02
AT3G59900	*ARGOS*	auxin-regulated gene involved in organ size	1.1	4.9E-01	6.3E-01	-2.8	9.6E-06	6.7E-04
AT3G55240	*AT3G55240*	Plant protein 1589 of unknown function	-1.8	1.6E-03	7.1E-03	-2.8	1.6E-06	2.0E-04
AT1G05700	*AT1G05700*	Leucine-rich repeat transmembrane protein kinase protein	-1.8	4.5E-02	1.1E-01	-2.8	1.3E-03	1.9E-02
AT4G27460	*CBSX5*	Cystathionine beta-synthase (CBS) family protein	-6.4	4.9E-06	5.5E-05	-2.8	2.3E-03	2.8E-02
AT1G30280	*AT1G30280*	Chaperone DnaJ-domain superfamily protein	-1.3	7.5E-02	1.6E-01	-2.7	3.5E-08	1.4E-05
AT1G68360	*AT1G68360*	C2H2 and C2HC zinc fingers superfamily protein	-2.7	3.3E-05	2.8E-04	-2.7	2.8E-05	1.3E-03
AT4G21745	*AT4G21745*	PAK-box/P21-Rho-binding family protein	-2.7	2.1E-04	1.3E-03	-2.7	2.0E-04	5.2E-03
AT2G23170	*GH3.3*	Auxin-responsive GH3 family protein	-6.6	2.0E-07	3.5E-06	-2.7	4.5E-04	9.1E-03
AT4G39700	*AT4G39700*	Heavy metal transport/detoxification superfamily protein	-1.4	1.2E-01	2.2E-01	-2.7	2.6E-04	6.3E-03
AT3G15356	*AT3G15356*	Legume lectin family protein	-1.2	1.4E-01	2.5E-01	-2.7	1.2E-07	3.1E-05
AT3G29370	*P1R3*	hypothetical protein	-3.3	5.7E-06	6.2E-05	-2.7	5.5E-05	2.1E-03
AT3G21330	*AT3G21330*	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	-3.1	5.1E-05	4.0E-04	-2.7	2.1E-04	5.4E-03
AT4G16892	*AT4G16892*		-1.5	2.9E-02	7.5E-02	-2.7	2.7E-06	2.8E-04
AT5G14780	*FDH*	formate dehydrogenase	-2.7	4.8E-08	1.0E-06	-2.7	4.4E-08	1.6E-05
AT1G72140	*AT1G72140*	Major facilitator superfamily protein	-1.1	4.8E-01	6.2E-01	-2.7	1.2E-05	7.8E-04
AT4G16780	*HB-2*	homeobox protein 2	-3.2	8.7E-04	4.4E-03	-2.7	3.6E-03	3.8E-02
AT2G33205	*AT2G33205*	Serinc-domain containing serine and sphingolipid biosynthesis protein	-1.7	3.5E-02	8.8E-02	-2.7	3.4E-04	7.5E-03
AT1G76240	*AT1G76240*	DUF241 domain protein (DUF241)	-1.3	1.7E-01	2.9E-01	-2.6	1.6E-06	1.9E-04
AT1G65310	*XTH17*	xyloglucan endotransglucosylase/hydrolase 17	-3.3	1.4E-05	1.3E-04	-2.6	1.8E-04	4.9E-03
AT3G29575	*AFP3*	ABI five binding protein 3	-1.8	3.2E-03	1.3E-02	-2.6	1.7E-05	9.9E-04
AT2G47010	*AT2G47010*	calcium/calcium/calmodulin-dependent Serine/Threonine-kinase	1.3	6.1E-02	1.3E-01	-2.6	2.8E-08	1.3E-05
AT3G42658	*SADHU3-2*	transposable_element_gene	-1.6	1.8E-02	5.2E-02	-2.6	4.4E-05	1.8E-03
AT1G52190	*AT1G52190*	Major facilitator superfamily protein	-2.3	8.9E-09	2.4E-07	-2.6	4.1E-10	6.8E-07
AT4G13280	*TPS12*	terpenoid synthase 12	-1.0	9.7E-01	9.9E-01	-2.6	8.3E-05	2.8E-03
AT5G47370	*HAT2*	Homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP protein	-2.3	5.5E-05	4.3E-04	-2.6	6.0E-06	4.9E-04
AT2G05518	*AT2G05518*		-1.8	1.5E-02	4.6E-02	-2.6	2.9E-04	6.7E-03
AT1G29510	*SAUR68*	SAUR-like auxin-responsive protein family	-1.0	9.3E-01	9.6E-01	-2.6	1.4E-05	8.5E-04
AT3G23030	*IAA2*	indole-3-acetic acid inducible 2	-1.2	1.4E-01	2.6E-01	-2.5	3.4E-08	1.4E-05
AT2G43050	*ATPMEPCRD*	Plant invertase/pectin methylesterase inhibitor superfamily	-2.9	1.9E-05	1.8E-04	-2.5	9.1E-05	3.0E-03
AT3G13980	*AT3G13980*	SKI/DACH domain protein	-2.0	3.5E-04	2.0E-03	-2.5	4.8E-06	4.2E-04
AT5G57240	*ORP4C*	OSBP(oxysterol binding protein)-related protein 4C	-5.0	3.0E-09	9.5E-08	-2.5	2.8E-05	1.3E-03
AT2G32990	*GH9B8*	glycosyl hydrolase 9B8	1.8	2.9E-03	1.2E-02	-2.5	3.3E-05	1.5E-03
AT4G28720	*YUC8*	Flavin-binding monooxygenase family protein	-2.5	3.6E-04	2.1E-03	-2.5	3.6E-04	7.8E-03
AT5G01740	*AT5G01740*	Nuclear transport factor 2 (NTF2) family protein	1.0	9.0E-01	9.4E-01	-2.5	4.3E-05	1.8E-03
AT5G51810	*GA20OX2*	gibberellin 20 oxidase 2	-2.0	1.8E-03	7.9E-03	-2.5	1.2E-04	3.7E-03
AT5G59010	*BSK5*	kinase with tetratricopeptide repeat domain-containing protein	-2.0	3.5E-07	5.7E-06	-2.5	2.4E-09	2.0E-06
AT3G20470	*GRP5*	glycine-rich protein 5	-2.2	1.5E-03	6.9E-03	-2.5	2.7E-04	6.4E-03
AT5G39865	*AT5G39865*	Glutaredoxin family protein	-2.4	4.4E-07	7.0E-06	-2.5	2.6E-07	5.1E-05
AT4G14640	*CAM8*	calmodulin 8	-2.0	8.9E-04	4.4E-03	-2.5	3.2E-05	1.5E-03
AT1G27670	*AT1G27670*	transmembrane protein	-1.8	1.3E-03	6.1E-03	-2.5	7.8E-06	5.9E-04
AT1G06080	*ADS1*	delta 9 desaturase 1	-4.6	5.9E-06	6.4E-05	-2.5	1.7E-03	2.2E-02
AT5G66390	*AT5G66390*	Peroxidase superfamily protein	1.2	2.1E-01	3.5E-01	-2.5	4.5E-08	1.6E-05
AT1G11120	*AT1G11120*	CTTNBP 2 amino-terminal-like protein	-3.4	1.2E-07	2.3E-06	-2.5	1.1E-05	7.5E-04
AT5G27660	*DEG14*	Trypsin family protein with PDZ domain-containing protein	1.1	5.2E-01	6.6E-01	-2.5	5.7E-06	4.7E-04
AT5G44260	*AT5G44260*	Zinc finger C-x8-C-x5-C-x3-H type family protein	-2.2	5.0E-04	2.8E-03	-2.5	9.3E-05	3.1E-03
AT1G62770	*AT1G62770*	Plant invertase/pectin methylesterase inhibitor superfamily protein	-5.1	1.9E-12	1.6E-10	-2.5	2.8E-07	5.4E-05
AT3G49820	*AT3G49820*	hypothetical protein	-1.4	1.5E-01	2.7E-01	-2.5	1.6E-03	2.1E-02
AT1G29440	*SAUR63*	SAUR-like auxin-responsive protein family	1.2	3.0E-01	4.5E-01	-2.5	7.3E-05	2.6E-03
AT5G62280	*AT5G62280*	DUF1442 family protein (DUF1442)	-2.3	2.0E-04	1.2E-03	-2.5	7.3E-05	2.6E-03
AT5G64770	*RGF9*	root meristem growth factor	1.9	6.1E-05	4.7E-04	-2.4	6.7E-07	1.0E-04
AT1G10560	*PUB18*	plant U-box 18	-3.1	1.7E-04	1.1E-03	-2.4	1.6E-03	2.2E-02
AT2G38530	*LTP2*	lipid transfer protein 2	-1.5	1.3E-01	2.5E-01	-2.4	3.0E-03	3.4E-02

AT5G01790	*AT5G01790*	hypothetical protein	1.8	1.6E-04	1.0E-03	-2.4	5.6E-07	9.1E-05
AT5G55780	*AT5G55780*	Cysteine/Histidine-rich C1 domain family protein	-3.6	1.5E-05	1.4E-04	-2.4	5.7E-04	1.1E-02
AT5G57760	*AT5G57760*	hypothetical protein	-1.6	9.8E-03	3.2E-02	-2.4	3.3E-05	1.5E-03
AT1G31040	*AT1G31040*	PLATZ transcription factor family protein	-2.2	6.2E-04	3.3E-03	-2.4	1.5E-04	4.3E-03
AT4G14140	*DMT2*	DNA methyltransferase 2	-2.0	1.7E-02	5.0E-02	-2.4	3.0E-03	3.3E-02
AT2G42990	*AT2G42990*	GDSL-like Lipase/Acylhydrolase superfamily protein	-5.1	2.0E-08	4.8E-07	-2.4	9.3E-05	3.1E-03
AT2G40610	*EXPA8*	expansin A8	-1.9	5.5E-04	3.0E-03	-2.4	6.5E-06	5.2E-04
AT5G53830	*AT5G53830*	VQ motif-containing protein	-2.0	8.0E-06	8.3E-05	-2.4	1.7E-07	3.8E-05
AT3G50800	*AT3G50800*	hypothetical protein	-2.2	3.2E-03	1.3E-02	-2.4	1.4E-03	2.0E-02
AT1G20450	*ERD10*	Dehydrin family protein	1.5	3.0E-03	1.2E-02	-2.4	1.8E-08	1.0E-05
AT5G23350	*AT5G23350*	GRAM domain protein/ABA-responsive-like protein	-1.3	5.6E-02	1.3E-01	-2.4	3.0E-07	5.6E-05
AT4G12730	*FLA2*	FASCICLIN-like arabinogalactan 2	-1.4	1.4E-02	4.1E-02	-2.4	5.0E-08	1.8E-05
AT4G37580	*HLS1*	Acyl-CoA N-acyltransferases (NAT) superfamily protein	-2.4	3.6E-04	2.1E-03	-2.4	3.5E-04	7.6E-03
AT5G46590	*NAC096*	NAC domain containing protein 96	1.1	7.3E-01	8.3E-01	-2.4	2.3E-04	5.8E-03
AT4G08040	*ACS11*	1-aminocyclopropane-1-carboxylate synthase 11	-1.9	8.4E-03	2.8E-02	-2.4	7.3E-04	1.3E-02
AT5G66580	*AT5G66580*	hypothetical protein	-1.4	7.3E-02	1.6E-01	-2.4	8.6E-05	2.9E-03
AT4G27260	*WES1*	Auxin-responsive GH3 family protein	-2.2	3.1E-06	3.8E-05	-2.4	6.2E-07	9.8E-05
AT5G10970	*AT5G10970*	C2H2 and C2HC zinc fingers superfamily protein	-1.5	4.1E-02	9.9E-02	-2.4	1.4E-04	4.1E-03
AT4G12470	*AZI1*	azelaic acid induced 1	1.2	2.9E-01	4.4E-01	-2.4	2.4E-04	6.0E-03
AT2G47015	*MIR408*		-2.0	1.8E-03	8.0E-03	-2.4	3.0E-04	7.0E-03
AT3G24715	*AT3G24715*	kinase superfamily with octicosapeptide/Phox/Bem1p domain-containing protein	-2.4	2.3E-10	1.1E-08	-2.3	3.0E-10	6.5E-07
AT1G15050	*IAA34*	indole-3-acetic acid inducible 34	-1.5	1.5E-01	2.7E-01	-2.3	2.6E-03	3.0E-02
AT2G25625	*AT2G25625*	histone deacetylase-like protein	1.5	1.4E-02	4.3E-02	-2.3	1.5E-05	9.2E-04
AT5G65390	*AGP7*	arabinogalactan protein 7	-3.3	6.4E-09	1.8E-07	-2.3	3.2E-06	3.1E-04
AT5G38005	*AT5G38005*		-1.2	3.4E-01	4.9E-01	-2.3	6.3E-04	1.2E-02
AT5G51200	*EMB3142*	nuclear pore complex protein (DUF3414)	-1.8	1.3E-03	6.1E-03	-2.3	2.7E-05	1.3E-03
AT5G66590	*AT5G66590*	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily	-1.9	1.7E-03	7.5E-03	-2.3	1.2E-04	3.7E-03
AT4G14380	*AT4G14380*	cotton fiber protein	-1.6	1.0E-02	3.3E-02	-2.3	3.5E-05	1.6E-03
AT5G39610	*NAC6*	NAC domain containing protein 6	-1.1	6.4E-01	7.6E-01	-2.3	2.2E-05	1.2E-03
AT2G18969	*AT2G18969*	transcription factor/transcription regulator	-1.5	1.9E-02	5.5E-02	-2.3	2.1E-05	1.1E-03
AT3G55230	*AT3G55230*	Disease resistance-responsive (dirigent-like protein) family protein	-1.1	5.5E-01	6.9E-01	-2.3	3.7E-06	3.4E-04
AT2G43060	*IBH1*	ILI1 binding bHLH 1	-1.4	5.3E-02	1.2E-01	-2.3	2.0E-05	1.1E-03
AT1G60030	*NAT7*	nucleobase-ascorbate transporter 7	-1.2	2.5E-01	4.0E-01	-2.3	1.1E-05	7.5E-04
AT5G02760	*AT5G02760*	Protein phosphatase 2C family protein	-2.7	1.5E-05	1.4E-04	-2.3	1.6E-04	4.4E-03
AT1G78815	*LSH7*	LIGHT-DEPENDENT SHORT HYPOCOTYLS-like protein (DUF640)	-1.7	6.2E-02	1.4E-01	-2.3	5.0E-03	4.7E-02
AT3G18200	*UMAMIT4*	nodulin MtN21 /EamA-like transporter family	-2.7	1.1E-08	3.0E-07	-2.3	2.6E-07	5.1E-05
AT4G11280	*ACS6*	1-aminocyclopropane-1-carboxylic acid (acc) synthase 6	-2.4	5.6E-04	3.0E-03	-2.3	9.0E-04	1.5E-02
AT5G51790	*AT5G51790*	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	-2.8	2.0E-07	3.4E-06	-2.3	6.4E-06	5.1E-04
AT2G39450	*MTP11*	Cation efflux family protein	1.3	2.5E-01	3.9E-01	-2.3	3.2E-04	7.2E-03
AT1G08500	*ENODL18*	early nodulin-like protein 18	-4.3	1.9E-13	2.2E-11	-2.3	4.1E-08	1.6E-05
AT2G27370	*CASP3*	Uncharacterized protein family (UPF0497)	-1.1	5.0E-01	6.4E-01	-2.3	2.6E-07	5.1E-05
AT1G61260	*AT1G61260*	cotton fiber (DUF761)	-2.0	3.8E-08	8.2E-07	-2.3	1.4E-09	1.7E-06
AT5G38020	*AT5G38020*	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	-1.1	7.0E-01	8.1E-01	-2.3	2.0E-03	2.5E-02
AT3G26170	*CYP71B19*	cytochrome P450, family 71, subfamily B, polypeptide 19	-2.9	6.4E-05	4.9E-04	-2.3	1.1E-03	1.7E-02
AT5G38970	*BR6OX1*	brassinosteroid-6-oxidase 1	-3.0	6.6E-11	3.4E-09	-2.2	3.0E-08	1.4E-05
AT1G09480	*AT1G09480*	NAD(P)-binding Rossmann-fold superfamily protein	-1.2	3.2E-01	4.7E-01	-2.2	1.2E-04	3.7E-03
AT1G75500	*WAT1*	Walls Are Thin 1	-1.7	1.6E-06	2.1E-05	-2.2	3.5E-10	6.8E-07
AT5G65980	*AT5G65980*	Auxin efflux carrier family protein	-1.1	7.3E-01	8.3E-01	-2.2	3.4E-03	3.6E-02
AT1G02670	*AT1G02670*	P-loop containing nucleoside triphosphate hydrolases superfamily protein	-1.6	4.8E-03	1.8E-02	-2.2	1.6E-05	9.2E-04
AT3G55840	*AT3G55840*	Hs1pro-1 protein	-2.5	2.1E-05	1.8E-04	-2.2	1.3E-04	3.9E-03
AT5G55730	*FLA1*	FASCICLIN-like arabinogalactan 1	-2.0	6.2E-07	9.3E-06	-2.2	2.8E-08	1.3E-05
AT1G17400	*AT1G17400*	hypothetical protein	1.3	2.6E-01	4.1E-01	-2.2	1.3E-03	1.9E-02
AT3G11550	*CASP2*	Uncharacterized protein family (UPF0497)	-1.1	3.6E-01	5.1E-01	-2.2	1.1E-07	3.0E-05
AT3G03240	*AT3G03240*	alpha/beta-Hydrolases superfamily protein	-1.7	4.3E-02	1.0E-01	-2.2	3.7E-03	3.8E-02
AT1G01120	*KCS1*	3-ketoacyl-CoA synthase 1	1.0	9.2E-01	9.5E-01	-2.2	6.2E-07	9.8E-05
AT5G47220	*ERF2*	ethylene responsive element binding factor 2	-1.8	3.3E-02	8.4E-02	-2.2	4.2E-03	4.2E-02
AT2G43290	*MSS3*	Calcium-binding EF-hand family protein	-1.7	1.3E-04	9.1E-04	-2.2	2.2E-07	4.6E-05
AT3G08660	*AT3G08660*	Phototropic-responsive NPH3 family protein	-1.1	6.4E-01	7.6E-01	-2.2	2.9E-06	2.9E-04
AT1G69570	*AT1G69570*	Dof-type zinc finger DNA-binding family protein	-1.6	4.1E-02	1.0E-01	-2.2	1.9E-03	2.5E-02
AT5G67090	*AT5G67090*	Subtilisin-like serine endopeptidase family protein	-1.2	2.8E-01	4.3E-01	-2.2	2.0E-06	2.3E-04
AT1G09310	*AT1G09310*	plant/protein (Protein of unknown function,	1.2	3.8E-01	5.3E-01	-2.2	5.0E-05	2.0E-03
AT1G05835	*AT1G05835*	PHD finger protein	-1.7	1.2E-02	3.8E-02	-2.2	4.4E-04	9.1E-03
AT1G36940	*AT1G36940*	myotubularin-like protein	-1.7	4.9E-04	2.7E-03	-2.2	4.5E-06	4.0E-04
AT1G62610	*AT1G62610*	NAD(P)-binding Rossmann-fold superfamily protein	-2.5	4.1E-08	8.8E-07	-2.2	4.9E-07	8.2E-05
AT1G01200	*RABA3*	RAB GTPase homolog A3	-1.6	6.0E-03	2.2E-02	-2.2	4.3E-05	1.8E-03
AT1G12070	*AT1G12070*	Immunoglobulin E-set superfamily protein	1.3	1.3E-01	2.4E-01	-2.2	2.4E-05	1.2E-03
AT5G04310	*AT5G04310*	Pectin lyase-like superfamily protein	-1.8	5.0E-06	5.6E-05	-2.2	2.2E-08	1.2E-05
AT5G20740	*AT5G20740*	Plant invertase/pectin methylesterase inhibitor superfamily protein	-1.6	9.2E-03	3.0E-02	-2.2	1.2E-04	3.6E-03
AT3G23450	*AT3G23450*	transmembrane protein	-1.6	3.4E-03	1.4E-02	-2.2	5.2E-06	4.5E-04
AT5G65800	*ACS5*	ACC synthase 5	-8.5	2.9E-08	6.6E-07	-2.2	4.2E-03	4.2E-02
AT5G01760	*AT5G01760*	ENTH/VHS/GAT family protein	1.1	6.6E-01	7.7E-01	-2.2	6.8E-04	1.2E-02

AT1G71740	*AT1G71740*	nucleolar protein	1.1	3.2E-01	4.7E-01	-2.2	2.8E-06	2.9E-04
AT4G13580	*AT4G13580*	Disease resistance-responsive (dirigent-like protein) family protein	-1.1	7.0E-01	8.1E-01	-2.1	7.8E-05	2.8E-03
AT2G28670	*ESB1*	Disease resistance-responsive (dirigent-like protein) family protein	-1.1	3.0E-01	4.5E-01	-2.1	1.2E-06	1.5E-04
AT1G29430	*AT1G29430*	SAUR-like auxin-responsive protein family	1.5	7.1E-03	2.5E-02	-2.1	3.0E-05	1.4E-03
AT4G13290	*CYP71A19*	cytochrome P450, family 71, subfamily A, polypeptide 19	1.2	1.1E-01	2.2E-01	-2.1	7.0E-06	5.4E-04
AT3G03820	*SAUR29*	SAUR-like auxin-responsive protein family	-1.4	8.0E-02	1.7E-01	-2.1	9.3E-04	1.5E-02
AT5G02200	*FHL*	far-red-elongated hypocotyl1-like protein	-2.6	4.1E-05	3.3E-04	-2.1	5.4E-04	1.0E-02
AT2G17880	*AT2G17880*	Chaperone DnaJ-domain superfamily protein	1.0	8.1E-01	8.9E-01	-2.1	1.9E-06	2.2E-04
AT1G62480	*AT1G62480*	Vacuolar calcium-binding protein-like protein	-2.2	6.9E-07	1.0E-05	-2.1	2.1E-06	2.4E-04
AT5G04190	*PKS4*	phytochrome kinase substrate 4	-2.3	2.3E-05	2.0E-04	-2.1	7.3E-05	2.6E-03
AT4G18290	*KAT2*	potassium channel KAT1-like protein	-1.2	1.2E-01	2.4E-01	-2.1	9.2E-06	6.5E-04
AT3G08570	*AT3G08570*	Phototropic-responsive NPH3 family protein	-1.7	1.5E-03	6.8E-03	-2.1	4.0E-05	1.7E-03
AT4G28900	*AT4G28900*	transposable_element_gene	-1.9	1.6E-04	1.0E-03	-2.1	2.5E-05	1.2E-03
AT5G49630	*AAP6*	amino acid permease 6	-1.7	1.5E-03	6.8E-03	-2.1	2.8E-05	1.3E-03
AT4G23670	*AT4G23670*	Polyketide cyclase/dehydrase and lipid transport superfamily protein	1.1	6.2E-01	7.5E-01	-2.1	2.1E-05	1.1E-03
AT5G02190	*PCS1*	Eukaryotic aspartyl protease family protein	-1.9	8.0E-03	2.7E-02	-2.1	3.4E-03	3.6E-02
AT1G54200	*AT1G54200*	DNA mismatch repair Msh6-like protein	-1.6	2.0E-04	1.2E-03	-2.1	7.4E-08	2.4E-05
AT1G61255	*AT1G61255*	hypothetical protein	-1.4	1.4E-01	2.6E-01	-2.1	1.8E-03	2.4E-02
AT2G37030	*AT2G37030*	SAUR-like auxin-responsive protein family	1.7	2.7E-02	7.1E-02	-2.1	5.2E-03	4.8E-02
AT4G37410	*CYP81F4*	cytochrome P450, family 81, subfamily F, polypeptide 4	1.1	7.0E-01	8.1E-01	-2.1	3.1E-05	1.5E-03
AT1G01130	*AT1G01130*	CBL-interacting Serine/Threonine-kinase	-1.3	2.6E-01	4.1E-01	-2.1	1.9E-03	2.5E-02
AT5G43660	*AT5G43660*	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	-1.2	3.4E-01	4.9E-01	-2.1	3.8E-04	8.1E-03
AT1G27030	*AT1G27030*	hypothetical protein	-1.5	4.3E-03	1.6E-02	-2.1	3.1E-06	3.0E-04
AT5G64870	*AT5G64870*	SPFH/Band 7/PHB domain-containing membrane-associated protein family	-2.0	1.3E-03	6.1E-03	-2.1	6.2E-04	1.2E-02
AT1G69840	*AT1G69840*	SPFH/Band 7/PHB domain-containing membrane-associated protein family	-1.7	2.4E-04	1.5E-03	-2.1	2.2E-06	2.5E-04
AT1G78490	*CYP708A3*	cytochrome P450, family 708, subfamily A, polypeptide 3	-1.7	4.6E-04	2.5E-03	-2.1	3.9E-06	3.6E-04
AT5G63810	*BGAL10*	beta-galactosidase 10	-2.3	5.1E-09	1.5E-07	-2.1	9.5E-08	2.7E-05
AT1G53700	*WAG1*	WAG 1	-3.7	4.4E-07	6.9E-06	-2.1	8.0E-04	1.4E-02
AT4G24265	*AT4G24265*	homeobox protein	-2.0	2.9E-04	1.7E-03	-2.1	2.3E-04	5.8E-03
AT1G66350	*RGL1*	RGA-like 1	-2.4	5.2E-08	1.1E-06	-2.1	1.4E-06	1.7E-04
AT4G38770	*PRP4*	proline-rich protein 4	-1.1	4.2E-01	5.7E-01	-2.1	1.2E-04	3.5E-03
AT4G20820	*AT4G20820*	FAD-binding Berberine family protein	1.5	1.0E-02	3.3E-02	-2.1	3.3E-05	1.5E-03
AT2G21100	*AT2G21100*	Disease resistance-responsive (dirigent-like protein) family protein	1.6	9.7E-03	3.2E-02	-2.1	2.8E-04	6.6E-03
AT1G11545	*XTH8*	xyloglucan endotransglucosylase/hydrolase 8	-3.2	1.0E-12	8.9E-11	-2.1	3.9E-08	1.5E-05
AT1G77400	*AT1G77400*	extensin-like protein	1.1	6.5E-01	7.7E-01	-2.1	3.5E-04	7.7E-03
AT4G32350	*AT4G32350*	Regulator of Vps4 activity in the MVB pathway protein	-1.3	5.8E-03	2.1E-02	-2.0	1.0E-10	3.1E-07
AT4G22690	*CYP706A1*	cytochrome P450, family 706, subfamily A, polypeptide 1	-1.1	7.1E-01	8.2E-01	-2.0	2.5E-04	6.1E-03
AT1G69490	*NAP*	NAC-like, activated by AP3/PI	-1.1	7.9E-01	8.7E-01	-2.0	2.7E-03	3.1E-02
AT5G63450	*CYP94B1*	cytochrome P450, family 94, subfamily B, polypeptide 1	1.3	6.2E-02	1.4E-01	-2.0	4.9E-05	2.0E-03
AT5G44670	*GALS2*	glycosyltransferase family protein (DUF23)	-1.7	1.3E-05	1.2E-04	-2.0	2.7E-08	1.3E-05
AT1G30750	*AT1G30750*	TPRXL	1.0	9.1E-01	9.5E-01	-2.0	9.9E-05	3.2E-03
AT5G15290	*CASP5*	Uncharacterized protein family (UPF0497)	-1.4	5.8E-02	1.3E-01	-2.0	2.5E-04	6.1E-03
AT1G04240	*SHY2*	AUX/IAA transcriptional regulator family protein	-1.9	2.8E-04	1.7E-03	-2.0	8.5E-05	2.9E-03
AT5G15900	*TBL19*	TRICHOME BIREFRINGENCE-LIKE 19	2.0	3.3E-04	1.9E-03	-2.0	6.2E-04	1.2E-02
AT1G64390	*GH9C2*	glycosyl hydrolase 9C2	-1.3	7.8E-02	1.6E-01	-2.0	3.2E-06	3.1E-04
AT3G04360	*AT3G04360*	Calcium-dependent lipid-binding (CaLB domain) family protein	-2.0	4.4E-03	1.7E-02	-2.0	2.7E-03	3.1E-02
AT4G39800	*MIPS1*	myo-inositol-1-phosphate synthase 1	-1.4	2.6E-02	6.9E-02	-2.0	6.8E-06	5.4E-04
AT1G52290	*PERK15*	Protein kinase superfamily protein	1.6	1.0E-05	1.0E-04	-2.0	4.3E-08	1.6E-05
AT3G50570	*AT3G50570*	hydroxyproline-rich glycoprotein family protein	1.4	3.9E-02	9.6E-02	-2.0	1.3E-04	3.9E-03
AT2G06850	*XTH4*	xyloglucan endotransglucosylase/hydrolase 4	-1.6	1.8E-03	8.1E-03	-2.0	3.6E-05	1.6E-03
AT4G09890	*AT4G09890*	mediator of RNA polymerase II transcription subunit, putative (DUF3511)	-1.6	1.3E-03	6.1E-03	-2.0	4.7E-06	4.2E-04
AT3G50890	*HB28*	homeobox protein 28	-2.1	7.0E-04	3.6E-03	-2.0	8.4E-04	1.4E-02
AT2G12462	*AT2G12462*	sterile alpha motif (SAM) domain protein	-1.3	1.6E-02	4.8E-02	-2.0	1.0E-07	2.8E-05
AT2G34490	*CYP710A2*	cytochrome P450, family 710, subfamily A, polypeptide 2	-1.2	4.4E-01	5.9E-01	-2.0	6.3E-04	1.2E-02
AT1G33170	*AT1G33170*	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	1.4	5.6E-02	1.3E-01	-2.0	1.2E-03	1.7E-02
AT1G64660	*MGL*	methionine gamma-lyase	-1.9	9.5E-04	4.7E-03	-2.0	3.1E-04	7.1E-03
AT2G43535	*AT2G43535*	Scorpion toxin-like knottin superfamily protein	-2.0	1.6E-03	7.1E-03	-2.0	1.5E-03	2.1E-02
AT1G72230	*AT1G72230*	Cupredoxin superfamily protein	-1.3	4.6E-02	1.1E-01	-2.0	4.9E-07	8.2E-05
AT5G44210	*ERF9*	erf domain protein 9	-2.0	1.3E-04	8.6E-04	-2.0	1.2E-04	3.5E-03
AT4G34710	*ADC2*	arginine decarboxylase 2	-1.3	9.0E-02	1.8E-01	-2.0	2.2E-05	1.1E-03
AT5G04370	*NAMT1*	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	-1.5	2.7E-02	7.1E-02	-2.0	3.8E-04	8.1E-03