

Supplementary Table S8. Overlapped genes between Cd and Cu stressors in different stress intensities.

Gene ID	Description	Average log ₂ FC value under mild				Average log ₂ FC value under			
		Al	Cd	Cu	Na	Al	Cd	Cu	Na
Common in severe and mild stress									
AT1G01680	U-box domain-containing protein 54	4.4	3.8	2.6	1.9	4.0	3.7	3.8	3.0
AT1G09080	protein BIP3	3.9	7.0	6.3	1.2	1.1	6.6	4.0	1.4
AT1G11925	stigma-specific stig1 family protein	2.9	3.3	6.0	-0.2	0.4	4.9	5.6	1.1
AT1G26420	FAD-binding and BBE domain-containing protein	2.5	3.2	2.4	2.0	2.3	4.5	3.6	3.0
AT1G35910	probable trehalose-phosphate phosphatase D	3.7	2.4	2.1	0.8	3.6	3.3	4.6	2.0
AT1G57630	Toll-Interleukin-Resistance domain-containing protein	3.7	4.0	4.2	1.8	2.4	4.5	5.1	2.9
AT1G64160	dirigent-like protein DIR5	4.3	5.4	6.6	3.3	2.6	6.0	5.1	4.1
AT1G66090	TIR-NBS class of disease resistance protein	4.0	3.0	2.2	0.2	1.4	3.4	3.9	3.0
AT1G68620	probable carboxylesterase 6	3.7	3.4	3.6	0.6	2.8	4.1	4.4	2.2
AT1G69490	NAC transcription factor protein family	4.8	3.6	3.5	0.9	2.4	4.2	5.2	1.6
AT1G70130	putative L-type lectin-domain containing receptor kinase V.2	5.9	4.5	6.4	1.0	2.9	5.8	5.7	4.5
AT1G70810	Calcium-dependent lipid-binding (CaLB domain) family protein	0.8	2.4	2.3	0.4	1.9	3.8	3.9	1.6
AT1G72900	Toll-Interleukin-Resistance domain-containing protein	1.6	2.8	2.7	1.1	1.9	4.5	3.8	1.6
AT1G73260	kunitz trypsin inhibitor 1	3.5	2.8	5.3	0.1	2.1	4.9	5.9	1.4
AT1G79680	wall-associated receptor kinase-like 10	3.7	2.9	5.9	2.1	0.4	3.0	3.4	0.8
AT2G02930	glutathione S-transferase F3	2.4	3.6	4.6	1.3	2.6	4.4	4.4	3.1
AT2G02990	ribonuclease 1	4.5	3.3	2.4	0.1	3.9	3.8	5.4	3.4
AT2G15780	Cupredoxin superfamily protein	4.6	4.4	6.3	0.6	2.2	6.3	5.9	3.8
AT2G18150	peroxidase 15	1.6	3.2	3.1	0.9	1.7	4.2	4.1	2.4
AT2G18690	hypothetical protein	2.0	2.6	2.1	-0.2	2.2	4.2	4.7	1.9
AT2G24850	tyrosine aminotransferase 3	4.4	4.1	4.5	1.4	2.5	4.3	4.6	2.9
AT2G26530	hypothetical protein	2.6	2.1	3.2	1.0	2.3	4.1	5.0	3.4
AT2G26560	phospholipase A 2A	3.5	4.4	5.7	1.6	2.1	6.0	7.1	1.7
AT2G29460	glutathione S-transferase tau 4	4.0	2.8	5.1	-0.1	5.9	6.3	6.5	3.2
AT2G35980	protein NDR1/HIN1-like 10	3.3	2.6	4.2	0.0	1.4	4.8	5.7	2.6
AT2G39400	alpha/beta-Hydrolases superfamily protein	3.1	3.1	2.3	0.9	2.4	4.7	5.4	3.3
AT2G42360	E3 ubiquitin-protein ligase ATL41	1.8	2.9	2.7	0.8	1.6	4.6	3.6	1.9
AT3G01420	alpha-dioxygenase	3.5	2.6	2.6	0.5	2.4	2.8	3.0	1.6
AT3G04070	NAC domain containing protein 47	4.7	3.6	3.2	0.1	4.1	3.6	4.5	1.5
AT3G12500	basic chitinase B	2.3	3.0	4.3	0.6	1.7	4.6	4.3	1.9
AT3G15500	ATAF-like NAC-domain transcription factor	6.0	3.7	5.4	-0.1	2.4	3.7	5.3	3.0
AT3G16530	legume lectin-like protein	4.2	2.3	5.1	1.0	1.7	3.7	5.9	2.0
AT3G21520	DUF679 domain membrane protein 1	3.8	3.9	4.6	0.2	0.6	3.5	4.8	0.5
AT3G22910	putative calcium-transporting ATPase 13	4.8	3.9	3.2	2.3	2.9	3.7	3.1	3.2
AT3G23250	myb domain protein 15	2.6	3.2	3.2	1.2	1.7	4.1	4.0	2.7
AT3G44860	farnesoic acid carboxyl-O-methyltransferase	4.5	4.1	6.0	1.1	1.2	3.9	4.5	3.4
AT3G44870	S-adenosyl-L-methionine-dependent methyltransferase	3.5	2.8	4.0	1.2	1.9	4.2	4.9	3.1
AT3G46080	zinc finger protein ZAT8	4.0	3.5	3.5	1.2	3.2	4.1	3.9	4.3
AT3G47340	asparagine synthetase [glutamine-hydrolyzing]	4.9	4.0	4.2	3.1	3.8	4.0	5.0	1.6
AT3G47480	putative calcium-binding protein CML47	4.3	3.8	2.8	1.1	3.8	4.7	4.0	2.5
AT3G55970	jasmonate-regulated protein JRG21	3.3	2.5	3.3	-0.1	2.0	3.8	3.4	1.8
AT3G60120	beta glucosidase 27	2.2	2.5	4.2	1.1	1.1	4.1	3.6	2.9
AT4G01360	BYPASS1-related protein	3.6	2.4	2.7	0.2	3.1	3.8	5.4	3.6
AT4G01870	tolB-related protein	1.6	2.2	2.1	0.6	1.8	4.3	3.4	2.6
AT4G02520	glutathione S-transferase F2	2.4	2.8	3.3	1.1	2.3	3.3	3.4	2.6
AT4G11170	putative disease resistance protein	1.6	3.6	2.4	1.2	0.3	3.7	3.3	1.8
AT4G11650	osmotin-like protein OSM34	2.7	3.2	4.4	0.9	2.2	4.8	5.0	1.6
AT4G16260	putative beta-1,3-endoglucanase	0.7	2.3	6.0	0.8	-0.4	5.7	6.0	2.6
AT4G21840	methionine sulfoxide reductase B8	1.9	2.7	3.1	0.5	1.5	3.8	3.6	1.5
AT4G22690	cytochrome P450, family 706, subfamily A, polypeptide 1	2.0	2.8	3.6	1.3	2.1	4.3	4.5	2.1

AT4G22710	cytochrome P450, family 706, subfamily A, polypeptide 2	2.0	2.3	2.8	1.4	1.7	3.5	3.5	1.9
AT4G36430	peroxidase 49	2.6	3.5	3.0	0.9	3.1	4.3	4.0	2.5
AT4G37290	hypothetical protein	3.9	2.8	4.3	1.8	1.0	3.6	4.4	0.8
AT5G05340	peroxidase 52	4.9	4.1	4.9	3.6	4.3	5.2	5.5	3.0
AT5G06720	peroxidase 53	2.7	2.7	2.7	0.4	2.3	3.5	3.6	1.0
AT5G06730	peroxidase 54	1.5	2.7	4.2	0.5	2.3	4.4	3.6	1.8
AT5G13080	putative WRKY transcription factor 75	5.2	4.5	5.2	0.7	3.4	6.4	6.3	2.4
AT5G13320	4-substituted benzoates-glutamate ligase GH3.12	2.7	3.1	2.6	0.6	3.4	3.8	3.6	2.9
AT5G19880	peroxidase	2.9	4.2	3.9	3.3	3.1	4.9	5.7	3.1
AT5G22300	bifunctional nitrilase/nitrile hydratase NIT4	3.4	2.9	4.6	1.4	3.6	4.3	5.2	3.2
AT5G39100	germin-like protein 6	2.0	5.5	5.7	1.6	2.6	5.7	3.8	2.6
AT5G39610	NAC-domain transcription factor	3.7	2.4	2.4	0.4	3.1	4.6	5.0	1.7
AT5G40000	AAA-type ATPase family protein	3.7	4.8	4.9	0.9	3.9	6.0	6.2	3.8
AT5G40010	AAA-ATPase 1	6.2	4.7	3.8	0.6	4.4	4.3	3.8	1.8
AT5G42380	calcium-binding protein CML37	4.1	2.8	2.9	0.8	1.7	3.7	3.6	3.6
AT5G43580	unusual seine protease inhibitor	2.5	2.1	2.7	0.0	1.8	3.6	6.0	0.9
AT5G44400	FAD-binding and BBE domain-containing protein	1.8	3.3	2.6	0.2	1.8	4.4	3.4	1.9
AT5G49450	basic leucine-zipper 1	4.4	2.9	4.3	0.8	1.6	3.6	4.4	1.9
AT5G52390	PAR1 protein	3.1	4.3	4.4	-0.3	3.1	5.8	6.3	3.1
AT5G52760	copper transport family protein	2.6	4.9	4.9	2.5	2.9	4.5	3.8	4.9

Specific in severe stress

AT1G01480	1-aminocyclopropane-1-carboxylate synthase 2	-1.6	0.6	1.4	0.1	0.2	3.2	4.0	2.1
AT1G02220	NAC domain-containing protein 3	1.7	2.0	1.9	0.3	0.9	3.2	3.3	1.1
AT1G02920	glutathione S-transferase F7	-0.2	1.8	2.1	1.5	0.9	4.0	4.1	1.9
AT1G02930	glutathione S-transferase F6	0.1	1.5	2.3	1.4	1.6	4.0	4.4	2.4
AT1G13340	Regulator of Vps4 activity in the MVB pathway protein	2.4	0.8	1.4	0.2	2.6	3.4	4.5	1.7
AT1G13520	hypothetical protein	2.7	1.8	1.8	0.4	1.4	3.0	3.9	1.8
AT1G14540	peroxidase 4	0.0	2.1	0.2	0.8	0.3	3.5	4.8	3.0
AT1G17170	glutathione S-transferase TAU 24	1.4	1.2	0.5	0.3	3.0	3.8	4.8	2.2
AT1G17380	protein TIFY 11A	1.4	0.2	2.5	0.1	1.8	3.0	4.2	2.5
AT1G18570	myb domain protein 51	0.5	1.4	1.6	0.6	1.4	3.3	3.7	1.8
AT1G19020	hypothetical protein	3.4	2.5	2.1	0.8	1.3	3.1	3.5	1.0
AT1G19180	jasmonate-zim-domain protein 1	0.8	0.4	1.7	-0.3	1.4	2.8	3.5	1.7
AT1G26380	FAD-binding and BBE domain-containing protein	0.1	2.6	1.9	2.0	0.7	3.3	4.9	2.3
AT1G26400	FAD-binding Berberine family protein	0.4	1.3	1.1	0.8	0.7	4.4	3.4	0.6
AT1G27730	zinc finger protein STZ/ZAT10	1.1	1.3	1.3	0.3	1.3	3.3	3.5	2.9
AT1G28190	hypothetical protein	0.9	0.9	1.4	0.5	1.8	3.2	4.0	1.3
AT1G28380	protein necrotic spotted lesions 1	0.7	0.9	0.9	0.2	0.4	2.8	3.1	1.5
AT1G28480	glutaredoxin-GRX480	2.0	1.8	2.7	0.5	2.7	3.5	3.8	3.6
AT1G29290	hypothetical protein	0.9	1.1	0.7	-0.1	1.6	3.0	3.9	1.0
AT1G30040	gibberellin 2-beta-dioxygenase 2	0.8	1.6	1.3	0.8	1.4	3.5	4.2	1.9
AT1G31290	argonaute 3	2.9	2.3	3.2	0.7	1.5	3.4	3.3	1.8
AT1G48000	myb domain protein 112	3.2	2.0	2.0	-0.2	3.1	3.7	3.5	1.6
AT1G55020	lipoxygenase 1	2.2	0.7	2.3	0.0	1.8	4.0	5.1	1.3
AT1G57990	purine permease 18	2.5	1.3	1.1	0.3	1.8	2.7	4.0	1.1
AT1G58420	hypothetical protein	0.3	1.9	1.8	0.4	0.5	3.4	4.3	2.1
AT1G60730	probable aldo-keto reductase 5	1.2	2.4	1.9	0.7	2.0	4.1	3.9	2.0
AT1G61820	beta glucosidase 46	2.0	1.0	2.3	-0.3	1.6	3.0	5.8	1.3
AT1G64660	methionine gamma-lyase	1.0	1.0	1.5	0.2	0.9	2.8	4.1	0.2
AT1G67810	sulfur E2	1.7	1.4	1.8	0.4	2.3	2.8	3.0	0.8
AT1G69920	glutathione S-transferase TAU 12	0.7	1.6	1.6	0.7	2.4	4.2	4.7	2.4
AT1G69930	glutathione S-transferase TAU 11	2.0	2.3	3.1	0.5	2.1	4.0	5.1	1.9
AT1G74360	putative LRR receptor-like serine/threonine-protein kinase	0.7	1.2	1.0	0.5	0.8	3.3	4.0	1.3
AT1G76600	hypothetical protein	1.3	1.3	1.3	0.4	1.9	3.9	5.0	3.4
AT1G76650	calcium-binding protein CML38	2.5	1.0	1.4	0.1	1.7	3.2	4.4	2.1
AT1G80840	putative WRKY transcription factor 40	0.7	2.0	3.4	0.6	1.1	3.9	4.0	2.8
AT2G22760		0.9	0.1	2.9	0.0	0.8	2.8	4.9	2.1
AT2G22860	phytosulfokine-beta	0.6	1.5	3.8	-0.3	0.6	4.3	3.8	2.2
AT2G24180	cytochrome P450 71B6	0.9	1.4	1.5	0.7	1.0	3.1	3.8	1.3

AT2G25460	hypothetical protein	2.2	1.6	1.7	0.2	1.9	3.9	4.1	2.4
AT2G26380	leucine-rich repeat-containing protein	2.3	1.0	4.3	0.5	2.0	4.3	5.2	2.4
AT2G29450	glutathione S-transferase tau 5	2.7	0.5	1.9	0.7	2.4	2.9	4.6	1.8
AT2G30140	UDP-glycosyltransferase 87A2	2.1	1.8	1.0	0.3	2.4	3.6	3.9	1.6
AT2G30750	cytochrome P450 71A12	-0.5	2.6	1.3	1.7	2.1	4.0	5.2	2.0
AT2G32190	hypothetical protein	3.6	1.7	1.6	0.4	2.9	3.0	4.0	1.6
AT2G38340	dehydration-responsive element-binding protein 2E	5.7	1.5	3.1	0.1	2.8	3.4	4.1	1.1
AT2G40000	HS1 PRO-1 2-like protein	3.0	1.4	2.2	0.2	2.7	3.4	4.4	2.3
AT2G41100	calmodulin-like protein 4	1.4	2.3	1.9	1.4	2.6	4.2	4.1	3.2
AT2G42980	aspartyl protease-like protein	-0.3	0.8	0.2	0.4	0.5	3.3	3.3	1.4
AT2G48090	hypothetical protein	2.2	1.4	2.4	0.1	2.3	3.3	2.9	1.0
AT3G02840	hypothetical protein	1.6	2.2	2.1	0.7	1.4	4.0	4.8	3.6
AT3G04720	pathogenesis-related 4	1.9	1.2	4.1	0.2	1.4	4.1	4.9	1.6
AT3G06490	putative transcription factor MYB108	3.2	1.6	2.1	-0.6	2.1	4.0	4.2	2.0
AT3G13650	disease resistance-responsive, dirigent domain-containing protein	1.2	1.5	1.7	0.1	2.0	2.9	4.5	0.9
AT3G21690	MATE efflux family protein	1.9	1.5	1.1	0.3	2.2	3.0	3.2	0.7
AT3G22160	VQ motif-containing protein	0.8	1.3	1.2	0.2	1.3	3.0	3.0	1.3
AT3G26830	protein PHYTOALEXIN DEFICIENT 3	0.8	1.6	2.7	0.7	1.4	4.1	3.6	2.2
AT3G28210	zinc finger (AN1-like) family protein	4.3	2.0	1.8	0.4	3.4	3.7	4.4	1.8
AT3G28580	AAA-type ATPase family protein	0.7	2.5	1.6	1.2	1.9	3.7	3.1	2.6
AT3G47380	plant invertase/pectin methylesterase inhibitor superfamily protein	-1.3	1.7	1.6	-0.5	-1.3	3.6	3.8	0.7
AT3G49620	2-oxoacid-dependent dioxygenase-like protein DIN11	-0.9	1.5	6.6	1.4	-0.2	5.7	5.4	4.3
AT3G53600	C2H2-type zinc finger protein	3.5	1.9	3.4	0.5	2.3	5.1	4.6	3.5
AT3G54150	S-adenosyl-L-methionine-dependent methyltransferase-like protein	2.1	2.5	2.2	0.9	3.1	4.1	4.5	2.1
AT3G62150	ABC transporter B family member 21	0.6	0.6	1.3	0.2	0.6	2.9	3.0	0.7
AT4G11280	1-aminocyclopropane-1-carboxylate synthase 6	0.2	0.6	0.9	-0.1	1.0	3.8	4.0	2.5
AT4G15610	hypothetical protein	1.6	0.9	0.5	0.1	1.5	2.6	3.6	0.6
AT4G17500	ethylene-responsive transcription factor 1A	1.3	1.3	1.7	-0.1	1.5	3.2	4.1	1.8
AT4G19460	UDP-glycosyltransferase family protein	-0.2	0.4	0.6	0.0	0.5	3.6	3.7	1.0
AT4G22610	protease inhibitor/seed storage/lipid transfer family protein	2.4	1.3	2.6	-0.2	2.9	4.0	4.6	3.4
AT4G24380	hypothetical protein	0.8	0.3	0.6	0.3	1.2	3.2	3.5	2.0
AT4G33050	calmodulin-binding protein	1.1	2.3	1.6	0.9	1.4	3.2	4.0	1.6
AT4G36500	hypothetical protein	0.5	0.9	1.4	0.5	1.0	3.0	3.8	1.8
AT4G37370	cytochrome P450, family 81, subfamily D, polypeptide 8	-0.8	1.0	0.4	0.4	1.4	4.3	4.3	3.3
AT5G01380	trihelix transcription factor GT-3a	3.3	2.1	1.9	0.6	2.9	4.0	4.6	3.3
AT5G06320	NDR1/HIN1-Like protein 3	3.8	1.6	1.1	0.3	2.8	3.4	4.0	1.8
AT5G08790	protein ATAF2	1.4	1.7	1.3	0.1	2.3	3.5	3.8	2.2
AT5G13220	protein TIFY 9	3.6	2.0	5.3	0.3	0.7	2.7	3.4	1.8
AT5G19110	Eukaryotic aspartyl protease family protein	1.3	0.4	3.0	0.1	1.3	2.9	4.5	2.7
AT5G24140	squalene monooxygenase 2	1.0	1.0	2.1	0.2	2.2	3.1	4.1	2.0
AT5G26340	sugar transport protein 13	2.3	1.3	2.8	0.6	2.3	2.9	4.5	1.6
AT5G28510	beta glucosidase 24	1.8	0.7	4.1	-1.1	1.8	4.4	5.3	1.9
AT5G35735	putative auxin-responsive protein	1.1	1.4	2.3	0.2	1.2	4.1	4.3	1.8
AT5G36970	NDR1/HIN1-like 25	3.7	2.1	3.5	1.3	0.7	3.2	4.0	0.5
AT5G39580	peroxidase 62	1.5	2.6	1.4	0.2	1.3	3.3	5.3	2.8
AT5G39670	putative calcium-binding protein CML45	2.6	2.8	1.6	1.2	3.1	3.9	3.3	2.3
AT5G44620	cytochrome P450, family 706, subfamily A, polypeptide 3	1.3	1.5	2.2	0.8	1.2	3.5	3.7	1.5
AT5G46350	putative WRKY transcription factor 8	3.3	1.3	3.0	0.7	1.4	3.1	3.7	2.5
AT5G47070	protein kinase family protein	0.8	1.2	0.8	0.3	1.6	3.4	3.4	1.6
AT5G49620	myb domain protein 78	3.5	1.4	2.7	-1.0	1.9	3.6	4.2	0.3
AT5G49690	UDP-glycosyltransferase 91C1	2.9	1.8	1.6	0.0	1.0	2.7	3.6	0.3
AT5G57220	cytochrome P450, family 81, subfamily F, polypeptide 2	-0.7	1.1	0.6	1.5	0.2	3.5	3.8	2.7
AT5G59490	haloacid dehalogenase-like hydrolase (HAD) superfamily protein	2.7	1.7	1.5	0.4	3.2	3.2	4.0	1.9

AT5G64750	ethylene-responsive transcription factor ABR1	1.8	0.7	0.5	0.2	1.9	2.9	3.1	1.5
AT5G65600	concanavalin A-like lectin kinase-like protein	1.3	2.0	2.1	1.4	0.5	3.4	3.1	1.5
AT5G67340	ARM repeat superfamily protein	1.6	2.5	1.8	0.4	2.2	4.2	3.9	1.6
specific in mild stress									
AT1G04370	ethylene-responsive transcription factor 14	1.8	2.1	5.1	-1.0	-0.1	2.6	1.6	0.6
AT1G06520	sn-glycerol-3-phosphate 2-O- acyltransferase	2.6	4.1	4.6	0.0	0.6	3.9	3.1	0.3
AT1G07900	LOB domain-containing protein 1	2.7	4.2	3.5	0.6	0.9	1.2	0.4	0.4
AT1G08050	C3HC4-type RING finger-containing protein	1.5	2.3	2.2	0.7	0.5	1.9	2.1	0.5
AT1G08080	alpha carbonic anhydrase 7	3.0	3.1	3.6	0.4	0.6	3.9	2.8	2.4
AT1G08100	nitrate transporter 2.2	1.4	4.1	3.1	0.8	1.3	3.5	0.5	0.9
AT1G08430	aluminum-activated malate transporter 1	6.5	3.8	3.4	1.3	6.3	-0.3	0.3	1.1
AT1G08630	threonine aldolase	0.4	2.7	4.2	1.0	-0.4	1.2	5.3	0.1
AT1G09935	phosphoglycerate mutase-like protein	0.9	2.4	3.7	0.0	0.0	1.9	0.5	1.0
AT1G11330	G-type lectin S-receptor-like serine/threonine-protein kinase	1.6	2.2	2.4	0.0	1.5	2.9	1.1	1.0
AT1G15610	hypothetical protein	4.4	5.2	4.5	0.7	0.3	0.4	0.1	-0.1
AT1G15620		1.1	3.3	2.9	0.9	0.2	2.3	1.4	-0.2
AT1G17420	lipoxygenase 3	2.6	2.6	4.1	0.4	0.5	2.2	5.3	2.4
AT1G18970	germin-like protein 4	1.9	3.8	3.6	1.1	1.0	3.3	2.8	1.7
AT1G18980	germin-like protein subfamily T member 2	2.7	3.0	2.6	0.6	1.4	3.1	2.5	1.3
AT1G19960	hypothetical protein	2.9	3.5	3.3	0.7	3.3	2.4	3.8	1.4
AT1G20180	hypothetical protein	5.5	2.5	5.2	0.3	0.3	0.5	0.8	0.0
AT1G20310	hypothetical protein	3.8	2.4	4.3	0.7	1.4	2.9	3.0	4.2
AT1G21240	wall-associated receptor kinase 3	0.1	4.1	3.8	-0.7	0.7	3.1	0.7	-0.4
AT1G21400	thiamin diphosphate-binding fold protein	5.1	3.9	4.8	1.1	1.8	2.5	5.5	0.9
AT1G23730	beta carbonic anhydrase 3	1.3	4.5	3.7	-0.3	-0.6	2.2	0.7	0.0
AT1G23840	hypothetical protein	1.5	3.0	2.5	0.0	0.4	3.3	0.5	0.3
AT1G26390	FAD-binding Berberine family protein	2.0	4.1	3.2	1.0	0.9	2.7	3.5	-0.2
AT1G26410	FAD-binding and BBE domain- containing protein	1.6	2.6	2.1	2.5	0.0	1.5	1.4	1.2
AT1G29860	putative WRKY transcription factor 71	2.1	3.1	2.3	1.2	1.0	3.9	1.6	1.9
AT1G30100	9-cis-epoxycarotenoid dioxygenase	0.8	2.4	2.4	-0.7	0.9	2.7	0.4	0.8
AT1G35210	hypothetical protein	1.8	2.4	2.6	1.1	0.6	2.9	2.5	1.5
AT1G35513		2.1	3.0	2.2	1.2	3.4	3.1	0.7	2.8
AT1G44010	hypothetical protein	-2.3	3.3	3.4	0.3	-1.2	0.9	-0.2	-0.3
AT1G47890	receptor like protein 7	2.8	3.1	2.6	1.1	1.8	4.4	2.1	0.1
AT1G52100	jacalin-like lectin domain-containing protein	1.3	3.2	2.9	0.0	0.0	2.2	2.2	0.4
AT1G52130	mannose-binding lectin-like protein	2.5	3.7	3.6	0.2	3.2	3.5	0.9	0.2
AT1G52890	NAC domain-containing protein 19	5.5	3.8	4.8	0.5	1.8	2.9	4.2	0.7
AT1G55230	hypothetical protein	6.0	5.3	5.5	2.3	3.8	3.5	1.2	0.9
AT1G58300	heme oxygenase 4	4.3	5.2	3.6	1.6	1.6	0.3	0.8	-0.1
AT1G61810	beta-glucosidase 45	1.1	2.4	3.2	0.0	0.2	0.7	3.4	0.2
AT1G65500	hypothetical protein	0.4	4.0	4.6	1.0	0.0	3.3	0.2	0.7
AT1G67980	caffeoyl-CoA 3-O-methyltransferase	3.1	2.5	3.2	1.3	0.9	3.0	4.8	1.4
AT1G70260	nodulin MtN21-like transporter UMAMIT36	2.5	3.9	3.5	2.2	0.1	-0.3	-0.3	0.3
AT1G73220	organic cation/carnitine transporter1	7.6	5.0	4.8	0.4	4.5	-0.7	-1.5	-1.1
AT1G73800	protein SAR Deficient 1	1.0	2.8	2.4	1.3	1.4	2.7	1.8	3.7
AT1G73805	protein SAR Deficient 1	2.5	3.8	3.2	1.8	0.1	0.6	0.4	0.8
AT1G73810	core-2/I-branching beta-1,6-N- acetylglucosaminyltransferase-like protein	4.9	3.4	2.5	1.1	0.6	2.0	0.7	0.2
AT1G74140	Rhomboid-related intramembrane serine protease family protein	1.9	3.9	3.1	-0.5	0.7	0.2	0.8	-0.7
AT1G74190	receptor like protein 15	1.5	2.6	2.9	0.2	-0.1	0.4	0.1	-0.1
AT1G74710	Isochorismate synthase 1	2.4	3.1	2.2	0.7	3.8	3.7	1.5	2.9
AT1G76430	putative inorganic phosphate transporter 1-9	1.3	3.6	3.1	0.9	-0.5	0.6	0.8	0.4
AT1G80160	GLYOXYLASE I 7	4.8	2.6	4.6	0.7	1.0	1.5	4.4	0.2

AT1G80590	putative WRKY transcription factor 66	2.1	3.3	4.9	0.4	0.3	1.4	0.8	0.0
AT2G02010	glutamate decarboxylase 4	2.1	2.9	3.7	0.9	0.8	2.4	3.3	1.8
AT2G02250	phloem protein 2-B2	3.8	3.4	2.8	0.4	2.5	2.2	1.0	0.7
AT2G17040	NAC transcription factor family protein NAC036	1.0	3.1	3.0	0.6	1.0	5.3	1.1	2.3
AT2G18660	plant natriuretic peptide A	1.7	4.8	4.9	2.3	1.4	4.2	0.2	2.0
AT2G25510	hypothetical protein	1.2	5.4	4.3	0.6	0.1	-0.2	0.5	-0.1
AT2G28270	cysteine/histidine-rich C1-like domain- containing protein	3.8	4.1	3.4	0.6	-0.6	-0.2	-0.9	1.2
AT2G29150	tropinone reductase-like protein	0.4	2.8	3.9	0.1	0.0	2.6	1.3	0.3
AT2G29470	glutathione S-transferase tau 3	4.1	3.1	4.7	-0.2	2.1	1.9	3.3	-1.0
AT2G30670	NAD(P)-binding Rossmann-fold superfamily protein	1.4	4.6	3.4	-1.9	1.5	2.0	1.1	-0.1
AT2G32130	hypothetical protein	2.8	2.2	2.2	0.7	1.2	0.8	2.7	0.9
AT2G32140	transmembrane receptor protein	3.6	2.8	2.7	1.1	2.6	3.5	5.4	2.5
AT2G34580	hypothetical protein	1.5	2.6	4.0	0.7	-0.1	0.5	0.3	0.0
AT2G38240	2-oxoglutarate (2OG) and Fe(II)- dependent oxygenase-like protein	5.1	3.4	4.0	1.0	1.8	3.8	5.4	1.4
AT2G43510	trypsin inhibitor protein 1	5.8	4.0	4.3	2.1	3.7	3.1	5.4	1.8
AT2G43580	chitinase family protein	4.4	2.3	3.7	0.2	1.2	0.4	0.8	1.1
AT2G43590	chitinase family protein	4.3	2.4	3.5	0.5	1.8	0.9	1.3	2.0
AT2G44460	beta glucosidase 28	1.9	5.8	2.6	0.2	0.1	3.0	0.8	0.1
AT2G44840	ethylene-responsive transcription factor 13	2.5	2.8	3.4	1.1	0.8	2.4	1.7	3.8
AT2G46400	putative WRKY transcription factor 46	2.5	2.2	2.3	0.5	1.2	1.0	1.3	1.7
AT3G03670	peroxidase	0.1	2.9	3.0	0.4	-1.7	1.8	3.0	1.8
AT3G04210	TIR-NBS class disease resistance protein	3.1	2.5	5.2	0.6	0.1	2.6	0.8	0.4
AT3G10930	hypothetical protein	2.5	2.7	2.9	0.6	1.5	4.5	3.4	3.1
AT3G12230	serine carboxypeptidase-like 14	4.1	5.4	5.4	1.9	3.1	1.9	1.6	-0.2
AT3G13950	hypothetical protein	3.8	3.6	2.7	1.3	0.3	0.5	0.3	0.1
AT3G23120	receptor like protein 38	0.4	3.9	3.1	-0.1	0.5	3.7	0.9	0.6
AT3G23240	ethylene-responsive transcription factor 1B	1.6	2.6	4.0	-0.8	0.3	3.3	2.1	0.5
AT3G26220	cytochrome P450 71B3	5.2	2.6	3.7	0.1	1.5	2.6	3.1	0.1
AT3G28510	AAA-type ATPase family protein	4.9	5.7	5.1	3.6	4.3	4.2	0.9	1.5
AT3G46090	zinc finger protein ZAT7	3.9	3.2	2.7	0.7	2.0	3.0	3.0	2.7
AT3G48580	probable xyloglucan endotransglucosylase/hydrolase 11	6.2	4.1	4.7	-1.3	2.8	2.8	3.2	0.4
AT3G48850	phosphate transporter 3;2	2.8	3.0	2.6	1.7	0.7	3.0	2.3	1.1
AT3G49120	peroxidase 34	3.2	2.2	2.1	1.2	2.2	2.5	3.1	1.4
AT3G52780	putative purple acid phosphatase 20	5.8	4.7	4.0	0.2	1.5	3.0	1.2	0.4
AT3G53770	late embryogenesis abundant 3 (LEA3) family protein	2.4	4.2	3.2	0.3	-0.9	1.0	0.0	0.1
AT3G53820	C2H2 and C2HC zinc fingers superfamily protein	1.2	2.7	3.1	0.0	0.6	3.3	3.1	0.6
AT3G55090	ABC transporter G family member 16	2.1	2.6	2.2	0.7	0.4	0.2	1.0	0.3
AT3G56710	sigma factor binding protein 1	0.3	2.5	3.0	0.0	0.0	1.6	0.5	0.8
AT3G60140	beta-glucosidase 30	5.9	4.3	4.7	0.8	1.0	1.9	3.9	0.1
AT4G04570	cysteine-rich receptor-like protein kinase 40	1.7	2.7	2.2	0.9	0.2	2.8	1.4	0.4
AT4G10500	oxidoreductase, 2OG-Fe(II) oxygenase family protein	1.4	4.0	3.5	0.7	1.8	3.6	2.4	1.4
AT4G11290	peroxidase 39	0.1	2.2	2.6	-0.3	0.1	3.4	2.0	-0.2
AT4G11340	TIR-NBS-LRR class disease resistance protein	2.8	5.2	4.6	0.7	0.7	2.6	0.9	1.7
AT4G11470	putative cysteine-rich receptor-like protein kinase 31	1.2	2.1	3.0	0.0	0.2	2.0	1.2	0.5
AT4G12290	copper amine oxidase family protein	3.3	2.7	2.6	0.7	1.3	1.6	1.0	0.2
AT4G12470	azelaic acid induced 1	-0.3	3.1	2.6	-0.5	0.2	0.5	0.8	0.0
AT4G13420	potassium transporter 5	3.9	3.4	2.9	-0.2	2.6	-1.1	0.8	4.0
AT4G13890	serine hydroxymethyltransferase 5	1.5	3.2	2.6	0.3	1.2	2.0	0.6	-0.1
AT4G15100	serine carboxypeptidase-like 30	3.5	2.4	5.5	0.6	0.2	0.8	2.7	0.4
AT4G17660	protein kinase family protein	2.9	4.1	3.8	0.5	0.6	2.6	0.6	0.4
AT4G19750	Glycosyl hydrolase family protein with chitinase insertion domain	5.2	5.2	5.4	-0.2	0.6	1.9	1.1	-0.9
AT4G19760	Glycosyl hydrolase family protein with chitinase insertion domain	3.6	4.3	4.7	0.4	0.5	1.6	0.5	-0.6

AT4G19800	Glycosyl hydrolase family protein with chitinase insertion domain	2.8	3.0	3.4	-0.7	-0.8	-1.5	-0.9	-2.1
AT4G21380	receptor kinase 3	1.2	4.8	2.3	1.6	1.2	5.2	3.4	2.0
AT4G21680	nitrate transporter 1.8	-0.4	2.8	3.6	0.2	-0.1	4.4	3.3	0.6
AT4G22020		1.1	2.8	3.1	-0.2	0.2	4.7	3.8	1.1
AT4G23990	cellulose synthase-like protein G3	-0.3	4.4	3.4	0.1	-0.1	0.2	0.1	0.0
AT4G25780	putative pathogenesis-related protein	0.0	3.4	6.6	0.3	-0.8	3.2	4.0	-1.5
AT4G27850	glycine-rich family protein	2.9	4.2	3.3	0.1	1.2	2.3	0.1	-0.5
AT4G29050	Concanavalin A-like lectin protein kinase family protein	2.0	2.8	2.4	1.1	1.5	2.6	2.3	1.8
	xyloglucan								
AT4G30270	endotransglucosylase/hydrolase protein 24	5.7	2.4	2.4	0.7	3.7	2.2	4.0	0.6
AT4G30430	tetraspanin9	4.9	3.3	3.5	0.8	0.8	1.8	2.7	1.1
AT4G31370	FASCICLIN-like arabinogalactan protein 5	3.2	2.5	3.3	0.2	0.0	0.4	0.1	0.1
AT4G32950	putative protein phosphatase 2C 61	3.9	3.4	2.7	0.8	1.4	1.9	2.2	0.8
AT4G33720	putative pathogenesis-related protein	-1.1	3.5	6.5	-0.5	-1.7	2.8	3.3	-2.4
AT4G35180	LYS/HIS transporter 7	1.3	3.6	3.1	1.5	0.4	1.7	1.4	0.7
AT4G35190	cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG5	2.4	3.8	3.1	-0.8	3.6	4.2	3.2	1.1
AT4G35770	senescence-associated protein DIN1	3.9	3.0	4.1	3.1	1.6	1.1	4.7	0.8
AT4G36880	cysteine proteinase1	4.8	2.8	4.4	1.8	2.4	0.5	1.2	1.0
AT4G37430	cytochrome P450 81F1	1.5	2.8	2.5	0.3	1.4	2.3	-0.1	0.7
AT4G37780	myb domain protein 87	0.1	2.8	2.5	0.2	-0.1	3.6	1.7	2.1
AT4G37990	cinnamyl alcohol dehydrogenase 8	3.5	2.7	2.7	-0.5	1.5	2.5	6.3	1.7
AT5G05390	laccase 12	2.4	3.2	2.8	1.2	0.2	0.0	0.9	0.4
AT5G06760	late embryogenesis abundant protein 4-5	5.2	4.1	3.2	-0.2	3.9	2.4	1.4	3.1
AT5G07570	glycine/proline-rich protein	3.8	3.6	3.8	0.6	0.3	-0.4	0.8	0.1
AT5G14760	L-aspartate oxidase	2.2	3.1	2.2	0.0	2.8	2.7	1.0	0.5
AT5G22380	NAC domain-containing protein	0.5	4.3	4.6	0.6	-0.2	1.4	0.7	1.9
AT5G22520	hypothetical protein	2.4	3.7	3.2	2.2	1.7	3.5	2.1	2.8
AT5G22530	hypothetical protein	2.6	4.2	4.3	2.1	1.9	4.1	1.9	2.6
AT5G22570	putative WRKY transcription factor 38	2.9	3.3	3.3	1.6	1.8	2.3	1.0	1.5
AT5G24550	beta glucosidase 32	2.3	2.4	2.9	0.5	0.7	0.9	1.2	1.4
AT5G26170	putative WRKY transcription factor 50	4.6	4.6	3.9	0.6	2.2	4.3	0.3	1.2
AT5G38200	class I glutamine amidotransferase-like protein	3.6	2.6	2.5	0.9	4.2	1.0	2.2	0.9
AT5G38900	Thioredoxin superfamily protein	2.3	3.2	2.6	1.0	1.9	3.4	2.8	1.9
AT5G38910	putative germin-like protein subfamily 1 member 9	7.2	7.1	7.1	1.0	4.4	4.5	1.5	0.4
AT5G39110	germin-like protein subfamily 1 member 14	0.1	4.9	5.6	1.1	0.0	3.0	0.8	0.6
AT5G39120	germin-like protein subfamily 1 member 15	0.6	4.8	5.8	0.5	0.0	1.6	0.1	0.1
AT5G39130	germin-like protein subfamily 1 member 16	1.1	3.5	4.4	0.6	0.2	1.3	0.4	0.5
AT5G39150	germin-like protein subfamily 1 member 17	0.7	5.7	6.6	1.2	1.1	5.3	2.4	2.1
AT5G39160	germin-like protein subfamily 1 member 18	1.2	3.4	4.2	0.4	0.2	1.4	0.2	0.6
AT5G39180	germin-like protein subfamily 1 member 19	0.6	5.0	5.5	1.1	1.1	5.0	2.1	2.0
AT5G39190	germin-like protein 2a	1.2	3.4	4.1	0.4	0.3	1.7	0.2	0.6
AT5G40990	GDSL lipase 1	1.0	3.2	3.9	2.8	0.5	2.9	2.1	2.6
AT5G43650	transcription factor bHLH92	3.9	2.8	3.6	1.3	1.1	2.2	2.1	3.6
AT5G46950	invertase/pectin methylesterase inhibitor family protein	0.4	2.3	2.9	-0.1	0.2	1.1	1.1	-0.4
AT5G47220	ethylene-responsive transcription factor 2	3.0	3.1	3.8	0.4	0.8	2.6	1.9	1.7
AT5G60770	nitrate transporter 2.4	1.6	3.1	2.9	0.0	0.1	-0.3	-0.5	0.3
AT5G64810	putative WRKY transcription factor 51	2.1	3.2	2.5	1.0	2.2	2.4	1.1	1.2
AT5G64870	SPFH/Band 7/PHB domain-containing membrane-associated protein family	1.9	3.0	2.6	0.5	-0.1	-0.6	0.7	0.2
AT5G66670	hypothetical protein	2.3	2.5	2.2	0.4	1.8	2.2	0.3	0.6

Averaged values of fold change in three microarray replicates were shown.