

Supplementary Table 1. Lists of identified DEGs under flooding stress in *Glycine soja* ($\log_2FC > |2|$ & $FDR < 0.05$ filtering).

Gene ID	\log_2 FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114383177	7.17833311	0.0160163	mRNA	alcohol dehydrogenase 1-like
LOC114407491	6.281064195	0.00226777	mRNA	mannan endo-1,4-beta-mannosidase 4-like, transcript variant X1
LOC114374838	5.971491166	0.0189764	mRNA	probable glutathione S-transferase parA
LOC114412220	5.806982622	0.00226777	mRNA	expansin-like B1
LOC114403694	5.716228923	0.0144323	mRNA	NAD(P)H-dependent 6'-deoxychalcone synthase-like
LOC114418576	5.367451738	0.00226777	mRNA	probable sulfate transporter 3.5
LOC114423609	5.325230305	0.0404779	mRNA	hydroquinone glucosyltransferase-like
LOC114406806	5.26712416	0.0118441	mRNA	dirigent protein 1-like
LOC114377381	5.257689149	0.00226777	mRNA	basic 7S globulin-like
LOC114413731	5.129971633	0.00226777	ncRNA	uncharacterized LOC114413731, transcript variant X1
LOC114396242	5.117984816	0.00226777	misc_RNA	uncharacterized LOC114396242, transcript variant X7
LOC114369366	5.09734214	0.00226777	mRNA	probable glutathione S-transferase
LOC114387086	5.041953084	0.0292127	mRNA	serine carboxypeptidase-like
LOC114386739	5.028911234	0.00536398	mRNA	isoflavone 2'-hydroxylase-like
LOC114379247	4.967813181	0.0210997	mRNA	LOB domain-containing protein 1-like
LOC114377295	4.950415454	0.00226777	mRNA	cytochrome P450 82A2
LOC114412825	4.912846408	0.00226777	mRNA	flavonoid 3',5'-methyltransferase-like, transcript variant X2
LOC114406771	4.903367601	0.0167884	mRNA	3,9-dihydroxypterocarpan 6A-monooxygenase
LOC114388688	4.860838222	0.00226777	mRNA	guanosine deaminase-like
LOC114388589	4.845732515	0.021824	mRNA	pleiotropic drug resistance protein 1-like
LOC114384622	4.825505619	0.0329675	mRNA	ethylene-responsive transcription factor ERF003-like, transcript variant X1
LOC114394659	4.807041562	0.0286553	mRNA	probable WRKY transcription factor 26
LOC114420000	4.797836668	0.00226777	mRNA	stress-induced protein SAM22
LOC114425361	4.780982799	0.00226777	mRNA	isoliquiritigenin 2'-O-methyltransferase-like, transcript variant X3
LOC114399435	4.712312175	0.0167884	mRNA	cytochrome P450 82A4-like
LOC114378019	4.70003753	0.0160163	mRNA	apoptosis-inducing factor homolog A-like
LOC114419999	4.689490264	0.00226777	mRNA	stress-induced protein SAM22
LOC114388557	4.667146099	0.00226777	mRNA	stem-specific protein TSJT1-like
LOC114421298	4.658288291	0.047745	mRNA	cytochrome P450 CYP82D47-like
LOC114422805	4.644495541	0.0144323	mRNA	UDP-glycosyltransferase 83A1-like
LOC114399391	4.59210811	0.0319435	ncRNA	uncharacterized LOC114399391
LOC114418616	4.555534738	0.0135986	mRNA	transcription factor BEE 1-like, transcript variant X1
LOC114413541	4.539615263	0.00226777	mRNA	uncharacterized LOC114413541
LOC114382508	4.514596827	0.00226777	mRNA	protein EARLY FLOWERING 4-like
LOC114381093	4.51407282	0.00226777	mRNA	endochitinase
LOC114386375	4.480481244	0.0324602	mRNA	glucan endo-1,3-beta-glucosidase, basic isoform-like
LOC114417220	4.472537016	0.00226777	mRNA	pectinesterase 2-like
LOC114425838	4.467640495	0.0345168	mRNA	isoflavone 2'-hydroxylase-like
LOC114386783	4.424054993	0.042315	mRNA	WRKY transcription factor 42-like
LOC114400814	4.413733236	0.0303111	mRNA	polygalacturonase inhibitor-like
LOC114397461	4.404330305	0.0183026	mRNA	ferritin-1, chloroplastic
LOC114417026	4.403631728	0.00226777	mRNA	uncharacterized LOC114417026, transcript variant X3
LOC114390648	4.397158947	0.0127546	mRNA	probable xyloglucan endotransglucosylase/hydrolase protein B

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114407041	4.357479864	0.00226777	mRNA	glutathione S-transferase L3-like
LOC114392584	4.329637464	0.0410216	mRNA	indole-3-acetic acid-amido synthetase GH3.3-like
LOC114367834	4.315921226	0.00226777	mRNA	repetitive proline-rich cell wall protein 1
LOC114392518	4.309357212	0.00226777	mRNA	stress-induced protein SAM22-like
LOC114395710	4.287785396	0.0175482	mRNA	cationic peroxidase 1-like
LOC114381274	4.24358647	0.0334467	mRNA	12-oxophytodienoate reductase 3-like
LOC114389607	4.239537095	0.021824	mRNA	tryptophan aminotransferase-related protein 4-like
LOC114423209	4.219154175	0.0467714	mRNA	bidirectional sugar transporter SWEET4-like, transcript variant X1
LOC114398414	4.181705695	0.0485337	mRNA	lysine histidine transporter 1-like
LOC114380437	4.172294156	0.00226777	misc_RNA	tropinone reductase-like
LOC114381509	4.123589309	0.0286553	mRNA	bifunctional aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase-like
LOC114369511	4.123222267	0.00226777	mRNA	zinc finger protein CONSTANS-LIKE 16-like
LOC114414800	4.123087081	0.0372252	mRNA	branched-chain-amino-acid aminotransferase 2, chloroplastic-like
LOC114374736	4.119440098	0.047745	mRNA	uncharacterized LOC114374736
LOC114382403	4.118635994	0.00226777	mRNA	cytochrome P450 82A3
LOC114423340	4.117288121	0.047745	mRNA	polygalacturonase inhibitor 2
LOC114394087	4.105878486	0.00226777	mRNA	cytochrome P450 711A1-like
LOC114406038	4.094901769	0.0225301	mRNA	dirigent protein 22-like
LOC114392988	4.089530808	0.00226777	ncRNA	uncharacterized LOC114392988, transcript variant X2
LOC114394516	4.060519322	0.0152251	mRNA	protein NRT1/ PTR FAMILY 7.1-like, transcript variant X3
LOC114399147	3.992787615	0.0473048	mRNA	F-box protein PP2-B15-like
LOC114392387	3.962934313	0.0418668	mRNA	expansin-like B1
LOC114423644	3.955433012	0.00226777	mRNA	kunitz-type trypsin inhibitor KTI1-like
LOC114424387	3.925902752	0.00226777	mRNA	ethylene-responsive transcription factor ERF113-like
LOC114379063	3.913423495	0.0144323	misc_RNA	protein SENSITIVE TO PROTON RHIZOTOXICITY 2-like, transcript variant X1
LOC114367253	3.909500099	0.0297945	mRNA	disease resistance response protein DRRG49-C-like
LOC114412379	3.905142352	0.0238743	mRNA	probable disease resistance protein At5g66900, transcript variant X1
LOC114367352	3.879713773	0.00226777	mRNA	putative uncharacterized protein DDB_G0286901
LOC114408165	3.877344967	0.00226777	mRNA	uncharacterized LOC114408165
LOC114381391	3.871103331	0.00226777	mRNA	mini zinc finger protein 2-like
LOC114399918	3.870051503	0.0481641	mRNA	protein PHYTOCHROME KINASE SUBSTRATE 4-like
LOC114424512	3.869095315	0.038705	mRNA	protein P21-like
LOC114400885	3.852627476	0.0494022	mRNA	histidine-containing phosphotransfer protein 1-like
LOC114387083	3.848560864	0.0414288	mRNA	uncharacterized LOC114387083
LOC114389636	3.847690063	0.00778722	mRNA	kunitz trypsin inhibitor 2-like
LOC114368831	3.847572141	0.00226777	mRNA	dehydrin DHN3-like
LOC114423902	3.843187497	0.0427524	mRNA	glutamate decarboxylase 1-like
LOC114375337	3.814726854	0.0281035	mRNA	1-aminocyclopropane-1-carboxylate synthase-like
LOC114396050	3.814506587	0.00226777	mRNA	uncharacterized LOC114396050
LOC114401336	3.805004193	0.00226777	mRNA	zinc finger protein CONSTANS-LIKE 16-like
LOC114406084	3.793348268	0.00226777	mRNA	ferritin-2, chloroplastic-like
LOC114401647	3.759044261	0.00226777	mRNA	glu S.griseus protease inhibitor-like

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114403842	3.756377242	0.0269311	mRNA	protein ALP1-like
LOC114387398	3.753737969	0.0274825	mRNA	GDSL esterase/lipase 5-like, transcript variant X2
LOC114401688	3.751325967	0.00536398	mRNA	ethylene-responsive transcription factor ERF107-like
LOC114399170	3.748030764	0.0382032	mRNA	lysine histidine transporter 1-like
LOC114382458	3.74760888	0.00226777	mRNA	linoleate 13S-lipoxygenase 2-1, chloroplastic-like
LOC114417018	3.744540047	0.00396241	mRNA	glycinol 4-dimethylallyltransferase-like
LOC114376019	3.732237628	0.00226777	mRNA	asparagine synthetase [glutamine-hydrolyzing] 2
LOC114417407	3.728351508	0.0356535	mRNA	hexose carrier protein HEX6-like, transcript variant X1
LOC114423572	3.726628637	0.00226777	mRNA	uncharacterized LOC114423572
LOC114416771	3.711821599	0.0269311	mRNA	probable LRR receptor-like serine/threonine-protein kinase At1g53430
LOC114390175	3.692191053	0.00396241	mRNA	gamma conglutin 1
LOC114424521	3.689014029	0.00226777	mRNA	thaumatin-like protein 1
LOC114384356	3.682011065	0.0319435	mRNA	vacuolar iron transporter homolog 3-like
LOC114395001	3.650982306	0.0391131	mRNA	MDIS1-interacting receptor like kinase 2-like, transcript variant X2
LOC114401776	3.649668672	0.00226777	mRNA	uncharacterized LOC114401776
LOC114375263	3.63969041	0.0494022	mRNA	uncharacterized LOC114375263
LOC114408635	3.638595421	0.00226777	mRNA	uncharacterized LOC114408635
LOC114406256	3.629596328	0.0203972	mRNA	laccase-7-like
LOC114416600	3.622195709	0.0498622	mRNA	exocyst complex component EXO70B1-like, transcript variant X1
LOC114409392	3.620279937	0.00226777	mRNA	polyphenol oxidase, chloroplastic-like
LOC114398928	3.610434751	0.00396241	mRNA	uncharacterized acetyltransferase At3g50280-like
LOC114374345	3.588198838	0.00226777	mRNA	isoflavone reductase-like
LOC114392737	3.580464418	0.0467714	mRNA	uncharacterized LOC114392737
LOC114386599	3.552682136	0.00226777	mRNA	uncharacterized LOC114386599
LOC114420090	3.541444799	0.00396241	mRNA	uncharacterized LOC114420090
LOC114372907	3.532848862	0.00226777	mRNA	isoflavone reductase-like
LOC114395484	3.518821932	0.0367182	mRNA	jasmonate O-methyltransferase-like, transcript variant X1
LOC114372227	3.515628167	0.0494022	mRNA	putative E3 ubiquitin-protein ligase LIN-1, transcript variant X2
LOC114383655	3.498172243	0.00226777	mRNA	uncharacterized LOC114383655
LOC114390628	3.478428528	0.00226777	mRNA	extensin-2-like
LOC114413229	3.475435309	0.00226777	mRNA	proline-rich extensin-like protein EPR1
LOC114425882	3.465687788	0.0109267	mRNA	cysteine-rich receptor-like protein kinase 7, transcript variant X2
LOC114417455	3.448315693	0.00885696	mRNA	GPI-anchored protein LLG1-like
LOC114393283	3.420252232	0.0449145	misc_RNA	G-type lectin S-receptor-like serine/threonine-protein kinase SD1-1, transcript variant X7
LOC114416399	3.417360899	0.00396241	mRNA	ferritin-2, chloroplastic
LOC114397614	3.412734757	0.00226777	mRNA	NAD(P)H-dependent 6'-deoxychalcone synthase-like
LOC114419470	3.402856197	0.0481641	mRNA	G-type lectin S-receptor-like serine/threonine-protein kinase B120
LOC114370245	3.401231567	0.00885696	mRNA	probable WRKY transcription factor 47, transcript variant X2
LOC114385107	3.390622925	0.00226777	mRNA	receptor-like protein Cf-9, transcript variant X2
LOC114385710	3.388899825	0.00226777	mRNA	serine carboxypeptidase-like 31
LOC114410359	3.387600706	0.00662383	mRNA	uncharacterized LOC114410359
LOC114382011	3.380731449	0.00226777	mRNA	probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 11

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114379397	3.375052618	0.0376697	mRNA	cyanogenic beta-glucosidase-like
LOC114389527	3.35472118	0.00226777	mRNA	cytochrome P450 CYP82D47-like
LOC114374372	3.352925078	0.00226777	mRNA	gibberellin 2-beta-dioxygenase 1-like
LOC114392104	3.346121829	0.00226777	mRNA	stress-induced protein SAM22-like
LOC114394484	3.345634574	0.00226777	mRNA	uncharacterized protein DDB_G0271670-like
LOC114393050	3.33398776	0.0203972	mRNA	uncharacterized LOC114393050, transcript variant X1
LOC114392353	3.333334385	0.00226777	mRNA	glutamate receptor 2.8-like
LOC114418984	3.294956169	0.00226777	mRNA	probable glutathione S-transferase
LOC114399612	3.293818874	0.00662383	mRNA	rapid alkalization factor-like
LOC114409944	3.285272811	0.00226777	mRNA	SNF1-related protein kinase regulatory subunit gamma-1-like
LOC114408763	3.254399699	0.00226777	mRNA	zinc finger protein ZAT10-like
LOC114396619	3.234173731	0.00226777	mRNA	probable serine/threonine-protein kinase WNK4, transcript variant X1
LOC114418536	3.232570819	0.00226777	mRNA	bark storage protein A-like
LOC114418873	3.232158004	0.00885696	mRNA	uncharacterized LOC114418873
LOC114370977	3.224015147	0.00536398	mRNA	ethylene-responsive transcription factor ERF107-like
LOC114385144	3.216363558	0.00226777	mRNA	NAD(P)H-dependent 6'-deoxychalcone synthase
LOC114398377	3.212527348	0.00226777	mRNA	mini zinc finger protein 2-like
LOC114402510	3.207758242	0.00885696	mRNA	uncharacterized LOC114402510
LOC114416557	3.207060154	0.00226777	mRNA	thioredoxin-like 1-2, chloroplastic
LOC114419114	3.201688285	0.00662383	mRNA	ferritin, chloroplastic-like
LOC114403898	3.199534779	0.00226777	mRNA	leucine-rich repeat extensin-like protein 6
LOC114399072	3.188063014	0.0175482	mRNA	heat stress transcription factor B-3-like, transcript variant X1
LOC114406809	3.186607183	0.00226777	mRNA	dirigent protein 22-like
LOC114383105	3.184545742	0.00226777	mRNA	ferritin-4, chloroplastic
LOC114420192	3.181982786	0.00662383	mRNA	WRKY transcription factor 6-like
LOC114415140	3.175139119	0.0329675	mRNA	uncharacterized LOC114415140, transcript variant X1
LOC114407533	3.169582555	0.00226777	mRNA	uncharacterized LOC114407533
LOC114393309	3.15857818	0.00396241	mRNA	CASP-like protein 1D1
LOC114422854	3.15693727	0.00226777	mRNA	extensin-like
LOC114397382	3.155657349	0.00885696	mRNA	uncharacterized LOC114397382
LOC114388268	3.154136343	0.00226777	mRNA	pleiotropic drug resistance protein 1-like
LOC114378500	3.129488766	0.00536398	mRNA	tropinone reductase homolog At5g06060-like
LOC114423048	3.127918644	0.00226777	mRNA	probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic
LOC114422590	3.116175102	0.00226777	mRNA	cytochrome P450 CYP736A12-like, transcript variant X2
LOC114397577	3.095758783	0.0109267	mRNA	protein NRT1/ PTR FAMILY 2.13-like
LOC114423812	3.089937668	0.00885696	mRNA	L-lactate dehydrogenase B-like
LOC114403385	3.087183431	0.00662383	mRNA	respiratory burst oxidase homolog protein B-like
LOC114396694	3.08533769	0.00226777	mRNA	proline dehydrogenase 2, mitochondrial-like
LOC114373520	3.083141365	0.00226777	mRNA	cytochrome P450 81E8-like
LOC114378137	3.080442301	0.00778722	mRNA	NAC domain-containing protein 72-like
LOC114400548	3.076691463	0.00885696	mRNA	respiratory burst oxidase homolog protein B-like
LOC114399954	3.075354598	0.00226777	mRNA	pro-hevein-like
LOC114385423	3.050213161	0.00226777	mRNA	E3 ubiquitin-protein ligase WAV3-like

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114375115	3.048094176	0.0127546	mRNA	fasciclin-like arabinogalactan protein 12
LOC114401628	3.046479683	0.0127546	mRNA	shikimate O-hydroxycinnamoyltransferase-like
LOC114378344	3.043355775	0.00226777	mRNA	uncharacterized LOC114378344
LOC114401563	3.03661569	0.0127546	mRNA	serine/threonine-protein kinase STY46-like, transcript variant X3
LOC114379160	3.031312402	0.00396241	mRNA	fasciclin-like arabinogalactan protein 12
LOC114388216	3.026810366	0.00226777	mRNA	protein EXORDIUM-like 2
LOC114372315	3.022865592	0.00885696	mRNA	ABC transporter C family member 10-like, transcript variant X1
LOC114401272	3.022103894	0.00396241	mRNA	ethylene-responsive transcription factor ERF107-like
LOC114380842	3.021025211	0.00226777	mRNA	uncharacterized LOC114380842
LOC114415501	3.005036914	0.00396241	mRNA	pathogen-related protein-like
LOC114368715	3.000457669	0.009937	mRNA	wall-associated receptor kinase-like 8
LOC114386859	2.990655107	0.00536398	mRNA	beta-fructofuranosidase, cell wall isozyme-like
LOC114412910	2.988276347	0.00226777	mRNA	F-box/kelch-repeat protein At1g15670-like
LOC114374554	2.983944326	0.00226777	mRNA	serine carboxypeptidase-like 31
LOC114376791	2.983775416	0.00226777	mRNA	WRKY transcription factor WRKY24-like
LOC114376983	2.974866131	0.00396241	mRNA	lysine histidine transporter-like 8
LOC114419267	2.973056609	0.00226777	mRNA	uncharacterized LOC114419267
LOC114415398	2.972096168	0.038705	mRNA	WAT1-related protein At4g08290-like, transcript variant X8
LOC114373868	2.968464504	0.0135986	mRNA	LOB domain-containing protein 1-like
LOC114376984	2.966558871	0.0135986	mRNA	uncharacterized LOC114376984
LOC114423542	2.962591482	0.00226777	mRNA	fasciclin-like arabinogalactan protein 11
LOC114395507	2.958150348	0.00226777	mRNA	non-specific lipid-transfer protein 1-like
LOC114386832	2.957096774	0.00226777	mRNA	stem-specific protein TSJT1-like
LOC114386286	2.956693094	0.0144323	mRNA	metacaspase-3-like, transcript variant X2
LOC114403083	2.949223972	0.00226777	mRNA	dormancy-associated protein homolog 3-like, transcript variant X1
LOC114421663	2.934043056	0.009937	mRNA	chalcone synthase 1-like
LOC114413140	2.933506965	0.00778722	mRNA	L-ascorbate oxidase-like
LOC114418985	2.92917977	0.00226777	mRNA	probable glutathione S-transferase
LOC114388866	2.922501188	0.0135986	mRNA	peroxidase 10-like
LOC114374211	2.922364509	0.0197131	mRNA	probable polyol transporter 3
LOC114384091	2.914628462	0.0183026	mRNA	ethylene-responsive transcription factor ABR1-like
LOC114386821	2.906212113	0.00226777	mRNA	pathogenesis-related protein 1-like
LOC114383563	2.899539155	0.021824	mRNA	glutamate dehydrogenase 1-like
LOC114381123	2.899198302	0.00662383	mRNA	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.3
LOC114413351	2.898611111	0.00226777	mRNA	protein P21-like
LOC114419649	2.895778387	0.00226777	mRNA	CCG-binding protein 1-like
LOC114388491	2.894700934	0.00226777	mRNA	pathogenesis-related protein 1-like
LOC114403900	2.890439064	0.00226777	mRNA	homocysteine S-methyltransferase 3-like
LOC114422452	2.889312136	0.00885696	mRNA	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.1
LOC114376771	2.882675317	0.00226777	mRNA	oxalate--CoA ligase-like
LOC114422982	2.879512083	0.00662383	mRNA	alpha-amylase/subtilisin inhibitor-like

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114388994	2.876065701	0.00226777	mRNA	CCG-binding protein 1-like
LOC114393213	2.874431128	0.0135986	mRNA	protein PPLZ02-like
LOC114374977	2.867531103	0.00396241	mRNA	fasciclin-like arabinogalactan protein 12
LOC114399297	2.865425554	0.00226777	mRNA	inorganic phosphate transporter 1-4-like
LOC114414832	2.850879602	0.0127546	mRNA	protein ALP1-like
LOC114395788	2.842433819	0.0183026	mRNA	transcription factor bHLH25-like
LOC114370403	2.837152928	0.0109267	mRNA	receptor-like cytosolic serine/threonine-protein kinase RBK2, transcript variant X1
LOC114377434	2.82618387	0.00226777	mRNA	beta-amylase 3, chloroplastic-like
LOC114418978	2.822739368	0.00226777	mRNA	uncharacterized LOC114418978
LOC114406444	2.818628203	0.0118441	mRNA	dynammin-related protein 1E-like
LOC114371093	2.814279074	0.0109267	mRNA	basic 7S globulin-like
LOC114425798	2.809625206	0.00885696	mRNA	uncharacterized protein At1g66480-like
LOC114370680	2.807863931	0.0127546	mRNA	metal-nicotianamine transporter YSL1-like
LOC114374458	2.800048152	0.0160163	mRNA	protein NRT1/ PTR FAMILY 6.2-like
LOC114384911	2.79925414	0.00226777	mRNA	uncharacterized LOC114384911
LOC114377786	2.798596796	0.0152251	mRNA	transcription factor MYB13-like
LOC114393778	2.792511035	0.0345168	mRNA	14 kDa proline-rich protein DC2.15-like
LOC114419944	2.79222441	0.0197131	mRNA	cell wall / vacuolar inhibitor of fructosidase 1-like
LOC114367125	2.792220162	0.0308439	mRNA	wall-associated receptor kinase-like 22
LOC114375127	2.790668533	0.0197131	mRNA	GABA transporter 1-like
LOC114415757	2.781763332	0.00885696	mRNA	RING-H2 finger protein ATL78-like
LOC114411818	2.781004506	0.00396241	mRNA	UDP-glucose 6-dehydrogenase 1-like, transcript variant X2
LOC114394221	2.78091963	0.0118441	mRNA	cytochrome b561 and DOMON domain-containing protein At5g47530-like
LOC114384993	2.779498089	0.0189764	mRNA	regulatory protein NPR3-like
LOC114387516	2.76989598	0.0189764	mRNA	GDSL esterase/lipase 5-like
LOC114399011	2.76964082	0.0175482	mRNA	uncharacterized LOC114399011
LOC114380153	2.768732245	0.00226777	mRNA	stem-specific protein TSJT1-like
LOC114386698	2.75882433	0.0238743	mRNA	cytochrome P450 82A2-like
LOC114368020	2.755955585	0.00226777	mRNA	ethylene-responsive transcription factor ERF071-like
LOC114386595	2.746355458	0.0329675	mRNA	G-type lectin S-receptor-like serine/threonine-protein kinase At1g67520, transcript variant X4
LOC114422989	2.741365563	0.0203972	mRNA	fructose-1,6-bisphosphatase, cytosolic-like, transcript variant X1
LOC114394915	2.739394806	0.00226777	mRNA	cationic peroxidase 1-like
LOC114394160	2.733806783	0.00226777	mRNA	protein NRT1/ PTR FAMILY 2.9-like
LOC114375149	2.729851649	0.0189764	mRNA	uncharacterized LOC114375149
LOC114374771	2.727074448	0.00226777	mRNA	fasciclin-like arabinogalactan protein 11
LOC114395333	2.725959014	0.0144323	mRNA	uncharacterized LOC114395333
LOC114368946	2.723839294	0.0410216	mRNA	phosphoenolpyruvate carboxykinase (ATP)-like
LOC114389501	2.722818428	0.00396241	mRNA	NAC domain-containing protein 2-like
LOC114366931	2.722132482	0.00226777	mRNA	pathogenesis-related protein 10
LOC114425380	2.720969692	0.0183026	mRNA	ethylene-responsive transcription factor ERF061-like
LOC114395495	2.719841034	0.0167884	mRNA	uncharacterized LOC114395495
LOC114367729	2.717736829	0.0175482	mRNA	protein LIR18B-like

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114422177	2.711565538	0.00226777	mRNA	protein EXORDIUM-like 2
LOC114402942	2.698183531	0.0274825	mRNA	putative receptor-like protein kinase At4g00960, transcript variant X3
LOC114417395	2.695707611	0.0308439	mRNA	phospholipid-transporting ATPase 1-like, transcript variant X2
LOC114367364	2.693606665	0.021824	ncRNA	uncharacterized LOC114367364
LOC114377234	2.688702763	0.00662383	ncRNA	uncharacterized LOC114377234
LOC114425419	2.686971309	0.00536398	mRNA	receptor-like protein kinase HSL1
LOC114395126	2.677238012	0.00662383	mRNA	ethylene-responsive transcription factor ERF113-like
LOC114381885	2.676557826	0.0189764	mRNA	epoxide hydrolase A-like
LOC114382553	2.675117644	0.00226777	mRNA	F-box protein SKP2B-like, transcript variant X1
LOC114394416	2.673588508	0.0160163	mRNA	uncharacterized LOC114394416
LOC114415580	2.66746049	0.00662383	mRNA	oligopeptide transporter 6-like
LOC114423927	2.666456939	0.0334467	mRNA	pectinesterase inhibitor 9
LOC114416718	2.662723771	0.00396241	mRNA	alanine--glyoxylate aminotransferase 2 homolog 2, mitochondrial-like
LOC114392640	2.660360823	0.00226777	mRNA	probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 11
LOC114376888	2.659498668	0.00226777	mRNA	pleiotropic drug resistance protein 1-like
LOC114395310	2.659240115	0.0292127	mRNA	vesicle-associated membrane protein 722-like
LOC114373641	2.65836643	0.0418668	mRNA	external alternative NAD(P)H-ubiquinone oxidoreductase B2, mitochondrial-like, transcript variant X1
LOC114390056	2.655031689	0.00226777	misc_RNA	protein TIME FOR COFFEE-like, transcript variant X2
LOC114388309	2.653690086	0.00226777	mRNA	ethylene-responsive transcription factor RAP2-3-like
LOC114397967	2.636697245	0.0251735	mRNA	probable aldo-keto reductase 1
LOC114403802	2.631526202	0.0427524	mRNA	ethylene receptor 2-like, transcript variant X2
LOC114409528	2.626482337	0.00885696	mRNA	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290, transcript variant X1
LOC114407457	2.620529689	0.0372252	mRNA	inositol oxygenase 2-like
LOC114419509	2.619832931	0.0269311	mRNA	serine carboxypeptidase-like 31
LOC114366829	2.619727374	0.00396241	mRNA	wall-associated receptor kinase-like 8
LOC114425794	2.618375531	0.00778722	mRNA	chalcone synthase 7
LOC114395860	2.61676101	0.0210997	mRNA	E3 ubiquitin-protein ligase WAV3-like
LOC114403343	2.61518099	0.00226777	mRNA	probable galactinol--sucrose galactosyltransferase 1
LOC114399911	2.613682707	0.00885696	mRNA	cytochrome P450 93A2
LOC114379092	2.612695403	0.00226777	mRNA	fasciclin-like arabinogalactan protein 11
LOC114425360	2.612655992	0.0281035	mRNA	probable WRKY transcription factor 41
LOC114388221	2.611557563	0.00226777	mRNA	ABC transporter G family member 35-like, transcript variant X1
LOC114406868	2.603361518	0.00226777	mRNA	protein MARD1-like
LOC114381267	2.600913814	0.0324602	mRNA	ankyrin repeat-containing protein BDA1-like
LOC114415810	2.59943356	0.00226777	mRNA	lipase-like PAD4
LOC114379207	2.59709143	0.025756	mRNA	fasciclin-like arabinogalactan protein 12
LOC114384656	2.595866988	0.0167884	mRNA	uncharacterized LOC114384656, transcript variant X2
LOC114411882	2.595682367	0.0274825	mRNA	protein SRG1-like
LOC114418471	2.592272392	0.00662383	mRNA	(+)-neomenthol dehydrogenase-like, transcript variant X2
LOC114418033	2.589127511	0.00226777	mRNA	uncharacterized LOC114418033, transcript variant X1
LOC114383356	2.58369842	0.00226777	mRNA	transcription factor PIF5-like
LOC114378507	2.578336217	0.0109267	mRNA	stem-specific protein TSJT1-like

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114425491	2.576832325	0.00226777	mRNA	vestitone reductase-like
LOC114367883	2.571757618	0.00226777	mRNA	probable WRKY transcription factor 31
LOC114397469	2.570719702	0.0382032	mRNA	60S ribosomal protein L10-like
LOC114396881	2.560476589	0.00885696	mRNA	zinc finger protein CONSTANS-LIKE 7-like
LOC114394179	2.559529297	0.00226777	mRNA	vacuolar-processing enzyme
LOC114391241	2.558438796	0.00226777	mRNA	zinc finger protein CONSTANS-LIKE 15-like
LOC114397468	2.554094927	0.00662383	mRNA	probable LRR receptor-like serine/threonine-protein kinase At1g06840
LOC114416709	2.552903204	0.0238743	mRNA	protein LURP-one-related 15-like
LOC114378483	2.546737525	0.025756	mRNA	probable L-type lectin-domain containing receptor kinase VII.2
LOC114393856	2.534966363	0.00226777	mRNA	peroxidase 50-like
LOC114410246	2.525081119	0.0197131	ncRNA	uncharacterized LOC114410246
LOC114385904	2.522496064	0.0395658	mRNA	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.8
LOC114372389	2.519819732	0.0281035	mRNA	uncharacterized LOC114372389
LOC114374564	2.507521359	0.00226777	mRNA	lysine-specific demethylase JMJ30-like, transcript variant X1
LOC114416956	2.507262092	0.0232107	mRNA	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290
LOC114374536	2.505080365	0.00226777	mRNA	protein CASPARIAN STRIP INTEGRITY FACTOR 1-like
LOC114374344	2.503874095	0.00778722	mRNA	isoflavone 3'-hydroxylase-like
LOC114410157	2.503401601	0.00662383	mRNA	peroxidase P7-like
LOC114392276	2.500683779	0.0449145	mRNA	cell wall / vacuolar inhibitor of fructosidase 1-like
LOC114417865	2.499717908	0.0286553	mRNA	protein LITTLE ZIPPER 2-like
LOC114408726	2.496668902	0.00885696	mRNA	ethylene-responsive transcription factor RAP2-1-like
LOC114372364	2.496393843	0.00226777	mRNA	dormancy-associated protein homolog 3-like
LOC114422304	2.490122251	0.00226777	mRNA	beta-galactosidase 1-like
LOC114420875	2.489006492	0.0245214	mRNA	G-box-binding factor 1-like, transcript variant X2
LOC114416013	2.488390938	0.025756	ncRNA	uncharacterized LOC114416013
LOC114391237	2.485512745	0.00226777	mRNA	peroxidase 12-like
LOC114417986	2.484936585	0.00226777	mRNA	ABC transporter G family member 36-like
LOC114422511	2.484000582	0.00226777	mRNA	uncharacterized LOC114422511, transcript variant X1
LOC114390278	2.477602926	0.00226777	mRNA	NAC transcription factor 47-like
LOC114379944	2.476644291	0.0339596	mRNA	cinnamoyl-CoA reductase 1-like
LOC114387431	2.47165251	0.0372252	mRNA	RING-H2 finger protein ATL1-like
LOC114366877	2.46627799	0.0334467	mRNA	cationic peroxidase 1-like
LOC114407365	2.464125794	0.00226777	mRNA	probable caffeoyl-CoA O-methyltransferase At4g26220, transcript variant X2
LOC114382281	2.454246643	0.00662383	mRNA	ABC transporter B family member 11-like
LOC114421388	2.45416768	0.00226777	mRNA	protein DMR6-LIKE OXYGENASE 2-like
LOC114395165	2.451234028	0.0339596	mRNA	putative clathrin assembly protein At4g40080
LOC114367958	2.450925064	0.0334467	mRNA	pectinesterase-like
LOC114369369	2.450442143	0.00396241	mRNA	putative receptor-like protein kinase At4g00960
LOC114398145	2.448016799	0.0339596	mRNA	MDIS1-interacting receptor like kinase 2-like
LOC114377097	2.443834137	0.00396241	mRNA	dormancy-associated protein 1-like, transcript variant X1
LOC114379864	2.443241019	0.00226777	mRNA	E3 ubiquitin-protein ligase RMA1H1-like, transcript variant X2
LOC114418635	2.442996737	0.0175482	mRNA	probable serine/threonine-protein kinase PBL3, transcript variant X3

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114373343	2.439389124	0.00396241	mRNA	uncharacterized LOC114373343
LOC114412449	2.438119481	0.0498622	mRNA	disease resistance protein RGA2-like, transcript variant X3
LOC114420002	2.436408676	0.009937	mRNA	pathogenesis-related protein STH-2-like
LOC114389261	2.436188437	0.00662383	mRNA	abscisic stress-ripening protein 2-like
LOC114422633	2.42296202	0.00536398	mRNA	probable LRR receptor-like serine/threonine-protein kinase At1g56130, transcript variant X2
LOC114423068	2.421835165	0.00226777	mRNA	protein DETOXIFICATION 16-like
LOC114413528	2.420759842	0.0308439	mRNA	inositol oxygenase 4-like
LOC114382533	2.418616367	0.0197131	mRNA	probable glutathione S-transferase, transcript variant X1
LOC114399007	2.417977387	0.0395658	mRNA	probable WRKY transcription factor 75
LOC114413382	2.414521641	0.0431737	mRNA	transcription factor EGL1-like
LOC114379086	2.413855365	0.00885696	mRNA	isocitrate lyase 2
LOC114410067	2.411332723	0.0303111	mRNA	amino-acid permease BAT1 homolog, transcript variant X2
LOC114413527	2.411301306	0.00396241	mRNA	zinc finger CCCH domain-containing protein 20-like
LOC114369194	2.41040347	0.00885696	ncRNA	uncharacterized LOC114369194
LOC114421337	2.40076801	0.00226777	mRNA	wall-associated receptor kinase-like 14
LOC114382540	2.399825844	0.00226777	mRNA	metal-nicotianamine transporter YSL1-like, transcript variant X1
LOC114400592	2.398841409	0.00226777	mRNA	protein MARD1-like
LOC114403659	2.3966903	0.00226777	mRNA	peroxidase 12-like
LOC114390092	2.395774541	0.0481641	mRNA	RING-H2 finger protein ATL8-like
LOC114407339	2.393002525	0.0431737	mRNA	monothiol glutaredoxin-S6-like
LOC114422377	2.390920235	0.00226777	mRNA	ABC transporter G family member 36-like
LOC114425681	2.390424306	0.0297945	mRNA	UDP-glycosyltransferase 13
LOC114415519	2.387940978	0.0400224	mRNA	probable WRKY transcription factor 53
LOC114418495	2.386950245	0.00226777	mRNA	uncharacterized LOC114418495, transcript variant X1
LOC114375209	2.385958393	0.038705	mRNA	uncharacterized LOC114375209
LOC114412826	2.385509814	0.0144323	mRNA	cytochrome P450 78A5-like
LOC114387521	2.381474801	0.00885696	mRNA	cytochrome P450 78A5-like
LOC114416639	2.379352424	0.0376697	mRNA	COBRA-like protein 4
LOC114416900	2.377881061	0.0127546	misc_RNA	NAC domain-containing protein 72-like
LOC114381249	2.377072737	0.00885696	mRNA	protein NRT1/ PTR FAMILY 4.5-like
LOC114412466	2.376648684	0.0210997	mRNA	peroxidase 50-like
LOC114406709	2.375097369	0.0391131	mRNA	heat stress transcription factor B-3-like
LOC114401711	2.371903862	0.025756	mRNA	uncharacterized protein At1g66480-like
LOC114393748	2.368801335	0.0319435	mRNA	uncharacterized LOC114393748, transcript variant X1
LOC114414526	2.36826878	0.0395658	mRNA	putative 12-oxophytodienoate reductase 11
LOC114373473	2.367344813	0.00226777	mRNA	uncharacterized LOC114373473
LOC114387028	2.36280845	0.0225301	mRNA	fasciclin-like arabinogalactan protein 11
LOC114395708	2.362258653	0.0391131	mRNA	adenine/guanine permease AZG1-like
LOC114422571	2.356921435	0.00396241	mRNA	phospholipid-transporting ATPase 1-like
LOC114367821	2.355625659	0.00226777	mRNA	wall-associated receptor kinase-like 8
LOC114399628	2.354556071	0.00396241	mRNA	ferritin-4, chloroplastic-like, transcript variant X1
LOC114417296	2.350231874	0.038705	mRNA	vascular-related unknown protein 1-like

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114390067	2.348772607	0.043595	mRNA	dormancy-associated protein homolog 3-like, transcript variant X1
LOC114388658	2.347071645	0.00226777	mRNA	probable WRKY transcription factor 40
LOC114376120	2.342957891	0.00226777	mRNA	asparagine synthetase [glutamine-hydrolyzing] 2
LOC114386975	2.342227892	0.0372252	mRNA	ethylene-responsive transcription factor 12-like
LOC114372533	2.337711002	0.0109267	mRNA	E3 ubiquitin-protein ligase ATL6
LOC114375110	2.336705765	0.00662383	mRNA	fasciclin-like arabinogalactan protein 12
LOC114423513	2.334448317	0.00226777	mRNA	purine permease 21-like
LOC114387988	2.333092855	0.00226777	mRNA	probable WRKY transcription factor 31
LOC114399039	2.332704893	0.0210997	mRNA	formate dehydrogenase 1, mitochondrial-like
LOC114374910	2.329784729	0.0175482	mRNA	fasciclin-like arabinogalactan protein 11
LOC114386733	2.329183359	0.00226777	mRNA	alpha-amylase/subtilisin inhibitor-like
LOC114376024	2.328754153	0.0135986	mRNA	receptor-like protein kinase 7
LOC114390429	2.32852601	0.0473048	mRNA	probable LRR receptor-like serine/threonine-protein kinase RKF3
LOC114416958	2.327165011	0.0494022	mRNA	G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290, transcript variant X3
LOC114377102	2.322382066	0.00662383	mRNA	organic cation/carnitine transporter 4-like
LOC114378636	2.318261942	0.0160163	mRNA	alpha-amylase/subtilisin inhibitor-like
LOC114412964	2.31355215	0.00396241	mRNA	fasciclin-like arabinogalactan protein 11
LOC114407860	2.313364372	0.0463397	mRNA	RING-H2 finger protein ATL3-like
LOC114420206	2.311989739	0.0286553	mRNA	1-aminocyclopropane-1-carboxylate oxidase-like
LOC114408809	2.311893249	0.00226777	mRNA	zinc finger CCCH domain-containing protein 23-like
LOC114398142	2.307362291	0.00778722	mRNA	F-box protein CPR1-like
LOC114414802	2.304920958	0.00396241	mRNA	zinc finger CCCH domain-containing protein 23-like
LOC114410333	2.299866352	0.043595	mRNA	protein MKS1-like
LOC114380743	2.295401329	0.0175482	mRNA	putative wall-associated receptor kinase-like 16
LOC114419442	2.294252794	0.0225301	mRNA	protein PLANT CADMIUM RESISTANCE 2-like, transcript variant X1
LOC114381545	2.292614756	0.0440433	mRNA	disease resistance protein TAO1-like
LOC114404121	2.288910458	0.0203972	mRNA	zeaxanthin epoxidase, chloroplastic-like, transcript variant X5
LOC114381120	2.281528602	0.00226777	mRNA	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.5
LOC114379309	2.279842558	0.0395658	mRNA	thioredoxin-like protein CXXS1
LOC114423096	2.279004487	0.0498622	mRNA	uncharacterized LOC114423096
LOC114380550	2.278920325	0.0167884	misc_RNA	transcription factor PCL1-like, transcript variant X3
LOC114416987	2.274957612	0.0329675	mRNA	probable aldo-keto reductase 2
LOC114423043	2.272671259	0.0459037	misc_RNA	metallothiol transferase FosB-like
LOC114418432	2.270084906	0.0160163	mRNA	U-box domain-containing protein 33-like, transcript variant X1
LOC114387997	2.268416868	0.0350813	mRNA	receptor-like serine/threonine-protein kinase SD1-8, transcript variant X1
LOC114379416	2.262922009	0.0498622	mRNA	leucine-rich repeat extensin-like protein 4
LOC114415502	2.261251056	0.00226777	mRNA	endoglucanase 25-like, transcript variant X2
LOC114419618	2.260825794	0.00226777	mRNA	ervatamin-B-like
LOC114409127	2.260146652	0.0152251	mRNA	probable mannitol dehydrogenase
LOC114422194	2.251698136	0.0118441	mRNA	cationic peroxidase 2-like
LOC114389649	2.250930929	0.042315	mRNA	39S ribosomal protein L46, mitochondrial-like, transcript variant X2

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114406551	2.249130255	0.0414288	mRNA	dnaJ protein homolog 1-like
LOC114420233	2.244875884	0.0167884	mRNA	microtubule-associated protein 70-5-like, transcript variant X2
LOC114393944	2.244452333	0.00226777	mRNA	stress-induced protein SAM22-like
LOC114416583	2.239634711	0.00226777	mRNA	dirigent protein 22-like
LOC114406218	2.23714472	0.00662383	mRNA	protein NRT1/ PTR FAMILY 5.6-like, transcript variant X2
LOC114407359	2.236079263	0.00396241	mRNA	heavy metal-associated isoprenylated plant protein 36-like
LOC114375099	2.236036736	0.0303111	mRNA	tryptophan synthase beta chain 1-like
LOC114387601	2.235844473	0.00226777	mRNA	probable ubiquitin-conjugating enzyme E2 24, transcript variant X2
LOC114406024	2.232345354	0.0467714	mRNA	probable WRKY transcription factor 33
LOC114418468	2.231076267	0.00396241	mRNA	(+)-neomenthol dehydrogenase-like, transcript variant X2
LOC114419804	2.228570964	0.00226777	mRNA	chaperone protein dnaJ 11, chloroplastic-like
LOC114391960	2.2278005	0.00536398	mRNA	nodulin-13-like
LOC114401367	2.226251282	0.009937	misc_RNA	NAD(P)H-dependent 6'-deoxychalcone synthase-like
LOC114378141	2.218888065	0.00226777	mRNA	uncharacterized LOC114378141
LOC114394465	2.213398994	0.00226777	mRNA	vestitone reductase-like
LOC114420112	2.209393113	0.00885696	mRNA	scopoletin glucosyltransferase-like
LOC114406037	2.208348611	0.0152251	mRNA	dirigent protein 22-like
LOC114414830	2.201614895	0.0210997	mRNA	uncharacterized LOC114414830
LOC114409172	2.195923453	0.0232107	mRNA	glutamyl-tRNA reductase 1, chloroplastic-like
LOC114378172	2.195634754	0.00226777	mRNA	uncharacterized LOC114378172
LOC114411638	2.192388612	0.00226777	mRNA	glucuronokinase 1-like
LOC114388019	2.18721151	0.043595	mRNA	protein SRG1-like
LOC114376216	2.185931577	0.00226777	mRNA	apoptosis-inducing factor homolog A-like
LOC114401335	2.18190889	0.00226777	mRNA	cytochrome P450 89A2-like
LOC114375749	2.177510339	0.00226777	mRNA	chalcone synthase
LOC114390866	2.17273886	0.00396241	mRNA	protein GIGANTEA-like, transcript variant X1
LOC114409479	2.168678112	0.0400224	ncRNA	uncharacterized LOC114409479, transcript variant X1
LOC114411783	2.167428556	0.0175482	mRNA	truncated transcription factor CAULIFLOWER A-like, transcript variant X2
LOC114382211	2.164329085	0.0232107	mRNA	protein-tyrosine-phosphatase MKP1-like, transcript variant X4
LOC114372304	2.157876376	0.00662383	misc_RNA	WRKY transcription factor 23-like, transcript variant X2
LOC114388930	2.156382375	0.0463397	mRNA	probable L-gulonolactone oxidase 6
LOC114373682	2.156205457	0.0251735	mRNA	fasciclin-like arabinogalactan protein 12
LOC114367342	2.155251622	0.00396241	mRNA	beta-D-xylosidase 1-like
LOC114381074	2.152281932	0.00536398	mRNA	RING-H2 finger protein ATL66-like
LOC114380812	2.151437743	0.0127546	mRNA	zinc transporter 8-like, transcript variant X2
LOC114417971	2.15062207	0.0467714	mRNA	inositol oxygenase 1-like
LOC114397104	2.146612571	0.00226777	mRNA	peroxidase 4-like
LOC114406728	2.145934515	0.00226777	mRNA	probable galactinol--sucrose galactosyltransferase 2, transcript variant X2
LOC114377058	2.145509992	0.00662383	mRNA	probable WRKY transcription factor 31
LOC114368661	2.143756568	0.00396241	mRNA	chloride channel protein CLC-c-like, transcript variant X2
LOC114406946	2.139570044	0.0203972	mRNA	MDIS1-interacting receptor like kinase 2-like
LOC114418747	2.138047604	0.00226777	mRNA	UPF0481 protein At3g47200-like
LOC114424753	2.137340644	0.00536398	mRNA	ABC transporter G family member 2-like

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114392235	2.127368922	0.00226777	mRNA	cell wall / vacuolar inhibitor of fructosidase 1-like
LOC114417434	2.123763092	0.00662383	mRNA	DNA damage-repair/toleration protein DRT100-like
LOC114376611	2.1223761	0.0152251	mRNA	probable ubiquitin-conjugating enzyme E2 24, transcript variant X2
LOC114414494	2.11979649	0.0232107	mRNA	organ-specific protein S2-like
LOC114388735	2.117083931	0.0372252	mRNA	protein trichome birefringence-like 10, transcript variant X1
LOC114385651	2.116081781	0.00778722	mRNA	gibberellin 2-beta-dioxygenase 1-like
LOC114384914	2.109933367	0.009937	mRNA	protein ELF4-LIKE 1-like, transcript variant X1
LOC114417293	2.107029095	0.0127546	mRNA	isocitrate lyase 1
LOC114386585	2.106143937	0.0118441	ncRNA	uncharacterized LOC114386585
LOC114390047	2.105815183	0.00226777	misc_RNA	uncharacterized LOC114390047
LOC114414493	2.105051742	0.00662383	mRNA	BURP domain-containing protein BNM2A-like
LOC114396967	2.099541056	0.00226777	mRNA	WRKY transcription factor WRKY24-like
LOC114367058	2.098648615	0.00885696	mRNA	uncharacterized LOC114367058
LOC114413817	2.087790909	0.00226777	mRNA	AP2/ERF and B3 domain-containing transcription repressor TEM1-like
LOC114416819	2.087355973	0.0189764	mRNA	uncharacterized LOC114416819
LOC114370056	2.085579517	0.00885696	mRNA	extensin-3-like
LOC114414762	2.085500814	0.0232107	mRNA	zinc finger protein ZAT10-like
LOC114376506	2.084914264	0.00396241	mRNA	probable ubiquitin-conjugating enzyme E2 24, transcript variant X1
LOC114411847	2.084639329	0.0167884	mRNA	NAC domain-containing protein 100-like
LOC114391247	2.082231906	0.00226777	mRNA	subtilisin-like protease SBT3.5, transcript variant X1
LOC114393252	2.080989868	0.00226777	mRNA	probable disease resistance protein At4g33300
LOC114403288	2.080771169	0.0376697	mRNA	LRR receptor-like serine/threonine-protein kinase
LOC114396222	2.079245381	0.00396241	misc_RNA	glycerophosphodiester phosphodiesterase GDPDL4-like, transcript variant X3
LOC114416209	2.076509907	0.00226777	mRNA	SNF1-related protein kinase regulatory subunit gamma-1-like, transcript variant X1
LOC114384517	2.076342715	0.00226777	mRNA	WRKY transcription factor WRKY24-like
LOC114394525	2.075763158	0.00662383	mRNA	vestitone reductase-like
LOC114423355	2.07212601	0.0118441	mRNA	fasciclin-like arabinogalactan protein 12
LOC114382702	2.067762054	0.0109267	mRNA	probable xyloglucan endotransglucosylase/hydrolase protein 23
LOC114422354	2.067733156	0.00885696	mRNA	inositol oxygenase 1-like
LOC114400370	2.061671857	0.0245214	mRNA	cytochrome P450 82A4-like
LOC114376737	2.06166525	0.009937	mRNA	fasciclin-like arabinogalactan protein 12
LOC114416767	2.059067285	0.0356535	mRNA	cellulose synthase A catalytic subunit 7 [UDP-forming]-like, transcript variant X2
LOC114381122	2.057029472	0.009937	mRNA	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.2, transcript variant X2
LOC114421396	2.053917838	0.00396241	mRNA	protein EXORDIUM-like 2
LOC114415743	2.047906136	0.00662383	mRNA	citrate-binding protein-like
LOC114370865	2.047284168	0.0144323	mRNA	protein LAZY 1-like
LOC114389944	2.046370661	0.0414288	misc_RNA	TMV resistance protein N-like
LOC114372106	2.046209405	0.00396241	mRNA	protein TIME FOR COFFEE-like, transcript variant X1
LOC114367998	2.044794754	0.0324602	mRNA	O-fucosyltransferase 20-like
LOC114423818	2.04382825	0.0127546	mRNA	extensin-2-like
LOC114422260	2.039587448	0.0118441	mRNA	probable receptor-like protein kinase At1g11050, transcript variant X1
LOC114377678	2.034724535	0.00226777	mRNA	uncharacterized LOC114377678

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114412959	2.033396484	0.0334467	mRNA	probable glutathione S-transferase
LOC114382032	2.032504105	0.00226777	mRNA	uncharacterized LOC114382032, transcript variant X2
LOC114413294	2.030987611	0.0109267	mRNA	putative amidase AmiD, transcript variant X4
LOC114386144	2.030528718	0.00226777	mRNA	U-box domain-containing protein 26-like, transcript variant X1
LOC114407421	2.02924198	0.021824	mRNA	probable LRR receptor-like serine/threonine-protein kinase At4g29180
LOC114373729	2.029070881	0.025756	mRNA	probable WRKY transcription factor 40
LOC114385463	2.028590455	0.0361745	mRNA	F-box/LRR-repeat protein 3-like, transcript variant X2
LOC114391974	2.023446632	0.00226777	mRNA	L-type lectin-domain containing receptor kinase IX.1-like
LOC114367323	2.01468998	0.0144323	mRNA	cytochrome P450 71A26-like
LOC114403853	2.012932002	0.0418668	mRNA	phenylalanine ammonia-lyase class 3, transcript variant X1
LOC114408375	2.010418615	0.0263571	mRNA	cellulose synthase-like protein D2
LOC114420398	2.009904643	0.0118441	mRNA	isoflavone reductase-like
LOC114376391	2.009854672	0.00226777	mRNA	formin-like protein 20
LOC114379987	2.009044087	0.00536398	mRNA	receptor-like protein kinase HSL1
LOC114390400	2.009016427	0.0189764	mRNA	protein SUPPRESSOR OF npr1-1, CONSTITUTIVE 1-like
LOC114396347	2.007430183	0.00226777	mRNA	disease resistance protein RPM1-like
LOC114367828	2.003326454	0.00536398	mRNA	sugar transport protein 13-like
LOC114425668	2.003071623	0.0183026	mRNA	vestitone reductase-like
LOC114376885	2.002228044	0.00536398	mRNA	stem-specific protein TSJT1-like
Down-regulation				
LOC114369581	-2.001571287	0.00226777	mRNA	light-harvesting complex-like protein OHP2, chloroplastic
LOC114394478	-2.001599197	0.00226777	mRNA	non-specific lipid transfer protein GPI-anchored 1-like
LOC114385309	-2.001881822	0.00778722	mRNA	uncharacterized LOC114385309, transcript variant X1
LOC114390519	-2.006275786	0.00226777	mRNA	UDP-glycosyltransferase 1
LOC114412555	-2.006362081	0.0281035	mRNA	GDSL esterase/lipase At5g33370-like
LOC114374685	-2.00872664	0.0251735	mRNA	probable carboxylesterase 15
LOC114374859	-2.00990117	0.00396241	mRNA	GDSL esterase/lipase At5g45910-like
LOC114389496	-2.015077715	0.00226777	mRNA	putative UDP-rhamnose:rhamnosyltransferase 1
LOC114397961	-2.015162435	0.00396241	mRNA	haloacid dehalogenase-like hydrolase domain-containing protein 3
LOC114395554	-2.018789271	0.00536398	mRNA	probable E3 ubiquitin-protein ligase XERICO
LOC114400554	-2.019561278	0.0152251	mRNA	chalcone synthase J-like
LOC114415652	-2.019795079	0.00536398	mRNA	protein RESPONSE TO LOW SULFUR 3-like
LOC114408597	-2.020508865	0.0127546	mRNA	aldehyde oxidase GLOX1-like
LOC114396288	-2.021863579	0.0367182	mRNA	heavy metal-associated isoprenylated plant protein 9-like, transcript variant X2
LOC114417861	-2.022541193	0.00226777	mRNA	uncharacterized LOC114417861, transcript variant X3
LOC114406661	-2.029055618	0.0485337	mRNA	transcription factor ORG3-like
LOC114381160	-2.030388443	0.00885696	mRNA	nitrate reductase [NADH] 2
LOC114374275	-2.033166666	0.0183026	mRNA	leucoanthocyanidin dioxygenase-like
LOC114424342	-2.033791457	0.0329675	mRNA	proline-rich protein 4-like, transcript variant X2
LOC114373628	-2.04416757	0.0269311	mRNA	tubulin-folding cofactor A-like, transcript variant X2
LOC114420034	-2.044628113	0.00226777	misc_RNA	B-box zinc finger protein 18-like, transcript variant X2
LOC114414013	-2.046096915	0.0274825	mRNA	uncharacterized LOC114414013
LOC114395358	-2.046457822	0.0245214	mRNA	polyphenol oxidase I, chloroplastic-like

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Down-regulation				
LOC114373703	-2.050350315	0.0175482	mRNA	uncharacterized LOC114373703
LOC114403080	-2.051774653	0.00885696	mRNA	uncharacterized protein sll0005-like, transcript variant X2
LOC114384926	-2.054983019	0.0160163	mRNA	ribulose biphosphate carboxylase/oxygenase activase, chloroplastic-like
LOC114381260	-2.058722525	0.00226777	mRNA	small heat shock protein, chloroplastic-like
LOC114422208	-2.060079473	0.00536398	mRNA	soyasaponin III rhamnosyltransferase
LOC114380961	-2.060635289	0.0232107	mRNA	xyloglucan endotransglucosylase/hydrolase 2-like
LOC114407834	-2.063971677	0.00885696	mRNA	probable L-gulonolactone oxidase 6
LOC114408563	-2.068080795	0.00396241	misc_RNA	uncharacterized LOC114408563
LOC114381549	-2.074514294	0.00536398	mRNA	naringenin,2-oxoglutarate 3-dioxygenase-like
LOC114411886	-2.080528815	0.00226777	mRNA	protein NRT1/ PTR FAMILY 4.6-like, transcript variant X2
LOC114396517	-2.097443431	0.00226777	mRNA	phenolic glucoside malonyltransferase 1-like
LOC114418284	-2.100750424	0.0245214	mRNA	ras-related protein RABA3-like
LOC114417277	-2.102137132	0.0232107	mRNA	zinc finger protein CONSTANS-LIKE 9-like
LOC114399226	-2.103225254	0.021824	mRNA	17.6 kDa class I heat shock protein-like
LOC114376554	-2.109503057	0.0175482	mRNA	unknown seed protein USP-like, transcript variant X1
LOC114399486	-2.109986264	0.00885696	mRNA	GDSL esterase/lipase At5g33370-like
LOC114406646	-2.117880821	0.00226777	mRNA	lycopene beta cyclase, chloroplastic-like
LOC114415913	-2.121720734	0.009937	mRNA	defensin-like protein, transcript variant X2
LOC114420918	-2.125422772	0.0367182	mRNA	ABC transporter G family member 5-like
LOC114392683	-2.127515861	0.0238743	mRNA	microtubule-associated protein RP/EB family member 1B, transcript variant X3
LOC114399063	-2.130683014	0.0238743	mRNA	phenolic glucoside malonyltransferase 1-like
LOC114413119	-2.14071649	0.00536398	mRNA	PLAT domain-containing protein 3-like
LOC114421931	-2.145721109	0.0152251	mRNA	uncharacterized LOC114421931
LOC114413465	-2.145923847	0.0118441	misc_RNA	uncharacterized LOC114413465, transcript variant X2
LOC114416612	-2.150466619	0.00226777	mRNA	flavonoid 3'-monooxygenase-like
LOC114379637	-2.150715376	0.0135986	mRNA	uncharacterized LOC114379637
LOC114424209	-2.152685773	0.00226777	mRNA	uncharacterized LOC114424209
LOC114373626	-2.153386504	0.00226777	mRNA	FCS-Like Zinc finger 2-like
LOC114385014	-2.155449618	0.0109267	mRNA	subtilisin-like protease Glyma18g48580
LOC114395027	-2.156051438	0.00396241	mRNA	omega-3 fatty acid desaturase, endoplasmic reticulum
LOC114387156	-2.156895945	0.00226777	mRNA	MLP-like protein 34
LOC114384892	-2.157933805	0.00226777	mRNA	asparagine synthetase [glutamine-hydrolyzing] 1
LOC114416720	-2.161873843	0.00536398	mRNA	gamma-interferon-responsive lysosomal thiol protein-like, transcript variant X1
LOC114384491	-2.163603372	0.0292127	mRNA	fructose-bisphosphate aldolase, cytoplasmic isozyme 1
LOC114372547	-2.166284074	0.00396241	mRNA	cysteine synthase-like, transcript variant X3
LOC114384289	-2.172407039	0.0109267	mRNA	putative uncharacterized protein DDB_G0290521
LOC114385680	-2.177662533	0.00226777	mRNA	berberine bridge enzyme-like 8
LOC114392466	-2.178005291	0.0251735	mRNA	CASP-like protein 2C1
LOC114383516	-2.178217367	0.00778722	mRNA	uncharacterized LOC114383516, transcript variant X2
LOC114422557	-2.178700526	0.00226777	mRNA	uncharacterized LOC114422557, transcript variant X1
LOC114422650	-2.180677115	0.00226777	mRNA	probable xyloglucan endotransglucosylase/hydrolase protein 6
LOC114389167	-2.190200692	0.00226777	mRNA	beta-carotene hydroxylase 2, chloroplastic-like
LOC114376567	-2.19170211	0.0175482	mRNA	auxin-responsive protein IAA17-like

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Down-regulation				
LOC114366997	-2.196937614	0.0144323	misc_RNA	uclacyanin 1-like
LOC114411828	-2.198380007	0.00396241	mRNA	flavin-containing monooxygenase FMO GS-OX-like 8
LOC114394117	-2.199876281	0.00885696	mRNA	probable isoaspartyl peptidase/L-asparaginase 2
LOC114380335	-2.202914797	0.00662383	mRNA	ferredoxin-A-like
LOC114423242	-2.204947155	0.0263571	mRNA	thioredoxin H2-like
LOC114374677	-2.205527942	0.0175482	mRNA	receptor-like serine/threonine-protein kinase ALE2, transcript variant X3
LOC114415196	-2.205897337	0.0109267	mRNA	uncharacterized LOC114415196
LOC114386847	-2.207847348	0.0109267	mRNA	pectinesterase inhibitor 3-like
LOC114411649	-2.215883026	0.00226777	mRNA	galactinol--sucrose galactosyltransferase
LOC114385289	-2.216022809	0.00226777	mRNA	peroxidase P7-like
LOC114394910	-2.220953462	0.00536398	mRNA	NAD(P)H-quinone oxidoreductase subunit N, chloroplastic-like
LOC114387514	-2.221272341	0.0308439	mRNA	uncharacterized LOC114387514
LOC114394105	-2.222646309	0.0135986	mRNA	calcium sensing receptor, chloroplastic-like
LOC114379111	-2.229120492	0.00396241	mRNA	aldehyde dehydrogenase family 3 member F1-like
LOC114413469	-2.229392409	0.00226777	mRNA	uncharacterized LOC114413469
LOC114403638	-2.229949578	0.00226777	mRNA	uncharacterized LOC114403638
LOC114404124	-2.230498844	0.0135986	mRNA	uncharacterized LOC114404124
LOC114394424	-2.23167403	0.0485337	mRNA	uncharacterized LOC114394424
LOC114395442	-2.233910658	0.0197131	mRNA	thioredoxin H2-like
LOC114379677	-2.242206635	0.0449145	mRNA	uncharacterized LOC114379677
LOC114413083	-2.24397876	0.047745	mRNA	bifunctional riboflavin biosynthesis protein RIBA 1, chloroplastic-like, transcript variant X5
LOC114412248	-2.253291834	0.0485337	mRNA	putative invertase inhibitor
LOC114399196	-2.256057722	0.00226777	mRNA	actin-97-like, transcript variant X3
LOC114372337	-2.260675384	0.00226777	mRNA	soyasaponin III rhamnosyltransferase-like
LOC114407446	-2.26237745	0.0339596	mRNA	long chain acyl-CoA synthetase 1-like, transcript variant X1
LOC114397668	-2.262721961	0.00226777	mRNA	carbonic anhydrase 2-like, transcript variant X1
LOC114423700	-2.269324017	0.009937	mRNA	chloroplast envelope quinone oxidoreductase homolog, transcript variant X1
LOC114413275	-2.276683009	0.0144323	mRNA	uncharacterized LOC114413275
LOC114385751	-2.280766406	0.00885696	ncRNA	uncharacterized LOC114385751
LOC114371740	-2.286818386	0.0463397	ncRNA	uncharacterized LOC114371740
LOC114379353	-2.287966261	0.00226777	ncRNA	uncharacterized LOC114379353
LOC114375992	-2.287998458	0.00662383	mRNA	organ-specific protein P4-like
LOC114376069	-2.294429917	0.00226777	mRNA	beta-galactosidase 8-like
LOC114389716	-2.298091924	0.0313617	mRNA	carboxylesterase 1-like
LOC114407128	-2.299487471	0.0144323	mRNA	UDP-glycosyltransferase 73C6-like
LOC114401718	-2.29996362	0.00226777	mRNA	uncharacterized LOC114401718
LOC114382526	-2.303049143	0.00226777	mRNA	ATP sulfurylase 2-like
LOC114376849	-2.304805539	0.00226777	mRNA	protein NRT1/ PTR FAMILY 6.3-like
LOC114381933	-2.305497238	0.047745	mRNA	probable glycerol-3-phosphate acyltransferase 2
LOC114407752	-2.307733039	0.0135986	mRNA	uncharacterized LOC114407752
LOC114418342	-2.317636586	0.00226777	mRNA	uncharacterized LOC114418342, transcript variant X1
LOC114396577	-2.318186417	0.0109267	mRNA	vacuolar cation/proton exchanger 3-like

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Down-regulation				
LOC114417382	-2.320324009	0.00226777	mRNA	protein ZINC INDUCED FACILITATOR-LIKE 1-like, transcript variant X1
LOC114402328	-2.321269395	0.0489955	mRNA	17.1 kDa class II heat shock protein-like
LOC114400268	-2.322206122	0.0175482	mRNA	endoglucanase 11-like
LOC114405707	-2.323126048	0.00226777	mRNA	protein DETOXIFICATION 21-like
LOC114424222	-2.323430844	0.00536398	mRNA	leucoanthocyanidin dioxygenase-like
LOC114369903	-2.341929709	0.00226777	misc_RNA	probable plastid-lipid-associated protein 12, chloroplastic
LOC114405709	-2.347542421	0.0313617	mRNA	probable 2-isopropylmalate synthase
LOC114370397	-2.351142906	0.0210997	mRNA	lectin DB58-like
LOC114388069	-2.353117553	0.0391131	mRNA	lysM domain receptor-like kinase 3, transcript variant X3
LOC114386914	-2.35613487	0.0118441	mRNA	uncharacterized LOC114386914
LOC114417471	-2.35768634	0.00396241	mRNA	probable sucrose-phosphate synthase 4
LOC114406967	-2.360093261	0.042315	mRNA	pleiotropic drug resistance protein 1-like
LOC114401551	-2.361390463	0.00778722	mRNA	beta-carotene hydroxylase 2, chloroplastic-like
LOC114389537	-2.361856753	0.00226777	mRNA	uncharacterized LOC114389537
LOC114381104	-2.366711782	0.00396241	mRNA	probable pectate lyase 5
LOC114410646	-2.366955309	0.00662383	mRNA	glutathione S-transferase U18-like
LOC114385351	-2.366971492	0.00396241	mRNA	transmembrane protein 136-like, transcript variant X2
LOC114400683	-2.367245407	0.0189764	mRNA	protein BIC1-like, transcript variant X1
LOC114371236	-2.36887512	0.0414288	mRNA	monothiol glutaredoxin-S6-like
LOC114387553	-2.371312416	0.0210997	mRNA	bidirectional sugar transporter SWEET17-like
LOC114392892	-2.371700669	0.0418668	mRNA	dihydroflavonol 4-reductase-like
LOC114412136	-2.372208001	0.0135986	mRNA	acid beta-fructofuranosidase
LOC114415520	-2.374326636	0.00226777	mRNA	RNA polymerase sigma factor sigE, chloroplastic/mitochondrial, transcript variant X1
LOC114372669	-2.378545243	0.043595	mRNA	soyasapogenol B glucuronide galactosyltransferase-like
LOC114395669	-2.385912906	0.0427524	mRNA	protein PHYTOCHROME KINASE SUBSTRATE 1-like
LOC114417193	-2.386236304	0.00226777	mRNA	O-acyltransferase WSD1-like, transcript variant X2
LOC114407845	-2.398974074	0.00778722	mRNA	protein LHY-like, transcript variant X4
LOC114402430	-2.403339291	0.0269311	mRNA	low-temperature-induced 65 kDa protein-like
LOC114402293	-2.409605264	0.0391131	mRNA	lupeol synthase, transcript variant X1
LOC114366873	-2.418966879	0.00226777	mRNA	ATP-dependent Clp protease adapter protein CLPS1, chloroplastic-like, transcript variant X1
LOC114417321	-2.427704494	0.00226777	ncRNA	uncharacterized LOC114417321
LOC114374382	-2.429706042	0.00536398	mRNA	polyphenol oxidase A1, chloroplastic-like
LOC114375558	-2.435173937	0.0225301	mRNA	protein trichome birefringence-like 19
LOC114372559	-2.44074303	0.0454029	mRNA	purine-uracil permease NCS1-like
LOC114406232	-2.440877869	0.047745	mRNA	probable glutathione S-transferase
LOC114379168	-2.452957718	0.00778722	mRNA	protein FANTASTIC FOUR 3-like
LOC114401751	-2.456450519	0.00226777	mRNA	light-harvesting complex-like protein OHP2, chloroplastic, transcript variant X2
LOC114393177	-2.45741293	0.00396241	mRNA	GDSL esterase/lipase EXL3-like
LOC114416840	-2.457969876	0.0303111	mRNA	squamosa promoter-binding protein 1-like
LOC114419573	-2.464062613	0.00226777	mRNA	18.5 kDa class I heat shock protein
LOC114379787	-2.465855264	0.0308439	ncRNA	uncharacterized LOC114379787
LOC114386762	-2.482659444	0.00226777	mRNA	patatin-like protein 7

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Down-regulation				
LOC114406007	-2.483436495	0.00226777	mRNA	non-specific lipid-transfer protein 1-like
LOC114383556	-2.491195283	0.0382032	mRNA	probable calcium-binding protein CML44
LOC114418023	-2.495305821	0.00662383	mRNA	B-box zinc finger protein 32-like
LOC114400867	-2.50159154	0.00226777	mRNA	UDP-glycosyltransferase 73C2-like
LOC114375242	-2.509092663	0.00226777	mRNA	non-symbiotic hemoglobin 1
LOC114383468	-2.523125489	0.00396241	mRNA	ABC transporter B family member 13-like
LOC114389172	-2.52351467	0.00536398	mRNA	protein PLASTID MOVEMENT IMPAIRED 1-like
LOC114424271	-2.525153237	0.0361745	mRNA	AP2-like ethylene-responsive transcription factor At1g79700
LOC114386632	-2.525951782	0.00226777	mRNA	soyasapogenol B glucuronide galactosyltransferase-like
LOC114392778	-2.536563836	0.0345168	mRNA	uncharacterized LOC114392778
LOC114418407	-2.539186374	0.0210997	mRNA	putative UDP-rhamnose:rhamnosyltransferase 1
LOC114418795	-2.542454718	0.0292127	mRNA	transcription factor bHLH25-like
LOC114395131	-2.546344944	0.0175482	mRNA	cinnamoyl-CoA reductase 1-like
LOC114375021	-2.549076672	0.0274825	mRNA	annexin D4-like
LOC114382830	-2.552232522	0.0303111	mRNA	glutathione S-transferase F11-like
LOC114418972	-2.553506655	0.0225301	mRNA	putative UDP-rhamnose:rhamnosyltransferase 1
LOC114392349	-2.555430037	0.00226777	mRNA	FCS-Like Zinc finger 10-like
LOC114367727	-2.556657081	0.00226777	mRNA	uncharacterized LOC114367727
LOC114412738	-2.57249828	0.0303111	mRNA	codeine O-demethylase-like
LOC114418467	-2.573310799	0.00396241	mRNA	protein NUCLEAR FUSION DEFECTIVE 4-like
LOC114369882	-2.575844677	0.00226777	mRNA	protein PROTON GRADIENT REGULATION 5, chloroplastic-like
LOC114380560	-2.589477121	0.00226777	mRNA	polygalacturonase 1 beta-like protein 3, transcript variant X1
LOC114387385	-2.592014627	0.00226777	mRNA	transcription factor ILR3-like
LOC114420165	-2.599072876	0.0245214	mRNA	uncharacterized LOC114420165
LOC114396562	-2.599602726	0.0313617	mRNA	cinnamoyl-CoA reductase 1-like
LOC114388712	-2.600212497	0.0356535	mRNA	protein LNK3-like
LOC114387390	-2.610615793	0.00226777	mRNA	GDSL esterase/lipase At5g45960-like
LOC114406882	-2.622349137	0.0245214	misc_RNA	heat stress transcription factor A-7a-like, transcript variant X1
LOC114407459	-2.629228523	0.0118441	mRNA	short-chain dehydrogenase reductase 3b-like
LOC114388555	-2.6324869	0.00226777	mRNA	ferredoxin--nitrite reductase, chloroplastic-like
LOC114410431	-2.63744474	0.0334467	mRNA	WAT1-related protein At4g08300-like
LOC114381336	-2.639358044	0.0329675	mRNA	probable E3 ubiquitin-protein ligase XERICO
LOC114381405	-2.645551275	0.0160163	mRNA	cyprosin-like, transcript variant X2
LOC114425369	-2.649027405	0.00226777	mRNA	abscisic acid 8'-hydroxylase 2
LOC114399649	-2.662144247	0.0238743	mRNA	GDSL esterase/lipase At5g33370-like
LOC114424699	-2.674131666	0.00536398	misc_RNA	probable phospholipid hydroperoxide glutathione peroxidase, transcript variant X2
LOC114417995	-2.675269005	0.0281035	mRNA	dehydration-responsive element-binding protein 3-like
LOC114415175	-2.680589434	0.0210997	mRNA	probable glutathione S-transferase
LOC114401622	-2.68705815	0.00226777	mRNA	phytoene synthase 2, chloroplastic-like
LOC114370561	-2.711303283	0.0152251	mRNA	peamaclein-like
LOC114424274	-2.7162983	0.0183026	mRNA	anthocyanidin 3-O-glucosyltransferase 7-like
LOC114378363	-2.719959103	0.00662383	mRNA	probable inactive purple acid phosphatase 27
LOC114372630	-2.727271245	0.0263571	mRNA	protein REVEILLE 8-like, transcript variant X2

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Down-regulation				
LOC114381264	-2.738236503	0.0210997	mRNA	purine-uracil permease NCS1-like
LOC114423373	-2.741165503	0.0152251	mRNA	spermidine hydroxycinnamoyl transferase-like
LOC114374707	-2.745496141	0.00226777	mRNA	NAD(P)H-quinone oxidoreductase subunit N, chloroplastic-like
LOC114374666	-2.747224951	0.00226777	mRNA	inorganic pyrophosphatase 2-like
LOC114414576	-2.757772596	0.00226777	mRNA	uncharacterized LOC114414576
LOC114388248	-2.763043854	0.00226777	mRNA	probable solanesyl-diphosphate synthase 3, chloroplastic
LOC114417194	-2.765291909	0.00226777	mRNA	O-acyltransferase WSD1-like
LOC114399413	-2.777593295	0.0251735	mRNA	alkane hydroxylase MAH1-like
LOC114370988	-2.792146286	0.00226777	mRNA	ammonium transporter 1 member 2-like
LOC114392759	-2.798712291	0.00396241	mRNA	myb-related protein 306-like
LOC114376580	-2.803368513	0.00226777	mRNA	probable solanesyl-diphosphate synthase 3, chloroplastic
LOC114420024	-2.809426164	0.00662383	mRNA	uncharacterized LOC114420024
LOC114380114	-2.810397248	0.00226777	mRNA	carotenoid 9,10(9',10')-cleavage dioxygenase 1-like, transcript variant X1
LOC114390821	-2.819271625	0.00226777	mRNA	aquaporin PIP2-2-like
LOC114422993	-2.84476231	0.00885696	mRNA	ABC transporter B family member 2-like
LOC114386703	-2.853429554	0.0144323	mRNA	uclacyanin 1-like
LOC114396815	-2.860412286	0.00226777	mRNA	serine/threonine-protein kinase STN8, chloroplastic-like, transcript variant X2
LOC114386729	-2.878489552	0.00226777	mRNA	cytochrome P450 71D10
LOC114375421	-2.892167717	0.00226777	mRNA	protein BIC2-like
LOC114381919	-2.901257235	0.00778722	mRNA	pathogenesis-related protein PR-1-like
LOC114392587	-2.901504087	0.0160163	mRNA	transmembrane protein 136-like
LOC114402534	-2.906412706	0.0109267	misc_RNA	cysteine synthase-like, transcript variant X2
LOC114374662	-2.913746484	0.00226777	mRNA	probable xyloglucan endotransglucosylase/hydrolase protein 6
LOC114383631	-2.919772434	0.00885696	mRNA	vacuolar cation/proton exchanger 3-like
LOC114374878	-2.920939058	0.00226777	mRNA	protein BIC1-like
LOC114375027	-2.923429382	0.0167884	mRNA	uncharacterized LOC114375027
LOC114394635	-2.925166702	0.00778722	mRNA	spermidine hydroxycinnamoyl transferase-like
LOC114374758	-2.927905839	0.00226777	mRNA	glucan endo-1,3-beta-glucosidase-like
LOC114382607	-2.930772097	0.00885696	mRNA	chlorophyll a-b binding protein CP29.3, chloroplastic-like
LOC114374480	-2.944495675	0.00778722	mRNA	polyphenol oxidase A1, chloroplastic-like
LOC114378505	-2.968724613	0.00226777	mRNA	uncharacterized LOC114378505
LOC114415082	-2.969074036	0.00226777	mRNA	gamma-glutamylcyclotransferase 2-1-like
LOC114367115	-2.991030898	0.00226777	mRNA	ferric reduction oxidase 7, chloroplastic-like
LOC114392755	-3.003556635	0.00226777	mRNA	uncharacterized LOC114392755
LOC114375708	-3.003857416	0.0339596	mRNA	UDP-glycosyltransferase 79B30-like
LOC114399406	-3.007932216	0.0152251	mRNA	dirigent protein 22-like
LOC114414965	-3.010773033	0.00226777	mRNA	lipid transfer protein EARLI 1-like
LOC114367251	-3.015421148	0.0183026	mRNA	NAD(P)H-quinone oxidoreductase subunit S, chloroplastic-like
LOC114419425	-3.017444066	0.0127546	mRNA	anthocyanidin 3-O-glucosyltransferase 7-like
LOC114367419	-3.03124104	0.00226777	mRNA	uncharacterized LOC114367419
LOC114389669	-3.056316161	0.00226777	mRNA	beta-carotene isomerase D27, chloroplastic-like, transcript variant X4
LOC114386942	-3.082738501	0.00885696	mRNA	boron transporter 4-like, transcript variant X2

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114396764	-3.091491764	0.00662383	mRNA	serine--glyoxylate aminotransferase-like
LOC114379813	-3.103403747	0.00226777	mRNA	actin-like, transcript variant X1
LOC114408827	-3.10677698	0.00226777	mRNA	heat shock factor protein HSF30-like, transcript variant X1
LOC114407246	-3.166821812	0.00226777	mRNA	transcription factor MYBS3-like
LOC114370989	-3.167251987	0.00226777	mRNA	ammonium transporter 1 member 2-like
LOC114374676	-3.187864101	0.00226777	mRNA	gibberellin 2-beta-dioxygenase 8-like, transcript variant X2
LOC114423581	-3.202227291	0.009937	mRNA	formyltetrahydrofolate deformylase 1, mitochondrial-like, transcript variant X2
LOC114410002	-3.247666912	0.0127546	mRNA	uncharacterized LOC114410002
LOC114402618	-3.270735426	0.00226777	mRNA	protein PROTON GRADIENT REGULATION 5, chloroplastic-like
LOC114423718	-3.286516396	0.00536398	mRNA	thioredoxin-like protein Clot
LOC114409796	-3.299382201	0.00226777	mRNA	uncharacterized protein At5g50100, chloroplastic-like
LOC114398133	-3.314651849	0.00226777	mRNA	uncharacterized LOC114398133
LOC114378408	-3.345999329	0.00226777	mRNA	beta-amylase-like, transcript variant X1
LOC114406190	-3.349237121	0.00885696	mRNA	ribulose biphosphate carboxylase/oxygenase activase 2, chloroplastic-like
LOC114395865	-3.352718261	0.042315	mRNA	ferric reduction oxidase 2-like
LOC114374526	-3.353512462	0.00226777	mRNA	uncharacterized LOC114374526
LOC114408849	-3.399782688	0.00226777	mRNA	17.1 kDa class II heat shock protein
LOC114395404	-3.428817372	0.00662383	mRNA	vacuolar cation/proton exchanger 3-like
LOC114383500	-3.45699337	0.0135986	mRNA	cucumisin-like, transcript variant X1
LOC114417322	-3.461838622	0.00226777	mRNA	aquaporin SIP1-1-like
LOC114413009	-3.470997317	0.00226777	mRNA	beta-amyrin 28-monoxygenase-like
LOC114380194	-3.481704391	0.0160163	mRNA	cyclin-U1-1-like, transcript variant X2
LOC114396684	-3.492487786	0.00226777	mRNA	asparagine synthetase, root [glutamine-hydrolyzing]-like
LOC114416308	-3.499334962	0.00226777	mRNA	TMV resistance protein N-like
LOC114403717	-3.502703142	0.0376697	mRNA	early light-induced protein, chloroplastic-like
LOC114395032	-3.512670553	0.00226777	mRNA	spermidine hydroxycinnamoyl transferase-like
LOC114407712	-3.530934355	0.0367182	mRNA	uncharacterized protein At2g34160-like, transcript variant X2
LOC114379393	-3.579943667	0.0329675	mRNA	transcription factor FER-LIKE IRON DEFICIENCY-INDUCED TRANSCRIPTION FACTOR-like
LOC114407425	-3.582254349	0.0313617	mRNA	cytochrome c oxidase subunit 5C-like, transcript variant X2
LOC114407129	-3.617929106	0.00226777	mRNA	UDP-glycosyltransferase 73C1-like
LOC114425520	-3.640632933	0.00226777	mRNA	berberine bridge enzyme-like 8
LOC114422188	-3.651121532	0.00226777	mRNA	protein CONSERVED IN THE GREEN LINEAGE AND DIATOMS 27, chloroplastic-like
LOC114369281	-3.741013108	0.00226777	mRNA	early light-induced protein, chloroplastic-like
LOC114383764	-3.759098026	0.00226777	mRNA	BURP domain protein RD22-like
LOC114386976	-3.822782542	0.00226777	mRNA	MLP-like protein 34
LOC114422664	-3.828454812	0.0189764	misc_RNA	uncharacterized LOC114422664, transcript variant X2
LOC114381794	-3.881853136	0.00226777	mRNA	beta-galactosidase 3-like
LOC114369295	-3.887301789	0.00226777	mRNA	spermidine hydroxycinnamoyl transferase-like
LOC114370132	-3.932920483	0.00226777	mRNA	protein BIC1-like
LOC114376233	-4.058803477	0.00226777	mRNA	actin
LOC114366946	-4.168161385	0.0334467	mRNA	polygalacturonase At1g48100-like, transcript variant X2

Supplementary Table 1. Continued.

Gene ID	log ₂ FoldChange	q-value (FDR)	feature	Gene name
Up-regulation				
LOC114389558	-4.226957883	0.0269311	mRNA	phospholipase A1-Igama1, chloroplastic-like
LOC114413262	-4.237070307	0.00226777	mRNA	uncharacterized LOC114413262, transcript variant X1
LOC114395880	-4.320095075	0.0494022	ncRNA	uncharacterized LOC114395880, transcript variant X1
LOC114395881	-4.361747601	0.00226777	ncRNA	uncharacterized LOC114395881, transcript variant X7
LOC114422279	-4.450255334	0.0263571	mRNA	seed linoleate 9S-lipoxygenase-like
LOC114419514	-4.525666369	0.00226777	mRNA	polyphenol oxidase I, chloroplastic-like
LOC114418777	-4.784098548	0.00662383	mRNA	patatin-like protein 3
LOC114395219	-4.820102047	0.00226777	mRNA	aureusidin synthase-like
LOC114379367	-4.87091934	0.00226777	mRNA	protein BIC1-like
LOC114415696	-4.945725278	0.00226777	mRNA	uncharacterized LOC114415696
LOC114394954	-4.966331982	0.00226777	mRNA	fatty acid desaturase 4, chloroplastic-like
LOC114424245	-5.24273022	0.0175482	mRNA	expansin-A7-like
LOC114409690	-5.747624642	0.00226777	mRNA	synaptotagmin-4-like, transcript variant X7
LOC114423382	-5.758672576	0.00226777	mRNA	spermidine hydroxycinnamoyl transferase-like
LOC114410166	-5.906065004	0.00226777	mRNA	uncharacterized LOC114410166
LOC114416970	-6.441036989	0.0152251	ncRNA	uncharacterized LOC114416970, transcript variant X6

Supplementary Table 2. List of major GO and KEGG annotations for identified DEGs under flooding stress in *Glycine soja* (p -value<0.05).

Category	GO ID	Term	p-value	Count	
Biological process	Up-regulation	GO:0006952	defense response	9.55121E-13	61
		GO:0009734	auxin-activated signaling pathway	0.00141607	48
		GO:0048544	recognition of pollen	2.28658E-24	46
		GO:0006979	response to oxidative stress	2.53767E-9	37
		GO:0042744	hydrogen peroxide catabolic process	1.3922E-12	36
		GO:0007165	signal transduction	8.97987E-5	35
		GO:0009873	ethylene-activated signaling pathway	5.19068E-12	27
		GO:0006865	amino acid transport	1.14167E-6	25
		GO:0016567	protein ubiquitination	0.00554728348	23
		GO:0006749	glutathione metabolic process	0.00014106807	17
		GO:0055085	transmembrane transport	0.0429153471	17
		GO:0009738	abscisic acid-activated signaling pathway	4.42833E-6	16
		GO:0030244	cellulose biosynthetic process	0.00107436124	12
		GO:0005992	trehalose biosynthetic process	0.000377408233	11
		GO:0016042	lipid catabolic process	0.0393506145	11
		GO:0015914	phospholipid transport	2.34185E-5	10
		GO:0046274	lignin catabolic process	0.00160802708	10
		GO:0009607	response to biotic stimulus	0.0215152401	10
		GO:0098542	defense response to other organism	0.00139148085	9
		GO:0042752	regulation of circadian rhythm	2.33843E-6	8
	GO:0009813	flavonoid biosynthetic process	0.000510127562	7	
	GO:0006826	iron ion transport	0.00012743617	6	
	GO:0006879	cellular iron ion homeostasis	0.000325585678	6	

Supplementary Table 2. Continued.

Category	GO ID	Term	p-value	Count	
Biological process	Up-regulation	GO:0006032	chitin catabolic process	0.00227255031	6
		GO:0009630	gravitropism	0.00227255031	6
		GO:2000031	regulation of salicylic acid mediated signaling pathway	0.00954030613	6
		GO:0048511	rhythmic process	0.0174541337	6
		GO:2000012	regulation of auxin polar transport	3.34882E-5	5
		GO:0009409	response to cold	0.000413669545	5
		GO:2000762	regulation of phenylpropanoid metabolic process	0.00247820382	5
		GO:0009638	phototropism	0.003434923	5
		GO:0009690	cytokinin metabolic process	0.00970184138	5
		GO:0019310	inositol catabolic process	0.00407342406	4
		GO:0009909	regulation of flower development	0.0211095816	4
		GO:0006536	glutamate metabolic process	0.0211095816	4
		GO:0019441	tryptophan catabolic process to kynurenine	0.0323566472	4
		GO:0010089	xylem development	0.0323566472	4
		GO:0042183	formate catabolic process	0.00767365361	3
		GO:2000022	regulation of jasmonic acid mediated signaling pathway	0.0238677331	3
		GO:0080037	negative regulation of cytokinin-activated signaling pathway	0.0238677331	3
		GO:0009862	systemic acquired resistance, salicylic acid mediated signaling pathway	0.0238677331	3
		GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	0.0345915574	3
		GO:0051260	protein homooligomerization	0.0345915574	3
GO:0042742	defense response to bacterium	0.0467988108	3		
Down-regulation	GO:0005975	carbohydrate metabolic process	0.000140390861	69	
	GO:0051301	cell division	1.4861E-8	42	
	GO:0007049	cell cycle	2.77485E-10	37	
	GO:0006629	lipid metabolic process	0.00264387837	26	
	GO:0006633	fatty acid biosynthetic process	0.0309443907	17	
	GO:0009058	biosynthetic process	0.020608062	15	
	GO:0006096	glycolytic process	0.00867071799	13	
	GO:0006869	lipid transport	0.0213917823	12	
	GO:0010052	guard cell differentiation	0.000162435794	11	
	GO:0010411	xyloglucan metabolic process	0.0126866217	10	
	GO:0009664	plant-type cell wall organization	0.0126866217	10	
	GO:0042546	cell wall biogenesis	0.0238174164	10	
	GO:0045893	positive regulation of transcription, DNA-templated	0.0245050234	9	
	GO:0007094	mitotic spindle assembly checkpoint	2.57132E-7	8	
	GO:0008610	lipid biosynthetic process	0.00540498681	8	
	GO:0015976	carbon utilization	7.27795E-6	7	
	GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	5.09541E-5	7	
	GO:0046148	pigment biosynthetic process	8.47019E-5	7	
	GO:0015977	carbon fixation	0.0157898957	7	
	GO:0006520	cellular amino acid metabolic process	0.0398638904	7	
	GO:0009785	blue light signaling pathway	4.12426E-6	6	
	GO:0006021	inositol biosynthetic process	7.44932E-5	6	
	GO:0009627	systemic acquired resistance	0.0227513338	6	

Supplementary Table 2. Continued.

Category		GO ID	Term	p-value	Count
Biological process	Down-regulation	GO:0007264	small GTPase mediated signal transduction	0.0431567287	6
		GO:0007059	chromosome segregation	0.00288735038	5
		GO:0007623	circadian rhythm	0.0125624013	5
		GO:0006662	glycerol ether metabolic process	0.0381282027	5
		GO:0033355	ascorbate glutathione cycle	0.00079263016	4
		GO:0042823	pyridoxal phosphate biosynthetic process	0.00362128625	4
		GO:0006546	glycine catabolic process	0.0132989106	4
		GO:0009636	response to toxic substance	0.0239043917	4
		GO:0006108	malate metabolic process	0.046214115	4
		GO:0098869	cellular oxidant detoxification	0.0101048644	3
		GO:1901671	positive regulation of superoxide dismutase activity	0.0194170986	3
		GO:0042262	DNA protection	0.0310991329	3
		GO:0006729	tetrahydrobiopterin biosynthetic process	0.0310991329	3
		GO:0006253	dCTP catabolic process	0.0310991329	3
		GO:0006597	spermine biosynthetic process	0.0448380563	3
GO:0019464	glycine decarboxylation via glycine cleavage system	0.0448380563	3		
GO:0006557	S-adenosylmethioninamine biosynthetic process	0.0448380563	3		
Cellular component	Up-regulation	GO:0016021	integral component of membrane	1.13736E-6	830
		GO:0005634	nucleus	1.20921E-5	337
		GO:0005576	extracellular region	4.83868E-8	72
		GO:0048046	apoplast	4.13997E-5	35
		GO:0031012	extracellular matrix	0.0143099889	6
		GO:0009326	formate dehydrogenase complex	0.010127	3
	Down-regulation	GO:0005576	extracellular region	0.000925639915	56
		GO:0005618	cell wall	2.04625E-5	53
		GO:0009507	chloroplast	0.000955824198	34
		GO:0048046	apoplast	0.000152278269	33
		GO:0031225	anchored component of membrane	0.000502447214	13
		GO:0009536	plastid	4.41492E-6	11
		GO:0009654	photosystem II oxygen evolving complex	0.00257757112	9
		GO:0009579	thylakoid	0.00206803907	8
		GO:0005856	cytoskeleton	0.0100021122	8
		GO:0019898	extrinsic component of membrane	0.0126791431	7
		GO:0005741	mitochondrial outer membrane	0.0182943252	6
		GO:0005667	transcription factor complex	0.0441681538	4
		GO:0033063	Rad51B-Rad51C-Rad51D-XRCC2 complex	0.00975320001	3
		GO:0000940	condensed chromosome outer kinetochore	0.0187547087	3
GO:0005960	glycine cleavage complex	0.0433692648	3		
Molecular function	Up-regulation	GO:0005524	ATP binding	2.17157E-10	403
		GO:0003700	transcription factor activity, sequence-specific DNA binding	1.79478E-33	216
		GO:0004672	protein kinase activity	5.24309E-11	150
		GO:0020037	heme binding	2.08988E-16	111
		GO:0043565	sequence-specific DNA binding	1.51977E-20	93
		GO:0004674	protein serine/threonine kinase activity	8.19598E-9	79

Supplementary Table 2. Continued.

Category	GO ID	Term	p-value	Count	
Molecular function	Up-regulation	GO:0005506	iron ion binding	3.83771E-9	76
		GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	2.30085E-10	69
		GO:0004497	monooxygenase activity	7.92702E-10	69
		GO:0030246	carbohydrate binding	3.11122E-8	60
		GO:0016491	oxidoreductase activity	0.0111251315	59
		GO:0043531	ADP binding	7.32507E-5	50
		GO:0004601	peroxidase activity	1.70261E-7	41
		GO:0008194	UDP-glycosyltransferase activity	0.000160993475	31
		GO:0030247	polysaccharide binding	3.0972E-14	30
		GO:0015293	symporter activity	4.37338E-6	28
		GO:0042626	ATPase activity, coupled to transmembrane movement of substances	0.00360311592	28
		GO:0003824	catalytic activity	0.014953818	28
		GO:0016747	transferase activity, transferring acyl groups other than amino-acyl groups	0.000169233184	24
		GO:0004842	ubiquitin-protein transferase activity	0.0351890138	24
		GO:0004864	protein phosphatase inhibitor activity	4.16734E-6	15
		GO:0042910	xenobiotic transporter activity	0.0318533761	14
		GO:0010427	abscisic acid binding	2.5251E-9	13
		GO:0038023	signaling receptor activity	2.5251E-9	13
		GO:0004568	chitinase activity	1.47368E-5	13
		GO:0016760	cellulose synthase (UDP-forming) activity	0.00955969174	11
		GO:0008171	O-methyltransferase activity	0.0128259575	11
		GO:0004866	endopeptidase inhibitor activity	0.00531927014	10
		GO:0052716	hydroquinone:oxygen oxidoreductase activity	0.00603558567	10
		GO:0005199	structural constituent of cell wall	7.05489E-5	7
		GO:0016210	naringenin-chalcone synthase activity	0.000409136591	7
		GO:0003825	alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity	0.00108889882	7
		GO:0008061	chitin binding	0.00570339194	7
		GO:0015145	monosaccharide transmembrane transporter activity	0.00570339194	7
		GO:0015276	ligand-gated ion channel activity	0.0296474578	7
		GO:0004322	ferroxidase activity	0.00052639276	6
		GO:0008199	ferric iron binding	0.000811295186	6
		GO:0051740	ethylene binding	0.0023834112	5
		GO:0038199	ethylene receptor activity	0.0023834112	5
		GO:0019139	cytokinin dehydrogenase activity	0.0189967112	5
		GO:0050664	oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	0.0280095274	5
		GO:0004659	prenyltransferase activity	0.0455828522	5
		GO:0004833	tryptophan 2,3-dioxygenase activity	0.00223699484	4
		GO:0050113	inositol oxygenase activity	0.00711711646	4
		GO:0004066	asparagine synthase (glutamine-hydrolyzing) activity	0.0155372542	4
		GO:0004351	glutamate decarboxylase activity	0.0353475173	4
GO:0008863	formate dehydrogenase (NAD+) activity	0.0112994668	3		
GO:0047780	citrate dehydratase activity	0.0497808608	3		
GO:0003994	aconitate hydratase activity	0.0497808608	3		
GO:0052634	C-19 gibberellin 2-beta-dioxygenase activity	0.0497808608	3		

Supplementary Table 2. Continued.

Category	GO ID	Term	p-value	Count	
Molecular function	Down-regulation	GO:0046872	metal ion binding	0.0428909759	192
		GO:0016491	oxidoreductase activity	6.54662E-8	80
		GO:0046983	protein dimerization activity	0.0306194804	63
		GO:0020037	heme binding	0.0350029232	61
		GO:0005506	iron ion binding	0.00264840469	55
		GO:0005509	calcium ion binding	0.033757221	41
		GO:0016788	hydrolase activity, acting on ester bonds	2.48658E-8	37
		GO:0008194	UDP-glycosyltransferase activity	4.55971E-7	37
		GO:0009055	electron carrier activity	6.65108E-5	24
		GO:0016747	transferase activity, transferring acyl groups other than amino-acyl groups	0.000147278913	24
		GO:0008289	lipid binding	0.0452527707	20
		GO:0004650	polygalacturonase activity	0.00032122059	19
		GO:0015267	channel activity	0.000189415811	16
		GO:0003993	acid phosphatase activity	1.71821E-5	15
		GO:0016791	phosphatase activity	0.0180999162	15
		GO:0008171	O-methyltransferase activity	0.000386189989	14
		GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	0.000377114542	13
		GO:0004364	glutathione transferase activity	0.00139071445	12
		GO:0097573	glutathione oxidoreductase activity	0.017308063	12
		GO:0004866	endopeptidase inhibitor activity	0.0050008417	10
		GO:0016762	xyloglucan:xyloglucosyl transferase activity	0.0153738728	10
		GO:0016746	transferase activity, transferring acyl groups	0.0337888829	10
		GO:0004089	carbonate dehydratase activity	0.000372269885	9
		GO:0052886	9,9'-dicis-carotene:quinone oxidoreductase activity	0.000747591473	9
		GO:0052887	7,9,9'-tricis-neurosporene:quinone oxidoreductase activity	0.000747591473	9
		GO:0016719	carotene 7,8-desaturase activity	0.000747591473	9
		GO:0005544	calcium-dependent phospholipid binding	0.00137999909	9
		GO:0048038	quinone binding	0.0343173819	9
		GO:0016717	oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	4.34149E-6	8
		GO:0016655	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor	9.62982E-6	7
		GO:0019901	protein kinase binding	0.000175072409	7
		GO:0004097	catechol oxidase activity	0.00544591159	7
		GO:0015035	protein disulfide oxidoreductase activity	0.0284639769	7
		GO:0042132	fructose 1,6-bisphosphate 1-phosphatase activity	0.000309676437	6
		GO:0005504	fatty acid binding	0.031386155	6
		GO:0051920	peroxiredoxin activity	0.00145188303	5
		GO:0015369	calcium:proton antiporter activity	0.0089805757	5
		GO:0004332	fructose-bisphosphate aldolase activity	0.0116526099	5
		GO:0045174	glutathione dehydrogenase (ascorbate) activity	0.000912725252	4
		GO:0004512	inositol-3-phosphate synthase activity	0.00217601119	4
GO:0004619	phosphoglycerate mutase activity	0.0105781488	4		
GO:0047911	galacturan 1,4-alpha-galacturonidase activity	0.0151412817	4		
GO:0004311	farnesyltranstransferase activity	0.034492593	4		

Supplementary Table 2. Continued.

Category		GO ID	Term	p-value	Count		
Molecular function	Down-regulation	GO:0000978	RNA polymerase II core promoter proximal region sequence-specific DNA binding	0.034492593	4		
		GO:0004506	squalene monooxygenase activity	0.0428176752	4		
		GO:0046914	transition metal ion binding	0.0212690998	3		
		GO:0002953	5'-deoxynucleotidase activity	0.0212690998	3		
		GO:0008124	4-alpha-hydroxytetrahydrobiopterin dehydratase activity	0.0339978255	3		
		GO:0004014	adenosylmethionine decarboxylase activity	0.0489212931	3		
		GO:0004673	protein histidine kinase activity	0.0489212931	3		
		GO:0044183	protein binding involved in protein folding	0.0489212931	3		
KEGG pathway	Up-regulation	gsj01100	Metabolic pathways	8.24986E-7	334		
		gsj01110	Biosynthesis of secondary metabolites	3.47592E-24	266		
		gsj04075	Plant hormone signal transduction	1.44995E-7	72		
		gsj04016	MAPK signaling pathway - plant	9.08653E-15	60		
		gsj04626	Plant-pathogen interaction	1.77277E-8	56		
		gsj00940	Phenylpropanoid biosynthesis	8.24342E-9	46		
		gsj00500	Starch and sucrose metabolism	0.0120872844	30		
		gsj02010	ABC transporters	8.39668E-8	24		
		gsj00943	Isoflavonoid biosynthesis	6.90958E-13	23		
		gsj00270	Cysteine and methionine metabolism	0.0433305987	22		
		gsj00941	Flavonoid biosynthesis	0.000277652556	18		
		gsj00480	Glutathione metabolism	0.0367179882	18		
		gsj00250	Alanine, aspartate and glutamate metabolism	0.000283816553	17		
		gsj00999	Biosynthesis of various plant secondary metabolites	0.000919927181	15		
		gsj00592	alpha-Linolenic acid metabolism	0.00281828319	15		
		gsj00908	Zeatin biosynthesis	2.16001E-5	14		
		gsj04712	Circadian rhythm - plant	0.0167202104	13		
		gsj00460	Cyanoamino acid metabolism	0.00764080442	12		
		gsj00410	beta-Alanine metabolism	0.0492303806	12		
		gsj00960	Tropane, piperidine and pyridine alkaloid biosynthesis	0.0155708141	10		
		gsj00430	Taurine and hypotaurine metabolism	0.0450421594	5		
		gsj00966	Glucosinolate biosynthesis	0.0491082695	4		
		Down-regulation	Down-regulation	gsj01100	Metabolic pathways	1.25641E-21	426
				gsj01110	Biosynthesis of secondary metabolites	2.56924E-20	279
				gsj01200	Carbon metabolism	6.1022E-8	69
				gsj01240	Biosynthesis of cofactors	0.036949815	46
gsj00710	Carbon fixation in photosynthetic organisms			1.10462E-10	33		
gsj00010	Glycolysis / Gluconeogenesis			0.00178771154	33		
gsj00940	Phenylpropanoid biosynthesis			0.0184905161	31		
gsj00941	Flavonoid biosynthesis			1.87174E-7	25		
gsj00630	Glyoxylate and dicarboxylate metabolism			5.95576E-6	25		
gsj00480	Glutathione metabolism			0.00359812324	23		
gsj00260	Glycine, serine and threonine metabolism			5.43413E-5	22		
gsj00380	Tryptophan metabolism			0.000272774931	19		
gsj00051	Fructose and mannose metabolism			0.00303723422	19		
gsj01232	Nucleotide metabolism			0.0455929997	18		

Supplementary Table 2. Continued.

Category	GO ID	Term	p-value	Count	
KEGG pathway	Down-regulation	gsj00350	Tyrosine metabolism	0.000450300174	17
		gsj00053	Ascorbate and aldarate metabolism	0.00748374443	17
		gsj00945	Stilbenoid, diarylheptanoid and gingerol biosynthesis	2.18604E-6	16
		gsj00030	Pentose phosphate pathway	0.01027323	16
		gsj00240	Pyrimidine metabolism	0.0273023954	16
		gsj00950	Isoquinoline alkaloid biosynthesis	3.03975E-6	15
		gsj00910	Nitrogen metabolism	0.00039102968	14
		gsj00906	Carotenoid biosynthesis	0.000462224253	14
		gsj00130	Ubiquinone and other terpenoid-quinone biosynthesis	0.0360994235	13
		gsj00750	Vitamin B6 metabolism	0.00166266452	8
		gsj00909	Sesquiterpenoid and triterpenoid biosynthesis	0.0143113692	7
		gsj00944	Flavone and flavonol biosynthesis	0.0102855089	6
		gsj00965	Betalain biosynthesis	0.0110249884	4