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APPENDICES

APPENDIX A
CHEMICAL SOLUTIONS

1. Modified WP No.2 nutrient solution (Vajrabhaya and Vajrabhaya, 1991)

Chemicals	Content (mg/L)
Macroelements	
Potassium nitrate (KNO ₃)	580
Calcium sulfate (CaSO ₄)	500
Magnesium sulfate (MgSO ₄ .7H ₂ O)	450
Triple superphosphate	250
Ammonium sulfate ((NH ₄) ₂ SO ₄)	100
Microelements	
Di-sodium ethylene diamine tetraacetate (Na ₂ EDTA) ^a	160
Ferrous sulfate (FeSO ₄ .7H ₂ O) ^a	120
Manganese sulfate (MnSO ₄ .H ₂ O)	15
Boric acid (H ₃ BO ₃)	5
Zinc sulfate (ZnSO ₄ .7H ₂ O)	1.5
Potassium iodide (KI)	1.0
Sodium molybdate (Na ₂ MoO ₄ . 2H ₂ O)	0.1
Copper sulfate(CuSO ₄ . 5H ₂ O)	0.05
Cobalt chloride (CoCl ₂ . 6H ₂ O)	0.05

^a Preparation of 30 g/L FeSO₄ stock solution

Na ₂ EDTA	40 g
FeSO ₄ .7H ₂ O	30 g

Stir each chemical separately in distilled water with a magnetic stirrer and adjust the total volume to 1 L



2. Solution preparation for proteomic analysis

2.1 Protein extraction

0.1% (w/v) SDS

2.2 Deoxycholate-trichloroacetic acid (DOC-TCA) precipitation

0.15% (w/v) DOC 950 μ l

72% (w/v) TCA 100 μ l

2.3 Lowry protein assay

Reagent A:

0.2% CuSO_4 + 0.4% tartaric acid 5 ml

20% Na_2CO_3 5 ml

0.8 N NaOH 10 ml

5% SDS 20 ml

Reagent B:

Folin-Ciocalteu phenol 10 ml

Distilled water 50 ml

2.4 Tris-glycine running buffer pH 8.3

Tris base 1.514 g

Glycine 7.2 g

SDS 0.5 g

Distilled water 850 ml

2.5 Protein loading buffer

50 mM Tris.HCl pH 6.8

2% SDS

10% Glycerol

12.5 mM EDTA

0.02 % Bromophenol Blue

2.6 Separating and Stacking gel preparation for SDS-PAGE analysis

Separating gel:

Reagents	Content (μ l)
40% (w/v) acrylamide/bis-acrylamide solution (29:1)	3125
1.5 M Tris.HCl pH 8.8	2500
10% SDS	125
10% ammonium persulfate (APS)	50
Tetramethylethylenediamine (TEMED)	6
Distilled water	4200

Stacking gel:

Reagents	Content (μ l)
40% (w/v) acrylamide/bis-acrylamide solution (29:1)	300
0.5 M Tris.HCl pH 6.8	742
10% SDS	30
10% ammonium persulfate (APS)	23
Tetramethylethylenediamine (TEMED)	3.5
Distilled water	1900

2.7 Coomassie brilliant blue staining

Coomassie brilliant blue R 250	5 g
Acetic acid	100 ml
Methanol	500 ml
Distilled water	400 ml

2.8 Destaining solution

Acetic acid	100 ml
Methanol	200 ml
Distilled water	700 ml



3. DNA and RNA electrophoresis

3.1 5x TBE

Tris base	54 g
Boric acid	27.5 g
0.5 M EDTA pH 8.0	20 ml

For 0.5x TBE diluted with sterile distilled water

3.2 DNA and RNA loading dyes

50% (v/v) glycerol in water
0.25% (w/v) bromophenol blue
0.25% (w/v) xylene cyanol FF

4. Genomic DNA extraction buffer

150 mM Tris pH 8.0
50 mM EDTA pH 8.0
500 mM NaCl
0.7% SDS
50 µg/ml DNase-free RNase A

5. 5x Second strand synthesis buffer

200 mM Tris.HCl pH 7.0
22 mM MgCl ₂
425 mM KCl



APPENDIX B
PROTEOMIC ANALYSIS

1. Protein Standard

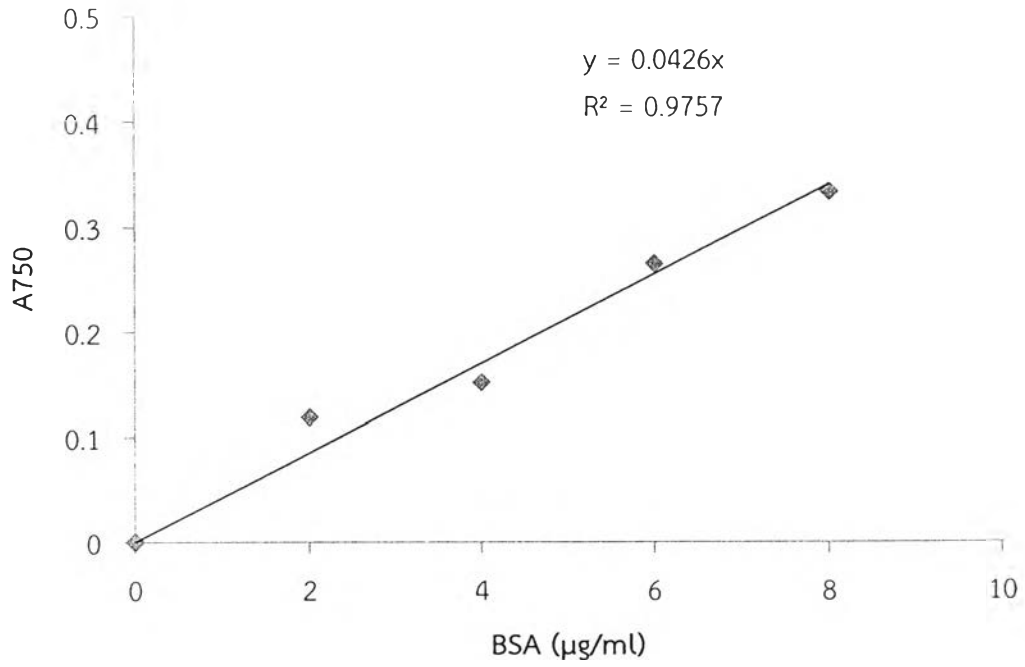


Figure B.1 Standard curve of standard protein (BSA)



2. One-dimensional SDS-PAGE of total protein extracts

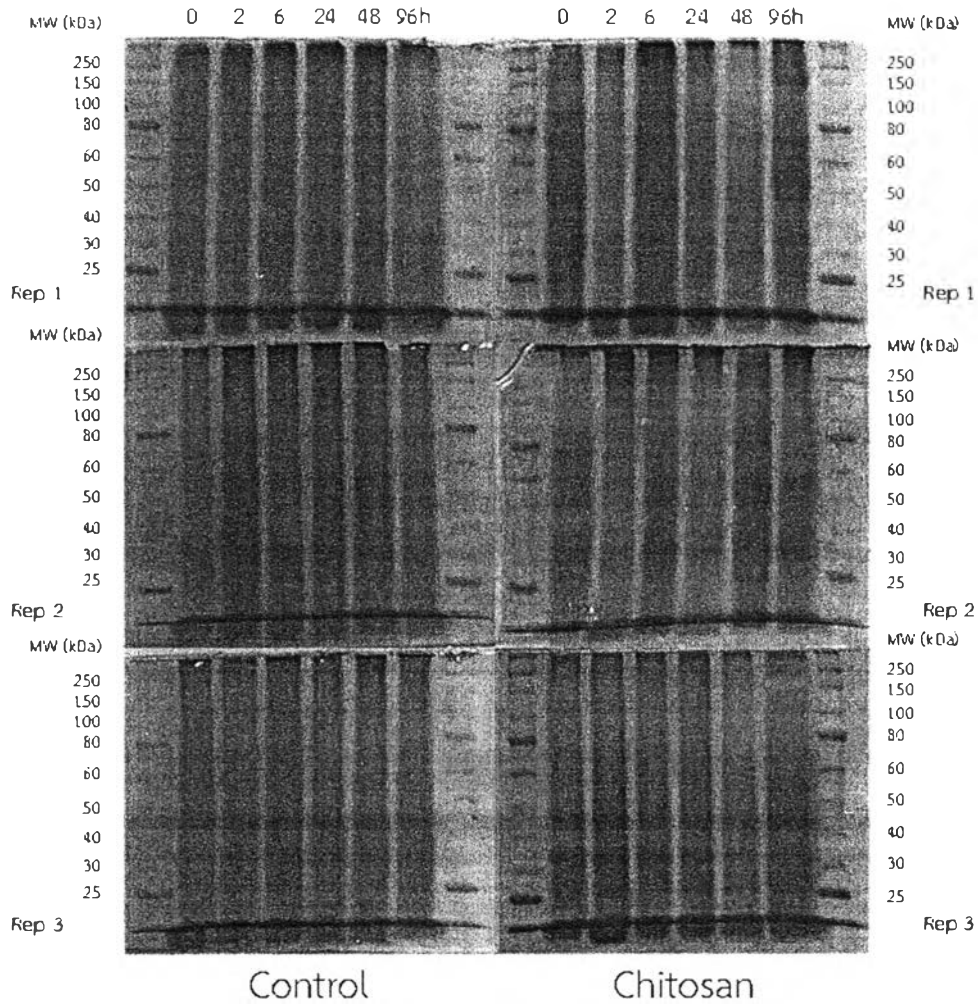


Figure B.2 The total protein extract of 'LPT123' leaves treated with water (left) or 40mg/L of chitosan O80 (right) at 0, 2, 6, 24, 48, and 96 hours after transferred to new freshly prepared nutrient solution with three independent biological replications. The protein were separated on 12.5% SDS-PAGE and visualized by coomassie blue staining. Only proteins from leaves of rice seedlings at 0 and 24 hours were analyzed by proteomic analysis for this study.

3. Protein ladder

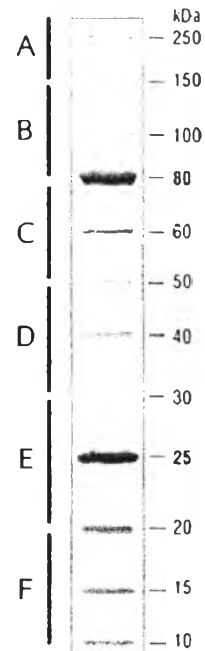


Figure B.3 Protein ladder (10-250 kDa, New England Biolabs). The letters indicated the range of protein size for markers; A (>150 kDa), B (80-150 kDa), C (50-80 kDa), D (30-50 kDa), E (20-30 kDa), and F (10-20 kDa).

4. Coomassie blue staining

Stain and destain solutions were freshly prepared prior to use. After gel electrophoresis, gel was stained for 2 hours at room temperature with gentle agitation. After that, gel was destained for an hour with changing the destain solution three times before overnight shaking until protein bands were seen and background color is clear.



LOC	Description	Function	ID Score	Mass (Da)	Peptide
LOC_Os11g13990	AAA-type ATPase family protein, putative, expressed	ATPase	13.48	563.847	AHIPK
LOC_Os11g47970	AAA-type ATPase family protein, putative, expressed	ATPase	53.86	1152.790	VPLILGIWGGK
LOC_Os04g41759	Wxpressed protein	carbohydrate metabolic process	9.41	627.189	VPQGAR
LOC_Os06g06560	Starch synthase	carbohydrate metabolic process	7.81	2270.303	DNIQFVMLGSGDPPGFEGWMR
LOC_Os01g74000	Glycerol-3-phosphate dehydrogenase, putative, expressed	carbohydrate metabolic process	7.31	578.901	AAIMR
LOC_Os02g14900	1,3-beta-glucan synthase component domain containing protein, expressed	carbohydrate metabolic process	15.16	519.304	SGSIR
LOC_Os04g16680	Fructose-1,6-bisphosphatase	carbohydrate metabolic process	32.14	1235.984	GIFTNVTSPYAK
LOC_Os04g38600	Glyceraldehyde-3-phosphate dehydrogenase, putative, expressed	carbohydrate metabolic process	87.70	1787.637	VIAWYDNEWGYSQR
LOC_Os06g40640	Fructose-bisphosphate aldolase isozyme, putative, expressed	carbohydrate metabolic process	76.18	1453.545	LASINVENVEPNR
LOC_Os07g10680	Polygalacturonase, putative, expressed	carbohydrate metabolic process	13.93	591.230	GGGSDAK
LOC_Os07g47120	Beta-amylase, putative, expressed	carbohydrate metabolic process	12.94	562.421	CGAVR
LOC_Os10g20650	Glucan endo-1,3-beta-glucosidase-related, putative, expressed	carbohydrate metabolic process	15.59	1217.357	QEPMAAAATRR
LOC_Os05g09620	SCC3, putative, expressed	cell division	8.21	521.173	ASGSNS
LOC_Os08g33430	Formin, putative, expressed	cellular component	7.78	580.147	GMAMR
LOC_Os04g38470	2-Cys peroxiredoxin BAS1, chloroplast precursor, putative, expressed	defense response	6.42	844.451	SMMFSAR
LOC_Os01g54510	MAC/Perforin domain containing protein, putative, expressed	defense response	11.23	772.344	YSLLNK
LOC_Os04g02030	RP1, expressed	defense response	16.80	1400.955	CPNLRALGEDQK
LOC_Os08g09770	DnaK family protein, putative, expressed	defense response	14.34	702.733	TMVPVR
LOC_Os09g20330	Annexin, putative, expressed	defense response	12.09	595.761	TTFAR
LOC_Os01g61880	Respiratory burst oxidase, putative, expressed	defense response	16.02	736.768	TTSSLAR
LOC_Os03g27460	Heat shock protein DnaJ	defense response	18.31	566.181	GGYGGR
LOC_Os04g58090	Harpin-induced protein 1 domain containing protein, expressed	defense response	6.24	870.619	STVSYGEK
LOC_Os10g25487	NBS-LRR disease resistance protein, putative, expressed	defense response	11.82	756.284	LPSSIIK
LOC_Os03g11040	Cyclin, putative, expressed	developmental process	9.10	746.281	QPAMSGR
LOC_Os03g31360	Glutelin, putative, expressed	developmental process	4.47	539.265	VVEHG
LOC_Os10g09990	Cytokinin-O-glucosyltransferase 3	developmental process	2.50	511.070	HVGAQ
LOC_Os01g05630	Core histone H2A/H2B/H3/H4 domain containing protein	DNA binding	70.35	1791.200	AMSIMNSFINDIFEK

5. List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis



5. (cont.) List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis

LOC	Description	Function	ID Score	Mass (Da)	Peptide
LOC_Os01g49270	XPA-binding protein 2	DNA repair	12.56	655.422	AHAEAR
LOC_Os07g38600	REX1 DNA Repair family protein, expressed	DNA repair	14.58	989.556	AENMVNAIK
LOC_Os12g18770	Oxysterol-binding protein	lipid metabolic process	16.87	1165.261	WVNYGKGWR
LOC_Os02g15230	GDSL-like lipase/acylhydrolase, putative, expressed	lipid metabolic process	13.15	533.374	MGAVR
LOC_Os04g55060	3-oxoacyl-synthase III, chloroplast precursor, putative, expressed	lipid metabolic process	12.13	459.021	GGGIR
LOC_Os07g38850	Prenyltransferase, putative, expressed	lipid metabolic process	10.00	2183.111	FLRPHTIRGTALGMSLVAR
LOC_Os01g04200	Metallo-beta-lactamase family protein, putative, expressed	metabolic process	15.48	616.828	NSGNEP
LOC_Os03g08999	Dehydrogenase, putative, expressed	metabolic process	6.29	519.434	DGTAR
LOC_Os06g17090	UDP-glycosyltransferase	metabolic process	8.71	537.740	AGAYR
LOC_Os06g37300	Cytochrome P450	metabolic process	9.34	1003.561	DAIMNALIK
LOC_Os08g43430	CXE carboxylesterase, putative, expressed	metabolic process	11.33	1225.576	GDVTAAPPSPDK
LOC_Os10g21266	ATP synthase subunit beta	metabolic process	48.36	1328.383	AHGGVSVFGGVGER
LOC_Os01g07530	Uncharacterized glycosyltransferase, putative, expressed	Metabolic process	17.95	540.398	VVAPR
LOC_Os01g11300	Cytochrome P450, putative, expressed	metabolic process	6.70	585.475	AEPIR
LOC_Os01g61380	Lactate/malate dehydrogenase, putative, expressed	metabolic process	11.23	677.069	QQAAATS
LOC_Os01g61460	Leaf senescence related protein, putative, expressed	metabolic process	13.78	514.296	TAAPR
LOC_Os01g62800	Methyltransferase	metabolic process	12.47	835.421	APIPWPR
LOC_Os01g66180	Cytochrome c, putative, expressed	metabolic process	11.44	483.845	AAGHK
LOC_Os01g74650	Cysteine synthase, mitochondrial precursor, putative, expressed	metabolic process	25.23	1114.988	IQGIGAGFVPR
LOC_Os02g26710	Cyclo-DOPA 5-O-glucosyltransferase, putative	metabolic process	13.24	617.363	GGSAVVK
LOC_Os03g14450	Enolase, putative, expressed	metabolic process	93.79	1573.714	VNQIGSVTESIEAVK
LOC_Os03g18640	Laccase precursor protein, putative, expressed	metabolic process	14.30	766.243	ATFGLEK
LOC_Os04g16740	ATP synthase subunit alpha, putative, expressed	metabolic process	33.60	1416.565	IAQIPVSEAYLGR
LOC_Os04g20260	UDP-glucuronosyl and UDP-glucosyl transferase	metabolic process	9.65	1031.019	DGAMSHQLR
LOC_Os05g33400	Basic 7S globulin precursor, putative, expressed	metabolic process	10.94	533.080	VASTR
LOC_Os06g02180	CSLD2 - cellulose synthase-like family D	metabolic process	5.46	761.359	ASSGGGGLR
LOC_Os06g04270	Transketolase, chloroplast precursor, putative, expressed	metabolic process	55.28	1085.794	AVTDKPTLIK



LOC	Description	Function	ID Score	Mass (Da)	Peptide
LOC_Os06g43490	Cytochrome P450, putative, expressed	metabolic process	4.00	525.208	VPLPV
LOC_Os06g48620	4-amino-4-deoxychorismate synthase, putative, expressed	metabolic process	10.27	758.590	ISSPOLK
LOC_Os07g38620	Pyridoxamine 5'-phosphate oxidase family protein, putative, expressed	metabolic process	5.20	883.025	FLHIKPK
LOC_Os07g44840	Bacterial transferase hexapeptide domain containing protein,	metabolic process	5.45	1833.725	GTGQAMDRLGSTIQGGLR
LOC_Os07g46852	Sex determination protein tasselseed-2, putative, expressed	metabolic process	16.50	589.541	VMAPR
LOC_Os07g46980	Sex determination protein tasselseed-2	metabolic process	16.50	589.541	VMAPR
LOC_Os08g01150	DTA2, putative, expressed	metabolic process	15.34	1030.859	MRGSSNNHK
LOC_Os08g01750	SAC domain containing protein, putative, expressed	metabolic process	22.08	957.119	FYLIGTSR
LOC_Os08g14180	Flavonol sulfotransferase, putative, expressed	metabolic process	15.34	710.817	GGGGLVPR
LOC_Os08g39694	cytochrome P450, putative, expressed	metabolic process	23.52	594.480	GGPAHR
LOC_Os08g40330	Sulfotransferase domain containing protein, expressed	metabolic process	15.43	1519.669	LLSTHMPPQLLPR
LOC_Os10g08550	Enolase, putative, expressed	metabolic process	44.03	1887.851	LAMQEFMILPTGAASFK
LOC_Os10g11140	Phosphoglucomutase, putative, expressed	metabolic process	19.89	773.482	DKPTVIT
LOC_Os10g31780	Oxidoreductase, short chain dehydrogenase/reductase family domain containing protein, expressed	metabolic process	11.90	697.693	IPAGAGGR
LOC_Os11g07020	Fructose-bisphosphate aldolase isozyme	metabolic process	64.39	1351.978	ATPEQVSDYTLK
LOC_Os11g26850	Erythronate-4-phosphate dehydrogenase, putative, expressed	metabolic process	43.24	827.966	IVLTIIR
LOC_Os01g31690	Oxygen-evolving enhancer protein 1, chloroplast precursor	photosynthesis	39.04	964.936	VPFLFTIK
LOC_Os02g01340	Ferredoxin--NADP reductase, chloroplast precursor	photosynthesis	8.03	833.001	RSSGNQVR
LOC_Os03g03720	Glyceraldehyde-3-phosphate dehydrogenase, putative, expressed	photosynthesis	41.91	1051.837	AVALVLPQLK
LOC_Os07g35860	Plastocyanin-like domain containing protein	photosynthesis	10.09	548.429	YGPVI
LOC_Os09g17740	Chlorophyll A-B binding protein	photosynthesis	49.36	983.512	FGEAVWFK
LOC_Os10g21268	ribulose biphosphate carboxylase large chain precursor, putative, expressed	photosynthesis	72.89	2410.059	LTYYPPEYETKDTDILAAFR
LOC_Os12g17600	ribulose biphosphate carboxylase small chain, chloroplast precursor	photosynthesis	28.13	1230.747	XQVWPIEGIK
LOC_Os12g19381	ribulose biphosphate carboxylase small chain, chloroplast precursor	photosynthesis	62.22	1597.297	LPMFGCTDATQVLK
LOC_Os02g17360	PPR repeat domain containing protein	post transcription	13.09	674.040	AAEGAGAK
LOC_Os01g04710	Aspartic proteinase, expressed	protein metabolic process	19.71	608.360	DAFVR

5. (cont.) List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis



LOC	Description	Function	ID Score	Mass (Da)	Peptide
LOC_Os01g16200	Serpin domain containing protein, putative, expressed	protein metabolic process	10.37	630.057	AGGPTAR
LOC_Os03g52070	OssSCP20 - Putative Serine Carboxypeptidase homologue, expressed	protein metabolic process	13.32	1446.205	LQGYIVGNPITGSK
LOC_Os03g58204	Ribosomal protein L4, putative, expressed	protein metabolic process	44.86	1282.937	NLPGVDVANVER
LOC_Os04g15790	Eukaryotic aspartyl protease domain containing protein, expressed	protein metabolic process	13.09	517.282	DGIGR
LOC_Os04g56400	Glutamine synthetase, catalytic domain containing protein, expressed	protein metabolic process	10.06	591.382	GCSIR
LOC_Os06g42810	UBA and UBX domain-containing protein	protein metabolic process	24.77	778.593	MAAGDAAR
LOC_Os07g09670	Galactosyltransferase family protein, putative, expressed	protein metabolic process	7.01	862.698	KLQSGSSR
LOC_Os11g13560	Serpin domain containing protein, putative, expressed	protein metabolic process	3.18	543.199	AVEPK
LOC_Os01g39810	Alg9-like mannosyltransferase protein	protein modification process	14.83	826.717	AANALLVR
LOC_Os02g01010	OsPDIL1-4 protein disulfide isomerase PDIL1-4, expressed	protein modification process	6.69	513.887	IWVGK
LOC_Os04g35680	U-box domain containing protein, expressed	protein modification process	14.17	558.501	APGGTR
LOC_Os08g32970	annexin, putative, expressed	protein modification process	16.31	761.971	CAESPAK
LOC_Os05g51550	DNA binding protein, putative, expressed	replication	30.94	790.850	MILLMR
LOC_Os08g07840	Poll-like DNA polymerase, putative, expressed	replication	14.28	2461.713	AAINAPQGSAADVAMCAMEIER
LOC_Os08g36330	POLE2B - Putative DNA polymerase epsilon complex subunit, expressed	replication	10.83	774.065	ATPSAATR
LOC_Os10g26280	ORC3 - Putative origin recognition complex subunit 3, expressed	replication	8.42	1882.610	SGDNMVDGLSELMNIQK
LOC_Os01g38740	Retrotransposon protein, , Ty1-copia subclass, expressed	retrotransposon	9.46	1176.152	LIKDNMVAR
LOC_Os03g17340	Retrotransposon protein, putative, unclassified, expressed	retrotransposon	12.63	932.826	SSPADYHR
LOC_Os03g30190	Retrotransposon protein, putative, unclassified, expressed	retrotransposon	16.40	861.993	GKTSQVSR
LOC_Os04g04530	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed	retrotransposon	4.98	585.304	VTPIR
LOC_Os05g21120	Retrotransposon protein, putative, unclassified, expressed	retrotransposon	27.09	902.509	KINLLSSK
LOC_Os05g38910	Retrotransposon protein, putative, unclassified, expressed	retrotransposon	20.34	534.053	VAGMR
LOC_Os06g26290	Retrotransposon protein, , Ty3-gypsy subclass, expressed	retrotransposon	8.16	1606.019	AAHMPTMAAEDDSAR
LOC_Os09g21650	Retrotransposon protein, putative, Ty3-gypsy subclass, expressed	retrotransposon	14.26	795.484	FMGNPGR
LOC_Os12g14020	Retrotransposon protein, Ty3-gypsy subclass, expressed	retrotransposon	9.36	498.817	GGPIR
LOC_Os12g25570	Retrotransposon protein, Ty3-gypsy subclass, expressed	retrotransposon	8.83	829.250	EPADVGNK
LOC_Os04g03260	Retrotransposon protein, Ty3-gypsy subclass, expressed	retrotransposon	7.70	589.229	GSVTPK

5. (cont.) List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis



LOC	Description	Function	ID Score	Mass (Da)	Peptide
LOC_Os10g09500	Retrotransposon protein, Ty3-gypsy subclass, expressed	retrotransposon	33.71	905.847	DEICKLK
LOC_Os12g23030	Retrotransposon protein, unclassified, expressed	retrotransposon	15.89	1294.879	VIVFGGDFRQR
LOC_Os01g71840	Retrotransposon protein, unclassified, expressed	retrotransposon	5.86	1758.548	SALPSVRFFGDMFIR
LOC_Os03g38284	Retrotransposon protein, unclassified, expressed	retrotransposon	5.12	525.780	PGVPR
LOC_Os03g41790	Retrotransposon, centromere-specific, expressed	retrotransposon	10.82	624.133	GAGQHR
LOC_Os04g27420	Retrotransposon protein, expressed	retrotransposon	14.41	824.592	ISIGNGHK
LOC_Os10g12630	Retrotransposon protein, Ty3-gypsy subclass, expressed	retrotransposon	18.00	928.293	ANVADALR
LOC_Os11g22160	Retrotransposon protein, unclassified, expressed	retrotransposon	7.73	729.026	VAGVGNR
LOC_Os11g30880	Retrotransposon protein, expressed	retrotransposon	6.95	599.822	AGVKPK
LOC_Os12g09480	Retrotransposon protein, Ty3-gypsy subclass, expressed	retrotransposon	8.30	1234.435	GVLNVENTVGSK
LOC_Os02g34030	Retrotransposon protein, unclassified, expressed	retrotransposon	6.18	905.380	NWASGSR
LOC_Os04g29120	Retrotransposon protein	retrotransposon	17.04	548.449	GGMER
LOC_Os06g38019	Retrotransposon protein, unclassified	retrotransposon	9.87	623.755	GEGGMR
LOC_Os11g17700	Retrotransposon protein, unclassified, expressed	retrotransposon	4.02	756.965	DPGPSEK
LOC_Os11g42630	Retrotransposon protein, Ty3-gypsy subclass, expressed	retrotransposon	18.91	668.357	ADGGGHR
LOC_Os12g09530	Retrotransposon protein, putative, unclassified, expressed	retrotransposon	1.25	831.026	SMGGMGFK
LOC_Os12g16840	Retrotransposon protein, Ty3-gypsy subclass, expressed	retrotransposon	10.43	604.419	GYAHR
LOC_Os01g22370	Peroxidase precursor, putative, expressed	ROS scavenging system	41.00	1146.127	LVQQAVAAAFK
LOC_Os02g14170	Peroxidase precursor, putative, expressed	ROS scavenging system	5.58	460.160	AVGGR
LOC_Os03g03910	Catalase domain containing protein, expressed	ROS scavenging system	69.36	1136.550	APGVQTPVIVR
LOC_Os06g51150	Catalase isozyme B, putative, expressed	ROS scavenging system	69.36	1136.550	APGVQTPVIVR
LOC_Os02g33450	Peroxiredoxin, putative, expressed	ROS scavenging system	19.90	1486.717	SFGLIPDQGIALLR
LOC_Os04g33970	2-Cys peroxiredoxin BAS1, chloroplast precursor, putative, expressed	ROS scavenging system	73.79	2508.231	GLFIIDKEGVIQHSTINLAIGR
LOC_Os12g08730	Thioredoxin	ROS scavenging system	24.69	1051.997	SIPTVLMFK
LOC_Os01g12390	Inactive receptor kinase At2g26730 precursor	signal transduction	19.70	773.322	EVSAGRR
LOC_Os03g62500	CGMC_GSK.5 - CGMC includes CDA, MAPK, GSK3, and CLKC kinases, expressed	signal transduction	17.05	1121.142	RQSLFMALR
LOC_Os04g08170	CBL-interacting protein kinase	signal transduction	3.79	461.540	AGGTR

5. (cont.) List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis



LOC	Description	Function	ID Score	Mass (Da)	Peptide
LOC_Os04g45170	Leucine-rich repeat family protein, putative, expressed	signal transduction	17.51	1722.726	MFACVDDDLLANVPK
LOC_Os08g01900	Armadillo/beta-catenin repeat family protein	signal transduction	14.34	749.208	SATSDIR
LOC_Os12g26940	CHASE domain containing protein, expressed	signal transduction	6.27	1837.149	QLLLVYELMAQGSLDK
LOC_Os12g34320	S-locus-like receptor protein kinase, putative, expressed	signal transduction	9.42	535.468	GTNSR
LOC_Os01g08140	Phototropic-responsive NPH3 family protein, putative, expressed	signal transduction	25.90	1140.856	GGAAGAAAATPTPK
LOC_Os01g62760	Protein phosphatase 2C, putative, expressed	signal transduction	9.07	809.973	ICSHHR
LOC_Os02g06090	Phytosulfokine receptor precursor	signal transduction	3.16	584.448	YGIMT
LOC_Os02g19550	Lectin-like receptor kinase	signal transduction	6.63	719.812	KSYPPK
LOC_Os02g21700	STE_MEKK_ste11_MAP3K.8 - STE kinases include homologs to sterile 7, sterile 11 and sterile 20 from yeast, expressed	signal transduction	19.86	1259.998	GTPMFLAPEAAR
LOC_Os02g39970	Regulatory subunit	signal transduction	3.85	649.257	GAVCSR
LOC_Os02g45320	OsFBX58 - F-box domain containing protein, expressed	signal transduction	9.27	1011.417	LHLGRPYR
LOC_Os03g15770	Tyrosine protein kinase domain containing protein, putative, expressed	signal transduction	4.60	479.509	VAGTM
LOC_Os03g49510	Phosphatidylinositol-4-phosphate 5-kinase	signal transduction	12.62	767.380	DSVYER
LOC_Os03g53100	Response regulator receiver domain containing protein, expressed	signal transduction	21.69	661.872	TTVVS
LOC_Os04g39160	RNA-dependent RNA polymerase, putative, expressed	signal transduction	5.82	832.440	KGFSIGPK
LOC_Os04g41950	Calcium-binding mitochondrial protein anon-60Da, putative, expressed	signal transduction	13.59	533.159	DTIGK
LOC_Os04g52600	SHR5-receptor-like kinase, putative, expressed	signal transduction	13.70	2216.139	MGLGSNHFNGSLPTELGNLIK
LOC_Os04g52840	Tyrosine protein kinase domain containing protein	signal transduction	7.28	594.879	SSNMR
LOC_Os04g54070	Receptor-like kinase, putative, expressed	signal transduction	13.44	734.887	GMLGDNK
LOC_Os05g43820	Ras-related protein, putative, expressed	signal transduction	5.86	1534.613	WPHGSTQNGIEDHG
LOC_Os06g21380	OsCttP3 - Putative C-terminal processing peptidase homologue	signal transduction	4.88	537.197	SKGSAS
LOC_Os06g47680	OsFBX205 - F-box domain containing protein, expressed	signal transduction	21.69	661.872	TTVVS
LOC_Os06g47740	phytosulfokine receptor precursor	signal transduction	4.40	636.598	VFSAGR
LOC_Os07g41910	DC1 domain-containing protein, putative, expressed	signal transduction	8.82	713.288	AATAQPR
LOC_Os08g25380	Serine/threonine-protein kinase BRI1-like 1 precursor, putative, expressed	signal transduction	12.12	554.019	HGSPR
LOC_Os08g30590	C1-like domain containing protein, expressed	signal transduction	10.32	1415.549	QEEEGPDHCCR

5. (cont.) List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis



LOC	Description	Function	ID Score	Mass (Da)	Peptide
LOC_Os08g31060	Phospholipase D alpha 1, putative, expressed	signal transduction	11.45	849.643	DGRMGAAR
LOC_Os08g39550	Polygalacturonase inhibitor 2 precursor, putative, expressed	signal transduction	20.11	786.571	LTGEIPR
LOC_Os09g02729	Phospholipase C, putative, expressed	signal transduction	16.56	576.162	GAAGSGR
LOC_Os09g09370	BTBN18 - Bric-a-Brac, Tramtrack, Broad Complex BTB domain with non-phototropic hypocotyl 3 NPH3 domain, expressed	signal transduction	17.40	629.859	RPTSGGG
LOC_Os09g13820	Pollen signalling protein with adenyl cyclase activity, putative, expressed	signal transduction	2.96	681.442	CNNSVS
LOC_Os09g36520	KI1 protein, putative, expressed	signal transduction	10.12	660.024	ARVDGAA
LOC_Os10g02720	OsWAK99 - OsWAK receptor-like protein kinase, expressed	signal transduction	17.96	516.828	VIVGK
LOC_Os10g04180	NB-ARC domain containing protein, expressed	signal transduction	8.34	864.431	QRMSGGGR
LOC_Os10g22484	RGH2B, putative, expressed	signal transduction	14.09	1539.183	GLQLLETMDMKT
LOC_Os10g25010	OsCML8 - Calmodulin-related calcium sensor protein	signal transduction	8.80	582.232	MSTVK
LOC_Os11g10340	OsFBX417 - F-box domain containing protein, expressed	signal transduction	27.67	846.236	LDADKER
LOC_Os11g44250	Protein kinase, putative, expressed	signal transduction	11.40	598.188	GTHGVK
LOC_Os11g45130	Pollen signalling protein with adenyl cyclase activity, putative, expressed	signal transduction	9.87	2199.340	TTLAQIYNDEKITGNFDK
LOC_Os12g31610	Lectin-like protein kinase, putative, expressed	signal transduction	10.24	991.116	SGLRGCDAR
LOC_Os12g32630	OsFBX448 - F-box domain containing protein, expressed	signal transduction	8.93	544.555	SPGAGR
LOC_Os12g39120	Protein phosphatase 2C, putative, expressed	signal transduction	28.21	801.128	AALTEAAR
LOC_Os12g41270	Cysteine-rich receptor-like protein kinase 20 precursor, putative, expressed	signal transduction	9.54	1032.051	GLLPEECSK
LOC_Os12g41490	Cysteine-rich receptor-like protein kinase 8 precursor	signal transduction	16.03	981.592	KEYASEVR
LOC_Os03g05270	RING finger and CHY zinc finger domain-containing protein 1, putative, expressed	transcription	9.80	1183.637	MASWPTSCTK
LOC_Os03g09820	transcription initiation factor IIB, putative, expressed	transcription	5.79	876.179	AAQTLEDK
LOC_Os03g42420	B3 DNA binding domain containing protein, expressed	transcription	7.21	1983.444	EVVMERGGGGGGDQWHVR
LOC_Os04g32600	Expressed protein Histone-fold TFIIID-31kDa	transcription	13.07	888.135	GKEPSSER
LOC_Os07g41910	Zinc finger, RING-type, putative, expressed	transcription	8.88	463.896	AGSTK
LOC_Os11g40210	Remorin C-terminal domain containing protein, putative, expressed	transcription	7.32	745.152	MITVHK
LOC_Os01g04800	B3 DNA binding domain containing protein, expressed	transcription	6.50	851.134	MTVSDIGK
LOC_Os01g11120	CID11, putative, expressed	transcription	14.64	688.525	AAVAGGSR

5. (cont.) List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis



5. (cont.) List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis

LOC	Description	Function	ID Score	Mass (Da)	Peptide
LOC_Os01g38710	Nucleic acid binding protein, putative, expressed	transcription	4.73	620.791	TAADDK
LOC_Os01g50040	DNA binding protein	transcription	10.41	543.037	PAAKR
LOC_Os01g63160	MYB family transcription factor, putative, expressed	transcription	10.98	499.035	GIPGR
LOC_Os01g74410	MY8 family transcription factor, putative, expressed	transcription	3.20	528.946	SIPGR
LOC_Os02g06584	Zinc finger C-x8-C-x5-C-x3-H type family protein, expressed	transcription	4.02	552.977	HSPGR
LOC_Os02g52960	PHD-finger domain containing protein, putative, expressed	transcription	10.80	2267.609	ARAEGLPEGAAPGVGDLYAQAR
LOC_Os03g02240	AT-GTL1, putative, expressed	transcription	6.86	1044.261	RGGGGIGGGGGGK
LOC_Os03g17060	RNA recognition motif containing protein	transcription	19.51	1497.169	MALSSLLHRLLR
LOC_Os03g27030	RNA recognition motif containing protein, expressed	transcription	15.09	547.704	TVDGR
LOC_Os03g40710	ZOS3-13 - C2H2 zinc finger protein, expressed	transcription	14.48	661.814	VATFPK
LOC_Os03g45450	WRKY60, expressed	transcription	17.35	473.453	GAGGGR
LOC_Os03g60130	Transcription elongation factor protein, putative, expressed	transcription	6.78	429.723	GGAPK
LOC_Os04g32940	Leucine Rich Repeat family protein, expressed	transcription	8.23	1489.994	ELPAEIPNLPQLR
LOC_Os07g40780	ZOS7-11 - C2H2 zinc finger protein, expressed	transcription	2.23	699.638	HASGGGGR
LOC_Os07g44030	MYB/SANT domain protein	transcription	25.16	767.603	QPNHSGK
LOC_Os07g45350	zinc finger, RING-type, putative, expressed	transcription	8.88	463.896	AGSTK
LOC_Os08g05510	MYB family transcription factor, putative, expressed	transcription	8.05	726.277	ADPPAEK
LOC_Os08g28214	Tesmin/TSO1-like CXC domain containing protein	transcription	5.46	875.697	NPAAFMPK
LOC_Os08g44910	DNA binding protein, putative, expressed	transcription	7.37	612.791	STTFR
LOC_Os09g32010	Ternary complex factor MIP1, putative, expressed	transcription	13.99	673.260	YVVHR
LOC_Os09g37910	HMG1/2, putative, expressed	transcription	8.15	447.651	AGGDK
LOC_Os10g30054	ENT domain containing protein, expressed	transcription	17.55	659.509	AMVPDK
LOC_Os10g30719	MYB family transcription factor, putative, expressed	transcription	10.86	530.964	GKAQK
LOC_Os11g48000	ZOS11-11 - C2H2 zinc finger protein	transcription	11.39	496.099	AVVHA
LOC_Os12g10250	Zinc finger family protein, putative, expressed	transcription	11.36	603.528	AMGGIR
LOC_Os12g31430	Helix-loop-helix DNA-binding domain containing protein, expressed	transcription	11.31	630.126	ATIPAR
LOC_Os01g61814	40S ribosomal protein S23, putative, expressed	translation	30.44	816.011	ILIIKSK



LOC	Description	Function	ID Score	Mass (Da)	Peptide
LOC_Os01g10820	Ribosomal protein L5	translation	30.53	1516.966	VLEQLSGQSPVFSK
LOC_Os04g28180	Ribosomal protein, putative, expressed	translation	10.22	473.276	GKGAAA
LOC_Os05g47630	Peptidyl-tRNA hydrolase, mitochondrial precursor protein, expressed	translation	15.60	520.379	SMVGK
LOC_Os06g43760	tRNA synthetase class I, putative, expressed	translation	5.82	711.817	GRHVSR
LOC_Os09g34070	RNA recognition motif containing protein, expressed	translation	4.08	550.542	GYGVR
LOC_Os01g08020	Boron transporter protein, putative, expressed	transport	2.50	511.070	HVGAQ
LOC_Os02g21630	SEC14 cytosolic factor family protein	transport	3.90	1106.014	KLSVDETVSK
LOC_Os06g36090	ABC-2 type transporter, putative, expressed	transport	7.39	576.303	AFIPK
LOC_Os09g21760	Proteasome subunit, putative, expressed	transport	8.67	1098.400	LQSAGSFLMK
LOC_Os10g02230	Expressed protein	transport	26.02	492.919	MGIGV
LOC_Os11g08980	Preprotein translocase secA family protein, putative, expressed	transport	12.43	729.704	TSSMMR
LOC_Os01g12680	C4-dicarboxylate transporter/malic acid transport protein, expressed	transport	9.78	515.839	DGAPR
LOC_Os01g61180	Exo70 exocyst complex subunit domain containing protein, expressed	transport	9.15	622.581	AACGSR
LOC_Os02g52060	Peptide transporter like protein, expressed	transport	6.17	1935.934	MAATTMAASDLVDQHSVR
LOC_Os03g08070	Copper-transporting ATPase PAA1, putative, expressed	transport	14.13	809.092	SHTGFML
LOC_Os04g04870	Retrotransposon protein, unclassified, expressed	transport	14.88	576.651	ASDER
LOC_Os04g41320	Nucleotide-sugar transporter family protein, putative, expressed	transport	23.47	679.454	KPLLPI
LOC_Os04g44810	Syntaxin-18	transport	4.35	448.323	GGSTK
LOC_Os07g01920	Nucleolar GTP-binding protein 1, putative, expressed	transport	16.46	490.678	SSIGK
LOC_Os09g03750	Ankyrin, putative, expressed	transport	17.70	535.256	TASTR
LOC_Os09g15330	Transporter family protein, putative, expressed	transport	11.27	726.927	LIAASPR
LOC_Os09g37300	Transporter, monovalent cation:proton antiporter-2 family, putative, expressed	transport	7.55	693.948	HVGPKR
LOC_Os11g09750	Transposon protein, putative, CACTA, En/Spm sub-class, expressed	transposon	11.98	537.487	GSAFR
LOC_Os03g37920	Transposon protein, unclassified, expressed	transposon	17.47	854.057	HATSVVLK
LOC_Os07g27470	Transposon protein, putative, CACTA, En/Spm sub-class, expressed	transposon	4.53	640.903	THTER
LOC_Os11g46290	Transposon protein, putative, unclassified, expressed	transposon	10.56	1053.677	EVMNMFKR

5. (cont.) List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis



LOC	Description	Function	ID Score	Mass (Da)	Peptide
LOC_Os01g15220	Expressed protein	unknown	15.69	1381.459	LLPLRALTAGLSR
LOC_Os01g31560	Expressed protein	unknown	14.97	604.213	GGGDAGGGG
LOC_Os01g37790	Expressed protein	unknown	11.66	617.457	SATSPR
LOC_Os02g13360	Expressed protein	unknown	16.23	459.366	GGGIR
LOC_Os02g50570	No Plant GOSlim ID has been assigned	unknown	12.63	932.826	SSPADYHR
LOC_Os03g04930	Expressed protein	unknown	7.01	538.332	GMTGR
LOC_Os03g08740	Expressed protein	unknown	6.77	554.874	SHGTR
LOC_Os03g10700	Expressed protein	unknown	18.47	560.853	DGGGVR
LOC_Os03g21530	AARP2CN domain containing protein, expressed	unknown	10.75	1376.612	FEGAAIRTVSGIR
LOC_Os03g21690	Lung seven transmembrane domain containing protein, putative, expressed	unknown	6.61	1127.154	SMAKLELYR
LOC_Os03g62660	No Plant GOSlim ID has been assigned	unknown	10.64	821.185	TLPSGMSK
LOC_Os04g22780	No Plant GOSlim ID has been assigned	unknown	13.25	1229.405	REAAGAEGGGGAAR
LOC_Os04g53660	Transposon protein, unclassified, expressed	unknown	4.61	969.758	HQSTLNIR
LOC_Os04g58100	Protein expressed protein	unknown	5.35	725.095	SVGYSGR
LOC_Os05g03140	Tetraspanin family protein	unknown	6.37	1009.312	TQPSRFQF
LOC_Os05g08730	Early fruit mRNA	unknown	2.62	720.350	KPSSSSK
LOC_Os05g40730	Expressed protein	unknown	8.47	481.907	SGGMN
LOC_Os05g49980	OsFBL26 - F-box domain and LRR containing protein, expressed	unknown	13.24	1207.440	MSRAQDEILK
LOC_Os06g12876	Expressed protein	unknown	2.64	741.440	ASMDFR
LOC_Os06g19750	Expressed protein	unknown	7.14	1051.860	ARGSGYSPTK
LOC_Os06g40130	Expressed protein	unknown	3.98	1179.418	WPMAMPCVR
LOC_Os07g01720	Expressed protein	unknown	13.04	615.870	SPALAR
LOC_Os07g12100	Expressed protein	unknown	10.52	773.497	DPNPSDK
LOC_Os07g29950	Expressed protein	unknown	30.18	691.491	TTEANR
LOC_Os07g33750	Expressed protein	unknown	6.30	584.471	AVGLPK
LOC_Os08g33170	Expressed protein	unknown	3.91	1959.027	SNSLEVAQAGADPPMSTGVK
LOC_Os08g35939	Expressed protein	unknown	16.52	819.227	MLLFPK

5. (cont.) List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis



LOC	Description	Function	ID Score	Mass (Da)	Peptide
I.LOC_Os08g37990	Expressed protein	unknown	9.80	632.818	AGKTEK
LOC_Os09g07520	Expressed protein	unknown	13.25	520.608	GRMAS
LOC_Os09g28470	Leucine-rich repeat family protein, putative, expressed	unknown	7.88	882.438	APGPLSWR
I.LOC_Os09g30060	Expressed protein	unknown	17.47	959.881	RSSPAGTQR
LOC_Os09g32940	Expressed protein	unknown	2.76	473.971	ATSVP
LOC_Os09g35540	Expressed protein	unknown	9.98	579.361	AMTIK
LOC_Os10g08830	Expressed protein	unknown	9.15	658.723	VSAARR
LOC_Os10g30270	Unknown	unknown	8.77	591.570	CGTVR
LOC_Os10g34120	No Plant GOSlim ID has been assigned	unknown	12.11	1150.337	MNMAIISKAR
LOC_Os12g19660	Expressed protein	unknown	7.05	751.599	ADGGGYGR
LOC_Os12g38540	Expressed protein	unknown	9.44	544.648	AVSIR
LOC_Os01g08750	Expressed protein	unknown	32.13	721.983	EMSLIK
LOC_Os01g09330	Expressed protein	unknown	1.44	657.233	IGLEPK
LOC_Os01g27030	hypothetical protein	unknown	11.27	525.981	VAAHK
LOC_Os01g56530	No Plant GOSlim ID has been assigned for	unknown	21.39	1028.676	GAAEFAAVHR
LOC_Os01g69240	CBS domain containing membrane protein, putative, expressed	unknown	7.28	506.017	SGPFV
LOC_Os02g28580	No Plant GOSlim ID has been assigned	unknown	9.67	741.716	NIVDGPK
LOC_Os02g32570	SNF2 family N-terminal domain containing protein, expressed	unknown	5.29	596.499	KSMSK
LOC_Os02g40110	Expressed protein	unknown	8.36	1540.139	LNPVAAAAAASASTK
LOC_Os02g50370	No Plant GOSlim ID has been assigned	unknown	10.27	1061.203	AFPGPSKDDK
LOC_Os03g23970	Diphthine synthase, putative, expressed	unknown	8.69	716.037	IVAGPMK
LOC_Os03g24090	No Plant GOSlim ID has been assigned	unknown	16.88	1611.150	MAVLVTDSSVGMTLR
LOC_Os03g35370	Expressed protein	unknown	10.94	545.663	NGAKR
LOC_Os03g38740	No Plant GOSlim ID has been assigned	unknown	15.21	751.968	DLIAGHK
LOC_Os03g40084	Expressed protein	unknown	21.81	917.240	DTEVRNGK
LOC_Os04g02350	No Plant GOSlim ID has been assigned	unknown	20.21	701.416	HAGMLR
LOC_Os04g07670	No Plant GOSlim ID has been assigned	unknown	10.45	577.281	FGGAAR

5. (cont.) List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis



LOC	Description	Function	ID Score	Mass (Da)	Peptide
LOC_Os04g09380	No Plant GOSlim ID has been assigned	unknown	3.14	846.684	DQMFYK
LOC_Os04g15510	No Plant GOSlim ID has been assigned	unknown	14.17	1822.125	TPTIPTCSKMEAAEGGR
LOC_Os04g19684	Methyl-CpG binding domain containing protein, expressed	unknown	18.87	677.995	EIIFR
LOC_Os04g19760	No Plant GOSlim ID has been assigned	unknown	7.46	642.529	SHKSGK
LOC_Os04g34600	Abscisic stress-ripening, putative, expressed	unknown	18.60	737.370	KHHLFG
LOC_Os04g49580	Nucleolar complex protein, putative, expressed	unknown	6.89	636.353	LRMVT
LOC_Os04g52950	Nitrate-induced NOI protein	unknown	9.89	725.850	MTTMDK
LOC_Os05g15700	Expressed protein	unknown	7.73	766.135	GCQNSV
LOC_Os05g31690	Expressed protein	unknown	13.27	597.890	FGAFR
LOC_Os05g32100	Expressed protein	unknown	6.21	628.867	GPRGSR
LOC_Os05g39190	Expressed protein	unknown	23.12	835.824	RLAHPSR
LOC_Os06g05560	Expressed protein	unknown	15.20	2231.996	TLSFVVYEADLSNGSRMWR
LOC_Os06g05580	OsFBDUF30 - F-box and DUF domain containing protein	unknown	15.20	2231.996	TLSFVVYEADLSNGSRMWR
LOC_Os06g07470	No Plant GOSlim ID has been assigned	unknown	24.09	679.361	DAGIFR
LOC_Os06g27800	Tm-1GCR237 protein, putative, expressed	unknown	16.86	811.520	TKSVLHK
LOC_Os06g36230	Expressed protein	unknown	14.81	1170.202	QVGTPEMGVPR
LOC_Os07g08040	Expressed protein	unknown	13.68	590.720	YGGHR
LOC_Os07g08290	Expressed protein	unknown	19.73	534.623	DGVSR
LOC_Os07g09530	Ankyrin repeat family protein, putative, expressed	unknown	3.98	784.225	PNLPSEK
LOC_Os07g11290	Expressed protein	unknown	6.66	807.863	FLTATVR
LOC_Os07g14910	Expressed protein	unknown	3.32	602.287	VAAGER
LOC_Os07g27760	Expressed protein	unknown	6.46	1569.340	FSNDGPDVQAEDFK
LOC_Os07g41270	No Plant GOSlim ID has been assigned	unknown	9.52	1071.831	GDGVYTGMR
LOC_Os07g48080	Expressed protein	unknown	4.41	638.985	AHAANR
LOC_Os08g17020	Expressed protein	unknown	12.02	983.277	AAAMNDHVR
LOC_Os08g17820	No Plant GOSlim ID has been assigned	unknown	5.84	785.943	LPGMRGR
LOC_Os08g43150	No Plant GOSlim ID has been assigned	unknown	9.44	617.936	ACGGTR

5. (cont.) List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis



LOC	Description	Function	ID Score	Mass (Da)	Peptide
LOC_Os08g43520	No Plant GOSlim ID has been assigned	unknown	31.84	814.312	LDTAGLPK
LOC_Os09g15200	No Plant GOSlim ID has been assigned	unknown	20.84	916.477	DGPDRSDR
LOC_Os09g15560	OsFBX314 - F-box domain containing protein, expressed	unknown	15.55	927.449	GLLLLLSKK
LOC_Os09g28060	MORN repeat domain containing protein, expressed	unknown	8.45	1299.840	MDGHGGGGGKLTR
LOC_Os09g28370	No Plant GOSlim ID has been assigned	unknown	5.00	679.115	IFTSVL
LOC_Os09g31230	Expressed protein	unknown	7.64	579.158	TSDGAK
LOC_Os09g37510	DUF292 domain containing protein	unknown	11.78	829.334	MMATAGSK
LOC_Os10g06910	No Plant GOSlim ID has been assigned	unknown	5.02	462.173	GPSSD
LOC_Os10g08530	Expressed protein	unknown	10.63	604.433	DIEAR
LOC_Os10g17940	No Plant GOSlim ID has been assigned	unknown	14.56	1092.643	KVAAPPGHCR
LOC_Os10g19980	conserved hypothetical protein	unknown	3.02	839.681	YGEGESAK
LOC_Os10g22030	No Plant GOSlim ID has been assigned	unknown	5.30	715.416	AGSIVIR
LOC_Os11g03550	Expressed protein	unknown	6.66	742.393	MASSAFK
LOC_Os11g05550	No Plant GOSlim ID has been assigned	unknown	12.59	848.360	MAADGGALK
LOC_Os11g06720	Abscisic stress-ripening, putative, expressed	unknown	19.21	737.963	KHHLFG
LOC_Os11g11730	No Plant GOSlim ID has been assigned	unknown	10.49	1105.456	DAIAAVQECK
LOC_Os11g12680	Expressed protein	unknown	6.42	874.135	GMAAASLPR
LOC_Os11g18070	No Plant GOSlim ID has been assigned	unknown	29.39	775.370	DIIIFR
LOC_Os11g22530	No Plant GOSlim ID has been assigned	unknown	13.85	1016.768	PSGTELQQR
LOC_Os11g38410	Expressed protein	unknown	12.18	539.819	RHGGL
LOC_Os11g42100	Leucine Rich Repeat family protein, expressed	unknown	16.72	761.468	ACLNAGR
LOC_Os11g42940	integral membrane protein, putative, expressed	unknown	9.99	621.560	MDGAAR
LOC_Os12g02050	No Plant GOSlim ID has been assigned	unknown	12.76	868.805	MENTSSGK
LOC_Os12g14500	Expressed protein	unknown	33.00	706.920	TSSLSGR
LOC_Os12g17120	No Plant GOSlim ID has been assigned	unknown	14.54	563.298	GSGGASK
LOC_Os12g29719	No Plant GOSlim ID has been assigned	unknown	15.45	710.364	IVAPPGR
LOC_Os12g40279	Protein kinase domain containing protein, expressed	unknown	7.97	787.187	ADVSGIPK

5. (cont.) List of all chitosan-responsive proteins in leaves of rice seedlings analyzed by proteomic analysis

6. Calculation of relative gene expression level

The level of gene expression was calculated by the ratio between the amount of target gene and an endogenous reference gene (*OsEF1 α*), which is present in all samples. The calibrator sample was the day 0 of treatment. The standard curve for each primer set was calculated using 5-fold dilution (1:1 to 1:625) of cDNA. The slope of the standard curve gives the efficiency (E) of the PCR reaction by the following equation: $E = 10^{(1/\text{slope})}$. Crossing point (CP) is defined as the cycle in which there is a significant increase above the threshold.

The relative expression level is calculated only from the PCR efficiencies and the crossing point deviation of an unknown sample versus a control.

$$\text{Relative gene expression level} = \frac{(E_{\text{target}})^{\Delta\text{CP}_{\text{target}} (\text{calibrator-sample})}}{(E_{\text{ref}})^{\Delta\text{CP}_{\text{ref}} (\text{calibrator-sample})}}$$

The relative gene expression level was subjected to Student's *t*-test statistic analysis to compare the difference of gene expression.

7. Primer for qPCR

Gene name	Primer name	Primer sequence (5'->3')
<i>Elongation factor 1-alpha (EF1α)</i>	OsEF1a-F	ATGGTTGTGGAGACCTTC
	OsEF1a-R	TCACCTGGCACC GGTTG
<i>Serine/threonine-protein kinase BRI1-like 1 precursor</i>	OsBRL1-F	CTTGATCTCTCACACAACCA
	OsBRL1-R	AATGTGATGAGCTGCCCTGA
<i>Phytosulfokine receptor precursor</i>	OsPSKR-F	CTCGTTGCTCTCGTCATCTT
	OsPSKR-R	GACTGCTCCAAAGACACGAT



APPENDIX C TRANSCRIPTOMIC ANALYSIS

1. RNA-seq library statistics

Library	Mapped reads ^a	Unique Reads ^b	%Mapped reads ^c
Control#1	10,703,588	9,159,350	85.6%
Control#2	12,101,404	10,756,647	88.9%
Chitosan#1	14,072,326	11,694,623	83.1%
Chitosan#2	11,934,265	10,398,454	87.1%

^aThe number of reads mapped to TAIR10

^bThe uniquely mapped reads as showed in the count script

^cPercentage of total mapped reads cDNA to all gene models

2. Adapter and barcode sequences

Library	Primer	Index	Sequence
Control#1	Bioo2	TGACCA	tgaccaAGATCGGAAGAGCGGTTTCAGCAGGAATGCCGAG
Control#2	Bioo5	CAGATC	cagatcAGATCGGAAGAGCGGTTTCAGCAGGAATGCCGAG
Chitosan#1	Bioo3	ACAGTG	acagtgAGATCGGAAGAGCGGTTTCAGCAGGAATGCCGAG
Chitosan#2	Bioo8	TTAGGC	ttaggcAGATCGGAAGAGCGGTTTCAGCAGGAATGCCGAG

3. Sequencing adaptor sequences (iiiiii indicates the position of the index)

primer A:

5' AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT 3'

primer B:

5' P-GATCGGAAGAGCACACGTCTGAACTCCAGTCACiiiiiiATCTCGTATGCCGTCTTCTGCTTG 3'



4. List of all significantly expressed genes of high dose chitosan-responsive gene in *Arabidopsis*

Biological function: cell organization

Gene ID	Alias	Gene name	Log ₂ FC	Component
At3g02480		Late embryogenesis abundant protein (LEA) family protein	4.26	unknown
At5g15500		Ankyrin repeat family protein	1.77	nucleus
At1g10340		Ankyrin repeat family protein	1.46	unknown
At5g58650	PSY1	Plant peptide containing sulfated tyrosine 1	1.08	unknown
At4g22240		Plastid-lipid associated protein PAP / fibrillin family protein	1.07	chloroplast
At2g38750	ANNAT4	Annexin 4	0.93	chloroplast
At1g58200	MSL3	MSCS-like 3	0.74	chloroplast
At5g56180	ARP8	Actin-related protein 8	0.67	cytoplasm
At1g64740	TUA1	Alpha-1 tubulin	0.66	cytoplasm
At2g37080	RIP3	ROP interactive partner 3	-0.68	chloroplast
At5g54710		Ankyrin repeat family protein	-0.69	unknown
At3g52750	FTSZ2-2	FTSZ2-2	-0.69	chloroplast
At2g36200		Kinesin motor protein-related	-0.70	cytoplasm
At5g60930		P-loop containing nucleoside triphosphate hydrolases superfamily protein	-0.71	nucleus
At4g26760	MAP65-2	Microtubule-associated protein 65-2	-0.71	unknown
At5g48600	SMC3	Structural maintenance of chromosome 3	-0.71	nucleus
At3g04630	WDL1	WVD2-LIKE 1	-0.71	cytoplasm
At3g19050	POK2	PHRAGMOPLAST ORIENTING KINESIN 2	-0.72	cytoplasm
At3g53750	ACT3	Actin 3	-0.72	cytoplasm
At2g24600		Ankyrin repeat family protein	-0.72	unknown
At3g23670	KINESIN-12B	Microtubule motor kinesin PAKRP1L/Kinesin-12B	-0.72	cytoplasm
At5g13840	FZR3	FIZZY-related 3	-0.73	nucleus
At2g28620		P-loop containing nucleoside triphosphate hydrolases superfamily protein	-0.73	nucleus
At3g44050		Kinesin motor protein-related	-0.74	cytoplasm
At1g03780	TPX2	Targeting protein for XKLP2	-0.75	nucleus
At5g06150	CYCB1;2	CYCLIN B1;2	-0.75	nucleus
At3g56480		Myosin heavy chain-related	-0.75	nucleus
At5g51550	EXL3	EXORDIUM like 3	-0.76	extracellular region
At2g31900	XIF	Myosin-like protein XIF	-0.78	cytoplasm
At1g70210	CYCD1;1	CYCLIN D1;1	-0.78	nucleus
At3g17360	POK1	PHRAGMOPLAST ORIENTING KINESIN 1	-0.78	nucleus
At5g51600	PLE	PLEIADE	-0.78	unknown
At2g22610		Kinesin motor protein-related	-0.78	cytoplasm
At5g55520		Kinesin-related	-0.79	chloroplast
At2g26760	CYCB1;4	CYCLIN B1;4	-0.81	nucleus
At5g66310		Kinesin motor family protein	-0.82	cytoplasm
At3g50240	KICP-02	KICP-02	-0.82	unknown
At5g48460		Actin binding Calponin homology (CH) domain-containing protein	-0.82	cytoplasm

Biological function: cell organization (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At2g36100	CASP1	Casparian strip membrane domain protein 1	-0.82	plasma membrane
At1g18370	HIK	HINKEL	-0.83	chloroplast
At2g47500		ATP binding / microtubule motor	-0.83	cytoplasm
At2g29890	VLN1	Villin-like 1	-0.85	cytoplasm
At5g15580	LNG1	Longifolia1	-0.85	cell wall
At3g12110	ACT11	Actin-11	-0.88	cytoplasm
At5g54670	ATK3	Kinesin 3	-0.88	unknown
At4g05190	ATK5	Kinesin 5	-0.90	nucleus
At5g54720		Ankyrin repeat family protein	-0.91	unknown
At1g75780	TUB1	Tubulin beta-1 chain	-0.91	vacuole
At4g21270	ATK1	Kinesin 1	-0.92	nucleus
At3g60840	MAP65-4	Microtubule-associated protein 65-4	-0.93	cytoplasm
At2g37420		ATP binding microtubule motor family protein	-0.97	nucleus
At4g38950		Kinesin motor family protein	-1.02	cytoplasm
At3g44730	KP1	Kinesin-like protein 1	-1.04	cytoplasm
At1g23720		Proline-rich extensin-like family protein	-1.07	unknown

Biological function: cell redox homeostasis

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At4g15700		Thioredoxin superfamily protein	1.99	endomembrane
At4g31870	GPX7	Glutathione peroxidase 7	1.86	chloroplast
At4g15690		Thioredoxin superfamily protein	1.67	endomembrane
At1g19570	DHAR1	Dehydroascorbate reductase	1.12	chloroplast
At1g20630	CAT1	Catalase 1	1.08	chloroplast
At3g10130		SOUL heme-binding family protein	0.94	chloroplast
At5g18600		Thioredoxin superfamily protein	0.83	mitochondria
At1g08570	ACHT4	Atypical CYS HIS rich thioredoxin 4	0.82	chloroplast
At2g25080	GPX1	Glutathione peroxidase 1	0.80	chloroplast
At5g55120	VTC5	Vitamin C defective 5	0.62	nucleus
At2g28190	CSD2	Copper/zinc superoxide dismutase 2	-0.73	chloroplast
At5g51010		Rubredoxin-like superfamily protein	-0.79	chloroplast
At2g46650	CB5-C	Cytochrome B5 isoform C	-0.79	unknown
At3g10520	HB2	Haemoglobin 2	-0.80	cytoplasm
At2g47880		Glutaredoxin family protein	-1.59	endomembrane
At1g06830		Glutaredoxin family protein	-1.62	cytoplasm

Biological function: cell wall modification

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At5g57550	XTH25	Xyloglucan endotransglucosylase/hydrolase 25	2.84	cell wall
At4g24000	CSLG2	Cellulose synthase like G2	2.70	Golgi apparatus
At5g14470		GHMP kinase family protein	2.13	extracellular region
At5g06870	PGIP2	Polygalacturonase inhibiting protein 2	2.07	cell wall
At5g49360	BXL1	Beta-xylosidase 1	1.76	extracellular region
At1g57590		Pectinacylesterase family protein	1.75	extracellular region
At1g67070	DIN9	Dark inducible 9	1.70	cytoplasm
At4g30270	XTH24	Xyloglucan endotransglucosylase/hydrolase 24	1.68	cell wall
At5g64570	XYL4	Beta-D-xylosidase 4	1.42	cell wall
At3g55500	EXPA16	Expansin A16	1.35	extracellular region
At2g15880		Extensin family protein	1.25	unknown
At4g25810	XTR6	Xyloglucan endotransglycosylase 6	1.24	cell wall
At3g43270		Plant invertase/pectin methylesterase inhibitor superfamily	1.24	cell wall
At4g16590	CSLA01	Cellulose synthase-like A01	1.14	Golgi apparatus
At1g24070	CSLA10	Cellulose synthase-like A10	1.10	Golgi apparatus
At5g06860	PGIP1	Polygalacturonase inhibiting protein 1	1.08	cell wall
At4g30280	XTH18	Xyloglucan endotransglucosylase/hydrolase 18	1.00	cell wall
At2g47550		Plant invertase/pectin methylesterase inhibitor superfamily	0.97	endomembrane
At2g32530	CSLB03	Cellulose synthase-like B3	0.95	Golgi apparatus
At1g12780	UGE1	UDP-D-glucose/UDP-D-galactose 4-epimerase 1	0.92	plasma membrane
At4g02330	PME41	Pectin methylesterase 41	0.88	cell wall
At1g76930	EXT4	Extensin 4	0.87	unknown
At2g01850	XTH27	Xyloglucan endotransglucosylase/hydrolase 27	0.79	cell wall
At5g44130	FLA13	FASCICLIN-like arabinogalactan protein 13 PRECURSOR	0.77	plasma membrane
At4g17030	EXLB1	Expansin-like B1	0.74	extracellular region
At4g19420		Pectinacylesterase family protein	0.73	extracellular region
At2g22470	AGP2	Arabinogalactan protein 2	0.67	cytoplasm
At1g67750		Pectate lyase family protein	-0.64	endomembrane
At1g04680		Pectate lyase family protein	0.65	cell wall
At4g23820		Pectin lyase-like superfamily protein	-0.67	endomembrane
At3g59010	PME61	Pectin methylesterase 61	-0.71	cell wall
At1g53830	PME2	Pectin methylesterase 2	-0.72	extracellular region
At3g62110		Pectin lyase-like superfamily protein	-0.73	vacuole
At2g37640	EXP3	Expansin 3	-0.76	extracellular region
At2g28950	EXPA6	Expansin A6	-0.77	extracellular region
At1g02730	CSLD5	Cellulose synthase-like D5	-0.77	Golgi apparatus
At1g03870	FLA9	FASCICLIN-like arabinogalactan 9	-0.78	plasma membrane
At5g22740	CSLA02	Cellulose synthase-like A02	-0.78	Golgi apparatus
At5g55730	FLA1	FASCICLIN-like arabinogalactan 1	-0.79	plasma membrane
At3g52370	FLA15	FASCICLIN-like arabinogalactan protein 15 PRECURSOR	-0.82	cell wall
At5g04960		Pectinesterase family protein	-0.83	cell wall
At2g45470	FLA8	FASCICLIN-like arabinogalactan protein 8	-0.83	cell wall
At1g60590		Pectin lyase-like superfamily protein	-0.86	extracellular region



Biological function: cell wall modification (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At4g26320	AGP13	Arabinogalactan protein 13	-0.86	plasma membrane
At5g63180		Pectate lyase family protein	-0.88	extracellular region
At1g60390	PG1	Polygalacturonase 1	-0.89	extracellular region
At5g44480	DUR	DEFECTIVE UGE IN ROOT	-0.90	Golgi apparatus
At3g44990	XTR8	Xyloglucan endotransglucosylase/hydrolase 31	-0.98	cell wall
At2g32990	GH9B8	Glycosyl hydrolase 9B8	-1.00	extracellular region
At4g13710		Pectate lyase family protein	-1.00	endomembrane
At4g03210	XTH9	Xyloglucan endotransglucosylase/hydrolase 9	-1.02	cell wall
At5g22940	F8H	FRA8 homolog	-1.04	Golgi apparatus
At1g11545	XTH8	Xyloglucan endotransglucosylase/hydrolase 8	-1.07	cell wall
At3g53190		Pectin lyase-like superfamily protein	-1.08	plasma membrane
At5g13870	XTH5	Xyloglucan endotransglucosylase/hydrolase 5	-1.09	chloroplast
At4g14130	XTH15	Xyloglucan endotransglucosylase/hydrolase 15	-1.10	cell wall
At3g07010		Pectin lyase-like superfamily protein	-1.11	extracellular region
At5g47500	PME5	Pectin methylesterase 5	-1.12	cell wall
At5g60490	FLA12	FASCICLIN-like arabinogalactan protein 12	-1.23	plasma membrane
At1g10640		Polygalacturonase	-1.24	extracellular region
At3g60900	FLA10	FASCICLIN-like arabinogalactan protein 10	-1.25	plasma membrane
At4g28250	EXPB3	Expansin B3	-1.29	extracellular region
At2g42800	RLP29	Receptor like protein 29	-1.38	cell wall
At1g65310	XTH17	Xyloglucan endotransglucosylase/hydrolase 17	-1.44	cell wall
At1g02810		Pectinesterase family protein	-1.46	cell wall
At4g15290	CSLB5	Cellulose synthase-like 5	-1.56	Golgi apparatus
At2g15370	FUT5	Fucosyltransferase 5	-1.59	Golgi apparatus
At2g40610	EXPA8	Expansin A8	-1.74	extracellular region
At1g26250		Proline-rich extensin-like family protein	3.19	unknown

Biological function: development

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At2g42560		Late embryogenesis abundant domain-containing protein	4.75	cytoplasm
At3g17520		Late embryogenesis abundant protein (LEA) family protein	4.03	unknown
At1g52690	LEA7	Late embryogenesis abundant 7	3.75	unknown
At3g49620	DIN11	Dark inducible 11	3.51	cytoplasm
At1g52890	NAC019	NAC domain containing protein 19	3.35	nucleus
At5g06760	LEA4-5	Late embryogenesis abundant 4-5	3.31	unknown
At4g35770	SEN1	Senescence 1	3.17	chloroplast
At5g01300		PEBP (phosphatidylethanolamine-binding protein) family protein	3.00	cytoplasm
At3g28007	SWEET4	Nodulin MtN3 family protein	2.74	plasma membrane
At1g15040		Glutamine amidotransferase type 1	2.59	unknown
At5g39610	NAC6	NAC domain containing protein 6	2.59	nucleus
At5g13170	SAG29	Senescence-associated gene 29	2.53	plasma membrane
At4g27410	RD26	Responsive to desiccation 26	2.14	nucleus

Biological function: development (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At1g09380		Nodulin MtN21-related	1.81	other membrane
At3g22640	PAP85	Low-molecular-weight cysteine-rich 78	1.79	extracellular region
At2g28120		Major facilitator superfamily protein	1.76	plasma membrane
At1g69490	NAC029	NAC domain containing protein 29	1.65	nucleus
At5g24780	VSP1	Vegetative storage protein 1	1.43	vacuole
At1g02820	LEA3	Late embryogenesis abundant 3	1.39	chloroplast
At2g26560	PLA2A	Phospholipase A 2A	1.32	cytoplasm
At1g01470	LEA14	Late embryogenesis abundant 14	1.29	cytoplasm
At4g08290		Nodulin MtN21 /EamA-like transporter family protein	1.28	extracellular region
At4g28040		Nodulin MtN21 /EamA-like transporter family protein	1.28	chloroplast
At5g20240	PI	PISTILLATA	1.15	nucleus
At1g13245	RTFL17	ROTUNDIFOLIA LIKE 17	1.11	mitochondria
At5g15850	COL1	CONSTANS-like 1	1.09	peroxisome
At5g52250	RUP1	Repressor of UV-B photomorphogenesis 1	0.98	chloroplast
At3g14770	SWEET2	Nodulin MtN3 family protein	0.97	plasma membrane
At1g01720	ATAF1	NAC domain containing protein 2	0.93	nucleus
At5g65380		MATE efflux family protein	0.91	plasma membrane
At2g39210		Major facilitator superfamily protein	0.90	chloroplast
At4g01026	RCAR2	Regulatory components of ABA receptor 2	0.87	nucleus
At5g22290	NAC089	NAC domain containing protein 89	0.87	unknown
At4g02380	SAG21	Senescence-associated gene 21	0.81	chloroplast
At3g49780	PSK4	Phytosulfokine 4 precursor	0.77	extracellular region
At3g28100		Nodulin MtN21 /EamA-like transporter family protein	0.75	other membrane
At1g21450	SCL1	Scarecrow-like 1	0.68	nucleus
At5g63790	NAC102	NAC domain containing protein 102	0.68	unknown
At4g37790	HAT22	Homeobox protein HAT22	0.67	nucleus
At1g28330	DYL1	Dormancy-associated protein-like 1	0.66	nucleus
At5g04040	SDP1	Sugar-dependent 1	0.65	unknown
At5g66040	STR16	Sulfurtransferase protein 16	0.63	chloroplast
At2g17040	NAC036	NAC domain containing protein 36	-0.63	unknown
At3g01930		Major facilitator superfamily protein	-0.64	plasma membrane
At1g04770		Tetratricopeptide repeat (TPR)-like superfamily protein	-0.65	unknown
At3g49670	BAM2	BARELY ANY MERISTEM 2	-0.68	plasma membrane
At3g07540		Actin-binding FH2 (formin homology 2) family protein	-0.75	plasma membrane
At5g54370		LEA protein-related	-0.75	unknown
At2g41660	MIZ1	MIZU-KUSSEI 1	-0.76	chloroplast
At2g37460		Nodulin MtN21 family protein	-0.76	cytoplasm
At3g63200	PLP9	PATATIN-LIKE PROTEIN 9	-0.78	extracellular region
At3g51280		Tetratricopeptide repeat (TPR)-like superfamily protein	-0.81	unknown
At1g78020		Senescence-associated protein-related	-0.86	nucleus
At5g66230		Chalcone-flavanone isomerase family protein	-0.87	chloroplast
At1g73590	PIN1	PIN1	-0.89	plasma membrane
At1g21880	LYM1	Lysm domain GPI-anchored protein 1 precursor	-0.89	plasma membrane
At5g09530	PRP10	Hydroxyproline-rich glycoprotein family protein	-0.91	extracellular region

Biological function: development (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At5g48360		Actin-binding FH2 (formin homology 2) family protein	-0.92	chloroplast
At1g66350	RGL1	RGA-like 1	0.94	nucleus
At5g66770		GRAS family transcription factor	-0.94	nucleus
At1g44800		Nodulin MtN21 family protein	-1.00	mitochondria
At3g06035		Glycoprotein membrane precursor GPI-anchored	-1.13	plasma membrane
At2g39510		Nodulin MtN21 family protein	-1.13	other membrane
At2g21045		Rhodanese-like	-1.13	cytoplasm
At4g12980		Auxin-responsive family protein	-1.14	chloroplast
At2g01950	BRL2	BRI1-LIKE 2	-1.16	plasma membrane
At4g17280		Auxin-responsive family protein	-1.17	extracellular region
At5g62210	ATS3	Embryo-specific protein 3	-1.18	plasma membrane
At4g37750	ANT	AINTEGUMENTA	-1.24	nucleus
At3g18200		Nodulin MtN21 /EamA-like transporter family protein	-1.40	chloroplast
At2g23630	SKS16	SKU5 similar 16	-1.41	extracellular region
At5g60520		LEA protein-related	-1.74	extracellular region
At3g19430		Late embryogenesis abundant protein-related	-1.89	nucleus
At3g25190	VIT	Vacuolar iron transporter (VIT) family protein	-2.00	unknown
At5g51720	NEET	NEET GROUP PROTEIN	-4.32	chloroplast

Biological function: DNA or RNA metabolic process

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At2g02990	RNS1	Ribonuclease 1	2.75	plasma membrane
At2g18050	HIS1-3	HISTONE H1-3	2.12	nucleus
At5g24280	GMI1	Gamma-irradiation and mitomycin c induced 1	1.11	nucleus
At4g16680		RNA helicase	1.06	nucleus
At2g23840		HNH endonuclease	0.84	nucleus
At5g13820	TBP1	Telomeric DNA binding protein 1	0.67	nucleus
At5g44680		DNA glycosylase superfamily protein	-0.68	nucleus
At3g44260	CAF1A	CCR4-associated factor 1A	-0.70	nucleus
At3g23890	TOPII	Topoisomerase II	-0.72	nucleus
At1g14210		Ribonuclease T2 family protein	-0.75	cytoplasm
At1g22330		RNA-binding (RRM/RBD/RNP motifs) family protein	-0.88	unknown
At3g54560	HTA11	Histone H2A 11	-0.98	nucleus
At1g05470	CVP2	Cotyledon vascular pattern 2	-1.05	cytoplasm
At3g13610		O-Glycosyl hydrolases family 17 protein	-1.09	cytoplasm
At3g54770		RNA recognition motif (RRM)-containing protein	-1.12	chloroplast
At3g12610	DRT100	DNA-damage repair/toleration 100	-1.13	plasma membrane
At2g01900		DNase I-like superfamily protein	-1.72	nucleus



Biological function: metabolic process

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At4g09600	GASA3	GAST1 protein homolog 3	5.07	extracellular region
At2g24850	TAT3	Tyrosine aminotransferase 3	4.70	cytoplasm
At5g59310	LTP4	Lipid transfer protein 4	4.34	extracellular region
At1g08630	THA1	Threonine Aldolase 1	3.44	cytoplasm
At5g59320	LTP3	Lipid transfer protein 3	3.33	cell wall
At3g47340	ASN1	Glutamine-dependent asparagine synthetase 1	3.18	cytoplasm
At2g19900	NADP-ME1	NADP-malic enzyme 1	3.11	cytoplasm
At4g26260	MIOX4	Myo-inositol oxygenase 4	3.07	cytoplasm
At1g10070	BCAT-2	Branched-chain amino acid aminotransferase 2	2.99	chloroplast
At5g04120		Phosphoglycerate mutase family protein	2.77	cytoplasm
At5g07010	ST2A	Sulfotransferase 2A	2.55	chloroplast
At2g38530	LTP2	Lipid transfer protein 2	2.49	plasma membrane
At5g14180	MPL1	Myzus persicae-induced lipase 1	2.48	unknown
At1g07430	HAI2	Highly ABA-induced PP2C gene 2	2.48	plasma membrane
At3g48520	CYP94B3	Cytochrome P450, family 94, subfamily B, polypeptide 3	2.41	extracellular region
At3g13784	CWINV5	Cell wall invertase 5	2.41	extracellular region
At1g21400		Thiamin diphosphate-binding fold (THDP-binding) superfamily protein	2.28	mitochondria
At5g57640		GCK domain-containing protein	2.28	nucleus
At4g33150	SDH	Lysine-ketoglutarate reductase	2.23	cytoplasm
At1g64660	MGL	Methionine gamma-lyase	2.20	cytoplasm
At2g21590	APL4	Glucose-1-phosphate adenyltransferase	2.12	chloroplast
At4g23600	CORI3	Coronatine induced 1	2.07	vacuole
At1g13700	PGL1	6-phosphogluconolactonase 1	1.96	chloroplast
At3g30775	ERD5	Early-responsive to dehydration 5	1.95	mitochondria
At2g39800	P5CS1	Delta1-pyrroline-5-carboxylate synthetase 1	1.93	chloroplast
At5g14780	FDH	Formate dehydrogenase	1.90	cytoplasm
At4g37370	CYP81D8	Cytochrome P450, family 81, subfamily D, polypeptide 8	1.88	ER
At2g37770	ChIAKR	NAD(P)-linked oxidoreductase superfamily protein	1.88	cytoplasm
At1g56600	GalS2	Galactinol synthase 2	1.86	nucleus
At3g57520	SIP2	Seed imbibition 2	1.86	cytoplasm
At4g11890	ARCK1	ABA- and osmotic-stress-inducible receptor-like cytosolic kinase 1	1.84	unknown
At5g56100		Glycine-rich protein / oleosin	1.80	nucleus
At4g08870	ARGAH2	Arginine amidohydrolase 2	1.79	mitochondria
At4g39210	APL3	Glucose-1-phosphate adenyltransferase	1.78	chloroplast
At5g36220	CYP81D1	Cytochrome p450, family 81, subfamily D, polypeptide 1	1.77	unknown
At4g25000	AMY1	Alpha-amylase-like	1.74	extracellular region
At1g75750	GASA1	GAST1 protein homolog 1	1.73	cell wall
At3g45300	IVDH	Isovaleryl-CoA dehydrogenase	1.72	mitochondria
At2g19800	MIOX2	Myo-inositol oxygenase 2	1.72	cytoplasm
At1g03090	MCCA	Methylcrotonoyl-CoA carboxylase	1.67	mitochondria
At4g02280	SUS3	Sucrose synthase 3	1.64	chloroplast
At3g19270	CYP707A4	Cytochrome P450, family 707, subfamily A, polypeptide 4	1.64	extracellular region
At4g17470		Alpha/beta-Hydrolases superfamily protein	1.59	chloroplast
At5g57655		Xylose isomerase family protein	1.58	vacuole

Biological function: metabolic process (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At5g43450		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1.57	cytoplasm
At5g24160	SQE6	Squalene monooxygenase 6	1.48	endomembrane
At5g53970	TAT7	Tyrosine aminotransferase 7	1.43	chloroplast
At5g07440	GDH2	Glutamate dehydrogenase 2	1.43	mitochondria
At1g68620		Alpha/beta-Hydrolases superfamily protein	1.38	nucleus
At3g13450	DIN4	Dark inducible 4	1.33	mitochondria
At3g21720	ICL	Isocitrate lyase	1.32	cytoplasm
At5g16370	AAE5	Acyl activating enzyme 5	1.30	extracellular region
At1g36180	ACC2	Acetyl-CoA carboxylase 2	1.30	chloroplast
At1g14250		Nucleoside phosphatase family protein	1.27	plasma membrane
At5g54080	HGO	Homogentisate 1,2-dioxygenase	1.26	cytoplasm
At3g21780	UGT71B6	UDP-glucosyltransferase 71B6	1.26	other membrane
At3g26280	CYP71B4	Cytochrome P450, family 71, subfamily B, polypeptide 4	1.25	chloroplast
At5g24420	PGL5	6-phosphogluconolactonase 5	1.24	chloroplast
At5g13200		GRAM domain family protein	1.24	cytoplasm
At3g08860	PYD4	PYRIMIDINE 4	1.22	mitochondria
At3g05640		Protein phosphatase 2C family protein	1.21	unknown
At4g26200	ACS7	1-Amino-cyclopropane-1-carboxylate synthase 7	1.20	cytoplasm
At1g53560		Ribosomal protein L18ae family	1.19	ribosome
At5g47240	NUDT8	Nudix hydrolase homolog 8	1.19	cytoplasm
At2g27150	AAO3	Abscisic aldehyde oxidase 3	1.18	cytoplasm
At5g43860	CLH2	Chlorophyllase 2	1.16	chloroplast
At5g10930	CIPK5	CBL-interacting protein kinase 5	1.15	plasma membrane
At2g38400	AGT3	Alanine:glyoxylate aminotransferase 3	1.14	mitochondria
At3g03470	CYP89A9	Cytochrome P450, family 87, subfamily A, polypeptide 9	1.14	unknown
At5g13800	PPH	Pheophytinase	1.13	chloroplast
At2g39400		Alpha/beta-Hydrolases superfamily protein	1.13	cytoplasm
At4g15530	PPDK	Pyruvate orthophosphate dikinase	1.12	chloroplast
At1g72770	HAB1	Homology to ABI1	1.10	unknown
At5g16010		3-oxo-5-alpha-steroid 4-dehydrogenase family protein	1.08	cytoplasm
At3g02875	ILR1	IAA-Leucine resistant 1	1.07	ER
At2g47180	GalS1	Galactinol synthase 1	1.06	unknown
At4g15210	BAM5	Beta-amylase 5	1.05	cytoplasm
At5g46180	DELTA-OAT	Ornithine-delta-aminotransferase	1.05	mitochondria
At3g26230	CYP71B24	Cytochrome P450, family 71, subfamily B, polypeptide 24	1.04	unknown
At3g06850	BCE2	Dihydrolipoamide branched chain acyltransferase	1.04	mitochondria
At3g23920	BAM1	Beta-amylase 1	1.02	nucleus
At4g27260	WES1	Indole-3-acetic acid amido synthetase	1.01	unknown
At3g48990	AAE3	Acyl-activating enzyme 3	1.00	chloroplast
At3g26210	CYP71B23	Cytochrome P450, family 71, subfamily B, polypeptide 23	0.98	unknown
At5g47880	ERF1-1	Eukaryotic release factor 1-1	0.98	cytoplasm
At5g41080	GDPD2	Glycerophosphoryldiester phosphodiesterase 2	0.97	cytoplasm
At4g24040	TRE1	Trehalase 1	0.97	plasma membrane

Biological function: metabolic process (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At2g30550		Alpha/beta-Hydrolases superfamily protein	0.97	chloroplast
At5g47330		Alpha/beta-Hydrolases superfamily protein	0.97	unknown
At1g09420	G6PD4	Glucose-6-phosphate dehydrogenase 4	0.97	chloroplast
At5g11520	ASP3	Aspartate aminotransferase 3	0.95	peroxisome
At4g15440	HPL1	Hydroperoxide lyase 1	0.94	chloroplast
At1g22370	UGT85A5	UDP-glucosyltransferase 85A5	0.94	chloroplast
At4g16760	ACX1	Acyl-CoA oxidase 1	0.93	peroxisome
At5g57630	CIPK21	CBL-interacting protein kinase 21	0.93	nucleus
At2g37760	AKR4C8	NAD(P)-linked oxidoreductase superfamily protein	0.92	cytoplasm
At5g19470	NUDT24	Nudix hydrolase homolog 24	0.92	nucleus
At1g12240	BETA-FRUCT4	Beta-fructofuranosidase/ hydrolase	0.91	vacuole
At5g53450	ORG1	OBP3-responsive gene 1	0.90	chloroplast
At1g64950	CYP89A5	Cytochrome P450, family 89, subfamily A, polypeptide 5	0.90	ER
At4g34030	MCCB	3-methylcrotonyl-CoA carboxylase	0.89	mitochondria
At4g24230	ACBP3	Acyl-CoA-binding domain 3	0.88	extracellular region
At1g55510	BCDH BETA1	Branched-chain alpha-keto acid decarboxylase E1 beta	0.88	unknown
At4g03320	Tic20-IV	Translocon at the inner envelope membrane of chloroplasts 20-IV	0.87	mitochondria
At2g18700	TPS11	Trehalose phosphatase/synthase 11	0.87	mitochondria
At3g06500	A/N-InvC	Plant neutral invertase family protein	0.87	extracellular region
At5g65010	ASN2	Asparagine synthetase 2	0.86	cytoplasm
At2g33150	PKT3	Peroxisomal 3-ketoacyl-CoA thiolase 3	0.84	mitochondria
At1g54740		Unknown protein	0.82	nucleus
At5g18630		Alpha/beta-Hydrolases superfamily protein	0.81	chloroplast
At3g14620	CYP72A8	Cytochrome P450, family 72, subfamily A, polypeptide 8	0.81	unknown
At5g60270		Concanavalin A-like lectin protein kinase family protein	0.81	plasma membrane
At4g31860		Protein phosphatase 2C family protein	0.80	plasma membrane
At3g22750		Protein kinase superfamily protein	0.80	nucleus
At2g39660	BIK1	Botrytis-induced kinase1	0.79	cytoplasm
At3g02040	SRG3	Senescence-related gene 3	0.79	cytoplasm
At3g47800		Galactose mutarotase-like superfamily protein	0.78	cytoplasm
At2g42790	CSY3	Citrate synthase 3	0.78	peroxisome
At4g33950	OST1	Open stomata 1	0.78	nucleus
At3g27060	TSO2	TSO meaning 'ugly' in Chinese 2	0.77	cytoplasm
At2g28630	KCS12	3-ketoacyl-CoA synthase 12	0.77	ER
At2g26980	CIPK3	CBL-interacting protein kinase 3	0.77	plasma membrane
At5g27320	GID1C	GA INSENSITIVE DWARF1C	0.76	nucleus
At1g23870	TPS9	Trehalose-phosphatase/synthase 9	0.75	nucleus
At3g01170		Ribosomal protein L34e superfamily protein	0.75	other membrane
At1g70290	TPS8	Trehalose-6-phosphatase synthase S8	0.75	nucleus
At3g51840	ACX4	Acyl-CoA oxidase 4	0.75	peroxisome
At1g75170		Sec14p-like phosphatidylinositol transfer family protein	0.74	plasma membrane
At5g62530	P5CDH	Delta1-pyrroline-5-carboxylate dehydrogenase	0.74	mitochondria
At3g06810	IBR3	IBA-response 3	0.74	unknown



2549742193

Biological function: metabolic process (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At1g60140	TPS10	Trehalose phosphate synthase	0.73	nucleus
At5g65110	ACX2	Acyl-CoA oxidase 2	0.72	peroxisome
At1g08650	PPCK1	Phosphoenolpyruvate carboxylase kinase 1	0.72	nucleus
At1g55810	UKL3	Uridine kinase-like 3	0.72	unknown
At4g27710	CYP709B3	Cytochrome P450, family 709, subfamily B, polypeptide 3	0.71	unknown
At5g22500	FAR1	Fatty acid reductase 1	0.71	chloroplast
At1g28960	NUDX15	Nudix hydrolase homolog 15	0.71	unknown
At1g64900	CYP89A2	Cytochrome P450, family 89, subfamily A, polypeptide 2	0.70	mitochondria
At1g05560	UGT75B1	UDP-glucosyl transferase 75B1	0.69	chloroplast
At3g48310	CYP71A22	Cytochrome P450, family 71, subfamily A, polypeptide 22	0.69	unknown
At5g58800		Quinone reductase family protein	0.68	plasma membrane
At3g16190		Isochorismatase hydrolase family protein	0.68	cytoplasm
At4g19170	NCED4	Nine-cis-epoxycarotenoid dioxygenase 4	0.68	chloroplast
At4g34120	LEJ1	LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 1	0.68	chloroplast
At1g03590		Protein phosphatase 2C family protein	0.67	plasma membrane
At3g14690	CYP72A15	Cytochrome P450, family 72, subfamily A, polypeptide 15	0.67	unknown
At4g37760	SQE3	Squalene epoxidase 3	0.67	extracellular region
At2g14170	ALDH16B2	Aldehyde dehydrogenase 6B2	0.67	mitochondria
At4g24450	PWD	Phosphoglucan, water dikinase	0.67	chloroplast
At5g21170	AKINBETA1	5'-AMP-activated protein kinase beta-2 subunit	0.66	cytoplasm
At3g46450		SEC14 cytosolic factor family protein	0.66	nucleus
At1g07720	KCS3	3-ketoacyl-CoA synthase 3	0.65	ER
At3g58750	CSY2	Citrate synthase 2	0.64	cytoplasm
At4g38470	STY46	Serine/threonine/tyrosine kinase 46	0.64	plasma membrane
At1g68020	TPS6	Trehalose-6-phosphatase synthase 56	0.63	mitochondria
At1g06690		NAD(P)-linked oxidoreductase superfamily protein	0.63	chloroplast
At1g78140		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	0.62	chloroplast
At5g59540		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	0.62	cytoplasm
At1g22360	UGT85A2	UDP-glucosyltransferase 85A2	0.62	unknown
At1g09430	ACLA-3	ATP-citrate lyase A-3	0.61	cytoplasm
At1g73920		Alpha/beta-Hydrolases superfamily protein	0.61	extracellular region
At2g34680	AIR9	Auxin-Induced in Root cultures 9	-0.61	plasma membrane
At1g77590	LACS9	Long chain acyl-CoA synthetase 9	-0.61	chloroplast
At4g01950	GPAT3	Glycerol-3-phosphate acyltransferase 3	-0.62	chloroplast
At5g18660	PCB2	PALE-GREEN AND CHLOROPHYLL B REDUCED 2	-0.64	chloroplast
At4g39710	PnsL4	PHOTOSYNTHETIC NDH SUBCOMPLEX L 4	-0.64	chloroplast
At5g15530	BCCP2	Biotin carboxyl carrier protein isoform 2	-0.64	chloroplast
At1g28130	GH3.17	Indole-3-acetic acid amido synthetase	-0.64	unknown
At1g60810	ACLA-2	ATP-citrate lyase A-2	-0.64	cytoplasm
At4g10120	ATSP54F	Sucrose-phosphate synthase	-0.69	nucleus
At5g61130	PDCB1	Plasmodesmata callose-binding protein 1	0.69	plasma membrane
At2g27510	FD3	Ferredoxin 3	-0.70	chloroplast



2549742163

Biological function: metabolic process (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At3g22790		Kinase interacting family protein	-0.70	plasma membrane
At5g13110	G6PD2	Glucose-6-phosphate dehydrogenase 2	-0.71	chloroplast
At1g06360		Fatty acid desaturase family protein	-0.72	mitochondria
At3g52720	ACA1	Alpha carbonic anhydrase	-0.73	cytoplasm
At1g30520	AAE14	Acyl-activating enzyme 14	-0.75	chloroplast
At2g47240	LACS1	Long-chain acyl-CoA synthetase 1	-0.76	nucleus
At2g21540	SFH3	SEC14-like 3	-0.77	Golgi apparatus
At1g78580	TPS1	Trehalose-6-phosphate synthase	-0.77	cytoplasm
At2g44830		Protein kinase superfamily protein	-0.79	nucleus
At4g37410	CYP81F4	Cytochrome P450, family 81, subfamily F, polypeptide 4	-0.79	ER
At1g55740	SIP1	Seed imbibition 1	-0.79	cytoplasm
At5g18860	NSH3	Nucleoside hydrolase 3	-0.83	cytoplasm
At1g28670	ARAB_1	GDSL-like Lipase/Acylhydrolase superfamily protein	-0.83	extracellular region
At5g07460	PMSR2	Peptidomethionine sulfoxide reductase 2	-0.83	chloroplast
At1g77690	LAX3	Like AUX1 3	-0.84	plasma membrane
At1g22690		Gibberellin-regulated family protein	-0.86	endomembrane
At3g44550	FAR5	Fatty acid reductase 5	-0.87	unknown
At5g41670		6-phosphogluconate dehydrogenase family protein	-0.88	mitochondria
At1g73540	NUDT21	Nudix hydrolase homolog 21	-0.89	chloroplast
At3g11430	GPAT5	Glycerol-3-phosphate acyltransferase 5	-0.90	unknown
At2g16750		Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	-0.90	plasma membrane
At5g14200	IMD1	Isopropylmalate dehydrogenase 1	-0.90	chloroplast
At1g78050	PGM	Phosphoglycerate/bisphosphoglycerate mutase	-0.90	chloroplast
At1g22650	A/N-InvD	Alkaline/neutral invertase D	-0.92	unknown
At1g66940		Protein kinase-related	-0.94	plasma membrane
At1g22170		Phosphoglycerate mutase family protein	-0.96	chloroplast
At5g02760		Protein phosphatase 2C family protein	-0.97	nucleus
At1g05570	CALS1	Callose synthase 1	-0.97	plasma membrane
At1g47840	HXK3	Hexokinase 3	-0.97	chloroplast
At1g58290	HEMA1	Glutamyl-tRNA reductase	-1.00	chloroplast
At3g56710	SIB1	Sigma factor binding protein	-1.01	nucleus
At4g13290	CYP71A19	Cytochrome P450, family 71, subfamily A, polypeptide 19	-1.02	unknown
At2g26710	BAS1	PHYB activation tagged suppressor 1	-1.02	unknown
At3g26330	CYP71B37	Cytochrome P450, family 71, subfamily B, polypeptide 37	-1.02	unknown
At1g53070		Legume lectin family protein	-1.05	cell wall
At1g80050	APT2	Adenine phosphoribosyl transferase 2	-1.05	plasma membrane
At2g30750	CYP71A12	Cytochrome P450, family 71, subfamily A, polypeptide 12	-1.07	unknown
At5g35580		Protein kinase superfamily protein	-1.07	plasma membrane
At5g12970		Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein	-1.08	extracellular region
At1g12740	CYP87A2	Cytochrome P450, family 87, subfamily A, polypeptide 2	-1.12	mitochondria
At3g44540	FAR4	Fatty acid reductase 4	-1.13	chloroplast
At5g14760	AO	L-aspartate oxidase	-1.15	endomembrane



Biological function: metabolic process (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At4g31940	CYP82C4	Cytochrome P450, family 82, subfamily C, polypeptide 4	-1.16	chloroplast
At1g50560	CYP705A25	Cytochrome P450, family 705, subfamily A, polypeptide 25	-1.17	extracellular region
At5g40850	UPM1	Urophorphyrin methylase 1	-1.17	chloroplast
At3g63110	IPT3	Isopentenyltransferase 3	-1.20	chloroplast
At1g08990	PGSIP5	Plant glycogenin-like starch initiation protein 5	-1.20	Golgi apparatus
At5g59530		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	-1.20	cytoplasm
At3g14940	PPC3	Phosphoenolpyruvate carboxylase	-1.21	cytoplasm
At4g20240	CYP71A27	Cytochrome P450, family 71, subfamily A, polypeptide 27	-1.23	unknown
At3g20110	CYP705A20	Cytochrome P450, family 705, subfamily A, polypeptide 20	-1.23	unknown
At3g14680	CYP72A14	Cytochrome P450, family 72, subfamily A, polypeptide 14	-1.27	unknown
At5g23190	CYP86B1	Cytochrome P450, family 86, subfamily B, polypeptide 1	-1.30	ER
At3g45410		Concanavalin A-like lectin protein kinase family protein	-1.31	plasma membrane
At4g15380	CYP705A4	Cytochrome P450, family 705, subfamily A, polypeptide 4	-1.31	unknown
At4g09160		SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	-1.33	nucleus
At1g24280	G6PD3	Glucose-6-phosphate dehydrogenase 3	-1.33	chloroplast
At5g58860	CYP86A1	Cytochrome P450, family 86, subfamily A, polypeptide 1	-1.34	vacuole
At1g50110	BCAT6	Branched-chain amino acid aminotransferase 6	-1.45	cytoplasm
At1g30510	RFNR2	Root FNR 2	-1.50	chloroplast
At4g04955	ALN	Allantoinase	-1.53	ER
At3g16150	ASPGB1	Asparaginase B1	-1.57	cytoplasm
At1g14185		Glucose-methanol-choline (GMC) oxidoreductase family protein	-1.58	chloroplast
At3g01260		Galactose mutarotase-like superfamily protein	-1.95	cytoplasm
At1g52820		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	-2.19	cytoplasm
At1g06120		Fatty acid desaturase family protein	-2.31	unknown
At5g16530	PIN5	PIN5	-2.33	nucleus
At3g46490		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	-2.57	cytoplasm
At1g01190	CYP78A8	Cytochrome P450, family 78, subfamily A, polypeptide 8	-2.89	unknown



Biological function: other

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At1g49570		Peroxidase superfamily protein	3.96	endomembrane
At2g39030	NATA1	Acyl-CoA N-acyltransferases 1	3.66	cytoplasm
At1g80160	GLY7	Glyoxalase I 7	3.33	cytoplasm
At2g29460	GSTU4	Glutathione S-transferase tau 4	2.87	cytoplasm
At2g29350	SAG13	Senescence-associated gene 13	2.70	chloroplast
At5g39580		Peroxidase superfamily protein	2.38	Golgi apparatus
At5g53870	ENODL1	Early nodulin-like protein 1	2.38	cytoplasm
At5g20230	BCB	Blue-copper-binding protein	2.21	plasma membrane
At3g60140	DIN2	Dark inducible 2	2.11	extracellular region
At3g04000		NAD(P)-binding Rossmann-fold superfamily protein	2.01	unknown
At4g08570		Heavy metal transport/detoxification superfamily protein	2.00	unknown
At1g22990	HIPP22	Heavy metal associated isoprenylated plant protein 22	1.94	unknown
At1g73040		Mannose-binding lectin superfamily protein	1.88	extracellular region
At1g54100	ALDH7B4	Aldehyde dehydrogenase 7B4	1.79	cytoplasm
At5g16970	AER	Alkenal reductase	1.75	nucleus
At1g09500		Cinnamyl-alcohol dehydrogenase family	1.74	unknown
At3g57260	BGL2	Beta-1,3-glucanase 2	1.61	cell wall
At2g34810		FAD-binding Berberine family protein	1.54	endomembrane
At1g47960	C/VIF1	Cell wall / vacuolar inhibitor of fructosidase 1	1.53	cell wall
At5g56870	BGAL4	beta-galactosidase 4	1.47	extracellular region
At1g02930	GSTF6	Glutathione S-transferase 6	1.44	cytoplasm
At4g37520	PER50	Peroxidase 50	1.44	cytoplasm
At3g09390	MT2A	Metallothionein 2A	1.44	unknown
At5g10300	MES5	Methyl esterase 5	1.40	cytoplasm
At5g16980		Zinc-binding dehydrogenase family protein	1.38	cytoplasm
At4g16690	MES16	Methyl esterase 16	1.38	cytoplasm
At1g14890		Plant invertase/pectin methylesterase inhibitor superfamily protein	1.31	mitochondria
At2g30140	UGT87A2	UDP-glucosyltransferase 87A2	1.27	cytoplasm
At1g02850	BGLU11	Beta glucosidase 11	1.26	extracellular region
At4g15260		UDP-glucuronosyl/UDP-glucosyl transferase family protein	1.23	unknown
At5g17220	GSTF12	Glutathione S-transferase phi 12	1.17	nucleus
At4g14090		UDP-glucuronosyl/UDP-glucosyl transferase family protein	1.16	chloroplast
At2g26740	SEH	Soluble epoxide hydrolase	1.15	nucleus
At5g64120		Peroxidase superfamily protein	1.15	apoplast
At2g36780		UDP-glucuronosyl/UDP-glucosyl transferase family protein	1.14	chloroplast
At3g61060	PP2-A13	Phloem protein 2-A13	1.12	nucleus
At3g17790	PAP17	Purple acid phosphatase 17	1.12	extracellular region
At1g10370	ERD9	Early-responsive to dehydration 9	1.06	chloroplast
At3g48000	ALDH2B4	Aldehyde dehydrogenase 2B4	1.06	chloroplast
At4g27830	BGLU10	Beta glucosidase 10	1.04	vacuole
At4g15490	UGT84A3	UDP-glucosyltransferase 84A3	1.03	unknown
At1g53580	GLY3	Glyoxalase II 3	0.99	mitochondria
At1g30720		FAD-binding Berberine family protein	0.99	endomembrane

Biological function: other (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At3g22370	AOX1A	Alternative oxidase 1A	0.93	mitochondria
At1g23020	FRO3	Ferric reduction oxidase 3	0.92	other membrane
At5g63800	MUM2	MUCILAGE-modified 2	0.90	cell wall
At4g20860		FAD-binding Berberine family protein	0.87	endomembrane
At1g73680	ALPHA DOX2	Alpha dioxygenase	0.86	unknown
At4g37530		Peroxidase superfamily protein	0.86	extracellular region
At3g46670	UGT76E11	UDP-glucosyltransferase 76E11	0.83	nucleus
At4g12290		Copper amine oxidase family protein	0.81	Goigi apparatus
At2g43400	ETFOQ	Electron-transfer flavoprotein:ubiquinone oxidoreductase	0.81	mitochondria
At1g30730		FAD-binding Berberine family protein	0.81	endomembrane
At5g17380		Pyruvate decarboxylase family protein	0.80	extracellular region
At2g29450	GSTU5	Glutathione S-transferase tau 5	0.80	cytoplasm
At3g51000		Alpha/beta-Hydrolases superfamily protein	0.77	nucleus
At3g26840	PES2	Phytol ester synthase 2	0.76	chloroplast
At3g20500	PAP18	Purple acid phosphatase 18	0.71	extracellular region
At4g15760	MO1	Monooxygenase 1	0.69	ER
At1g66240	ATX1	Homolog of anti-oxidant 1	0.69	plasma membrane
At1g65610	KOR2	Korrigan 2	0.68	plasma membrane
At5g41210	GSTT1	Glutathione S-transferase THETA 1	0.68	peroxisome
At5g17000		Zinc-binding dehydrogenase family protein	0.67	cytoplasm
At2g02390	GSTZ1	Glutathione S-transferase zeta 1	0.66	cytoplasm
At4g21580		Oxidoreductase, zinc-binding dehydrogenase family protein	0.65	cytoplasm
At1g45130	BGAL5	Beta-galactosidase 5	-0.61	extracellular region
At2g05790		O-Glycosyl hydrolases family 17 protein	-0.62	plasma membrane
At1g01580	FRO2	Ferric reduction oxidase 2	-0.67	plasma membrane
At1g21110	IGMT3	Indole glucosinolate O-methyltransferase 3	-0.69	cytoplasm
At3g07320		O-Glycosyl hydrolases family 17 protein	-0.72	plasma membrane
At5g42720		Glycosyl hydrolase family 17 protein	-0.72	other membrane
At5g49270	SHV2	SHAVEN 2	-0.74	other membrane
At5g42180	PER64	Peroxidase 64	-0.76	cell wall
At1g70710	GH9B1	Glycosyl hydrolase 9B1	-0.78	chloroplast
At1g31690		Copper amine oxidase family protein	-0.78	chloroplast
At5g55180		O-Glycosyl hydrolases family 17 protein	-0.78	plasma membrane
At3g01190	PER27	Peroxidase 27	-0.79	extracellular region
At5g66390	PER72	Peroxidase 72	-0.79	extracellular region
At5g50740		Heavy metal transport/detoxification superfamily protein	-0.79	nucleus
At3g53100		GDSL-like Lipase/Acylhydrolase superfamily protein	-0.81	extracellular region
At2g01890	PAP8	Purple acid phosphatase 8	-0.83	extracellular region
At3g13560		O-Glycosyl hydrolases family 17 protein	-0.85	plasma membrane
At4g29360		O-Glycosyl hydrolases family 17 protein	-0.87	plasma membrane
At4g16260		Glycosyl hydrolase superfamily protein	-0.88	cell wall
At1g33811		GDSL-like Lipase/Acylhydrolase superfamily protein	-0.89	extracellular region
At4g26010		Peroxidase superfamily protein	-0.95	extracellular region



Biological function: other (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At4g29270		HAD superfamily, subfamily IIIB acid phosphatase	-0.96	chloroplast
At1g78370	GSTU20	Glutathione S-transferase TAU 20	-0.99	cytoplasm
At1g21100	IGMT1	Indole glucosinolate O-methyltransferase 1	-0.99	cytoplasm
At2g28080		UDP-Glycosyltransferase superfamily protein	-1.03	unknown
At1g68850		Peroxidase superfamily protein	-1.06	extracellular region
At4g00080	UNE11	Unfertilized embryo sac 11	-1.06	endomembrane
At5g45670		GDSL-like Lipase/Acylhydrolase superfamily protein	-1.07	extracellular region
At3g16410	NSP4	Nitrile-specifier protein 4	-1.07	cytoplasm
At1g31710		Copper amine oxidase family protein	-1.10	extracellular region
At4g14940	AO1	Amine oxidase 1	-1.15	cell wall
At3g55710		UDP-glucuronosyl/UDP-glucosyl transferase family protein	-1.16	unknown
At4g25240	SKS1	SKU5 similar 1	-1.18	plasma membrane
At5g37690		SGNH hydrolase-type esterase superfamily protein	-1.18	extracellular region
At5g07475		Cupredoxin superfamily protein	-1.19	plasma membrane
At4g18970		GDSL-like Lipase/Acylhydrolase superfamily protein	-1.21	extracellular region
At4g15500	UGT84A4	UDP-glucosyltransferase 84A4	-1.23	unknown
At3g43670		Copper amine oxidase	-1.25	unknown
At1g02800	CEL2	Cellulase 2	-1.25	unknown
At5g44400		FAD-binding Berberine family protein	-1.27	cell wall
At1g19900		Glyoxal oxidase-related protein	-1.34	extracellular region
At4g15960		Alpha/beta-Hydrolases superfamily protein	-1.40	unknown
At4g37160	SKS15	SKU5 similar 15	-1.46	extracellular region
At4g30140	CDEF1	Cuticle destructing factor 1	-1.51	extracellular region
At5g24580		Heavy metal transport/detoxification superfamily protein	-1.52	nucleus
At5g58310	MES18	Methyl esterase 18	-1.54	cytoplasm
At5g16570	GLN1;4	Glutamine synthetase 1;4	-1.66	plasma membrane
At3g49110	PRX33	Peroxidase 33	-1.68	cell wall
At1g14430		Glyoxal oxidase-related protein	-1.77	extracellular region
At2g38390		Peroxidase superfamily protein	-1.92	extracellular region
At5g56080	NAS2	Nicotianamine synthase 2	-2.05	unknown
At4g12270		Copper amine oxidase family protein	-2.47	unknown
At1g49860	GSTF14	Glutathione S-transferase (class phi) 14	-4.10	cytoplasm

Biological function: photosynthesis

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At1g61800	GPT2	Glucose-6-phosphate/phosphate translocator 2	2.15	chloroplast
At1g64810	APO1	Accumulation of photosystem one 1	0.95	chloroplast
At3g15840	PIF1	Post-illumination chlorophyll fluorescence increase	0.82	chloroplast
Atcg00520	YCF4	YCF4	-0.63	chloroplast
Atcg01050	NDHD	NAD(P)H dehydrogenase complex	-0.64	chloroplast
Atcg01040	YCF5	Hypothetical protein	-0.64	chloroplast
Atcg00730	PETD	Photosynthetic electron transfer D	-0.66	chloroplast
Atcg00180	RPOC1	RNA polymerase beta' subunit-1	-0.67	chloroplast
Atcg01110	NDHH	NAD(P)H dehydrogenase subunit H	-0.71	chloroplast
Atcg00500	ACCD	Acetyl-CoA carboxylase carboxyl transferase subunit beta	-0.76	chloroplast
At3g18890	Tic62	Translocon at the inner envelope membrane of chloroplasts 62	-0.77	chloroplast
At3g62030	ROC4	Rotamase CYP 4	-0.78	chloroplast
Atcg00710	PSBH	Photosystem II reaction center protein H	-0.86	chloroplast
Atcg01010	NDHF	NADH dehydrogenase unit F	-0.90	chloroplast
At3g56090	FER3	Ferritin 3	-0.91	chloroplast
Atcg00220	PSBM	Photosystem II reaction center protein M	-0.97	chloroplast
At5g64040	PSAN	Photosystem I reaction center subunit PSI-N	-0.97	chloroplast
At3g46780	PTAC16	Plastid transcriptionally active 16	-1.02	chloroplast
At4g26530		Fructose-bisphosphate aldolase 5	-1.05	chloroplast
At3g27690	LHCB2.4	Photosystem II light harvesting complex gene 2.3	-1.06	chloroplast
At2g40100	LHCB4.3	Light harvesting complex of photosystem II	-1.10	chloroplast
At5g17170	ENH1	Enhancer of SOS3-1	-1.40	chloroplast
At5g10170	MIPS3	Myo-inositol-1-phosphate synthase 3	-1.48	cytoplasm
At2g40300	FER4	Ferritin4	-2.26	chloroplast

Biological function: protein degradation

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At1g64110	DAA1	DUO1-activated ATPase 1	3.17	plasma membrane
At1g17870	EGY3	Ethylene-dependent gravitropism-deficient and yellow-green-like 3	1.84	chloroplast
At1g76410	ATL8	RING/U-box superfamily protein	1.76	nucleus
At1g60190	PUB19	Plant U-box 19	1.72	nucleus
At2g42360		Zinc finger (C3HC4-type RING finger) family protein	1.51	nucleus
At2g18193		AAA-type ATPase family protein	1.49	ER
At1g80110	PP2-B11	Phloem protein 2-B11	1.42	nucleus
At1g62710	BETA-VPE	Beta vacuolar processing enzyme	1.29	unknown
At3g59940		Galactose oxidase/kelch repeat superfamily protein	1.28	cytoplasm
At5g01520	AIRP2	ABA insensitive RING protein 2	1.27	nucleus
At4g19700	RING	RING	1.24	nucleus
At4g03510	RMA1	RING membrane-anchor 1	1.16	ER
At5g51070	ERD1	Early-responsive to dehydration 1	1.11	chloroplast
At1g23390		Kelch repeat-containing F-box family protein	1.07	nucleus
At5g22860		Serine carboxypeptidase S28 family protein	1.07	chloroplast
At1g21410	SKP2A	SKP2-like	1.03	nucleus
At3g10450	SCPL7	Serine carboxypeptidase-like 7	1.02	extracellular region
At4g16190		Cysteine proteinases superfamily protein	1.00	vacuole
At1g26930		Kelch repeat-containing F-box family protein	0.97	peroxisome
At5g01720		RNI-like superfamily protein	0.93	nucleus
At4g17245		RING/U-box superfamily protein	0.93	unknown
At1g20160	AT5BT5.2	Serine-type endopeptidase	0.92	apoplast
At5g05110		Cystatin/monellin family protein	0.90	extracellular region
At5g57900	SKIP1	SKIP1 interacting partner 1	0.89	cytoplasm
At4g35480	RHA3B	RING-H2 finger A3B	0.84	unknown
At4g01610		Cathepsin B-like cysteine protease	0.81	extracellular region
At1g01650	SPPL4	Signal peptide peptidase-like 4	0.80	plasma membrane
At5g22920		Zinc finger (C3HC4-type RING finger) family protein	0.77	nucleus
At5g63160	BT1	BTB AND TAZ domain protein 1	0.77	nucleus
At3g17000	UBC32	Ubiquitin-conjugating enzyme 32	0.77	nucleus
At2g27310		F-box family protein	0.76	unknown
At4g16520	ATG8F	Autophagy 8F	0.75	unknown
At1g06430	FTSH8	FTSH protease 8	0.73	chloroplast
At1g76390		ARM repeat superfamily protein	0.72	plasma membrane
At2g39710		Eukaryotic aspartyl protease family protein	0.71	extracellular region
At1g80440		Galactose oxidase/kelch repeat superfamily protein	0.71	nucleus
At1g55000		Peptidoglycan-binding LysM domain-containing protein	0.66	cell wall
At4g03030		Galactose oxidase/kelch repeat superfamily protein	0.65	chloroplast
At4g03190	GRH1	GRR1-like protein 1	-0.62	unknown
At4g34980	SLP2	Subtilisin-like serine protease 2	-0.63	cell wall
At5g51750	SBT1.3	Subtilase 1.3	-0.69	cell wall
At5g59090	SBT4.12	Subtilase 4.12	-0.70	extracellular region
At3g20015		Eukaryotic aspartyl protease family protein	-0.73	extracellular region



Biological function: protein degradation

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At5g47050		SBP (S-ribonuclease binding protein) family protein	-0.73	nucleus
At3g50930	BCS1	Cytochrome BC1 synthesis	-0.75	plasma membrane
At3g54720	AMP1	Altered meristem program 1	-0.76	plasma membrane
At1g01900	SBT1.1	Subtilisin-like serine protease	-0.77	apoplast
At4g20070	AAH	Allantoate Amidohydrolase	-0.79	chloroplast
At3g06140		RING/U-box superfamily protein	-0.86	cytoplasm
At1g72200		RING/U-box superfamily protein	-0.86	unknown
At5g56530		Unknown protein	-0.91	extracellular region
At2g39850		Subtilisin-like serine endopeptidase family protein	-1.01	cell wall
At3g63470	scpl40	Serine carboxypeptidase-like 40	-1.03	extracellular region
At4g11320		Papain family cysteine protease	-1.05	extracellular region
At4g21650		Subtilase family protein	-1.08	extracellular region
At1g25510		Eukaryotic aspartyl protease family protein	-1.09	extracellular region
At4g20430		Subtilase family protein	-1.12	cell wall
At5g08260	scpl35	Serine carboxypeptidase-like 35	-1.21	extracellular region
At2g03200		Eukaryotic aspartyl protease family protein	-1.28	extracellular region
At3g43960		Cysteine proteinases superfamily protein	-1.33	plasma membrane
At2g35770	scpl28	Serine carboxypeptidase-like 28	-1.40	extracellular region
At2g27420		Cysteine proteinases superfamily protein	-1.41	unknown
At2g35000	ATL9	TOXICOS EN LEVADURA 9	-1.44	extracellular region
At5g45650		Subtilase family protein	-1.57	cell wall
At3g51330		Eukaryotic aspartyl protease family protein	-1.70	plasma membrane
At1g11080	SCPL31	Serine carboxypeptidase-like 31	-1.73	extracellular region
At3g51350		Eukaryotic aspartyl protease family protein	-2.28	plasma membrane

Biological function: regulation of transcription

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At1g43160	RAP2.6	Related to AP2 6	2.61	nucleus
At1g48000	MYB112	MYB domain protein 112	2.38	nucleus
At5g13220	JAZ10	Jasmonate-zim-domain protein 10	2.35	nucleus
At3g61890	HB12	Homeobox 12	2.31	nucleus
At2g46680	HB7	Homeobox 7	2.19	nucleus
At2g38250		DNA-binding protein-related	1.95	nucleus
At5g13330	Rap2.6L	Related to AP2 6L	1.94	nucleus
At4g18170	WRKY28	WRKY DNA-binding protein 28	1.93	nucleus
At3g56970	ORG2	OBP3-responsive gene 2	1.83	nucleus
At1g76590		PLATZ transcription factor family protein	1.83	mitochondria
At3g01600	NAC044	NAC domain containing protein 44	1.83	unknown
At3g15500	NAC55	NAC domain containing protein 55	1.72	nucleus
At3g04070	NAC047	NAC domain containing protein 47	1.72	nucleus
At1g75490		DREB subfamily A-2 of ERF/AP2 transcription factor family	1.68	nucleus

Biological function: regulation of transcription (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At3g56980	ORG3	OBP3-responsive gene 3	1.65	nucleus
At3g01970	WRKY45	WRKY DNA-binding protein 45	1.64	nucleus
At5g49700		Predicted AT-hook DNA-binding family protein	1.58	nucleus
At4g39780		AP2 domain-containing transcription factor	1.57	nucleus
At1g71030	MYBL2	MYB-like 2	1.56	nucleus
At3g02150	TFPD	Plastid transcription factor 1	1.53	chloroplast
At5g07100	WRKY26	WRKY DNA-binding protein 26	1.45	nucleus
At3g23250	MYB15	MYB domain protein 15	1.39	nucleus
At1g62300	WRKY6	WRKY DNA-binding protein 6	1.35	nucleus
At1g70810		Calcium-dependent lipid-binding (CaLB domain) family protein	1.34	unknown
At3g61630	CRF6	Cytokinin response factor 6	1.32	cytoplasm
At2g19810	OZF1	Oxidation-related zinc finger 1	1.28	nucleus
At1g70700	JAZ9	Jasmonate-zim-domain protein 9	1.26	nucleus
At1g54160	NFYA5	Nuclear factor Y, subunit A5	1.22	nucleus
At2g41870		Remorin family protein	1.17	cytoplasm
At2g46270	GBF3	G-box binding factor 3	1.14	nucleus
At1g06180	MYB13	MYB domain protein 13	1.11	nucleus
At5g44260		Zinc finger (CCCH-type) family protein	1.08	nucleus
At1g17380	JAZ5	Jasmonate-zim-domain protein 5	1.08	nucleus
At4g37180		MYB family transcription factor	1.06	nucleus
At5g25830	GATA12	GATA transcription factor 12	1.04	nucleus
At4g09820	TT8	TRANSPARENT TESTA 8	1.00	nucleus
At5g24120	SIGE	Sigma factor E	0.96	mitochondria
At5g27280		Zinc finger (DNL type) family protein	0.95	chloroplast
At4g36900	RAP2.10	Related to AP2 10	0.95	nucleus
At2g31380	STH	Salt tolerance homologue	0.94	nucleus
At3g47600	MYB94	MYB domain protein 94	0.93	nucleus
At5g57660	COL5	CONSTANS-like 5	0.89	nucleus
At3g47500	CDF3	Cycling DOF factor 3	0.88	nucleus
At4g22820		A20/AN1-like zinc finger family protein	0.87	nucleus
At3g14020		Nuclear factor Y, subunit A6	0.87	nucleus
At4g29190	OZF2	Oxidation-related zinc finger 2	0.87	nucleus
At1g21000		PLATZ transcription factor family protein	0.86	mitochondria
At2g30250	WRKY25	WRKY DNA-binding protein 25	0.84	nucleus
At4g01250	WRKY22	WRKY DNA-binding protein 22	0.84	nucleus
At3g17860	JAZ3	Jasmonate-zim-domain protein 3	0.83	chloroplast
At5g67480	BT4	BTB and TAZ domain protein	0.82	cytoplasm
At2g45660	AGL20	AGAMOUS-like 20	0.81	nucleus
At2g25900	TZF1	Tandem zinc finger protein 1	0.81	nucleus
At1g36060		AP2 domain-containing transcription factor	0.79	nucleus
At5g20900	JAZ12	Jasmonate-zim-domain protein 12	0.76	nucleus
At5g37540		Eukaryotic aspartyl protease family protein	0.76	extracellular region
At5g49520	WRKY48	WRKY DNA-binding protein 48	0.75	nucleus
At1g74950	JAZ2	Jasmonate-zim-domain protein 2	0.75	nucleus



Biological function: regulation of transcription (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At1g55110	IDD7	Indeterminate(ID)-Domain 7	0.72	nucleus
At5g23750		Remorin family protein	0.71	nucleus
At1g30320		Remorin family protein	0.71	unknown
At1g28520	VOZ1	Vascular plant one zinc finger protein	0.71	unknown
At5g02810	PRR7	Pseudo-response regulator 7	0.70	nucleus
At1g04990		Zinc finger (CCCH-type) family protein	0.69	nucleus
At3g15790		Methyl-CpG binding	0.69	nucleus
At1g51140	FBH3	FLOWERING BHLH 3	0.67	nucleus
At2g35940	BLH1	BEL-like homeodomain 1	0.67	nucleus
At2g23320	WRKY15	WRKY DNA-binding protein 15	0.65	nucleus
At5g17300		MYB family transcription factor	0.63	plasma membrane
At1g52150	ATHB-15	Class III HD-ZIP protein family	-0.62	nucleus
At4g37260	MYB73	MYB domain protein 73	-0.66	nucleus
At5g65630	GTE7	Global transcription factor group E7	-0.70	nucleus
At4g17460	HAT1	Homeobox protein HAT1	-0.73	nucleus
At5g07030		Eukaryotic aspartyl protease family protein	-0.75	cell wall
At5g11510	MYB3R4	MYB domain protein 3R-4	-0.77	nucleus
At1g14350	MYB124	MYB domain protein 124	-0.77	nucleus
At3g58120	BZIP61	bZIP transcription factor family protein 61	-0.78	nucleus
At5g03150	JKD	JACKDAW	-0.82	nucleus
At1g21740		Unknown protein	-0.82	unknown
At5g19520	MSL9	Mechanosensitive channel of small conductance-like 9	-0.94	chloroplast
At1g63100		GRAS family transcription factor	-0.95	nucleus
At2g38090		MYB family transcription factor	-0.98	nucleus
At1g24260	SEP3	SEPALATA3	-1.01	nucleus
At1g73870	COL7	B-box type zinc finger protein with CCT domain	-1.02	nucleus
At1g04240	IAA3	Indole-3-acetic acid inducible 3	-1.03	nucleus
At2g42380	BZIP34	bZIP transcription factor family protein	-1.04	nucleus
At5g05790		MYB family transcription factor	-1.05	nucleus
At5g15150	HB3	Homeobox 3	-1.06	nucleus
At3g22760	SOL1	TSO1-like protein 1	-1.07	nucleus
At1g09750		Eukaryotic aspartyl protease family protein	-1.18	cell wall
At3g61950		Basic helix-loop-helix (bHLH) family protein	-1.19	nucleus
At5g22890		Zinc finger (C2H2 type) family protein	-1.23	nucleus
At1g34670	MYB93	MYB domain protein 93	-1.26	nucleus
At2g34620		Mitochondrial transcription termination factor family protein	-1.32	chloroplast
At2g40750	WRKY54	WRKY DNA-binding protein 54	-1.34	nucleus
At3g56400	WRKY70	WRKY DNA-binding protein 70	-1.42	nucleus
At1g33760		AP2 domain-containing transcription factor	-2.08	nucleus



Biological function: secondary metabolism

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At4g37990	ELI3-2	Elicitor-activated gene 3-2	3.76	cytoplasm
At2g38240		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	3.18	cytoplasm
At1g61120	TPS4	Terpene synthase 04	2.93	chloroplast
At3g44300	NIT2	Nitrilase 2	2.58	plasma membrane
At3g45130	LAS1	Lanosterol synthase	2.19	unknown
At1g56650	MYB75	MYB domain protein 75	1.56	nucleus
At1g54020		GDSL-like Lipase/Acylhydrolase superfamily protein	1.50	vacuole
At5g39050	PMAT1	HXXXD-type acyl-transferase family protein	1.49	cytoplasm
At3g51450		Calcium-dependent phosphotriesterase superfamily protein	1.40	chloroplast
At4g22880	TT18	Leucoanthocyanidin dioxygenase	1.28	cytoplasm
At5g42800	DFR	Dihydroflavonol 4-reductase	1.21	ER
At4g34230	CAD5	Cinnamyl alcohol dehydrogenase 5	1.21	cytoplasm
At1g72680	CAD1	Cinnamyl-alcohol dehydrogenase	1.19	cytoplasm
At1g03940		HXXXD-type acyl-transferase family protein	1.19	cytoplasm
At3g29590	AT5MAT	O-malonyltransferase/ transferase	1.18	cytoplasm
At5g54060	UF3GT	UDP-glucose:flavonoid 3-O-glucosyltransferase	1.16	cytoplasm
At3g51440		Calcium-dependent phosphotriesterase superfamily protein	1.13	ER
At3g51430	YLS2	YELLOW-LEAF-SPECIFIC GENE 2	1.05	chloroplast
At2g29340		NAD-dependent epimerase/dehydratase family protein	0.96	unknown
At2g33590		Cinnamoyl-CoA reductase family	0.95	unknown
At5g52570	BETA-OHASE2	Beta-carotene hydroxylase 2	0.88	chloroplast
At4g37980	ELI3-1	Elicitor-activated gene 3-1	0.80	cytoplasm
At1g62540	FMO GS-OX2	Flavin-monooxygenase glucosinolate S-oxygenase 2	0.79	nucleus
At1g54040	EPS	Epithiospecifier protein	0.72	nucleus
At4g12300	CYP706A4	Cytochrome P450, family 706, subfamily A, polypeptide 4	0.67	chloroplast
At1g57770		Amine oxidase family	0.66	chloroplast
At3g23490	CYN	Cyanase	0.63	cytoplasm
At5g23020	IMS2	2-isopropylmalate synthase	-0.70	chloroplast
At1g18570	MYB51	MYB domain protein 51	-0.72	nucleus
At2g30210	LAC3	Laccase 3	-0.73	apoplast
At5g01040	LAC8	Laccase 8	-0.73	apoplast
At2g29730	UGT71D1	UDP-glucosyltransferase 71D1	-0.73	unknown
At5g66690	UGT72E2	UDP-glucosyltransferase 72E2	-0.79	unknown
At1g16400	CYP79F2	Cytochrome P450, family 79, subfamily F, polypeptide 2	-0.85	ER
At3g50740	UGT72E1	UDP-glucosyltransferase 72E1	-0.98	unknown
At4g24670	TAR2	Tryptophan aminotransferase related 2	-0.99	unknown
At3g09220	LAC7	Laccase 7	-1.05	apoplast
At4g31910		HXXXD-type acyl-transferase family protein	-1.07	nucleus
At2g29130	LAC2	Laccase 2	-1.14	apoplast
At2g18570		UDP-glucuronosyl/UDP-glucosyl transferase family protein	-1.15	cytoplasm
At1g78970	LUP1	Lupeol synthase 1	-1.17	nucleus
At1g18140	LAC1	Laccase 1	-1.20	apoplast
At2g29750	UGT71C1	UDP-glucosyltransferase 71C1	-1.22	unknown



Biological function: secondary metabolism (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At5g07130	LAC13	Laccase 13	-1.23	apoplast
At4g35160		O-methyltransferase family protein	-1.32	nucleus
At2g40230		HXXXD-type acyl-transferase family protein	-1.32	cytoplasm
At4g12330	CYP706A7	Cytochrome P450, family 706, subfamily A, polypeptide 7	-1.35	unknown
At1g34040		Alliinase family protein	-1.41	extracellular region
At1g01390		UDP-glucuronosyl/UDP-glucosyl transferase family protein	-1.49	unknown
At1g77520		O-methyltransferase family 2 protein	-1.53	nucleus

Biological function: signaling

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At2g33380	RD20	Responsive to desiccation 20	2.40	vacuole
At1g51820		Leucine-rich repeat protein kinase family protein	2.18	plasma membrane
At5g52390		PAR1 protein	2.02	plasma membrane
At3g24982	RLP40	Receptor like protein 40	2.01	chloroplast
At4g23210	CRK13	Cysteine-rich RLK (RECEPTOR-like protein kinase) 13	1.65	extracellular region
At3g50770	CML41	Calmodulin-like 41	1.57	unknown
At1g66920		Protein kinase superfamily protein	1.40	plasma membrane
At1g07390	RLP1	Receptor like protein 1	1.39	unknown
At2g02710	PLPB	PAS/LOV PROTEIN B	1.21	plasma membrane
At3g46280		Protein kinase-related	1.14	extracellular region
At5g09440	EXL4	EXORDIUM like 4	1.14	other membrane
At1g52410	TSA1	TSK-associating protein 1	1.08	peroxisome
At5g01540	LECRKA4.1	Lectin receptor kinase subfamily A4	0.99	plasma membrane
At1g61380	SD1-29	S-DOMAIN-1 29	0.98	plasma membrane
At1g09530	PIF3	Phytochrome interacting factor 3	0.98	nucleus
At5g58350	WNK4	With no lysine (K) kinase 4	0.96	cytoplasm
At4g23220	CRK14	Cysteine-rich RLK (RECEPTOR-like protein kinase) 14	0.92	unknown
At3g59700	HLECRK	Lectin-receptor kinase	0.88	endomembrane
At5g20480	EFR	EF-TU receptor	0.88	plasma membrane
At2g29120	GLR2.7	Glutamate receptor 2.7	0.82	vacuole
At4g35750		SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	0.80	cytoplasm
At3g50840		Phototropic-responsive NPH3 family protein	0.80	plasma membrane
At4g23190	CRK11	Cysteine-rich RLK (RECEPTOR-like protein kinase) 11	0.80	extracellular region
At4g38810		Calcium-binding EF-hand family protein	0.77	nucleus
At4g23050		PAS domain-containing protein tyrosine kinase family protein	0.76	cytoplasm
At1g16110	WAKL6	Wall associated kinase-like 6	0.75	extracellular region
At2g18170	MPK7	MAP kinase 7	0.74	nucleus
At5g05930	GC1	Guanylyl cyclase 1	0.71	nucleus
At3g51740	IMK2	Inflorescence meristem receptor-like kinase 2	-0.63	plasma membrane



Biological function: signaling (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At3g56370		Leucine-rich repeat protein kinase family protein	-0.65	cell wall
At1g75820	CLV1	CLAVATA 1	-0.66	plasma membrane
At5g16590	LRR1	Leucine-rich repeat protein kinase family protein	-0.69	plasma membrane
At5g61600	ERF104	Ethylene response factor 104	-0.70	nucleus
At5g07580		ERF (ethylene response factor) subfamily B-3	-0.71	nucleus
At3g49260	iqd21	IQ-domain 21	-0.71	nucleus
At1g54820		Protein kinase superfamily protein	-0.72	plasma membrane
At1g35710		Leucine-rich repeat transmembrane protein kinase	-0.73	plasma membrane
At5g43020		Leucine-rich repeat protein kinase family protein	-0.74	plasma membrane
At3g47570		Leucine-rich repeat protein kinase family protein	-0.74	plasma membrane
At5g62710		Leucine-rich repeat protein kinase family protein	-0.75	plasma membrane
At2g27030	CAM5	Calmodulin 5	-0.76	nucleus
At4g20940	GHR1	Guard cell hydrogen peroxide-resistant 1	-0.76	plasma membrane
At1g21250	WAK1	Cell wall-associated kinase	-0.76	plasma membrane
At4g27280		Calcium-binding EF-hand family protein	-0.77	plasma membrane
At2g23770	LYK4	LysM domain-containing receptor-like kinase 4	-0.81	plasma membrane
At4g35380		SEC7-like guanine nucleotide exchange family protein	-0.84	cytoplasm
At1g76650	CML38	calmodulin-like 38	-0.85	nucleus
At2g41820		Leucine-rich repeat protein kinase family protein	-0.86	plasma membrane
At5g27100	GLR2.1	Glutamate receptor 2.1	-0.89	extracellular region
At1g51860		Leucine-rich repeat protein kinase family protein	-0.90	extracellular region
At4g11900		S-locus lectin protein kinase family protein	-0.90	plasma membrane
At1g48480	RKL1	Receptor-like kinase 1	-0.91	plasma membrane
At4g03100		Rho GTPase activating protein	-0.92	cytoplasm
At3g54040		PAR1 protein	-0.96	chloroplast
At3g24240		LRR receptor-like protein kinase family protein	-0.97	chloroplast
At1g08590		CLAVATA1 receptor kinase	-0.98	plasma membrane
At2g17230	EXL5	EXORDIUM like 5	-0.99	extracellular region
At4g18640	MRH1	Morphogenesis of root hair 1	-1.01	chloroplast
At5g12940		Leucine-rich repeat (LRR) family protein	-1.05	extracellular region
At3g17640		Leucine-rich repeat (LRR) family protein	-1.08	unknown
At2g01210		Leucine-rich repeat protein kinase family protein	-1.20	chloroplast
At4g05200	CRK25	Cysteine-rich RLK (RECEPTOR-like protein kinase) 25	-1.25	extracellular region
At2g28250	NCRK	Protein kinase superfamily protein	-1.26	plasma membrane
At2g28960		Leucine-rich repeat protein kinase family protein	-1.34	plasma membrane
At3g45860	CRK4	Cysteine-rich RLK (RECEPTOR-like protein kinase) 4	-1.40	extracellular region
At2g36570		Leucine-rich repeat protein kinase family protein	-1.41	plasma membrane
At5g66330		Leucine-rich repeat (LRR) family protein	-1.50	plasma membrane
At1g51840		Protein kinase-related	-1.51	extracellular region
At1g07560		Leucine-rich repeat protein kinase family protein	-1.59	plasma membrane
At1g51830		Leucine-rich repeat protein kinase family protein	-1.66	unknown
At2g41090		Calcium-binding EF-hand family protein	-1.80	plasma membrane
At1g78990		HXXXD-type acyl-transferase family protein	-1.82	cytoplasm

Biological function: signaling (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At5g59670		Leucine-rich repeat protein kinase family protein	-1.84	plasma membrane
At5g59680		Leucine-rich repeat protein kinase family protein	-2.02	plasma membrane
At1g05700		Leucine-rich repeat transmembrane protein kinase protein	-2.08	plasma membrane

Biological function: stress

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At5g44420	PDF1.2A	Plant defensin 1.2	6.25	cell wall
At2g26010	PDF1.3	Plant defensin 1.3	5.10	cell wall
At5g66400	RAB18	Responsive to ABA 18	4.33	unknown
At4g27670	HSP21	Heat shock protein 21	3.95	unknown
At5g12020	HSP17.6II	17.6 kDa class II heat shock protein	3.74	cytoplasm
At5g15960	KIN1	Stress-responsive protein	3.54	chloroplast
At5g43840	HSFA6A	Heat shock transcription factor A6A	3.53	nucleus
At2g47770	TSPO	Tryptophan-rich sensory protein	3.49	Golgi apparatus
At5g52300	RD29B	Responsive to desiccation 29B	3.31	cytoplasm
At3g46230	HSP17.4	Heat shock protein 17.4	2.85	unknown
At1g19610	PDF1.4	Plant defensin 1.4	2.80	extracellular region
At3g55970	JRG21	Jasmonate-regulated gene 21	2.68	cytoplasm
At5g05600		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	2.64	cytoplasm
At1g16850		Unknown protein	2.62	ER
At2g45570	CYP76C2	Cytochrome P450, family 76, subfamily C, polypeptide 2	2.59	extracellular region
At1g33960	AIG1	AVRRPT2-induced gene 1	2.42	chloroplast
At3g25760	AOC1	Allene oxide cyclase 1	2.35	chloroplast
At2g42540	COR15A	Cold-regulated 15A	2.32	chloroplast
At2g43510	TI1	Trypsin inhibitor protein 1	2.32	extracellular region
At5g59220	HAI1	Highly ABA-induced PP2C gene 1	2.28	nucleus
At5g52310	RD29A	Responsive to desiccation 29A	2.16	nucleus
At1g18710	MYB47	MYB domain protein 47	2.13	nucleus
At1g69930	GSTU11	Glutathione S-transferase TAU 11	2.11	unknown
At3g59930		Defensin-like (DEFL) family protein	2.11	extracellular region
At1g44350	ILL6	IAA-leucine resistant (ILR)-like gene 6	2.09	extracellular region
At2g43620		Chitinase family protein	2.07	apoplast
At1g07400		HSP20-like chaperones superfamily protein	1.97	cytoplasm
At1g13609		Defensin-like (DEFL) family protein	1.97	mitochondria
At1g69260	AFP1	ABI five binding protein 1	1.96	nucleus
At1g80130		Tetratricopeptide repeat (TPR)-like superfamily protein	1.92	other membrane
At1g56150		SAUR-like auxin-responsive protein family	1.90	unknown
At1g52040	MBP1	Myrosinase-binding protein 1	1.81	vacuole
At1g16510		SAUR-like auxin-responsive protein family	1.79	unknown
At1g05680	UGT74E2	UDP-glucosyltransferase 74E2	1.78	unknown



Biological function: stress (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At5g15970	COR6.6	Cold-responsive 6.6	1.75	plasma membrane
At3g28740	CYP81D11	Cytochrome P450, family 81, subfamily D, polypeptide 11	1.74	unknown
At1g22400	UGT85A1	UDP-glucosyltransferase 85A1	1.71	unknown
At3g22840	ELIP1	EARLY LIGHT-INDUCIBLE PROTEIN	1.70	chloroplast
At5g04150	BHLH101	Basic helix-loop-helix protein 101	1.69	nucleus
At3g14440	NCED3	Nine-cis-epoxycarotenoid dioxygenase 3	1.68	chloroplast
At1g73480		Alpha/beta-Hydrolases superfamily protein	1.65	cytoplasm
At2g34930		Disease resistance family protein	1.62	cell wall
At1g52000		Mannose-binding lectin superfamily protein	1.61	unknown
At2g41240	BHLH100	Basic helix-loop-helix protein 100	1.58	nucleus
At3g50970	LTI30	Low temperature-induced 30	1.58	other membrane
At3g16770	EBP	Ethylene responsive element binding protein	1.57	nucleus
At4g12470	AZ11	Azelaic acid induced 1	1.57	extracellular region
At3g50480	HR4	Homolog of RPW8 4	1.53	chloroplast
At1g12480	pEARL1 1	Early arabidopsis aluminum induced 1	1.52	extracellular region
At3g22060		Receptor-like protein kinase-related family protein	1.51	vacuole
At5g02020	SIS	Salt induced serine rich	1.50	nucleus
At1g19670	CLH1	Chlorophyllase 1	1.47	vacuole
At1g06570	PDS1	Phytoene desaturation 1	1.45	chloroplast
At2g25450		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1.43	cytoplasm
At2g43530		Scorpion toxin-like knottin superfamily protein	1.40	extracellular region
At2g36750	UGT73C1	UDP-glucosyltransferase 73C1	1.40	chloroplast
At1g17020	SRG1	Senescence-related gene 1	1.40	cytoplasm
At2g45210		SAUR-like auxin-responsive protein family	1.33	mitochondria
At1g77120	ADH1	Alcohol dehydrogenase 1	1.31	plasma membrane
At2g36080		Plant-specific B3 DNA-binding domain transcription factor	1.31	unknown
At5g25610	RD22	Responsive to desiccation 22	1.30	Golgi apparatus
At5g56550	OXS3	Oxidative stress 3	1.30	nucleus
At3g25770	AOC2	Allene oxide cyclase 2	1.29	chloroplast
At5g13370		Auxin-responsive GH3 family protein	1.29	cytoplasm
At5g57050	ABI2	ABA insensitive 2	1.28	unknown
At2g39200	MLO12	Mildew resistance locus O 12	1.27	plasma membrane
At1g52100		Mannose-binding lectin superfamily protein	1.26	other membrane
At3g26290	CYP71B26	Cytochrome P450, family 71, subfamily B, polypeptide 26	1.25	unknown
At3g60690		SAUR-like auxin-responsive protein family	1.25	mitochondria
At4g15910	DI21	Drought-induced 21	1.24	chloroplast
At3g44880	ACD1	Accelerated cell death 1	1.23	chloroplast
At1g45616	RLP6	Receptor like protein 6	1.21	other membrane
At1g80920	TOC12	Chaperone DnaJ-domain superfamily protein	1.19	nucleus
At2g33830		Dormancy/auxin associated family protein	1.17	nucleus
At3g26220	CYP71B3	Cytochrome P450, family 71, subfamily B, polypeptide 3	1.16	unknown
At3g15450		Unknown protein	1.15	chloroplast
At5g61560		U-box domain-containing protein kinase family protein	1.13	nucleus



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Biological function: stress (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At2g43570	CHI	Chitinase	1.12	apoplast
At3g29575	AFP3	ABI five binding protein 3	1.11	nucleus
At1g17420	LOX3	Lipoxygenase 3	1.08	chloroplast
At5g25110	CIPK25	CBL-interacting protein kinase 25	1.07	plasma membrane
At1g78070		Transducin/WD40 repeat-like superfamily protein	1.07	cytoplasm
At4g27450		Unknown protein	1.07	plasma membrane
At1g51760	IAR3	IAA-Alanine resistant 3	1.06	chloroplast
At1g58180	BCA6	Beta carbonic anhydrase 6	1.06	chloroplast
At1g62810	CUAO1	Copper amine oxidase 1	1.05	extracellular region
At3g46690		UDP-glucuronosyl/UDP-glucosyl transferase family protein	1.05	unknown
At3g11930		Adenine nucleotide alpha hydrolases-like superfamily protein	1.04	cytoplasm
At4g19230	CYP707A1	Cytochrome P450, family 707, subfamily A, polypeptide 1	1.04	extracellular region
At4g23680		Polyketide cyclase/dehydrase and lipid transport superfamily protein	1.04	unknown
At4g23300	CRK22	Cysteine-rich RLK (RECEPTOR-like protein kinase) 22	1.03	extracellular region
At1g16030	Hsp70b	Heat shock protein 70B	1.01	cytoplasm
At1g60730		Aldo/keto reductase family protein	0.98	cytoplasm
At1g19180	JAZ1	Jasmonate-zim-domain protein 1	0.97	nucleus
At1g18810		Phytochrome kinase substrate-related	0.96	plasma membrane
At5g42650	AOS	Allene oxide synthase	0.95	chloroplast
At2g38870		Protease inhibitor	0.93	cell wall
At4g26080	ABI1	ABA insensitive 1	0.91	nucleus
At1g58270	ZW9	ZW9	0.91	cytoplasm
At1g03495		HXXXD-type acyl-transferase family protein	0.91	cytoplasm
At2g03760	SOT12	Sulphotransferase 12	0.90	cytoplasm
At3g62550		Adenine nucleotide alpha hydrolases-like superfamily protein	0.90	nucleus
At3g21790		UDP-glucuronosyl/UDP-glucosyl transferase family protein	0.86	unknown
At2g23170	GH3.3	Indole-3-acetic acid amido synthetase	0.86	unknown
At1g72830	NF-YA3	Nuclear factor Y, subunit A3	0.86	nucleus
At1g54010		GDSL-like Lipase/Acylhydrolase superfamily protein	0.85	vacuole
At2g42750		DNAJ heat shock N-terminal domain-containing protein	0.84	chloroplast
At1g71040	LPR2	Low Phosphate Root2	0.84	Golgi apparatus
At3g19290	ABF4	ABRE binding factor 4	0.83	nucleus
At1g73260	KTI1	Kunitz trypsin inhibitor 1	0.82	extracellular region
At5g43260		Chaperone protein dnaJ-related	0.82	chloroplast
At5g42900	COR27	Cold-regulated gene 27	0.81	nucleus
At1g01140	CIPK9	CBL-interacting protein kinase 9	0.80	plasma membrane
At5g20150	SPX1	SPX domain gene 1	0.80	cytoplasm
At3g04720	PR4	Pathogenesis-related 4	0.79	extracellular region
At4g36040	J11	Chaperone DnaJ-domain superfamily protein	0.78	nucleus
At3g55610	P5CS2	Delta1-pyrroline-5-carboxylate synthetase 2	0.77	chloroplast
At2g43820	UGT74F2	UDP-glucosyltransferase 74F2	0.76	cytoplasm
At3g46700		UDP-glucuronosyl/UDP-glucosyl transferase family protein	0.76	unknown

Biological function: stress (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At5g43440		2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	0.75	cytoplasm
At1g66160	CMPG1	CYS, MET, PRO, and GLY protein 1	0.73	cytoplasm
At2g39980		HXXXD-type acyl-transferase family protein	0.72	cytoplasm
At4g13010		Oxidoreductase, zinc-binding dehydrogenase family protein	0.72	chloroplast
At2g23120		Late embryogenesis abundant protein, group 6	0.72	plasma membrane
At2g41940		Zinc finger protein 8	0.70	nucleus
At5g38020	UGT87A2	UDP-glucosyltransferase 87A2	0.70	nucleus
At1g13930		Nodulin-related protein 1	0.69	chloroplast
At3g18280		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	0.68	extracellular region
At4g28240		Wound-responsive family protein	0.67	nucleus
At2g36800	UGT73C5	UDP-glucosyltransferase 73C5	0.64	chloroplast
At2g06050	OPR3	Oxophytodienoate reductase 3	0.63	peroxisome
At3g55230		Disease resistance-responsive (dirigent-like protein) family protein	-0.61	extracellular region
At3g61820		Eukaryotic aspartyl protease family protein	-0.62	cell wall
At1g55210		Disease resistance-responsive (dirigent-like protein) family protein	-0.62	extracellular region
At1g04040		HAD superfamily, subfamily IIIB acid phosphatase	-0.63	cell wall
At2g22670	IAA8	Indoleacetic acid-induced protein 8	-0.65	unknown
At2g39430		Disease resistance-responsive (dirigent-like protein) family protein	-0.65	extracellular region
At4g22120		Early-responsive to dehydration protein-related	-0.66	plasma membrane
At1g31540		Disease resistance protein (TIR-NBS-LRR class) family	-0.66	other membrane
At4g08390	SAPX	Stromal ascorbate peroxidase	-0.67	chloroplast
At3g16920	CTL2	Chitinase-like protein 2	-0.69	unknown
At5g65210	TGA1	TGA1 transcription factor	-0.69	nucleus
At5g01810	CIPK15	CBL-interacting protein kinase 15	-0.69	plasma membrane
At4g23800	3xHMG-box2	High mobility group (HMG1/2) family protein	-0.73	nucleus
At1g52070		Mannose-binding lectin superfamily protein	-0.73	extracellular region
At1g51850		Leucine-rich repeat protein kinase family protein	-0.73	plasma membrane
At4g08685	SAH7	SAH7	-0.74	endomembrane
At3g48090	EDS1	Enhanced disease susceptibility 1	-0.74	chloroplast
At5g58900		MYB family transcription factor	-0.75	nucleus
At2g47440		Tetratricopeptide repeat (TPR)-like superfamily protein	-0.75	unknown
At5g04060		Dehydration-responsive protein-related	-0.76	Golgi apparatus
At1g66090		Disease resistance protein (TIR-NBS class)	-0.76	chloroplast
At1g68400		Leucine-rich repeat protein kinase family protein	-0.76	extracellular region
At3g49960		Peroxidase superfamily protein	-0.77	extracellular region
At4g00880		SAUR-like auxin-responsive protein family	-0.79	mitochondria
At1g02360		Chitinase family protein	-0.81	extracellular region
At2g45750		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	-0.82	Golgi apparatus
At3g24020		Disease resistance-responsive family protein	-0.83	chloroplast

Biological function: stress (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At5g51060	RHD2	Root hair defective 2	0.84	nucleus
At5g08330	TCP11	TCP domain protein 11	-0.85	nucleus
At4g38660		Pathogenesis-related thaumatin superfamily protein	-0.85	extracellular region
At1g21270	WAK2	Wall-associated kinase 2	-0.85	plasma membrane
At2g01530	MLP329	MLP-like protein 329	-0.86	nucleus
At5g45070	PP2-A8	Phloem protein 2-A8	-0.88	mitochondria
At5g15780		Pollen Ole e 1 allergen and extensin family protein	-0.91	nucleus
At4g29030		Putative membrane lipoprotein	-0.91	unknown
At5g41750		Disease resistance protein (TIR-NBS-LRR class) family	-0.91	nucleus
At4g25100	FSD1	Fe superoxide dismutase 1	-0.92	chloroplast
At1g75640		Leucine-rich receptor-like protein kinase family protein	-0.93	plasma membrane
At1g31580	ECS1	ECS1	-0.95	cell wall
At2g02130	PDF2.3	Plant defensin 2.3	-0.95	cell wall
At4g19530		Disease resistance protein (TIR-NBS-LRR class) family	-0.98	unknown
At1g56540		Disease resistance protein (TIR-NBS-LRR class) family	-0.98	nucleus
At1g71400	RLP12	Receptor like protein 12	-0.98	unknown
At1g28290	AGP31	Arabinogalactan protein 31	-0.99	plasma membrane
At1g29020		Calcium-binding EF-hand family protein	-1.00	vacuole
At1g56520		Disease resistance protein (TIR-NBS-LRR class) family	-1.01	cytoplasm
At2g02820	MYB88	MYB domain protein 88	-1.02	nucleus
At3g52910	GRF4	Growth-regulating factor 4	-1.03	nucleus
At5g45340	CYP707A3	Cytochrome P450, family 707, subfamily A, polypeptide 3	-1.04	cytoplasm
At3g04210		Disease resistance protein (TIR-NBS class)	-1.05	cytoplasm
At5g41740		Disease resistance protein (TIR-NBS-LRR class) family	-1.06	nucleus
At2g40130		Heat shock protein-related	-1.06	nucleus
At1g18970	GLP4	Germin-like protein 4	-1.07	apoplast
At2g19590	ACO1	ACC oxidase 1	-1.07	cytoplasm
At5g67450	AZF1	Zinc-finger protein 1	-1.08	nucleus
At2g15620	NIR1	Nitrite reductase 1	-1.09	chloroplast
At5g51190		AP2 domain-containing transcription factor	-1.10	nucleus
At2g21840		Cysteine/Histidine-rich C1 domain family protein	-1.11	nucleus
At3g05727	SLR1	S locus-related glycoprotein 1	-1.13	endomembrane
At3g50060	MYB77	MYB domain protein 77	-1.13	nucleus
At2g40370	LAC5	Laccase 5	-1.13	apoplast
At5g36910	THI2.2	Thionin 2.2	-1.13	extracellular region
At1g72910		Toll-Interleukin-Resistance (TIR) domain-containing protein	-1.15	cytoplasm
At5g03350		Legume lectin family protein	-1.16	cell wall
At1g18250	ATLP-1	Thaumatococcus-like protein	-1.19	extracellular region
At5g10130		Pollen Ole e 1 allergen and extensin family protein	-1.23	unknown
At2g23540		GDSL-like Lipase/Acylhydrolase superfamily protein	-1.24	extracellular region
At2g43590		Chitinase family protein	-1.24	extracellular region
At2g28160	FIT1	FER-like regulator of iron uptake	-1.25	nucleus
At1g70830	MLP28	MLP-like protein 28	-1.25	nucleus



Biological function: stress (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At3g23800	SBP3	Selenium-binding protein 3	-1.26	nucleus
At5g50760		SAUR-like auxin-responsive protein family	-1.27	chloroplast
At4g14400	ACD6	Accelerated cell death 6	-1.27	other membrane
At5g65970	MLO10	Mildew resistance locus O 10	-1.33	mitochondria
At3g55150	EXO70H1	Exocyst subunit exo70 family protein H1	-1.34	nucleus
At1g72230		Cupredoxin superfamily protein	-1.37	plasma membrane
At1g52060		Mannose-binding lectin superfamily protein	-1.41	extracellular region
At1g74460		GDSL-like Lipase/Acylhydrolase superfamily protein	-1.42	extracellular region
At3g23290	LSH4	Light sensitive hypocotyls 4	-1.46	mitochondria
At5g06740		Concanavalin A-like lectin protein kinase family protein	-1.47	plasma membrane
At4g22212		Defensin-like (DEFL) family protein	-1.49	endomembrane
At2g35380	PER20	Peroxidase 20	-1.51	extracellular region
At1g52050		Mannose-binding lectin superfamily protein	-1.53	extracellular region
At1g33170		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	-1.53	unknown
At4g29080	PAP2	Phytochrome-associated protein 2	-1.54	nucleus
At2g25980		Mannose-binding lectin superfamily protein	-1.56	cytoplasm
At2g21100		Disease resistance-responsive (dirigent-like protein) family protein	-1.57	unknown
At2g32160		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	-1.63	nucleus
At2g19970		Pathogenesis-related protein	-1.69	extracellular region
At2g33790	AGP30	Arabinogalactan protein 30	-1.70	extracellular region
At3g25790		MYB family transcription factor	-1.81	nucleus
At4g20230		Terpenoid cyclases/Protein prenyltransferases superfamily protein	-1.87	cytoplasm
At4g25090		respiratory burst oxidase	-1.98	vacuole
At4g02290	GH9B13	Glycosyl hydrolase 9B13	-1.99	extracellular region
At4g14630	GLP9	Germin-like protein 9	-2.01	plasma membrane
At3g22231	PCC1	PATHOGEN AND CIRCADIAN CONTROLLED 1	-2.09	plasma membrane
At2g01520	MLP328	MLP-like protein 328	-2.09	nucleus
At2g39040		Peroxidase superfamily protein	-2.13	extracellular region
At1g08430	ALMT1	Aluminum-activated malate transporter 1	-2.18	nucleus
At1g18980		RmlC-like cupins superfamily protein	-2.24	apoplast
At5g45080	PP2-A6	Phloem protein 2-A6	-2.68	cytoplasm



Biological function: transport

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At4g21680	NRT1.8	Nitrate transporter 1.8	3.17	plasma membrane
At2g37870		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	3.13	extracellular region
At4g22470		Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	2.99	unknown
At4g36670	PMT6	Polyol/monosaccharide transporter 6	2.37	plasma membrane
At1g62510		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	2.25	unknown
At2g04050		MATE efflux family protein	2.12	plasma membrane
At1g30220	INT2	Inositol transporter	2.11	plasma membrane
At2g41190		Amino acid transporter family protein	2.10	vacuole
At5g46050	PTR3	Peptide transporter 3	1.99	plasma membrane
At5g26340	MSS1	High-affinity hydrogen:glucose symporter	1.81	plasma membrane
At2g04040	DTX1	Detoxification 1	1.74	plasma membrane
At1g15520	PDR12	Pleiotropic drug resistance 12	1.67	plasma membrane
At1g66760		MATE efflux family protein	1.63	plasma membrane
At1g68570		Major facilitator superfamily protein	1.61	plasma membrane
At4g33550		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	1.61	extracellular region
At1g71890	SUC5	Sucrose-proton symporter 5	1.58	plasma membrane
At5g17860	CAX7	Calcium exchanger 7	1.53	cytoplasm
At1g11260	STP1	Sugar transporter 1	1.51	plasma membrane
At4g12490		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	1.50	unknown
At4g21910		MATE efflux family protein	1.49	plasma membrane
At4g21120	AAT1	Amino acid transporter 1	1.49	plasma membrane
At3g20660	OCT4	Organic cation/carnitine transporter 4	1.45	plasma membrane
At5g47560	TDT	Tonoplast dicarboxylate transporter	1.43	vacuole
At1g69480		EXS (ERD1/XPR1/SYG1) family protein	1.40	plasma membrane
At4g13800		Permease-related	1.36	plasma membrane
At1g69870	NRT1.7	Nitrate transporter 1.7	1.30	plasma membrane
At1g58360	AAP1	Amino acid permease 1	1.29	plasma membrane
At3g51860	CAX3	Cation exchanger 3	1.28	vacuole
At1g79360	OCT2	Organic cation/carnitine transporter 2	1.26	plasma membrane
At3g27870		ATPase E1-E2 type family protein	1.26	other membrane
At1g77210	STP14	Sugar transport protein 14	1.15	plasma membrane
At1g65730	YSL7	YELLOW STRIPE LIKE 7	1.13	extracellular region
At3g53980		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	1.12	extracellular region
At1g22570		Major facilitator superfamily protein	1.11	plasma membrane
At1g79520		Cation efflux family protein	1.08	plasma membrane
At5g17850		Sodium/calcium exchanger family protein	1.05	chloroplast
At2g35060	KUP11	K ⁺ uptake permease 11	1.04	plasma membrane
At5g18840		Major facilitator superfamily protein	1.04	cytoplasm
At5g06530	ABCG22	ATP-binding cassette G22	0.99	plasma membrane

Biological function: transport (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At1g75220	ERDL6	ERD6-like 6	0.98	plasma membrane
At5g40780	LHT1	Lysine histidine transporter 1	0.93	plasma membrane
At5g55930	OPT1	Oligopeptide transporter 1	0.92	other membrane
At2g23150	NRAMP3	Natural resistance-associated macrophage protein 3	0.92	vacuole
At5g13740	ZIF1	Zinc induced facilitator 1	0.90	plasma membrane
At5g20380	PHIT4;5	Phosphate transporter 4;5	0.89	chloroplast
At3g22120	CWLP	Cell wall-plasma membrane linker protein homolog	0.88	plasma membrane
At5g67330	NRAMP4	Natural resistance associated macrophage protein 4	0.88	vacuole
At4g18210	PUP10	Purine permease 10	0.87	cytoplasm
At2g47600	MHX1	Magnesium/proton exchanger	0.87	vacuole
At1g61890		MATE efflux family protein	0.87	chloroplast
At5g41800		Transmembrane amino acid transporter family protein	0.85	plasma membrane
At5g58070	TIL	Temperature-induced lipocalin	0.85	plasma membrane
At4g28390	AAC3	ADP/ATP carrier 3	0.85	mitochondria
At2g48020		Major facilitator superfamily protein	0.85	vacuole
At1g31820		Amino acid permease family protein	0.81	other membrane
At1g08230	GAT1	Amino acid transporter family protein	0.80	plasma membrane
At2g40420		Amino acid transporter family protein	0.77	plasma membrane
At3g21670	NTP3	Nitrate transporter	0.77	plasma membrane
At5g57350	AHA3	H ⁽⁺⁾ -ATPase 3	0.76	plasma membrane
At3g55130	WBC19	White-Brown Complex homolog 19	0.74	vacuole
At1g67300		Major facilitator superfamily protein	0.74	other membrane
At5g27520	PNC2	Peroxisomal adenine nucleotide carrier 2	0.74	peroxisome
At5g24380	YSL2	YELLOW STRIPE like 2	0.73	plasma membrane
At3g54140	PTR1	Peptide transporter 1	0.70	plasma membrane
At3g47420	G3Pp1	Glycerol-3-phosphate permease	0.70	other membrane
At5g15410	DND1	DEFENSE NO DEATH 1	0.69	plasma membrane
At5g27350	SFP1	Sugar:hydrogen symporter	0.67	plasma membrane
At5g65990		Amino acid transporter family protein	0.67	plasma membrane
At5g24030	SLAH3	SLAC1 homologue 3	0.62	plasma membrane
At1g12500		Nucleotide-sugar transporter family protein	-0.62	cell wall
At4g22490		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-0.64	extracellular region
At2g22500	UCP5	Uncoupling protein 5	-0.66	mitochondria
At3g28860	ABC19	ATP binding cassette subfamily B19	-0.67	plasma membrane
At2g47160	BOR1	Requires high boron 1	-0.70	plasma membrane
At3g22620		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-0.71	plasma membrane
At2g16850	PIP2,8	Plasma membrane intrinsic protein 2,8	-0.72	cytoplasm
At5g60800		Heavy metal transport/detoxification superfamily protein	-0.72	plasma membrane
At5g09220	AAP2	Amino acid permease 2	-0.77	plasma membrane
At4g30110	HMA2	Heavy metal ATPase 2	-0.80	plasma membrane
At2g21050	LAX2	Like AUXIN RESISTANT 2	-0.83	other membrane
At5g59520	ZIP2	ZRT/IRT-like protein 2	-0.87	plasma membrane



Biological function: transport (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At2g34190		Xanthine/uracil permease family protein	-0.87	other membrane
At3g16180		Major facilitator superfamily protein	-0.88	plasma membrane
At4g22485		Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-0.88	unknown
At4g15160		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-0.88	unknown
At2g37360	ABCG2	ABC transporter family protein	-0.89	other membrane
At2g13820	XYP2	Xylogen protein 2	-0.90	plasma membrane
At3g06130		Heavy metal transport/detoxification superfamily protein	-0.91	cytoplasm
At1g80760	NIP6,1	Nod26-like intrinsic protein 6,1	-0.92	plasma membrane
At1g15210	PDR7	Pleiotropic drug resistance 7	-0.93	plasma membrane
At3g58810	MTPA2	Metal tolerance protein A2	-0.93	vacuole
At4g22505		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-0.93	unknown
At5g46890		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-0.94	extracellular region
At1g64780	AMT1,2	Ammonium transporter 1,2	-0.98	plasma membrane
At1g62500		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-1.01	unknown
At5g05960		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-1.01	extracellular region
At2g48140	EDA4	Embryo sac development arrest 4	-1.03	plasma membrane
At2g24610	CNGC14	Cyclic nucleotide-gated channel	-1.05	plasma membrane
At4g29140	ADS1	Activated disease susceptibility 1	-1.05	plasma membrane
At2g46750	GULLO2	L- γ -glutono-1,4-lactone oxidase 2	-1.09	other membrane
At5g26220		ChaC-like family protein	-1.09	cytoplasm
At2g02020		Peptide transporter 4	-1.10	other membrane
At3g45650	NAXT1	Nitrate excretion transporter1	-1.14	plasma membrane
At3g45710		Major facilitator superfamily protein	-1.17	plasma membrane
At2g32270	ZIP3	Zinc transporter 3 precursor	-1.19	plasma membrane
At3g06370	NHX4	Sodium hydrogen exchanger 4	-1.22	vacuole
At5g13580	ABCG6	ATP-binding cassette G6	-1.24	plasma membrane
At5g19410	ABCG23	ATP-binding cassette G23	-1.24	chloroplast
At3g62270		HCO ₃ ⁻ transporter family	-1.26	other membrane
At1g12110	NRT1.1	Nitrate transporter 1.1	-1.26	plasma membrane
At1g30840	PUP4	Purine permease 4	-1.31	other membrane
At2g48130		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-1.35	plasma membrane
At4g12510		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-1.36	extracellular region
At5g49630	AAP6	Amino acid permease 6	-1.37	plasma membrane
At2g46440	CNGC11	Cyclic nucleotide-gated channels	-1.39	plasma membrane
At1g71870		MATE efflux family protein	-1.42	plasma membrane
At5g46900		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-1.46	extracellular region
At1g52190		Major facilitator superfamily protein	-1.61	plasma membrane

Biological function: transport (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At2g18480		Major facilitator superfamily protein	-1.61	plasma membrane
At2g46740	GULLOS	L -gulono-1,4-lactone oxidase 5	-1.62	cell wall
At4g12500		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-1.74	extracellular region
At4g12545		Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	-1.75	extracellular region
At3g28345	ABCB15	ATP-binding cassette B15	-1.88	plasma membrane
At3g24300	AMT1;3	Ammonium transporter 1;3	-2.04	plasma membrane
At5g19600	SULTR3;5	Sulfate transporter 3;5	-2.15	peroxisome
At5g65980		Auxin efflux carrier family protein	-2.50	endomembrane
At4g12550	AIR1	Auxin-induced in Root cultures 1	-2.75	extracellular region
At4g13420	HAK5	High affinity K ⁺ transporter 5	-3.64	plasma membrane

Biological function: unknown

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At5g35660		Glycine-rich protein family	4.79	unknown
At4g33467		Unknown protein	3.35	nucleus
At1g62420		Unknown protein	3.32	unknown
At4g02360		Unknown protein	3.15	extracellular region
At3g44860	FAMT	Farnesoic acid carboxyl-O-methyltransferase	3.13	chloroplast
At4g01985		Unknown protein	3.06	unknown
At5g50360		Unknown protein	3.05	nucleus
At3g28220		TRAF-like family protein	2.97	cytoplasm
At2g35070		Unknown protein	2.88	chloroplast
At5g39520		Unknown protein	2.79	nucleus
At3g27250		Unknown protein	2.71	nucleus
At5g63350		Unknown protein	2.35	unknown
At3g28270		Unknown protein	2.34	unknown
At5g40800		Unknown protein	2.30	unknown
At5g44575		Unknown protein	2.14	mitochondria
At2g05510		Glycine-rich protein family	2.11	unknown
At2g05540		Glycine-rich protein family	2.06	extracellular region
At4g16240		Unknown protein	2.03	unknown
At4g36700		Cupin family protein	2.02	unknown
At1g47395		Unknown protein	1.95	unknown
At4g01870		TolB protein-related	1.94	nucleus
At5g22460		Alpha/beta-Hydrolases superfamily protein	1.93	vacuole
At1g54575		Unknown protein	1.91	nucleus
At1g76960		Unknown protein	1.87	mitochondria
At5g45310		Unknown protein	1.84	Golgi apparatus
At4g36850		PQ-loop repeat family protein / transmembrane family protein	1.84	other membrane



Biological function: unknown (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At2g39518		Unknown protein	1.82	chloroplast
At1g05340		Unknown protein	1.82	nucleus
At1g07985		Expressed protein	1.81	chloroplast
At2g05380	GRP35	Glycine-rich protein 3 short isoform	1.81	extracellular region
At1g65500		Unknown protein	1.80	mitochondria
At1g47400		Unknown protein	1.76	unknown
At2g05520	GRP3	Glycine rich protein 3	1.74	extracellular region
At3g45730		Unknown protein	1.74	mitochondria
At5g25260		SPFH/Band 7/PHB domain-containing membrane-associated protein family	1.73	plasma membrane
At1g12030		Unknown protein	1.70	unknown
At1g15010		Unknown protein	1.65	mitochondria
At4g26288		Unknown protein	1.60	nucleus
At2g21640		Unknown protein	1.55	mitochondria
At4g18280		Glycine-rich cell wall protein-related	1.48	unknown
At3g58270		Phospholipase-like protein (PEARL1 4) with TRAF-like domain	1.46	nucleus
At1g13990		Unknown protein	1.45	chloroplast
At2g14247		Expressed protein	1.45	chloroplast
At1g24530		Transducin/WD40 repeat-like superfamily protein	1.44	plasma membrane
At2g34070	TBL37	TRICHOME BIREFRINGENCE-LIKE 37	1.44	unknown
At1g65845		Unknown protein	1.43	plasma membrane
At5g10625		Unknown protein	1.43	unknown
At1g10140		Uncharacterised conserved protein UCP031279	1.40	plasma membrane
At3g51660		Tautomerase/MIF superfamily protein	1.39	peroxisome
At1g67920		Unknown protein	1.38	nucleus
At3g14060		Unknown protein	1.36	cell wall
At1g29195		Unknown protein	1.34	chloroplast
At1g19380		Unknown protein	1.33	unknown
At4g15610		Integral membrane family protein	1.33	Golgi apparatus
At1g07040		Unknown protein	1.32	chloroplast
At2g25625		Unknown protein	1.31	unknown
At5g44572		Unknown protein	1.30	extracellular region
At4g14020		Rapid alkalization factor (RALF) family protein	1.29	nucleus
At4g33540		Metallo-beta-lactamase family protein	1.25	unknown
At3g07350		Unknown protein	1.25	mitochondria
At2g15960		Unknown protein	1.22	unknown
At5g22270		Unknown protein	1.22	nucleus
At3g48390		MA3 domain-containing protein	1.21	unknown
At2g25460		Unknown protein	1.19	nucleus
At2g25200		Unknown protein	1.19	chloroplast
At1g65510		Unknown protein	1.18	extracellular region
At2g41250		Haloacid dehalogenase-like hydrolase family protein	1.17	unknown
At5g61820		Unknown protein	1.16	chloroplast
At1g29640		Unknown protein	1.16	nucleus



Biological function: unknown (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At3g15780		Unknown protein	1.15	mitochondria
At1g69610		Unknown protein	1.15	ribosome
At2g28400		Unknown protein	1.13	unknown
At4g16670		Phosphoinositide binding	1.09	nucleus
At2g31945		Unknown protein	1.08	unknown
At1g28260		Telomerase activating protein	1.07	nucleus
At1g49032		Unknown protein	1.07	mitochondria
At4g03410		Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	1.07	mitochondria
At5g51390		Unknown protein	1.07	mitochondria
At2g32150		Haloacid dehalogenase-like hydrolase family protein	1.06	unknown
At5g44005		Unknown protein	1.03	plasma membrane
At1g03990		Alcohol dehydrogenase family protein	1.03	unknown
At4g21620		Subtilase family protein	1.03	extracellular region
At5g03230		Unknown protein	1.01	nucleus
At4g39955		Alpha/beta-Hydrolases superfamily protein	1.00	plasma membrane
At1g25275		Unknown protein	1.00	extracellular region
At4g19390		Unknown protein	1.00	plasma membrane
At2g20670		Unknown protein	0.99	nucleus
At1g73750		Unknown protein	0.99	unknown
At4g21570		Unknown protein	0.99	chloroplast
At2g16990		Major facilitator superfamily protein	0.98	other membrane
At2g38820		Unknown protein	0.96	nucleus
At5g54170		Polyketide cyclase/dehydrase and lipid transport superfamily protein	0.96	unknown
At2g30600		BTB/POZ domain-containing protein	0.96	cytoplasm
At5g64230		Unknown protein	0.96	unknown
At1g23050		Hydroxyproline-rich glycoprotein family protein	0.96	unknown
At3g03150		Unknown protein	0.96	mitochondria
At1g01240		Unknown protein	0.96	unknown
At1g79510		Unknown protein	0.96	chloroplast
At2g30766		Unknown protein	0.95	unknown
At3g20270		Lipid-binding serum glycoprotein family protein	0.94	nucleus
At4g17840		Unknown protein	0.94	chloroplast
At4g30460		Glycine-rich protein family	0.94	unknown
At1g69890		Unknown protein	0.94	nucleus
At1g21670		Unknown protein	0.91	cell wall
At3g22160		VQ motif-containing protein	0.91	nucleus
At3g24420		Alpha/beta-Hydrolases superfamily protein	0.89	cytoplasm
At4g03420		Unknown protein	0.89	nucleus
At1g03610		Unknown protein	0.89	nucleus
At1g49500		Unknown protein	0.89	unknown
At2g24100	ASG1	Altered seed germination 1	0.88	nucleus
At3g20470	GRP5	Glycine-rich protein 5	0.88	cell wall
At1g11210		Unknown protein	0.87	unknown
At4g22920	NYE1	NON-YELLOWING 1	0.87	unknown



Biological function: unknown (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At3g16660		Pollen Ole e 1 allergen and extensin family protein	0.86	extracellular region
At4g32480		Unknown protein	0.86	nucleus
At4g14270		Protein containing PAM2 motif	0.85	nucleus
At4g27990	YLMG1-2	YGGT family protein	0.85	chloroplast
At2g15890	MEE14	Maternal effect embryo arrest 14	0.85	chloroplast
At1g22890		Unknown protein	0.85	endomembrane
At5g05250		Unknown protein	0.85	unknown
At2g46220		Unknown protein	0.84	chloroplast
At3g26510		Octisapeptide/Phox/Bem1p family protein	0.83	nucleus
At1g15230		Unknown protein	0.82	cytoplasm
At1g13390		Unknown protein	0.82	nucleus
At5g24460		Unknown protein	0.80	cell wall
At5g43850	ARD4	Acireductone dioxygenase (iron(II)-requiring)/ metal ion binding	0.80	plasma membrane
At5g06370		NAC domain-containing protein-related	0.79	unknown
At1g80180		Unknown protein	0.79	plasma membrane
At1g48840		Unknown protein	0.78	unknown
At3g07700		Protein kinase superfamily protein	0.78	plasma membrane
At5g45350		Proline-rich family protein	0.77	extracellular region
At3g49790		Carbohydrate-binding protein	0.77	unknown
At1g16320		Unknown protein	0.77	unknown
At5g18130		Unknown protein	0.76	chloroplast
At2g39570		ACT domain-containing protein	0.76	nucleus
At3g13062		Unknown protein	0.76	mitochondria
At1g18270		Ketose-bisphosphate aldolase class-II family protein	0.76	mitochondria
At1g52342		Unknown protein	0.75	nucleus
At2g46100		Nuclear transport factor 2 family protein	0.75	unknown
At5g47860		Unknown protein	0.74	chloroplast
At5g12010		Unknown protein	0.74	unknown
At5g19230		Unknown protein	0.74	plasma membrane
At5g39590		TLD domain containing nucleolar protein	0.73	nucleus
At5g02940		Unknown protein	0.73	chloroplast
At5g11840		Unknown protein	0.73	unknown
At3g03870		Unknown protein	0.73	nucleus
At5g64170		Dentin sialophosphoprotein-related	0.73	nucleus
At1g13360		Unknown protein	0.72	nucleus
At1g78890		Unknown protein	0.72	chloroplast
At5g26260		TRAF-like family protein	0.71	chloroplast
At1g69360		Unknown protein	0.71	unknown
At1g63010		SPX (SYG1/Pho81/XPR1) domain-containing protein	0.68	vacuole
At4g15630		Integral membrane family protein	0.68	plasma membrane
At4g29950		Ypt/Rab-GAP domain of gyp1p superfamily protein	0.68	cytoplasm
At3g10020		Unknown protein	0.68	nucleus
At2g37200		Unknown protein	0.68	other membrane
At3g03990		Alpha/beta-Hydrolases superfamily protein	0.68	cytoplasm

Biological function: unknown (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At4g30750		Unknown protein	0.67	chloroplast
At1g70160		Unknown protein	0.67	extracellular region
At3g15630		Unknown protein	0.67	nucleus
At5g04830		Nuclear transport factor 2 family protein	0.66	nucleus
At5g43745		Phosphotransferase-related	0.65	chloroplast
At2g34310		Unknown protein	0.65	nucleus
At4g36210		Unknown protein	0.64	chloroplast
At1g48440		B-cell receptor-associated 31-like	0.64	ER
At5g25630		Tetrapeptide repeat (TPR)-like superfamily protein	0.64	chloroplast
At4g13530		Unknown protein	0.64	nucleus
At5g60680		Unknown protein	0.64	nucleus
At5g42850		Thioredoxin superfamily protein	0.63	unknown
At4g25170		Unknown protein	0.63	unknown
At4g28025		Unknown protein	0.62	chloroplast
At3g20250	PUM5	Pumilio 5	0.61	cytoplasm
At3g47070		Unknown protein	-0.62	chloroplast
At2g35860	FLA16	FASCICLIN-like arabinogalactan protein 16 precursor	-0.65	endomembrane
At5g53500		WD-40 repeat family protein	-0.65	cytoplasm
At5g19090		Heavy-metal-associated domain-containing protein	-0.65	nucleus
At2g32690	GRP23	Glycine-rich protein 23	-0.65	unknown
At5g17160		Unknown protein	-0.66	plasma membrane
At3g17330	ECT6	Evolutionarily conserved C-terminal region 6	-0.67	nucleus
At5g19240		Unknown protein	-0.68	nucleus
At1g32080		Membrane protein	-0.70	chloroplast
At4g39970		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	-0.71	chloroplast
At5g19250		Unknown protein	-0.71	plasma membrane
At5g44060		Unknown protein	-0.71	mitochondria
At5g12470		Unknown protein	-0.71	unknown
At2g33570		Unknown protein	-0.72	unknown
At4g14200		Pentapeptide repeat (PPR) superfamily protein	-0.72	nucleus
At3g19680		Unknown protein	-0.73	plasma membrane
At1g27210		ARM repeat superfamily protein	-0.74	chloroplast
At5g11420		Unknown protein	-0.75	unknown
At3g19370		Unknown protein	-0.75	plasma membrane
At5g16250		Unknown protein	-0.75	extracellular region
At5g16720		Unknown protein	-0.75	nucleus
At5g57070		Hydroxyproline-rich glycoprotein family protein	-0.75	nucleus
At4g15093		Catalytic LigB subunit of aromatic ring-opening dioxygenase family	-0.77	cytoplasm
At3g51720		Unknown protein	-0.77	extracellular region
At1g12380		Unknown protein	-0.77	nucleus
At5g16030		Unknown protein	-0.77	chloroplast
At3g01670	SEOa	Sieve element occlusion A	-0.78	chloroplast
At2g33850		Unknown protein	-0.78	extracellular region
At1g04520	PDLP2	Plasmodesmata-located protein 2	-0.79	extracellular region



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Biological function: unknown (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At2g30010	TBL45	TRICHOME BIREFRINGENCE-LIKE 45	-0.79	unknown
At2g05440	GRP9	Glycine rich protein 9	-0.79	unknown
At3g18050		Unknown protein	-0.79	plasma membrane
At5g58000		Reticulon family protein	-0.80	ER
At5g41140		Unknown protein	-0.80	unknown
At5g05180		Unknown protein	-0.82	cytoplasm
At4g23490		Fringe-related protein	-0.83	Golgi apparatus
At5g42860		Unknown protein	-0.84	nucleus
At1g74770		Zinc ion binding	-0.84	nucleus
At5g59050		Unknown protein	-0.85	nucleus
At3g15550		Unknown protein	-0.85	cytoplasm
At1g80690		PPPDE putative thiol peptidase family protein	-0.86	cytoplasm
At2g35960	NHL12	NDR1/HIN1-like 12	-0.87	plasma membrane
At2g22510		Hydroxyproline-rich glycoprotein family protein	-0.88	mitochondria
At1g16630		Unknown protein	-0.88	chloroplast
At4g29310		Unknown protein	-0.90	nucleus
At3g61870		Unknown protein	-0.92	chloroplast
At3g61270		Unknown protein	-0.92	extracellular region
At3g52360		Unknown protein	-0.93	unknown
At5g17350		Unknown protein	-0.97	cell wall
At5g40510		Sucrase/ferredoxin-like family protein	-0.97	unknown
At3g11550	CASP2	Casparian strip membrane domain protein 2	-0.97	plasma membrane
At2g21850		Cysteine/Histidine-rich C1 domain family protein	-0.98	nucleus
At3g56810		Unknown protein	-0.98	mitochondria
At4g37240		Unknown protein	-0.99	unknown
At4g19430		Unknown protein	-1.01	mitochondria
At4g14465	AHL20	AT-hook motif nuclear-localized protein 20	-1.01	unknown
At2g39650		Unknown protein	-1.02	nucleus
At2g28780		Unknown protein	-1.03	plasma membrane
At4g28940		Phosphorylase superfamily protein	-1.04	plasma membrane
At2g16270		Unknown protein	-1.04	nucleus
At4g38080		Hydroxyproline-rich glycoprotein family protein	-1.04	unknown
At1g64360		Unknown protein	-1.05	nucleus
At1g49750		Leucine-rich repeat (LRR) family protein	-1.05	plasma membrane
At2g39530		Unknown protein	-1.05	other membrane
At5g62550		Unknown protein	-1.06	plasma membrane
Atmg00030	ORF107A	Hypothetical protein	-1.06	mitochondria
At2g34510		Unknown protein	-1.07	other membrane
At3g50800		Unknown protein	-1.08	unknown
At3g23175		Lesion inducing protein-related	-1.09	chloroplast
At5g48290		Heavy metal transport/detoxification superfamily protein	-1.10	nucleus
At1g22030		Unknown protein	-1.11	unknown
At3g54260	TBL36	TRICHOME BIREFRINGENCE-LIKE 36	-1.11	unknown
At1g61260		Unknown protein	-1.11	chloroplast

Biological function: unknown (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At1g62870		Unknown protein	-1.13	chloroplast
At3g06070		Unknown protein	-1.13	unknown
At4g33610		Glycine-rich protein family	-1.14	cytoplasm
At5g19260	FAF3	FANTASTIC FOUR 3	-1.15	chloroplast
At3g62040		Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	-1.16	nucleus
At1g78120	TPR12	Tetratricopeptide repeat 12	-1.17	mitochondria
At1g67865		Unknown protein	-1.17	unknown
At3g25130		Unknown protein	-1.18	chloroplast
At5g09520		Hydroxyproline-rich glycoprotein family protein	-1.18	unknown
At4g14650		Unknown protein	-1.18	nucleus
At1g05540		Unknown protein	-1.20	mitochondria
At4g00700		C2 domain-containing protein	-1.20	unknown
At1g68330		Unknown protein	-1.20	nucleus
At5g44550		Integral membrane family protein	-1.21	extracellular region
At2g25510		Unknown protein	-1.23	mitochondria
At3g47980		Integral membrane HPP family protein	-1.24	chloroplast
At5g49350		Glycine-rich protein family	-1.24	chloroplast
At2g41990		Unknown protein	-1.24	unknown
At4g15390		HXXXD-type acyl-transferase family protein	-1.29	cytoplasm
At2g40480		Unknown protein	-1.31	unknown
At4g24140		Alpha/beta-Hydrolases superfamily protein	-1.31	cytoplasm
At3g06390		Unknown protein	1.33	nucleus
At5g25460	DGR2	DUF642 L-GALL responsive gene 2	-1.34	cell wall
At5g19970		Unknown protein	-1.35	ER
At1g55990		Glycine-rich protein family	-1.39	unknown
At5g22580		Stress responsive A/B Barrel Domain	-1.40	chloroplast
At3g45160		Unknown protein	1.45	unknown
At2g42610	LSH10	Light sensitive hypocotyls 10	-1.45	nucleus
At3g63430	TRM5	TON1 recruiting motif 5	-1.46	nucleus
At1g80280		Alpha/beta-Hydrolases superfamily protein	-1.46	cytoplasm
At4g02850		Phenazine biosynthesis PhzC/PhzF family protein	-1.47	unknown
At3g59370		Unknown protein	-1.50	unknown
At4g30670		Unknown protein	-1.54	mitochondria
At1g80240	DGR1	DUF642 L-GALL responsive gene 1	-1.54	cell wall
At3g23170		Unknown protein	-1.61	chloroplast
At4g20390		Integral membrane family protein	-1.62	unknown
At2g48080		oxidoreductase, 2OG-Fe(II) oxygenase family protein	-1.62	nucleus
At5g09480		Hydroxyproline-rich glycoprotein family protein	-1.69	unknown
At1g69230	SP1L2	SPIRAL1-LIKE2	-1.72	plasma membrane
At5g42530		Unknown protein	-1.76	mitochondria
At3g20380		TRAF-like family protein	-1.91	extracellular region
At1g12080		Vacuolar calcium-binding protein-related	-1.93	unknown
At2g14560	LURP1	Late upregulated in response to Hyaloperonospora parasitica	2.01	unknown
At2g36885		Unknown protein	-2.09	chloroplast

Biological function: unknown (cont.)

Gene ID	Alias	Gene name	Log ₂ FC	Cell component
At5g52790		CBS domain-containing protein-related	-2.10	plasma membrane
At3g13760		Cysteine/Histidine-rich C1 domain family protein	-2.16	nucleus
At5g10210		Unknown protein	-2.34	unknown
At2g18328	RL4	RAD-like 4	-2.82	nucleus
At5g26300		TRAF-like family protein	-3.27	extracellular region



APPENDIX D
CHITOSAN MUTANT ANALYSIS

1. Library statistics

Library	# of Reads ^a	Aligned read ^b	Unique read ^c	Percent (%)
Col x 106A	52,691,418	52,122,175	29,496,197	56.59
Col x 161A	42,724,719	41,800,322	24,159,166	57.80

^a The number of reads after quality filter

^b The number of reads mapped aligned to TAIR10

^c The uniquely mapped that were removed clonal reads

^d Percentage of unique reads to aligned read

2. Adapter and barcode sequences

Library	Primer	Index	Sequence
Col x 106A	Bioo2	TGACCA	tgaccaAGATCGGAAGAGCGGTT CAGCAGGAATGCCGAG
Col x 161A	Bioo35	CATTTT	cattttAGATCGGAAGAGCGGTT CAGCAGGAATGCCGAG

3. Sequencing adaptor sequences (iiiiii indicates the position of the index)

primer A:

5' AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATCT 3'

primer B:

5' P-GATCGGAAGAGCACACGTCTGAACTCCAGTCACiiiiiiATCTCGTATGCCGTCTTCTGCTTG 3'



4. List of predicted point mutation in candidate mutants

4.1 Predicted gene mutation in recessive pool of F₂ progeny of Col x 106A

Locus	Position	Chr	Type	Amino acid change	Effect	SIFT	Candidate status
At1g16800	5748420	Chr1	CT	A1338T	MISSENSE	0.57	
At1g59820	22018067	Chr1	GA	V761I	MISSENSE	0.53	
At1g74800	28102370	Chr1	GA	P624S	MISSENSE	0.49	
At1g67560	25321985	Chr1	GA	A344T	MISSENSE	0.46	
At1g61350	22635404	Chr1	GA	E436K	MISSENSE	0.29	
At1g25580	8998415	Chr1	CT	R150H	MISSENSE	0.15	
At1g04160	1091101	Chr1	CT	L620F	MISSENSE	0.01	good
At1g03905	995380	Chr1	CT	A220V	MISSENSE	0.84	low
At1g04920	1393569	Chr1	CT	V566I	MISSENSE	0.29	low
At1g03360	825776	Chr1	CT	P189L	MISSENSE	0.02	low
At1g01250	105096	Chr1	CT	G72R	MISSENSE	0.01	medium
At2g47700	19552682	Chr2	GA	P301S	MISSENSE	0.88	
At2g06040	2355029	Chr2	CT	V131I	MISSENSE	0.72	
At2g25490	10849421	Chr2	CT	A162T	MISSENSE	0.71	
At2g43700	18117238	Chr2	GA	R239K	MISSENSE	0.42	
At2g33260	14102033	Chr2	CT	E74K	MISSENSE	0.40	
At2g25940	11064685	Chr2	CT	A228T	MISSENSE	0.32	
At2g18450	7999566	Chr2	CT	V221I	MISSENSE	0.10	
At2g02180	561419	Chr2	CT	R97C	MISSENSE	0.00	good
At2g47800	19577281	Chr2	GA	E752K	MISSENSE	0.03	low
At2g04740	1657299	Chr2	CT	L55F	MISSENSE	0.02	low
At2g47220	19384892	Chr2	GA		SPLSIT_acc	0.00	low
At2g16250	7040622	Chr2	CT	G674E	MISSENSE	0.00	low
At3g46290	17013978	Chr3	GA	D324N	MISSENSE	0.91	
At3g58960	21788068	Chr3	GA	P247L	MISSENSE	0.69	
At3g51460	19093095	Chr3	GA	G30D	MISSENSE	0.52	
At3g56740	21017358	Chr3	GA	A181T	MISSENSE	0.31	
At3g48430	17936747	Chr3	GA	A314T	MISSENSE	0.26	
At3g06010	1803823	Chr3	CT	G671E	MISSENSE	0.08	
At3g56980	21086917	Chr3	GA	Q158*	NONSENSE	0.00	low
At4g00752	319435	Chr4	GA	P270S	MISSENSE	0.73	
At4g33060	15951088	Chr4	GA	G361S	MISSENSE	0.64	
At4g05620	2985293	Chr4	GA	L53F	MISSENSE	0.39	

Chr: chromosome number

Type: nucleotide base change

Effect: type of mutation

SIFT: SIFT score

Candidate status: determination of candidate mutation



1.1 (cont.) Predicted gene mutation in recessive pool of F₂ progeny of Col x 106A

Locus	Position	Chr	Type	Amino acid change	Effect	SIFT	Candidate status
At4g13960	8061732	Chr4	GA	S153L	MISSENSE	0.37	
At4g38640	18062066	Chr4	GA	T9I	MISSENSE	0.20	
At4g08470	5385026	Chr4	GA	L411F	MISSENSE	0.01	medium
At5g49152	19928072	Chr5	CT	S912L	MISSENSE	10	
At5g57590	23321479	Chr5	CT	E342K	MISSENSE	1.00	
At5g25790	8978420	Chr5	CT	S179N	MISSENSE	1.00	
At5g01990	378416	Chr5	GA	A213V	MISSENSE	0.32	
At5g64410	25751114	Chr5	CT	W666*	NONSENSE	0.00	good
At5g56740	22953584	Chr5	CT	V277I	MISSENSE	0.55	low
At5g54730	22234613	Chr5	GA	S609F	MISSENSE	0.08	low
At5g03650	934779	Chr5	GA	A333T	MISSENSE	0.00	medium

Chr: chromosome number

Type: nucleotide base change

Effect: type of mutation

SIFT: SIFT score

Candidate status: determination of candidate mutation



4.2 Predicted gene mutation in recessive pool of F₂ progeny of Col x 161A

Locus	Position	Chr	Type	Amino acid change	Effect	SIFT	Candidate status
At1g72440	27270014	Chr1	GA	L593F	MISSENSE	0.66	
At1g64310	23866743	Chr1	GA	A231T	MISSENSE	0.57	
At1g05260	1530873	Chr1	GA	V195I	MISSENSE	0.48	
At1g26390	9130354	Chr1	GA	A468V	MISSENSE	0.29	
At1g69295	26051224	Chr1	GA	T104I	MISSENSE	0.18	
At1g54240	20254346	Chr1	GA	S206N	MISSENSE	0.13	
At1g54780	20439842	Chr1	GA	A104T	MISSENSE	0.04	good
At1g23800	8412435	Chr1	CT	D470N	MISSENSE	0.68	low
At1g19600	6779434	Chr1	GA	S65N	MISSENSE	0.46	low
At1g28640	10068153	Chr1	GA	T219M	MISSENSE	0.06	low
At1g16780	5743502	Chr1	GA	P72L	MISSENSE	0.05	medium
At1g69710	26222774	Chr1	GA		SPLSIT_acc	0.00	medium
At1g72920	27438411	Chr1	GA		SPLSIT_don	0.00	medium
At1g18040	6208018	Chr1	GA	P208S	MISSENSE	0.00	medium
At2g39330	16420338	Chr2	GA	P308L	MISSENSE	0.30	
At2g25430	10823803	Chr2	GA	S363N	MISSENSE	0.09	
At2g02050	490375	Chr2	GA		SPLSIT_don	0.00	low
At2g32680	13859991	Chr2	GA	P875L	MISSENSE	0.68	
At3g60270	22278120	Chr3	GA	A158V	MISSENSE	0.22	
At4g20960	5492473	Chr4	GA	Q528*	NONSENSE	0.00	low

Chr: chromosome number

Type: nucleotide base change

Effect: type of mutation

SIFT: SIFT score

Candidate status: determination of candidate mutation



5. Primers for ABRC mutant confirmation

Gene name	Primer name	Primer sequence (5'→3')
<i>Myosin XI B (XIB)</i>	LP1	CAGAAGCAACCCACTTCAGTC
	RP1	GCTACCGAAGGAAGGACTGTC
<i>Cyclin-dependent kinase D1;3 (CDKD1;3)</i>	LP2	ATGTTTTTCGGTAGCCATGTG
	RP2	AACATGAGGCCATTACAGTGC
<i>Toll-Interleukin-Resistance (TIR) domain family protein</i>	LP3	TCGCTAACTTTCCAAAGTTGG
	RP3	AAGATAGGCATCACGGTGATG
<i>Type II H⁺-PPases (VHP2;2)</i>	LP4	GAAGTTGGACGCTGAATCTTG
	RP4	GGGAATTTCTTCGATTTCTGC
<i>MAPK/ERK kinase kinase 3 (MEKK3)</i>	LP5	ATGTCAGTGGGATAAGCGATG
	RP5	CTTCTATGGAGTTCCCGGATC
<i>Tobamovirus multiplication protein 3 (TOM3)</i>	LP6	AGCCCAGAAAAGAACCAGAAG
	RP6	AGGACTCTTGATGTTGGGCC
<i>DREB subfamily A-4 of ERF/AP2 transcription factor family</i>	LP7	ATCAGGGGAAAAGTAAAAGC
	RP7	CAGAGATATCCAAGTCGCAGC
<i>Oligopeptide transporter 4 (OPT4)</i>	LP8	ACCTGAACCGTGATTTGAGTG
	RP8	AGAATCCTGAAGCGGTAAAGC
<i>Thylakoid lumen protein 18.3 (TLP18.3)</i>	LP9	TCCAAAACCTGGTCTGCATAC
	RP9	ACCACATGTCACGCTCTAGTG
Left Border	LBb1.3	ATTTTGCCGATITCGGAAC



6. Primers for RT-PCR

Gene name	Primer name	Primer sequence (5'→3')
<i>Elongation factor 1-alpha (EF1α)</i>	AtEF1 α -F	TTCTCCGAGTACCCACCTTT
	AtEF1 α -R	ATTTGGCACCCCTTCTTCACT
<i>Myosin XI B (XIB)</i>	AtMYOxI-F	GAAATGCTGGGAAATCTGCT
	AtMYOxI-R	CTCTGATTCAAAGCACTTCC
<i>Cyclin-dependent kinase D1;3 (CDKD1;3)</i>	AtCDKD1.3-F	CACAGGTACTTCACTTCTGC
	AtCDKD1.3-R	GCTCAGGCATCACTCTTCTA
<i>Toll-Interleukin-Resistance (TIR) domain family protein</i>	AtTIR-F	GGACCTAGTTGGGATTGATA
	AtTIR-R	ACCAACCTTCAACCAATGAC
<i>Type II H⁺-PPases (VHP2;2)</i>	AtPPase-F	CACTGGTCATGGAACCAATA
	AtPPase-R	CACCTGCATTATCAGCTATG
<i>MAPK/ERK kinase kinase 3 (MEKK3)</i>	AtMEKK3-F	TGCTGGGTTGAATTATCTCC
	AtMEKK3-R	CGGAGCCATCCAAAATAATG
<i>Tobamovirus multiplication protein 3 (TOM3)</i>	AtTOM3-F	ATTGTTGCTGCCCTTGGAT
	AtTOM3-R	CGAAAGCAGCAAAGCACATC
<i>DREB subfamily A-4 of ERF/AP2 transcription factor family</i>	AtDREBA4-F	GATGATGACGTGGCAGGAAT
	AtDREBA4-R	GATACTGATACAAGTCTCCG
<i>Oligopeptide transporter 4 (OPT4)</i>	AtOPT4-F	CGCAACAACCTAACCAACAC
	AtOPT4-R	ATCTAGGTGGGATCTTCATG



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VITA

Miss Nontalee Chamnanmanoontham was born on May 2, 1986 in Bangkok. After she finished the high school in 2004 from Saint Joseph Convent School, she enrolled in the Department of Botany in the genetics program at Chulalongkorn University and graduated with the degree of Bachelor of Science in 2008. After that, she continued on the Master of Science in Biotechnology program at Chulalongkorn University from 2008 to 2010. Then, she has been supported by the scholarship from The Royal Golden Jubilee Ph.D program to study for the degree of Doctor of Philosophy in Biological Sciences program at Chulalongkorn University since 2010. During the Ph.D. study, NC had the great opportunity to visit Comai Lab to achieve her research including genomic study, RNA sequencing, and EMS mutagenesis analysis.

