Supplemental Table 1. Complete list of tunicamycin-responsive genes

Cluster I						
AGI code	Description	Tunicamycin treatment				Cis-elements
		0h	2h	5h	10h	
At1g49930	similar to aminoacyl-tRNA synthetase family protein	1.00	0.94	2.81	1.96	
At5g22800	EMB1030 (EMBRYO DEFECTIVE 1030); ATP binding / alanine-tRNA ligase/ ligase	1.00	0.94	2.49	1.67	
At5g06690	THIOREDOXIN-LIKE 5	1.00	1.50	2.41	4.24	AAAATATCT
At2g32130	similar to UNE1 (unfertilized embryo sac 1)	1.00	1.31	1.76	2.54	
At4g08040	ACS11, encodes an aminotransferase that belongs to ACC synthase gene family structurally	0.93	1.31	2.16	3.51	
At2g40080	EARLY FLOWERING 4, ELF4	1.00	1.46	2.15	3.26	
At3g26740	CCL, CCR-LIKE	0.99	2.01	3.37	6.40	AAAATATCT
At2g40670	ARR16	0.98	1.42	3.18	5.57	
At2g44840	ATERF13	0.99	1.20	1.79	2.97	
At3g55970	oxidoreductase, 2OG-Fe(II) oxygenase family protein	0.81	1.06	2.16	4.91	
At5g01380	similar to DNA-binding protein-related	1.00	1.13	2.01	2.96	
At5g53450	ORG1 (OBP3-RESPONSIVE GENE 1); kinase	1.00	1.07	1.75	2.65	UPRE
At3g17690	ATCNGC19, member of Cyclic nucleotide gated channel family	1.00	0.99	1.63	2.56	
At5g53240	similar to unknown protein	0.99	0.97	1.48	2.86	
At3g20810	transcription factor jumonji (jmjC) domain-containing protein	0.99	0.95	1.69	4.20	AAAATATCT
At2g15490	UDP-glycosyltransferase/ transferase, transferring glycosyl groups	0.91	0.77	1.46	2.96	
At5g26170	ATWRKY50	1.00	0.67	2.03	6.27	
At1g36180	acetyl-CoA carboxylase 2 (ACC2)	1.00	0.85	2.07	4.87	
At2g40880 [a]	cysteine proteinase inhibitor homolog	1.00	0.89	3.90	4.08	
At4g05380	AAA-type ATPase family protein	0.95	0.85	4.23	3.46	
At5g40010	AAA-type ATPase family protein	1.00	0.91	7.63	12.95	AAAATATCT
At4g36710	scarecrow transcription factor family protein	1.00	0.87	2.50	3.11	
At1g13340	similar to unknown protein	0.99	0.75	3.71	5.32	
At5g05250	similar to unknown protein	0.94	0.86	1.90	2.42	
At3g28210	PMZ	1.00	0.85	4.30	5.21	
At1g14010 [a]	emp24/gp25L/p24 family protein	1.00	0.91	2.33	2.74	AAAATATCT
At5g43860	ATCLH2; Encodes a chlorophyllase,	0.99	0.63	3.99	5.24	
At1g78290	serine/threonine protein kinase, putative; similar to OST1/P44/SNRK2-6/SRK2E	1.00	0.67	3.96	4.91	
At1g23550	SRO2 (Similar to RCD-One 2)	0.99	0.75	2.65	3.38	AAAATATCT
At1g17960	threonyl-tRNA synthetase, putative	0.96	0.47	4.07	5.11	
At3g03640 [a]	beta-glucosidase (GLUC)	1.00	0.57	4.68	10.21	
At5g03720	AT-HSFA3	1.00	1.34	3.49	3.94	UPRE
At1g80110	ATPP2-B11, Identical to F-box protein PP2-B11	0.98	1.23	3.26	3.74	
At5g58710 [c]	ROC7	1.00	1.41	3.42	4.27	ERSE, UPRE
At1g78340	ATGSTU22, glutathione transferase	0.96	1.57	6.35	9.14	
At1g42480	similar to Saposin B	1.00	1.39	3.45	4.30	
At1g56340 [c]	CRT1	0.99	1.46	4.07	4.93	ERSE, UPREx2
At5g10695	unknown protein	1.00	1.29	3.02	3.78	UPRE
At4g24690	ubiquitin-associated (UBA)/TS-N domain-containing protein	1.00	1.19	2.47	2.56	AAAATATCTx2
At3g23280	zinc finger (C3HC4-type RING finger) family protein	1.00	1.35	3.24	3.27	
At2g05630 [a]	ATG8D	1.00	1.29	2.79	2.83	
At3g54960 [a]	PDI1	1.00	1.29	3.91	3.74	
At3g46090	ZAT7; nucleic acid binding	0.99	1.06	2.51	3.37	
At5g42900	unknown protein	0.99	1.04	4.56	7.96	UPRE, AAAATATCTx2
At5g16360	NC domain-containing protein	1.00	1.16	2.73	3.74	
At3g57090	BIGYIN; binding; similar to binding	1.00	1.09	2.09	2.56	AAAATATCT
At3g46080	zinc finger (C2H2 type) family protein; similar to ZAT7	1.00	1.17	3.51	5.59	

At2g21430	cysteine proteinase A494	1.00	1.14	2.20	2.54	ERSE
At2g19460	unknown protein	1.00	1.15	3.94	5.09	
At3g05880	RCI2A, Induced by low temperatures, dehydration and salt stress and ABA	1.00	1.21	2.54	3.29	AAAATATCT
Cluster II						
AGI code	Description	Tunicamycin treatment				Cis-elements
		0h	2h	5h	10h	
At5g54860	integral membrane transporter family protein	1.00	2.55	2.64	2.54	
At5g35080 [a]	unknown protein	1.00	5.30	5.60	5.27	ERSE
At4g24920	Sec61 gamma	1.00	3.80	4.18	3.68	
At1g67960	unknown protein	1.00	3.38	3.63	3.22	ERSE
At1g72280	ERO1	0.99	9.66	13.36	11.88	
At1g09080 [a b c]	BiP3	0.99	77.84	118.37	104.81	ERSEx2
At3g05230	Signal peptidase subunit	1.00	4.34	5.12	4.93	
At3g04070	ANAN047	1.00	2.46	2.85	2.54	
At1g24460	myosin-related	1.00	2.41	2.76	2.42	
At3g53670	unknown protein	1.00	3.37	3.44	3.57	
At1g42990	AtbZIP60	1.00	7.73	8.30	8.83	
At4g17420	unknown protein	1.00	2.88	2.83	2.92	ERSE
At4g34630 [a b]	unknown protein	1.00	7.76	7.43	8.65	
At2g02810 [a b c]	AtUTR1	0.99	7.76	10.30	12.24	
At3g03790	RCC1 family protein	1.00	2.12	2.37	2.53	
At1g27330 [c]	unknown protein	1.00	4.28	5.02	5.47	ERSE
At1g14360	AtUTR3	1.00	5.73	6.93	8.04	ERSE
At1g27350 [a b c]	unknown protein	0.99	3.85	5.02	4.99	ERSE
At4g29520	unknown protein	1.00	5.05	6.80	6.80	
At1g29310 [c]	Sec61 alpha	0.99	5.18	7.20	6.77	ERSE
At5g42050	unknown protein	1.00	4.60	6.14	5.75	UPRE
At5g07340 [a b c]	CNX2	1.00	3.34	4.52	4.38	
At4g29960	expressed protein	1.00	2.69	3.50	3.38	ERSE
At4g21180	ERdj2B	1.00	2.88	3.89	3.44	
At3g63060	EDL3 (EID1-LIKE 3), F-box protein	1.00	2.86	2.59	2.38	AAAATATCT
At5g22290	ANAC089	1.00	8.28	6.69	5.94	UPRE, AAAATATCT
At2g25460	unknown protein	1.00	10.12	8.61	6.63	ERSE
At5g13100	unknown protein, contains domain NADH oxidase/flavin reductase (SSF55469)	1.00	2.78	2.50	2.20	
At3g49530	ANAC062	1.00	4.94	3.75	3.50	
At3g17000	UBC32 (ubiquitin-conjugating enzyme)	1.00	4.03	3.96	3.55	UPREx2
At5g64510 [c]	unknown protein	1.00	31.38	26.77	23.64	UPREx3
At3g55700	UDP-glucosyltransferase family protein	1.00	8.02	7.59	6.82	
At4g29330	Der1-like	1.00	2.57	2.51	2.41	ERSE
At3g24090	glutamine:fructose-6-phosphate transaminase, putative	1.00	7.79	7.07	6.22	ERSE, UPRE
At3g51980 [c]	similar to SIL1	1.00	9.64	8.33	7.65	ERSE
At3g08970	ERdj3A	1.00	28.83	23.93	23.14	
At5g47420	unknown protein	1.00	4.78	4.26	4.27	ERSE
At5g24470	APRR5	1.00	2.38	3.46	2.29	AAAATATCT
At1g62020 [a]	coatomer protein complex, subunit alpha, putative, ER-to Golgi transport	1.00	2.84	3.15	2.44	
At3g51000	epoxide hydrolase, putative	1.00	2.18	2.62	2.10	
At5g64060	ANAC103	1.00	4.61	6.61	4.14	
At3g15980	coatomer protein complex, subunit beta 2	1.00	5.05	6.69	4.65	
At5g45080	ATPP2-A6 (Phloem protein 2-A6); transmembrane receptor	0.99	2.52	2.35	4.04	
At1g29290	expressed protein	1.00	2.36	2.25	2.84	
At2g41870	remorin family protein	1.00	4.48	2.72	2.74	
At4g05010	F-box family protein	0.99	9.33	5.09	5.31	ERSE

At3g53800	armadillo/beta-catenin repeat family protein	1.00	1.71	2.62	2.06	AAAATATCT
At1g10630	ARF GTPase	1.00	2.28	3.88	2.99	
At3g44340	Sec23	1.00	2.15	3.85	3.03	
At4g32670	zinc-ion binding	1.00	2.49	4.96	3.53	
At5g14670	ARF GTPase	1.00	3.68	6.30	4.38	
At4g21820	calmodulin-binding family protein	1.00	3.69	6.68	4.62	
At3g18750	WNK6, protein kinase	1.00	2.31	3.44	2.66	
At1g70490	ARF GTPase	1.00	4.33	8.91	6.28	ERSE
At1g52540	putative protein kinase	1.00	1.97	2.60	2.25	
At5g23575	CLPTM1-like	1.00	4.79	9.45	6.99	
At1g21900	emp24/gp25L/p24 family protein	1.00	2.33	3.51	3.79	
At2g25110 [a c]	MIR domain-containing protein	1.00	3.32	5.98	6.55	
At1g67970	HsfA8	1.00	2.44	3.70	4.06	AAAATATCTx2
At3g46640	myb family transcription factor	1.00	1.94	2.75	2.90	ERSE, AAAATATCT
At5g50460 [c]	Sec61 gamma	1.00	2.72	4.54	5.04	
At5g02220	unknown protein	0.99	3.31	5.83	6.09	UPRE
At5g47120 [c]	BI-1	1.00	2.84	4.58	4.87	ERSE
At1g04980 [c]	PDI10	0.99	4.28	8.88	9.43	ERSE
At5g03080	phosphatidic acid phosphatase-related	1.00	1.89	2.60	2.51	
At1g56300	DnaJ, putative	1.00	3.45	6.18	5.72	
At2g34250 [a c]	Sec61 alpha	1.00	2.14	3.08	3.04	
At1g61780	postsynaptic protein-related	1.00	1.97	2.62	2.56	ERSE
At5g42020 [a b]	BiP2	0.99	5.17	9.38	11.02	ERSE-II, UPRE
At5g28540 [a b c]	BiP1	0.99	4.96	8.80	9.47	ERSE-II, UPRE
At5g61790 [a b c]	CNX1	1.00	4.18	7.03	6.90	ERSE, UPRE
At2g45070 [a]	Sec61 beta	1.00	2.71	3.97	3.90	AAAATATCT
At3g60540	Sec61 beta	1.00	3.67	5.75	5.79	ERSEx2
At1g18260 [c]	SEL-1 protein-related	1.00	2.97	4.05	4.13	ERSE
At2g34430	Photosystem II type I chlorophyll a/b-binding protein	0.99	3.32	6.39	5.10	
At4g01810 [a]	Sec23, putative	1.00	1.97	2.84	2.59	UPRE
At2g32920 [a c]	PDI9	1.00	3.66	8.64	7.51	
At5g15190	unknown protein	1.00	3.97	5.34	6.31	AAAATATCT
At4g30500	Protein of unknown function (DUF788)	1.00	2.90	3.72	4.21	
At5g64260	phosphate-responsive protein, putative, phi-1 like	1.00	2.19	2.47	2.94	UPRE, AAAATATCT
At3g29575	unknown protein	0.99	1.88	2.24	2.69	
At2g17840	dehydration-associated protein-related (ERD7)	1.00	1.66	2.14	2.52	
At4g14420	esion inducing protein-related similar to ORF, able to induce HR-like lesions	1.00	2.07	5.44	6.80	
At1g76690	12-oxophytodienoate reductase (OPR2)	1.00	1.45	2.25	2.53	
At4g33980	unknown protein	1.00	1.87	3.90	4.96	UPRE, AAAATATCT
At5g66880	a member of SNF1-related protein kinases (SnRK2	1.00	1.44	2.29	2.91	
At5g60100	APRR3	1.00	1.91	3.69	4.96	UPREx2
At1g07050	unknown protein	1.00	3.63	14.06	28.14	
At5g26340	Encodes a protein with high affinity, hexose-specific/H+ symporter activity.	0.99	1.40	2.71	2.75	ERSE, AAAATATCT
At5g17760	AAA-type ATPase family protein (BCS1-like)	1.00	1.75	4.49	4.64	
At2g47470 [a c]	PDI11	1.00	1.84	4.32	4.90	UPRE
At1g21750 [a b]	PDI5	1.00	2.12	6.03	6.46	ERSEx2, UPRE
At3g51400	Protein of unknown function DUF241	0.98	2.35	5.21	5.77	AAAATATCT
At2g27690	CYP94C	0.99	1.91	3.97	4.35	
At3g07680 [c]	emp24/gp25L/p24 family protein	1.00	1.78	3.37	3.57	ERSE, UPRE
At1g53280	DJ-1 family protein	1.00	1.61	2.69	2.82	ERSE
At1g56330	Sar1	1.00	1.57	2.58	2.62	UPRE
At1g52600	Signal peptidase	1.00	1.92	3.24	3.72	UPREx3
At4g16660 [a b]	HSP70-like, containing HDEL	0.99	2.94	6.04	6.14	ERSE, UPRE

At1g77510 [c]	PDI6	0.99	4.16	11.90	10.97	ERSE
At3g62600	ERdj3B	1.00	3.13	7.52	8.09	ERSE
At1g09210 [a,b,c]	CRT2	1.00	2.98	7.11	7.44	ERSE
At4g24190 [a,b,c]	GRP94	0.99	3.72	11.28	11.59	ERSE, UPRE
At2g03120 [a]	signal peptide peptidase	1.00	2.00	3.75	3.64	
At3g29320	plastidic alpha-glucan phosphorylase	1.00	1.68	2.74	2.57	ERSE
At1g30120	putative plastid pyruvate dehydrogenase E1 beta subunit	1.00	1.54	2.56	2.15	ERSE
At1g56580 [c]	unknown protein	1.00	2.79	8.80	6.99	
At2g40340	AP2-EREBP	0.97	1.98	8.13	6.14	UPRE
At2g28720	Histone H2B, putative	1.00	1.41	2.67	2.45	UPREx2
At2g02230	ATPP2-B1 (Phloem protein 2-B1)	1.00	1.36	5.53	4.38	
At1g78920 [a]	vacuolar-pyrophosphatase like protein (AVPL1)	1.00	1.32	2.95	2.52	
At1g01380	myb family transcription factor ETC1	1.00	2.00	8.48	5.01	
Cluster III						
AGI code	Description	Tunicamycin treatment				Cis-elements
		0h	2h	5h	10h	
At5g37260	CIR1	1.00	1.02	0.98	3.14	
At4g26530	fructose-bisphosphate aldolase, putative	1.00	0.77	0.63	5.41	AAAATATCTx2
At1g69930	ATGSTU11, glutathione transferase	1.00	1.18	1.26	2.63	
At5g49360	ATBXL1, a beta-xylosidase located in the extracellular matrix.	1.00	0.36	1.50	1.91	
At4g17090 [a]	BAM3, beta-amylase	0.99	0.50	1.51	2.65	
At1g22500	zinc finger (C3HC4-type RING finger) family protein	1.00	0.30	1.10	0.97	
Cluster IV						
AGI code	Description	Tunicamycin treatment				Cis-elements
		0h	2h	5h	10h	
At2g28630 [a]	KCS12	0.98	3.77	4.39	1.61	
At1g56170 [a]	Hap5b	1.00	3.29	3.02	2.01	
At5g10550	Global transcription factor group E 2 (GTE2)	1.00	2.53	1.61	1.41	UPRE
At5g65630	Global transcription factor group E 7 (GTE7)	1.00	2.59	1.56	1.39	
At2g38470 [a]	WRKY33	1.00	3.55	1.90	1.77	
At3g52450	PLANT U-BOX 22 (PUB22)	1.00	2.57	1.39	1.40	
At2g34620	mitochondrial transcription termination factor-related	1.00	2.88	1.45	1.37	
At4g18430	Rab GTPase homolog A1e (AtRABA1e)	1.00	2.59	1.13	1.21	
At1g52200	unknown protein	0.99	2.84	1.82	1.07	AAAATATCTx2
Cluster V						
AGI code	Description	Tunicamycin treatment				Cis-elements
		0h	2h	5h	10h	
At3g14210	epithiospecifier modifier 1 (ESM1)	1.00	0.16	0.28	0.52	
At5g65380	ripening-responsive protein, putative	1.00	0.26	0.40	0.61	
At3g21690	MATE efflux family protein	1.00	0.33	0.44	0.67	
At1g34060	alliinase family protein	1.00	0.31	0.51	0.64	
At4g17340	TONOPLAST INTRINSIC PROTEIN 2;2 (TIP2;2)	0.99	0.28	0.47	0.77	ERSE
At3g14067	subtilase family protein	1.00	0.22	0.37	0.73	
At3g21670	nitrate transporter (NTP3)	1.00	0.29	0.36	0.79	
At1g55260	unknown protein	1.00	0.37	0.48	0.78	
At3g10410	serine carboxypeptidase-like 49 (scpl49)	1.00	0.37	0.47	0.77	
At5g45280	pectinacetylesterase, putative	1.00	0.37	0.41	0.70	
At1g17100	SOUL heme-binding family protein	1.00	0.24	0.27	0.61	
At3g06510	SENSITIVE TO FREEZING 2 (SFR2)	1.00	0.38	0.51	0.97	
At2g01320	ABC transporter family protein	1.00	0.37	0.62	0.80	
At5g53860	embryo defective 2737 (emb2737)	1.00	0.36	0.59	0.81	
At1g70160 [a]	unknown protein	1.00	0.34	0.59	0.75	
At1g30400	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 1 (MRP1)	1.00	0.37	0.62	0.77	
At1g72610	GERMIN-LIKE PROTEIN 1 (GLP1)	1.00	0.13	0.45	0.70	

At1g33600	leucine-rich repeat family protein	1.00	0.29	0.64	0.69	
At4g19410	pectinacetylesterase, putative	1.00	0.37	0.47	0.61	
At4g38220	aminoacylase, putative	1.00	0.37	0.42	0.59	
At3g53420	PLASMA MEMBRANE INTRINSIC PROTEIN 2A (PIP2A)	1.00	0.34	0.32	0.43	
At1g64900	CYP89A2	1.00	0.38	0.41	0.48	
At5g66590	allergen V5/Tpx-1-related family protein	1.00	0.38	0.44	0.55	
At2g22170	lipid-associated family protein	1.00	0.26	0.31	0.40	UPRE
At4g27520	plastocyanin-like domain-containing protein	0.99	0.35	0.52	0.55	
At1g15180	MATE efflux family protein	1.00	0.38	0.54	0.57	
At1g34040	alliinase family protein	1.00	0.22	0.39	0.45	
At1g27940	P-GLYCOPROTEIN 13 (PGP13)	1.00	0.34	0.52	0.51	
At2g38170	cation exchanger 1 (CAX1)	1.00	0.36	0.58	0.58	
At2g24280	serine carboxypeptidase S28 family protein	1.00	0.47	0.38	0.85	
At3g47430	PEX11B	1.00	0.49	0.36	0.93	
At3g62410	CP12 DOMAIN-CONTAINING PROTEIN 1 (CP12)	0.99	0.69	0.39	1.61	
At4g28080	unknown protein	1.00	0.68	0.38	0.71	
At1g52400	BETA GLUCOSIDASE 18 (BGLU18)	0.79	0.69	0.29	0.74	
Cluster VI						
AGI code	Description	Tunicamycin treatment				Cis-elements
		0h	2h	5h	10h	
At1g14960	major latex protein-related	0.97	0.83	0.29	0.23	
At5g10180	SULFATE TRANSPORTER 2;1 (SULTR2;1)	0.98	0.87	0.44	0.39	
At5g37970	S-adenosyl-L-methionine:carboxyl methyltransferase family protein	0.93	0.79	0.36	0.32	
At5g37990	S-adenosylmethionine-dependent methyltransferase	0.94	0.79	0.29	0.30	
At4g12870	GILT family protein	0.99	0.75	0.31	0.31	
At1g03130	photosystem I subunit D-2 (PSAD-2)	1.00	0.81	0.37	0.38	
At5g54270	IGHT-HARVESTING CHLOROPHYLL B-BINDING PROTEIN 3 (LHCB3)	1.00	0.82	0.40	0.39	
At3g08770	LIPID TRANSFER PROTEIN 6 (LTP6)	0.99	0.81	0.47	0.39	
At3g54500	unknown protein	1.00	0.73	0.38	0.30	UPRE
At5g25190	a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family	1.00	0.74	0.43	0.34	AAAATATCT
At1g29920	CHLOROPHYLL A/B-BINDING PROTEIN 2 (CAB2)	1.00	0.59	0.23	0.17	
At1g07180	ALTERNATIVE NAD(P)H DEHYDROGENASE 1 (NDA1)	1.00	0.67	0.33	0.29	
At1g20160	ATSBT5.2	1.00	0.57	0.23	0.26	
At2g31380	SALT TOLERANCE HOMOLOGUE (STH)	1.00	0.66	0.41	0.38	
At1g01060 [c]	LATE ELONGATED HYPOCOTYL (LHY)	1.00	0.49	0.18	0.17	
At2g38530 [a]	LIPID TRANSFER PROTEIN 2 (LTP2)	1.00	0.51	0.26	0.25	
At5g51720	unknown protein	0.99	1.07	0.50	0.31	
At3g01060	unknown protein	1.00	0.95	0.46	0.27	
At3g54260	unknown protein	1.00	0.93	0.54	0.38	
At3g12320	unknown protein	1.00	0.91	0.48	0.34	ERSE-II
At2g37460	nodulin MtN21 family protein	1.00	0.90	0.41	0.31	
At2g46830	CIRCADIAN CLOCK ASSOCIATED 1 (CCA1)	1.00	1.00	0.30	0.21	
At5g20830	SUCROSE SYNTHASE 1 (SUS1)	1.00	0.77	0.39	0.26	
At1g73870	zinc finger (B-box type) family protein	1.00	1.38	0.49	0.37	
At5g51460	ATTPPA	1.00	0.71	0.57	0.38	
At1g73600	phosphoethanolamine N-methyltransferase	0.99	0.63	0.52	0.33	
At3g16670	unknown protein	1.00	0.69	0.47	0.34	
At2g43610	glycoside hydrolase family 19 protein	1.00	0.35	0.16	0.09	
At1g05660	polygalacturonase, putative	0.99	0.87	0.62	0.36	
At4g26010	peroxidase, putative	1.00	0.71	0.57	0.28	
At3g47500	CYCLING DOF FACTOR 3 (CDF3)	1.00	0.73	0.56	0.31	
At4g35880	aspartyl protease family protein	1.00	0.84	0.87	0.37	
At2g39430	disease resistance-responsive protein-related	1.00	0.71	0.72	0.33	

At5g42200	zinc finger (C3HC4-type RING finger) family protein	1.00	0.37	0.35	0.32	
At2g43620	chitinase, putative	1.00	0.21	0.18	0.16	
At1g54000[a]	myrosinase-associated protein, putative	0.99	0.18	0.21	0.18	AAAATATCT
At3g27170	CHLORIDE CHANNEL B (CLC-B)	1.00	0.40	0.51	0.35	
At1g05250	peroxidase, putative	1.00	0.37	0.29	0.19	
At5g10430	ARABINOGALACTAN PROTEIN 4 (AGP4)	1.00	0.59	0.49	0.39	
At1g62710	BETA VACUOLAR PROCESSING ENZYME (BETA-VPE)	1.00	0.43	0.32	0.23	
At1g23205	invertase/pectin methylesterase inhibitor family protein	1.00	0.40	0.26	0.23	
At5g60950	COBRA-LIKE PROTEIN 5 PRECURSOR (COBL5)	1.00	0.44	0.36	0.31	
At2g25510[a]	unknown protein	1.00	0.28	0.15	0.27	
At4g21960[a]	PRXR1	1.00	0.43	0.33	0.45	
At1g64500	glutaredoxin family protein	1.00	0.44	0.28	0.46	
At1g54010[a]	myrosinase-associated protein, putative	1.00	0.36	0.23	0.42	
At2g38380	peroxidase 22 (PER22) (P22) (PRXEA)	1.00	0.61	0.26	0.39	
At2g38390	peroxidase, putative	1.00	0.71	0.28	0.42	AAAATATCT

[a] Genes reported in Martinez and Chrispeels (2003) *Plant Cell* 15: 561-76.

[b] Genes reported in Noh et al. (2003) *Gene* 311: 81-91.

[c] Genes reported in Kamauchi et al. (2005) *FEBS J* 272: 3461-76.