Supplementary Table S5
Genes significantly up-regulated ≥ 2-fold specifically in ACE seeds treated with PEG.

AGI number	Fold change	Description (TAIR)	Biological process (Nick's classification)
At5g08670	2.16	ATP synthase beta chain 1	biosynthesis, nucleic acid metabolism
At1g02640	2.18	glycosyl hydrolase family 3 protein	carbohydrate metabolism
At5g49360	2.36	glycosyl hydrolase family 3 protein	carbohydrate metabolism
At2g43590	3.93	chitinase	carbohydrate metabolism, catabolism, response to stress
At5g09870	2.26	cellulose synthase	carbohydrate metabolism, cell organization and biogenesis
At3g55260	2.4	beta-N-acetylhexosaminidase-like protein	carbohydrate metabolism, transport
At4g10610	2.1	RNA-binding protein	cell growth and/or maintenance
At1g06760	2.81	histone H1-1 (partial)	cell organization and biogenesis
At3g48140	2.08	B12D-like protein	development
At4g27440	2.66	protochlorophyllide reductase precursor (F27G19.40)	development
At5g46700	2.56	putative senescence-associated protein	development
At1g77510	3.91	protein disulfide isomerase	electron transport
At4g28750	2.16	photosystem I subunit IV precursor (psaE1 gene)	electron transport
At5g54500	2.42	1,4-benzoquinone reductase-like protein	electron transport
At3g12780	3.38	phosphoglycerate kinase	energy pathways
At3g50520	2.37	phosphoglycerate/bisphosphoglycerate mutase family	energy pathways, carbohydrate metabolism, metabolism
At3g02360	2.47	6-phosphogluconate dehydrogenase	energy pathways, metabolism
At4g35790	2.09	phospholipase D delta	lipid metabolism, metabolism
At1g10670	2.3	putative ATP citrate-lyase	metabolism
At1g37130	2.15	nitrate reductase	metabolism
At1g48430	2.03	dihydroxyacetone kinase	metabolism
At1g62180	2	putative 5'-adenylylphosphosulfate reductase	metabolism
At1g65960	2.26	glutamate decarboxylase 2 (GAD2)	metabolism
At1g79750	2	malate oxidoreductase	metabolism
At3g12120	2.9	omega-6 fatty acid desaturase, fatty acid biosynthesis	metabolism
At3g58610	2.32	putative ketol-acid reductoisomerase	metabolism
At4g02520	4.21	glutathione S-transferase	metabolism
At4g15560	3.38	1-deoxy-D-xylulose-5-phosphate synthase	metabolism
At5g04740	2.05	ACT domain-containing protein	metabolism
At5g10860	2.09	CBS domain-containing protein	metabolism
At5g17920	2.09	cobalamin-independent methionine synthase (ATCIMS)	metabolism
At5g53460	2.34	glutamate synthase (NADH)	metabolism
At5g54810	2.19	tryptophan synthase beta chain 1	metabolism
At4g25100	3.06	putative Fe superoxide dismutase	metabolism, behavior

At2g30970	2.02	aspartate aminotransferase	metabolism, biosynthesis
At1g30380	2.94	photosystem I reaction center subunit psaK	photosynthesis
At1g52230	2.08	photosystem I subunit VI precursor (psaH2 gene)	photosynthesis
At1g55670	2.3	putative photosystem I subunit V precursor	photosynthesis
At3g61470	2.07	chlorophyll A-B binding protein (LHCA2)	photosynthesis
At5g47110	2.02	lil3 protein, putative	photosynthesis
At1g61740	2.21	unknown protein	physiological process
At1g30230	2.84	elongation factor 1-beta	protein biosynthesis
At1g70600	2.13	60S ribosomal protein L27A	protein biosynthesis
At1g74060	2.12	putative 60S ribosomal protein L6 (F2P9.7)	protein biosynthesis
At5g19510	2.86	putative elongation factor 1B alpha-subunit	protein biosynthesis
At5g35620	2.35	eIF4Eiso protein	protein biosynthesis
At5g20290	2.12	40S ribosomal protein	protein biosynthesis, cell organization and biogenesis
At5g65220	5.04	putative 50S ribosomal protein L29	protein biosynthesis, cell organization and biogenesis
At1g57720	2.73	elongation factor 1-gamma 2	protein biosynthesis, metabolism
At1g56300	3.64	DNAJ heat shock N-terminal domain-containing protein	protein metabolism
At1g79920	2.1	putative heat-shock protein	protein metabolism
At3g22630	2.19	20S proteasome beta subunit PBD1 (PBD1)	protein metabolism
At3g27080	2.18	mitochondrial preprotein receptor TOM20-3	protein metabolism
At4g01610	2.24	putative cathepsin B cysteine protease	protein metabolism
At4g08980	3.2	F-box family protein	protein metabolism
At5g05740	2.51	peptidase M50 family protein	protein metabolism
At5g41700	2.18	putative E2 ubiquitin-conjugating enzyme UBC8	protein metabolism
At5g50920	2	ATP-dependent Clp protease ATP-binding subunit	protein metabolism
At2g29960	2.24	cyclophilin	protein metabolism, cell organization and biogenesis
At1g72150	2.06	putative cytosolic factor	protein metabolism, transport
At1g64230	2.08	ubiquitin-conjugating enzyme	protein modification
At2g40730	2.39	HEAT repeat-containing protein	protein modification
At3g13670	2.21	putative casein kinase	protein modification
At5g10520	3.17	putative Pto kinase interactor	protein modification
At5g63940	2.66	unknown protein	protein modification
At1g28440	2.29	putative receptor protein kinase	protein modification, signal transduction
At5g62690	2.97	tubulin beta-2/beta-3 chain	response to abiotic stimulus
At4g02380	2.33	late embryogenesis abundant protein homolog (SAG21)	response to abiotic stimulus, embryonic development
At5g56220	2.41	unknown protein	response to biotic stimulus, cell death
At3g26450	2.1	major latex protein-related	secondary metabolism
At4g23670	2.06	major latex protein-related	secondary metabolism
At4g34050	3.48	caffeoyl-CoA 3-O-methyltransferase	secondary metabolism
At5g25980	2.2	glycosyl hydrolase family 1 protein	secondary metabolism
At1g35160	2.93	14-3-3 protein GF14 phi (grf4)	signal transduction
At2g33340	2.34	transducin family protein	signal transduction
At5g61790	3.4	calnexin 1 (CNX1)	signal transduction
At1g17470	2.12	developmentally regulated GTP binding	signal transduction, cell growth and/or

		protein (AtDRG1)	maintenance
At4g14640	2.15	calmodulin-8 (CAM8)	signal transduction, response to abiotic stimulus
At5g14920	2	gibberellin-regulated family protein	signal transduction, response to endogenous stimulus
At1g14350	2.36	putative transcription factor MYB124 (MYB124)	transcription
At2g18160	2.1	transcription factor GBF5 (GBF5)	transcription
At5g10650	2.49	zinc finger (C3HC4-type RING finger) family protein	transcription
At5g44800	2.48	chromodomain-helicase-DNA-binding family protein	transcription, cell organization and biogenesis
At1g10450	2.16	paired amphipathic helix repeat-containing protein	transcription, transport
At1g11260	4.94	glucose transporter (STP1)	transport
At1g15500	2.43	AATP2, chloroplast ADP, ATP carrier	transport
At2g13820	2.08	protease inhibitor/seed storage/lipid transfer protein	transport
At2g38530	5.22	non-specific lipid transfer protein 2	transport
At2g38540	3.14	non-specific lipid transfer protein 1	transport
At3g01390	2.59	vacuolar ATP synthase subunit G 1	transport
At3g16240	2.23	delta tonoplast integral protein	transport
At3g21670	2.1	nitrate transporter partial	transport
At4g27140	2.02	2S albumin 1 precursor	transport
At4g35100	2.13	plasma membrane intrinsic protein (SIMIP)	transport
At4g37880	2.22	unknown protein	transport
At3g08580	3.16	mitochondrial ADP/ATP carrier protein 1	transport, biological process
At3g26520	2.46	tonoplast intrinsic protein	transport, physiological process
At1g59870	2.16	ABC transporter family protein	transport, protein metabolism, response to abiotic stimulus
At3g48970	2.18	copper-binding family protein	transport, response to abiotic stimulus
At5g40890	2.27	voltage-gated chloride channel	transport, response to abiotic stimulus
At1g03220	2.16	extracellular dermal glycoprotein	unknown
At1g05020	2.34	clathrin assembly protein-related	unknown
At1g05320	2	myosin-related	unknown
At1g17860	2.01	trypsin and protease inhibitor family protein	unknown
At1g20370	2.48	tRNA pseudouridine synthase family protein	unknown
At1g21660	2.08	unknown protein	unknown
At1g48300	2.04	unknown protein	unknown
At1g49600	2.49	RNA-binding protein 47	unknown
At1g70830	3.11	Bet v I allergen family protein	unknown
At1g78850	2.35	curculin-like (mannose-binding) lectin family protein	unknown
At2g15240	3.02	UNC-50 family protein	unknown
At2g21870	2.01	putative ATP synthase	unknown
At2g28840	2.15	RING zinc finger ankyrin protein	unknown
At2g36320	2.06	zinc finger (AN1-like) family protein	unknown
At3g08030	3.02	unknown protein	unknown
At3g13460	2.14	unknown protein	unknown
At3g14100	2.19	oligouridylate-binding protein	unknown
At3g18780	2.19	actin 2 (ACT2)	unknown

At3g27750	2.38	unknown protein	unknown
At3g29240	2.51	unknown protein	unknown
At3g33530	2.09	transducin family protein	unknown
At3g46200	2.13	MutT/nudix family protein	unknown
At3g56940	2.3	putative dicarboxylate diiron protein (Crd1)	unknown
At4g09620	4.21	unknown protein	unknown
At4g14990	8.96	unknown protein	unknown
At4g16410	2.03	unknown protein	unknown
At4g18120	2.33	RNA recognition motif (RRM)-containing protein	unknown
At4g18970	2.3	GDSL-motif lipase/hydrolase family protein	unknown
At4g25580	2.5	stress-responsive protein-related	unknown
At5g05100	2.46	unknown protein	unknown
At5g09410	2.41	calmodulin-binding protein	unknown
At5g09440	3.43	phosphate-responsive protein	unknown
At5g23060	2.05	unknown protein	unknown
At5g33370	4.76	GDSL-motif lipase/hydrolase family protein	unknown
At5g35440	2.18	unknown protein	unknown
At5g40450	2.34	unknown protein	unknown
At5g44120	4.13	12S seed storage protein (CRA1)	unknown
At5g45950	3.79	GDSL-motif lipase/hydrolase family protein	unknown
At5g53160	2.59	unknown protein	unknown
At5g57580	2.08	putative calmodulin-binding protein	unknown
At5g61820	2.07	unknown protein	unknown
At5g64260	8.91	phosphate-responsive protein	unknown
NO_HIT_ORF	2.75	24622 CD4-13 Arabidopsis thaliana cDNA clone E6A11T7	unknown
NO_HIT_ORF	2.21	21233 CD4-14 Arabidopsis thaliana cDNA clone F5F7T7	unknown
NO_HIT_ORF	2.2	18080 Lambda-PRL2 Arabidopsis thaliana cDNA clone 193J5T7	unknown
NO_HIT_ORF	2.05	20630 Lambda-PRL2 Arabidopsis thaliana cDNA clone 238H10T7	unknown
NO_HIT_ORF	2.15	20635 Lambda-PRL2 Arabidopsis thaliana cDNA clone 239A3T7	unknown
NO_HIT_ORF	2.46	20637 Lambda-PRL2 Arabidopsis thaliana cDNA clone 239B7T7	unknown
NO_HIT_ORF	2.11	20620 Lambda-PRL2 Arabidopsis thaliana cDNA clone 237H12T7	unknown
NO_HIT_ORF	2.24	24773 CD4-16 Arabidopsis thaliana cDNA clone H10F7T7	unknown
NO_HIT_ORF	2.15	14242 Lambda-PRL2 Arabidopsis thaliana cDNA clone 175A4T7	unknown
NO_HIT_ORF	2.15	20622 Lambda-PRL2 Arabidopsis thaliana cDNA clone 237H3T7	unknown
NO_HIT_ORF	2.1	20870 Lambda-PRL2 Arabidopsis thaliana cDNA clone 239H2T7	unknown
NO_HIT_ORF	2.85	22898 CD4-15 A. cDNA clone G12H3T7	unknown