Supplemental Table S1. Significant APA genes with $|\triangle \mathrm{PSU}| \geq 0.2$ and $padj < 0.05$

Locus Identifier	Gene Model Description	Gene Model Type	All Gene Symbols
AT4G26810	SWIB/MDM2 domain superfamily protein	protein_coding	
AT5G02540	NAD(P)-binding Rossmann-fold superfamily protein	protein_coding	
AT5G61530	small G protein family protein / RhoGAP family protein	protein_coding	
AT1G26300	BSD domain-containing protein	protein_coding	
AT3G58200	TRAF-like family protein	protein_coding	
AT3G47040	Glycosyl hydrolase family protein	protein_coding	
AT3G04450	Homeodomain-like superfamily protein	protein_coding	
AT4G10890	DDE family endonuclease	protein_coding	
AT3G09925	Pollen Ole e 1 allergen and extensin family protein	protein_coding	
AT1G64180	intracellular protein transport protein USO1-like protein	protein_coding	
AT3G01516	transmembrane protein	protein_coding	
AT1G10780	F-box/RNI-like superfamily protein	protein_coding	
AT4G00750	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	protein_coding	
AT3G56210	ARM repeat superfamily protein	protein_coding	
AT3G54000	TIP41-like protein	protein_coding	
AT4G01570	Tetratricopeptide repeat (TPR)-like superfamily protein	protein_coding	
AT4G03935	None	other_rna	
AT3G23740	hypothetical protein	protein_coding	
AT3G44120	F-box and associated interaction domains-containing protein	protein_coding	
AT3G55910	ADP-ribosylation factor GTPase-activating protein	protein_coding	
AT3G15518	hypothetical protein	protein_coding	
AT3G49710	Pentatricopeptide repeat (PPR) superfamily protein	protein_coding	
AT2G04378	Beta-galactosidase related protein	protein_coding	
AT2G26630	transposable_element_gene;transposase IS4 family protein, contains Pfam profile: PF01609 transposase DDE domain;(source:TAIR10)	transposable_element_gene	

AT4G32440	Plant Tudor-like RNA-binding protein	protein_coding	
AT1G34315	transmembrane protein	protein_coding	
AT1G63855	Putative methyltransferase family protein	protein_coding	
AT1G52060	Mannose-binding lectin superfamily protein	protein_coding	
AT2G29500	HSP20-like chaperones superfamily protein	protein_coding	(HSP17.6B)
AT1G06490	Encodes Callose Synthase 7 (CalS7), a phloem-specific callose synthase responsible for callose deposition in developing sieve elements during phloem formation and in mature phloem induced by wounding.	protein_coding	ARABIDOPSIS THALIANA GLUCAN SYNTHASE-LIKE 7 (ATGSL07); (gsl07);CALLOSE SYNTHASE 7 (CalS7);GLUCAN SYNTHASE-LIKE 7 (GSL07);GLUCAN SYNTHASE-LIKE 7 (GSL7); (atgsl7)
AT4G25830	Uncharacterized protein family (UPF0497)	protein_coding	CASP-LIKE PROTEIN 2C1 (CASPL2C1)
AT2G21730	cinnamyl alcohol dehydrogenase homolog 2	protein_coding	CINNAMYL ALCOHOL DEHYDROGENASE HOMOLOG 2 (CAD2); (ATCAD2)
AT3G60620	cytidinediphosphate diacylglycerol synthase 5	protein_coding	CYTIDINEDIPHOSPHATE DIACYLGLYCEROL SYNTHASE 5 (CDS5)
AT2G44520	cytochrome c oxidase 10	protein_coding	CYTOCHROME C OXIDASE 10 (COX10)
AT5G61600	encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5. Involved in regulating root architecture.	protein_coding	ETHYLENE RESPONSE FACTOR 104 (ERF104)
AT1G10270	glutamine-rich protein 23	protein_coding	GLYCINE-RICH PROTEIN 23 (GRP23);GLUTAMINE-RICH PROTEIN 23 (GRP23)
AT1G02950	Encodes glutathione transferase belonging to the phi class of GSTs. Naming convention according to Wagner et al. (2002).	protein_coding	GLUTATHIONE S-TRANSFERASE F4 (ATGSTF4);GLUTATHIONE S-TRANSFERASE F4 (GSTF4);GLUTATHIONE S-TRANSFERASE 31 (GST31)

AT5G41080	Encodes a member of the glycerophosphodiester phosphodiesterase (GDPD) family.	protein_coding	(AtGDPD2);GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE 2 (GDPD2)
AT1G08280	Encodes a glycosyltransferase (GT) GALT29A, which belongs to the Carbohydrate Active Enzyme family GT29. GALT29A co-expresses with other arabinogalactan GTs, GALT31A and GLCAT14A. The recombinant GALT29A expressed in Nicotiana benthamiana demonstrated a galactosyltransferase activity, transferring galactose from UDP-galactose to a mixture of various oligosaccharides derived from arabinogalactan proteins.	protein_coding	GLYCOSYLTRANSFERASE 29A (GALT29A)
AT1G71920	Encodes a protein that is believed to act as a histidinol-phosphate transaminase involved in histidine biosynthesis. If the gene encoding the other protein shown to have this function, HISN6A (AT5G10330), is disrupted, a residual level of histidine biosynthesis continues, suggesting that HISN6B can somewhat compensate for the loss of HISN6A.	protein_coding	HISTIDINE BIOSYNTHESIS 6B (HISN6B)
AT1G18670	Encodes a cyclin-dependent kinase-like protein with a ser/thr protein kinase domain and an N-terminal myristoylation sequence. Mutants in this gene are unable to express female sterility in response to beta-aminobutyric acid, as wild type plants do.	protein_coding	IMPAIRED IN BABA-INDUCED STERILITY 1 (IBS1)
AT3G27940	LOB domain-containing protein 26	protein_coding	LOB DOMAIN-CONTAINING PROTEIN 26 (LBD26)

AT2G28230	Encodes one of the subunits of the head domain of the MEDIATOR complex. The complex conveys transcriptional signals by acting as an intermediary between transcription factors and RNA polymerase II. Together with MED18, MED20 is proposed to control the balance of salicylic acid and jasmonate associated defense pathways. It is involved in miRNA biogenesis by recruiting Pol II to promoters of miRNA genes.	protein_coding	MEDIATOR 20 (MED20);MEDIATOR 20A (MED20A)
AT5G67300	Member of the R2R3 factor MYB gene family involved in mediating plant responses to a variety of abiotic stimiuli. The mRNA is cell-to-cell mobile.	protein_coding	(ATMYBR1);MYB DOMAIN PROTEIN R1 (MYBR1); (MYB44);ARABIDOPSIS THALIANA MYB DOMAIN PROTEIN 44 (ATMYB44)
AT3G04070	NAC domain containing protein 47	protein_coding	NAC DOMAIN CONTAINING PROTEIN 47 (anac047);SPEEDY HYPONASTIC GROWTH (SHYG);SPEEDY HYPONASTIC GROWTH (SHG);NAC DOMAIN CONTAINING PROTEIN 47 (NAC047)
AT1G58602	LRR and NB-ARC domains-containing disease resistance protein	protein_coding	RECOGNITION OF PERONOSPORA PARASITICA 7 (RPP7)
AT3G27670	A novel protein, did not show high similarity to any protein of known function; reveals a novel genetic connection between lipid synthesis and embryo development. Expressed in all tissues examined including leaves, flowers, roots, stems, and siliques, but accumulation levels were not correlated with the degree to which different organs appeared affected by the mutation. Mutant plants showed alterations in the cuticular wax profiles and embryo development. The mRNA is cell-to-cell mobile.	protein_coding	ECERIFERUM 13 (CER13);RESURRECTION1 (RST1); (CER13)

AT1G72530	Member of MORF family consisting of of nine full-length proteins encoded in the nuclear genome. MORF proteins are required for all RNA editing events in plastids and for many, possibly also all, sites in mitochondria. Potential link between the RNA binding PPR protein and the protein contributing the enzymatic activity in RNA editing.	protein_coding	MULTIPLE ORGANELLAR RNA EDITING FACTOR 7 (MORF7);RNA EDITING-INTERACTING PROTEIN (RIP7)
AT2G43190	Encodes a protein involved in rRNA but not tRNA maturation.	protein_coding	SIMILAR TO YEAST POP4 (POP4)
AT5G16830	member of SYP2 Gene Family. Over-expression of the gene in tobacco protoplasts leads to a disruption of vacuolar transport from the prevacuolar compartment (PVC) to the vacuole, but not from the Golgi apparatus to the plasma membrane.	protein_coding	SYNTAXIN OF PLANTS 21 (SYP21); (ATSYP21); (PEP12P); (ATPEP12); (PEP12)
AT3G11910	Ubiquitin-specific protease, which together with UBP12 deubiquitinates DA1, DAR1 and DAR2, hence reducing their peptidase activity. Works upstream of DA1, DAR1 and DAR2 to restrict their protease activity and hence fine-tune plant growth and development.	protein_coding	(AtUBP13);UBIQUITIN-SPECIFIC PROTEASE 13 (UBP13)
AT3G03340	LUC7 related protein	protein_coding	LETHAL UNLESS CBC 7 A (LUC7A);UNFERTILIZED EMBRYO SAC 6 (UNE6)
AT5G33290	Acts as a xylogalacturonan xylosyltransferase within the XGA biosynthesis pathway. Involved in pectin biosynthesis.	protein_coding	XYLOGALACTURONAN DEFICIENT 1 (XGD1)