

Supplemental Table S4: List of the *Arabidopsis* sequences from the pistil data set described at the article of Swanson et al. (2005), for which there are ‘true homologous’ sequences in the TOBEST database.

Query	TOBEST ID	Gene Description (Function or Comment)
At3g09350	C003H02	armadillo/beta-catenin repeat family protein
At3g12390	C007F02	nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative
At5g14030	C009A04	translocon-associated protein beta (TRAPB) family protein
At1g30510	C013C06	ATRFNR2 (root FNR 2); oxidoreductase
At5g40370	C013H11	glutaredoxin, putative
At3g08640	C014C07	alphavirus core protein family
At3g09390	C017F05	ATMT-K, ATMT-1, MT2, MT2A (metallothionein 2A)
At2g02850	C017H10	ARPN (plantacyanin); copper ion binding
At1g44575	C018C06	PSBS, NPQ4 (nonphotochemical quenching)
At3g16140	C018G07	PSAH-1 (photosystem I subunit H-1)
At1g70330	C018H01	ENT1, AT (equilibrative nucleotide transporter 1); nucleoside transporter
At4g02890	C018H09	UBQ14 (ubiquitin 14); protein binding
At3g18280	C023D01	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
At2g24940	C025D02	ATMAPR2 (<i>Arabidopsis thaliana</i> membrane-associated progesterone binding protein 2); heme binding/transition metal ion
At5g47030	C027E12	ATP synthase delta' chain, mitochondrial
At5g53300	C028D10	UBC10 (ubiquitin-conjugating enzyme 10); ubiquitin-protein ligase
At1g64660	C031E08	ATMGL; catalytic/ methionine gamma-lyase
At1g51980	C032B03	mitochondrial processing peptidase alpha subunit, putative
At4g11600	C033G09	PHGPX, LSC803, ATGPX6 (glutathione peroxidase 6); glutathione peroxidase
At2g45290	C035E09	transketolase, putative
At1g76200	C037B06	similar to conserved hypothetical protein [<i>Medicago truncatula</i>] (GB:ABE89059.1)
At2g37110	C041E09	similar to unknown protein [<i>Arabidopsis thaliana</i>] (TAIR:AT2G40935.1); similar to uncharacterized Cys-rich domain [<i>Medicago truncatula</i>]
At3g46450	C046E11	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein
At1g27400	C047C11	60S ribosomal protein L17 (RPL17A)
At5g43330	C049A05	malate dehydrogenase, cytosolic, putative
At1g53130	C054D09	stigma-specific Stig1 family protein
At5g51970	C056B05	sorbitol dehydrogenase, putative / L-iditol 2-dehydrogenase, putative
At3g51250	C057D08	senescence/dehydration-associated protein-related
At1g72650	C058A01	TRFL6 (TRF-LIKE 6); DNA binding / transcription factor
At4g35000	C059C07	APX3 (ascorbate peroxidase 3); L-ascorbate peroxidase
At3g20320	C062D04	TGD2 (trigalactosyldiacylglycerol2)
At4g17670	C064E12	senescence-associated protein-related
At1g16210	C078E10	similar to cupin family protein [<i>Arabidopsis thaliana</i>] (TAIR:AT2G18540.1);
At4g35100	C085F10	PIP3A, PIP2;7, SIMIP, PIP3 (plasma membrane intrinsic protein 3); water channel
At4g34265	C087D06	similar to unknown protein [<i>Arabidopsis thaliana</i>] (TAIR:AT2G15000.5)
At1g64670	C092C05	BDG1 (BODYGUARD1); hydrolase
At2g30570	C095D06	PSBW photosystem II reaction center W (PsbW) protein-related
At5g53920	C095H09	ribosomal protein L11 methyltransferase-related
At5g54770	C096F01	TZ, THI1 THI1 (thiazole requiring)
At1g08830	C100B03	CSD1 (copper/zinc superoxide dismutase 1)
At4g08240	C102E08	similar to Os02g0567000 [<i>Oryza sativa</i> (japonica cultivar-group)]
At2g37170 ^a	C103C08	PIP2;2, PIP2B (plasma membrane intrinsic protein 2;2); water channel
At2g20340 ^a	C104G09	tyrosine decarboxylase, putative
At1g32230	C105C07	CEO, ATP8, CEO1, RCD1 RCD1 (radical-induced cell death1)
At1g70370	C107C01	BURP domain-containing protein / polygalacturonase, putative
At4g00360	C107D01	ATT1, CYP86A2 CYP86A2 (aberrant induction of type three genes 1); oxygen binding
At3g48690	C109A07	similar to unknown protein [<i>Arabidopsis thaliana</i>] (TAIR:AT3G48700.1); similar to Esterase/lipase/thioesterase [<i>Medicago truncatula</i>]
At1g55810	C113D09	uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative
At1g14450	C113H11	similar to unknown protein [<i>Arabidopsis thaliana</i>] (TAIR:AT2G02510.1)
At1g35720	C114E01	OXY5, ATOXY5, ANNAT1 (annexin <i>Arabidopsis</i> 1); calcium ion binding/calcium-dependent phospholipid binding
At1g24260	C118G09	AGL9, SEP3 (SEPALLATA3); transcription factor
At1g06680	C129E02	OEE2, PSBP-1 (oxygen-evolving enhancer protein 2); calcium ion binding

At4g09800	C132G05	RPS18C (S18 ribosomal protein); structural constituent of ribosome
At3g53990	S001A09	universal stress protein (USP) family protein
At3g48860	S003D07	similar to unknown protein [<i>Arabidopsis thaliana</i>] (TAIR:AT5G23700.1); similar to Esterase/lipase/thioesterase [<i>Medicago truncatula</i>]
At5g52590	S003E03	RabGAP/TBC domain-containing protein
At3g22845	S003G12	emp24/gp25L/p24 protein-related
At3g58460	S004C02	rhomboid family protein / ubiquitin-associated (UBA)/TS-N domain-containing protein
At4g24190	S005F01	SHD (SHEPHERD); ATP binding
At4g38460	S008C08	GGR (geranylgeranyl reductase); farnesyltransferase
At5g13430	S008E11	ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative
At3g01320	S009A03	similar to paired amphipathic helix repeat-containing protein [<i>Arabidopsis thaliana</i>] (TAIR:At1g70060.1); similar to ATSIN3/SIN3 (<i>Arabidopsis thaliana</i>)
At4g37760	S010B05	squalene monooxygenase, putative / squalene epoxidase, putative
At4g30960	S013C10	SIP3, SnRK3.14, CIPK6 CIPK6 (cbl-interacting protein kinase 6); kinase
At5g01410	S013E03	ATPDX1.3, RSR4, PDX1 (pyridoxine biosynthesis 1.3); protein heterodimerization / protein homodimerization
At3g17810	S014A12	dihydroorotate dehydrogenase family protein / dihydroorotate oxidase family protein
At2g41410	S016F03	calmodulin, putative
At5g35360	S018G10	CAC2 (acetyl co-enzyme A carboxylase biotin carboxylase subunit)
At4g24690	S021D03	ubiquitin-associated (UBA)/TS-N domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein
At1g80360	S021H02	aminotransferase class I and II family protein
At4g38770 ^a	S022C10	ATPRP4, PRP4 (proline-rich protein 4)
At5g11200	S024F01	DEAD/DEAH box helicase, putative
At1g65445	S024H04	transferase-related
At5g09230	S026C08	SRT2
At3g59920	S027H03	ATGDI2 (rab gdp dissociation inhibitor 2); RAB GDP-dissociation inhibitor
At1g19300	S029F12	GATL1/GLZ1/PARVUS (Galacturonosyltransferase-like 1); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase,
At1g14820	S029H06	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein
At1g16890	S031D02	UBC36; ubiquitin-protein ligase
At4g00790	S034E08	protein binding / zinc ion binding
At3g10410	S035G09	SCPL49 (serine carboxypeptidase-like 49); serine carboxypeptidase
At1g03140	S036B08	splicing factor Prp18 family protein
At5g42960	S038F12	similar to unknown protein [<i>Arabidopsis thaliana</i>] (TAIR:At1g45170.1); similar to pore protein of 24 kD (OEP24) [<i>Pisum sativum</i>] (GB:CAA04468.1)
At3g03450	S040B05	RGL2 (RGA-LIKE 2); transcription factor
At3g52870	S043C07	calmodulin-binding family protein E
At4g36810	S045G04	GGPS1 (geranylgeranyl pyrophosphate synthase 1); farnesyltransferase
At5g23540	S047C02	26S proteasome regulatory subunit, putative
At4g26860	S048C04	alanine racemase family protein
At1g48090	S051A12	C2 domain-containing protein
At3g18790	S052E10	similar to 2 coiled coil domains of eukaryotic ori (GB:BAD19345.1); contains InterPro domain Isy1-like splicing; (InterPro:IPR009360)
At1g55690	S056A10	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein
At1g15820	S057H12	CP24, LHCB6 (light harvesting complex PSII); chlorophyll binding
At5g27990	S059C03	similar to unknown protein [<i>Arabidopsis thaliana</i>] (TAIR:At3g22510.1)
At5g15530	S061G01	CAC1-B BCCP2 (biotin carboxyl carrier protein 2); biotin binding
At2g34480	S063C11	60S ribosomal protein L18A (RPL18aB)
At4g38510	S063H08	(vacuolar ATP synthase subunit B2); hydrogen ion transporting ATP synthase
At1g65290	S065A06	acyl carrier family protein / ACP family protein
At3g07220	S068A01	transcriptional activator, putative
At5g59613	S070A03	similar to unknown protein [<i>Arabidopsis thaliana</i>] (TAIR:At3g46430.1); similar to mitochondrial ATP synthase 6 KD subunit [<i>Oryza sativa</i> (japonica cultivar-group)]
At3g19020	S073B03	leucine-rich repeat family protein / extensin family protein
At2g30970	S074F10	ASP1 (aspartate aminotransferase 1)
At5g47720	S077F08	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative
At1g72150	S084A10	PATL1 (PATELLIN 1); transporter
At1g30380	S089A11	PSAK (photosystem i subunit K)
At1g44542	S092C04	cyclase family protein
At5g20180	S093F10	ribosomal protein L36 family protein
At4g07390	S094B12	PQ-loop repeat family protein / transmembrane family protein
At1g79340	S095F07	latex-abundant protein, putative (AMC7) / caspase family protein
At2g05990	S098E05	ENR1, MOD1 (mosaic death 1); enoyl-[acyl-carrier-protein] reductase (NADH)/ oxidoreductase
At3g12260	S102A12	complex 1 family protein / LVR family protein

At4g01050	S103D02	hydroxyproline-rich glycoprotein family protein
At5g21105	S105A09	L-ascorbate oxidase/ copper ion binding
At5g10290	S109C05	leucine-rich repeat family protein / protein kinase family protein
At4g03280	S109G09	PGR1, PETC (photosynthetic electron transfer C)
At2g25530	S114B12	AFG1-like ATPase family protein
At2g13360	S114H07	AGT1, AGT (alanine:glyoxylate aminotransferase)
At4g39980	S119F03	DHS1 (3-deoxy-d-arabino-heptulosonate 7-phosphate synthase 1); 3-deoxy-7-phosphoheptulonate synthase
At2g40540	S121F01	ATKT2, SHY3, KUP2, ATKUP2, TRK2, KT2 (potassium transporter 2); potassium ion transporter
At2g17880	S122C03	DNAJ heat shock protein, putative
At3g27820	S122E12	ATMDAR4 (monodehydroascorbate reductase 4); monodehydroascorbate reductase (NADH)
At4g16360	S124F09	5'-AMP-activated protein kinase beta-2 subunit, putative
At3g22660	S129B05	rRNA processing protein-related
At5g47840	S130D09	adenylate kinase, chloroplast, putative / ATP-AMP transphosphorylase, putative
At5g57900	S130H05	SKIP1 (SKP1 interacting partner 1)
At1g11840	S132D06	ATGLX1 (glyoxalase I homolog); lactoylglutathione lyase

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- a. Genes up-regulated in stigma relative to ovary (cDNA subtraction, 32 top genes) (Table 1 from Swanson et al., 2005).