

SUPPLEMENTARY TABLE S10

Gene ID	log2-Fold Change M:F		Arabidopsis Homolog Name	Description	Category	Type	Notes on function	Source	Heterozygote Dominance Deviation		Percent distance from additive mean	p-value
	FDR											
Sapu_001G000400.3	-1.068	1.347E-01	PUR ALPHA-1	transcription factor Pur-alpha 1	Transcription	trans	binds telomeric repeat sequence	UniProt	-0.004015503	-26.76%	0.43996014	
Sapu_001G003600.1	1.424	1.390E-10	HRE2	AP2/ERF domain transcription factor	Transcription	trans	senescence	TAIR; Uniprot	-0.236415777	-48.39%	0.203024626	
Sapu_001G054400.1	-0.010	9.913E-01	LEP	AP2/ERF domain transcription factor	Transcription	trans	Positive regulator of gibberellin induced germination	TAIR	0.129477972	651.68%	0.000344165	
Sapu_001G069800.1	-0.071	8.485E-01	Dof-type zinc finger DNA-binding family protein	Transcription	trans	-	-	-	-0.008440334	-32.28%	0.415962781	
Sapu_001G136800.1	0.434	2.579E-01	CRF4	cytokinin response factor 4	Signaling	trans	cytokinins signaling, transcriptional activator, cotyledon, leaf and embryo development	UniProt	-0.59777885	-91.11%	0.000594206	
Sapu_001G178800.1	1.095	2.915E-04	EDF2,RAP2.8,RAV2,TEM2	B3 DNA-binding domain protein	Transcription	trans	repressor of flowering in long-day plants, activator of stress signal transduction pathways	UniProt	-0.391598244	-100.00%	0	
Sapu_002G007100.1	-1.278	1.980E-28	anthranilate N-benzoyltransferase, putative	Secondary Metabolism	trans	involved upstream of phytoalexin production	UniProt	-0.342897914	-30.44%	0.281239997		
Sapu_002G025600.1	0.286	2.109E-03	DFR,M318,TT3	dihydroflavonol 4-reductase	Secondary Metabolism	trans	Flavonoid metabolism	UniProt	-7.901753163	-18.12%	0.337520992	
Sapu_002G081900.1	-5.566	6.980E-118	transcription factor bHLH96	Transcription	trans	-	-	-	-0.003698966	-0.35%	0.496852821	
Sapu_002G137700.1	-1.189	4.190E-08	ATOMT1,OMT1	caffeinic acid O-methyltransferase	Secondary Metabolism	trans	Converts quercetin into isorhamnetin, methylates flavonoids and monoglucosides	UniProt	0.148111307	26.08%	0.403629538	
Sapu_003G027300.1	1.633	7.580E-116	Homeodomain-like superfamily protein	Transcription	trans	-	-	-	-5.508204805	-19.64%	0.0400617	
Sapu_003G047200.1	-0.214	1.302E-01	1	Myb-like transcription factor 2, putative	Transcription	trans	Involved in epidermal cell fate specification in roots and hypocotyl	UniProt	2.466524275	17.63%	0.410301084	
Sapu_003G069200.1	0.013	9.132E-01	ANACD02,ATAF1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	Transcription	trans	Response to wounding and abscisic acid	TAIR	-0.326061428	-21.65%	0.237971133	
Sapu_003G085800.1	-0.492	3.490E-01	AP2/ERF domain transcription factor	Transcription	trans	-	-	-	-0.400666216	-51.09%	0.400473393	
Sapu_003G115100.1	-0.786	2.550E-01	ATMYB67,ATY53,MYB67	transcription factor Myb protein	Transcription	trans	-	-	-0.005143045	-34.67%	0.416216558	
Sapu_003G133600.1	-1.086	1.620E-16	ATCHS,OH5,T4	chalcone synthase	Secondary Metabolism	trans	flavonoid biosynthesis, naringenin synthesis	UniProt	1.974074992	21.24%	0.362919979	
Sapu_003G149400.1	0.114	2.799E-01	ATST2A,ST2A	flavonol 4'-sulfotransferase, putative	Secondary Metabolism	trans	jasmonic acid metabolism	UniProt	8.272934231	10.03%	0.363014037	
Sapu_003G155500.1	-1.059	1.780E-53	SC1-3,SC1-3	saccharose-like 3	Transcription	trans	auxillary meristem regulation during vegetative and reproductive growth	TAIR; Uniprot	0.445794996	7.86%	0.364659646	
Sapu_004G007600.1	-0.886	3.280E-30	ADT1	aromatic dehydratase 1	Secondary Metabolism	trans	catalyzes aromatic to phenylalanine	TAIR; Uniprot	-1.013531596	-13.47%	0.361525243	
Sapu_004G013400.1	0.104	2.693E-01	CPC	Homeodomain-like superfamily protein	Transcription	trans	Determines epidermal cell fate, suppresses WER	UniProt	15.54322919	18.84%	0.337273285	
Sapu_004G016000.2	-0.124	8.633E-01	transcription factor bHLH123	Transcription	trans	-	-	-	-0.04558561	-56.93%	0.181542539	
Sapu_004G078800.1	-0.109	3.935E-01	CYP82G1	cytochrome P450, family 82, subfamily G, polypeptide 1	Secondary Metabolism	trans	homopetene biosynthesis, floral herbivory response	UniProt	0.067209669	1.37%	0.463605998	
Sapu_004G082600.1	-1.242	1.480E-27	LuxR transcriptional regulator, putative	Transcription	trans	-	-	-	0.088921054	1.89%	0.485279809	
Sapu_004G088900.1	-0.629	3.636E-01	ATWRKY7,WRKY7	WRKY DNA-binding protein 7	Transcription	trans	Calmodulin binding protein	TAIR	-0.061916709	-41.11%	0.358660197	
Sapu_004G089000.1	-0.370	6.169E-01	RRTF1	AP2/ERF domain transcription factor	Transcription	trans	-	-	0.145538835	433.93%	0.243465321	
Sapu_004G103400.1	-1.147	1.159E-04	AGL29	AGAMOUS-like 29	Transcription	trans	transcription factor, activated by MKC genes, suppresses 76 genes, suppressed by AGL18, high expression levels in pollen	TAIR; Verelst et al.	2007	-0.0091499	-1.20%	0.49441233
Sapu_004G104400.1	-1.565	1.640E-179	ATHB30,HB30,ZHD3	homeobox protein 30	Transcription	trans	-	-	0.759563089	2.07%	0.4841976	
Sapu_004G110200.1	-0.451	6.700E-05	MIF2	mini zinc finger 2	Transcription	trans	Ovary development and floral meristem determination	TAIR	-0.214518422	-1.44%	0.486538161	
Sapu_004G112000.3	0.056	NA	REM39,VRN1	B3 domain transcription factor VRN1	Transcription	trans	vernalization response and regulation of flower development	TAIR	-0.012603913	-27.86%	0.410562213	
Sapu_004G117100.1	-0.277	2.016E-01	ATRL6,RL6,RSM3	RAD-like 6	Transcription	trans	-	-	0.394572724	4.38%	0.480637996	
Sapu_004G124000.1	0.491	3.210E-06	SAUR-like auxin-responsive protein family	Hormone signaling	trans	-	-	-	21.31586427	41.21%	0.270397116	
Sapu_004G124300.1	0.147	1.876E-08	SAUR-like auxin-responsive protein family	Hormone signaling	trans	-	-	-	0.439203741	41.03%	0.385145291	
Sapu_004G124600.1	1.465	1.040E-08	SAUR-like auxin-responsive protein family	Hormone signaling	trans	-	-	-	-1.455155409	-23.51%	0.37049335	
Sapu_005G022400.1	-0.454	2.390E-05	ALY1,ATALY1	DIRP Myb-like DNA-binding domain	Transcription	trans	-	-	-0.212068128	-4.34%	0.469163483	
Sapu_005G057900.1	-1.987	1.976E-30	ATMYB93,MYB93	Myb-like DNA-binding domain protein	Transcription	trans	negative regulator of lateral root development, auxin response	UniProt	0.082635585	179.41%	0.317986668	
Sapu_005G077400.1	3.986	4.150E-30	anoc42,NAC042	NAC transcription factor 030	Transcription	trans	delays senescence	TAIR; Uniprot	-0.081157811	-38.19%	0.384642785	
Sapu_005G093200.1	-0.167	4.482E-01	winged-helix DNA-binding transcription factor family protein	Transcription	trans	-	-	-	-0.256349999	-6.48%	0.436227979	
Sapu_005G191800.1	0.401	3.373E-04	GASA1	gibberellin-regulated protein	Transcription	trans	xlym formation and secondary cell wall biosynthesis	UniProt	0.007492507	13.81%	0.445713995	
Sapu_006G089400.1	-0.919	7.050E-05	ATWRKY70,WRKY70	WRKY transcription factor	Transcription	trans	Involvement in seed germination and maturation and flowering	UniProt	-4.51255671	-60.65%	1.37E-09	
Sapu_006G118600.1	-0.145	1.640E-05	mediator of RNA polymerase II transcription subunit 20, putative	Transcription	trans	stress response, salicylic acid and jasmonic acid signalling	UniProt	0.885807794	32.67%	0.359298838		
Sapu_006G140600.1	0.860	5.430E-77	ATCOL5,COLS	CONSTANS-like 5	Development	trans	regulation of floral development	UniProt	-2.191113938	-10.90%	0.220112544	
Sapu_007G068100.1	-0.836	5.804E-03	ABS,AGL32,TT16	MADS-box DNA-binding domain transcription factor	Transcription; Floral Development	trans	regulates proanthocyanidin biosynthesis, involved in seed coat and ovule development, maternal role in fertilization and seed development,	TAIR	-0.034349935	-67.03%	0.221130563	
Sapu_007G074000.1	-1.407	4.500E-07	ATWRKY13,WRKY13	WRKY transcription factor, putative	Transcription	trans	transcription factor	TAIR	0.054450975	96.54%	0.185400858	
Sapu_008G107000.1	-0.608	8.200E-52	RGA,RGA1	DELLA domain GRAS family transcription factor GAI	Transcription; Hormone Signaling	trans	positive regulation of transcription, repressor of GA response, DELLA protein, restrains cell proliferation and expansion, represses vegetative and floral growth	TAIR; UniProt	4.825409314	18.72%	0.168531199	
Sapu_009G026400.1	0.034	7.898E-01	SAUR-like	gibberellin-regulated protein	Hormone signaling	trans	-	-	-0.351131744	-3.85%	0.459347878	
Sapu_009G039400.1	3.305	2.540E-17	ANACD02,ATAF1	NAC domain protein	Transcription	trans	Response to wounding and abscisic acid	TAIR	-0.071824254	-48.63%	0.30521124	
Sapu_009G044100.1	0.701	2.830E-24	cinnamyl-alcohol dehydrogenase-like protein	Secondary Metabolism	trans	in floral stem lignin biosynthesis	UniProt	-0.032843057	-86.43%	0.077113497		
Sapu_009G078200.1	0.008	9.008E-01	CCoAOMT1	caffeyl-CoA 3-O-methyltransferase	Secondary Metabolism	trans	phenylpropanoid biosynthesis	UniProt	-45.38773416	-13.72%	0.153140855	
Sapu_010G016400.1	2.353	1.050E-193	flavonol synthase/flavanone 3-hydroxylase, putative	Secondary Metabolism	trans	flavonols from dihydroflavonols, oxidation of naringenin to dihydrokaempferol, dihydrokaempferol to kaempferol	UniProt	-5.036553	-75.91%	1.43E-08		
Sapu_010G023900.1	-1.277	9.776E-02	DRN-LIKE_DRNLRS2,SOB2	DORNROSCHEIN-like	Transcription	trans	embryo patterning, gibberellin signaling	UniProt	0.060502114	271.92%	0.198818424	
Sapu_010G039800.1	0.444	3.700E-26	bHLH104	helix loop helix DNA-binding domain protein, putative	Transcription	trans	-	-	-0.246633148	-4.96%	0.410178102	
Sapu_010G040000.1	-0.065	9.536E-01	ethylene-responsive transcription factor ERF098, putative	Transcription	trans	stress response	UniProt	-0.030673055	-36.19%	0.376793639		
Sapu_010G076600.1	-1.287	3.400E-39	bHLH-MYC/R2R3-MYB transcription factor amino-terminal protein	Transcription	trans	-	-	-	2.242483938	3.99%	0.433517091	
Sapu_010G128900.1	5.719	0.000E+00	AGL30	AGAMOUS-like 30	Transcription	trans	pollen maturation and pollen tube growth	UniProt	-12.65705924	-91.60%	0	
Sapu_010G137700.4	0.045	NA	AS2	asymmetric leaves protein, putative	Transcription	trans	leaf symmetry and venation	UniProt	-0.002724643	-18.98%	0.474896427	
Sapu_010G139800.1	-1.163	1.350E-32	skiminate/quinate hydroxycinnamoyltransferase	Secondary Metabolism	trans	synthesizing and catabolizing hydroxycinnamoyesters. Influences flavonoid involved in transition to flowering, affects FLC expression levels, necessary for male development	UniProt	1.250874845	11.89%	0.424961582		
Sapu_010G149000.6	-1.362	3.850E-03	P90A1,DWF3	cytochrome P450 family 90 monoxygenase, putative	Secondary Metabolism	trans	TFL, positive regulation of transcription, negative regulation of FLC/MAF and positive regulation of FT, vegetative to reproductive phase transition, promotes flowering	TAIR; Dreni and Zhang 2016	0.077455955	189.65%	0.149530569	
Sapu_010G149700.1	-1.770	1.090E-09	AUX1,MAP1,PIR1,WAV5	auxin influx carrier-like protein	Hormone signaling	trans	Mediates auxin gradient in developing leaves	UniProt	-0.015571514	-29.05%	0.377083799	
Sapu_012G009500.1	-5.385	2.340E-119	LAS,SC1L	GRAS family transcription factor lateral protein	Transcription	trans	auxillary meristem regulation during vegetative and reproductive growth	TAIR; Uniprot	-0.013251576	-1.89%	0.473686538	
Sapu_012G020100.1	0.706	1.010E-20	CRF4	cytokinin response factor 4	Transcription	trans	cytokinin signaling, transcriptional activator, cotyledon, leaf and embryo development	UniProt	-1.06095952	-10.30%	0.354314831	
Sapu_012G062200.1	-0.895	1.291E-04	LOB	lateral organ boundaries-like protein	Transcription	trans	lateral organ development	TAIR	0.166310562	128.99%	0.155738116	
Sapu_012G096400.1	-3.575	1.630E-65	ABS,AGL32,TT16	MADS-box DNA-binding domain transcription factor	Transcription; Floral Development	trans	regulates proanthocyanidin biosynthesis, involved in seed coat and ovule development, maternal role in fertilization and seed development, transcription factor	TAIR	1.663209688	105.37%	0.106391536	
Sapu_012G120200.1	0.379	1.581E-01	AGL6	AGAMOUS-like 6	Transcription; Floral Development	trans	-	-	-	-	-	
Sapu_013G014002.0	0.437	1.247E-02	transcription factor VIP2, putative	Transcription	trans	Regulates gamma-tocopherol synthesis	UniProt	-0.024350455	-57.88%	0.305385573		
Sapu_013G099600.3	-4.206	3.980E-57	AGL11,STK	agamous MADS box factor transcription factor	Transcription; Floral Development	trans	Maternal control of endothelial formation and female gametophyte development	UniProt	0.180494016	34.52%	0.378988347	
Sapu_014G006800.1	-1.022	1.910E-142	WLM1	LIM transcription factor	Transcription	trans	Cytoskeleton organization	TAIR	-20.11691212	-13.32%	0.353855873	
Sapu_014G027100.1	-1.573	8.900E-07	CYP82C4	cytochrome P450 family protein	Secondary Metabolism	trans	flavonol glucoside biosynthesis	UniProt	1.963748981	12.85%	0.353394587	
Sapu_014G058300.1	-0.593	3.892E-01	HYR1	AP2/B3-like transcriptional factor family protein	Transcription	trans	flavonol glucoside biosynthesis	UniProt	-1.426100907	-13.14%	0.336091687	
Sapu_014G068900.1	0.069	6.019E-01	myb/SANT-like DNA-binding domain protein	Transcription	trans	-	-	-	1.614254318	29.21%	0.377476678	
Sapu_016G114900.1	-1.171	9.760E-88	LHW	transcription factor-related	Transcription	trans	Regulates root development and promotes stеле production	UniProt	8.469974273	29.3%	0.245840539	
Sapu_016G174500.3	0.054	NA	WLM1	transcription factor LIM1	Transcription	trans	Cytoskeleton organization	TAIR	0.069664186	880.30%	0.013696545	
Sapu_016G184400.1	-2.628	5.808E-05	ATTP521,TP521	terpene synthase 21	Secondary Metabolism	trans	Sesquiterpene synthases, produces beta-caryophyllene and alpha-humulene	TAIR	-0.05427384	-61.77%	0.29304533	
Sapu_016G273800.1	-0.516	5.710E-07	SCL5	scarecrow-like 5	Transcription	trans	Involved in plant development	UniProt	-2.685639609	-26.48%	0.1381	

Sapu.016G274000.1	-0.404	7.670E-07	PAT1	GRAS family transcription factor	Transcription	trans	mRNA decapping	TAIR	0.048750239	0.46%	0.494543761
Sapu.017G008600.1	-0.117	2.097E-01	ATGLK1,GLK1,GPRI1	golden-like transcription factor, putative	Transcription	trans	regulates chloroplast development	TAIR	-0.408862145	-6.90%	0.398002416
Sapu.017G014200.1	-1.142	3.480E-06	SGR7,SHR	GRAS family transcription factor	Transcription	trans	quiescent center cell specification	UniProt	0.158284491	79.53%	0.188161619
Sapu.017G015700.1	-0.769	7.520E-08	SGR7,SHR	GRAS family transcription factor	Transcription	trans	quiescent center cell specification	UniProt	-0.085590236	-9.65%	0.421828771
Sapu.017G067900.2	0.107	8.718E-01	ATHB13	Homeobox-leucine zipper protein family	Transcription	trans	involved in seed to seedling transition	TAIR	0.060825254	261.60%	0.076923906
Sapu.017G107600.1	-1.178	4.740E-34	AIMYB43,MYB43	myb domain protein 43	Transcription	trans	phenylpropanoid biosynthesis	TAIR	1.145767164	37.76%	0.182486866
Sapu.018G062500.1	-1.591	9.370E-64	TINY2	AP2/ERF domain transcription factor	Transcription	trans	stress response	UniProt	-1.008529935	-19.21%	0.314412226
Sapu.019G065400.1	1.678	5.130E-124	CYP71AA1	cytochrome P450 family protein	Hormone singaling	trans	Inactivation of early gibberellin intermediates	UniProt	-15.67688143	-46.21%	0.000609148
Sapu.019G074900.8	-5.779	5.380E-126	AGL11,STK	agamous MADS box factor transcription factor	Transcription; Floral Development	trans	Maternal control of endothelium formation and female gametophyte development	UniProt	0.913434876	203.65%	0.051954672
Sapu.019G112300.1	0.993	6.270E-85	BZIP transcription factor	Transcription	trans	-	-	-	-10.02029276	-25.77%	0.01178972
Sapu.015WG01900.1	-0.355	3.420E-44	ATO	splicing factor 3a subunit 3, putative	RNA splicing and regulation	trans	pre-splicosome formation, necessary for gametic cell fate determination component of RISC, involved in RNA post-transcriptional silencing via 21-22 nt RNAs	UniProt	-0.362459118	-0.85%	0.479573968
Sapu.15WG022500.3	0.018	NA	AGO1	argonaute protein 1B	RNA splicing and regulation	cis	-	UniProt	0.015845775	146.21%	0.260401514
Sapu.15WG023500.1	-0.594	8.810E-27	ATBT1F3,BTF3	basic transcription factor 3	Transcription	cis	seed development	TAIR; UniProt	-1.011411406	-0.81%	0.48800724
Sapu.15WG023800.1	-1.228	1.580E-20	anac057,NAC057	NAC transcription factor	Transcription	cis	-	-	-0.005397820	-0.68%	0.495612738
Sapu.15WG024100.1	-0.456	3.180E-19	EPRL1,VET7	Homeodomain-like superfamily protein	Transcription	cis	Modification of cell-wall structure	UniProt	2.190480682	13.38%	0.27192435
Sapu.15WG026400.1	1.645	1.470E-59	ATMBY52,BW52,MYB52	myb domain protein 52	Transcription	cis	Drought tolerance, secondary cell wall biosynthesis	UniProt	-0.227529133	-7.30%	0.463064695
Sapu.15WG031800.1	-5.340	1.360E-109	AIMYB6,MYB6	MYB-like transcription factor	Transcription	cis	-	-	-0.032636883	-4.84%	0.487818481
Sapu.15WG032500.1	-0.646	2.420E-48	AIMYB4R1,MYB4R1	Myb transcription factor, putative	Transcription	cis	regulates accumulation of UV protectant sinapoylmalate	TAIR; UniProt	-0.947710667	-17.94%	0.155123552
Sapu.15WG038800.1	-6.149	4.490E-292	PLATZ transcription factor family protein	Transcription	cis	-	-	-	NA	NA	NA
Sapu.15WG039100.1	-6.183	8.940E-158	PLATZ transcription factor family protein	Transcription	cis	-	-	-	NA	NA	NA
Sapu.15WG039400.1	-5.732	8.450E-124	PLATZ transcription factor family protein	Transcription	cis	-	-	-	-0.19635684	-20.22%	0.57106592
Sapu.15WG039600.1	-1.732	8.980E-29	PLATZ transcription factor family protein	Transcription	cis	-	-	-	0.408051975	17.42%	0.353073949
Sapu.15WG039700.1	-5.549	1.810E-115	PLATZ transcription factor family protein	Transcription	cis	-	-	-	0.971295514	68.66%	0.190619934
Sapu.15WG039800.1	-4.194	2.320E-62	PLATZ transcription factor family protein	Transcription	cis	-	-	-	0.294703766	20.73%	0.378742442
Sapu.15WG042400.1	-2.176	1.860E-138	ADT2	arogenate dehydratase 2	Secondary Metabolism	cis	catalyzes arogenate to phenylalanine	TAIR	-0.818118927	-56.55%	0.99424545
Sapu.15WG045900.1	-1.427	3.510E-09	anac058,NAC058	NAC transcription factor 005	Transcription	cis	nuclear and plasma membrane targeting	TAIR	0.025452877	13.36%	0.449794577
Sapu.15WG046800.1	-5.814	1.110E-143	WOX1	WUSCHEL related homeobox 1	Transcription; Floral Development	cis	Plant development	UniProt	0.995119791	55.44%	0.106423415
Sapu.15WG056200.1	-2.058	8.710E-12	ARR2,RR22	response regulator 22	Hormone singaling	cis	Involved in two-component cytokinin response	TAIR	-0.139820947	-61.12%	0.763291721
Sapu.15WG056300.1	-4.640	3.620E-83	WOX1	WUSCHEL related homeobox 1	Transcription; Floral Development	cis	Plant development	UniProt	0.320026593	69.74%	0.126632321
Sapu.15WG057600.1	-6.250	2.250E-148	ATTCP18,BRC1,TC18	transcription factor TCP24	Transcription	cis	regulates bud growth	TAIR; UniProt	0.542541753	82.82%	0.11704887
Sapu.15WG058800.1	-1.113	2.180E-20	constans-like zinc finger protein	Transcription; Floral Development	cis	constans-like zinc finger protein	TAIR; UniProt	-1.077553494	-35.55%	0.872601211	
Sapu.15WG060600.1	-1.119	8.240E-09	IDN2,RDM12	transcription factor XI-like protein	Transcription	cis	RDDM pathway, AGO4 dependent binding of lnc-RNA	UniProt	-0.015823678	-15.07%	0.602052562
Sapu.15WG062800.1	-7.630	4.500E-231	GATA15	GATA transcription factor 15	Transcription; Floral Development	cis	transcription factor, floral and vegetative development	TAIR	1.358814322	19.85%	0.291359137
Sapu.15WG065500.1	-0.066	7.959E-01	AtbZIP70,bZIP70	bZIP transcription factor	Transcription	cis	-	-	-0.500457344	-42.25%	0.77813865
Sapu.15WG073900.1	-2.847	3.750E-23	ARR17,RR17	response regulator 17	Hormone singaling	cis	Type-A cytokinin response regulator	TAIR	0.044790833	22.78%	0.410801924
Sapu.15WG074000.1	-4.056	3.410E-56	ARR17,RR17	response regulator 17	Hormone singaling	cis	Type-A cytokinin response regulator	TAIR	0.025216631	4.13%	0.475121304
Sapu.15WG074200.1	-2.806	5.030E-19	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase	Secondary Metabolism	cis	lignin biosynthesis	UniProt	-0.038179274	-42.04%	0.75570537
Sapu.15WG074400.1	-7.937	2.430E-24	AGO4,OCP11	Arogenate family protein	RNA splicing and regulation	cis	RDDM pathway	TAIR	0.472315512	12.44%	0.403556959
Sapu.15WG075200.1	-4.031	3.510E-55	ARR17,RR17	response regulator 17	Hormone singaling	cis	Type-A cytokinin response regulator	TAIR	0.033180883	5.46%	0.467423277
Sapu.15WG079800.1	-0.672	5.640E-64	APRR1,ATO1,PRR1,TOC1	timing of cab expression 1/PRR response regulator 1	Development	cis	Two component cytokinin response	UniProt	-5.345270439	-18.70%	0.933899357
Sapu.15WG084600.1	0.932	1.070E-47	1.HD-ZIP-1	homeobox 1	Transcription	trans	Leaf development, transcriptional activator	UniProt	8.681407324	17.29%	0.333599221
Sapu.15WG088100.2	0.522	1.380E-05	MYB	MYB transcription factor, putative	Transcription	trans	-	-	0.24983345	36.02%	0.329170612
Sapu.15WG100700.1	-0.308	3.618E-04	ATMBY86,MYB86	R2R3-MYB transcription factor, putative	Transcription	trans	sinapate ester production	UniProt	-0.124090837	-6.11%	0.572955811
Sapu.15WG121000.1	-0.657	1.280E-35	ARF1-BP,ARF2,HSS,ORE14	auxin response factor 2	Hormone Signaling; Floral Development	trans	promotes flowering and stamen development	UniProt	12.25471372	8.57%	0.35917787
Sapu.15ZG033300.5	-2.114	3.790E-15	ATPIN1,PN1	auxin efflux carrier component 1	Hormone Signaling	cis	Auxin gradient formation during organogenesis	UniProt	0.017395467	27.70%	0.379957203
Sapu.15ZG035700.1	-1.305	2.310E-24	AIMYB6,MYB6	MYB-like transcription factor	Transcription	cis	-	-	0.500036709	33.96%	0.24995866
Sapu.15ZG039200.1	-0.314	2.745E-03	ADT2	arogenate dehydratase 2	Secondary Metabolism	cis	catalyzes arogenate to phenylalanine	TAIR	0.040965123	2.49%	0.470061794
Sapu.15ZG048100.1	1.519	2.800E-07	anac058,NAC058	NAC transcription factor 005	Transcription	cis	nuclear and plasma membrane targeting	TAIR	0.811795248	140.34%	0.20895275
Sapu.15ZG048600.1	-7.267	0.000E+00	BEE3	transcription factor BEE	Transcription	cis	brassinosteroid signalling	TAIR; UniProt	3.927664448	24.30%	0.259643207
Sapu.15ZG053700.1	2.310	1.240E-34	AtbZIP70,bZIP70	bZIP transcription factor	Transcription	cis	-	-	1.064744139	35.48%	0.392857871
Sapu.15ZG055400.1	0.578	9.180E-08	ATTCP18,BRC1,TC18	transcription factor TCP24	Transcription	cis	Delays axillary bud outgrowth and development	UniProt	-0.090461807	-8.88%	0.56140319
Sapu.15ZG055800.1	0.658	4.020E-72	AP2/B3-like transcription factor family protein	Transcription	cis	-	-	-	-0.294764643	-2.76%	0.538203755
Sapu.T004700.1	-0.758	1.240E-17	AtWRKY20,WRKY20	WRKY transcription factor	Transcription	trans	-	-	2.558173434	14.98%	0.022182773
Sapu.T004800.2	-1.076	9.248E-04	SCL5	scarecrow-like 5	Transcription	trans	Involved in plant development	UniProt	0.037533222	128.96%	0.132970903
Sapu.T077300.1	1.342	1.290E-12	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3	Secondary Metabolism	trans	xanthophyll biosynthesis, hydroxylates beta rings of beta carotene	UniProt	0.149471863	4.47%	0.476844747
Sapu.T078000.1	1.440	2.950E-28	ATO	splicing factor-related	RNA splicing and regulation	trans	pre-splicosome formation, necessary for gametic cell fate determination	UniProt	0.553787679	33.24%	0.325143777
Sapu.T078100.1	1.418	1.060E-07	CYP97B3	cytochrome P450, family 97, subfamily B, polypeptide 3	Secondary Metabolism	trans	xanthophyll biosynthesis, hydroxylates beta rings of beta carotene	UniProt	0.018230052	2.13%	0.490838807
Sapu.T168300.1	-0.211	9.064E-01	PLATZ transcription factor family protein	Transcription	trans	-	-	-	-0.000894472	-16.26%	0.522513077