

Sapur.016G274000.1	-0.404	7.670E-07	PAT1	GRAS family transcription factor	Transcription	trans	mRNA decapping	TAIR	0.048750239	0.46%	0.494543761
Sapur.017G008600.1	-0.117	2.097E-01	ATGLK1,GLK1,GPR11	golden-like transcription factor, putative	Transcription	trans	regulates chloroplast development	TAIR	-0.408862145	-6.90%	0.398002416
Sapur.017G014200.1	-1.142	3.480E-06	SGR7,SHR	GRAS family transcription factor	Transcription	trans	quiescent center cell specification	UniProt	0.158284491	79.23%	0.18851619
Sapur.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
Sapur.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%	0.076929306
Sapur.017G107600.1	-1.178	4.740E-34	ATMYB43,MYB43	myb domain protein 43	Transcription	trans	phenylpropanoid biosynthesis	TAIR	1.145767164	37.76%	0.182486866
Sapur.018G062500.1	-1.591	9.370E-64	TW2	AP2/ERF domain transcription factor	Transcription	trans	stress response	UniProt	-1.008529935	-19.21%	0.314412226
Sapur.019G065400.1	1.678	5.130E-124	CYP74A1	cytochrome P450 family protein	Hormone signaling	trans	Inactivation of early gibberellin intermediates	UniProt	-15.67688143	-46.21%	0.000609148
Sapur.019G074900.8	-5.779	5.390E-126	AGL11,STK	agnamous 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
Sapur.019G112000.1	0.993	6.270E-85		BZIP transcription factor	Transcription	trans		-	-10.02029276	-25.77%	0.011738972
Sapur.15WG012900.1	-0.355	3.420E-44	ATO	splicing factor 3a subunit 3, putative	RNA splicing and regulation	trans	pre-spliceosome 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
Sapur.15WG022500.3	0.018	NA	AGO1	argonate protein 1B	RNA splicing and regulation	cis	regulates bud growth	UniProt	0.015845775	146.21%	0.26040154
Sapur.15WG023500.1	-0.594	8.810E-27	ATBTF3,BTF3	basic transcription factor 3	Transcription	cis	seed development	TAIR; UniProt	-1.011411406	-0.81%	0.48800724
Sapur.15WG023800.1	-1.228	1.580E-20	anak057,NAC057	NAC transcription factor	Transcription	cis		-	-0.00539782	-0.68%	0.495612738
Sapur.15WG024100.1	-0.456	3.180E-19	EP1,VE7	Homeodomain-like superfamily protein	Transcription	cis	Modification of cell-wall structure	UniProt	2.190480682	13.38%	0.27192435
Sapur.15WG026400.1	1.645	1.470E-59	ATMYB52,BWS2,MYB52	myb domain protein 52	Transcription	cis	Drought tolerance, secondary cell wall biosynthesis	UniProt	-0.227529133	-7.30%	0.463064695
Sapur.15WG031800.1	-5.340	1.360E-109	ATMYB6,MYB6	MYB-like transcription factor	Transcription	cis		-	-0.032636883	-4.84%	0.487818481
Sapur.15WG032500.1	-0.646	2.420E-48	ATMYB41,MYB41	Myb transcription factor, putative	Transcription	cis	regulates accumulation of UV protectant sinapoylmalate	TAIR; UniProt	-0.947710667	-17.94%	0.155123552
Sapur.15WG038800.1	-6.149	4.490E-292		PLATZ transcription factor family protein	Transcription	cis		-	NA	NA	NA
Sapur.15WG039100.1	-6.183	8.940E-158		PLATZ transcription factor family protein	Transcription	cis		-	NA	NA	NA
Sapur.15WG039400.1	-5.732	8.450E-124		PLATZ transcription factor family protein	Transcription	cis		-	-0.19635684	-20.72%	0.57106592
Sapur.15WG039600.1	-1.732	8.980E-29		PLATZ transcription factor family protein	Transcription	cis		-	0.408051975	17.42%	0.353073949
Sapur.15WG039700.1	-5.549	1.810E-115		PLATZ transcription factor family protein	Transcription	cis		-	0.971295514	68.66%	0.19061934
Sapur.15WG039800.1	-4.194	2.320E-62		PLATZ transcription factor family protein	Transcription	cis		-	0.294703766	20.73%	0.378742442
Sapur.15WG042400.1	-2.176	1.860E-138	ADT2	argonate dehydratase 2	Secondary Metabolism	cis	catalyzes argenolate to phenylalanine	TAIR	-0.818118927	-56.55%	0.994724545
Sapur.15WG045900.1	-1.427	3.510E-09	anak058,NAC058	NAC transcription factor 005	Transcription	cis	nuclear and plasma membrane targeting	TAIR	0.025452877	13.96%	0.449794577
Sapur.15WG046800.1	-5.814	1.110E-143	WDX1	WUSCHEL related homeobox 1	Transcription; Floral Development	cis	Plant development	UniProt	0.995119791	55.44%	0.106423415
Sapur.15WG056200.1	-2.058	8.710E-12	ARR2,RR22	response regulator 22	Hormone signaling	cis	Involved in two-component cytokinin response	TAIR	-0.139820947	-61.12%	0.763291721
Sapur.15WG056300.1	-4.640	3.620E-83	WDX1	WUSCHEL related homeobox 1	Transcription; Floral Development	cis	Plant development	UniProt	0.320026593	69.74%	0.126632321
Sapur.15WG057600.1	6.250	2.350E-148	ATTCP18,BRC1,TCP18	transcription factor TCP24	Transcription	cis	regulates bud growth	TAIR; UniProt	0.542541753	82.82%	0.117104887
Sapur.15WG058800.1	-1.113	2.180E-20		constans-like zinc finger protein	Transcription; Floral Development	cis	transcription factor, regulation of flowering, acts on SOC1, FT, TFL, photoreceptor regulated, could be sexually antagonistic gene, upstream of flowering pathway, could be regulating many other genes	TAIR; UniProt	-1.077559494	-35.75%	0.87260121
Sapur.15WG060600.1	-1.119	8.240E-09	IDN2,ADM12	transcription factor X1-like protein	Transcription	cis	RDDM pathway, AGO4 dependant binding of Inc-RNA	UniProt	-0.015823678	-15.07%	0.602052562
Sapur.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
Sapur.15WG065500.1	-0.066	7.959E-01	AtbZIP70,bZIP70	bZIP transcription factor	Transcription	cis		-	-0.500457344	-42.25%	0.77813865
Sapur.15WG073900.1	-2.847	3.750E-23	ARR17,RR17	response regulator 17	Hormone signaling	cis	Type-A cytokinin response regulator	TAIR	0.044790833	22.78%	0.410801924
Sapur.15WG074000.1	-4.056	3.410E-56	ARR17,RR17	response regulator 17	Hormone signaling	cis	Type-A cytokinin response regulator	TAIR	0.025216631	4.13%	0.475112304
Sapur.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
Sapur.15WG074400.1	-7.937	2.430E-240	AGO4,DCP11	Argonaute family protein	RNA splicing and regulation	cis	RDDM pathway	TAIR	0.472315512	12.44%	0.403356956
Sapur.15WG075200.1	-4.031	3.510E-55	ARR17,RR17	response regulator 17	Hormone signaling	cis	Type-A cytokinin response regulator	TAIR	0.033180883	5.46%	0.467423277
Sapur.15WG079800.1	-0.672	5.640E-64	APRR1,ATDCL1,PRR1,TOC1	timing of cab expression 1/PRR response regulator 1	Transcription; Floral Development	cis	Two component cytokinin response	UniProt	-5.345270439	-18.70%	0.933899357
Sapur.15WG084600.1	0.932	1.070E-47	1,HD-ZIP1	homeobox 1	Transcription	trans	Leaf development, transcriptional activator	UniProt	8.681407324	17.29%	0.333599211
Sapur.15WG088100.2	0.522	1.380E-05		MYB transcription factor, putative	Transcription	trans		-	0.24983345	36.02%	0.329170612
Sapur.15WG100700.1	-0.308	3.618E-04	ATMYB86,MYB86	R2R3-MYB transcription factor, putative	Transcription	trans	sinapate ester production	UniProt	-0.124090837	-6.11%	0.572955811
Sapur.15WG112100.1	-0.657	1.280E-35	ARR1-8P,ARR2,HSS,ORE14	auxin response factor 2	Hormone Signaling; Floral Development	trans	promotes flowering and stamen development	UniProt	12.25471372	8.57%	0.35917787
Sapur.15ZG033300.5	-2.114	3.790E-15	ATPIN1,PIN1	auxin efflux carrier component 1	Hormone Signaling	cis	Auxin gradient formation during organogenesis	UniProt	0.017399467	27.70%	0.379957203
Sapur.15ZG035700.1	-1.305	2.310E-24	ATMYB6,MYB6	MYB-like transcription factor	Transcription	cis		-	0.500036709	33.96%	0.24995866
Sapur.15ZG039200.1	-0.314	2.745E-03	ADT2	argonate dehydratase 2	Secondary Metabolism	cis	catalyzes argenolate to phenylalanine	TAIR	0.040965123	2.49%	0.470061794
Sapur.15ZG048100.1	1.519	2.800E-07	anak058,NAC058	NAC transcription factor 005	Transcription	cis	nuclear and plasma membrane targeting	TAIR	0.811795248	140.34%	0.209895275
Sapur.15ZG048600.1	-7.267	0.000E+00	BEE3	transcription factor BEE	Transcription	cis	brassinosteroid signalling	TAIR; UniProt	3.927666448	24.30%	0.259643207
Sapur.15ZG053700.1	2.310	1.240E-34	AtbZIP70,bZIP70	bZIP transcription factor	Transcription	cis		-	1.064744139	35.48%	0.392857871
Sapur.15ZG055400.1	0.578	9.180E-08	ATTCP18,BRC1,TCP18	transcription factor TCP24	Transcription	cis	Delays axillary bud outgrowth and development	UniProt	-0.090461807	-8.88%	0.569140319
Sapur.15ZG055800.1	0.658	4.020E-72		AP2/B3-like transcriptional factor family protein	Transcription	cis		-	-0.294764643	-2.76%	0.538203755
Sapur.T004700.1	-0.758	1.240E-137	ATWRK20,WRKY20	WRKY transcription factor	Transcription	trans		-	2.558173434	14.98%	0.022182773
Sapur.T004800.2	-1.076	9.248E-04	SC5	scarecrow-like 5	Transcription	trans	Involved in plant development	UniProt	0.037533222	128.96%	0.132970903
Sapur.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
Sapur.T078000.1	1.440	2.950E-28	ATO	splicing factor-related	RNA splicing and regulation	trans	pre-spliceosome formation, necessary for gametic cell fate determination	UniProt	0.553787679	33.24%	0.325143777
Sapur.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
Sapur.T168300.1	-0.211	9.064E-03		PLATZ transcription factor family protein	Transcription	trans		-	-0.000894472	-16.26%	0.522513077