

AGI	Annotation	Log2FC	pvalue	Description	REF6-binding site	epigenetic profile	Ethylene	Induced during
AT3G48350	CEP3	-6.7517	1E-40	Involved in starvation-related responses	Y	single H3K27me3		Y
AT3G48740	SWEET11	-5.0262	2E-108	member of the SWEET sucrose efflux transporter family proteins	Y	single H3K27me3		Y
AT1G34510		-4.7075	4E-06	Peroxidase superfamily protein	Y	single H3K27me3		
AT1G78090	TPPB	-4.6542	1E-16	homologous to the C-terminal part of microbial trehalose-6-phosphate phosphatases	Y	single H3K27me3		
AT3G56620	UMAMIT10	-3.6672	1E-134	nodulin MtN21-like transporter family protein	Y	single H3K27me3	Y	Y
AT3G30180	CYP85A2	-3.3989	0	cytochrome p450 enzyme that catalyzes the last reaction in the production of brassinolide	Y	single H3K27me3	Y	Y
AT1G47510	5PTASE11	-3.2795	2E-07	phosphatidylinositol polyphosphate 5-phosphatase	Y	single H3K27me3		
AT5G49270	COBL9	-3.257	0.0082	Involved in successfully establishing tip growth in root hairs	Y	single H3K27me3		
AT1G05240	PR9	-3.0429	4E-07	Peroxidase superfamily protein	Y	single H3K27me3	Y	
AT5G49770		-2.9563	2E-11	Leucine rich receptor kinase	Y	single H3K27me3		Y
AT1G30990		-2.9397	0.0325	Polyketide cyclase/dehydrase and lipid transport superfamily protein	Y	single H3K27me3		
AT5G45090	PP2-A7	-2.8767	2E-10	phloem protein 2-A7	Y	single H3K27me3		
AT3G26210	CYP71B23	-2.7183	4E-74	putative cytochrome P450	Y	single H3K27me3		Y
AT2G39410	MAGL7	-2.6411	4E-08	alpha/beta-Hydrolases superfamily protein	Y	single H3K27me3		
AT2G47540		-2.4988	0.0305	Pollen Ole e 1 allergen and extensin family protein	Y	single H3K27me3		
AT4G37070	PLP1	-2.4772	0.0009	Patatin-related phospholipase A	Y	single H3K27me3		
AT4G23450	AIRP1	-2.4157	6E-12	C3H2C3-type RING E3 Ub ligase	Y	single H3K27me3		
AT1G70440	SRO3	-2.318	4E-24	protein with similarity to RCD1 but without the WWE domain	Y	single H3K27me3		
AT4G34580	COW1	-2.297	0.0013	phosphatidylinositol transfer protein	Y	single H3K27me3		
AT1G74080	MYB122	-2.2785	7E-08	putative transcription factor, member of the R2R3 factor gene family	Y	single H3K27me3		
AT1G07690		-2.1702	1E-80	transmembrane protein	Y	single H3K27me3		Y
AT5G46960	INVINH1	-2.1555	0	Pectin methylesterase inhibitor that is involved in resistance to Botrytis cinerea	Y	single H3K27me3		
AT2G35585		-2.133	1E-15	cystic fibrosis transmembrane conductance regulator	Y	single H3K27me3		
AT5G44390	BBE25	-2.12	4E-16	FAD-binding Berberine family protein	Y	single H3K27me3	Y	
AT2G38940	PHT1;4	-2.0429	4E-219	member of the Pht1 family of phosphate transporters	Y	single H3K27me3		Y
AT5G47330		-2.0184	1E-12	alpha/beta-Hydrolases superfamily protein	Y	single H3K27me3	Y	Y
AT1G21360	GLTP2	-1.9427	0.0029	glycolipid transfer protein	Y	single H3K27me3	Y	Y
AT2G26290	ARSK1	-1.9085	3E-16	root-specific kinase 1	Y	single H3K27me3		Y
AT2G32150		-1.8523	2E-184	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	Y	single H3K27me3		Y
AT3G49580	LSU1	-1.83	6E-13	response to low sulfur 1	Y	single H3K27me3		
AT3G52920		-1.8191	1E-74	transcriptional activator	Y	single H3K27me3		Y
AT1G53990	GLIP3	-1.794	8E-08	Contains lipase signature motif and GDSL domain	Y	single H3K27me3		
AT4G02075	PIT1	-1.7851	5E-09	RING/FYVE/PHD zinc finger superfamily protein	Y	single H3K27me3		Y
AT3G16470	JR1	-1.6975	0.0379	JA-responsive gene that coordinates with GRP7	Y	single H3K27me3		
AT1G75580	SAUR51	-1.6813	1E-21	SAUR-like auxin-responsive protein family	Y	single H3K27me3	Y	Y
AT3G47540		-1.6665	9E-33	Chitinase family protein	Y	single H3K27me3		Y
AT5G04230	PAL1	-1.6036	3E-27	Phenylalanine ammonialyase (PAL) gene family	Y	single H3K27me3		Y
AT1G61740		-1.6011	3E-79	Sulfite exporter TauE/SafE family protein	Y	single H3K27me3		Y
AT3G22740	HMT3	-1.5418	0.012	homocysteine S-methyltransferase	Y	single H3K27me3		
AT2G41380		-1.517	3E-35	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	Y	single H3K27me3		Y
AT5G11060	KNAT4	-1.4592	6E-06	member of Class II KN1-like homeodomain transcription factors	Y	single H3K27me3		
AT5G38010		-1.324	0.0391	UDP-Glycosyltransferase superfamily protein	Y	single H3K27me3		
AT1G28190		-1.2967	2E-10	hypothetical protein	Y	single H3K27me3	Y	Y
AT5G51580		-1.291	0.0456	hypothetical protein	Y	single H3K27me3		
AT1G05000	PFA-DSP1	-1.2769	1E-91	atypical dual-specificity phosphatase	Y	single H3K27me3	Y	Y
AT3G21230	4CL5	-1.276	0.0008	4-coumarate coenzyme A ligase being able to use sinapate as substrate	Y	single H3K27me3		
AT2G39350	ABCG1	-1.2717	6E-60	Belongs to a clade of five Arabidopsis thaliana ABCG half-transporters	Y	single H3K27me3	Y	Y
AT1G72490	DRO1	-1.2631	0.0004	member of the IGT gene family	Y	single H3K27me3		
AT1G31540		-1.2506	1E-80	Disease resistance protein (TIR-NBS-LRR class) family	Y	single H3K27me3		
AT4G19810	CHIC	-1.2502	1E-118	Class V chitinase that is a part of glycoside hydrolase family 18 based on CAZy groupings	Y	single H3K27me3		Y
AT1G14890		-1.2493	5E-11	Plant invertase/pectin methylesterase inhibitor superfamily protein	Y	single H3K27me3	Y	
AT1G13260	EDF4	-1.2457	1E-75	AP2/B3 domain transcription factor	Y	single H3K27me3		Y
AT3G51720		-1.2409	5E-27	WEB family protein	Y	single H3K27me3		Y
AT1G66090		-1.2273	6E-15	Disease resistance protein (TIR-NBS class)	Y	single H3K27me3		Y
AT2G17540		-1.1944	9E-15	hypothetical protein	Y	single H3K27me3		
AT4G13345	MEE5	-1.1732	2E-51	Serinc-domain containing serine and sphingolipid biosynthesis protein	Y	single H3K27me3	Y	Y
AT2G23770	LYK4	-1.1561	4E-19	putative LysM-containing receptor-like kinase	Y	single H3K27me3		Y
AT5G02780	GSTL1	-1.064	0.0002	member of the lambda family of glutathione transferases	Y	single H3K27me3		Y
AT3G49110	PRX33	-1.0159	0.0356	Class III peroxidase	Y	single H3K27me3		
AT4G19230	CYP707A1	0.66799	2E-16	CYTOCHROME P450	Y	no	Y	Y
AT2G29090	CYP707A2	2.55868	5E-48	CYTOCHROME P450		no	Y	
AT5G45340	CYP707A3	0.88362	0.0024	CYTOCHROME P450	Y	no		Y
AT3G19270	CYP707A4	0.7237	1	CYTOCHROME P450		double H3K27me3/H3K9me2		
AT2G19590	ACO1	-0.0543	0.5298	ACC oxidase 1	Y	no	Y	Y
AT1G62380	ACO2	-2.2565	3E-183	ACC oxidase 2	Y	no	Y	
AT1G12010	ACO3	-0.4554	1	ACC oxidase 3		no	Y	
AT1G05010	ACO4	-2.5025	1E-239	ACC oxidase 4	Y	no	Y	Y
AT1G77330	ACO5	-1.9734	1E-85	ACC oxidase 5	Y	no	Y	Y
AT3G61510	ACS1	-0.032	1	ACC synthase 1		no		
AT1G01480	ACS2	0.73224	0.044	ACC synthase 2		no		
AT5G28360	ACS3	-	-	ACC synthase 3		no		
AT2G22810	ACS4	1.51337	0.6134	ACC synthase 4		single H3K27me3		
AT5G65800	ACS5	0.01979	1	ACC synthase 5	Y	double H3K27me3/H3K9me2	Y	
AT4G11280	ACS6	0.2446	0.0002	ACC synthase 6		no		Y
AT4G26200	ACS7	-0.6353	3E-20	ACC synthase 7		no		Y
AT4G37770	ACS8	0.10458	1	ACC synthase 8		no		
AT3G49700	ACS9	-0.032	1	ACC synthase 9	Y	no		
AT1G62960	ACS10	0.02626	1	ACC synthase 10	Y	no		Y
AT4G08040	ACS11	-0.6882	1	ACC synthase 11	Y	no		
AT5G51690	ACS12	-0.0056	1	ACC synthase 12		no		