

Supplementary Table S1. Blue module genes that were significantly correlated with CsESE3 in WT and DEV.

Gene TD	Gene Name	DEV.c or.ES E3	WT. Cor. ESE3	Annotation	Pathway	KO.N umber	BestHit in Arabidopsis
Cs7g06120	ESE3	1	1	Ethylene-responsive transcription factor	Wax	-	AT5G25190
Wax biosynthesis							
Cs1g02760	CER1	0.94	0.90	Protein WAX2	Wax	K15404	AT1G02205
Cs4g02580	CER3	0.93	0.92	Long-chain-alcohol O-fatty-acyltransferase family Oleoyl-acyl	Wax		
Cs4g09520	AT5	0.97	0.94	carrier protein thioesterase Fatty acyl-CoA reductase 2	Wax	-	AT5G55340
Cs5g27720	FATA	0.93	0.72		Wax	K10782	AT3G25110
Cs6g12890	FAR	1.00	0.73		Wax	K13356	AT3G11980
Jasmonic acid related genes							
Cs1g17210	JAZ1(b)	1.00	0.61	Linoleate 13S-lipoxygenase 3-1	Jasmonic Acid	K13464	AT1G19180
Cs1g17220	JAZ1(a)	1.00	0.49	Alpha/beta-hydrolase domain-containing protein	Jasmonic Acid	K13464	AT1G19180
Cs1g17380	LOX3	0.96	0.37	Alpha/beta-hydrolase domain-containing protein	Jasmonic Acid	K13464	AT1G17420
Cs2g03240	JAZ8	1.00	0.60	Allene oxide	Jasmonic Acid	-	AT1G30135

Cs2g28830	PLIP1	0.98	0.56	Jasmonate O-methyltransferase 12-	ic Acid_	-	AT3G61680
orange1.1t0165	PLIP2	0.99	0.37	oxophytodi enoate reductase 2 Putative 12-	ic Acid_	-	AT1G02660
Cs3g24230	AOS	0.98	0.47	oxophytodi enoate reductase 12-	ic Acid_K01723		AT5G42650
Cs3g25140	JMT	0.99	0.43	oxophytodi enoate reductase 2	ic Acid_	-	AT1G19640
Cs5g17900	OPR	0.95	0.36	Protein TIFY 10A	ic Acid_K05894		AT1G76690
Cs5g17920	OPR	0.97	0.36	Protein TIFY 10A	ic Acid_K05894		AT1G76690
Cs5g30350	DAD1-like	0.87	0.52	Protein TIFY 5A	ic Acid_	-	AT1G06800
Cs7g02820	JAZ10	0.97	0.36	Protein TIFY 9	ic Acid_K13464		AT5G13220

Phospholipid metabolism

Cs3g14580	Lipase	0.93	0.26	Alpha/beta -hydrolase domain- containing protein	Lipase	-	AT3G05600
Cs3g23440	Lipase	1.00	0.60	Lipase	Lipase	-	AT5G42930
Cs7g09100	Lipase	0.98	0.55	Alpha/beta -hydrolase domain- containing protein Palmitoyl- monogalact osyldiacylg lycerol delta-7 desaturase	Lipase	-	AT1G10740
Cs1g12430	FAD5	0.93	0.60		Lipid_K20416		AT3G15850

Cs2g13110	LPP3	0.99	0.87	Lipid phosphate phosphatase 3,	Lipid K18693	AT3G02600
Cs2g13440	PSS1	0.98	0.27	Phosphatidylserine synthase 2	Lipid K08730	AT1G15110
Cs5g11570	DGK	0.93	0.31	Diacylglycerol kinase	Lipid K00901	AT5G07920
Ethylene biosynthesis						
Cs1g21210	ACS8	0.97	0.75	1-aminocyclopropane-1-carboxylate synthase 8	ethylene_re K01762	AT4G37770
Cs4g13490	ACS7	0.95	0.64	1-aminocyclopropane-1-carboxylate synthase 1	ethylene_re -	AT4G26200
Others						
Cs6g21350	GALT1	0.98	0.85		Other K14413	AT1G26810
Cs6g22150	UGT	-0.87	0.00		Other	AT3G02100
Cs7g25890	UDP-glycosyltransferase 89B1;	0.97	0.41		Other	AT1G73880
Cs2g25450	Peroxidase 55	1.00	0.61	Phenylpropanoid b	K00430	AT5G14130
Cs4g03740	Peroxidase 16	0.98	0.52	Phenylpropanoid b	K00430	AT2G18980
Cs5g18010	Flavone 3'-O-methyltransferase 1	0.94	0.45	Phenylpropanoid b	K13066	AT5G54160
Cs5g18050	Flavone 3'-O-methyltransferase 1	0.90	-0.25	Phenylpropanoid b	K13066	AT5G54160
Cs7g08070	Peroxidase 6	0.99	0.40	Phenylpropanoid b	-	AT1G24110
Cs1g18240	INV	0.87	0.52	Starch and sucrose	K01193	AT3G13790
Cs2g07720	GPT2	1.00	0.38	Starch and sucrose	K05350	AT1G61800
Cs4g02730	ATTPS11	0.93	0.34	Starch and sucrose	K16055	AT2G18700
Cs5g19060	SPS4	1.00	1.00	Starch and sucrose	K00696	AT4G10120

Cs1g20580	TPS	0.94	0.52	TerpenoidK23232	AT4G37990
Cs2g08460	LUP2	0.99	0.68	TerpenoidK15813	AT1G78960
orange1.1t0563	TPS	0.89	0.93	Terpenoid	- AT5G23960
Cs1g21000	Transcription factor bHLH25	1.00	0.56	TF_bHLH	- AT4G37850
Cs9g08460	bHLH92	1.00	0.46	TF_bHLH	- AT5G43650
Cs4g09770	ERF7	0.77	0.80	TF_ERF	K09286 AT3G20310
Cs5g02340	ERG061	0.92	0.61	TF_ERF	- AT1G64380
Cs5g33540	ERFRap2-3	0.63	0.95	TF_ERF	K09286 AT3G16770
Cs8g05910	ERF109	0.99	0.56	TF_ERF	- AT4G34410
Cs9g16820	ERF026	0.90	0.56	TF_ERF	- AT5G52020
orange1.1t0529	ERF114	0.71	0.54	TF_ERF	- AT5G61890
Cs3g21660	ERF112	1.00	0.40	TF_ERF1	- AT2G33710
Cs3g23270	RAP2-1	0.93	0.72	TF_ERF1	K09286 AT1G46768
Cs3g23070	myb domain protein	0.81	0.97	TF_Myb	K09422 AT5G67300
Cs4g12760	Myb63	0.96	0.52	TF_Myb	K09422 AT1G79180
orange1.1t0033	MYB39	-0.96	-0.86	TF_Myb	K09422 AT3G61250
Cs1g08440	NAC	0.97	0.41	TF_NAC	- AT1G01720
Cs5g26150	NAC100	0.77	0.45	TF_NAC	- AT5G18270
Cs2g02790	WRKY42	1.00	0.60	TF_WRK	- AT4G04450
Cs2g06950	Myb102	0.99	0.34	TF_WRK	K09422 AT4G21440
Cs2g07040	Mb4	0.98	0.63	TF_WRK	K09422 AT2G31180
Cs5g02440	WRKY30	0.98	0.42	TF_WRK	- AT4G11070
Cs5g24240	wrk19	1.00	0.79	TF_WRK	- AT4G12010
Cs9g02040	WRKY 48	0.99	0.66	TF_WRK	- AT5G49520

Cs6g09960	LTP	0.99	0.87	Transport	-	AT2G38540
Cs5g09390	LTP	0.91	0.48	Transport	-	AT1G62790
Cs6g15290	ABG39	0.99	0.41	Transport	-	AT1G66950
Cs6g18090	ABC transporter	0.84	0.80	Transport	-	AT3G03280
orange1.1t0176	ABCB	0.99	0.65	Transport	K05658	AT2G47000
Cs1g20510	UGT	0.98	0.55	UGT	-	AT2G22590
Cs3g18090	UGT85A2	0.89	0.27	UGT	-	AT1G22360
Cs8g05320	UGT73B4	0.75	0.37	UGT	K14595	AT2G15490
Cs8g19260	UGT76E2	0.98	0.83	UGT	-	AT5G59590
Cs9g16640	UGT76B1	1.00	0.84	UGT	-	AT3G11340
Cs2g03270	NCED5	0.92	0.54	ABA_rela	K09840	AT1G30100
Cs6g19380	Abscisic acid 8'-hydroxylase	1.00	0.92	ABA_rela	K09843	AT4G19230
Cs2g28730	CSLC4	0.99	0.92	Cell Wall	K20887	AT3G28180
Cs3g09000	CSLD3	0.97	0.49	Cell Wall	K20924	AT3G03050
Cs4g03050	XTH23(a)	1.00	0.98	Cell Wall	K14504	AT4G25810
Cs4g03130	XTH23(b)	1.00	1.00	Cell Wall	K14504	AT4G25810
Cs4g03140	XTH22	1.00	0.97	Cell Wall	K14504	AT5G57560
Cs1g22140	GH3.1	1.00	0.91	IAA_signal	K14487	AT2G14960
Cs8g04610	GH3.1	0.76	0.24	IAA_signal	K14487	AT2G14960