

Involvement of the miR156/SPL module in flooding response in *Medicago sativa*

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Table S1. List of primers used in the study

No.	Gene name	Abbreviation	Forward primer sequence	Reverse primer sequence	Plant	Use	Source
1	miR156	miR156	cctatctctgctgtgacct	agcaccacctccaataacata	<i>Arabidopsis</i>	qRT-PCR	
2	KIN10 (At3g01090)	KIN10	agaatgatggcactgtgacg	acaggtgaagcaacgctt	<i>Arabidopsis</i>	qRT-PCR	Baena-González et al., 2007
3	KIN11(At3g29160)	KIN11	ccgtgtccaagtggtactc	acatgtcaggaatccagtg	<i>Arabidopsis</i>	qRT-PCR	Baena-González et al., 2008
4	senescence-associated protein 1, DIN1 (At4g35770)	DIN1	cagagtcggatcaggaatgg	atttgaccgtctccaacc	<i>Arabidopsis</i>	qRT-PCR	Baena-González et al., 2009
5	DIN3 (At3g06850)	DIN3	tcagctcgtcatctgtttgc	atcaaatgtggagggtgaac	<i>Arabidopsis</i>	qRT-PCR	Baena-González et al., 2010
6	glutamine-dependent asparagine synthetase dark inducible 6 (At3g47340)	DIN6	aacttgcgcagatcaagg	ggaacacgtgccttagtcc	<i>Arabidopsis</i>	qRT-PCR	Baena-González et al., 2011
7	raffinose synthase familydarkinducible 10 (At5g20250)	DIN10	gattcttctgtctgctgacct	ttagcaagctgacaccatcac	<i>Arabidopsis</i>	qRT-PCR	Baena-González et al., 2012
8	SNF1-related kinase (Medtr1g034030)	SnRK1	ggagaccctgcacagagaat	ctgaaactgctcgttgtt	<i>M. truncatula</i>	qRT-PCR	
9	SNF1 alpha kin 11 (Medtr6g048250)	SnRK1-KIN11	ttctggttgagccgtatcc	gttgctctattcctactctt	<i>M. truncatula</i>	qRT-PCR	
10	SNF1-related kinase beta (Medtr5g098510)	SnRK1-b1	ggccttctaagagtaggtcaa	actcaggagcatgtgtccatt	<i>M. truncatula</i>	qRT-PCR	
11	SNF1-related kinase beta 2 (Medtr2g095290)	SnRK1-b2	tcggctactctgtaatgct	gcgatgagtgatcccaag	<i>M. truncatula</i>	qRT-PCR	
12	SNF1 gamma subunit (Medtr4g103550)	SnRK1-g	tttcatgggctcctgctt	aaccaagtctaccacaggaac	<i>M. truncatula</i>	qRT-PCR	
13	SNF2, helicase and zinc finger protein (Medtr2g012830)	SnRK2	aagaccaaaagcacacga	aaagaggaaacccagca	<i>M. truncatula</i>	qRT-PCR	
14	Snorkel	SnorkelERF	ttccagaggagggtagttaaga	ttgggtgcacagatgattcc	<i>M. sativa</i>	qRT-PCR	
15	MsSPL1 (Medtr2g046550)	MsSPL1	agggttggagatgaacgatg	cacaggcgaatcttgtct	<i>M. truncatula</i>	qRT-PCR	
16	MsSPL1a (Medtr7g110320)	MsSPL1a	gtgaggagaatagcaggcagt	cccacagcatcaggtctaaa	<i>M. truncatula</i>	qRT-PCR	
17	MsSPL2	MsSPL2	gtagaagaggaggagggtgatg	gcaacagggtgggaaacac	<i>M. sativa</i>	qRT-PCR	Gao et al., 2016
18	MsSPL2a (Medtr8g080680)	MsSPL2a	gctgcagacgacaacttca	catctgttctcccacac	<i>M. truncatula</i>	qRT-PCR	
19	MsSPL4	MsSPL4	atgcaaaagcacctaccgt	cctctcattatgccagcca	<i>Msativa</i>	qRT-PCR	Gao et al., 2016
20	MsSPI7 (Medtr2g020620)	MsSPL7	ccctgaactcgtatcttgt	gccgtgatgatagccttca	<i>M. truncatula</i>	qRT-PCR	
21	MsSPL7a (Medtr7g444860)	MsSPL7a	cagggcacacatgagagaaga	gccatgatcagtcagat	<i>M. truncatula</i>	qRT-PCR	
22	MsSPL8 (Medtr8g005960)	MsSPL8	tggccgacctactctctct	aaccttggctgacaccta	<i>M. truncatula</i>	qRT-PCR	
23	MsSPL9	MsSPL9	ggaagaggtggctcagttca	acagtaaacgttggcacttag	<i>Msativa</i>	qRT-PCR	Aung et al., 2015b
24	MsSPL13	MsSPL13	caccatggagtggaattgaaagc	ctattcccattgataggaaatagt	<i>Msativa</i>	qRT-PCR	Aung et al., 2015b
25	MsSPL13a (Medtr8g096780)	MsSPL13a	cttgggttggaggatgtt	gctgctggttgaagatgtt	<i>M. truncatula</i>	qRT-PCR	
26	MsSPL14 (Medtr1g035010)	MsSPL14	gatctccaacatcggtctca	gagcttcgcaaccttatga	<i>M. truncatula</i>	qRT-PCR	
27	MsSPI16 (Medtr7g028740)	MsSPI16	tttgactcgggtgtgctct	cgttcacagcaagattgtg	<i>M. truncatula</i>	qRT-PCR	
28	MsSPL7a (Medtr7g444860)	MsSPL7aGSP	gagctcccattgattctgtt	-	<i>M. truncatula</i>	5' RLM-RACE	
29	MsSPL7a (Medtr7g444860)	MsSPL7aGIP	-	cctagccattatcgtatctc	<i>M. truncatula</i>	5' RLM-RACE	
30	MsSPL7a (Medtr7g444860)	MsSPL7aGOP	-	ctgcaaatgccattctctgtct	<i>M. truncatula</i>	5' RLM-RACE	
31	MsSPL8 (Medtr8g005960)	MsSPL8GSP	atggagggtcatcaactgct	-	<i>M. truncatula</i>	5' RLM-RACE	
32	MsSPL8 (Medtr8g005960)	MsSPL8GIP	-	cacgaagtcaatggctctgt	<i>M. truncatula</i>	5' RLM-RACE	
33	MsSPL8 (Medtr8g005960)	MsSPL8GOP	-	ttcgaagaacctgtggaacc	<i>M. truncatula</i>	5' RLM-RACE	
34	MsSPL13a (Medtr8g096780)	MsSPL13aGSP	tcctagatcgcacgttttag	-	<i>M. truncatula</i>	5' RLM-RACE	
35	MsSPL13a (Medtr8g096780)	MsSPL13aGIP	-	caggatgatcatgttgtt	<i>M. truncatula</i>	5' RLM-RACE	
36	MsSPL13a (Medtr8g096780)	MsSPL13aGOP	-	ccactctgatcattgaacca	<i>M. truncatula</i>	5' RLM-RACE	
37	Zinc finger protein SERRATE (SE) (Medtr8g043980)	SE	caccatggcagaagtctcacc	tatcacggtagctcttctgt	<i>M. truncatula</i>	Yeast-two-hybrid	
38	Zinc finger protein SERRATE (SE) (Medtr3g006760.1)	SE	caccatggccgaagtcgaaaaatct	gtcttgataactccgatcc	<i>M. truncatula</i>	Yeast-two-hybrid	
39	DCL protein (Medtr3g102270.2)	DCL1	caccatggccgcaccactctct	ccaacaggccttagtactctg	<i>M. truncatula</i>	Yeast-two-hybrid	
40	SNF1-related kinase (Medtr1g034030.1)	SnRK1	caccatggatcctactatgaacca	ctctgctcattctctatcga	<i>M. truncatula</i>	Yeast-two-hybrid	
41	Acetyl CoA Carboxylase I	<i>Acc1</i>	gatcagtgaaactcgcaaaagtac	caacgacgtgaacactacaac	<i>M. sativa</i>	qRT-PCR	
42	Actin	<i>Actin</i>	tcaatgtcctgcatgtatgt	actcacacctcaccagaatcc	<i>M. sativa</i>	qRT-PCR	

Table S2. The matching gene IDs of the newly identified MsSPLs in the tetraploid alfalfa genome

MsSPL	Chromosome	Gene ID	MsSPL	Chromosome	Gene ID
1	2.1	MS.gene98509	7a	7.4	MS.gene93246
1	2.2	MS.gene033954	8	8.2	MS.gene61571
1	2.3	MS.gene59294	8	8.3	MS.gene000259
1	2.4	MS.gene76798	8	8.4	MS.gene022540
1a	7.1	MS.gene050425	8	8.4	MS.gene62778
1a	7.2	MS.gene28650	13a	4.1	MS.gene40685
1a	7.3	MS.gene050856	13a	4.2	MS.gene030560
1a	7.4	MS.gene043764	13a	4.3	MS.gene79945
2a	4.2	MS.gene023425	13a	4.4	MS.gene030453
7	2.1	MS.gene002799	14	1.1	MS.gene026366
7	2.2	MS.gene96180	14	1.2	MS.gene040800
7	2.3	MS.gene00967	14	1.3	MS.gene061710
7	2.4	MS.gene004483	14	1.4	MS.gene061104
7a	7.1	MS.gene36181	16	7.1	MS.gene000446
7a	7.2	MS.gene010796	16	7.2	MS.gene99828
7a	7.3	MS.gene38329	16	7.3	MS.gene001948

Table S3 coding sequences used for yeast-two-hybrid assay between SnRK1 and miR156 biogenesis genes

>Medtr8g043980.1 (zinc finger protein SERRATE (SE) (Medtr8g043980)

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atggcagaagtctcccccattccctccgattccctccgacaaatctccccaccaccacctccccccaccaccgctcccaaccaccacaatcacctctcccacctccgccccgattccgatctccctaccaccaccacaatctctccgcccgcaga
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>Medtr3g006760.1 C2H2 zinc finger protein SERRATE (SE) (Medtr3g006760.1)

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>Medtr3g102270.2 DCL protein (Medtr3g102270.2)

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>Medtr1g034030.1 SNF1-related kinase (Medtr1g034030.1)

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The whole protein coding sequences of SnRK1 (Medtr1g034030.1), DICER-LIKE (DCL) (Medtr3g102270.2), and zinc finger protein SERRATE (SE) (Medtr8g043980) were amplified using gene specific primers (Table S1). The amplified coding sequences were cloned into the pENTR™ /D-TOPO® vector (Invitrogen) and transformed into *E. coli* by heat shock (42 °C for 90s). For subsequent Y2H assay, we used the ProQuest™ Two-Hybrid System (Invitrogen).

Table S4. Analysis of variance from physiological data obtained from the field experiment laid at Agriculture and Agri-Food Canada (AAFC) Research Centre in Kentville, Nova Scotia, Canada

Source	d.f.	Plant Ht, cm, 6wk post flood	Vigor, 0-4, 6wk post flood	DM, gm, 6wk post flood	Plant Ht, cm, 12wk post flood	Vigor, 0-4, 12wk post flood	DM, gm, 12wk post flood
Block:Plot stratum	*	-	-	-	-	-	-
Flood	1	ns	0.089	ns	ns	0.059	ns
Residual	6	-	-	-	-	-	-
Block:Plot:Tray_ePlot stratum	*	-	-	-	-	-	-
Cultivar	15	0.003	0.096	<0.001	0.066	<0.001	0.005
Flood:Cultivar	15	ns	ns	ns	ns	ns	ns
Residual	90	-	-	-	-	-	-
Block:Plot:Tray_ePlot:Pouch:Plant stratum	*	-	-	-	-	-	-
PPlant	7	ns	0.060	<0.001	ns	0.003	0.006
Flood:PPlant	7	0.091	ns	ns	ns	ns	0.082
Cultivar:PPlant	105	0.076	ns	<0.001	<0.001	0.034	<0.001
Flood:Cultivar:PPlant	105	0.091	ns	<0.001	ns	ns	0.061
Residual	667	-	-	-	-	-	-
Total	1018	-	-	-	-	-	-

Table S5. Analysis of variance of hormone profiles in flood stressed and control alfalfa plants

Hormone	Genotype	trt	Genotype*trt
ABA	0.0123	NS	NS
ABAGE	7.23E-07	2.57E-07	0.0305
PA	0.00488	7.74E-06	0.02528
Total ABA	0.00655	NS	0.04869
IAA	NS	NS	NS
Totalauxin	NS	0.0151	NS
GA19	NS	NS	0.0076
TotalGA	0.041	NS	NS
TotalCy	0.0253	8.40E-09	0.00988
DPA	0.014654	0.000275	0.042277
7OHABA	0.014654	0.000275	0.042277
tABA	NS	NS	0.0229
cZOG	8.38E-05	NS	NS
cZR	0.0277	1.99E-09	0.0105
iPR	0.03413	2.39E-08	0.00908
IAAAsp	7.54E-05	5.49E-10	0.000512

NS: Not significant at p<0.05

Table S6. UHPLC-MS profiled hormones in ng/g dry weight up on flood stress in alfalfa leaf tissues

Phytohormones	Abbreviations	Wild-type		AAC-Trueman		A8 (miR156OE)		<i>SPL13RNAi</i>	
		Control	Flood	Control	Flood	Control	Flood	Control	Flood
ABA metabolites	ABA	6129.42	2879.37	3436.01	2494.99	1118.73	1871.10	2795.64	3319.30
	DPA	308.11	334.79	223.85	730.86	105.05	324.19	133.04	368.09
	ABAGE	50.40	373.88	401.74	1073.29	110.15	423.27	47.52	329.98
	PA	2724.02	2883.30	1173.19	3470.77	607.34	2252.90	758.16	2835.76
	7'OH-ABA	183.18	158.16	64.38	116.98	66.46	91.75	76.90	80.92
	neo-PA	8.74	ND	4.45	ND	ND	ND	3.90	4.00
	t-ABA	82.56	43.31	73.83	67.06	35.73	62.06	40.39	79.38
Cytokinins	t-ZOG	ND	ND	1.76	ND	2.64	2.23	2.89	1.62
	c-ZOG	18.75	17.43	6.69	9.59	13.49	14.02	16.47	14.97
	t-ZR	1.00	ND	0.95	0.90	2.40	1.50	1.00	ND
	c-ZR	109.14	13.91	74.15	18.77	60.00	14.70	69.54	21.36
	dhZR	2.45	1.23	3.13	ND	2.14	1.40	3.99	1.30
	iP	1.13	1.10	1.35	1.00	ND	1.35	1.70	ND
	iPR	220.17	22.62	149.02	32.71	105.67	26.38	133.81	50.74
Auxins	IAA	87.56	174.55	130.75	181.39	134.61	102.40	145.66	191.95
	IAA-Asp	171.57	46.59	84.02	13.33	95.34	47.98	181.67	29.20
Gibberellins	GA1	ND	ND	ND	ND	ND	ND	9.65	ND
	GA3	3.90	4.00	8.45	ND	ND	ND	ND	ND
	GA7	ND	ND	3.90	ND	7.40	5.90	3.95	ND
	GA8	29.04	6.05	40.81	4.76	13.29	5.95	55.02	4.90
	GA19	66.54	131.06	83.96	129.10	94.89	45.97	94.30	108.96
	GA29	29.10	23.64	24.96	16.15	26.20	18.37	22.18	13.67
	GA34	ND	ND	ND	3.70	ND	ND	ND	4.00
GA53	3.90	8.28	4.28	9.45	7.40	5.60	4.27	6.33	

Table S7. List of significantly affected ABA-related genes fold-changes from well-drained control plants

Gene name	Gene ID	Genotypes				
		Wild-type	AC-Caribou	AAC-Trueman	miROE (A8)	SPL13RNAi-6
PYL9	Medtr3g090980		1.468333339	1.940415079	1.313445512	1.610158038
	Medtr8g027805		1.480644153			1.361084937
	Medtr1g028380	4.963729546	16.94250381	4.410731563	8.915831456	10.64340389
PYR1	Medtr5g030500		0.551276568			0.631988256
ABA-receptor	Medtr7g070050		0.288305364			0.668773116
	Medtr1g016480	1.726137604	2.34850122	2.170072974	1.451561869	2.76464643
	Medtr5g083270		0.284645612	2.802468962	2.302822132	
	Medtr4g014460		0.386710299	2.074601331		
ABA induced bHLH	Medtr8g027495		0.44730769		0.627963112	0.681350829
	Medtr7g117670	0.578658563	0.504039594		0.609460569	0.662601162
	Medtr7g096350				1.353689034	
ABA/WDS Induced protein	Medtr1g098680	0.509854126	0.45983657	0.456389774	0.558366393	0.664104756
XDH1	Medtr2g098030	1.708143437	1.753770481	2.182169255	1.587031141	1.952980022
zeta-Carotene isomerase	Medtr3g084950					0.621969659
	Medtr8g097190			2.35743112		
Beta-Carotene Isomerase	Medtr7g095920					0.375806719
ABA-responsive protein	Medtr2g035190	4.476207756	8.025441393			
ABA-responsive (TB2/DP1, HVA22) family protein	Medtr1g024930	0.28821008	0.200650313	0.319513604	0.643970772	0.208526515
ABA response element-binding factor	Medtr4g085910	2.105747729	3.727460438	3.134374429	1.783055573	3.572943355
ABA-responsive-like protein	Medtr8g100065			1.788690853		1.77213165
	Medtr1g114640				2.661306098	
	Medtr7g083570			2.125450176	1.697723951	
	Medtr6g077990		4.409943923			
	Medtr8g100065		1.574540283			
ABA induced plasma membrane protein	Medtr4g117600	0.450860822				0.379373122
PSY	Medtr5g076620					0.652151143
	Medtr3g450510	0.411986337	0.227360821		0.705058323	0.299838299
	Medtr5g090780	0.455543133	0.274667972		0.575679144	0.194748945
PDS	Medtr3g084830		1.482103143	1.526032664		1.377339249
LCY-e	Medtr2g040060	0.27241664	0.332762581	0.574271942	0.563130472	0.278468961
LCY-b	Medtr7g090150		0.688293753			
	Medtr8g465870			1.697438637		
CHY	Medtr1g100070	0.368081354	0.241712735	0.608144239	0.667732718	0.248853736
	Medtr6g048440		1.489852257			
CCD1	Medtr3g109610		4.074932125	25.13738121		20.97763582
	Medtr8g037315			1.915333133	1.366102418	
CCD4	Medtr5g025270	0.246985367	0.283622967	0.172140204	0.405135074	0.428300805
	Medtr5g025230	0.289981861	0.338459135	0.184447256	0.433233598	0.40454507
ZEP	Medtr4g022850	4.03297979	7.705559819	2.67311853	2.210951765	6.096039107
	Medtr5g017350	3.03308126	3.232068708	2.438581712	2.083075313	5.613112534
VDE	Medtr8g092050		0.618185962			0.62706794
	Medtr7g116630	0.568931294	0.561403722		0.708757417	0.532251204
NSY	Medtr7g007280	0.459825004	0.340076773	0.348227281	0.651375774	0.346068728
	Medtr6g025680					3.126790208
	Medtr6g018550	4.045066625				
NCED3	Medtr2g070460	1.852418586	6.703907087	4.751628254	1.628771003	6.492220275
Cytochrome P450 family ABA- 8 hydroxylase	Medtr5g025610	0.518542824			0.618119458	1.890076358
	Medtr1g019410	3.375806092	11.55971202	5.120935372	2.245986502	6.127579653
	Medtr4g086040		0.551399468	0.584319511	0.59505537	0.516336322
	Medtr8g072260	0.278184042	0.209947451		1.809095309	0.615951388
	Medtr1g037580			0.49768187	1.835384513	
sucrose nonfermenting 1(SNF1)-related kinase	Medtr1g034030	2.780324005	2.711466533	2.343780998	1.778232373	3.525850452
	Medtr8g079560		1.916094332	1.743409131		1.705262408
	Medtr4g099240		1.790565027	1.619925849	1.454628246	
	Medtr5g018050				1.424120656	
SNF1-related kinase regulatory subunit beta-2	Medtr5g098510	6.884094008	9.97537076	7.161091135	6.328153516	10.14232325
	Medtr2g095290	1.921102765	2.2018862	1.848043183	1.541646047	1.703699503
	Medtr2g026695	0.600141087	0.535881509	0.510054311		0.578046214
SNF1-related kinase catalytic subunit alpha KIN11	Medtr6g048250		2.103369823			1.648765123
	Medtr6g012990		1.844837154			1.357621649
SNF1-related kinase regulatory subunit gamma 1	Medtr4g103550		3.003721173			1.564202386
Snf1-related kinase interactor 1, putative	Medtr4g007700		2.444608079	1.97123124		2.363397456
SNF2 family amino-terminal protein	Medtr4g118720		1.585782026			1.591472075
	Medtr7g050445	0.27928081	0.186708251			0.14658971
SNF2, helicase and zinc finger protein	Medtr2g012830	1.541181957	2.142240877	1.697455189	1.340032077	1.643170672

Table S8. DEG associated with phenylpropanoid pathway fold change in SPL13RNAi plants

Control	Flooded	Fold change	Gene name	Gene ID	Gene annotation
0.157259	1.79351	11.55	CHS	Meditr2g01700	chalcone and stilbene synthase family protein
0.863899	68.4215	79.20	CHS	Meditr2g083910	chalcone and stilbene synthase family protein
1.13824	19.3975	17.04	CHS	Meditr5g007713	chalcone and stilbene synthase family protein
0.853317	3.76625	4.41	CHS	Meditr2g097935	chalcone and stilbene synthase family protein
2.46825	5.57545	3.88	CHS	Meditr2g083920	chalcone and stilbene synthase family protein
0.184781	0.580756	3.14	CHS	Meditr2g097910	chalcone and stilbene synthase family protein
0.43232	1.1666	2.70	CHS	Meditr2g098140	chalcone and stilbene synthase family protein
281.474	496.147	1.76	CHS	Meditr2g084300	chalcone and stilbene synthase family protein
132.399	225.551	1.70	CHI	Meditr2g093980	chalcone-flavanone isomerase family protein
24.5176	15.9105	0.65	CHI	Meditr2g075150	chalcone-flavanone isomerase family protein
39.1902	20.4897	0.52	CHI	Meditr2g094980	chalcone-flavanone isomerase family protein
12.245	4.41102	0.36	CHI	Meditr2g115840	chalcone-flavanone isomerase family protein
28.1494	2.50074	0.09	CHI	Meditr2g075950	chalcone-flavanone isomerase family protein
8.46837	1.74168	0.21	CHI	Meditr2g022010	chalcone-flavanone isomerase family protein, putative
4.43879	170.01	38.30	LDGX	Meditr5g011250	leucoanthocyanidin dioxygenase-like protein
26.495	17.8889	0.68	LDGX	Meditr2g015790	leucoanthocyanidin dioxygenase-like protein
15.7654	5.08904	0.32	LDGX	Meditr2g070860	leucoanthocyanidin dioxygenase-like protein
20.2361	2.12126	0.16	LDGX	Meditr2g086560	leucoanthocyanidin dioxygenase-like protein
0.818886	29.0492	35.47	F3H	Meditr2g075830	naringenin 3-dioxygenase (flavanone-3-hydroxylase)
10.4318	6.88297	0.66	F3H	Meditr2g058610	naringenin 3-dioxygenase (flavanone-3-hydroxylase)
1.39805	30.1875	21.59	FLS	Meditr2g091330	flavonol synthase/flavanone 3-hydroxylase
0.353812	6.74808	19.07	FLS	Meditr2g055680	flavonol synthase/flavanone 3-hydroxylase
2.22346	10.4189	4.69	FLS	Meditr5g055690	flavonol synthase/flavanone 3-hydroxylase
7.03461	15.7578	2.24	FLS	Meditr5g059130	flavonol synthase/flavanone 3-hydroxylase
8.76692	12.9497	1.48	FLS	Meditr5g048580	flavonol synthase/flavanone 3-hydroxylase
23.4646	12.9946	0.55	FLS	Meditr5g050100	flavonol synthase/flavanone 3-hydroxylase
0.132358	14.2242	107.47	HID	Meditr2g450680	2-hydroxyisoflavone dehydratase
0.474388	1.42907	3.01	HID	Meditr2g051020	2-hydroxyisoflavone dehydratase
10.8869	22.6469	2.08	HID	Meditr2g104930	2-hydroxyisoflavone dehydratase
0.674841	7.71548	11.48	IFR	Meditr2g070340	isoflavanone reductase-like protein
0.117758	0.857928	7.29	IFR	Meditr5g020760	isoflavanone reductase-like protein
11.8543	71.9415	6.07	DFR	Meditr2g022440	dihydroflavonol 4-reductase-like protein
6.69756	3.9136	0.58	DFR	Meditr2g013250	dihydroflavonol 4-reductase-like protein
0.757991	41.0798	54.22	F3H	Meditr2g109470	flavonoid hydroxylase
0.046738	0.740955	15.57	F3H	Meditr2g045700	flavonoid hydroxylase
4.49419	23.6299	5.26	FGT	Meditr2g084520	flavonoid glucosyltransferase
6.48035	16.63	2.57	FGT	Meditr2g084530	flavonoid glucosyltransferase
15.9971	61.729	3.86	FGT	Meditr2g128690	flavonoid glucosyltransferase
80.5089	102.809	0.13	FGT	Meditr2g455630	flavonoid glucosyltransferase
72.6701	5.51536	0.08	FGT	Meditr2g031800	flavonoid glucosyltransferase
4.47777	0.841314	0.19	FOMT	Meditr2g083620	flavonoid O-methyltransferase-like protein
0.168525	0.587252	3.48	AAT	Meditr2g089560	anthocyanin 5-aromatic acyltransferase
15.963	36.3294	2.28	AAT	Meditr2g089570	anthocyanin 5-aromatic acyltransferase
24.5972	53.9455	2.19	AAT	Meditr2g051180	anthocyanin 5-aromatic acyltransferase
26.359	17.3893	0.66	AAT	Meditr2g104205	anthocyanin 5-aromatic acyltransferase
6.63988	2.36659	0.36	AAT	Meditr2g015860	anthocyanin 5-aromatic acyltransferase
14.1224	1.5501	0.11	AAT	Meditr2g089570	anthocyanin 5-aromatic acyltransferase
84.2219	60.3209	0.72	AAT	Meditr2g018590	1-O-acetylglucose-anthocyanin acyltransferase
0.606445	1.25578	2.07	PAL	Meditr5g098720	phenylalanine ammonia-lyase-like protein
17.7626	10.6099	0.60	PAL	Meditr2g101395	phenylalanine ammonia-lyase-like protein
21.4047	12.6183	0.60	PAL	Meditr2g101425	phenylalanine ammonia-lyase-like protein
0.514246	0.833333	0.16	PAL	Meditr2g464495	shikimate/quisate hydroxycinnamoyltransferase
11.9181	21.1793	1.78	CCR	Meditr2g090040	cinnamoyl-CoA reductase
37.5393	75.3853	2.01	CCR	Meditr2g076200	cinnamoyl-CoA reductase-like protein
522.729	888.859	1.70	CCR	Meditr2g031650	cinnamoyl-CoA reductase-like protein
23.5755	11.8414	0.50	CCR	Meditr2g077100	cinnamoyl-CoA reductase-like protein
14.717	6.24377	0.42	CCR	Meditr2g069940	cinnamoyl-CoA reductase-like protein
71.2782	342.814	2.00	CADL	Meditr2g107425	cinnamyl alcohol dehydrogenase-like protein
49.2539	72.7787	1.57	CADL	Meditr2g050170	cinnamyl alcohol dehydrogenase-like protein
12.3828	18.3453	1.48	CADL	Meditr5g031180	cinnamyl alcohol dehydrogenase-like protein
11.4937	4.75367	0.41	CADL	Meditr2g115300	cinnamyl alcohol dehydrogenase-like protein
101.33	37.7547	0.37	CADL	Meditr2g029590	cinnamyl alcohol dehydrogenase-like protein
1.01223	0.364236	0.36	CADL	Meditr2g031140	cinnamyl alcohol dehydrogenase-like protein
240.397	59.0809	0.25	CADL	Meditr5g031190	cinnamyl alcohol dehydrogenase-like protein
3.15267	8.28627	2.63	4CL	Meditr2g073180	4-coumarate:CoA ligase-like protein
1.36185	9.28901	6.82	4CL	Meditr2g057730	4-coumarate:CoA ligase-like protein
11.3113	17.619	1.56	4CL	Meditr5g007640	4-coumarate:CoA ligase-like protein
42.3478	57.6463	1.36	4CL	Meditr2g128337	4-coumarate:CoA ligase-like protein
31.8462	19.3249	0.61	4CL	Meditr2g009730	4-coumarate:CoA ligase-like protein
110.624	66.179	0.60	4CL	Meditr2g105710	4-coumarate:CoA ligase-like protein
0.365712	0.0424932	0.12	4CL	Meditr2g063110	4-coumarate:CoA ligase-like protein
13.5551	22.704	1.67	MCD	Meditr2g043310	malonyl-CoA decarboxylase
1.81981	27.6218	15.18	MCD	Meditr2g015830	malonyl-CoA:isoflavone 7-O-glucoside malonyltransferase
0.118006	0.454966	3.83	MCD	Meditr2g013315	malonyl-CoA:isoflavone 7-O-glucoside malonyltransferase
0.937934	2.29464	2.45	MCD	Meditr2g013330	malonyl-CoA:isoflavone 7-O-glucoside malonyltransferase
6.86031	2.93338	0.43	MCD	Meditr2g031380	malonyl-CoA-acyl carrier transacylase
1.70143	5.00687	2.94	FNS II	Meditr2g088160	cytochrome P450 family flavone synthase
0.137557	0.919824	6.69	UGT	Meditr2g059425	UDP-glucosyltransferase family protein
0.350648	1.66457	4.75	UGT	Meditr2g040530	UDP-glucosyltransferase family protein
196.293	928.746	4.73	UGT	Meditr2g179470	UDP-glucosyltransferase family protein
6.33138	22.235	4.17	UGT	Meditr2g105560	UDP-glucosyltransferase family protein
1.2037	4.83554	4.02	UGT	Meditr2g083430	UDP-glucosyltransferase family protein
0.158481	0.615249	3.88	UGT	Meditr2g071050	UDP-glucosyltransferase family protein
2.68234	8.55554	3.19	UGT	Meditr2g064987	UDP-glucosyltransferase family protein
2.94393	9.27543	3.15	UGT	Meditr2g113200	UDP-glucosyltransferase family protein
4.52185	13.4526	2.98	UGT	Meditr2g009490	UDP-glucosyltransferase family protein
13.5481	32.2392	2.38	UGT	Meditr2g046490	UDP-glucosyltransferase family protein
2.79832	6.62039	2.37	UGT	Meditr2g142170	UDP-glucosyltransferase family protein
2.21141	4.91576	2.22	UGT	Meditr2g095040	UDP-glucosyltransferase family protein
0.697333	1.46894	2.11	UGT	Meditr2g0840030	UDP-glucosyltransferase family protein
15.7726	32.9981	2.09	UGT	Meditr2g070040	UDP-glucosyltransferase family protein
31.7106	63.4933	2.00	UGT	Meditr2g009730	UDP-glucosyltransferase family protein
0.521214	1.03023	1.96	UGT	Meditr2g466240	UDP-glucosyltransferase family protein
8.72568	17.0294	1.95	UGT	Meditr2g006710	UDP-glucosyltransferase family protein
140.744	263.264	1.87	UGT	Meditr2g117170	UDP-glucosyltransferase family protein
2.13248	3.63389	1.70	UGT	Meditr2g071070	UDP-glucosyltransferase family protein
4.84927	7.40883	1.53	UGT	Meditr2g116180	UDP-glucosyltransferase family protein
30.7221	43.9453	1.43	UGT	Meditr2g013553	UDP-glucosyltransferase family protein
69.8163	46.0608	0.66	UGT	Meditr5g067170	UDP-glucosyltransferase family protein
7.21762	4.68116	0.65	UGT	Meditr2g072860	UDP-glucosyltransferase family protein
37.1886	23.8406	0.64	UGT	Meditr2g046620	UDP-glucosyltransferase family protein
16.2584	9.52955	0.59	UGT	Meditr5g029800	UDP-glucosyltransferase family protein
6.43999	3.7057	0.58	UGT	Meditr2g090055	UDP-glucosyltransferase family protein
29.8741	16.7492	0.56	UGT	Meditr2g027870	UDP-glucosyltransferase family protein
67.8708	36.7269	0.54	UGT	Meditr2g0780010	UDP-glucosyltransferase family protein
7.9155	4.20799	0.53	UGT	Meditr2g080010	UDP-glucosyltransferase family protein
1.78859	0.948812	0.53	UGT	Meditr2g047030	UDP-glucosyltransferase family protein
6.07381	2.92499	0.48	UGT	Meditr2g102490	UDP-glucosyltransferase family protein
14.6454	6.9002	0.47	UGT	Meditr2g042310	UDP-glucosyltransferase family protein
3.33218	1.54762	0.47	UGT	Meditr2g082490	UDP-glucosyltransferase family protein
2.77768	1.23336	0.44	UGT	Meditr2g024020	UDP-glucosyltransferase family protein
11.0104	4.84754	0.44	UGT	Meditr2g0360010	UDP-glucosyltransferase family protein
9.06752	3.95663	0.44	UGT	Meditr2g014250	UDP-glucosyltransferase family protein
1.13569	0.542325	0.41	UGT	Meditr2g077960	UDP-glucosyltransferase family protein
2.46584	0.97921	0.40	UGT	Meditr2g107325	UDP-glucosyltransferase family protein
18.3859	7.18924	0.39	UGT	Meditr2g035295	UDP-glucosyltransferase family protein
0.946443	0.358983	0.38	UGT	Meditr2g005600	UDP-glucosyltransferase family protein
8.7515	3.25115	0.37	UGT	Meditr2g080870	UDP-glucosyltransferase family protein
7.1097	2.47922	0.35	UGT	Meditr2g068330	UDP-glucosyltransferase family protein
7.86048	2.56268	0.33	UGT	Meditr2g008210	UDP-glucosyltransferase family protein

3.6433	1.16332	0.32	Medr2g083380	UDP-glucosyltransferase family protein
1.48236	0.468547	0.32	Medr6g083800	UDP-glucosyltransferase family protein
3.9875	1.00155	0.29	Medr6g062600	UDP-glucosyltransferase family protein
3.9818	1.13242	0.28	Medr2g012120	UDP-glucosyltransferase family protein
3.986	0.829804	0.21	Medr3g069690	UDP-glucosyltransferase family protein
7.38548	1.46819	0.20	Medr8g068340	UDP-glucosyltransferase family protein
59.3483	11.625	0.20	Medr5g015500	UDP-glucosyltransferase family protein
32.2985	6.01307	0.19	Medr3g016560	UDP-glucosyltransferase family protein
37.4396	6.72904	0.18	Medr2g034990	UDP-glucosyltransferase family protein
19.8098	3.47176	0.18	Medr4g117890	UDP-glucosyltransferase family protein
0.999749	0.167898	0.17	Medr0g0810010	UDP-glucosyltransferase family protein
5.80386	8.9703	0.17	Medr7g057710	UDP-glucosyltransferase family protein
6.41592	0.879345	0.14	Medr6g078320	UDP-glucosyltransferase family protein
10.7019	1.42278	0.13	Medr2g008226	UDP-glucosyltransferase family protein
1.52347	0.202059	0.13	Medr4g059370	UDP-glucosyltransferase family protein
25.0363	2.31422	0.13	Medr4g04140	UDP-glucosyltransferase family protein
98.5232	6.06681	0.06	Medr2g008220	UDP-glucosyltransferase family protein
2.63237	0.0364904	0.01	Medr5g075440	UDP-glucosyltransferase family protein
12.2024	45.3894	3.77	Medr6g033675	UDP-glucosyltransferase 88A1
0.367654	0.987389	2.69	Medr3g021725	UDP-glucosyltransferase 88A1
33.3904	61.4334	1.84	Medr4g485640	UDP-glucosyltransferase 73B2
115.392	191.329	1.66	Medr1g088480	UDP-glucuronic acid decarboxylase-like protein
10.4702	6.57739	0.63	Medr3g095910	UDP-glucuronate-xylan alpha-glucuronosyltransferase
3.85051	2.26533	0.60	Medr1g015130	UDP-glucuronate-xylan alpha-glucuronosyltransferase
33.2139	54.163	1.63	Medr5g090580	UDP-glucose flavonoid 3-O-glucosyltransferase
9.65266	5.39069	0.56	Medr5g089830	UDP-glucose flavonoid 3-O-glucosyltransferase
19.9753	31.709	1.57	Medr7g076310	UDP-galactose transporter 1
11.4605	16.2493	1.42	Medr3g098640	UDP-glucose-6-phosphate 4-epimerase
16.6317	11.0046	0.66	Medr4g46850	UDP-glucac-adenosine triphosphate glucac-1-P-transferase
121.813	59.2811	0.49	Medr5g043970	UDP-glucose 6-dehydrogenase family protein
132.319	63.7785	0.48	Medr7g012950	UDP-glucose 6-dehydrogenase family protein
71.2601	38.6445	0.54	Medr2g096660	UDP-glucuronic acid decarboxylase
0.120398	8.52013	70.77	MYB	Medr5g079670 myb transcription factor
0.432767	24.86	57.44	MYB	Medr1g086510 myb transcription factor
0.230764	4.84289	20.99	MYB	Medr2g033170 myb transcription factor
0.079506	1.51186	19.02	MYB	Medr3g110460 myb transcription factor
0.550735	6.25846	11.36	MYB	Medr4g123040 myb transcription factor
35.8314	237.333	6.62	MYB	Medr2g096380 myb transcription factor
0.530137	6.12412	5.89	MYB	Medr3g083540 myb transcription factor
0.124816	0.669176	6.36	MYB	Medr4g074520 myb transcription factor
49.1599	204.177	4.15	MYB	Medr5g016510 myb transcription factor
0.17398	0.682151	3.92	MYB	Medr5g005460 myb transcription factor
14.7859	65.1316	4.40	MYB	Medr4g098982 myb transcription factor
0.578214	1.48385	2.58	MYB	Medr3g100720 myb transcription factor
1.11895	3.08061	2.75	MYB	Medr2g011660 myb transcription factor
84.5599	229.053	2.71	MYB	Medr4g063100 myb transcription factor
12.2639	27.9997	2.28	MYB	Medr7g087130 myb transcription factor
7.45783	14.8842	2.00	MYB	Medr3g028555 myb transcription factor
28.7948	54.8752	1.91	MYB	Medr01233070 myb transcription factor
2.53256	4.33654	1.71	MYB	Medr8g095390 myb transcription factor
10.7008	16.371	1.53	MYB	Medr3g064500 myb transcription factor
16.1631	21.335	1.44	MYB	Medr3g02130 myb transcription factor
170.1372	127.593	0.75	MYB	Medr1g067000 myb transcription factor
44.9463	28.9646	0.64	MYB	Medr6g477860 myb transcription factor
12.8452	7.70599	0.60	MYB	Medr4g102380 myb transcription factor
3.35322	1.8376	0.59	MYB	Medr6g013790 myb transcription factor
1.30247	0.703915	0.54	MYB	Medr3g028740 myb transcription factor
23.5059	12.6929	0.54	MYB	Medr4g073420 myb transcription factor
41.6862	20.7641	0.50	MYB	Medr1g063940 myb transcription factor
4.51862	2.17317	0.48	MYB	Medr8g098860 myb transcription factor
5.79459	2.70077	0.47	MYB	Medr3g049017 myb transcription factor
2.0004	0.869425	0.43	MYB	Medr8g468380 myb transcription factor
1.60222	0.661824	0.41	MYB	Medr2g097910 myb transcription factor
17.9481	6.43035	0.36	MYB	Medr7g061550 myb transcription factor
1.89876	0.67792	0.36	MYB	Medr3g087140 myb transcription factor
1.14311	0.406191	0.36	MYB	Medr7g096930 myb transcription factor
2.11574	0.639308	0.30	MYB	Medr1g085040 myb transcription factor
0.640971	0.148424	0.23	MYB	Medr7g117730 myb transcription factor
1.96408	0.408359	0.21	MYB	Medr3g085010 myb transcription factor
0.699955	0.144624	0.21	MYB	Medr5g082910 myb transcription factor
0.844207	0.0969873	0.11	MYB	Medr4g082040 myb transcription factor
15.173	0.817636	0.05	MYB	Medr4g214460 myb transcription factor
5.80551	0.277499	0.05	MYB	Medr3g061790 myb transcription factor
108.368	3.02779	0.03	MYB	Medr2g023100 myb transcription factor
4.71002	2.80708	0.60	MYB	Medr1g086180 MYB family transcription factor
27.6694	16.3007	0.59	MYB	Medr2g02290 MYB family transcription factor
314.802	52.1533	0.17	MYB	Medr6g077420 MYB family transcription factor
1.7983	0.197476	0.11	MYB	Medr3g119320 MYB family transcription factor
12.7126	0.980649	0.08	MYB	Medr3g111880 MYB family transcription factor
56.0058	3.2274	0.06	MYB	Medr7g089210 MYB family transcription factor
35.2036	0.908802	0.03	MYB	Medr6g077990 MYB family transcription factor
10.8536	3.60458	0.33	MYB5	Medr1g026870 transcription repressor MYB5
11.7042	1.78489	0.15	MYB5	Medr3g110028 transcription repressor MYB5
17.2453	26.0005	1.51	MYB51	Medr5g081860 MYB transcription factor MYB51
17.6979	25.733	1.45	MYB51	Medr7g067080 MYB transcription factor MYB51
11.7448	16.7709	1.43	MYB51	Medr3g462790 MYB transcription factor MYB51
7.93977	2.27366	0.29	MYB64	Medr7g110830 myb transcription factor MYB64
44.9035	203.915	4.54	MYB	Medr5g037080 MYB-like transcription factor family protein
15.7197	59.8905	3.81	MYB	Medr4g081710 myb-like transcription factor family protein
11.9827	29.8953	2.70	MYB	Medr2g086450 myb-like transcription factor family protein
7.66715	17.6767	2.31	MYB	Medr1g111830 MYB-like transcription factor family protein
23.2199	53.217	2.29	MYB	Medr7g115530 myb-like transcription factor family protein
31.2609	67.6386	2.16	MYB	Medr6g449880 myb-like transcription factor family protein
1.65447	5.50801	2.12	MYB	Medr6g086410 MYB-like transcription factor family protein
10.4112	21.8071	2.09	MYB	Medr6g032990 myb-like transcription factor family protein
0.566713	1.15656	2.04	MYB	Medr1g053835 myb-like transcription factor family protein
0.952566	1.92501	2.02	MYB	Medr7g069660 MYB-like transcription factor family protein
4.61434	9.18373	1.99	MYB	Medr4g111140 myb-like transcription factor family protein
37.7677	65.5914	1.74	MYB	Medr7g088070 myb-like transcription factor family protein
21.7583	30.0845	1.38	MYB	Medr2g027860 myb-like transcription factor family protein
33.209	45.1914	1.36	MYB	Medr7g098250 myb-like transcription factor family protein
13.4695	8.48777	0.63	MYB	Medr6g086835 myb-like transcription factor family protein
25.1176	15.6944	0.62	MYB	Medr4g111975 MYB-like transcription factor family protein
20.6778	11.8119	0.57	MYB	Medr1g090670 myb-like transcription factor family protein
2.04156	0.999157	0.49	MYB	Medr3g093080 myb-like transcription factor family protein
24.6511	17.4084	0.71	MYB	Medr6g077990 Myb transcription factor-like protein
0.196743	2.14551	10.41	Myb/SANT	Medr7g105890 Myb/SANT-like DNA-binding domain protein
1.21298	8.49433	7.00	Myb/SANT	Medr4g128540 Myb/SANT-like DNA-binding domain protein
1.79056	11.6691	6.52	Myb/SANT	Medr06930050 Myb/SANT-like DNA-binding domain protein
0.084772	0.470761	5.55	Myb/SANT	Medr3g161370 Myb/SANT-like DNA-binding domain protein
1.64831	5.59186	1.39	Myb/SANT	Medr7g020870 Myb/SANT-like DNA-binding domain protein
4.24087	2.5629	0.60	Myb/SANT	Medr2g026725 Myb/SANT-like DNA-binding domain protein
21.9766	7.86686	0.36	Myb/SANT	Medr6g035370 myb/SANT-like DNA-binding domain protein
1.27208	0.355906	0.28	Myb/SANT	Medr7g061640 Myb/SANT-like DNA-binding domain protein
6.90884	1.26822	0.18	Myb/SANT	Medr7g114860 Myb/SANT-like DNA-binding domain protein
0.64763	0.094147	0.15	Myb/SANT	Medr8g085310 Myb/SANT-like DNA-binding domain protein
1.5387	0.156707	0.10	Myb/SANT	Medr1g094045 Myb/SANT-like DNA-binding domain protein
0.179537	3.0709	17.10	R2R3-myb	Medr5g078860 R2R3-myb transcription factor
0.704362	11.7703	6.71	R2R3-myb	Medr3g076910 R2R3-myb transcription factor
8.07993	4.9244	0.61	R2R3-myb	Medr6g012180 R2R3-myb transcription factor
1.58705	0.736946	0.46	R2R3-myb	Medr3g039990 R2R3-myb transcription factor
4.21645	1.91166	0.45	R2R3-myb	Medr01400030 R2R3-myb transcription factor

8.00167	13.9304	1.74	Medtr3g100180	myb-like DNA-binding domain protein
0.16105	0.659837	4.10	Medtr2g084230	myb-like DNA-binding domain, shaqhyf class protein
0.837505	2.54894	3.04	Medtr3g050110	myb-like DNA-binding domain, shaqhyf class protein
3.52187	5.91887	1.68	Medtr3g071625	myb-like DNA-binding domain, shaqhyf class protein
1.65367	0.882482	0.53	Medtr1g112370	myb-like DNA-binding domain, shaqhyf class protein
0.49824	0.159056	0.32	Medtr2g016220	myb-like DNA-binding domain, shaqhyf class protein
4.2808	1.24676	0.29	Medtr0g11980	myb-like DNA-binding domain, shaqhyf class protein
3.0424	0.617461	0.20	Medtr0230040	myb-like DNA-binding domain, shaqhyf class protein
0.987074	2.32545	2.36	Medtr1g100653	myb transcription factor MKTA-like protein
8.20835	3.35286	0.41	Medtr7g011170	myb transcription factor mika-like protein
18.249	5.89435	0.32	Medtr6g012990	myb transcription factor MKTA-like protein
1.45991	0.333044	0.23	Medtr3g013360	myb transcription factor MKTA-like protein
0.11246	1.37871	12.26	LBM1	myb-related transcription factor LBM1
0.158576	0.95577	62.78	WD40	transducin/WD40 repeat protein
48.1375	120.24	2.50	WD40	transducin/WD40 repeat protein
8.21249	17.562	2.14	WD40	transducin/WD40 repeat protein
4.25151	7.86745	1.85	WD40	transducin/WD40 repeat protein
64.3551	102.99	1.60	WD40	transducin/WD40 repeat protein
17.4037	24.994	1.44	WD40	transducin/WD40 repeat protein
16.468	23.409	1.42	WD40	transducin/WD40 repeat protein
19.8835	27.1718	1.37	WD40	transducin/WD40 repeat protein
38.735	52.7972	1.36	WD40	transducin/WD40 repeat protein
32.6727	44.437	1.36	WD40	transducin/WD40 repeat protein
9.49086	6.52318	0.69	WD40	transducin/WD40 repeat protein
7.25918	4.88408	0.67	WD40	transducin/WD40 repeat protein
8.55168	5.67702	0.66	WD40	transducin/WD40 repeat protein
10.9794	6.82827	0.62	WD40	transducin/WD40 repeat protein
4.02492	2.42562	0.60	WD40	transducin/WD40 repeat protein
9.03513	5.39885	0.60	WD40	transducin/WD40 repeat protein
9.52219	4.53135	0.48	WD40	transducin/WD40 repeat protein
1.62882	0.448949	0.28	WD40	transducin/WD40 repeat protein
3.2979	0.535583	0.17	WD40	transducin/WD40 domain protein
12.6325	8.58941	0.68	Medtr6g004040	katatin p80 WD40 repeat subunit B1-like protein
13.0724	17.4139	1.33	Medtr1g087120	WD40/YVTN repeat containing domain-containing protein
0.482652	9.73325	20.17	bHLH	Medtr1g072320 bHLH transcription factor
9.29101	16.4404	1.77	bHLH	Medtr5g048860 bHLH transcription factor
15.1871	26.152	1.72	bHLH	Medtr4g108360 bHLH transcription factor
27.9724	40.992	1.47	bHLH	Medtr3g131160 bHLH transcription factor
7.58623	2.23027	0.49	bHLH	Medtr3g096605 bHLH transcription factor
13.6047	1.83974	0.14	bHLH	Medtr3g116770 bHLH transcription factor
23.8017	90.6247	3.81	bHLH147	Medtr1g084160 transcription factor bHLH147
72.744	52.8237	0.73	bHLH137	Medtr3g098285 transcription factor bHLH137
10.6712	0.15754	0.26	bHLH93	Medtr5g003770 transcription factor bHLH93
23.9212	49.2664	2.09	bHLH	Medtr7g077470 transcription factor bHLH93-like protein
0.481536	0.0864422	0.18	bHLH	Medtr4g079760 transcription factor bHLH107-like protein
40.0829	83.2713	2.08	bHLH	Medtr3g088100 bHLH transcription factor-like protein
19.4702	38.817	1.99	bHLH	Medtr3g103605 bHLH transcription factor-like protein
32.0128	61.6959	1.93	bHLH	Medtr2g101520 bHLH transcription factor-like protein
3.1696	6.02474	1.82	bHLH	Medtr7g063470 bHLH transcription factor-like protein
12.6943	18.2201	1.44	bHLH	Medtr7g096650 bHLH transcription factor-like protein
23.6729	32.3027	1.36	bHLH	Medtr4g051505 bHLH transcription factor-like protein
41.6825	27.7763	0.67	bHLH	Medtr4g087300 bHLH transcription factor-like protein
2.72595	0.94114	0.35	bHLH	Medtr3g112170 bHLH transcription factor-like protein
3.71394	6.28639	1.69	bHLH	Medtr3g052470 transcription factor bHLH122-like protein
24.1379	39.2204	1.61	bHLH	Medtr3g050470 transcription factor bHLH122-like protein
37.5145	65.6528	1.75	bHLH	Medtr1g070870 basic helix loop helix protein bHLH4
3.04939	17.4671	5.73	bHLH	Medtr8g099880 basic helix loop helix protein bHLH8
28.1758	15.0457	0.53	bHLH	Medtr7g083900 basic helix loop helix protein bHLH23
16.5088	23.4003	1.42	bHLH	Medtr3g043430 bHLH domain class transcription factor
22.6827	33.1024	1.46	bHLH	Medtr3g001770 basic helix loop helix (bHLH) family transcription factor
16.5506	10.7003	0.65	bHLH	Medtr8g067280 basic helix loop helix (bHLH) family transcription factor
8.81645	4.70374	0.53	bHLH	Medtr8g024790 basic helix loop helix (bHLH) family transcription factor
0.21782	1.11105	5.10	Medtr3g094762	basic helix loop helix (bHLH) DNA-binding family protein
33.564	16.5108	0.49	Medtr3g014210	basic helix loop helix (bHLH) DNA-binding family protein
3.26047	1.4972	0.46	Medtr024660020	basic helix loop helix (bHLH) DNA-binding family protein
12.2783	5.43255	0.44	Medtr5g014600	basic helix loop helix (bHLH) DNA-binding family protein
13.8229	4.75374	0.31	Medtr3g093750	basic helix loop helix (bHLH) DNA-binding family protein
0.748242	0.230026	0.21	Medtr3g093750	basic helix loop helix (bHLH) DNA-binding family protein
1.96269	0.320185	0.16	Medtr2g022280	basic helix loop helix (bHLH) DNA-binding family protein
1.14533	2.07771	1.81	bZIP	Medtr4g012430 bZIP protein
10.7869	15.1678	1.41	bZIP	Medtr2g102050 bZIP protein
8.35676	1.03161	0.12	bZIP	Medtr3g019450 bZIP protein
0.075122	0.862346	11.48	bZIP	Medtr2g086340 bZIP transcription factor
0.724958	7.2286	9.97	bZIP	Medtr3g109310 bZIP transcription factor
16.4438	64.7385	3.94	bZIP	Medtr3g080990 bZIP transcription factor
7.33424	15.2449	0.28	bZIP	Medtr3g080990 bZIP transcription factor
7.47561	15.3233	2.05	bZIP	Medtr3g078830 bZIP transcription factor
11.0567	22.0465	1.99	bZIP	Medtr6g034945 bZIP transcription factor
47.7718	83.2262	1.74	bZIP	Medtr5g038550 bZIP transcription factor
18.1531	30.1794	1.66	bZIP	Medtr3g023690 bZIP transcription factor
18.0279	28.3531	1.52	bZIP	Medtr3g090950 bZIP transcription factor
14.4279	21.0393	1.46	bZIP	Medtr3g436010 bZIP transcription factor
3.15742	2.04794	0.65	bZIP	Medtr8g091250 bZIP transcription factor
16.3044	30.2419	0.63	bZIP	Medtr4g072090 bZIP transcription factor
18.4919	9.12766	0.50	bZIP	Medtr3g094020 bZIP transcription factor
18.584	6.23088	0.34	bZIP	Medtr5g075390 bZIP transcription factor
5.32053	1.69353	0.32	bZIP	Medtr5g087740 bZIP transcription factor
14.6869	4.54229	0.31	bZIP	Medtr2g047120 bZIP transcription factor
1.18751	0.35049	0.20	bZIP	Medtr3g014210 bZIP transcription factor
2.10162	0.368046	0.18	bZIP	Medtr6g016375 bZIP transcription factor
13.3568	22.6691	1.70	bZIP	Medtr8g091650 bZIP family transcription factor
39.776	61.8403	1.57	bZIP	Medtr8g040120 bZIP family transcription factor
0.171538	0.62132	0.61	bZIP	Medtr3g092750 bZIP family transcription factor
7.1997	24.1693	3.36	bZIP	Medtr5g060950 bZIP family transcription factor
0.06184	0.346624	5.61	bZIP	Medtr01260080 bZIP family transcription factor
0.267177	1.28501	4.81	bZIP	Medtr2g086420 bZIP family transcription factor
20.1294	1.62464	0.08	bZIP	Medtr3g079500 bZIP family transcription factor
8.44693	0.614546	0.07	bZIP	Medtr2g090900 bZIP family transcription factor
67.0252	375.604	5.60	bZIP124	Medtr4g070860 bZIP transcription factor bZIP124
30.9631	116.475	3.76	bZIP124	Medtr3g117120 bZIP transcription factor bZIP124
26.9435	17.6029	0.68	bZIP90	Medtr7g081705 bZIP transcription factor bZIP90
14.249	2.38044	0.17	bZIP98	Medtr7g115120 transcription factor bZIP98
3.84622	11.8769	3.09	bZIP	Medtr8g028150 bZIP transcription factor family protein
41.7014	84.3009	2.02	bZIP	Medtr7g116890 bZIP transcription factor family protein
33.7726	24.8979	0.74	bZIP	Medtr3g077950 bZIP transcription factor family protein
0.463323	4.68381	10.11	GST	Medtr3g080440 glutathione S-transferase
0.973524	13.4098	13.77	GST	Medtr1g115195 glutathione S-transferase
50.4936	100.29	1.99	GST	Medtr1g067170 glutathione S-transferase
26.1468	48.6235	1.86	GST	Medtr3g090910 glutathione S-transferase
1.68396	9.01346	1.85	GST	Medtr7g100320 glutathione S-transferase
40.9017	57.9545	1.42	GST	Medtr3g450790 glutathione S-transferase
369.912	105.272	0.28	GST	Medtr1g115500 glutathione S-transferase
25.7497	14.2299	0.55	Medtr2g072120	glutathione S-transferase tau
15.8005	53.8127	0.41	GSTUS	Medtr4g134380 glutathione S-transferase tau 5
13.6054	30.2248	2.22	Medtr4g134370	glutathione S-transferase tau 5
0.989109	12.1507	12.28	Medtr1g090150	glutathione S-transferase, amino-terminal domain protein
8.03876	458.188	57.00	Medtr3g064700	glutathione S-transferase, amino-terminal domain protein
0.903146	21.6331	23.95	Medtr3g090600	glutathione S-transferase, amino-terminal domain protein
3.50749	31.068	8.86	Medtr7g050265	glutathione S-transferase, amino-terminal domain protein
3.79018	24.5397	6.47	Medtr7g065230	glutathione S-transferase, amino-terminal domain protein
7.72919	44.3179	5.80	Medtr2g067070	glutathione S-transferase, amino-terminal domain protein
6.26214	28.0683	4.48	Medtr3g099757	glutathione S-transferase, amino-terminal domain protein
0.207468	0.775324	3.73	Medtr2g070120	glutathione S-transferase, amino-terminal domain protein
0.419894	1.09915	2.62	Medtr3g467420	glutathione S-transferase, amino-terminal domain protein
3.59599	8.75863	2.44	Medtr3g061950	glutathione S-transferase, amino-terminal domain protein
13.2277	25.8655	1.91	Medtr3g088635	glutathione S-transferase, amino-terminal domain protein
4.09234	6.59916	1.61	Medtr4g019780	glutathione S-transferase, amino-terminal domain protein
23.5805	37.5887	1.59	Medtr3g059970	glutathione S-transferase, amino-terminal domain protein
80.0303	42.5945	0.53	Medtr3g060600	glutathione S-transferase, amino-terminal domain protein
1.80519	0.947428	0.47	Medtr3g057020	glutathione S-transferase, amino-terminal domain protein
22.2606	10.5267	0.47	Medtr2g070060	glutathione S-transferase, amino-terminal domain protein
3.49344	1.50116	0.43	Medtr8g098430	glutathione S-transferase, amino-terminal domain protein
19.2616	7.21202	0.37	Medtr1g026140	glutathione S-transferase, amino-terminal domain protein
9.42449	3.23428	0.34	Medtr2g070210	glutathione S-transferase, amino-terminal domain protein
64.2695	15.2161	0.24	Medtr3g037390	glutathione S-transferase, amino-terminal domain protein

Table S9. Coding sequences of SPLs with conserved squamosa binding domain from different plants used for phylogenetic analysis

>AtSPL1
tgtcaggtcgaaaactgtgaagctgatcttagttaaagttaaaggattatcatagacgccataaagttctgtgagatgcaatccaaggctactagtccactgtcggaggtatcttgcagcgttttgcagcaatgtagtaggttccatctctcaggagtttgatgaaggaagagaagt
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>AtSPL5
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Table S10. DEG associated with glycolysis and TCA fold change in SPL13RNAi plants

Control	Flooded	Gene name	Gene ID	Gene annotation
0.292283	4.07574	ACS	Medtr7g079080	1-aminocyclopropane-1-carboxylate synthase
1.23672	2.54512	ACS	Medtr8g028600	1-aminocyclopropane-1-carboxylate synthase
33.2025	22.6475	ACS	Medtr8g098930	1-aminocyclopropane-1-carboxylate synthase
0.407777	0.046786	ACS	Medtr4g097540	1-aminocyclopropane-1-carboxylate synthase
52.2622	336.989	ACO	Medtr5g085330	1-aminocyclopropane-1-carboxylate oxidase
46.8868	165.751	ACO	Medtr3g083370	1-aminocyclopropane-1-carboxylate oxidase
14.4589	42.9741	ACO	Medtr2g025120	1-aminocyclopropane-1-carboxylate oxidase
7.47745	19.7655	ACO	Medtr3g088565	1-aminocyclopropane-1-carboxylate oxidase
1.17664	0.189009	ACO	Medtr1g043760	1-aminocyclopropane-1-carboxylate oxidase
5.80576	0.381962	ACO	Medtr8g024120	1-aminocyclopropane-1-carboxylate oxidase
6.46515	0.357816	ACO	Medtr1g070120	aminocyclopropanecarboxylate oxidase
0.05795	7.51682	ACO-L	Medtr8g028435	1-aminocyclopropane-1-carboxylate oxidase-like protein
1.59279	48.2452	ACO-L	Medtr1g032220	1-aminocyclopropane-1-carboxylate oxidase-like protein
1.16709	23.3807	ACO-L	Medtr1g032250	1-aminocyclopropane-1-carboxylate oxidase-like protein
0.05876	0.44284	ACO-L	Medtr1g032140	1-aminocyclopropane-1-carboxylate oxidase-like protein
4.21246	8.38377	ACO-L	Medtr4g099390	1-aminocyclopropane-1-carboxylate oxidase-like protein
46.4123	15.3528	ACO-L	Medtr4g117880	1-aminocyclopropane-1-carboxylate oxidase-like protein
60.8768	43.9499	GPI	Medtr5g065880	glucose-6-phosphate isomerase
46.6782	29.2285	GPI	Medtr6g009330	glucose-6-phosphate isomerase
21.9428	78.6897	GPI-L	Medtr7g116910	glucose-6-phosphate 1-epimerase-like protein
4.77392	0.722638	GPI-L	Medtr4g092780	glucose-6-phosphate 1-epimerase-like protein
62.6073	41.0816	G6PDH	Medtr1034s0010	glucose-6-phosphate 1-dehydrogenase
24.1502	14.5054	G6PDH	Medtr0590s0010	glucose-6-phosphate 1-dehydrogenase
21.5236	11.1966	G6PDH	Medtr7g111760	glucose-6-phosphate 1-dehydrogenase
20.9832	11.2963	G6PDH	Medtr0275s0010	glucose-6-phosphate 1-dehydrogenase
7.75127	378.812	GlgC	Medtr4g070430	glucose-1-phosphate adenyltransferase family protein
15.2253	99.1674	GlgC	Medtr3g116860	glucose-1-phosphate adenyltransferase family protein
118.531	208.528	GlgC	Medtr5g097010	glucose-1-phosphate adenyltransferase family protein
64.9239	48.9034	GlgC	Medtr3g082150	glucose-1-phosphate adenyltransferase family protein
145.958	34.3167	GlgC	Medtr4g131760	glucose-1-phosphate adenyltransferase family protein
0.806535	0.182397	GlgC	Medtr7g111020	glucose-1-phosphate adenyltransferase family protein
9.28271	560.857	APE2	Medtr2g022700	glucose-6-phosphate/phosphate translocator-like protein
433.367	174.379	FBPase	Medtr7g066120	fructose-1,6-bisphosphatase
25.979	13.2709	FBPase	Medtr4g093620	fructose-1,6-bisphosphatase
250.3	72.776	FBPase	Medtr6g035305	fructose-1,6-bisphosphatase, cytosolic-like protein
0.501292	0.087603	FBPase	Medtr2g008030	fructose-1,6-bisphosphatase, cytosolic-like protein
28.2472	47.7547	FBA	Medtr1g061050	fructose-bisphosphate aldolase
193.732	129.19	FBA	Medtr5g069050	fructose-bisphosphate aldolase
108.064	8.29535	FBA	Medtr5g096670	fructose-bisphosphate aldolase
255.707	147.846	cFBA	Medtr4g057670	fructose-bisphosphate aldolase class I
2805.73	1255.73	cFBA	Medtr4g071860	fructose-bisphosphate aldolase class I
39.8398	55.0008	pFBA	Medtr6g069660	fructose-bisphosphate aldolase class-II protein
49.3714	22.8812	FKFBP	Medtr3g464770	fructose-6-phosphate-2-kinase/fructose-2, 6-bisphosphatase
4.64322	2.48202	FKFBP	Medtr8g066450	fructose-6-phosphate-2-kinase/fructose-2, 6-bisphosphatase
43.0044	18.6331	FKFBP	Medtr5g071900	fructose-6-phosphate-2-kinase/fructose-2, 6-bisphosphatase
32.9084	64.1851	PPF	Medtr4g132700	pyrophosphate-fructose-6-phosphate 1-phosphotransferase
86.4387	43.6765	PPF	Medtr1g035230	pyrophosphate-fructose-6-phosphate 1-phosphotransferase
75.3817	32.4042	PPF	Medtr2g025020	pyrophosphate-fructose-6-phosphate 1-phosphotransferase
11.5014	7.90297	GFAT	Medtr7g080270	glucosamine-fructose-6-phosphate aminotransferase
1.50605	19.7827	LKR/SDH	Medtr4g124470	lysine-ketoglutarate reductase/saccharopine dehydrogenase
21.416	60.8072	DUF707-L	Medtr2g012570	lysine ketoglutarate reductase trans-splicing-like protein
0.188594	0.683537	DUF707-L	Medtr4g058800	lysine ketoglutarate reductase trans-splicing-like protein
4.72316	9.38377	DUF707-L	Medtr2g005330	lysine ketoglutarate reductase trans-splicing-like protein
3.76927	8.40902	DUF707	Medtr8g089820	lysine ketoglutarate reductase trans-splicing protein
22.9177	40.6687	DUF707	Medtr3g086610	lysine ketoglutarate reductase trans-splicing protein
0.036409	0.391954	GLR	Medtr2g015310	glutamate receptor 27
1.61681	2.70688	GLR	Medtr3g105595	glutamate receptor 32
16.0473	25.5125	GLR	Medtr2g088450	glutamate receptor 32
28.4751	43.982	GLR	Medtr5g024350	glutamate receptor 32
1.72447	0.8265	FPGS	Medtr1g028510	tetrahydrofolylpolyglutamate synthase
30.2332	21.5555	GLT	Medtr1g027020	NADH glutamate synthase
375.259	225.587	GLSF	Medtr7g089970	ferredoxin-dependent glutamate synthase
10.0575	33.0235	GAD	Medtr3g064740	glutamate decarboxylase
10.6646	1.87683	GDH	Medtr6g029460	NADP-specific glutamate dehydrogenase
40.4652	11.2278	GDH	Medtr7g085630	NADP-specific glutamate dehydrogenase
1.18988	4.42316	NodGS	Medtr1g062710	nodulin/glutamate-ammonia ligase-like protein
1354.52	613.394	GGAT	Medtr5g033230	glutamate-glyoxylate aminotransferase
303.199	87.6004	GASA1	Medtr3g118070	glutamate-1-semialdehyde 2,1-aminomutase
13.6836	40.2263	GABARAP	Medtr2g023430	gaba-receptor-associated protein ubiquitin domain protein
59.1437	92.2045	GABARAP	Medtr2g088230	gaba-receptor-associated protein ubiquitin domain protein
78.0739	116.506	GABARAP	Medtr4g101090	gaba-receptor-associated protein ubiquitin domain protein
64.168	88.8288	GABARAP	Medtr4g048510	gaba-receptor-associated protein ubiquitin domain protein
30.1675	158.107	TPS	Medtr1g109620	trehalose-6-phosphate synthase domain protein
29.0621	129.856	TPS	Medtr1g032730	trehalose-6-phosphate synthase domain protein
20.2449	49.7794	TPS	Medtr0034s0170	trehalose-6-phosphate synthase
13.8054	21.4043	TPS	Medtr2g073260	trehalose-6-phosphate synthase
22.4012	16.7394	TPS	Medtr4g080160	trehalose-6-phosphate synthase domain protein
4.28908	2.14877	TPS	Medtr4g129270	trehalose-6-phosphate synthase domain protein
8.04799	3.02819	TPS	Medtr8g105740	trehalose-6-phosphate synthase domain protein
50.7712	20.4159	TPP	Medtr4g036090	trehalose-phosphate phosphatase
2.23129	4.37979	TPP	Medtr4g101600	trehalose-phosphate phosphatase
9.57638	5.49931	HK	Medtr8g014530	hexokinase
10.9137	5.73095	HK	Medtr6g088795	hexokinase
3.38202	13.023	PFK	Medtr2g100710	6-phosphofructokinase
0.525803	1.31515	PFK	Medtr5g032570	6-phosphofructokinase
11.2548	26.9884	PFK	Medtr4g134290	6-phosphofructokinase
24.4676	54.5847	PFK	Medtr8g102190	6-phosphofructokinase
23.1086	47.2095	PFK	Medtr6g090130	6-phosphofructokinase

11.2702	50.4042	PGM	Medtr8g006290	phosphoglycerate mutase family protein
18.34	13.0719	PGM	Medtr4g092840	phosphoglycerate mutase family protein
75.32	38.3234	PGM	Medtr2g013570	phosphoglycerate mutase
44.0105	22.3197	PGM	Medtr3g111310	phosphoglycerate mutase family protein
1.90495	0.857637	PGK	Medtr6g018680	phosphoglycerate kinase
7.66652	3.45295	PGK	Medtr2g095260	2-phosphoglycerate kinase
0.469678	1.00654	PGK	Medtr1g056720	2-phosphoglycerate kinase
1536.74	327.218	PGK	Medtr2g066610	phosphoglycerate kinase-like protein
1.86224	0.826396	PGK	Medtr6g011290	phosphoglycerate mutase-like protein
13.4134	7.83134	PGK	Medtr7g009060	phosphoglycerate mutase-like protein
682.462	299.553	GLP	Medtr7g080530	phosphoglycolate phosphatase-like protein
56.0631	30.1008	PGDH	Medtr1g107480	D-3-phosphoglycerate dehydrogenase family protein
17.7314	52.2952	ALMT	Medtr5g014310	aluminum activated malate transporter family protein
2.89802	7.83636	ALMT	Medtr4g051575	aluminum activated malate transporter family protein
3.08243	7.52092	ALMT	Medtr4g098570	aluminum activated malate transporter family protein
119.282	44.3424	OMT	Medtr2g009220	2-oxoglutarate/malate translocator
164.826	35.2882	OMT	Medtr4g065007	2-oxoglutarate/malate translocator
45.4885	24.525	IPMS	Medtr1g116500	2-isopropylmalate synthase
51.0659	19.3914	IPMDH	Medtr2g104610	3-isopropylmalate dehydrogenase
464.035	112.462	gMDH	Medtr4g092690	glyoxysomal malate dehydrogenase
286.01	171.914	MDH	Medtr8g463760	malate dehydrogenase
190.785	108.574	MDH	Medtr1g076130	cytoplasmic-like malate dehydrogenase
265.539	150.151	MDH	Medtr1g043040	cytoplasmic-like malate dehydrogenase
11.191	4.49178	MDH	Medtr8g005980	cytoplasmic-like malate dehydrogenase
189.87	92.4863	ACLY	Medtr2g034090	ATP:citrate lyase
187.941	55.8366	ACLA-1	Medtr2g062920	ATP-citrate synthase alpha chain protein
30.176	48.9079	CSY3	Medtr3g048920	citrate synthase 3, peroxisomal protein
92.3021	123.627	IDH	Medtr5g077070	NADP-dependent isocitrate dehydrogenase
28.3778	9.77807	ASS	Medtr4g103680	argininosuccinate synthase
50.8709	23.5838	ADSL	Medtr7g092860	adenylosuccinate lyase
5.10698	2.51499	ADSL	Medtr5g081750	adenylosuccinate lyase
81.2238	48.7435	GLYR	Medtr8g028120	glyoxylate/succinic semialdehyde reductase
50.2928	13.4202	GLYR	Medtr2g099910	glyoxylate/succinic semialdehyde reductase
83.4239	177.931	SDH	Medtr5g020050	succinate dehydrogenase [ubiquinone] flavoprotein subunit
31.5611	45.7821	SDHB	Medtr1g492610	succinate dehydrogenase [ubiquinone] iron-sulfur subunit
59.6711	80.7958	SDHB	Medtr0018s0260	succinate dehydrogenase [ubiquinone] iron-sulfur subunit
53.2723	28.1818	ALPHA-SCS2	Medtr6g077820	succinyl-CoA ligase [ADP-forming] subunit alpha-2
12.9651	22.6348	BCCP	Medtr2g103280	biotin carboxyl carrier acetyl-CoA carboxylase
18.1025	9.43557	BCCP	Medtr6g015020	biotin carboxyl carrier acetyl-CoA carboxylase
28.0631	14.3313	BCCP	Medtr7g013100	biotin carboxyl carrier acetyl-CoA carboxylase
144.061	71.1014	BCCP	Medtr7g080290	biotin carboxyl carrier acetyl-CoA carboxylase
74.3424	36.076	ACC	Medtr8g101330	acetyl-CoA carboxylase biotin carboxylase subunit
5.35096	1.0041	accD	Medtr4g050863	acetyl-coA carboxylase carboxyltransferase beta subunit
64.9331	119.341	ACO	Medtr5g022940	cytoplasmic-like aconitate hydratase
13.7291	18.5585	ACO	Medtr4g048190	cytoplasmic-like aconitate hydratase
164.29	108.477	PGM	Medtr8g104540	cytoplasmic phosphoglucomutase
18.7936	36.5541	HPPD	Medtr5g091060	4-hydroxyphenylpyruvate dioxygenase
6.32472	9.93728	HPPD	Medtr5g090980	4-hydroxyphenylpyruvate dioxygenase
9.35988	18.592	PGLS	Medtr5g045000	glucosamine-6-phosphate isomerase/6-phosphogluconolactonase
57.3965	19.8764	PGLS	Medtr1g028320	glucosamine-6-phosphate isomerase/6-phosphogluconolactonase
51.7187	13.3864	PGLS	Medtr1g028330	glucosamine-6-phosphate isomerase/6-phosphogluconolactonase
159.017	116.395	PGD	Medtr7g017900	decarboxylating-like 6-phosphogluconate dehydrogenase
75.4566	53.3728	PGD	Medtr8g099185	decarboxylating-like 6-phosphogluconate dehydrogenase
6.74328	4.37057	PGDH	Medtr8g088900	6-phosphogluconate dehydrogenase-like protein
57.4216	24.6736	FH	Medtr1g087900	fumarate hydratase
2130.43	652.241	GAPDH	Medtr3g115920	glyceraldehyde-3-phosphate dehydrogenase B
4855.69	1115.1	GAPDH	Medtr7g084800	glyceraldehyde-3-phosphate dehydrogenase
0.687058	3.07768	NADP-GAPDH	Medtr1g014320	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
1028.75	443.604	RPE	Medtr4g108800	ribulose-phosphate 3-epimerase
58.0905	27.4291	Rubisco	Medtr4g021210	ribulose biphosphate carboxylase/oxygenase activase
92.5537	29.1866	Rubisco	Medtr2g105480	ribulose biphosphate carboxylase/oxygenase activase
86.8246	5.19883	RBCS	Medtr7g007200	ribulose biphosphate carboxylase small chain
128.607	6.21938	RBCS	Medtr7g007120	ribulose biphosphate carboxylase small chain
40.1342	0.88186	RBCS	Medtr7g007230	ribulose biphosphate carboxylase small chain
25.8692	7.63572	RBCL	Medtr4g051270	ribulose biphosphate carboxylase large chain domain protein
0.780575	0.198257	RBCL	Medtr6g055010	ribulose biphosphate carboxylase large chain domain protein
19.7333	70.6749	PEPEC	Medtr2g092930	phosphoenolpyruvate carboxylase
45.8304	66.0523	PEPEC	Medtr1g094010	phosphoenolpyruvate carboxylase
38.4137	54.632	PEPEC	Medtr2g076670	phosphoenolpyruvate carboxylase
57.0682	78.2569	PEPEC	Medtr1g094000	phosphoenolpyruvate carboxylase
69.6138	40.679	PEPEC	Medtr8g463920	phosphoenolpyruvate carboxylase
3.28823	1.25575	PEPEC	Medtr4g079860	phosphoenolpyruvate carboxylase
0.529471	1.03165	PCKA	Medtr5g430730	phosphoenolpyruvate carboxykinase [ATP] protein
3.70197	5.69649	PDC	Medtr2g015560	pyruvate decarboxylase
0.339392	0.108399	PDC	Medtr7g069540	pyruvate decarboxylase
0.607883	0.043344	PDC	Medtr2g009330	pyruvate decarboxylase
0.385012	0.159089	PDC	Medtr5g046610	pyruvate decarboxylase
28.2199	20.0905	PK	Medtr6g004020	pyruvate kinase family protein
54.5871	25.9717	PK	Medtr1g076540	pyruvate kinase family protein
47.2312	18.8652	PK	Medtr6g034195	pyruvate kinase family protein
18.1967	5.07857	PK	Medtr1g105965	pyruvate kinase family protein
1.95628	0.242755	PK	Medtr4g083340	pyruvate kinase family protein
7.92729	25.968	PPDK	Medtr4g118350	pyruvate orthophosphate dikinase
20.3592	53.9382	Enolase	Medtr6g060570	phosphopyruvate hydratase
339.055	243.955	Enolase	Medtr7g103620	phosphopyruvate hydratase
47.4263	26.195	PDK	Medtr7g024460	pyruvate dehydrogenase (acetyl-transferring) kinase
14.3581	7.59767	PDH2	Medtr3g076630	pyruvate dehydrogenase E1 beta subunit
40.6262	60.0095	PDHA1	Medtr5g036600	pyruvate dehydrogenase complex E1 alpha subunit
312.049	89.3826	GRHPR	Medtr1g112510	D-glycerate dehydrogenase/hydroxypyruvate reductase
0.732055	0.155978	GRHPR	Medtr4g013135	D-glycerate dehydrogenase/hydroxypyruvate reductase
34.4808	68.0237	GRHPR	Medtr6g007170	D-glycerate dehydrogenase/hydroxypyruvate reductase