

Table S1. Primer sequences used for real-time quantitative PCR

Gene ID	Primer name	Primer sequence (5'-3')	Experimental Use
MD04G1003300	<i>CHS-F</i>	CTAGTGACACCCACCTTGAYAG	RT-PCR
	<i>CHS-R</i>	AGAAGAGYGAGTTCCAGTCYGA	
MD01G1118100	<i>CHI-F</i>	GGTCCGTTTGAGAAATTCATTC	RT-PCR
	<i>CHI-R</i>	KGTTTTCTATCACCRYGTTTGC	
MD15G1353800	<i>F3H-F</i>	TCAACCAGTGGAAGGAGCTT	RT-PCR
	<i>F3H-R</i>	GTCCTGCAGTTGCTGTTCTT	
MD15G1024100	<i>DFR-F</i>	AGTCCGAATCCGTTTGTGTC	RT-PCR
	<i>DFR-R</i>	TTGTGGGCTTGATCACTTCA	
MD03G1001100	<i>ANS -F</i>	CACCTTCATCCTCCACAACAT	RT-PCR
	<i>ANS - R</i>	ATGTGCTCAGCAAAAGTTCGT	
MD15G1215500	<i>MYB114-F</i>	GAAGACCTTGTTAGAAGACGACGATATA	RT-PCR
	<i>MYB114-R</i>	TATGATCTTGCCGACTGTTGCATAT	
MD03G1266300	<i>bHLHA-like-F</i>	AACTAAGGGCCAAGGTGAAGG	RT-PCR
	<i>bHLHA-like-R</i>	CTGCTTATCCTAAATCGTCCTGC	
MD07G1137500	<i>bHLH33-F</i>	ATGTTTTTGCGACGGAGAGAGCA	RT-PCR
	<i>bHLH33-R</i>	TAGGCGAGTGAACACCATAACATTAAGG	
MD09G1193500	<i>MSI4-1F</i>	CCAGGCGTGATGTCTCCTTT	RT-PCR
	<i>MSI4-1R</i>	GCTGTCTTAGCGGACTGGTT	
JX162681	<i>MYB10-F</i>	ACGCCACCACAAACGTCGTCG	RT-PCR
	<i>MYB10-R</i>	GGCGCATGATCTTGGCGACAGT	
DQ341382	<i>18SR-F</i>	GAGCCTGAGAAACGGCTACC	RT-PCR
	<i>18SR-R</i>	GTCACTACCTCCCCGTGTCA	

Table S2. Transcription factors identified among the differentially regulated genes

Gene ID	log2 Ratio (RT/UIT)	FDR	Annotation
MD00G1000500	2.12	0.032445	MYB family transcription factor PHL11 [<i>Pyrus x bretschneideri</i>]
MD01G1054800	1.26	0.013987	MYB-related protein MYB4-like [<i>Malus domestica</i>]
MD01G1084400	4.51	2.98E-06	MYB-related protein 308-like [<i>Malus domestica</i>]
MD01G1144700	1.64	0.001018	transcription factor MYB86-like [<i>Malus domestica</i>]
MD01G1155100	2.98	0.006279	transcriptional activator MYB-like [<i>Malus domestica</i>]
MD02G1076300	-1.87	1.01E-05	MYB-like protein J [<i>Malus domestica</i>]
MD02G1087700	8.51	1.50E-51	transcription repressor MYB5-like [<i>Pyrus x bretschneideri</i>]
MD02G1179000	2.66	1.65E-240	transcription factor MYB44-like [<i>Malus domestica</i>]
MD03G1176000	3.17	0.003131	transcription factor MYB46-like [<i>Pyrus x bretschneideri</i>]
MD04G1060200	4.26	1.22E-27	transcription factor MYB114-like [<i>Malus domestica</i>]
MD04G1142200	1.41	8.14E-22	transcription factor MYB59-like [<i>Malus domestica</i>]
MD05G1089600	2.89	1.26E-28	transcription factor MYB44-like [<i>Malus domestica</i>]
MD05G1197600	4.14	5.01E-108	MYB-related protein MYB4-like [<i>Malus domestica</i>]
MD05G1224100	4.92	1.25E-07	MYB-related protein MYB4-like [<i>Malus domestica</i>]
MD05G1327500	4.58	1.78E-06	MYB-related protein MYB4-like [<i>Malus domestica</i>]
MD06G1054100	1.06	7.35E-20	MYBR domain class transcription factor [<i>Malus domestica</i>]
MD06G1192900	-1.37	2.06E-14	MYB-related protein 306-like [<i>Malus domestica</i>]
MD06G1229700	4.47	8.48E-11	MYB-related protein 308-like [<i>Malus domestica</i>]

Gene ID	log2 Ratio (RIT/UIT)	FDR	Annotation
MD07G1140400	6.67	1.81E-16	MYB-related protein Hv1 [<i>Malus domestica</i>]
MD07G1153200	7.63	1.08E-41	MYB-related protein 308-like [<i>Pyrus x bretschneideri</i>]
MD07G1224200	2.34	0.002668	transcription factor MYB23-like [<i>Malus domestica</i>]
MD08G1070800	2.29	3.29E-06	transcription repressor MYB6-like [<i>Malus domestica</i>]
MD08G1092000	2.58	0	transcription factor MYB44-like [<i>Malus domestica</i>]
MD08G1107400	7.11	4.92E-50	transcriptional activator MYB-like [<i>Malus domestica</i>]
MD09G1051000	2.03	8.20E-11	MYB-related protein 306 [<i>Malus domestica</i>]
MD10G1184100	7.61	2.11E-23	MYB-related protein MYB4 [<i>Malus domestica</i>]
MD10G1216700	-1.24	7.58E-27	MYB family transcription factor APL-like [<i>Pyrus x bretschneideri</i>]
MD12G1012700	4.94	1.95E-13	transcription factor MYB122 [<i>Malus domestica</i>]
MD12G1198600	2.41	2.33E-12	transcription factor MYB86-like [<i>Malus domestica</i>]
MD13G1039900	7.50	1.20E-22	MYB-related protein 305 [<i>Malus domestica</i>]
MD13G1075000	1.04	1.06E-10	transcription factor MYB51 isoform X1 [<i>Malus domestica</i>]
MD13G1148200	2.65	0.016425	transcription factor MYB108-like [<i>Malus domestica</i>]
MD14G1010600	3.65	8.23E-06	MYB-like protein Q [<i>Malus domestica</i>]
MD14G1172900	1.80	0.002607	transcription factor MYB86-like [<i>Pyrus x bretschneideri</i>]
MD14G1200100	-2.38	6.30E-20	MYB-related protein 306-like [<i>Pyrus x bretschneideri</i>]
MD14G1227500	5.06	0	transcription factor MYB108-like [<i>Malus domestica</i>]
MD14G1234500	2.26	1.12E-60	MYB-related protein Zm38-like [<i>Malus domestica</i>]
MD14G1234600	1.09	6.83E-11	MYB-related protein 308-like [<i>Malus domestica</i>]
MD15G1050300	2.69	0.008004	transcription factor MYB114-like [<i>Malus domestica</i>]
MD15G1062400	2.00	0.001084	transcription factor MYB36-like [<i>Malus domestica</i>]
MD15G1076600	2.75	0	transcription factor MYB44-like [<i>Malus domestica</i>]
MD15G1088000	3.98	5.79E-12	transcription factor MYB44-like [<i>Malus domestica</i>]
MD15G1168900	2.44	0.030753	transcription factor MYB82 [<i>Malus domestica</i>]
MD15G1204700	-1.64	2.81E-20	MYB-like protein J [<i>Malus domestica</i>]
MD15G1215500	5.86	4.65E-51	transcription factor MYB12 isoform X2 [<i>Malus domestica</i>]
MD15G1411200	1.79	1.856E-23	MYB transcription factor 3, partial [<i>Malus domestica</i>]
MD16G1010100	6.71	9.46E-17	putative MYB family transcription factor At1g14600 [<i>Malus domestica</i>]
MD16G1029400	1.43	3.33E-43	MYB-related protein 308-like [<i>Malus domestica</i>]
MD16G1040800	4.14	1.56E-13	transcription factor MYB21 [<i>Malus domestica</i>]
MD16G1076100	2.28	2.45E-21	transcription factor MYB88 [<i>Malus domestica</i>]
MD16G1148300	7.01	1.26E-18	transcription factor MYB108-like [<i>Malus domestica</i>]
MD16G1228600	2.53	5.25E-13	transcription factor MYB21-like [<i>Pyrus x bretschneideri</i>]
MD17G1051700	-1.49	0.000259	transcription factor MYB34-like [<i>Malus domestica</i>]
MD17G1261000	4.10	3.36E-10	transcription factor MYB114-like [<i>Malus domestica</i>]
MD17G1279200	1.82	0.017582	transcription factor MYB108-like [<i>Malus domestica</i>]
NEWGene_4845	4.76	4.49E-07	putative MYB family transcription factor At1g14600 [<i>Malus domestica</i>]
MD01G1037100	2.38	0.027946	transcription factor bHLH94-like [<i>Pyrus x bretschneideri</i>]
MD01G1045500	5.75	3.33E-64	transcription factor bHLH93 [<i>Malus domestica</i>]
MD01G1047200	7.07	2.97E-19	transcription factor bHLH18-like [<i>Malus domestica</i>]
MD01G1047400	3.52	3.04E-80	transcription factor bHLH18-like isoform X1 [<i>Malus domestica</i>]
MD01G1086900	3.44	1.11E-45	transcription factor bHLH14-like [<i>Malus domestica</i>]
MD01G1089300	2.65	1.45E-09	transcription factor bHLH57-like isoform X1 [<i>Malus domestica</i>]
MD01G1191700	4.28	1.30E-05	transcription factor bHLH120-like [<i>Malus domestica</i>]
MD02G1009200	1.12	0.003169	transcription factor bHLH66-like [<i>Malus domestica</i>]
MD03G1266300	1.84	2.38E-124	basic helix-loop-helix protein A-like [<i>Malus domestica</i>]
MD04G1161800	5.34	8.97E-13	transcription factor bHLH140-like [<i>Pyrus x bretschneideri</i>]
MD04G1208700	1.37	0.000596	transcription factor bHLH96-like [<i>Malus domestica</i>]
MD05G1065100	-3.03	1.83E-67	transcription factor bHLH49-like isoform X2 [<i>Malus domestica</i>]
MD05G1113000	1.51	8.45E-09	transcription factor bHLH18-like [<i>Malus domestica</i>]
MD05G1165800	1.17	6.09E-17	transcription factor bHLH62-like [<i>Malus domestica</i>]
MD05G1302400	6.60	5.79E-16	transcription factor bHLH30-like [<i>Malus domestica</i>]
MD06G1133200	2.29	9.14E-116	transcription factor bHLH137 [<i>Malus domestica</i>]
MD07G1151000	1.18	2.44E-41	transcription factor bHLH13 [<i>Malus domestica</i>]

Gene ID	log2 Ratio (RIT/UIT)	FDR	Annotation
MD08G1077000	1.34	6.88E-24	transcription factor bHLH74-like [<i>Malus domestica</i>]
MD08G1190500	2.84	0.000879	transcription factor bHLH96-like [<i>Malus domestica</i>]
MD08G1207700	5.14	3.59E-148	transcription factor bHLH61-like [<i>Malus domestica</i>]
MD10G1074000	-1.19	3.45E-29	transcription factor bHLH63 isoform X1 [<i>Malus domestica</i>]
MD10G1115500	3.56	2.83E-41	transcription factor bHLH18-like [<i>Pyrus x bretschneideri</i>]
MD10G1156100	3.72	1.15E-31	transcription factor bHLH62 [<i>Malus domestica</i>]
MD10G1281100	-1.24	6.39E-53	transcription factor bHLH30-like [<i>Malus domestica</i>]
MD12G1062600	-1.25	4.22E-15	transcription factor bHLH130-like [<i>Malus domestica</i>]
MD12G1063900	1.93	1.86E-17	transcription factor bHLH48-like [<i>Malus domestica</i>]
MD12G1223000	7.84	1.76E-36	transcription factor bHLH94-like [<i>Malus domestica</i>]
MD13G1083200	9.45	1.95E-130	transcription factor bHLH79-like [<i>Malus domestica</i>]
MD14G1063300	-1.60	1.38E-27	transcription factor bHLH130-like [<i>Malus domestica</i>]
MD14G1091000	-1.09	0.003271	transcription factor bHLH106-like [<i>Malus domestica</i>]
MD14G1149600	2.93	8.14E-51	transcription factor bHLH137-like [<i>Malus domestica</i>]
MD15G1154600	1.04	2.58E-21	transcription factor bHLH66-like [<i>Pyrus x bretschneideri</i>]
MD15G1208900	-1.22	7.29E-14	putative transcription factor bHLH041 isoform X1 [<i>Malus domestica</i>]
MD15G1392100	5.27	2.65E-15	transcription factor bHLH93-like [<i>Malus domestica</i>]
MD16G1082000	8.97	8.32E-138	transcription factor bHLH79-like [<i>Malus domestica</i>]
MD07G1137500	3.23	4.42E-71	bHLH33 [<i>Malus domestica</i>]
MD09G1193500	1.57	0.006595	WD-40 repeat-containing protein MSI4-like [<i>Malus domestica</i>]

Table S3. The results of GO term significant enrichment among DEGs (KS≤0.01).

GO_ID	Term	Annotated	Significant	KS
GO:0015979	photosynthesis	242	152	3.60E-20
GO:0055114	oxidation-reduction process	1726	603	6.90E-13
GO:0009765	photosynthesis, light harvesting	35	26	7.50E-11
GO:0006098	pentose-phosphate shunt	103	52	2.60E-10
GO:0010027	thylakoid membrane organization	97	51	6.40E-10
GO:0019252	starch biosynthetic process	77	41	1.90E-08
GO:0000023	maltose metabolic process	62	35	1.90E-08
GO:0010207	photosystem II assembly	65	34	2.10E-07
GO:0035304	regulation of protein dephosphorylation	35	23	7.00E-07
GO:0015995	chlorophyll biosynthetic process	68	35	9.50E-07
GO:0009902	chloroplast relocation	45	26	4.00E-06
GO:0016117	carotenoid biosynthetic process	62	32	9.80E-06
GO:0019344	cysteine biosynthetic process	66	32	2.00E-05
GO:0019288	isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway	108	44	3.30E-05
GO:0009773	photosynthetic electron transport in photosystem I	14	11	4.00E-05
GO:0030003	cellular cation homeostasis	42	22	5.40E-05
GO:0009595	detection of biotic stimulus	15	12	6.00E-05
GO:0009073	aromatic amino acid family biosynthetic process	60	26	6.10E-05
GO:0006730	one-carbon metabolic process	32	18	6.60E-05
GO:0019684	photosynthesis, light reaction	148	89	7.50E-05
GO:0009862	systemic acquired resistance, salicylic acid mediated signaling pathway	23	14	0.00013
GO:0006364	rRNA processing	146	56	0.00016
GO:0009637	response to blue light	46	22	0.00027
GO:0009611	response to wounding	60	28	0.0003
GO:0010264	myo-inositol hexakisphosphate biosynthetic process	23	14	0.00048
GO:0009867	jasmonic acid mediated signaling pathway	31	17	0.00076

GO_ID	Term	Annotated	Significant	KS
GO:0009813	flavonoid biosynthetic process	60	30	0.00079
GO:0015976	carbon utilization	9	7	0.00083
GO:0046148	pigment biosynthetic process	174	85	0.0009
GO:0010103	stomatal complex morphogenesis	45	23	0.00094
GO:0051186	cofactor metabolic process	370	153	0.0011
GO:0005975	carbohydrate metabolic process	1190	381	0.0012
GO:0009697	salicylic acid biosynthetic process	28	14	0.00138
GO:0009805	coumarin biosynthetic process	19	14	0.00141
GO:0010310	regulation of hydrogen peroxide metabolic process	24	14	0.00144
GO:1901617	organic hydroxy compound biosynthetic process	158	72	0.00159
GO:0052315	phytoalexin biosynthetic process	11	8	0.00168
GO:1901884	4-hydroxycoumarin biosynthetic process	9	7	0.00192
GO:1901886	2-hydroxybenzoyl-CoA catabolic process	9	7	0.00192
GO:0008299	isoprenoid biosynthetic process	242	100	0.00197
GO:0019761	glucosinolate biosynthetic process	36	17	0.00224
GO:0007568	aging	40	15	0.00229
GO:0006855	drug transmembrane transport	44	23	0.00237
GO:0044710	single-organism metabolic process	4340	1319	0.00295
GO:0009684	indoleacetic acid biosynthetic process	21	12	0.00304
GO:0030001	metal ion transport	290	94	0.00329
GO:0010114	response to red light	36	17	0.004
GO:0009693	ethylene biosynthetic process	27	15	0.00402
GO:0046417	chorismate metabolic process	15	8	0.00433
GO:0010218	response to far red light	38	17	0.00434
GO:0009698	phenylpropanoid metabolic process	101	42	0.00447
GO:0044550	secondary metabolite biosynthetic process	100	49	0.00561
GO:0006559	L-phenylalanine catabolic process	6	4	0.00587
GO:0006569	tryptophan catabolic process	19	11	0.00623
GO:0006032	chitin catabolic process	18	7	0.00729
GO:0006694	steroid biosynthetic process	75	29	0.00738
GO:0046394	carboxylic acid biosynthetic process	528	196	0.00767
GO:0043086	negative regulation of catalytic activity	117	38	0.00836
GO:0009617	response to bacterium	146	47	0.00853
GO:0009226	nucleotide-sugar biosynthetic process	15	9	0.00872
GO:0009695	jasmonic acid biosynthetic process	18	11	0.00876
GO:0010304	PSII associated light-harvesting complex II catabolic process	11	7	0.00934
GO:0045087	innate immune response	147	36	0.00953
GO:0009535	chloroplast thylakoid membrane	164	94	6.50E-18
GO:0009570	chloroplast stroma	318	141	1.50E-13
GO:0009654	photosystem II oxygen evolving complex	20	18	1.30E-09
GO:0009543	chloroplast thylakoid lumen	47	31	2.20E-09
GO:0009941	chloroplast envelope	299	118	2.30E-09
GO:0048046	apoplast	175	76	3.40E-07
GO:0022625	cytosolic large ribosomal subunit	79	41	3.30E-06
GO:0010287	plastoglobule	29	17	1.20E-05
GO:0009538	photosystem I reaction center	11	8	2.00E-05
GO:0010598	NAD(P)H dehydrogenase complex (plastoquinone)	6	6	4.50E-05
GO:0009523	photosystem II	49	36	0.00024
GO:0005618	cell wall	266	106	0.00025
GO:0009533	chloroplast stromal thylakoid	14	9	0.00028

GO_ID	Term	Annotated	Significant	KS
GO:0030076	light-harvesting complex	11	8	0.00055
GO:0009534	chloroplast thylakoid	213	121	0.00113
GO:0030095	chloroplast photosystem II	6	5	0.00124
GO:0009522	photosystem I	27	17	0.00126
GO:0043231	intracellular membrane-bounded organelle	3726	910	0.00131
GO:0044464	cell part	5776	1444	0.00136
GO:0009505	plant-type cell wall	72	32	0.00159
GO:0009579	thylakoid	317	175	0.00166
GO:0044444	cytoplasmic part	3280	839	0.00211
GO:0005886	plasma membrane	779	208	0.0024
GO:0009507	chloroplast	1086	384	0.00528
GO:0000786	nucleosome	82	25	0.00545
GO:0010319	stromule	22	12	0.0056
GO:0005945	6-phosphofructokinase complex	15	8	0.00595
GO:0043229	intracellular organelle	4238	1045	0.00628
GO:0046658	anchored component of plasma membrane	17	10	0.00635
GO:0020037	heme binding	282	118	7.00E-10
GO:0005506	iron ion binding	288	116	2.20E-06
GO:0016774	phosphotransferase activity, carboxyl group as acceptor	8	8	8.10E-06
GO:0070330	aromatase activity	16	13	9.60E-06
GO:0005507	copper ion binding	193	71	1.70E-05
GO:0009055	electron carrier activity	335	127	1.80E-05
GO:0004332	fructose-bisphosphate aldolase activity	12	8	8.40E-05
GO:0008666	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase activity	7	7	9.00E-05
GO:0004601	peroxidase activity	132	51	0.00023
GO:0043531	ADP binding	83	13	0.00025
GO:0016168	chlorophyll binding	18	11	0.00026
GO:0004097	catechol oxidase activity	18	10	0.00029
GO:0008171	O-methyltransferase activity	49	18	0.00035
GO:0003939	L-iditol 2-dehydrogenase activity	18	9	0.00041
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	342	141	0.00046
GO:0050661	NADP binding	79	36	0.0005
GO:0004420	hydroxymethylglutaryl-CoA reductase (NADPH) activity	10	8	0.00055
GO:0016838	carbon-oxygen lyase activity, acting on phosphates	21	13	0.0007
GO:0003854	3-beta-hydroxy-delta5-steroid dehydrogenase activity	15	7	0.00078
GO:0015297	antiporter activity	92	44	0.00079
GO:0016857	racemase and epimerase activity, acting on carbohydrates and derivatives	20	12	0.00088
GO:0008447	L-ascorbate oxidase activity	19	10	0.00094
GO:0004089	carbonate dehydratase activity	9	7	0.00101
GO:0003735	structural constituent of ribosome	407	133	0.0013
GO:0004857	enzyme inhibitor activity	66	28	0.00144
GO:0033815	biphenyl synthase activity	9	7	0.00176
GO:0090599	alpha-glucosidase activity	7	6	0.00222
GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	95	43	0.00231
GO:0047617	acyl-CoA hydrolase activity	6	2	0.00251
GO:0010181	FMN binding	29	15	0.00256
GO:0016210	naringenin-chalcone synthase activity	7	4	0.0026

GO_ID	Term	Annotated	Significant	KS
GO:0008422	beta-glucosidase activity	52	18	0.00291
GO:0050662	coenzyme binding	363	132	0.00321
GO:0004497	monooxygenase activity	222	91	0.00339
GO:0016762	xyloglucan:xyloglucosyl transferase activity	33	17	0.00379
GO:0016841	ammonia-lyase activity	10	6	0.00391
GO:0015301	anion:anion antiporter activity	13	8	0.00443
GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	84	36	0.00443
GO:0016706	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	108	43	0.00467
GO:0016710	trans-cinnamate 4-monooxygenase activity	6	5	0.00493
GO:0046527	glucosyltransferase activity	86	33	0.00565
GO:0003849	3-deoxy-7-phosphoheptulonate synthase activity	10	4	0.00608
GO:0005509	calcium ion binding	251	81	0.00614
GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	58	26	0.00651
GO:0016731	oxidoreductase activity, acting on iron-sulfur proteins as donors, NAD or NADP as acceptor	6	5	0.00659
GO:0004565	beta-galactosidase activity	23	12	0.00782
GO:0004620	phospholipase activity	32	12	0.00915
GO:0000062	fatty-acyl-CoA binding	7	3	0.00946
GO:0003872	6-phosphofructokinase activity	15	8	0.00962
GO:0045430	chalcone isomerase activity	8	6	0.00972

Table S4. Latin comparison table of the known *MYB* genes that regulate anthocyanin biosynthesis.

Latin Name of Species	The Known <i>MYB</i> Genes that Regulate Anthocyanin Biosynthesis Term
<i>Liquidambar formosana</i>	<i>LfMYB113</i>
<i>Ipomoea purpurea</i>	<i>IpMYB1</i>
<i>Arabidopsis thaliana</i>	<i>AtMYB90 ,AtMYB75 and AtMYB113</i>
<i>Nicotiana tabacum</i>	<i>NtAN2</i>
<i>Petunia hybrid</i>	<i>PhAN2</i>
<i>Lycopersicon esculentum</i>	<i>LeANT1</i>
<i>Vitis vinifera</i>	<i>VvMYBA1 and VvMYBA2</i>
<i>Antirrhinum majus</i>	<i>AmROSEA1</i>
<i>Myrica rubra</i>	<i>MrMYB1</i>
<i>Malus domestica</i>	<i>MdMYB110a and MdMYBA</i>
<i>Malus hybrid cultivar</i>	<i>McMYB10</i>

Table S5. Latin comparison table of the known *bHLH* genes that regulate anthocyanin biosynthesis.

Latin Name of Species	The Known <i>bHLH</i> Genes that Regulate Anthocyanin Biosynthesis Term
<i>Arabidopsis thaliana</i>	<i>AtGL3, AtEGL3, and AtTT8</i>
<i>Nicotiana tabacum</i>	<i>NtAn1a and NtAn1b</i>
<i>Petunia hybrida</i>	<i>PhAN1 and PhJAF13</i>
<i>Vitis vinifera</i>	<i>VvMYCA1 and VvMYC1</i>
<i>Dahlia pinnata</i>	<i>DvIVS</i>
<i>Malus domestica</i>	<i>MdbHLH3 and MdbHLH33</i>
<i>Lotus japonicas</i>	<i>LjTT8</i>
<i>Ipomoea nil</i>	<i>InIVS</i>
<i>Litchi chinensis</i>	<i>LcbHLH3 and LcbHLH1</i>