Table 1 Suppl. The anthocyanin synthesis related genes in some species used in this study.

Gene name	Origin	Genbank accession number
ThF3'5'H	*Torenia hybrida*	AB012925
VwF3'5'H	*Viola × wittrockiana*	AB332097
DgF3'5'H	*Delphinium grandiflorum*	AB818395
PhF3'5'H	*Petunia hybrida*	AB270615
NtF3'5'H	*Nicotiana tomentosiformis*	XM_009621551
NtTTG1	*Nicotiana tabacum*	FJ346578
BbF3'5'H	*Brunfelsia brasiliensis*	JQ678765
LuF3'5'H	*Lycium ruthenicum*	KC161969
IcF3'5'H	*Iochroma cyaneum*	KJ094354
StF3'5'H	*Solanum tuberosum*	HQ860267
PsF3'5'H	*Penstemon spectabilis*	KM576703
AkF3'5'H	*Antirrhinum kelloggii*	AB547160
CpF3'5'H	*Cyclamen persicum*	GQ891056
GmF3'5'H	*Clycine max*	NM001249703
VaF3'5'H	*Vitis amurensis*	KC753779
EeF3'5'H	*Eustoma exaltatum*	AB383117
EgF3'5'H	*Eustoma grandiflorum*	U72654
EsF3'5'H	*Epimedium sagittatum*	HM011055
AcF3'5'H	*Aconitum carmichaelii*	JN625708
DhF3'5'H	*Dendrobium hybrida*	KC345017
PhAN11	*Petunia hybrida*	PXU94748
StWD40	*Solanum tuberosum*	JX848661
IhWD40	*Ipomoea hochstetteri*	ADZ24791
NtTTG1	*Nicotiana tabacum*	FJ346578
ZmLC	*Zea mays*	NM_001111869
ZmB	*Zea mays*	NM_001105706
NtAN2	*Nicotiana tabacum*	FJ472650
PpMYB10	*Pyrus pyrifolia*	GU253310
VvMYBA1	*Vitis vinifera*	AB073013
VvMYBA2	*Vitis vinifera*	AB097924
PsMYB	*Phalaenopsis schilleriana*	FJ039862
OgMYB1	*Oncidium Gower*	EF570115
OsMYB	*Oryza sativa*	AY569615
PhJAF13	*Petunia hybrida*	AAC39455
PhAN1	*Petunia hybrida*	AAG25927
PhPH1	*Petunia hybrid*	KF690732
PhPH5	*Petunia hybrida*	DQ888719

Table 2 Suppl. The primers for reverse-transcription PCR in *Phalaenopsis* spp.

Gene name		5'-primer (stock number-sequences)	3'-primer (stock number-sequences)
Actin		AAGGCTGGATTTGCTGGTGA	CGCAGTGGTTGTGAAAGAGTAT
CHS	*CHS-1*	128-CCTCAAGGAGAAGTTCAAGCG	129-GGAAGGATGGTTTGGGAAGC
	CHS-2	144-GTGGAACGAAGACCTTCTCAGAG	145-CTCGTGAGCCGCCTCATTTGG
	CHS-3	142-TGTGACAAGACGGCAATCAG	143-GGCACCATCGGCAAATAAAG
	CHS-4	146-CTGGAACGAGGAATTTCTCAC	147-CAGCCGCCTCATCTGGATCAG
CHI	*CHI*	26-TGGAGGGAGTGAAGTTTCCG	27-AAGATGATGGAGGTGCCTGG
F3H	*F3H*	56-TCGGAAGCCATGGGACTAGATC	57-GCCTTTGCTCCAGTAACCTCAG
F3'H	*F3'H-1*	122-GAACGCTTGTGCGACTGATG	123-TGTGCTTGATGTGGTGTCCG
	F3'H-2	124-CCAAACCCTTCAGCACCTATC	33-GCTCCGCTAATATCCATTCTACTG
	F3'H-3	282-GCAGGGACTGAAACTACTTC	283-CCCAGCACCGAATGGTATTA
	F3'H-4	30-CCTCTACAAGCTCTCCCAAACC	31-CTCTATCAGCACGCTTAGCAGAT
F3'5'H	*F3'5'H*	58-GGACGAAGCTTTCTCCATGTCC	59-GAACGGTATCAGCTCAAAATCG
FLS	*FLS*	148-AGTTCAATCCATCGCCTCC	149-TTTCATCACCACCCAAAGC
DFR	*DFR*	22-TCAGGGCTACAGTCAGAGAC	91-GTACCTACCATTTGCGTCCGG
LDOX/ANS	*LDOX*	24-GGGACAGATACAGGGCTATG	25-TTGTGAAGGATGAAGGAGAGG
WD40	*WD40-1*	270-GTATCCTCCCACCAAGACCAT	271-TTCCAACCAAGGCGAACGAG
	WD40-2	42-GCGCATGATTCTCCACTAAACC	43-CCTGGTTACTGTCCATAAGAATGG
	WD40-3	272-ACAACAACAAATCGCCCGAG	273-CACAGGAACAGCAGGAGAAC
WRKY	*WRKY*	276-CTTTGCTTACCATTCCTCCTG	277-AGTCTCATCTCCATCACCATC
bHLH	*bHLH-1*	274-TCGGAGTTGATGGAGATTGGG	275-TCTTCTTCAGTGTCCTGGCAG
	bHLH-2	152-TGACTCCTTTGCTCCCAACA	153-TCTGCCTCTGCTTTCCAAGT
	bHLH-3	48-TCCCAGGTCATTAGAGTGGAATG	49-GTGAACTTGTGATGGCTCATTAG
R2R3-MYB	*MYB1*	116-TCGTCTTCATTGTCTCCTCGG	117-TTAGTTCCACTGCTCGCATCT
	MYB2	166-CGAAGGAAGGGCTCAACAAG	167-CAATGGTGCTGGCTTTGGTG
	MYB3	112-CTGGCTTGTTGAGATGTGGG	113-CTGCTTTCCTCTTCTTCGCC
	MYB11	108-GGTCTCAATAGGCGTGGAAAG	109-TGCTGGCTCATTTGTTGGGT
	MYB12	104-CCAGAAAGCAGGGCTAAACAG	105-CACCATCCAAACAGTCCAAATC
	MYB13	164-GAAGACGCATTGCTCACCAG	165-CGATGACGACCCTTTCCCTT
	MYB14	162-AGGAGCATACCAACAAGTGG	163-CCGAACCCAAGTAATGATTCAC
	MYB15	114-CGATAAGAAGGGGCTGAAGAAG	115-ACCTGTTTCCAATGGTGGAATG
	MYB17	110-GAAGAATGGGCTGAGGAAAGG	111-GCGACGACAAAGGTGAGAGT
R3-MYB	*MYBx-1*	192-ATGTTAGAAGGTCTCTTCTTGGTG	193-GACTTCCAATACTTCTCAATCTCC
	MYBx-2	194-CAGAGGGCGCTTCTGTTAATTC	195-AGCTGGGAAACAATACATACTCA
MADS	*MADS*	154-TCTGCGATGCTGAGGTTTCG	155-ATGTGAGACCCGTCATTTGC
LBD	*LBD-1*	156-AGCGTCCTGCTCTGTTTCAG	157-ATTTAGAAGCCTCGGACGGC
	LBD-2	158-CAATGGCTGCCGAGTTCTTC	159-CCTTCTCTTCCGTCACAGGT
Other regulators	*COP*	278-TAGTATCCAGTGGGCGTAGC	279-AGCATTGATGGTTCTGTCCG
	RIF	280-CCGCCACCACATCAGAATAG	281-TTTAGGCTGCTTGCCCTTCG

Table 3 Suppl. The primers for reverse-transcription quantitative PCR in *Phalaenopsis* spp.

Primer name	5'-primer (stock number-sequences)	3'-primer (stock number-sequences)
CHS-1	284-CACCTTCCACCTACTCAAAGAC	285-AGTCAGCGAGCACATTTCTAC
CHI	286-TGACGAGAGTGACGATGCTG	287-AAGATGATGGAGGTGCCTGG
F3H	288-AATCTCCTCGGCGTGCTATC	289-TTTACCGTCGTCCTTGGTGG
F3'H-1	290-AATCTATTCGCAGCAGGAACG	291-GGGATGTAGGCGGAAGGTTT
F3'5'H-1	291-GAATCCGACATACCAAATCTCCC	292-ACTCCAATGGCTTCTCCCAC
DFR	293-CAAGAGGTCAGGCAGCGTAA	294-CTTTCACGAACTCCCAAGCAG
LDOX	295-TACAGGGCTATGGGAGCAAG	296-AAGACCGAGGGAGAGTATGGA
Actin	CTCTTTCACAACCACTGCGG	TGGGCACCTAAATCTCTCAGC

Table 4 Suppl. The constructs used in this study.

Number of constructs	Gene	Vector	Purpose
5	*F3′5′H (Phalaenopsis)*	pDONR207	entry construct (with Stop codon)
6	*F3'5'H (Phalaenopsis)*	pK2GW2.0/rfa	overexpression
8	*VwF3′5′H (Viola)*	pK2GW2.0/rfa	overexpression
31	*MYB2 (Phalaenopsis)*	pDONR207	entry construct (with stop codon)
32	*MYB11 (Phalaenopsis)*	pDONR207	entry construct (with stop codon)
33	*MYB12 (Phalaenopsis)*	pDONR207	entry construct (with stop codon)
34	*MYB2 (Phalaenopsis)*	pK2GW2.0/rfa	overexpression
35	*MYB11 (Phalaenopsis)*	pK2GW2.0/rfa	overexpression
36	*MYB12 (Phalaenopsis)*	pK2GW2.0/rfa	overexpression
96	*AN1 (Petunia)*	pGBKT7/GW	yeast two -hybrid
97	*AN1 (Petunia)*	pGADT7/GW	yeast two -hybrid
100	*AN11 (Petunia)*	pGBKT7/GW	yeast two -hybrid
101	*AN11 (Petunia)*	pGADT7/GW	yeast two -hybrid
156	*MYB2 (Phalaenopsis)*	pDONR207	entry constructs (without stop codon)
157	*MYB2 (Phalaenopsis)*	pGBKT7/GW	yeast two-hybrid
158	*MYB2 (Phalaenopsis)*	pGADT7/GW	yeast two -hybrid
159	*MYB11 (Phalaenopsis)*	pDONR207	entry construct (without stop codon)
160	*MYB11 (Phalaenopsis)*	pGBKT7/GW	yeast two -hybrid
161	*MYB11 (Phalaenopsis)*	pGADT7/GW	yeast two -hybrid
162	*MYB12 (Phalaenopsis)*	pDONR207	entry construct (without stop codon)
163	*MYB12 (Phalaenopsis)*	pGBKT7/GW	yeast two -hybrid
164	*MYB12 (Phalaenopsis)*	pGADT7/GW	yeast two -hybrid

Suppl. Table 5. The primers for reverse transcription PCR in petunia.

Primer name	5'-primer (stock number-sequences)	3'-primer (stock number-sequences)
Actin	219b-CTACGAGGGTTATGCTTTGCC	220b-GCTGGAATGTGCTAAGGGATG
AN2	284-GCTTCATAAGCTTCTAGGCAAC	285-TAAGGCTGCTTTCAGCATTTAC
PH4	286-CATGGACACCAGAAGAAGATGA	287-AATGGCTTGTGAGTTCTAGGATC
PHZ	288-TAAGGCCACACATAAAGAGAGG	289-GGATCGACTTGTACTTGGGATAC
DPL1	290-CGGAGGAAGTGGACCTTATTC	291-GTTGTTATCTCTCGATACGACTTC
DPL2	292-TCTCTCCAGATGAAGTGGATCTT	293-TTGGCTTCTCGATGATAATTTCC
CHSa	350-CAGTGAGCACAAGACTGATC	351-TGGAGGACAACAGTCTCAAC
CHIa	352-ACGCTTTCGCACCGACCG	353-GTAGATTTCTCGGTCTCCG
F3H	354-CCAACAAGGGCAAGAGACT	355-GCTATTTGAGTTCACCACTGC
DFR	356-ACAATGTTCACGCTACTGTTC	357-GTAGGAACATAGTACTCTGG
LDOX	358-AGGAGTTGAAGAAAGCAGCC	359-ACACACTTAGCAGTTACCCAC
AN9	360-GGGAAGCAAACTAACAGGAAC	361- CTGGGATAGACACTGCTTCA
AAT	362-GTCTTATGCGAGTGGTGAGG	363-GGCATAGAACTAAACTCCACA

Table 6 Suppl. Anthocyanin synthesis related genes identified in *Phalaenopsis* genome.

Gene classification	Gene function	Gene designation	*Arabidopsis*	*Petunia*	*Phalaenopsis* genome number and gene name	Genome location	Orchid transcript database
Structural genes (14 members)	chalcone synthase	*CHS*	TT4 (At5G13930)	>7	PEQU_20125 *PeCHS-1*	scaffold000008	PATC124207
					PEQU_06483 *PeCHS-2*	scaffold000036	PATC125905
					PEQU_06485 *PeCHS-3*	scaffold000036	PATC124475
					PEQU_06486 *PeCHS-4*	scaffold000036	
	chalcone isomerase	*CHI*	TT5 (At3G55120)	3	PEQU_17251 *PeCHI*	scaffold000392	PATC143796
	flavanone 3-hydroxylase	*F3H*	TT6 (At3G51240)	1	PEQU_38891 *PeF3H*	scaffold218306	PATC151410
	flavonoid 3'-hydroxylase	*F3'H* (CYP75B1)	TT7 (At5G07990)	1	PEQU_00400 *PeF3'H-1*	scaffold000002	PATC194953
					PEQU_11493 *PeF3'H-2*	scaffold000873	PATC143258
					PEQU_11491 *PeF3'H-3*	scaffold000873	PATC157768 PATC158017
					PEQU_12719 *PeF3'H-4*	scaffold000061	PATC124290
	flavonoid 3', 5'-hydroxylase	*F3'5'H*		1	PEQU_18442 *PeF3'5'H*	scaffold000400	PATC137570
	flavonol synthase	*FLS1*	FLS1 (At5G08640)		PEQU_17337 *PeFLS*	scaffold000078	PATC138594
		FLS2	FLS2 (At5G63580)				
		FLS3	FLS3 (At5G63590)				
		FLS4	FLS4 (AT5G63595)				
		FLS5	FLS5 (AT5G63600)				
		FLS6	FLS6 (AT5G43935)				
	dihydroflavonol reductase	*DFR*	TT3 (At5G42800)	>3	PEQU_34933 *PeDFR*	scaffold233672	PATC148351
	leucoanthocyanidin dioxygenase/anthocyanidin synthase	*LDOX/ANS*	TT18 (At4G22880)		PEQU_25924 *PeLDOX*	scaffold000076	PATC213596
Modification and Transferring genes (9 members)	anthocyanin 5-O-glucosyltransferase	*UGT75C1*	At4G14090		PEQU_17545 *PeGT-1*	scaffold000210	PATC128032
	anthocyanin 3-O-glucoside: 2"-O-xylosyltransferase	*UGT79B1*	At5G54060		PEQU_06326 *PeGT-2*	scaffold000094	PATC112902
	UDP-glucose glucosyltransferase	*UGT84A2*	AT3G21560		PEQU_12598 *PeGT-3*	scaffold000359	PATC141084
	anthocyanin 3-O-6"-O-coumaroylglucoside: glucosyltransferase	*BGLU10*	At4G27830		PEQU_04044 *PeGT-4*	scaffold000002	PATC149204 PATC131922
	Methyltransferase	*OMT1*	At5G54160		PEQU_17856 *PeMT-1*	scaffold000204	PATC154210
				KJ639935.1	PEQU_02006 *PeMT-2*	scaffold000002	PATC132053
				KJ639934.1	PEQU_31160 *PeMT-3*	scaffold000869	PATC157288
					PEQU_31161 *PeMT-4*	scaffold000869	PATC131750 PATC143296

	anthocyanin 5-aromatic acyltransferase	*A5GlcMalT*	At3G29590		no hit			
	anthocyanin coumaroyltransferase (BAHD)	*A3GlcCouT*	At1G03495		no hit			
		A3GlcCouT	At1G03940		no hit			
	anthocyanin sinapoyltransferase (SCPL)	A3Glc2"XylSinT (*SCPL10*)	At2G23000		no hit			
	glutathione S-transferase	*GSTF12*	TT19 (At5G17220)		no hit			
	multi-drug and toxic efflux (MATE) transporter	*TT12*	At3G59030		no hit			
	transparent Testa 9	*TT9*	AT3G28430		PEQU_17601	*PeAT*	scaffold000263	PATC128565
Regulatory genes (26 members)	WD40	*TTG1*	AT5G24520	*AN11*	PEQU_07807	*PeWD40-1*	scaffold000297	PATC125923
					PEQU_40013	*PeWD40-2*	scaffold197238	PATC142255
					PEQU_10345	*PeWD40-3*	scaffold000090	
					PEQU_03426	*PeWD40-4*	scaffold000002	PATC128885
	bHLH	*TT8*	AT4G09820	*AN1*	PEQU_19744 ((partial CDS))	*PebHLH-1*	scaffold000545 (749735-750257)	PATC147535
					PEQU_19747 (partial CDS)		scaffold000545 (761837-778862)	
		GL3	AT5G41315	*JAF13*	PEQU_00717	*PebHLH-2*	scaffold000002	PATC144366
		AtEGL3	AT1G63650		PEQU_26133	*PebHLH-3*	scaffold001058	PATC128898
	R2R3-MYB	*AtMYB11*	AT3G62610		PEQU_30611	*PeMYB3*	scaffold226954	PATC153632
		AtMYB12	AT2G47460		PEQU_14880 (partial CDS)	*PeMYB17*	scaffold000436	PATC056759
		AtMYB111	AT5G49330					
					PEQU_34075 (partial CDS)	*PeMYB18*	scaffold001342	PATC041804
		MYB5		*PH4*	PEQU_16344	*PeMYB14*	scaffold000504	PATC064572
					PEQU_39447	*PeMYB1a*	scaffold210401	PATC129648
					PEQU_40997	*PeMYB1b*	scaffold204963	
					PEQU_14547	*PeMYB13*	scaffold000413	PATC071507
		AtMYB113	AT1G66370	*AN2*				
		AtMYB114	AT1G66380	*PHZ*				
		MYB75 (*PAP1*)	AT1G56650	*DPL*				
		MYB90 (*PAP2*)	AT1G66390					
		MYB123 (*TT2*)	AT5G35550		PEQU_11292	*PeMYB2*	scaffold000347	PATC095567
					PEQU_10361	*PeMYB11a*	scaffold000090	PATC151122
					PEQU_10362	*PeMYB11b*	scaffold000090	PATC055158
					PEQU_20333	*PeMYB12*	scaffold000221	No hit
	R3-MYB	*CPC*	AT2G46410	*MYBx*	PEQU_06243	*PeMYBx-1*	scaffold000094	PATC069281

					PEQU_30334	*PeMYBx-2*	scaffold001055	No found
		AtMYBL2	AT1G71030		no hit			
	WRKY	*TTG2*	AT2G37260	*PH3*	PEQU_09833	*PeWRKY*	scaffold000240	PATC151849
	Zn-finger	*TT1*	AT1G34790		no hit			
	MADS	*TT16*	AT5G23260		PEQU_18912	*PeMADS*	scaffold000672	PATC138350
	LOB-domain protein	*AtLBD37*	AT5G67420		PEQU_15233	*PeLBD-1*	scaffold000421	PATC153211
		AtLBD38	AT3G49940				scaffold001303	PATC148635
		AtLBD39	AT4G37540		PEQU_19038	*PeLBD-2*	scaffold191247	PATC152029
		COP1	AT2G32950		PEQU_18985	*PeCOP*	scaffold000191	PATC139502
	other regulators	R-interacting factor1 (In maize, NM_001112584)			PEQU_14989	*PeRIF*	scaffold000191	PATC144759
pH regulatory genes	P-type H$^+$-ATPase	*AHA10*	At1G17260 (TT13)	*PH5*	PEQU_23488 (More similar with AHA7)			PATC132361
				PH1	no hit			

Suppl. Table 7. The gene pairs that are involved in anthocyanin synthesis in *Phalaenopsis*

Gene pairs	Gene name	*Phalaenopsis* genome number	Genome location
CHS	*PeCHS-3*	PEQU_06485	scaffold000036
	PeCHS-4	PEQU_06486	scaffold000036
F3'H	*PeF3'H-2*	PEQU_11493	scaffold000873
	PeF3'H-3	PEQU_11491	scaffold000873
MT	*PeMT-3*	PEQU_31160	scaffold000869
	PeMT-4	PEQU_31161	scaffold000869
R2R3-MYB	*PeMYB1a*	PEQU_39447	scaffold210401
	PeMYB1b	PEQU_40997	scaffold204963
	PeMYB11a	PEQU_10361	scaffold000090 (352908- 354157)
	PeMYB11b	PEQU_10362	scaffold000090 (359313-360404)
WD40	*PeWD40-2*	PEQU_40013	scaffold197238
	PeWD40-3	PEQU_10345	scaffold000090

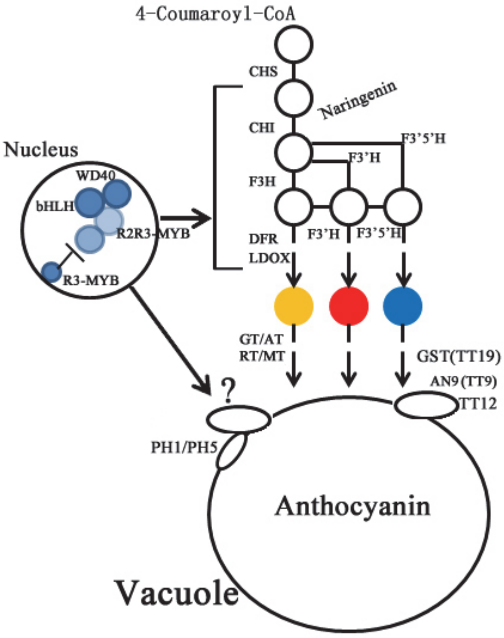


Fig. 1 Suppl. The model of anthocyanin biosynthetic pathway.

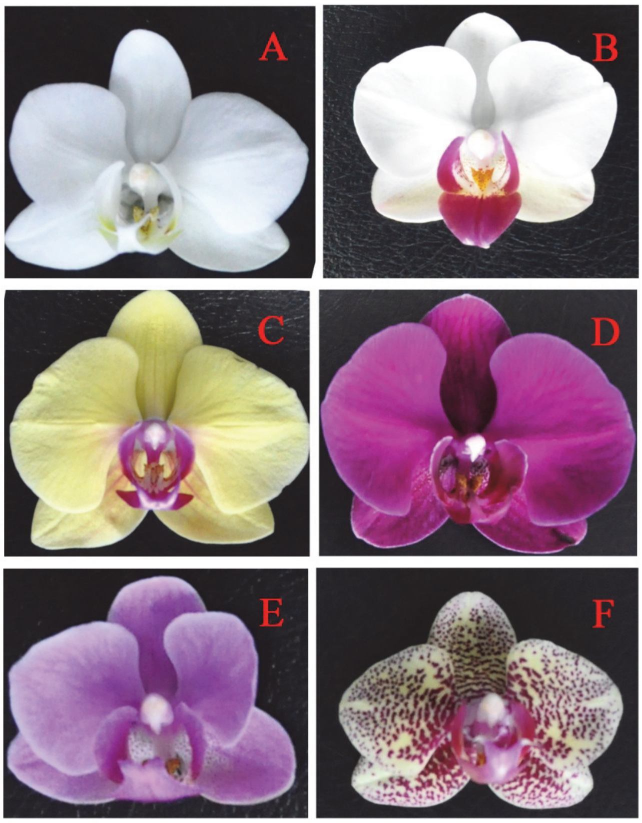


Fig. 2 Suppl. *Phalaenopsis* species used in this study. *A* - *Phalaenopsis* cv. Sogo Yukidian V3, *B* - cv. Sogo Lit-Sunny, *C* - cv. Fuller's Sunset, *D* - cv. Big Chili, *E* - cv. Wedding Promenade , *F* - cv. Sogo Passat.

Fig. 3 Suppl. The flower development stage of *Phalaenopsis*: *A* - stage 1, *B* - stage 2, *C* - stage 3, *D* - stage 4, and *E* - stage 5. *Red bar* means the scale of 10 mm.

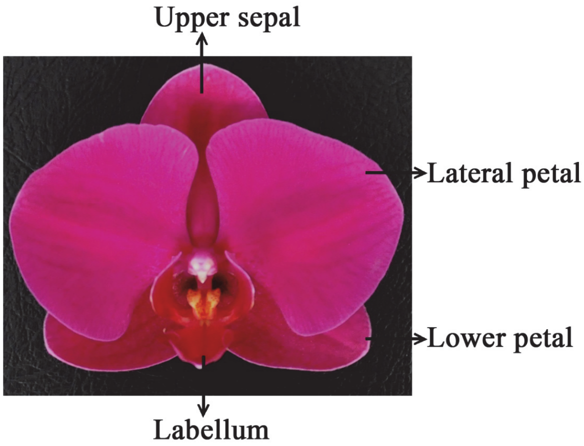
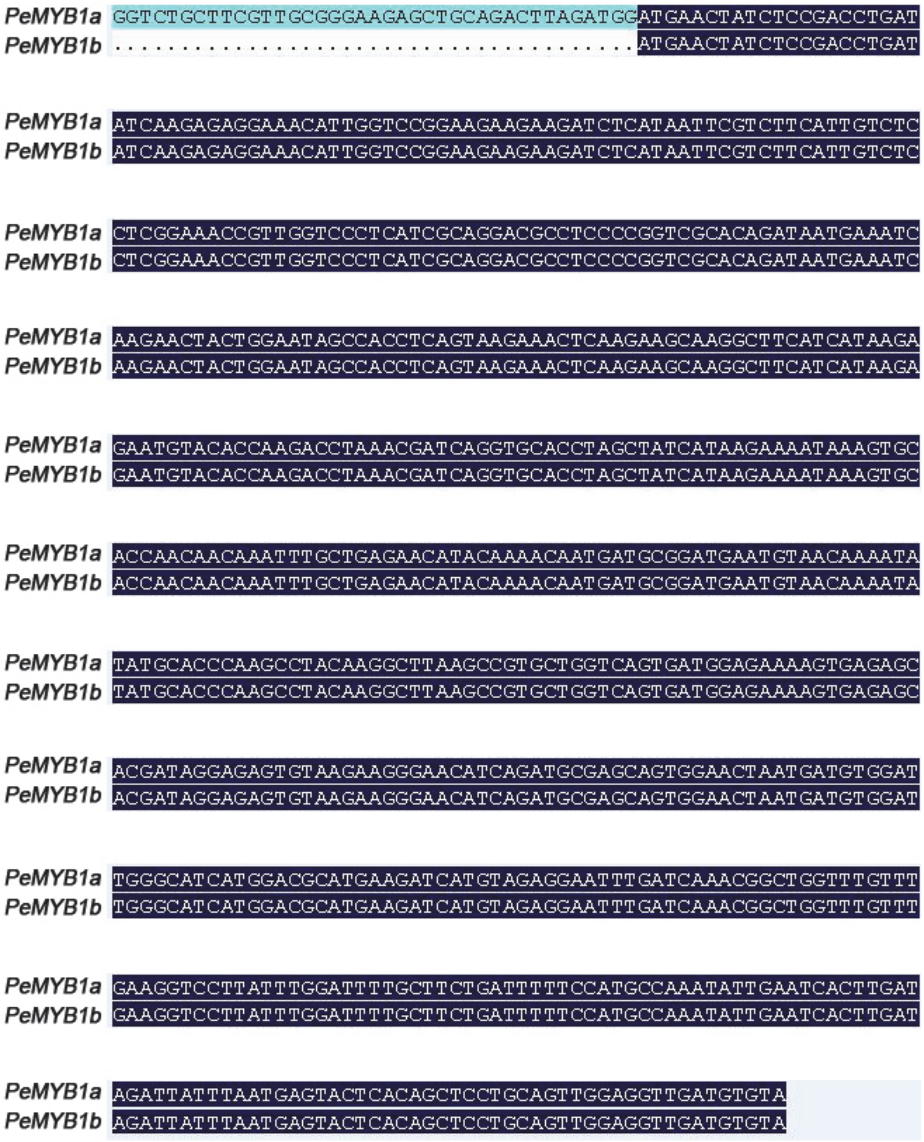


Fig. 4 Suppl. The flower floral organs of *Phalaenopsis*.



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PeMYB1b ATCAAGAGAGGAAACATTGGTCCGGAAGAAGAAGATCTCATAATTCGTCTTCATTGTCTC

PeMYB1a CTCGGAAACCGTTGGTCCCTCATCGCAGGACGCCTCCCCGGTCGCACAGATAATGAAATC
PeMYB1b CTCGGAAACCGTTGGTCCCTCATCGCAGGACGCCTCCCCGGTCGCACAGATAATGAAATC

PeMYB1a AAGAACTACTGGAATAGCCACCTCAGTAAGAAACTCAAGAAGCAAGGCTTCATCATAAGA
PeMYB1b AAGAACTACTGGAATAGCCACCTCAGTAAGAAACTCAAGAAGCAAGGCTTCATCATAAGA

PeMYB1a GAATGTACACCAAGACCTAAACGATCAGGTGCACCTAGCTATCATAAGAAAATAAAGTGC
PeMYB1b GAATGTACACCAAGACCTAAACGATCAGGTGCACCTAGCTATCATAAGAAAATAAAGTGC

PeMYB1a ACCAACAACAAATTTGCTGAGAACATACAAAACAATGATGCGGATGAATGTAACAAAATA
PeMYB1b ACCAACAACAAATTTGCTGAGAACATACAAAACAATGATGCGGATGAATGTAACAAAATA

PeMYB1a TATGCACCCAAGCCTACAAGGCTTAAGCCGTGCTGGTCAGTGATGGAGAAAGTGAGAGC
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PeMYB1a ACGATAGGAGAGTGTAAGAAGGGAACATCAGATGCGAGCAGTGGAACTAATGATGTGGAT
PeMYB1b ACGATAGGAGAGTGTAAGAAGGGAACATCAGATGCGAGCAGTGGAACTAATGATGTGGAT

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PeMYB1b TGGGCATCATGGACGCATGAAGATCATGTAGAGGAATTTGATCAAACGGCTGGTTTGTTT

PeMYB1a GAAGGTCCTTATTTGGATTTTGCTTCTGATTTTTCCATGCCAAATATTGAATCACTTGAT
PeMYB1b GAAGGTCCTTATTTGGATTTTGCTTCTGATTTTTCCATGCCAAATATTGAATCACTTGAT

PeMYB1a AGATTATTTAATGAGTACTCACAGCTCCTGCAGTTGGAGGTTGATGTGTA
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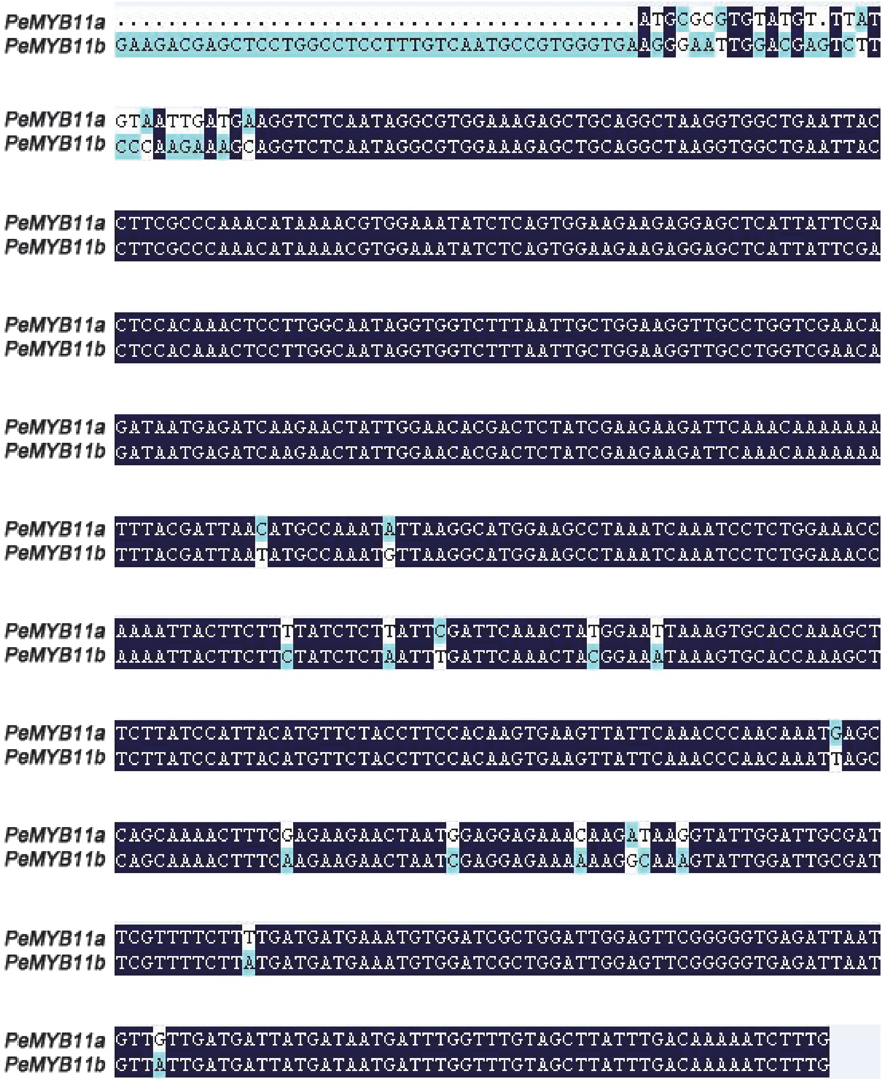
Fig. 5 Suppl. Comparison of sequences of two *PeMYB1* gene pairs.



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PeMYB11a GTAATTGATGAAGGTCTCAATAGGCGTGGAAAGAGCTGCAGGCTAAGGTGGCTGAATTAC
PeMYB11b CCCAAGAAAGCAGGTCTCAATAGGCGTGGAAAGAGCTGCAGGCTAAGGTGGCTGAATTAC

PeMYB11a CTTCGCCCAAACATAAAACGTGGAAATATCTCAGTGGAAGAAGAGGAGCTCATTATTCGA
PeMYB11b CTTCGCCCAAACATAAAACGTGGAAATATCTCAGTGGAAGAAGAGGAGCTCATTATTCGA

PeMYB11a CTCCACAAACTCCTTGGCAATAGGTGGTCTTTAATTGCTGGAAGGTTGCCTGGTCGAACA
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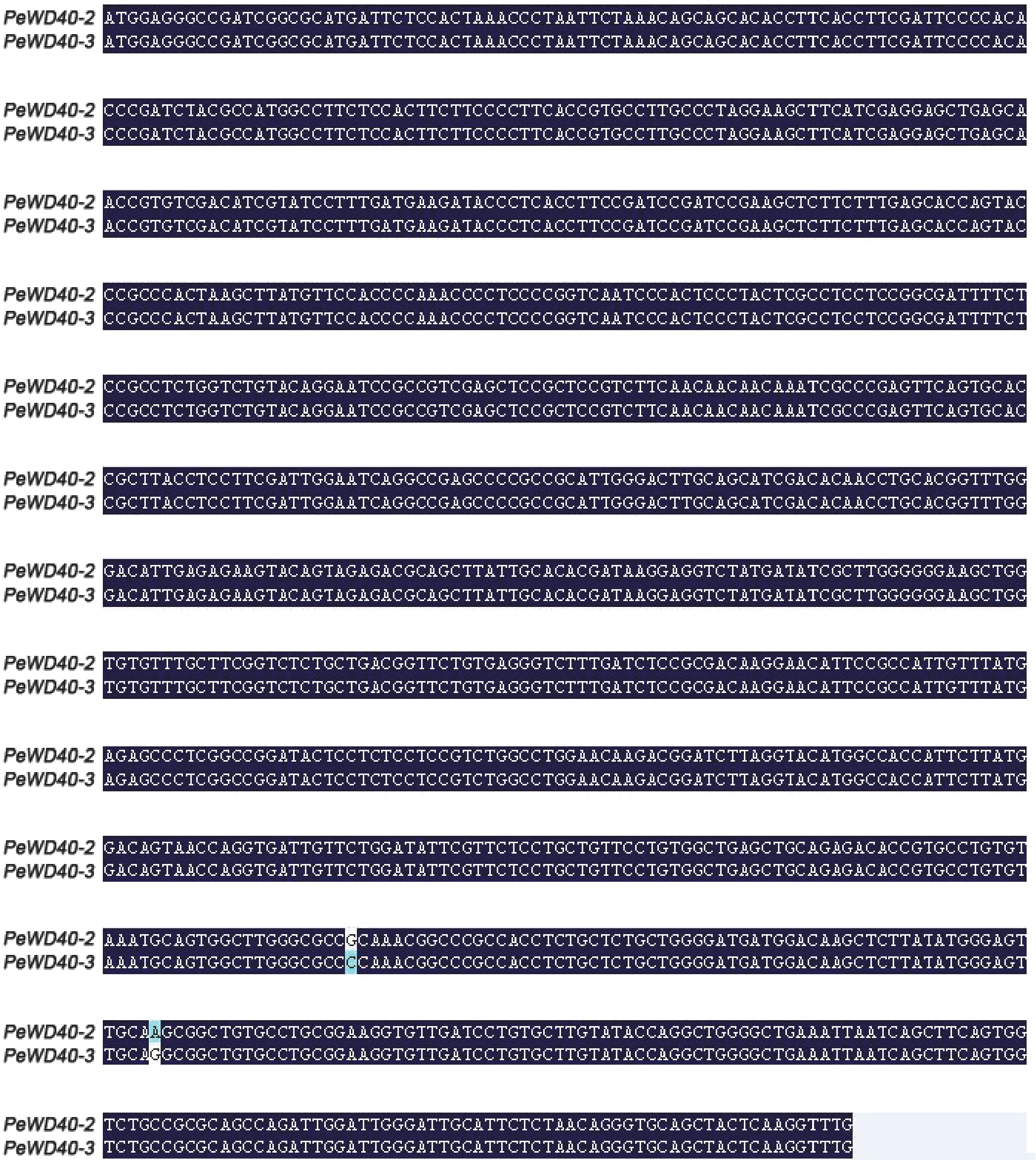
Fig. 6 Suppl. Comparison of sequences of two *PeMYB11* gene pairs.



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PeWD40-2 CCGCCCACTAAGCTTATGTTCCACCCCAAACCCCTCCCCGGTCAATCCCACTCCCTACTCGCCTCCTCCGGCGATTTTCT
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Fig. 7 Suppl. Comparison of sequences of *PeWD40-2* and *3*.

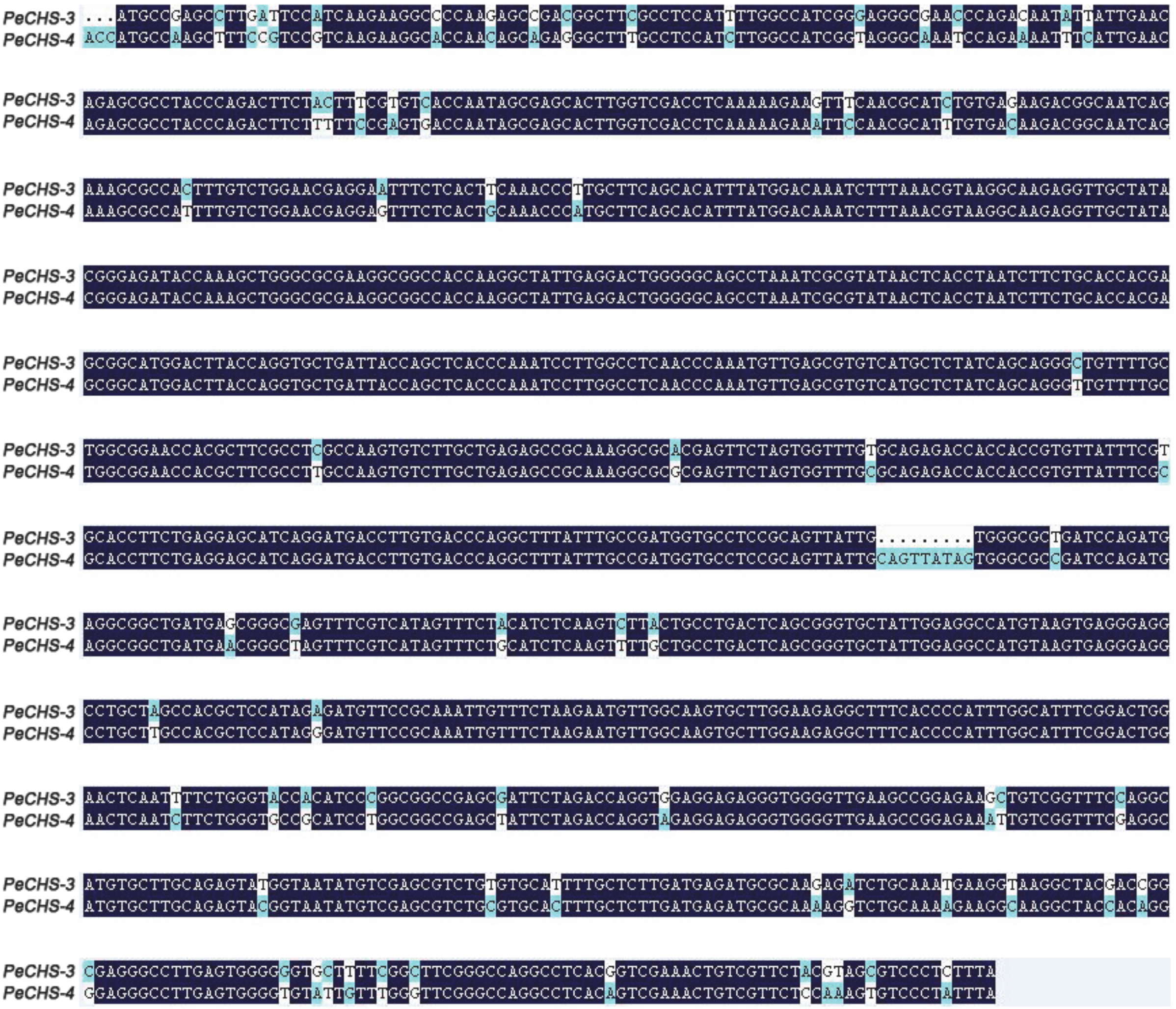

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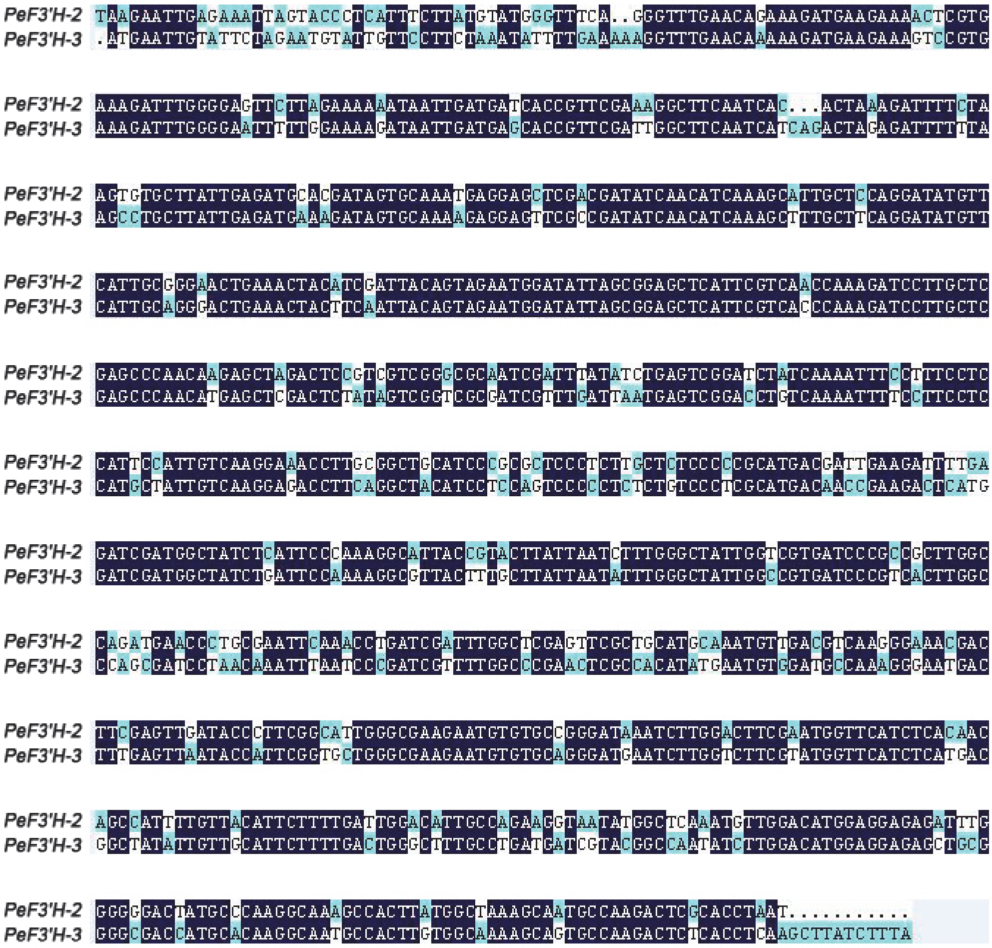
Fig. 8 Suppl. Comparison of sequences of *PeCHS-3* and *4*.



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PeF3'H-2 AAAGATTTGGGGAGTTCTTAGAAAAAATAATTGATGATCACCGTTCGAAAGGCTTCAATCAC...ACTAAAGATTTTCTA
PeF3'H-3 AAAGATTTGGGGAATTTTTGGAAAAGATAATTGATGAGCACCGTTCGATTGGCTTCAATCATCAGACTAGAGATTTTTTA

PeF3'H-2 AGTGTGCTTATTGAGATGCACGATAGTGCAAATGAGGAGCTCGACGATATCAACATCAAAGCATTGCTCCAGGATATGTT
PeF3'H-3 AGCCTGCTTATTGAGATGAAAGATAGTGCAAAAGAGGAGTTCGCCGATATCAACATCAAAGCTTTGCTTCAGGATATGTT

PeF3'H-2 CATTGCGGGAACTGAAACTACATCGATTACAGTAGAATGGATATTAGCGGAGCTCATTCGTCAACCAAAGATCCTTGCTC
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PeF3'H-2 GATCGATGGCTATCTCATTCCCAAAGGCATTACCGTACTTATTAATCTTTGGGCTATTGGTCGTGATCCCGCCGCTTGGC
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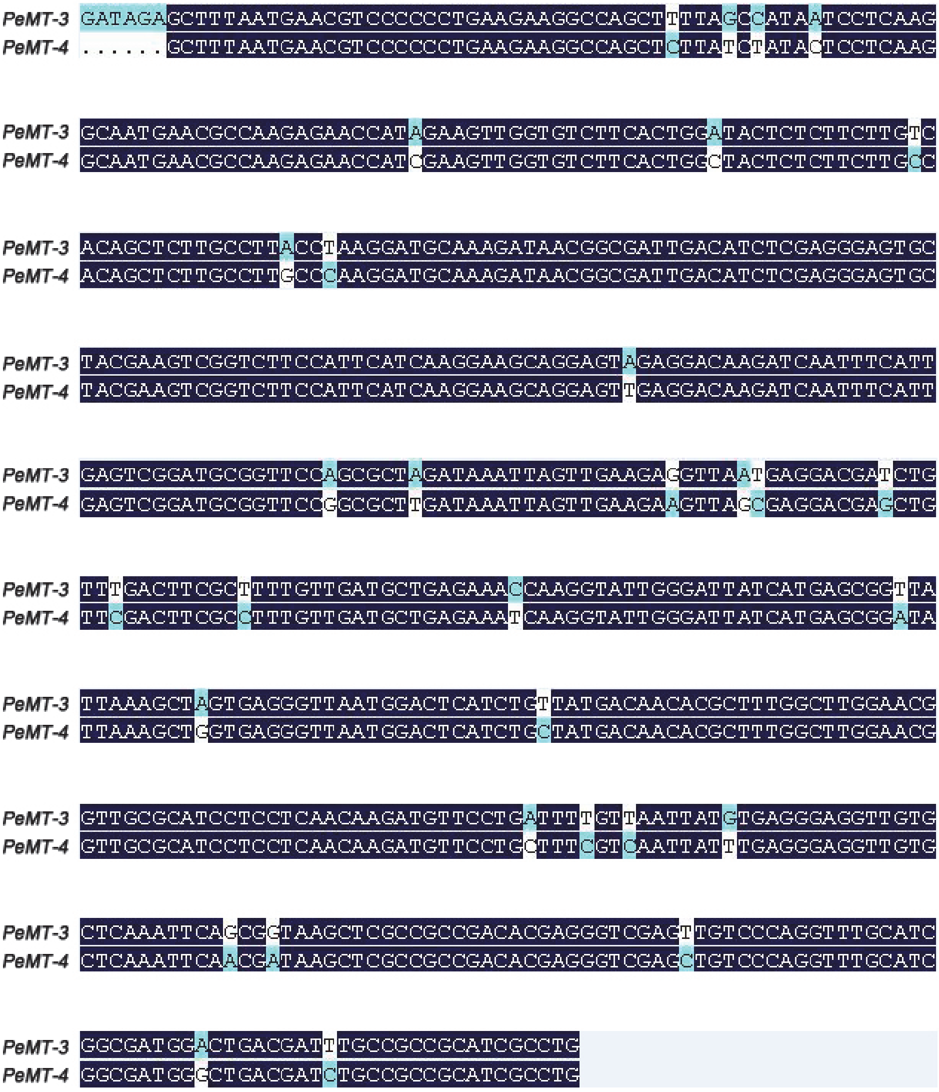
Fig. 9 Suppl. Comparison of sequences of *PeF3'H-2* and *3*.



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PeMT-3 ACAGCTCTTGCCTTACCTAAGGATGCAAAGATAACGGCGATTGACATCTCGAGGGAGTGC
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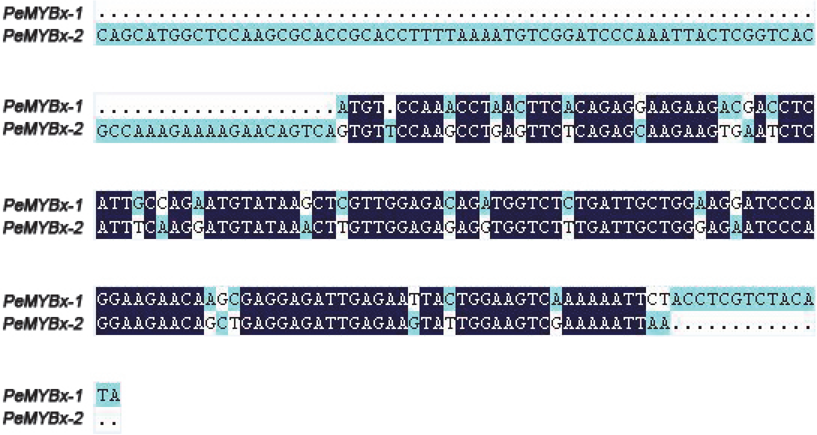
Fig. 10 Suppl. Comparison of sequences of *PeMET-3* and *4*.



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PeMYBx-1 ATTGCCAGAATGTATAAGCTCGTTGGAGACAGATGGTCTCTGATTGCTGGAAGGATCCCA
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PeMYBx-1 GGAAGAACAAGCGAGGAGATTGAGAATTACTGGAAGTCAAAAAATTCTACCTCGTCTACA
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PeMYBx-1 TA
PeMYBx-2 ..
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Fig. 11 Suppl. Comparison of sequences of *PeMYBx-1* and *2*.

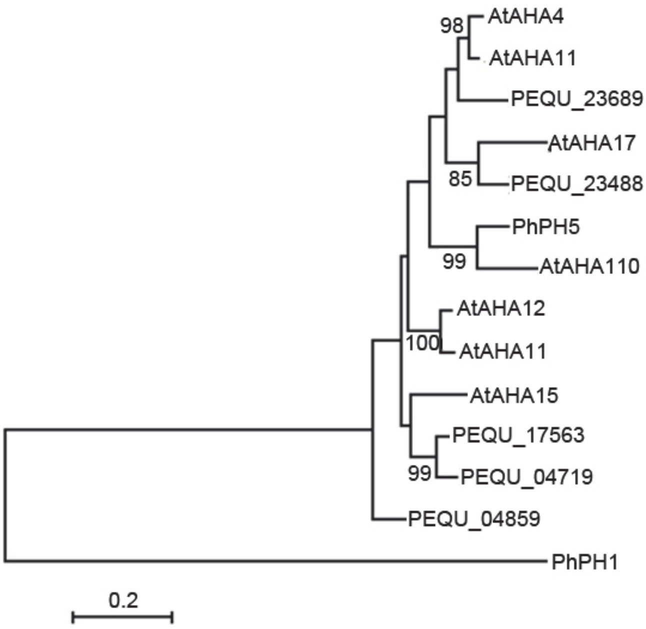

Fig. 12 Suppl. Phylogenetic tree of the genes encoding P-type H$^+$-ATPase in *Arabidopsis, Petunia*, and *Phalaenopsis.*

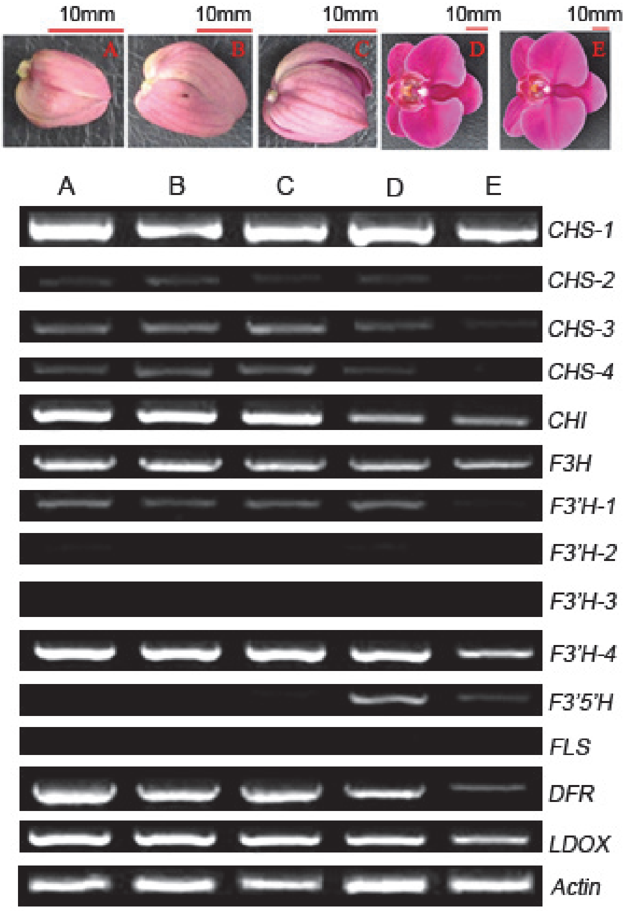

Fig. 13 Suppl. Comparative expression pattern analysis of anthocyanin synthesis structural genes in *Phalaenopsis* cv. Big Chili at different flower development stage.

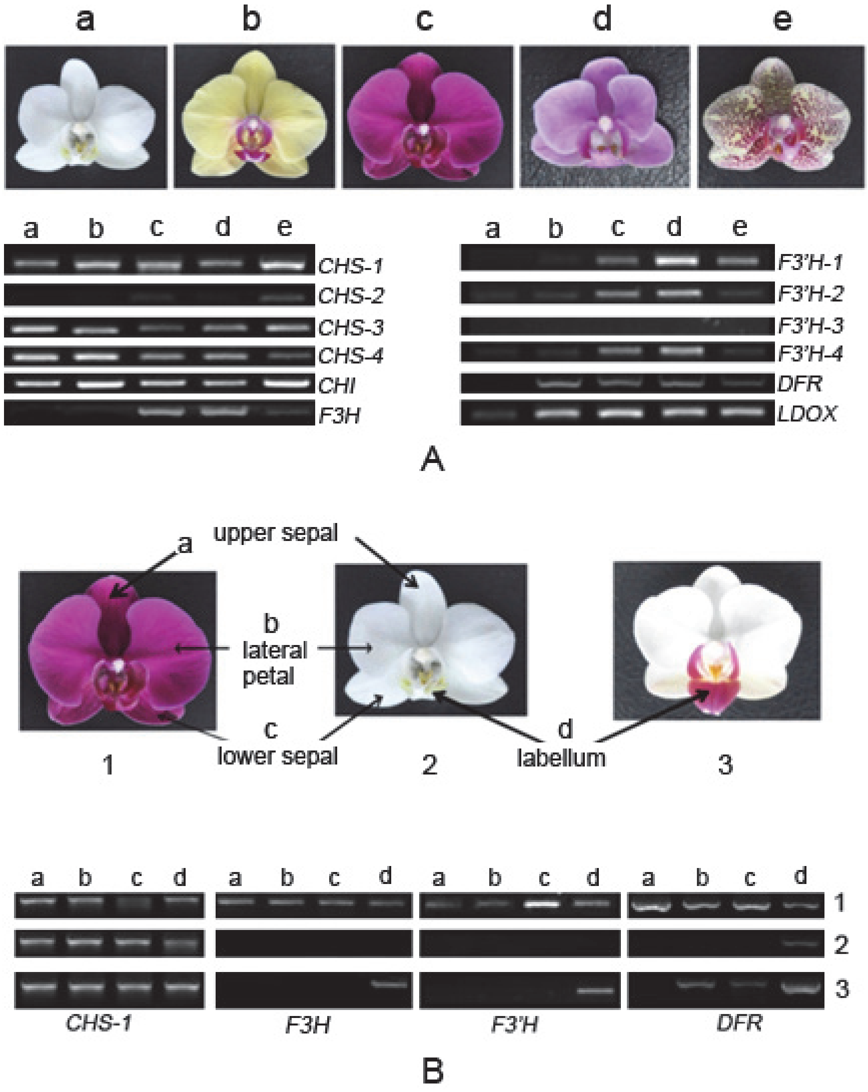

Fig. 14 Suppl. Expression patterns of anthocyanin synthesis structural genes in *Phalaenopsis* (a - cv. Sogo Yukidian V3, b - cv. Fuller's Sunset, c - cv. Big Chili, d - cv. Wedding Promenade, e - cv. Sogo Passat) with flowers of different colour (*A*) and in different flower organs (*B*).

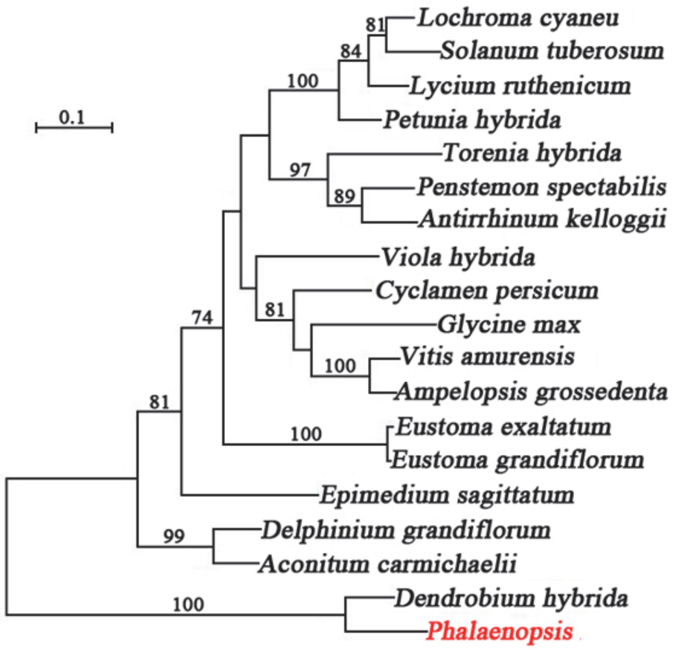

Fig. 15 Suppl. Phylogenetic tree of the genes encoding F3′5′H in *Phalaenopsis* and other plants.

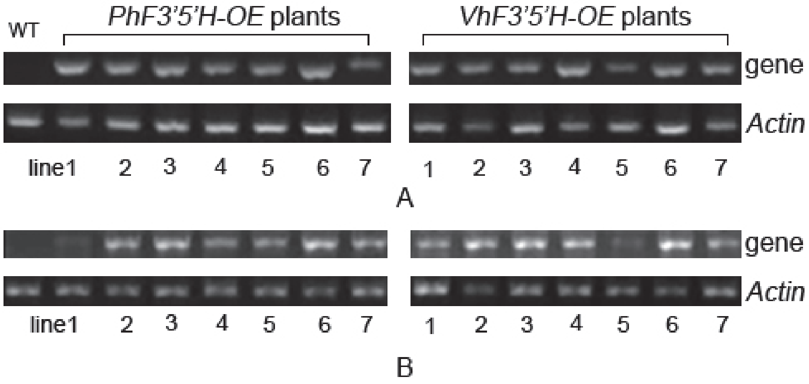

Fig. 16 Suppl. Identification of the *F3′5′H*-OE transgenic plants by PCR from DNA (*A*) and RT-PCR from cDNA (*B*).

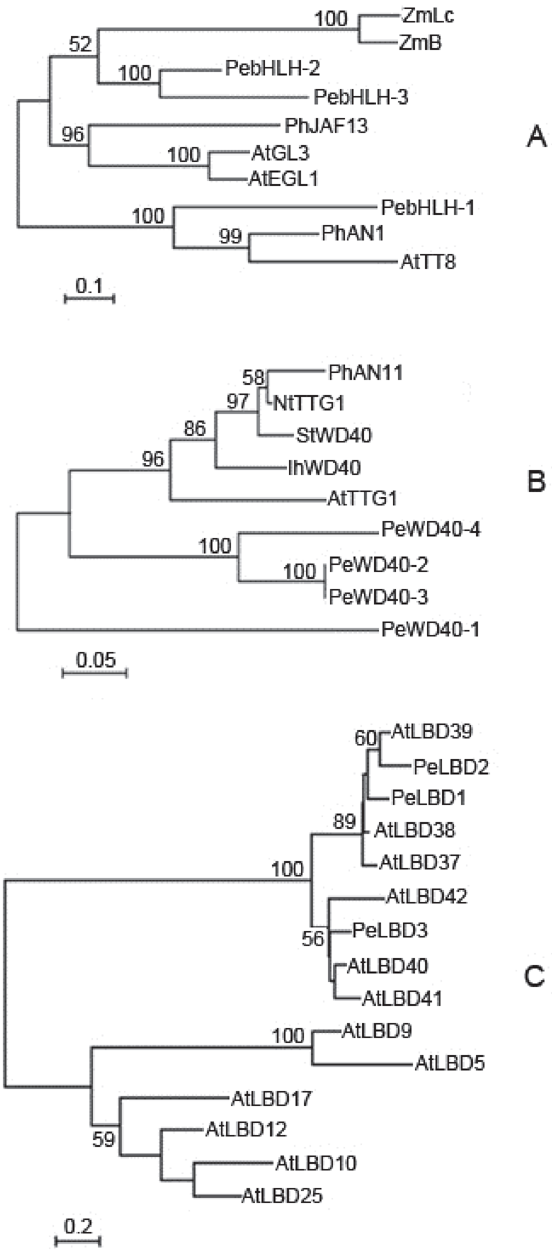

Fig. 17 Suppl. Phylogenetic tree of the genes encoding WD, bHLH, and LBD proteins in relation to regulating anthocyanin synthesis.

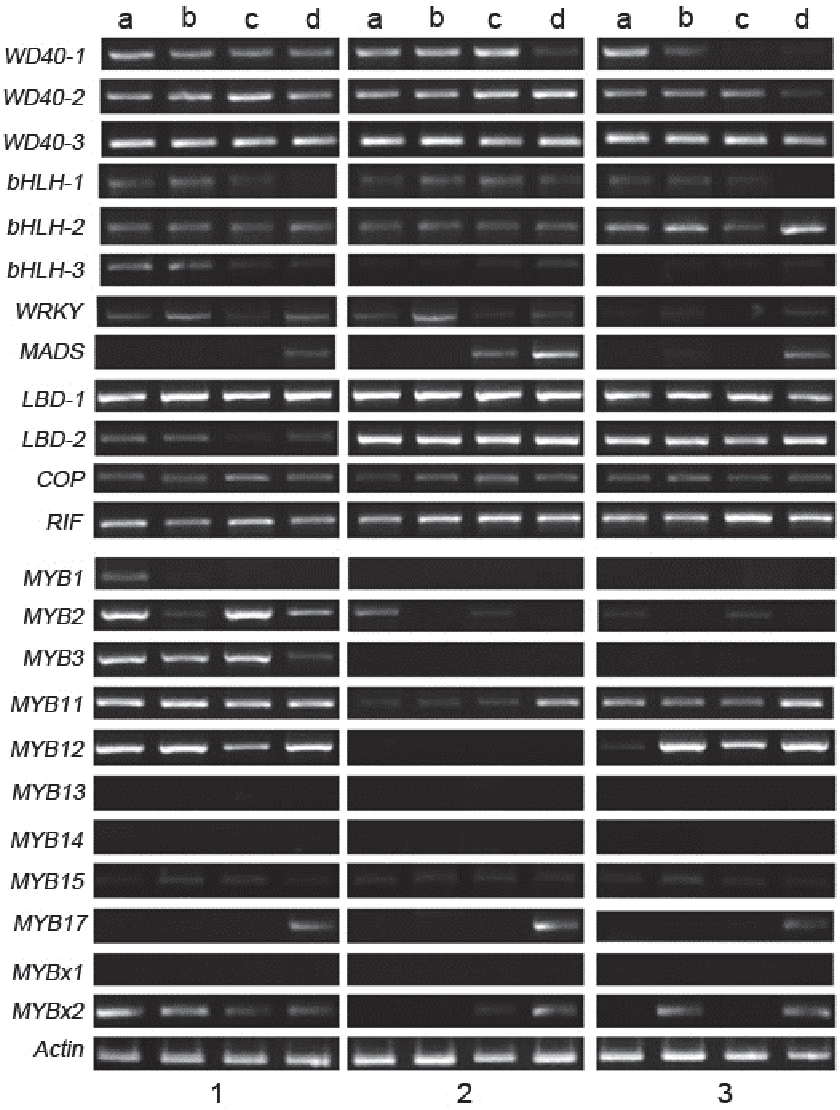

Fig. 18 Suppl. Comparative expression pattern analysis of regulatory genes in different corolla tissues: a - upper sepal, b - lateral petal, c - lower sepal, and d - labellum. Different *Phalaenopsis* spp. (1 - cv. Big Chili, 2 - cv. Sogo Yukidian V3, and 3 -cv. Sogo lit-sunny) were used.

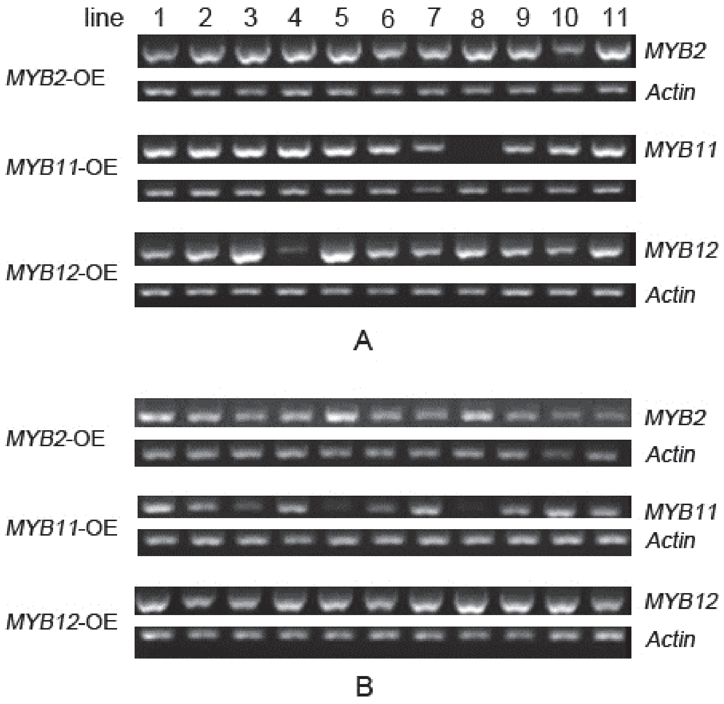

Fig. 19 Suppl. Identification of the *MYB2*-OE, *MYB11*-OE, and *MYB12*-OE transgenic plants by PCR from DNA (*A*) and RT-PCR from cDNA (*B*).