

SUPPLEMENTARY DATA

FIG. S1. Alignment of SsGAMYB amino acids and the homologous genes in *A. thaliana*, *O. sativa* and *H. vulgare*. The asterisks mark the R2R3 domain and BOX 1, 2 and 3 of SsGAMYB.

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SsGAMYB	(1)	MTSESE—EWMIS—KNGIDSPSDVSSGG—NVGANGPLKKGWPTS AEDAILVDYVVKHGE GNWNA	
AtMYB33	(1)	MSYTTSDSD—HNESPAADDNGSDCRS—RWDGHALKKGWSSAEDDILIDYVVKHGE GNWNA	
AtMYB65	(1)	MSYTTATADSDGMHSSIHNE SPAPDSISNGCRS—RGRSVLKKGPWTS TEDGILIDYVVKHGE GNWNA	
AtMYB101	(1)	MDGGGETTATATMEGRGLKKGWPTTDEDAILTEYVVKHGE GNWNA	
OsGAMYB	(1)	MYRVKSESDCEMIHQE—QMDSPVADDGSSGG—SPHRGGG—PPLKKGWPTS AEDAILVDYVVKHGE GNWNA	
HvGAMYB	(1)	MYRVKSESDCEMHQED—QMDSPVGGDGGSSGGSPHRGGG—PPLKKGWPTS AEDAILVDYVVKHGE GNWNA	
			***** R2R3 *****
SsGAMYB	(61)	VQKHSGLARCGKSCRLRWANHLRPNLKKGAFSPPEERHITELHAKMGNKWARMAAELPGRTDNEIKNYWN	
AtMYB33	(60)	VQKHTSLPRCGKSCRLRWANHLRPNLKKGAFSQEEELIVELHAKMGNKWARMAAHLPGRTDNEIKNYWN	
AtMYB65	(69)	VQKHTSLARCGKSCRLRWANHLRPNLKKGAFSQEEELIVELHAKMGNKWARMAAHLPGRTDNEIKNYWN	
AtMYB101	(46)	VQKNSGLRRCGKSCRLRWANHLRPNLKKGAFSTPEEKIITLHAKLGNKWARMAAHLPGRTDNEIKNYWN	
OsGAMYB	(68)	VQKNTGLPRCGKSCRLRWANHLRPNLKKGAFITPEERLITLHAKMGNKWARMAAHLPGRTDNEIKNYWN	
HvGAMYB	(70)	VQKNTGLPRCGKSCRLRWANHLRPNLKKGAFITPEERLITLHAKMGNKWARMAAHLPGRTDNEIKNYWN	
			***** ** BOX1 **
SsGAMYB	(131)	TRIKRRQRAGLPITYPPDICTQAFNDNQNEDMAAFSSGDVHHPDFLPINNFEIPAVEFKLELNQQLHPQ	
AtMYB33	(130)	TRIKRRQRAGLPITYPEMHVEALEWSQE—YAKSRVMGEDRR—HQDFLQLGSCESNVFFDTLNFT	
AtMYB65	(139)	TRIKRRQRAGLPITYPEIYVDDLHWSEE—YTKSNIIRVDRRRRHQDFLQLGNSKDNVLFDDLNF	
AtMYB101	(116)	TRIKRRQRAGLPITYPEIQHQGIDIDDE—FEFD—ITS—FQFQNDLQDHNHQM	
OsGAMYB	(138)	TRIKRQRAGLPITYPTSVCGSSNEDQQ—CSSDFDCGENLS—NDLLNANGLYLPDFTCDNFIAN	
HvGAMYB	(140)	TRIKRQRAGLPITYPASVCGSSNEDQQ—GSSDFRCGENLS—SDLLNGLYLPDFTCDNFIAN	
SsGAMYB	(201)	AFLDIPANSLLDIPASSLLAQLNSSYPNKVLLSTIYPSKFRGSESLFGLSAAVGSTLPDSNQYQSDG	
AtMYB33	(192)	D—MVPGTPDLADMTAYKNMGNCASSPRYENFMPTIIPSSKRLWESELLYPGCSSTIKQEFSSPEQFRNTS	
AtMYB65	(203)	ASLLPAASDLSLVACNMLGTGASSRYSYEMPPILPSPKQIWESGSRFPCCSSNIKHEFQSPHFQNTA	
AtMYB101	(166)	IQYTNSSNTSSSSSSFSSSSQSKRLRPDFLVSTNPLNIPDSSMDFQMFSLYNNLENDNNQFGFSV	
OsGAMYB	(200)	SEALPYAPHLSAVSISNLLGQSFAS—KSCSFMQVNVQTG—MLKQSDGVLPGLSDTINGVLISSVDQFSNDS	
HvGAMYB	(202)	SEALSYAPQLSAVSISNLLGQSFAS—KNCQFMQVNVQAG—MLKQSDPLPGLSDTINGALSSVDQFSNDS	
SsGAMYB	(271)	SVEIFQPSVFSAYDHNSTPDHASS—SVLPGSHAILNGNTSSSEPTTWAMKLELPSLQTHMG—S	
AtMYB33	(261)	PQTISKTCSPVPCDVEHPLYGNRHS—PVMIPDSHTPTDGLVPYSKPLYGAVKLELPSFQYSET—TFDQ	
AtMYB65	(273)	VQKNRSCSIS—POVDVHHPYENQHSMMMPDSHTVYGMHPTSKPLFGAVKLELPSFQYSETSAFDQ	
AtMYB101	(236)	PLS—SSSSNEVCNPNHILEYISEN—SDTRNTKKDIDAMSYSSLVGDLEIRSSSPFLGLDNSVLE	
OsGAMYB	(268)	EK—LKQAVGFDYLHEANSTKIIAPFGGALNGSHAFLNGNFSASRPTSGLKME LPSLQDTE S—DPNS	
HvGAMYB	(270)	EK—LKQALGFDYLHEANSSKIIAPFGGALNGSHAFLNGNFTSRTINGFLKME LPSLQDTE S—DPNS	
			***** ** BOX2 **
SsGAMYB	(334)	VGSPSSP—LPSLESVDITLQITPPV—EHPHSSNLSSQNSGLLDAVLYESHSMK—NSKNSFQQTSHAS	
AtMYB33	(328)	WKSSSPPH—SDLLDPFDITIQSPPPP—TGEEESDLYSNFDTGLLDMLLLEAKIRNNSTKNNLYRSCASTI	
AtMYB65	(342)	WKTTPSPPH—SDLLDSVDAYIQSPPPP—SQVEESDQFSSCDTGLLDMLLLEAKIKT—SAKHSLLMSSPQKS	
AtMYB101	(301)	LPSNQRPHTSPSSPIIDNGVHLEPP—SGNSGLLDALLDESQLS—RGLPKDVRVSSS	
OsGAMYB	(334)	WLKYTVAPA—LQPTLVDPYVQSPAA—TPSVKSEPCASPRNSGLLEELLHEAQLR—SGKNQQTSVISSSS	
HvGAMYB	(336)	WLKYTVAPA—MQPTLVDPYVQSPTA—TPSVKSEPCASPRNSGLLEELLHEAQLR—SGKNKQLSVRSSSS	
SsGAMYB	(398)	IMPVDMINTSSQDLHEADWVFAEPI SPLGRSSSSVFSSECTPISGSS—FDELQSVFMPVKEEAADRLVL	
AtMYB33	(397)	PSADLQGVTVSQTKSEFDNSLKS—FLVHSEMS—TQNADE	
AtMYB65	(409)	FSSITCTTNTQNVPRGSENLKSGE—YEDSQYLGRSEITSPSQLSAGGFSSAFAGNVVKTTEELDQ	
AtMYB101	(358)	DLCEVQDKRYKDFENLLIDHLNS—SNHSSLGANPNHNKYNPTMVKVTVDDDDLEL	
OsGAMYB	(401)	SVGTFCNTTVLSPFDMCQYWEEQHPGPF LNDCAPFSGNSPTESTPPVSAASPDIFQLSRVSPAQSTSM	
HvGAMYB	(403)	SVSTPCDITTVSPFDFLCOYWEER—LNEYAPFSGNSLTGSTAPMSAASPDVFLSKISPAQSPSL	
SsGAMYB	(467)	MKYDERAETTQMI FSRPDLFLASN—CFVSMNTHNEHCLLKDATGTPICDDLKDKQMDTA—AASSA	
AtMYB33	(435)	TP—PSELLFTLPSLEIVC—	
AtMYB65	(475)	VWE—PKRVDITRPDVLASSWLDQGCYGI VSDTSSMSDALALLGGDIGNSYVTVGSS—SGQAP	
AtMYB101	(415)	TS—LLNFPSTTTPLPDWYRVTEMQNEASYLAPPSGILMGNHQGNRVEPPTVPPSSSVD	
OsGAMYB	(471)	GSGEQVMGPKYEP—GDTSPHFENFRPDALFSGNTADPSVFNNATAMLGNDLSIDCRPV LGD—GIMFN	
HvGAMYB	(468)	GSGEQAMEPAYEPGAGDTSSHENLRPDAPFSGNTADSSVFNNATAMLGNDMNTCECKPVFGD—GIMFD	
			*BOX3*
SsGAMYB	(534)	QHGPDNCAVNAFPTV—	
AtMYB33	(452)	—	
AtMYB65	(537)	RGVGSY—GVINMPVWSL—	
AtMYB101	(474)	PMA SLGSCYWSNMPSIC—	
OsGAMYB	(537)	SSS—WSNMPHACEMSEFK—	
HvGAMYB	(536)	TSV—WSNLPHACQMSEEPK—	

FIG. S2. Alignment of *SsLFY* nucleotide and its homologous genes in *A. thaliana* and *S. lycopersicum*.

<i>SsLFY</i>	(1)	GAAGTAGCACGTGGCAAAAAGAACGGCCTTAGATTATCTGTTCCATCTGTACGAGCAGTGCCGCGAGTTCT
<i>AtLFY</i>	(730)	GAAGTGGCACGTGGCAAAAAGAACGGCTTAGATTATCTGTTCCACTGTACGAACAATGCCGTGAGTTCC
<i>SILFY</i>	(746)	GAAGTAGCACGTGGCAAAAAGAACGGCCTTAGATTATCTGTTCCATCTGTACGAACAATGCCGTGATTTCT

<i>SsLFY</i>	(71)	TGATCCAAGTTCAGAAATATTGCCAAGGAAGAGGTGAAAAATGCCCTACCAAGGTGACGAA
<i>AtLFY</i>	(860)	TTCITTCAGGTCCAGACAATTGCTAAAGACCGTGGCGAAAAATGCCCTACCAAGGTGACGAA
<i>SILFY</i>	(846)	TGATCCAAGTTCAGACTATTGCTAAGGAACGAGGTGAAAAATGCCCTACCAAGGTGACGAA

FIG. S3. Relative expression levels of *AP1* and *AP3* in abnormal flower organs of transgenic lines compared to WT using real-time quantitative RT-PCR. Relative expression levels are normalized using  $\beta$ -actin and WT levels are set at 1 using the software of Mastercycler ep realplex (Eppendorf, Hamburg, Germany).

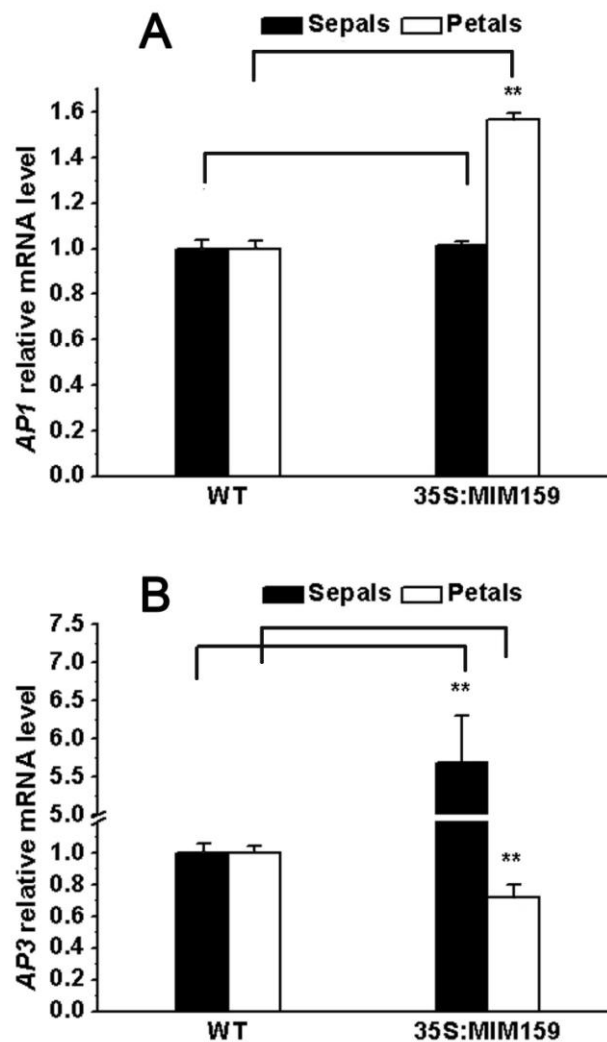


FIG. S4. Expression patterns of *API*, *AP3*, *AG* and *GAMYB* in various tissues of wild type gloxinia by semi-quantitative RT-PCR.

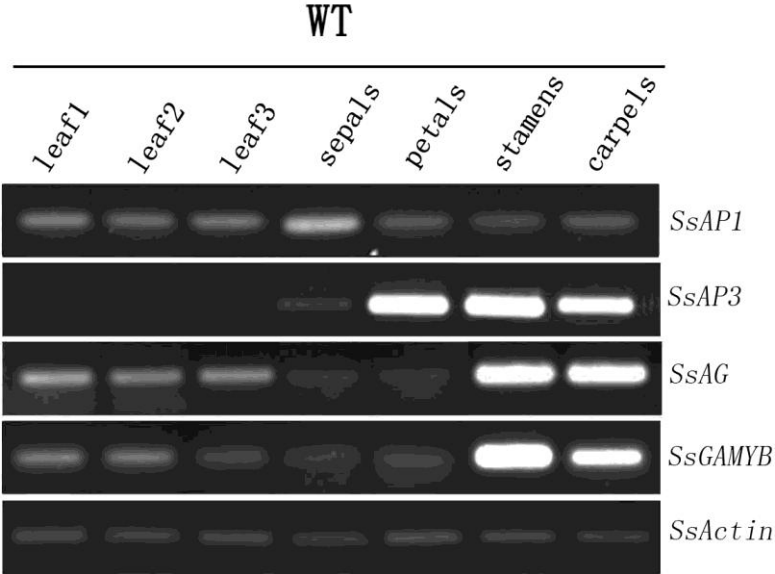


TABLE S1. Primers used in the experiments

	Primers
MIM159-I	CTTTTGGATTGAtagGGGAGCTCTATTTCTAGAGGGAGATAA
MIM159-II	AATAGAGCTCCCCctaTCAATCCAAAAGCTTCGGTTCCCCTCG
miR159a-Stem-loop primer	GTTGGCTCTGGTGCAGGGTCCGAGGTATTTCGCACcagagccaACTAGAGCTC
miR159a Forward	GCGGCGGTTTGGATTGAAG
UPM	GTGCAGGGTCCGAGGT
SsU6-UP	GACATCCGATAAAAATTGGAACGATA
SsU6-DN	ATTTTGGACCATTCTCGATTTGT
SsGAMYB-UP	GTATGACTAGTGAAAGTGAGGAATGG
SsGAMYB-DN	GACAGTAGGCATAGCATTCCAAGCAC
SsActin-UP	CAATAAATTGCGTGTTGCTCCTGAG
SsActin-DN	TGTTTCCGTACCGATCCTTTCTGATA
IPS1-UP	GGGTACCCAAACACCACAAAACAAAAGA
IPS1-DN	CGGATCCACTATAAAGAGAATCGGAAGCA
SsLFY-UP	GAAGTRGCACGTGGCAAAAAGAACG
SsLFY-DN	TTCGTCACCTTSGTRGGGCATTTTTC
SsGAMYB-qRT-UP	CAACACTTCTTCTTCAGAGCCTACT
SsGAMYB-qRT-DN	GCCACTGTTTTGAGATGAAAGAT
SsActin-qRT-UP	TTCTCCTTTACATCACGAACAATTT
SsActin-qRT-DN	ATCCAGGCTGTCTTTTCATTGTAT
SsLFY-qRT-UP	GAAGTTGCACGTGGCAAAAAGAACG
SsLFY-qRT-DN	TTCGTCACCTTCGTTGGGCATTTTTC
SsAG1-qRT-UP	CTGATTGTCTTCTCTAGCAGAGGCCGCC
SsAG1-qRT-DN	GCACCCAAAGATTCACCAAGCATGTTCC
SsAP1-qRT-UP	TACTCAAGGCTCCGATTGGCAGGCGAC
SsAP1-qRT-DN	TCTCGCATGGACAGGATTCTTGAGAGG
SsAP3-qRT-UP	GACTTTTGCAGCCCTTCTACGACGTTGG
SsAP3-qRT-DN	TCCAAGTGCAGTTGGCGCAGCTTGAAT

TABLE S2. Sequence of MIM159 (the artificial miR159a sequence is in red)

AAACACCACAAAACAAAAGAAAATGGCCATCCCCTAGCTAGGTGAAGAAGAATGA AAACCTCTAATTTATCTAGAGGTTATTCATCTTTTAGGGGATGGCCTAAATACAAAATG AAAACCTCTCTAGTTAAGTGGTTTTGTGTTTCATGTAAGGAAAGCGTTTTAAGATATGGAG CAATGAAGACTGCAGAAGGCTGATTCAGACTGCGAGTTTTGTTTATCTCCCTCTAGAAA <b>TAGAGCTCCCCctaTCAATCCAAA</b> AGCTTCGGTTCCCCTCGGAATCAGCAGATTATGTA TCTTTAATTTTGTAATACTCTCTCTTCTCTATGCTTTGTTTTTCTTCATTATGTTTGGG TTGTACCCACTCCCGCGCGTTGTGTGTTCTTTGTGTGAGGAATAAAAAAATATTCGGAT TTGAGAACTAAACTAGAGTAGTTTTATTGATATTCTTGTTTTTCATTTAGTATCTAATA AGTTTGGAGAATAGTCAGACCAGTGCATGTAAATTTGCTTCCGATTCTCTTTATAGTG
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