

# A regulatory mechanism on pathways: modulating roles of MYC2 and BBX21 in the flavonoid network

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**Table S1** Primers for genes of *A. thaliana*.

Experiment	Primer	Sequence of primer (5' → 3') <sup>a</sup>	Note
Complementary transformation	MYC2-BglII-5f	gcctgaagatctcATGACTGATTACCGGCTACAA	
	MYC2-Pst-3r	gcctgactgcagTTAACCGATTTTTGAAATCAAAC TTGCT	
EMSA	MYC2-BglII-F	agatctgATGACTGATTACCGGCTACAACCAA	domain only
	MYC2-NcoI-R GL3-KpnI-F GL3-SalI-R	ccatggcTTAACCGATTTTTGAAATCAAAC TT ggtaccATGCAGAAAGAGAAGTTAATGTTGGA gtcgacCTTCATCGTCATCGTCCCA	
BiFC	MYC2-Clal-5f	atcgatATGACTGATTACCGGCTACAA	
	MYC2-KpnI-3r GL3-XbaI-F GL3-BamHI-3r	ggtaccACCGATTTTTGAAATCAAAC TTGCT tctagaATGGCTACCGGACAAAACAGAAC ggatccACAGATCCATGCAACCC	
Dual LUC assays	p-AtCHS-728	Zhu et al. 2015	Reporter
	CHI-PRO-1105-KpnI-5f	gaagatggtaccGAGTCTATTAAATTTTTTGCCATTTTGT	
	CHI-PRO-1105-NcoI-3r	gaagatccatggTGTTGAGTCGGTTGGAATTTC	
	F3H-pro-495	Zhu et al. 2015	
	F3'H-pro-876		
	ANS-pro-503		
	BAN-pro-667		
	DFR-pro-KpnI-5f		
	DFR-pro-NcoI-3r		
	P-3GT-tested-5F-KpnI	gaagatggtaccATCAATCTGAGAAGATAAGAATTATACCAA	
	P-3GT-tested-3R-NcoI	gaagatccatggTTTTGTGGTTATATGATAGATTGTGCTTTG	
		caagctaattcgagctcgggtaccGAATTTAAGGTGTGCATAATATCTG	
	P-TTG1-KpnI-5f	tttatgttttggcgtcttccatggGGTGCGAGTAATGAAGAAGA	
	P-TTG1-NcoI-3r	gcctgaggtaccGCTTTTCATCATATTTAGTGGTTAG	
	P-GL3-KpnI-5f	gcctgacctggGGAATGTGTGGTGTGATT	
	P-GL3-NcoI-3r	gcctgaggtaccCGATCACTCAAATAGTAATAAGAC	
	PAP1-pro-KpnI-5f	gcctgacctggTGTTTCTCATCCCTATATCCCA	
	PAP1-pro-NcoI-3r	gaagatggtaccTACAGTGGCGGATCAACGTTAAT	
	MYC2-pro-KpnI-5f	gaagatccatggGGAACAAAGATAGATACGTAAATATATAAAC	
	MYC2-pro-NcoI-3r	ggtaccGTTAGGAGTAATGGGACCATATTG	
	P-MYBL2-KpnI-5f	ccatggaTCCATAAACCGGTGACCGGT	
	P-MYBL2-NcoI-3r	gcctgaggtaccGGCATTGCAGATATTGGACCA	
	TT2-pro-964-KpnI-5f	gcctgacctggGTCTTTTCAAAGTGAGATTGGTTGA	
	TT2-pro-964-NcoI-3r	gaagatggtaccGGTTTACCGGAATTGTATGTCAA	
	P-HY5-KpnI-5f	gaagatccatggTCTCACTTTTCTCTCTCTGTG	
	P-HY5-NcoI-3r	gcctgaggtaccCAGAAGATCAAAACGACCCAC	
		gcctgacctggTTTTCTACTCTTTGAAGATCGATCAG	
	P-BBX21-1000-5F-KpnI	accgctaattcgagctcgggtaccTAATTATTGATGTAGAAGGAAAGACTC	
	P-BBX21-1000-3R-NcoI	tatgtttttggcgtcttccatggCGATCGATTAAAGAGAGAGATAG	
	P-SPL9-1000-5F-KpnI	caagctaattcgagctcgggtaccCCAATTAGAGAATTATATCCACATG	
	P-SPL9-1000-NcoI	tttatgttttggcgtcttccatggGTTGGTTTCCTCTTACTCAGA	
	MYC2-NcoI-5f	gaagatccATGGCGATGACTGATTACCGGCTAACAA	
	MYC2-BglII-3r	gaagatagatctgtTTAACCGATTTTTGAAATCAAAC TTGCT	
	BBX21-CDS-NcoI-5F	cagcccaagcttcacctggcgATGAAGATCAGGTGCGACGT	
	BBX21-CDS-SalI-3r	aattccccgggatccgtcgacTTACCAGAAAGATCTAAACTTTTTATTAGA	
	SPL9-163-5f	ggacagcccaagcttcacctggcgATGGAGATGGGTTCCAACTC	
	SPL9-163-3r	ttcagcgtaccgaattccccgggatccTCAGAGAGACCAGTTGGTATG	
	HY5-163-5f	ggacagcccaagcttcacctggcgATGCAGGAACAAGCGACTAGCT	
	HY5-163-3r	ttcagcgtaccgaattccccgggatccTCAAAGGCTTGATCAGCATTAGA	
	BBX22-163-5f	ggacagcccaagcttcacctggcgATGAAGATTCAGTGTAACGTTTGTGA	
	BBX22-163-3r	ttcagcgtaccgaattccccgggatccTAGAACCGTCGCCG	
	PIF3-163-5f	ggacagcccaagcttcacctggcgATGCCTCTGTTTGAGCTTTTCAG	
	PIF3-163-3r	ttcagcgtaccgaattccccgggatccTCACGACGATCCACAAAAC TGAT	
Y2H	MYC2-BglII-f	agatctATGACTGATTACCGGCTACAACCAA	
	MYC2-PstI-r	ctgcagTTAACCGATTTTTGAAATCAAAC TT	
	GL3-CDS-SalI-5f	gtcgactaATGGCTACCGGACAAAACAGAAC	
	GL3-CDS-PstI-3r	ctgcagTCAACAGATCCATGCAACCC	
	BBX21-AD-EcoRI-5F	atcctctgctagcagagaattcATGAAGATCAGGTGCGACGT	
	BBX21-AD-SalI-3r	tatagggtcttagagtcgacTTACCAGAAAGATCTAAACTTTTTATTAGA	
	PAP1-BglII-5f	agatctATGGAGGGTT CGTCCAAA	
	PAP1-PstI-3r	ctgcagtCTAATCAAAT TTCACAGTCT CTC	
	TTG1-NdeIF	agcatatgATGGATAATTCAAGTCCAGAT	
	TTG1-SacIR	acgagctcTCAAAC TCTAAGGAGCTGCAT	
Y1H	CHS-pro-1500-EcoRI-5f	gaagatgaattcGCGAATTTTGCAAGAGATGAAGA	Reporter
	CHS-pro-1500-MluI-3r	gaagatacgctTATAGTATACCAACTTGGGTTTATT	
	CHI-pro-1105-EcoRI-5f	gaagatgaattcGAGTCTATTAAATTTTTTGCCATTTTGT	
	CHI-pro-1105-MluI-3r	gaagatacgctTGTTGAGTCGGTTGGAATTC	
	F3H-pro-1492-EcoRI-5f	gaagatgaattcACCATGAACCCCTGAAGGAG	
	F3H-pro-1492-MluI-3r	gaagatacgctTGTAATTACGAAGACAAAAGACTAAATTAAG	
	F3'H-pro-876-EcoRI-5f	gaagatgaattcAAACTAATGAACTGTAACCTCTTTTTTC	
	F3'H-pro-876-MluI-3r	gaagatacgctAGTGTGGGTTTGAATGGTAAG	
	DFR-pro-EcoRI-5f	gcctgagaattcATCAATCTGAGAAGATAAGAATTATACCAA	
	DFR-pro- MluI-3r	gcctgaacgcgtTTTTGTGGTTATATGATAGATTGTGCTTTG	
	ANS-pro-569-EcoRI-5f	gaagatgaattcATTGATCCACATACAATTGTCTATTTG	
	ANS-pro-569--MluI-3r	gaagatacgctCTTCTTTAGTCTTCTGTTTAAAGCT	
	3GT-pro-836-EcoRI-5f	gaagatgaattcCAACGGAACATTTTTGGCC	
	3GT-836-pro-MluI-3r	gaagatacgctTTTCTTGGA CTCTCTGTATTTTAC	
	PAP1-pro-EcoRI-5f	gcctgagaattcTACAGTGGCGGATCAACGTTAAT	
	PAP1-pro- MluI-3r	gcctgaacgcgtGGAACAAAGATAGATACGTAAATATATAAAC	
CoIP	MYC2-KpnI-5F	catttggagaggacaggggtaccATGACTGATTACCGGCTACAA	
	MYC2-SalI-3R	gaacatcgatatgggtagtcgacACCGATTTTTGAAATCAAAC TTGCT	
	SPL9-KpnI-5F	catttggagaggacaggggtaccATGGAGATGGGTTCCAACTC	
	SPL9-SalI-3r	gaacatcgatatgggtagtcgacGAGAGACCAGTTGGTATGGT	
	BBX21-KpnI-5F	ggtaccATGAAGATCAGGTGCGACGT	
	BBX21-SalI-3r	gtcgacCCAGAAAGATCTAAACTTTTTATTAGA	
	HY5-KpnI-5f	ggtaccATGCAGGAACAAGCGACTAG	
	HY5-XbaI-3r	tctagaAAGGCTTG CATCAGCATTAGA	
	PAP1-KpnI-5F	catttggagaggacaggggtaccATGGAGGGTTCGTCCAAA	
	PAP1-SalI-3r	gaacatcgatatgggtagtcgacATCAAATTTACAGTCTCTC	
	GL3-KpnI-5F	catttggagaggacaggggtaccATGGCTACCGGACAAAACAGAAC	
	GL3-SalI-3r	agatgagtttctgctctgacACAGATCCATGCAACCC	
Transcript quantification	CHS-CDS-5f	ATGGTGATGGCTGGTGCT	Standard
	CHS-CDS-3r	TTAGAGAGGAACGCTGTGCA	
	F3H-CDS-5f	ATGGCTCCAGGAAC TTGAC	
	F3H-CDS-3r	CTAAGCGAAGATTGGTCGACA	
	F3'H-CDS-5f	ATGGCAACTCTATTTCTCACAATC	
	F3'H-CDS-3r	TTAACCCGACCCGAGTC	
	DFR-CDS-5f	ATGGTTAGTCAGAAAGAGACCGT	
	DFR-CDS-3r	CTAGGCACACATCTGTTGTG	
	ANS-CDS-5f	ATGGTTGCGGTTGAAAGAGTTG	
	ANS-CDS-3r	TTAATCATTTTTCTCGGATACCAATTCC	
	3GT-head	ATGACCAAACCTCCGAC	
	3GT-end	TCAAATAATGTTTACA ACTGCATCCAAC	
	CHS-e1f	GACCGACCTCAAGGAGAAGTTCAA	
	CHS-e2r	GAGAAGGAGCCATGTAAGCACACAT	
	F3H-e1f	CTCGTCTCGCTCGTGACTTCTT	
	F3H-e2r	CACCGTGAGTAGTCTCTGTTTCTCA	
	F3pH-e1f	GACACCGATGGAGACTGTTGAGAA	
	F3pH-e2r	CGTTGACTACACACATGTTCAACCACT	
	DFR-e1f	GTTCTGCCACCGTTTCGAGAT	
	DFR-e2r	CATCATCGTAGCTTCCTTCTCAGAT	
	ANS-e1f	GCGTATCCTGAAGAGAAGAGAGATCTA	
	ANS-e2r	CGACAGAGAGAGCCTTGAAGACTT	
	3GT-e1f	CTCTGCTCATCTCTACACAGATCTCAT	
	3GT-e2r	CTCCTTCTGGTGATCTTTGACTCTGAT	
	PAP1-e2f	GAAGTCGATCTTCTTCTTCGCCTTCAT	
	PAP1-e3r2	GATGAGTGTTCCAGTAATTCTTGACGT CAT	
	GL3-e1f	GGTCTGTCTCTGCTTCTCAGTCT	
	GL3-e2r2	GATCAGCTTTGATCTCCGAAGCTTGAAT	
	MYBL2-e2f	GATCTCATCCTCAAGCTTCATGCACTT	
	MYBL2-e3r	GTCGGTTTCGTCTGGCAATCTT	
	TTG1-206f	CGAATCTCTCCTTCGAGCATCCTTAT	
	TTG1-363r	CGAGATTGGCTCGACGGTTGAT	
	MYC2-251f	TACGCTATATTCTGGCAACCGTCGTAT	
	MYC2-391r	GAGTAGAAAACGGCGGCGAACT	
	BBx21-e2f	CTAAGAGTGGTGATGATGATGGAGTGTTA	
	BBx21-e3r	GTATGAAGAAGGAAGAGTTTGGAATCTGA	
	SPL9-e2f	GCACCTTCGCTTTACGAAAATGGTGAT	
	SPL9-e3r	TGCCATGACGGTGACGACACT	
	PIF3-e1f	CAGGCTCACCAAAGCTAAGCTT	
	PIF3-e2r	GTTCTCTGATCTACTTGACTGACTT	
	HY5-e1f	GTCATCAAGCTCTGCTCCACATT	
	HY5-e2r	CGACAGCTTCTCCTCCAAACT	
	JAZ1-e1f	GACGTGTAGTCGATTGAGTCA GTAT	
	JAZ1-e2r	GCTGACGTGAGTTGCCTAAAGTT	

<sup>a</sup> Sequence in lower case is for enzyme-cutting and linker sites.

**Table S2.** Primers for genes of *O. sativa*.

Gene	Primer	Sequence of primer (5' → 3') <sup>a</sup>
<i>OsMYC2</i>	OsMYC2-HindIII-5F	<u>AAGCTT</u> ATGTGGGTTTTGTTATCTCCTCT
	OsMYC2-EcoRI-3R	<u>GAATTC</u> TACCGGGCGGCGG
<i>OsC1</i>	OsC1-163-HindIII-F	<u>ATACCCAAGCTT</u> ATGGGGAGGAGAGCTTGCTGC
	OsC1-163-EcoRI-R	<u>GATCCGGAATTCT</u> CACGCACACAAGTTCCAGGC
<i>OsB2</i>	OsB2-163-HindIII-F	<u>ATACCCAAGCTT</u> ATGGCATCTGCTCCTCCAGTT
	OsB2-163-EcoRI-R	<u>GATCCGGAATTCT</u> TACGGCGCCTTCCCCTGT
<i>OsPAC1(TTG1)</i>	OsPAC1-163-Sall-F	<u>ACGTCGACG</u> ATGGAGCAGCCCAAGCCG
	OsPAC1-163-EcoRI-R	<u>ACGAATTCT</u> CAGACCCTGAGAAGCTGGA
<i>OsC1pro</i>	OsC1-pro-KpnI-5f	<u>GGTACCG</u> ATATGAGCATTATCCGTCCG
	OsC1-pro-BamHI-3R	<u>GGATCCT</u> CTCCCTCTCTCTCTCT
<i>OsCHSpro</i>	OsCHSpro_5	<u>CAAGCTAATTCGAGCTCGGTACC</u> GTGCATATATACCAACTAAATAGTCATC
	OsCHSpro_3	<u>GTCTTCCATGGATCCGTCGACCTCTCTCG</u> ACTAATTCACCAG
<i>OsCHIpro</i>	OsCHIpro-1Kfb	<u>CAAGCTAATTCGAGCTCGGTACC</u> CTCGTCATTTCCACAAGCCTA
	OsCHIpro-R	<u>GTCTTCCATGGATCCGTCGACGG</u> ATACAGGATCGGGTGAGC
<i>OsF3Hpro</i>	OsF3Hpro-KpnI-F	<u>GAGCTCGGTACCC</u> AACCTACGATCTGATCACAC
	OsF3Hpro-NcoI-R	<u>CGTCTTCCATGGCTCG</u> ATCGATCGACCCGATGC
<i>OsF3'Hpro</i>	OsF3pHpro-F	<u>CAAGCTAATTCGAGCTCGGTACC</u> GATTATACGTGAGCCGAATATGCATG
	OsF3pHpro-R	<u>CGTCTTCCATGGATCCGTCGACAAGCTT</u> GACCGTATGATCCGCTCGCT
<i>OsDFRpro</i>	OsDFRpro0921-F	<u>CAAGCTAATTCGAGCTCGGTACC</u> GACAGGACTTCTATAGATTATAAA
	OsDFRpro0921-R	<u>GTCTTCCATGGATCCGTCGACGG</u> CGTACCGTGCGTGATC
<i>OsANSpro</i>	OsANSpro-o6_5	<u>CAAGCTAATTCGAGCTCGGTACC</u> TAGGATGGCAATCTGTGGATGAT
	OsANSpro-o6_3	<u>GTCTTCCATGGATCCGTCGACGT</u> CGCCCTCCCGAAGTA

<sup>a</sup> The underlined sequence is for enzyme cut and linker.

**A**

**MYC2** (AT1G32640, 624 aa)

MTDYRLQPTMNLWTTDDNASMMEAFMSSSDISTLWPPASTTTTTATTETTPTPAMEIPAQAGFNQETLQQRILQALIEGTHEG  
WTYAIFWQPSYDFSGASVLGWGDGYKGEEDKANPRRRSSSPFSTPADQEYRKKVLRELNSLISGGVAPSDDAVDEEVTDT  
EWWFFLVSMTQSFACGAGLAGKAFATGNAVWVSGSDQLSGSGCERAKQGGVFGMHTIACIP SANGVVEVGSTAPIRQSSDLIN  
KVRILFNFDGGAGDLSGLNWNLDPDQGENDPMSWINDPIGTPGSNEPGNGAPSSSSQLFSKSIQFENGSSSTITENPNLDPT  
PSPVHSQTQNPKNNTFSRELNFSTSSSTLVKPRSGEILNFGDEGKRSSGNPDPSYSGQTQFENKRKRSMVLNEDKVLSFG  
DKTAGESDHSDDLEASVVKEVAVEKRPKKRGRKPANGREEPLNHVEAERQRREKLNQRFYALRAVVPNVSKMDKASLLGDAIA  
YINELKSKVVKTESEKLQIKNQLEE VKLELAGRKASASGGDMSSSSCSSIKPVGMEIEVKIIIGWDAMIRVESSKRNHPAARLM  
SALMDLELEVNHASMSVNDLMIQQATVKMGFRIYTTQEQLRASLISKIG

**B**

**GL3** (AT5G17050, 638 aa)

MATGQNRTTVPENLKKHLAVSVRNIQWSYGIFWSVSASQSGVLEWGDGYNGDIKTRKTIQASEIKADQLGLRRSEQLSELYESL  
SVAESSSSGVAAGSQVTRRASAAALSPEDLADTEWYYLVCMSFVFNIGEGMPGRTFANGAPIWL CNAHTADSKVFSRSL LAKSAA  
VKTVVCFPFLGGVVEIGTTEHITEDMNVIQCVKTSFLEAPDPYATILPARSDYHIDNVLDPQQILGDEIYAPMFSTEPFPTASPS  
RTTNGFDQEHEQVADDHDSFMTERITGGASQVQSWQLMDDLSNCVHQSLNSSDCVSTQTFVEGAAGRVAYGARKSRVQRLGQIQE  
QQRNVKTL SFDPRNDDVHYQSVISTIFKTNHQLILGPLFRNC DKQSSFTRWKSSSSSSSGTATVTAPSQGMLKKIIFDVPRVHQK  
EKLMLDSPEARDETNHAVLEKKRREKLNERFM TLRKIIPSINKIDKVSILDDTIEYLOELERRVOELESCRESTDTETRGTMT  
KRKKPCDAGERTSANCANNETGNGKKVSVNNVGEAEPADTGFTGLTDNL RIGSFGNEVVIELRCAWREGV LLEIMDVISDLHLDS  
HSVQSSTGDGLLCLTVNCKHKGSKIATPGMIKEALQ R VAWIC

**C**

**PAP1** (AT5G35550, 249 aa)

MEGSSKGLRKGAWTTEEDSLLRQCINKYGEKGWHQVPVRAGLNR CRKSCRLRWLN YLKPSIKRGKLSSDEV DLLLLRLHRL LGNRW  
SLIAGRLPGRTANDVKNYWNTHLSKKHEPCCKIKMKKR DITPIPTTPALKNNVYKPRPRSFTVNNDCNHLNAPPKVDVNP PCLGL  
NINNVCDNSIIYNKDKKKDQLVNNLIDGDNMWLEKFLEESQEVDILVPEATTTEKGD TLAFDVDQLWSLFDGETVKFD

**JAZ1** (AT1G19180, 254 aa)

MSSSMECSEFVGSRRTGKKPSFSQTC SRLSQYLKENG SFGDLSLGMACKPDVNGTLGNSRQPTTTMSLFPCEASNMDSMVQDVK  
PTNLFPRQPSFSSSSSSSLPKEDVLKMTQTTRS VKPESQTAPLTIFYAGQVIVFNDFS AEKAKEVINLASKGTANS LAKNQTDIRS  
NIATIANQVPHPRKTTTQEPIQSSPTPLTELPIARRASLHRFLEK RKDRVTSKAPYQLCDPAKASSNPQTTGNMSWLGLAAEI

**BBX21** (AT1G75540, 332 aa)

MKIRCDVCDKEEASVFCTADEASLCGGCDHQVHHANKLASKHLRFSLLYPSSSNTSSPLCDICQDKKALLFCQQDRAILCKDCDS  
SIHAANEHTKKHDRFLLTG VKLSATSSVYKPTSKSSSSSSSNQDFSVP GSSISNPPPLKKPLSAPPQSNKI QPFSKINGGDASVN  
QWGSTSTISEYLMDTLPGWHVEDFLDSSLPTYGFSKSGDDDGVL PYMEPEDDNNTKRNNNNNNNNNNNTVSLPSKNLGIWVPQIP  
QTL PSSYPNQYFSQDNNIQFGMYNKETSPEVVSFAPIQNMKQQGQNNKRWYDDGGFTVPQITPPPLSSNKKFRSFW

**SPL9** (AT2G42200, 376 aa)

MEMGSNSGPGHGPQAE SGGSSSTESSFSGGLMFGQKIYFEDGGGGSGSSSSGGRSNRRVRGGSGQSGQIPRCQVEGCGMDLTN  
AKGYYSRHRVCGVH SKTPKVTVAGIEQRFCQQCSR FHQLPEFDLEKRSCRRRLAGHNERRRKPQPASLSVLASRYGRIAPSLYEN  
GDAGMNGSFLGNQEIGWPSSRTL DTRVMRRPVSSPSWQINPMNVFSQGSVGGGGTSFSSPEIMDTKLESYKGIGDSNCALSL SN  
PHQPHDNNNNNNNNNNNNNTWRASSGFGPMTVTMAQPPAPSQH QYLNPPWVFKDNDNDMS PVLNLGRYTEPDNCQISSGTAMG  
EFELSDHHHQSR RQYMEDENTRAYDSSSHHTNWSL

**PIF3** (AT1G09530, 525 aa)

MPLFELFRLTKAKLESAQDRNPSPPVDEVVELVWENGQISTQSQSSRSRNI PPPQANSSRAREIGNGSKTTMVDEIPMSVP SLMT  
GLSQDDDDFVPWLNHHPSLDGYCSDFLRDVSSPVTVNEQESDMAVNQTAFPLFQRRKDGNESAPAASSSQYNGFQSHSLYGS DRAR  
DLPSQQTNPD RFTQTQEPLITSNKPSLVNFSHFLRPATFAKT'TNNNLHDTKEKSPQSPPNVFQTRVLGAKDSEDKVLNESVASAT  
PKDNQKACLISEDSCRKDQESEKAVVCSSVSGNSLDGPSESPSLSLKRKHSNIQDIDCHSEDVEEESGDGRKEAGPSRTGLGSK  
RSRSAEVHNLSERRRRDRINEKMRA LQELIPNCNKVDKASMLDEAIEYLKSLQLQVQIMSMASGYLPPAVMFP PGMGHYPAAAA  
AMAMGMGMPYAMGLPDL SRGGSSVNHGPQFQVSGMQQQPVAMGIPRVSGGGIFAGSSTIGNGSTRDLSGSKDQTTTNNNSNLKPI  
KRKQGSSDQFCGSS

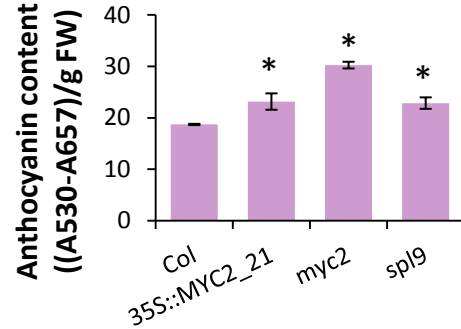
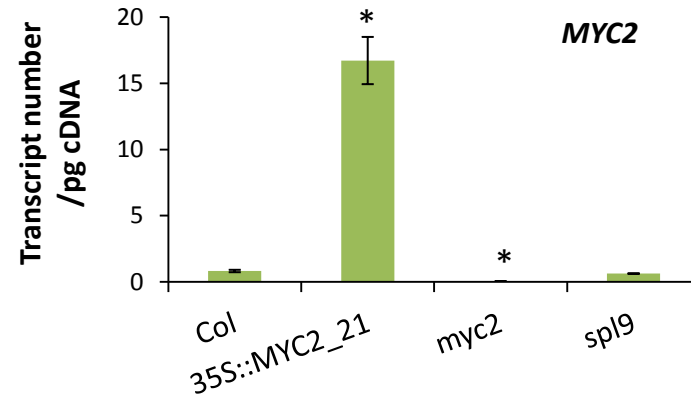
**HY5** (AT5G11260, 169 aa)

MQEQTATSSLAASSLPSSSERSSSSAPHLEIKEGIESDEEIRRVP EFGGEAVGKETSGRESGSATGQERTQATVGESQRKRGRTPA  
EKENKRLKRLLRNRVSAQQARERKKAYLSELENRVKDLENKNSELEERLSTLQENQMLRHILKNTTGNKRGGGGGSNADASL

**TTG1** (AT5G24520, 342 aa)

MDNSAPDSLRSSETAVTYDSPYPLYAMAFSSLRSSSGHRIAVGSFLEDYNNRIDILSFDSDSMTVKPLPNLSFEHPYPPTKLMFS  
PPSLRRPSSGDL LASSGDFLRLWEINEDSSTVEPISVLNNSKTSEFCAPLTSFDWNDVEPKRLGTCSIDT'TCTIWDIEKSVVETQ  
LIAHDKEVHDIAWGEARVFASVSADGSVRI FDLRDKEHSTIIYESPQPDTPLLRLAWN KQDLRYMATILMDSNKVVILDIRSPTM  
PVAELERHQASVNAIAWAPQSKCHICSGGDDTQALIWELPTVAGPNGIDPMSVYSAGSEINQLQWSSSQPDWIGIAFANKMQLLR  
V

**Figure S1.** Coding regions of regulatory genes examined in this study. **(A)** MYC2. The coding region of MYC2. **(B)** GL3. The coding region of GL3. The region of DNA-binding domain expressed and used in EMSA tests is underlined. **(C)** Amino acid sequences of other regulators.

**A****B****C**

**Figure S2.** Phenotype of transformation of *myc2* in 2021. **(A)** Comparison of phenotypes across 3-d seedlings of lines. Seeds of three lines (Col, 35S::MYC2\_21, and *myc2*) were grown on the MS medium with 3% sucrose. **(B)** Anthocyanin content of seedlings (shoots only) at 96 hrs. All lines were sampled in three replicates, with the standard error bars shown. The three lines to the right had significantly high anthocyanin contents than Col (one-tailed *t*-tests; \*,  $P \leq 0.05$ ). **(C)** Level of *MYC2*'s transcription in seedlings of lines in (A). Two replicates for *myc2* (*myc2*) and 35S::MYC2\_21 but three for *col-0* (Col) and *spl9* (*spl9*) are shown in the standard error bars. Comparisons of *myc2* and 35S::MYC2\_21 to Col are significant (one-tailed *t*-tests; \*,  $P < 0.05$ ).

**CHS-5'** region (AT5G13930, 728 bp, 5' → 3')

GTTTGGAAAGCGCAAATAGGGCAGATTTTTCAGACAGATATCACTATGATGGGGGTGAGAGAAAGAAACGAGGCGTACCTAATGTAACTACT  
TTAATTAGTCGTTAGTTATAGGACTTTTTTTTTTGTGTTGGGCCTAGTTATAGGATCATAAGGTAAAAATGAAGAATGAATATTAGATTAGTAGG  
AGCTAATGATGGAGTTAAGTATG**CACCGTGT**TAAGAACTGGGAAGTGAAACCTCCTGTATGGTGAAGAACTATACAACAAAGCCCTTTGTTGGT  
GTATACGTATTAAATTTTTATTCTTTATCACAAAGCGATACGTATCTTAAAGACATAATAAATATATATCTTACTCATATAAATATCTTAAGAT  
ATATATACAGTATACACCTGTATATATATAATAAAATAGGCATATAGTAGAAATTAATATGAGTTGTTGTTGTTGCAAATATATAAATCAATCA  
AAAGATTTAAACCCACCATTCAATCTTGGTAAGTAACGAAAAAAAGGGAAGCAAGAAGAACACAGAAAAGGGGGCTAACAACTAGAC**CACG**  
**TAG**ATCTTCATCTGCCCGTCCATCTAACCTACACACTCTCATCTTCTTTTTCCCGTGTCTAGTTTGTTATATAAGCTCTCAGCTCTCCGGTATA  
TTTCCAAATACACCTAACTTGTTTAGTACACAACAGCAACATCAAACCTCTAATAAACCCAAGTTGGTGTATACTATA

**CHI-5'** region (AT3G55120, 1105 bp, 5' → 3')

GAGTCTATTAAATTTTTTGCCATTTTTGTTTTTTGTGTTTTTTCAGTGACAAACTCACATGGATTTTCATTTTCAGATTTCAGTTAGATTTTATTATA  
CTTCAGCCCAGTGTAGGAACAACCGGAACCCAAAATCTAGAGAGCATTTCATGGTGGGGTTCAATAGCCCATGTAATAGCCCCTTCCCGGCAT  
CAGAACTGACAAATCCAAAATTGAATTGAAATGTGTTTATAACCCGATTAGTTTTAATATTACGGAACAAACAAATCAAACCATAACTCAAA  
CTAAACGAAGTCATATAATAGATATGATAAAATTTATATTAAACGTTTTATTAATATAAAAGAGTGTTAAAAGTTTTTATTTATCTAAAATGA  
ACATAGTTAAACGAAAACCCAACCAAATCTAAGTACAATTGTTTCAAACCAAAGTGAACCAAGTTGAATTATTGTTTTTAATTCACAAAACGA  
TTTGTTGAAATAAGGGCTGAAGTCGTAGAAGCTTTAATAGATAAGAAAAGAAAGAGATATGTTGATATTGAGAATACCCAAAAAAGTAGGATT  
TCTGAATATTAGAACTAGAGAACGTAAGAAATCTTTGATTTTTTCTTTGATTTTCCGAAAGTAAGAATTAGAGAATACTTTTTCTGAAAAG  
CTATTTTTTTTTTTTTTAATTTTATTGATCAATCAACTGAATACACTGAATACAAAAGAAAACCTGATTTATTTATAATAAAACTCAATTTATTT  
ATAATATAAATCTCAAAAACCTAGATAAAACTCTAAAATAACTATATAAATTTATCTCAAATAACCAAATATATAAATCAATAATATGAAAGATAA  
CGATAGAAAATATTTGAAATTATCTTAACCTAT**GTGCTCT**CGCATATTTAAGGGCTCAAAGCTTCAACCACCAATTGTCAATGCATCTCCCAATC  
AAAATATAAAAAAAGAGACGAAAACGAAAGTAC**CACCGTGT**CTTACACATCCAACACTCGTAATCGTAACCTATTGCTACCTACCCTTCTCTCTTCT  
ACTTAACCCCAAAGGCCCCAAAAACACAATCAAGAAAAGCTCTGTAACATTATTATCAATCGAAATTCCAACCGACTCAACA

**F3H-5'** region (AT3G51240, 1492 bp, 5' → 3')

ACCATGAACCCCTGAAGGAGGTGTCTGCATCGTTAGACCCACGATCGGTGAGTCGTTGGTTATGTGCGATTAGTGCAGACCTGTCTTCTTCTTTT  
CTTTGGTCGATGCTCGAATCCTCTGTTTTGTCTGAGCCAAAAAGCAAAGAAAAGGATTAGGTTTCAGAAAGATCGAGTCTATCTATGTTACTTTA  
TAAATAACTAATTACTCTGCAGATGCTTTAAGGCTAAAGAACTACAAGAACCTAAAAAAGAAGATGGGAAAGACAAACATACTTGATGATGA  
AAAGGGAACCTTTGAAGTCAGAATCAGAGTCGTTGATTGCAGAGATAGCCTGTGATCTAGTGACCCTTTTGGCTGATGATGGAGTCTCCATTG  
AATTTTCGAGTTCTTGTAAACAACAACGAAACTGAATGAAAGAGAATTTGGGAAAAACAAAGATGTAATGAAGTCTGTTTAGTTCGCAGTG  
TTATAACGTTTTTATAACTAACTTAGCCGTTGTGGCTCCTCTCTTGCAAAGTGGAAGATGAGCCGTTCCGTTACCGTTCCGTTAGTAAACCCA  
CGAATTATTTTTCTTCCAAAAGTAGCCGTTGGATCCGTTCTCTCATGGAAAAAGTAGACGTCTTTGTTCTGTATGGGCCTTTGACTAACTAAA  
TGGCCCGAGCCCGTTTCATAACATTAATCATTTAAAAAATCACATTGATGGTATAACACTAATTTTTTTTTTTTTCACAGGTGTATAACCAACTAATA  
TAAATATGCACATTCACCTTAAAATTAATAATATCATAAAGAGTATTATGGCGTCTGTTTTATTGTTTATCCATAACTACATCAATCAAATCC  
AAGTTGATATACTAGTTTAGAACCTAATACTTTACAAATCCGATCATTAAATTTATCTTGTCTGCTTAAGATTTTTTTTTTTTGTGAATAAGGTTTA  
ATTTATCTCATCAATACGATTTAGTAAAAAGTCTGTGCAAAAATTAATGACGATTGGGATTTTTGTAACGCAAGCCCGTACCAGAACATGTCTC  
CGCC**CACGTG**ATTTCTCCACAGACCACAAGCATTTTTAAGACGTGGCTTTCTATCAACCGTTAAAAACGTAAATCATATTAAAC**CATGTGT**CTAC  
TACCTACGGTGTAAACGAAACTGTATAACGTCCCTATCATATAATAGTAATGTGATACGTTGGAATGTAGCCAAAAAGCATAAAAAATAAATA  
GATAATTAAGTTTATAATGTTTTCTACAAAATATTATTATACCGTATGTATTTTTTATTTTATTTTCTGAAGTTAAAAACAGATGTAGTTAG  
TTGAGTAAATTGTGTTCTAGAAAAGAGAAGAGAGAGCAGTAGTACCGTGGTAGGTAGCTAGCGACCTCTCGTTTCGTCTAGTCATCACAAAGCTTT  
GAAAGATTTTCAGCTACCCTCTCTCCTTTATATATTTCATTACACATCTCTTCTTCTATATCTCTCTTAATTTAGTCTTTTGTCTTCGTAAT  
TACA

**F3'H-5'** region (AT5G07990, 870 bp, 5' → 3')

AAACTAATGAACTGTAACCTCTTTTTCTTTTCTTTTTTGTAAAGGATTATGAACTGTAACCTAGAAATGCTTGGTTTGTGGGCAGTGTAAT  
ATATGACACACATGCATTTTTTTTTGTGTTGTCAAATAGGAAGACTTCTTTTTTCTTTTATCAACTTCCTTATTTTTCATAAAACAAAACACTGAAA  
AAAGTACAGATGTT**TCTCACGTACGTACCGTGTACATACAT**ATATATTAGACCCTATATAATAAGATATGAAGTGTTAGGTTTAAATCAATTA  
ACGAATCCCATCCAAATGATGAAACAGTTAAACAAGAAATCAAATAGTTTATTAGGGTTACAATGATTTTATACTTTTAAAGAAATCTTAGAAC  
CTATCACTTACAAATGAGTAAATGACCATTACTCCTCGAGAATCTAAGGCGCTTAAGGAAGCATTGCGAATCGGGTGTGAAAAAGATCTATTT  
TTGAATTATTTTCACACAATTTCTTAATGTCAATTTTCGATGCTCCCATATCTCTCCACGGTTTAAAGCAAGATTGGTGGGAAAGGGATATTCTC  
GCATCGATTACAAATGAAATATGGGTTGAAAAAAATAAAAAATTACTCAATG**TTGACAC**CAAAACCGAAAAACTCTAAGTTGCGCTAATAAA  
AAAAAAGTTTATAAACCCCAACATCAAACCAAAACCGTACTAAACTGTCCCATATGAGATTTAGCTTTTAAATAAATTAGTACTTCTCATAAACGA  
TAACTAAATTAATTTCCCTAGCCAAGACATACATATAGTTTGATTGACAAAAAATAAAACTCCTCTATTTATAGCTTGTGTTTTGTTTTCT  
CTCATTTTTTCACTTACCATTCAAACCAACACT

**DFR-5'** region (AT5G42800, 1554 bp, 5' → 3')

ATCAATCTGAGAAGATAAGAATTATACCAACACTGATTCTGATTCTGATTCTTTCATAGAAGAAGAGAGCCACTAAAAAAGAATCTATATCCAA  
GTTTCTAACTAGAGAATCTAAACCAAACCTTTTATAAAGCTAAAAAGTCAATGACGGCGAGAATCTGAACTACTTTTTTTTCAAAGTTCATCAGA  
CTTGCTTTAACTTTTACAGGATTCAAAGGAAGAGAGATCGAAGAAGAAGAGACTAACAAAAAGTGGAGAAGATCCAGCGTAAGCAAGAACGA  
GATTGGCACCACCTTCGCCCTCTGTAATCCAATCTGATGCATCTTCTCCTCCAAAATCATCTCCATGCGATACAAAATTCTTCGATTTTTAA  
AATCGAAATCAAGCGAAGATCTGATCAAAATCAATTACCAGAATTTTGCTAACGCAATGCAATTGAATAGAGAACGAAGATTTCTAGTGTTG  
AAGAAGAAGAAGAGAGAGCTTTGAAGTATTCTTCTCTCTCGCTCGAGCTGCA**AAACGTGTG**GTGGTGGAATACACCAAGACGCTTGGCTTACTTT  
GTCTCTCTGTTTTGGAGGAGAGTCAAAATTAAGCTGACCTCTTCTCTGACGTCTTACGATACAACAAATTGAAAATACAAGAGTTATATTGATT  
CTGTGTTTTAGAAAT**CCACGTGG**ACGAGGTAACCAC**CACGTG**TTATTTCTTACTTTATGAGATTAAGTGATTCACTGTCTCTTCTAATTTTATTT  
TATTTTCTTTGCGAAAAGCTGGAAATAAATAAATTTTTGAAAACAATATTTTAACATATCAATTATTTTTTATAATAATTTCGTGAAATAATAATG  
AAAAAGCTGACATGGGACACAATTGGATAATTACATCTTTTAAAGTTTTAGTTTATGTATTTTATGTAATGCTTATAATATTTAGATTGCAA  
TAAATCTAGAAGTCATATTTATAAATTAATATGTTTTATAATTTTACAATTTTGTAATAAGAAACTCCTAATTCATAAATCTAAAAATATAAAC  
ATATTTTTTCATTTAAGCTTTTCCAAGATTTTATAATTATTTTAGGTGTCTGATTTTTTAGATTTCAATTTAAAATTAATAATTACTTTAAGTAAAA  
TGTATTTCTGTATATATTCTATCAAAATGTTAATTTGTTTAGACAAATTTTGATTTATTTTCGTAAAAGTGGGTGGGGAACAAAAACAAAAACA  
AACTGAACTGAAGTCACCCA**CACGTCT**CACCAACAAATCGAAGTCAACGTATTTCAACCACCGGTACAACAACAAAATACACACCTAAGGAA  
ATAATAAAATCAACTTACCAGATTGTTACGTACCACACATCTCTTTAGTCCTTCGT**CAACCAACGTTCCCCACGTGCTTCTCCGGTTGGTACT**  
**CACGTGACCGGCAGCTTCTCGT**TCTTATTATCTGTTTTTCTTCAATAACGATTCATAAATCTCTAGTGCTTATTTTATAATGTCTTCACATCACA  
AAGATTTGTACCGAACATACATAGTTGAATCTTTCCCAAAGCACAAATCTATCATATAACCACAAAA

**ANS-5'** region (AT4G22880, 503 bp, 5' → 3')

TCCAAACTACAAAAAGAAAATGTGGTTAGTAGAAGAAGTCTAGAGAGTGAAC**CACGTGGAGACACGCTTAAAGCACGCGACGAAGAACACGTTG**  
**ATAGCGAT**TATGGGTTTAATTTCTATTGGGCCTTTTCTGGGAGTCTAGACCCAAGCCCATATAGTAGTAATCTTTTTTGACCAATCAGTCAACCC  
AACCATCCTCTCCCGTTGACCGTGAAGTGAGTCACGCACCTTACCTCACACAATAGCACTAACCACCGGTAGCTCTACAATGTCTCTTAGTTC  
GGTAACAAACTCTTCTAACTAAAAGTATAGTAAAACTTTGCTATATAAGAAAGAGTCTTTGCACATTTCAATTTACTTTGCAACCAATTACAAA  
AAAGAGTGTAAGAAGAAAAACAAAACAAATCCATTTTTTTTATTACTCTGTTTTTCCCTGTTTTTAAGTTTATTTACTTCTTACTCTGTTT  
TCTGCTCTGTTTTAGCTTTAAACAGAAGACTAAAGAAG

**3GT-5'** region (AT5G17050, 1005 bp, 5' → 3')

GAATTTAAGGT**GTGCA**TAATATCTGAATTTGAACACCCAATCGTTAGTAATAATTTGAACCAGTATCCGAATGTATATCCTAACATACCTACA  
ATTTAAGTACATAGTAATAAATTATTATTAGCATTTATATTTATAATAATTTTAGTGTCAAAATATTAGGATTTTAAAAATATTTTAGATATTT  
TTGGGTATTTAATCTATTTTTGAATAAATTTGGGTAAAAATGTTCAAATTTTATAGATGTTTGTATACTTTCTAGGAGTTTAGATAGATTTCG  
TTTATAAAAAAGTTGATTTTTTGGGAAGTTCGGATAATCCAAATTCGAAATATTCTGACCAACCCACAATATAGAATTATCCGAATAGATTTT  
ATACCTCTAAATTTGAAAACCTAAAAATCTAAAATATTTCGATCTGAATTCAAACGGATACTCTAACTCCCACCCTTTTGTCTAGTGTATATAAT  
TTCCTATTTTTTCAACGGATGATCATAAAAAACAAAAGTCTACTACTTTGTTGACGGGTAAAATAGATTATTTTCTTTTATTTTTTCCCTCTA  
AAGTCTTAAAATAAATCATTCACCAATCT**TA**ATCTTATGACAAATCAATAATTTTTTATTTTTTGGTTGAAAAAATAATCTAATAATTGCTTT  
ATTAAGATAT**CATGTACAAAGTACAG**ATACAAATACAATCCTAAAAATGTCCTTCTATAAGAAGAAAATTACATAAAAAAACAAAAACATTT  
TCTCTGAAAAAAGAAAAATATCAAAAACGATTTTGTATTAAATTTGTCGTTTCATAAAAAAATTTGATTAAAAAAGTTGTTTACTTGTTA  
TATAAAGAAAGAGAAGAGATCGGTACCAACCAGAAACAGAGCTTTACACTTGCTCGGTGGTTCATTTACGACCACACTCTCTCTCTCTTT  
AGCCCTCTCCTCTCTATTTATTTCTCCAACAACTCTCTCTCTCTTTTCAAGTCTTCTTCTTCATTACTCGCACC

**BAN-5'** region (AT1G61720, 667 bp, 5' → 3')

GAATGCTATTGCCAATGCCTTCTTTTGTTCGATTTAGGATTTACCCCTCTCTTTTTTTTGTCTTCTTCACTTTTTTATCTTTCAATGTAACCTT  
TCTGGTTATTTTTATCTTTGTTTAACTCTGTTATGGATTTGTAGCTTAAATATGATAAAATTGCTTAAAGGCCAGATTCTGTGAAACATGGACAA  
GAACAGAGCAAGTTATGTTGAATTGA**TCGTG**TAATTCGTGAAACAGAACATAGCAAGTCCAAGTTGTGTTAAAAACTGCAGAGAATTTGACA  
GATTGGTGGAAGTAAAAAGCATTCTTTTGCAACTCATTTTAAGATCGGCAAAGAAAAAATTGAAGTAACAGAACCTTACTGTAACACTATTCTG  
TTACTCTAAAGCTGTGTTATATTGTTTAGAGACAGAAATAATCAAACCT**CTTGTG**GATAATTTGGTAGATGATAACAAATCAGAACTCTGAAGGT  
CAATCTTTTTTGATTCTTAGGTGAAGACAAGTTGGTTATTTCAAAGAT**CACGTG**CTTACCTTCTAAACAGCCTTATTGATCTACTGTTGTAC  
CTAATGAGCAAGGACTATTTGCAAAATCTTTTACTTCTTATATAGAAGTCTCAAGACGATAAACTCATAACAACTAAATCTCTATCTCTGTAA  
TTTCAAAAGTACAATC

**Figure S3.** 5’ regions of structural genes of the anthocyanin pathway and proanthocyanidin pathway in *Arabidopsis thaliana* examined in this study. The sequences are ones immediately before ATG codon, covering at least partial promoters. All sequences have been confirmed via Sanger’s sequencing. One nucleotide in **3GT** (shown in red) differs from the standard genomic sequence. The G-box and its variants are shown in blue, and sequence underlined or in rectangle indicate those of probes tested in EMSAs.

**PAP1-5'** region (AT1G56650, 1548 bp, 5'→3')

TACAGTGGCGGATCAACGTTAATGAGGCAAATTTGGTTCAAATTCATCTAAATAAGACTAGAGTTTCACAGGTTTCGATTCTCTCTTATAACAATTTGCTCCCAC  
CAATTTTTTTTGGCTGGGTCCGCCCTGGTTATATATATACTTTCTACACCAGGTTTGGGTTTCGAGTCCACACATAATTAACGACACAATTATATAGTGCACGATA  
GAATGAACTAAAACAGCTAGAGCGTAGAGGGCTCATTGTCTATAAAAAATCCTTCGTTAACCTTGCAAGAAACCAAGAGTAGAGGGCTCACACTTAAGTCTCCT  
ACATGACGATTATATTTTCGTCAAAAAAGAAGCAATTAGTTAGCTTTACAGCATATCATTTCGCCTAGGTTTTCCATCGTACACGTAAATTTTCATGCAAGAAA  
GCAGAAATATACAAATACTAATCTTTAGATACTGAAAAATGAGATCAGATTCTAGTCAAATTTTGTTAAAAGTATTTATAAAATTTAAATGCAAGTCTCTCAA  
AAAGTACGACTAAAAATGCTTTTTCTTAGAAAATGATAATAAACCGGCGTTTTATATATAAGTGTTTCTTTTTCTCTTCTGTCGAGAAGTAAATCATTAAGAA  
CCAATATGGCTTTTTCTTAACTAATCTCCGTGATAATCAAATCTTTGATCATTTCTCCACACAATCCCATCAACAACATCGATCTCAGTATAGTGCACCAACAA  
TGATTCTAATCGGCACTACTAACTATAGAGATAGTTGTGCCAAAAAAGGATTAAGTAACTAGAGAGATAAATCATATTTCAATACATGTACTATTTCTTA  
CTATACTTAAGAAAAATTTGTATACCACTATCTTAACTCTTAACACTGAACATACTATACACTATCTTAACTCCCAACTCTTGTAAGAAATATCTAATTTTAA  
AGAAAAGACTTCAAATGCTTGTTAAATTTCTAGTGAAGATGCACATTCTAAAACTGGTAAAAATGGTAAGAAAAAATATATAAAAAAATAGCCTTATTAAA  
ATTTATATCTCTCTATTTCTCTATCCAACTACACGGATGAAGCTTATTGTTATTCATCCACCCTTTTTCTCAATTCTGTCTCTATTTCTTGTGCATGAACTT  
CTCCATCTTGTAAATCGGATAAATCATACCCAAATTTTTCTTTCTGAAAACATATATACCCGAACATTAATTAATCTATCGTCTCTTCTCCTAATTTTGTAAAG  
AAACATGTTTGTGTTTTGTTTAGTACTGAAAAAGGATGGAGATACCTTGCTAGATTCCTTAAGCCTTTTTCTCTAGGACAAATCAGTAACCAACAAATAACTT  
AGCAAATTAAGCACGACAGCTAATACATAAAATGTGGATATCAAACATGACGCTCACTTCTTTTTTCCGTCACGCTGTTTTTATAAAATTTTCTCACATACTC  
ACACTCTCTATAAGACCTCCAATCATTTGTGAACCATACTATATATACCCTCTTCTTGACCAATTTACTTTATACCTTTTACAATTTGTTTATATATTTTA  
CGTATCTATCTTTGTTC

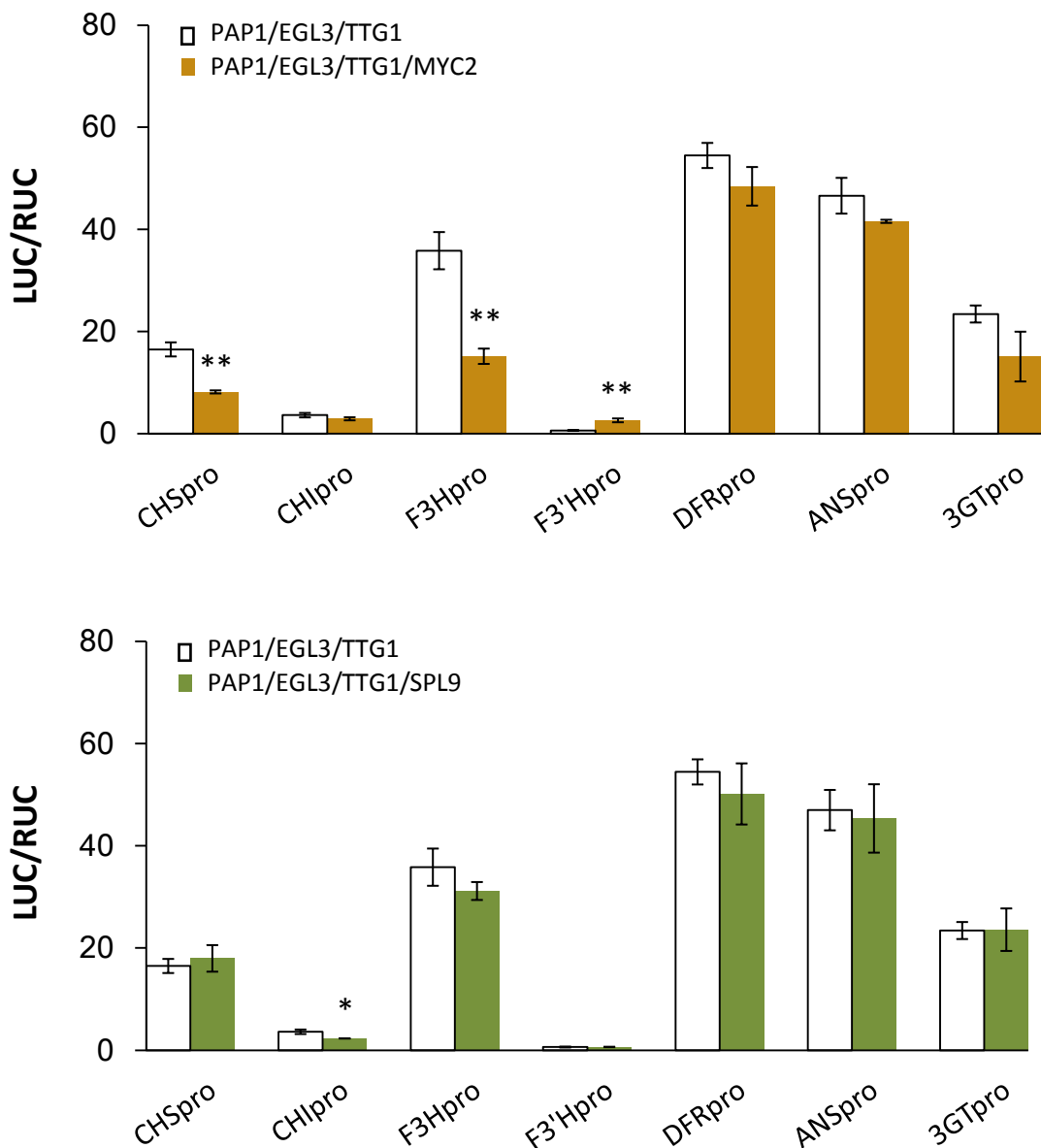
**GL3-5'** region (AT5G41315, 989 bp, 5'→3')

CGATCACTCAAATAGTAATAAGACTGATTAGATTATACAAAAAGAAAGAAATCATACGATGCTGGTTAGATTGGACTTGATCAGTAATGGTATTCTA  
GTCAACATTGCTTCAAAGATCTAATAGTCAAGGAAACAAATTTTTTTTTTTTGGTATCAGTGGGGATATTAAAGTGAGGGAACATTTTTTTTCAAGAATAGA  
TGGGTGAAAAGTTACGCTTGACGTGATAACATTTAACTTTAAAAATCAGTGTTGGAAGAGACACAAATGATTCAATATTCCCAAAAAAAGAGATCTCTA  
GAACCACAAAGAGACTGAATAGAGAATTTATTGAAGACAAGACCACAACAATGGACATTGTAGTTTCATTGTCTTAAAAAAGGTTGTCTTCCCAATGAGG  
AACTAATCAATCAACTCAAGATAAAAAGGAGGAACAATCAATCAACATCAGCGTTTTGCTTTTTTCTCTACTTTTGTATCCTTTTTTTTTTCTCATAAATCA  
TTAAAAAATTATAAGTACTTTTTTATTTTTCGTGATAAAATGTCTTGTGTTTTGTTCTGTACACAACAAAGATGATATCGTCAATTTCAAAGAAAAAAGGATTC  
GTAGACAGTTCTTCTAGTCTTTTCGAGTTCAAGCTCAAACAACAACAAATTAATATTCAAACAACATTAATAAAAAAAGTATGGAGTGACCAAAGAAAA  
AAAAAACTCTCAAACATTTCTCTGTTTGTTCGGCGGAAAACGGCAACTGTTTCATCAAATGACAAAACAAAAACCTTAACATCTAGTTGTATCCTCTCTG  
ATACTTCAAAAAAAATGTAAAGAGTTACAAGTTTCCCTTTTTCTTTCTTTTTTAGGCTATAAATTAACATAGTATCTTATTTCTTTCTAAATCAGGACAAA  
AAGTTTGATTTTTTTCTTTCTTTTCTTTTCCCTGTGTGTGGTTTCATGGGATATAGGGATGAAGAAACA

**TTG1-5'** region (AT5G24520, 968 bp, 5'→3')

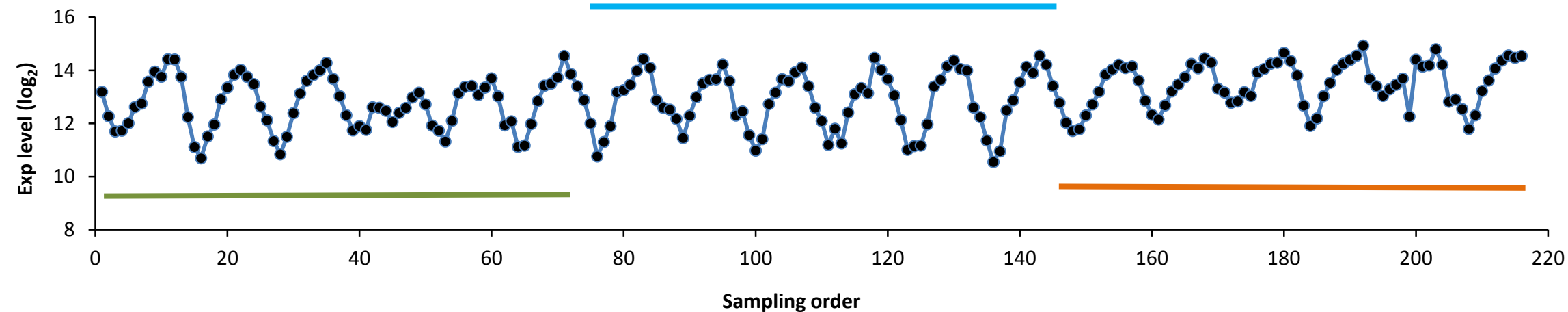
GCTTTTCATCATATTTAGTGGTTAGTTTTTATTATTTATTTATTGATTTCATGACTTATGCTAGATTATGATAAGAATTTATGTTACCCTTGATAAATCCTC  
CATTTGACATGTGTTAATGCTAGATTTATATTGTCTCCAAATTTACAACCTTCGATGTCTTATGATAAATGCCAACAAACCAATTTTCAGATAAAGATTAGCA  
GACTTAACCTAAGCTTATTTATTCACCTTGCAAGGTGGAGTGATGTTGAAAGAACCCTCACAGACACGTCATTTGGGAAGACTAAATCTCTTTTTAGCACGTTACAC  
CTTTGAGATCGCGTTTATTTCCATATGGAGAGAGAGCAACAATACGAGACATGGAGAGGCACCATTAACCGCGCGCACTGCTTCCAAATATTGACAAACAA  
ATTTGAATCTGGATTTCTCTATTTCTGTGAACAAGGAGATAGAAGCTACGATGAATGCATGGAAGCTTGTTGCTTTAATATAAAACACTAAAGGGGAGTAGA  
ACTTTCTTGAAAAATTTGTATGCAAATTTATTTACCGAATGTTAAAAGCTTTTTTTCGAATAAATTTTACATTTTCTTAATAATAATAATAAAAAAGGATTGTTG  
ATTATCTTAATCACAAACAATTTATTTTAGCTGAATTAGACAATTTGTTAGTAAAATGATTAGAGTGTACATATTAATGTTGTTAGTGTTCATGTCATCCT  
AGTGATCCAATAATTAGGCCATTCTATAGCTCTTAACGTTAAAAATAAAGGCCATTATCTGAATATACAGAAGGCCATTATCAATAGATACATTAAAGAT  
ACTGATTAATCCAGAGGGTTTATATCTACGCCGTCTCCATTGATTATTTCTCCGTCTCTTGAAAAATCCGACTGACACTGACCTCAAACCTCTCCTCTCACT  
TTCGTCGTGAAGAAGCCAAATCTCGAATCGAATCAGCACCACACATTTCC

**Figure S4.** 5' regions of the MBW genes examined in dual LUC assays. The sequences are 5' → 3', immediately before ATG codon. They have been verified via Sanger's sequencing. The sequence underlined is for the probe tested in EMSAs. The elements in blue are G-box and its variant.



**Figure S5.** Effects of MYC2 on the structural genes in the presence of PAP1/EGL3/TTG1 complex in dual LUC assays. The results are based on biological replicates ranging from 2 to 10, with the bars representing standard errors. Significant effects of MYC2 or SPL9 are shown (one-tailed t-tests, \*,  $P < 0.05$ ; \*\*,  $P < 0.01$ ).





**Figure S6.** Expression pattern of *OsMYC2* (Os10g0575000) in Nipponbare leaves of *O. sativa*. Data are based on GSE36040 reported by Sato et al. ([63]). A total of 216 sampling points (dots) are presented here (without redundancy), grouped into three developmental stages. The bars show different stages of leaf sampling (green for vegetative growth, blue for flowering stage, and orange for seed maturation stage). The first data point was collected at 10 am, following by 71 data points sampled at a 2-hr interval within each developmental stage. Data were corrected for background signal, normalized using quantile method ([109]), transformed by log of base 2, and concatenated across three developmental stages with samples taken at the same time averaged.

***OsC1*-5' region (Os06g10350, 997 bp, 5' → 3')**  
GATATGAGCATTATCCGTCCGTATCCGCTCCGTTTTTCATCCCTATATGTAATTATAATTTATTTTGGTTATGAGTTATTTTATCACTCAAAGCACTTG  
AAATTTTGAATAAGACAAATGTTCAAACATATGTTTAAAGTCAACGATATCATCTATTAACGAGGGAGTATTAATATGTTGATTTGTTGG  
TGAGAGAAATGGAGAGAGAGTGCATTGAAACTTTCAAAGGAGTTGTAACATGAGGTTATCCTCTTAGTAGAAAACTCCAAATATACATAGAAATTA  
TTATTTCCATGAAATTCCTTTGAACCAAGACTAGCATTCAAAGACTCTCAAAGGATTTTTTCCCCCTATGGATTCTATTACTCCATATATATTTTCAT  
ACAAATTTTCGTCCAATCTAAAAGGACTCCTAAGCACTGATTTTTTTTTCTTTAAAAAAAAGAACCCAAAGTTAACATGCGAAAAGACAGGGGCCTAT  
AATTAATACTCCCTCCGTCCCAAAATATAAGCATTTTTTAGAATAGTGTCAAGTCAAACTTTTTAAATTTTGAGTATTAGTAGCAAAAATTTTAGAAA  
GATTAATCATGTAAATTTGATCTTACTATATTTATCATTAACGAACATATCATAACATGCAACTCTTTTTATTTAAACATTCTACTTTTATAGATA  
TTGTTGGTCAAAATAGTATCTCGAAAACCGTGTCAAGACCAAAATACTTATATTTTGGGACGGAGGGGTAGTATTCAATTGATTCTCTCCATCCGTA  
GCAGCCAAGTCCCATGGATGGTTGCATGTGACCACATCGTACGGGGCTACAGGTGGTGTGTATTTCATGCCACACCGTTGCATGTATAAGTACAGC  
GCAAAAGTGGTAGAACGAGAGGCTCTGATGCGCACCAGATCGCTCAGTCTCACACCGCACAGAGACAGAGAAGAGCTCTAGAGAGAACGAGAGAGAG  
AGACAGAGAGAGAGAGAGAGAGGGAGA

***OsCHS1*-5' region (Os11g32650, 1Kb, 5' → 3')**  
GTGCATATATACCACTAAATAGTCATCAAAGGATTTGAAAATTTTTCTGGCAAGATAGATTAATATAAAAAATATATAGCACTCTACAAACATGCAAG  
TTAAAAATTCAACTTGTACAAGTTGTAACAAAAATAGCAAACATAGATGCGAATGTACGTTAACTATTTTCGGTGTGATTTGTTCTTTTTTGTGTA  
ACCTGTAGAAGTCAAATTTGGTCTTGTATGTTTGTATAGTGGTGTATTTTCATGTTAATATATATTATCATTTTTTTCAATTTTTTTAACTATTTTACT  
TCCTCCGTTTTATGTTATAATACATTTTAACTTTGGTCAAAATTAACCTGCTTTAAGTTTGACCAAATTTATAGAGAAAAGTAGTAATTTTTCAAC  
CTAGGATAAAATTTATATGAAAATATATTGAATTATTGATTTAATGAACTAATTTAGTATATAAAATATTTTACTATATTTATCTATATATTTAGT  
CAAACTTAAAACAGTTTAATTTTGTTCAAAATCAAACGACTTATAATCTAAAACTGAGGAAGTAGATGACATATAAACAAACGAGAGTACATTCCC  
ACGGAGGAATGAAAATCCATCTCCGAAGAAAAGCTTTAGCTTTGGTAGAGCGAGCGAGAGCTGCATTGGCCACGCGAGCCAACCTAACCCCTCCGAGT  
CCAGGCCGGTTGGTACACGTGTCGCCGCCGCCGTCCGTTTCCACCCCGAGCCACGTGGCCGCCATCCGCCCGTCCGCCCGACCTAACACCCCCC  
TCCCCCCCCGCGCTATATATATCAGCAGCGCCCCACCAGCTTTGCCAACCCAGCAGCAGCAAGCAGCGCACAGCCCCAGCACCAGCAAGCTGC  
CTCTCATCATCAGCGAGAGCTAGCTAGTGTGTGCCACTTACACTGCTGCTGCTGCTGTTCTAGCTAAGCTCACCAGATCGTCGTCTTCGTGCATC  
GCCGTTGACCTGGTGAATTAGTCGAGAGAG

***OsCHI*-5' region (Os03g60509, 986 bp, 5' → 3')**  
GACTAATTTCCACGTCCCAATTGCTCCCAACCATCCTAACCATGCTTCGTATGGACCGTAATAAAAAAAAAAACAGCCTTCCAAAGTGAAGACACTC  
GCCAAGAATCTCAAGGAAAATACCAGTACCTTCTTATAGCACACAAAACAATACTCAACTCTAGCCAACCTACTCCTTCGTTCCAAAACAAATGTAAT  
TTCGCACTATTCTTATCTAATGTTTGACATTTTCATCTTATTTAAATTTTTTTTATGATTAGTATTTTTATTGTTATTAGATGATAAATCATAAATAGT  
ATTTTATGTGTGACTAATATTTTAAATTTTTTTTATAGATTTTTTTTAAATAAGACAGACGGTCAAACGTTGGATACAGATATCCTCGGCTACATTTA  
TTTTGGGATGGATATAGTAGTAACAATAAACAGTAACAGAGTCCAACGCAAAAATCAACTTGATATAAAAGTGGCATGATAGCTCTAATTTACGAA  
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GTGTTGTTGCCCATCCCATCAATTTAGCAGCTGCGATGTACCACCACAACATTTCATTATAGCCACCCAGCTAACACCATCTCGTGCGCTCGTGGC  
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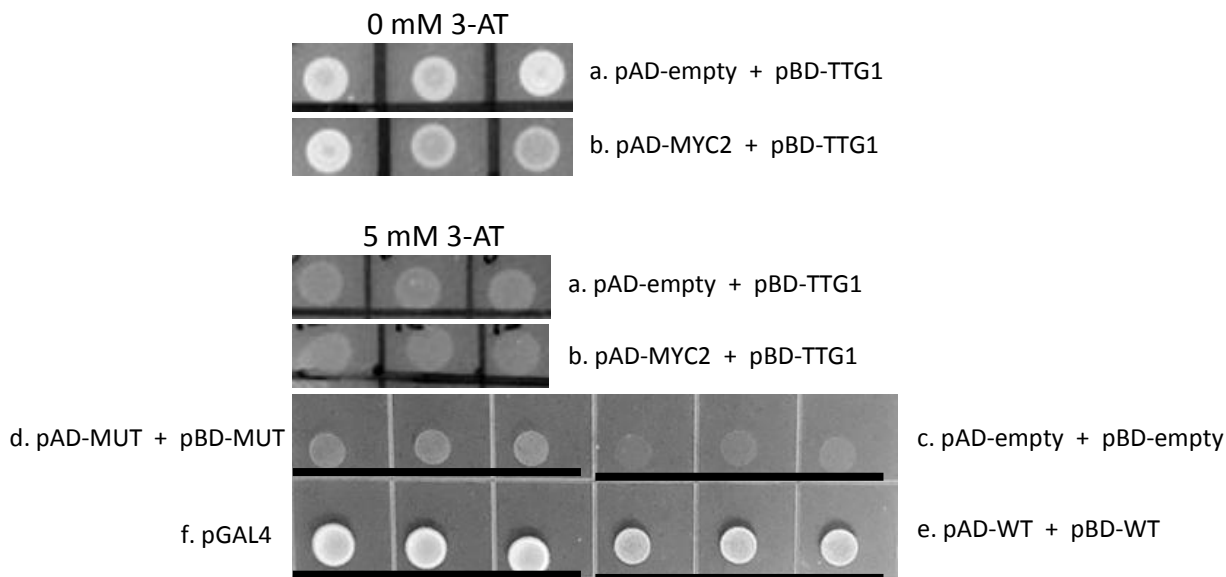
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ATAACTGTATGTTTCACTTGTGTAGTTAACTGGAAACATTTGACTGACCGATTTTTTTTGCATCTGCATACAGGTGGTGTGATGACGTGTAAACA  
GTCCGGCGCTCCGATTCTTGGTGGAATATCGGACGTCCGATCGGGATCATCTCCCGTAGTTGCCGTTGCCAATTTTTTTCTACAGTAACATAACA  
TCTCTGATATGGACAAAAATCCAAACTATTTAGGTGAGTTTCTGTTTATGGAAGAAGCTGCAGCTGTTAAAAACTCTCCCAAACATATCCAAAGATA  
TTTCTACGCTCATCTCTAGGATATTTGTAGGTATTGTAGGGCTAGTTTAGCTCCCATAGTCCCATTGAAGCGTACGTGCACACAACCAAAAATGTT  
TGCTGGAGCAGTGGAGAGCACGGAATGTTAGATAGCACCTACCCTTCCACGTCAAATCGGAACCTACCTAAGCTTATCGATCGGGTGATCAGTTATGC  
TAAAGGCCTGCAGCTAGCTAGAGAACACAAACGCATCGATGAGTAGTAGTTGGAACGTGCCACTGCCACTGCACGACTTTAGTTCTTCGACCCTGT  
GTGAGTAGTAGCGAACCAGCCTCTCTATGTAGCGTGCTCCACCCGTACAGTACGCCCTCCCTATATACGGATGATCACGCAGTACACGCTCTCCC  
TATCGTAAACCCGCGAAAACCACAACCGAAACGCAAGGGTCGATCCATCCACGCCTATCGCGCGCGCTGCATCGGGTCGATCGATCGAG

***OsF3'H*-5' region (Os10g17260, 934 bp, 5' → 3')**  
TACTTTGAGTTTTTTGAGATTTGAGACCATGCATAAAGCCAACGGCTCGTAACTTTTCAAATTCCTAGAAAAATAATTTCTATAGGAAATGTTTTTA  
AAATCCATATTAATCTATTGTCTTTCAAGTTTTTATAAGCTAATAATGCTTAATTAATCATGTGGTAACCTCACTCTATTTTGCGTGTGGGAGGGA  
AGGGTTCAGATCCCGTAGCTAGGTCTGAACACACCCAGATTGTATCAGGGTTCACTAATTCGATTTAAAATTTAGATTCCAAATATAGCAATATGGCT  
TTTTTTTACCAAAATTTGATATTTTTTATTAATTTGGTTTAAATTTTACAATTTCAAATTTGAATTCTTGAAAACTATTCCAAATTTCACTCAAAAT  
CTACTTTTGTCCCAAGTTGGAACATCGAAATTGCGTTGTTTTCAATCCGTTTTGGCTGAAAACATAGACCCTGGTTAGTAATGACCCCGACGATCAT  
TTATCCTGGATTTCGCCCTGGTAAAAACGGATGGAGTATTGAATTTGTTGATATCCGGGACAATCTCGTGTCAATGATGAAATTTTCTTTGATAAAA  
AAGGTGAAAGTTGCACCACTACATGCTGTGACATATTTTTCTTTACTCATTTTGAAACAAGTTGATTTCTATGATATGTGCCAAGTAGTCGAGAGCCAA  
ATAAAATAAAATTATTAGTGATTGCAACAGGTGGGCTGGTTTTGCGTCAATTTGACCAGTACACAGCCACACATGCCATGAGGAGAAAAGGAATCAAG  
CAAACAACCTTTGGTACCTGTTCCGGTGGTAGGTACGAAGGGTAGTTTGTTAGCTGCACAGCAGCGCGGGGTACCGTGTATATATCAACTACCCAGTC  
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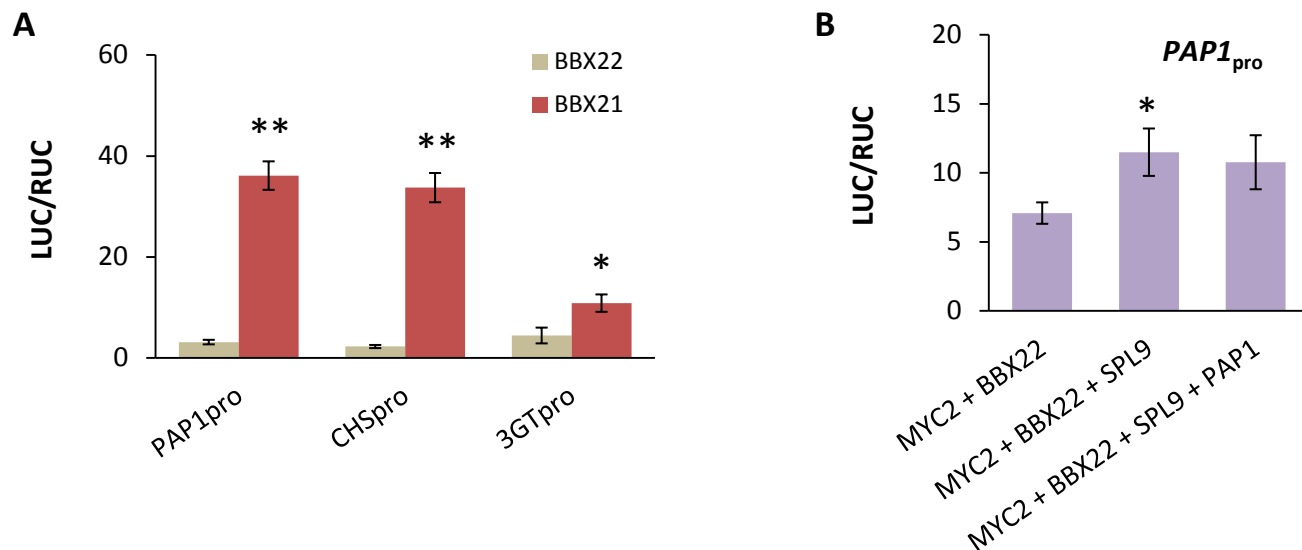
***OsDFR*-5' region (Os01g44260, 1042 bp, 5' → 3')**  
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AAGGAGCAGAGTAATGATGGTTAAAAACTATAAGAACGAAACAGTGATGGTTTGATTTTTAAGGTACCAAGAACAATCAATAGAAATGGTGGCCAGC  
CAGGCAAGCAGCTGGAGGAGCTACAAGGAGAGGGGTGGCGCCCAATGCGACTTTTAAACATATAAAATTATAAAGTTGGTAATGATAATGTTAATTT  
TAAAAAATATCATGTGGAATGAGTTGACCTTTTACAAATTTTCAAGAAAAATAAAGGGTAAAAAATTAGATGATTTTATATCGGTGCTAGATGTACA  
AATGCGTGGGCCAACCTACTAGTTTTTGGCTGAATCTGAACAATTTTGAACCGTCCAAAAAAACCGGTTCAATTCTGTCTCCTTTGCCTGTGCTCACG  
CTGTCTACACGCTGCGGATGCAGCGTACTAAACGCACCGGCCCTTTCAAACAAGAACCGGCCGGTGTGCAGGTGCACGTAGCTCAAACCTACCTATCA  
AAACGCTGGTCATTTCTGTCTACTCCATCCGACCCCAAAAAAAAAAAGACAAACCCCTGATTTTCGTGTCTAACGTTTGACCGTCCGTCTTATTTAAGAA  
AATTATGAAAAAAATTAATAAAACAAGTCACACATAAAATATTAATCATGTTTTATCATCTAACAAATAATGAAAATACGAATTATAAAAAAATTTTCA  
ATATAAGACGGACAGTCAAAGTTGGACACGGAAACCTAGAGTAACTTGTTAGGCAGTACAAGTGTGTGTAGCTATACTCCCCCTGTCTGTACACAGC  
TTATATATATAGGCGAGCCAACGAGCGAGGCCATCACCAAGTGCAAGGTAGCTATCATATATTTCTGCGAATCCAACACAAGCACCGCCGCGTAGTA  
CTACTACTTTGCGCGCGCGTGTTAGATTTCGCGTGCGAATCCAACACAAGCAGATCGATCACGCACGGTACGCC

***OsANS1*-5' region (Os01g27490, 942 bp, 5' → 3')**  
AAATCAAACCCGTGATATGAAGCTTTTAGTTTTTCCAGACTTTTGTAGTACTACTATTTGCTAGATGATTCTGAGTAGATACAATTGCTGATGGTTTT  
GATTAATTTTTTAGACAATGTGATAGTTTTGTACTTTTTCTTAAATATATTTTCATATATGACATGGATCAAAATGGACAGAAATTTGGGAAATTTAATTT  
GATTAACATGAATTTAATAATTTTATTAACACAAATTTTATAGTGCCGTAGCGTTAGCACGGACAGATTACTAGTAGTGTAATAATTTTAAATCTTCTT  
GTAAATTTTAGAAGCACGAGGACTAAAATGAGAAGTGCCCAAAAGGGTAGGTTTTTTTTTAGAGGTGTTGCCTCAGCGCCTACCTGTTATTTGAGGCC  
ATTGGATAGGAGTGGGCCTATATTGTTTCATGCCCTCGTGCGCGTACACAATCATAGTTTCACATAGTAGAAATGGTGCTTAAGACTTTTAACTTTTCA  
GTTCTTCAAGTCTCAAATATAGTCAATTAAGTTTGGAAACTAGAAAACAATAGAAAAAATCAACTACAAAATAAGTTCTACAATTTAAATTTCTA  
ACTTGTAAAAGTCAAATTTCTGTTATATGCTTTATAGGCTAACGAGCATGCAATGAGTTTATACATACGCTCGTATCATCTGAATTAAGAAACAAC  
AGGGGCATTATTGACAGGGACCAATCAACCAATGTTACGAACCGGCACGCGATTGATGGATGGAGCTAACCGCGCGTGCCCGACACCGCTGGTTGTT  
GTTAGCTACAAACGTAACACATGCATGCACCGATCCATGGATGGAGCAAAGCGGCGCGCAGCGCCGGAGTATAAATCTACCCGCGCTCTGCCTGCCTC  
GCCATCACCGGCCGCCGATCGAGTACGTGCGCACGCAGCTCATCTACTAGCCTACTTCGGGAGGGCGAC

**Figure S7.** 5’ regions of the anthocyanin-pathway genes of *Oryza sativa* tested in this study. They were obtained from Heidao, verified via Sanger’s sequencing and examined in dual LUC assays.

**A****B**

**Figure S8.** Detection of protein interactions of MYC2 with GL3 and TTG1 in Y2H. **(A)** Interaction of MYC2 and GL3. Results show growth of yeast strain under high concentrations of 3-AT in three biological replicates. Co-transformed yeast by vectors indicated by a (negative control) and b (trial), respectively, grew on SD-medium deficient in three amino acids (Leu, His, Trp) and added with 3-AT of 40 mM or 80 mM. **(B)** Interaction between MYC2 and TTG1. The background growth on the three-deficit medium as in (A) was inhibited at the concentration of 5 mM 3-AT. Controls for no interaction (c) and positive interactions at different levels (d—f) are shown in three biological replicates.



**Figure S9.** Impacts of BBX21 and BBX22 on transcriptions of anthocyanin genes in dual LUC assays. **(A)** Comparisons of single effects of BBX21 and BBX22 on transcriptions of three genes. For pPAP1<sub>pro</sub>, effector and reporter were supplied in 4 µg/each in co-transformations. For pCHS<sub>pro</sub> and p3GT<sub>pro</sub>, 4 µg pBBX21 or 6 µg pBBX22 were provided in 1:1 ratio for each co-transformation. Biological replicates (n) in the standard errors varied: For effects on PAP1<sub>pro</sub>, n = 9 for BBX22 and 27 for BBX21; for CHS<sub>pro</sub>, n = 5 for both BBX21 and BBX22; for 3GT<sub>pro</sub>, n is 6 for BBX21 but 2 for BBX22. Higher impacts of BBX21 than BBX22 are shown (one sided *t*-tests, \*, *P* < 0.05; \*\*, *P* < 0.01). **(B)** Combined effects of activations of PAP1 by BBX22, MYC2, and SPL9. Vectors were added in 1:1 ratio (4 µg each) in each co-transformation that had at least 10 biological replicates. Data were normalized across tests. A significant effect of adding SPL9 is suggested by one sided *t*-test (\*, *P* = 0.017) but no effect of adding additional PAP1 can be detected (one sided *t*-test, *P* = 0.39).

**MYBL2**-5' region (AT1G71030, 1038 bp, 5'→3')

GGCATTGCAGATATTGGACCATGAAGACAATATGATGATGAGGCCCTTTGCAATGGTGCATATAATTCTAAAACGAAAACAATTTACAATTACGAGTG  
CAGAATACAAACGAGTTGATATAGATTGAGATTTAGATTACATAAATATCTTATACAGAAAGTGTTAAAAGATAATTTCGATTGGATTGATGTTATA  
TCTCTATCATTGTTTTT**CACCTTG**GCCTCGGAGATTAGAAGCAGCTTGTAAATGGGCTTTTAACAGTTACGGGCTTTAACGGGCCCAATAACAAAAC  
CTTTTGCTTCTTATATGATTTTGGAGTAGATGTAAGTGAGTAGGGAAGTGGTGAGTGAAATTAGAAAAATTCCTCGTATACAAAGTCCTAACCCACC  
AGTCAAATTCGAATGCTCCCATGTTTCTCCCTTATCTGTTCTGAACCTACACTCTTTAATTTTCATGGTTCCCTATTTTCTCTTAATTTGTTT  
ATTTTCATGTCATATTCGGAAGCTTCAGATATTTTATCAAATAATGCATCCAAATAATTTTGAGCCACTAGTCAAATATCTTCTTCGTTCTTCTTCTT  
GCTTAATATATATTTTAGTGAATCTATTATTGATACCACACACATCTTTGATATTTACAAAAGGTATCTATCGGAGCCGTACATATATTTTACG  
AAAATGTGGATAAGAGCGAGATTGGATTGGTATTGGTAAGGCAAATTAATGCGACACACTTCCACATTCATGATTCCACAAATTCATATGGATTT  
GAACAAATATGGGACCAATTTTTATTTGTTTCACTCCTAAATGTGGGACCAATTAACAAGGTTGATGTATTCTTCTGTTCTTCTCCTCGTTCATTAA  
TAGTTTGATTGAGCATGCACGCTCTCTCAACCCACCAGTCCAAGTCAAACCTCCTCAAGCCATCCCCAATCCTATATATCAGTTTCTTCTCGCAA  
ACCACCTCACAATCTATCAACAGTTTTTAAAAAAGACATAACTCAACCAATCTCACTTTGAAAAAGAC

**TT2**-5' region (AT5G35550, 964 bp, 5'→3')

GGTTTACCGAATTGTATGTCAATGGTGTTAAAC**CACATG**CAGTCCTATACTTCATATATGTGGTCATGTAATACATCTACTTCGTGTCTACTTCGTG  
TAGCTGGATATACAATGTATAGTAGGTATGTGTGACCATGTATTCTCTTATACTTTGTTTACCTAGCAATCTTTTTTTTTAAATTAAAATAAATATGC  
GGTTTAGATATGAAACTACCCAACAAATTTAACATTTTTAAACGTTTCATAACGTAAAACGACGTCGTTATAGACACATATTTTCCATGTGTCTGCTGA  
CTTATCATCTTCACGGAGTTGACTAACACCCGTTACTTTGACTCTGAATTTTGTACTTTTTCTTAAGTTGAGGTATGAAATTCAAATAAATATGCGG  
TTAATATATGAAAAACCCAACAAATTTTTTTGGATACGAAAATACACTCAGAAAATAGTACGGGTATGAAAATACCCTTTTCCCGTATTTGATACA  
TGTCTAATTCGGTTCAAATAAACCGAATATGAAAATTTTCAGTTTATTTTCGGAAGTTAAATAAATCTAGATAACCGACCTGAAAAACCCGAGTCCC  
GACCGAACCGAACCAGAAATTAATTCGGTTTTAATTCGGAAGCATTTCCAAAAACCGAAATTCCTTAAACCGAATAACCCGACCCGATTAACCGAT  
TTGCCGAACCTCCAGGCCTAAATTCACACTTGGCTTAGAAAAACTCTTTGTAGATGTTAAAATTCGGTAAAATTAACCTCACCAAAGCTAATTATTA  
**CCAGGTG**AAGAAAGCATTAATAATTTCAAAGTGTGTATGACAGAGGTTTTAGAAAGCGACTGATGTACGGACATATCAACAACCTCCCTATAAAGATA  
CTCAGCTAAACACAAAAACAGAATCTATTCTCAACACAACACTAAAGACAATTGTACCAACCACACAACCACAAGAGAGAGAAAAGTGAGA

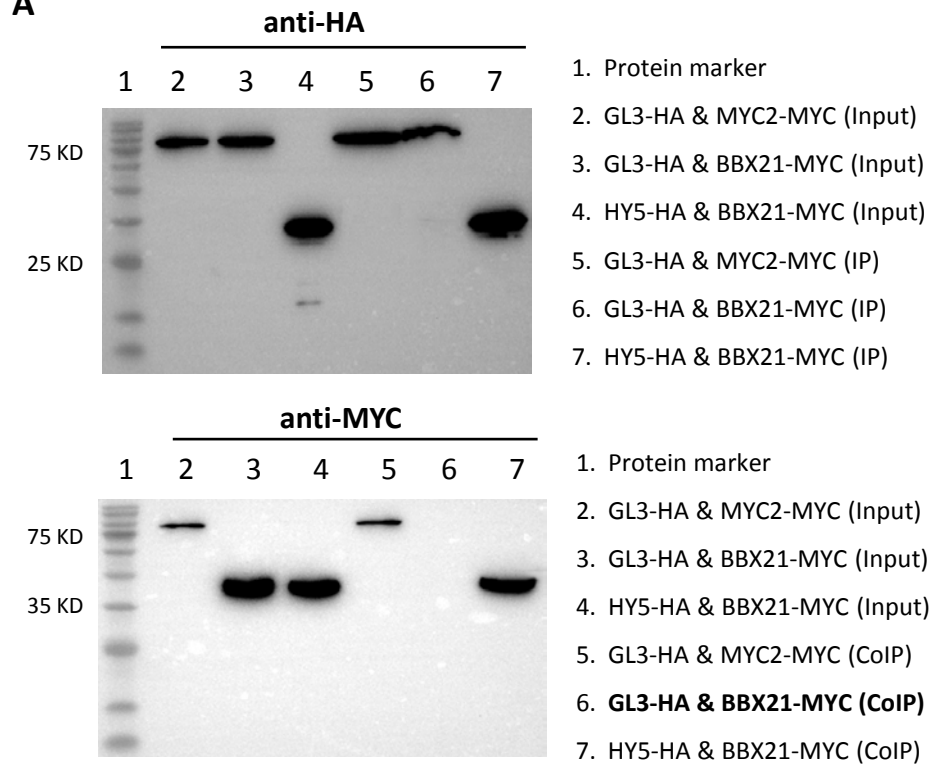
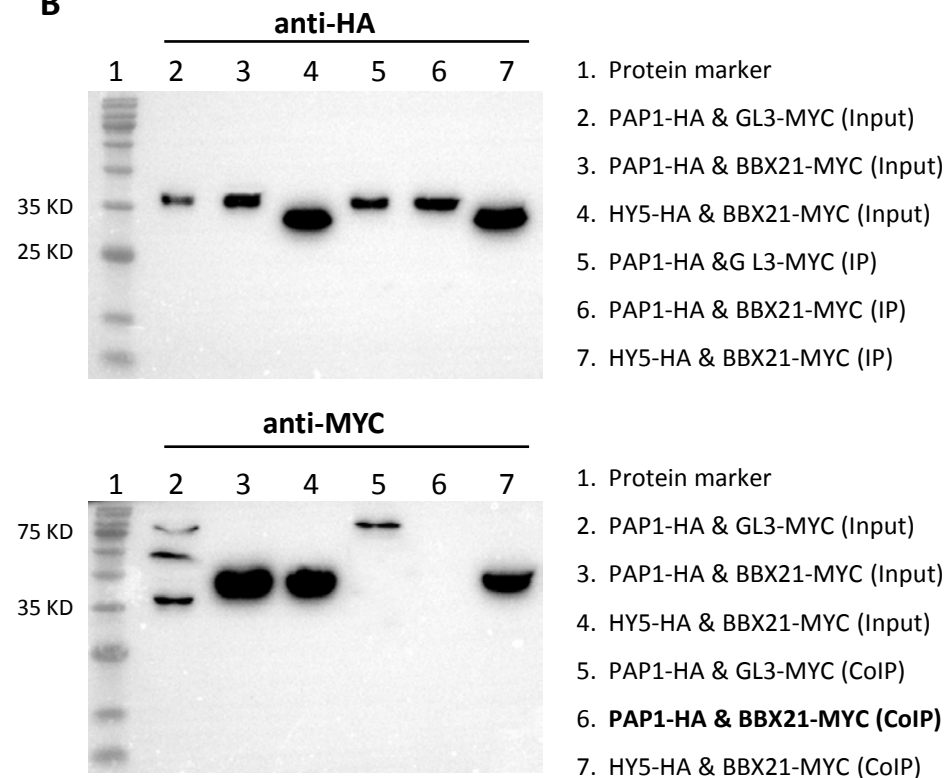
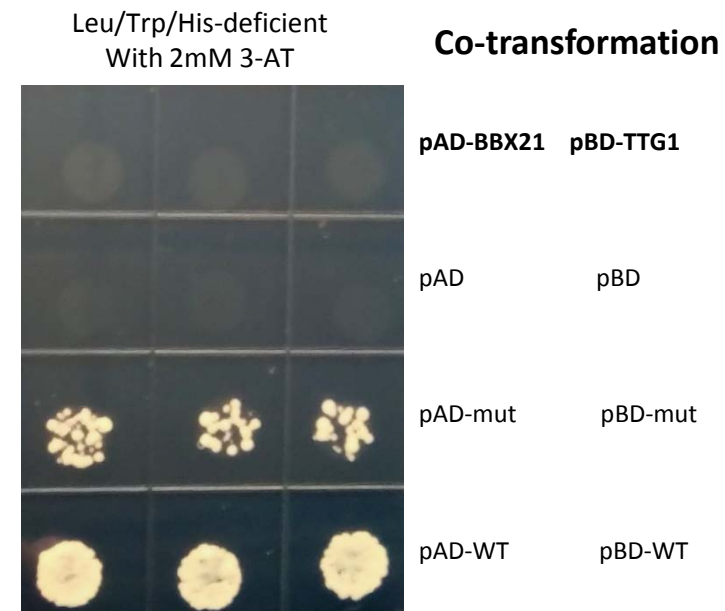
**HY5**-5' region (AT5G11260, 998 bp, 5'→3')

CAGAAGATCAAAACGACCCACTGTAAGGATTCTCCTTTTACATTTGAATCAATTTCTATGTTACTTGAATGCTCTATCTCACATATGATCATGTTTG  
ATGATGCTGTGAATAGAATGCTGTGGTTAGCAGCATTGTT**CAAGTG**ACCAATCTTCCAAGGAAGCGAGTTTTGAAGTGGTTCGAAGATAAAAGAGCA  
GAAGACGGAGTTCCAGATAAGCGAGCTCCATATCAAGCTCCGGTTTGATCTAATGTTAACGTTGAGATGGCAATGATTTGTATACTTGATTCTCAGA  
AACTCATCAACATTGTGTCAGCAAGGACAAGTTTTTTTGGTGATACGAGGAGTGTTTATAGTAGTAGATTCTGTCCAATGGTGTGGCTGGATATGTTGG  
ACTATGAAATTTTAGGATATCTTGTATTAGTTTTAGTTATTTTCTTGTGAGATTGTGCTTGTAGAAAACCGTTTTCAACTTTGTTTGGTTTTATG  
GCGGTATATAAGTTTAATTTTATGTCATGACAAAAACAAATCACCAAAAAATAAAATAAATTACTTTTACGACACTTTTGAAAGCACTGCCCTAGGCG  
TGGGC**CATGTG**ACAGAATGAAAGAACTCAGACCAAACTTTTCTGTCCAAGGACAGGAATGGGGCCACCCAATTAGCTCCCCTATCCATTATTCACC  
GTAAGATGCTAACCAGATCTAACGGCTAAAATCCACCC**CACGTT**CCAATCTCAATTGCCTTTGGATCCTTGTATTTCTCAAGGCTCACCTTTCTCCA  
CGATTCACCTCTCGATATCCGTTTCGATTCTTCAGAGATCTGACGGCGGTAGCCAGAGTAATCTATTCTTCCCAAAATGTCTCGCAATTAGATTCTTT  
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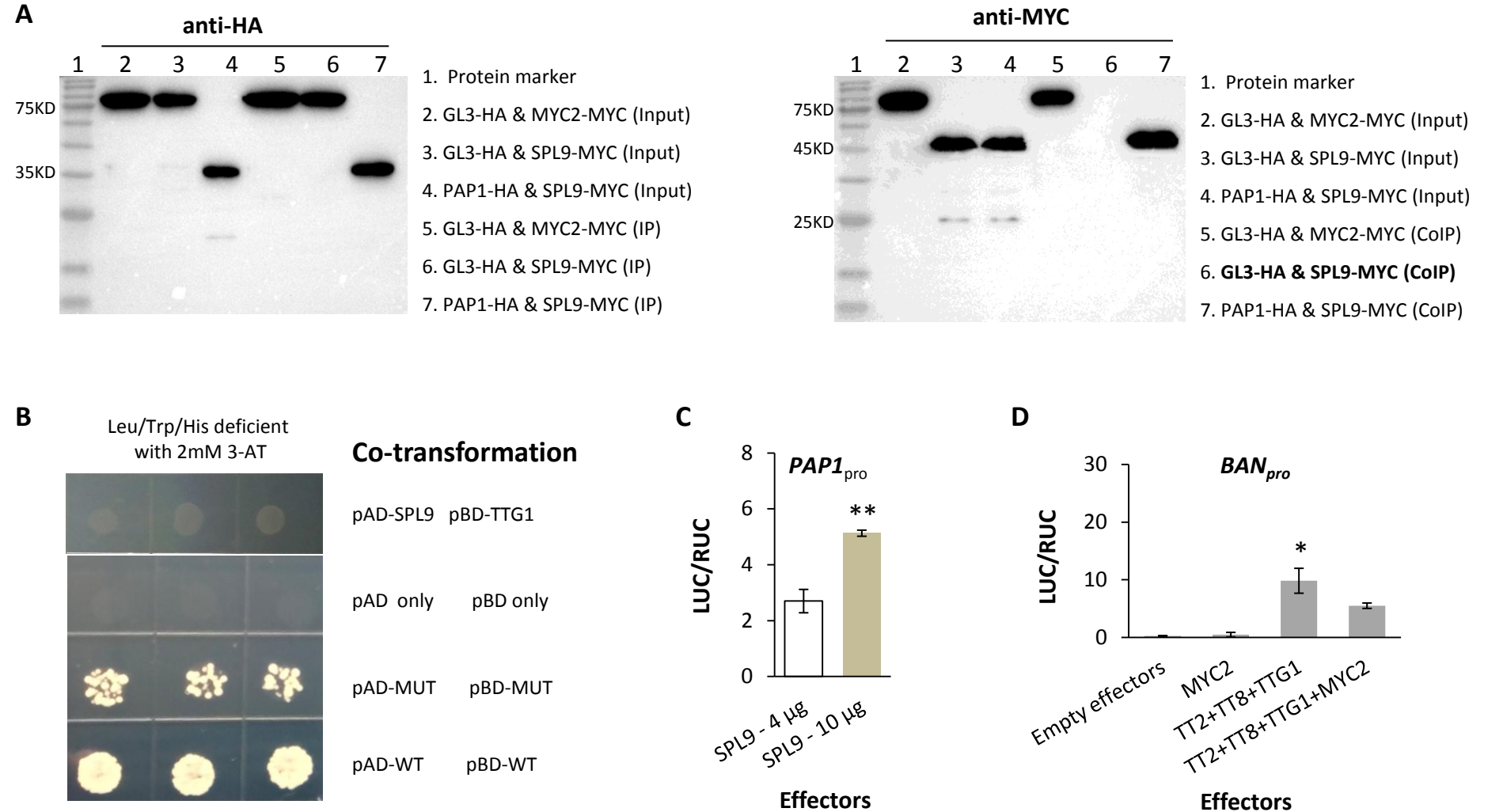
**MYC2**-5' region (AT1G32640, 1055 bp, 5'→3')

GTTAGGAGTAATGGGACCATATTGGTGGCATGCTAAATTATTGTGATAAATTTATGCATGGAGGAAAAGATGCCAAATGATTTATGTTATTTCACTCA  
TACTCACCTAATGACCTAATCCTTGAATTATTGTTTGAACCTTTAAAAATAAAATTTTAAATATTGTAATTAACAAACAATATAACGTTGTTAGCAT  
GTGTTTATCGTGAAATGTGAATGTAACATAAAATATTATAAAGGAGTTCTTCCTTTCTTAAAGCATATGCTAATAATAGCGTTTGGTCAAATTAATA  
AATTTATAGTTTATTTAGTCGTCAACAAATTAATTAGTTAAGCAGACAAGAATCGTTTTTGGAGATAGAGATTCTCACTTGCATTTCACTCTCTTGC  
AATTTAACATATTAAGACAAACACAAATTTTTGCTTTAGTGAATTATTAGCAACGACT**CACGTT**TATATAGATATGCAATCTCAAAATTAATTAAGC  
TAAGACACAGTATTTGATAATTGAGATTACAAATCTTAAATTTTGATTTTAAATATTTTAAATAACATTATAAAATAAGTAATTAATCTGTTATAA  
AAAAATATATTCTAAAAGTTGACAAAACAGCAAAATATAAATCGAAAAATAGTGAAAGTGTATAGTAAAGTGTTTTTCCACTGAGCTCACAGTTTAC  
TCTTTGGTACAAAAGAAACAATCAGTTAAATCTAAGTCAATCATTAAGAGCGTGTGATA**CACGTG**CGACCAAAACAGCCGTACGATCTCACTCACT  
TCCGGTCTTAATTTCTACCGCGTCGATCCAACAGTCGATGGGGTTAAATCGGGATGTGAGTTTCATCGAAGCTTCTCTCTCTCTTACAACCATC**CACG**  
**TT**TCCCAATGAAATCTCGC**CACGTA**ATATCCCTAACACAAATTTACACATTCACCCTCAAGATCAGTTACACATATAAATAATCGCAGACGCTCTCC  
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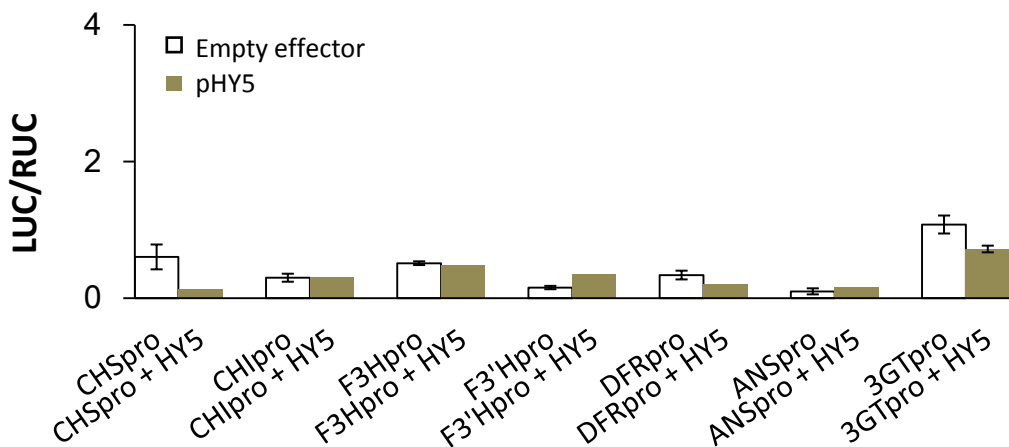
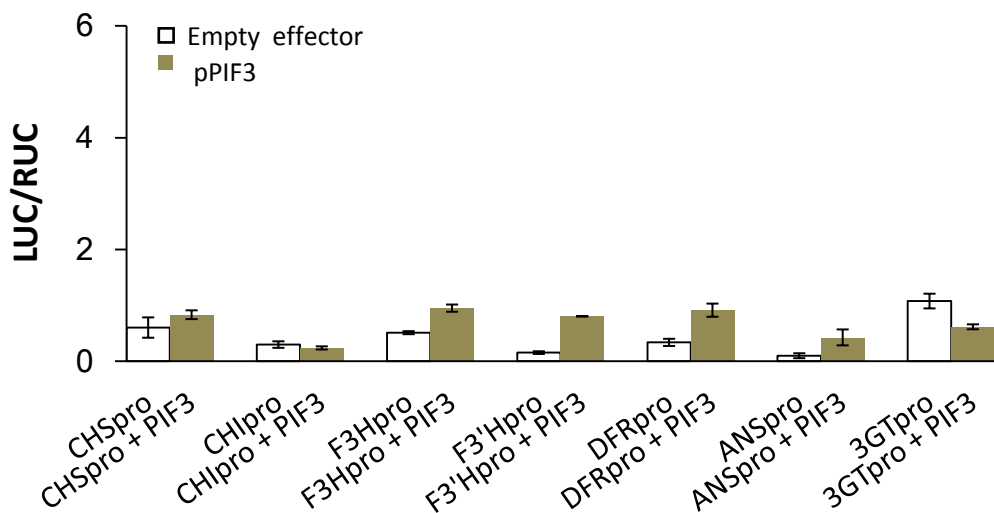
**Figure S10.** 5' regions of regulatory genes examined in this study. Sequence is immediately before ATG codon for each gene. G-box and its variants are in blue.

**A****B****C**

**Figure S11.** Lack of interactions of BBX21 with PAP1, GL3, or TTG1 in CoIP or Y2H. **(A)** Tests on interaction between GL3 and BBX21 in CoIP. The upper panel shows the examinations of the input cells (Input) and extracted proteins by the antibody targeting HA (IP), as shown to the right. The lower panel shows the results of antibody targeting MYC against the same input and isolated proteins via HA-beads. The label of the targeted test is in bold. **(B)** Testing interaction between PAP1 and BBX21 in CoIP. The format follows (A). **(C)** Testing interaction between BBX21 and TTG1 in Y2H. The selective medium (SD agar) lacks three amino acids (Leu, Trp, His) and was added with 2mM 3-AT to curb the leaky expression of *HIS3*. The first row is for targeted interaction, against the negative (the 2<sup>nd</sup> row) and positive controls (the 3<sup>rd</sup> and 4<sup>th</sup> rows).



**Figure S12.** Relationships of SPL9 with GL3, TTG1, and MYC2. **(A)** CoIP concerning SPL9. Experimental condition followed Figure 3A, with protein expressions shown in the left panel and 2-4 lanes of the right panel. Protein-protein interactions are shown in the 5-7 lanes of the right panel. **(B)** Interaction between SPL9 and TTG1 in Y2H. The negative control is co-transformed vectors of pAD and pBD without inserts, and positive controls are co-transformations of mutated (pAD-MUT & pBD-MUT) and wild-type (pAD-WT & pBD-WT) vectors provided in the HybriZAP kit. Lack of interaction is shown in the top row in three biological replicates. **(C)** Dosage effect of SPL9 on *PAP1<sub>pro</sub>* in dual LUC assays. pSPL9 was provided in 4 µg or 10 µg along with the same quantity of reporter p*PAP1<sub>pro</sub>*. The standard error bars are based on biological replicates of 22 and 2, respectively. The difference between treatment is highly significant (one-sided *t*-test, \*\*,  $P < 0.001$ ). **(D)** Activation of *BAN* in dual luciferase assays. With the exception of background activity (4 µg/vector), other treatment used 2 µg/vector type. Biological replicates are two for each treatment and included in the error bar. Effect of MYC2 alone is not significant (one-sided *t*-test,  $P = 0.4$ ) and that of the MBW complex (TT2/TT8/TTG1) is significant ( $P = 0.01$ ) whereas adding MYC2 with the complex caused a non-significant change in the promoter activity ( $P = 0.14$ ).

**A****B**

**Figure S13.** Single effects of HY5 and PIF3 on anthocyanin structural genes in dual LUC assays. **(A)** Activations of the structural genes by HY5. Vectors in 6  $\mu$ g each were introduced for each test except 3GTpro (4  $\mu$ g each). The standard error bars include at least two biological replicates. Data were normalized. The comparable test on 3GTpro is not significant for HY5 (two-tailed  $t$ -test,  $P = 0.099$ ). **(B)** Activations of structural genes by PIF3. Tests were performed as in (A). Data were normalized across tests. The comparable test on 3GTpro is not significant for PIF3 (two-tailed  $t$ -test,  $P = 0.072$ ).