

Supplementary Data

	R2	
AtMYB32	MGRSPCCEKDHTNKGAWTKEEDKLIISYIKAHGEGCWRSLPFRSAGLQRCGKSCRLRWINYLRPD	64
AtMYB7	MGRSPCCEKEFMNKGAWTKEEDERIVSYIKSHGEGCWRSLPFRAAGLIRCGKSCRLRWINYLRPD	64
FtMYB15	MGRSPCCEKAHTNKGAWTKEEDDRILAYIKTHGEGCWRSLPKAAGLIRCGKSCRLRWINYLRPD	64
FtMYB14	MGRSPCCEKAHTNKGAWTKEEDDRITAYIRAHGEGCWRSLPKAAGLIRCGKSCRLRWINYLRPD	64
FtMYB16	MGRSPCCEKEHTNKGAWSKEEDERILINYINSHGEGSWRSLPKHAGLQRCGKSCRLRWINYLRPD	64
FtMYB13	MGRAPCCSKVGLHRCGPWTPKEDSIITNYIQTHGEGCWRSLPKNAGLIRCGKSCRLRMNYLRPD	64
FtMYB11	MASSSSRKDLRIKGWPWSPEEDEIILQKLVDKHCPRNWSLISKSIP.GRSGKSCRLWCNQLSPE	63
AtMYB3	MGRSPCCEKAHMNKGAWTKEEDDQIIVDYIRKHGEGCWRSLPFRAAGLQRCGKSCRLRMNYLRPD	64
AtMYB4	MGRSPCCEKAHTNKGAWTKEEDERIVAYIKAHGEGCWRSLPKAAGLIRCGKSCRLRWINYLRPD	64
Consensus	mgrspcckahtnkgawtkeeddrilayikahgegcwrslpkaagllrcgkscrlrwinylrpd	
	R3	
AtMYB32	LKRGNFTELEDDIIIKLHSIGGNKWSLIAATRLPGRTDNEIKNYWNNTVKRKLRLKGIDPATHRP	128
AtMYB7	LKRGNFTHDEDEIIIKLHSIGGNKWSLIAARLPGRTDNEIKNYWNTHIKRKLLSKGIDPATHRG	128
FtMYB15	LKRGNFTEEEDEIIIKLHSIGGNKWSLIAGRRLPGRTDNEIKNYWNTHIKRKLLSRGIDPITHRS	128
FtMYB14	LKRGNFSDDEDEIIIKLHSIGGNKWSLIAGRRLPGRTDNEIKNYWNTHIKRKLLSRGIDPVTHR	128
FtMYB16	LKRGNFHQEDDEIIIDLHTLIGNWSEIAARLPGRTDNEIKNYWNTHIKRRLLARRQSFTRKDN	128
FtMYB13	IKRGNISPEDDIIRLHALIGNWSEIAGRRLPGRTDNEIKNYWNTHLSKKLRSQGTDPTNTHKK	128
FtMYB11	VEHRPFPTPDEAAITVQAHARGNWKATIARMIVGRTDNAIKNHWNSTLKRKCSSMSGDFNFDL	127
AtMYB3	LKRGNFTEEEDEIIIKLHSIGGNKWSLIAGRRLPGRTDNEIKNYWNTHIKRKLLSRGIDPNSHRL	128
AtMYB4	LKRGNFTEEEDEIIIKLHSIGGNKWSLIAGRRLPGRTDNEIKNYWNTHIRRKLINRGIDPTSHRP	128
Consensus	lkrgnfteeedeliiklhsllgnkwsliagrlnpgrtndneiknywnthirkrlsrgidp thrp	
AtMYB32	INETKTTSQDSSDSSKTEDPLVK....ILSFG..PQLEKIANFG..DERIQKRV.....EY	175
AtMYB7	INEAKIS....DLKTKDQIVK....DVSFV..TKFEETDKSG..DQKQNKYIRNGLVCKEER	179
FtMYB15	VNEVEVEGEVIPSPTP.TTTTSISFGATIP...KLEQD.LHDHNLMNTNSRFAAIT.GSKSEERN	186
FtMYB14	LNEASSPTNTTNTNSNTRTSSTKTTTISFASNLKQEPLLQNIITTRLLSSSSPGSKLRSTN	192
FtMYB16	VTTTASS.....ILHFAPTSN.....NIT.....TKVLHHGPVDVGVSG.....HYHD	166
FtMYB13	LSLDPIPPIPCKPSKPKKRTPQTNNKKQKGSDPSAQNKTKVHQPKPVRTSLSLTRNNNSNTSFES	192
FtMYB11	HANPPPLKR..SASVGPATNVSG...LNFN.PGSPSGSDISDSGGSLSHVYRPVPLSVVPFSRE	185
AtMYB3	INESVVS....PSSLQNDVVEL....IHLDIFSGPVKPEPVREEIGMVNNCESSG....TTSEKD	180
AtMYB4	IQEASSASQ...DSKPTQLEPVTSNT.INISFTSAPKVETFHESISFPGKSEKISMLTFKEEKDE	188
Consensus	ine s dsskt dttvs nisf s pk evhdsg d k gsk see	
	EAR	
AtMYB32	SVVEERC....LDLNLELRISPPWQDKLHDERNLRFG..RVKYRCSACRFGFNGKECSCNNVK	233
AtMYB7	VVVEKIG....PDLNLELRISPPWQNO.....REISTCTASRFYMENDMECSSETVK	228
FtMYB15	PGY.....RCPDLNLELRISPPS.HQHQPEQLKSGGIIVNSNPCKFCSEGMQSGQVCKCNTFD	243
FtMYB14	SGLGFEIRDQSLLDNLDLKIISPPSHHQHQPEQLKIG.....VMCFKCNLGLQNSQDCSCNIFG	250
FtMYB16	SNN.....SNLNEISLISIPTSTN.....NMQEHERFTLW	195
FtMYB13	NLTSVSTP..TSQGGGPPIVPPTYWQPYD.....LTTSGVFLIGCEEEDDVAGLVVQ	244
FtMYB11	ITPKIE.....EPETALSLSLPGFDSEG.....SNQCQGSVDMLSQTSCPVVPEK	231
AtMYB3	YGNEED....WVLNLELSVGPSPYRES.....TRKVSVDASAESTRRWGSELF	225
AtMYB4	CPVQEKF....PDLNLELRISLPDDVDRLQGHG...K..STTPRCFKCSLGMINGMECTRCGRMR	243
Consensus	sgvee pdlnlelrissps q e rcfkcsfgmengaecscntfk	
	SID-domain	
AtMYB32	CQTEDSSSSSYSSSTDISSSS.IGYDFLGLNN...TRVLDF.....STLEMK.....	274
AtMYB7	CQTENSSSSYSSIDISSSNVGYDFLGLK...TRILDF.....RSLEMK.....	269
FtMYB15	SKG.NSS....ECSNIGFH....DFLGLRG...SATLDY.....RTLEMK.....	276
FtMYB14	NKT.NASN...DHSNIGIH....DFLGLRV...SANLDF.....RSLEMK.....	284
FtMYB16	RESSNAT.....TS.....	204
FtMYB13	EQGVMEELVSDQSDMLDK.LYDEYLQLIKADDHGFLDFDDLDSDQARELDSFAESLL	302
FtMYB11	VFGPF\$RELLSVMQDMIRQEVRYMDQQGGGTCTYNQTEAISNAMMNRGMNSVE...	285
AtMYB3	AHESDAVC...LCCRIGLF....RNESCRN...CRVSDV.....RTH.....	257
AtMYB4	CDVVGSS...KGSDMSNG...FDFLGLAKKETTSILLGF.....RSLEMK.....	282
Consensus	cqg nsss sdig dfglr tr ldf rslemk	

Fig. S1. Amino acid sequence alignment of a clade of subgroup 4 R2R3-MYB TFs from *F. tataricum* with subgroup 4 R2R3-MYB TFs from *Arabidopsis*. Sequences were aligned using the clustalW and MEGA version 5. FtMYB11 (KU498041), FtMYB13 (KY290579), FtMYB14 (KY290580), FtMYB15 (KY290581), FtMYB16 (KY290582).

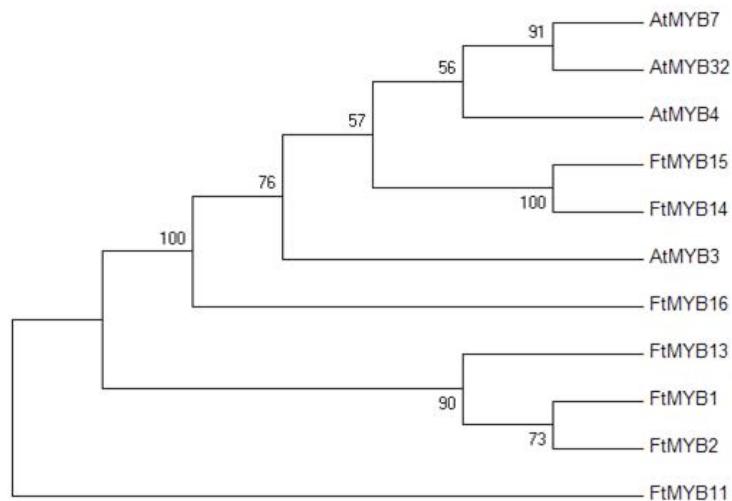


Fig. S2. Phylogeny of R2R3-MYB TFs including two activators: FtMYB1 (JF313345) and FtMYB2 (JF313347) from *F. tataricum* with subgroup 4 R2R3-MYB TFs from *Arabidopsis*. Phylogenetic tree is based on alignment of complete protein sequences.

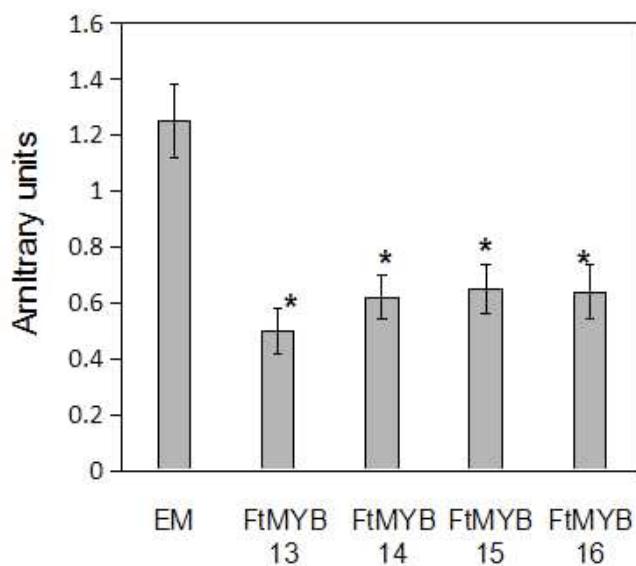


Fig. S3. Transcriptional repression activity assays of FtMYB13, FtMYB14, FtMYB15 and FtMYB16. The transformed yeasts were selected on SD/-W media and then β -galactosidase activity assays (Arbitrary units) were performed. Empty pAS2.1 vector was used as a negative control. The mean value is from three independent measurements, and error bars indicate \pm SD.

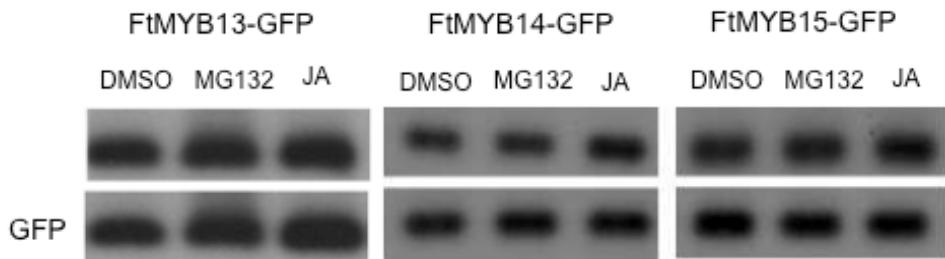


Fig. S4. Immunoblot analysis with anti-GFP antibodies of total protein extracts from *Arabidopsis coi-1* leaf protoplasts transiently co-expressing GFP and FtMYB13-GFP, FtMYB14-GFP or FtMYB15-GFP. *Arabidopsis* protoplasts were harvested 18 hrs after transformation of protoplasts treated for 4 hrs with the solvent DMSO at 0.1% (v/v) final concentration or with 50 μ M of the 26S proteasome inhibitor MG132 or with 50 μ M MeJA.

	SID-motif
AtMYB4	G--FDFL--GL
AtMYB7	G--YDFL--GL
AtMYB32	G--YDFL--GL
FtMYB13	G--LDFLDL
FtMYB14	G IHDFL--GL
FtMYB15	GFHDFL--GL
Consensus	GxxDFxxxG/DL

Fig. S5. Amino acid sequence alignment of the SID domain of FtMYB13, FtMYB14 and FtMYB15 with AtMYB4, AtMYB7 and AtMYB32. Sequences were aligned using the clustalW and MEGA version 5.

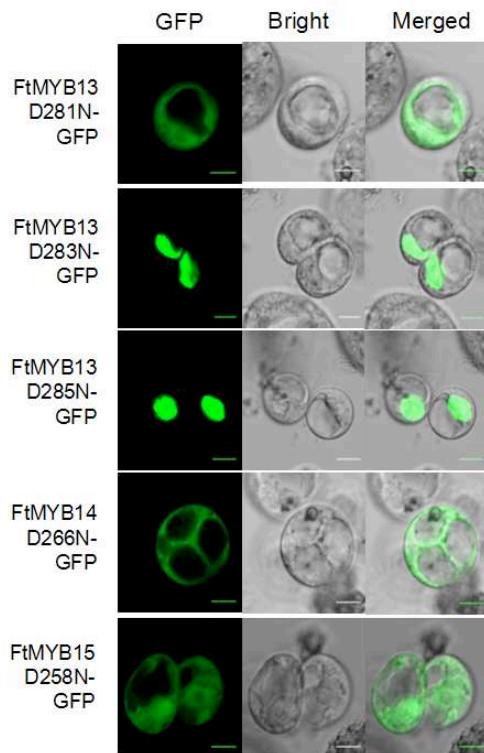


Fig. S6. Subcellular localization of FtMYB13D281N-GFP, FtMYB13D283N-GFP, FtMYB13D285N-GFP, FtMYB14D266N-GFP or FtMYB15D258N-GFP in Arabidopsis protoplasts. Scale bar=20 μ m.

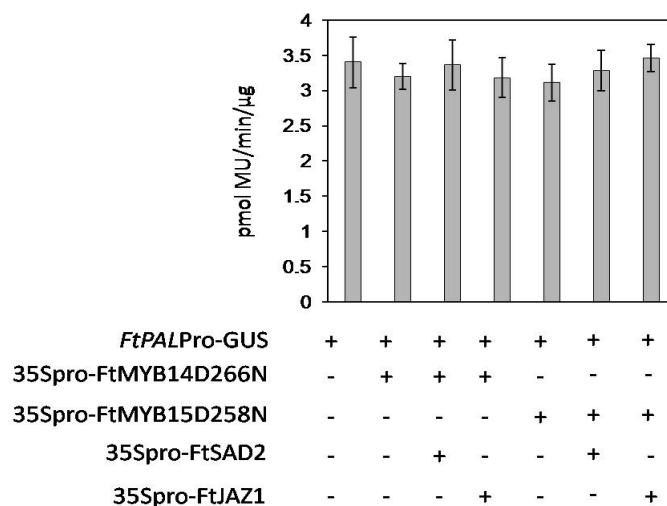


Fig. S7. The transcriptional activity of $FtMYB14^{D266N}$ or $FtMYB15^{D258N}$ was not affected by $FtSAD2$ or $FtJAZ1$. Arabidopsis protoplasts were co-transformed with 2 μ g reporter construct of $FtPAlpro$ -GUS and 2 μ g of effector plasmids. The effector constructs consisted of an expression vector carrying the CaMV 35S promoter without or with the $FtMYB14^{D266N}$, $FtMYB15^{D258N}$, $FtSAD2$ or $FtJAZ1$ genes. Values represent means \pm SE of triplicate experiments.

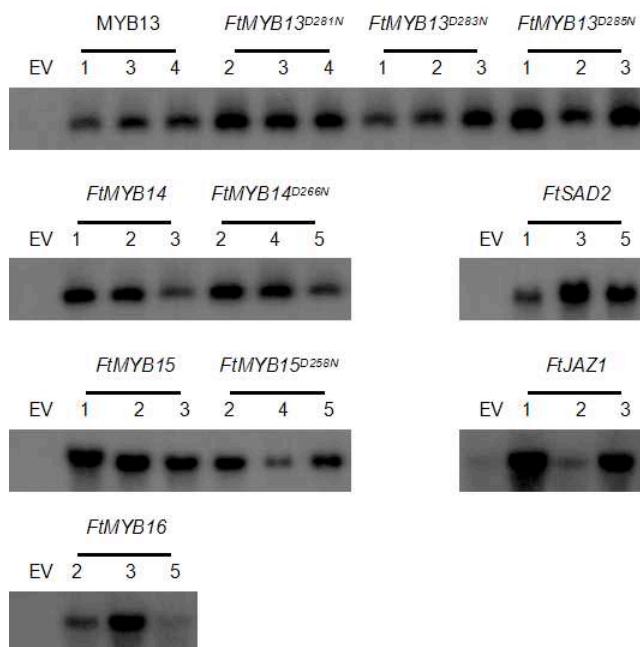


Fig. S8. Immunoblot analysis with anti-HA antibodies of total protein extracts from *FtMYB13-HA*, *FtMYB13^{D281N}-HA*, *FtMYB13^{D283N}-HA*, *FtMYB13^{D285N}-HA*, *FtMYB14-HA*, *FtMYB14^{D266N}-HA*, *FtMYB15-HA*, *FtMYB15^{D258N}-HA*, *FtMYB16-HA*, *FtSAD2-HA* or *FtJAZ1-HA* overexpressing hairy root lines of *F. tataricum* as indicated. 5 µg protein were loaded for each sample.



Fig. S9. Immunoblot analysis with anti-HA antibodies of total protein extracts from *F. tataricum* hairy roots expressing *FtMYB13-HA*, *FtMYB13D281N-HA*, *FtMYB13D283N-HA* and *FtMYB13D285N-HA*. The 20 days hairy root lines were harvested 12 hrs after treated with the solvent DMSO at 0.1% (v/v) final concentration or with 50 µM MeJA. 5 µg protein were loaded for each sample.



Fig. S10 Immunoblot analysis with anti-GFP antibodies of total protein extracts from *Arabidopsis* cell suspension protoplasts transiently co-expressing GFP and *FtMYB13ΔC-GFP*, *FtMYB14ΔC-GFP*, *FtMYB15ΔC-GFP* or *FtMYB16ΔC-GFP*. *Arabidopsis* protoplasts were harvested 18 hrs after transformation of protoplasts treated for 4 hrs with the solvent DMSO at 0.1% (v/v) final concentration or with 50 μ M MeJA.

Table S1. List of primers used in this study.

Genes	Primers
Primers used for qRT-PCR	
FtMYB13	Fw: 5'-GCCGTACGATCTGACGACGAG-3' Rv: 5'-GTCCATGATCATCATCCGC-3'
FtMYB14	Fw: 5'-CGAGATAAGAGATCAAAGC-3' Rv: 5'-CTATGATCATTACTAGCAT-3'
FtMYB15	Fw: 5'-CATCAGCCAGAACAACTG-3' Rv: 5'-CATGGAAGCCAATGTTGC-3'
FtMYB16	Fw: 5'-ACGTCGGAGTATCCGGTC-3' Rv: 5'-GCTTGTGTGGCATTAG-3'
FtSAD2	Fw: 5'-GATCCTGTGGAGCAATCTAAG-3' Rv: 5'-AGACCCTGCCATTGCTCG-3'
FtH3	Fw: 5'-GAAATTGCAAGTACCAAGAAGAG-3' Rv: 5'-CCAACAAGGTATGCCTCAGC-3'
Primers used for yeast two hybrid	
FtMYB13	ADFw: 5'- <u>GCCCCGGGGATGGGAAGAGACTCCTTGTG</u> -3' ADRv: 5'- <u>AGCTCGAGTCAGATGAGCAAAGACTCAGC</u> -3'
FtMYB14	ADFw: 5'- <u>GCCCCGGGGATGGGTAGATCTCCATGTTGTG</u> -3' ADRv: 5'- <u>AGCTCGAGTCATTCATCTCCAATGATC</u> -3'
FtMYB15	ADFw: 5'- <u>GCCCCGGGGATGGGTCGATCTCCATGTTGC</u> -3' ADRv: 5'- <u>AGCTCGAGTCATTCATCTCCAAAGTTCTATAG</u> -3'
FtMYB16	ADFw: 5'- <u>GCCCCGGGGATGGGGAGATCACCTTGCTGC</u> -3' ADRv: 5'- <u>AGCTCGAGCTAGCTTGTGGCATTAGAAG</u> -3'
FtSAD2	BDFw: 5'- <u>CTCATATGGATCTCCAAGCCTCGCT</u> -3'

	BDRv: 5'-CCGTCGACTCAAGAGAGTTCTCGAGCAT-3'
FtJAZ1	ABDFw: 5'-TGCCATGGAGATGAACTTGTTCCACTGAAAG-3' ABDRv: 5'-CGGGATCCTCAGGGCTGAATCGACGTCCG-3'
FtJAZ2	ABDFw: 5'-CTCATATGATGGTGAATTGTCGGCTTCC-3' ABDRv: 5'-CCGTCGACTCAAGAACGTGGATTAGCAGC-3'
Primers used for yeast one hybrid	
FtMYB13	BDFw: 5'-CTCATATGGGAAGAGAGCTCCTTGTGC-3' BDRv: 5'-CCGTCGACTCAGATGAGCAAAGACTCAGC-3'
FtMYB14	BDFw: 5'-CTCATATGGGTAGATCTCCATGTTGTG-3' BDRv: 5'-CCGTCGACTCATTTCATCTCCAATGATC-3'
FtMYB15	BDFw: 5'-CTCATATGGGTCGATCTCCATGTTGC-3' BDRv: 5'-CCGTCGACTCATTTCATCTCCAAAGTTCTATAG-3'
FtMYB16	BDFw: 5'-CTCATATGGGGAGATCACCTTGCTGC-3' BDRv: 5'-CGGGATCCCTAGCTTGTGGCATTAGAAG-3'
<i>FtPALpro</i>	Fw: 5'-CGGCGGCCGCGTCAAATATCGTTAAAAT-3' Rv: 5'-TGCCCCGGGCCACCCCAACGGATCCTGCAC-3'
Primers used for protoplast transactivation assays	
FtMYB13-HA	RT101Fw: 5'-AGCTCGAGATGGGAAGAGAGCTCCTTGTGC-3' RT101Rv: 5'-TGTCTAGATTAGGCGTAGTCAGGCACGTCGTAAGG GATGAGCAAAGACTCAGC-3'
FtMYB14-HA	RT101Fw: 5'-AGCTCGAGATGGGTAGATCTCCATGTTGTG-3' RT101Rv: 5'-TGTCTAGATTAGGCGTAGTCAGGCACGTCGTAAGG TTTCATCTCCAATGATC-3'
FtMYB15-HA	RT101Fw: 5'-AGCTCGAGATGGGTCGATCTCCATGTTGC-3' RT101Rv: 5'-TGTCTAGATTAGGCGTAGTCAGGCACGTCGTAAGG

	TTTCATCTCCAAAGTTCTATAG-3'
FtMYB16-HA	RT101Fw: 5'- <u>AGCTCGAGATGGGGAGATCACCTGCTGC</u> -3' RT101Rv: 5'- <u>TGTCTAGATTAGGCGTAGTCAGGCACGTCGTAAGG</u> <u>GCTTGTGTCATTAGAAG</u> -3'
FtSAD2-HA	RT101Fw: 5'- <u>AGCTCGAGATGGATCTCCAAGCCTCGCT</u> -3' RT101Rv: 5'- <u>TGTCTAGATTAGGCGTAGTCAGGCACGTCGTAAGGGT</u> <u>CAAGAGAGTTCTCGAGCAT</u> -3'
FtJAZ1-HA	RT101Fw: 5'- <u>AGCTCGAGATGAACTTGTTCCCCTGAAAGAG</u> -3' RT101Rv: 5'- <u>CCGGTACCTCAGGGCTGAATCGACGTCCG</u> -3'
<i>FtPALpro</i>	GUSXXFw: 5'- <u>CGGGATCCCGTCAAATATCGTTAAAAT</u> -3' GUSXXRv: 5'- <u>TGCCATGGCCACCCCCAACGGATCCTGCAC</u> -3'
Primers used for BiFC	
FtMYB13	pRTL2-HAYCFw: 5'- <u>CCGTCGACAATGGGAAGAGACTCCTTGTG</u> -3' pRTL2-HAYCRv: 5'- <u>GCAAGCGGCCGCGATGAGCAAAGACTCAGC</u> -3' GFPFw: 5'- <u>TCGTCGACATGGGAAGAGACTCCTTGTG</u> -3' GFPΔNFw: 5'- <u>TCGTCGACATGTCGGATCAGAGTGACATG</u> -3' GFPΔCRv: 5'- <u>TCGTCGACCATGTCACTCTGATCCGACAT</u> -3' GFPRv: 5'- <u>TCGTCGACGATGAGCAAAGACTCAGC</u> -3'
FtMYB14	pRTL2-HAYCFw: 5'- <u>CCGTCGACAATGGGTAGATCTCCATGTTGTG</u> -3' pRTL2-HAYCRv: 5'- <u>GCAAGCGGCCGCTTCATCTCCAATGATC</u> -3' GFPFw: 5'- <u>TCGTCGACATGGGTAGATCTCCATGTTGTG</u> -3' GFPΔNFw: 5'- <u>TCGTCGACATGTTAGGGTTGCAAAACAGC</u> -3' GFPΔCRv: 5'- <u>TCGTCGACGCTGTTGCAACCCTAACAT</u> -3' GFPRv: 5'- <u>TCGTCGACTTCATCTCCAATGATC</u> -3'

FtMYB15	pRTL2-HAYCFw: 5'-CCGTCGACA ATGGGTCGATCTCCATGTTGC-3' pRTL2-HAYCRv: 5'-GCAAG <u>GCGGCCGC</u> TTTCATCTCAAAGTTCTATAG-3' GFPFw: 5'- TCGTCGACATGGGTCGATCTCCATGTTGC-3' GFPΔNFw: 5'- TCGTCGACATGAGTTGGTATGCAAAGTG-3' GFPΔCRv: 5'-TCGTCGACCACTTGCATACCAAAACTCAT-3' GFPRv: 5'- TCGTCGAC TTTCATCTCAAAGTTCTATAG-3'
FtMYB16	pRTL2-YNEEFw: 5'- CCGG <u>ACTAGT</u> ATGGGGAGATCACCTGCTGC-3' pRTL2-YNEERv: 5'- CGGG <u>ATCC</u> CTAGCTTGTGTGGCATTAGAAG-3' GFPΔNFw: 5'- TCGTCGACATGGTTGACGTCGGAGTATCC-3' GFPΔCRv: 5'-TCGTCGACGGATACTCCGACGTCAACCAT-3' GFPRv: 5'- TCGTCGACGCTTGTGTGGCATTAGAAG-3'
FtSAD2	pRTL2-HAYCFw: 5'-CCGTCGACAATGGATCTCCAAGCCTCGCT-3' pRTL2-HAYCRv: 5'-GCAAG <u>GCGGCCGCGTCAAGAGAGTTCTCGAGCAT</u> -3'
FtJAZ1	pRTL2-HAYCFw: 5'-CCGTCGACAATGAACTTGTTCCCCTGAAAGAG-3' pRTL2-HAYCRv: 5'-GCAAG <u>GCGGCCGCGTCAAGGGCTGAATCGACGTCCG</u> -3'