

Table 1 Suppl. Primer sequences used for TD-PCR, RACE, real-time PCR, ORF cloning, and gene walking.

Primer types	Primer names	Sequences (5'-3')
TD-PCR primers	GmMYB-TD-F	GRTGYGGVAARAGCTGYAGACTMMG
	GmMYB-TD-R	TYTCATTGKCWGTTCCTCCWGGHAR
RACE primers	3'RACE F1	GGAAGAAACAATCATCAAGTTAC
	3'RACE F2	ATGAACTTCTTGAAACAGATGGTC
	5'RACE F1	TCCGATGAGTTTCCGCCGTTG
	5'RACE F2	GGAAGCACCATTTGTCAACTCCACCT
ORF cloning primers	LeMYB1-ORF-F	GACTCTAGAATGGTGAGAGCACCATGTTGTG
	LeMYB1-ORF-R	GGTGGATCCCGGGCCCGCTACTGATTTTCCAGC
Real-time PCR primers	LeMYB1-Q-F	GGGCCATGGACTACTGAAGAGG
	LeMYB1-Q-R	CCGGCCTTAGATAGTTTATCCACC
	GAPDH-Q-F	ACCGTCCACTCCATTACCG
	GAPDH-Q-R	ATGAGGCAGCCCTTCCACC
Universal primers	adaptor-oligo(dT15)	CTGATCTAGAGGTACCGGATCC-T ₁₅
	adaptor	CTGATCTAGAGGTACCGGATCC
Gene walking	GSP1	TGTICTTCCAGGTAATCTTGTGC
	GSP2	AAGTTTCCACGTTTGATATCCGGCC
	GSP3	CTGTTCTTCCAGGTAATCTTGTTC

	R2																														R3																																																																								
AtMYB4	T	N	K	G	A	W	T	E	E	D	E	R	V	A	Y	I	K	A	H	G	E	G	W	R	S	L	P	K	A	A	G	L	R	C	G	K	S	C	R	L	R	W	N	Y	L	R	P	D	L	K	R	G	N	F	T	E	E	D	E	L	I	I	K	L	H	S	L	L	G	N	K	W	S	L	I	A	G	R	L	P	G	R	T	D	N	E	I	K	N	Y	W	N	T	H	L	R	R	K	L	105			
AtMYB75	L	R	K	G	A	W	T	E	E	D	S	L	R	Q	C	I	N	K	Y	G	E	G	W	H	Q	V	P	V	R	A	G	L	N	R	C	R	K	S	C	R	L	R	W	N	Y	L	K	P	S	I	K	R	G	L	S	S	D	E	V	D	L	L	R	L	H	R	L	L	G	N	R	W	S	L	I	A	G	R	L	P	G	R	T	A	N	D	V	K	N	Y	W	N	T	H	L	S	K	K	H	105			
AtMYB90	L	R	K	G	A	W	T	E	E	D	S	L	R	L	C	I	D	K	Y	G	E	G	W	H	Q	V	P	L	R	A	G	L	N	R	C	R	K	S	C	R	L	R	W	N	Y	L	K	P	S	I	K	R	G	L	S	N	D	E	V	D	L	L	R	L	H	R	L	L	G	N	R	W	S	L	I	A	G	R	L	P	G	R	T	A	N	D	V	K	N	Y	W	N	T	H	L	S	K	K	H	105			
FaMYB1	T	T	K	G	A	S	I	Q	E	D	Q	K	L	I	D	Y	I	Q	K	H	G	E	G	W	H	Q	V	P	L	R	A	G	L	N	R	C	R	K	S	C	R	L	R	W	N	Y	L	R	P	D	L	K	R	G	S	F	G	E	D	E	D	L	I	T	R	L	H	K	L	L	G	N	R	W	S	L	I	A	G	R	L	P	G	R	T	D	N	E	V	K	N	Y	W	N	T	H	L	S	K	K	I	105	
GbMYB1	L	R	K	G	A	W	T	E	E	D	M	L	L	K	N	C	I	A	K	Y	G	E	G	W	H	L	V	P	L	R	A	G	L	N	R	C	R	K	S	C	R	L	R	W	N	Y	L	R	P	D	L	K	R	G	D	F	G	E	D	E	V	D	L	M	L	R	L	H	K	L	L	G	N	K	W	S	L	I	A	G	R	L	P	G	R	T	A	N	D	V	K	N	Y	W	N	T	H	L	R	S	R	S	105
MdMYB1	V	R	K	G	A	W	T	E	E	D	N	L	R	Q	C	V	E	I	H	G	E	G	W	N	Q	V	S	Y	K	A	G	L	N	R	C	R	K	S	C	R	L	R	W	N	Y	L	K	P	N	I	K	R	G	D	F	G	E	D	E	V	D	L	I	T	R	L	H	R	L	L	G	N	R	W	S	L	I	A	G	R	L	P	G	R	T	A	N	D	V	K	N	Y	W	N	T	H	L	R	I	D	S	105	
PmMBF1	L	N	K	G	A	S	I	Q	E	D	S	L	L	G	K	Y	I	Q	T	H	G	E	G	W	H	Q	V	P	L	R	A	G	L	N	R	C	R	K	S	C	R	L	R	W	N	Y	L	R	P	D	L	K	R	G	N	I	T	A	D	E	E	L	I	I	R	M	H	A	L	L	G	N	R	W	S	L	I	A	G	R	V	P	G	R	T	D	N	E	I	K	N	Y	W	N	T	H	L	S	K	K	L	105	
VvMYB5a	L	K	R	G	P	W	T	E	E	D	E	L	L	A	N	Y	V	K	R	E	G	E	G	R	W	T	L	P	K	R	A	G	L	L	R	C	G	K	S	C	R	L	R	W	N	Y	L	R	P	S	V	K	R	G	Q	A	P	D	E	E	D	L	I	L	R	L	H	R	L	L	G	N	R	W	S	L	I	A	G	R	L	P	G	R	T	D	N	E	I	K	N	Y	W	N	T	H	L	S	K	K	L	105	
VvMYB5b	L	K	R	G	P	W	T	E	E	D	E	L	L	A	N	Y	V	K	R	E	G	E	G	R	W	T	L	P	K	R	A	G	L	L	R	C	G	K	S	C	R	L	R	W	N	Y	L	R	P	S	V	K	R	G	Q	A	P	D	E	E	D	L	I	L	R	L	H	R	L	L	G	N	R	W	S	L	I	A	G	R	L	P	G	R	T	D	N	E	I	K	N	Y	W	N	T	H	L	S	K	K	L	105	
VvMYBPA1	L	H	R	G	S	W	T	A	R	E	D	T	L	L	T	K	Y	I	Q	A	H	G	E	G	W	H	Q	V	P	L	R	A	G	L	L	R	C	G	K	S	C	R	L	R	W	N	Y	L	R	P	D	L	K	R	G	N	I	T	P	D	E	D	L	I	I	R	L	H	S	L	L	G	N	R	W	S	L	I	A	G	R	L	P	G	R	T	D	N	E	I	K	N	Y	W	N	T	H	L	S	K	K	L	105
ZmC1	V	K	R	G	A	W	T	S	K	E	D	D	A	L	A	Y	V	K	A	H	G	E	G	W	H	Q	V	P	L	R	A	G	L	L	R	C	G	K	S	C	R	L	R	W	N	Y	L	R	P	D	L	K	R	G	N	I	S	Y	D	E	E	D	L	I	I	R	L	H	R	L	L	G	N	R	W	S	L	I	A	G	R	L	P	G	R	T	D	N	E	I	K	N	Y	W	N	T	H	L	S	K	K	L	105
LeMYB1	V	K	K	G	P	W	T	E	E	D	Q	I	L	I	S	Y	I	C	R	Y	G	H	D	N	W	R	A	L	P	K	Q	A	G	L	L	R	C	G	K	S	C	R	L	R	W	N	Y	L	R	P	D	L	K	R	G	N	F	S	K	E	E	E	T	I	I	K	L	H	E	L	L	G	N	R	W	S	L	I	A	T	R	L	P	G	R	T	D	N	E	I	K	N	F	W	N	T	H	L	S	K	K	L	105

Fig. 1 Suppl. The comparison of the deduced amino acids of LeMYB1 (KC818628) with AtMYB29 (NP_196386), AtMYB122 (NP_177548), VvMYB5a (AY555190), VvMYB5b (AY899404), AtMYB4 (BAA21619), FaMYB1 (AAK84064), NtMYBJS1 (AB236951), NaMYB8 (ADD59978), AtMYB12 (AF062864), LjMYB12 (BAF74782), VvMYBF1 (FJ948477), VvMYBPA1 (AM259482), DkMYB4 (BAI49721), MdMYB1 (ABK58136), ZmC1 (AAA33482), GbMYB1 (AB550244), AtMYB90 (NP_176813), and AtMYB75 (NP_17605). Identical amino acids are *shaded in black*, and the R2R3 domain is indicated by the *dark lines* upon the sequences. Sequences are aligned using the *DNAMAN v. 5.2.2.* program