

Fig. S1. Multiple alignment of monocot OsMyb4-like protein sequences. Red boxes indicate conserved sequences. The three subgroups related to the three rice Myb are indicated: I (TaMyb2, TaMyb2B, TaMyb7, Bradi5g15760, Sb06g022660, ZmMyb4, GRMZM2G048295, OsMyb4); II (TaMyb73, TaMyb32, TaMyb33, Bradi3g49190, Bradi3g49180, Sb04g026480, GRMZM2G095904, ZmMyb39, LOC_Os02g41510); and III (Bradi3g28830, OsMyb8, Sb01g019270, GRMZM2G147346).

TaMyb2	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
TaMyb2B	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
TaMyb7	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
Bradi5g15760	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
Sb06g022660	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
ZmMyb4	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
GRMZM2G048295	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
OsMyb4	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
TaMyb73	MVRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
TaMyb32	MVRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
TaMyb33	MVRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
Bradi3g49190	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
Bradi3g49180	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
Sb04g026480	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
GRMZM2G095904	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
ZmMyb39	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
LOC_Os02g41510	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
Bradi3g28830	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
OsMyb8	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
Sb01g019270	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
GRMZM2G147346	MGRAPCCCEMGLKRGWTFEEDKILVAHISGHGHNWRLPKQAGLLRCGKSCRLRWINYLRPDIKRGNTFDEEQSIQLHQLLGNRWSAIAARLPGRDNEIKNVWHTLKKRDPGA
TaMyb2	-----QEQ-LEFAAARKKKPP-----AAAARKKEGKIMKRLDALAKAAPVLSSPDRSVSTLTSTSTASAAEQHNGSGSSAS-----ASASVKECFPTSS--
TaMyb2B	-----QEQ-LEFAAARKKKPP-----AAAARKKEGKIMKRLDALAKAAPVLSSPDRSVSTLTSTSTASAAEQHNGSGSSAS-----TSASVKECFPTSS--
TaMyb7	-----QEQ-HQEA-----KRRKKP-----AAAARKKEGKIMKRLDALAKAAPVLSSPDRSVSTLTSTSTASAAEQHNGSGSSAS-----ASASVKECFPTSS--
Bradi5g15760	SA-----QCHDEEGQANKKKPP-----AAASKKK-----PAATAPVSS-PEPSVST-----STVTESSMAVEHNGSGSSA-----VSVEESFTSAS
Sb06g022660	K-----PEQHGGAQAG-----AGKKHRP-----KRG-AAKKTADD-----VAVPATTAPVS-PEPSASSSVTSSSTTQEQEQNTGSSA-----GGFPKEESFTSSA
ZmMyb4	QKL-EQEQHGAHAGGAARKKSRP-----KRA--GAKKTTT-----AAVAPATTAPAS-PERSAASSSVTSSSTTQEQEQNTGSSA-----GGFPKEESFTSSA
GRMZM2G048295	QK-----QQQHQHTTFAAG-AGKKHRPAAAKRGGGKATANADAVVPAPATAAPAS-PERSAASSSVTSSSTTQEQEQNTGSSA-----GGFPKEESFTSSA
OsMyb4	QG-----GHVAAAG--GKKHKK-----PKS--AKFPAA-----AAAAPAS-PERS-ASSSVTSSMASSVAEHNAGISS-----ASASVCAKEESFTSS--
TaMyb73	-----FESQAG-----AAPKKRKK-----FAVAG-SALEGP-----TSEPASSPGQ-LSMSPQSLSTSSAA-YS-----MAS-----SLENTGSSSS--
TaMyb32	-----FESQAG-----AAPKKRKK-----FAVAA-SALEGP-----TSEPASSPGQ-LSMSPQSLSTSSAA-YS-----MAS-----SLENTGSSSS--
TaMyb33	S-----KTSQG-----AAPKKRKK-----FVAAA-STADGP-----TSEPASSPGQ-LSMSPQSLSTSSAA-YS-----MAS-----SLENTGSSSS--
Bradi3g49190	S-----GTATQ-----APAKRKKK-----HVASVNTTLQQQ-----QQGPVSSVPVS-----PEQSLSTSSSTNDNC-----MAS-----SLENTGSSSS--
Bradi3g49180	QG-----GGQAG-----AAPKKRKK-----FVAVTSRTEVP-----TSVPVSPQ-----SLSTSSGAGYS-----MEAP-----SLENTGSSSS--
Sb04g026480	-----KFAAQ-----APKRRP-KKQQQ-PEAVTLAA-----TGAVPVSPQ-----TSTTTTDDYS-----AASS-----MENNADSSSTEE
GRMZM2G095904	-----KTAATQ-----APKRRP-KKQQQ-PEAVTLAA-----TGAVPVSPQ-----TSTTTTDDYS-----AASS-----MENNADSSSTEE
ZmMyb39	-----KFAAQ-----APKRRP-KKQQQ-PEAVTLAA-----TGAVPVSPQ-----TSTTTTDDYS-----AASS-----MENNADSSSTEE
LOC_Os02g41510	-----KPSGREAAPKRRKATKKAATAVAIDVPT-----TVPSPEQSLST-----TTSATTEYSYSSMASSA-----DHNTTDSFTSE--
Bradi3g28830	-----QKTTFGDGRQRKK-----RKQAKA-----TKSAPVSVKHEQLSPGRSS-----SSVTYNSTVETAPVSS-----SPAITSSASH-----DLVKEESFSS--
OsMyb8	-----KLAAAGGGGRRPH-----TRQPKA-----AKSAAAVKREATPSVVDVT-----SSGVTCTVTETSSPSADGHRHQOQTOH-----AAVKEESFSSG
Sb01g019270	-----DGEDKKAARKSKPAAAKRSSAAKKTADANAVDNNSQQPFLTASPLSSSVSGVTFSTATDSAAVSS--ADNAATTSHQEQEQEQ-----EQEQLGASKAEMMEME
GRMZM2G147346	-----HGEKK--ARKGKP-----AAKKAADA--VGRSSEHG-PFLTASPLSS--SGVT-FSAADSAAVSSSADNAATTSHHF-----QQVGASKAESSLELD
TaMyb2	E-----ESEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
TaMyb2B	E-----ESEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
TaMyb7	E-----ESEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
Bradi5g15760	E-----ESEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
Sb06g022660	E-----ESEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
ZmMyb4	E-----ESEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
GRMZM2G048295	E-----ESEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
OsMyb4	E-----ESEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
TaMyb73	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
TaMyb32	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
TaMyb33	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
Bradi3g49190	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
Bradi3g49180	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
Sb04g026480	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
GRMZM2G095904	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
ZmMyb39	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
LOC_Os02g41510	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
Bradi3g28830	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
OsMyb8	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
Sb01g019270	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277
GRMZM2G147346	-----SEEFQDDESFWSETLSTPL-----DDINDVC--MEPHD--AFG-----KPA-----DKDMD-YWLKVFMEGGDD--NNDGALDLPQI--277