



Supplementary Figure 1. Sequence analysis of conservative motifs in CqR2R3-MYB proteins. Different color represents different amino acid residues, and larger font sizes represent higher frequencies.

CaMYB2R09	... NSN SPVDRI KCPWSFEEEDRI IRLVQKHGRNWI L SKSI GR SGSKSCRLRNWQLS	57
AmYB73	NSN TP SKN WEL KCPWSFEEEDRI IRLVQKHGRNWI L SKSI GR SGSKSCRLRNWQLS	60
Consensus	r k r i g g p w s e e d d i r l v q k h g r n w l i s k s i g r s g s k s c r l r n w q l s	
CaMYB2R09	P VEHRAITFTEEDITRI RAHAR ENCKWATIRILRLSGRTDNAIKNHWNS TLRKCK SAVSS	117
AmYB73	P VEHRAITFTEEDITRI RAHAR ENCKWATIRILRLSGRTDNAIKNHWNS TLRKCK SAVSS	120
Consensus	p v e h r a i t f t e e d i t r i r a h a r e n c k w a t i r i l r l s g r t d n a i k n h w n s t l r k c k s a v s s	
CaMYB2R09	A PDDFDEFPDPPPKKEASLEGAVILRNVSGLSTINNNNNNGSPGSDADSDSHVFRF	177
AmYB73	C DFGQGGYGDNLGEEQPKLRKTSGGGVSTGLVSPG...SLSGSDVPSGSGHVF	178
Consensus	g l i l y p p s s s g h v f p	
CaMYB2R09	VPI PGPIVPPPVLSLADQLSSLSLIGSGSECVSS...DHEPNTSPIQVITSSP	232
AmYB73	T RSRENTASSSGEDPGLSSLSLITLFTVRVSPVQLNQNTVIGSGTAEILVRKE	236
Consensus	v p t l s l s l p d e t l f t v r v s p v q l n q n t v i g g t a e i l v r k e	
CaMYB2R09	V MEFPPPPP...AFSGEGLVLAQMEIKTEVRVYLGVEVNSNG...IGSGGGGCSQ	283
AmYB73	V MEFVEEVEEAKGI SGGGGEGGLVLAQMEIKTEVRVYALDQLRQNGSGGGGCSNP	296
Consensus	v m e f v e e e a k g i s g g g e g g l v l a q m e i k t e v r y m n g g g g g c s n p	
CaMYB2R09	A AD...GVRAAMSRLTGRF	301
AmYB73	Q SVNSRRIRFEPINQILGRM	319
Consensus	g i g i g k	

[illegible][illegible]

CqMYB2R62	N RRPFD Q KKKKGKVPWTFEED I LV Y QHCHGPGNRAVPTNGLIRKSSKSRILWNTV	60
AtMYB30	N RRPFD Q KKKKGKVPWTFEED I LV Y QHCHGPGNRAVPTNGLIRKSSKSRILWNTV	60
Consensus	m r p p c d k g y k g k g p w t f e e d i l v y i q h c h g p g n r a v p t n g l i r e s s k s r i l w n t v	
CqMYB2R62	L RPQ I KRGNET TD EE KK VL I HLQALLGNRWAA AS YLP Q RTDND I KNYWNT HLKKKLRR KD	120
AtMYB30	L RPQ I KRGNET TD EE KK VL I HLQALLGNRWAA AS YLP Q RTDND I KNYWNT HLKKKLRR KD	120
Consensus	l r p q i k r g n e t e e k m h l q a l l g n r w a a s y l p r t d n d i k n y w n t h l k k l r k d	
CqMYB2R62	S NNH IK SS SG DF VS SP EN ST SS SP EN ST SS SG WERLL Q TD IA AK AL CA LS TD MD K Q SS	180
AtMYB30	S NNH IK SS SG DF VS SP EN ST SS SP EN ST SS SG WERLL Q TD IA AK AL CA LS TD MD K Q SS	180
Consensus	d s s s s s s r g q w e r l l q t d i a k a l a l s	
CqMYB2R62	N MPDS MS Q SK I SL NS S NNNN K Q G T ASS I Y ASS T EN I AK LL Q GW NN SP K Q ESS VS	240
AtMYB30	N MPDS MS Q SK I SL NS S NNNN K Q G T ASS I Y ASS T EN I AK LL Q GW NN SP K Q ESS VS	240
Consensus	s s s s s s s g l r t g e t s y a s s e n i a l l g w s p k	
CqMYB2R62	TD HL SL CS TS VE Y GH EP K PK AS D HH FS K NE AF LS GL FT ES SP SS VS Q TS VS PE A	300
AtMYB30	TD HL SL CS TS VE Y GH EP K PK AS D HH FS K NE AF LS GL FT ES SP SS VS Q TS VS PE A	300
Consensus	a d i o a s t e v k c k s d d c e a g a f s s f e d h s y q o a g	
CqMYB2R62	S FE FF HL SG TS GG GS SS OW SL KE W LF EL DS QH CH Q SG SOV MDL NP RT AD AL	350
AtMYB30	S FE FF HL SG TS GG GS SS OW SL KE W LF EL DS QH CH Q SG SOV MDL NP RT AD AL	350
Consensus	h e k p s e k w l f e l d s g q d l e e f	

[illegible]

Supplementary Figure 2. Multi-sequence alignment of R2R3-MYB proteins of *Arabidopsis* and quinoa. Amino acid sequence alignment of CqMYB2R09 and AtMYB73 (A), CqMYB2R16 and AtMYB42 (B), CqMYB2R25 and AtMYB49 (C), CqMYB2R62 and AtMYB30 (D), and CqMYB2R49 and tomato MYB49 (E). Black background represents sequence identities = 100%. Red box highlights nuclear localization signals (NLSs).