

Supplementary Information

RgMYB24	: -MKERQWRPFDALRSYRQYEP-RDHLVSEHMNEPLNRDAKSGLERWKNYLPKGIKKGSLTEEEQCLVHLQAKHGKPKKIAAEVPGRTAKRLGKWWVEVFKE-	: 105	} Group I
RgMYB25	: -MKERQWRPFDALRSYRQYEP-RDNLISQRMGKPLDRDPKSGLERWKNYLPKGIKKGSLTEEEQCLVHLQAKHGKPKKIAAEVPGRTAKRLGKWWVEVFKE-	: 105	
RgMYB15	: -----MIFWLCYVVG--LRRTGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 78	
RgMYB16	: TELRRGWLEEDDNLIQYISCHPE-GRNSLARCAG--LRRTGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 127	
RgMYB17	: TELRRGWLEEDDNLIQYISCHPE-GRNSLARCAG--LRRTGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 127	
RgMYB6	: ANVRKGVWPEEDDEQIKYIDRHTGGNIALPQKAG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 114	
RgMYB12	: NGLRKGWPEEDDNLKRAYILRYEH-WNRLLPKFAG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 112	
RgMYB13	: NGMRKGVWPEEDDNLKRAYILRYEH-WNRLLPKYAG--VSRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 113	
RgMYB14	: NGMRKGVWPEEDDNLKRAYILRYEH-WNRLLPKYAG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 113	
RgMYB5	: NELNRGVWAEEDDRKAEYIYQYEA-RQITIAAKAE--LNRCAKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 122	
RgMYB8	: IGVKRGWPEEDDNLVSYIQENHP-GNRVAVPASTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 113	
RgMYB9	: IGMKRGWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 113	
RgMYB10	: MGMRKGVWAEEDDNLIDYINRNEH-DNRALPKRAG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 113	
RgMYB11	: ERLKRGWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 113	
RgMYB7	: TRVKRGWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 115	
RgMYB4	: QKLRGLWPEEDDEKIKHTRYEH-GCSSVPKLAG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 113	
RgMYB3	: ENVRKGVWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 113	
RgMYB1	: VGLRRGWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 113	
RgMYB2	: TYTRKGVWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 113	
RgMYB20	: PGKIRGVWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 110	
RgMYB21	: SDRIRGVWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 112	
RgMYB22	: MDRIRGVWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 107	
RgMYB23	: MDRIRGVWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 114	
RgMYB19	: KGVKRGWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 139	
RgMYB18	: SKSGGGWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 161	
RgMYB26	: PDLVKGWPEEDDNLVSYIQENHP-GNRVAVPNTG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 183	
RgMYB38	: IPKSESVDDEHDFLEAQLQFD--RDKK---IEDFVG-----SKTVYQIRSHAKYFLVQKN-----GTVAVHVPVPRP-	: 96	
RgMYB35	: DPKPLRWVSDLHDFVDAVTKLE--GPDKATPKTIRVMVMGK-----GLTYHLKSHLQRYRLGQQPT-----KFSVDHSMKQD-	: 103	
RgMYB36	: DPKPLRWVSDLHDFVDAVTKLE--GPDKATPKTIRVMVMGK-----GLTYHLKSHLQRYRLGQQPT-----KKNGLNLENKE-	: 95	
RgMYB37	: QRKAARPEEDDHLFLIQLQYVYK-GDGRK---ISRYM-VL-----TRSPAQVASHAKRYVERLEKE--EP-----NKK-	: 166	
RgMYB39	: ERKRGVWPEEDDHLFLIQLQYVYK-GDGRK---ISRYM-VL-----TRSPAQVASHAKRYVERLEKE--EP-----NKK-	: 114	
RgMYB40	: ERKRGVWPEEDDHLFLIQLQYVYK-GDGRK---ISRYM-VL-----TRSPAQVASHAKRYVERLEKE--EP-----NKK-	: 114	
RgMYB27	: QRRIRPEESVAVVEAVGAEKLET-GRDRD---VRIGA-FE-----NADHRTYVDLKRW-----	: 634	
RgMYB30	: RRRKRRPWSLSVVKVVEGVARYEA-GNISE---IKRLA-FA-----SYSYRTSVDLKRW-----	: 543	
RgMYB28	: RRRKRRPWSLSVVKVVEGVARYEA-GNISE---IKRLA-FA-----SYSYRTSVDLKRW-----	: 511	
RgMYB29	: RRRKHIVMIAVVRKIDGVSQYEV-GRGSR---IKKLF-FS-----ASAHTSVDLKRW-----	: 151	
RgMYB31	: MGAPKQWPEEDDNLKRAYILRYEH-WNRLLPKFAG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 68	
RgMYB32	: MGAPKQWPEEDDNLKRAYILRYEH-WNRLLPKFAG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 68	
RgMYB33	: MGAPKQWPEEDDNLKRAYILRYEH-WNRLLPKFAG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 68	
RgMYB34	: MGAPKQWPEEDDNLKRAYILRYEH-WNRLLPKFAG--LRRCGKSCSLRWVNYLHPGLKRGKMTPEHERLVLQLHSHKGNRWSRTIARLPGRTDNEIKNYWRTRVQ-	: 68	

Figure S1. Conserved amino acid residues are present among the 40 proteins of the *R. glutinosa* MYBs. The amino acid sequences are aligned, and gaps (dots) have been introduced to maximize the alignment. The shading of the alignment presents identical residues in black, conserved residues in dark gray, and similar residues in light gray.

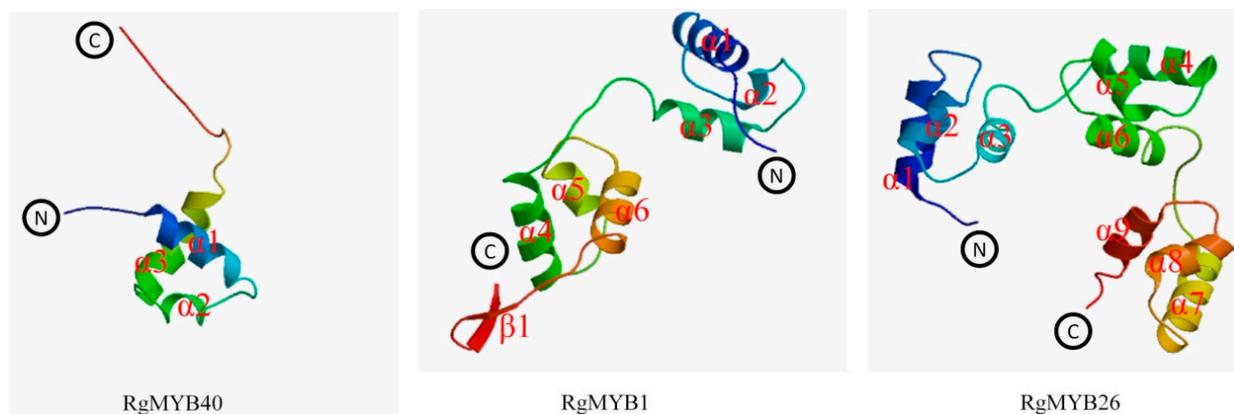


Figure S2. 3-D structure analysis of RgMYB transcription factors. C, C-terminal; N, N-terminal; α , α helix; β , β sheet.

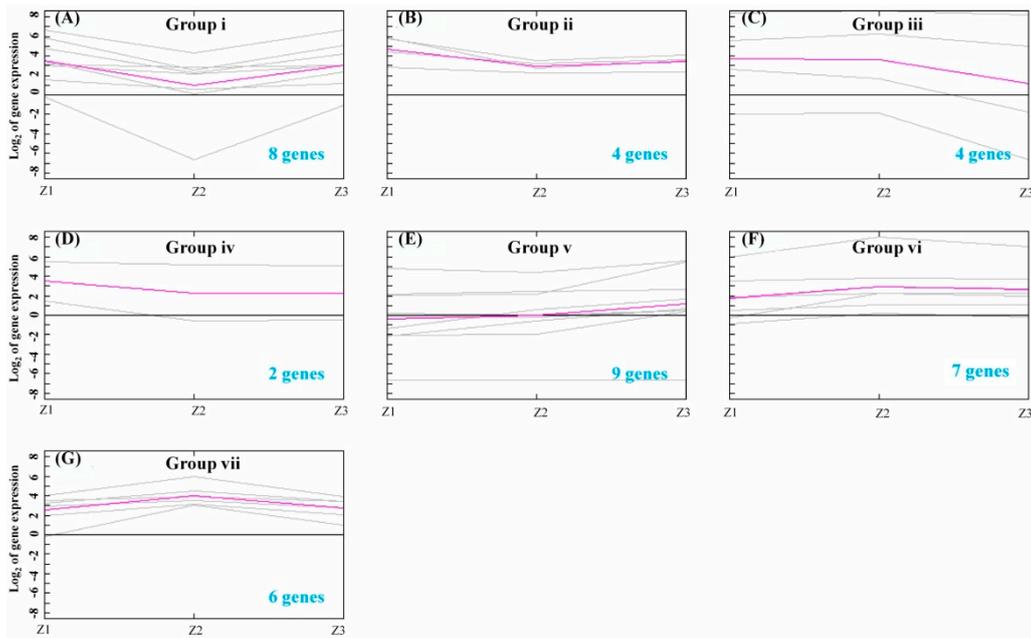


Figure S3. Expression patterns of 40 *R. glutinosa* MYB family genes in tuberous roots at different stages. (A–G) Seven expression patterns were identified to represent genes up- or down-regulated at Z1, Z2, and Z3 stage. Gene expression profiles of individual genes are depicted in gray lines, and average expression profiles for each pattern are depicted in pink lines. The line charts were generated by MultiExperiment Viewer (MeV).

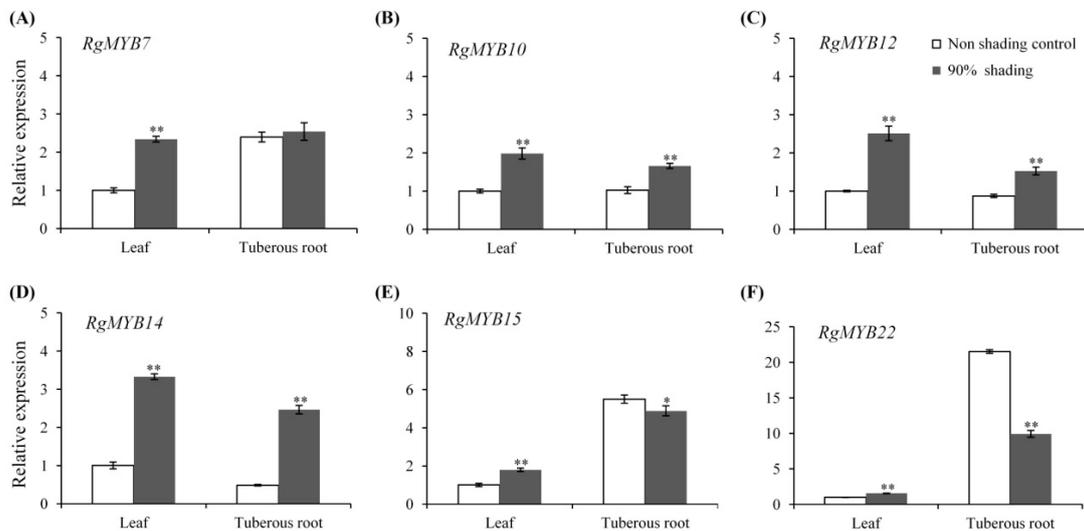


Figure S4. Quantitative RT-PCR analysis of transcript abundance of MYB family genes in leaf and tuberous root of *R. glutinosa* under 90% shading. (A–F) The expression levels of *RgMYB7* (A); *RgMYB10* (B); *RgMYB12* (C); *RgMYB14* (D); *RgMYB15* (E); and *RgMYB22* (F) under shading and non-shading conditions. The relative expression level of genes in control leaves were used as references. Mean values from three independent experiments are shown. Each independent experiment was performed with three technical replicates. Error bars represent standard deviations. For statistical analysis, 2-tailed *t*-test was performed to determine the significance of difference. * and ** indicate significant difference at $p < 0.05$ and $p < 0.01$, respectively.

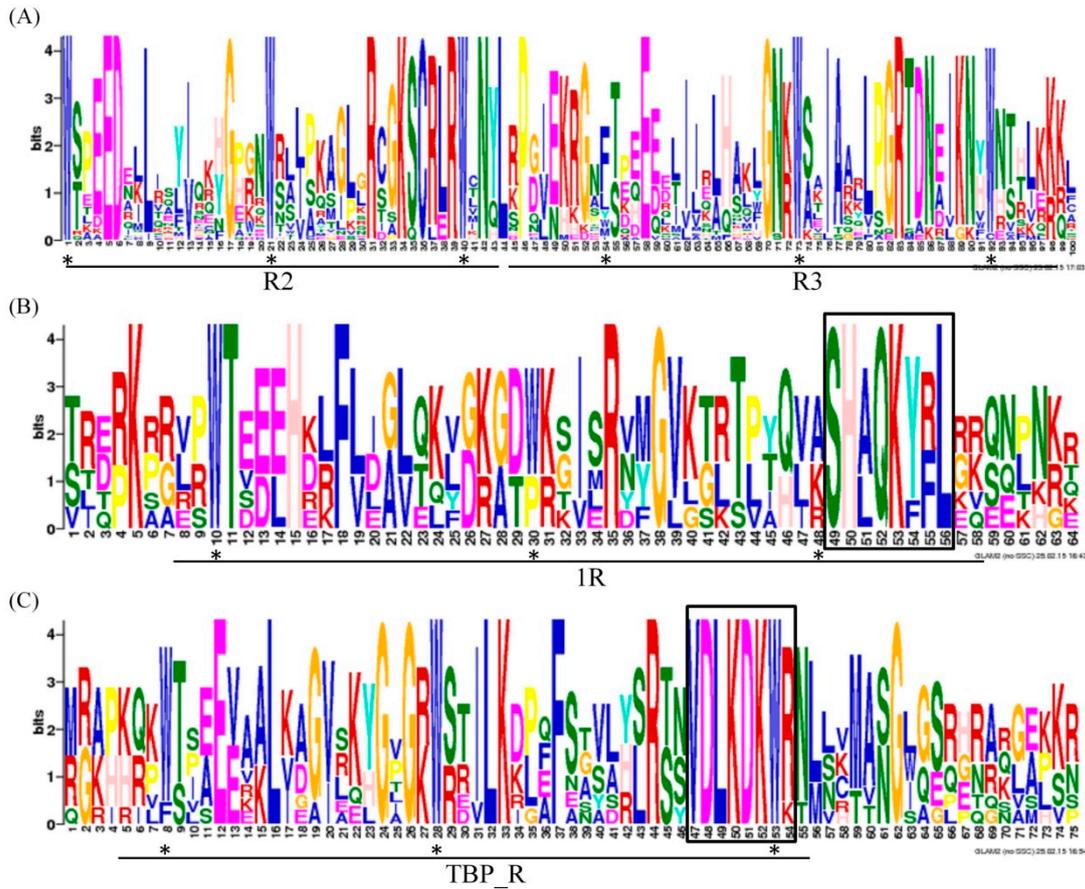


Figure S5. Conserved sequences of *R. glutinosa* MYB DNA binding domain (DBD). (A–C) Sequence logos of the 25 MYBs with R2R3 domains (A); 6 MYBs with 1R domains (B) and 8 MYBs with TRB domains (C). The bit score indicates the information content for each position in the sequence. Asterisks indicate the conserved tryptophan residues (Trp) in the MYB domain. The width of the amino acid positions indicates the probability of insertions (wider) and deletions (narrower). The highly conserved SHAQKYF motifs in 1R and VDLKDKWR motif in TBP_R are boxed. Logos were generated using the method described by Frith *et al.*, (2008), available at GLAM2 [64].