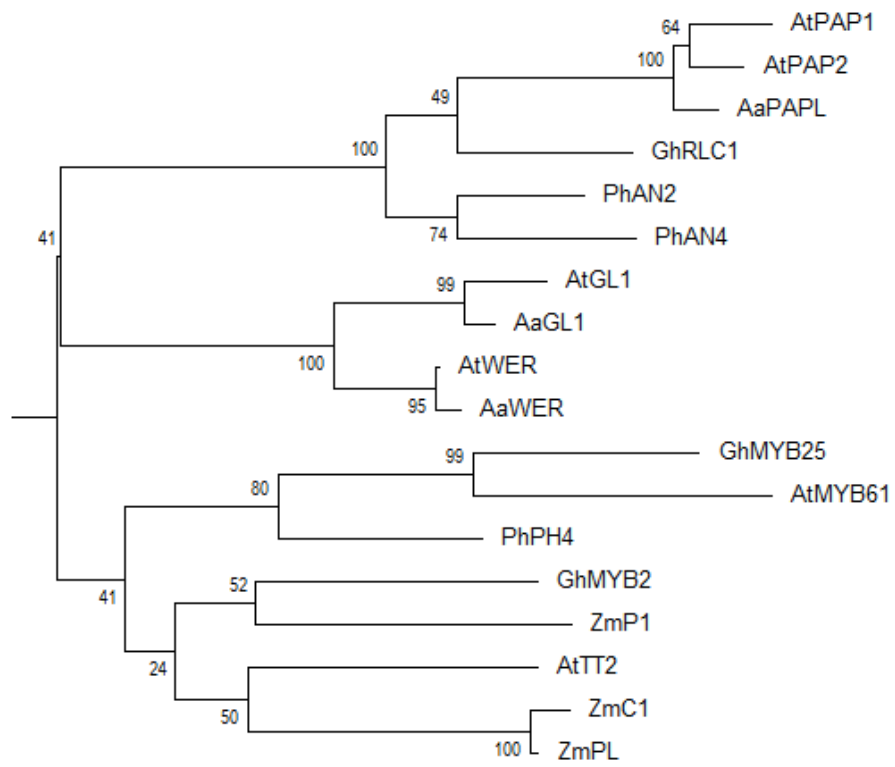


Figure S1

A



B

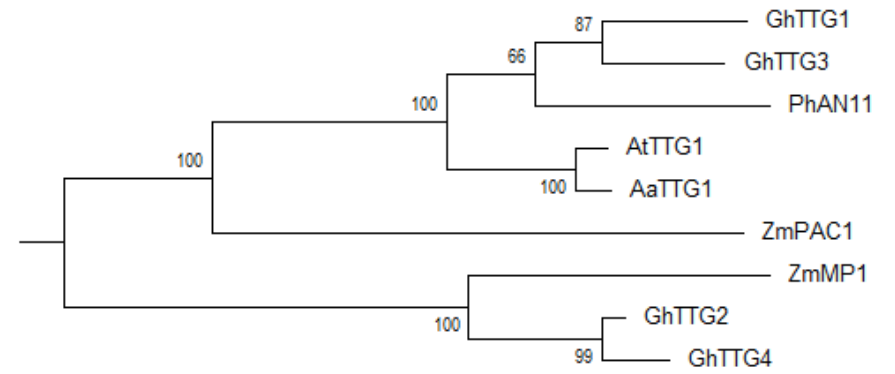
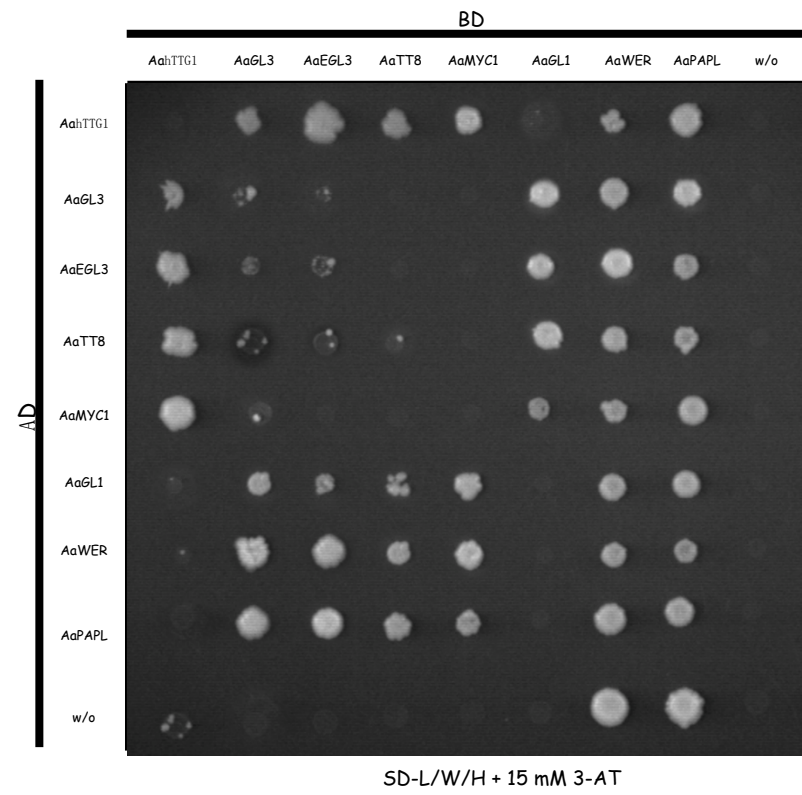
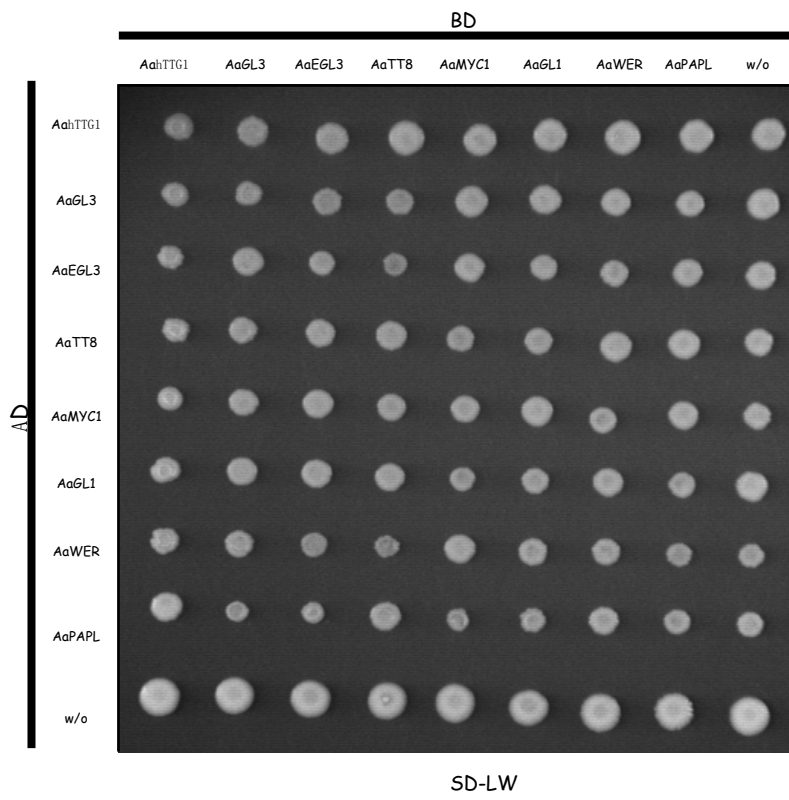


Figure S1: Phylogenetic tree of WD40 and R2R3 MYB proteins used in this study.

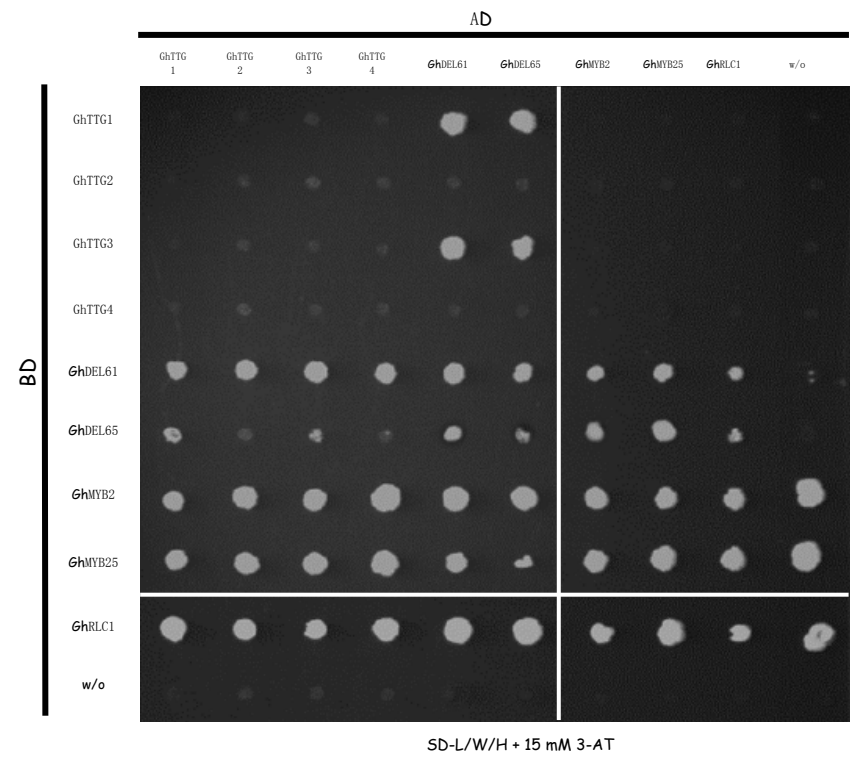
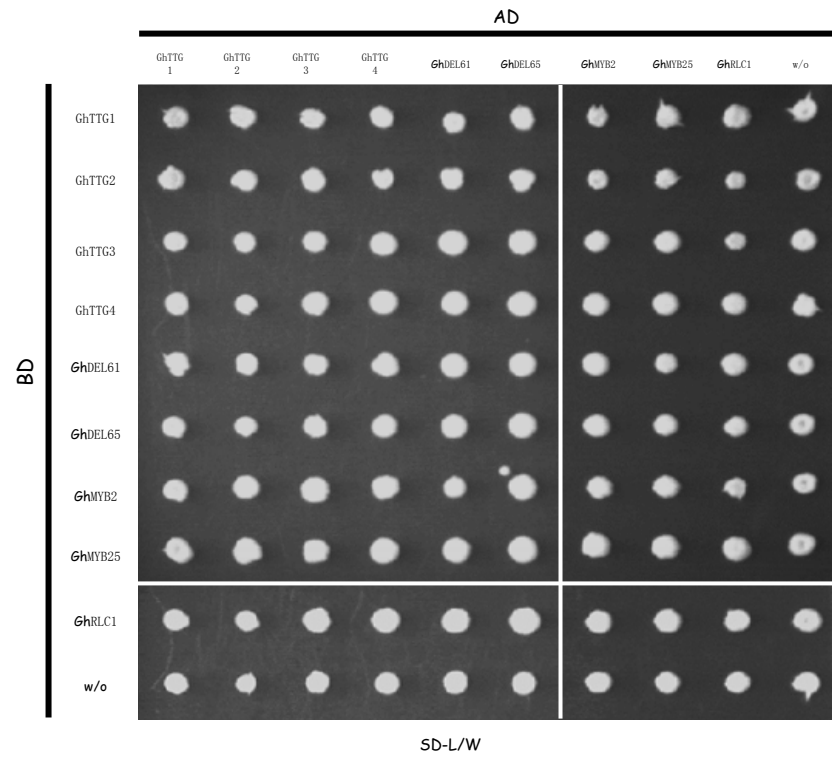
The phylogenetic trees were constructed using the aligned full length of the WD40 and R2R3 MYB proteins. The tree was drawn to scale with branch lengths measured in the number of substitutions per site. The phylogenetic tree was created by mid point rooting. Bootstrap values from 500 bootstrap repetitions are provided at the branch nodes. A) Phylogenetic tree of R2R3 MYB proteins used in this study. B) Phylogenetic tree of WD40 proteins used in this study.

Figure S2

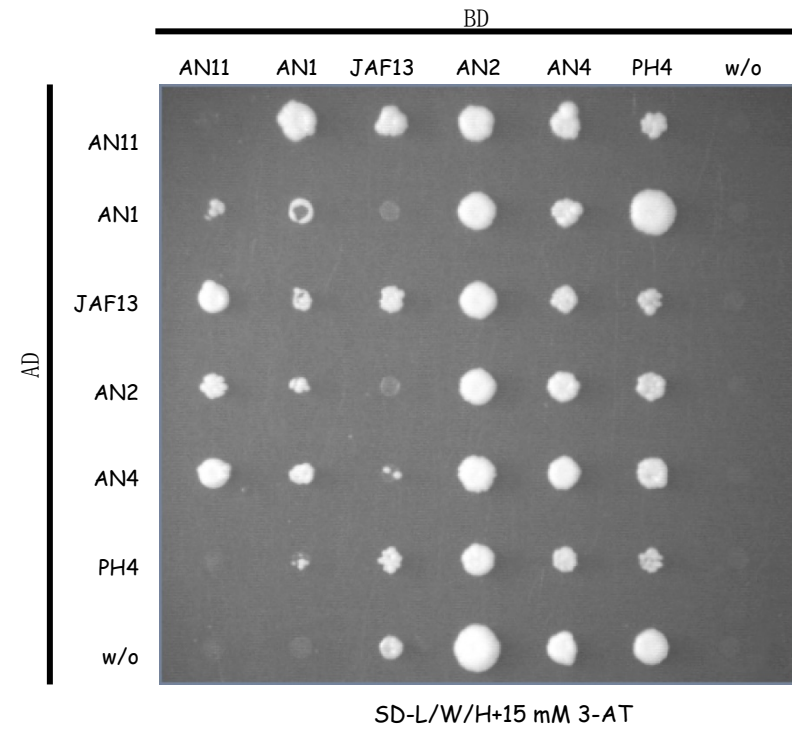
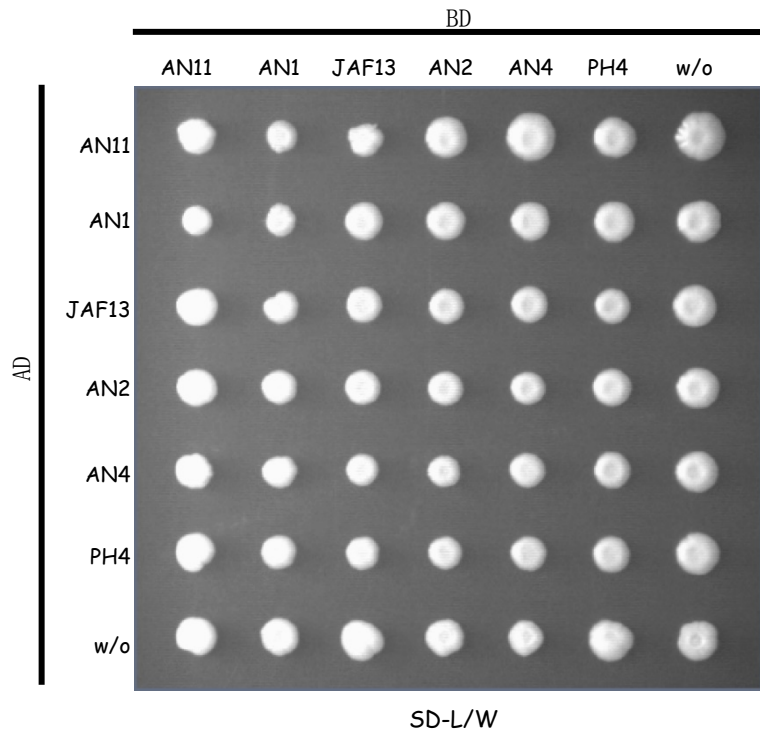
A



B



C



D

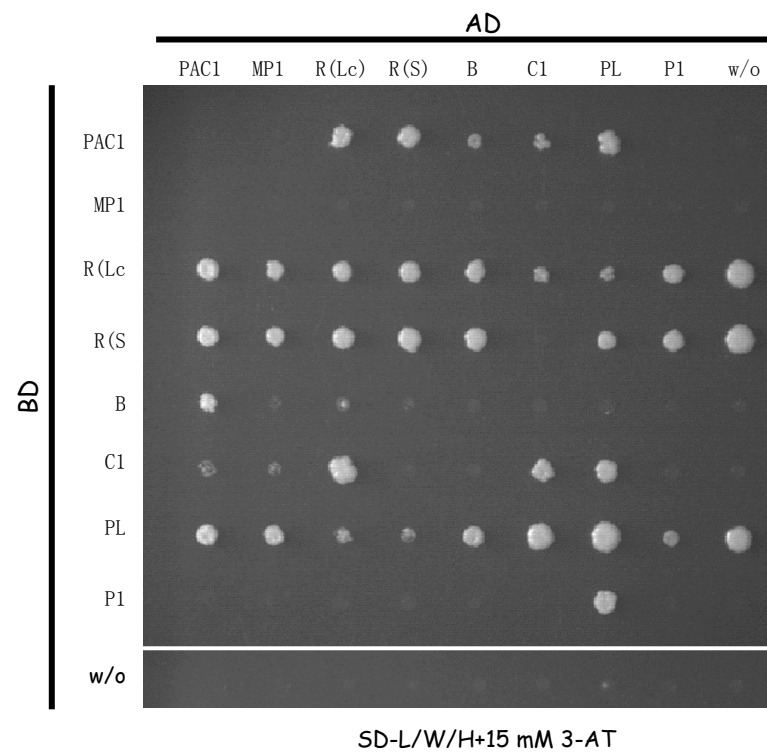
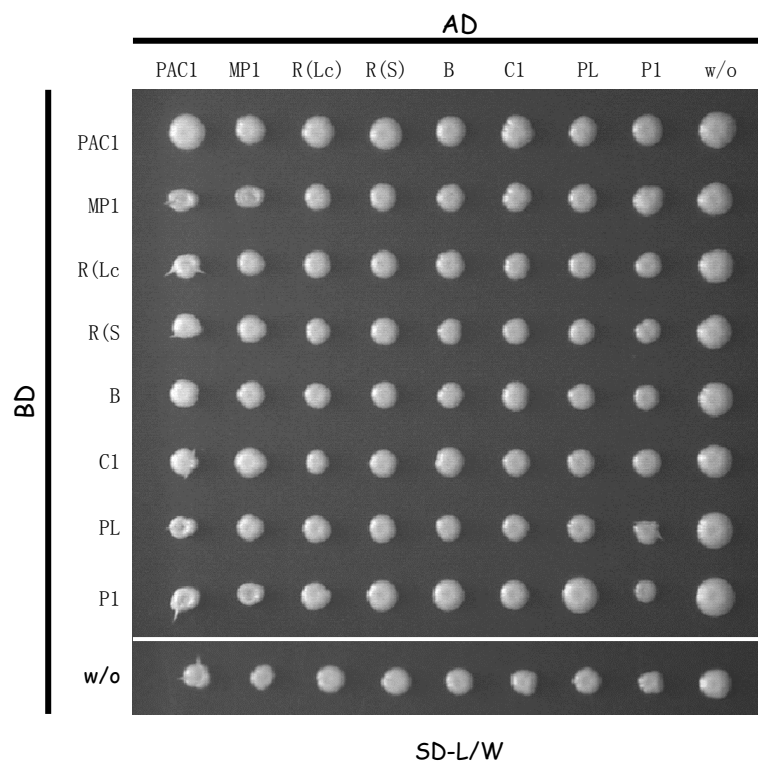
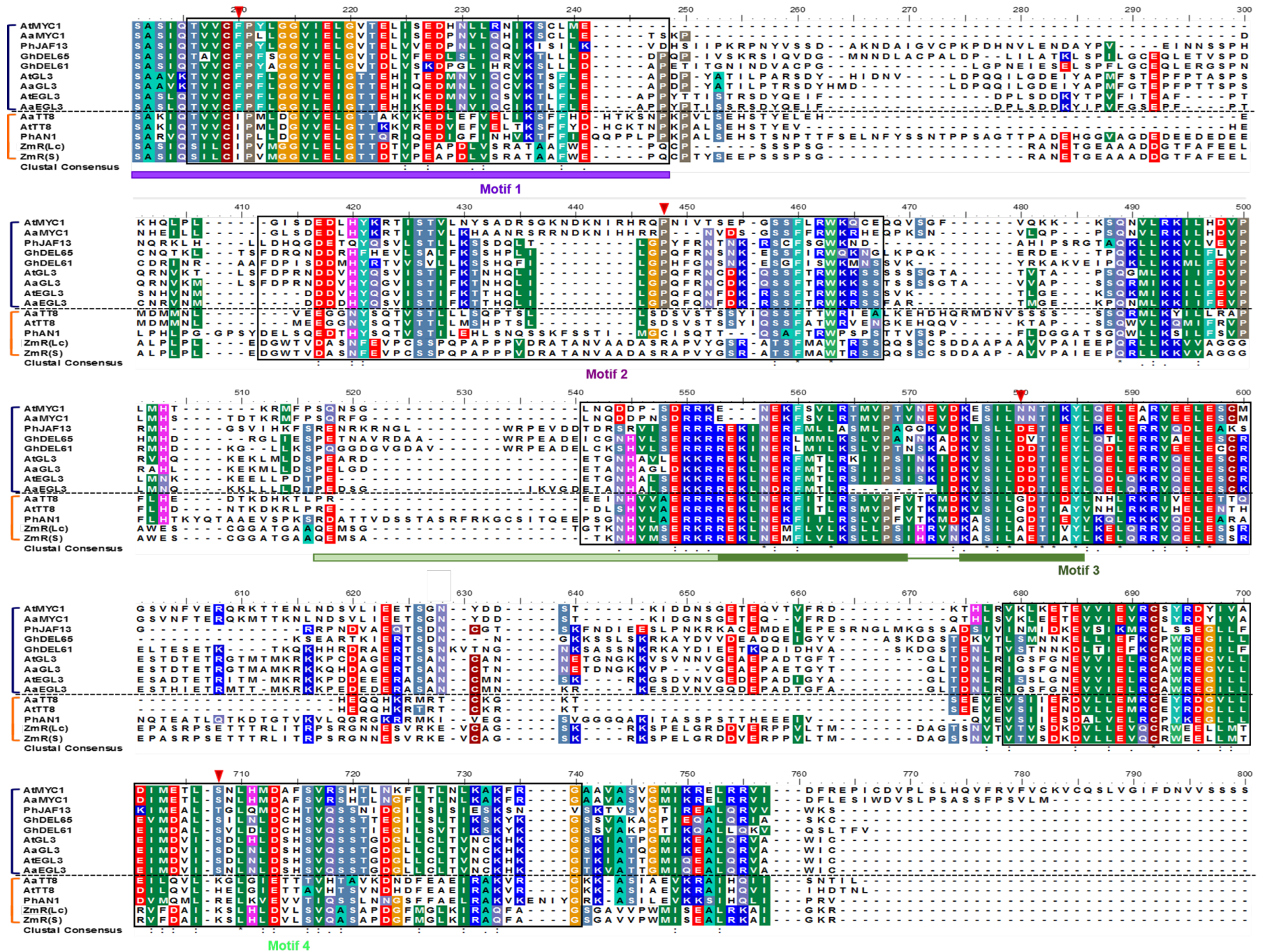


Figure S2: Protein–protein interactions among members of the MBW regulatory complex in *A. alpina* (A), *G. hirsutum* (B), *P. hybrid* (C) and *Z. mays* (D) determined by yeast two hybrids assays.

Left: Growth on synthetic defined (SD) selective medium lacking Leu, Trp (SD-L/W) for 5 days at 30°C. Right: Growth on SD interaction medium lacking Leu, Trp, and His supplemented with 15 mM 3-AT for 5 days at 30°C. AD: GAL4 activation domain; BD: GAL4 DNA binding domain.

Figure S3



Transcription factor MYC/Myb N-terminal

basic Helix-Loop-Helix (bHLH) domain

Figure S3: Comparison of bHLH proteins

Sequence alignment of bHLH proteins from five plant species. Red triangles indicate amino acids that differ between the two clades and that are candidates for mediating differences between competitive complex formation behavior. Blue bracket indicates the clade of bHLH proteins displaying competitive complex formation. The orange bracket indicates the clade that does not show competitive complex formation.

Figure S4

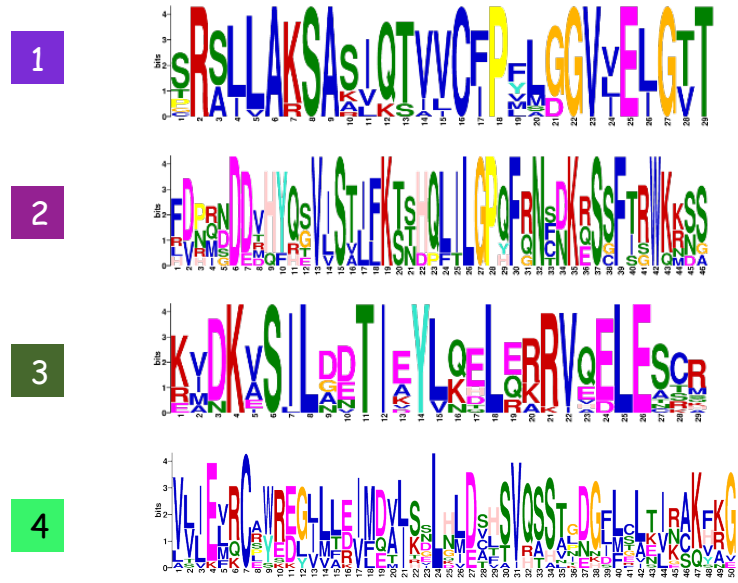


Figure S4: Common motifs in bHLH proteins

Sequences of bHLH motifs are shown. The size of the letters indicates the conservation of the respective amino acids.