

Figure S1. The proportions of representative lineages in Asteraceae species and *Arabidopsis thaliana*. The rows and columns respectively indicate different species and lineages.

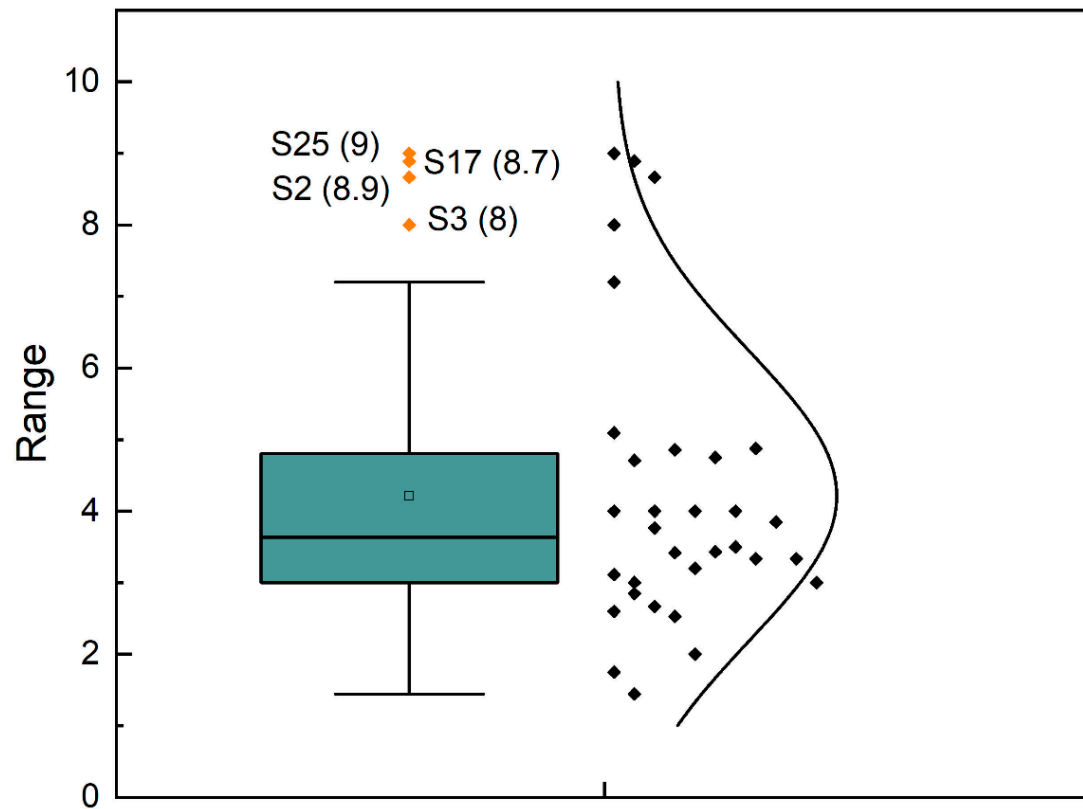


Figure S2. Boxplot of the ratio of *MYB* genes between *C. ×morifolium* and wild *Chrysanthemum* species in each lineage. Obvious outliers are marked in yellow.

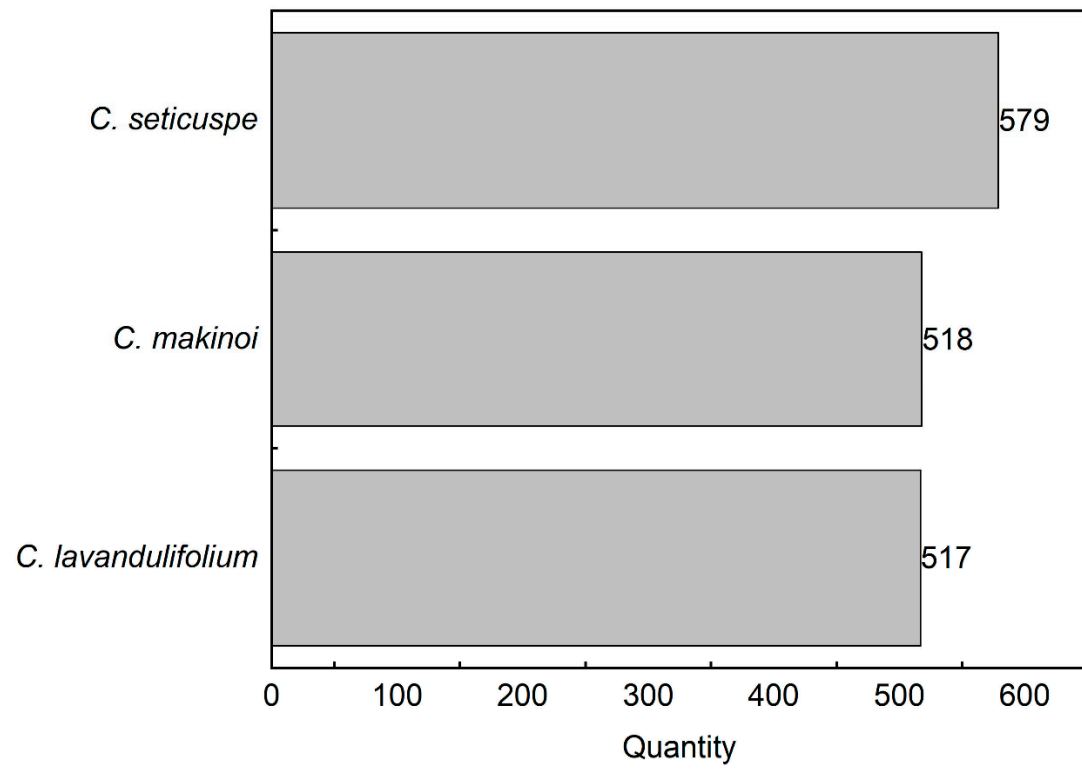


Figure S3. Statistics of syntenic *MYB* gene numbers between *C. ×morifolium* and wild *Chrysanthemum* species.

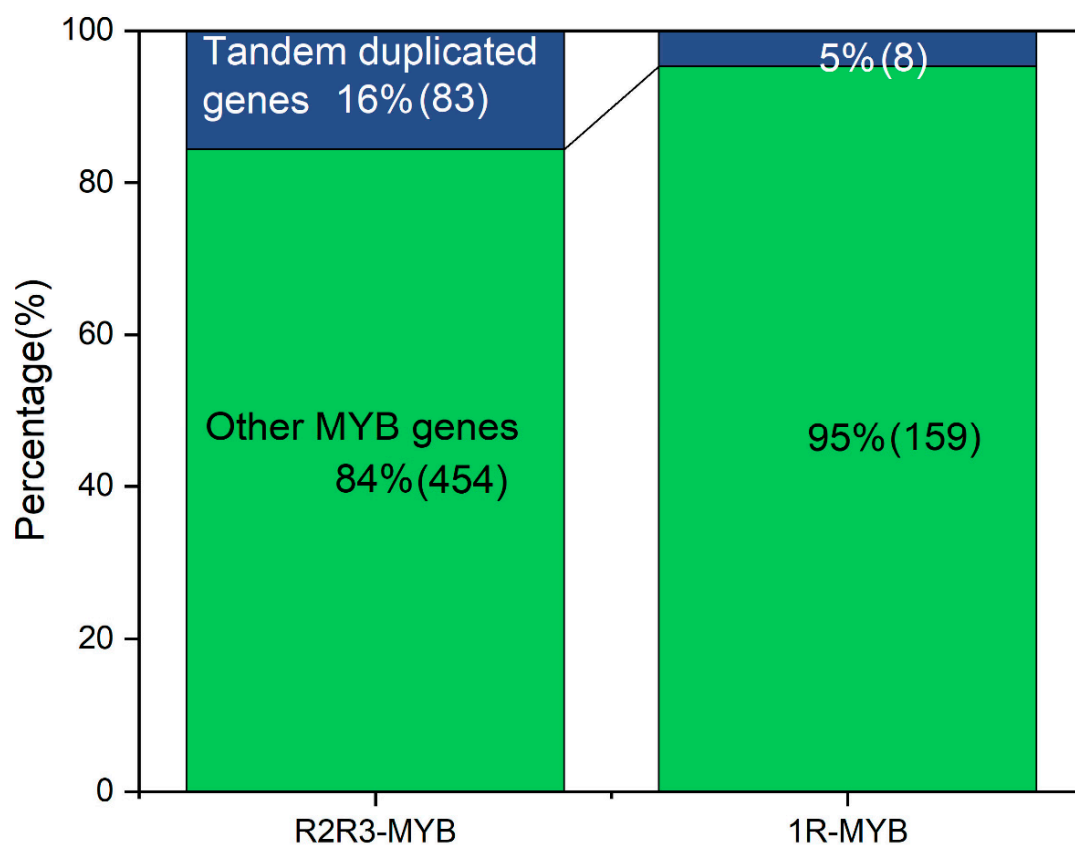
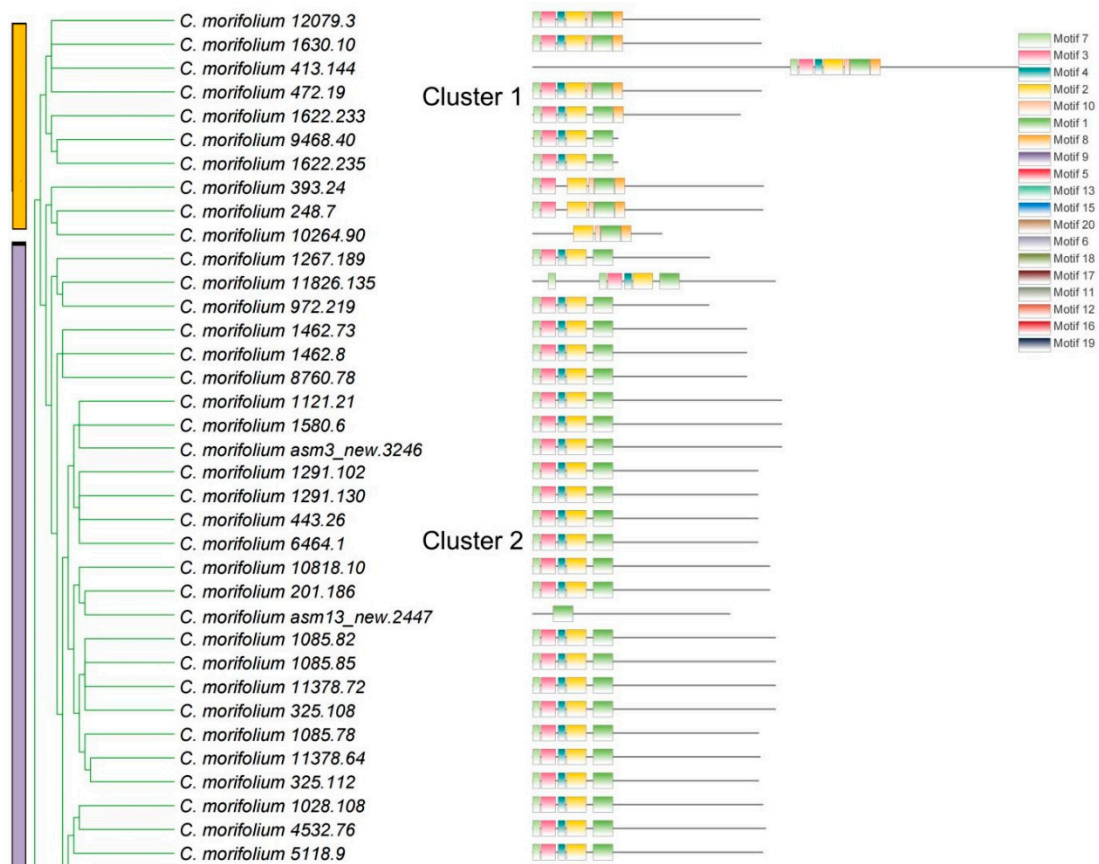
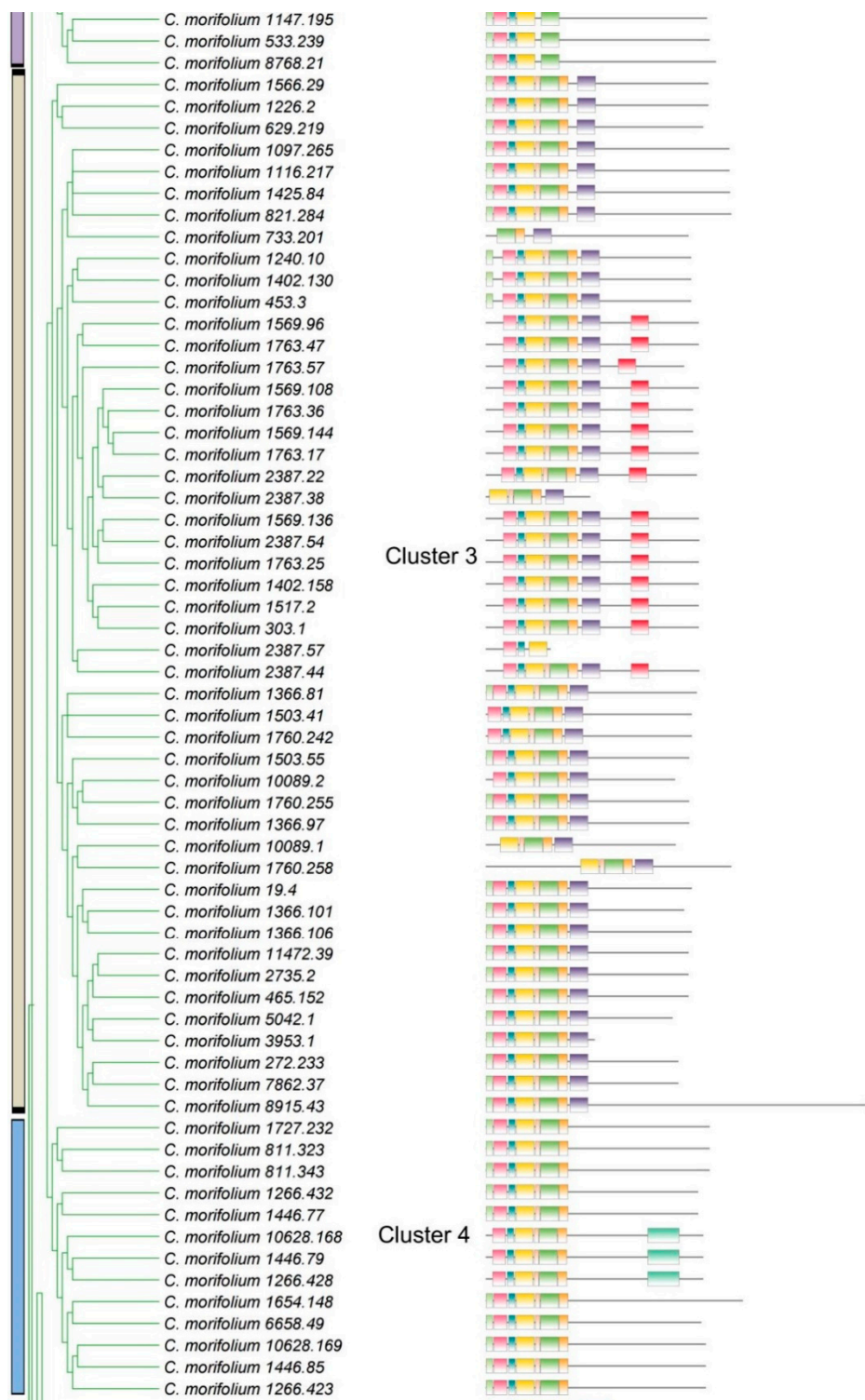
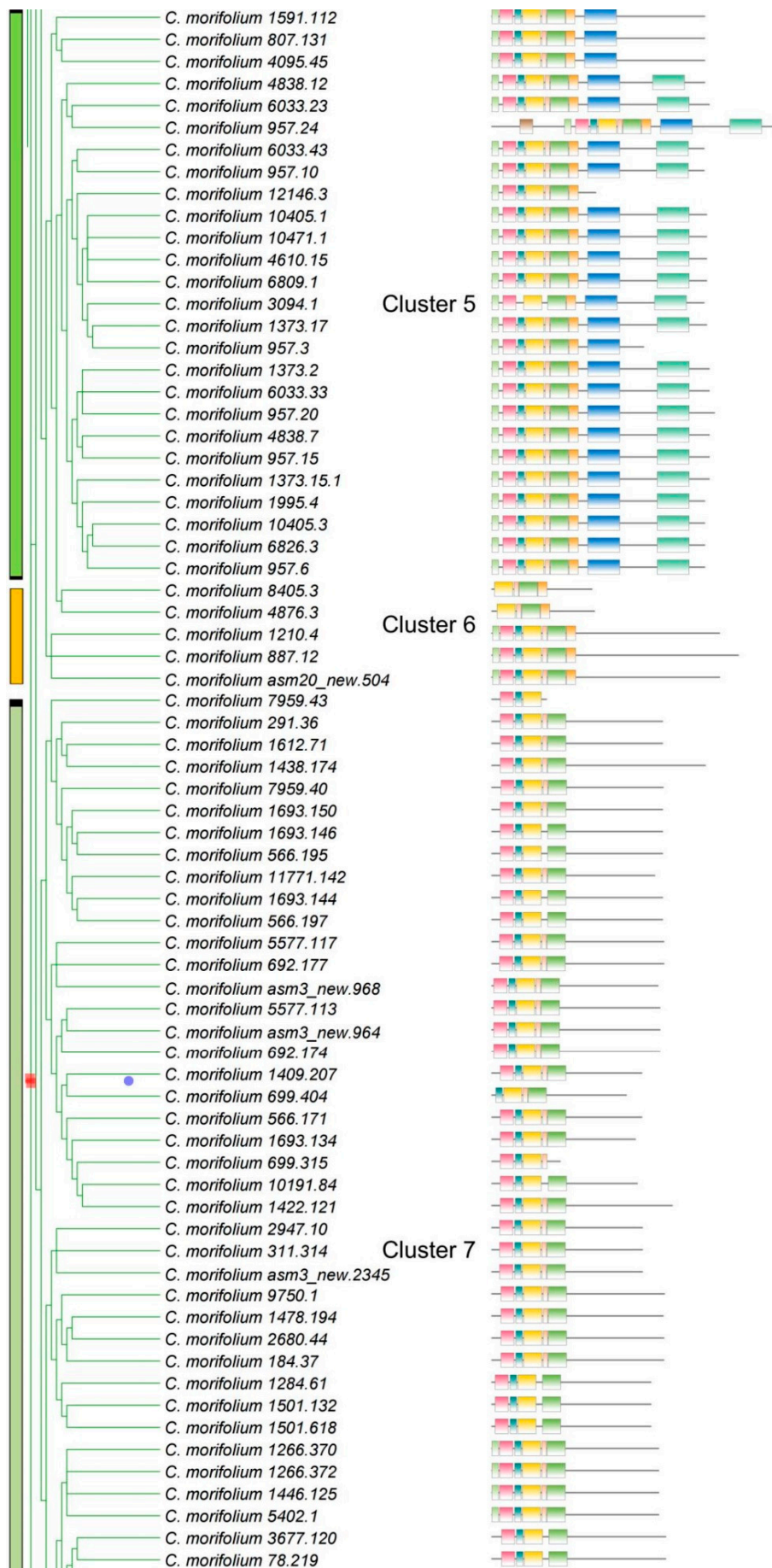
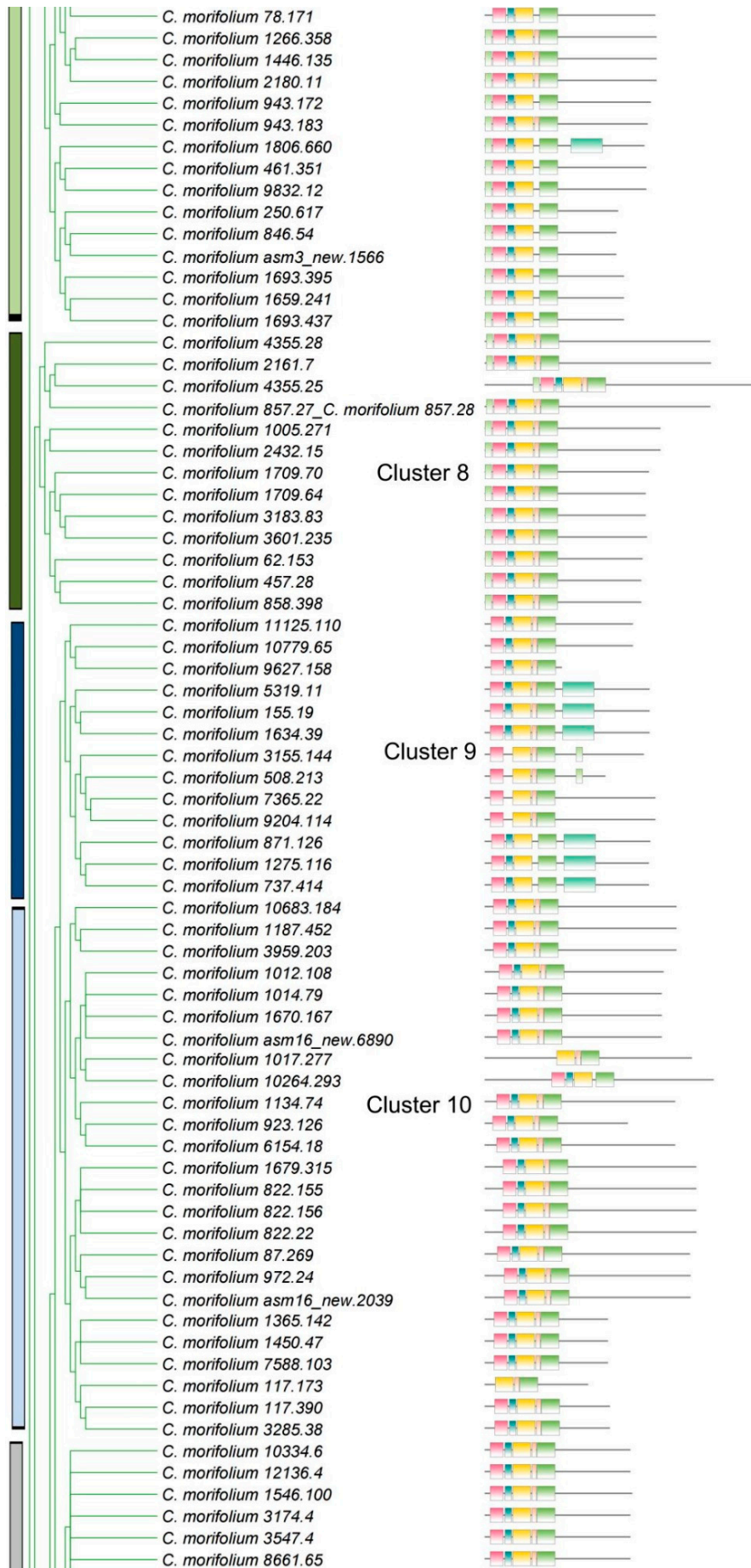


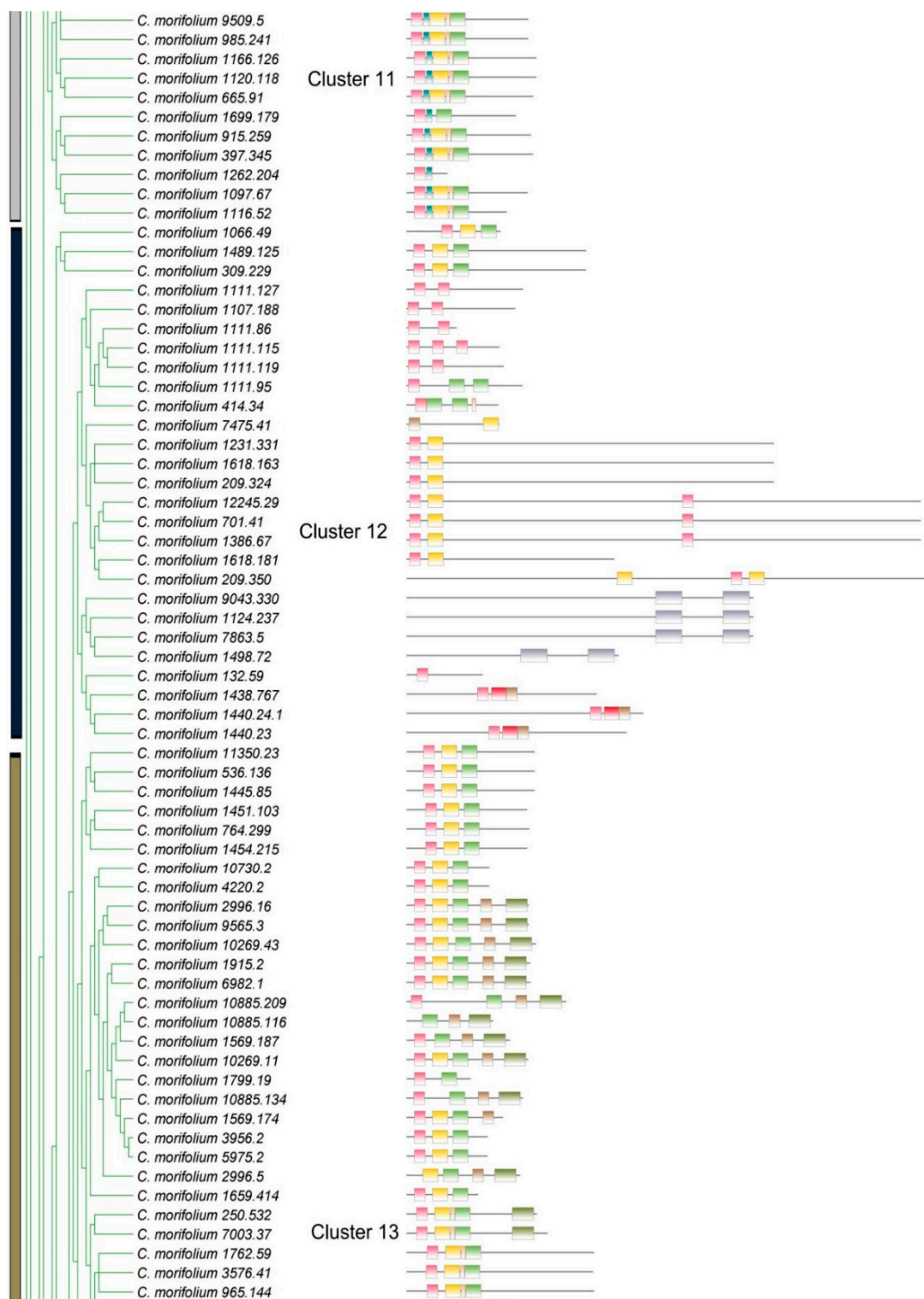
Figure S4. Number and proportion of tandem duplicated genes in R2R3-MYB and 1R-MYB in *C. ×morifolium*.

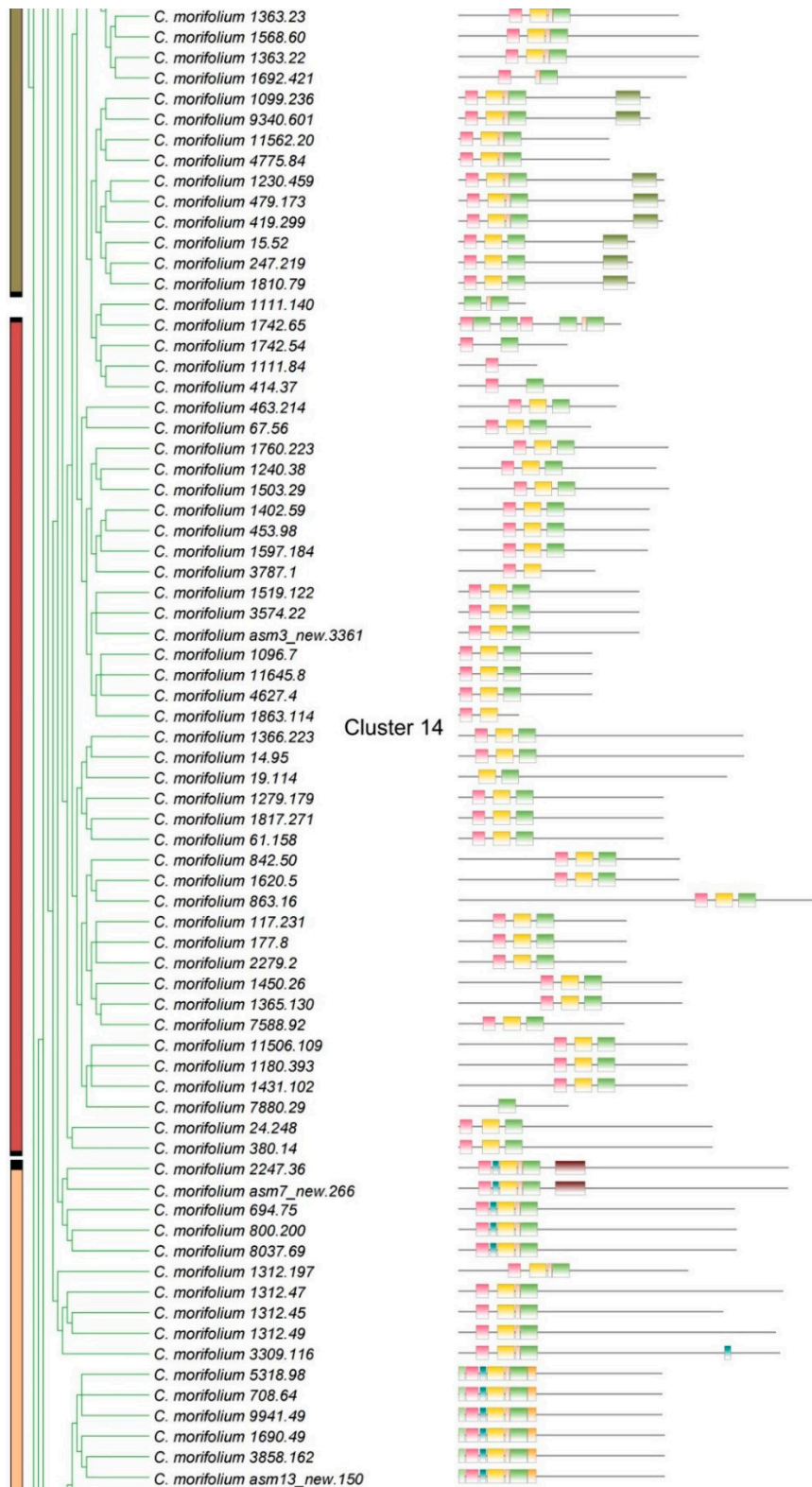


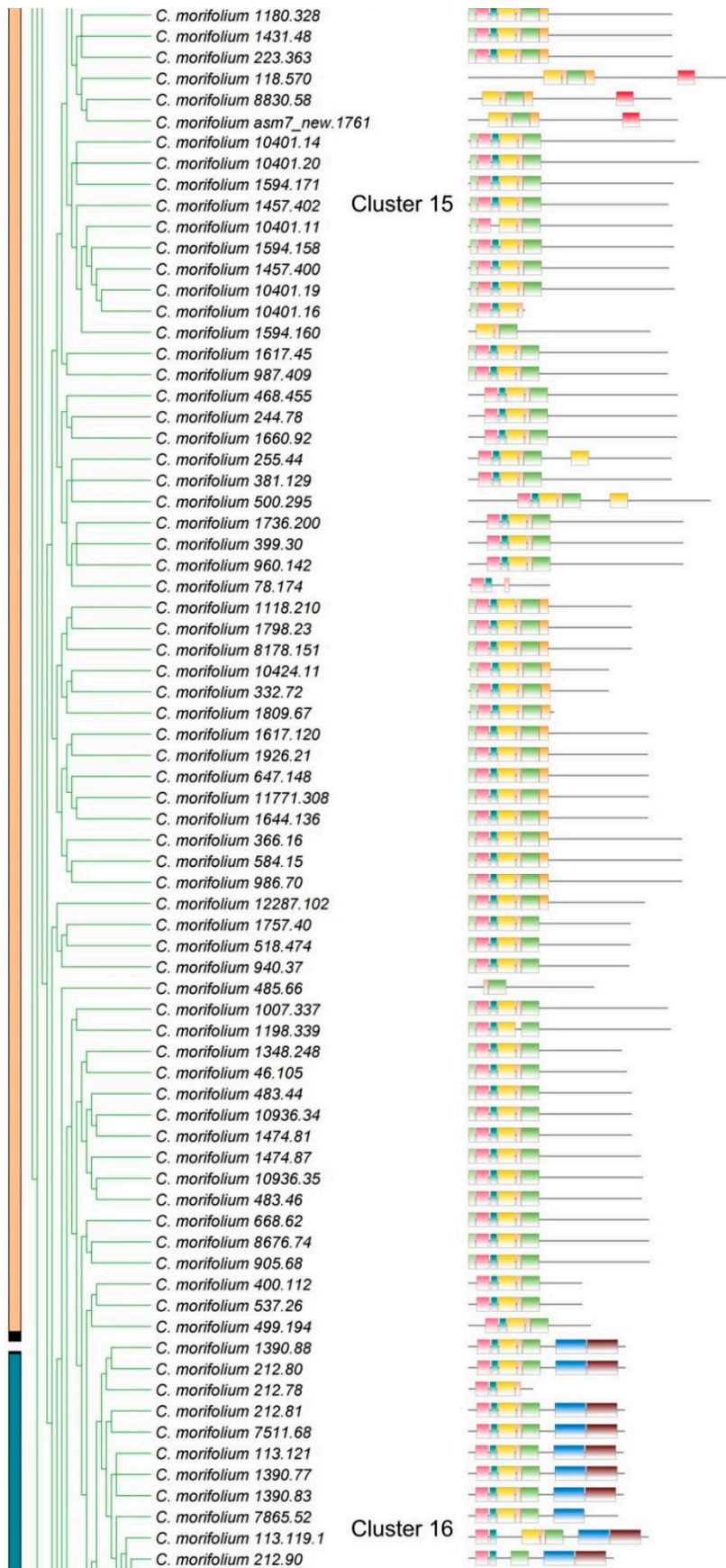












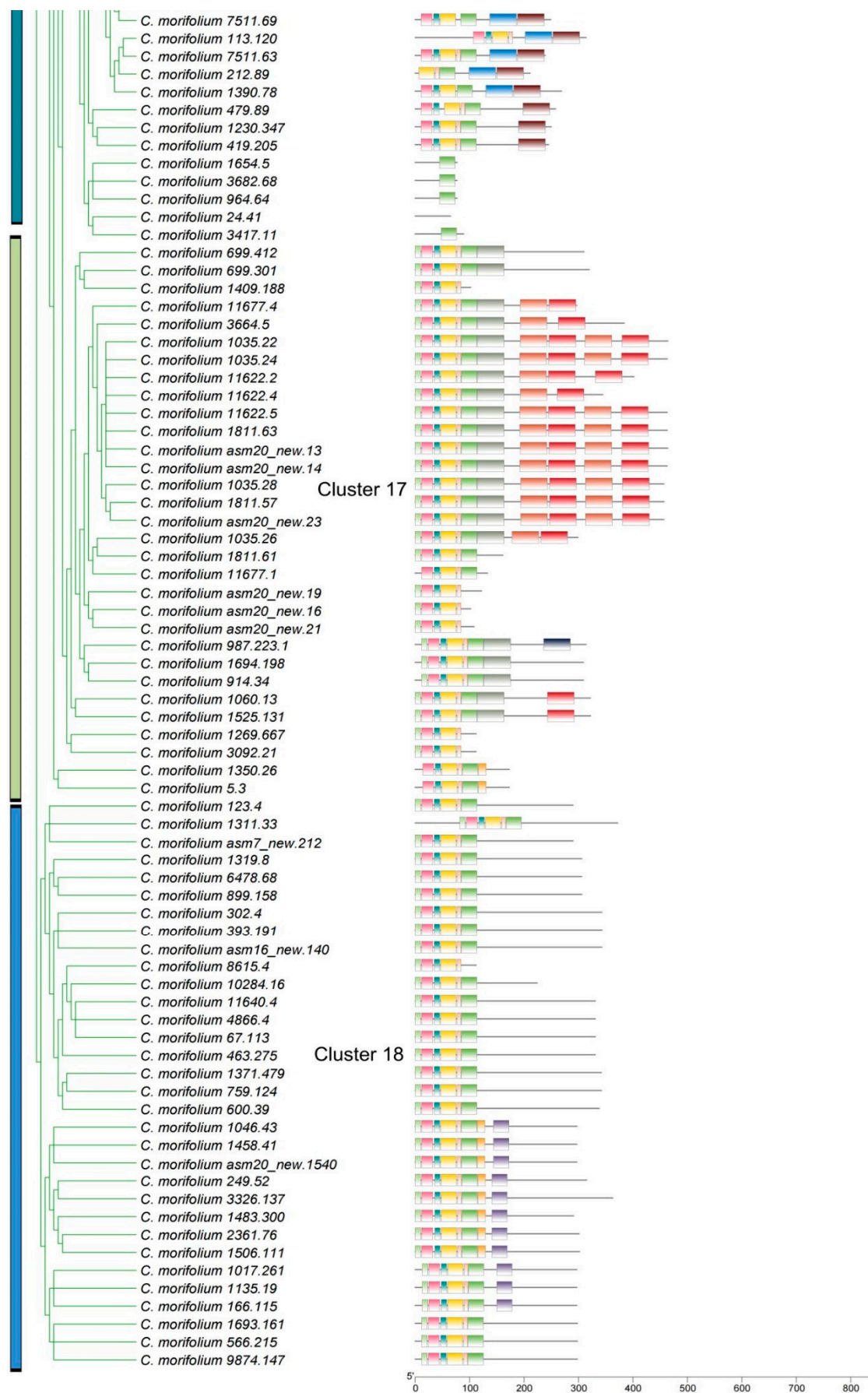
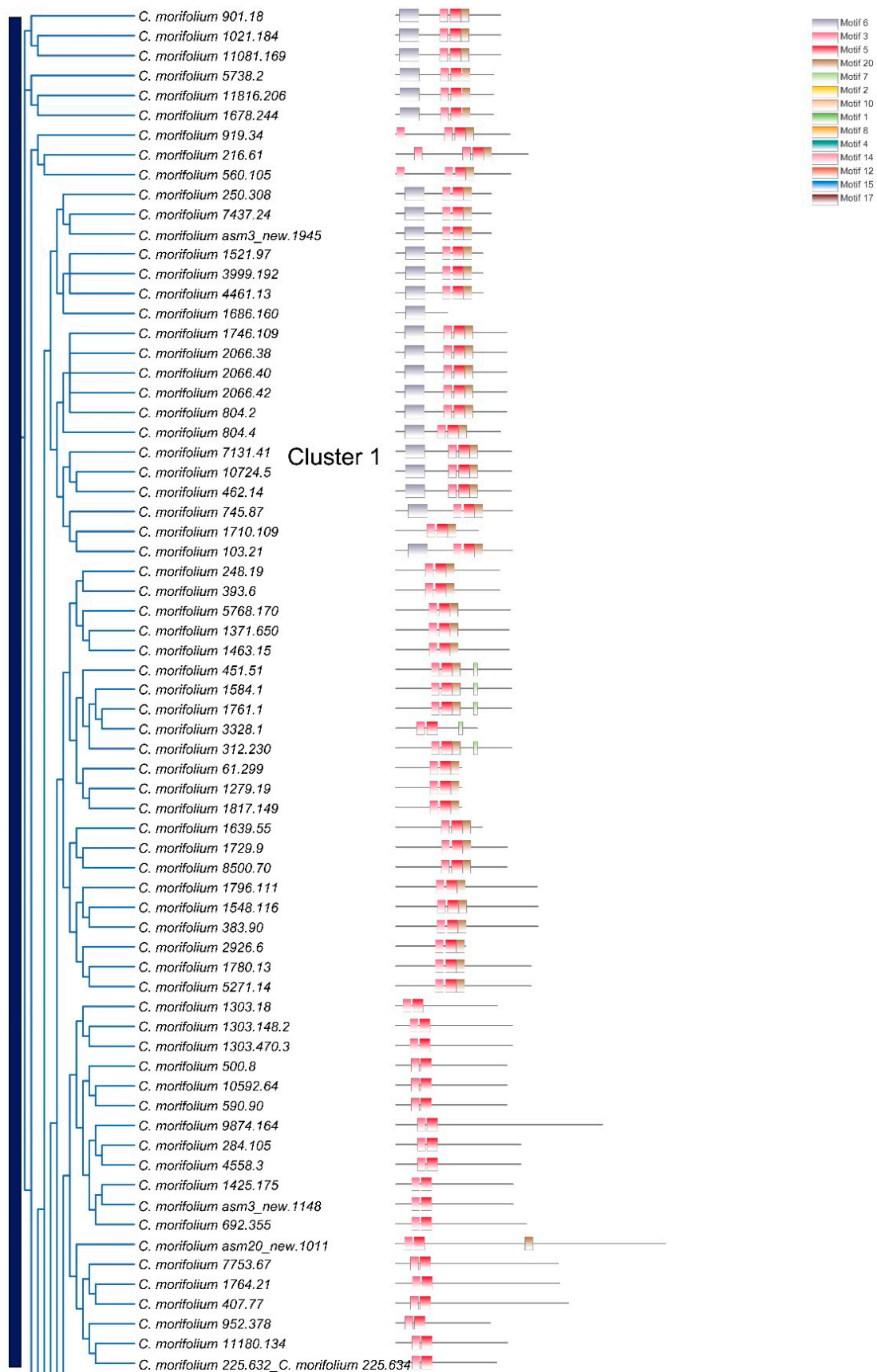


Figure S5. Sequence structure analysis of the R2R3-MYB subfamily. 19/20 conserved motifs exist in R2R3-MYBs.



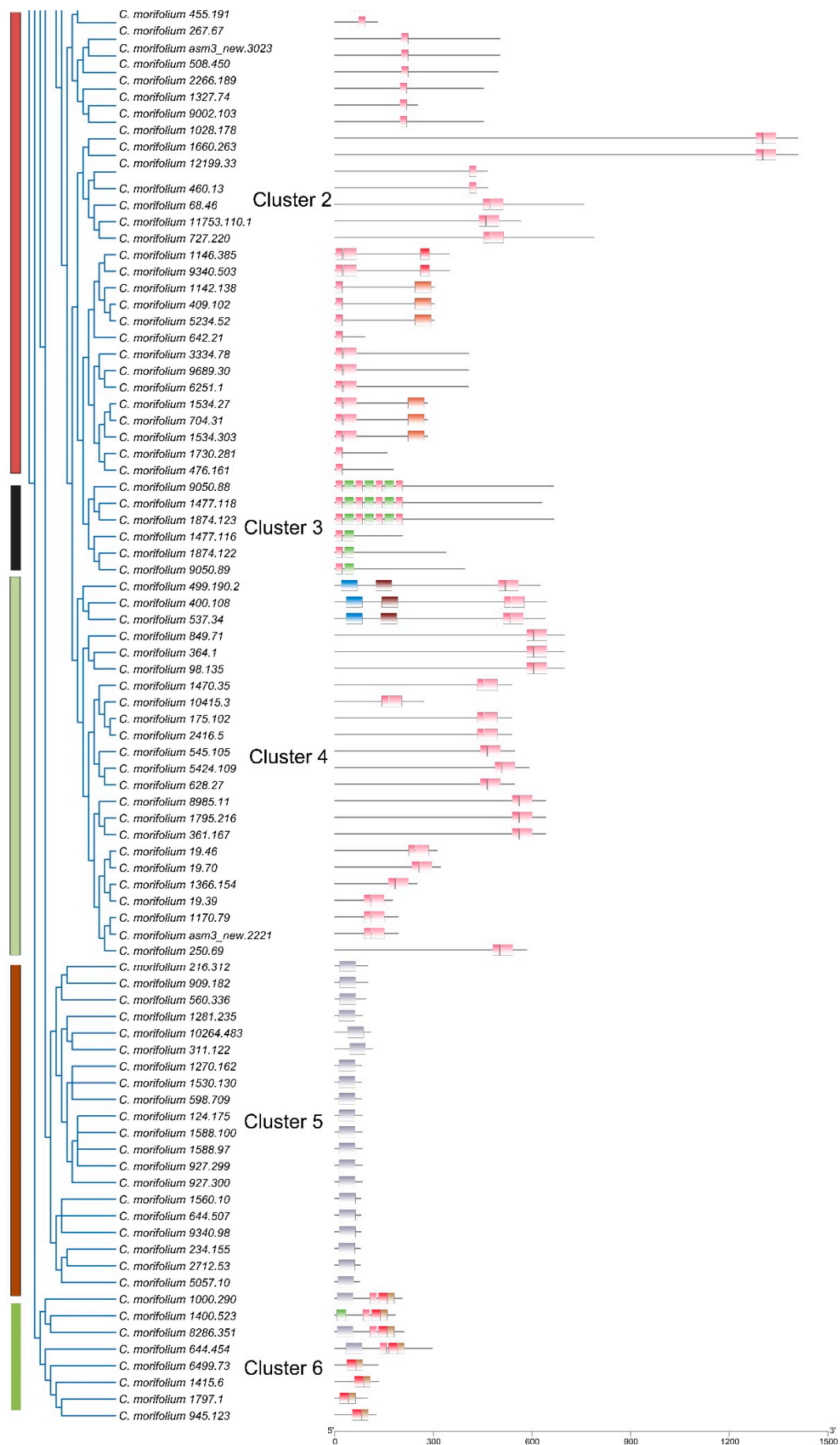


Figure S6. Sequence structure analysis of the 1R-MYB subfamily. 14/20 conserved motifs exist in 1R-MYBs.

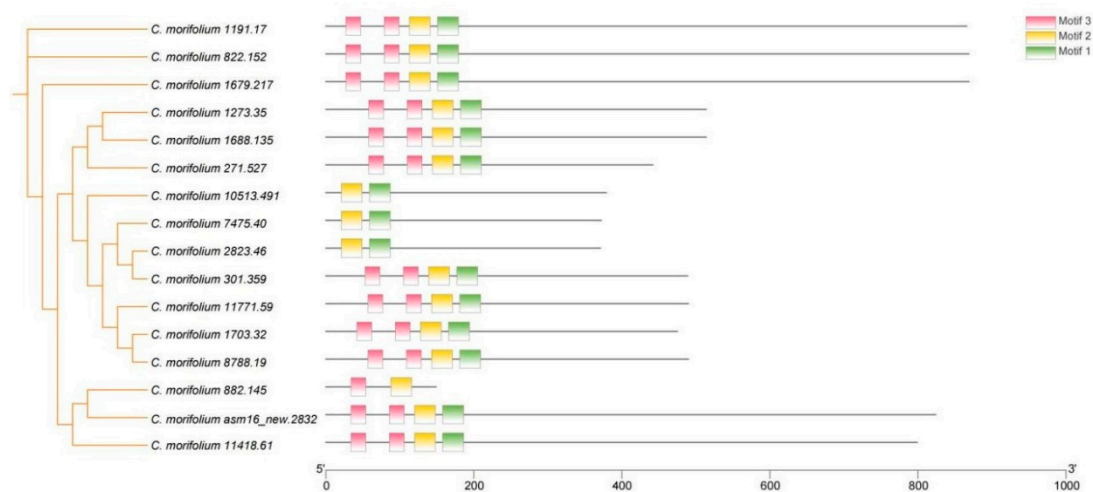


Figure S7. Sequence structure analysis of the 3R-MYB subfamily. 3/20 conserved motifs exist in 3R-MYBs.

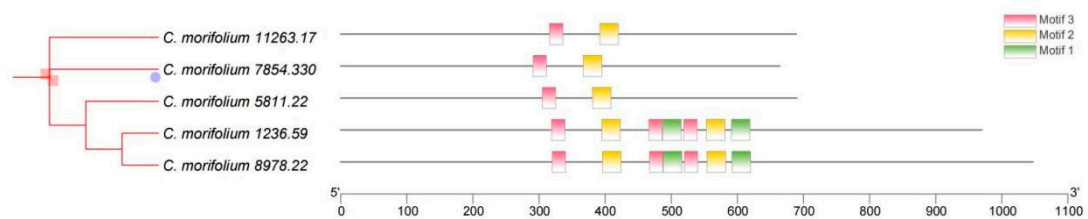


Figure S8. Sequence structure analysis of the 4R-MYB subfamily. 3/20 conserved motifs exist in 4R-MYBs.

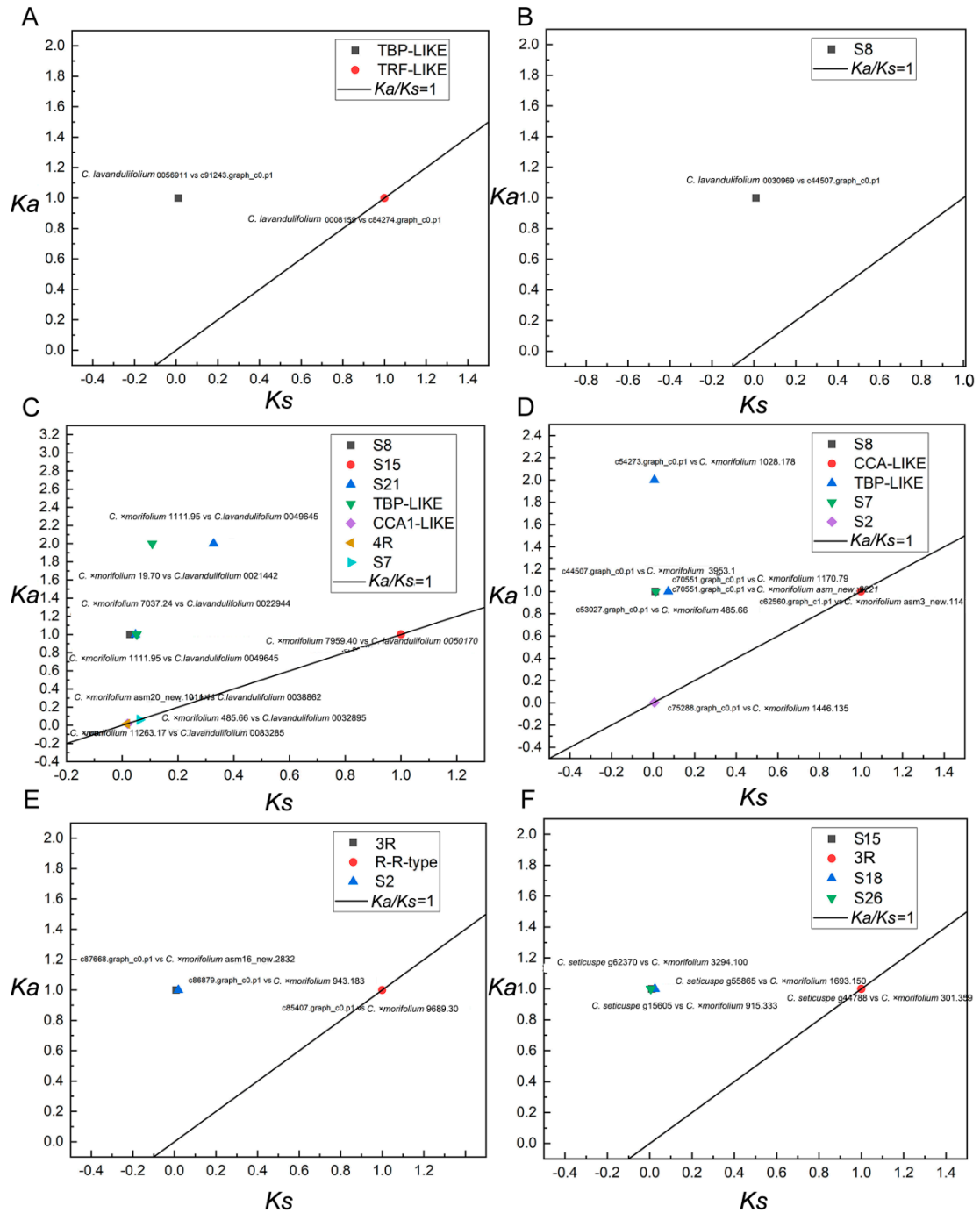


Figure S9. Comparative analysis of homologous MYB genes that were subjected to positive selection between *Chrysanthemum* species. (A) *C. lavandulifolium* vs. *C. vestitum*; (B) *C. lavandulifolium* vs. *C. indicum*; (C) *C. lavandulifolium* vs. *C. ×morifolium*; (D) *C. indicum* vs. *C. ×morifolium*; (E) *C. ×morifolium* vs. *C. vestitum*; (F) *C. seticuspe* vs. *C. ×morifolium*. The horizontal and vertical axes represent K_s and K_a values, respectively. The K_a/K_s values of each lineage are marked by different symbols.

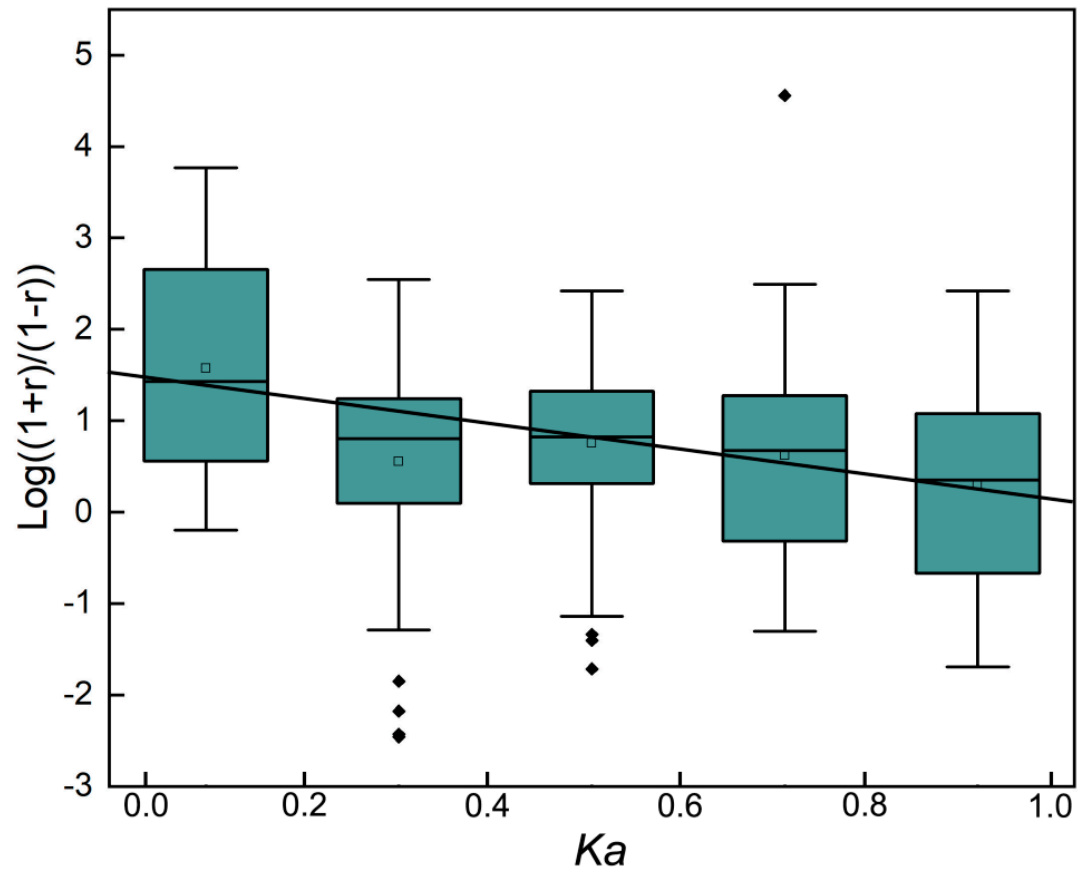


Figure S10. Correlations of expression patterns between homologous genes and Ka values in the *MYB* gene family.
Fitting function = $\text{Log} [(1 + r) / (1 - r)] = 1.5 - 0.25 \cdot Ka$.

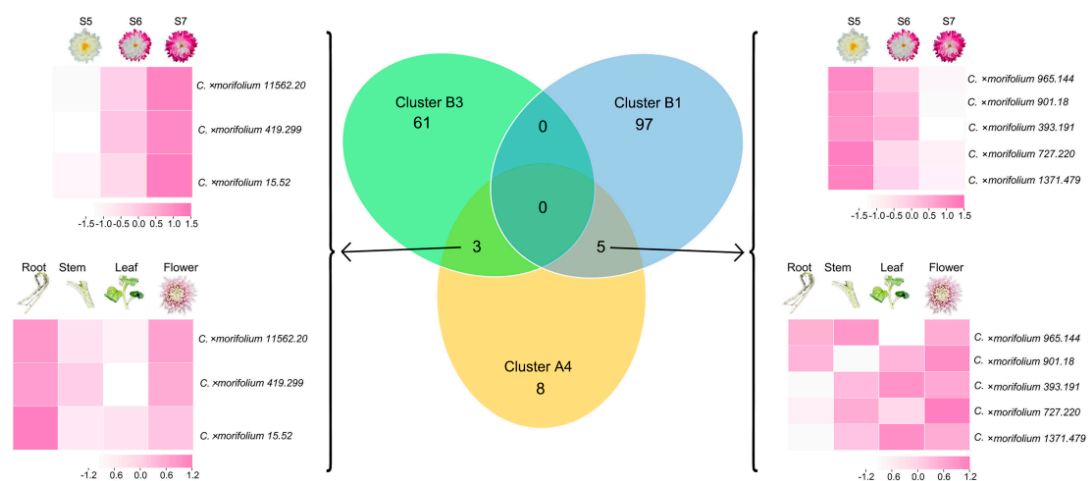


Figure S11. The expression of candidate genes that may regulate anthocyanin biosynthesis in *C. x morifolium*. S5, S6, and S7 respectively indicate the early, middle, and late stages of anthocyanin accumulation in the capitulum of the cultivated chrysanthemum 'f23'. Numbers in the Venn diagram indicate gene numbers.

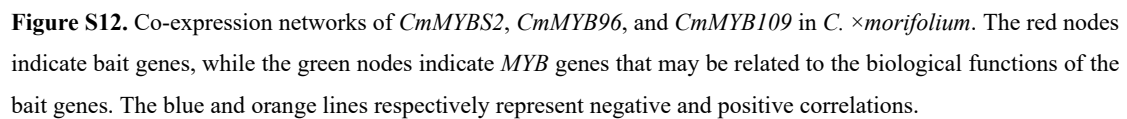


Figure S12. Co-expression networks of *CmMYBS2*, *CmMYB96*, and *CmMYB109* in *C. ×morifolium*. The red nodes indicate bait genes, while the green nodes indicate *MYB* genes that may be related to the biological functions of the bait genes. The blue and orange lines respectively represent negative and positive correlations.