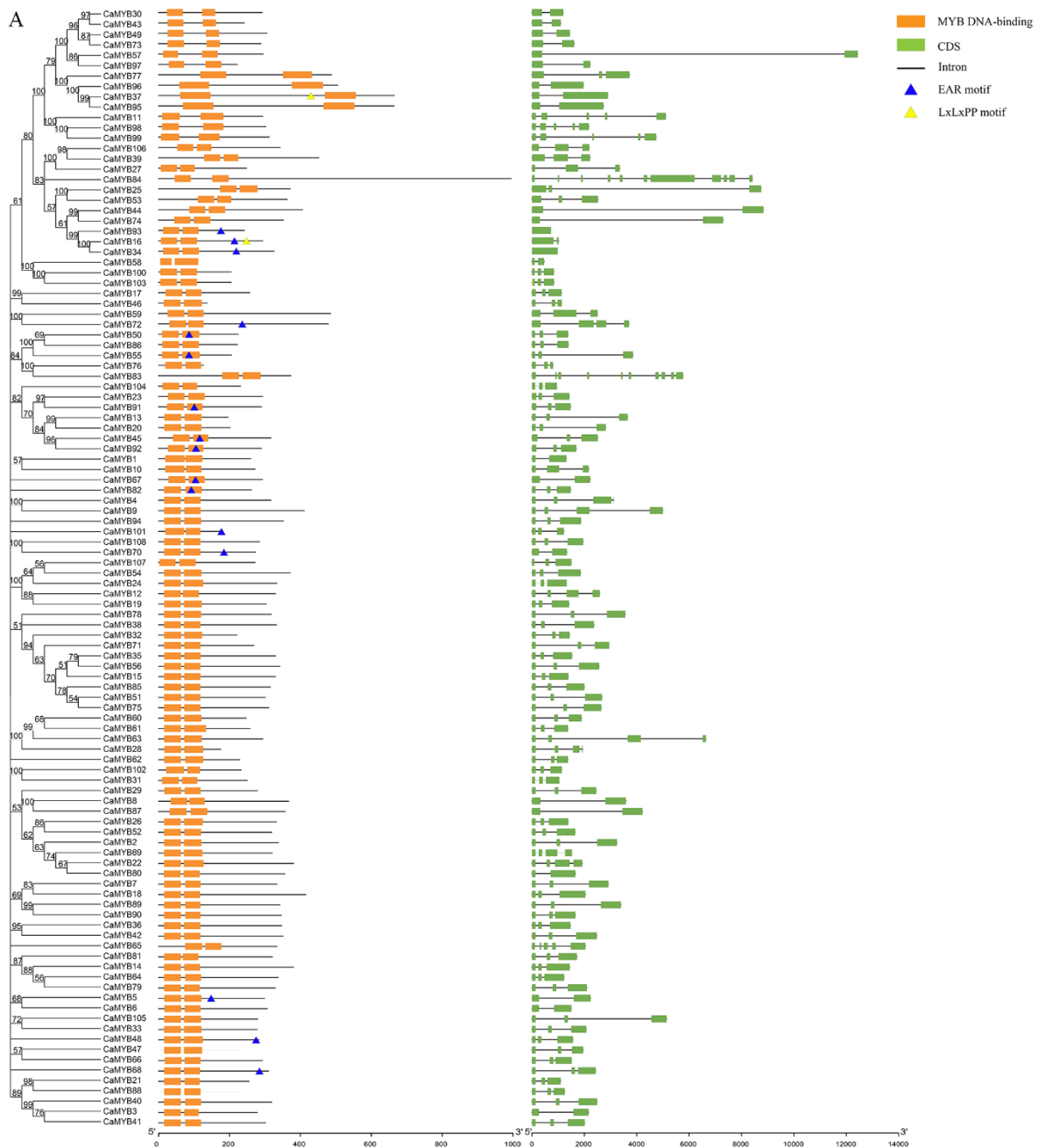
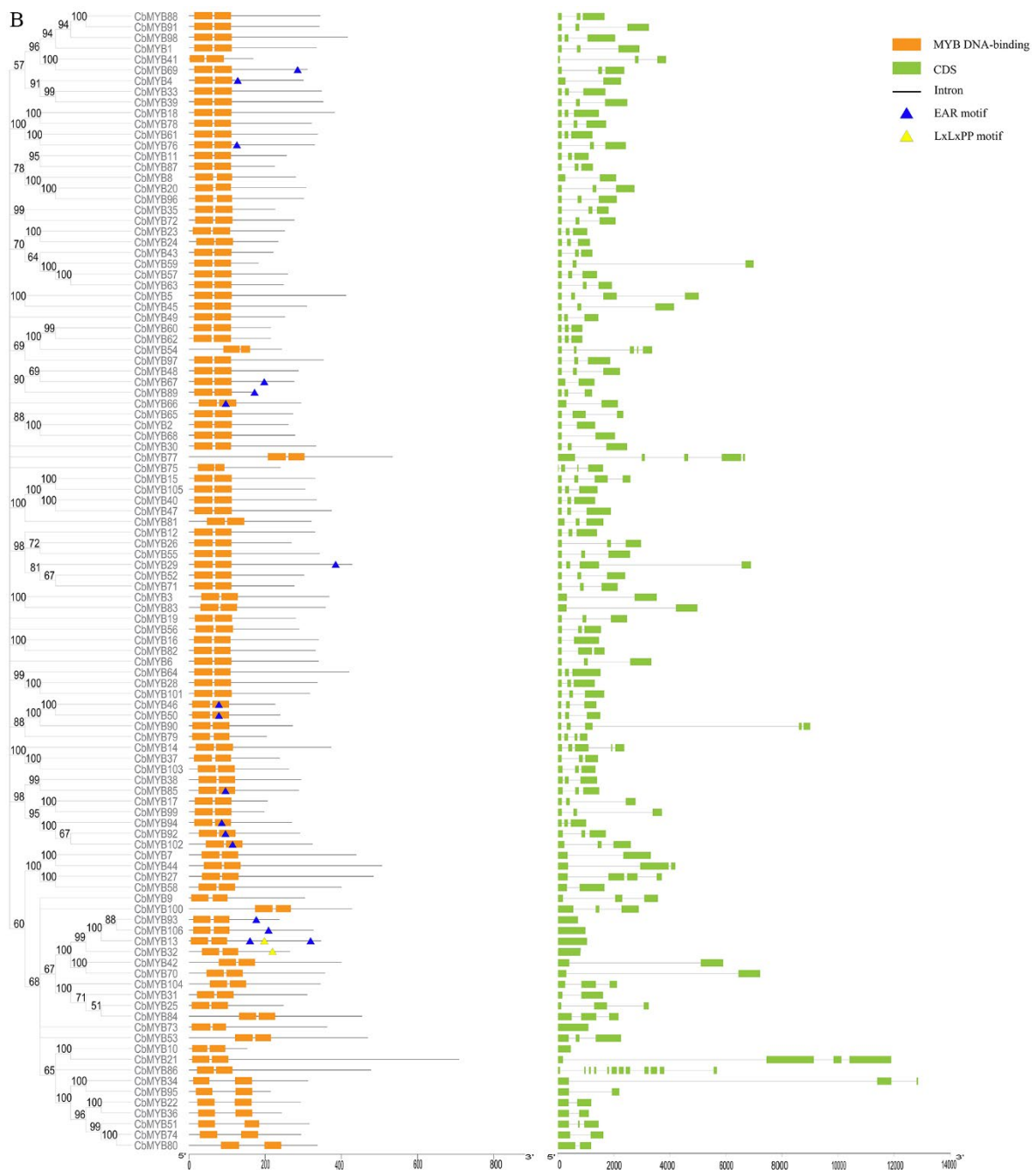


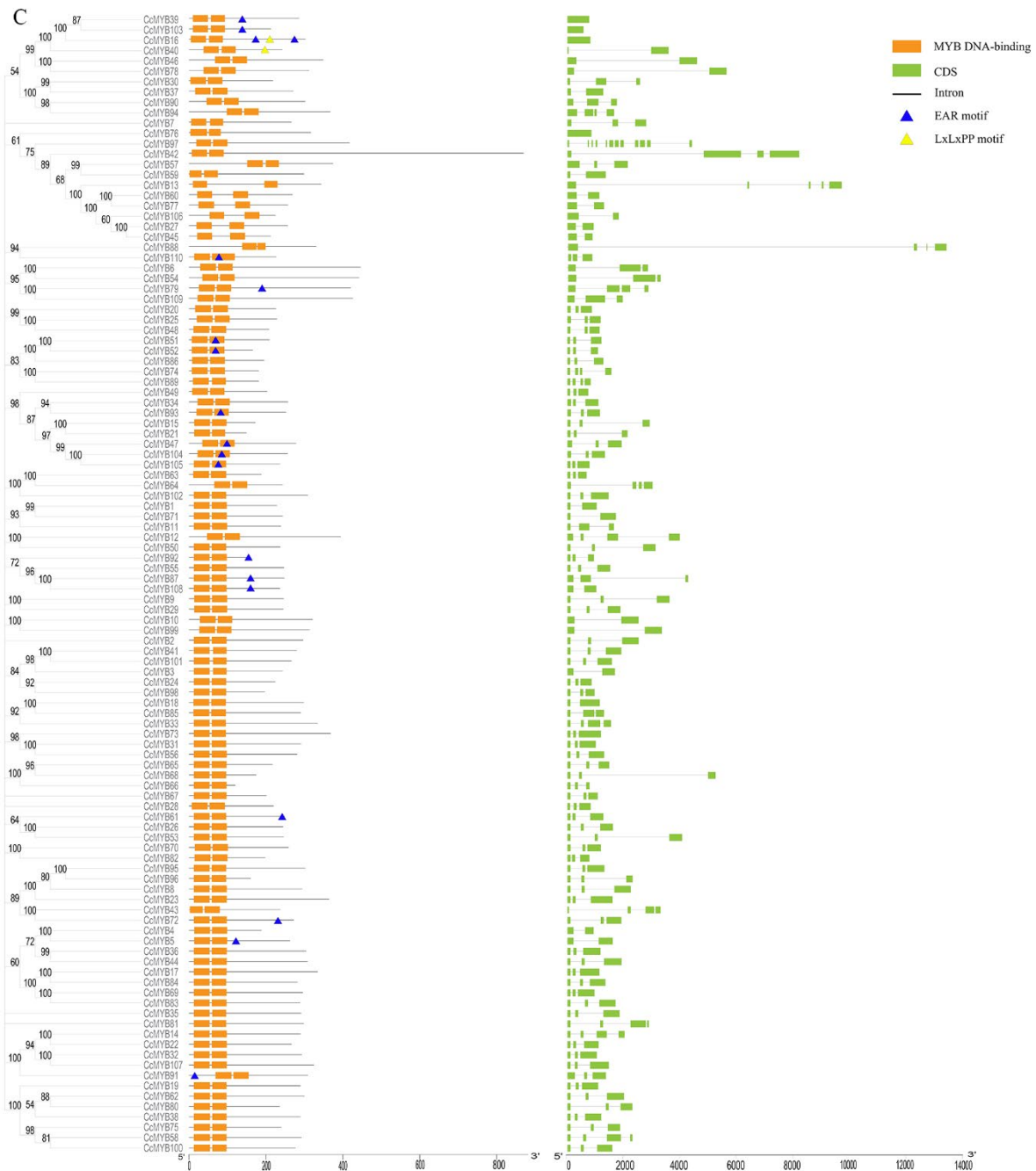
Supplemental Figures

Supplementary Figure 1 Phylogenetic relationships, conserved motifs, and gene structural analysis of R2R3-MYBs in (A) *Capsicum annuum*, (B) *Capsicum baccatum* and (C) *Capsicum chinense*.

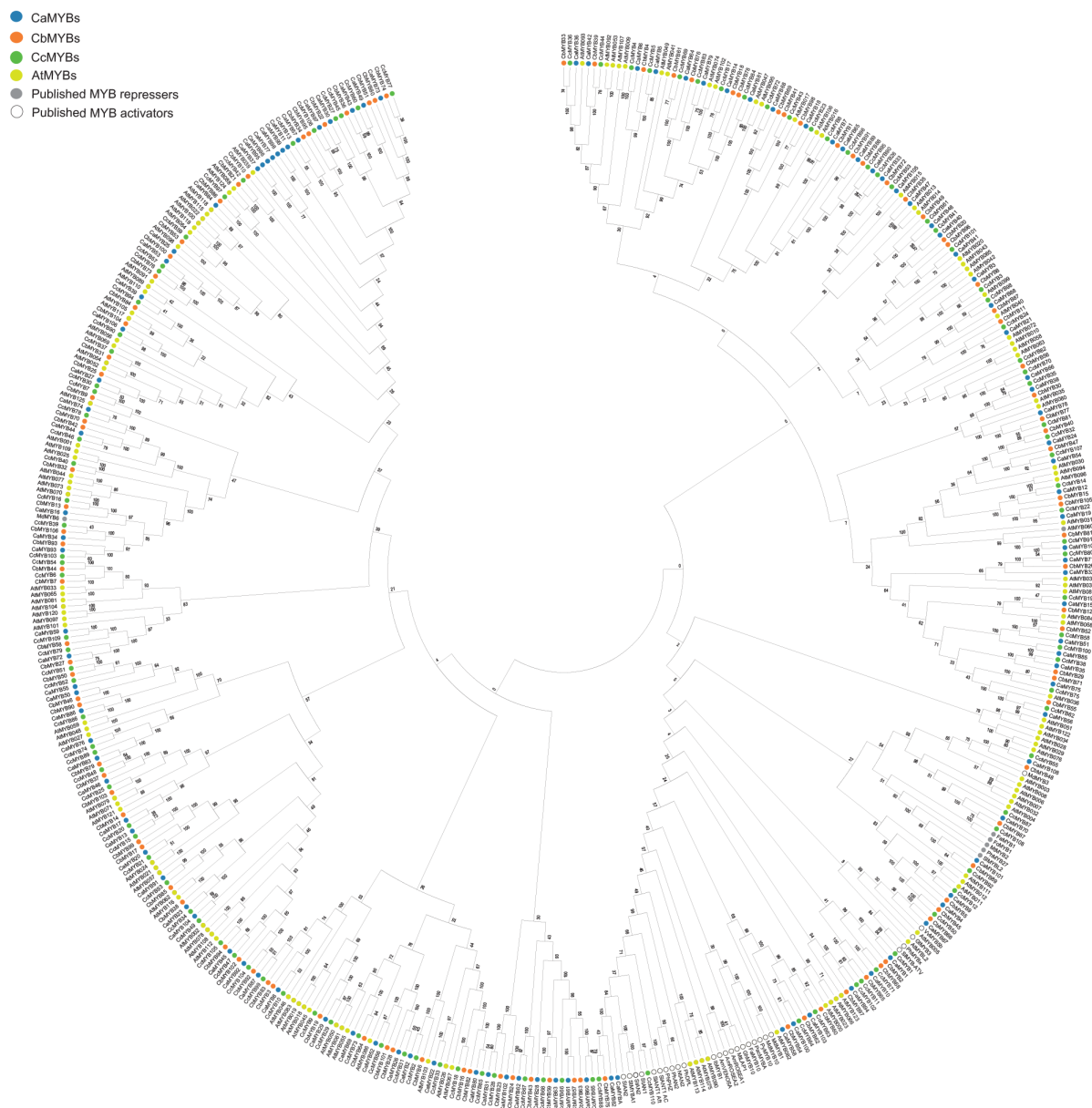
Supplementary Figure 2 Phylogenetic analyses of all *Capsicum* R2R3-MYB transcription factors with Arabidopsis R2R3-MYBs and anthocyanin-related MYB transcription factors from other plant species.







Supplementary Figure 1. Phylogenetic relationships, conserved motifs, and gene structural analysis of R2R3-MYBs in (A) *Capsicum annuum*, (B) *Capsicum baccatum* and (C) *Capsicum chinense*. Complete alignments of all *Capsicum* R2R3-MYB proteins were used to construct the phylogenetic tree using the neighbor-joining method. The bootstrap values are indicated on the nodes of the branches. The scale at the bottom provides a size reference. The repression motifs are marked with solid triangles.



Supplementary Figure 2. Phylogenetic analyses of the *Capsicum* R2R3-MYB transcription factors with anthocyanin-related MYB transcription factors from other plant species. The composite phylogenetic tree that included all *Capsicum* and *Arabidopsis* R2R3-MYB transcription factors and anthocyanin-related MYB transcription factors from *Arabidopsis thaliana*, rice (*Oryza sativa*), soybean (*Glycine max*), tomato (*Solanum lycopersicum*), strawberry (*Fragaria x ananassa*), *Gentiana triflora*, *Ipomoea batatas*, apple (*Malus domestica*), barrelclover (*Medicago truncatula*), Tobacco (*Nicotiana tabacum*), Petunia and grape (*Vitis vinifera*) were constructed by the neighbor-Joining method. The bootstrap values are indicated on the nodes of the branches. The anthocyanin-related MYB transcription factors are in bold.