Supplementary Information

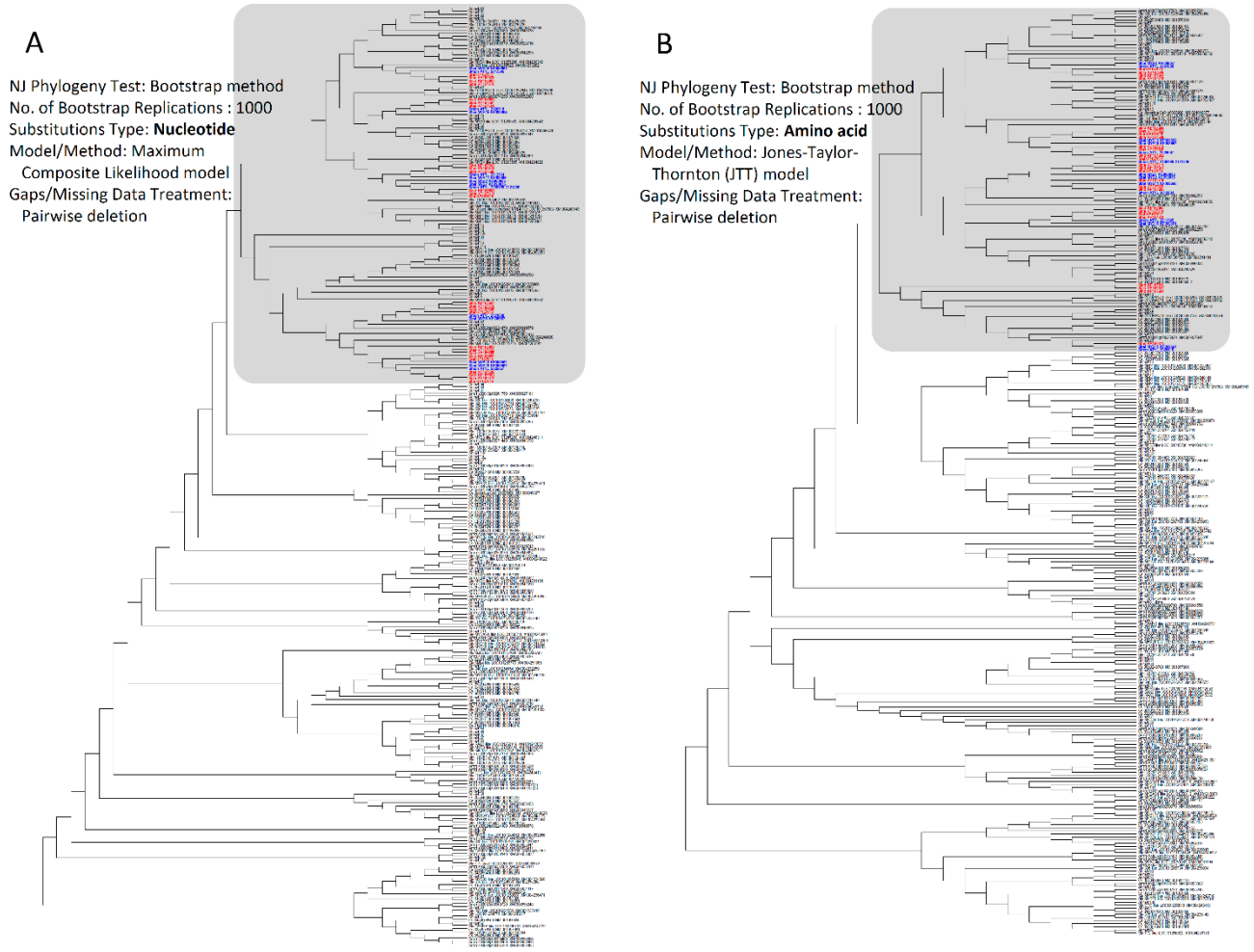

Figure S1. *Cont.*

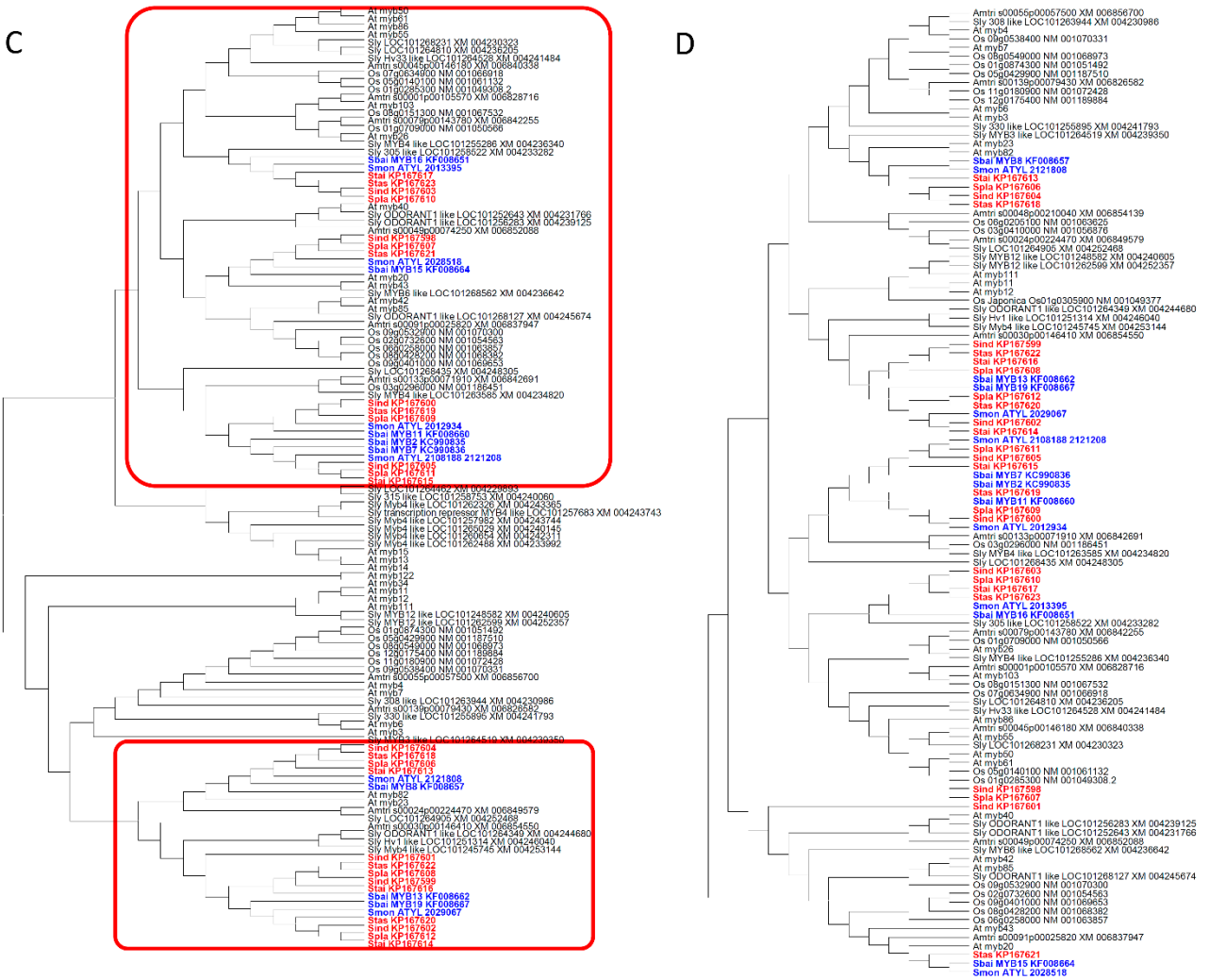

Figure S1. Cladogram of the *Scutellaria* R2R3-MYBs extracted from the inflorescence-bud transcriptomic library of *Scutellaria* and the published R2R3-MYBs from GenBank. (**A**) Neighbor-joining tree reconstructed based on the nucleotide sequences; (**B**) Neighbor-joining tree reconstructed based on the amino acid sequences. The gray boxes are the clade including the *Scutellaria* R2R3-MYBs and the corresponding sequences of *Amborella trichopoda* (Amtri), *Arabidopsis thaliana* (At), *Oryza sativa* (Os), and *Solanum lycopersicum* (Sly); (**C**) and (**D**) are enlargements of the gray areas of Figure S1A,B, respectively. Based on Figure S1C, the *Scutellaria* R2R3-MYBs and the sequences that were grouped with *Scutellaria* R2R3-MYBs were selected (the red frames) and realigned to re-perform the NJ analysis shown in Figure 1. Sbai: *Scutellaria baicalensis*; Sind: *Scutellaria indica*; Smon: *Scutellaria montana*; Spla: *Scutellaria playfairii*; Stai: *Scutellaria taiwanensis*; Stas: *Scutellaria tashiroi*.

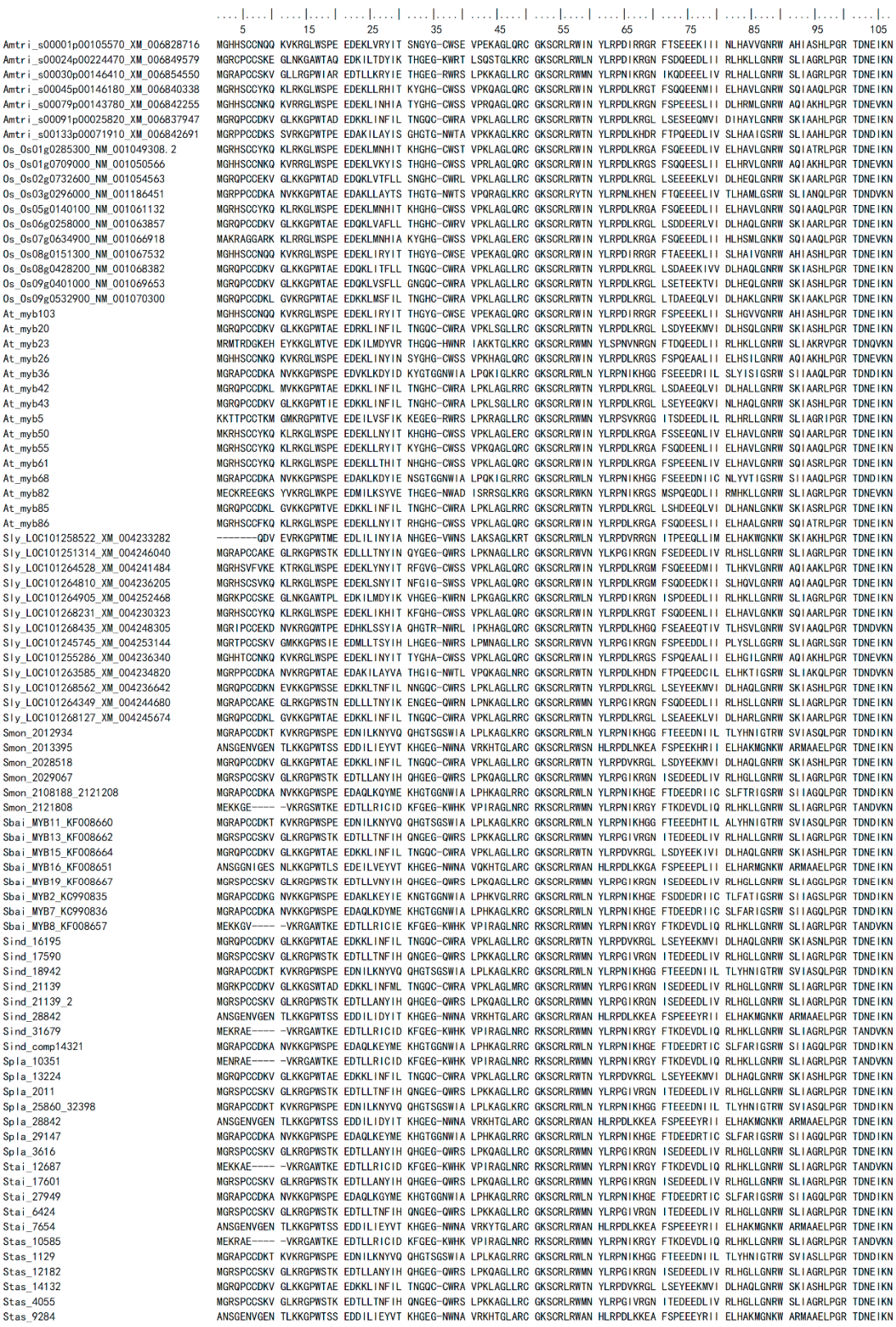

Figure S2. Amino acid alignments of the conserved region of the R2R3 Myb genes used for the NJ tree reconstruction in Figure 1. Amtri: *Amborella trichopoda*; At: *Arabidopsis thaliana*; Os: *Oryza sativa*; Sbai: *Scutellaria baicalensis*; Sind: *Scutellaria indica*; Sly: *Solanum lycopersicum*; Smon: *Scutellaria montana*; Spla: *Scutellaria playfairii*; Stai: *Scutellaria taiwanensis*; Stas: *Scutellaria tashiroi*.