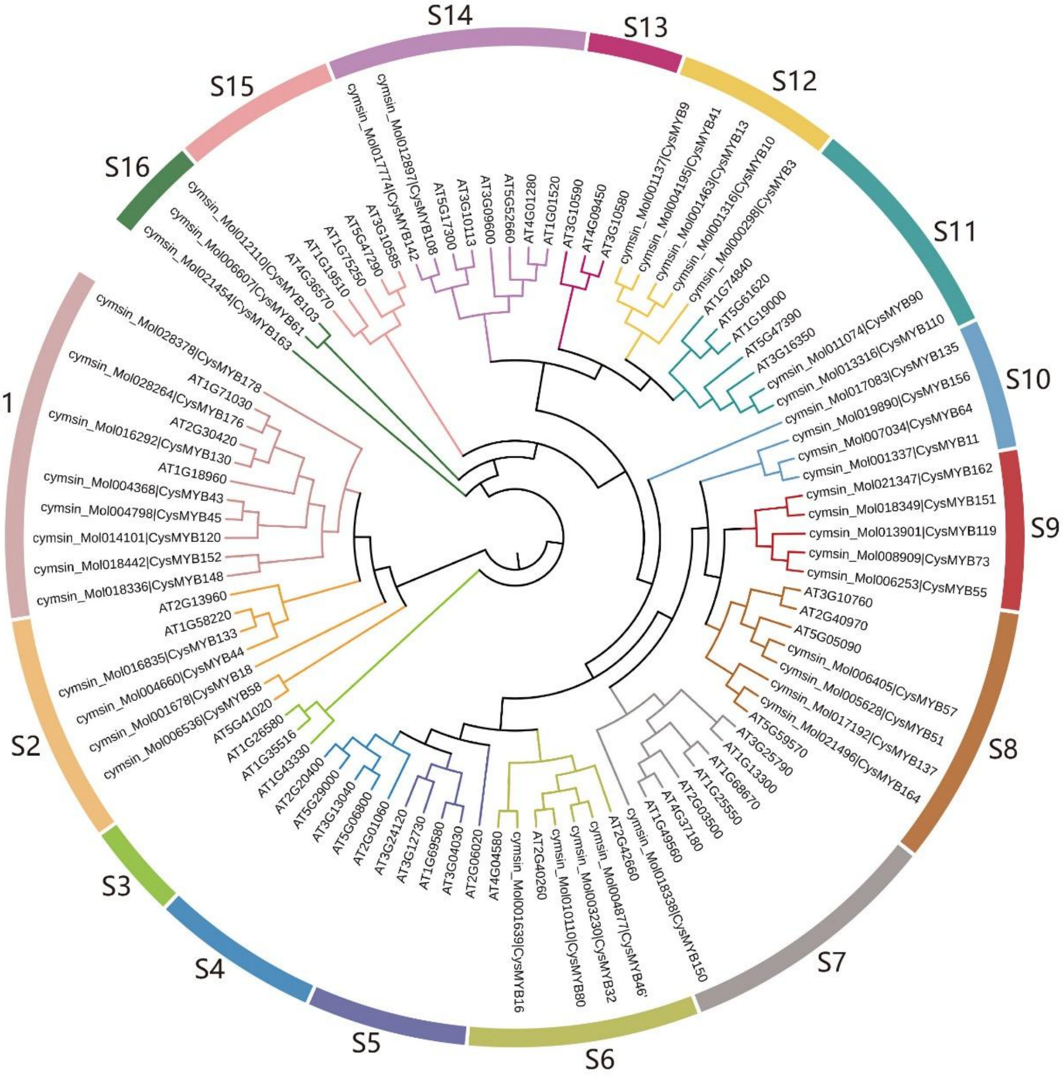

Figure S1 Phylogenetic tree of the 1R-MYB proteins from *C. sinense* and *A. thaliana*. The phylogenetic trees were constructed using MEGA X (V10.0) by the Maximum-likelihood (ML) method with 1,000 bootstrap replicates. The tree was classified into 16 phylogenetic subgroups (S1-S16) indicated with different colors.