Figure S3. ML phylogenetic tree of 157 typical maize R2R3-MYB family genes. The unrooted tree was constructed by the maximum likelihood (ML) method based on the alignment of the corresponding MYB DNA binding domains. Boot strapping values are indicated as percentages along the branches in ML analysis. The MYB proteins are clustered into 19 subgroups (designated as C1 to C19) and the corresponding subgroups in NJ tree (Fig.2) were listed in round bracket, for reference.