













Figure S5. Maximum likelihood (ML) tree of the R2R3-MYB proteins from maize (Zm), *Arabidopsis* (At) and other plants. The unrooted tree was constructed by the Maximum likelihood (ML) method based on the alignment of the corresponding MYB domains. Boot strapping values

are indicated as percentages along the branches in ML analysis. The MYB proteins are clustered into 37 subgroups (designated as C1 to C37) and the corresponding subfamilies in NJ tree (Fig.5) were listed in round bracket, for reference.