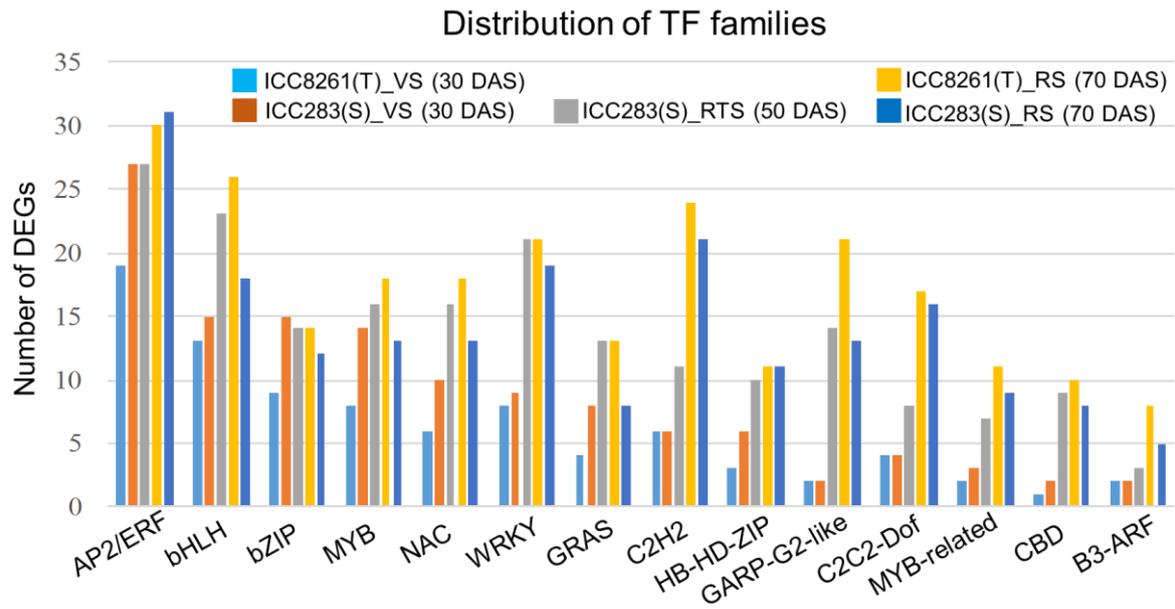


Supplementary Figure S1: qRT-PCR validation of DEGs during three developmental stages VS, RTS, RS. The correlation between fold change obtained by using qRT-PCR (x-axis) and RNA-Seq (y-axis).



Supplementary Figure S2: Top TF families represented in DEGs across vegetative stage (VS), reproductive transition stage (RTS) and reproductive stage (RS) in tolerant (T, ICC8261) and sensitive (S, ICC283) genotypes.