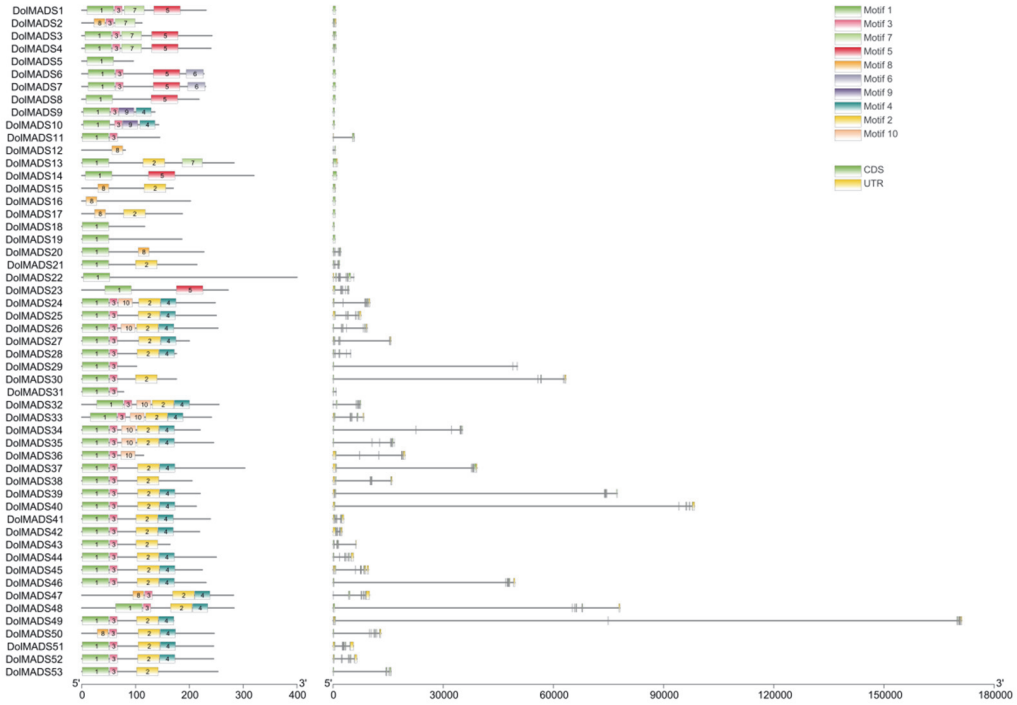


Figure S1. Conserved motifs and gene structure of DolMADSs.

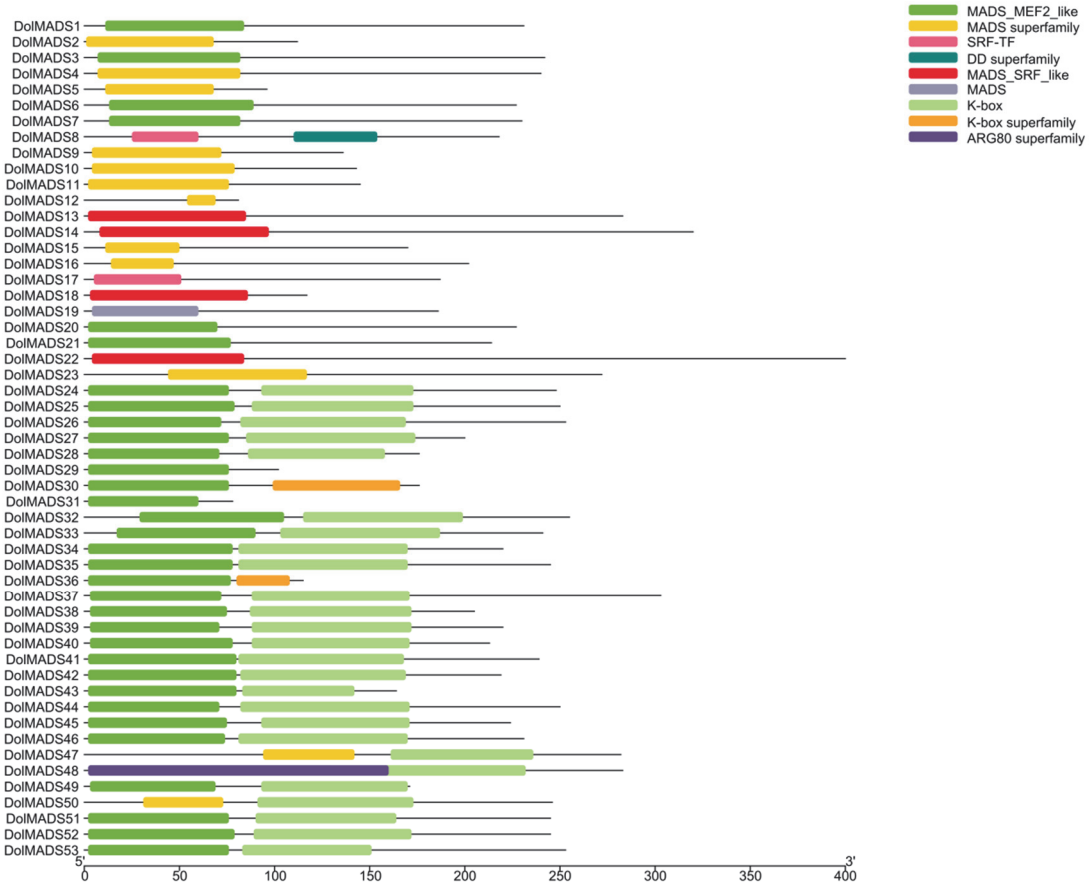


Figure S2. Conserved domains of DolMADSs.



Figure S3. Prediction of cis-regulatory elements in the promoter regions of DolMADS gene family

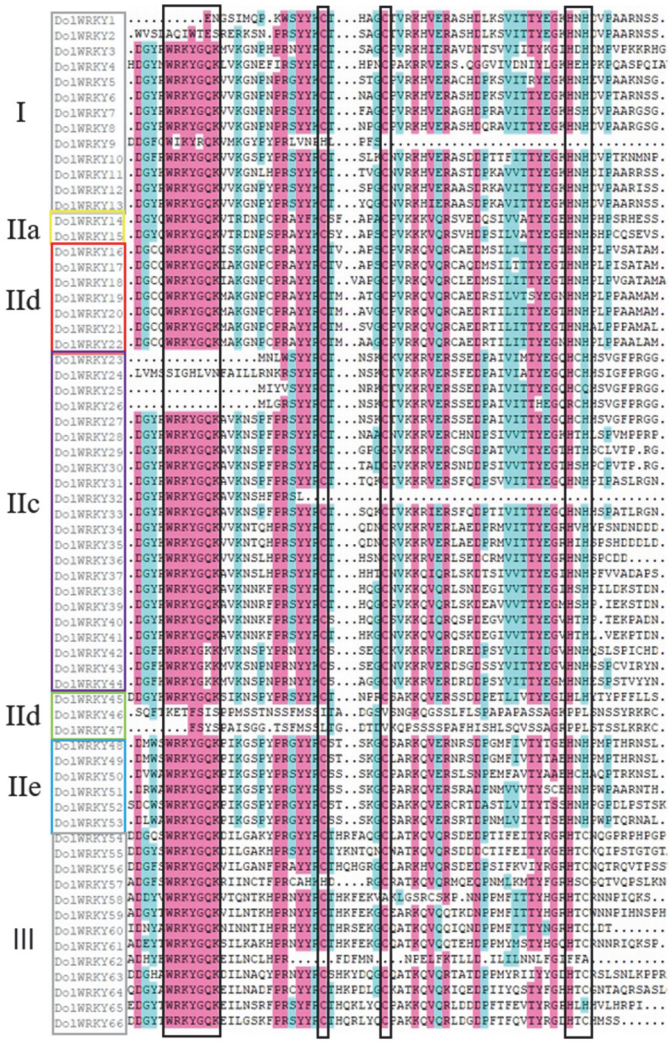


Figure S4. Multiple sequence alignment of DolWRKYs

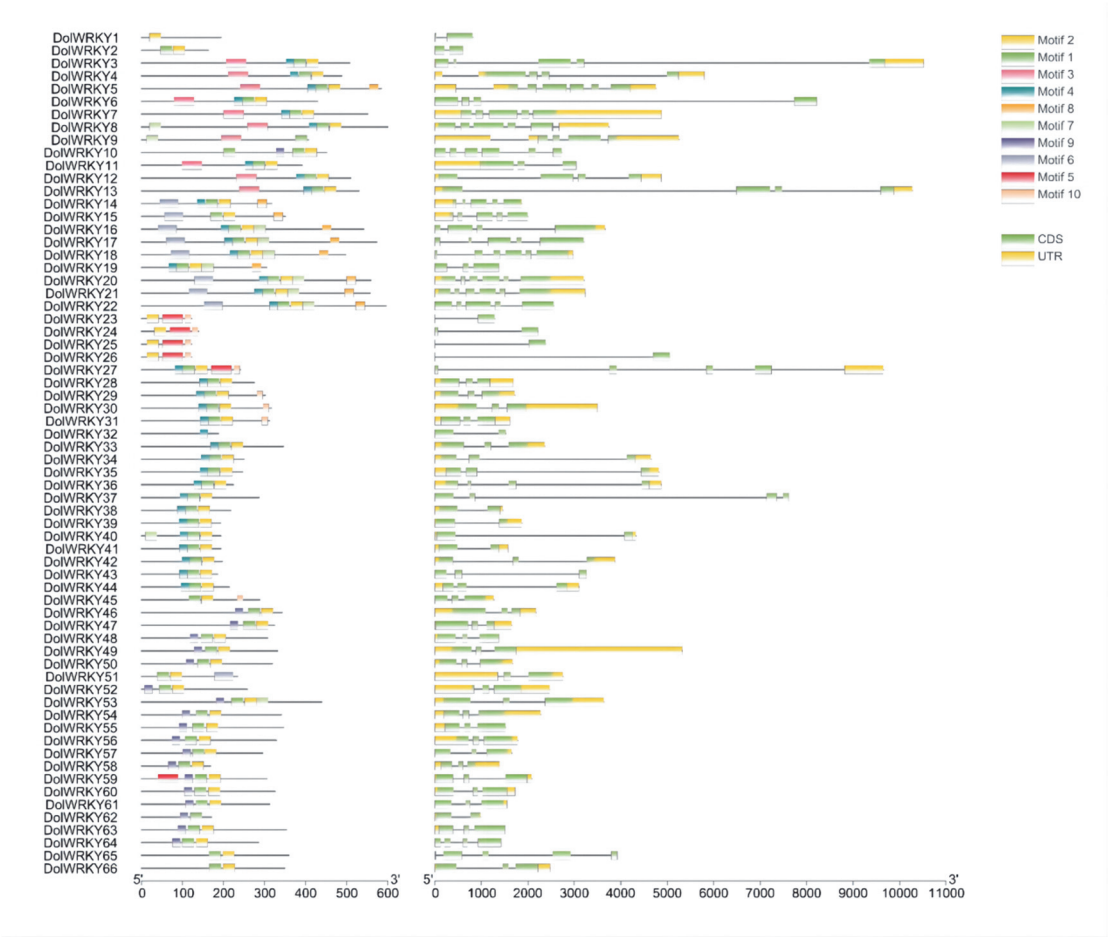


Figure S5. Conserved motifs and gene structure of DolWRKYs.

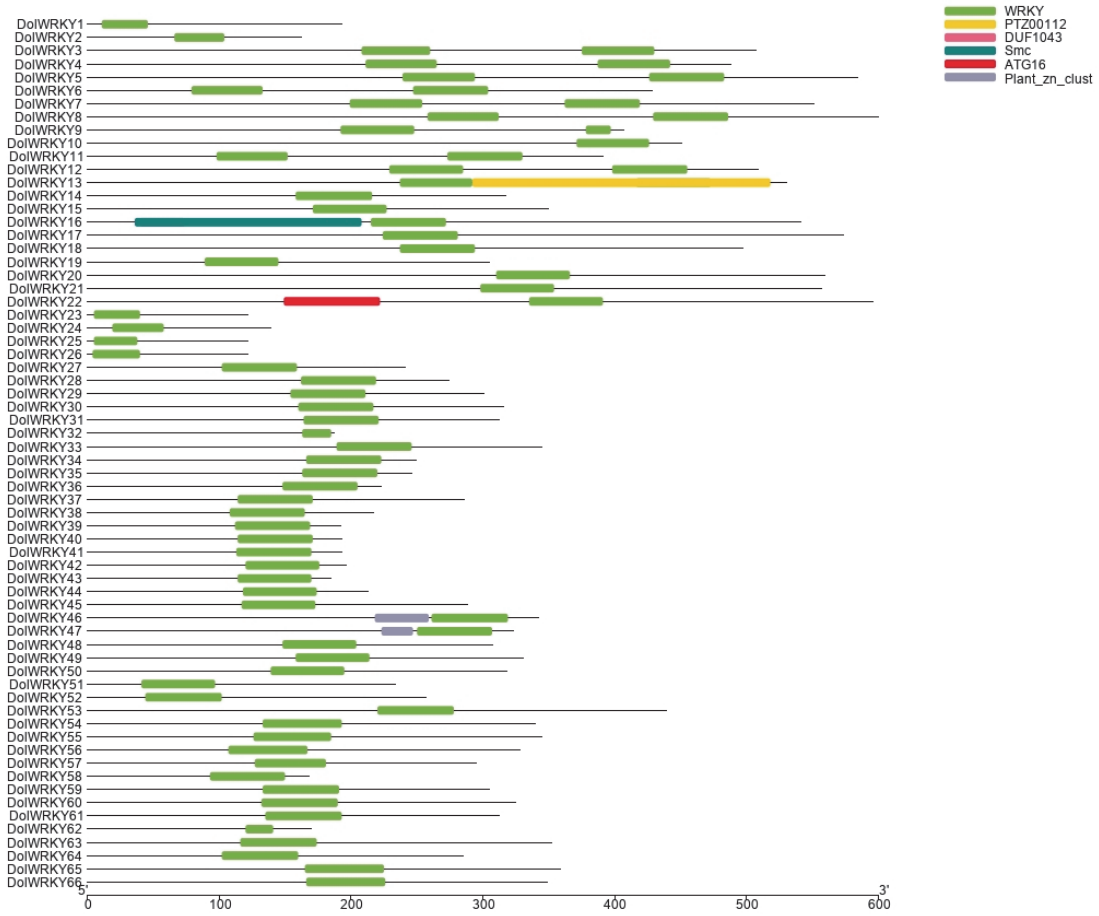


Figure S6. Conserved domains of DolWRKYs.



Figure S7. Prediction of cis-regulatory elements in the promoter regions of DolWRKY gene family.

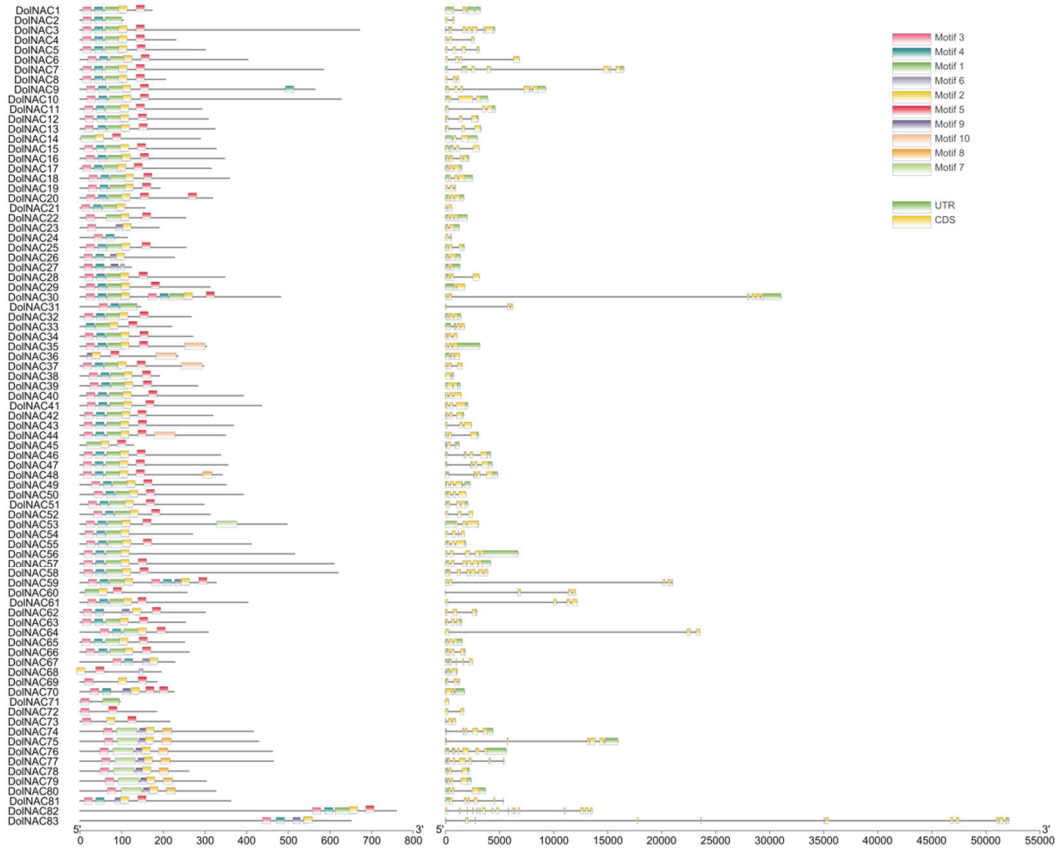


Figure S8. Conserved motifs and gene structure of DolNACs.

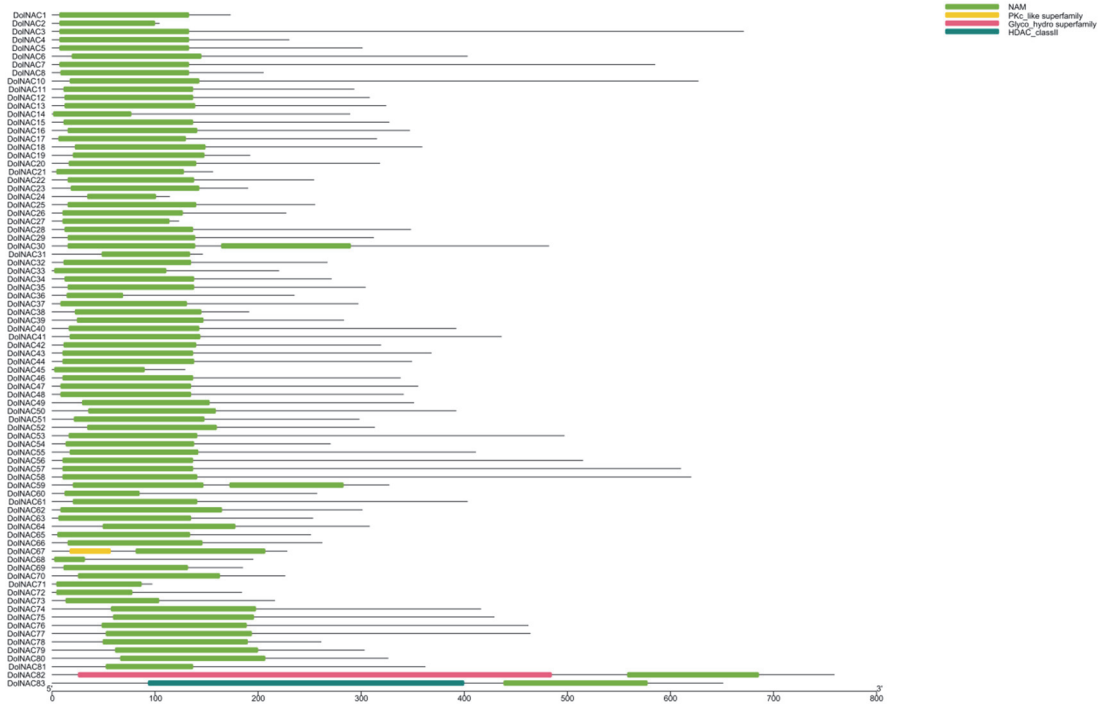


Figure S9. Conserved domains of DolNACs.

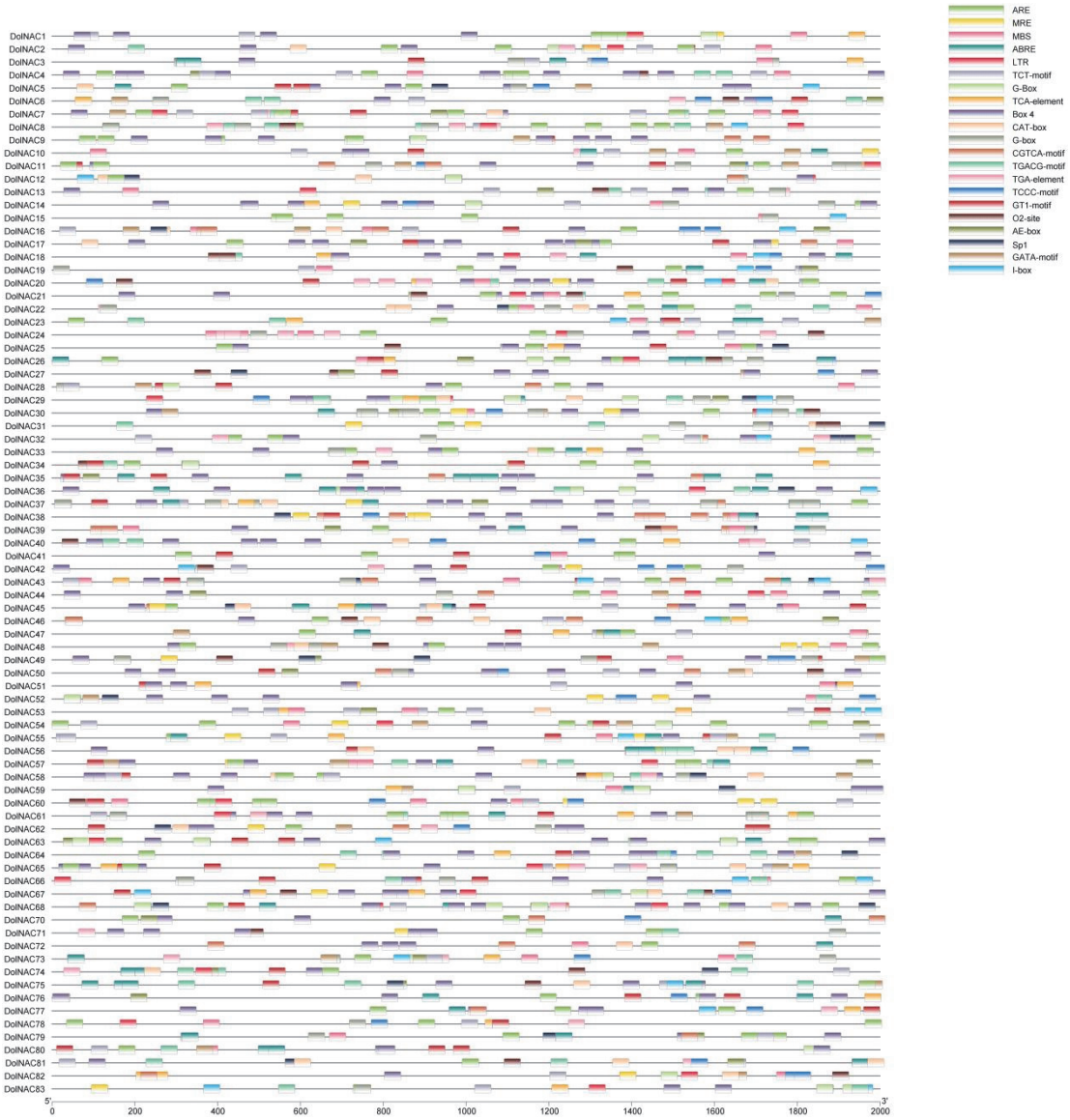


Figure S10. Prediction of cis-regulatory elements in the promoter regions of DolNAC gene family.

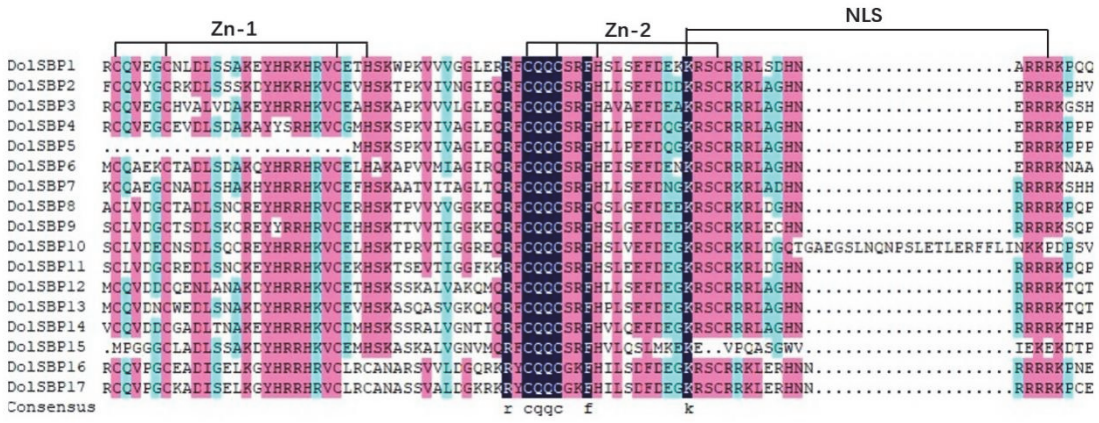


Figure S11. Multiple sequence alignment of DolSBPs.

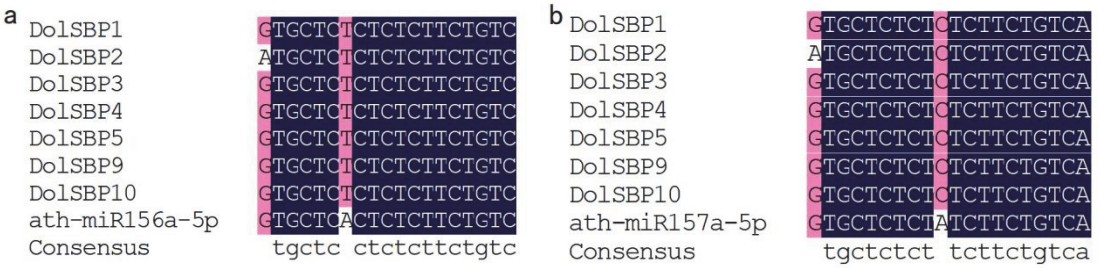


Figure S12. Sequence alignment of miR156 and miR157 with their complementary sequences of DolSBPs.

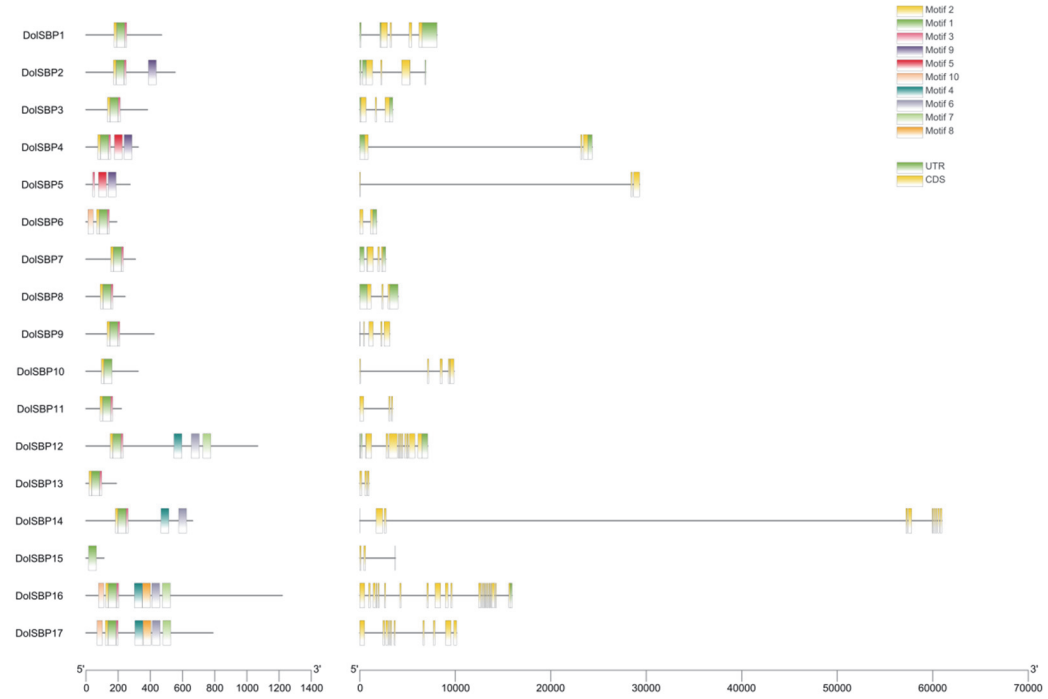


Figure S13. Conserved motifs and gene structure of DolSBPs.

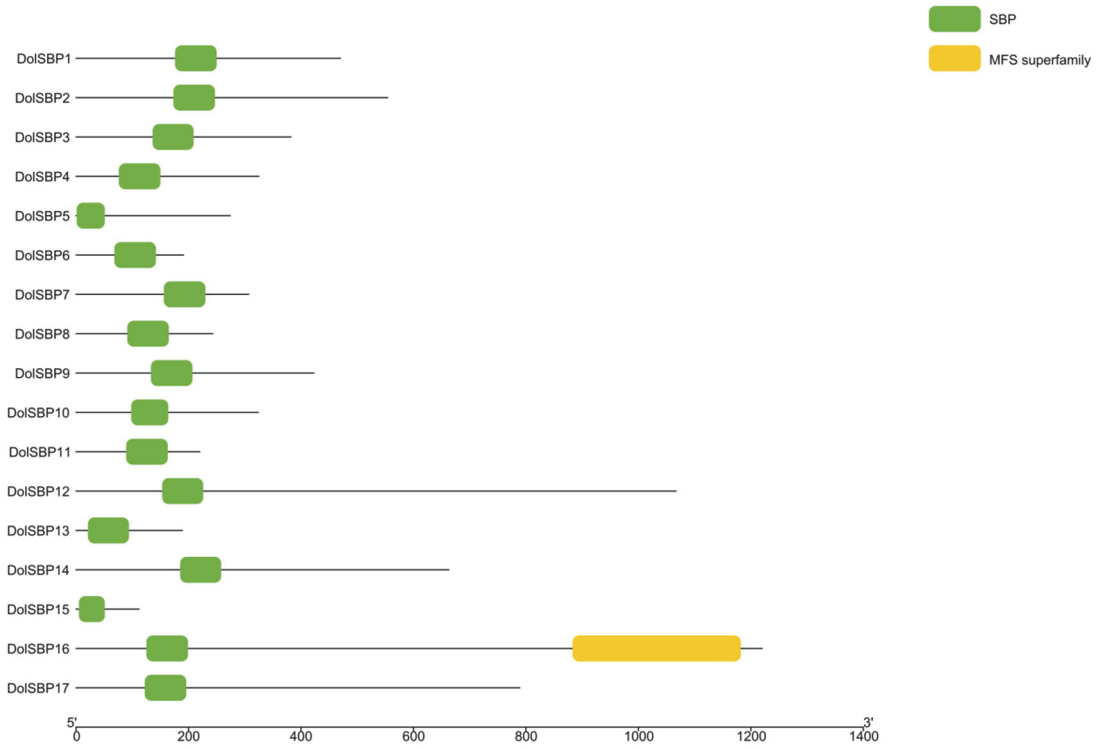


Figure S14. Conserved domains of DolSBPs.

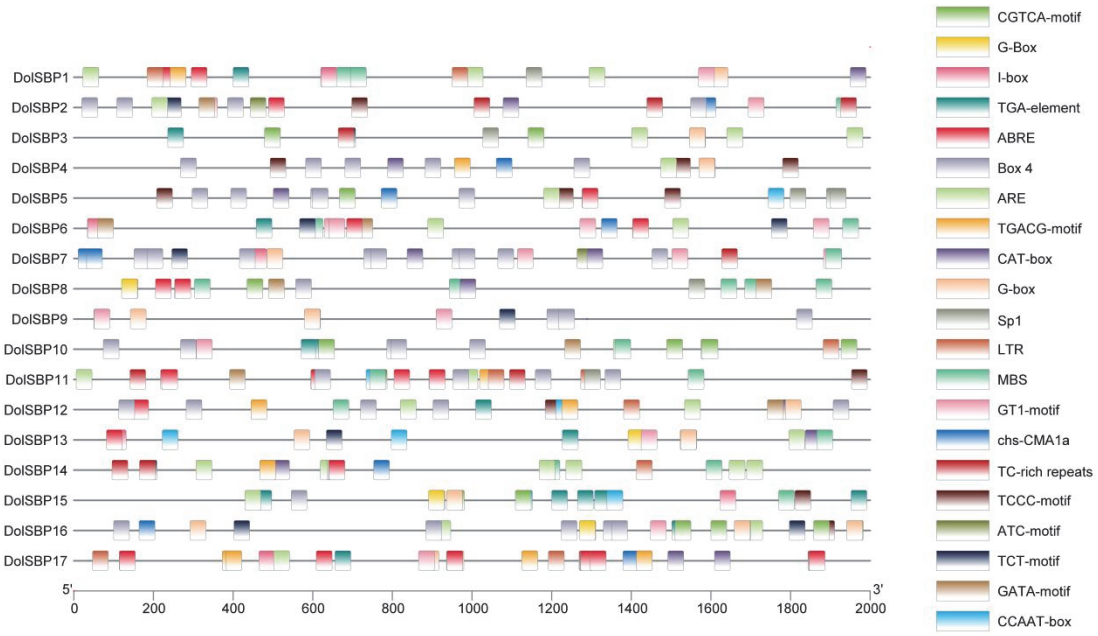


Figure S15. Prediction of cis-regulatory elements in the promoter regions of DolSBP gene family.

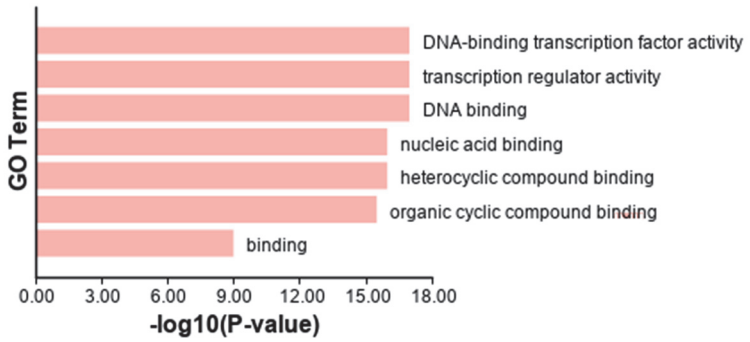


Figure S16. Gene ontology (GO) enrichment analysis of DolMADSs, DolWRKYs, DolNACs, and DolSBPs. The *x*-axis was $\log_{10}$ (*p-value*), and the *y*-axis was the GO term.