



Fig. S 3 HY5 sequence homogeneity. (a) Amino acid sequence alignment of HY5 in *Arabidopsis thaliana* (AthHY5) and that in *Pogostemon cablin* (PathHY5). (b) Representative structures in PDB of transcription factor HY5 from *Arabidopsis thaliana*. (c) Mosel building of transcription factor HY5 from *Pogostemon cablin* base on AlphaFold DB model of HY5_SOLLG (gene: *HY5*, organism: *Solanum lycopersicum*) using SWISS-MODEL tool. GMQE 0.69; Seq Identity 83.97%; Coverage 0.99; the darker the blue, the higher the confidence; the darker the orange, the lower the confidence. (d) PathHY5 Phylogenetic tree. Animo acid sequence of PathHY5 is aligned with that of common medicinal plants and model plants using maximum likelihood method. (e) Functional motifs analysis. The kpLogo output consists of two distinct panels: the upper panel illustrates the $-\log_{10}(P)$ values for each amino acid at specific positions, indicating their statistical significance, while the lower panel displays the amino acid composition, with size and color denoting their frequency across the analyzed sequences.