

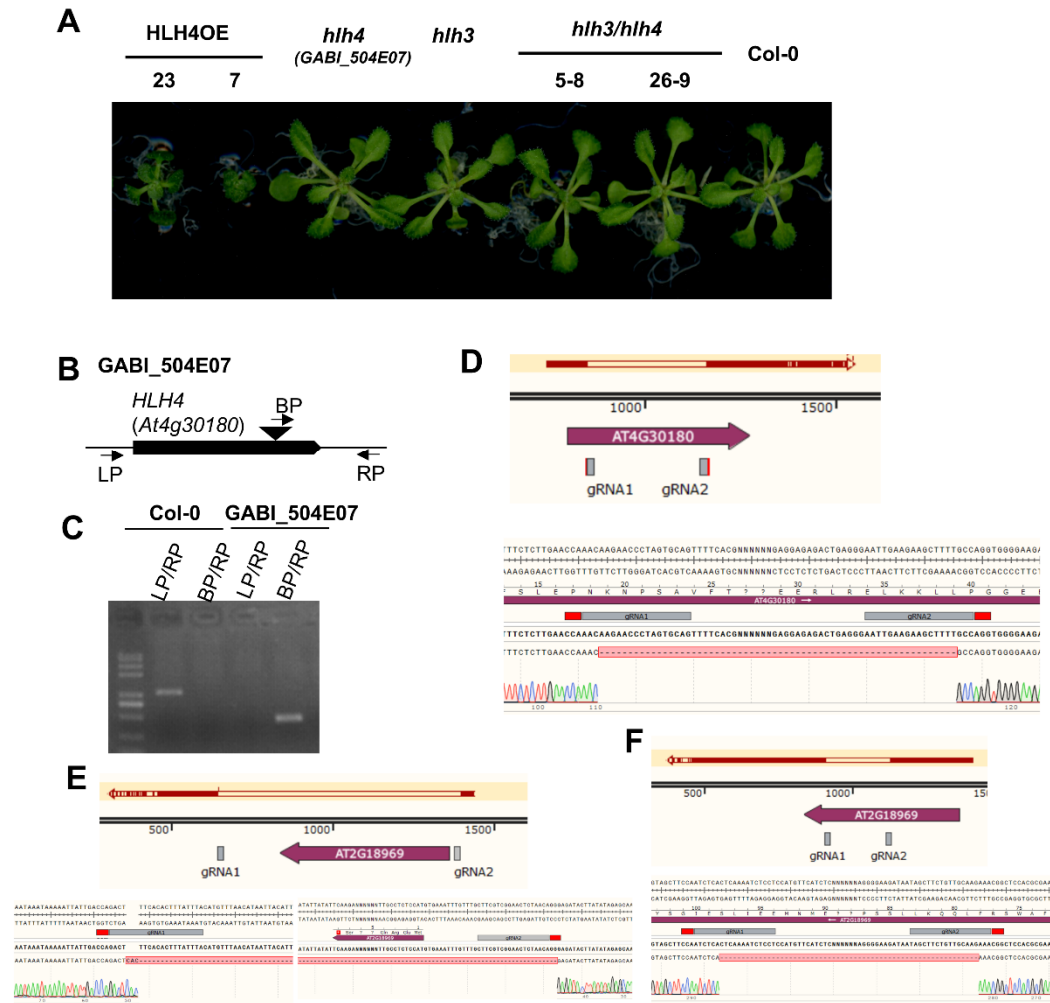


Figure S1. Phenotyping and genotyping the *hlh4*, *hlh3*, *hlh3/hlh4*. **(A)** Phenotypes of 3-week HLH4 overexpression -23 and -7, *hlh4*, *hlh3*, *hlh3/hlh4* and wildtype plants grown on $\frac{1}{2}$ MS medium. **(B)** Schematic representation of the *hlh4* mutant (GABI_504E07). **(C)** Genotyping of the *hlh4* mutant. **(D)** Sequencing analysis of the *HLH4* locus of the *hlh4* mutant generated by CRISPR/Cas9. **(E)** Sequencing analysis of the *hlh3* mutant generated by CRISPR/Cas9. **(F)** Sequencing analysis of the *HLH3* locus of *hlh3/hlh4* mutant generated by CRISPR/Cas9. This *hlh3* mutation cross with *hlh4* mutant (GABI_504E07) results in the *hlh3/hlh4* mutant (5-8) and cross with *hlh4* mutant shown in D results in the *hlh3/hlh4* mutant (26-9) .

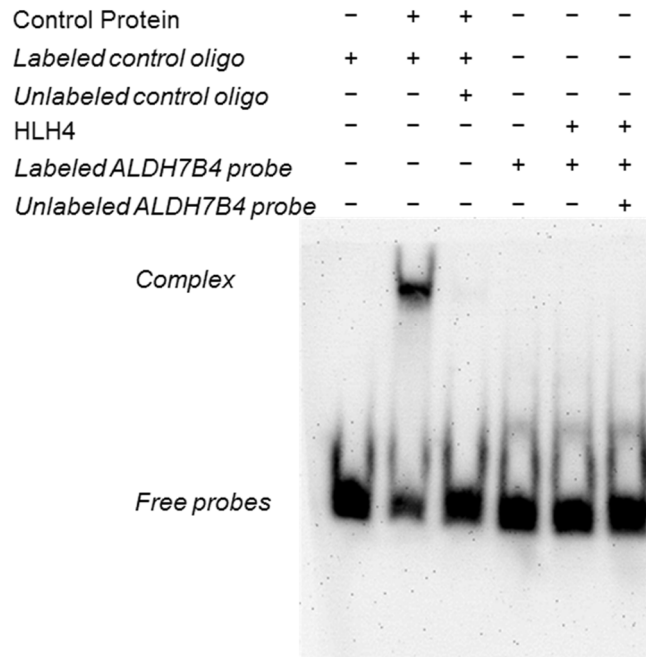


Figure S2. EMSA showing HLH4 dose not bind a G-box containing *ALDH7B4* promoter probe.

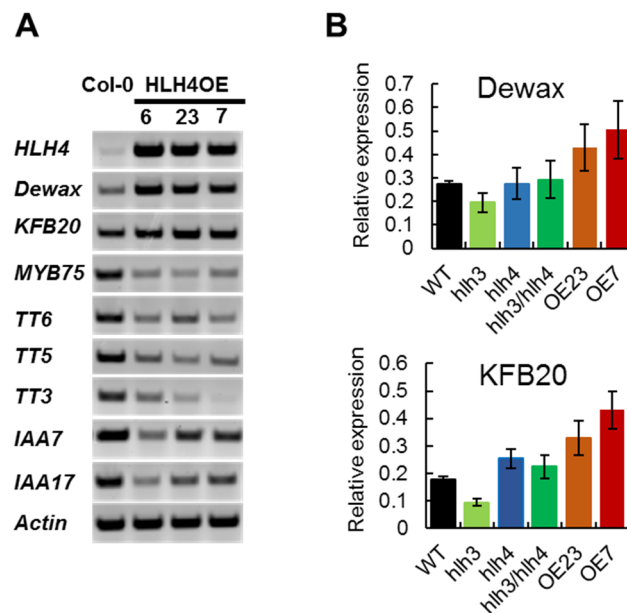


Figure S3. Validation of DEGs identified from RNA_seq by RT-PCR (A) and RT-qPCR (B) analyses.

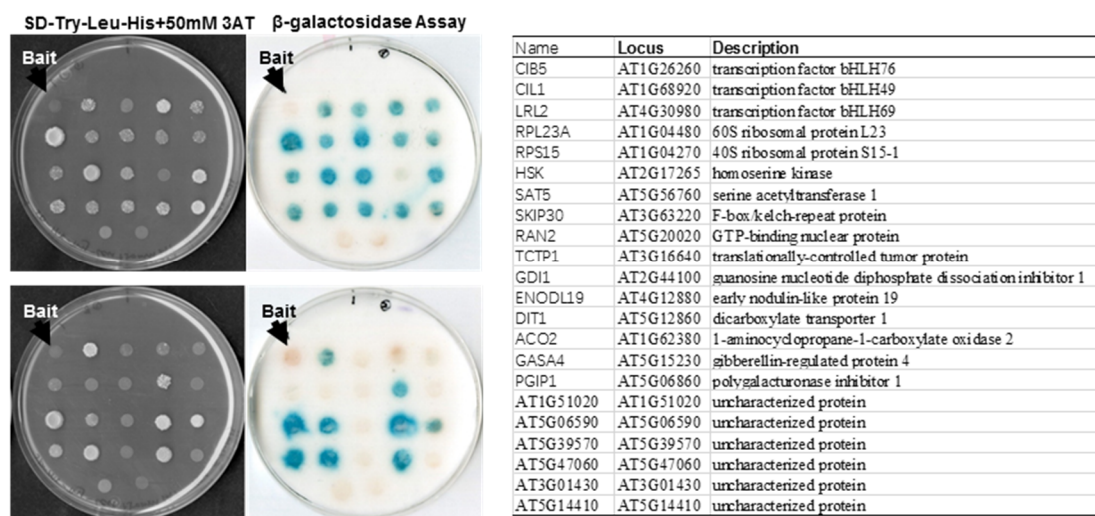


Figure S4. Proteins identified as HLH4 interactors by Y2H library screening.

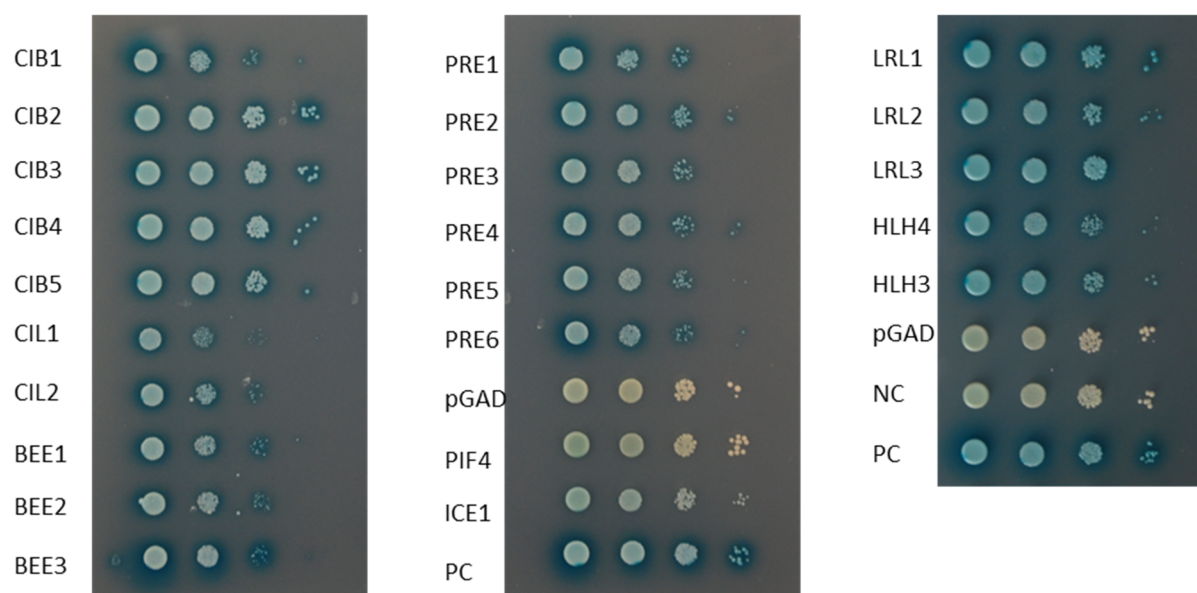


Figure S5. Y2H to show HLH4 interacts with other bHLH proteins. HLH4 coding sequence was fused with GAL4 BD as bait, while other bHLH proteins were fused with GAL4 AD as preys.

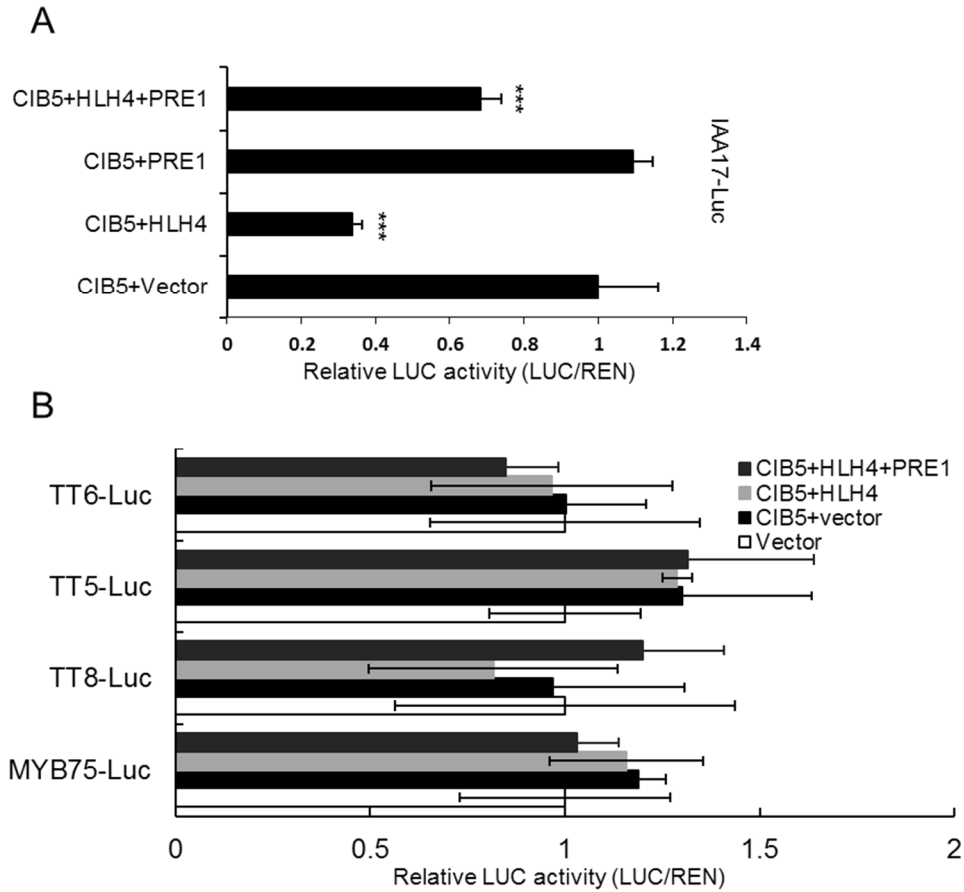


Figure S6. Relative luciferase activities detected in *A.thaliana* protoplasts co-transformed with the plasmids shown in Figure 6A. (A) The LUC reporter was driven by the *IAA17* promoter. (B) The LUC reporter was driven by *TT5*, *TT6*, *TT8* and *MYB75* promoters. Data represent mean $\pm$ SD of three biological replicates with three technical replicates ($n = 9$). Asterisks indicate significant differences (** $p < 0.001$).