

Figure 1 AP2/ERF transcription factor comparisons among different species. Different colors represent each family domain in the AP2/ERF superfamily. The colored sections represent the number of transcription factor domains identified in a species. Gray represents the absence of a domain.

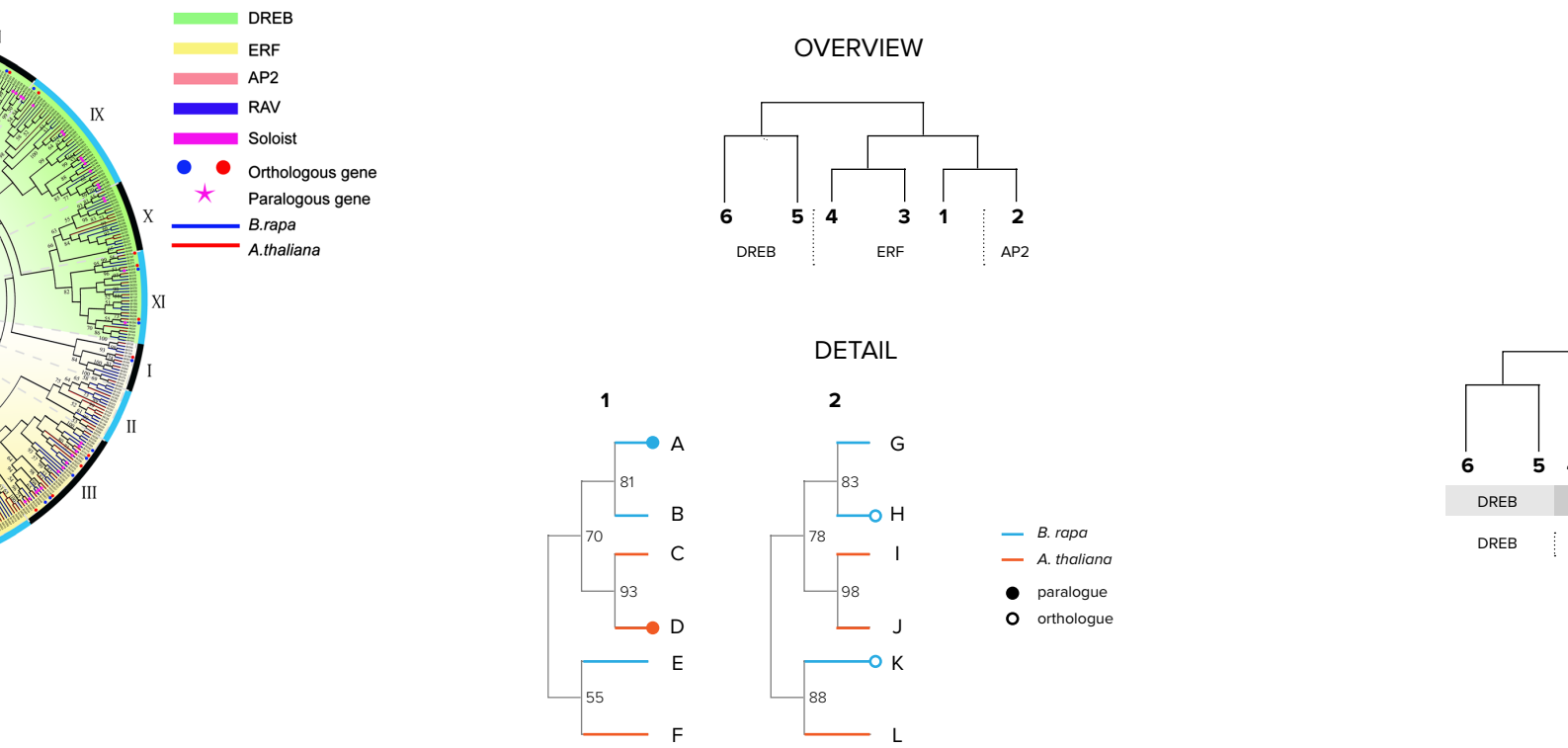


Figure 2 Phylogenetic tree constructed from the neighbor-joining method using AP2/ERF transcription factor domains in Chinese cabbage and Arabidopsis. The tree was divided into 15 groups, which contained ERF (DREB and ERF subfamily), AP2, RAV and Soloist family. The pentagram represents paralogous genes of Chinese cabbage. Circles represent orthologous genes from Chinese cabbage (blue) and Arabidopsis (red). The phylogenetic tree was constructed using MEGA5. The numbers are bootstrap values based on 1000 iterations. Only bootstrap values larger than 50% support are indicated.