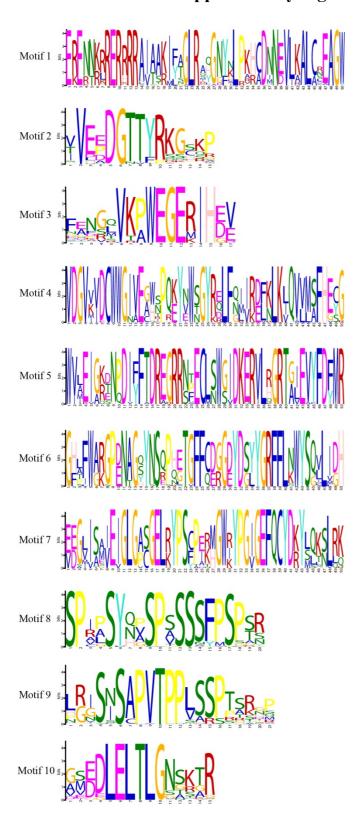
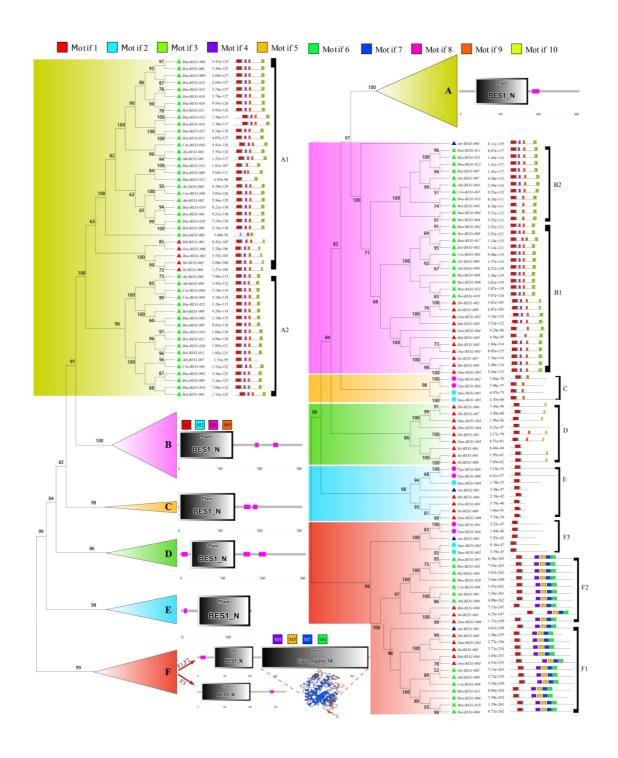
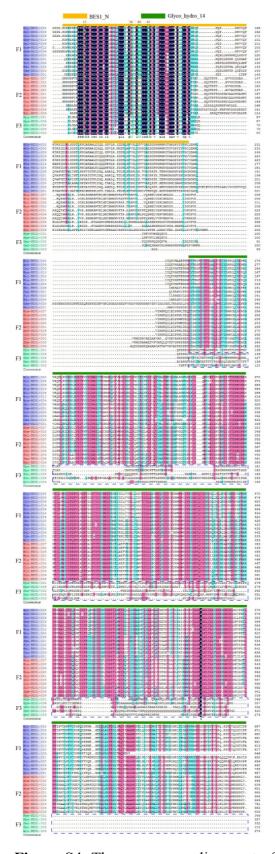
## **Supplementary Figure S2-S15**



**Figure S2.** The sequences of motif 1 to motif 10 of BES1 gene family among examined species.



**Figure S3.** The conversed motifs (M1 to M10) analyses for each group using the MEME program.



**Figure S4.** The sequences alignment of F1, F2, and F3 subgroups among examined species. The Glyco\_hydro\_14 domain contained in F1 and F2 subgroups is marked using the blue dashed box in F3 subgroup.

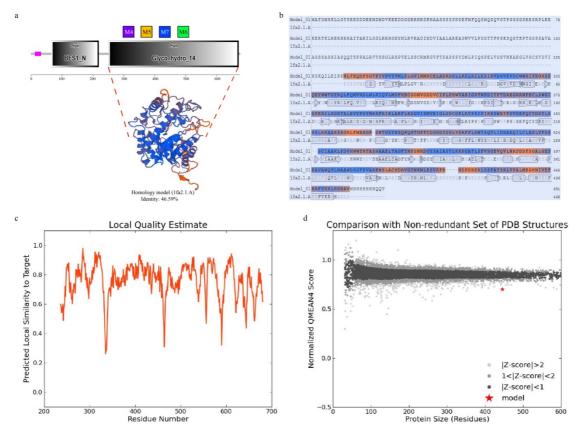


Figure S5. The analyses of Glyco\_hydro\_14 domain, including (a) protein structure, (b) alignment with the homology model (1fa2.1.A), (c) prediction of local similarity to target, (d) comparison with non-redundant set of PDB structures.

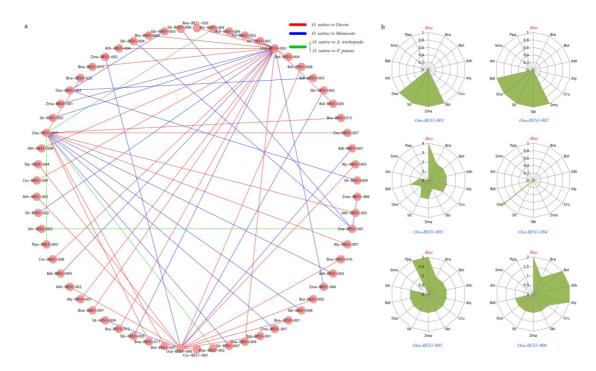
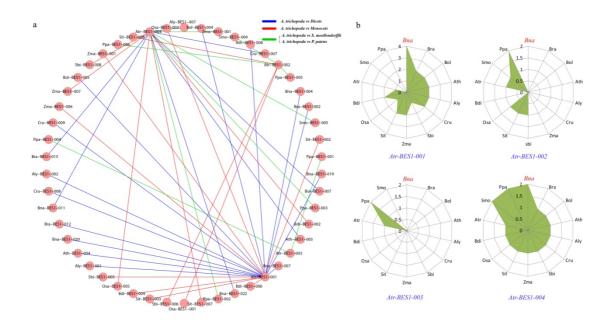
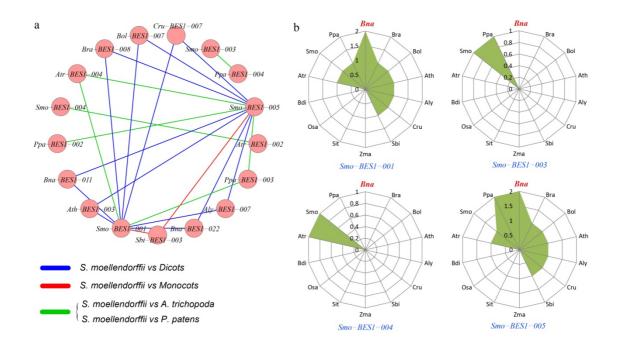


Figure S6. The analyses of orthologous *BES1* genes between *O. sativa* and other examined species. (a) The interaction network constructed using the orthologous gene pairs between *O. sativa* and other species. (b) The number of orthologous genes in each species with 6 *O. sativa BES1* genes.



**Figure S7.** The analyses of orthologous *BES1* genes between *A. trichopoda* and other examined species. (a) The interaction network constructed using the orthologous gene pairs between *A. trichopoda* and other species. (b) The number of orthologous genes in each species with 4 *A. trichopoda BES1* genes.



**Figure S8.** The analyses of orthologous *BES1* genes between *S. moellendorffii* and other examined species. (a) The interaction network constructed using the orthologous gene pairs between *S. moellendorffii* and other species. (b) The number of orthologous genes in each species with 4 *S. moellendorffii BES1* genes.

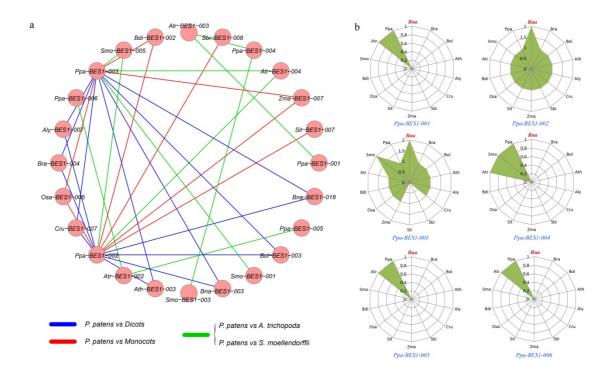
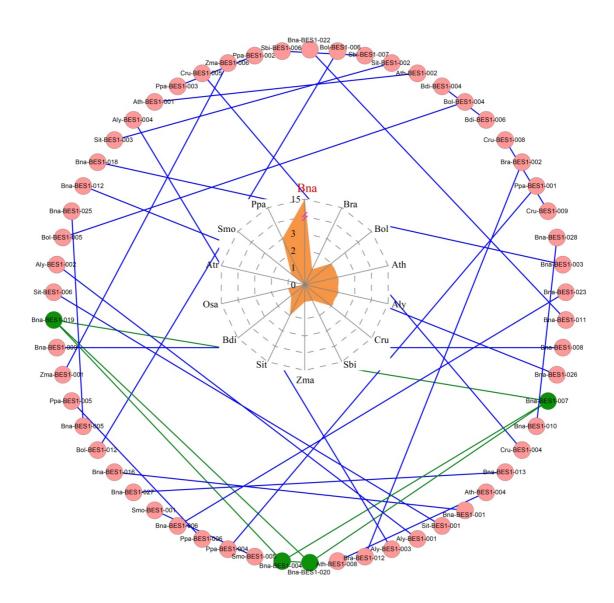
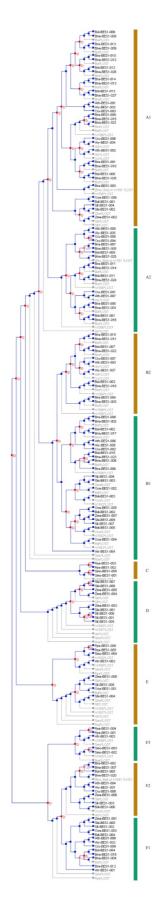


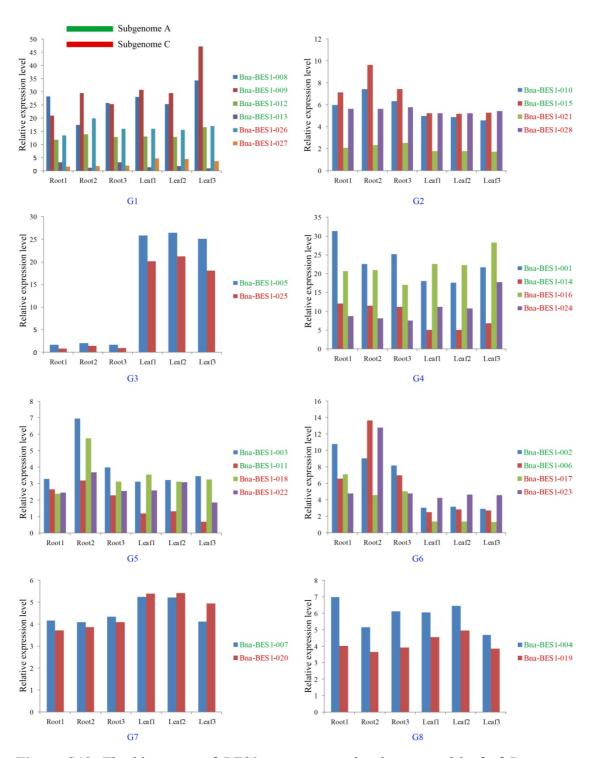
Figure S9. The analyses of orthologous *BES1* genes between *P. patens* and other examined species. (a) The interaction network constructed using the orthologous gene pairs between *P. patens* and other species. (b) The number of orthologous genes in each species with 6 *P. patens BES1* genes.



**Figure S10.** The analyses of paralogous *BES1* genes in each of the examined species. The green lines indicated the 4 *B. napus BES1* genes, which had more than 1 paralogous genes.



**Figure S11.** The reconstructed phylogenetic tree according to the duplication and losses of *BES1* genes at different stages of plant evolution.



**Figure S12.** The histogram of *BES1* genes expression in root and leaf of *B. napus*. The genes marked with green located subgenome A, and red located subgenome C of *B. napus*.