

Supplementary Figure S2-S15

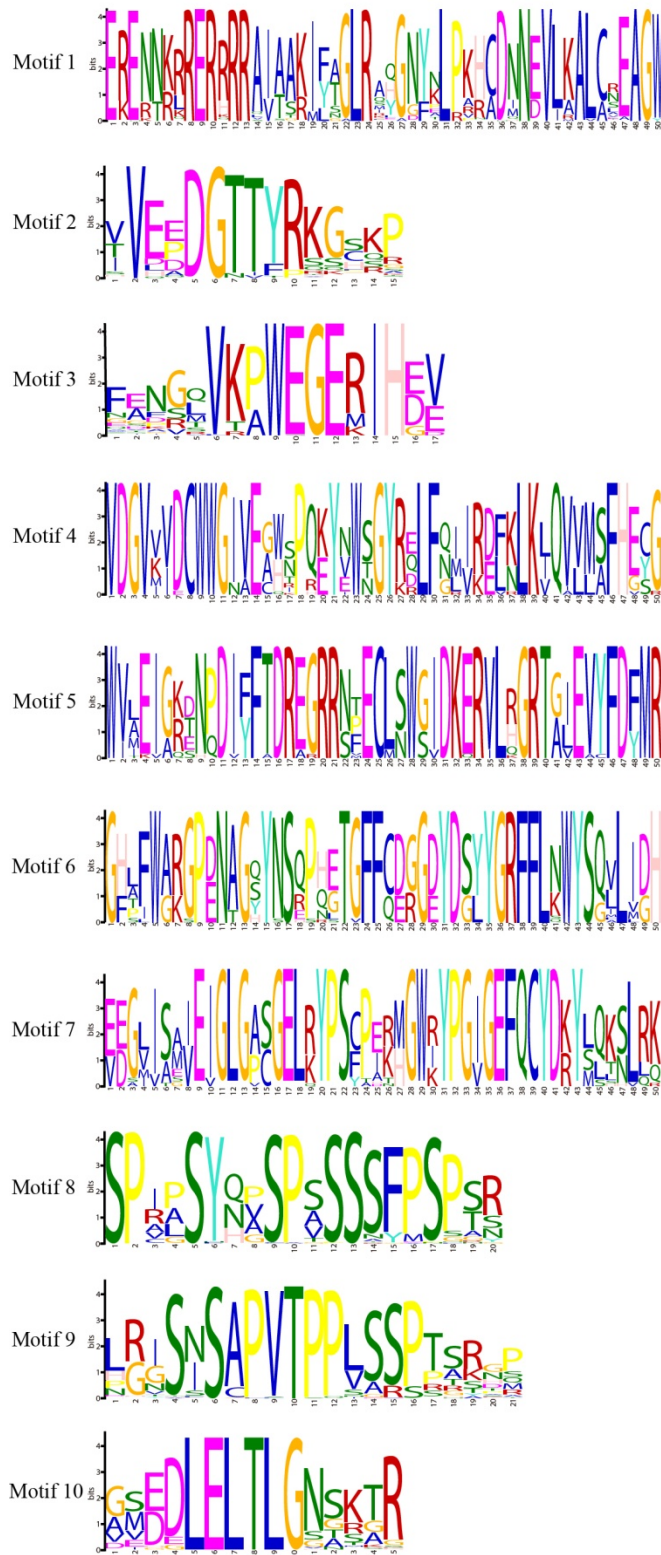


Figure S2. The sequences of motif 1 to motif 10 of BES1 gene family among examined species.

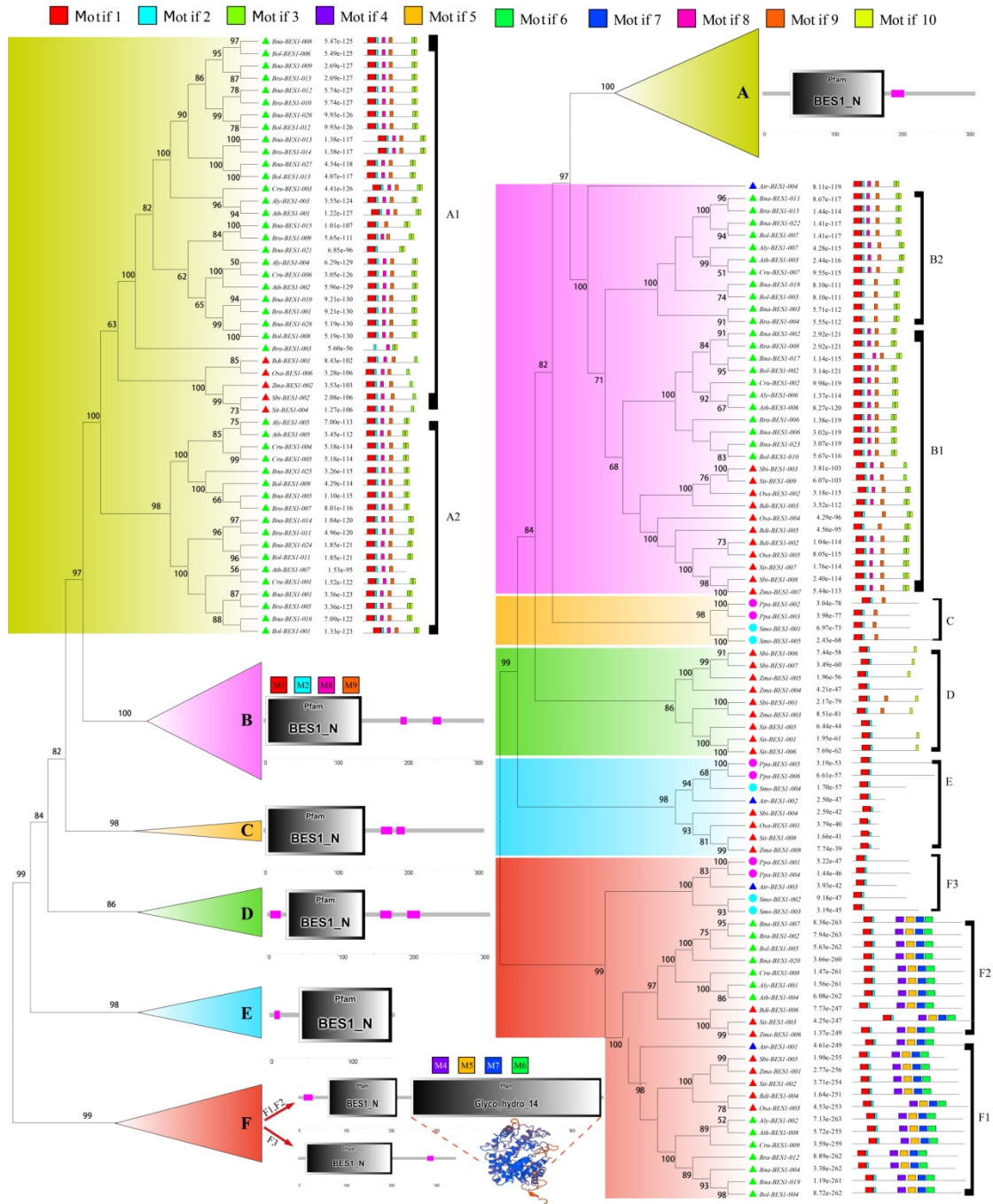


Figure S3. The converted motifs (M1 to M10) analyses for each group using the MEME program.

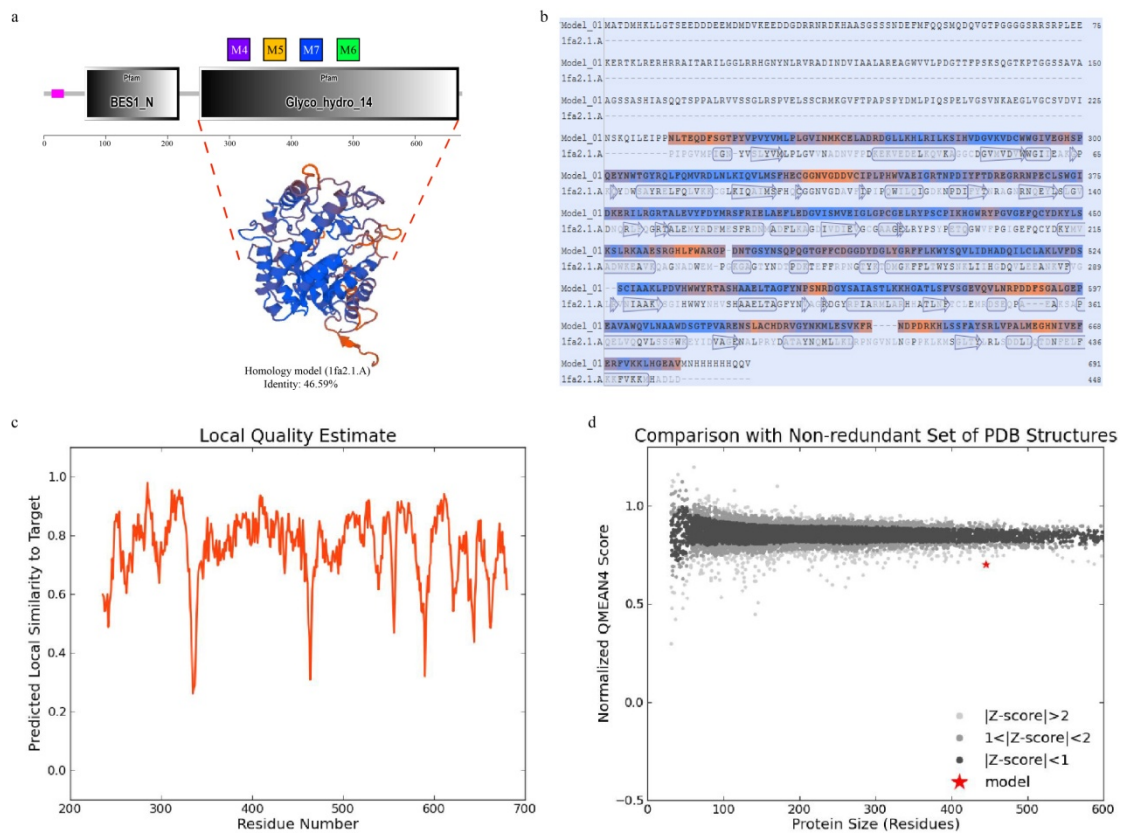


Figure S5. The analyses of Glyco_hydro_14 domain, including (a) protein structure, (b) alignment with the homology model (1fa2.1.A), (c) prediction of local similarity to target, (d) comparison with non-redundant set of PDB structures.

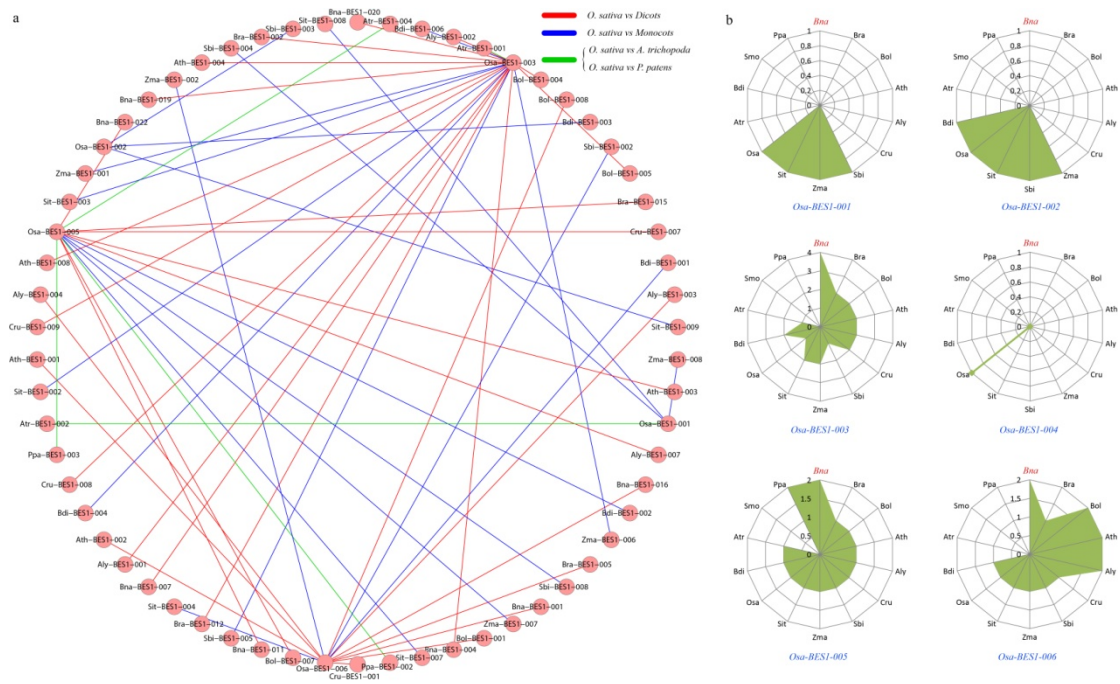


Figure S6. The analyses of orthologous *BES1* genes between *O. sativa* and other examined species. (a) The interaction network constructed using the orthologous gene pairs between *O. sativa* and other species. (b) The number of orthologous genes in each species with 6 *O. sativa* *BES1* genes.

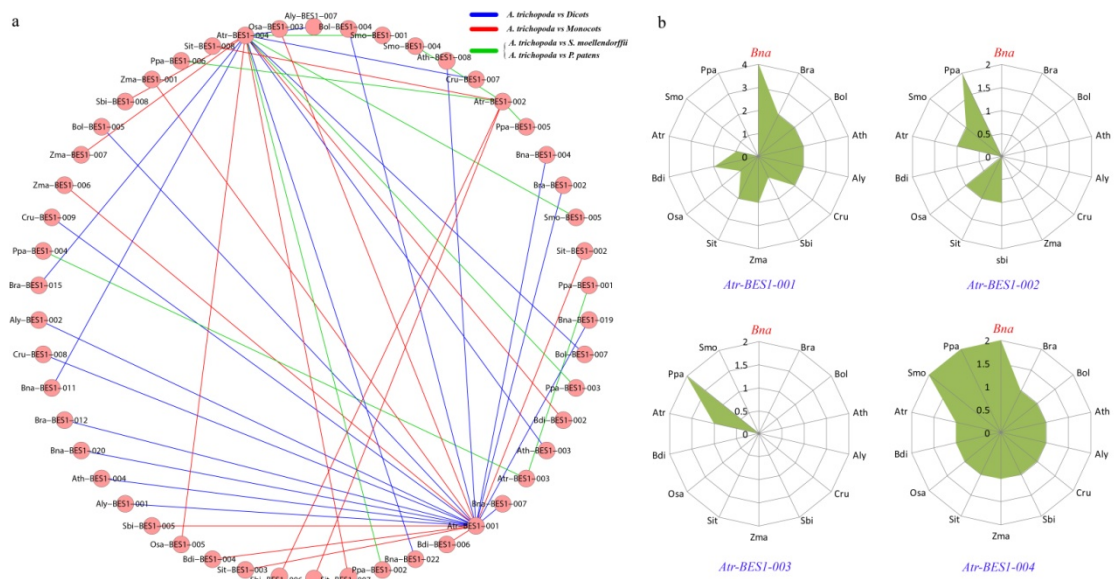


Figure S7. The analyses of orthologous *BES1* genes between *A. trichopoda* and other examined species. (a) The interaction network constructed using the orthologous gene pairs between *A. trichopoda* and other species. (b) The number of orthologous genes in each species with 4 *A. trichopoda* *BES1*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

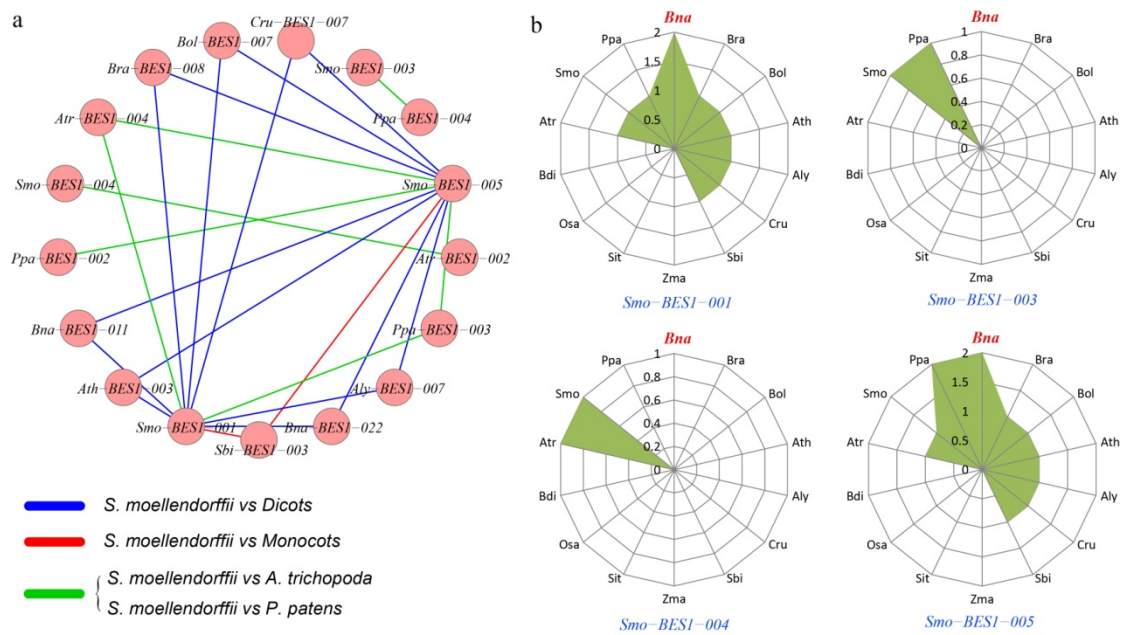


Figure S8. The analyses of orthologous *BES1* genes between *S. moellendorffii* and other examined species. (a) The interaction network constructed using the orthologous gene pairs between *S. moellendorffii* and other species. (b) The number of orthologous genes in each species with 4 *S. moellendorffii*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

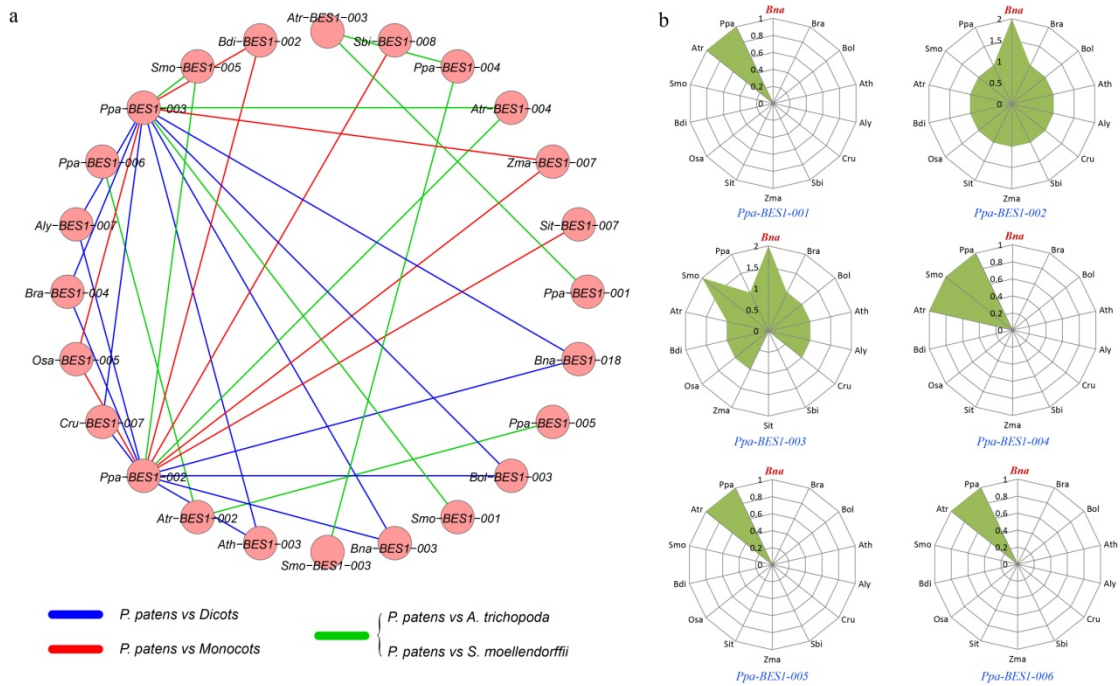


Figure S9. The analyses of orthologous *BES1* genes between *P. patens* and other examined species. **(a)** The interaction network constructed using the orthologous gene pairs between *P. patens* and other species. **(b)** The number of orthologous genes in each species with 6 *P. patens* *BES1* genes.

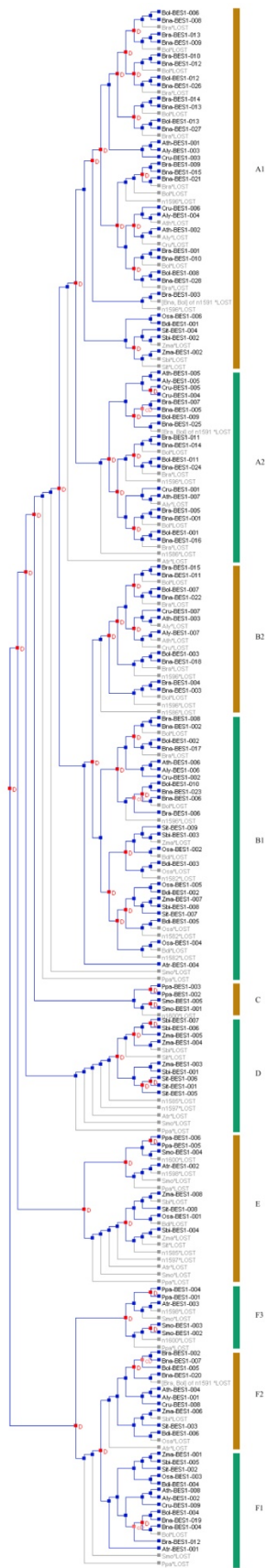


Figure S11. The reconstructed phylogenetic tree according to the duplication and losses of *BES1* genes at different stages of plant evolution.

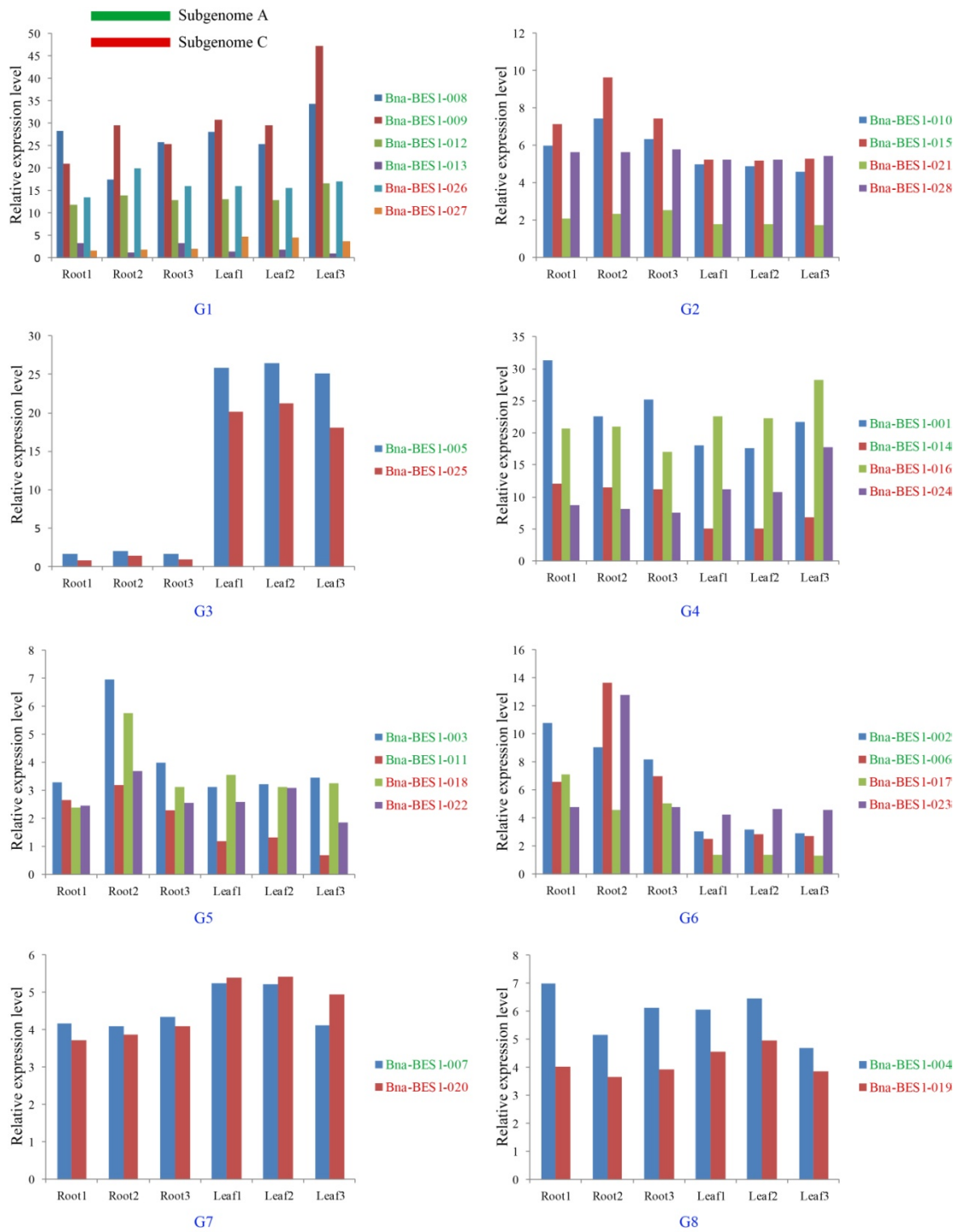


Figure S12. The histogram of *BES1* genes expression in root and leaf of *B. napus*. The genes marked with green located subgenome A, and red located subgenome C of *B. napus*.