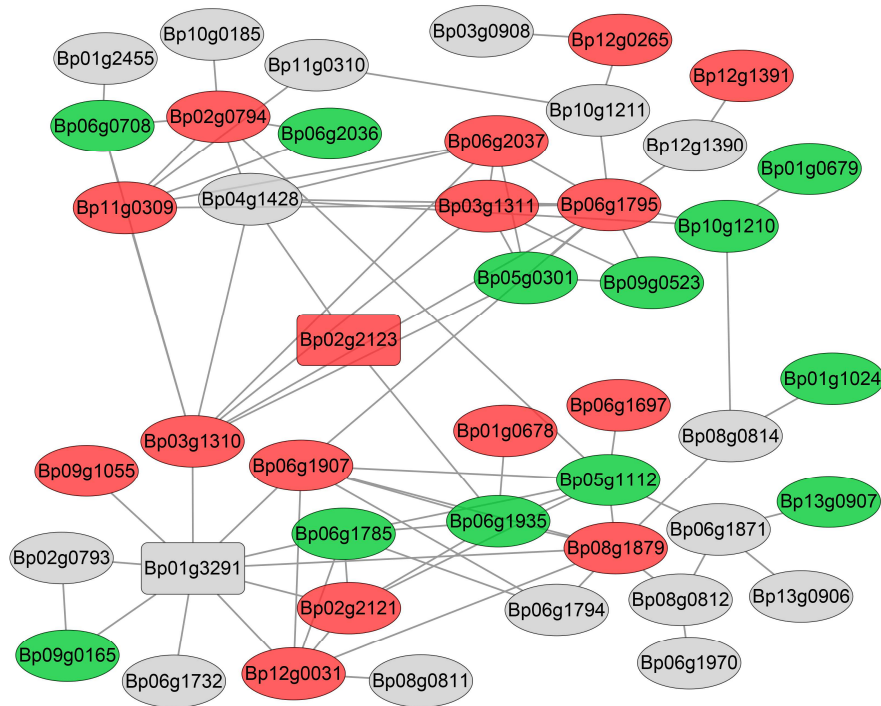
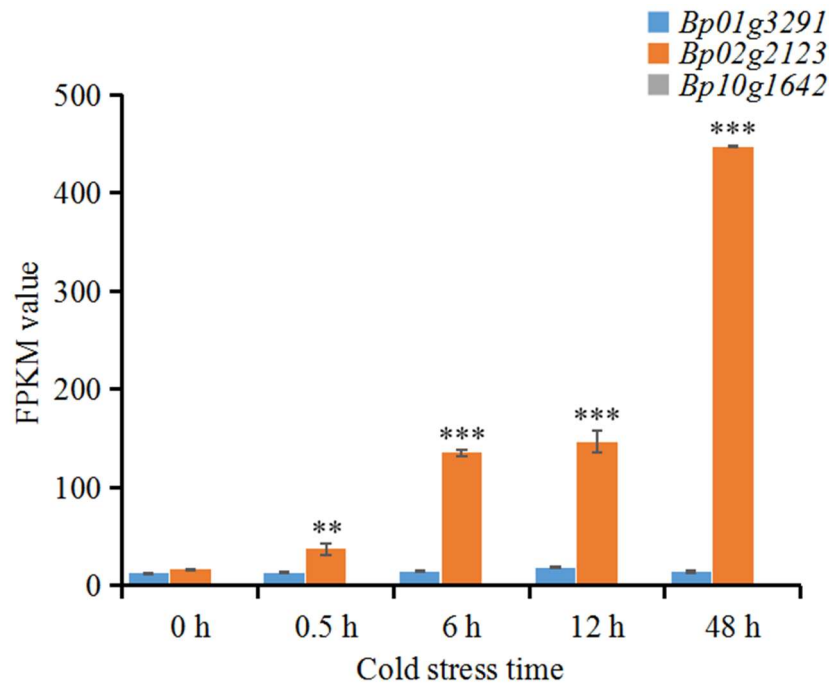


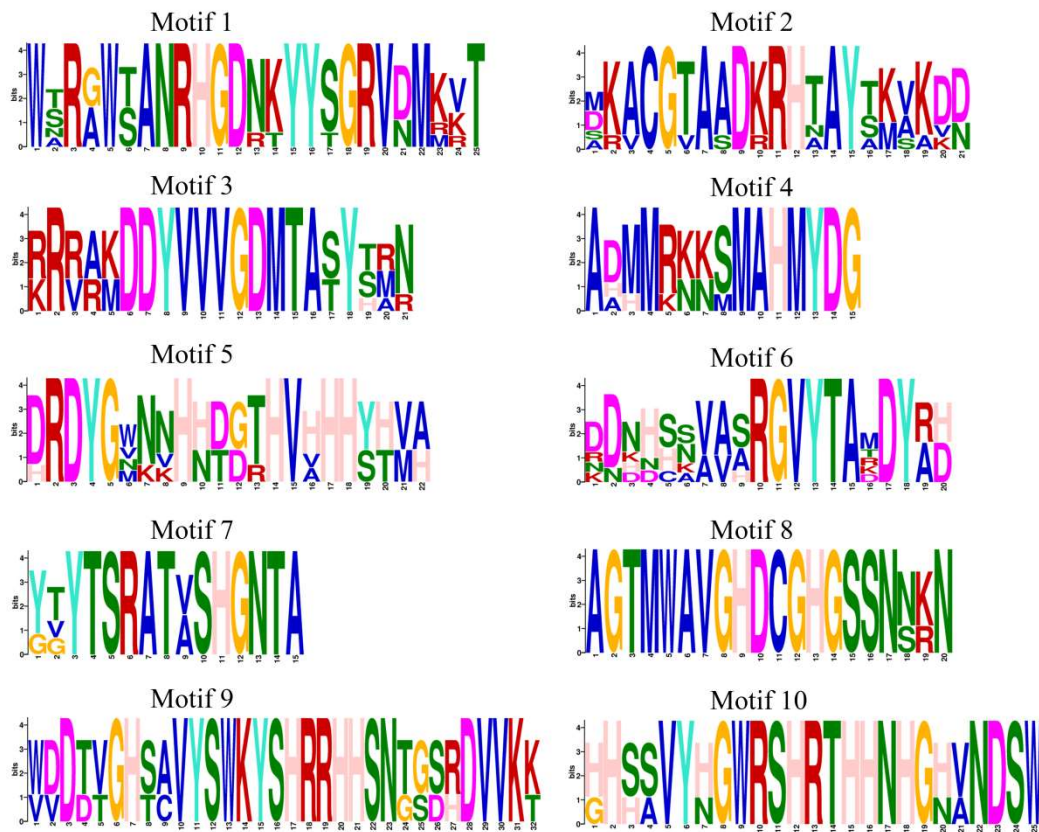
Yanmin Hu, Xianjun Peng and Shihua Shen



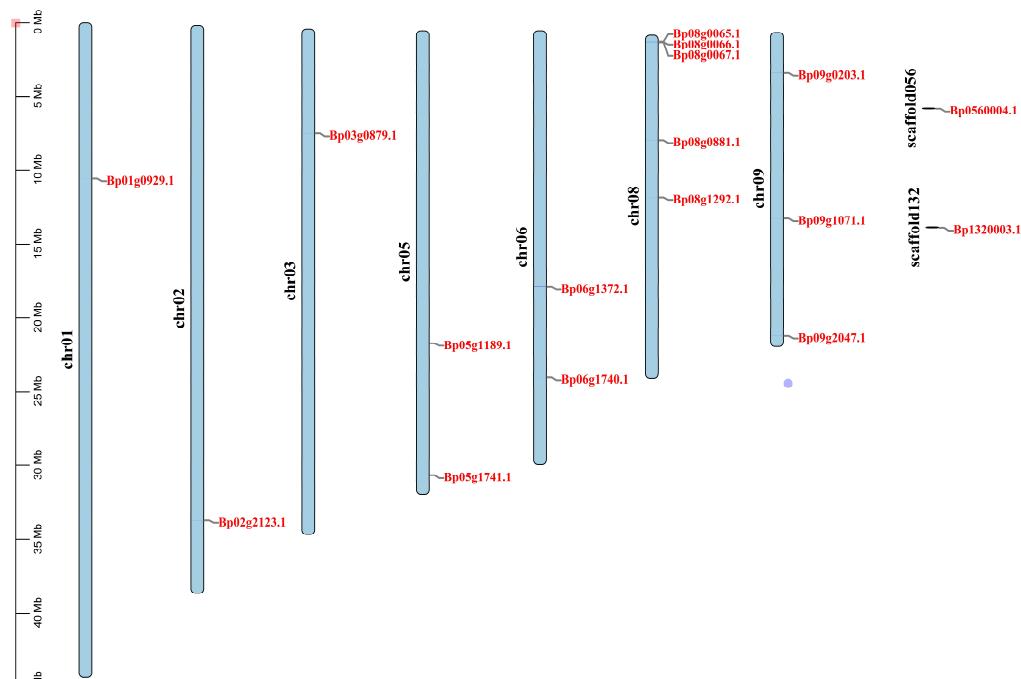
**Figure S3.** Protein-protein interaction analysis of the associated genes identified by GWAS of hundred-seed weight. The read color represents the related genes up-regulated under cold stress, the green color represents the related genes down-regulated under cold stress, and the gray color represents that the expression level of the related genes did not change under cold stress.



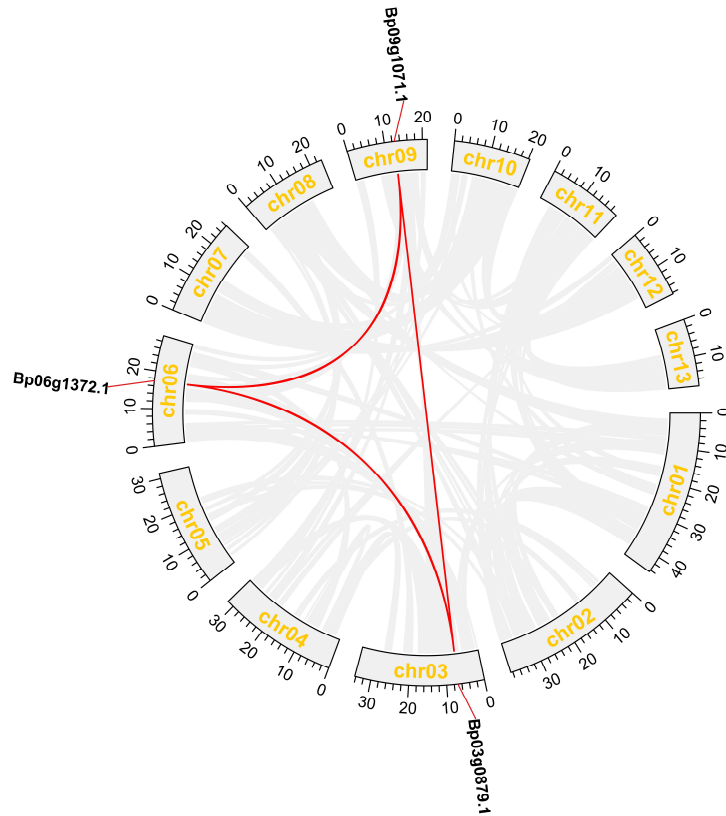
**Figure S4.** Expression patterns of *Bp01g3291*, *Bp02g2123* and *Bp10g1642* in paper mulberry under 4°C treated with different times based on the FPKM values. 0 h, 0.5 h, 6 h, 12 h and 48 h represent 4°C treated with different times. \*\* represents  $p < 0.01$ , \*\*\* represents  $p < 0.001$ .



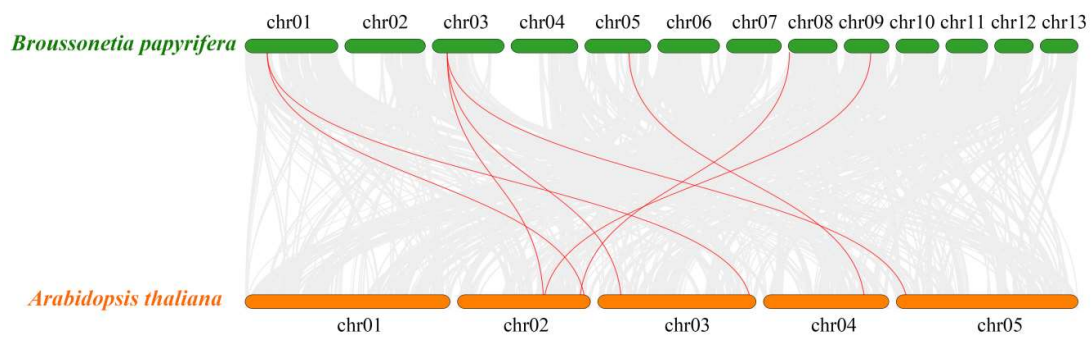
**Figure S5.** The ten conserved motifs of BpFAD proteins in paper mulberry, which were identified through the online analysis tool MEME (version 5.4.1).



**Figure S6.** Chromosomal distribution of FAD genes from paper mulberry. Based on the paper mulberry genome data, the 17 FAD genes were mapped on 7 chromosomes and 2 scaffolds.



**Figure S7.** Duplication analysis of the *FAD* genes in paper mulberry, and the red lines represent the three pairs of duplicated genes.



**Figure S8.** Collinearity analysis of the *FAD* genes in paper mulberry and *Arabidopsis*.