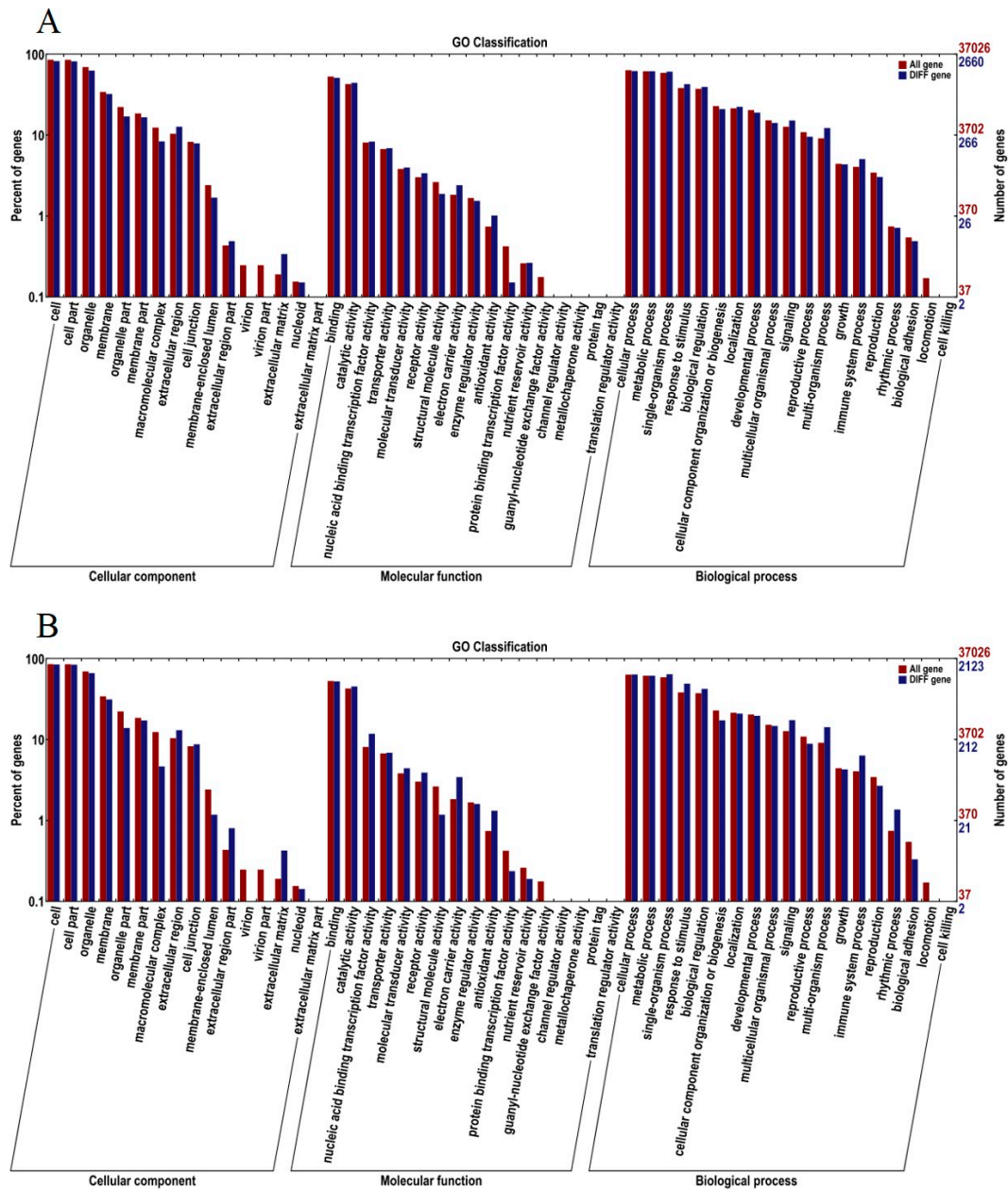
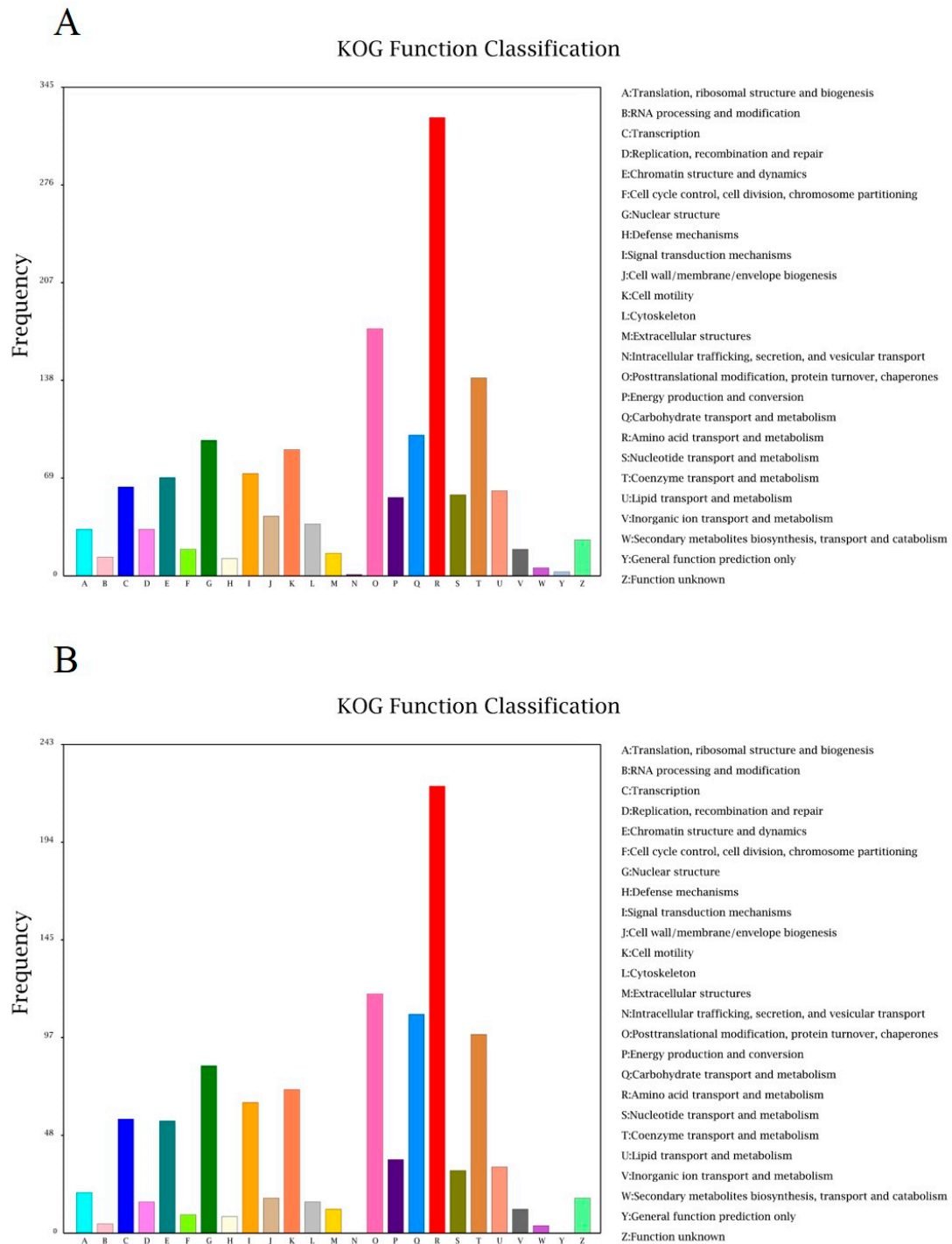


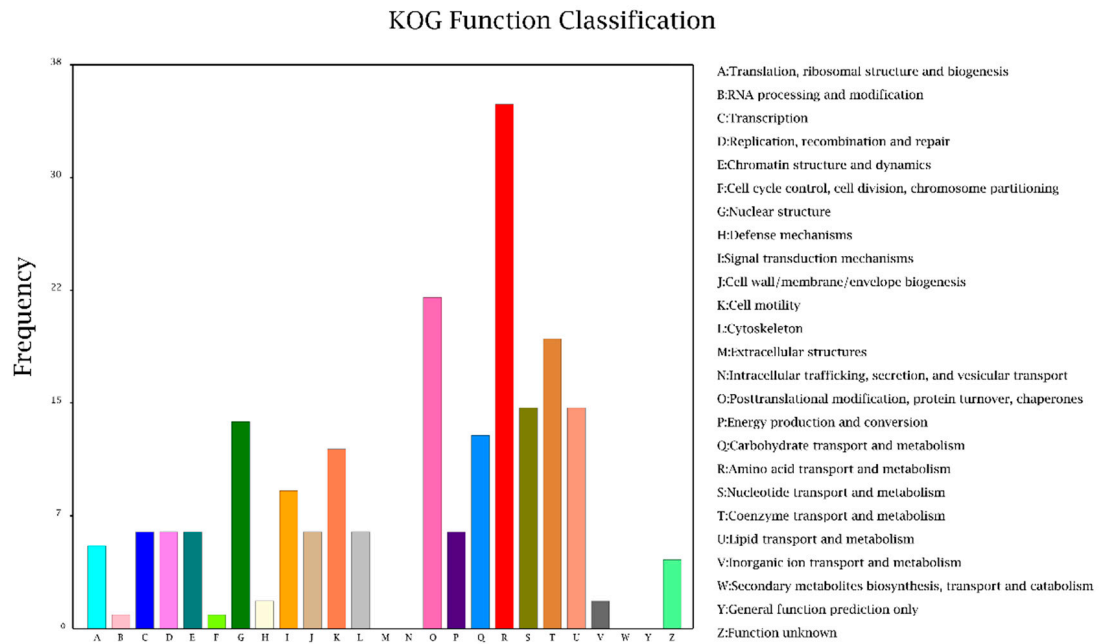
**Figure S1.** KOG function classification analysis of candidate genes identified by the association analysis of BSA-Seq.



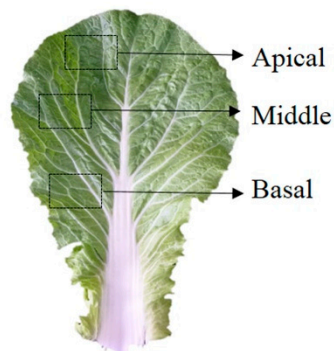
**Figure S2.** Gene Ontology (GO) enrichment analysis of differentially expressed genes (DEGs) between two set pairs of cDNA sequencing bulks of BSR-Seq analysis. All genes and the DEGs were assigned to the three GO categories: biological processes, cell components, and molecular functions. (A) T01 vs. T02. (B) T03 vs. T04.



**Figure S3.** KOG function classification analysis of differentially expression genes (DEGs) between four cDNA sequencing bulks. (A) T01 VS. T02. (B) T03 VS. T04.



**Figure S4.** KOG function classification analysis of candidate genes identified by the association analysis of BSR-Seq.



**Figure S5.** Three sampling locations for mature leaves.