

## Supplementary

### **Comprehensive transcriptome analysis reveals heat-responsive genes in flowering Chinese cabbage (*Brassica campestris* L. ssp. *chinensis*) using RNA sequencing**

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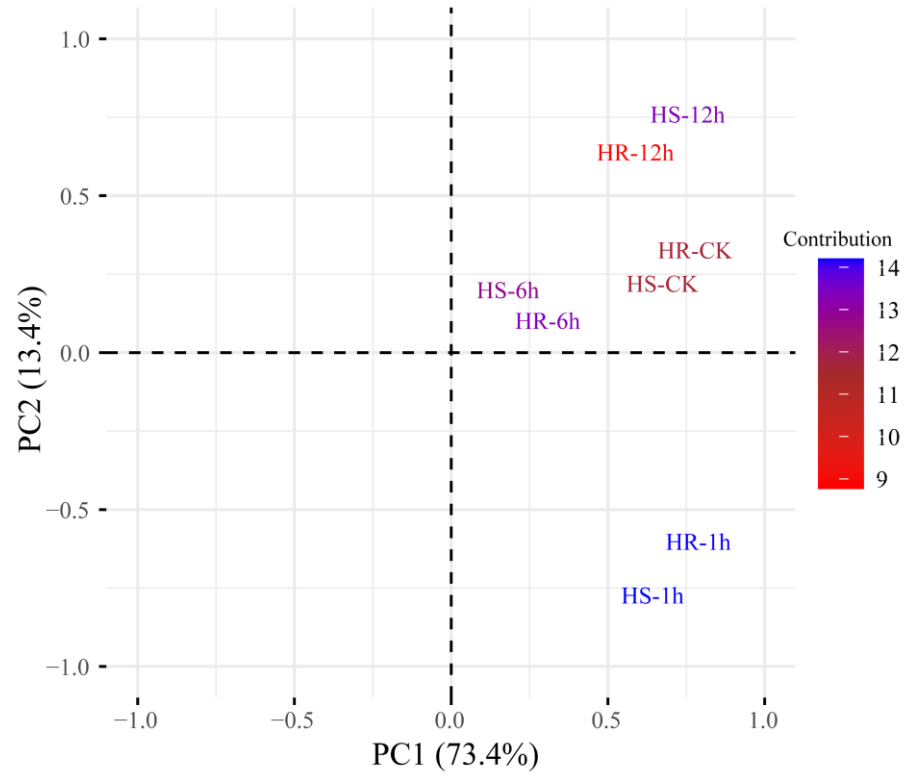
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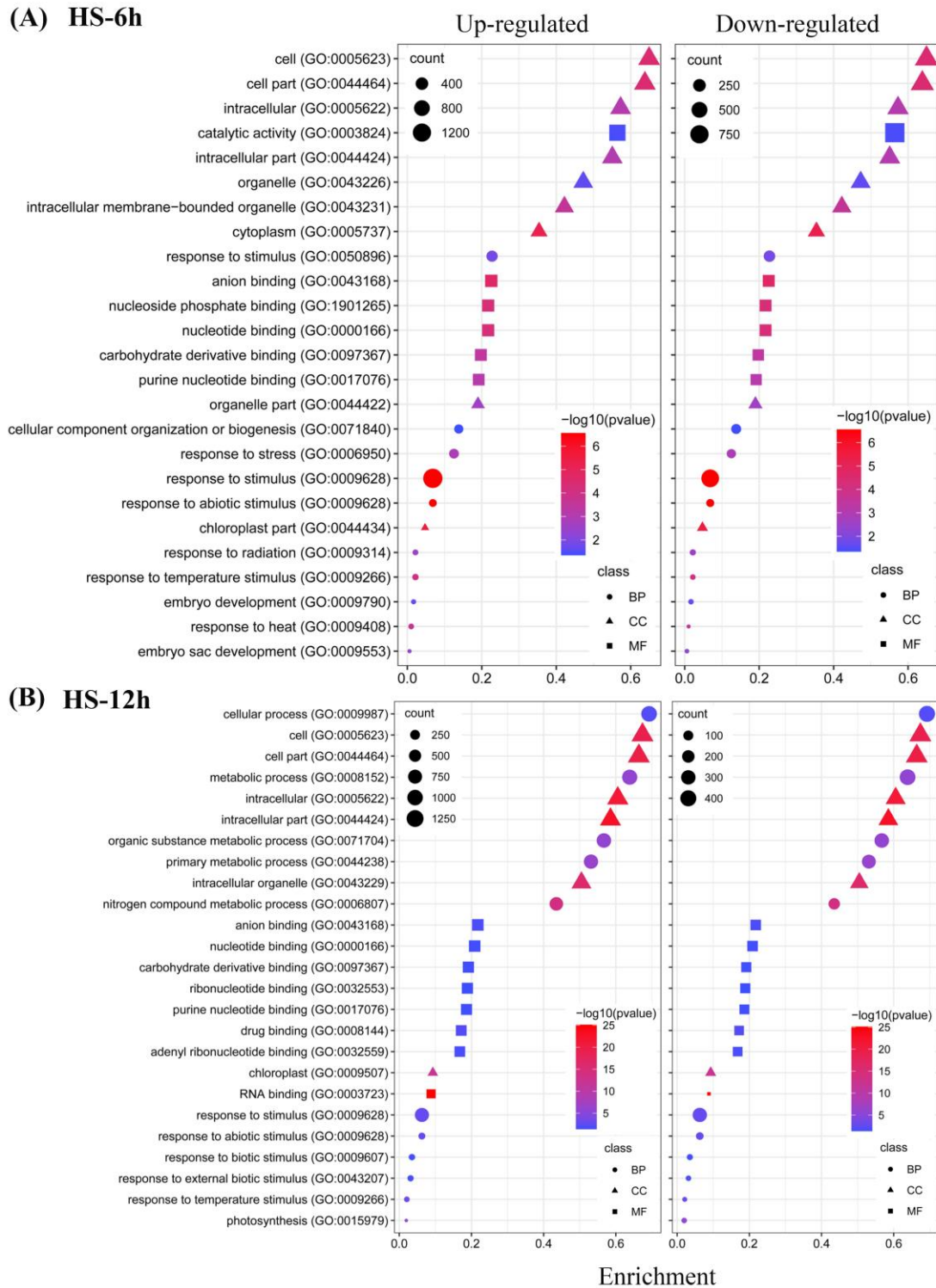
[xiayanshi922@163.com](mailto:xiayanshi922@163.com)

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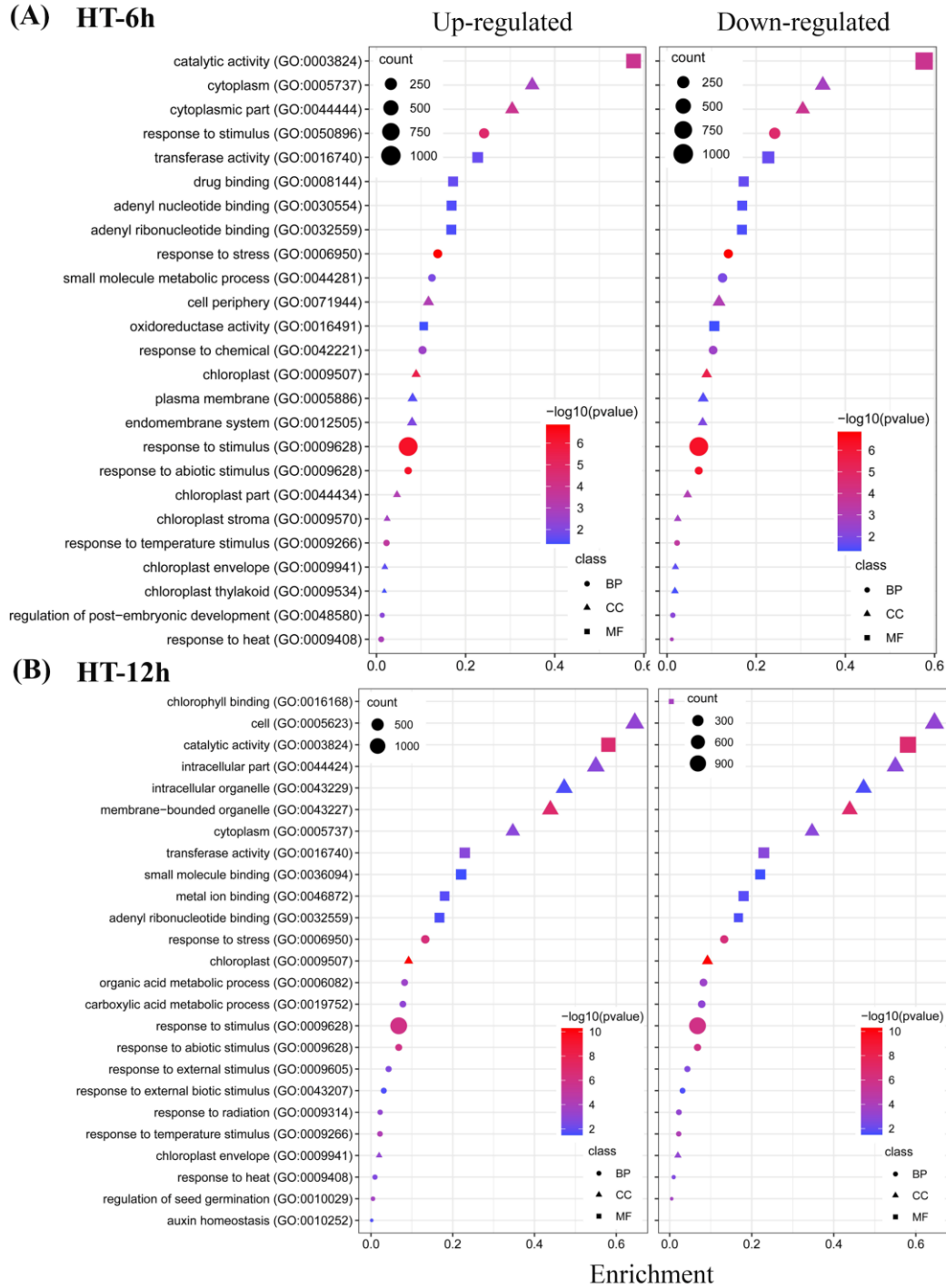
Figures S1-S5



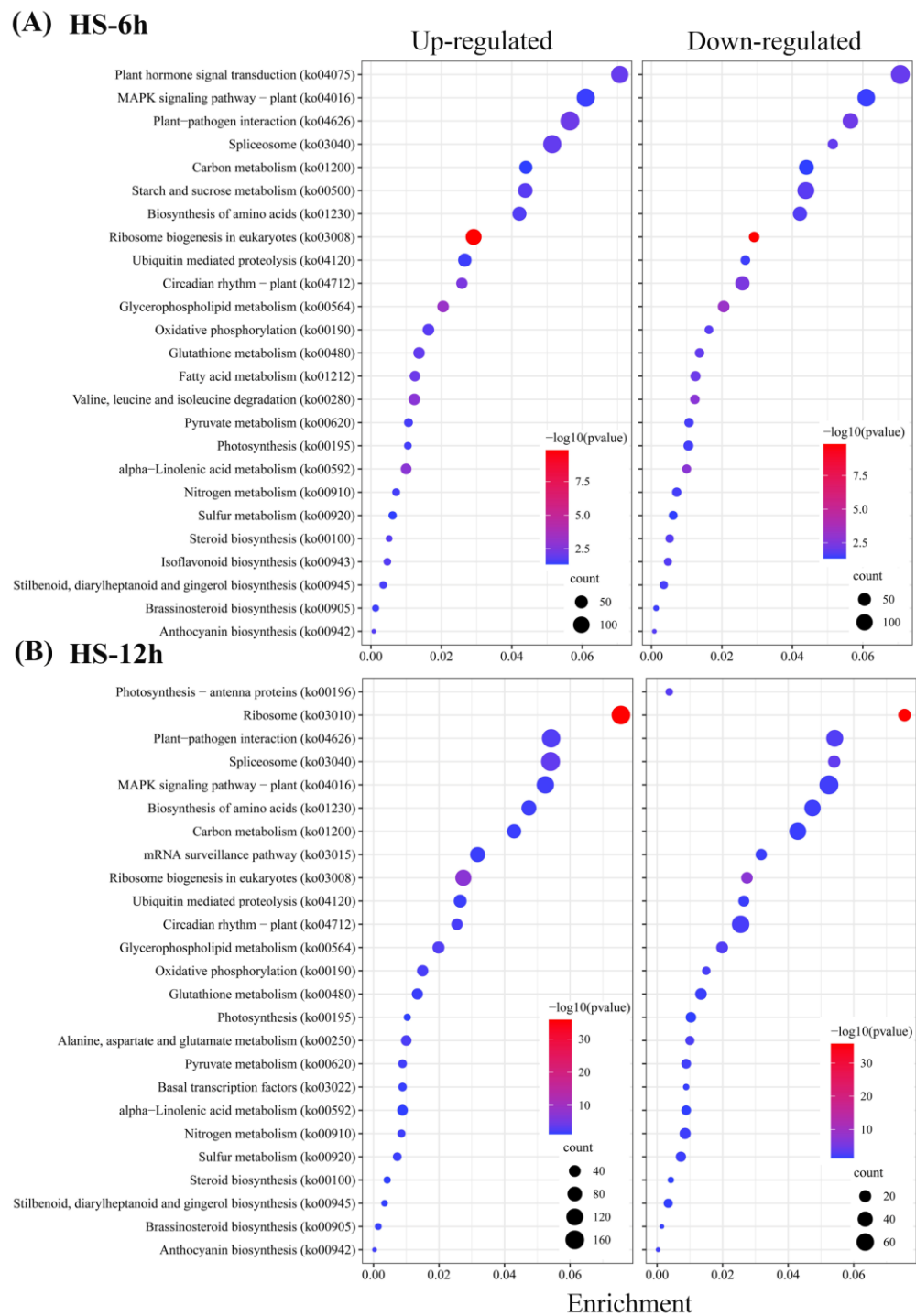
**Figure S1. Principal component analysis using FPKM values of heat-sensitive and heat-tolerant flowering Chinese cabbage varieties.**



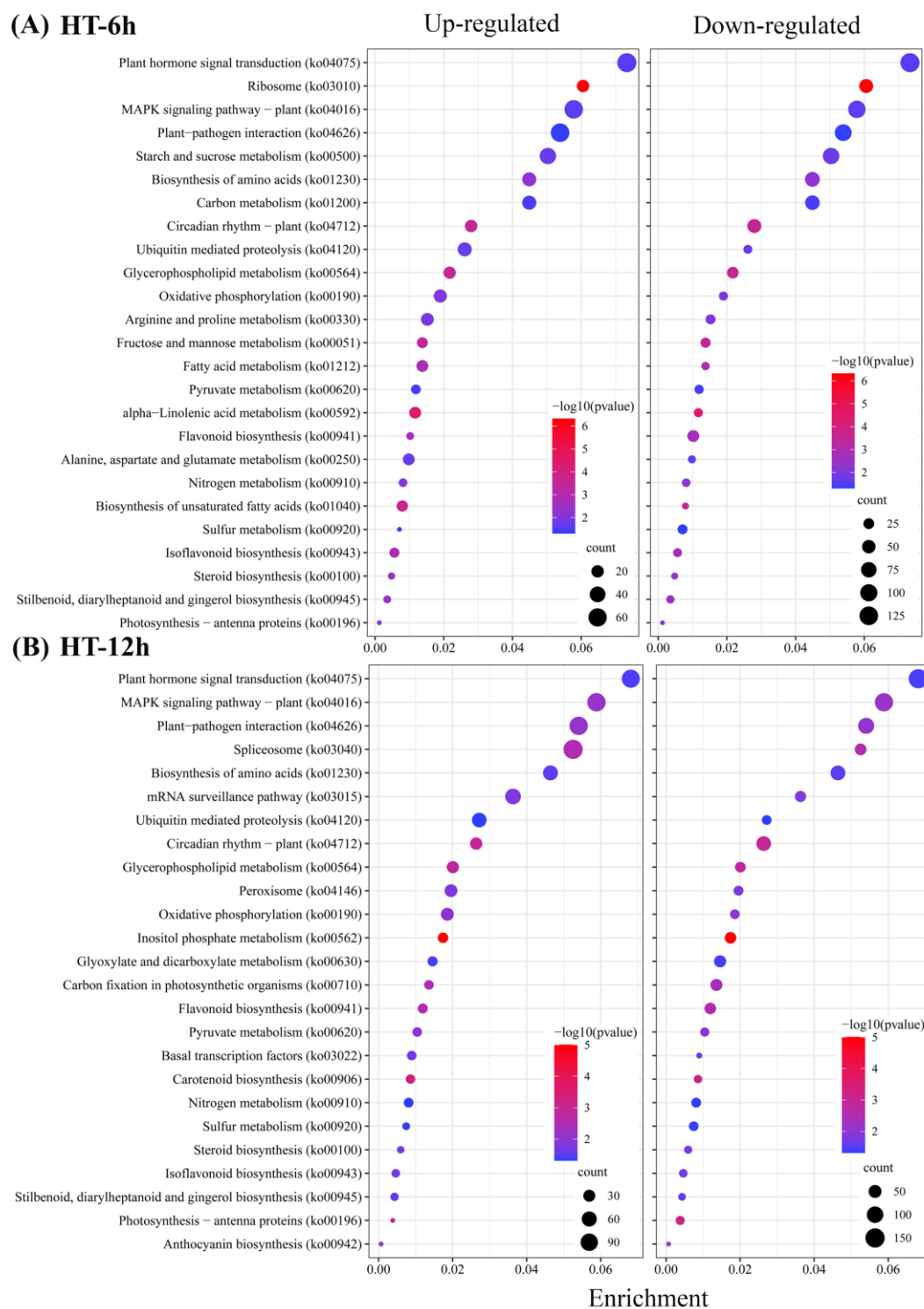
**Figure S2. GO enrichment analysis of up- and down-regulated genes in heat-sensitive (3T-6) flowering Chinese cabbage.** The top 25 GO terms in three categories are listed as (A) HS-CK vs. HS-6h and (B) HS-CK vs. HS-12h at  $P \leq 0.05$ .



**Figure S3. GO enrichment analysis of up- and down-regulated genes of heat-tolerant (Youlu-501) flowering Chinese cabbage.** The top 25 GO terms in three categories are listed as (A) HT-CK vs. HT-6h and (B) HT-CK vs. HT-12h at  $P \leq 0.05$ .



**Figure S4. KEGG enrichment analysis of up- and down-regulated genes of heat-sensitive (3T-6) flowering Chinese cabbage.** The top 25 pathways are listed as (A) HS-CK vs. HS-6h and (B) HS-CK vs. HS-12h at  $P \leq 0.05$ .



**Figure S5. KEGG enrichment analysis of up- and down-regulated genes of heat-tolerant (Youlu-501) flowering Chinese cabbage.** The top 25 pathways are listed as (A) HT-CK vs. HT-6h and (B) HT-CK vs. HT-12h at  $P \leq 0.05$ .