

# ***Supplementary Figures***

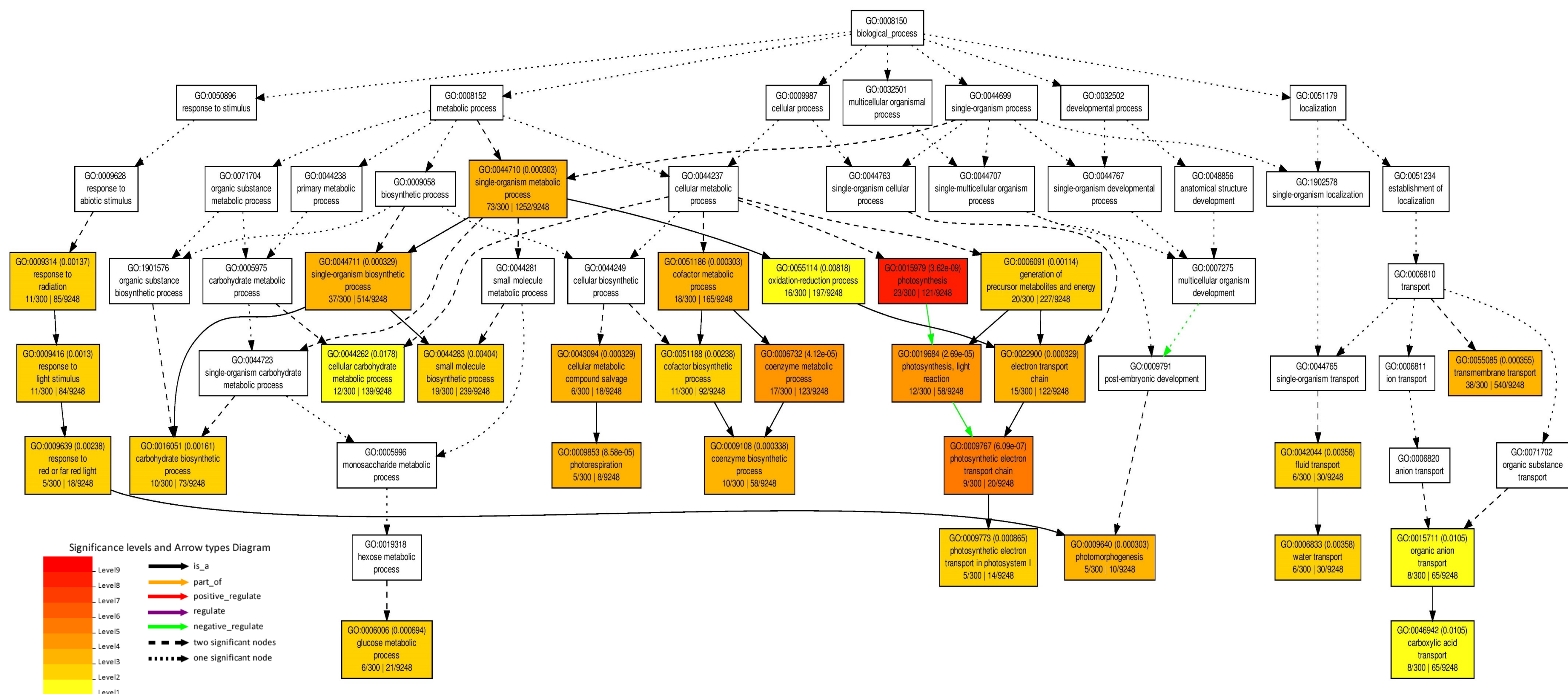
## **Genome-Wide Transcriptional Analysis of Rapeseed (*Brassica napus* L.) Responses to Heat Stress: An Integrated RNA-Seq Meta-Analysis, Gene Co-Expression, and Gene Regulatory Network Study**

**Masoud Shahsavari <sup>a,\*</sup>, Martin Raspor <sup>b</sup>, Valiollah Mohammadi <sup>a</sup>**

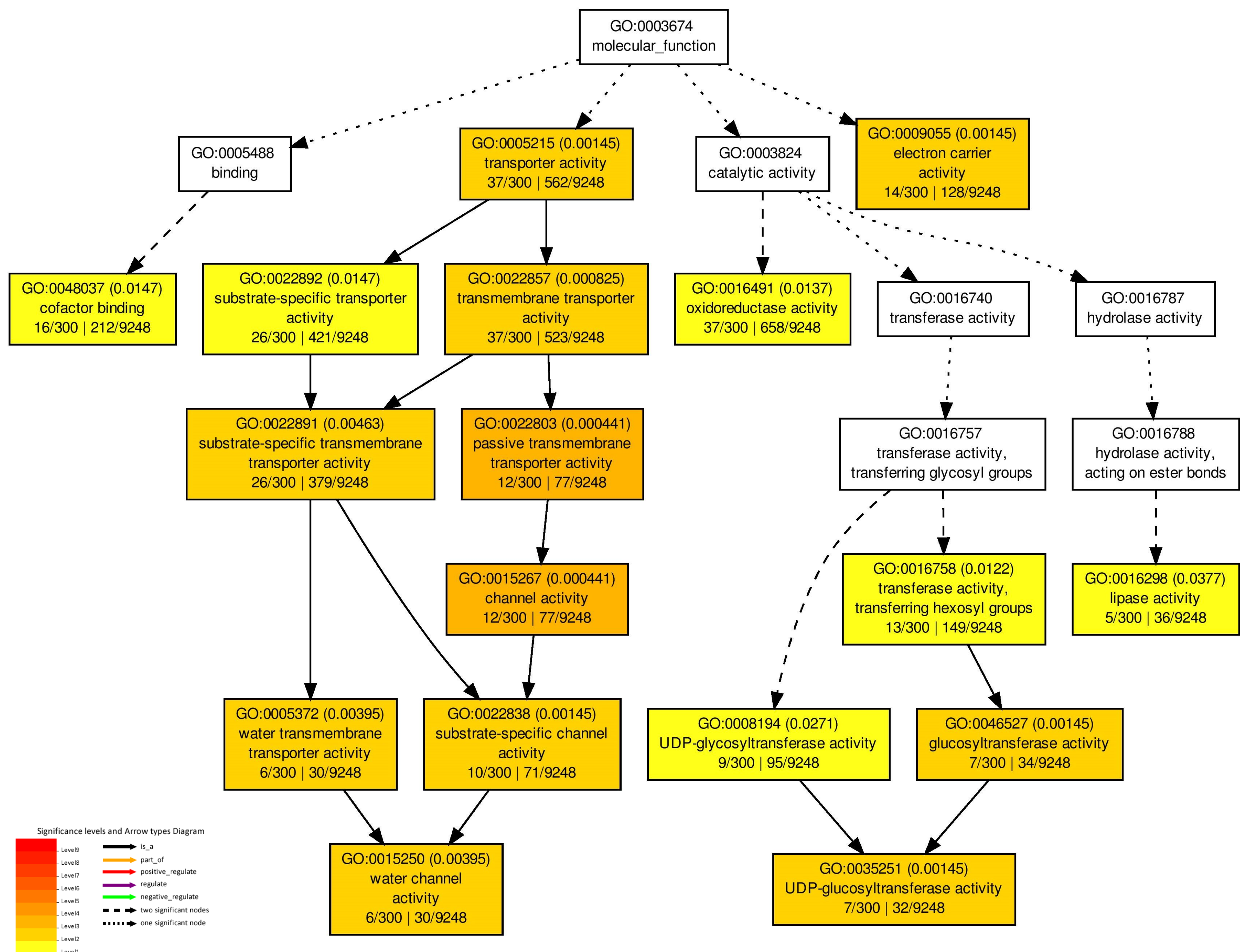
<sup>a</sup> Department of Agronomy and Plant Breeding, College of Agriculture and Natural Resources,  
University of Tehran, Karaj, Iran.

<sup>b</sup> Department of Plant Physiology, Institute for Biological Research “Siniša Stanković” – National  
Institute of the Republic of Serbia, University of Belgrade, Belgrade, Serbia.

\* Corresponding author: *Mobile:* +989352326448. *E-mail addresses:* [mshahsavari@ut.ac.ir](mailto:mshahsavari@ut.ac.ir)  
(M.Shahsavari).

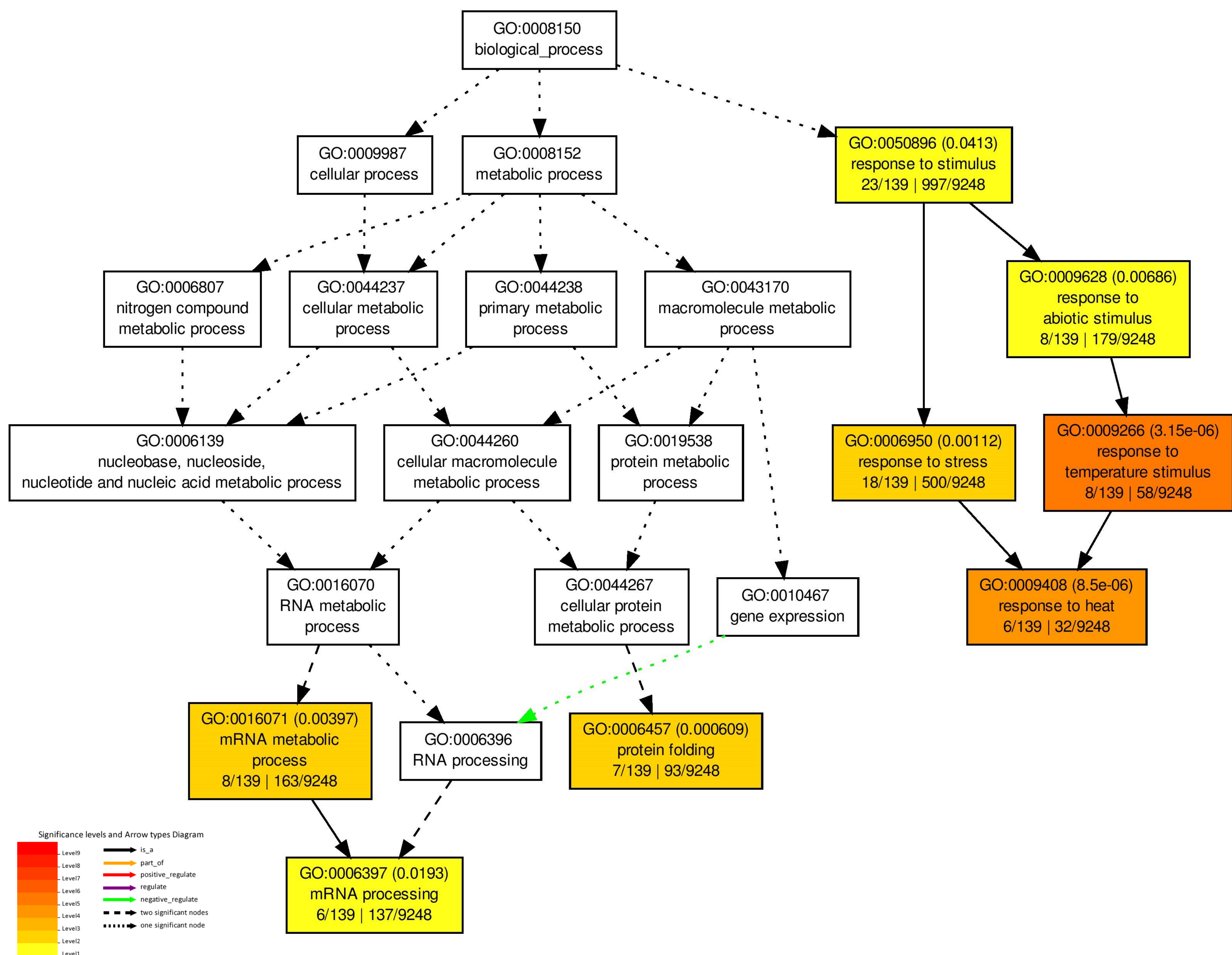


**Figure S1** Gene set enrichment analysis (GSEA) of biological processes for DEGs in the black co-expression module.

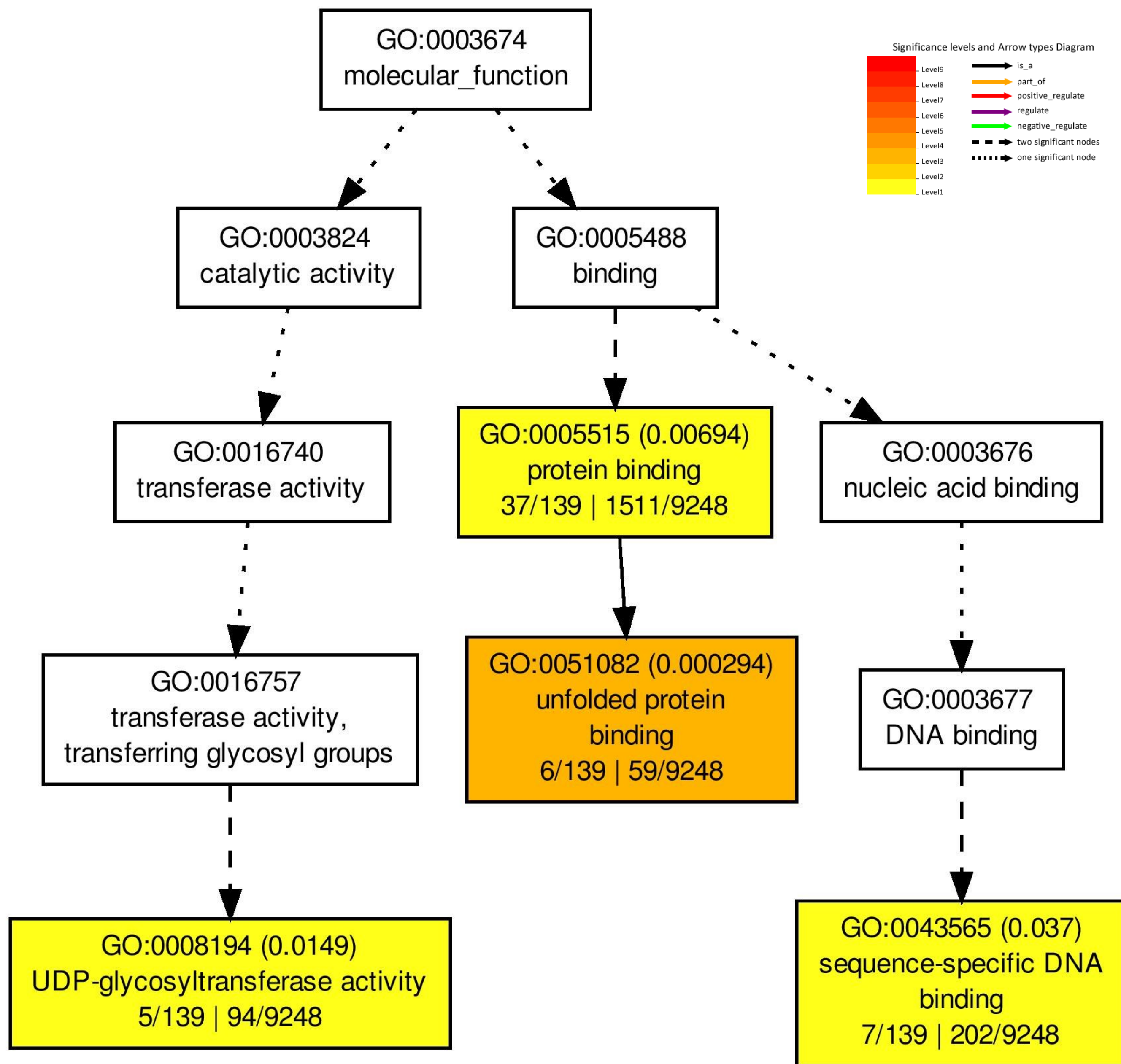


**Figure S2** Gene set enrichment analysis (GSEA) of molecular functions for DEGs in the black co-expression module.

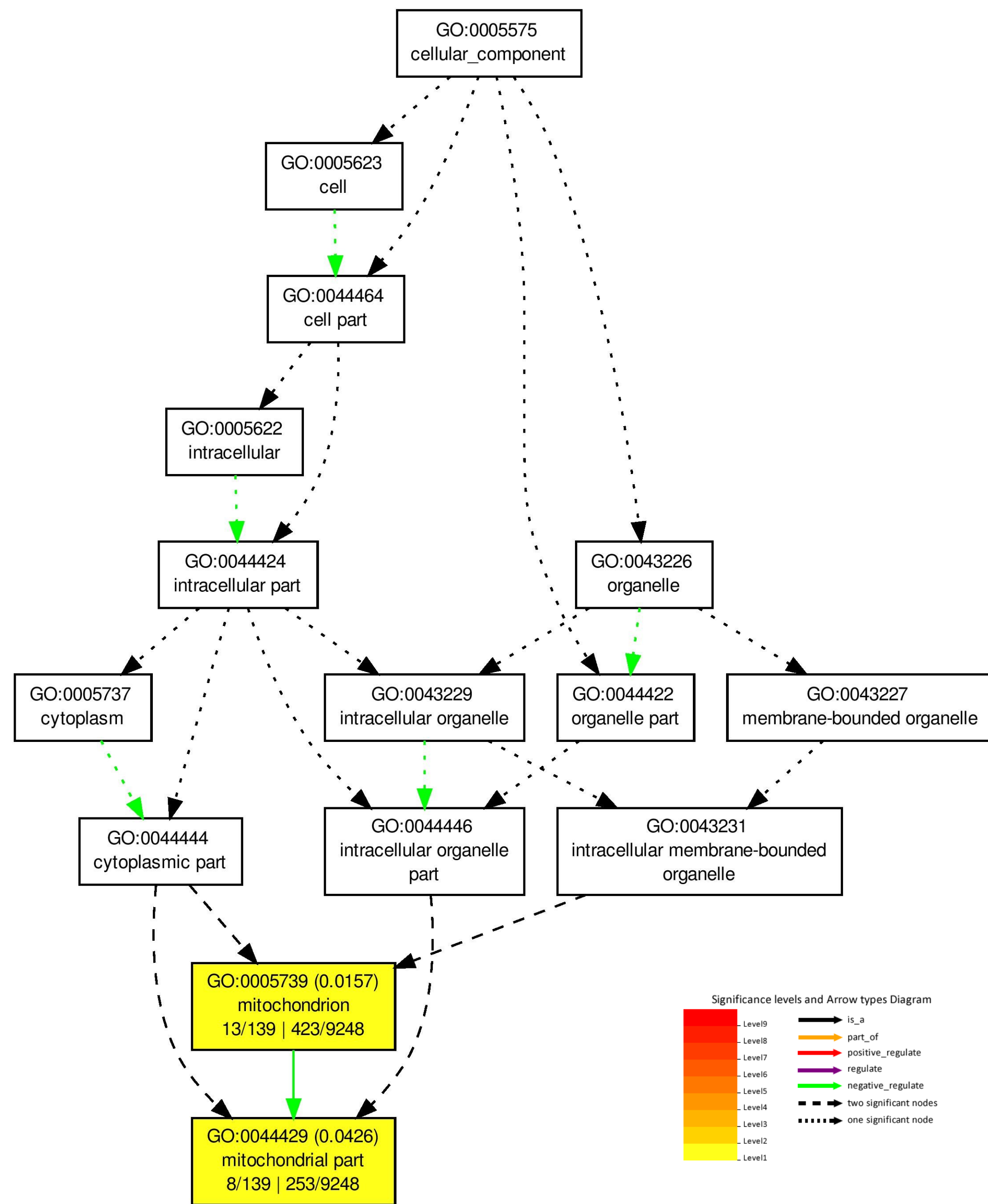




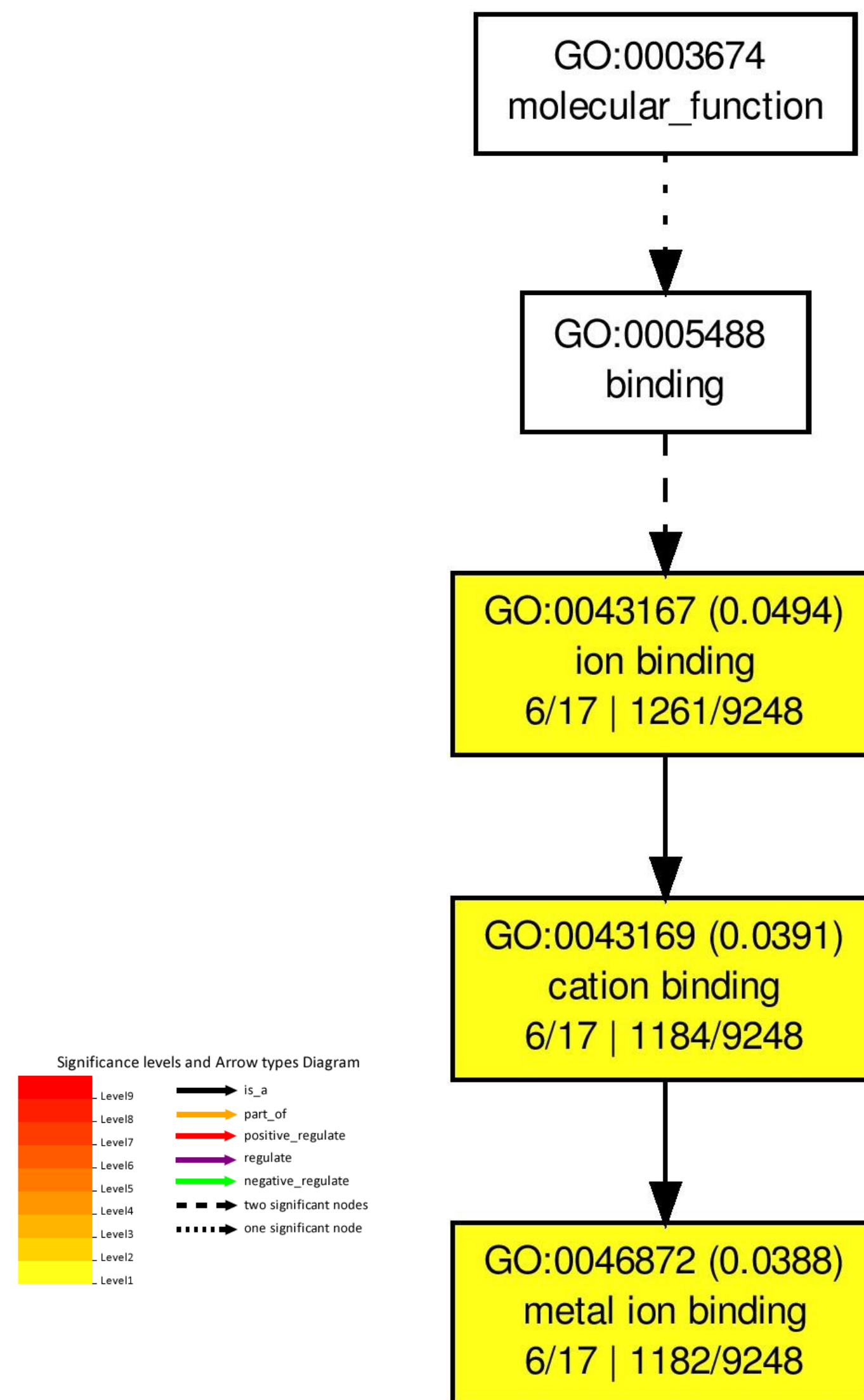
**Figure S4** Gene set enrichment analysis (GSEA) of biological processes for DEGs in the green co-expression module.



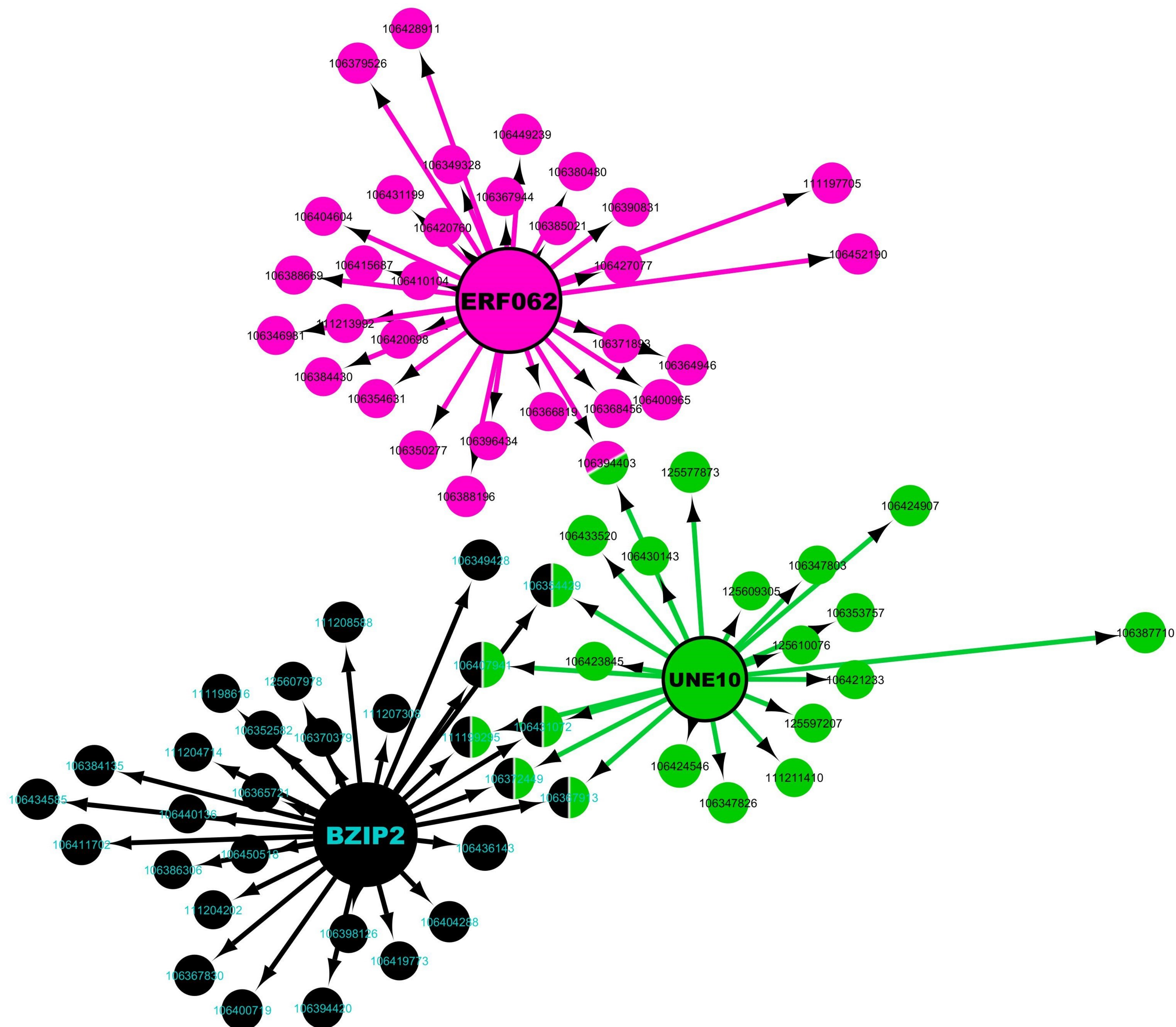
**Figure S5** Gene set enrichment analysis (GSEA) of molecular functions for DEGs in the green co-expression module.



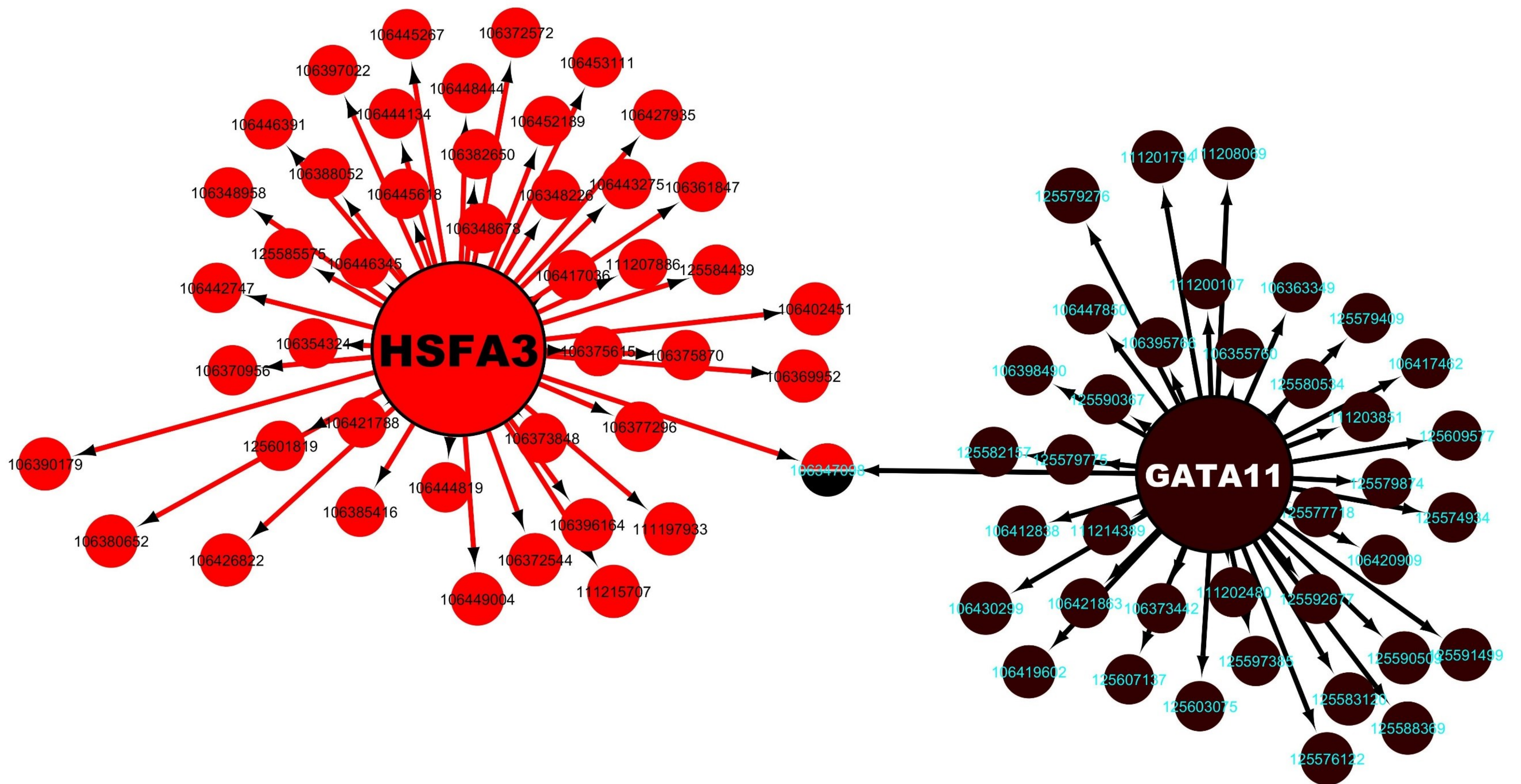
**Figure S6** Gene set enrichment analysis (GSEA) of cellular components for DEGs in the green co-expression module.



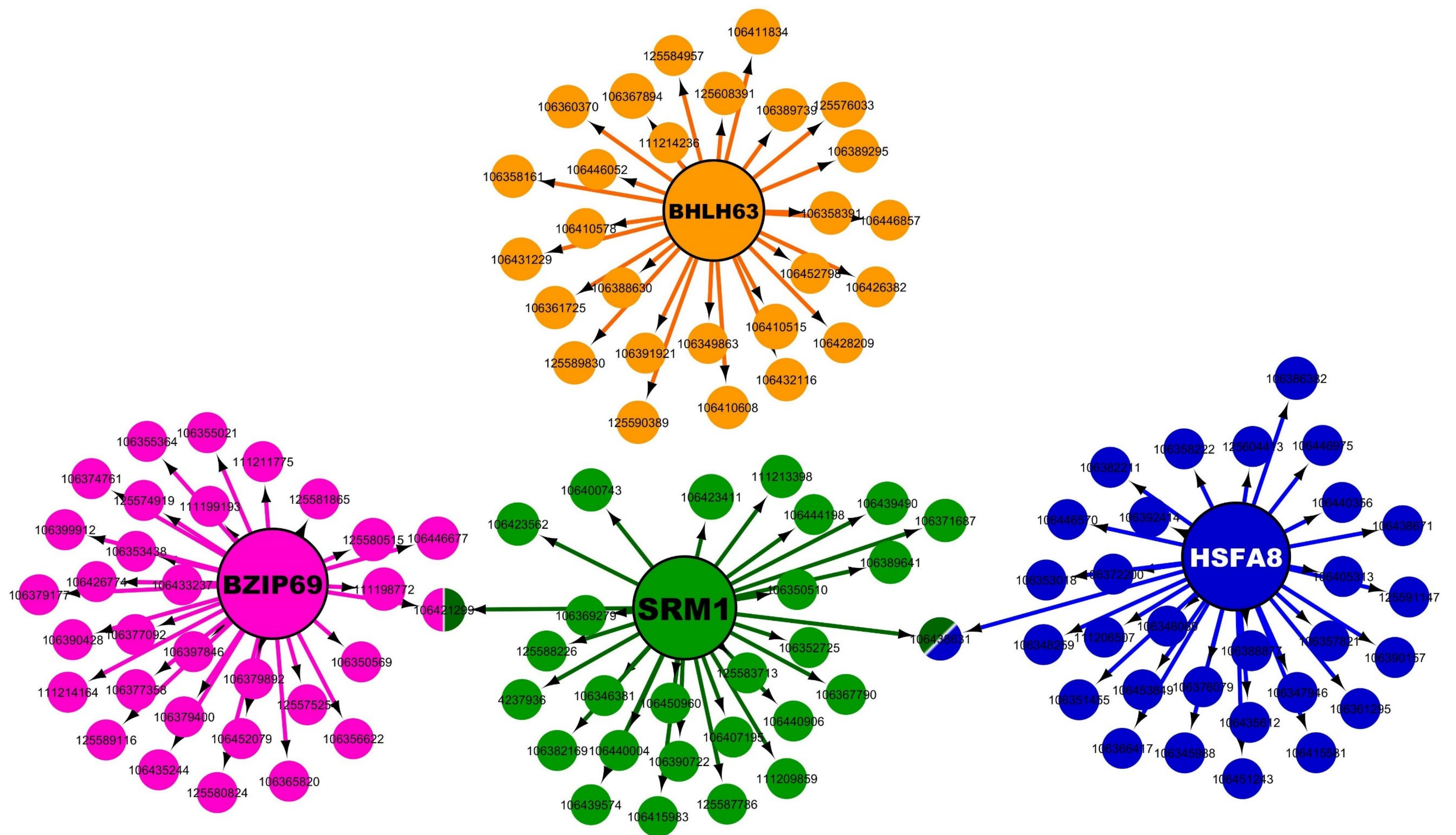
**Figure S7** Gene set enrichment analysis (GSEA) of molecular functions for DEGs in the brown co-expression module.



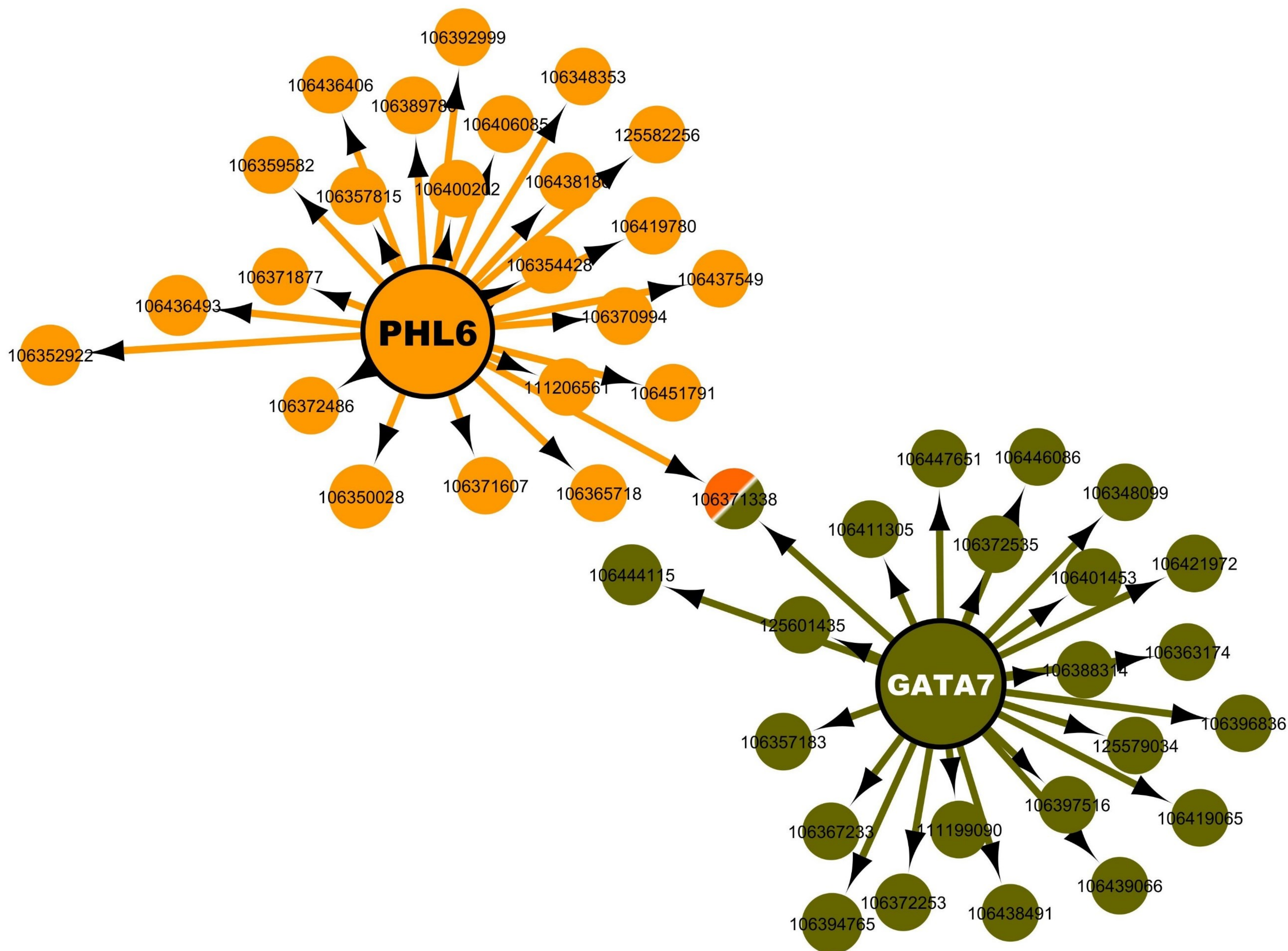
**Figure S8** Regulatory networks of ERF062, BZIP2, and UNE10 transcription factors.



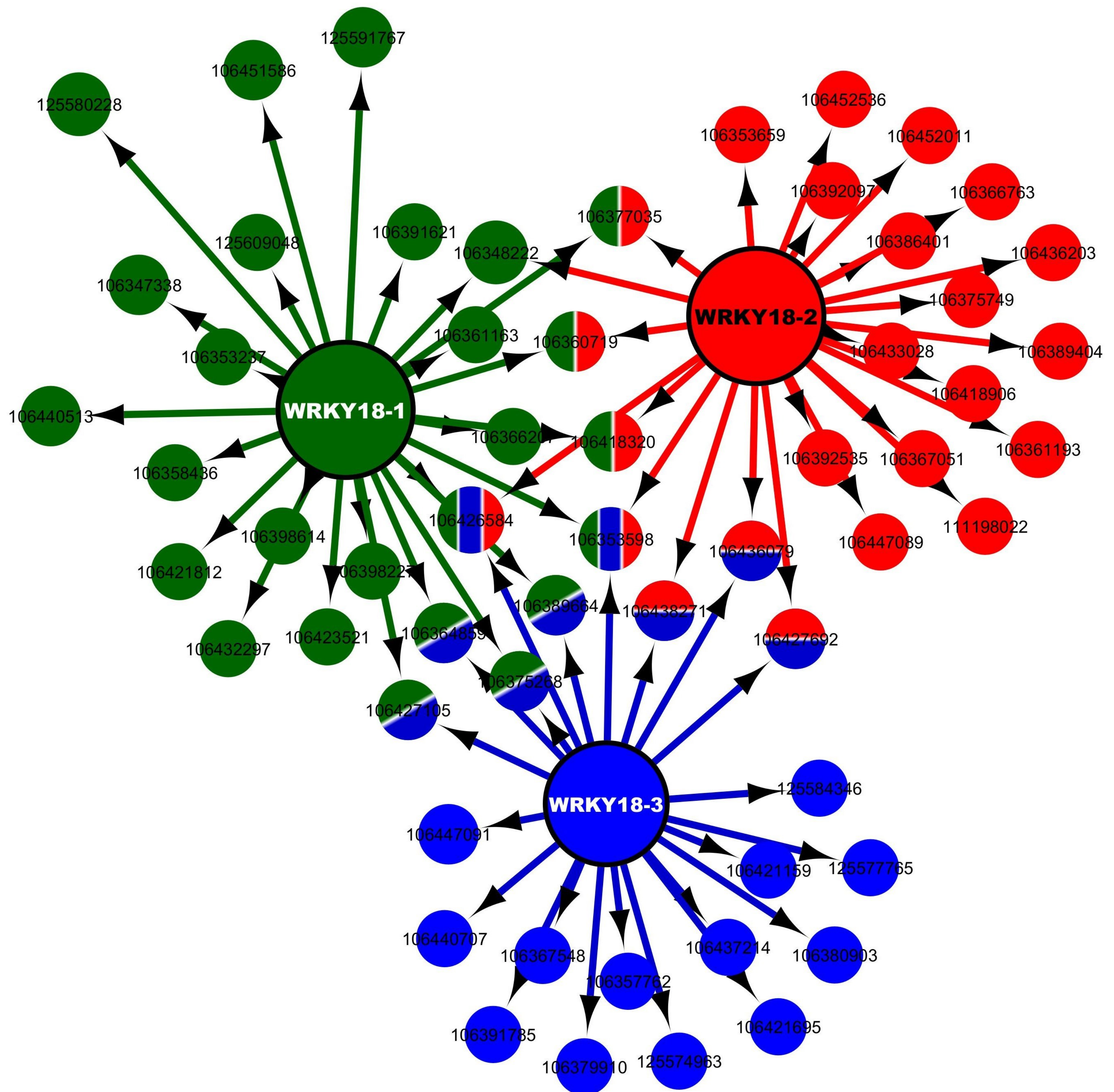
**Figure S9** Regulatory networks of HSFA3 and GATA11 transcription factors.



**Figure S10** Regulatory networks of BHLH63, BZIP69, SRM1, and HSFA8 transcription factors.



**Figure S11** Regulatory networks of PHL6 and GATA7 transcription factors.



**Figure S12** Regulatory networks of WRKY18-1/2/3 transcription factors.