

**Temporal expression profiles reveal potential targets during postembryonic development of forensically important *Sarcophaga peregrina* (Diptera: Sarcophagidae)**

**Figure S1.** The life cycle of *S. peregrina*.

**Figure S2.** Clustering analysis between samples.

**Figure S3.** PCA based on the expression level of genes.

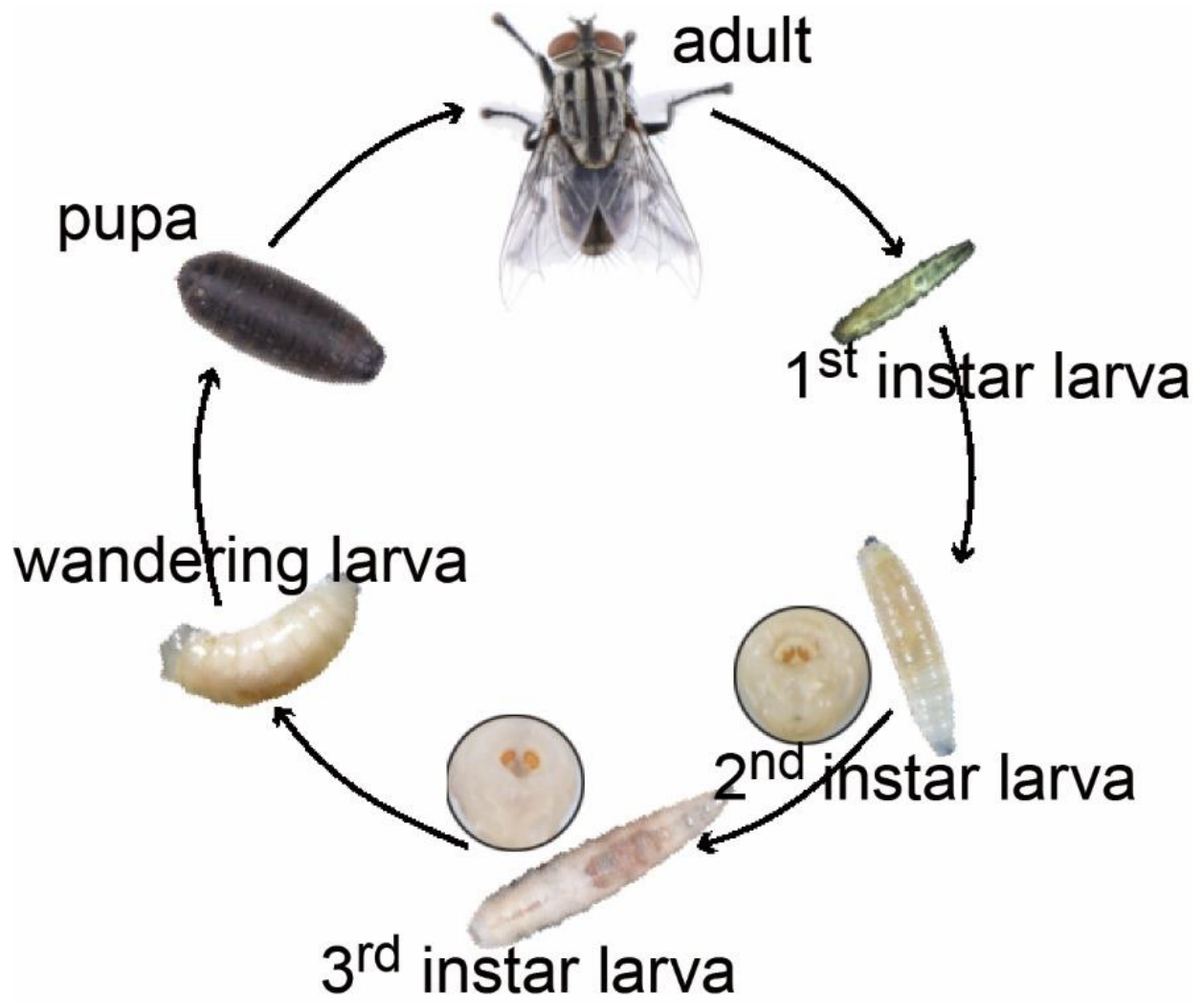
**Figure S4.** Similarity analysis between samples (Heat map).

**Figure S5.** Heat map of differentially expressed genes (DEGs).

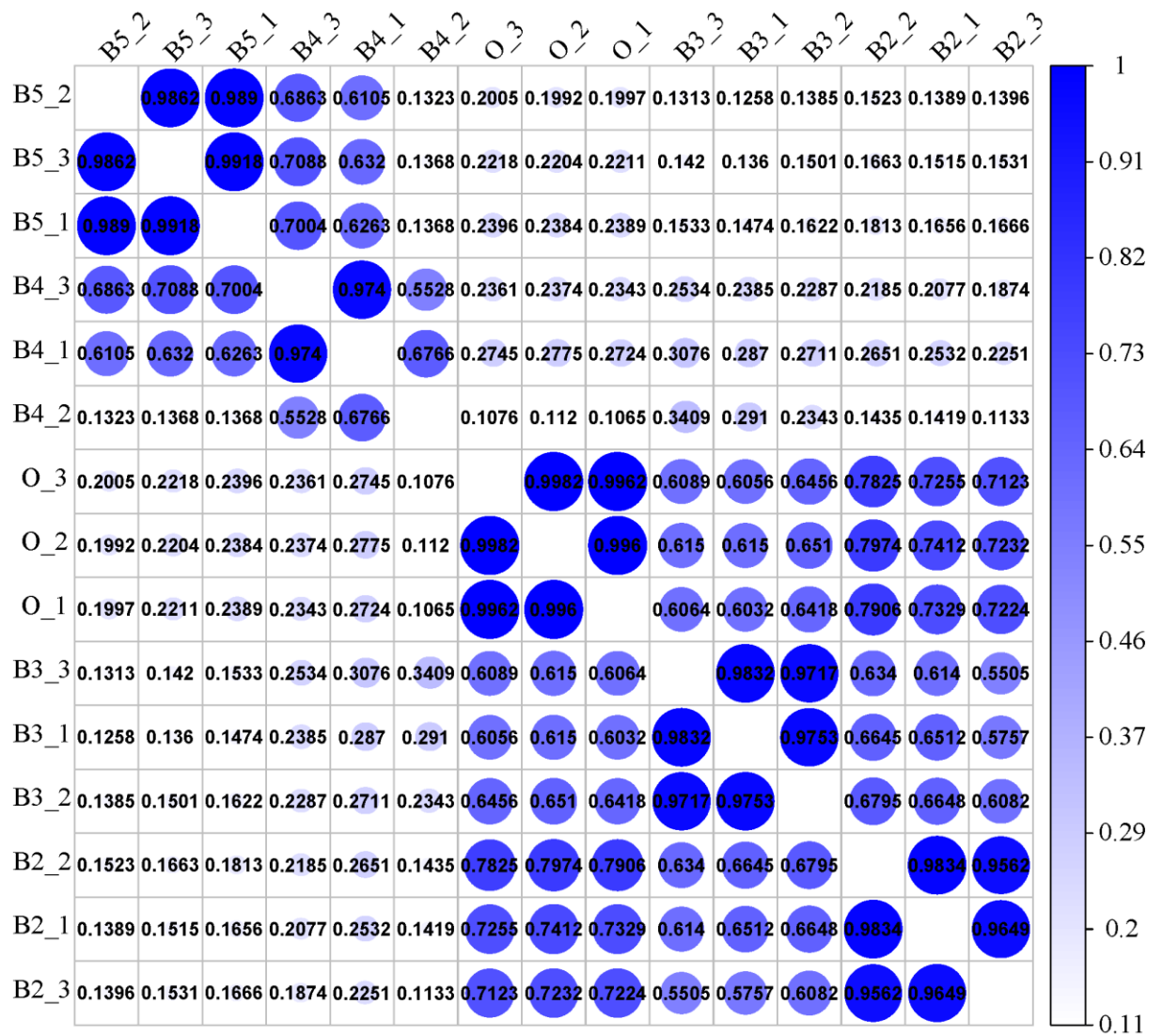
**Figure S6.** GO significant enrichment analysis for differentially expressed genes (DEGs) during postembryonic development. **a)** B2 vs. O; **b)** B3 vs. B2; **c)** B4 vs. B3; **d)** B5 vs. B4.

**Figure S7.** KEGG enrichment analysis of DEGs during postembryonic development. The numbers above bars represent the number of enriched genes. **a)** B2 vs. O; **b)** B3 vs. B2; **c)** B4 vs. B3; **d)** B5 vs. B4.

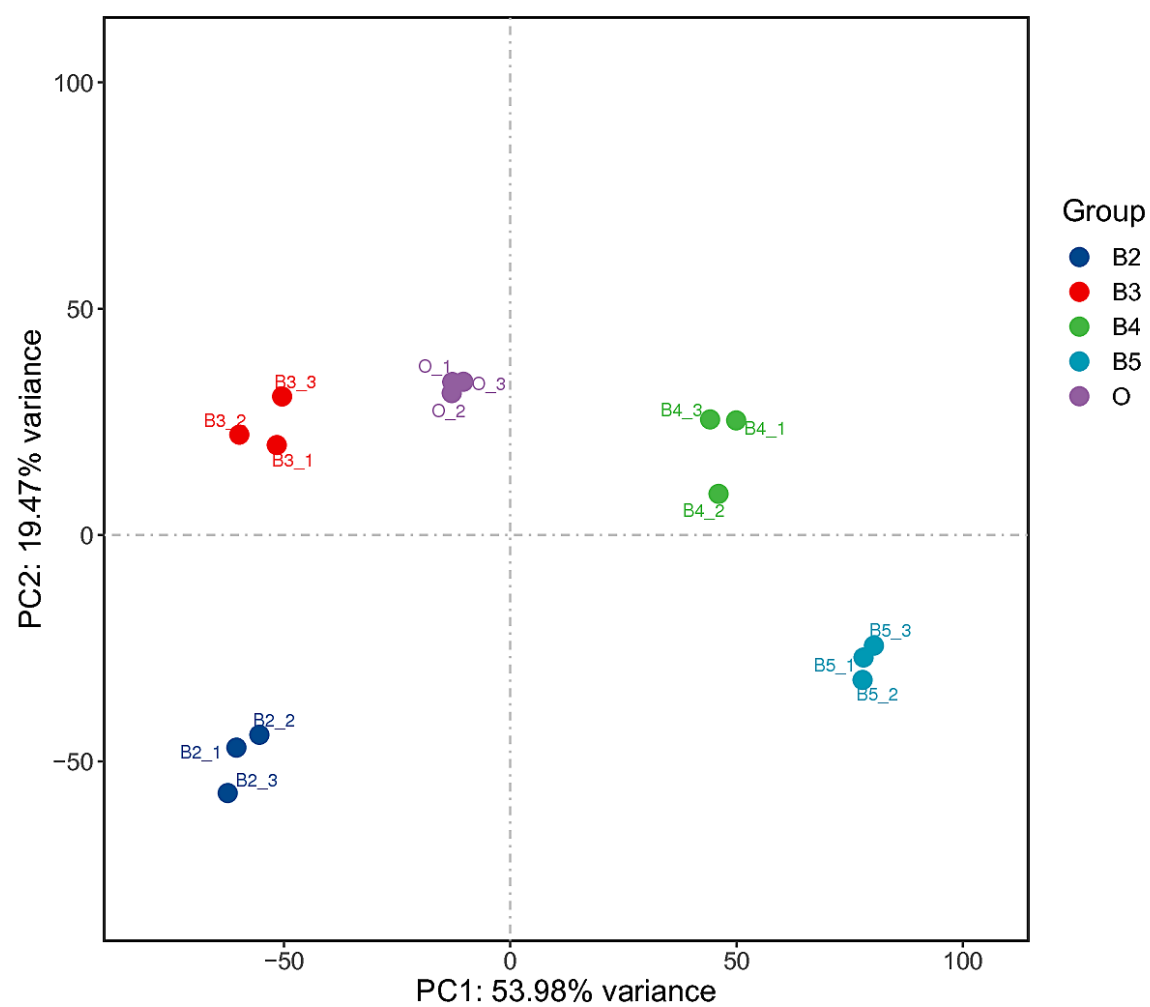
**Figure S8.** KEGG significant enrichment analysis for differentially expressed genes (DEGs) during postembryonic development. **a)** B2 vs. O; **b)** B3 vs. B2; **c)** B4 vs. B3; **d)** B5 vs. B4.



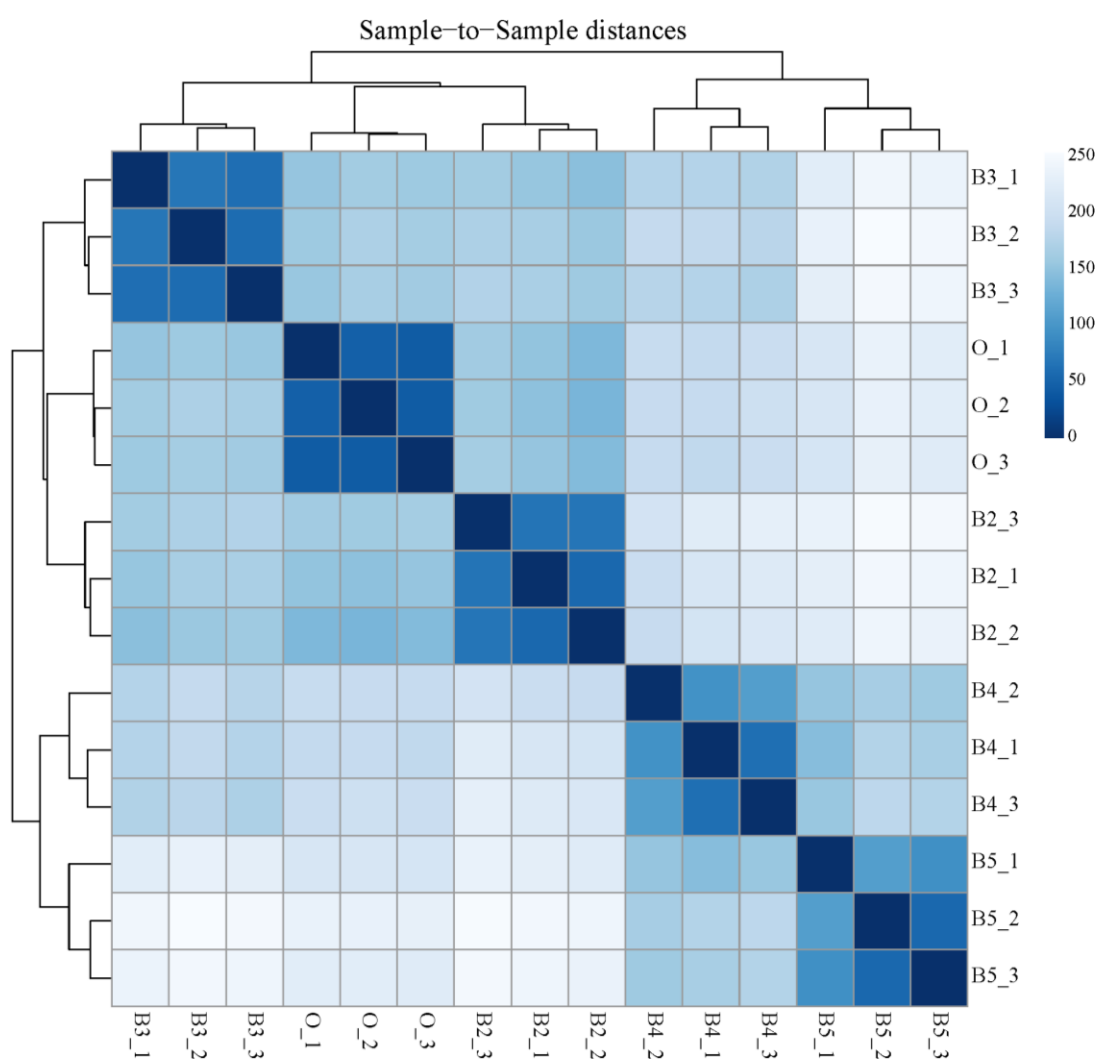
**Figure S1.** The life cycle of *S. peregrina*.



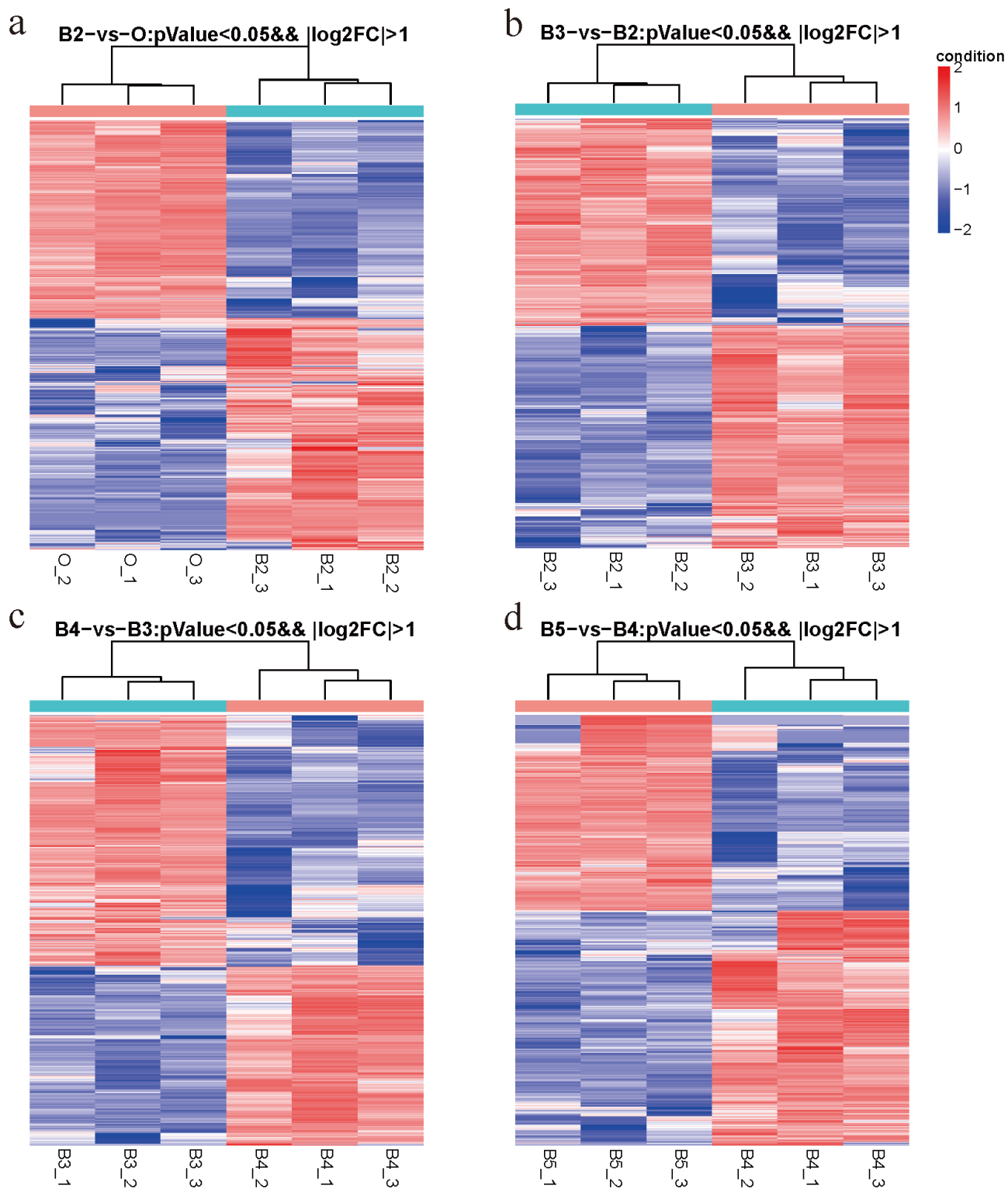
**Figure S2.** Heat map of correlation analysis between samples. The correlation of biological replicates reflects the degree of similarity between samples. The closer the correlation coefficient is to 1, the higher the similarity between samples is, and the smaller the difference between samples is. X-axis represents the name of the sample, Y-axis represents the name of the corresponding sample, and the scale represents the size of the correlation coefficient.



**Figure S3.** PCA based on the expression level of genes. The closer the PCA variance is, the more similar the samples are.

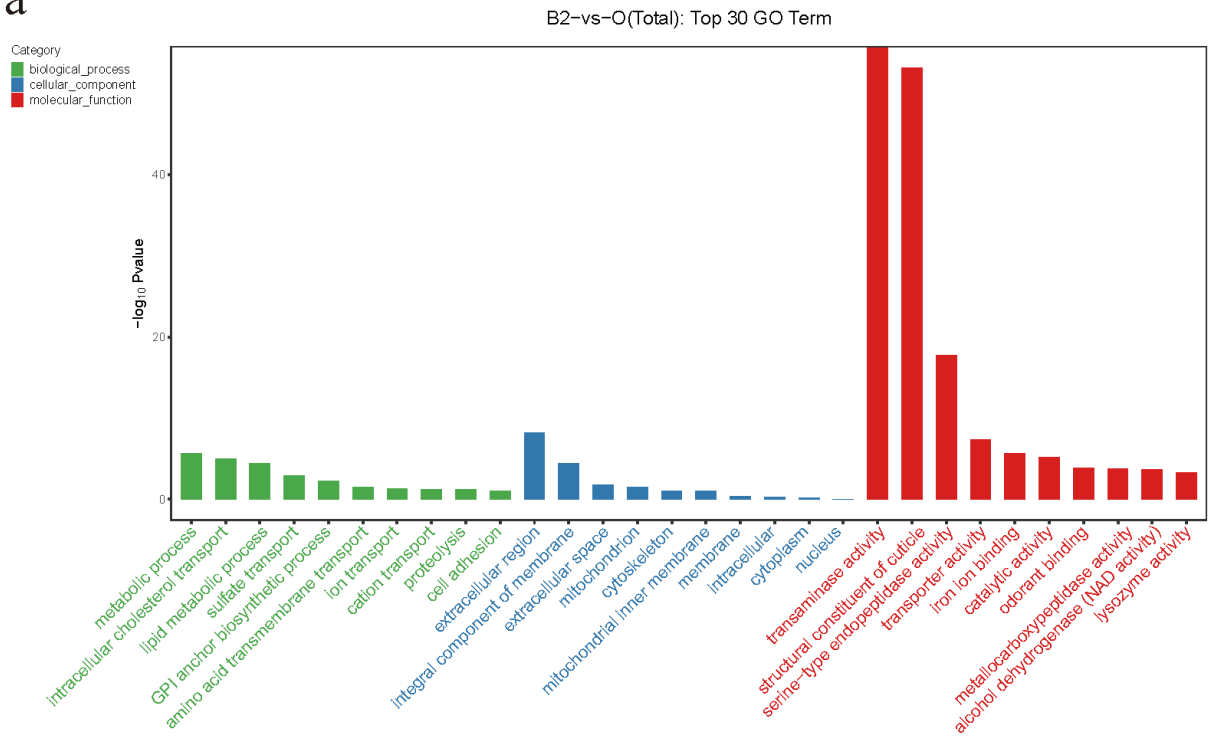


**Figure S4.** Similarity analysis between samples (Heat map). The analysis can accurately reflect the situation of experimental design, and the distances between samples belonging to the same design are close to each other and preferentially clustered together. X-axis represents the name of the sample, Y-axis represents the name of the corresponding sample, and the scale represents the size of the correlation coefficient.

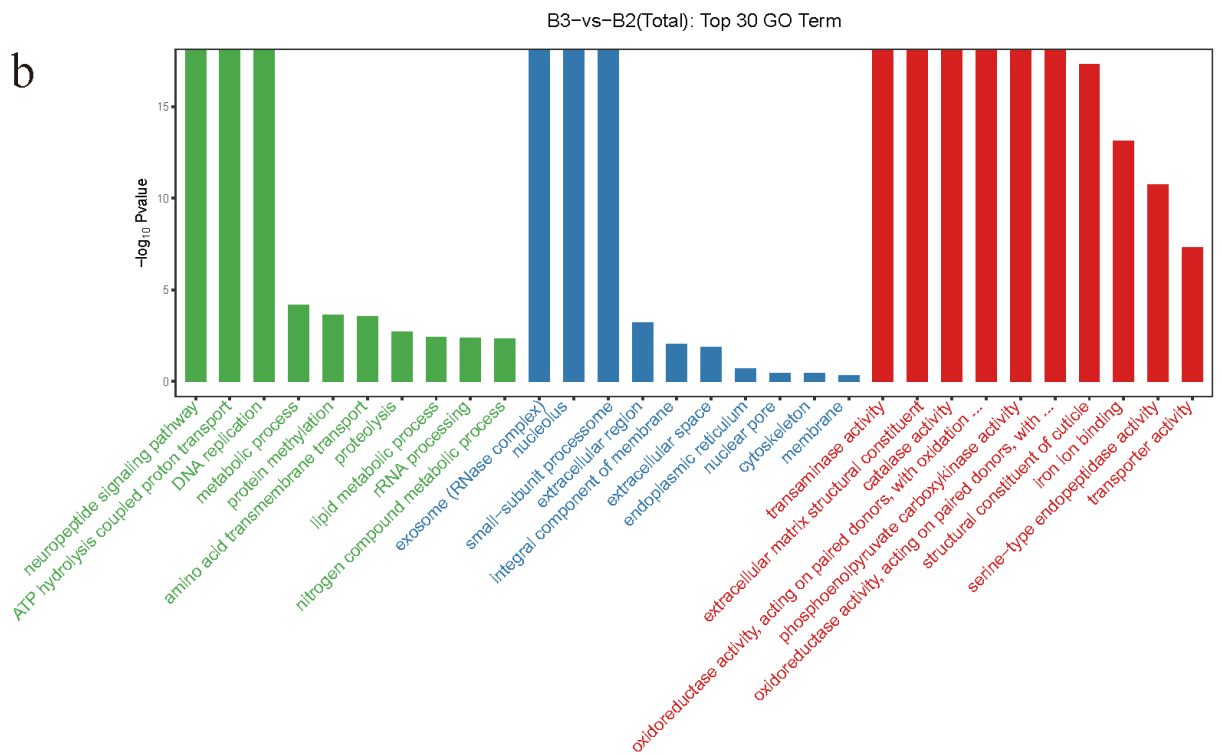


**Figure S5.** Heat map of differentially expressed genes (DEGs).

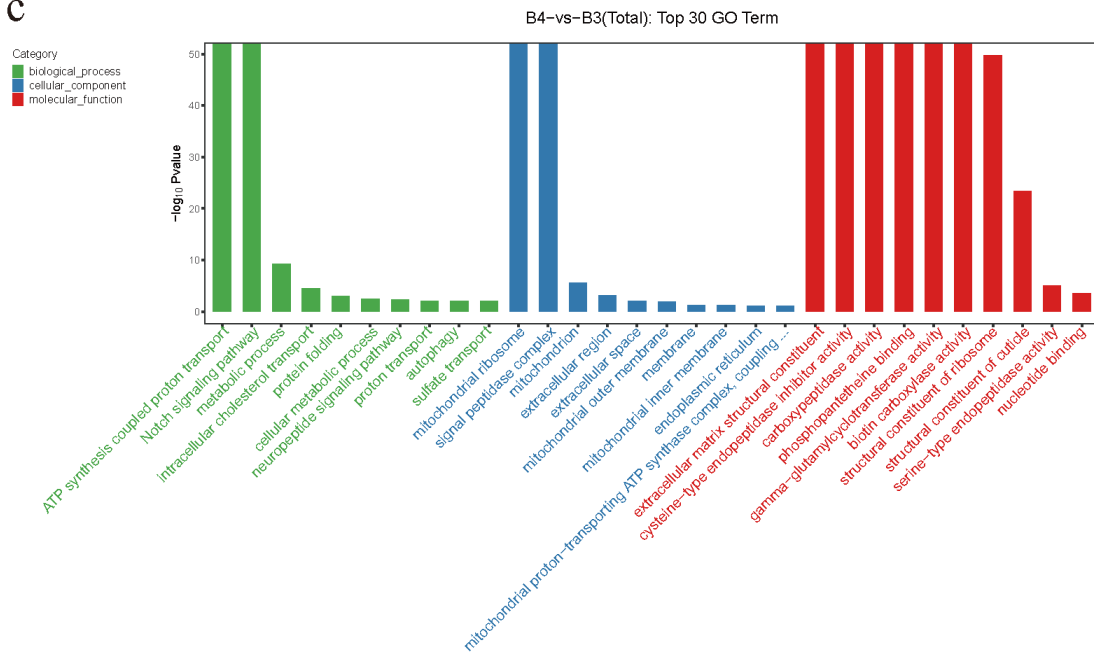
a



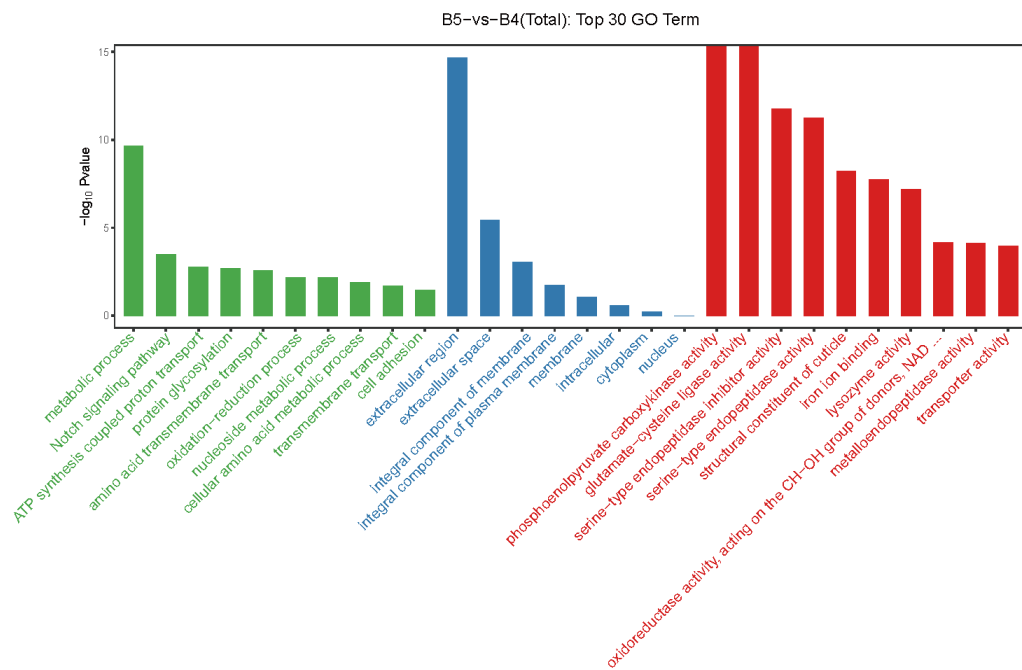
b



**c**



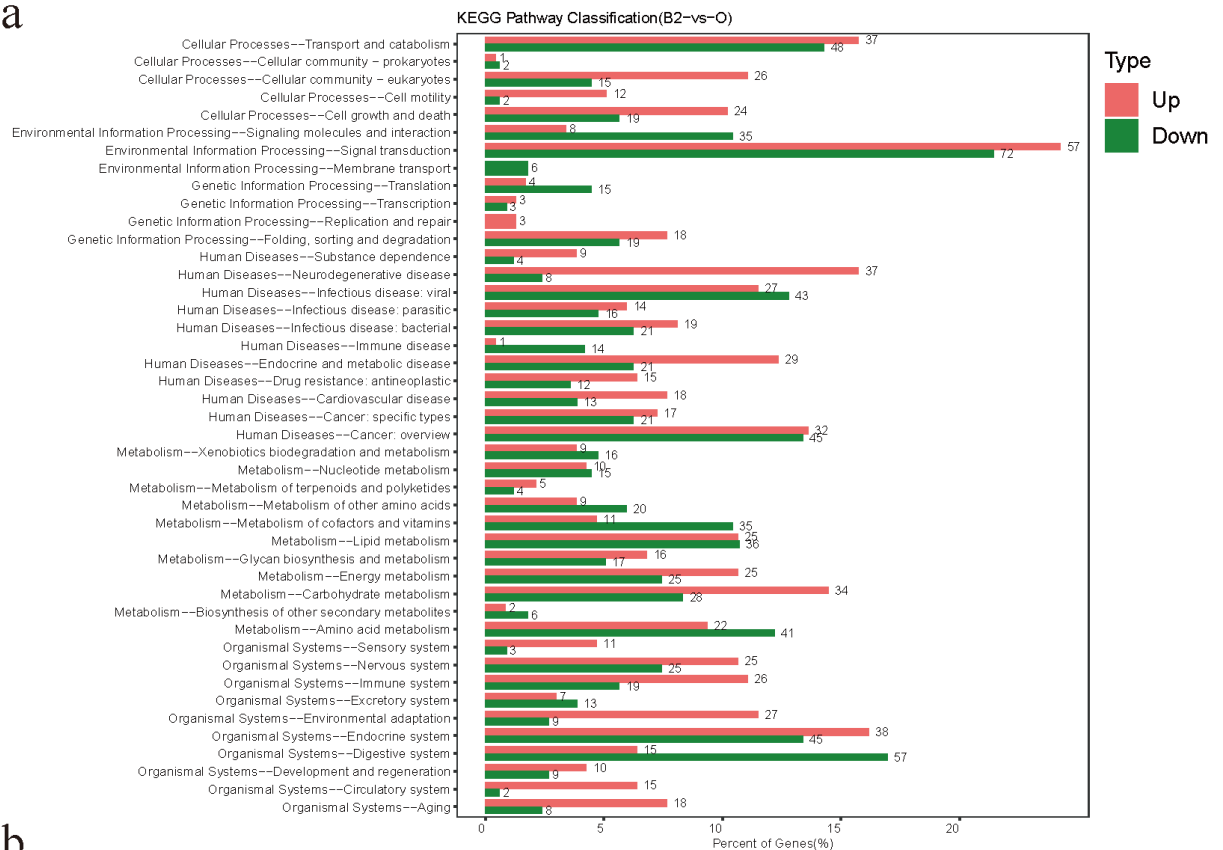
**d**



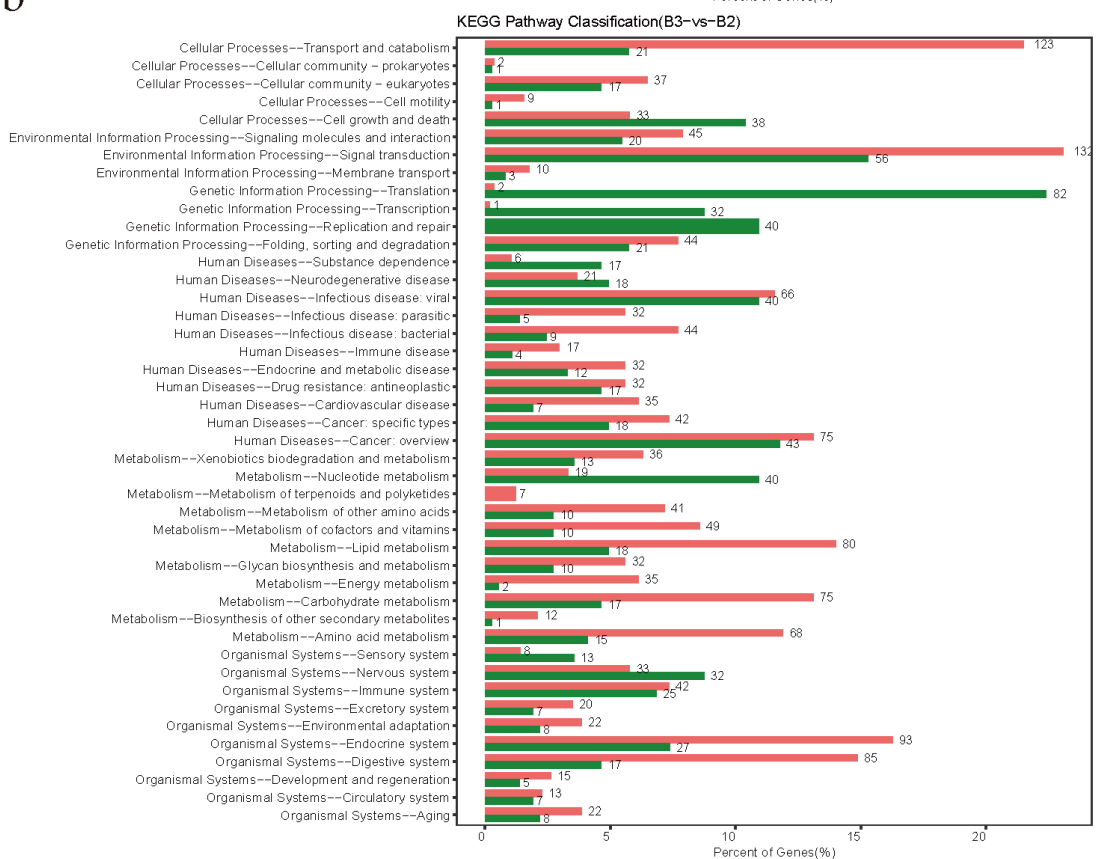
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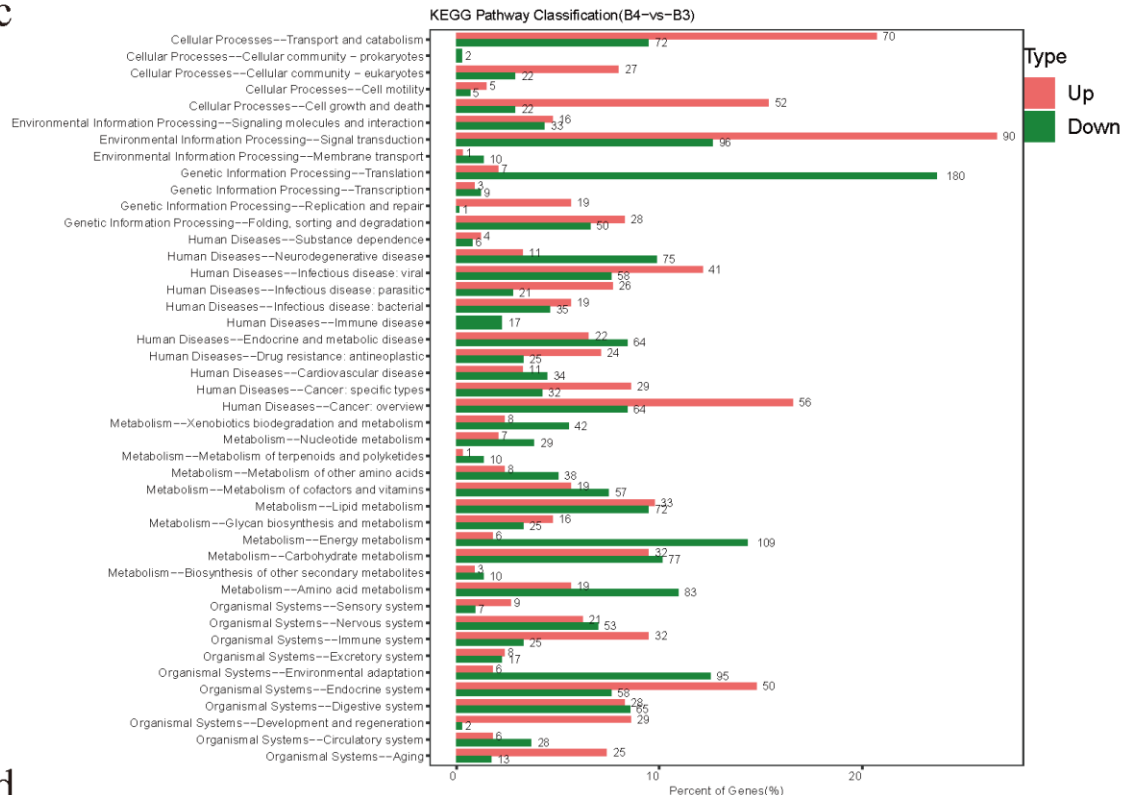
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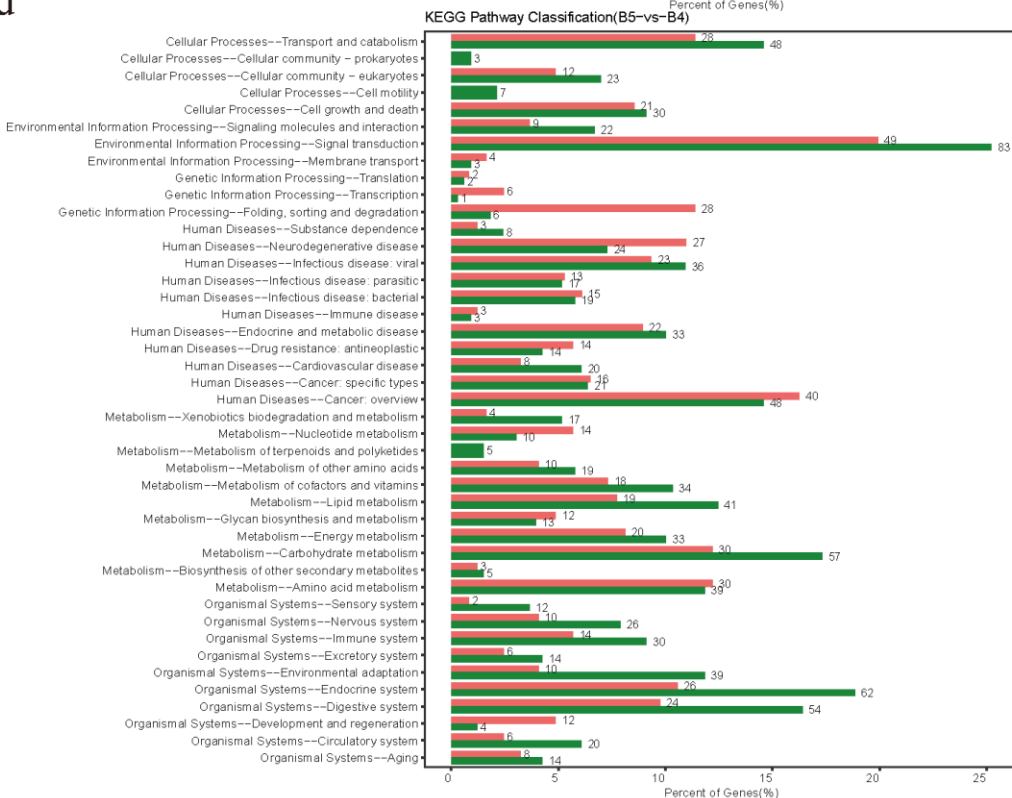
b



C



d

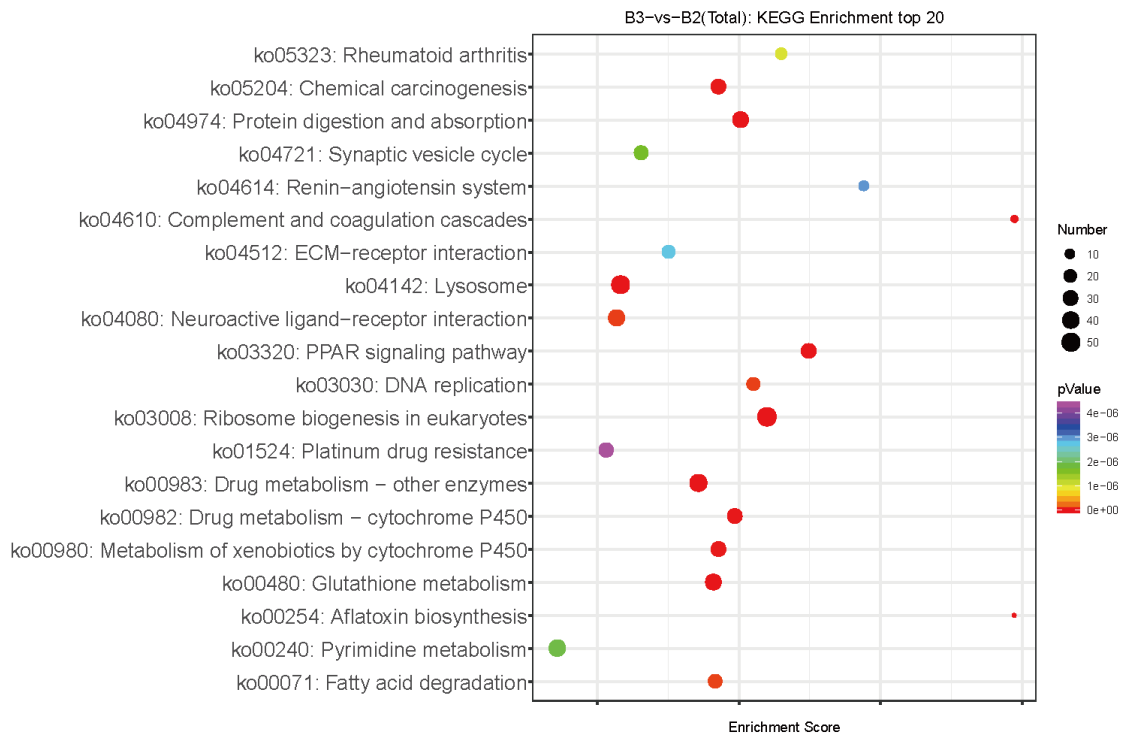


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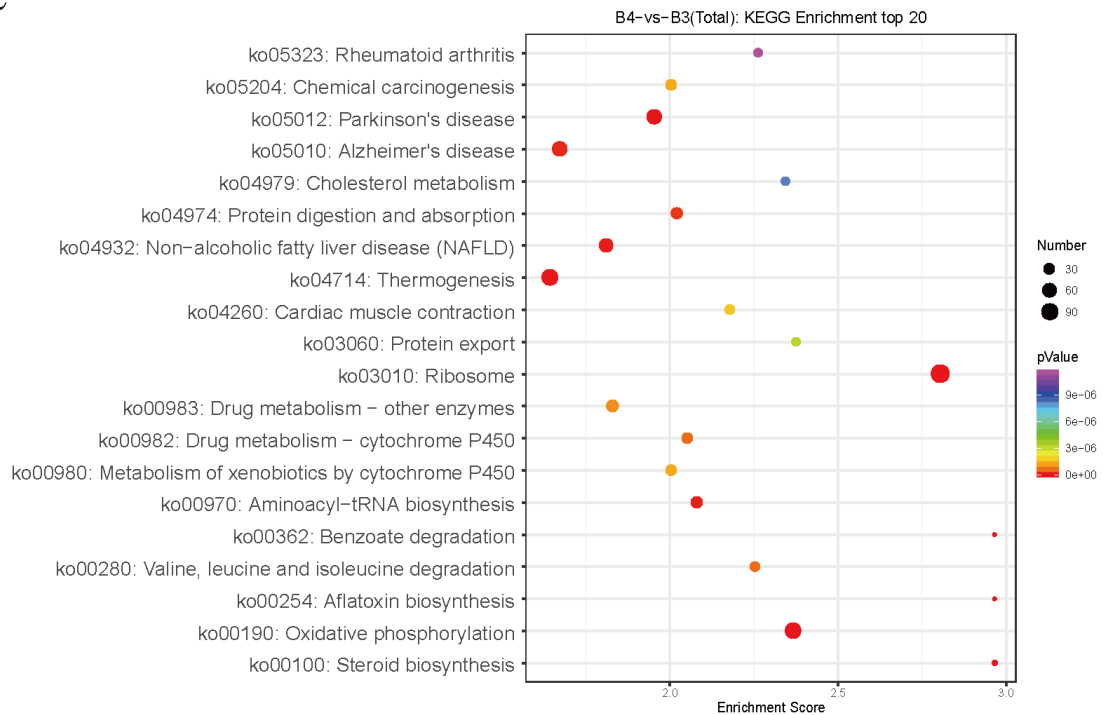
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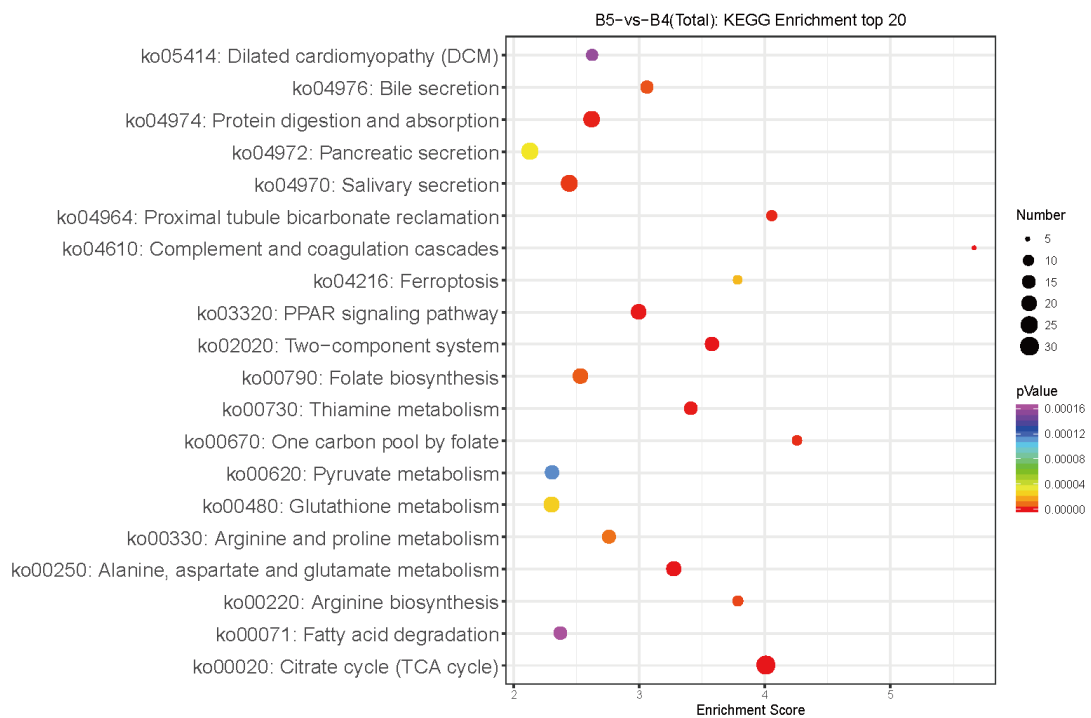
b



c



d



**Figure S8.** KEGG significant enrichment analysis for differentially expressed genes (DEGs) during postembryonic development. **a)** B2 vs. O; **b)** B3 vs. B2; **c)** B4 vs. B3; **d)** B5 vs. B4.