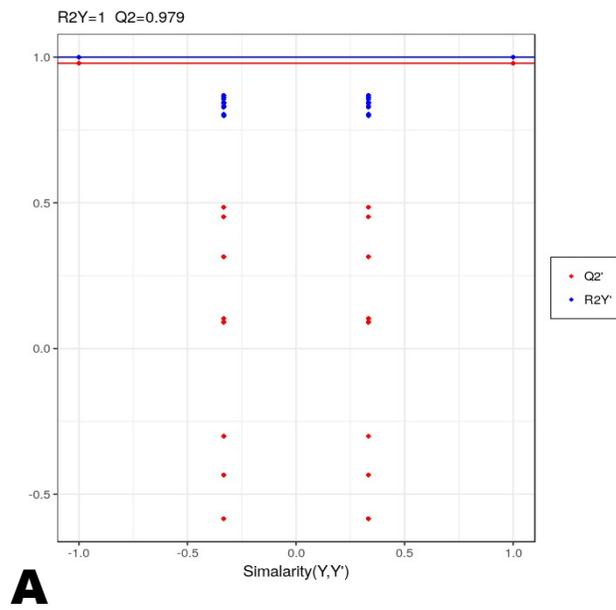
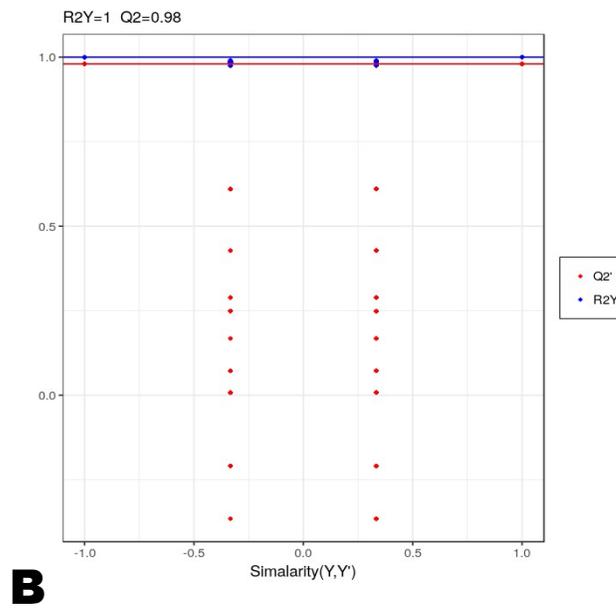


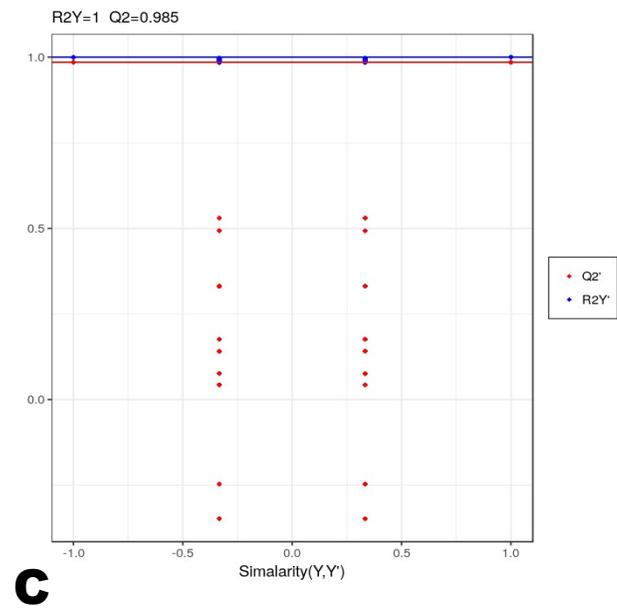
Figure S1. Correlation analysis of samples based on the relative content of the metabolites.



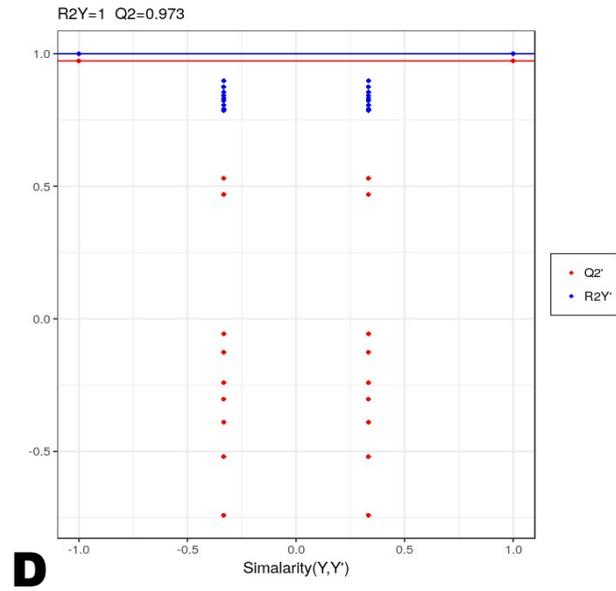
A



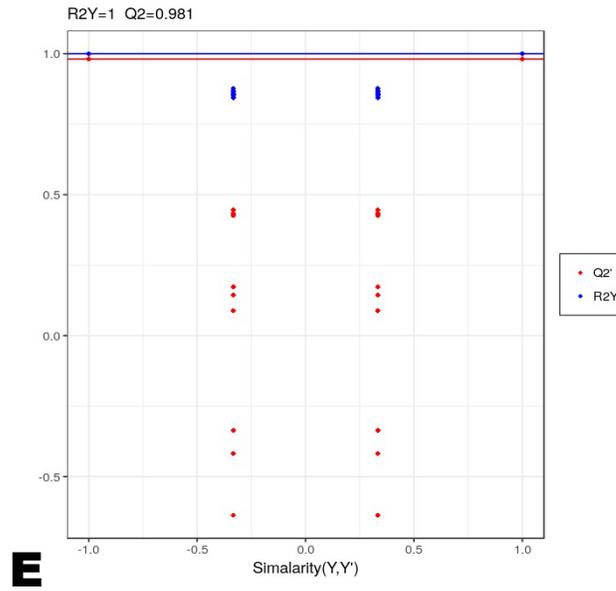
B



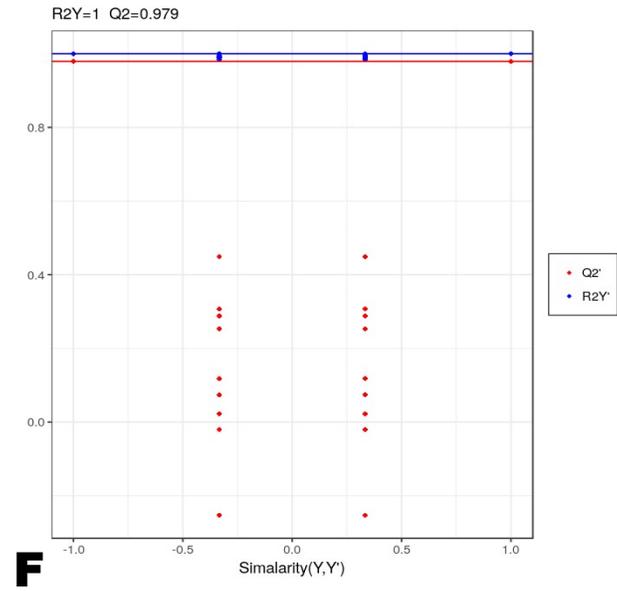
C



D



E



F

Figure S2. OPLS-DA plots of pairwise comparison between (A) K1102_vs_262; (B) K1102_vs_1392; (C) K1102_vs_K115; (D) 1392_vs_262; (E) K115_vs_262; (F) K115_vs_1392.

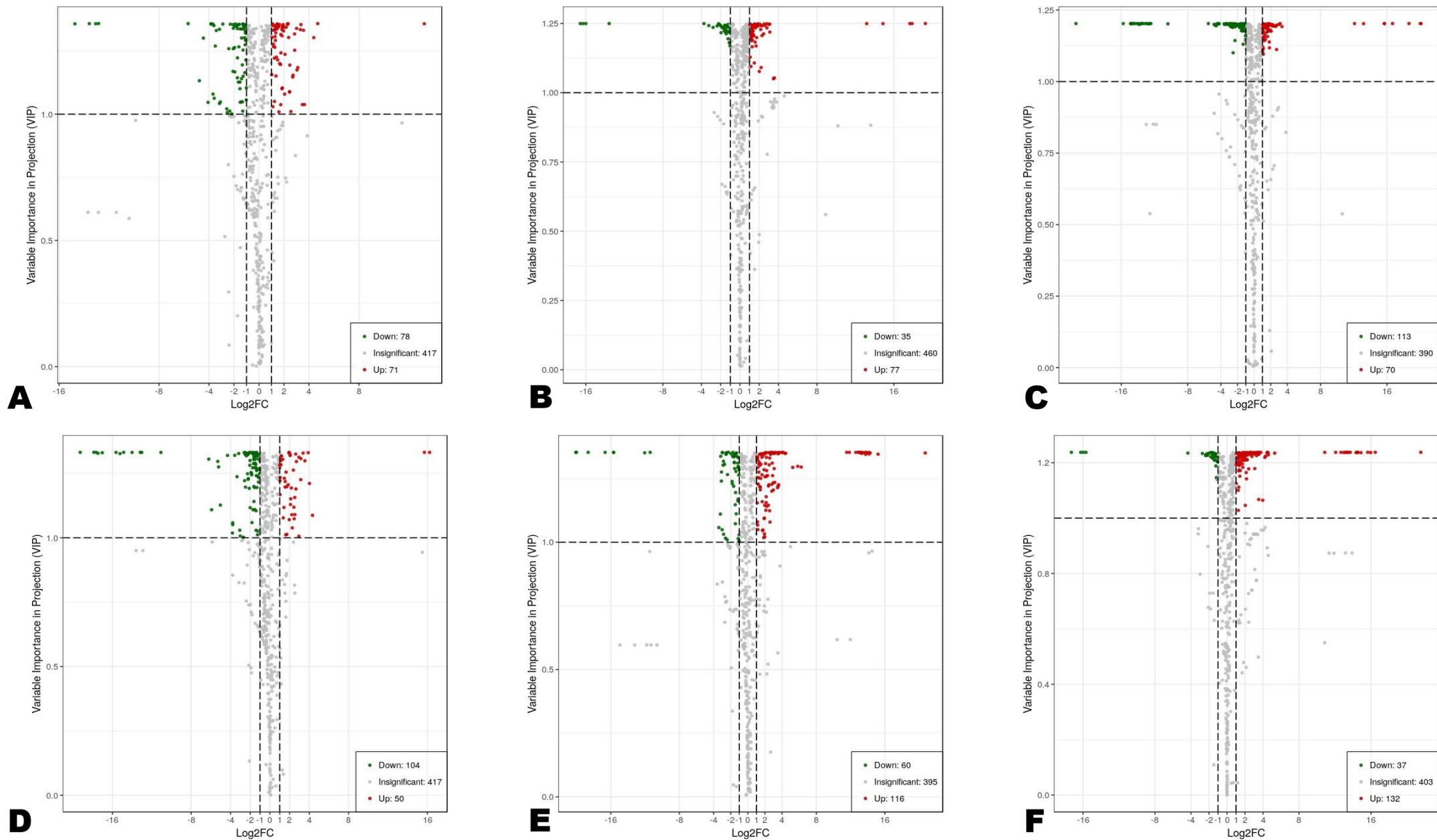


Figure S3. Volcano plots of the DAMs in pairwise comparison between (A) K1102_vs_262; (B) K1102_vs_1392; (C) K1102_vs_K115; (D) 1392_vs_262; (E) K115_vs_262; (F) K115_vs_1392.

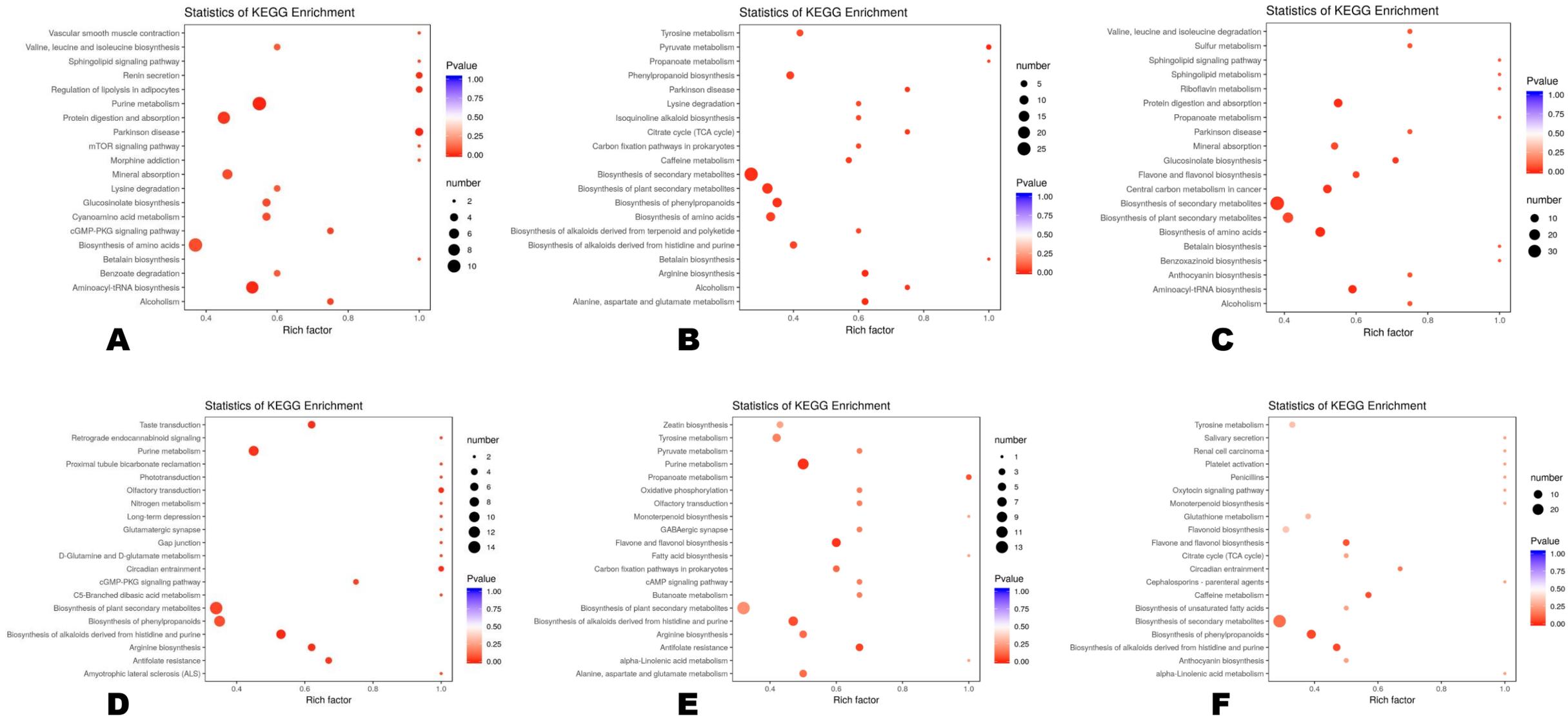
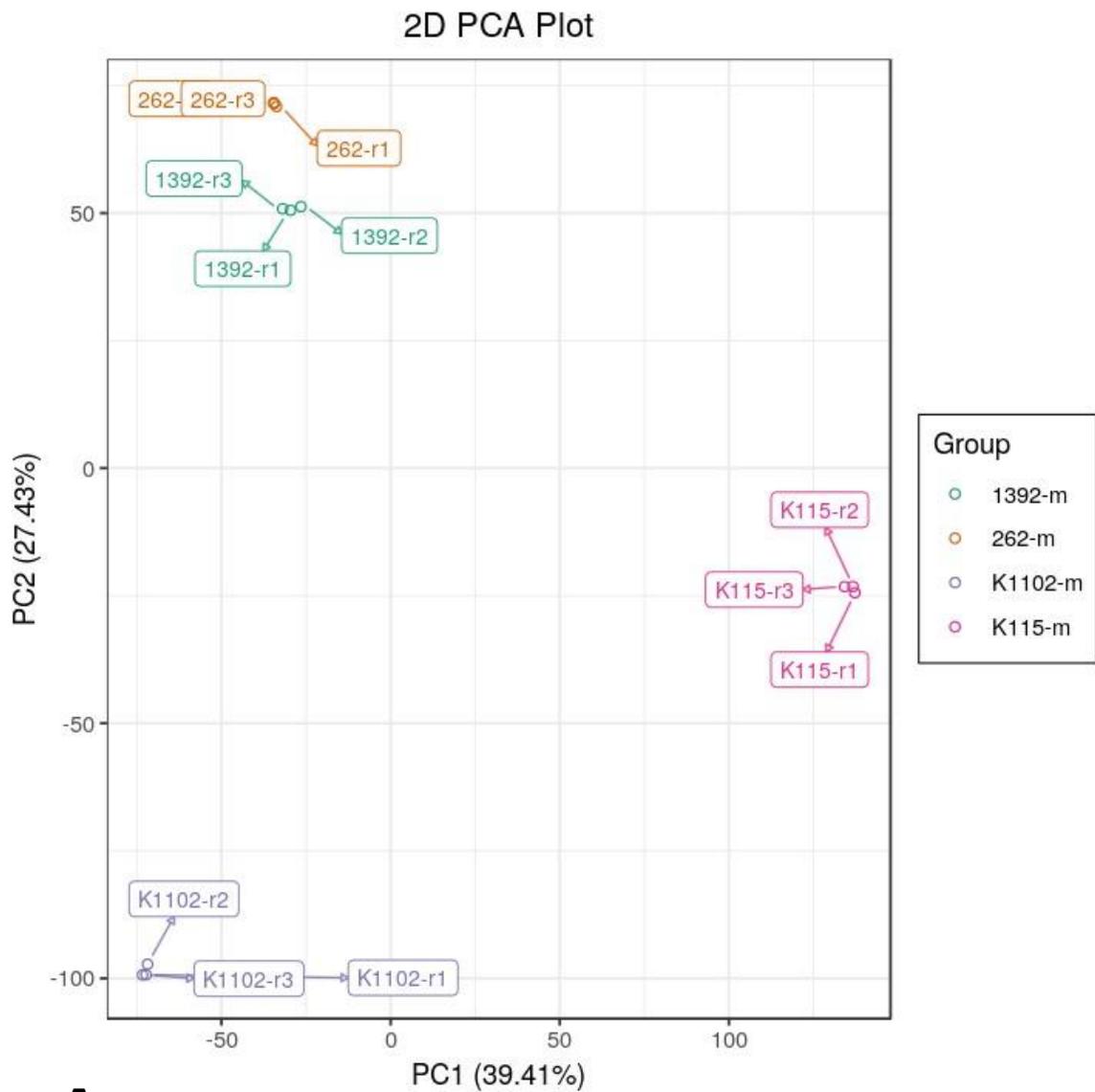


Figure S4. KEGG annotation and enrichment plots of the DAMs in pairwise comparison between (A) K1102_vs_262; (B) K1102_vs_1392; (C) K1102_vs_K115; (D) 1392_vs_262; (E) K115_vs_262; (F) K115_vs_1392.



A

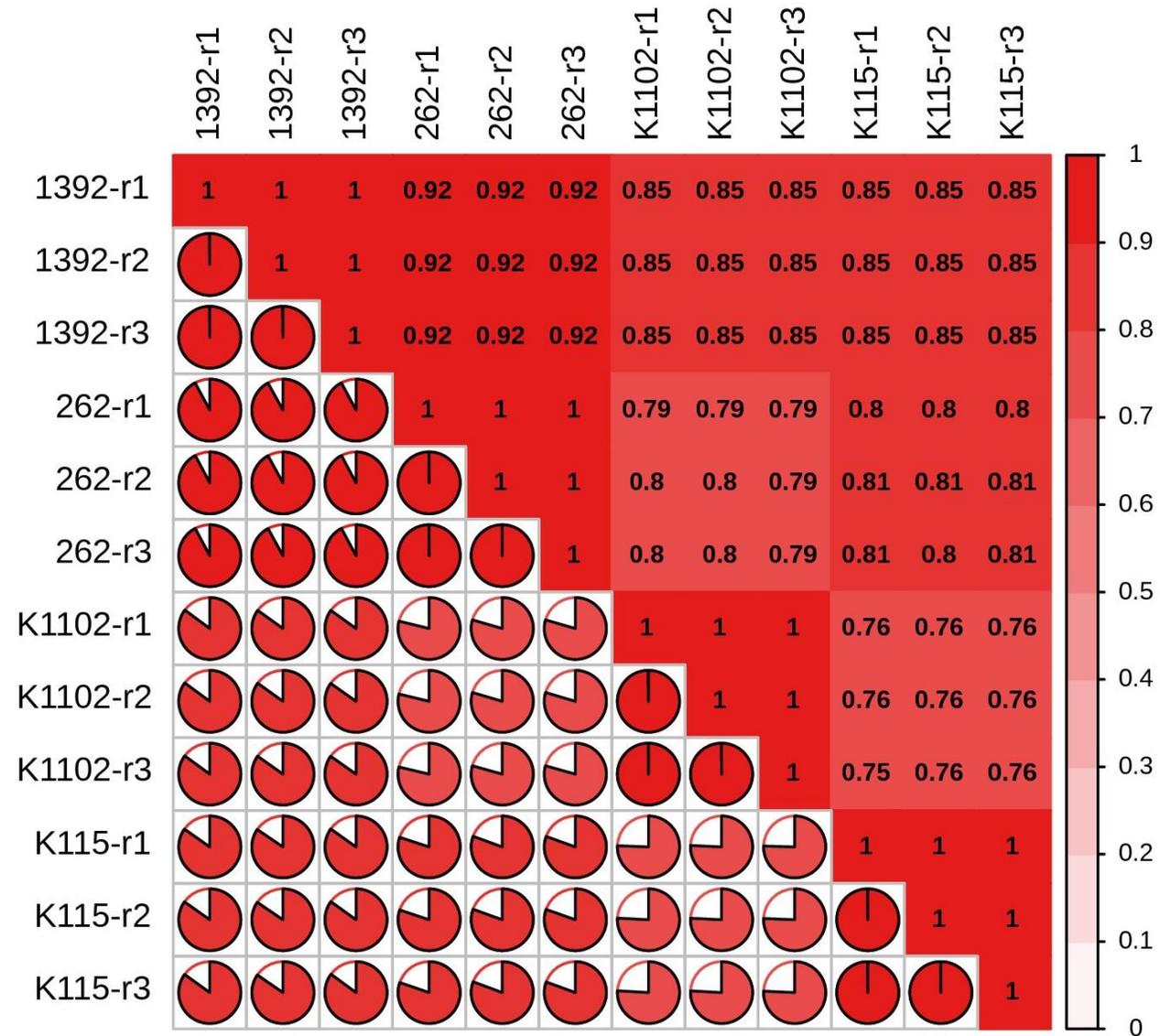


Figure S5. PCA (A) and correlation (B) analyses of samples based on the FPKM values of all genes from the transcriptome sequencing.

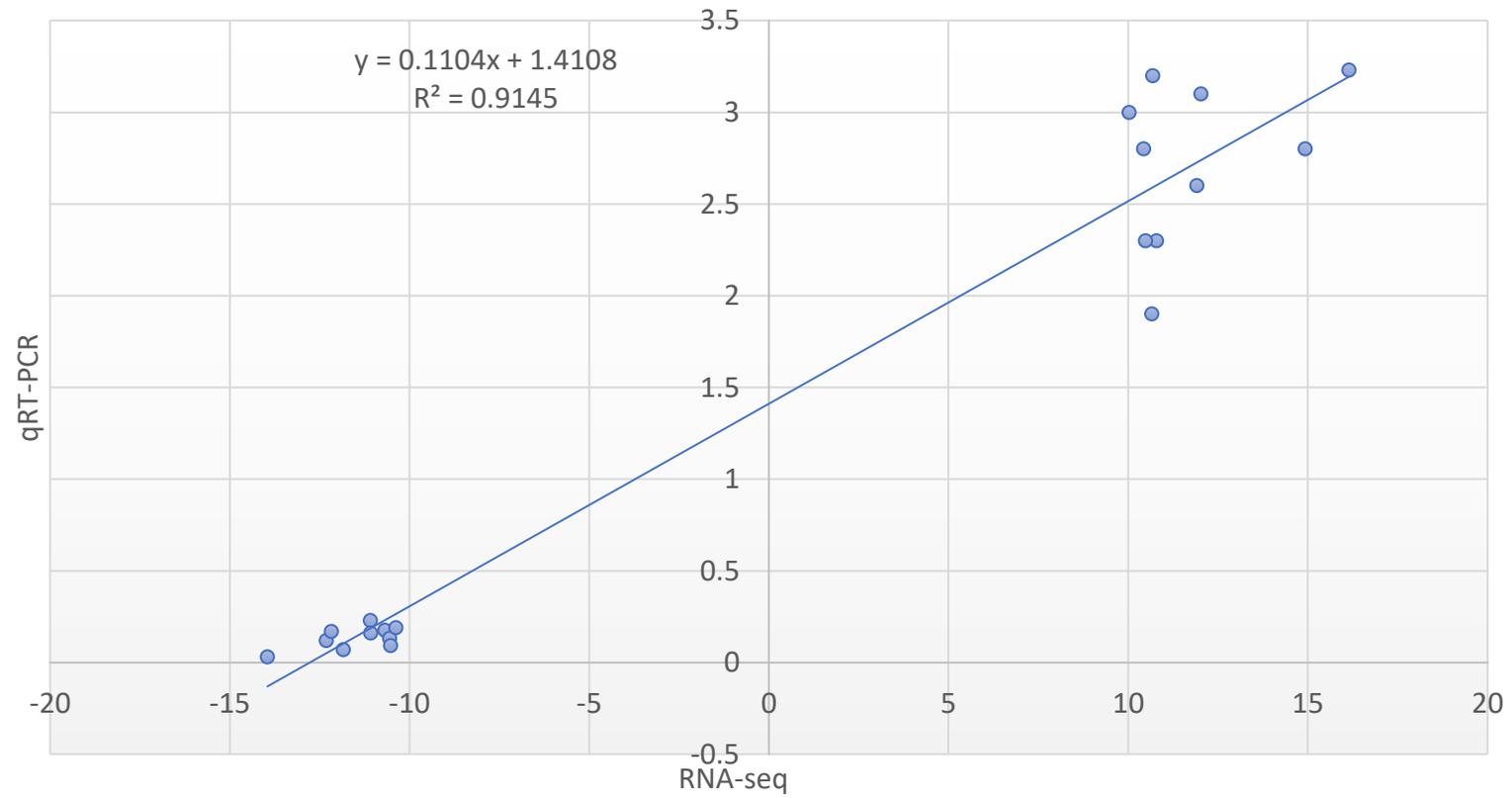
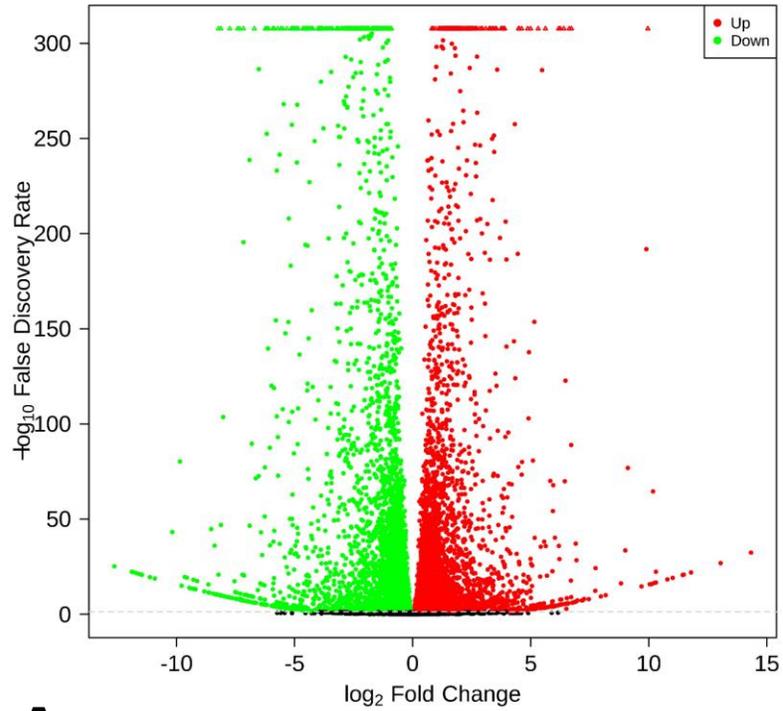


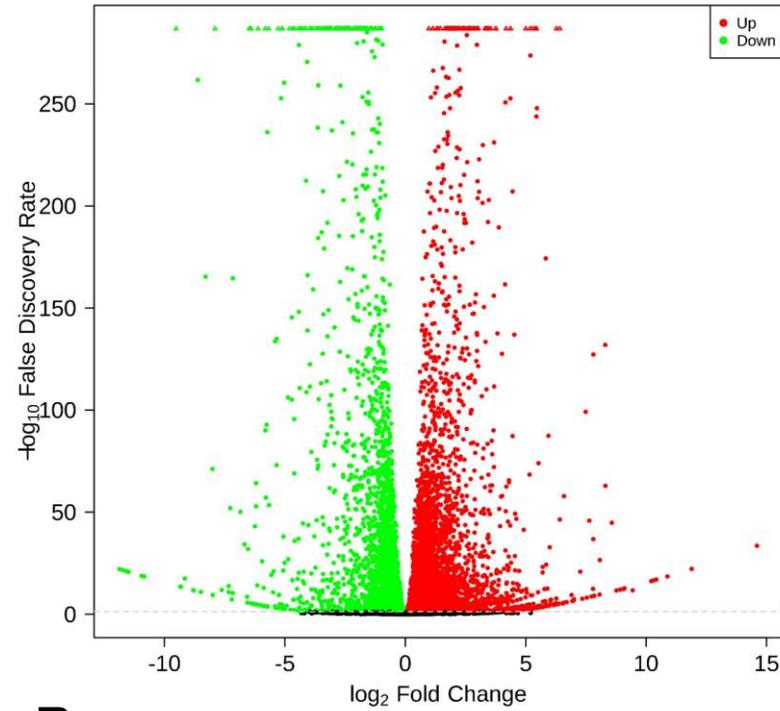
Figure S6. qRT-PCR validation of the transcriptome data.

Volcano plot - K1102r vs 262r



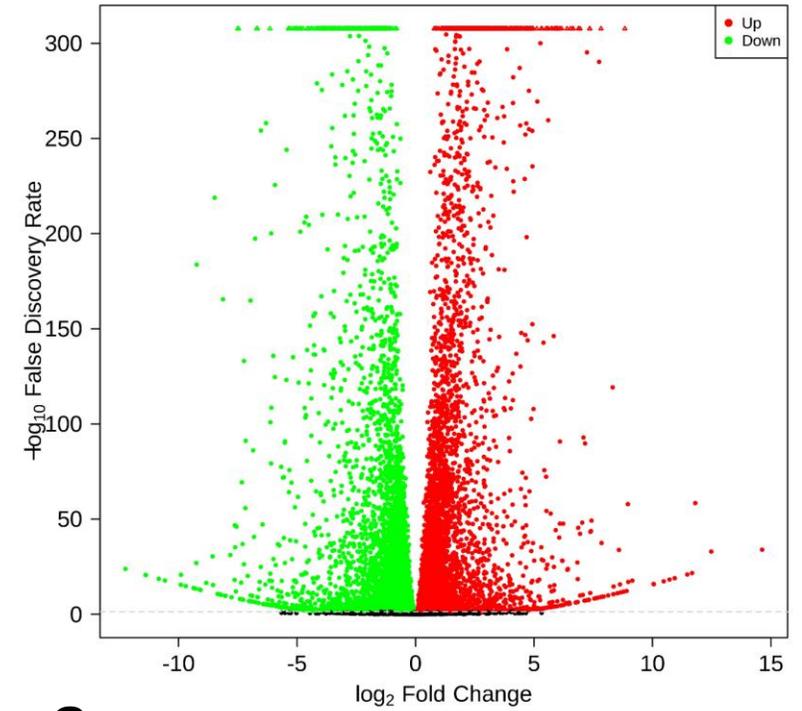
A

Volcano plot - K1102r vs 1392r



B

Volcano plot - K1102r vs K115r



C

Figure S7. Volcano plots of the DEGs in pairwise comparison between (A) K1102_vs_262; (B) K1102_vs_1392; (C) K1102_vs_K115.

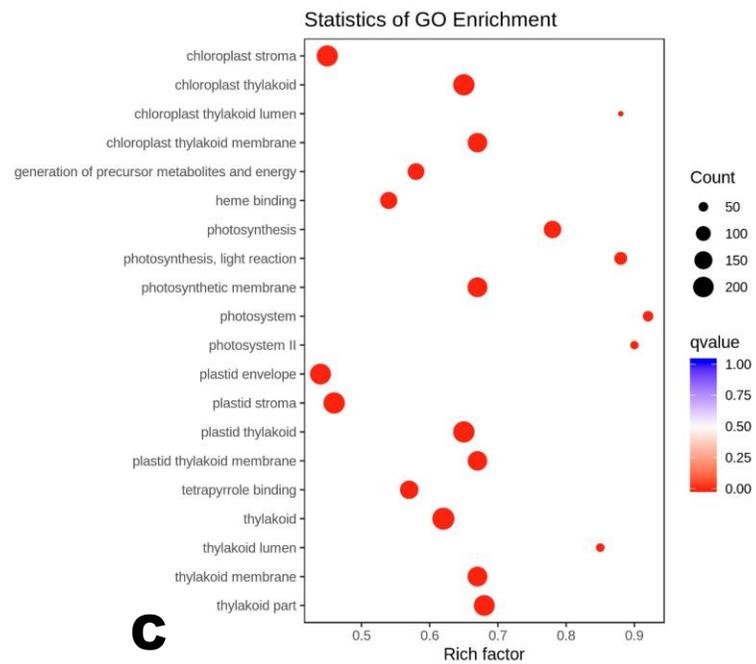
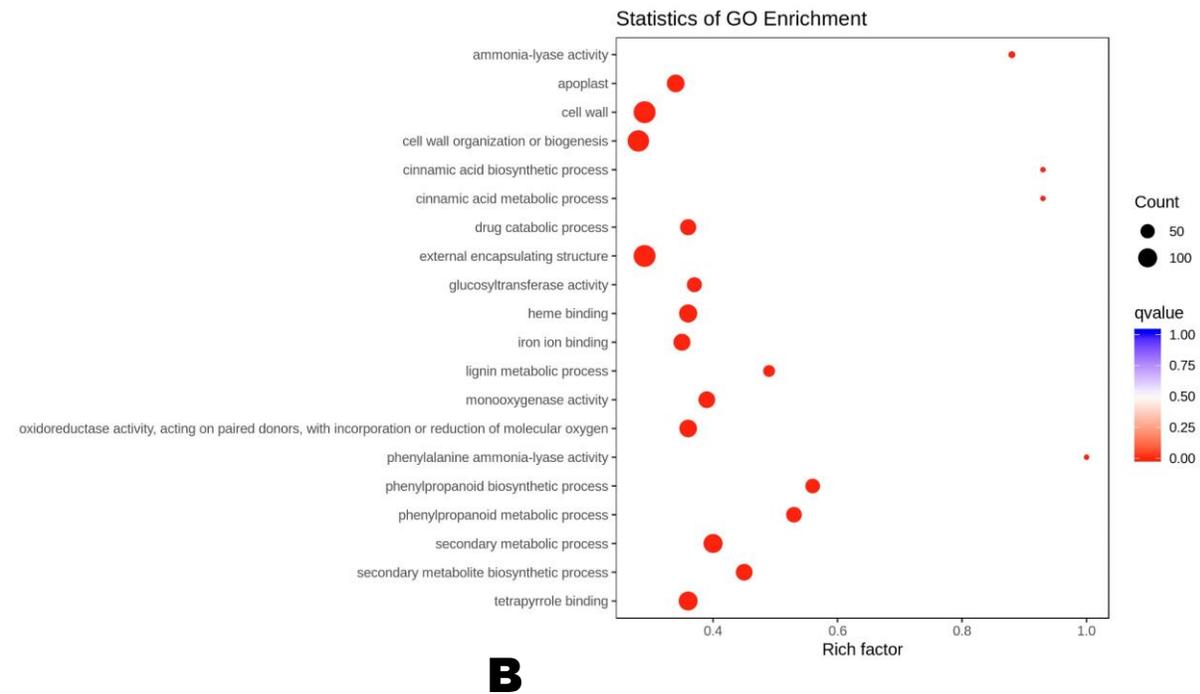
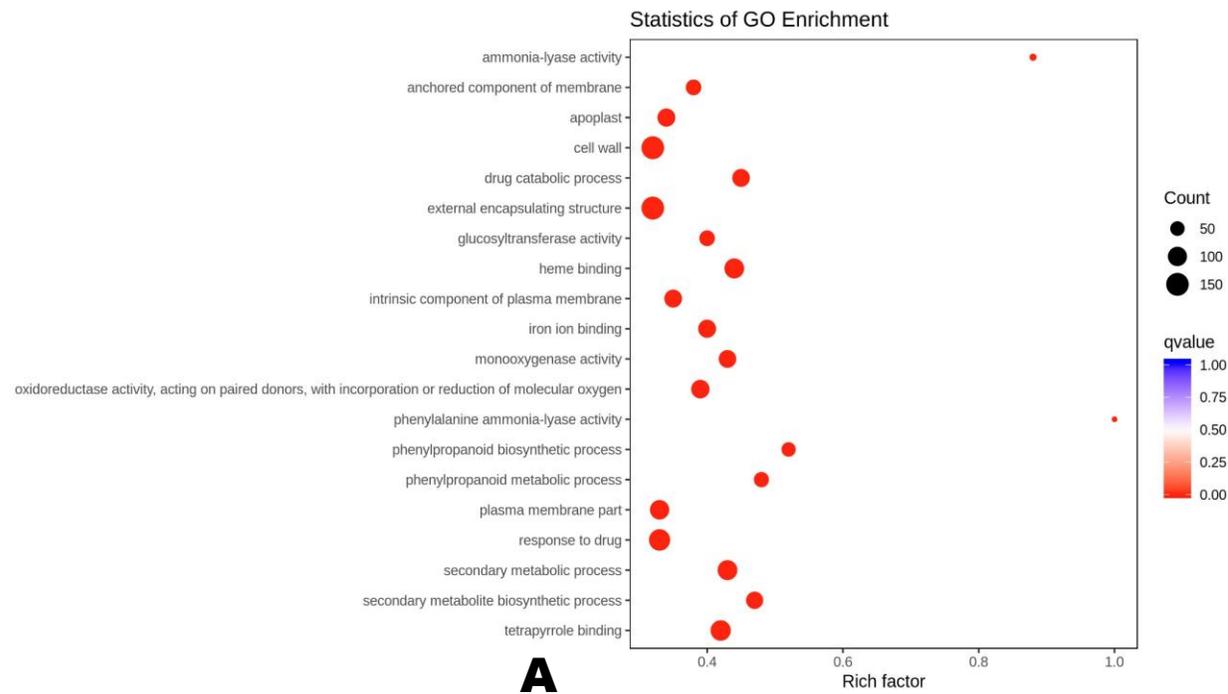


Figure S8. GO annotation and enrichment plots of the DEGs in pairwise comparison between (A) K1102_vs_262; (B) K1102_vs_1392; (C) K1102_vs_K115.

Statistics of KEGG Enrichment

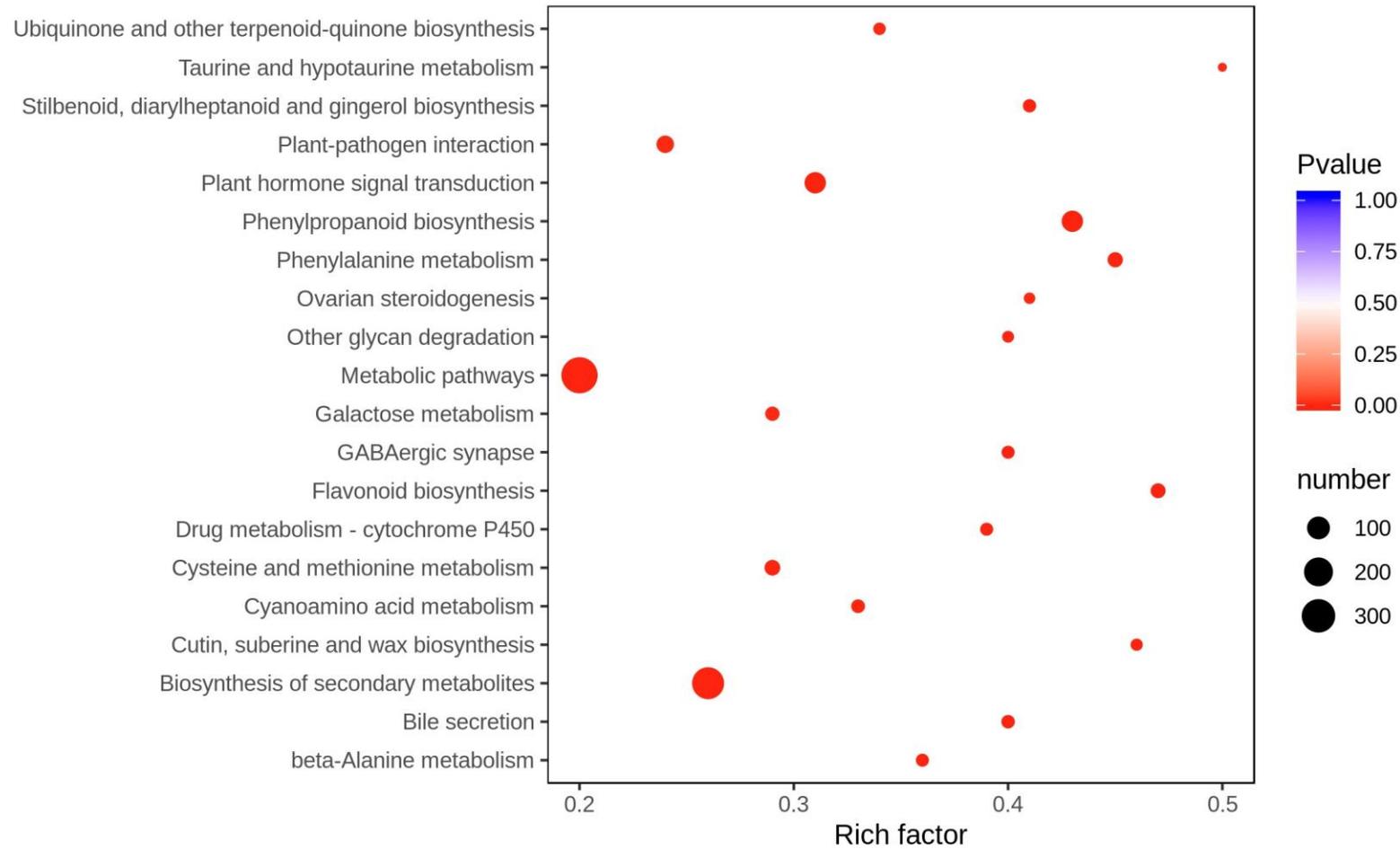


Figure S9. KEGG annotation and enrichment plots of the DEGs in pairwise comparison K1102_vs_262.

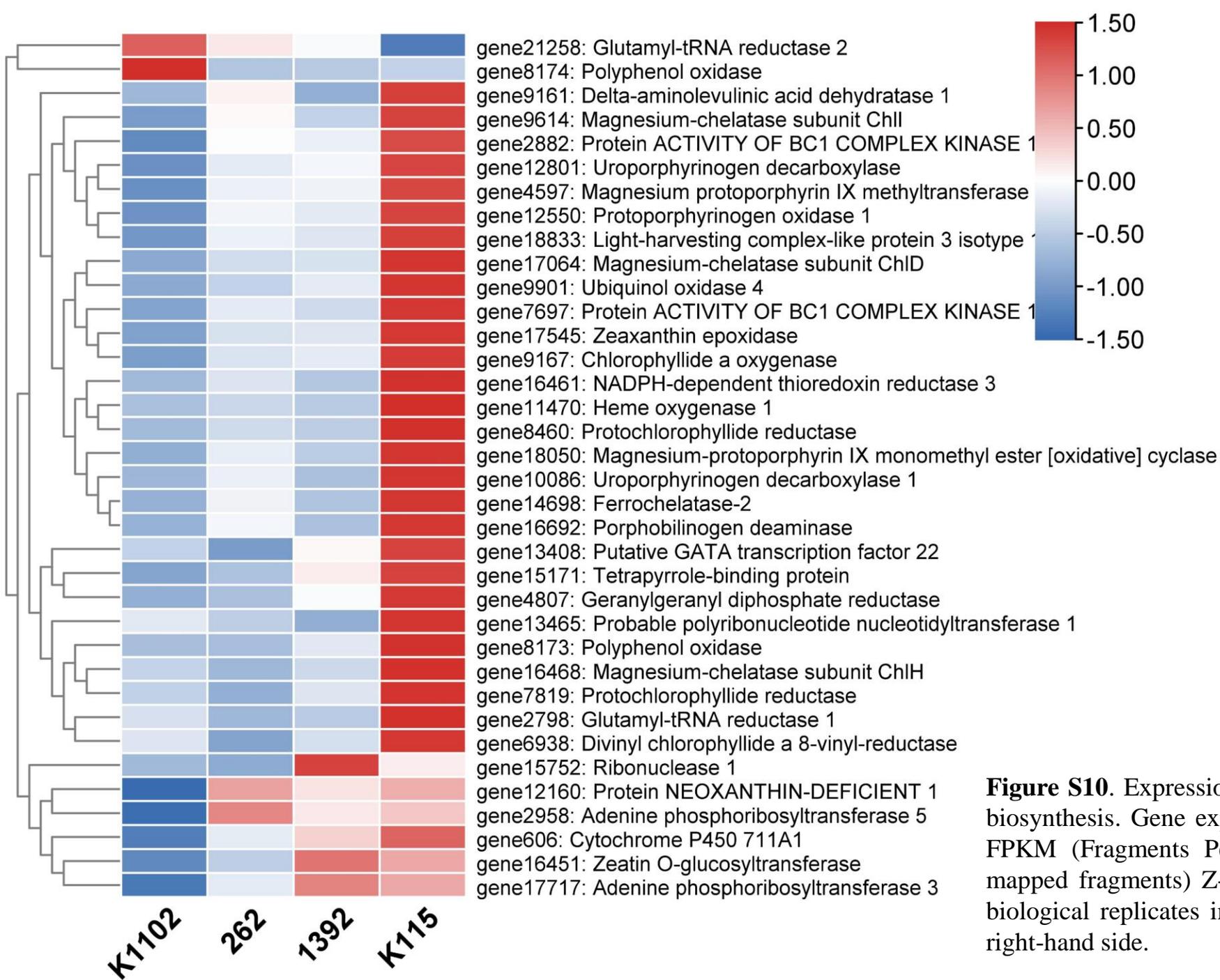


Figure S10. Expression patterns of other DEGs related pigment biosynthesis. Gene expression was scaled in this analysis using FPKM (Fragments Per Kilobase of exon model per Million mapped fragments) Z-scores based on the mean value of three biological replicates in the heatmap. The key is located on the right-hand side.

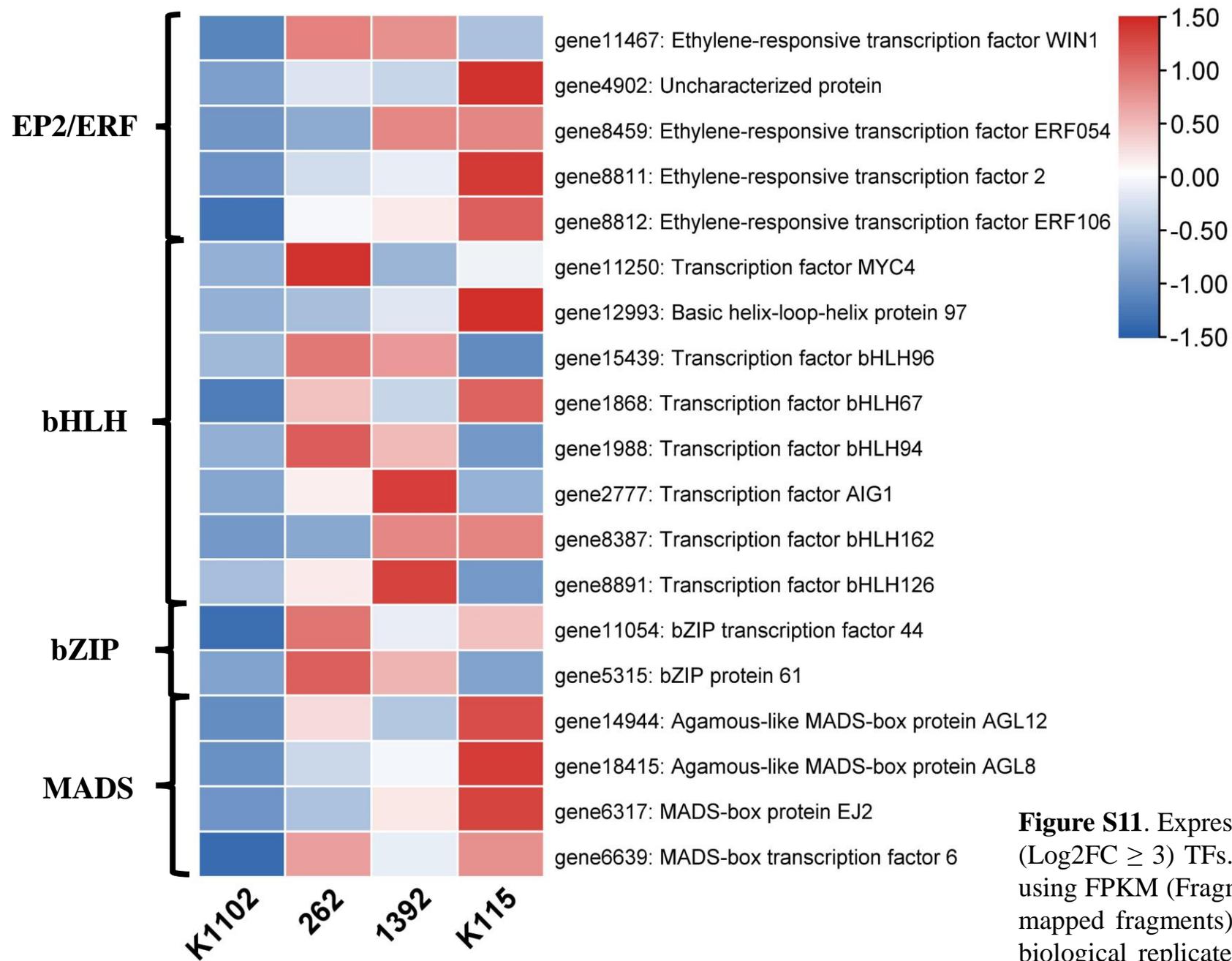


Figure S11. Expression patterns of other key highly up-regulated ($\text{Log}_2\text{FC} \geq 3$) TFs. Gene expression was scaled in this analysis using FPKM (Fragments Per Kilobase of exon model per Million mapped fragments) Z-scores based on the mean value of three biological replicates in the heatmap. The key is located on the right-hand side.