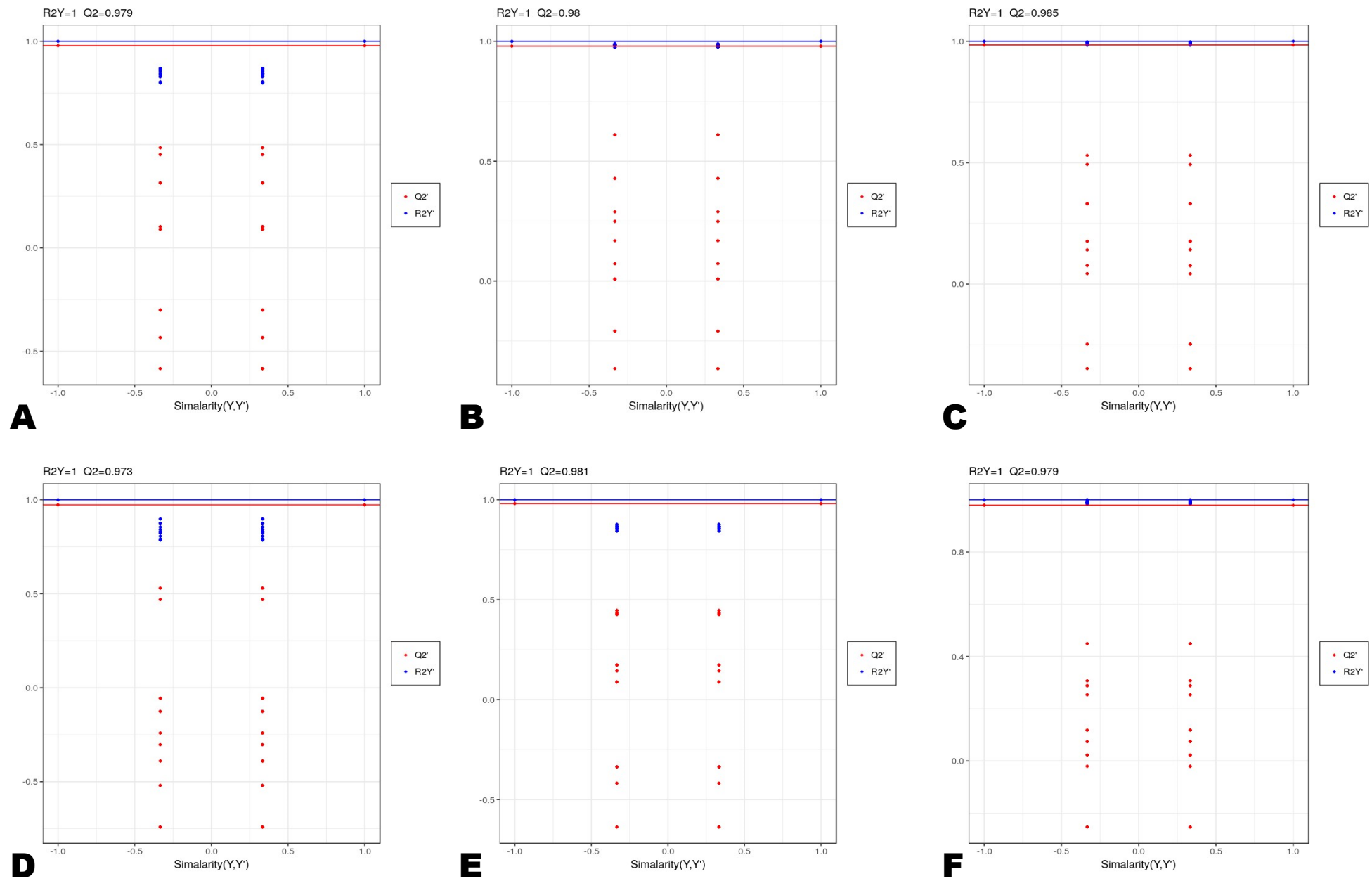
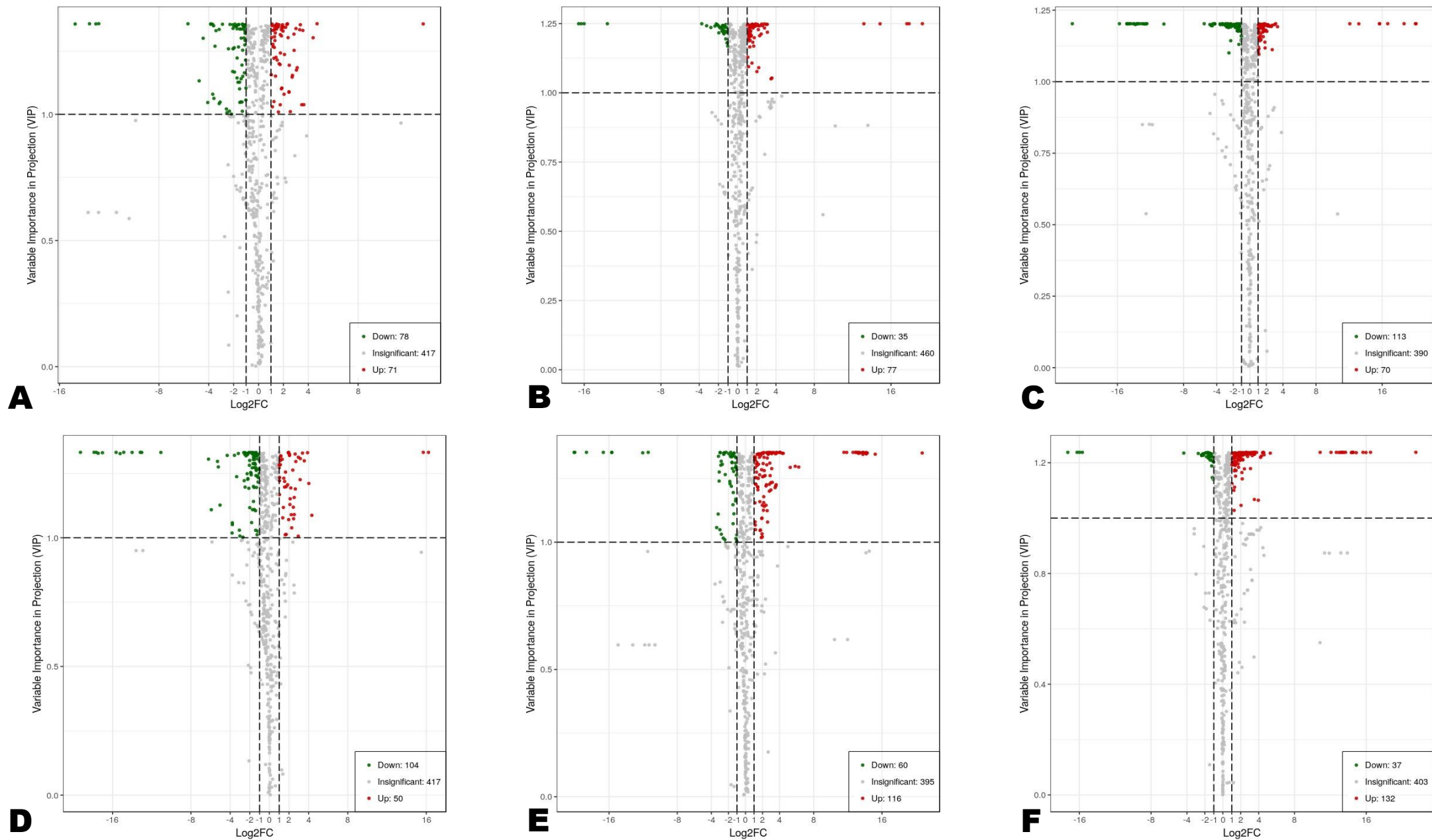


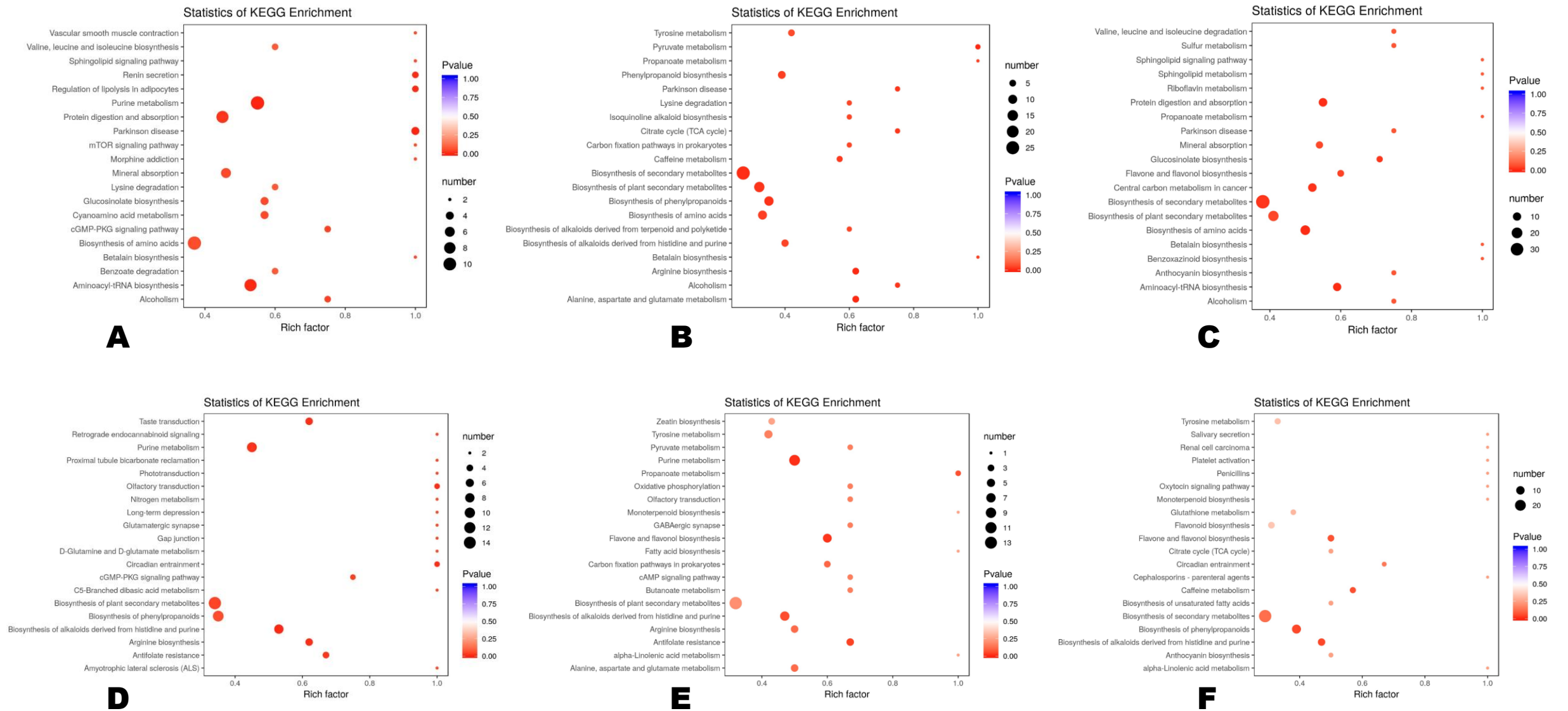
**Figure S1.** Correlation analysis of samples based on the relative content of the metabolites.



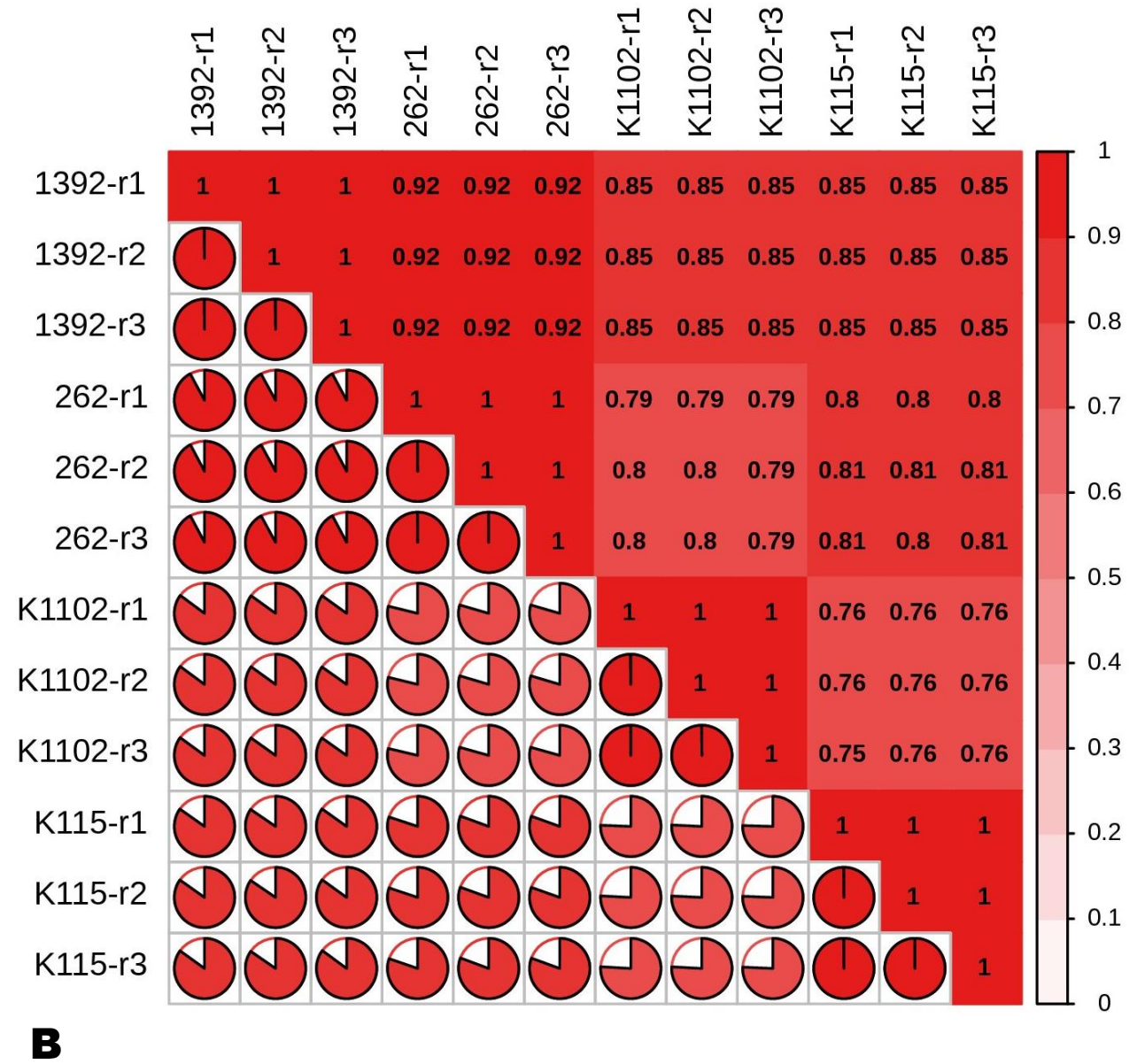
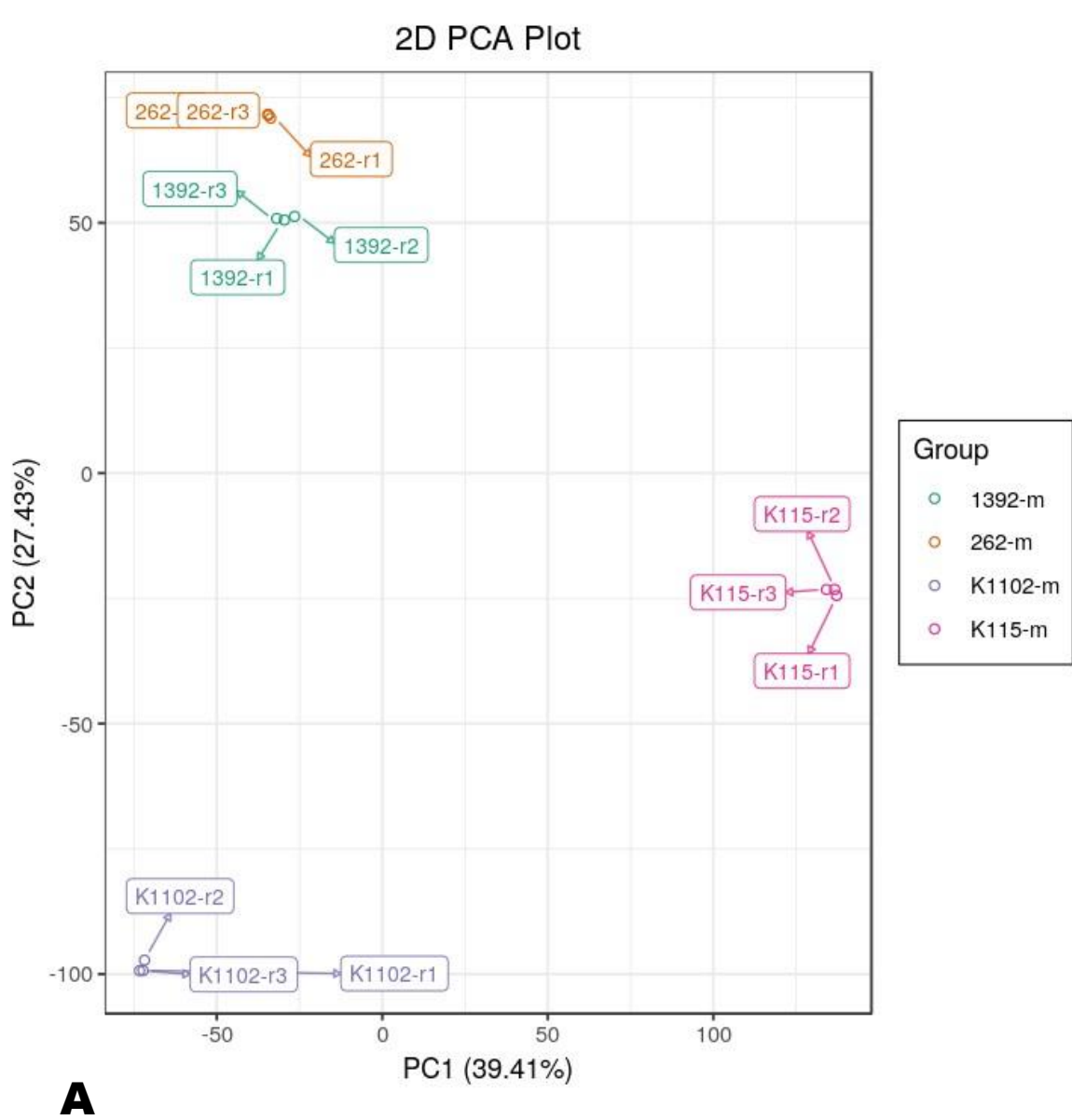
**Figure S2.** OPLS-DA plots of pairwise comparison between (A) K1102\_vs\_262; (B) K1102\_vs\_1392; (C) K1102\_vs\_K115; (D) 1392\_vs\_262; (E) K115\_vs\_262; (F) K115\_vs\_1392.



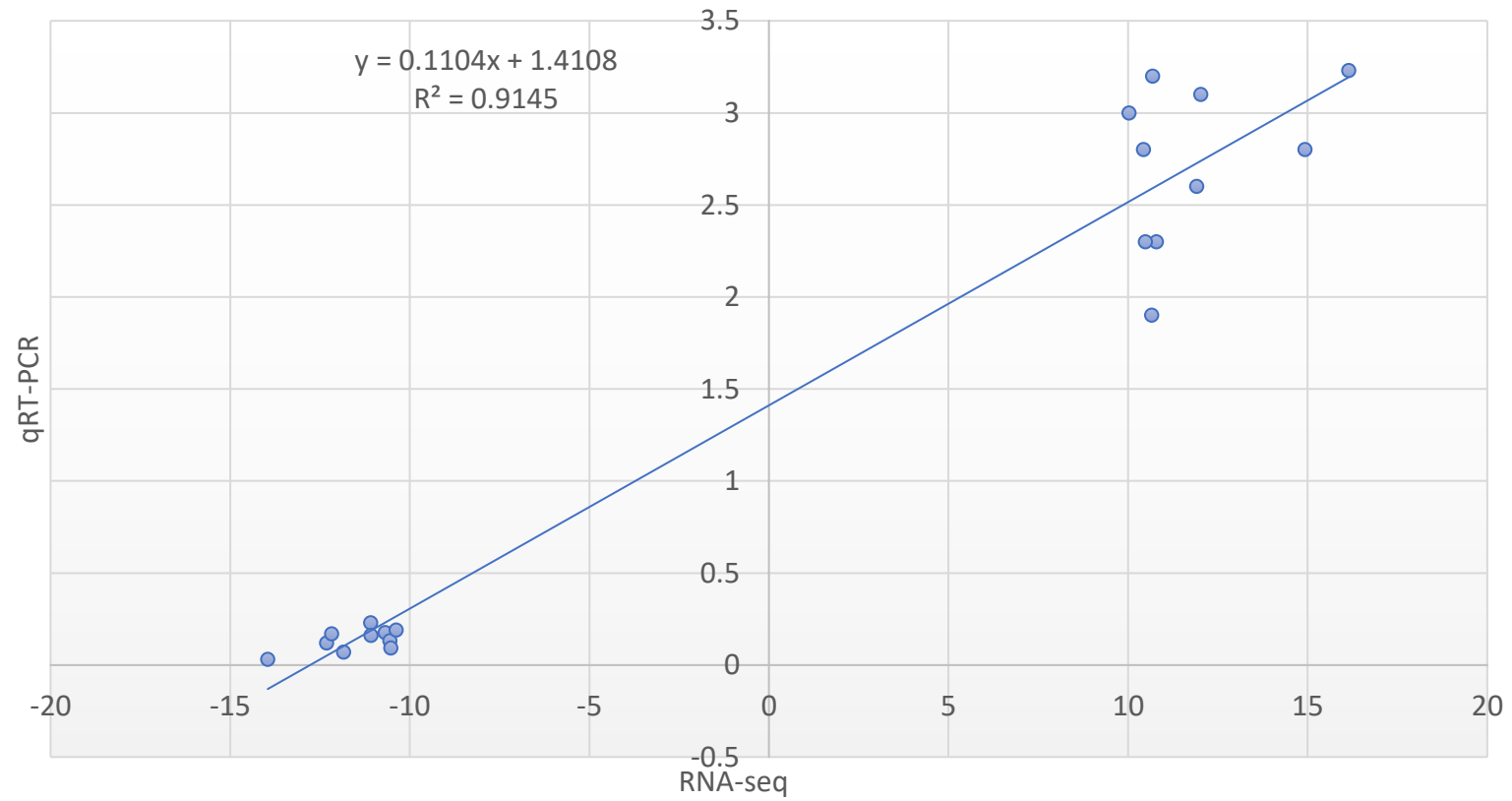
**Figure S3.** Volcano plots of the DAMs in pairwise comparison between (A) K1102\_vs\_262; (B) K1102\_vs\_1392; (C) K1102\_vs\_K115; (D) 1392\_vs\_262; (E) K115\_vs\_262; (F) K115\_vs\_1392.



**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.



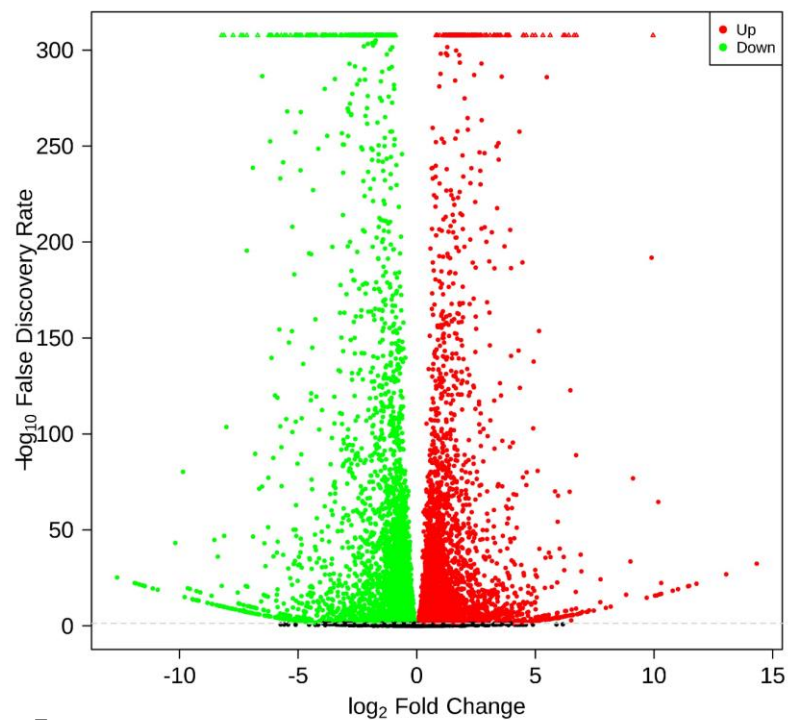
**Figure S5.** PCA (A) and correlation (B) analyses of samples based on the FPKM values of all genes from the transcriptome sequencing.



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

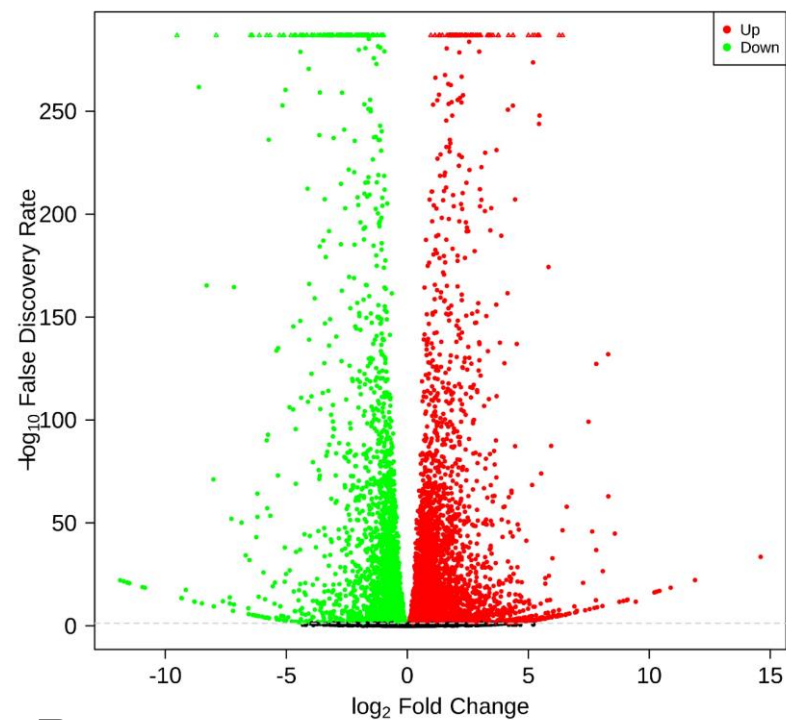


Volcano plot - K1102r vs 262r



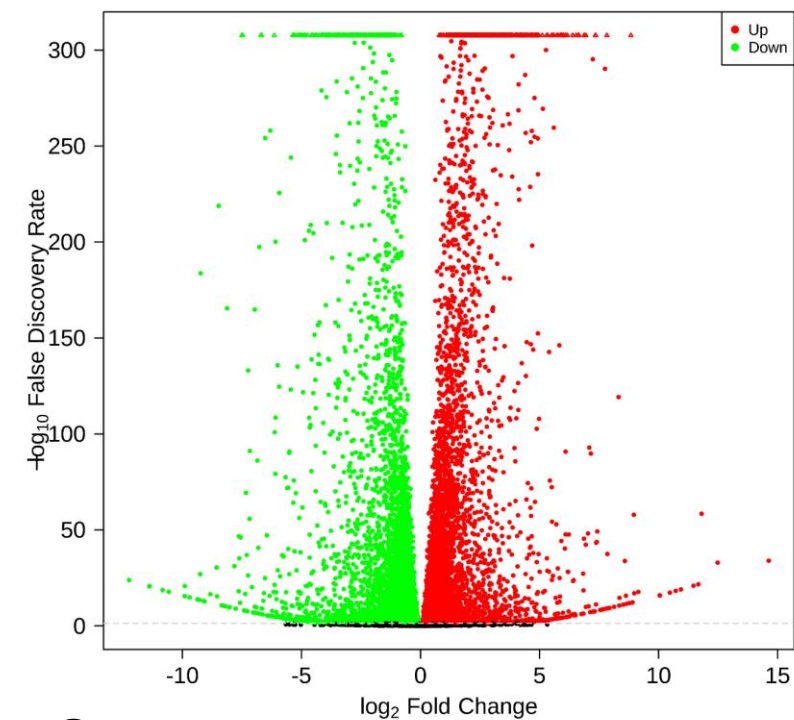
**A**

Volcano plot - K1102r vs 1392r



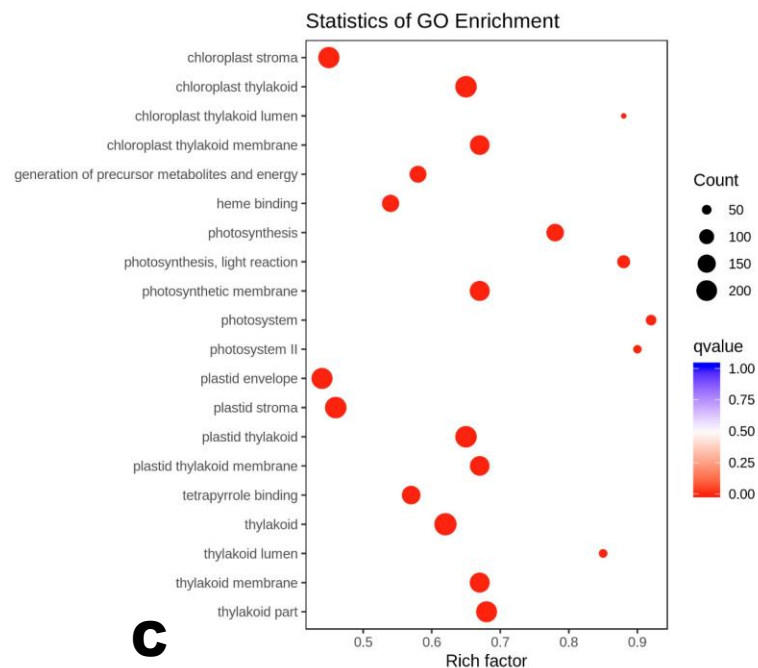
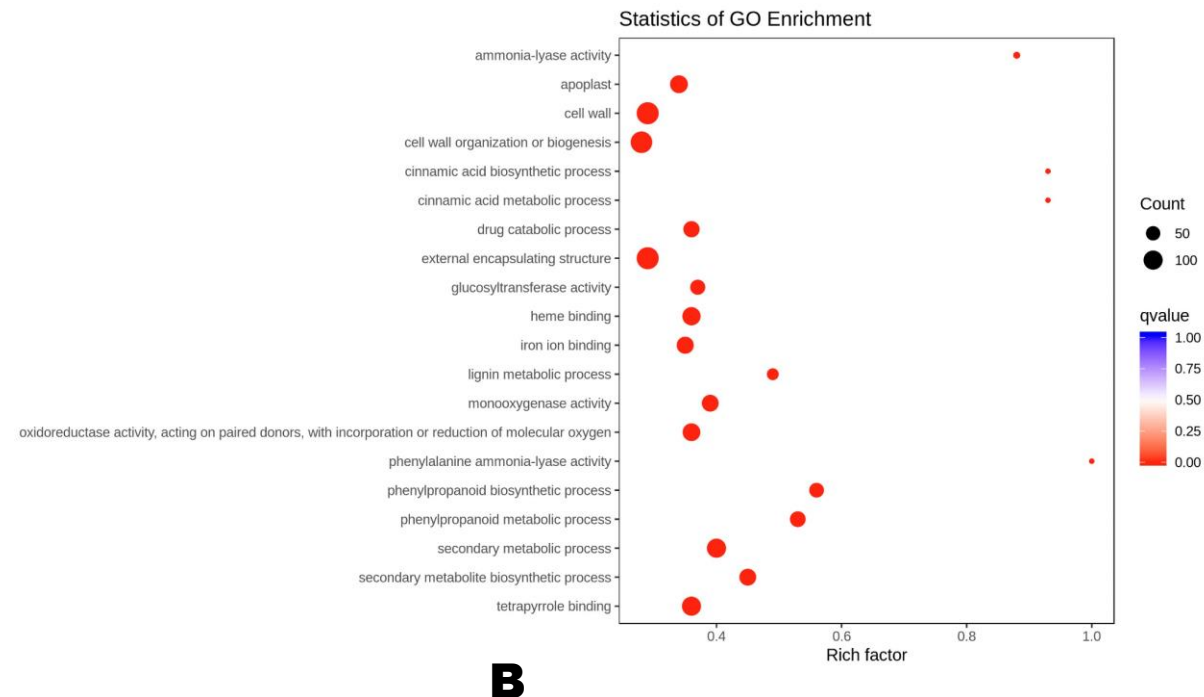
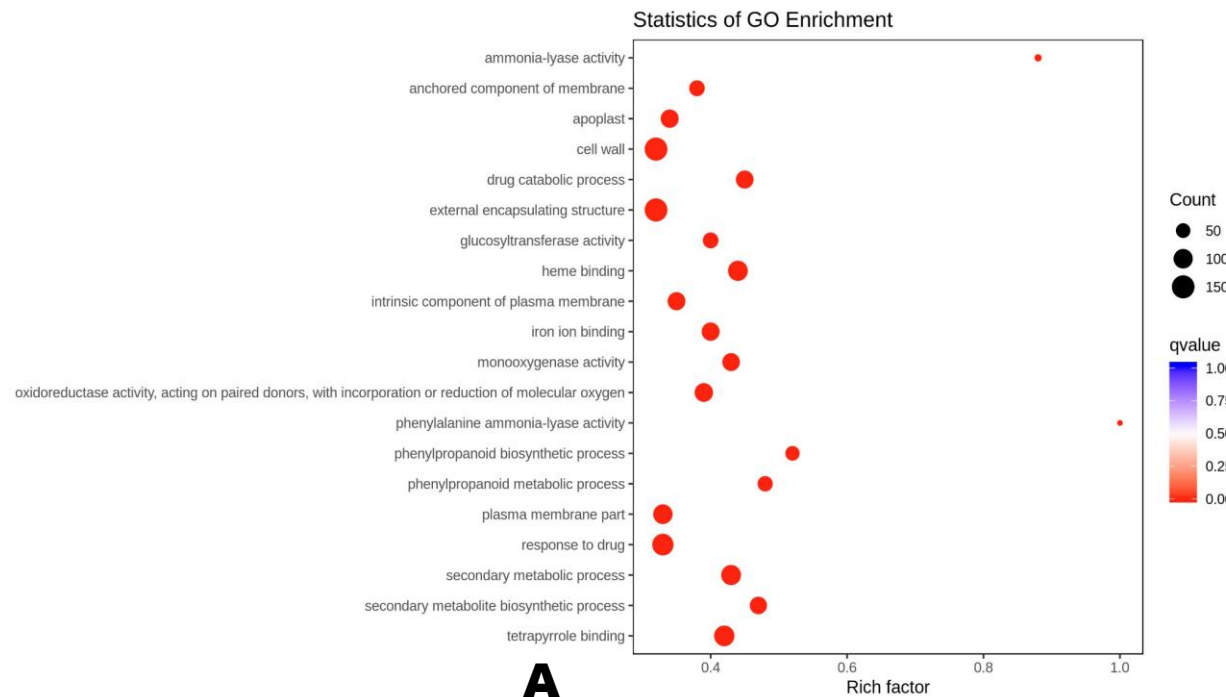
**B**

Volcano plot - K1102r vs K115r



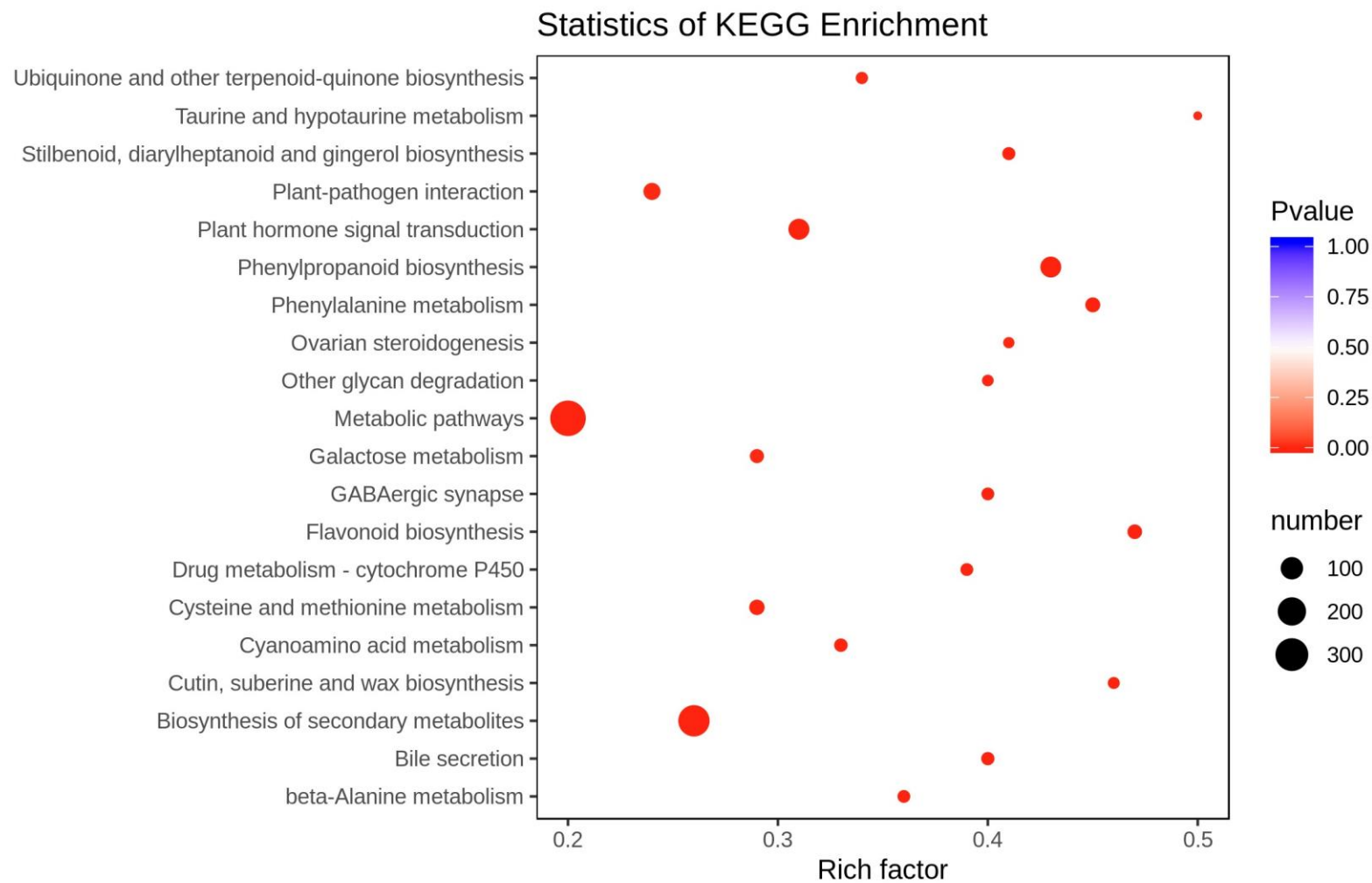
**C**

**Figure S7.** Volcano plots of the DEGs in pairwise comparison between (A) K1102\_vs\_262; (B) K1102\_vs\_1392; (C) K1102\_vs\_K115.

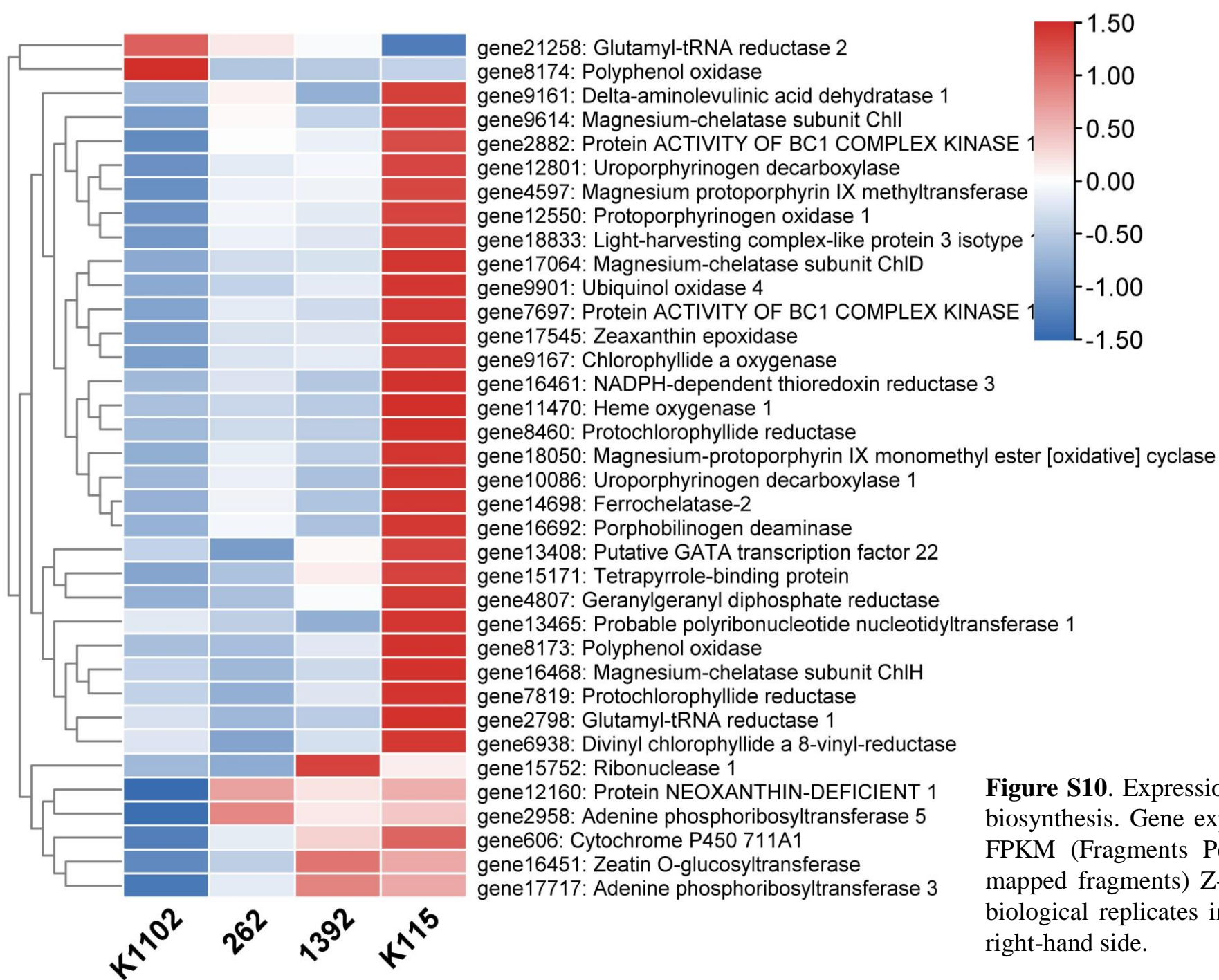


**Figure S8.** GO annotation and enrichment plots of the DEGs in pairwise comparison between (A) K1102\_vs\_262; (B) K1102\_vs\_1392; (C) K1102\_vs\_K115.

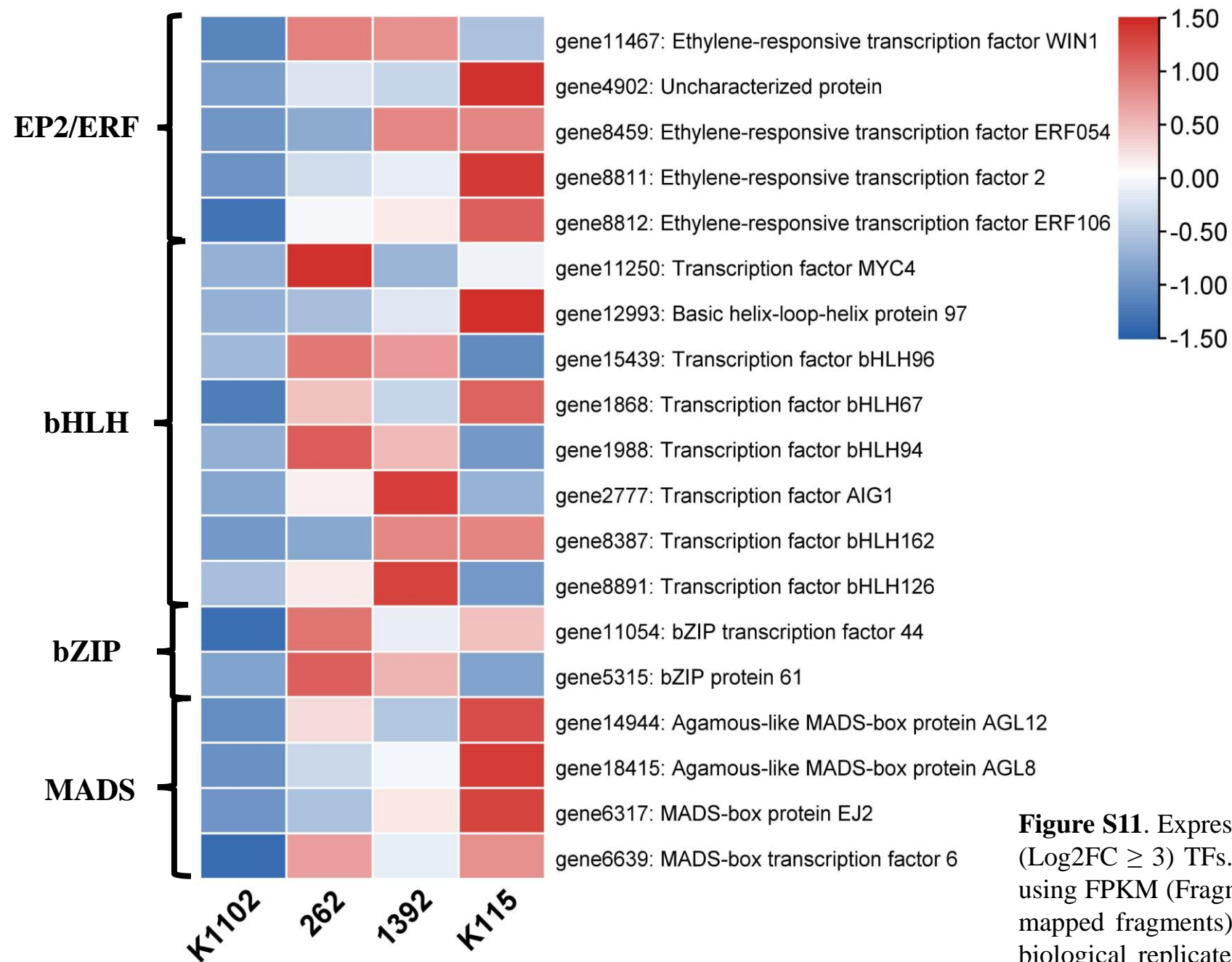




**Figure S9.** KEGG annotation and enrichment plots of the DEGs in pairwise comparison K1102\_vs\_262.



**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 ( $\text{Log2FC} \geq 3$ ) 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.