Supplemental information

Proteome-wide Mendelian randomization

and functional studies uncover therapeutic targets

for polycystic ovarian syndrome

Feida Ni, Feixia Wang, Jing Sun, Mixue Tu, Jianpeng Chen, Xiling Shen, Xiaohang Ye, Ruixue Chen, Yifeng Liu, Xiao Sun, Jianhua Chen, Xue Li, and Dan Zhang
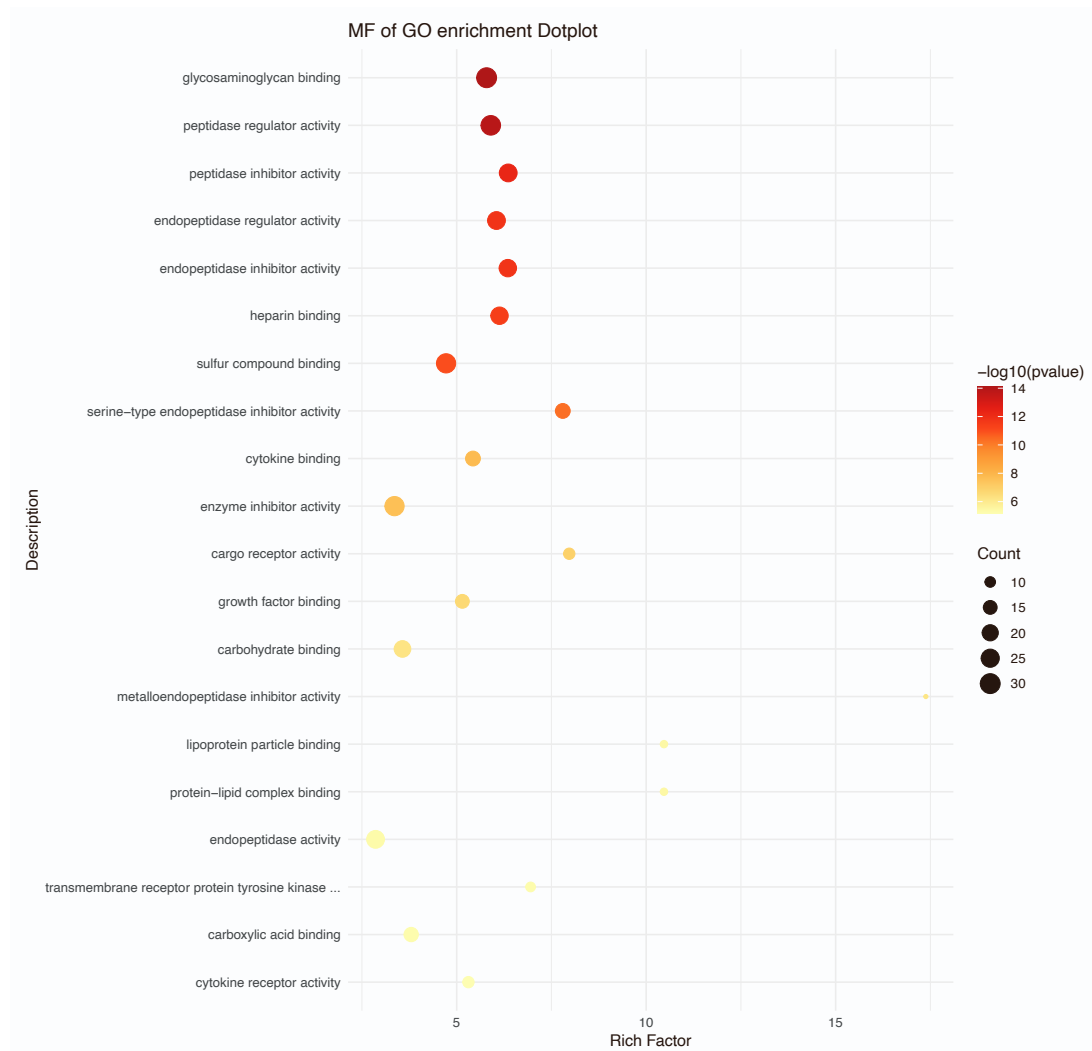
MF of GO enrichment Dotplot

Figure S1.

A scatter plot of the enriched molecular function GO terms in the GO enrichment analysis for potential therapeutic targets for PCOS. Abscissa, Rich factor. Rich factor indicates the ratio of the number of differential GO genes (S gene number) to the total number of GO genes (B gene number). The larger the Rich factor, the greater the GO enrichment. Ordinate, GO_Term (the GO function comment). In the scatter plot, the dot size represents the number of genes with a significant difference in the S gene number matched to a single GO. The dot color represents the p value of the enrichment analysis. The p value ≤ 0.05 was used as the threshold to select GO terms, which represents significant enrichment. GO, Gene Ontology.
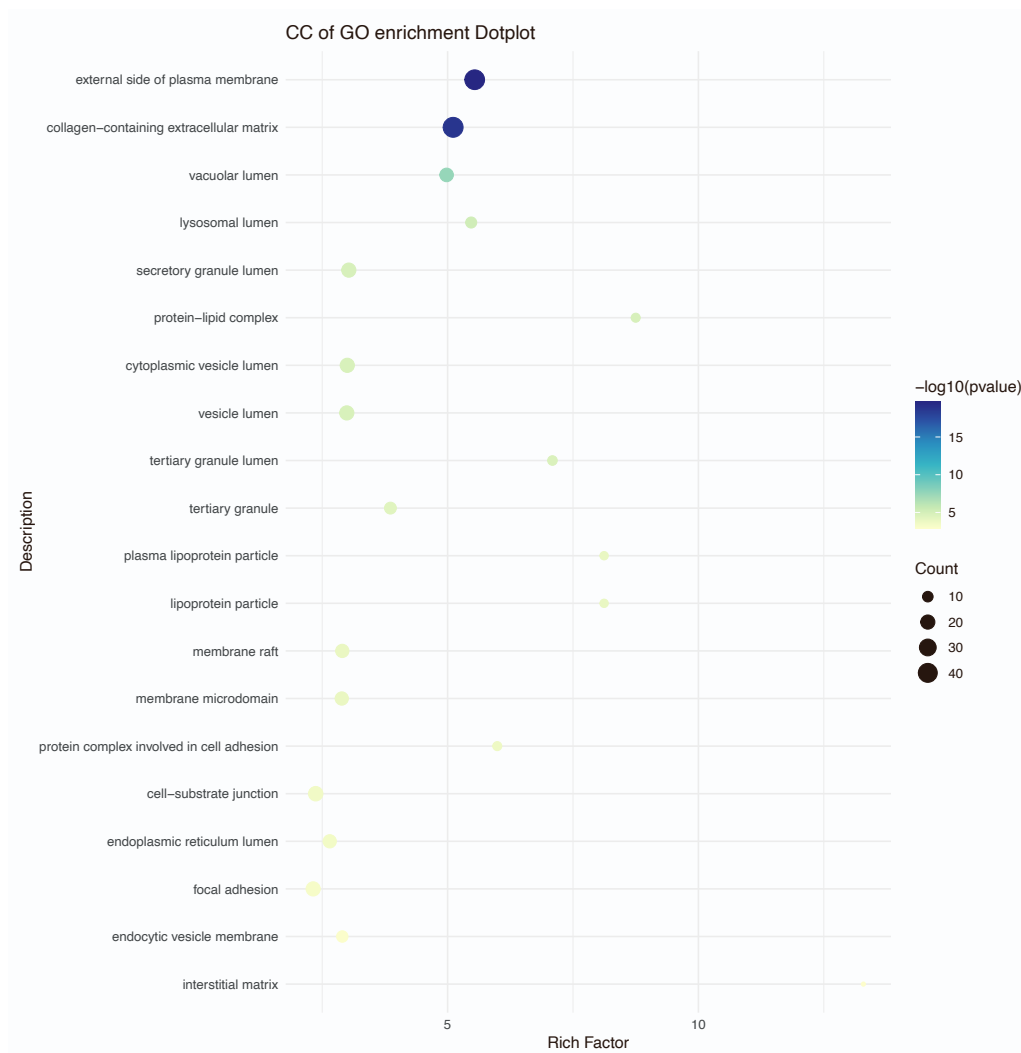
CC of GO enrichment Dotplot

Figure S2.

A scatter plot of the enriched cellular component GO terms in the GO enrichment analysis for potential therapeutic targets for PCOS. Abscissa, Rich factor. Rich factor indicates the ratio of the number of differential GO genes (S gene number) to the total number of GO genes (B gene number). The larger the Rich factor, the greater the GO enrichment. Ordinate, GO_Term (the GO function comment). In the scatter plot, the dot size represents the number of genes with a significant difference in the S gene number matched to a single GO. The dot color represents the p value of the enrichment analysis. The p value ≤ 0.05 was used as the threshold to select GO terms, which represents significant enrichment. GO, Gene Ontology.
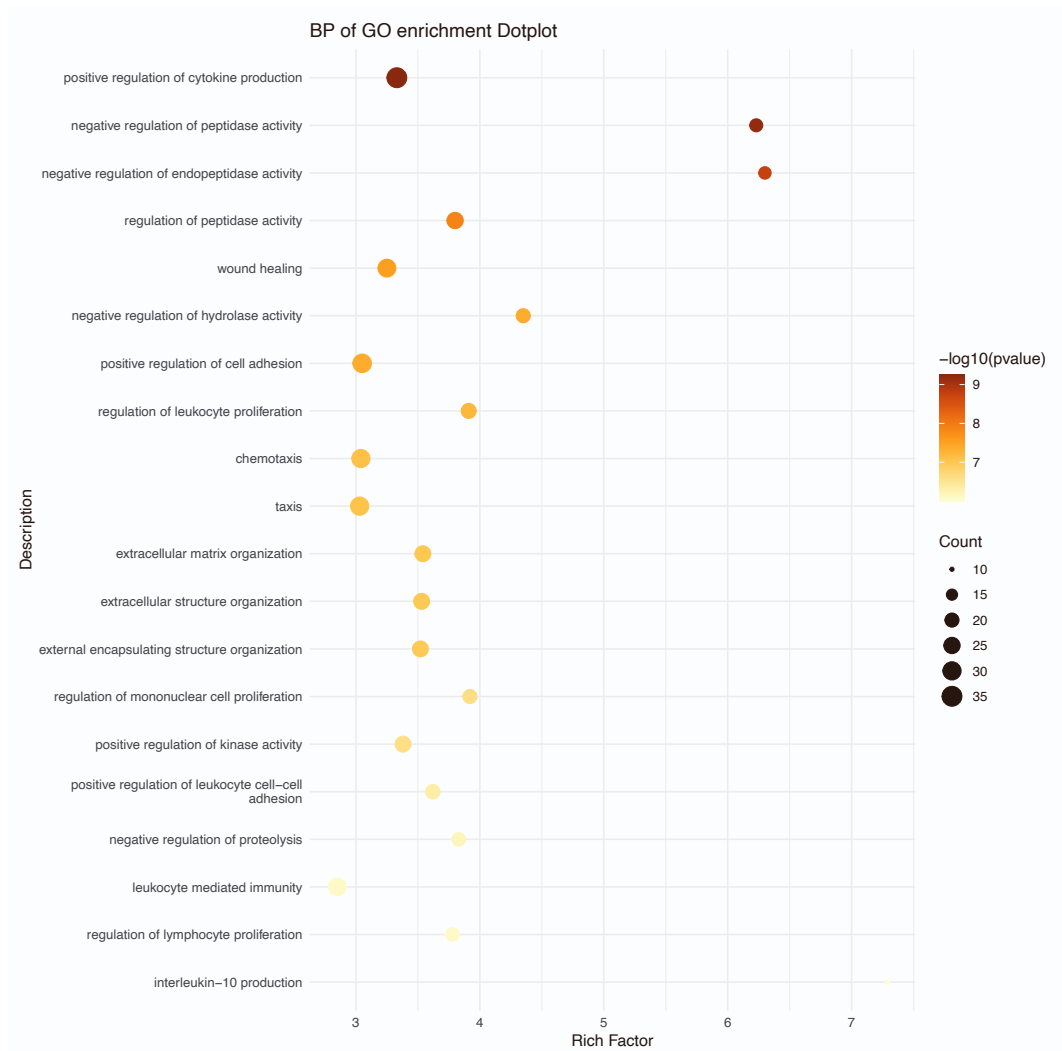
Figure S3.

A scatter plot of the enriched biological process GO terms in the GO enrichment analysis for potential therapeutic targets for PCOS. Abscissa, Rich factor. Rich factor indicates the ratio of the number of differential GO genes (S gene number) to the total number of GO genes (B gene number). The larger the Rich factor, the greater the GO enrichment. Ordinate, GO_Term (the GO function comment). In the scatter plot, the dot size represents the number of genes with a significant difference in the S gene number matched to a single GO. The dot color represents the p value of the enrichment analysis. The p value ≤ 0.05 was used as the threshold to select GO terms, which represents significant enrichment. GO, Gene Ontology.
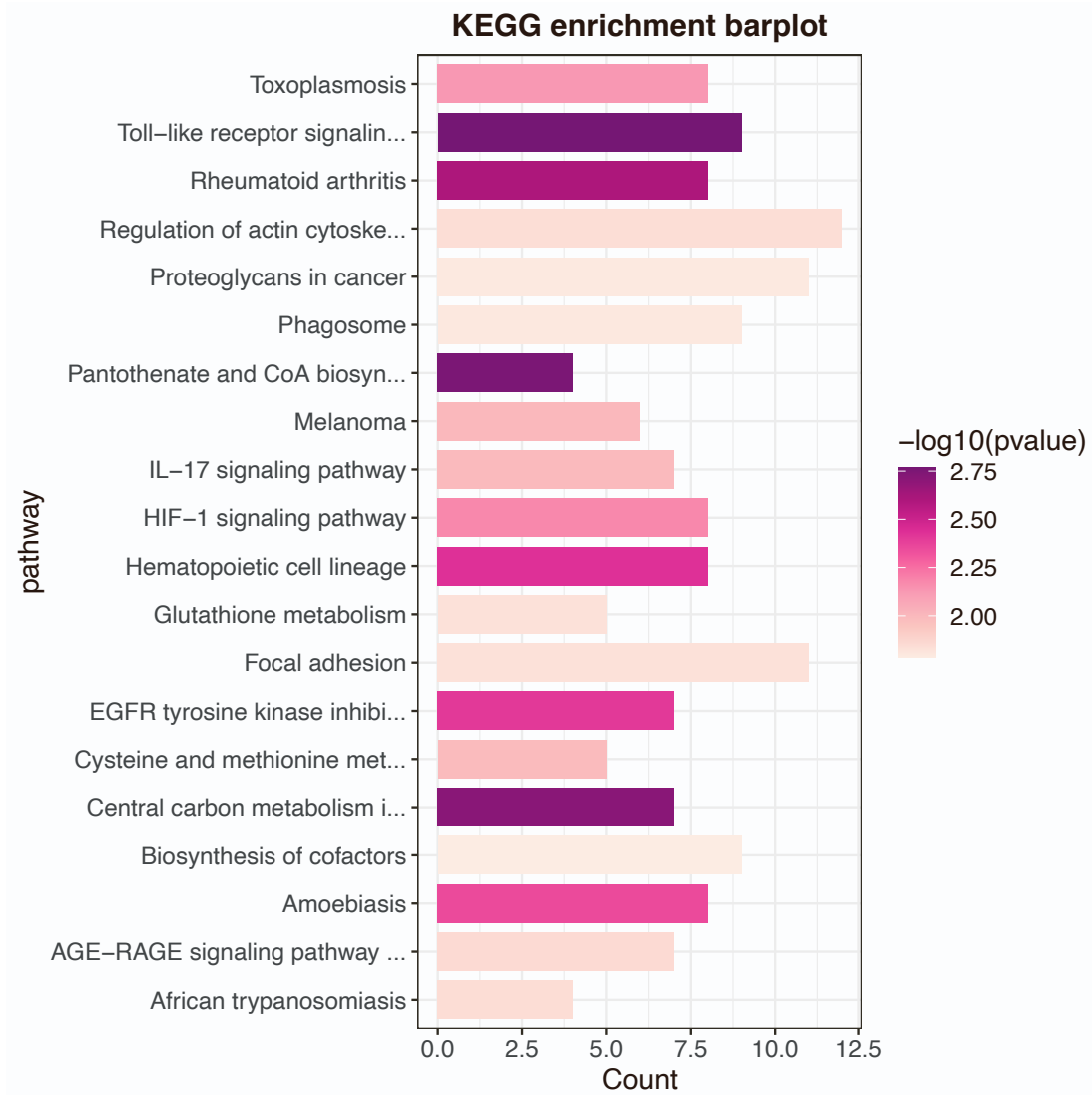
KEGG enrichment barplot

Figure S4.

A histogram of the KEGG pathway enrichment analysis of potential therapeutic targets for PCOS. Abscissa, the number of genes; ordinate, pathway term (the KEGG metabolic pathway). The dot color represents the *p* value of the enrichment analysis. The *p* value ≤ 0.05 was used as the threshold to select KEGG terms, which represents significant enrichment. KEGG, Kyoto Encyclopedia of Genes and Genomes.