

Supplementary Information

Supplementary Table Legends

Supplementary Table 1. Go functional enrichment analysis of DEGs.

Supplementary Table 2. KEGG pathway enrichment analysis of DEGs.

Supplementary Table 3. KEGG pathway enrichment analysis of each module.

Supplementary Table 4. The selection of hub genes based on MNC and MCC methods.

Supplementary Table 5. KEGG pathway enrichment analysis of 17 hub genes.

Supplementary Table 6. The primer sequences of IL17R, CD8A, CD3D, CD48, CCL2, LEP and β -actin.

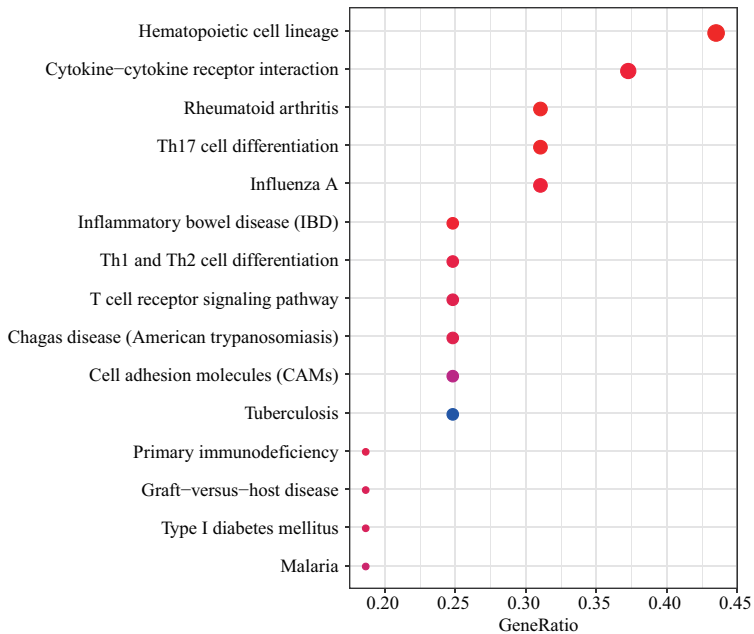
Supplementary Figure Legends

Supplementary Figure 1. KEGG pathway enrichment analysis of 17 hub genes. (A) The dot plot of KEGG pathway enrichment results. (B) The connections of hub genes and KEGG pathways.

Supplementary Figure 2. Genes expression changes between PE and normal tissues.

IL17R, CD8A, CD3D, CD48 and CCL2 mRNA expression levels were significantly downregulated in the placenta of patients with PE, and LEP mRNA level was upregulated using RT-qPCR. N = 5/group, * p-value < 0.05, ** p-value < 0.01, *** p-value < 0.001 vs. NC and analyzed by Student's t-test.

A



B

