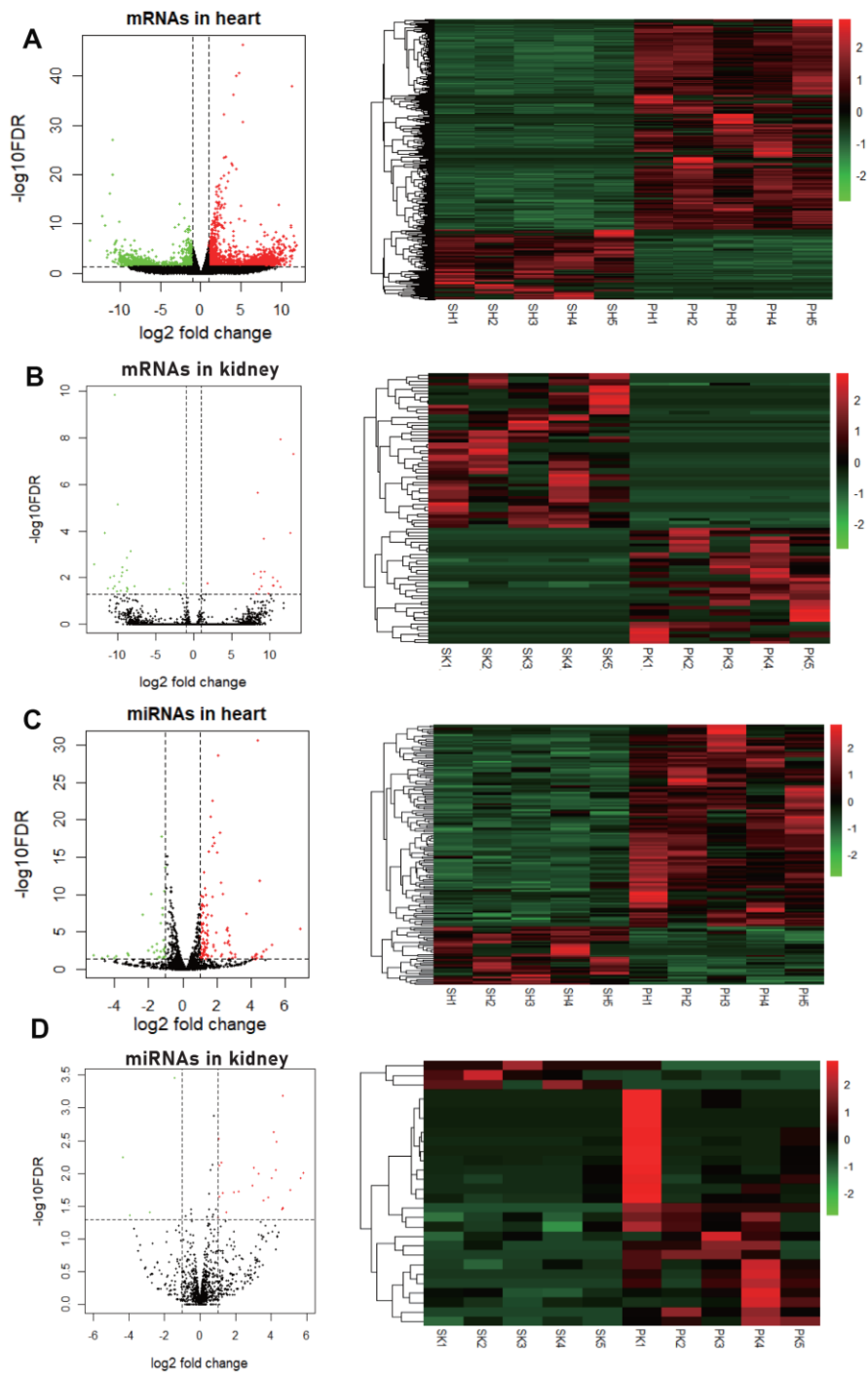
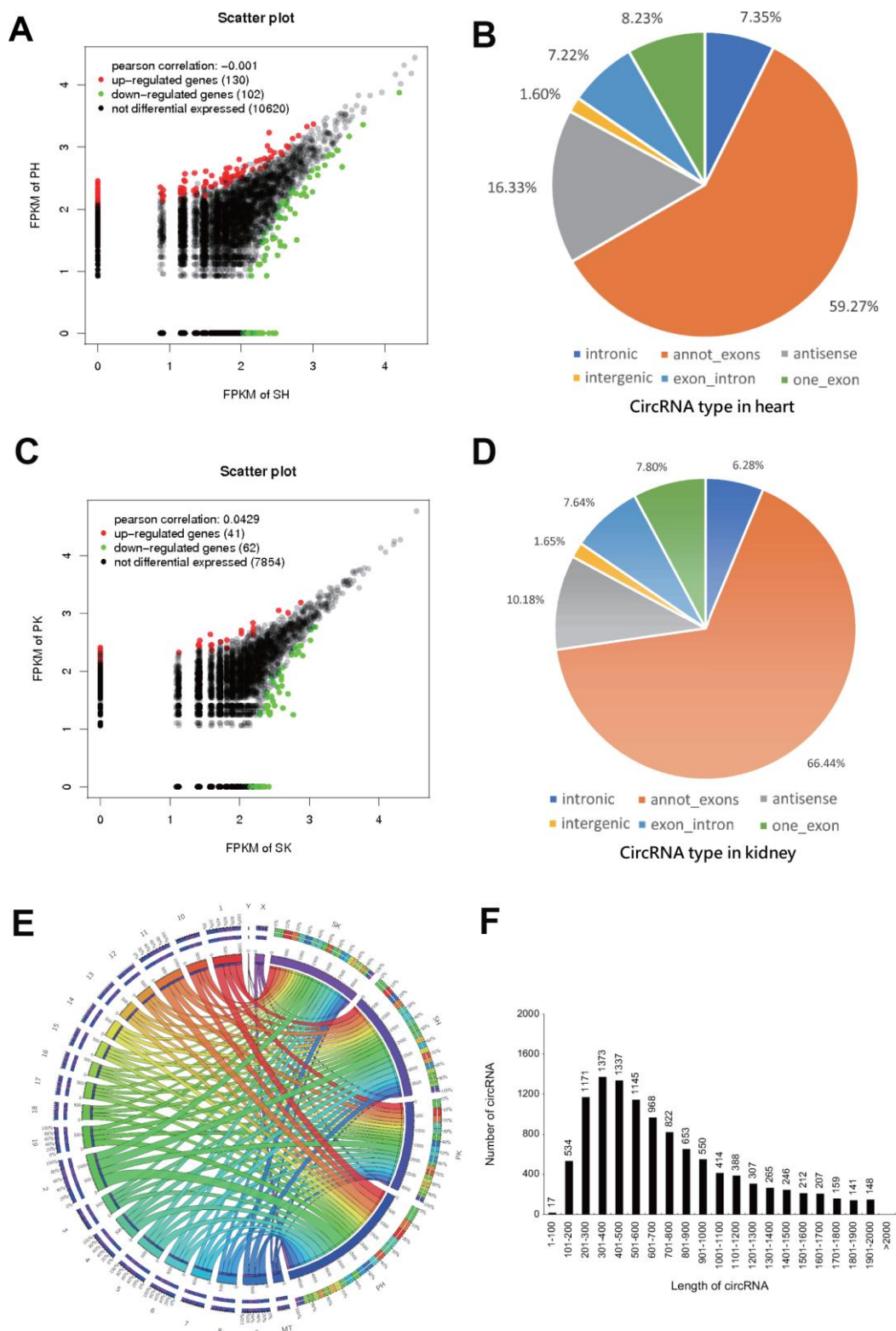


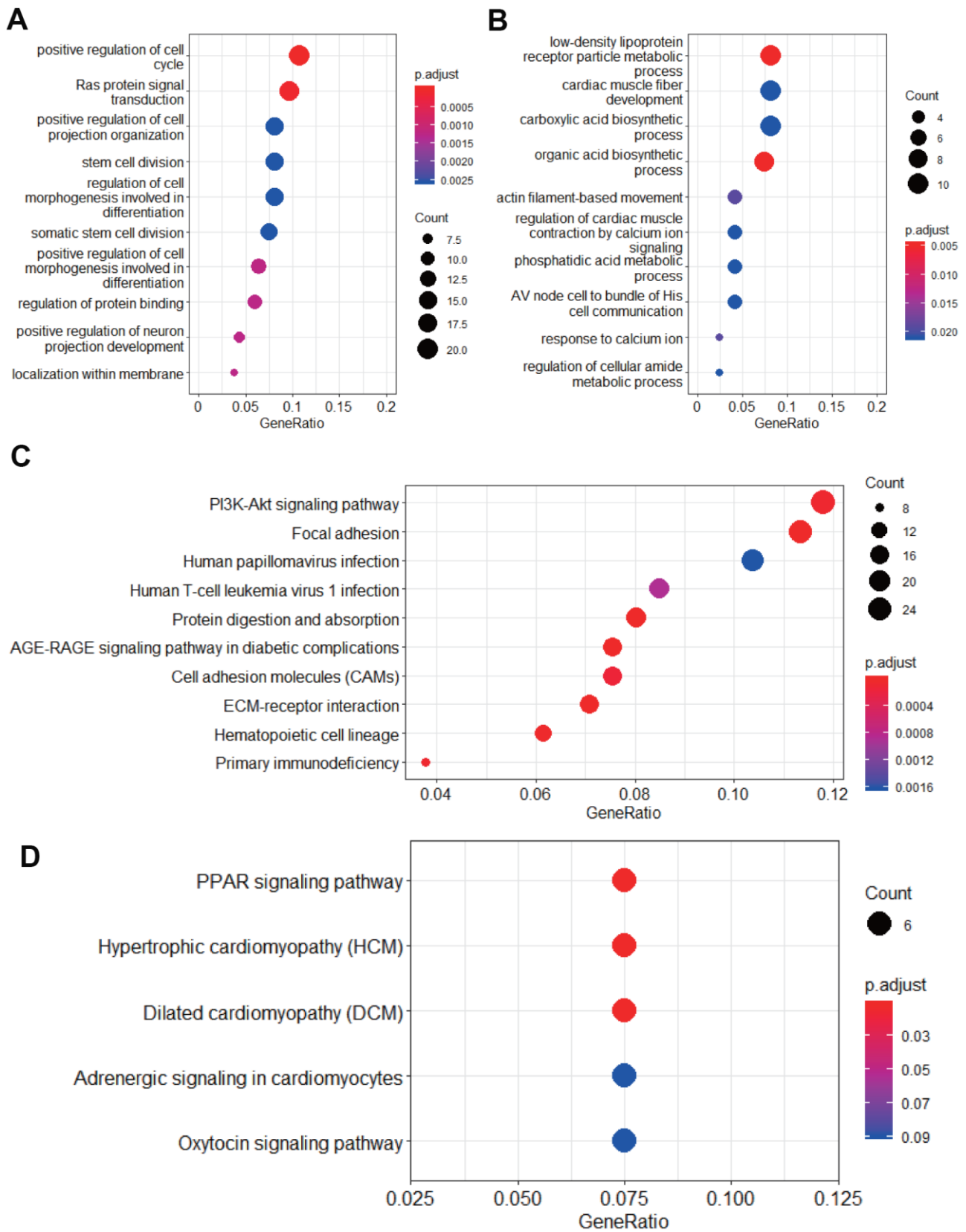
SUPPLEMENTARY FIGURES



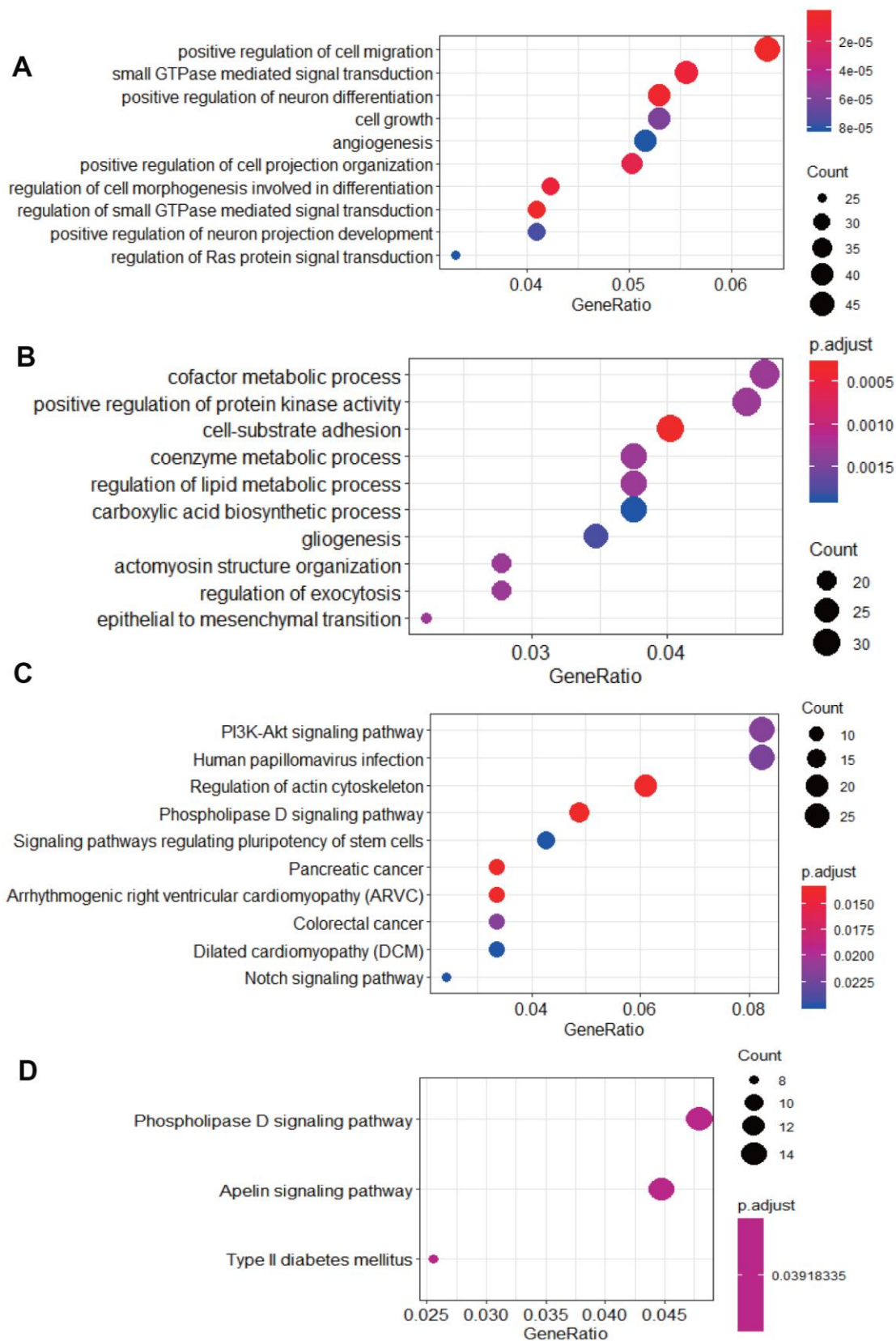
Supplementary Figure 1. Differential expression of mRNAs and miRNAs. (A, B) Volcano plot and hierarchically clustered heat map illustrating differentially expressed ($FDR \leq 0.05$ and the abstract value of $\log_2(\text{Fold Change}) \geq 1.0$) mRNAs of RV and renal tissue samples between sham and PAC group. (C, D) Volcano plot and hierarchically clustered heat map illustrating differentially expressed miRNAs of RV and renal tissue samples between sham and PAC group. Up-regulated mRNAs and miRNAs are denoted in red and down-regulated ones in green. SH: the RV tissue sample of the sham group; PH: the RV tissue sample of the PAC group; SK: the kidney tissue sample of the sham group; PK: the kidney tissue sample of the PAC group; PAC: pulmonary artery constriction.



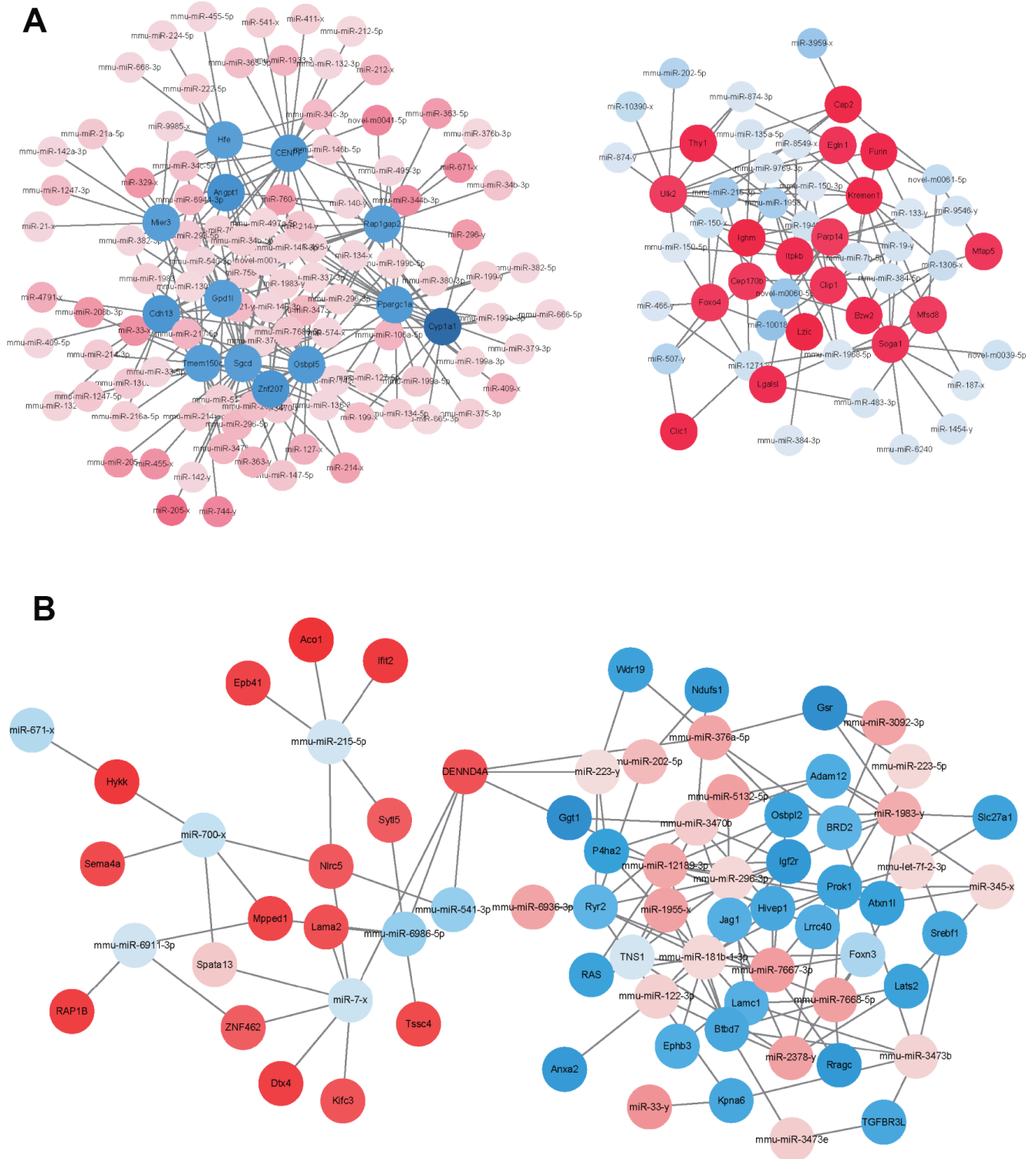
Supplementary Figure 2. Differential expression of circRNAs. (A) Scatter plot of the upregulated and downregulated circRNAs in the RV tissue samples between sham and PAC group; (B) Subgroups of the DEcircRNAs according to their genomic locations and effect; (C) Scatter plot of the upregulated and downregulated circRNAs in the renal tissue samples between sham and PAC group; (D) Subgroups of the DEcircRNAs according to their genomic locations and effect; (E) Chromosome distribution of the circRNAs; (F) The length distribution of circRNAs. SH: the RV tissue sample of the sham group; PH: the RV tissue sample of the PAC group; SK: the kidney tissue sample of the sham group; PK: the kidney tissue sample of the PAC group; PAC: pulmonary artery constriction.



Supplementary Figure 3. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis of up- and down-regulated mRNAs in RV tissue. (A, B) GO analysis of the biological functions of differentially expressed mRNAs that were significantly up- and down-regulated in the RV tissue; (C, D) KEGG pathway analysis of the up- and down-regulated mRNAs in the RV tissue.



Supplementary Figure 4. GO and KEGG analysis of up- and down-regulated mRNAs in renal tissue. (A, B) GO analysis of the biological functions of differentially expressed mRNAs that were significantly up- and down-regulated in the renal tissue; (C, D) KEGG pathway analysis of the up- and down-regulated mRNAs in the renal tissue.



Supplementary Figure 5. Co-expression miRNA-mRNA network. (A) The regulatory network of significantly differentially expressed miRNAs (FDR < 0.05 and the absolute value of $\log_2(\text{Fold Change}) \geq 10.0$) and 34 potential target mRNAs; **(B)** The regulatory network of metabolic pathway-related miRNAs and 11 target mRNAs. The red nodes represent up-regulated miRNAs and mRNAs and blue nodes represent down-regulated miRNAs and mRNAs. The $\log_2(\text{Fold Change})$ values of the miRNA and target mRNA are shown by the node color. The figures were generated using Cytoscape (Shannon et al., 2003).