**Figure S1. Analysis of lncRNA and mRNA expression profile of pancreas tissue from mouse with acute pancreatitis.**

**A.** Bar plot showing the up-regulated and down-regulated numbers of DEmRNA,When analyzing the differential expression of genes, the software we used was DESeq2.Pvalue≤0.05, FC(fold change) ≥ 1.5 or ≤1.5.

**B.** Principal component analysis (PCA) based on FPKM value of all DEmRNA. The ellipse for each group is the confidence ellipse.

**C.** The Heatmap showing the expression of DEmRNA.

**D-E.**Bar plot showing the up-regulated and down-regulated numbers of DEmRNA,When analyzing the differential expression of genes, the software we used was DESeq2.Pvalue≤0.05, FC(fold change) ≥ 1.5 or ≤1.5.

**F-G.**Bar plot exhibited the most enriched GO biological process results of D7 up and down.

**H-I.**Bar plot exhibited the most enriched GO biological process results of D14 up and down.

**Figure S2. Expression correlation analysis of lncRNAs and mRNAs in pancreas tissue from mouse with acute pancreatitis.**

**A.** Bar plot showing the top 10 enriched KEGG pathways of the up and down overlap in Fig2C-D.

**B.** Bar plot showing the top 10 enriched KEGG pathways of the D7 specific DElncRNA co expressed DEmRNA in Fig2C-D.

**Figure S3. Co-expression analysis (WGCNA) of lncRNAs and mRNAs in pancreas tissue from mouse with acute pancreatitis.**

A-C. Eigengene bar plot of three advanced assoiciated modules.

D-F. Bar plot showing the top 10 enriched KEGG pathways of the three modules.