SUPPLEMENTARY MATERIAL

RNA-Seq Analyses of the Role of miR-21 in Acute Pancreatitis

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Supplementary Figure 1. Top IPA interaction network analysis of significant DEGs in the pancreas between WT and KO mice treated with caerulein and the identification of cell death, chemotaxis, and inflammatory response as the top regulated network. (A) The top five networks were analyzed by IPA and merged into one figure. Downregulated (green) and upregulated (red) genes were identified in the network. Genes in the network without any color were analyzed by IPA to show potential connectivity. (B) Cell death networks were analyzed by IPA. (C) Interaction networks, including chemotaxis (left) and inflammatory response (right), were analyzed by IPA.

Supplementary Figure 2. (A) IPA interaction network analyses of 16 selected significant DEGs.

A

WDFY3 ATG5 ATG16L1 **RGCC** ATG7 ATG10 SQSTM1 PIAS3 IL1RL1 PMS2 ICOS BARD1 ELAVL1XAF1 CASP9 T3 LEFT GATA3 KPNA2 El24 KPNB Gm21596/Hmgb1 NANOG HDAC5 NOS2 GLB1 RBFOX2 PIEN PPP2R1A LLTAW CSEIL APART D1 IL9R KIFC1 HNRNPH1CDKN2A CDKN1A
PP2A STRN3 ELF5
THRS1 CASP3 ESR1 CONTACTOR OF COLUMN TO THE COLUMN THRSE CASP3 ESR1 CONTACTOR OF COLUMN THRSE COLUMN THRS SMAD7 CXCL13 ERBB2 TP53 CD47 LIMA1 Hsp90 YWHAQ KAT5 GSN PDCD10 NME1 Alpha actin CCM2 C8orf44-SGK3/SGK3 CFL1 NFATCERBB4 EREGSRE KRIT1 miR-21-5p (and other miRNAs w/seed AGCUUAU)