

SUPPLEMENTARY MATERIAL

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

Xun Li^a Zhanwen Lin^a Lei Wang^a Qin Liu^a Zhi Cao^b
Zhujuan Huang^b Mingtian Zhong^b Shuxian Peng^b
Yingheng Zhang^b Yong Li^c Xiaodong Ma^a

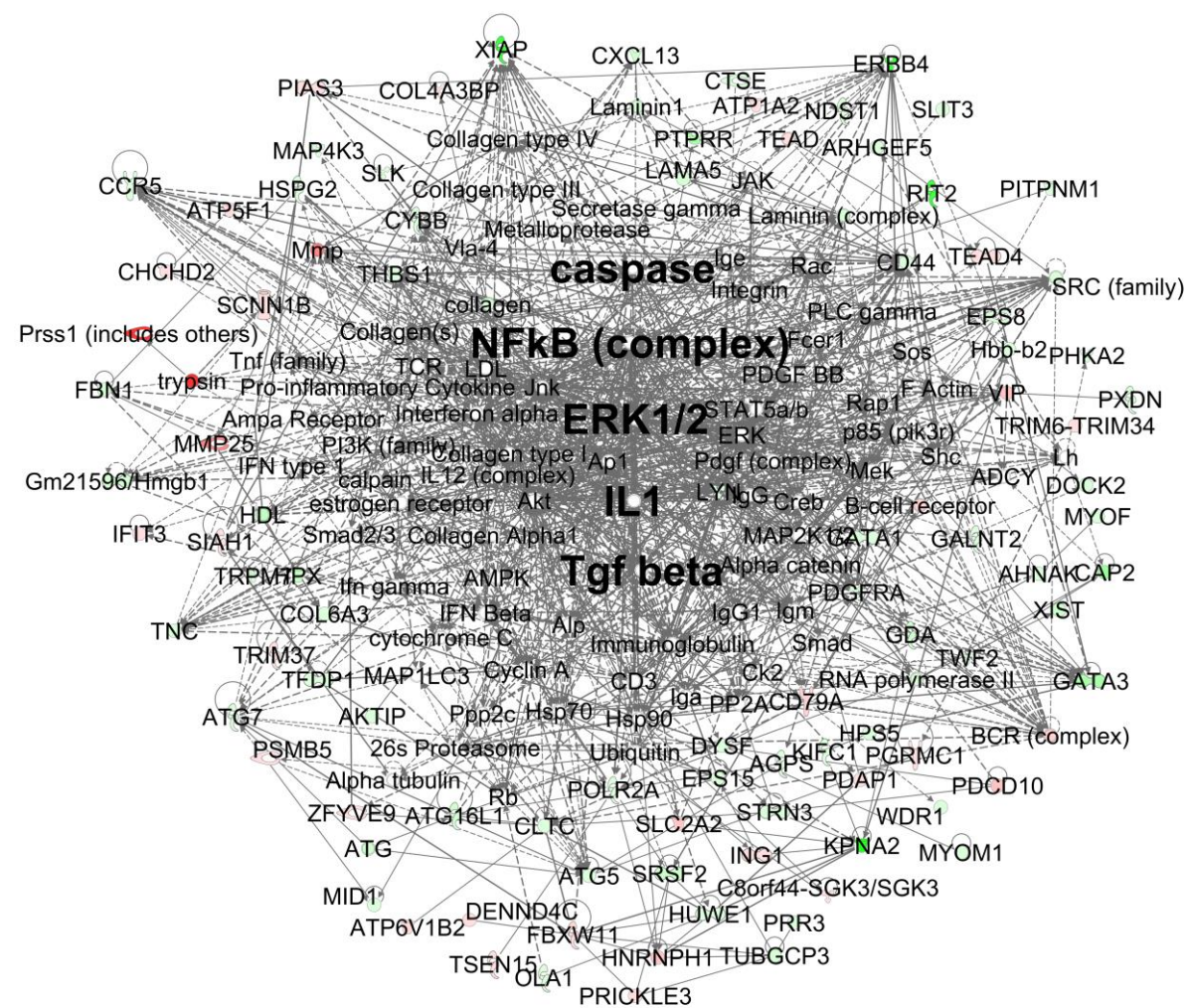
^aInstitute for Brain Research and Rehabilitation, Guangdong Key Laboratory of Mental Health and Cognitive Science, Center for Studies of Psychological Application, South China Normal University, Guangzhou, ^bThe Research Center of Basic Integrative Medicine, Guangzhou University of Chinese Medicine, Guangzhou, China,

^cDepartment of Cancer Biology, Lerner Research Institute, Cleveland Clinic, Cleveland, USA

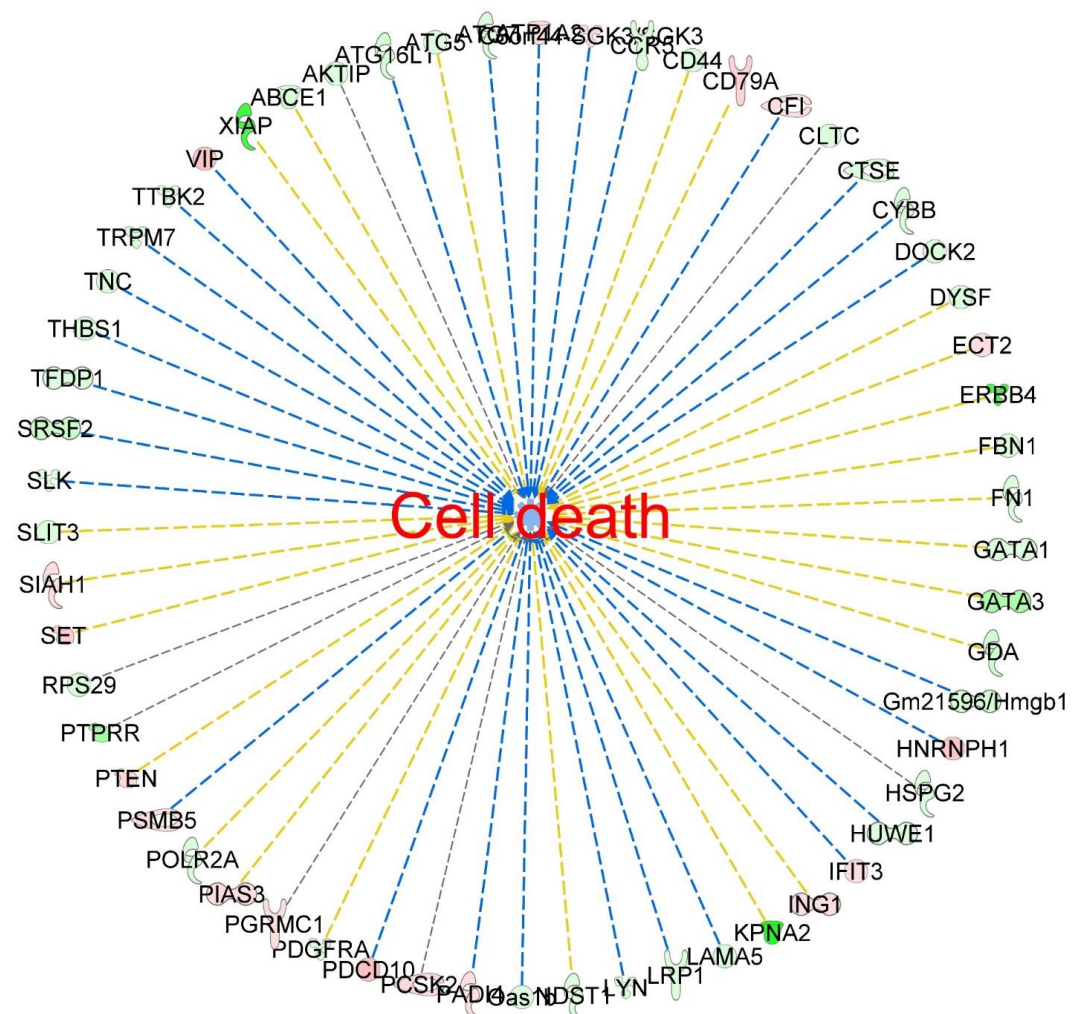
Supplementary Figure 1. Top IPA interaction network analysis of significant DEGs in the pancreas between WT and KO mice treated with caerulein and the identification of cell death, chemotaxis, and inflammatory response as the top regulated network. (A) The top five networks were analyzed by IPA and merged 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.

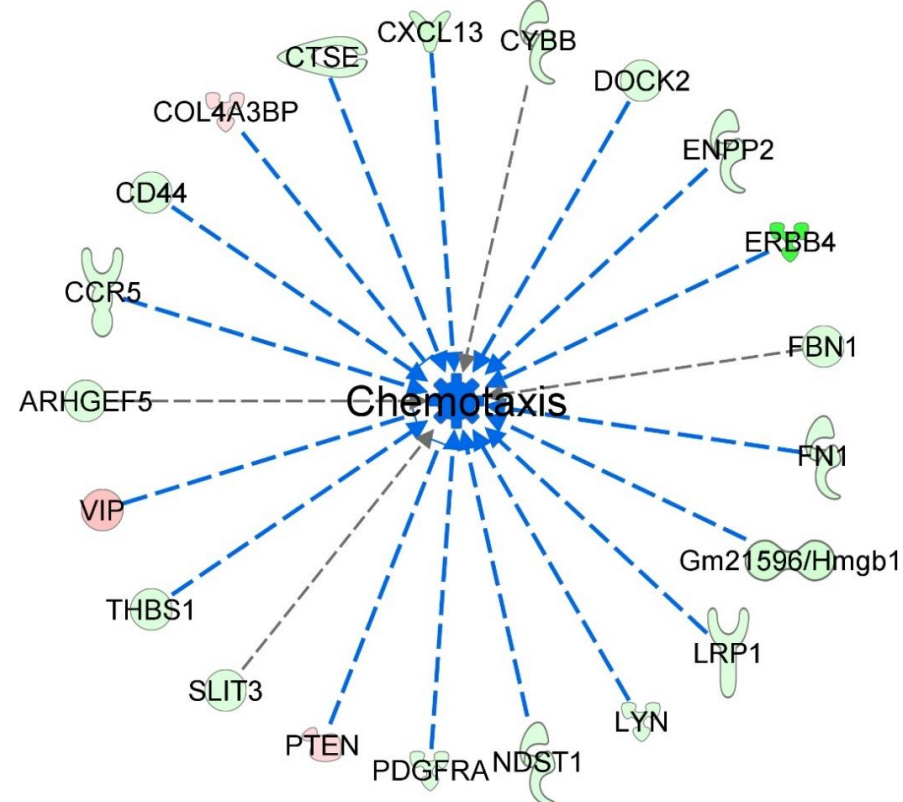
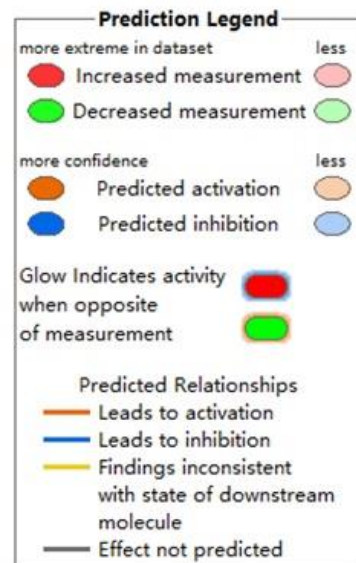
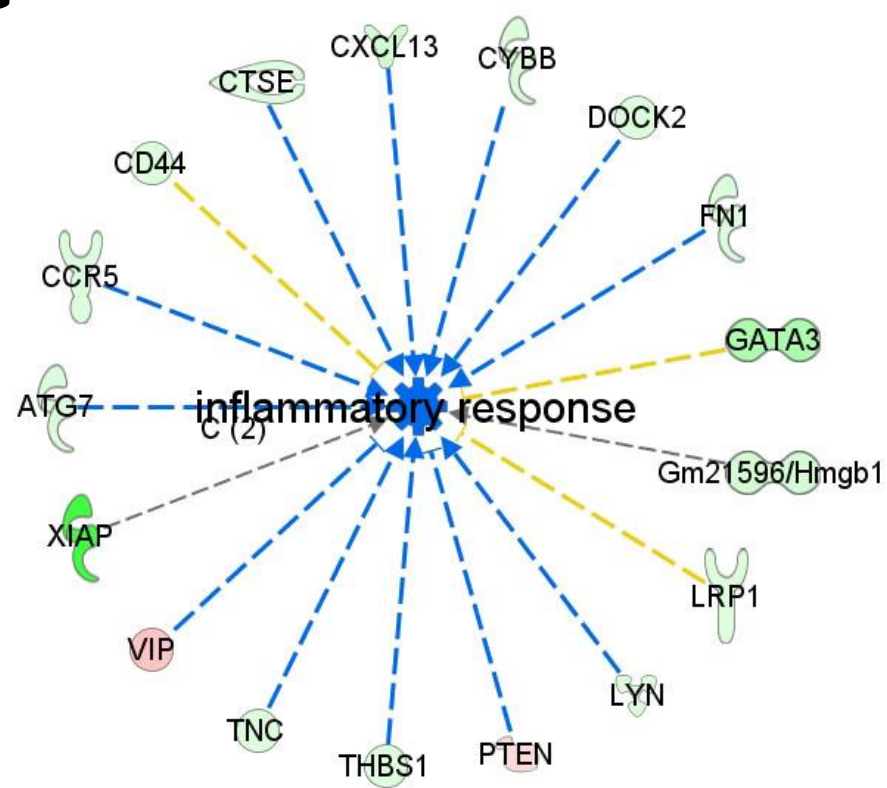
A



B



C



A

