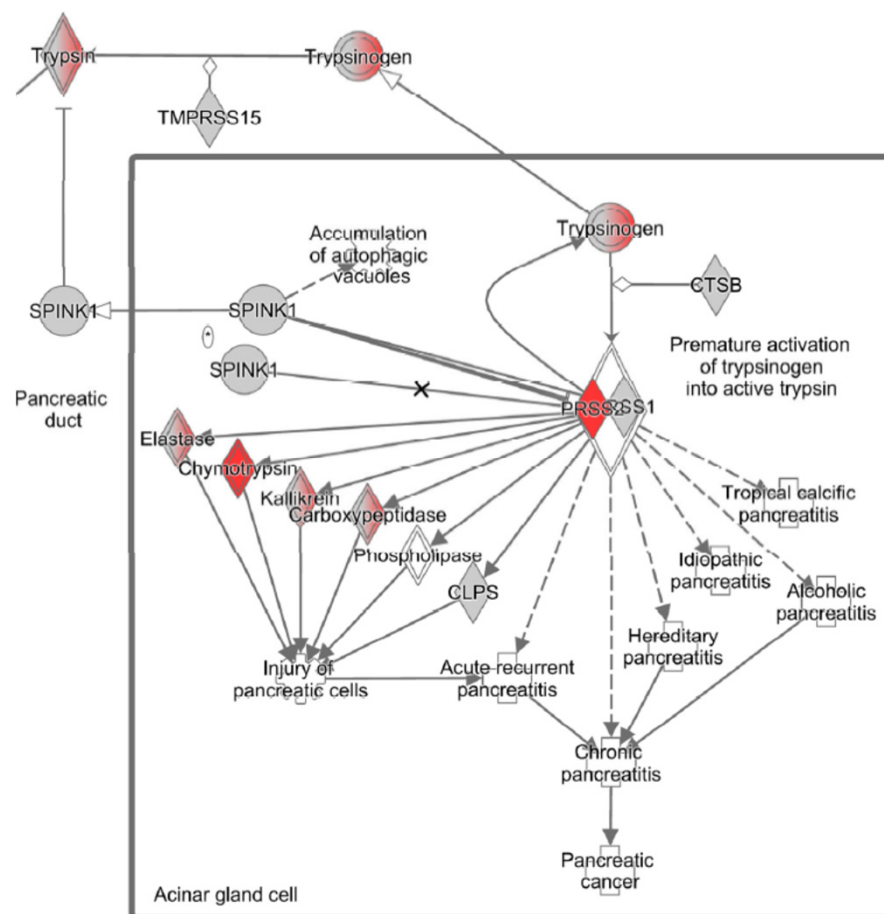
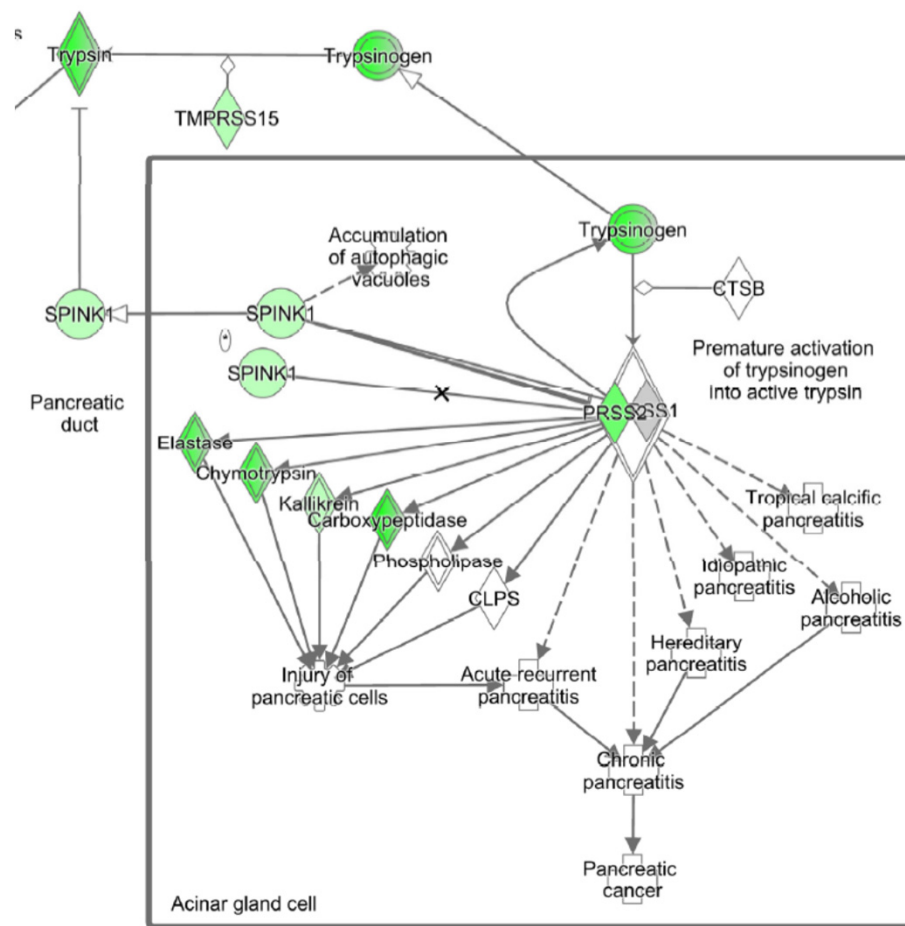


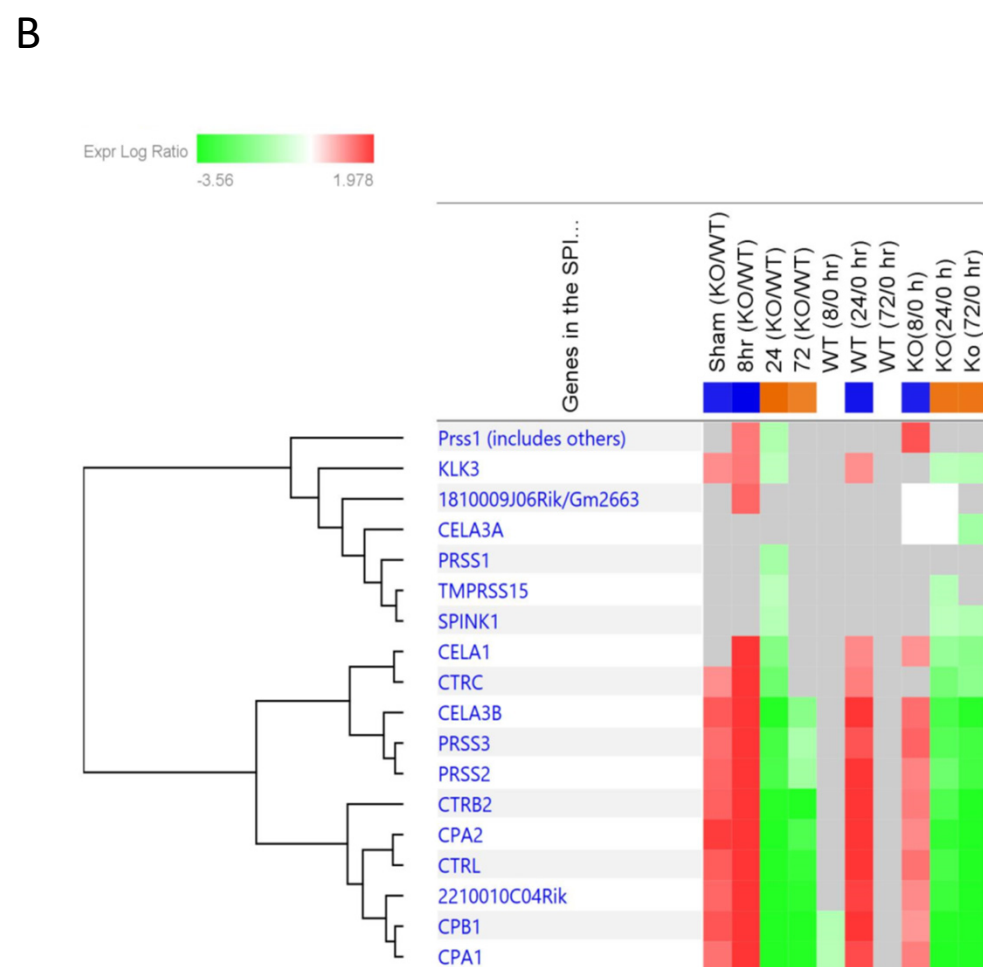
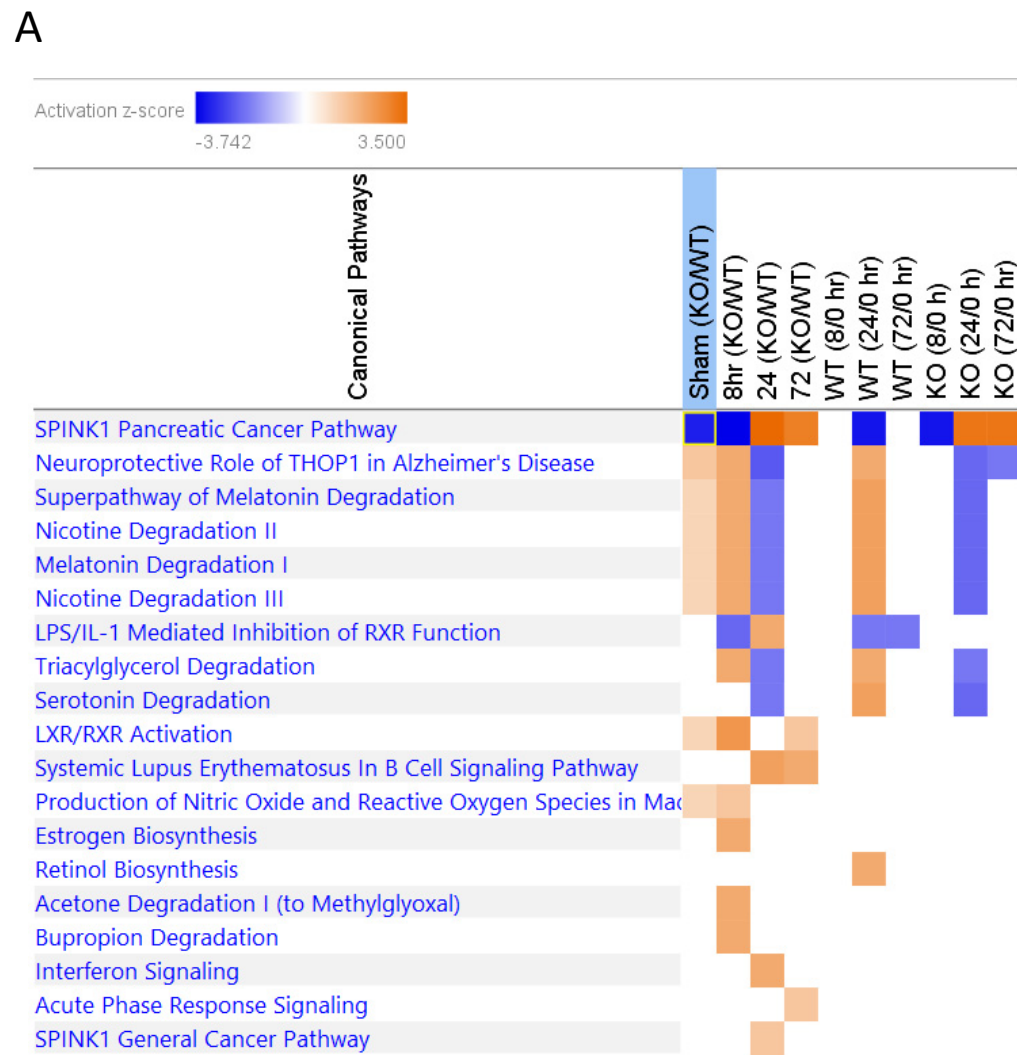
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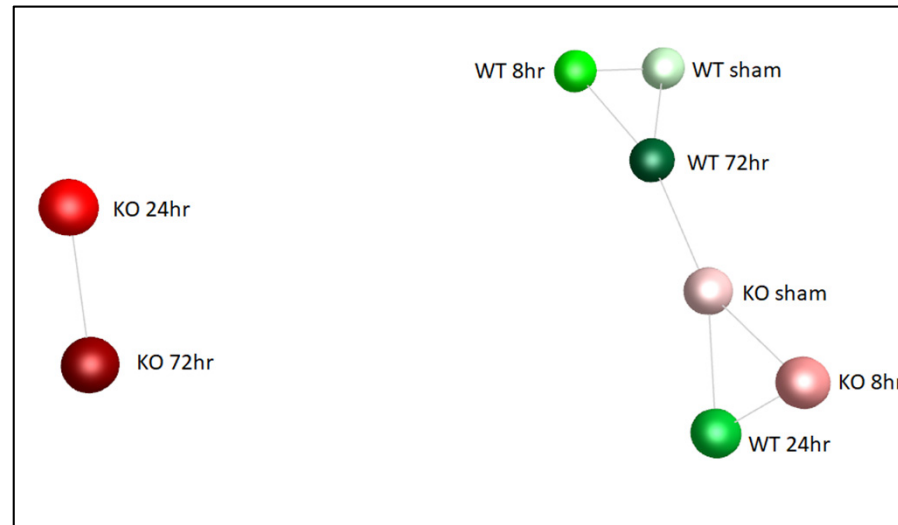
B



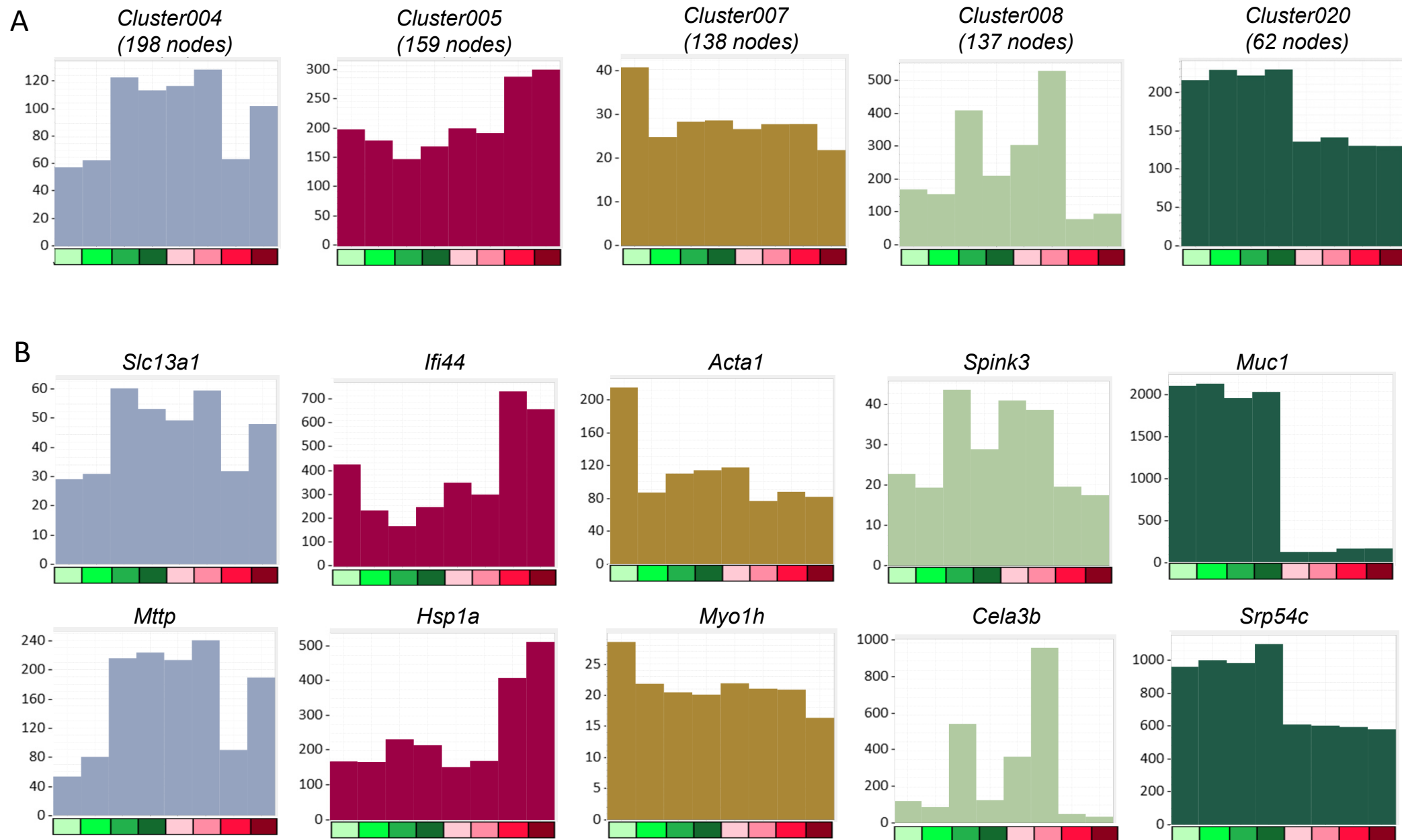
**Sup Figure 1:** Diagrams of SPINK 1 pancreatic cancer pathway between gastric *Muc1*<sup>-/-</sup> vs WT in response to *H. pylori* infection. (A) Increased the expression of the target genes are showed in red at 8 h infection. (B) Decreased the expression of the target genes are showed in green at 72 h infection.



**Sup Figure 2:** (A) Z-scored heat map of canonical pathways associated with time-course of changes between gastric *Muc1*<sup>-/-</sup> vs WT (KO/ WT) or gastric WT mice or gastric *Muc1*<sup>-/-</sup>(KO) mice in response to *H. pylori* infection. (B) Heat map of DE genes associated with IPA terms canonical pathways associated with SPINK1 pancreatic cancer pathway in our data set.



**Sup Figure 3:** Sample-to-sample analysis of the *H. pylori* infection time course in WT and *Muc1*<sup>-/-</sup> samples. In this analysis (similar to a principal components analysis) nodes (spheres) represent samples and the edges (lines) show correlations between samples of  $\geq 0.95$ . The network layout shows the similarity of samples based on the expression of all genes in the sample.



**Sup Figure 4:** Gene coexpression network analysis. The network was developed at a correlation coefficient threshold of 0.87 and clustering was performed using the Markov clustering algorithm at an inflation value of 1.7. X axis shows the time course samples colour coded as for Sup Figure 3; green – WT; red – *Muc1*<sup>-/-</sup>. Y axis shows the expression (relative intensity). **(A)** The expression pattern of GCN cluster004, 005, 007, 008 and 020. **(B)** Examples of genes of interest from GCN cluster004, 005, 007, 008 and 020, coloured as for the clusters in **(A)**.