

Supplementary Materials

scGENA: A single-cell gene co-expression network analysis framework for clustering cell types and revealing biological mechanisms

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1. Co-expression Networks construction

These networks are constructed for only randomly selected 25 genes in each cell types modules.

Alpha-cells:

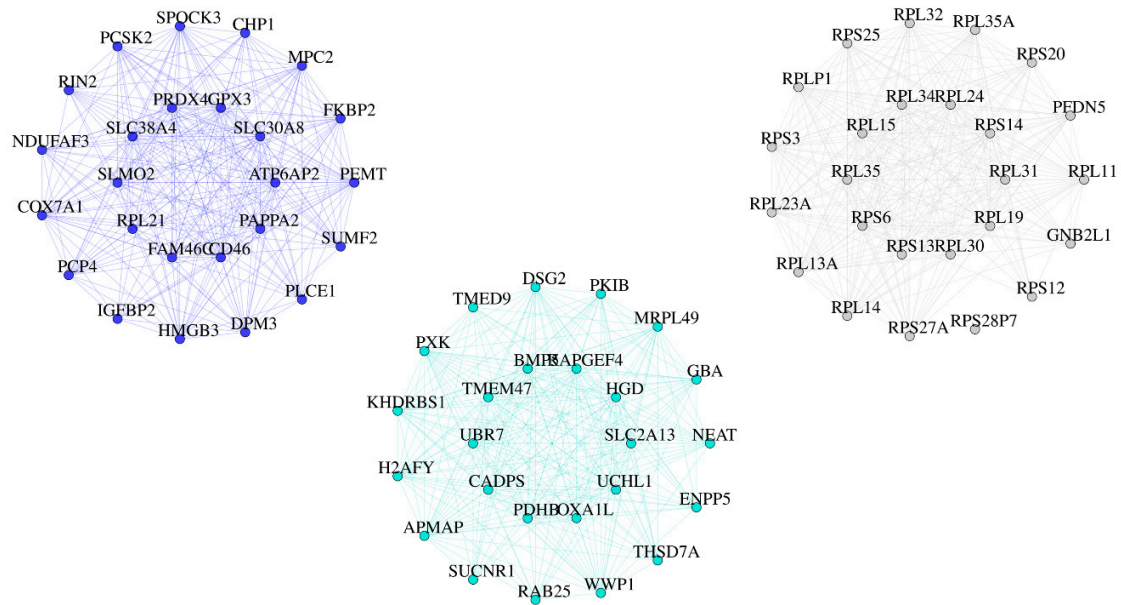


Figure S1: Gene co-expression networks in Alpha.

Delta-Cells

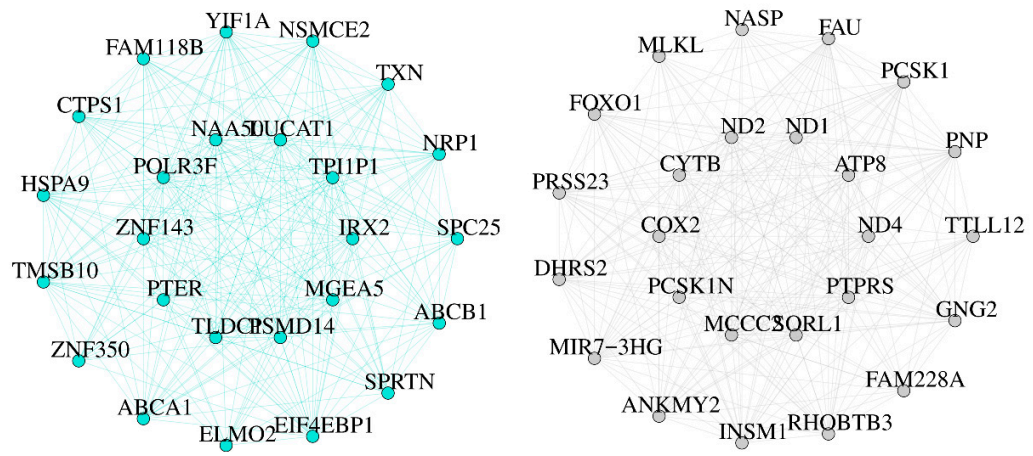


Figure S2: Gene co-expression networks in Delta.

Gamma/PP Cells

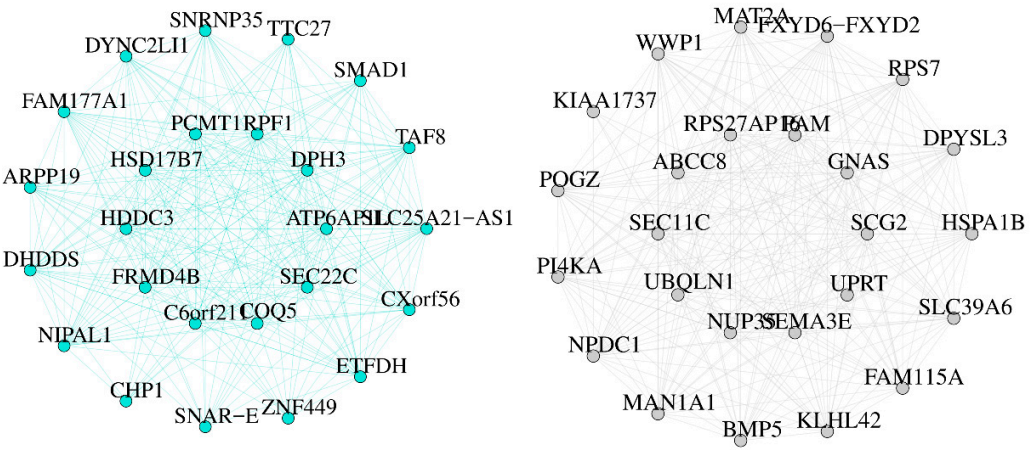


Figure S3: Gene co-expression networks in Delta.

2. Differential Co-Expression Analysis

In this step, we identify the differential co-expression genes in all cells type in the islet human pancreatic data. The heatmaps are plotted by MODA package in R.

Alpha genes heatmap:

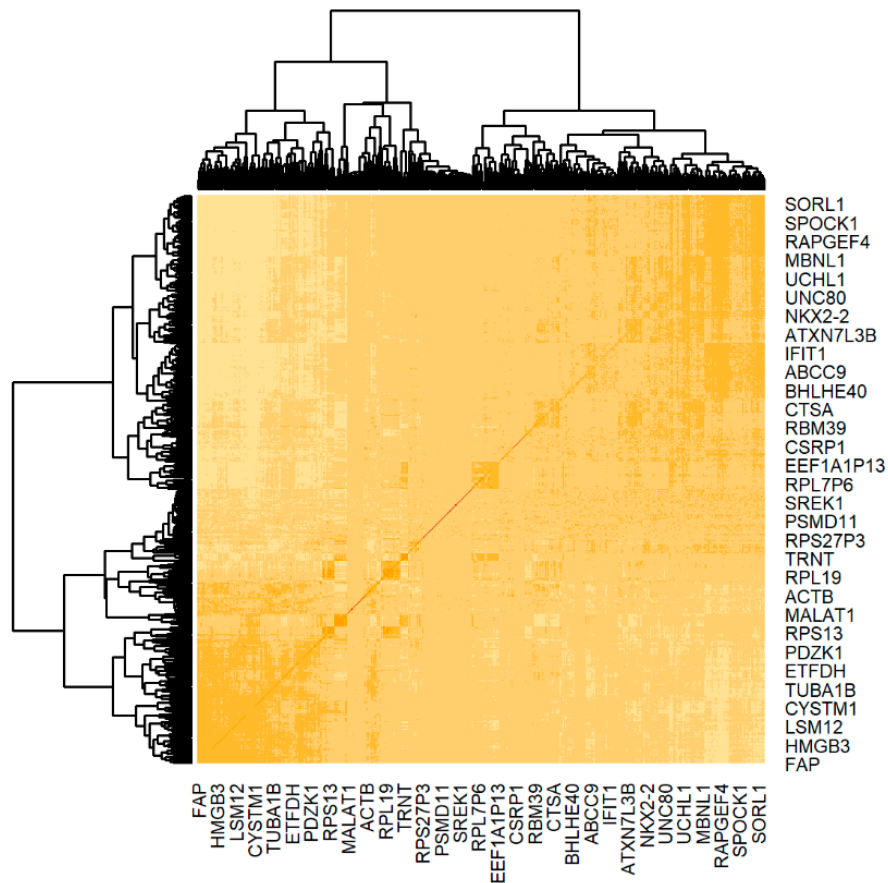


Figure S4: Differential co-expression heatmap for correlated genes in Alpha cells.

Delta genes heatmap:

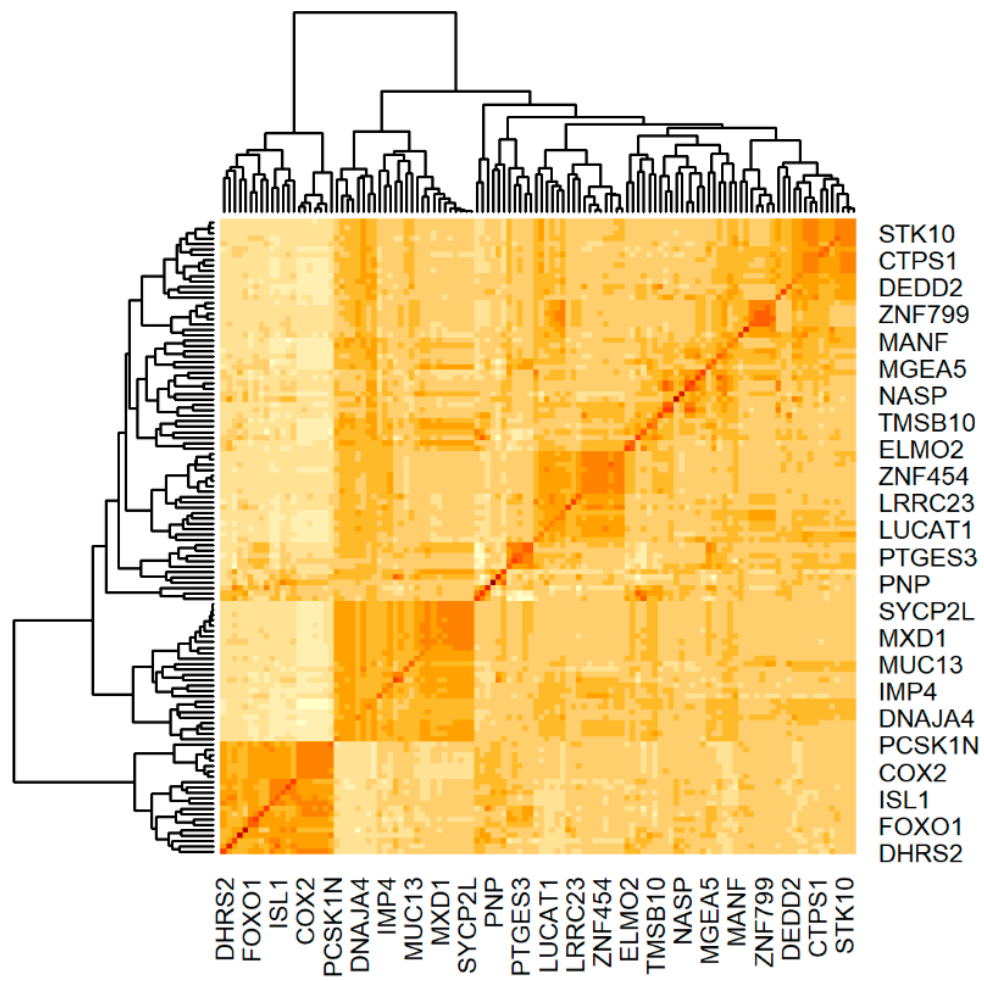


Figure S5: Differential co-expression heatmap for correlated genes in Delta cells.

Gamma genes heatmap:

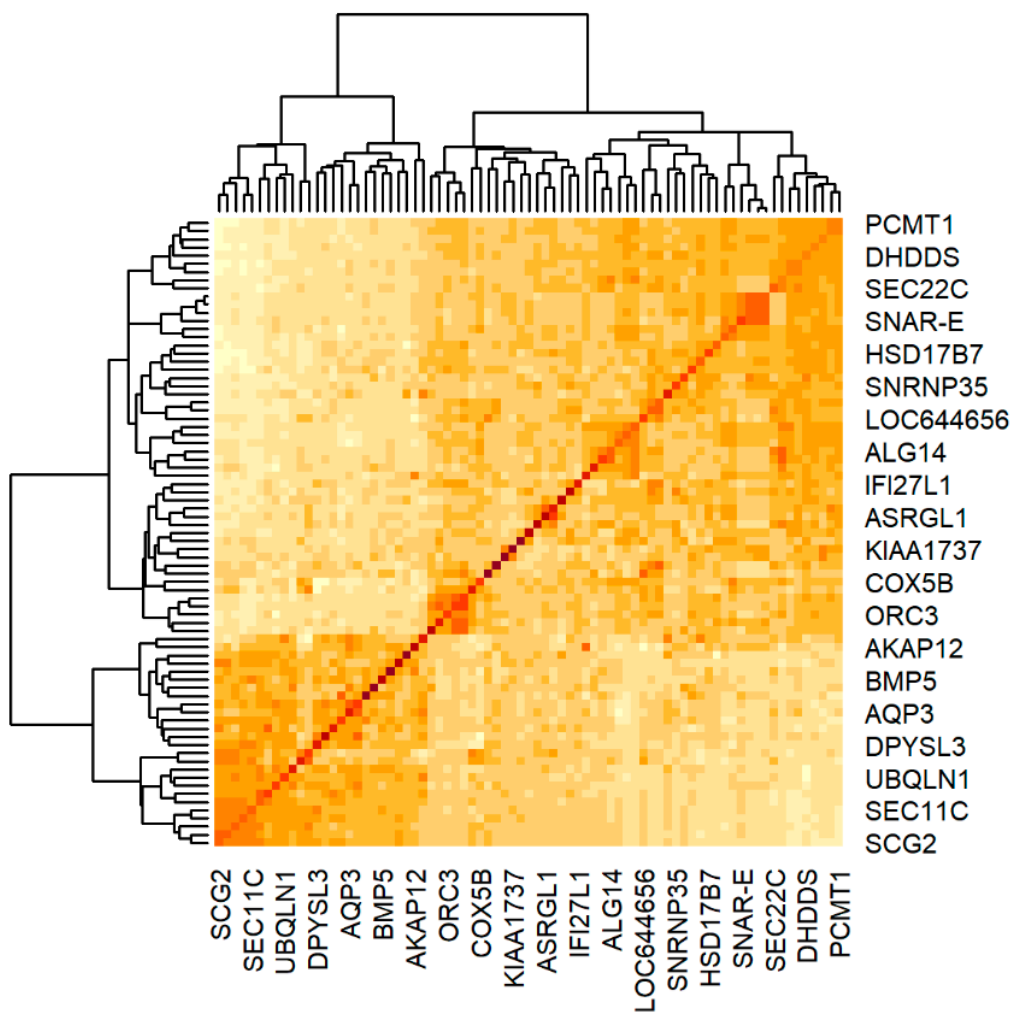


Figure S6: Differential co-expression heatmap for correlated genes in Gamma Cells.