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

Yousif A. Algabri [1], Lingyu Li [1] and Zhi-Ping Liu [1]*

[1]Department of Biomedical Engineering, School of Control Science and Engineering, Shandong University, Jinan, Shandong 250061, China; algabri@mail.sdu.edu.cn, lingyuli@mail.sdu.edu.cn, zpliu@sdu.edu.cn

*Correspondence: zpliu@sdu.edu.cn

Supplementary Materials 2

1. Co-expression Networks construction

These networks are constructed for only random selected 25 genes in each cell types modules.
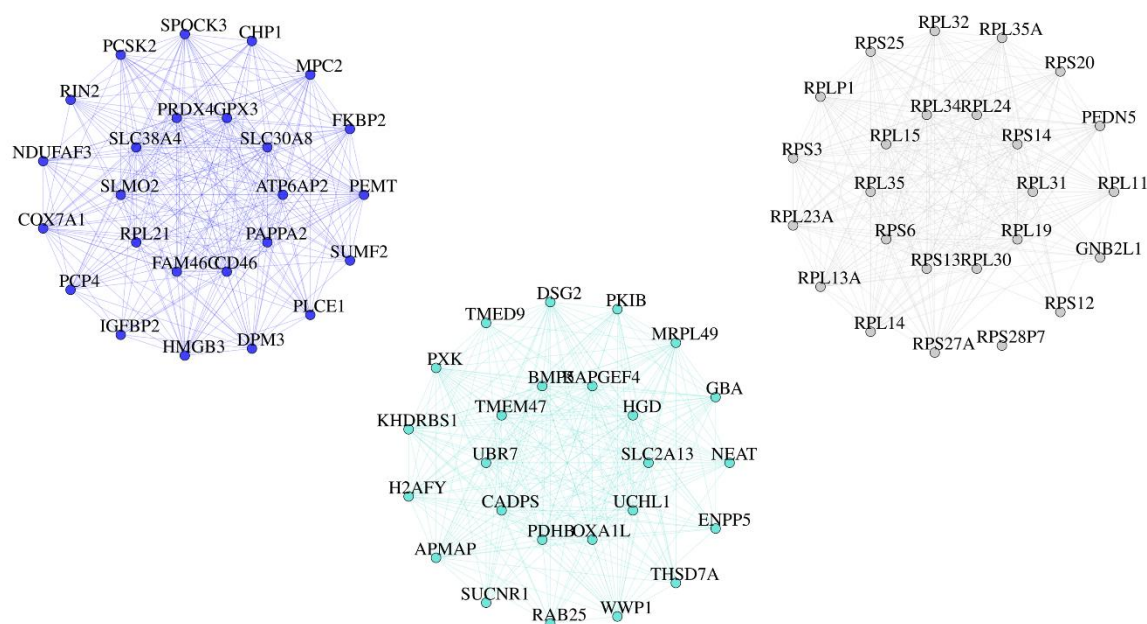
Alpha-cells:

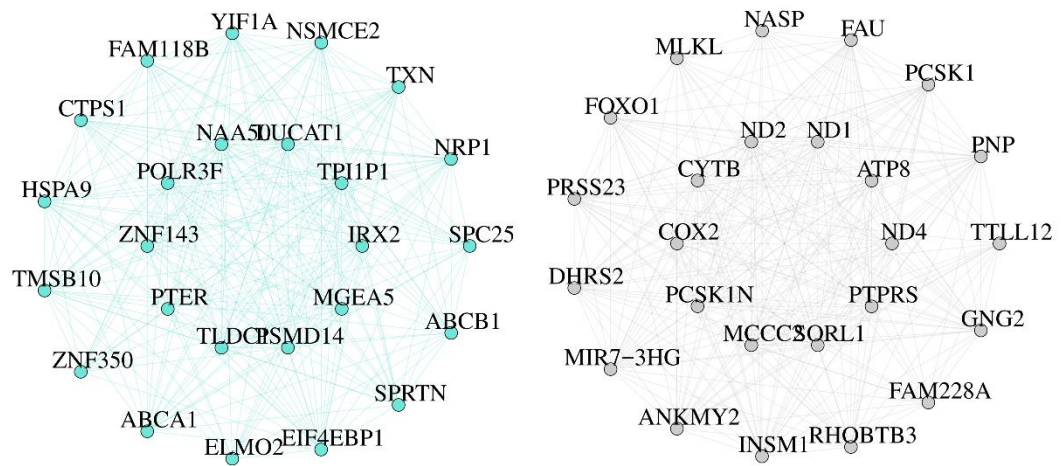Figure S1: Gene co-expression networks in Alpha

Delta-Cells

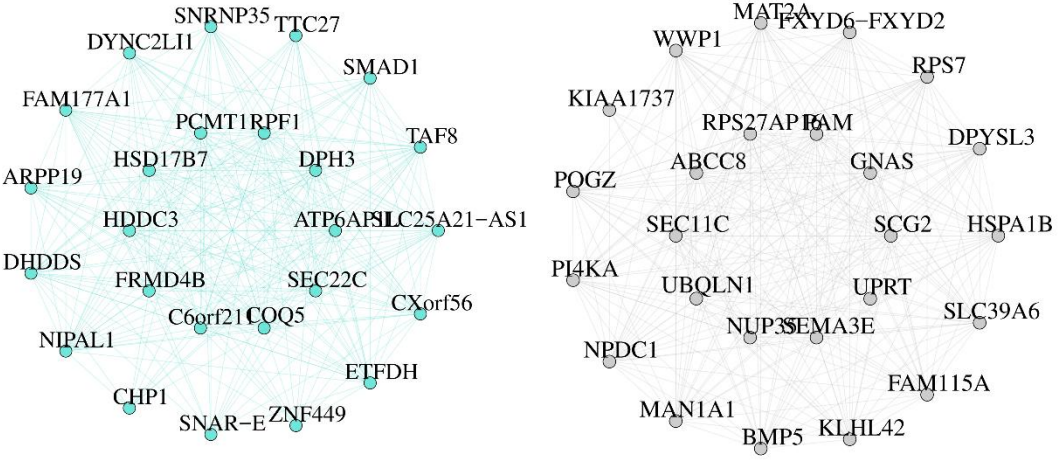Figure S2: Gene co-expression networks in Delta

Gamma Cells

Figure S3: Gene co-expression networks in Delta

2. Co-expression networks for all genes in each cell-type modules

Beta-cell: based on the analysis, there are four modules of genes in beta cells

Figure S4: Co-expression networks for all genes in four presented modules in beta cells

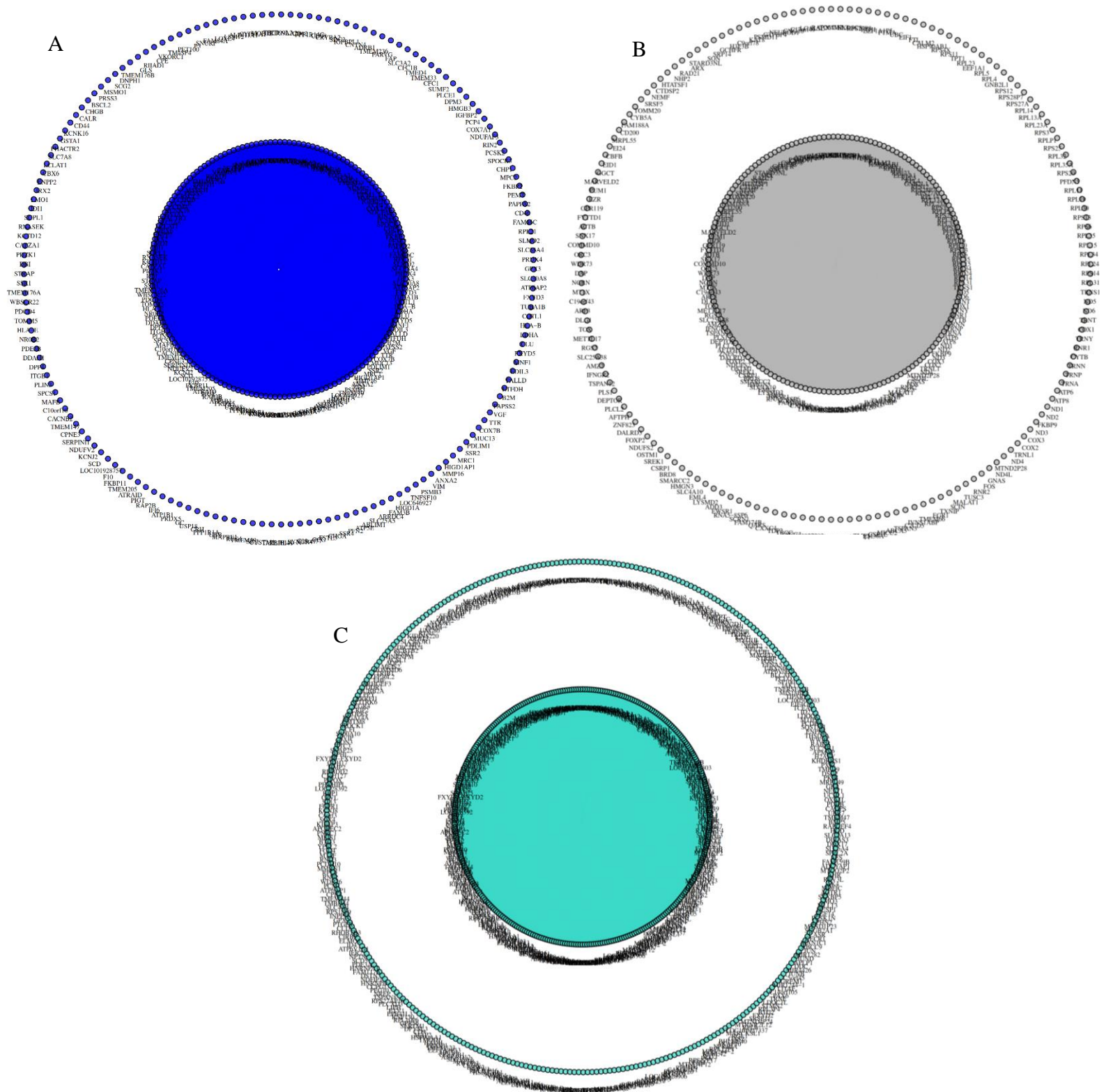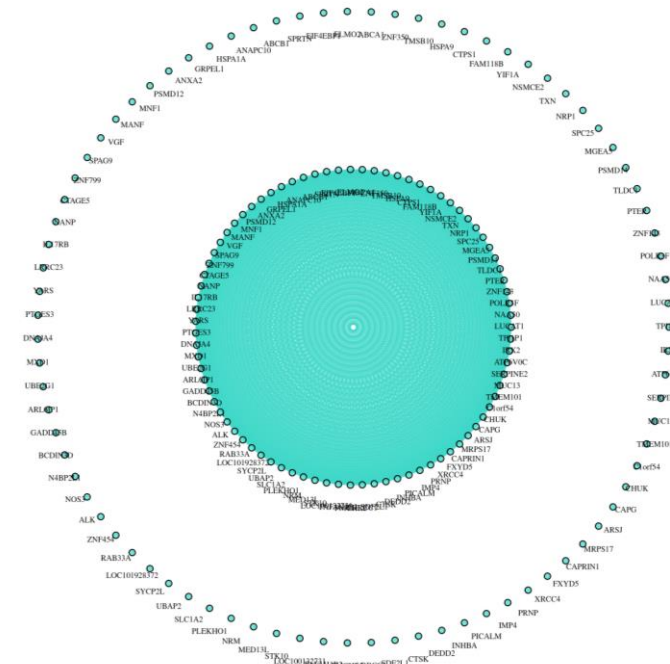**Alpha cell:** The analysis exhibit three modules of genes

Figure S5: Co-expression networks for all genes in three presented modules in Alpha cells
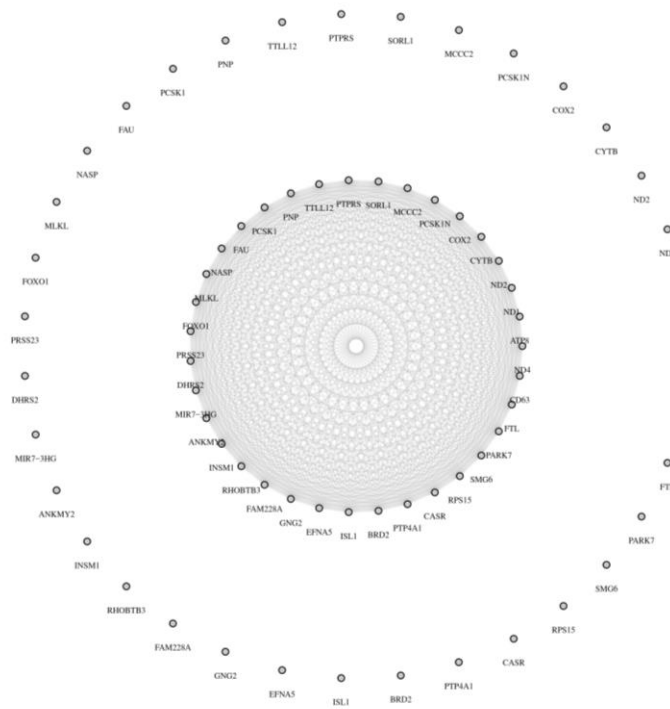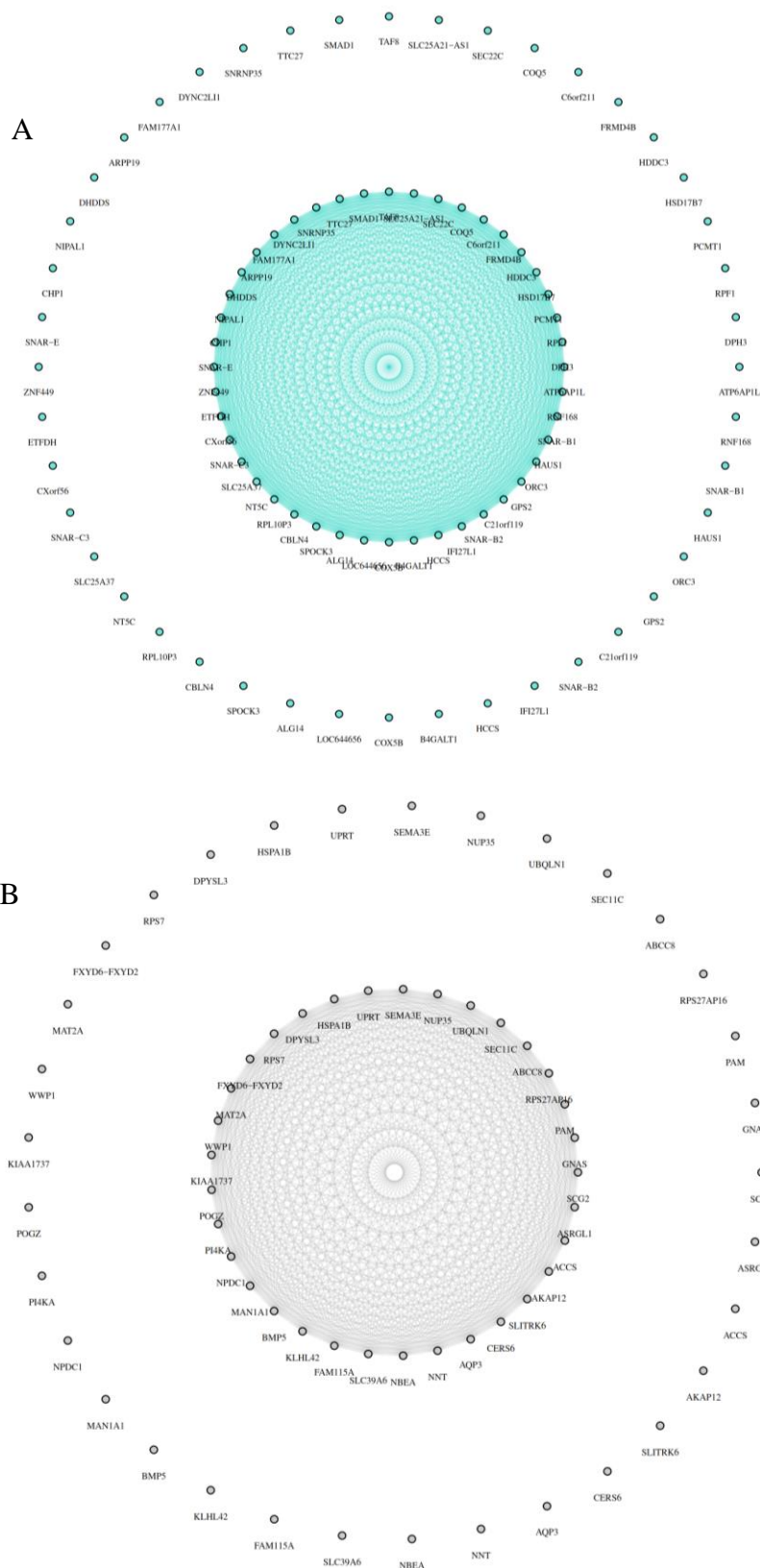
Delta cells

A

B

Figure S6: Co-expression networks for all genes in two presented modules in Delta cells

Gamma cell

Figure S6: Co-expression networks for all genes in two presented modules in Gamma cells

3. 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 using MODA package in R.
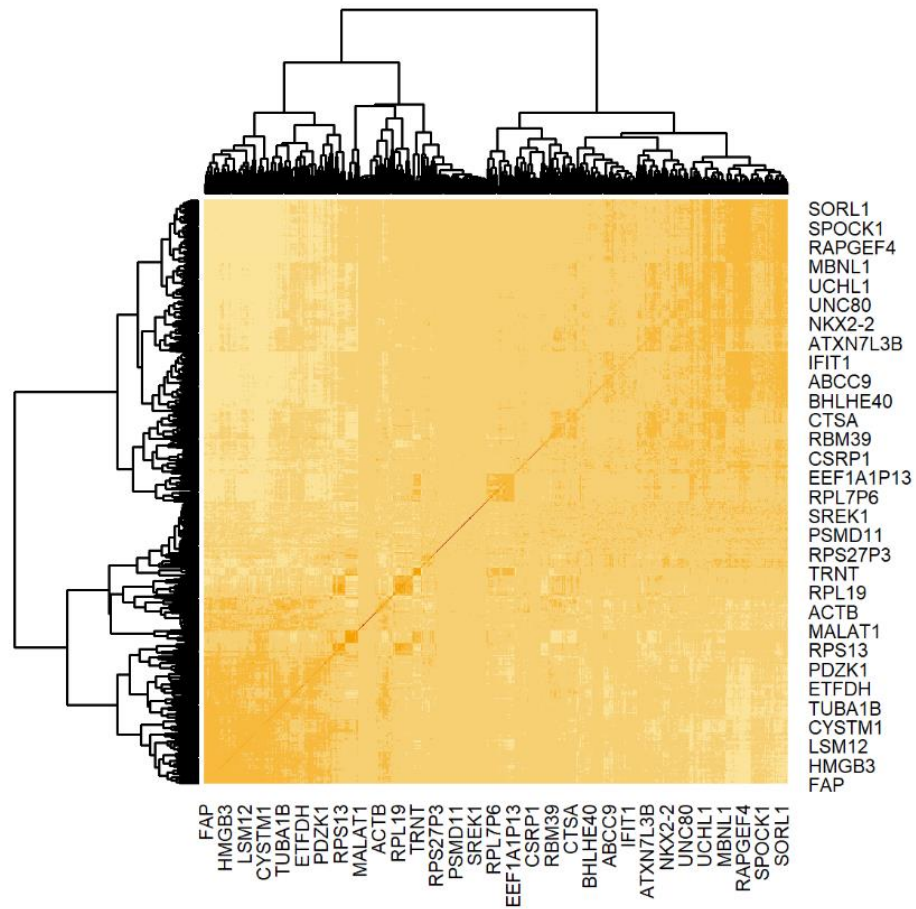
Alpha genes heatmap

Figure S7: Differential co-expression heatmap for correlated genes in Alpha cells
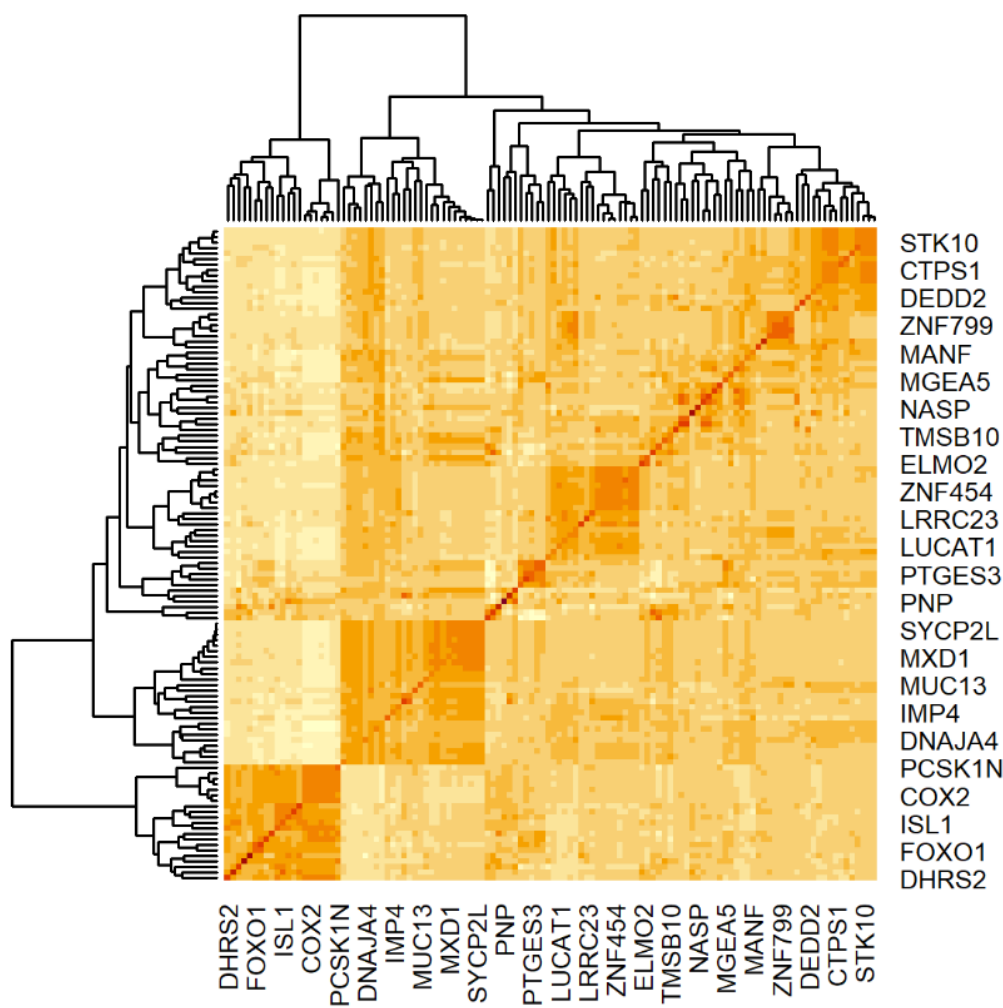
Delta genes heatmap:

Figure S7: Differential co-expression heatmap for correlated genes in Delta cells
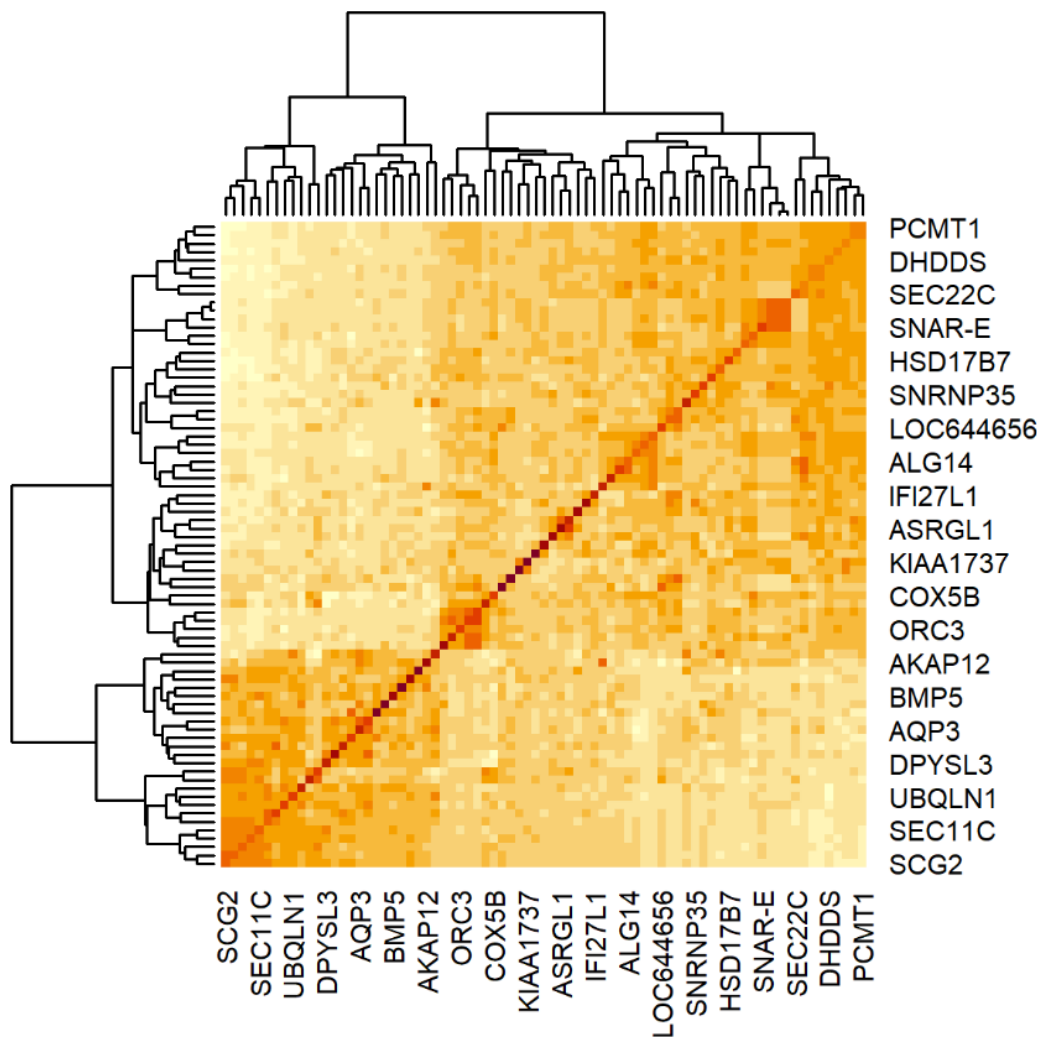
Gamma genes heatmap:

Figure S7: Differential co-expression heatmap for correlated genes in Gamma Cells