

Supplemental information

Single cell atlas of human gastric muscle immune cells and macrophage-driven changes in idiopathic gastroparesis

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Supplementary Figure 1

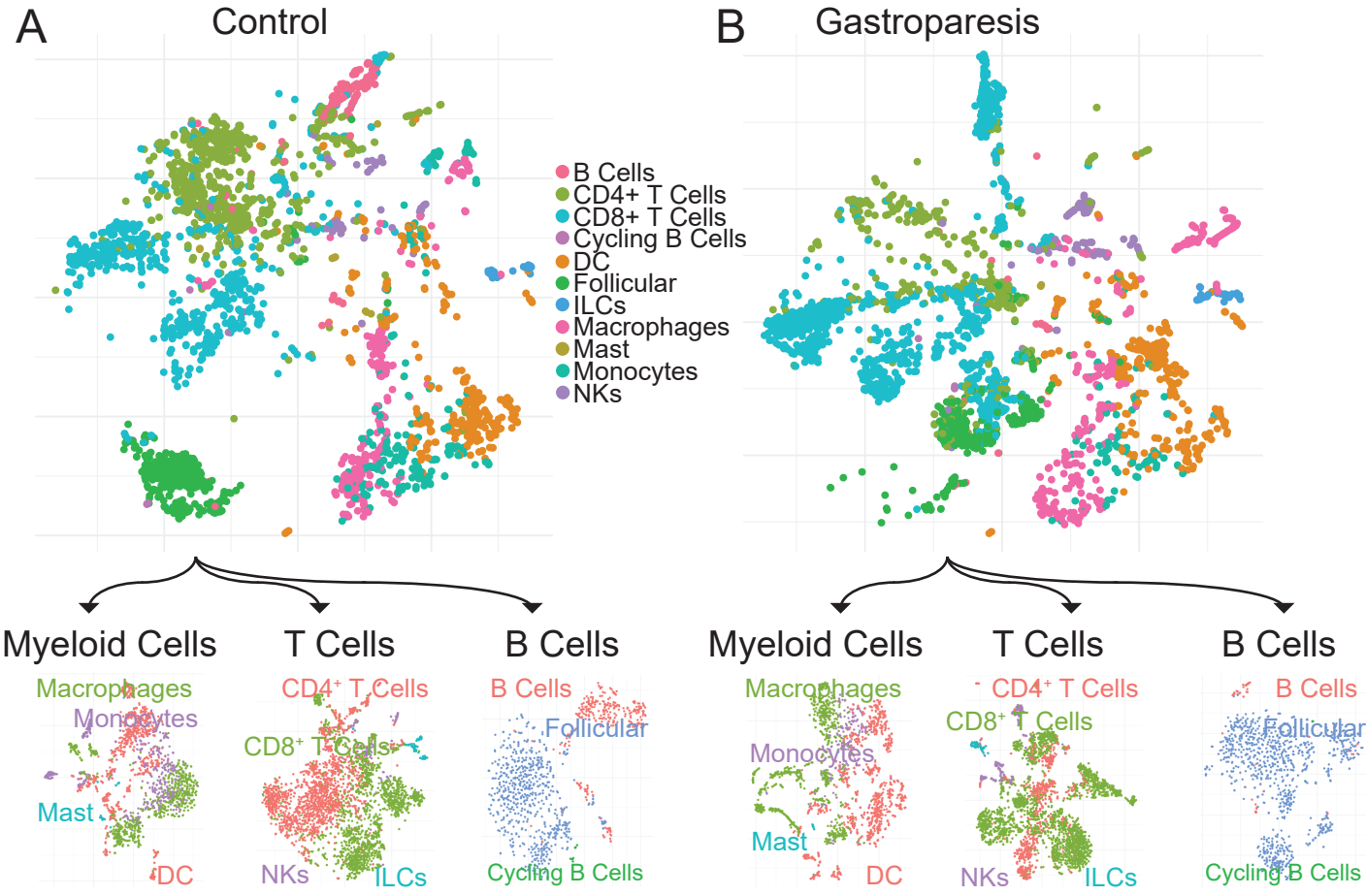


Figure S1: tSNE distribution of clusters using cells from idiopathic gastroparesis and healthy volunteers (down scaled to numbers matching idiopathic gastroparesis)

(A) T-sne plot of all samples from the control patients colored by cell type. Additional t-sne plots of cells specific to Myeloid, T cell, and B cell subtypes. (B) T-sne plot of all samples from the gastroparesis patients colored by cell type. Additional t-sne plots of cells specific to Myeloid, T cell, and B cell subtypes. Related to Figure 1.

Supplementary Figure 2

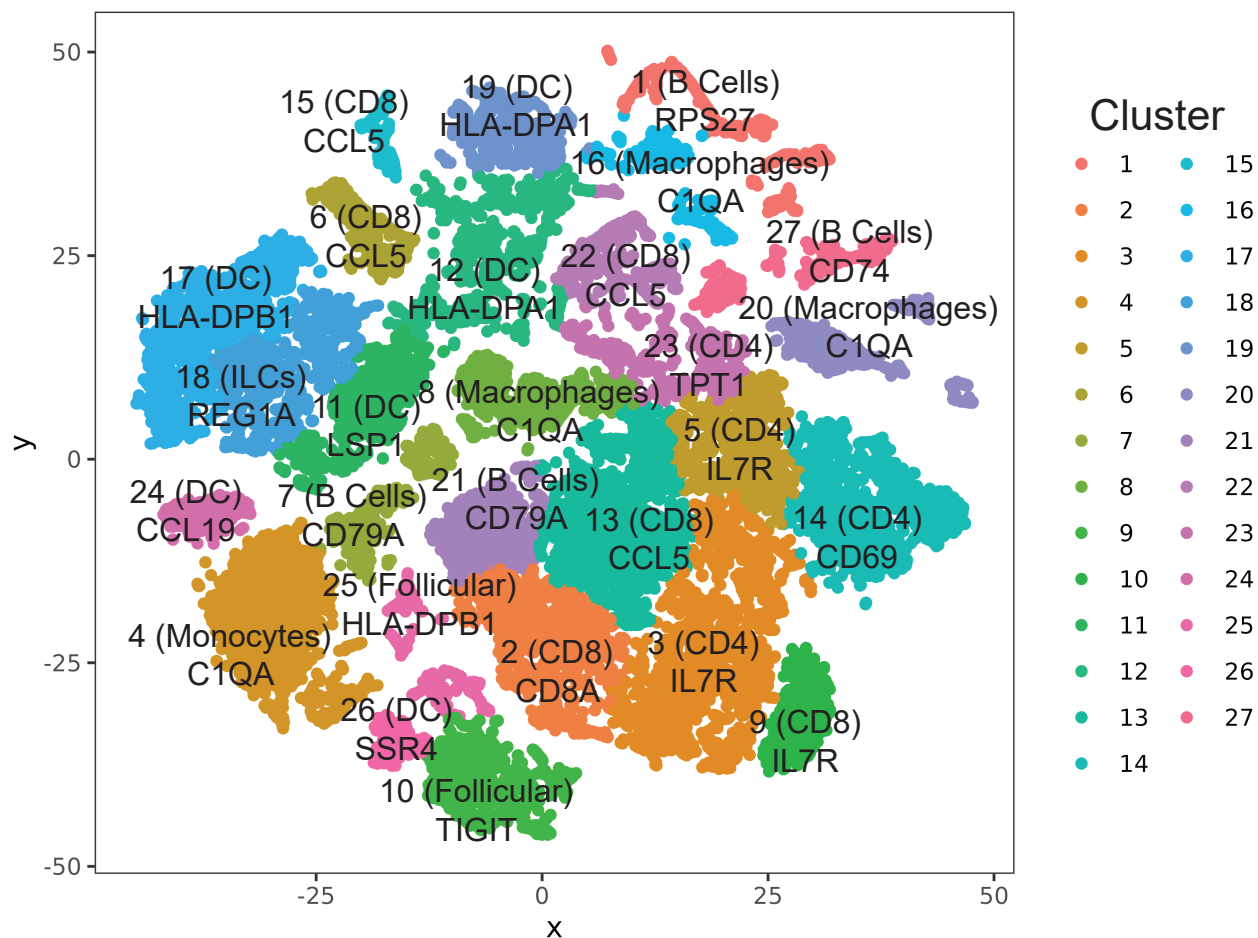


Figure S2: tSNE distribution of unsupervised clusters with cell assignments from Tabula Sapiens based on enriched gene expression
 (A) tSNE plot of all samples from the patients colored by unsupervised cluster assignment (number). The most abundant cell type is listed next to each cluster. Enriched gene expression calculated against all other clusters was compared to Tabula Sapiens small intestine immune cell types and the top relevant gene is listed next to each cluster. Related to Figure 1.

Supplementary Figure 3

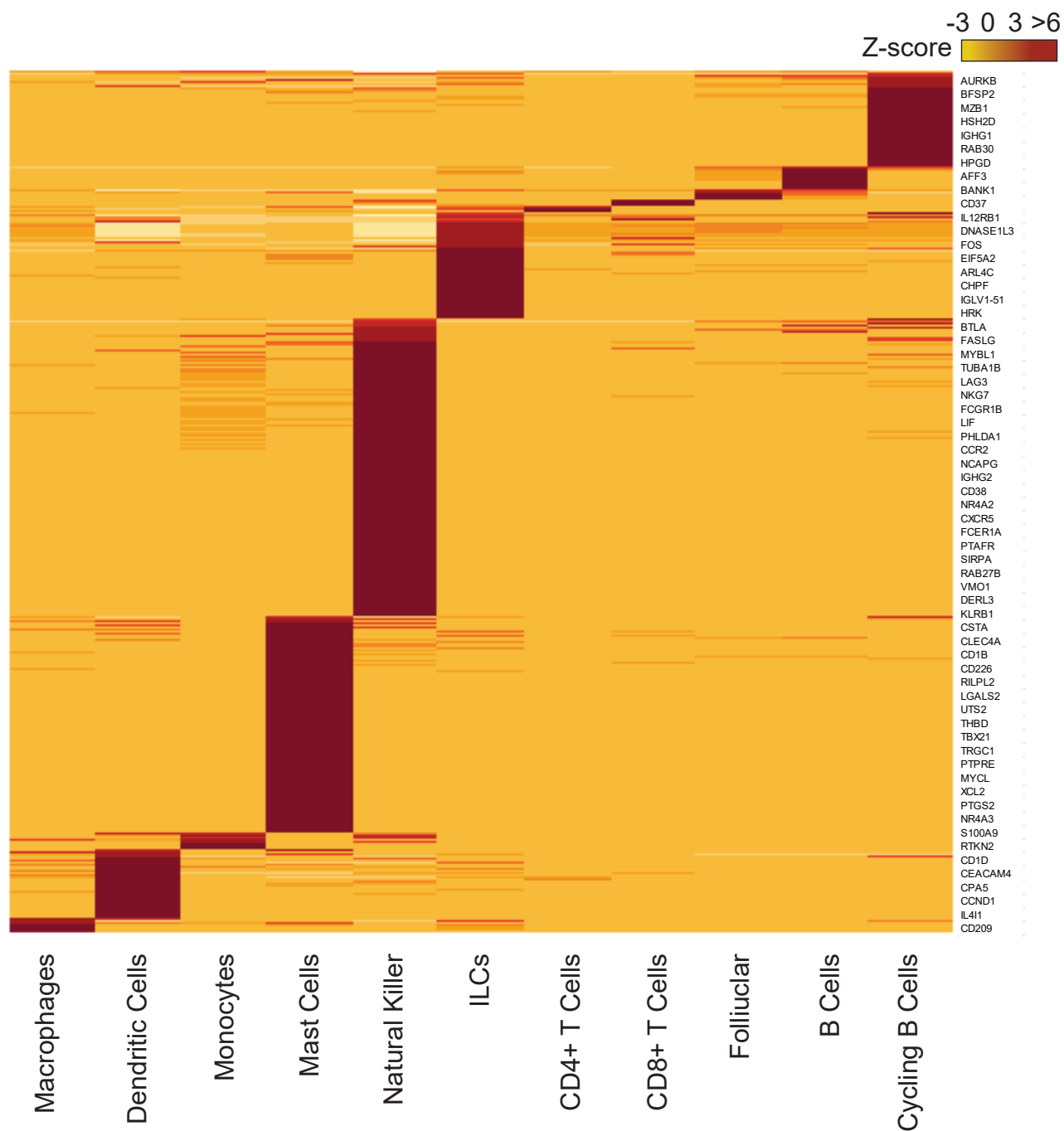


Figure S3: Heatmap of cell type specific genes (544 genes) expression (Zscore logTP10K+1) for all cell types called.
 Ordering of genes was predetermined based on known cell type. Y-axis labels for selected genes of the 544 plotted genes. Related to Figure 1.

Supplementary Figure 4

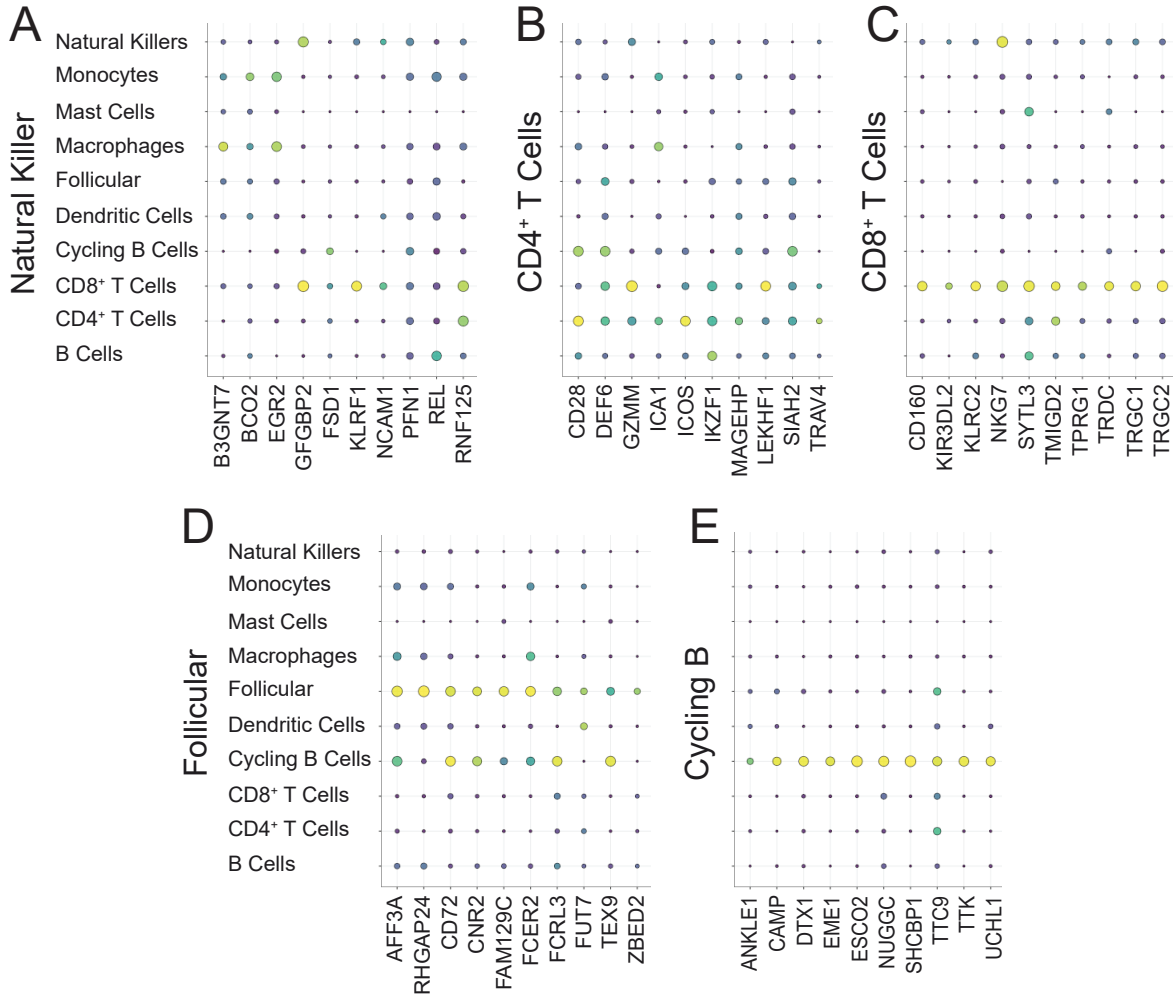


Figure S4: Bubble plots of genes associated with specific cell types.

In order: (A) Natural Killers, (B) CD4+ T cells, (C) CD8+ T cells, (D) Follicular, (E) Cycling B cells. Gene expression (log TP10K+1) is represented by color (yellow high, purple low) and fraction of cells expressing the gene (log TP10K+1 > 0.5) is represented by size of the bubble. Genes were selected by calculating a Zscore for the associated cell type against all other cell types, and genes with the highest Zscore were plotted. Related to Figure 2.