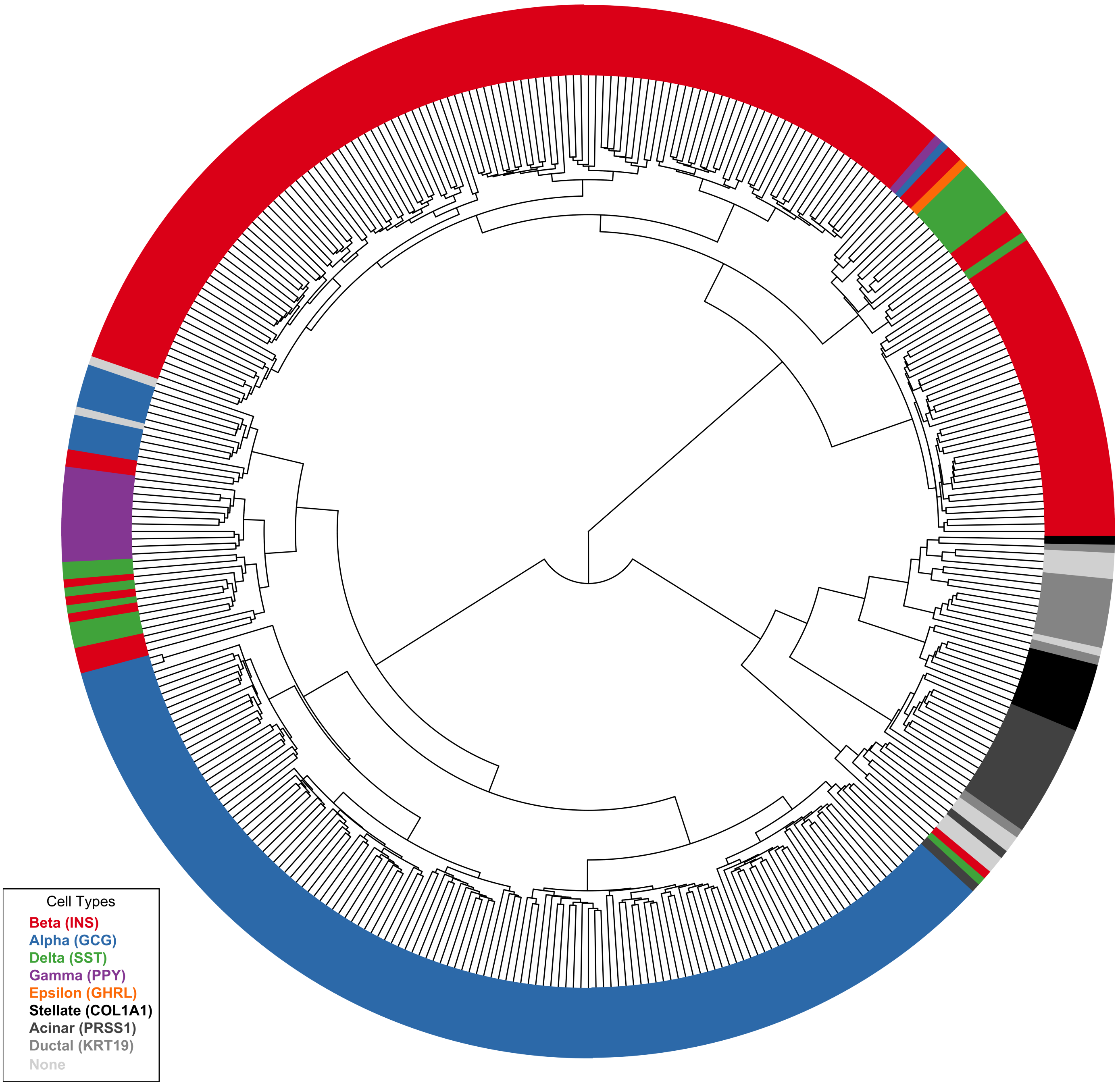
Cell Types
Beta (INS)
Alpha (GCG)
Delta (SST)
Gamma (PPY)
Epsilon (GHRL)
Stellate (COL1A1)
Acinar (PRSS1)
Ductal (KRT19)
None

Supplemental_Fig_S8: Unsupervised hierarchical clustering of non-diabetic single cell transcriptomes is not driven by marker gene expression.

Circular dendrogram illustrates unsupervised clustering of samples by cell type even after excluding marker genes (*INS, GCG, SST, PPY, GHRL, COL1A1, PRSS1*, and *KRT19*) from analysis. 1816 highly expressed genes with $\log_2$(CPM) > 10.5 were used in the analysis and the color labels remained the same as shown in Figure 3B.