



Supplemental_Fig_S17: Reduction of non-diabetic and Type 2 diabetic single cell transcriptomes to two dimensions via unsupervised t-SNE shows robust grouping by cell types regardless of disease state.

Scatter plot of non-diabetic and Type 2 diabetic single cell samples after t-SNE dimensionality reduction. Similar to the hierarchical clustering analysis, 2754 highly expressed genes with $\log_2(\text{CPM}) > 10.5$ were used. Cell type identities, coloring, and disease state information were labeled after the t-SNE analysis. Circular points correspond to non-diabetic single cells while triangular points correspond to Type 2 diabetic single cells.