iScience, Volume 25

## Supplemental information

Human alpha cell transcriptomic

## signatures of types 1 and 2 diabetes highlight

## disease-specific dysfunction pathways

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Supplementary Figure 1 - Pipeline for the identification of high-quality cells The figure illustrates the steps implemented to define high- and low-quality cells.

Supplementary Figure 2 - UMAP representation of T1D with confounders The single-cells from the T1D dataset are reported with cells color-labeled according to the single-cell technology used for sample preparation (left) and the HPAP ID of the donor (right).

Supplementary Figure 3 - UMAP representation of T2D with confounders The single-cells from the T2D dataset are reported with cells color-labeled according to the single-cell technology used for sample preparation (left) and the HPAP ID of the donor (right).

Supplementary Figure 4 - Expression of genes involved in Glycolysis in T1D and T2D datasets The KEGG map of the Glycolysis pathway (hsa00010) is reported with the enzymes colored according to the fold-change of the corresponding genes in T1D (left) and T2D (right) datasets.

Supplementary Figure 5 - Expression of genes involved in Insulin Signaling in T1D and T2D datasets The KEGG map of the Insulin Signaling pathway (hsa04910) is reported with the enzymes coloured according to the fold-change of the corresponding genes in T1D (top) and T2D (bottom) datasets.

Supplementary Figure 6 - Expression of genes involved in Unfolded Protein Response in T1D and T2D datasets

The KEGG map of the Unfolded Protein Response pathway (hsa04141) is reported with the enzymes colored according to the fold-change of the corresponding genes in T1D (left) and T2D (right) datasets.



0.6 0.8 Mitochondrial fraction

Number of mapped reads











Down-regulated Up-regulated



