Electronic Supplementary Material (ESI) for Molecular Omics.

Supplementary File 1:

Supplementary Figure 1: Experimental protocol

Supplementary Figure 2: Heatmap showing the expression level of selected genes in the INS+/UCN3+ (β1-cells), INS+/CD9+ (β2-cells), INS+/ST8SIA1+ (β3-cells), INS+/GRHL+, INS+/ARX/GCG+, INS+/PPY+, INS+/STT+ populations extracted from Loupe browser analysis.

Supplementary Figure 3: Heatmap showing the expression levels of top 10 highly expressed genes in the 10 clusters identified from the data driven analysis from Loupe browser analysis.

Supplementary Figure 4: Enriched KEGG pathways identified by the top 200 representative genes of the PPY+/IAPP+ subpopulation.

Supplementary Figure 5: Enriched KEGG pathways identified by the top 200 representative genes of the DPP4+/KDR+ subpopulation.

Supplementary Figure 6: Enriched KEGG pathways identified by the top 200 representative genes of the TTR+/GCG+/STT+ subpopulation.

Supplementary Figure 7: Enriched GO biological processes identified by the top 200 representative genes of the cycling cell subpopulation.

Supplementary Figure 8: (A) Enriched GO biological processes characterized by the top 200 representative genes in the CD9+/SPARC+/REST+ subpopulation. (B) Network of enriched biological processes in the CD9+/SPARC+/REST+ subpopulation.

Supplementary Figure 9: Enriched KEGG pathways by the top 200 genes of CD9+/SPARC+/REST+ cell subpopulation

Supplementary Figure 10: Enriched KEGG pathways by the top 200 genes of SOX2+/NEUROG3+ subpopulation

Supplementary Figure 11: Enriched KEGG pathways by the top 200 genes of HNF1A+/APOA2+ subpopulation

Supplementary Figure 12: Enriched KEGG pathways by the top 200 genes of KCNJ3+/TPH1+/MYH4+ subpopulation.

Supplementary File 2:

Supplementary file 2: word file of additional information on bioinformatics analysis

Supplementary File 3:

Supplementary file 3: Excel file with cell subpopulation clustering using knowledge-based markers

Supplementary File 4:

Supplementary file 4: Excel file with cell subpopulation clustering using data driven analysis by K-means

Supplementary File 5:

Supplementary file 5: Excel file with cell subpopulation re-clustering from K-means cluster CD9+/SPARC+/REST+ subpopulation