

Appendix to “Single-cell transcriptomes reveal characteristic features of human pancreatic islet cell types”

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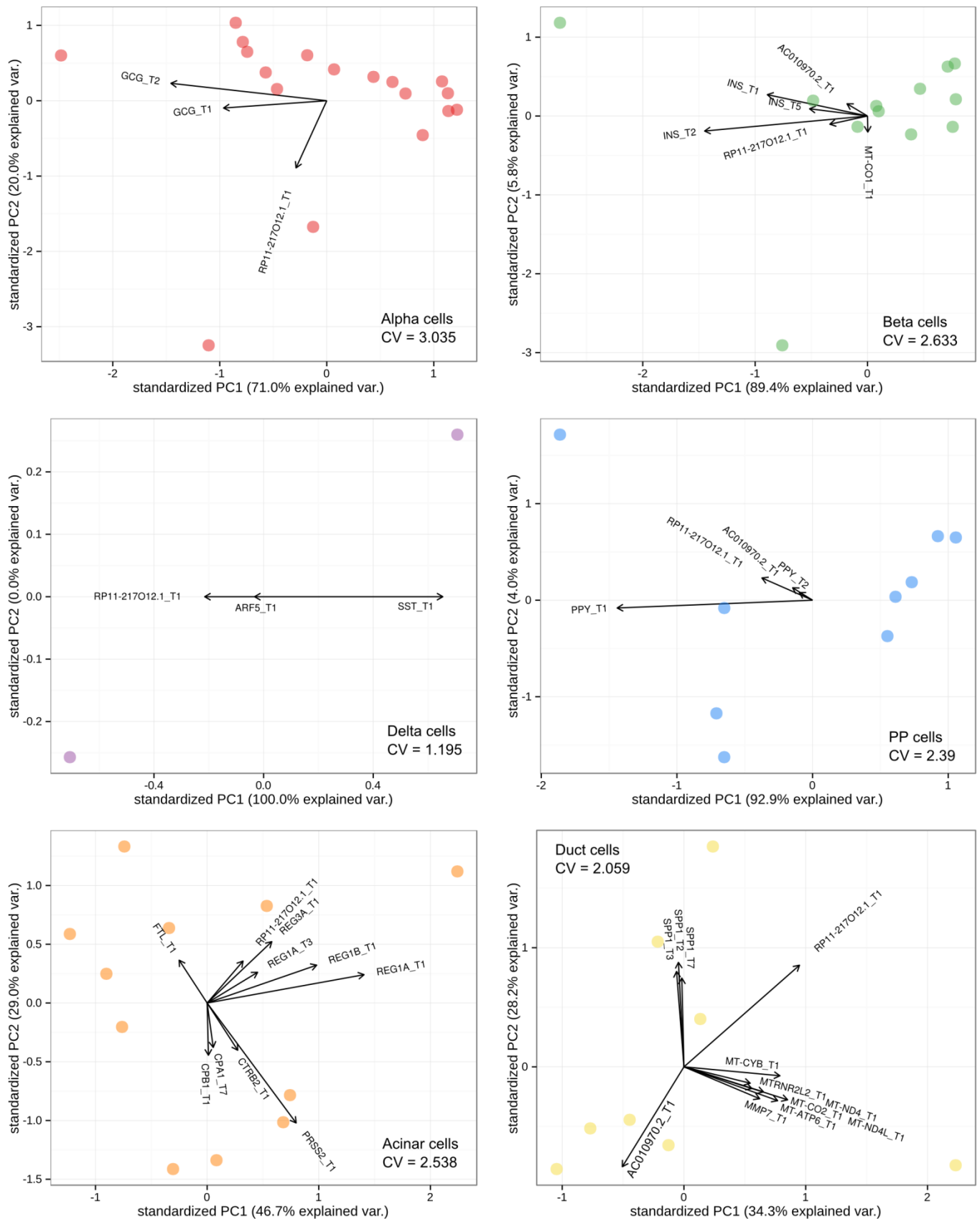
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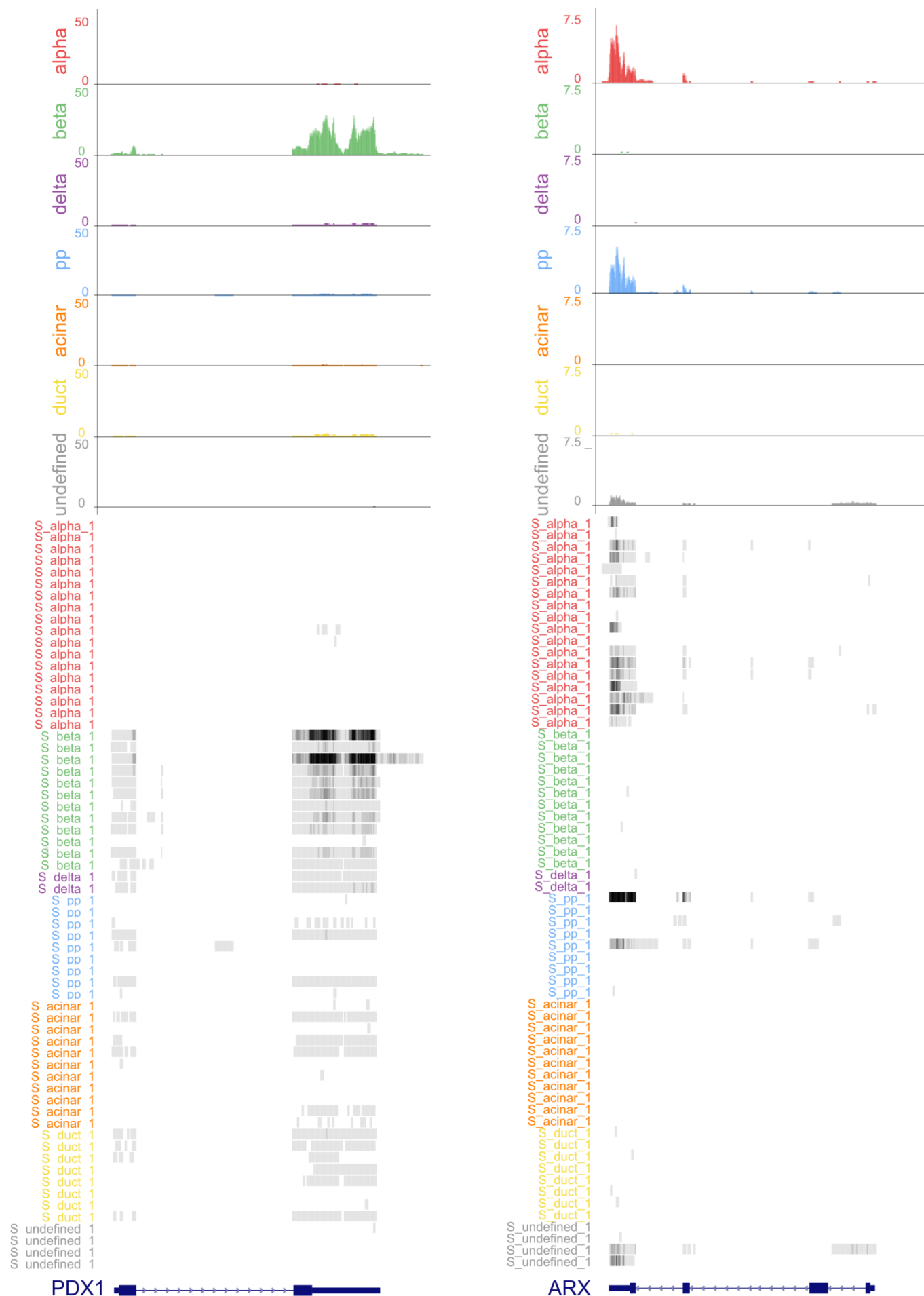
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Appendix Figure S1: Assessment of heterogeneity within each identified human islet cell type

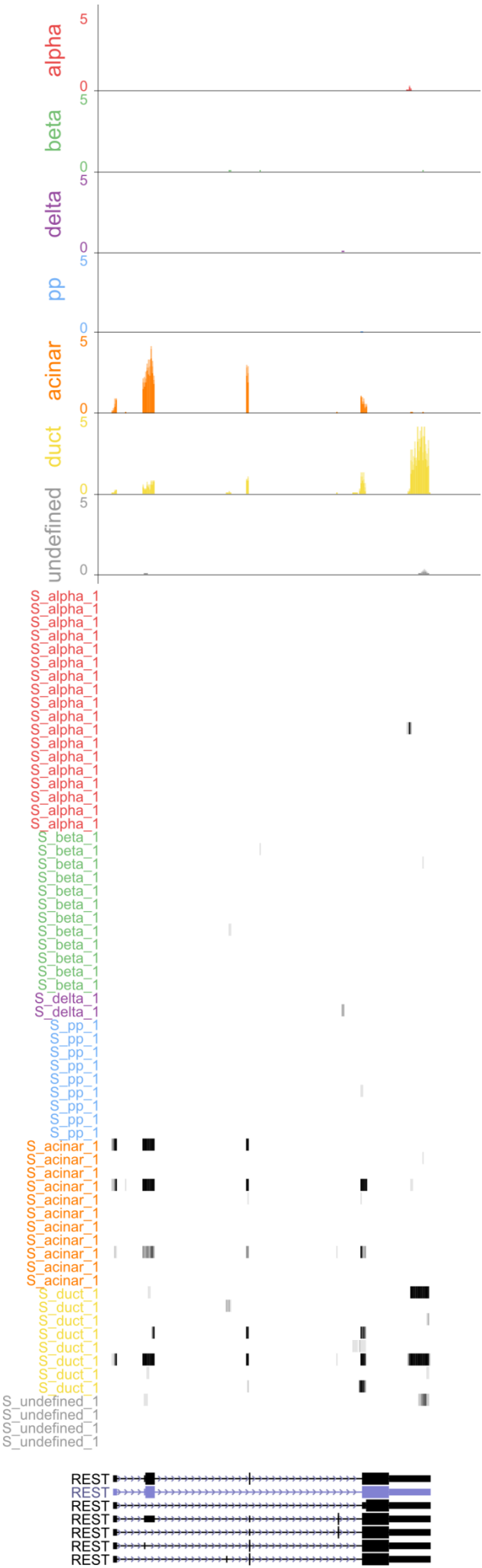
Separate biplots for each of the six identified human islet cell types show considerable variability within cell types. Only the most loaded eigenvectors (transcripts) are displayed. The coefficient of variance (CV) was calculated per cell type based on all transcripts that were expressed in at least one of the single-cells of the respective cell type.

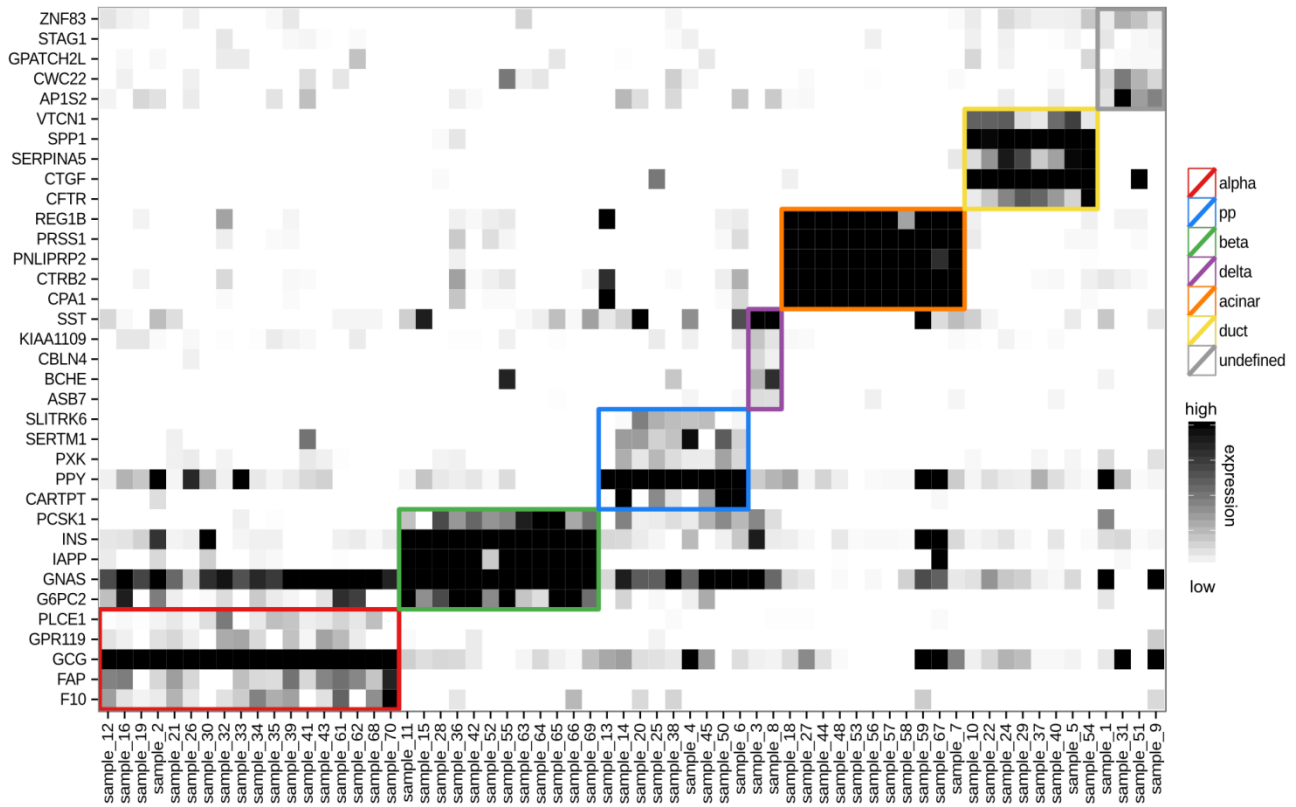


Appendix Figure S2: Single cell expression of PDX1 and ARX

UCSC Genome Browser tracks of PDX1 and ARX for all single-cells as well as merged tracks for each cell type. The scales for individual cells are 0-250 counts for PDX1 and 0-50 counts for ARX.

Appendix Figure S3: Single cell expression of REST
UCSC Genome Browser tracks of REST for all single-cells as well as merged tracks for each cell type. The scales for individual cells are 0-10 counts.

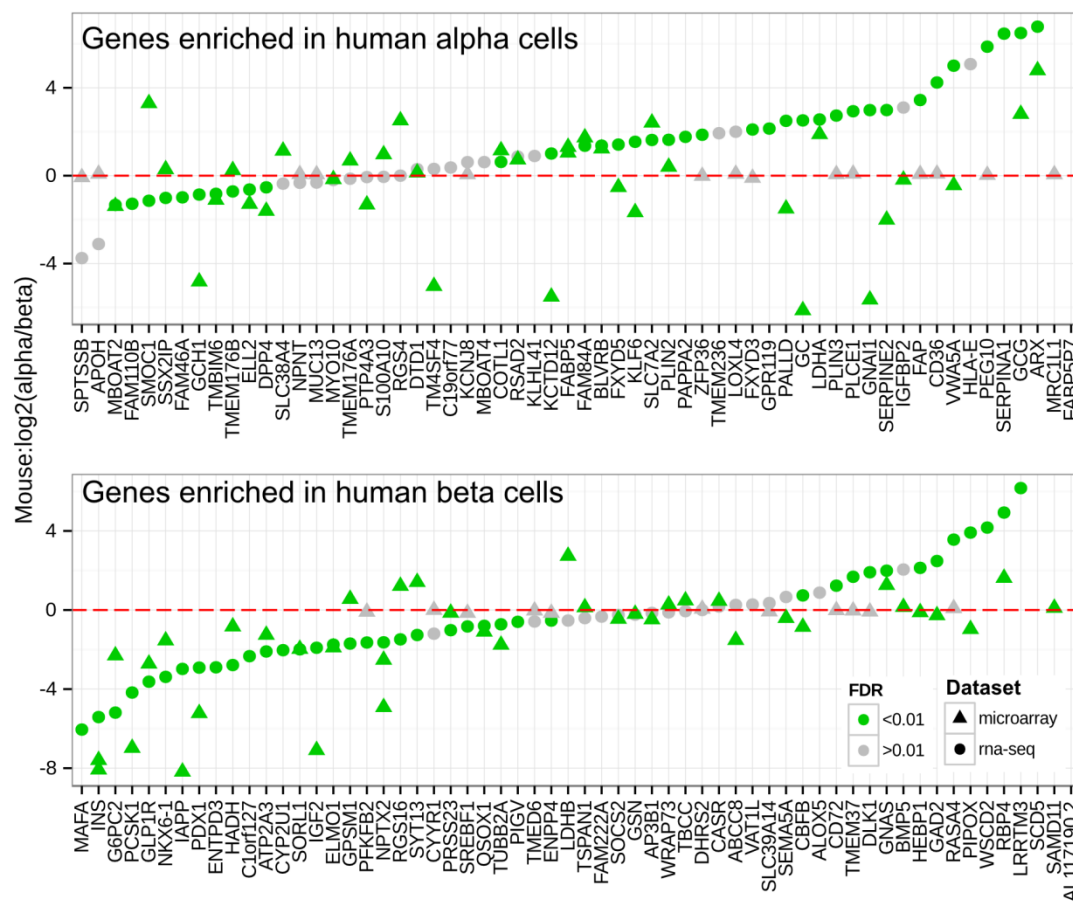




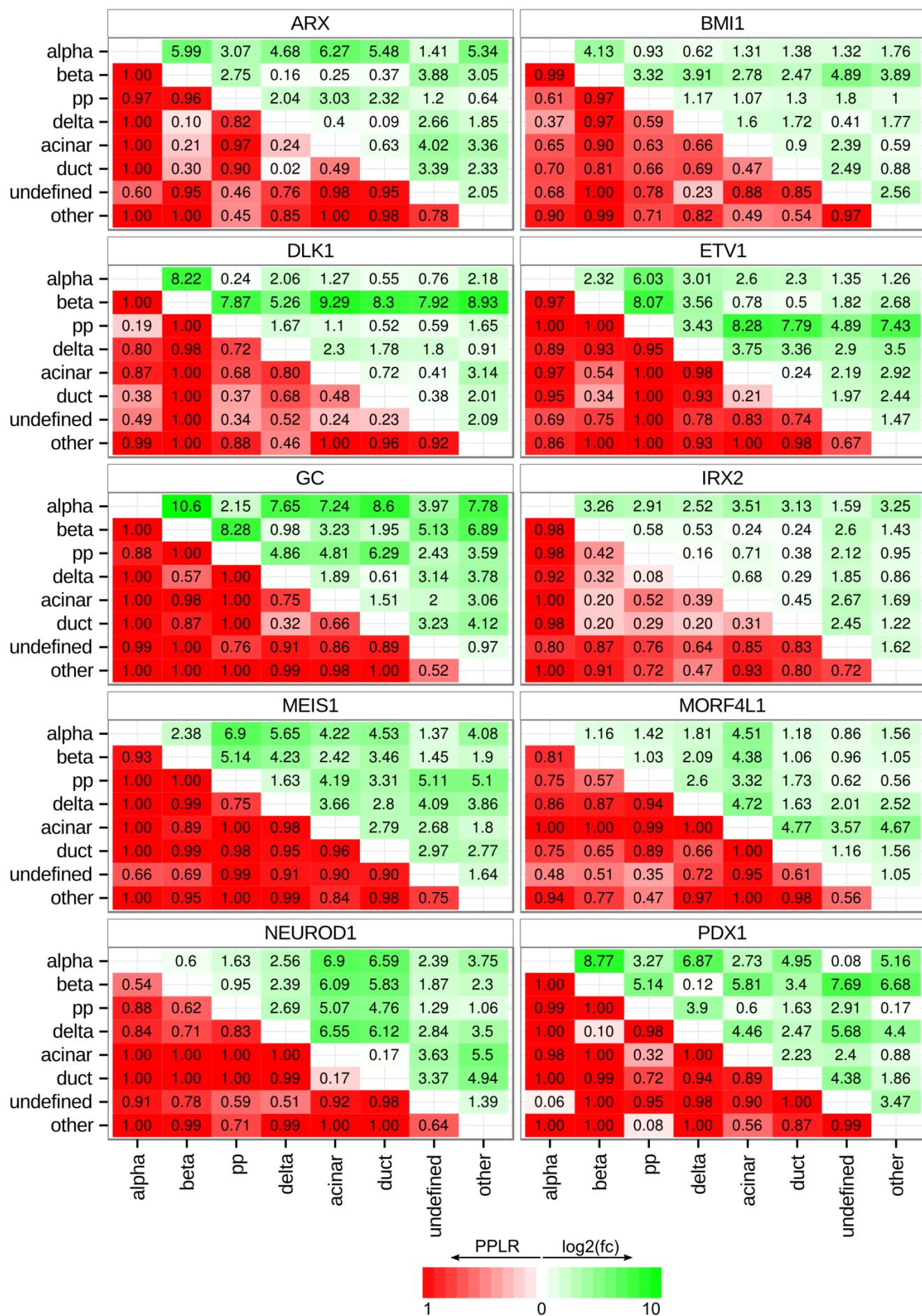
Appendix Figure S4: Identification of cell type specific transcripts

Heatmap displaying the expression patterns (scaled RPKM values) across all single cells for the top five cell type specific genes as determined by pairwise differential expression analysis.

B

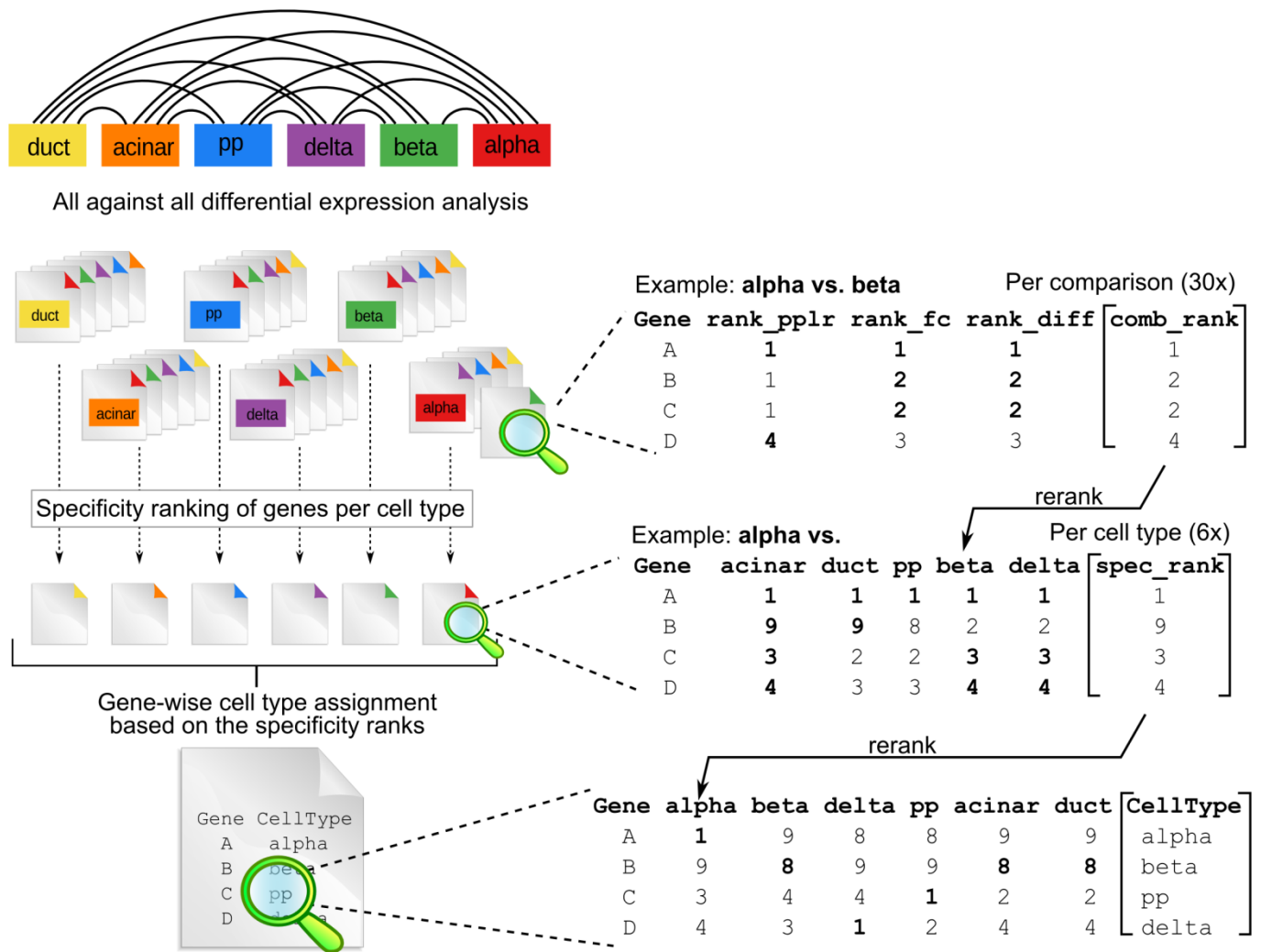


**Appendix
Figure S5:
Comparing
alpha cell and
beta cell
specific genes
between
human and
mouse**
(A) Log fold
change in RNA
expression
between human
alpha and beta
single-cells for
genes identified
as the 60 most
alpha or beta
cell specific
genes in mouse.
(B) Log fold
change in RNA
expression
between mouse
alpha and beta
cells for genes
identified as the
60 most alpha or
beta cell specific
genes in human
single-cells.
PPLR:
probability of
positive log
ratio; FDR: false
discovery rate.



Appendix Figure S6: Statistical significance of differential gene expression

Matrix showing the scaled probability of positive log-ratio (pplr: lower left) and log2 fold change (log2(fc): upper right) of pairwise differential expression analysis for individual genes displayed in Fig. 2C-F and Fig. 3D. "Other" signifies the comparison to all other cell types taken together.



Appendix Figure S7: Rank-based approach for defining cell type specific genes

Illustration of the rank based approach of defining cell type specific genes and assigning cell types to genes. PPLR: Probability of Positive Log Ratio; FC: Fold Change (expression); Diff: absolute difference (expression).