



Supplemental Figure 5. A,B) General quality assessment of selected published datasets (table S) prior to Seurat processing and SCUREL analysis, before filtering (A) and after (B). C) Uniform Manifold Approximation and Projection (UMAP) of the different samples after normalisation, scaling and annotation by gating using scGate. 'Multi' indicates cells annotated by different scGate models. D) scRNAseq annotation summarised per dataset (top) or by cell categories (bottom). Only cells of interest are summed up. E) Barplots presenting number of shortening (left) or lengthening (right) exons in the different comparisons after SCUREL analysis. F) Venn diagram showing the overlap of genes whose length is reverted between A-seq2 and scRNAseq/SCUREL analysis.