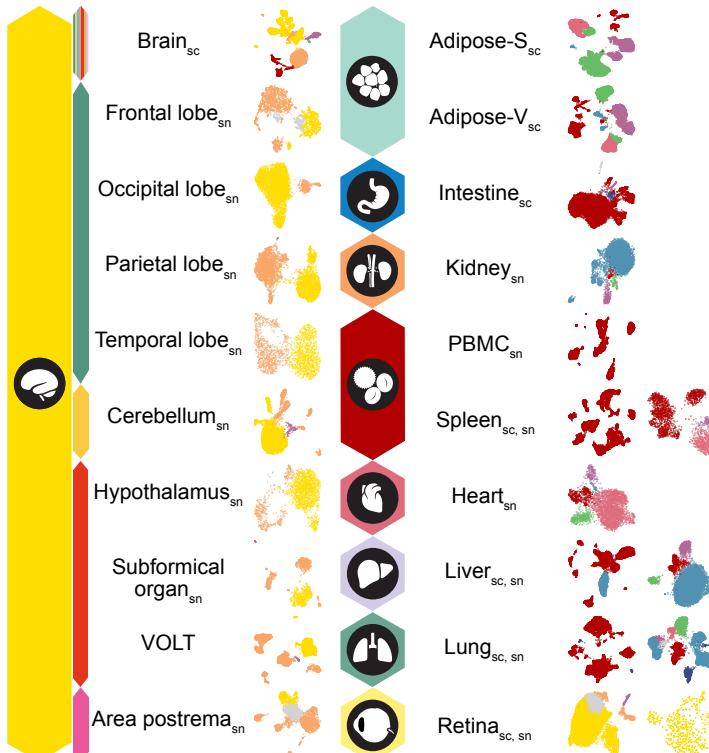
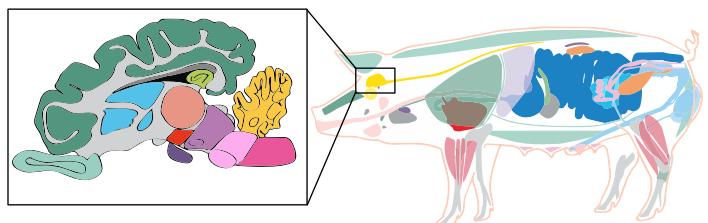
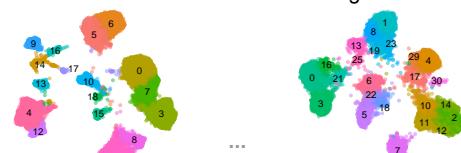
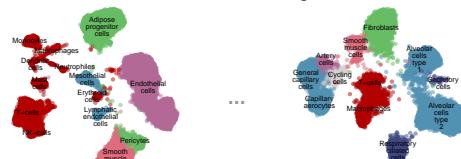


A**B**

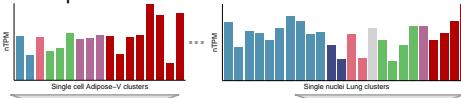
Clustering 24 single cell transcriptomic libraries from 11 tissues and 9 brain regions.



Manual annotation of 191,987 single cells by cluster labelling



Pooling into 469 cell cluster libraries and expression data normalisation into nTPM



QC filtering and weighted average pooling into unique 190 unique cell types across samples.



Aggregate nTPM into 66 unique cell types



Figure 1. Overview of the single cell transcriptomic data processing. **A)** Overview of the datasets used for the generation of the single cell atlas. In total 24 tissues stemming from 11 organs and 9 brain tissues were processed. Note, the brain sample, includes sections of the neocortex (cerebral cortex), cerebellar cortex (cerebellum), caudate nucleus (basal ganglia), thalamus, hypothalamus, hippocampus, hypothalamus, and pons. Illustrations of the pig and the brain, as well as the tissue symbols are taken from Human Protein Atlas. **B)** Schematic overview of the pooling strategy applied to generate the normalised cell type expression matrix for each gene and each single cell library.