

Supplementary information, Fig. S1

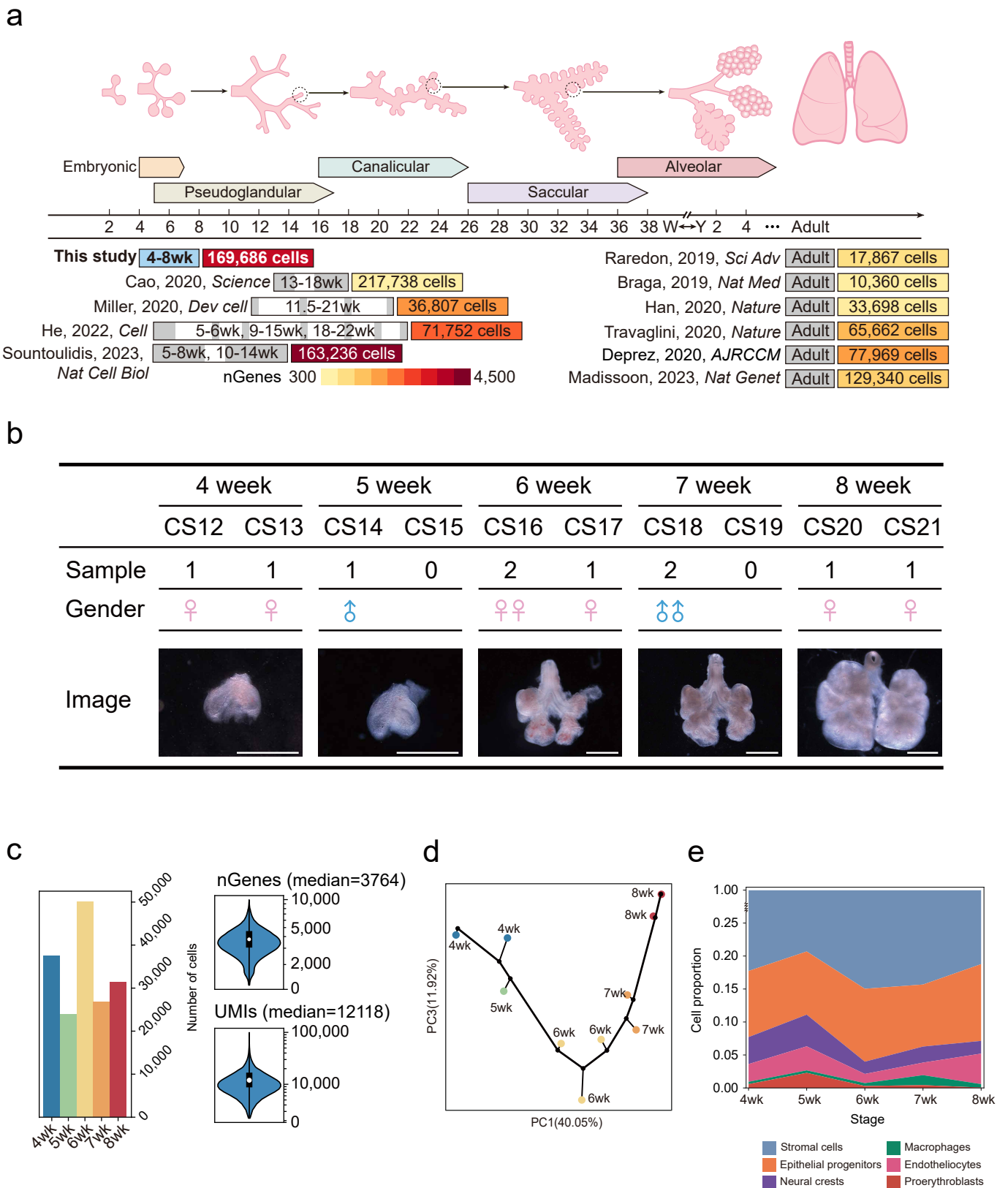


Fig. S1 Tissue images and data quality.

(a) Comparison of single cell studies for human lung development.

(b) Representative human embryonic lung image, Carnegie stage, and sample size of scRNA-seq experiments. Scale bar, 1mm.

(c) Histograms showing the number of cells sequenced at each timepoint. The distribution of detected genes (nGenes) and counts (UMIs) across all samples were shown in violin plots.

(d) PCA of pseudo-bulk RNA-seq profiles demonstrating a concordance collection time of samples along the PC components.

(e) Stack plot showing the proportion of cell types over time.