Supplementary information, Fig. S2

a

b

Epithelial progenitors

CTNND2/NKX2.1/DAPI
SPINT1/NKX2.1/DAPI

Stromal cells

TSHZ3/TCF21/DAPI

CRLF1/NKX2.1/DAPI
PERP/NKX2.1/DAPI

Neural crests

KIF1A/SOX10/DAPI

Endotheliocytes

ESAM/PECAM1/DAPI
CD93/PECAM1/DAPI

Macrophages

ADAP2/MRC1/DAPI

c

Stromal cells
① SC_Early
② SC_TOP2A+
③ SC_COL9A2+
④ SC_BDNF+
⑤ SC_CRABP1+
⑥ ASMC
⑦ VSMC

Epithelial progenitors
① EPI_SOX2hi/ETV5lo
② EPI_TOP2A+
③ EPI_SOX9hi/ETV5hi
④ EPI_DTL+
⑤ Neuroendocrine cells

Neural crests
① NC_S100B+
② NC_TOP2A+
③ NC_TAC3+
④ NC_VWDE+
⑤ NC_OLIG3+
⑥ NC_PDGFRA+

Endotheliocytes
① EC_CA4+
② EC_TOP2A+
③ EC_TAL1+
④ EC_Artery
⑤ EC_Lymphatic
⑥ EC_RSPO2+

Macrophages
① MP_LILRB5+
② MP_PLAC8+
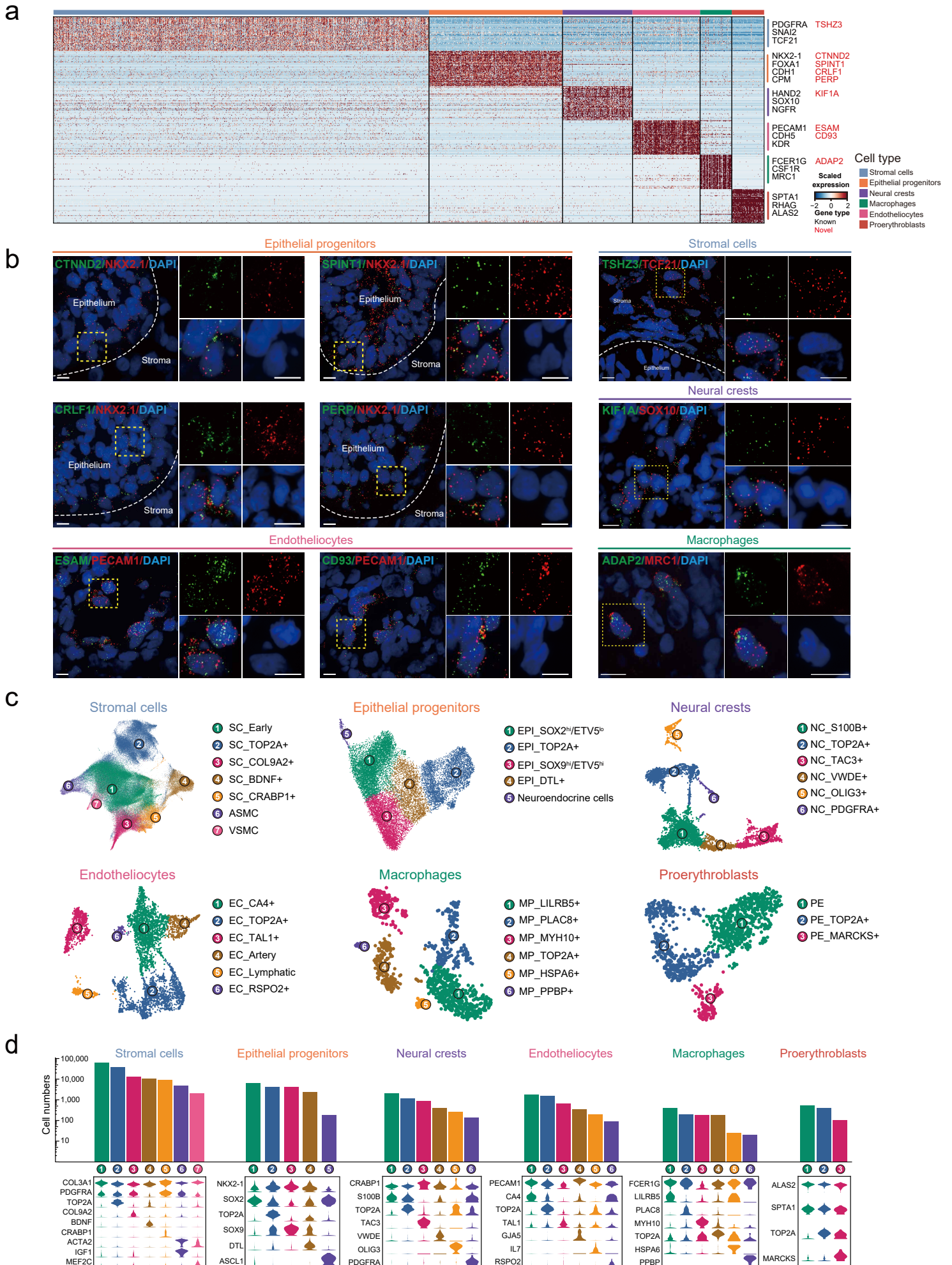③ MP_MYH10+
④ MP_TOP2A+
⑤ MP_HSPA6+
⑥ MP_PPBP+

Proerythroblasts
① PE
② PE_TOP2A+
③ PE_MARCKS+

d

Fig. S2 Human embryonic lung cell atlas.

(a) Heatmap showed scaled expression of differentially expressed genes (DEGs) among six major cell types (p-value<0.01, Wilcoxon rank-sum test). Genes marked in black are the known cell type markers, in red are the newly identified markers in this study.

(b) smiFISH staining in 8 weeks' lung tissue showing epithelial (i.e., *NKX2-1*, *CTNND2*, *SPINT1*, *CRLF1*, *PERP*), stromal (i.e., *TSHZ3*, *TCF21*), neural crest (i.e., *KIF1A*, *SOX10*), endothelial (i.e., *ESAM*, *PECAM1*), and macrophage (i.e., *ADAP2*, *MRC1*) markers. Data are representative of at least two independent smiFISH experiments. Scale bar, 10µm.

(c) Further clustering of the six major cell types, yielding 33 cell subtypes. Cell subtypes of each major cell types are projected on UMAP layout, respectively.

(d) Bar plot showing the log10-transformed cell number of 33 cell subtypes (upper). Violin plot showing the distribution of shared and specific markers of these cell subtypes (lower).