Fig. S1

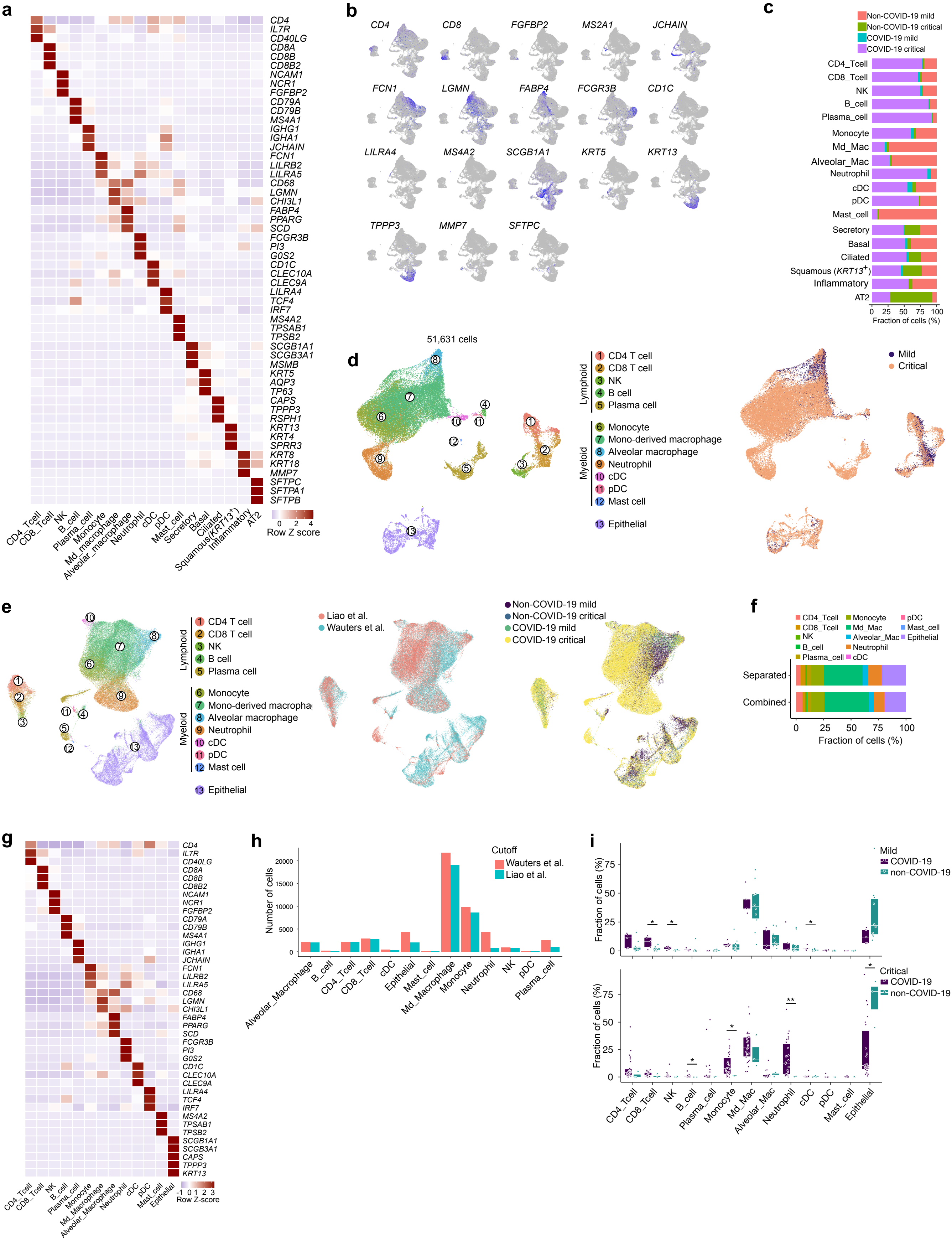
a
CD4
IL7R
CD40LG
CD8A
CD8B
CD8B2
NCAM1
NCR1
FGFBP2
CD79A
CD79B
MS4A1
IGHG1
IGHA1
JCHAIN
FCN1
LILRB2
LILRA5
CD68
LGMN
CHI3L1
FABP4
PPARG
SCD
FCGR3B
PI3
G0S2
CD1C
CLEC10A
CLEC9A
LILRA4
TCF4
IRF7
MS4A2
TPSAB1
TPSB2
SCGB1A1
SCGB3A1
MSMB
KRT5
AQP3
TP63
CAPS
TPPP3
RSPH1
KRT13
KRT4
SPRR3
KRT8
KRT18
MMP7
SFTPC
SFTPA1
SFTPB
CD4_Tcell
CD8_Tcell
NK
B_cell
Plasma_cell
Monocyte
Md_macrophage
Alveolar_macrophage
Neutrophil
cDC
pDC
Mast_cell
Secretory
Basal
Ciliated
Squamous(KRT13+)
Inflammatory
AT2
0 2 4
Row Z score
b
CD4
CD8
FGFBP2
MS2A1
JCHAIN
FCN1
LGMN
FABP4
FCGR3B
CD1C
LILRA4
MS4A2
SCGB1A1
KRT5
KRT13
TPPP3
MMP7
SFTPC
c
Non-COVID-19 mild
Non-COVID-19 critical
COVID-19 mild
COVID-19 critical
CD4_Tcell
CD8_Tcell
NK
B_cell
Plasma_cell
Monocyte
Md_Mac
Alveolar_Mac
Neutrophil
cDC
pDC
Mast_cell
Secretory
Basal
Ciliated
Squamous (KRT13+)
Inflammatory
AT2
0 25 50 75 100
Fraction of cells (%)
d
51,631 cells
Lymphoid
1 CD4 T cell
2 CD8 T cell
3 NK
4 B cell
5 Plasma cell
Myeloid
6 Monocyte
7 Mono-derived macrophage
8 Alveolar macrophage
9 Neutrophil
10 cDC
11 pDC
12 Mast cell
13 Epithelial
Mild
Critical
e
Lymphoid
1 CD4 T cell
2 CD8 T cell
3 NK
4 B cell
5 Plasma cell
Myeloid
6 Monocyte
7 Mono-derived macropha
8 Alveolar macrophage
9 Neutrophil
10 cDC
11 pDC
12 Mast cell
13 Epithelial
Liao et al.
Wauters et al.
Non-COVID-19 mild
Non-COVID-19 critical
COVID-19 mild
COVID-19 critical
f
CD4_Tcell
CD8_Tcell
NK
B_cell
Plasma_cell
Monocyte
Md_Mac
Alveolar_Mac
Neutrophil
cDC
pDC
Mast_cell
Epithelial
Separated
Combined
0 25 50 75 100
Fraction of cells (%)
g
CD4
IL7R
CD40LG
CD8A
CD8B
CD8B2
NCAM1
NCR1
FGFBP2
CD79A
CD79B
MS4A1
IGHG1
IGHA1
JCHAIN
FCN1
LILRB2
LILRA5
CD68
LGMN
CHI3L1
FABP4
PPARG
SCD
FCGR3B
PI3
G0S2
CD1C
CLEC10A
CLEC9A
LILRA4
TCF4
IRF7
MS4A2
TPSAB1
TPSB2
SCGB1A1
SCGB3A1
CAPS
TPPP3
KRT13
CD4_Tcell
CD8_Tcell
NK
B_cell
Plasma_cell
Monocyte
Md_Macrophage
Alveolar_Macrophage
Neutrophil
cDC
pDC
Mast_cell
Epithelial
-1 0 1 2 3
Row Z-score
h
Number of cells
0
5000
10000
15000
20000
Cutoff
Wauters et al.
Liao et al.
Alveolar_Macrophage
B_cell
CD4_Tcell
CD8_Tcell
cDC
Epithelial
Mast_cell
Md_Macrophage
Monocyte
Neutrophil
NK
pDC
Plasma_cell
i
Fraction of cells (%)
0
25
50
75
Mild
COVID-19
non-COVID-19
*
*
*
*
Critical
COVID-19
non-COVID-19
*
*
**
*
CD4_Tcell
CD8_Tcell
NK
B_cell
Plasma_cell
Monocyte
Md_Mac
Alveolar_Mac
Neutrophil
cDC
pDC
Mast_cell
Epithelial

Fig. S1 Cell type annotation and clustering of scRNA-seq data by Liao et al.

a-b Heatmap showing the expression of 3 marker genes (**a**) and feature plots showing 1 marker gene (**b**) for each of the different cell types. **c** Fraction of cell type per disease (COVID-19 vs non-COVID-19) and severity of the disease (mild vs critical). **d** UMAP showing 51,631 cells identified in scRNA-seq data by Liao et al., color-coded per cell type (left) and per disease severity status (right). **e** UMAP representation of merged datasets (Liao et al., and Wauters et al.) by scRNA-seq color-coded for the indicated cell type (left), the dataset (middle) and the disease (right). **f** Fraction of each cell type as determined by clustering both datasets separately or together. **g** Heatmap showing cell types with corresponding marker genes and functional gene sets. **h** Number of cells detected for each cell type using two quality cutoffs: the cutoff described in Wauters et al. vs the cutoff described in Liao et al. **i** Relative contribution of each cell type (in %) in COVID-19 vs non-COVID-19 in mild (upper panel) and critical disease (lower panel).