Fig. S2

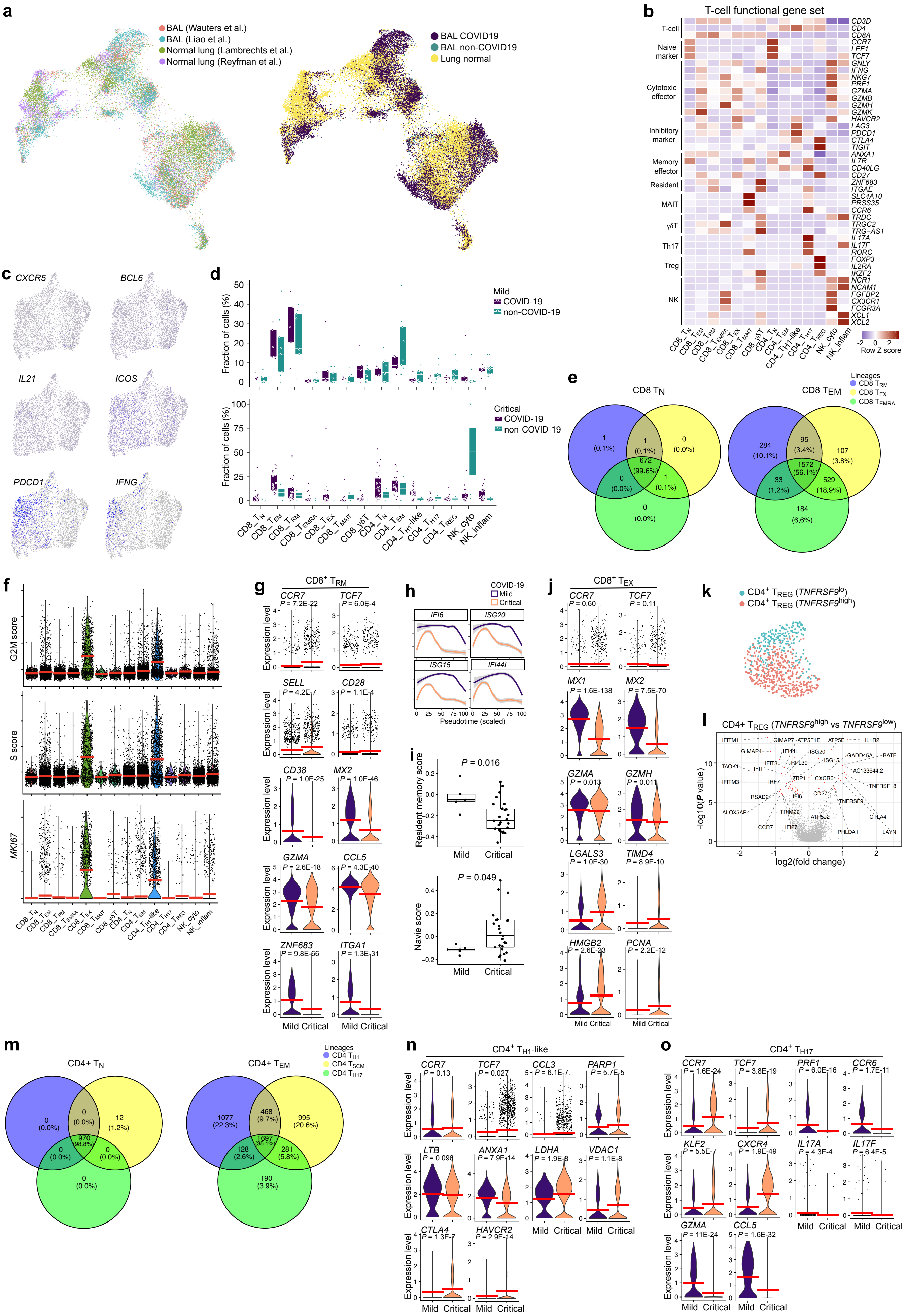
a
BAL (Wauters et al.)
BAL (Liao et al.)
Normal lung (Lambrechts et al.)
Normal lung (Reyfman et al.)
BAL COVID19
BAL non-COVID19
Lung normal
b
T-cell functional gene set
T-cell
Naive marker
Cytotoxic effector
Inhibitory marker
Memory effector
Resident
MAIT
γδT
Th17
Treg
NK
CD3D CD4 CD8A CCR7 LEF1 TCF7 GNLY IFNG NKG7 PRF1 GZMA GZMB GZMH GZMK HAVCR2 LAG3 PDCD1 CTLA4 TIGIT ANXA1 IL7R CD40LG CD27 ZNF683 ITGAE SLC4A10 PRSS35 CCR6 TRDC TRGC2 TRG-AS1 IL17A IL17F RORC FOXP3 IL2RA IKZF2 NCR1 NCAM1 FGFBP2 CX3CR1 FCGR3A XCL1 XCL2
Row Z score
-2 0 2
c
CXCR5
BCL6
IL21
ICOS
PDCD1
IFNG
d
Fraction of cells (%)
Mild
COVID-19
non-COVID-19
Critical
COVID-19
non-COVID-19
CD8_TN CD8_TEM CD8_TRM CD8_TEMRA CD8_TEX CD8_TMAIT CD8_γδT CD4_TN CD4_TEM CD4_TH1-like CD4_TH17 CD4_TREG NK_cyto NK_inflam
e
CD8 TN
CD8 TEM
Lineages
CD8 TRM
CD8 TEX
CD8 TEMRA
1 (0.1%)
0 (0.0%)
1 (0.1%)
672 (99.6%)
0 (0.0%)
1 (0.1%)
0 (0.0%)
284 (10.1%)
95 (3.4%)
107 (3.8%)
1572 (56.1%)
33 (1.2%)
529 (18.9%)
184 (6.6%)
f
G2M score
S score
MKI67
g
CD8+ TRM
CCR7 P = 7.2E-22
TCF7 P = 6.0E-4
SELL P = 4.2E-7
CD28 P = 1.1E-4
CD38 P = 1.0E-25
MX2 P = 1.0E-46
GZMA P = 2.6E-18
CCL5 P = 4.3E-40
ZNF683 P = 9.8E-66
ITGA1 P = 1.3E-31
Expression level
Mild Critical
h
COVID-19
Mild
Critical
IFI6
ISG20
ISG15
IFI44L
Pseudotime (scaled)
i
Resident memory score
P = 0.016
Navie score
P = 0.049
Mild
Critical
j
CD8+ TEX
CCR7 P = 0.60
TCF7 P = 0.11
MX1 P = 1.6E-138
MX2 P = 7.5E-70
GZMA P = 0.013
GZMH P = 0.011
LGALS3 P = 1.0E-30
TIMD4 P = 8.9E-10
HMGB2 P = 2.6E-23
PCNA P = 2.2E-12
Mild Critical
k
CD4+ TREG (TNFRSF9lo)
CD4+ TREG (TNFRSF9high)
l
CD4+ TREG (TNFRSF9high vs TNFRSF9low)
-log10(P value)
log2(fold change)
IFITM1 GIMAP7 ATP5F1E ATP5E IL1R2 GIMAP4 IFI44L ISG20 GADD45A BATF TAOK1 IFIT3 RPL39 ISG15 IFIT1 AC133644.2 IFITM3 IRF7 ZBP1 CXCR6 TNFRSF18 RSAD2 IFI6 CD27 TNFRSF9 ALOX5AP TRIM22 ATP5J2 CTLA4 CCR7 IFI27 PHLDA1 LAYN
m
CD4+ TN
CD4+ TEM
Lineages
CD4 TH1
CD4 TSCM
CD4 TH17
0 (0.0%)
0 (0.0%)
12 (1.2%)
970 (98.8%)
0 (0.0%)
0 (0.0%)
0 (0.0%)
1077 (22.3%)
468 (9.7%)
995 (20.6%)
1697 (35.1%)
128 (2.6%)
281 (5.8%)
190 (3.9%)
n
CD4+ TH1-like
CCR7 P = 0.13
TCF7 P = 0.027
CCL3 P = 6.1E-7
PARP1 P = 5.7E-5
LTB P = 0.096
ANXA1 P = 7.9E-14
LDHA P = 1.9E-8
VDAC1 P = 1.1E-8
CTLA4 P = 1.3E-7
HAVCR2 P = 2.9E-14
Expression level
Mild Critical
o
CD4+ TH17
CCR7 P = 1.6E-24
TCF7 P = 3.8E-19
PRF1 P = 6.0E-16
CCR6 P = 1.7E-11
KLF2 P = 5.5E-7
CXCR4 P = 1.9E-49
IL17A P = 4.3E-4
IL17F P = 6.4E-5
GZMA P = 11E-24
CCL5 P = 1.6E-32
Expression level
Mild Critical

Fig. S2 Single-cell profiling of T-/NK-cell phenotypes

a UMAP showing 23,468 T-/NK-cells color-coded per data origin (left) and per COVID-19 disease status (right). **b** Heatmap showing T-/NK-cell phenotypes with corresponding marker genes and functional gene sets. **c** UMAP for the expression of key T_{FH} markers (*CXCR5*, *BCL6*, *IL21*, and *ICOS*) and other helper T-cell markers (*PDCD1*, *IFNG*), suggesting a lack of T_{FH}-cells. **d** Relative contribution of each cell type (in %) in mild (upper panel) and critical (lower panel) pneumonia patients comparing COVID-19 vs non-COVID-19. **e** Numbers and percentages of CD8+ T_N (left) and T_{EM} (right) T-cells shared by three $CD8^+$ T cell lineages. **f** Violin plot showing scores of cell cycle scores (G2M and S) and *MKI67* expression of T cell clusters. **g** Violin plot showing differential expression of genes in T-cells belonging to the $CD8^+$ T_{RM} lineage in mild vs critical COVID-19 patients. **h** Expression of interferon response genes along the $CD8^+$ T_{RM} trajectory. **i** Box plot showing ‘resident memory’ and ‘naïve T-cell’ scores of the CD8+ T_{RM} lineage from mild-moderate and critical patients. **j** Violin plot showing differential expression of genes in T-cells belonging to the $CD8^+$ T_{EX} lineage in mild vs critical COVID-19 patients. **k** UMAP of CD4+ T_{REG} subclusters. **l** Volcano plot showing differentially expressed genes between *TNFRSF9*^{high} and *TNFRSF9*^{low} T_{REG} subclusters. **m** Numbers and percentages of CD4+ T_{h1}-like (left) and T_{h17} (right) T-cells shared by three $CD4^+$ T cell lineages. **n** Violin plot showing differential expression of genes in T-cells belonging to the $CD4^+$ T_{H1}-like lineage in mild vs critical COVID-19 patients. **o** Violin plot showing differential expression of genes in T-cells belonging to the $CD4^+$ T_{H17} lineage in mild vs critical COVID-19 patients.