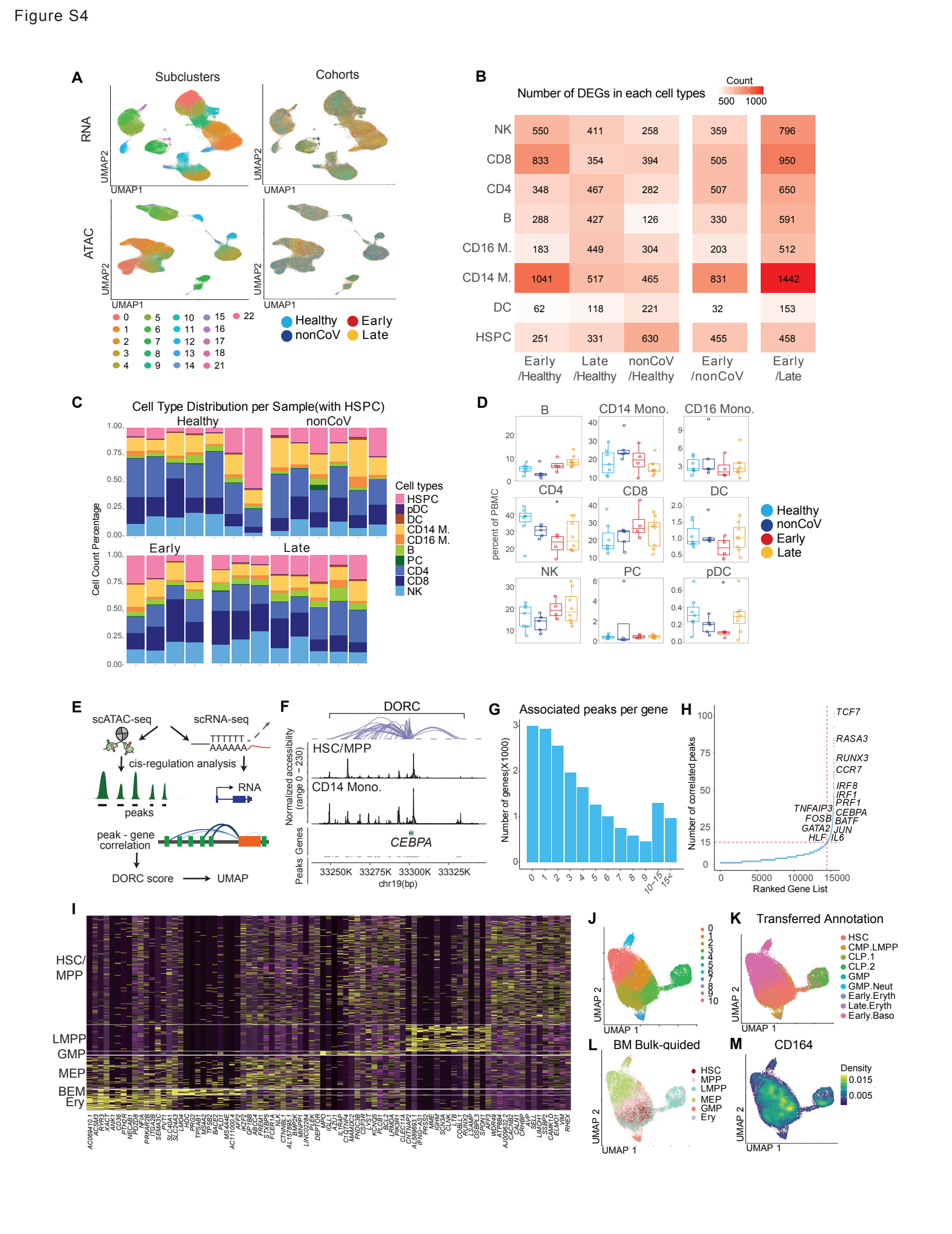
Figure S4


A
Subclusters
Cohorts
RNA
ATAC
UMAP1
UMAP2
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 21 22
Healthy
nonCoV
Early
Late
B
Number of DEGs in each cell types
Count
500 1000
NK 550 411 258 359 796
CD8 833 354 394 505 950
CD4 348 467 282 507 650
B 288 427 126 330 591
CD16 M. 183 449 304 203 512
CD14 M. 1041 517 465 831 1442
DC 62 118 221 32 153
HSPC 251 331 630 455 458
Early /Healthy
Late /Healthy
nonCoV /Healthy
Early /nonCoV
Early /Late
C
Cell Type Distribution per Sample(with HSPC)
Healthy
nonCoV
Early
Late
Cell Count Percentage
Cell types
HSPC
pDC
DC
CD14 M.
CD16 M.
B
PC
CD4
CD8
NK
D
B
CD14 Mono.
CD16 Mono.
CD4
CD8
DC
NK
PC
pDC
percent of PBMC
Healthy
nonCoV
Early
Late
E
scATAC-seq
scRNA-seq
TTTTTT
AAAAAA
cis-regulation analysis
peaks
RNA
peak - gene correlation
DORC score
UMAP
F
DORC
HSC/MPP
CD14 Mono.
CEBPA
Normalized accessibility (range 0 – 230)
Peaks Genes
33250K 33275K 33300K 33325K
chr19(bp)
G
Associated peaks per gene
Number of genes(X1000)
0 1 2 3 4 5 6 7 8 9 10~15 15<
H
Number of correlated peaks
Ranked Gene List
TCF7
RASA3
RUNX3
CCR7
IRF8
IRF1
PRF1
CEBPA
BATF
JUN
IL6
TNFAIP3
FOSB
GATA2
HLF
I
HSC/ MPP
LMPP
GMP
MEP
BEM
Ery
J
UMAP 1
UMAP 2
K
Transferred Annotation
HSC
CMP.LMPP
CLP.1
CLP.2
GMP
GMP.Neut
Early.Eryth
Late.Eryth
Early.Baso
L
BM Bulk-guided
HSC
MPP
LMPP
MEP
GMP
Ery
M
CD164
Density
0.015
0.005