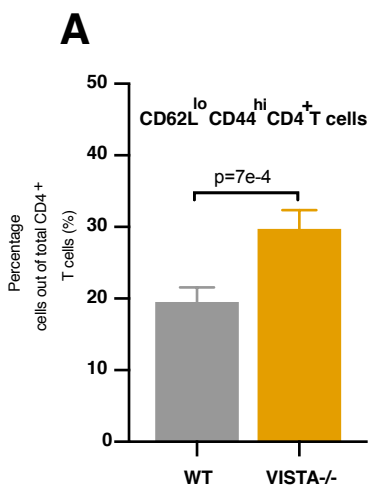
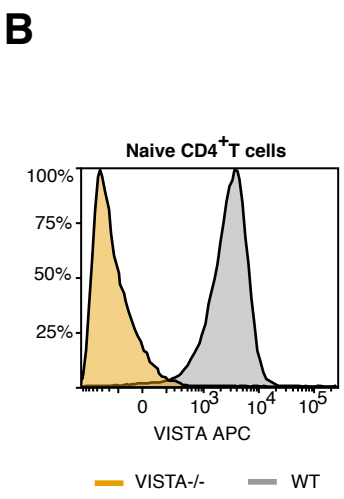
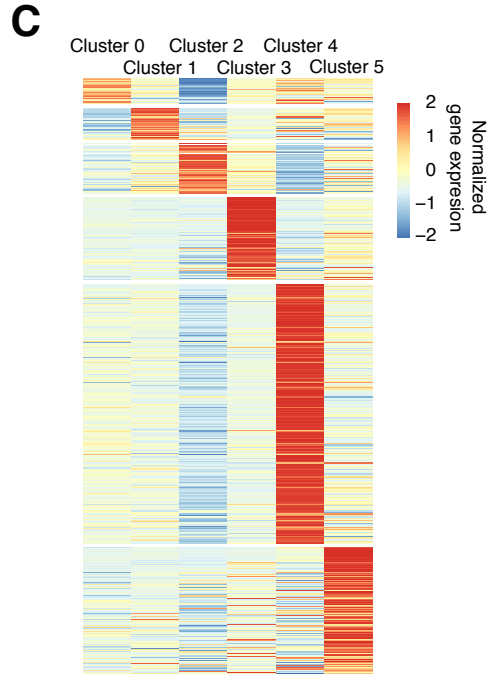
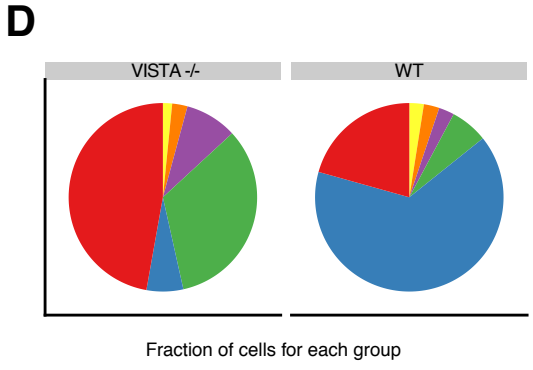
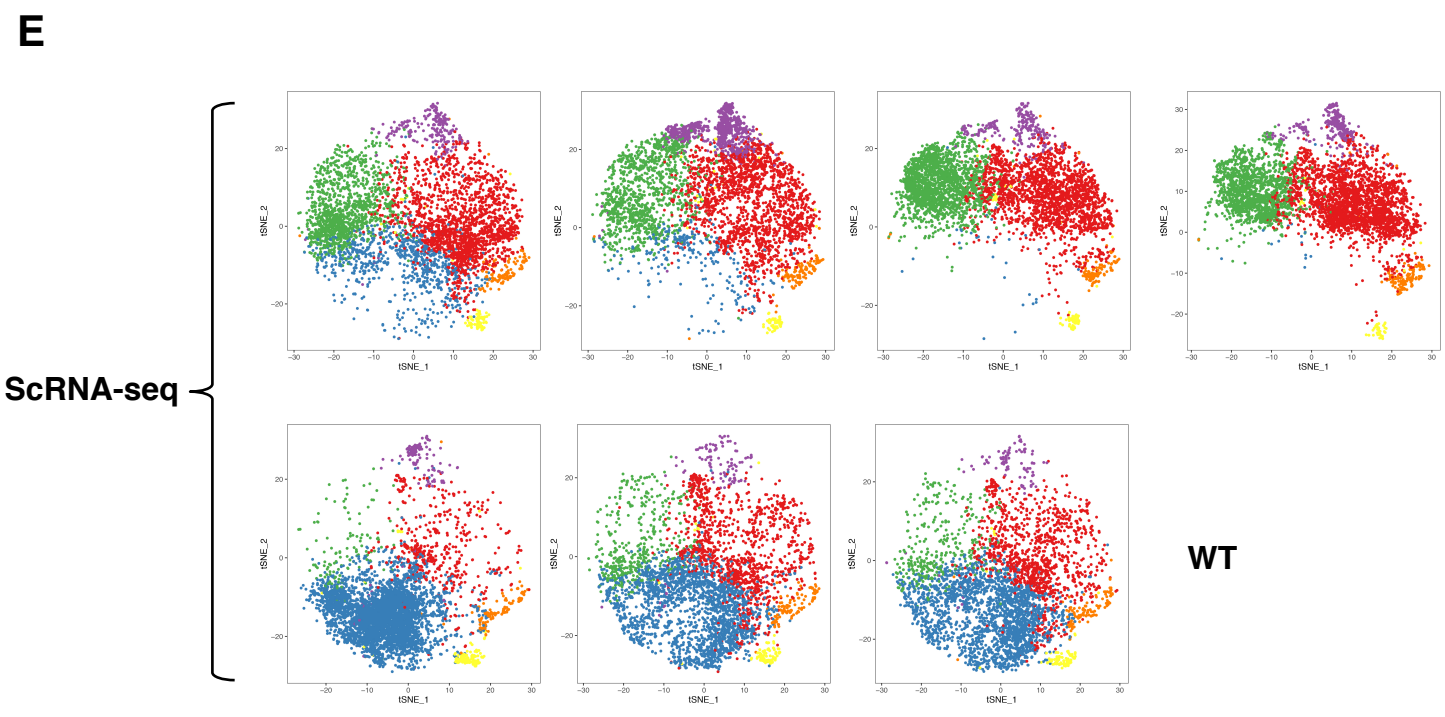
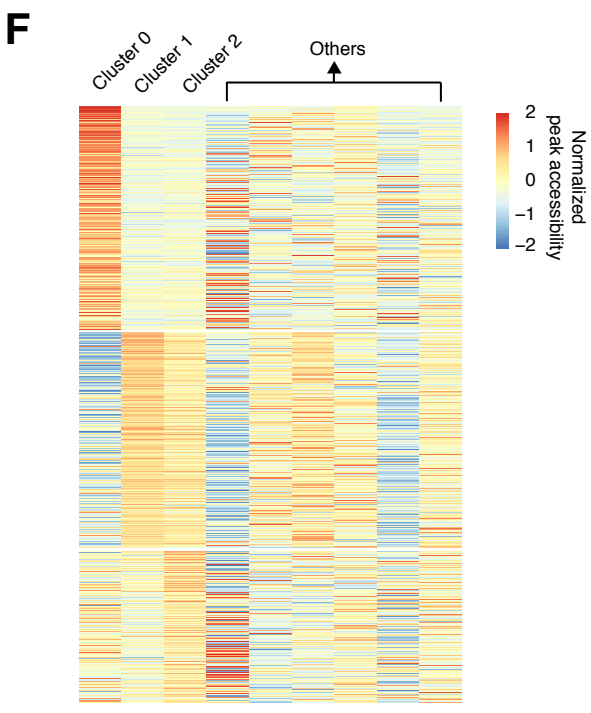

A
CD62L lo CD44 hi CD4 + T cells
p=7e-4
Percentage cells out of total CD4 + T cells (%)
50
40
30
20
10
0
WT
VISTA-/-

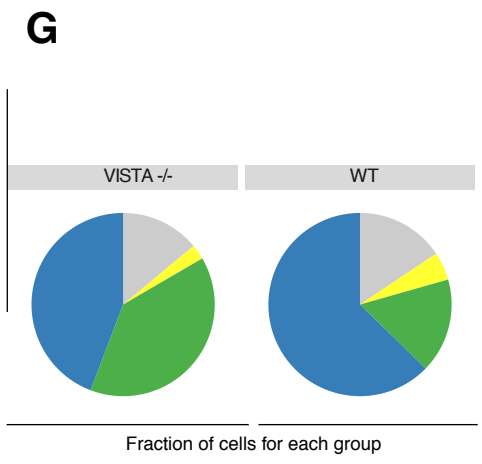

B
Naive CD4 + T cells
100%
75%
50%
25%
0
10 3
10 4
10 5
VISTA APC
VISTA-/-
WT

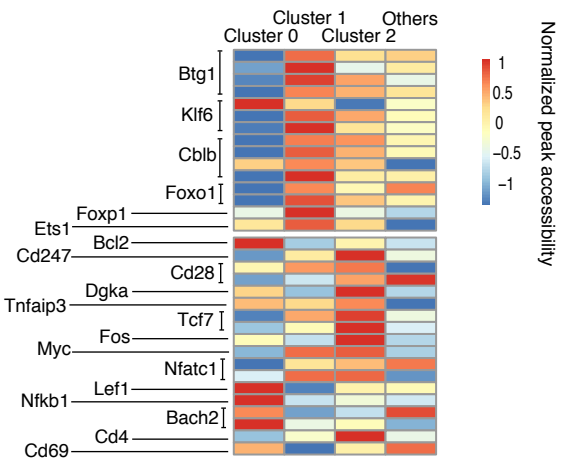

C
Cluster 0
Cluster 1
Cluster 2
Cluster 3
Cluster 4
Cluster 5
Normalized gene expresion
2
1
0
−1
−2

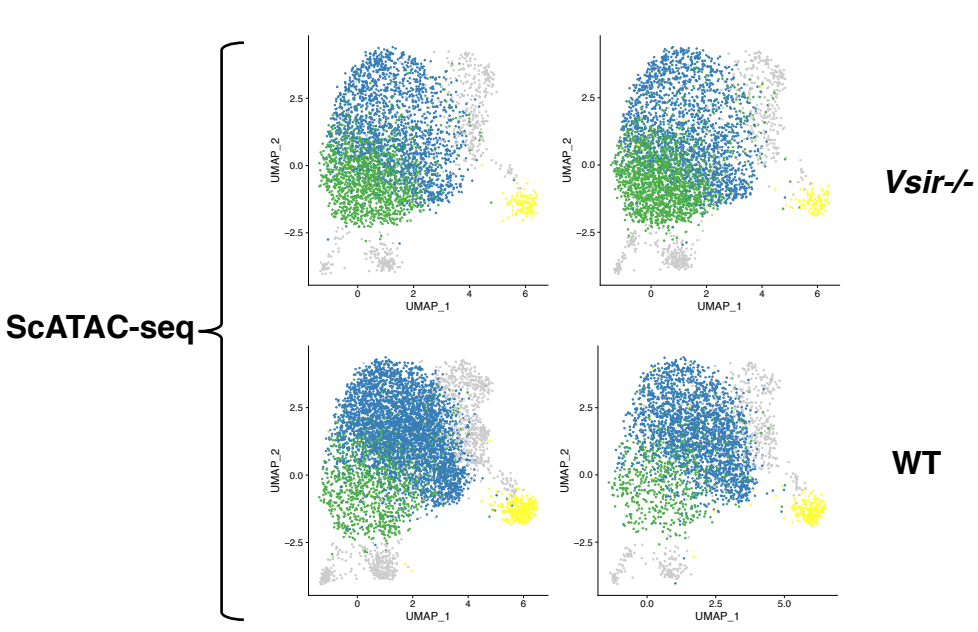

D
VISTA -/-
WT
Fraction of cells for each group

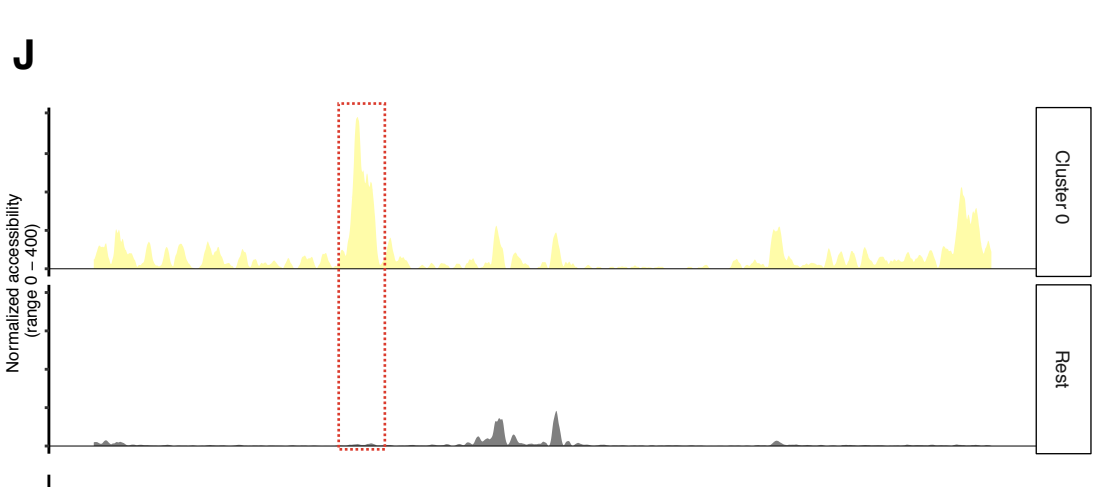

E
ScRNA-seq
Vsir-/-
WT
tSNE_1
tSNE_2

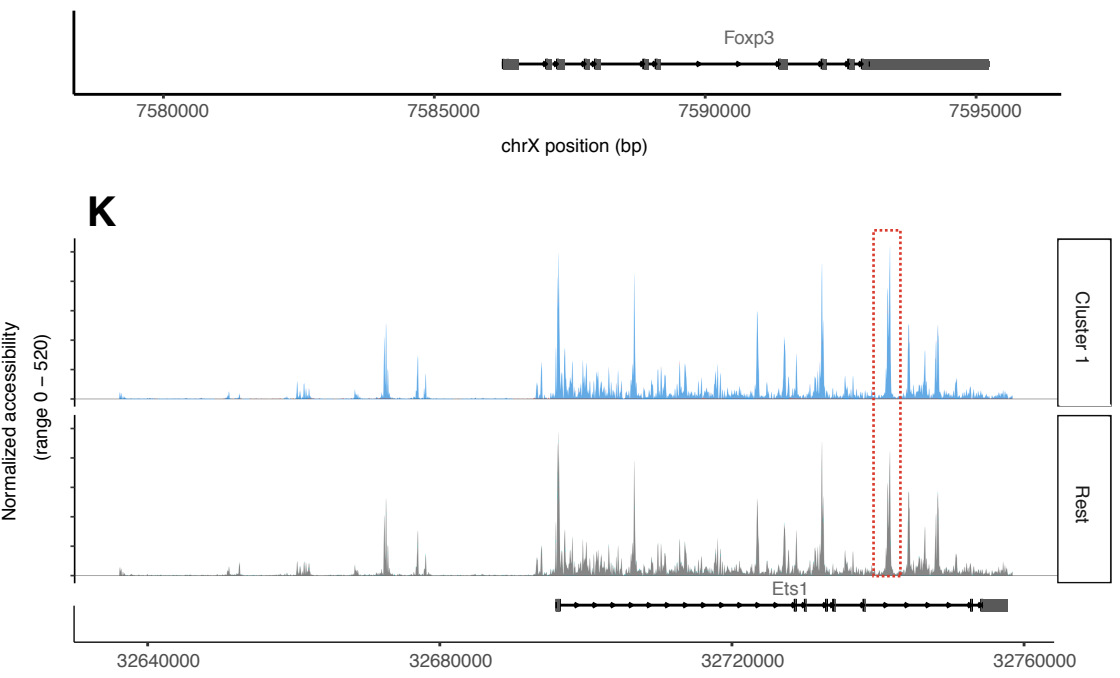

F
Cluster 0
Cluster 1
Cluster 2
Others
Normalized peak accessibility
2
1
0
−1
−2

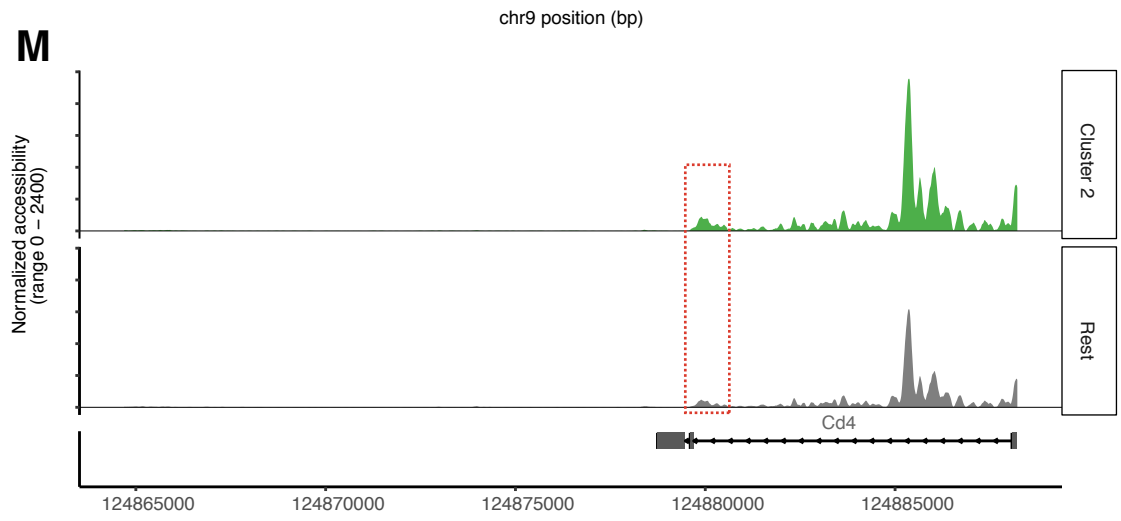

G
VISTA -/-
WT
Fraction of cells for each group

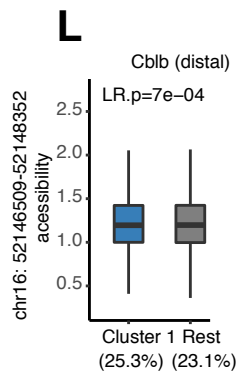

H
Cluster 0
Cluster 1
Cluster 2
Others
Btg1
Klf6
Cblb
Foxo1
Foxp1
Ets1
Bcl2
Cd247
Cd28
Dgka
Tnfaip3
Tcf7
Fos
Myc
Nfatc1
Lef1
Nfkb1
Bach2
Cd4
Cd69
Normalized peak accessibility
1
0.5
0
−0.5
−1

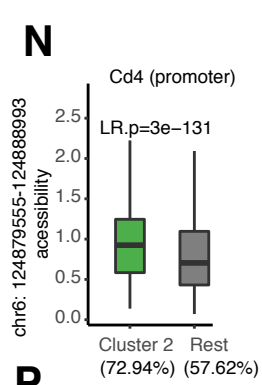

I
ScATAC-seq
Vsir-/-
WT
UMAP_1
UMAP_2

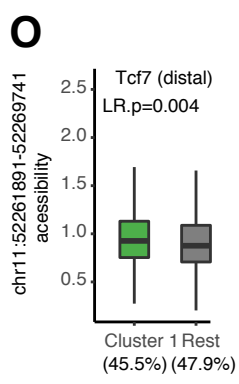

J
Normalized accessibility (range 0 – 400)
Cluster 0
Rest
Foxp3
7580000
7585000
7590000
7595000
chrX position (bp)

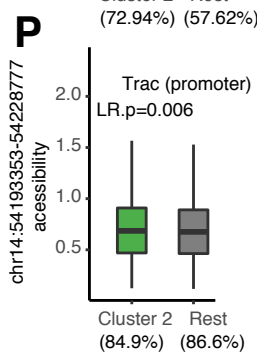

K
Normalized accessibility (range 0 – 520)
Cluster 1
Rest
Ets1
32640000
32680000
32720000
32760000
chr9 position (bp)

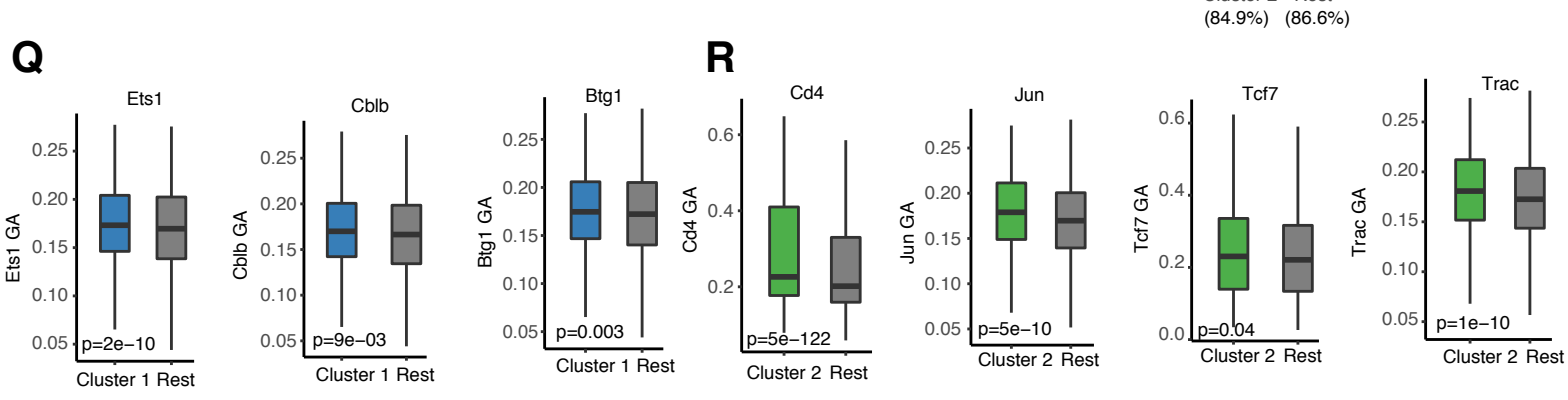

M
Normalized accessibility (range 0 – 2400)
Cluster 2
Rest
Cd4
124865000
124870000
124875000
124880000
124885000
chr6 position (bp)


L
Cblb (distal)
LR.p=7e−04
chr16: 52146509-52148352 acessibility
Cluster 1 (25.3%)
Rest (23.1%)


N
Cd4 (promoter)
LR.p=3e−131
chr6: 124879555-124888993 acessibility
Cluster 2 (72.94%)
Rest (57.62%)


O
Tcf7 (distal)
LR.p=0.004
chr11:52261891-52269741 acessibility
Cluster 1 (45.5%)
Rest (47.9%)


P
Trac (promoter)
LR.p=0.006
chr14:54193353-54228777 acessibility
Cluster 2 (84.9%)
Rest (86.6%)


Q
Ets1
Cblb
Btg1
p=2e−10
p=9e−03
p=0.003
Cluster 1 Rest
R
Cd4
Jun
Tcf7
Trac
p=5e−122
p=5e−10
p=0.04
p=1e−10
Cluster 2 Rest