AML1

jtrincado

2022-02-08 15:31:19

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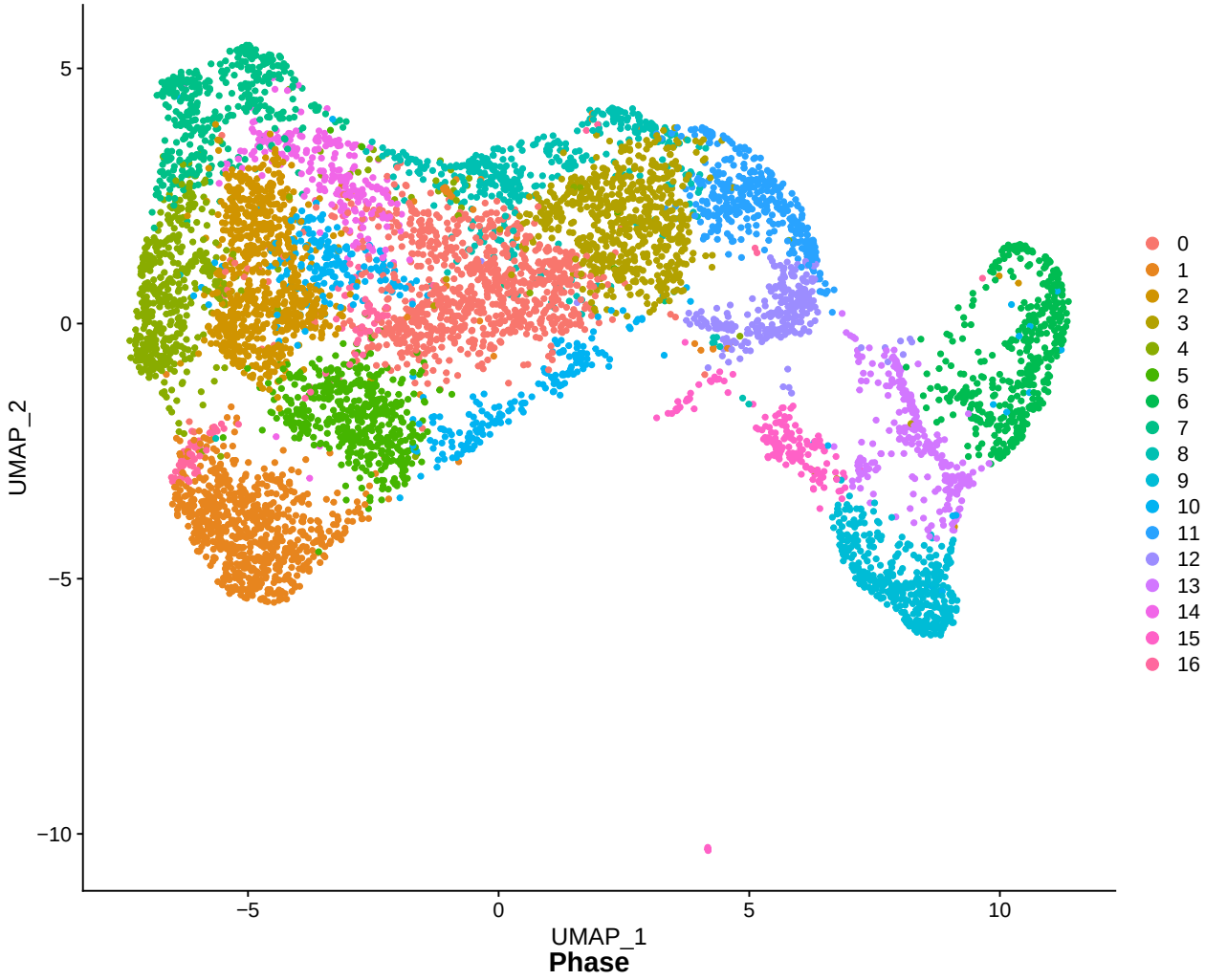
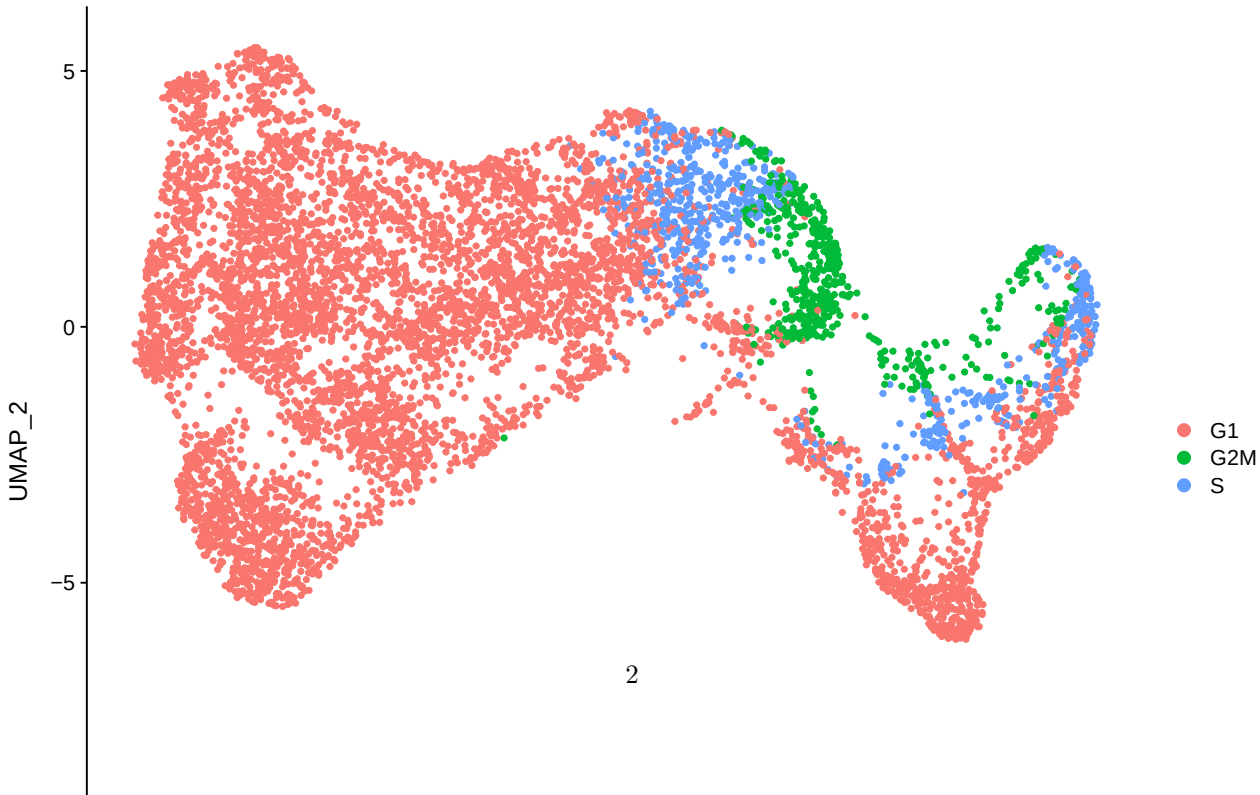
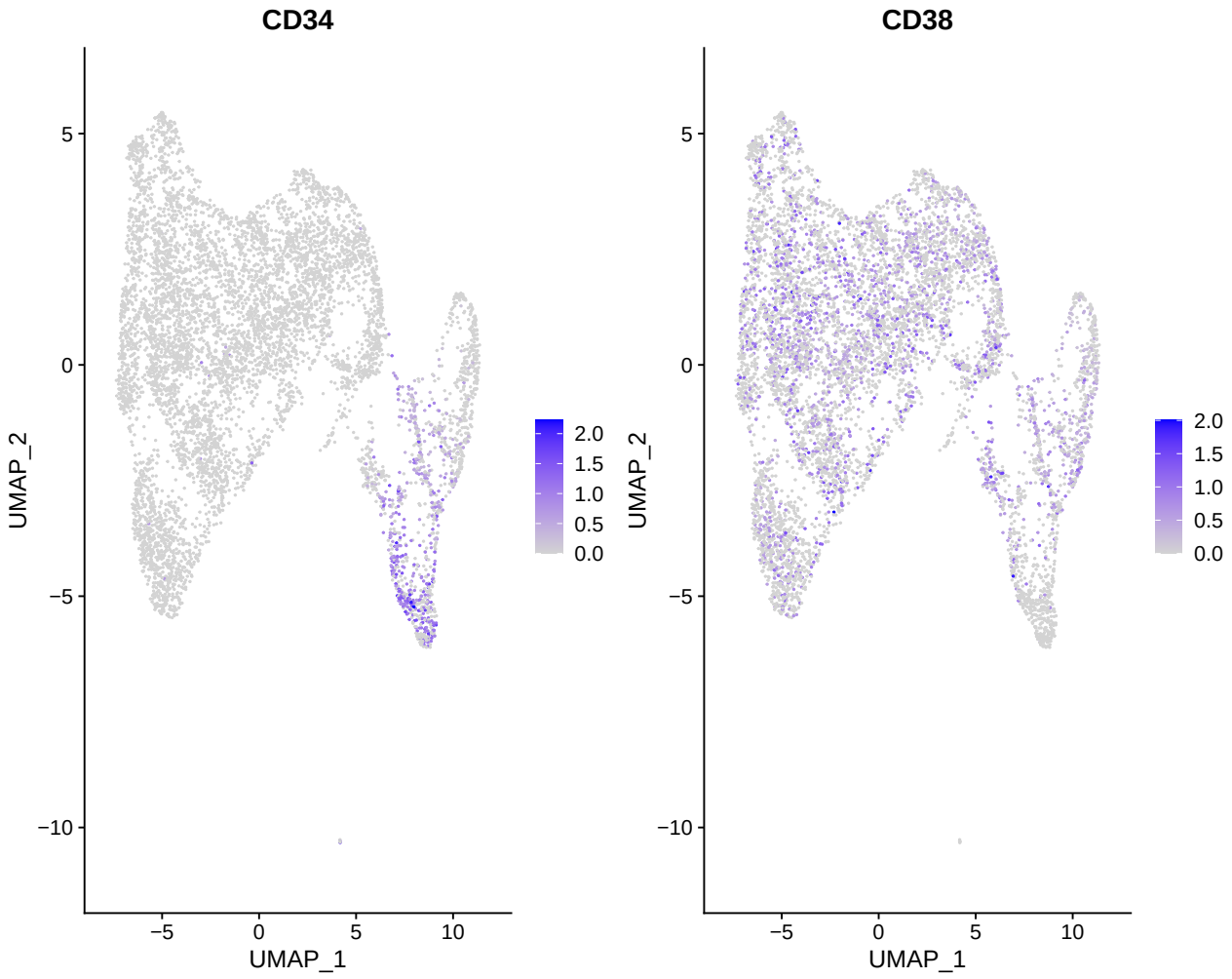
1. Put together both 34 and 38 libraries. Apply QC and dimensionality reduction.

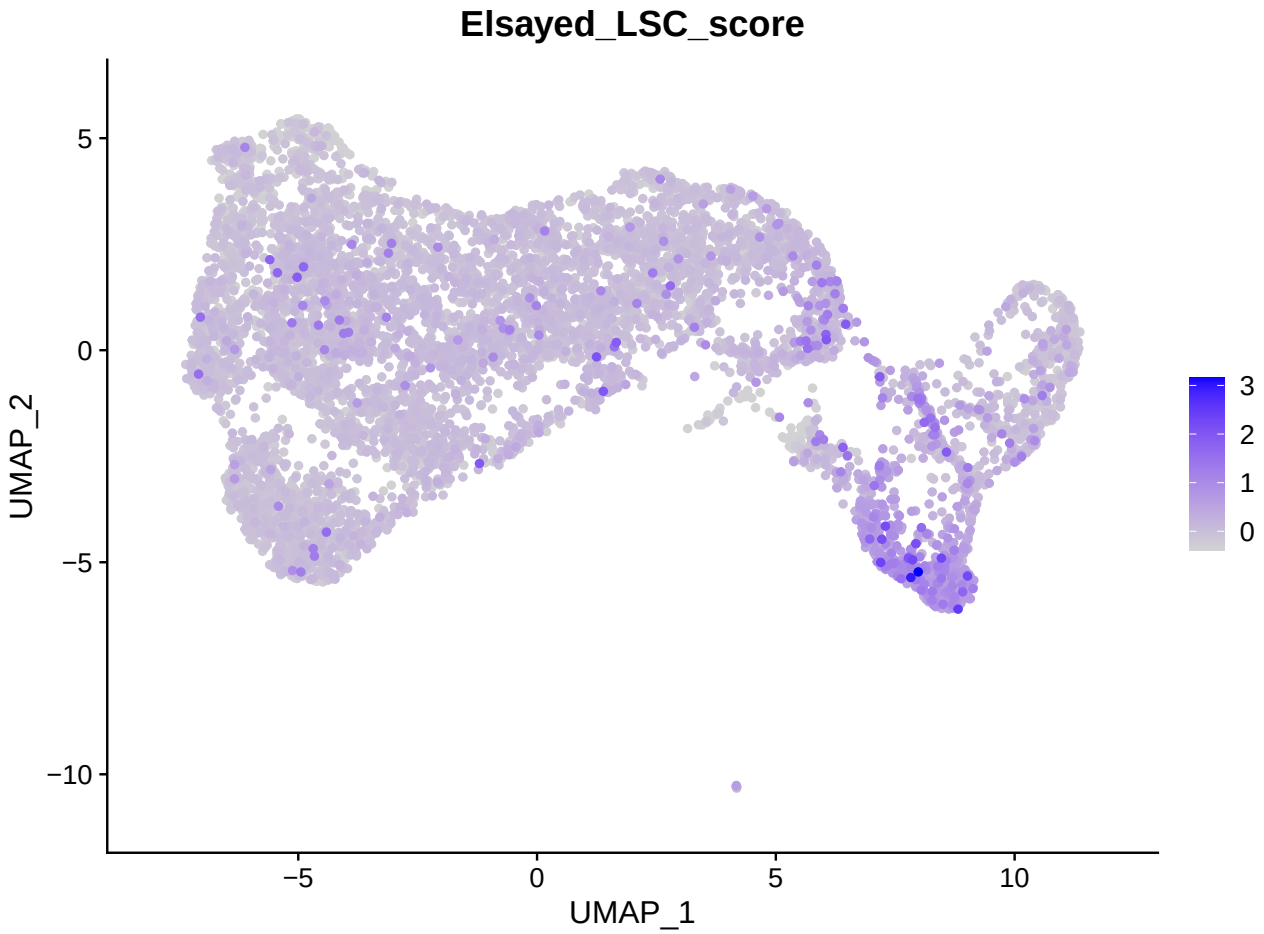


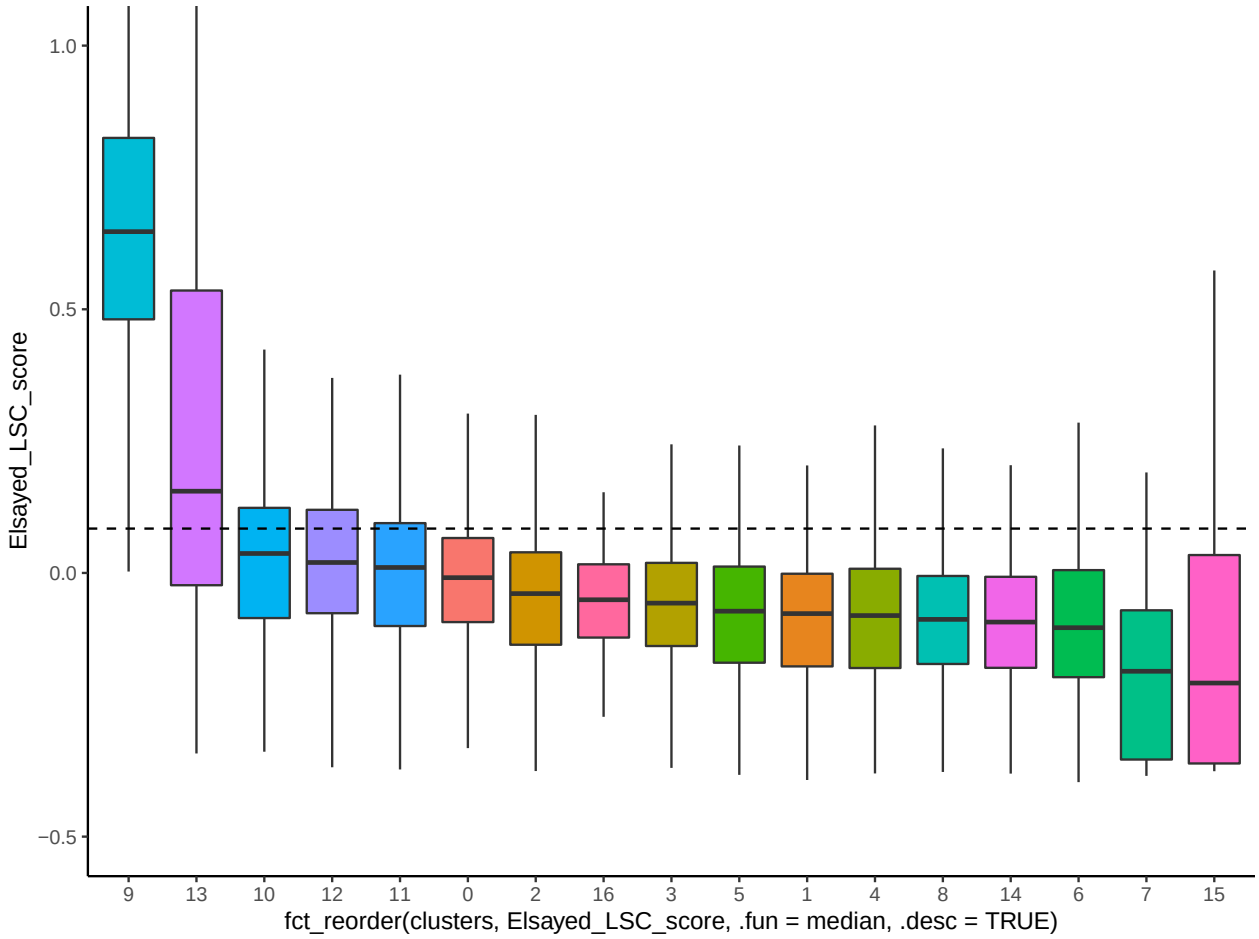




2. Get the LSC6 score

```
## [1] "CD34"   "SPINK2" "SOCS2"  "FAM30A" "ADGRG1" "DNMT3B"
```

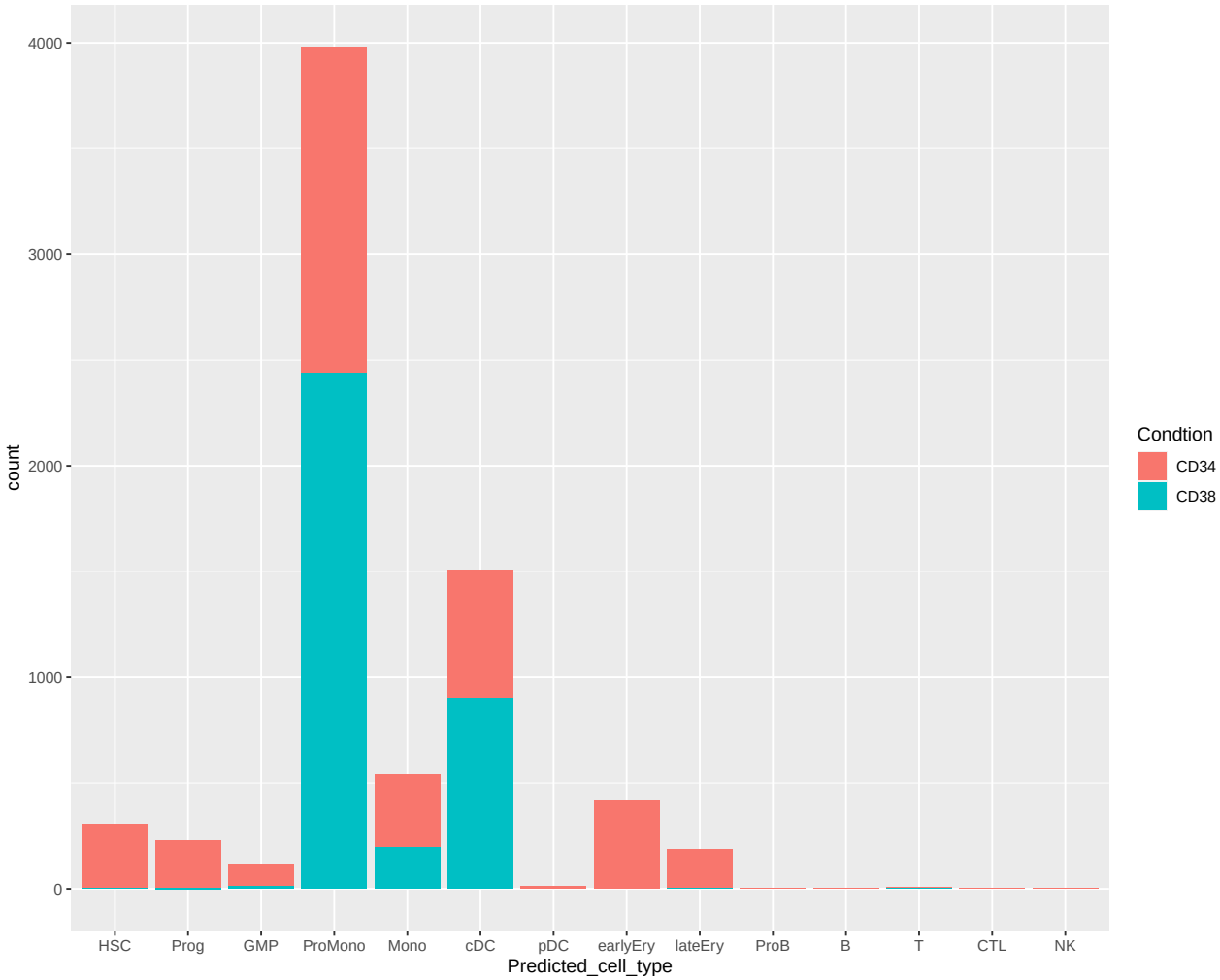

Elsayed_LSC_score
5
0
−5
−10
UMAP_2
−5
0
5
10
UMAP_1
3
2
1
0

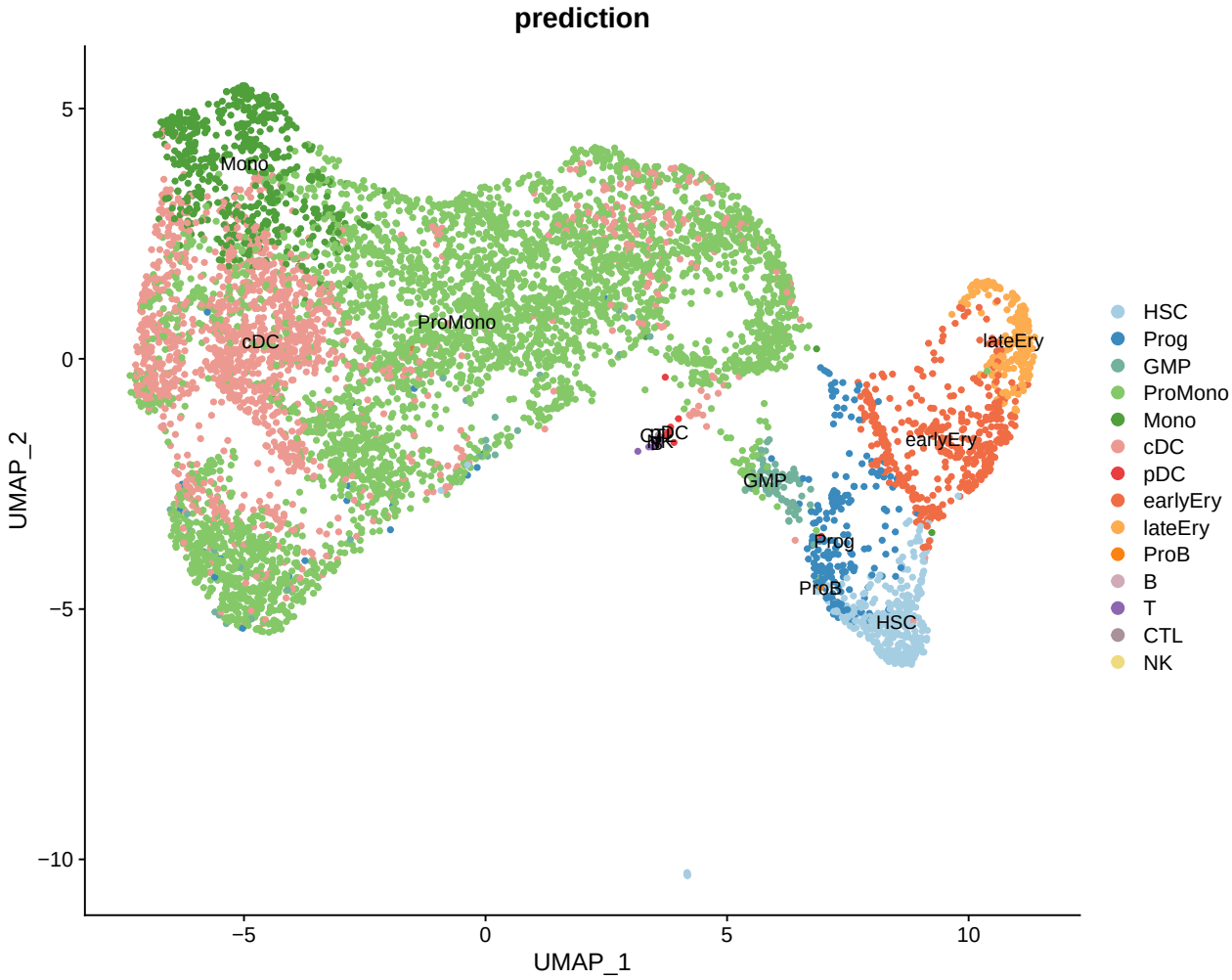


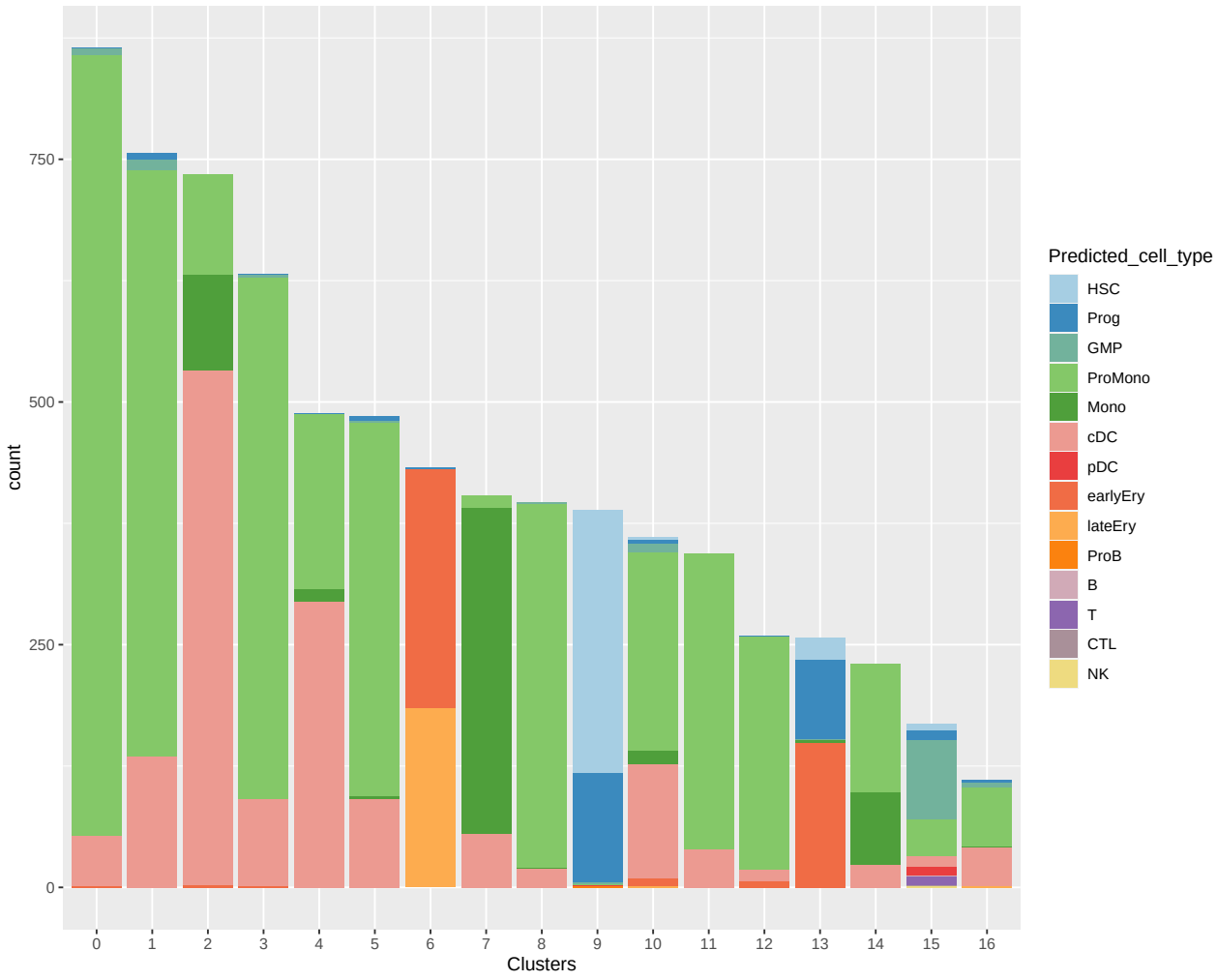
3. Predict the class of the cells using the markers and the expression of the BM cells form Van_Galen paper

```
## Performing PCA on the provided reference using 1821 features as input.
## Projecting cell embeddings
## Finding neighborhoods
## Finding anchors
##  Found 3478 anchors
## Filtering anchors
##  Retained 2498 anchors
## Finding integration vectors
## Finding integration vector weights
## Predicting cell labels
##
##         HSC Prog  GMP ProMono Mono  cDC  pDC earlyEry lateEry ProB    B Plasma
##   CD34  303  224  110    1542  347  607   10      414     184    1    1      0
##   CD38    1    5   11    2440  194  902    0        0       2    0    0      0
```

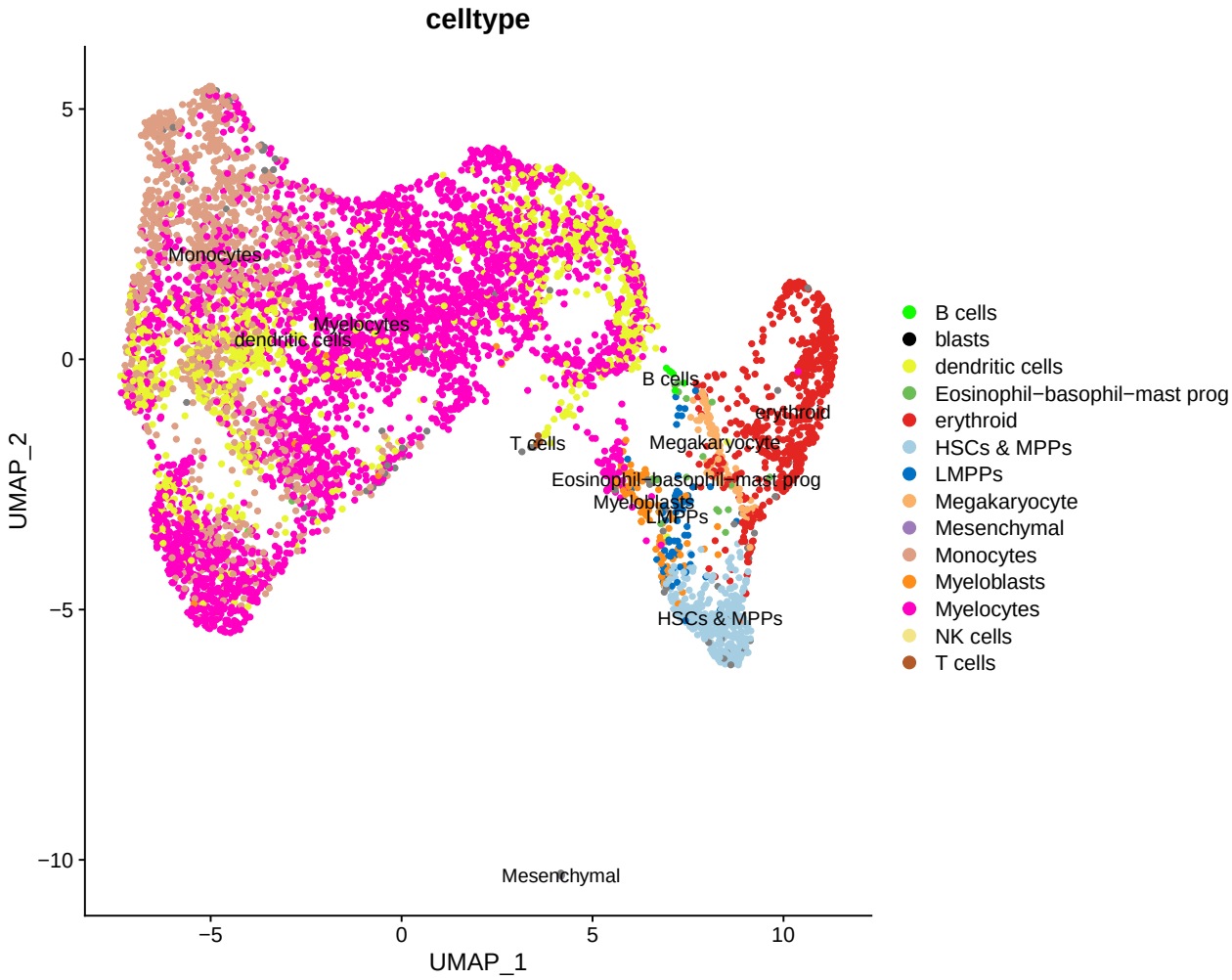
```
##
##          T  CTL   NK
##    CD34  5    1    1
##    CD38  4    0    0
```

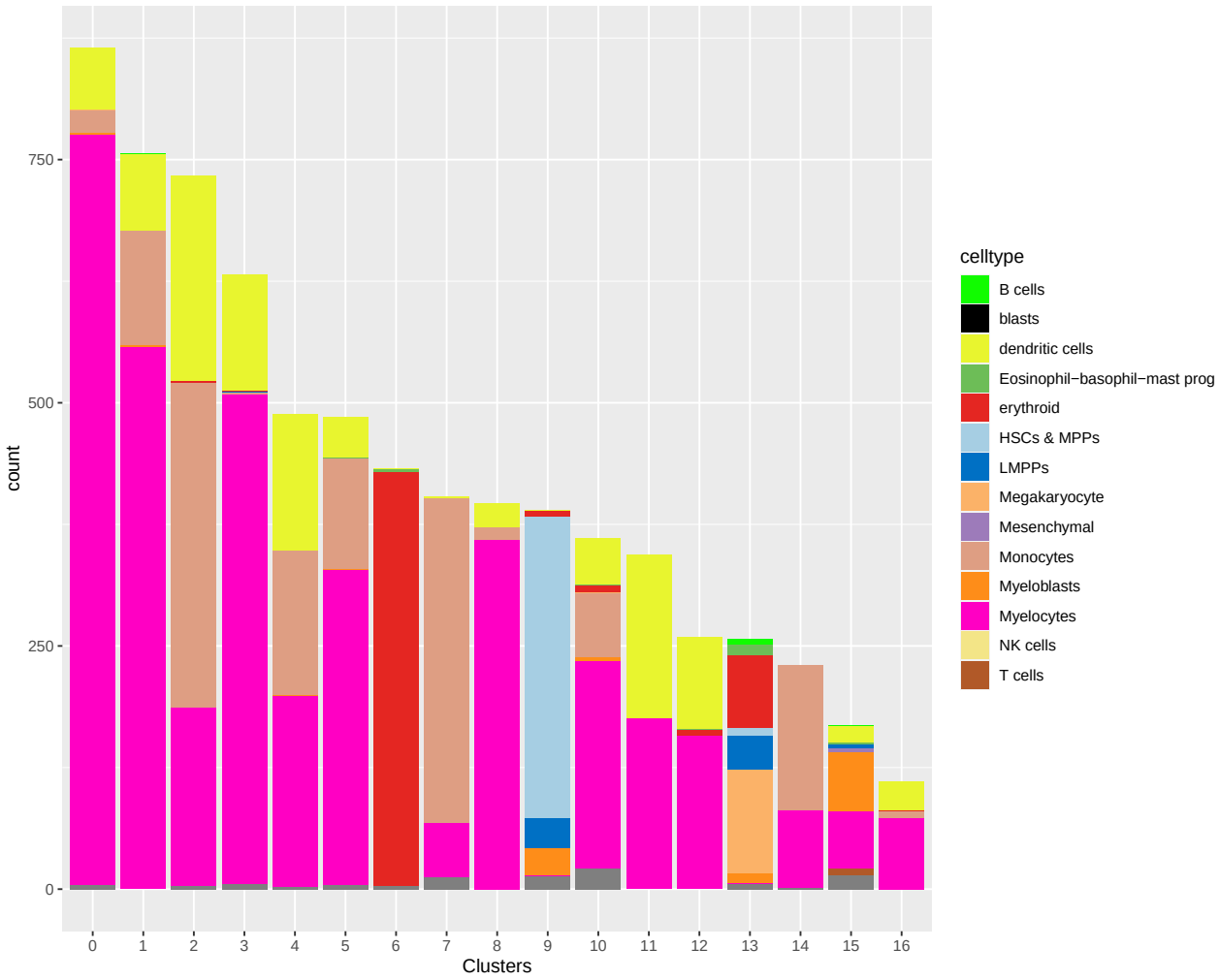



prediction
Mono
cDC
ProMono
pDC
GMP
Prog
ProB
HSC
earlyEry
lateEry
HSC
Prog
GMP
ProMono
Mono
cDC
pDC
earlyEry
lateEry
ProB
B
T
CTL
NK
UMAP_2
UMAP_1
5
0
−5
−10
−5
0
5
10


count
750
500
250
0
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
Clusters
Predicted_cell_type
HSC
Prog
GMP
ProMono
Mono
cDC
pDC
earlyEry
lateEry
ProB
B
T
CTL
NK

4. Project the predictions from Velten onto our UMAP





Cluster 9 seems the most likely to be enriched in LSC