AML10_Rx

jtrincado

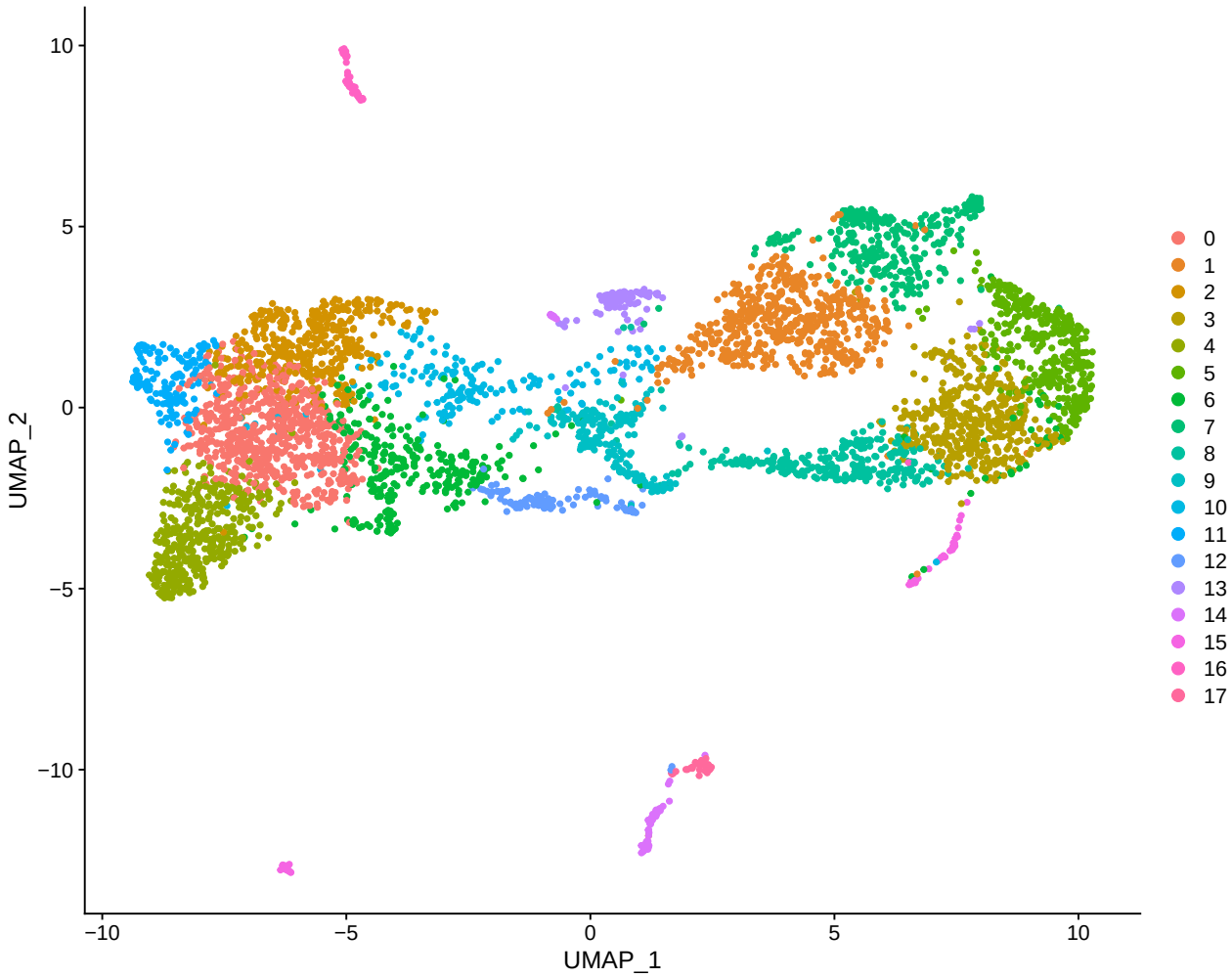
2022-02-09 10:58:54

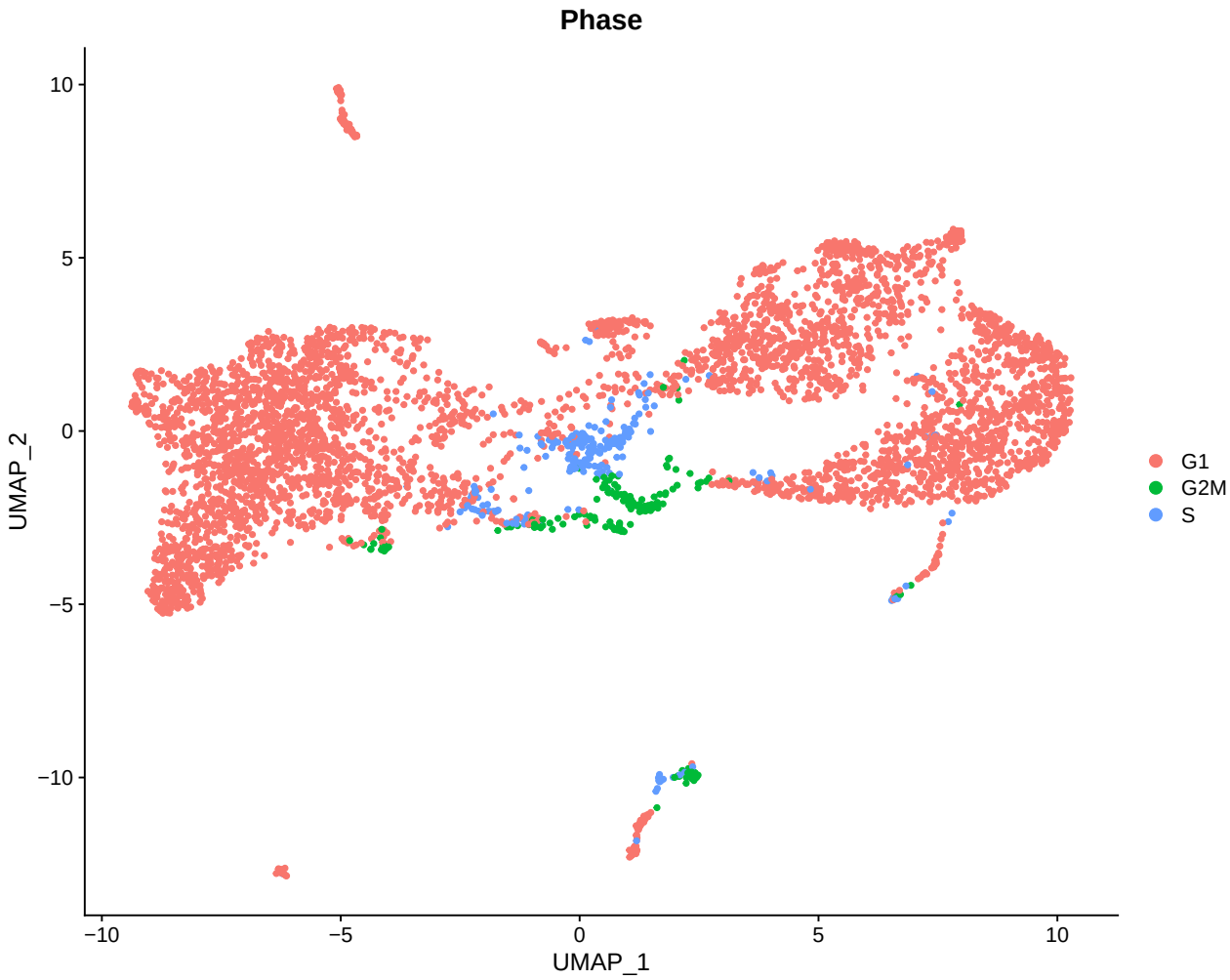
Contents

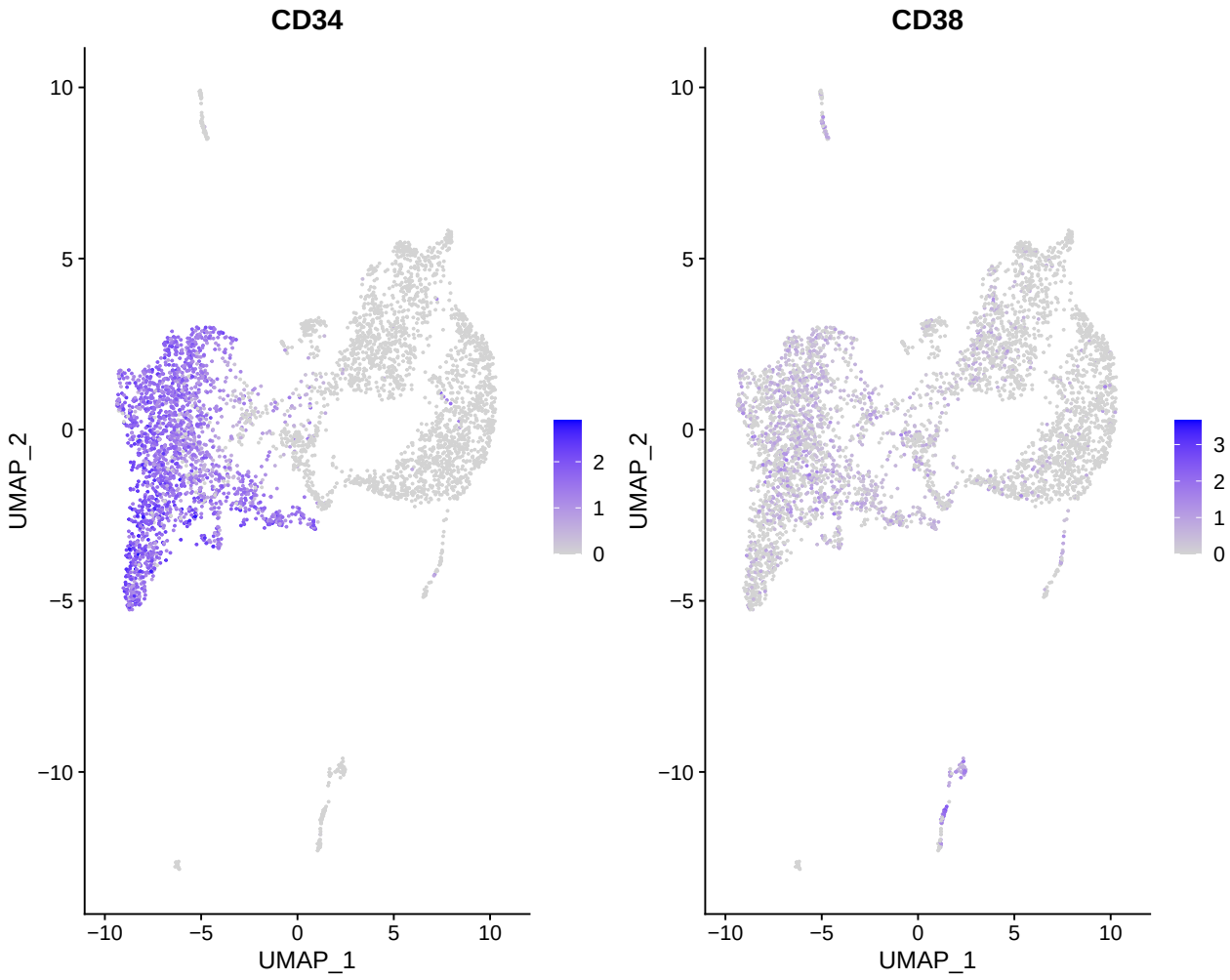
1. Put together both 34 and 38 libraries. Apply QC and dimensionality reduction. 1
2. Get the LSC6 score 4
3. Predict the class of the cells using the markers and the expression of the BM cells form Van_Galen paper 6
4. Project the predictions from Velten onto our UMAP 10

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

```
## Warning: The default method for RunUMAP has changed from calling Python UMAP via reticulate to the R
## To use Python UMAP via reticulate, set umap.method to 'umap-learn' and metric to 'correlation'
## This message will be shown once per session
```

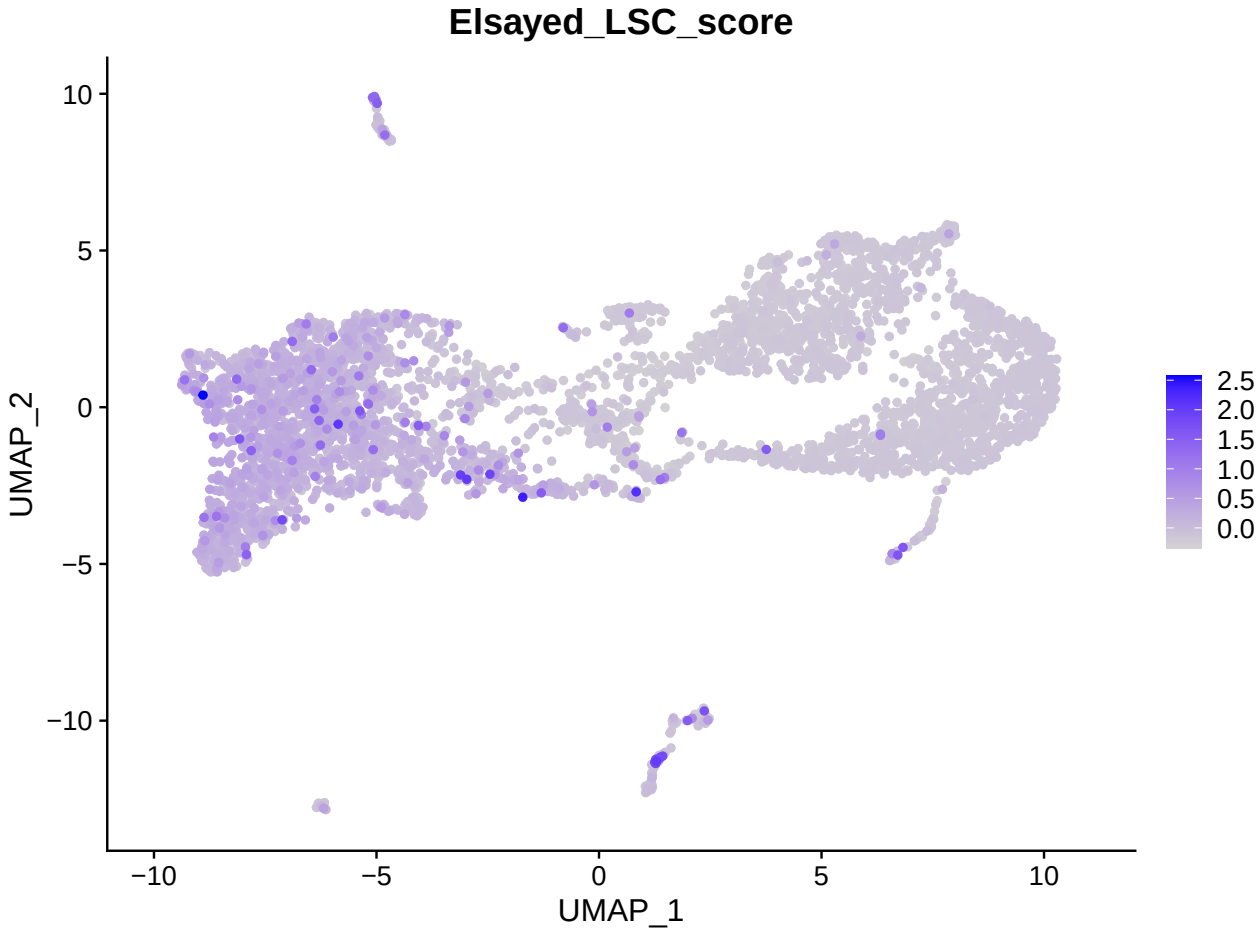

10
5
0
−5
−10
UMAP_2
−10
−5
0
5
10
UMAP_1
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17

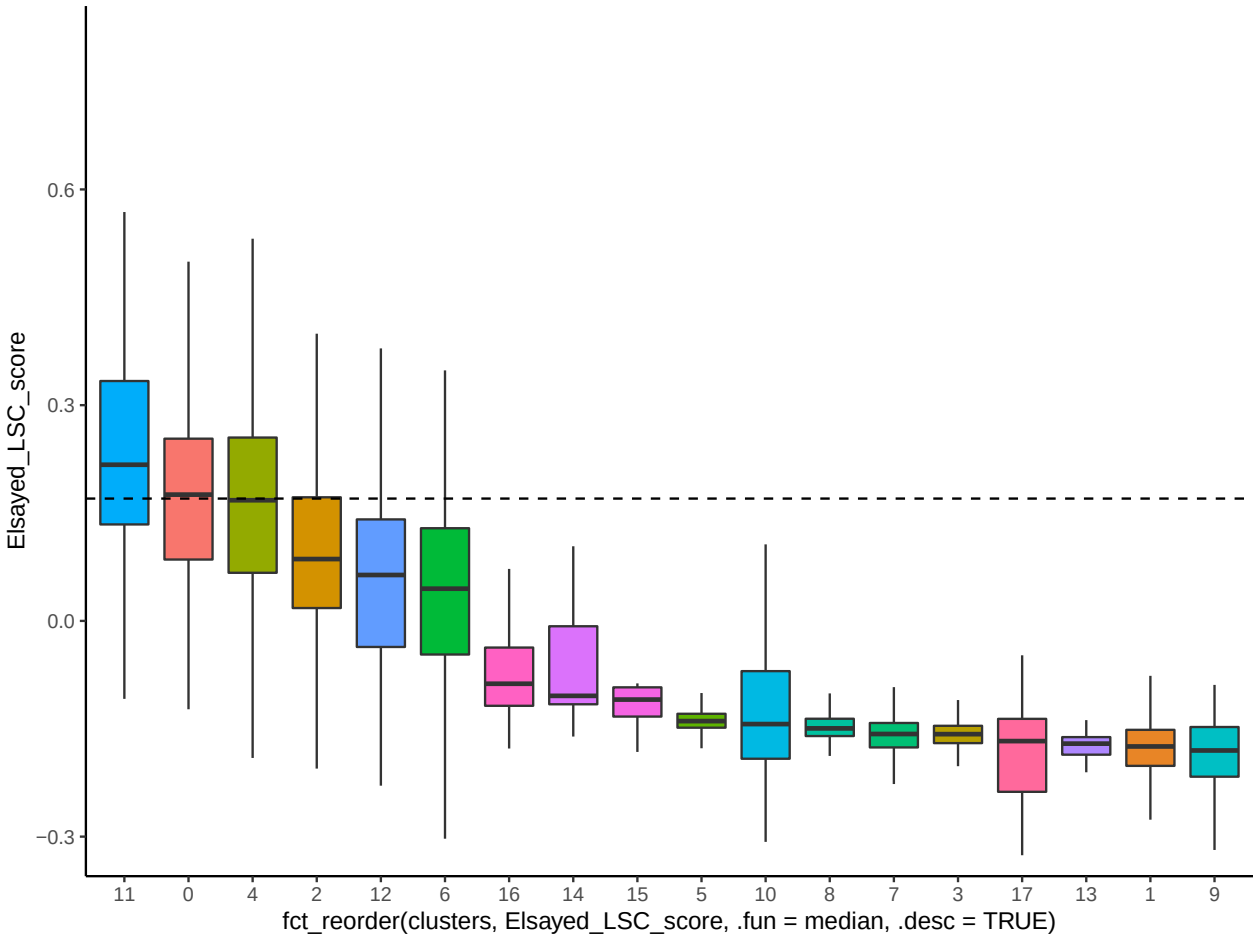

Phase
10
5
0
−5
−10
UMAP_2
−10
−5
0
5
10
UMAP_1
G1
G2M
S



2. Get the LSC6 score

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

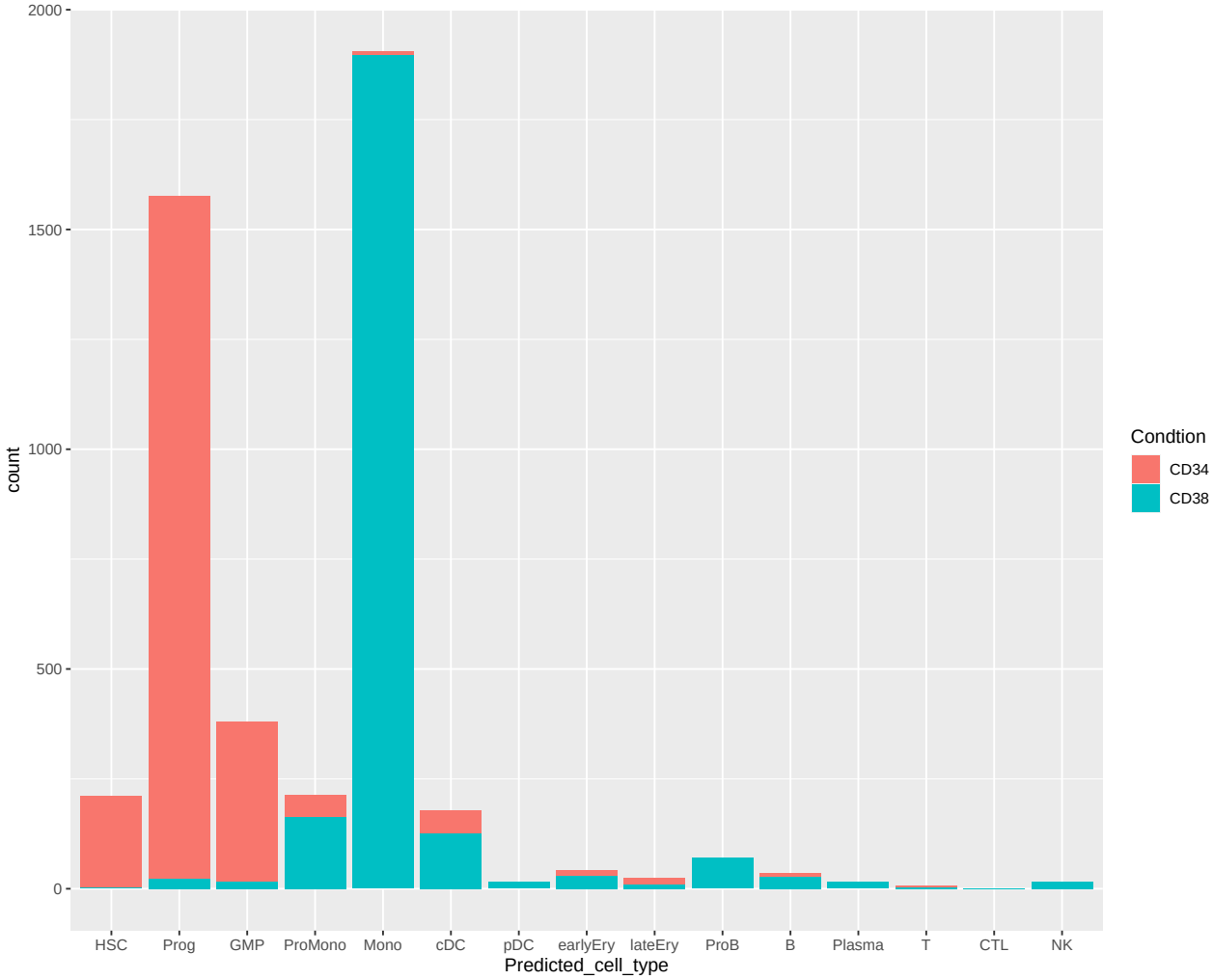

Elsayed_LSC_score
10
5
0
−5
−10
UMAP_2
−10
−5
0
5
10
UMAP_1
2.5
2.0
1.5
1.0
0.5
0.0

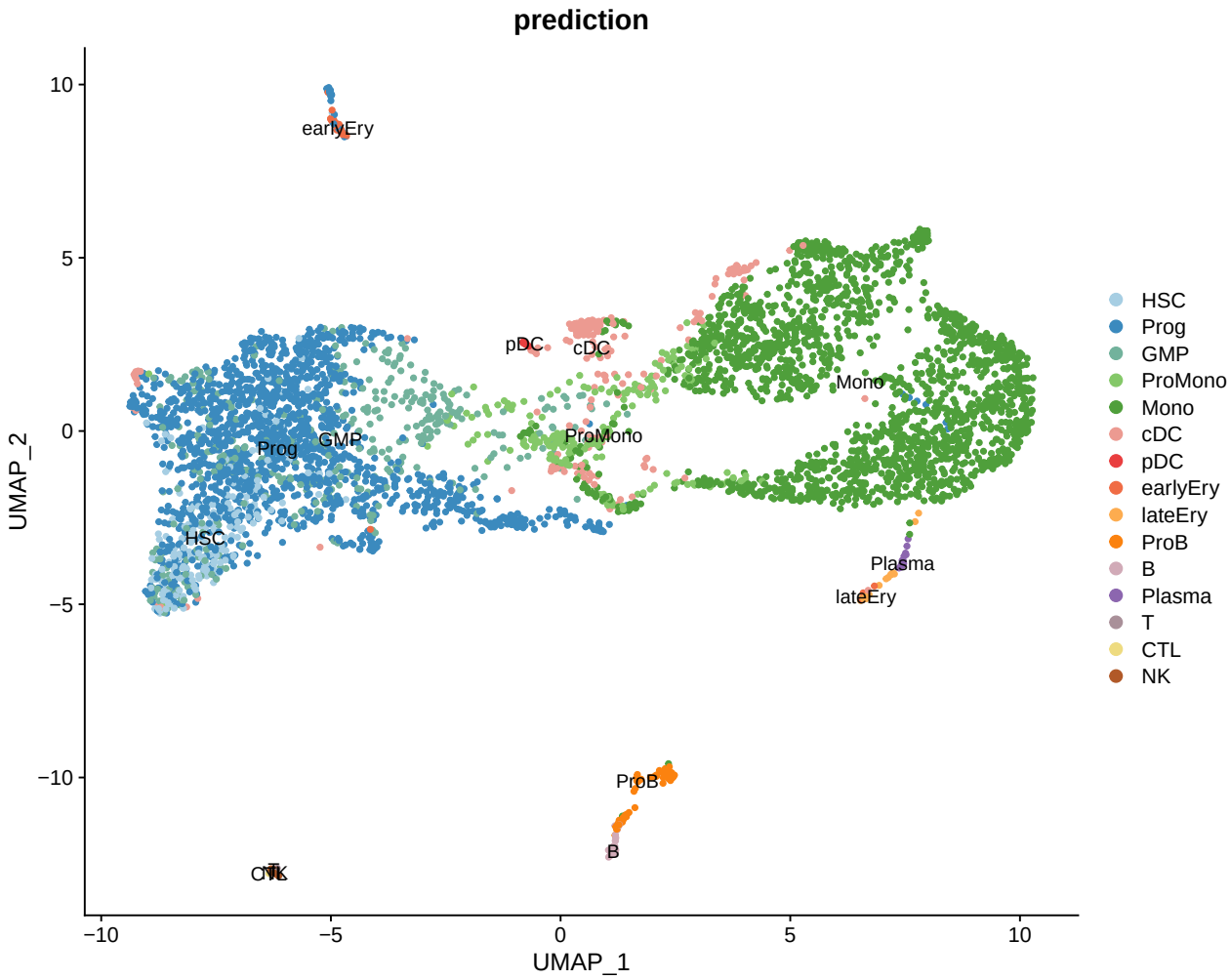


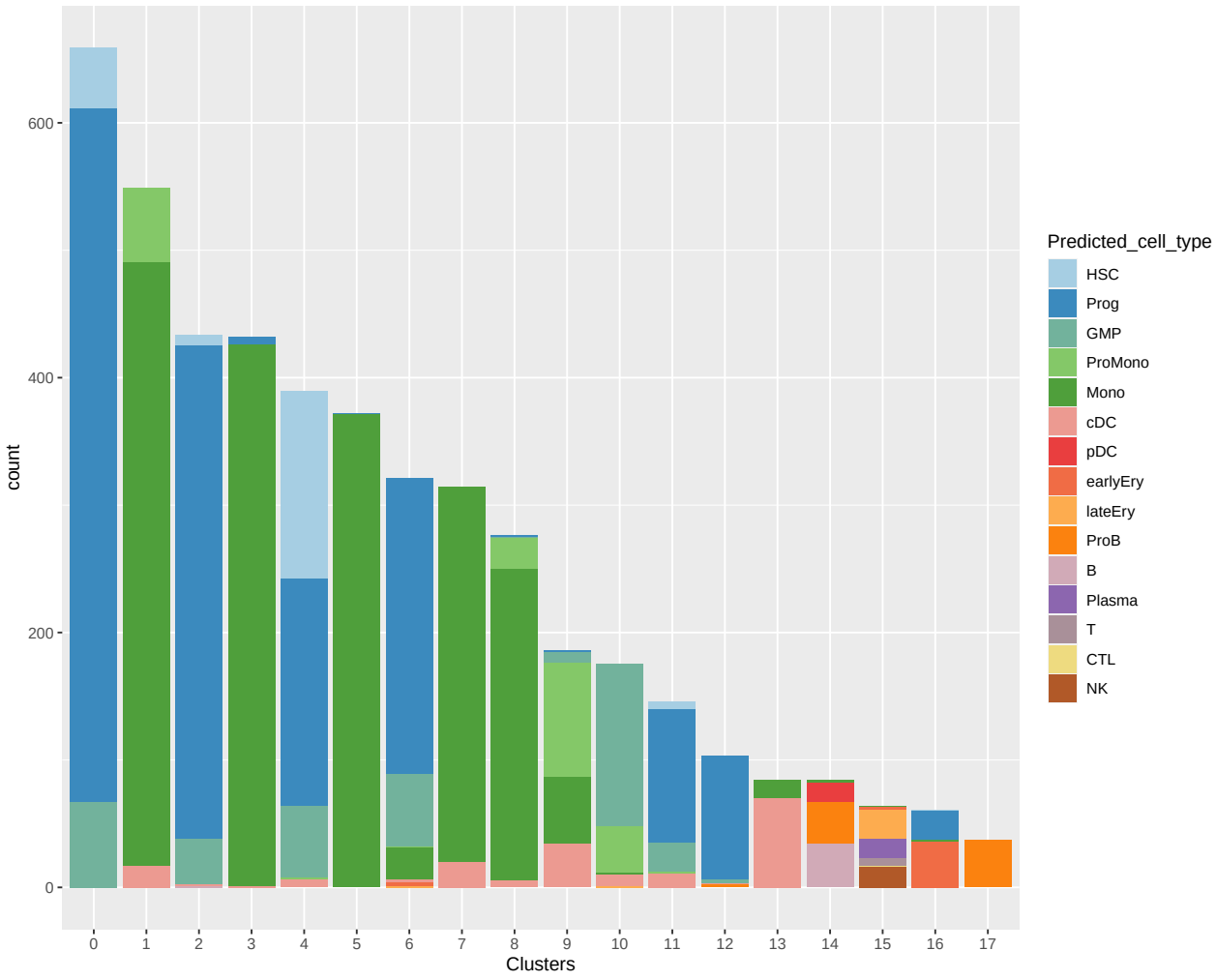
3. Predict the class of the cells using the markers and the expression of the BM cells form Van_Galen paper

```
## Performing PCA on the provided reference using 1821 features as input.
## Projecting cell embeddings
## Finding neighborhoods
## Finding anchors
##  Found 3632 anchors
## Filtering anchors
##  Retained 2622 anchors
## Finding integration vectors
## Finding integration vector weights
## Predicting cell labels
##
##         HSC Prog  GMP ProMono Mono  cDC  pDC earlyEry lateEry ProB    B Plasma
##   CD34  210 1552  363      49    9   51    0       12      16    2    7      0
##   CD38    2   23   16     164 1896  126   15       29       9   70   28     15
```

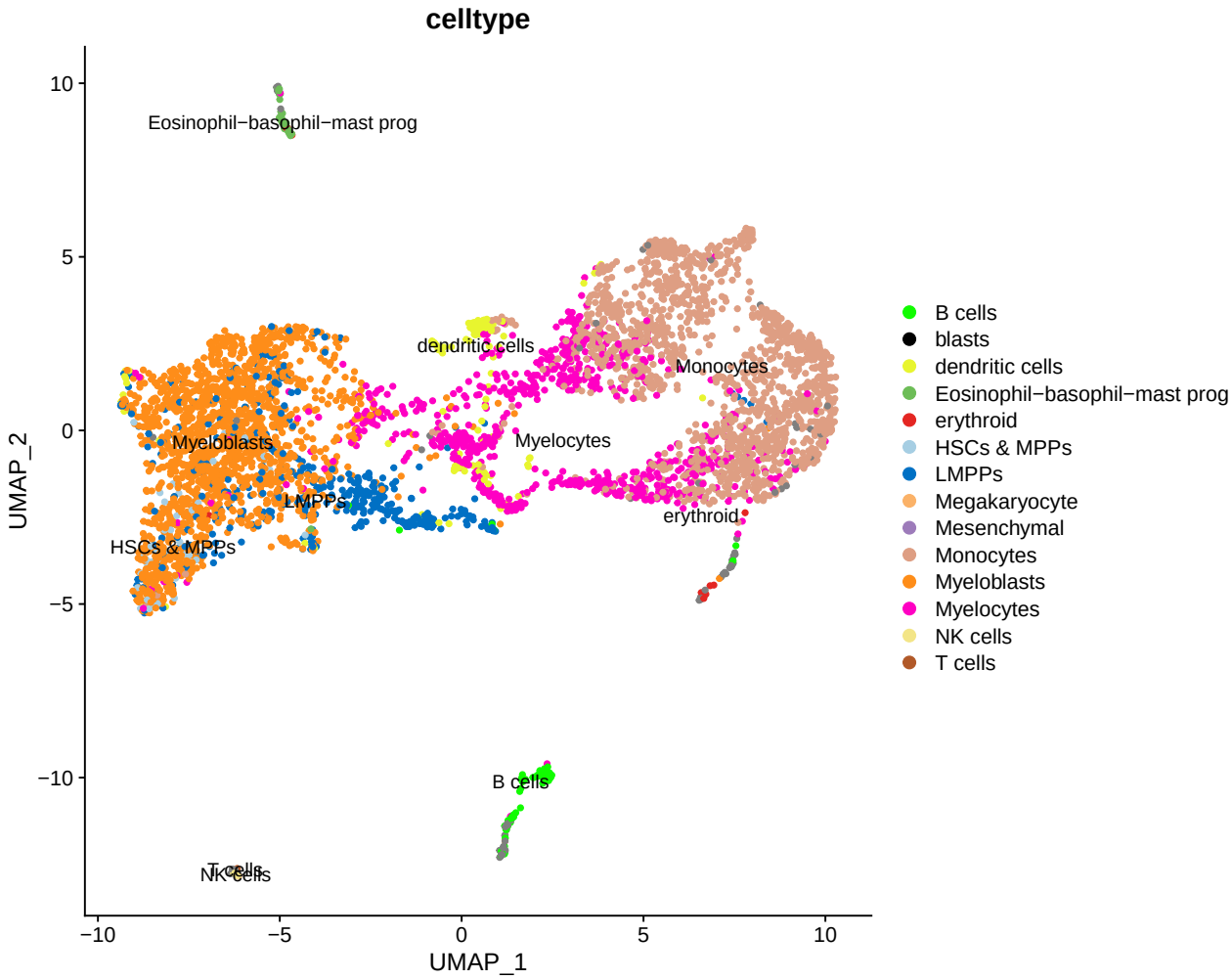
```
##
##             T  CTL   NK
##    CD34     3    0    0
##    CD38     3    1   16
```

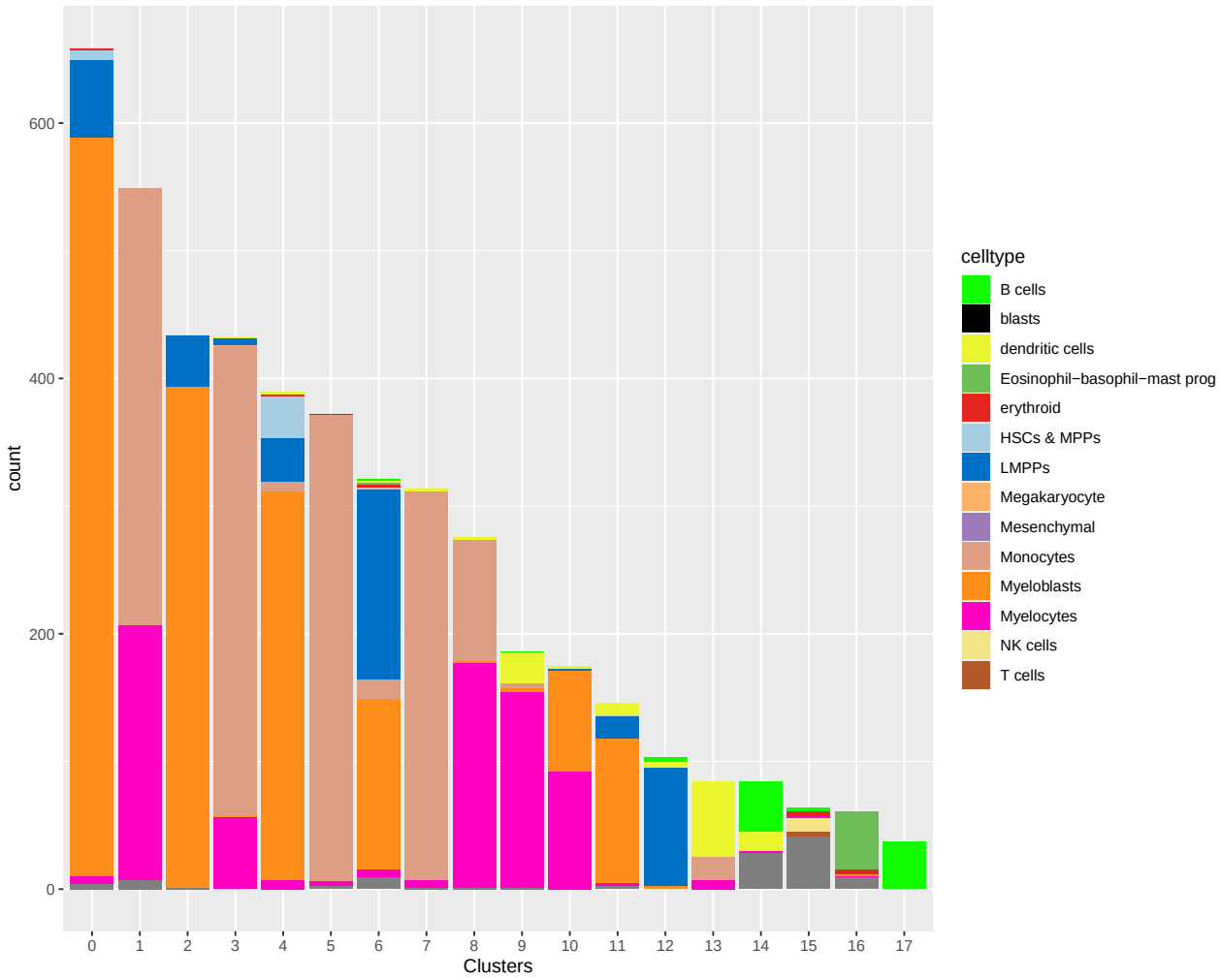



prediction
earlyEry
pDC
cDC
Mono
Prog
GMP
ProMono
HSC
Plasma
lateEry
ProB
B
CTL
NK
HSC
Prog
GMP
ProMono
Mono
cDC
pDC
earlyEry
lateEry
ProB
B
Plasma
T
CTL
NK
UMAP_2
UMAP_1
10
5
0
−5
−10
−10
−5
0
5
10


count
600
400
200
0
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
Clusters
Predicted_cell_type
HSC
Prog
GMP
ProMono
Mono
cDC
pDC
earlyEry
lateEry
ProB
B
Plasma
T
CTL
NK

4. Project the predictions from Velten onto our UMAP





Cluster 11 and 0 are the ones above the D10 threshold. Nevertheless, cluster 4 has more HSC predicted cells. In addition, is this cluster 4 the ones that colocalizes with cluster 5 LSC from the paired Dx sample. Therefore, we propose cluster 4 as the more likely to have enrichment of LSC