AML11_Dx

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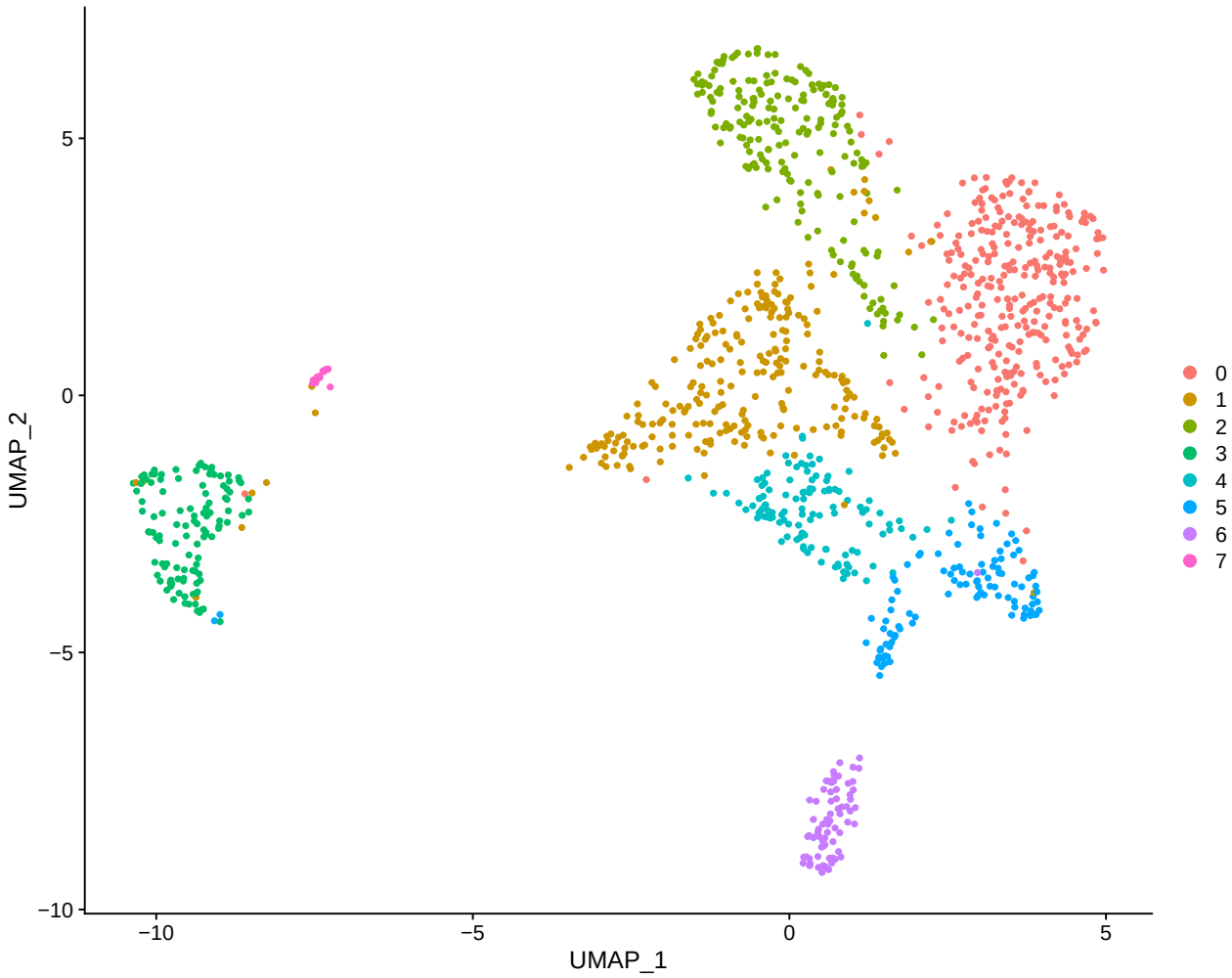
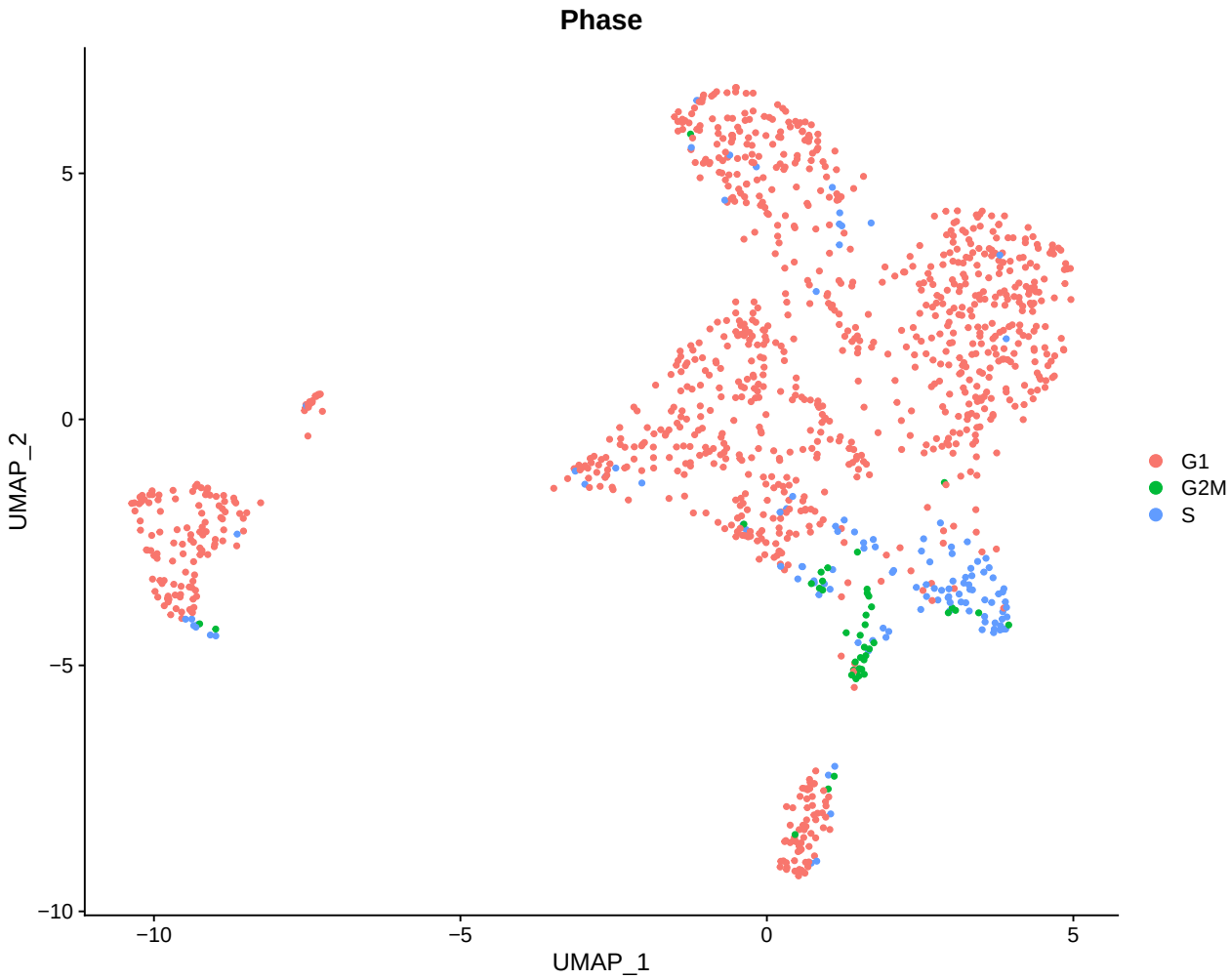
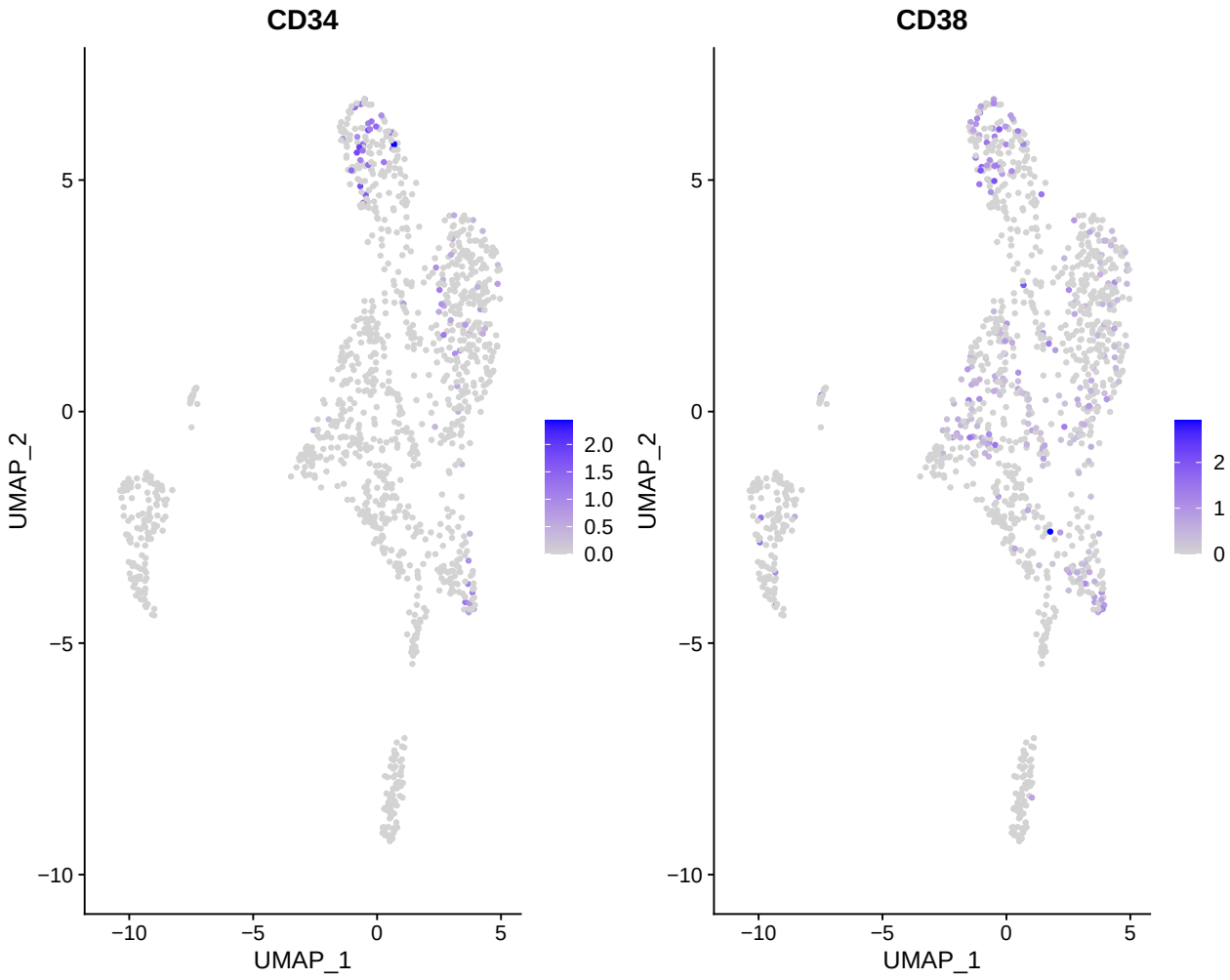
1. Put together both 34 and 38 libraries. Apply QC and dimensionality reduction.

```
## 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
```

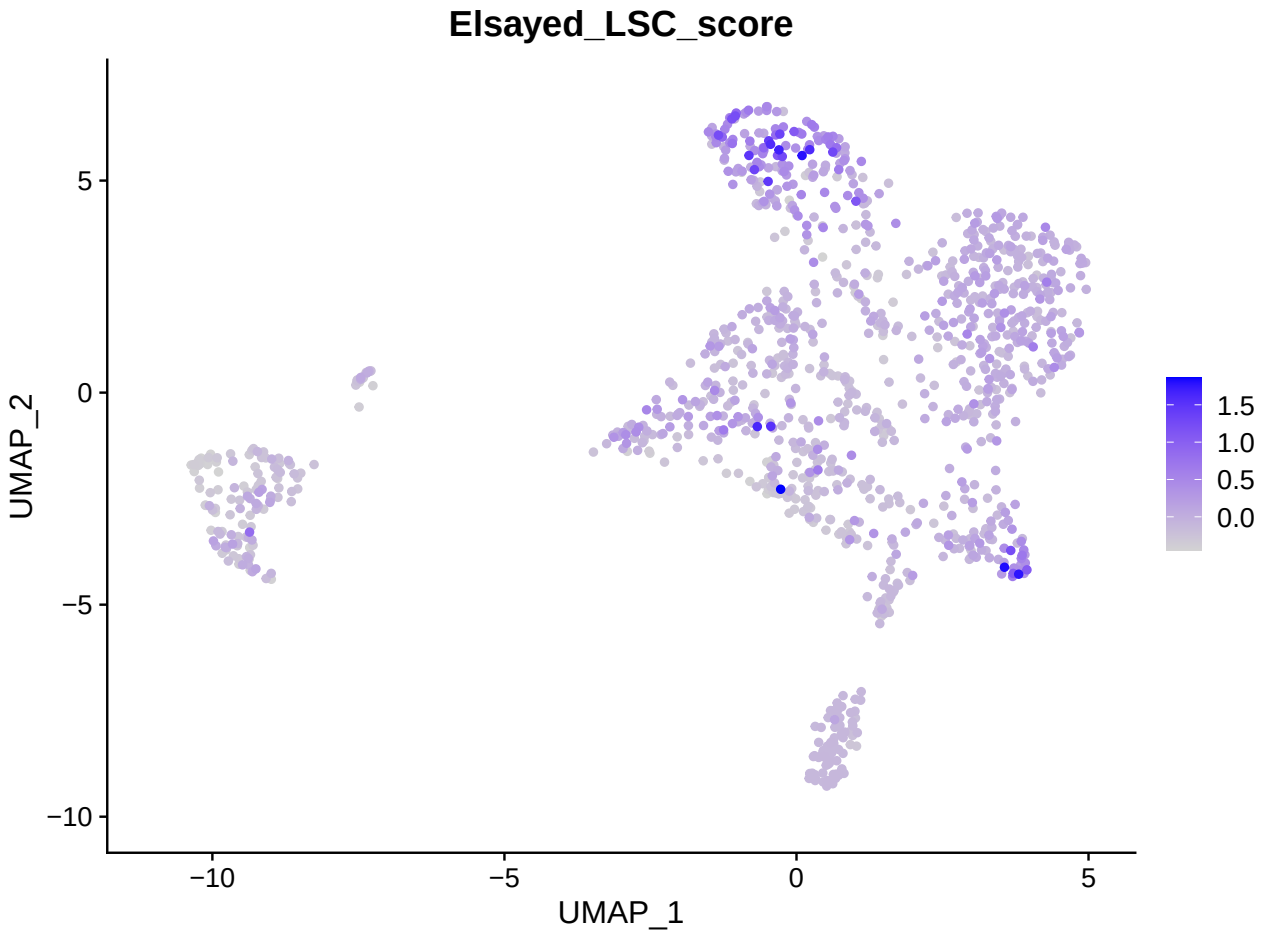

UMAP_2
UMAP_1
5
0
−5
−10
−10
−5
0
5
0
1
2
3
4
5
6
7

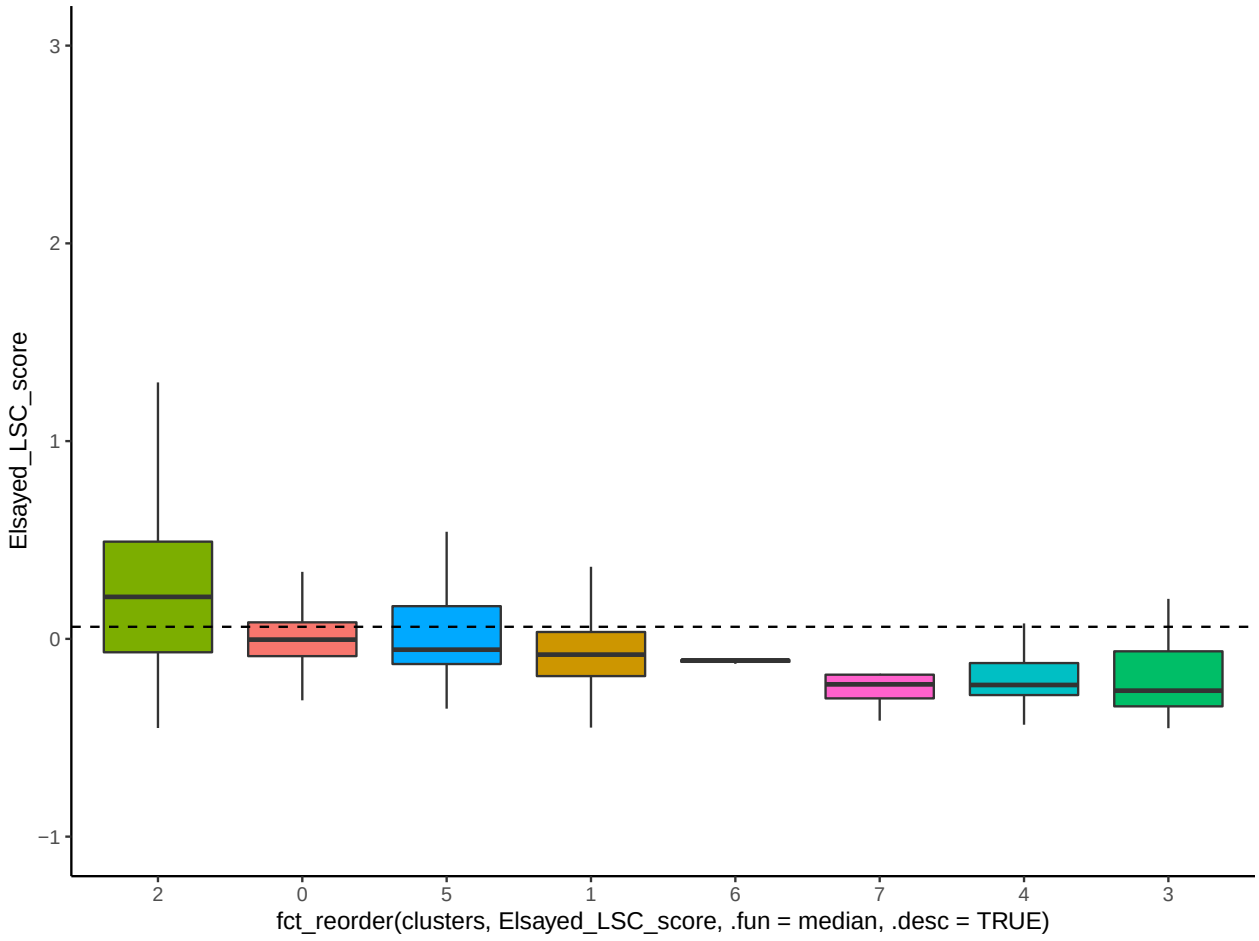

Phase
UMAP_2
UMAP_1
5
0
−5
−10
−10
−5
0
5
G1
G2M
S



2. Get the LSC6 score

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

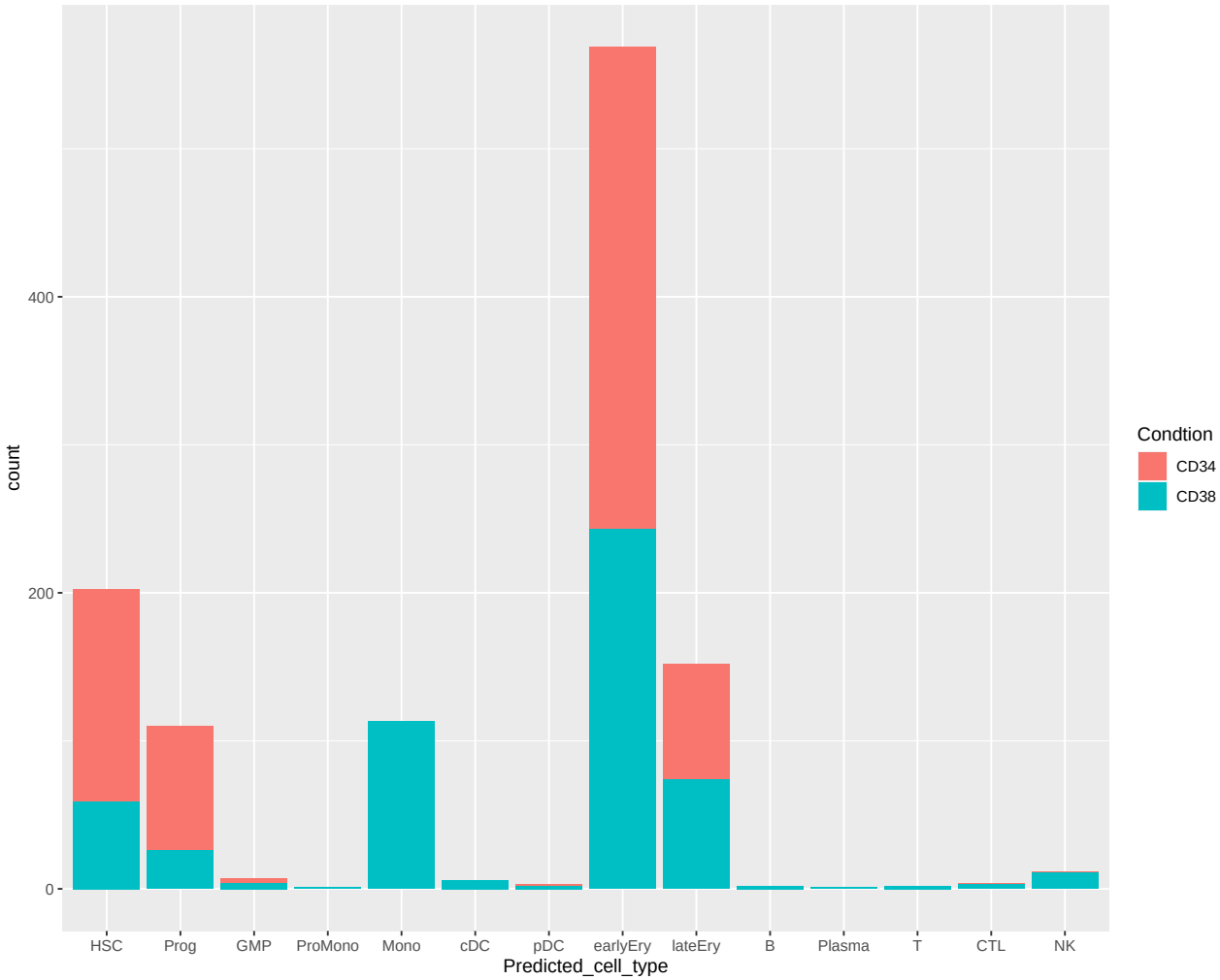

Elsayed_LSC_score
5
0
−5
−10
UMAP_2
−10
−5
0
5
UMAP_1
1.5
1.0
0.5
0.0

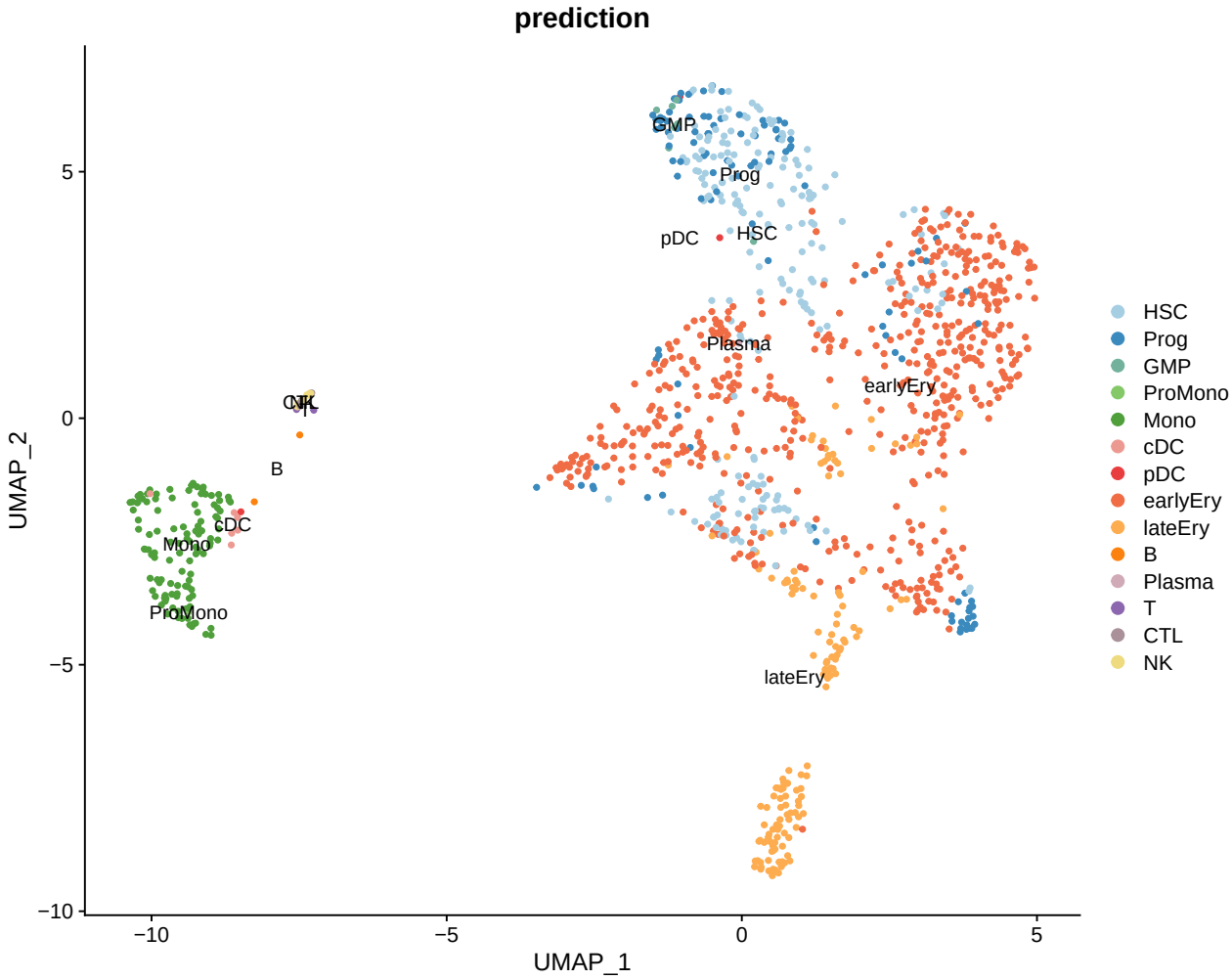


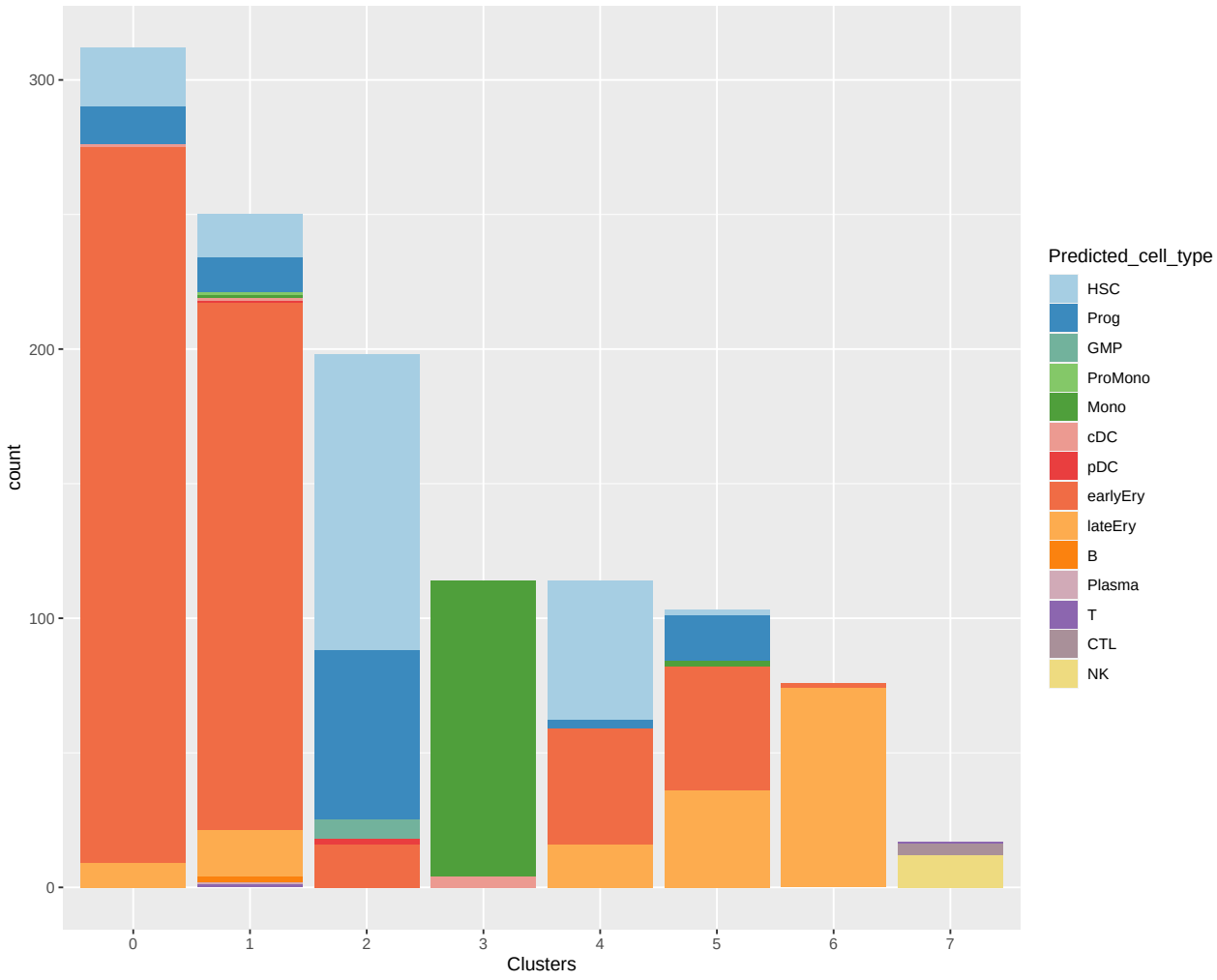
3. Predict the class of the cells using the markers and the expression of the BM cells form Van_Galen paper

```
## Performing PCA on the provided reference using 1821 features as input.
## Projecting cell embeddings
## Finding neighborhoods
## Finding anchors
##  Found 1317 anchors
## Filtering anchors
##  Retained 1057 anchors
## Finding integration vectors
## Finding integration vector weights
## Predicting cell labels
##
##        HSC Prog GMP ProMono Mono cDC pDC earlyEry lateEry ProB   B Plasma   T
##   CD34 143   84   3       0    0   0   1      326      78    0   0      0   0
##   CD38  59   26   4       1  113   6   2      243      74    0   2      1   2
```

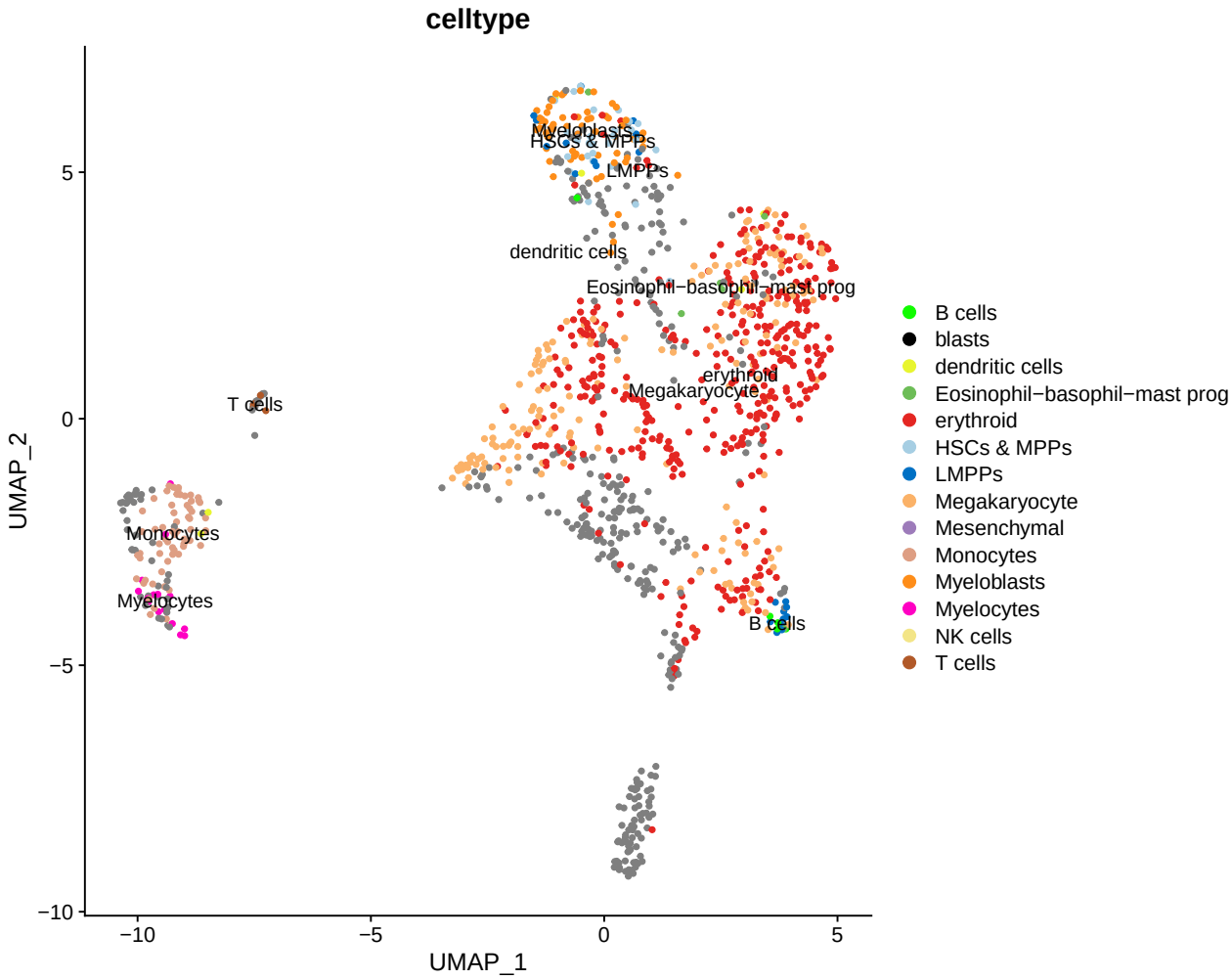
```
##
##         CTL  NK
##    CD34   1   1
##    CD38   3  11
```

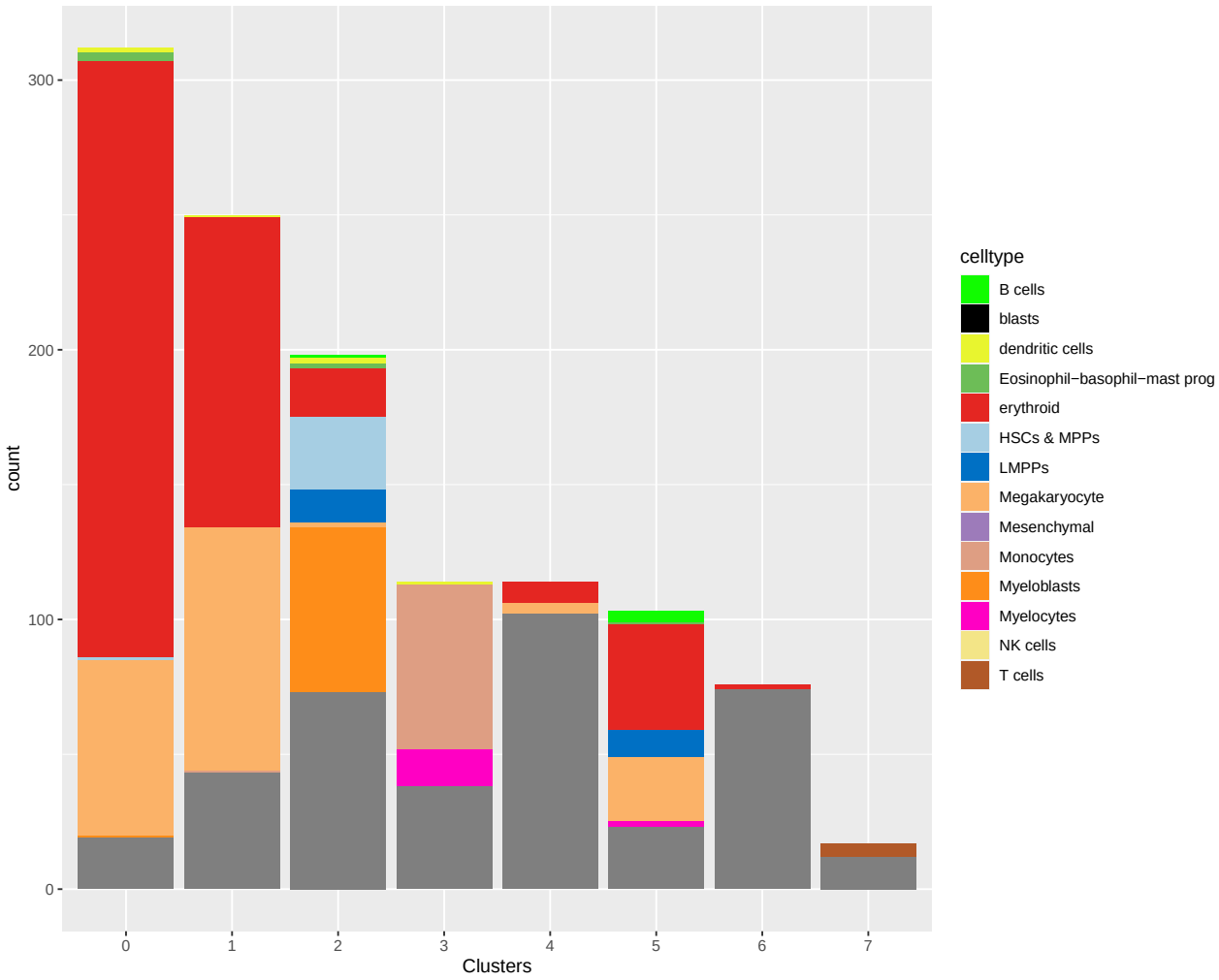



prediction
GMP
Prog
pDC
HSC
Plasma
earlyEry
CTL
NK
B
cDC
Mono
ProMono
lateEry
UMAP_2
UMAP_1
5
0
−5
−10
−10
−5
0
5
HSC
Prog
GMP
ProMono
Mono
cDC
pDC
earlyEry
lateEry
B
Plasma
T
CTL
NK


300
200
100
0
count
0
1
2
3
4
5
6
7
Clusters
Predicted_cell_type
HSC
Prog
GMP
ProMono
Mono
cDC
pDC
earlyEry
lateEry
B
Plasma
T
CTL
NK

4. Project the predictions from Velten onto our UMAP





Cluster 2 seems the one with greater LSC6 score