AML8_Dx

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2022-02-08 10:11:44

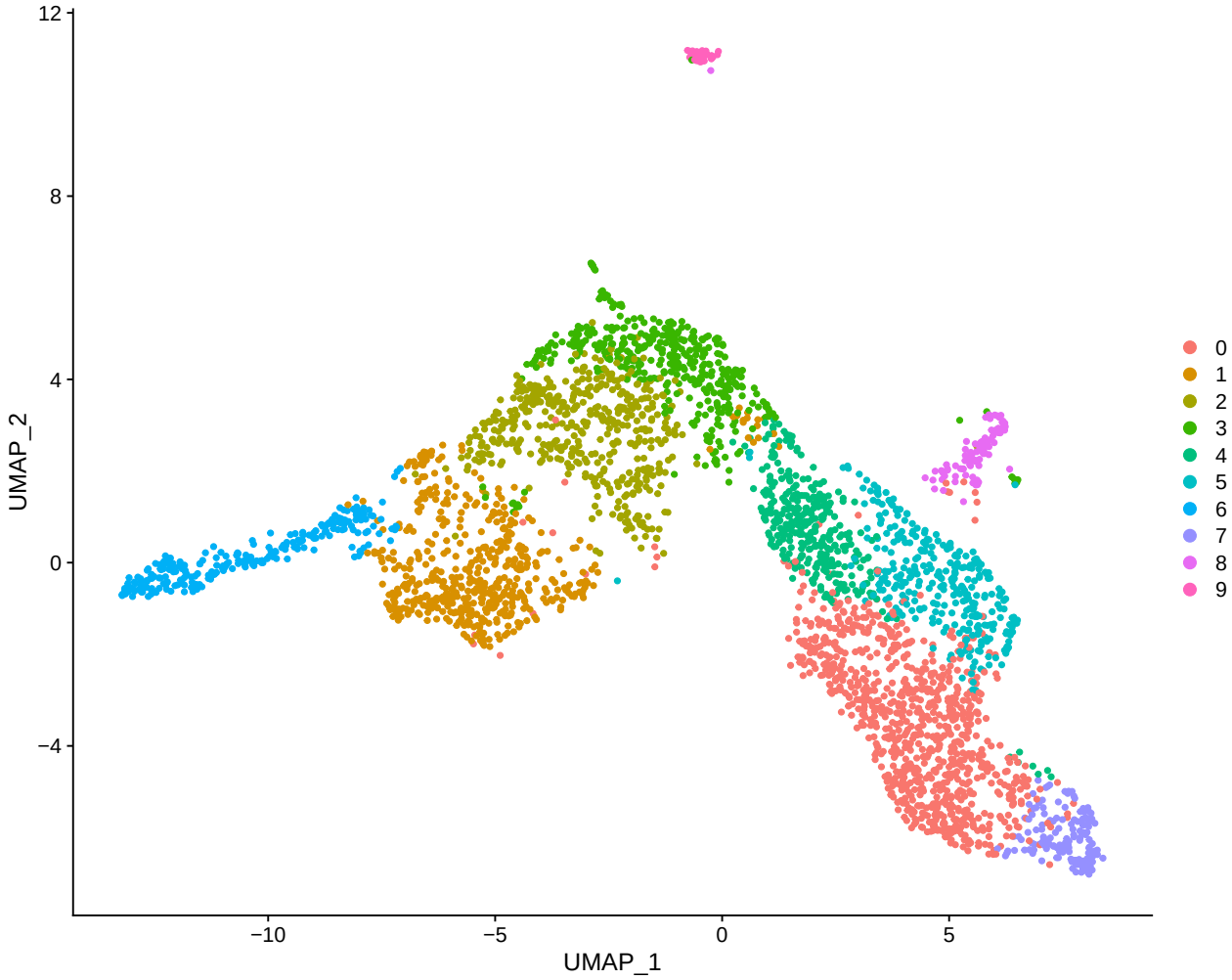
Contents

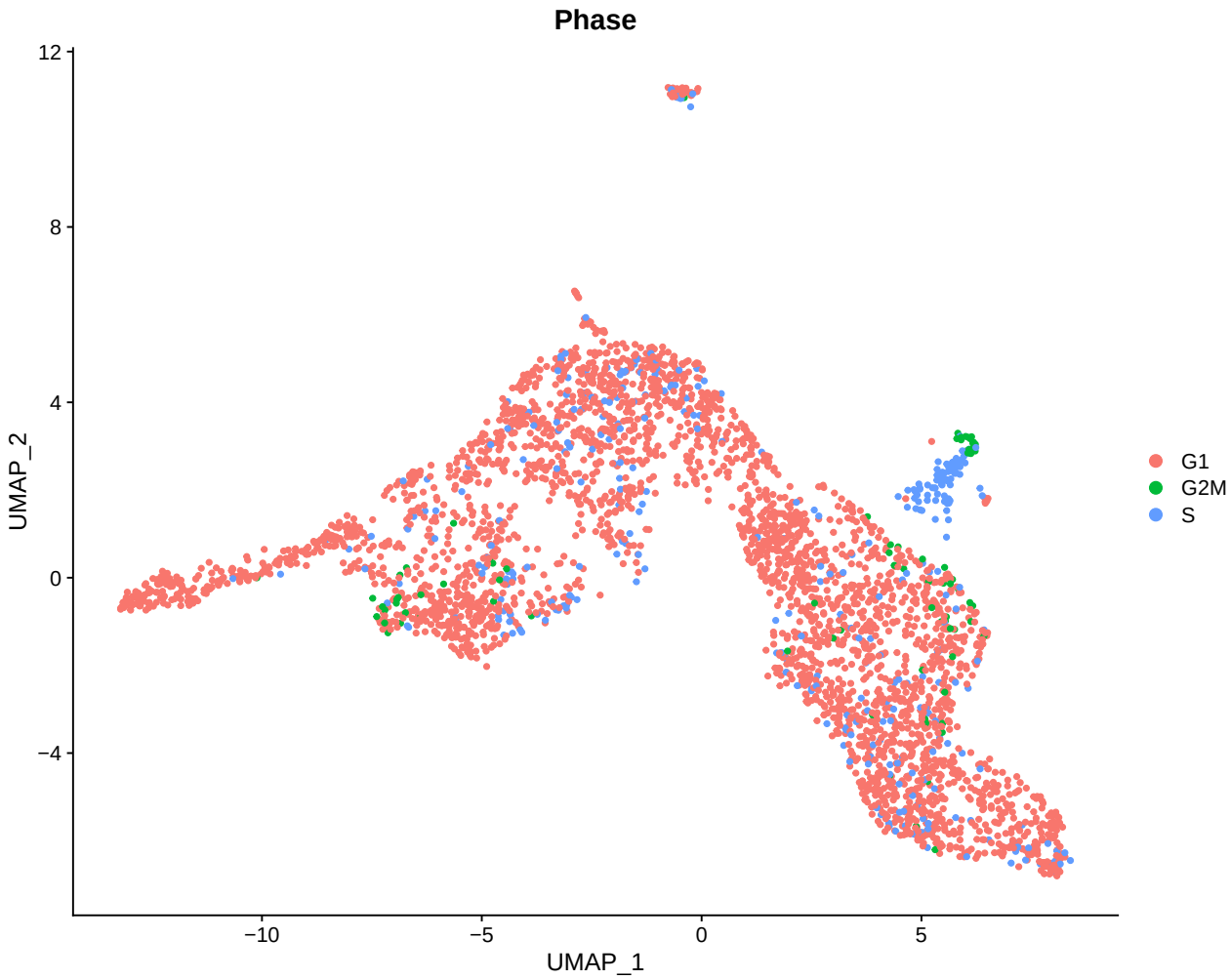
1. Put together both 34 and 38 libraries. Apply QC and dimensionality reduction.

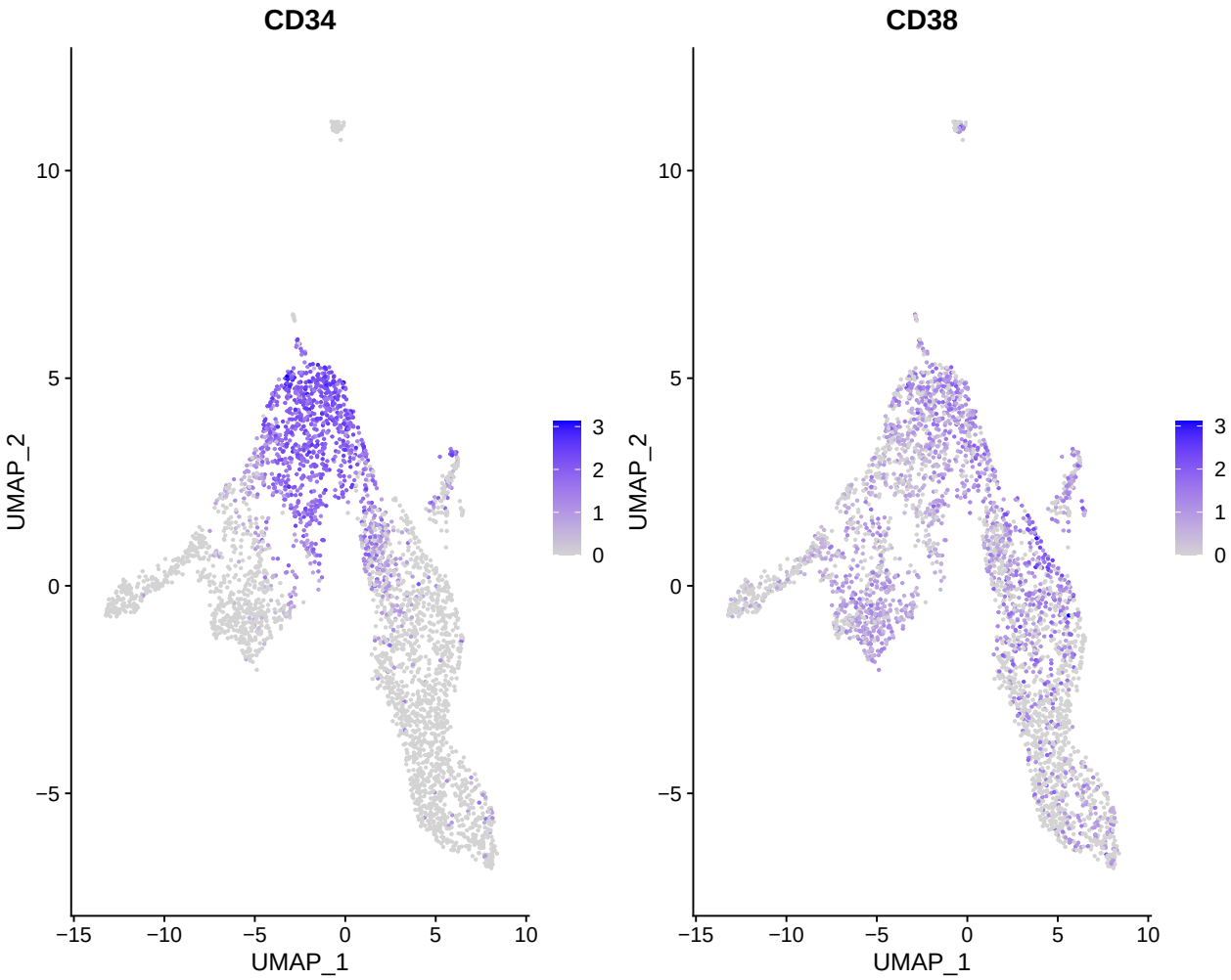
```
## CD34_AAACCCACAGCAGTTT-1 CD34_AAACCCAGTAATGCGG-1 CD34_AAACCCAGTATCGCAT-1
##                       3                       1                       0
## CD34_AAACCCATCACCCTTG-1 CD34_AAACGAAGTGTGCTTA-1
##                       4                       4
## Levels: 0 1 2 3 4 5 6 7 8 9
```

```
##
##          0   1   2   3   4   5   6   7   8   9
##   CD34  35  79 451 391 309  55   8  45  35   0
##   CD38 812 420   7  19  23 267 263 109  56  43
```

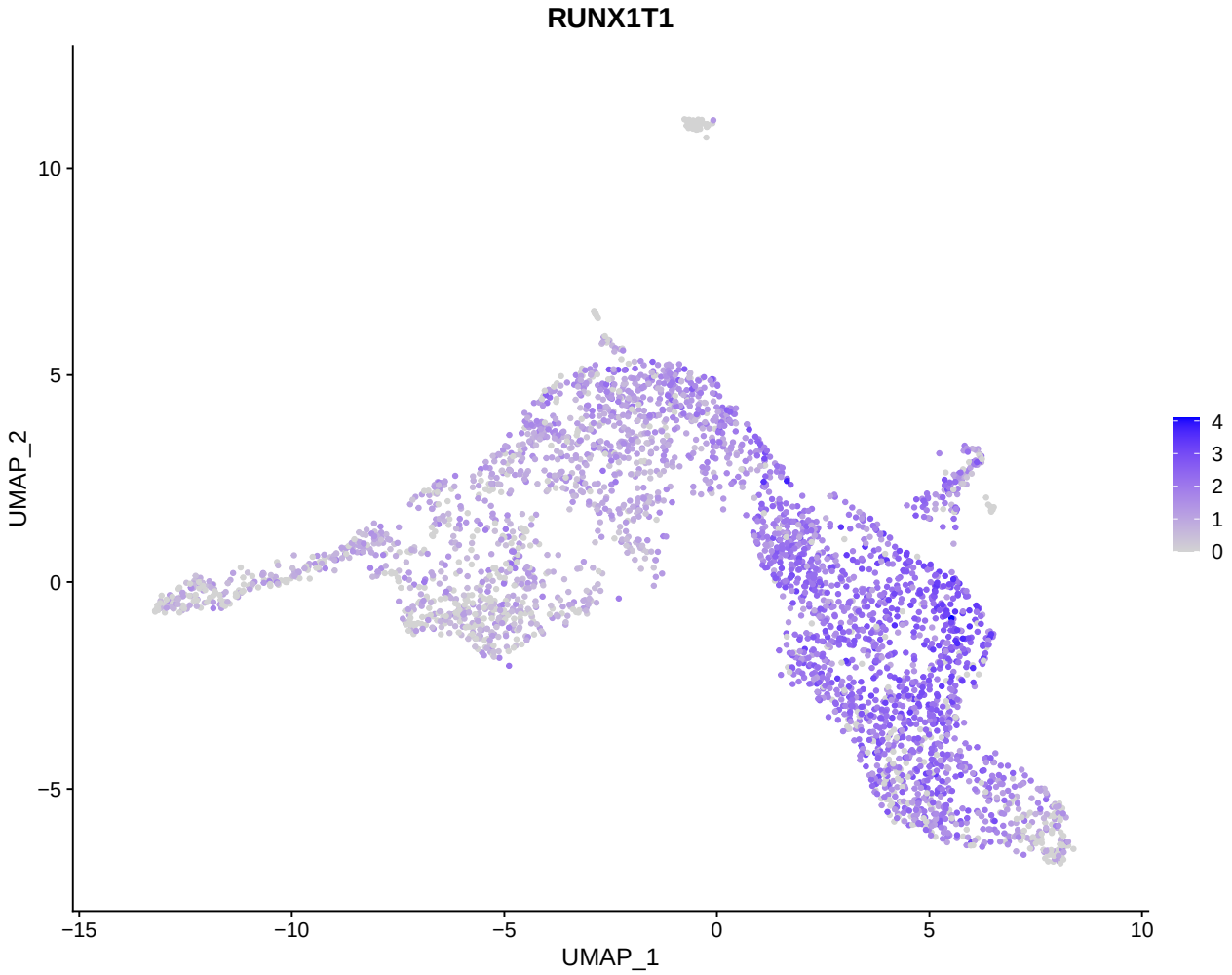
```
## Warning: The default method for RunUMAP has changed from calling Python UMAP via reticulate to the R
## To use Python UMAP via reticulate, set umap.method to 'umap-learn' and metric to 'correlation'
## This message will be shown once per session
```


12
8
4
0
−4
UMAP_2
−10
−5
0
5
UMAP_1
0
1
2
3
4
5
6
7
8
9


Phase
12
8
4
0
−4
UMAP_2
−10
−5
0
5
UMAP_1
G1
G2M
S

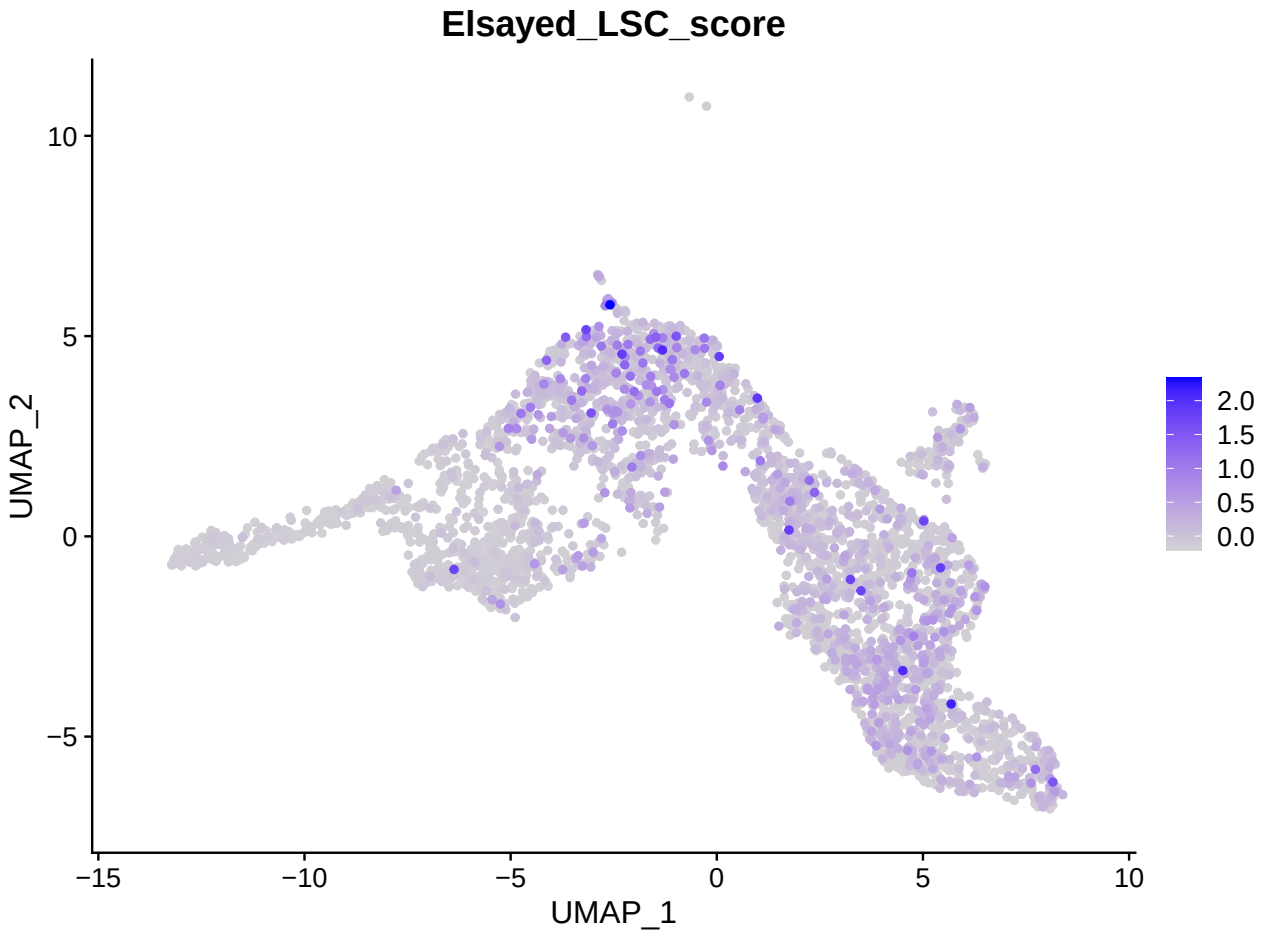


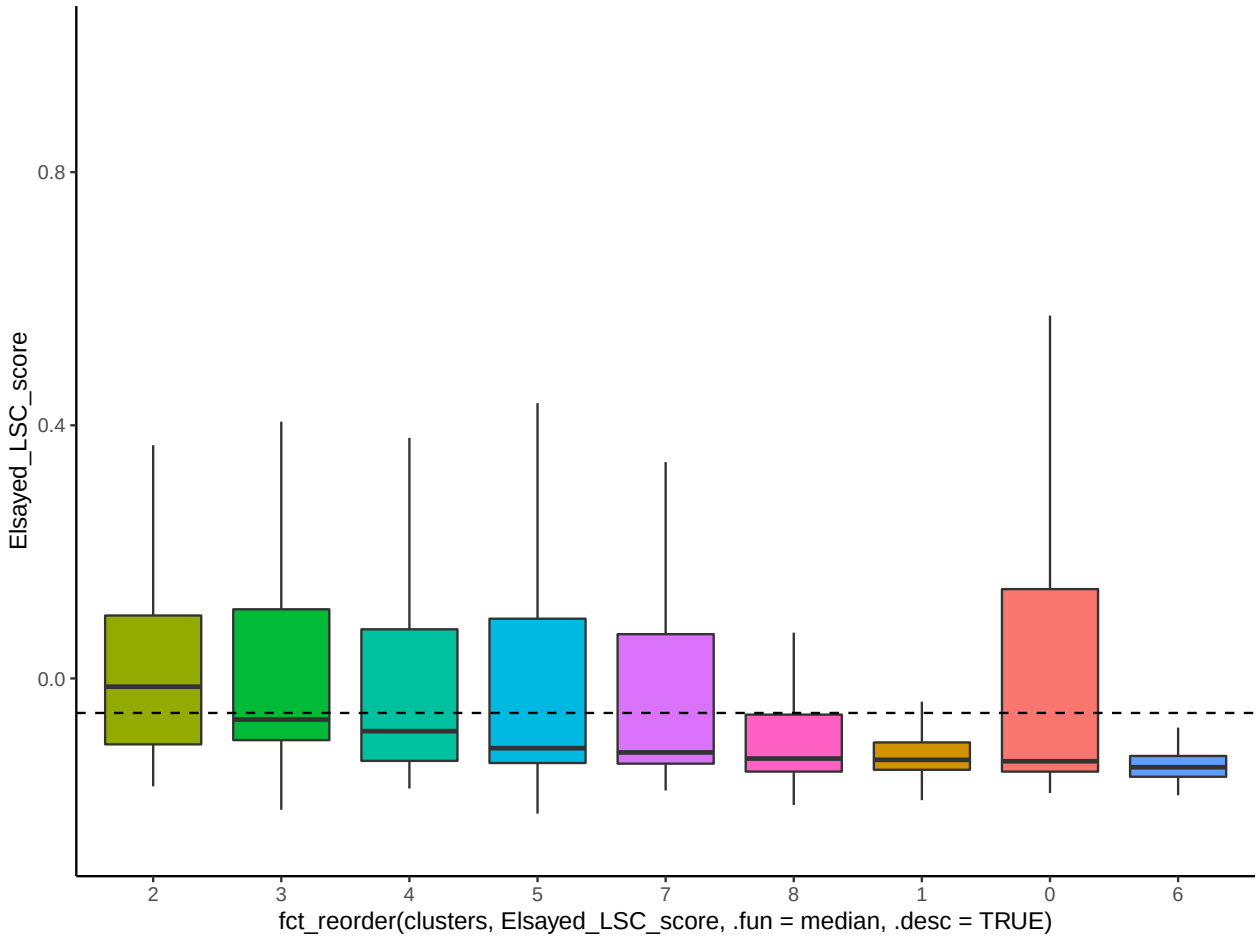

```
## Check for expression of malignant marker for t(8;21) RUNX1T1
```



2. Get the LSC6 score

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

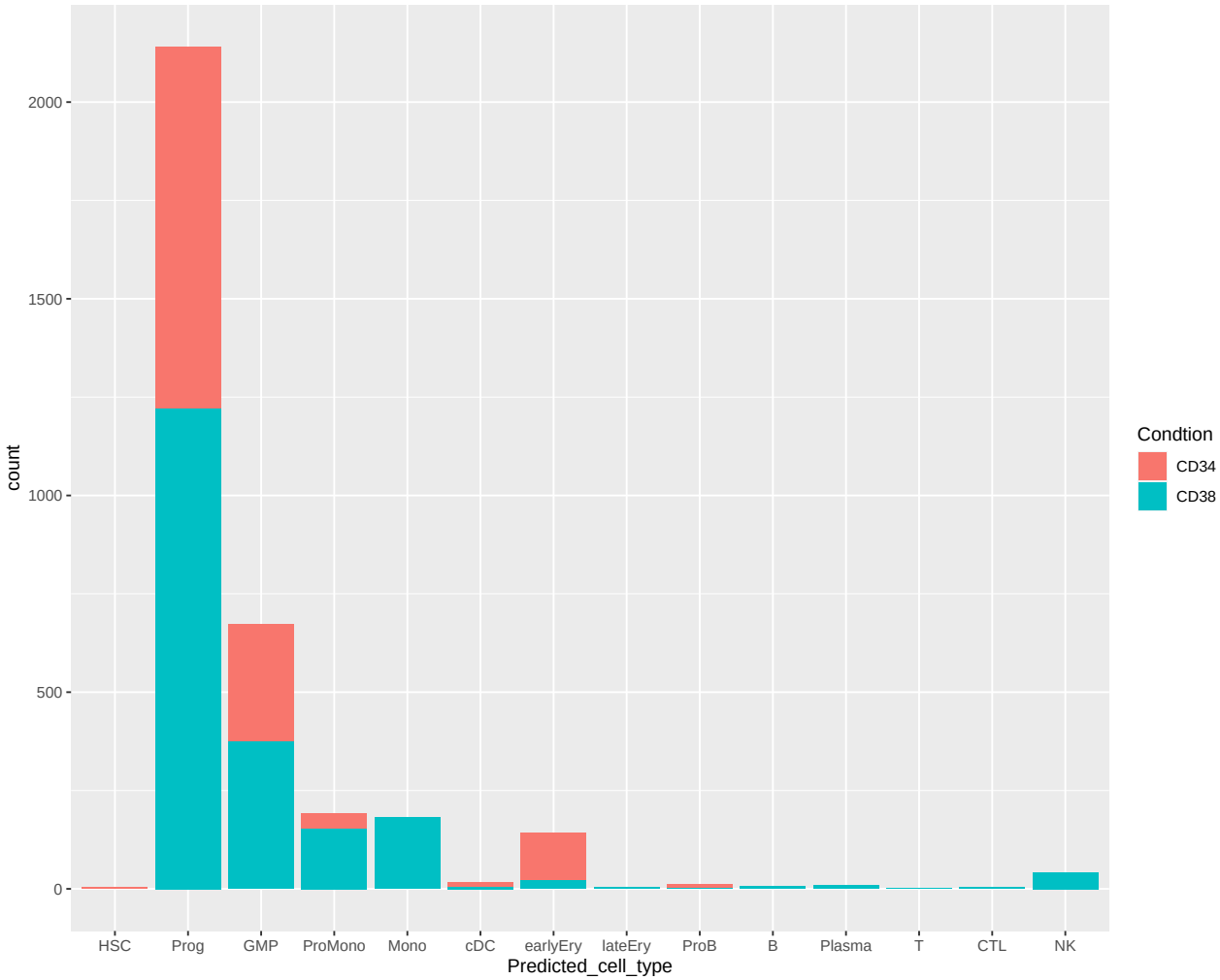

Elsayed_LSC_score
10
5
0
−5
UMAP_2
−15
−10
−5
0
5
10
UMAP_1
2.0
1.5
1.0
0.5
0.0

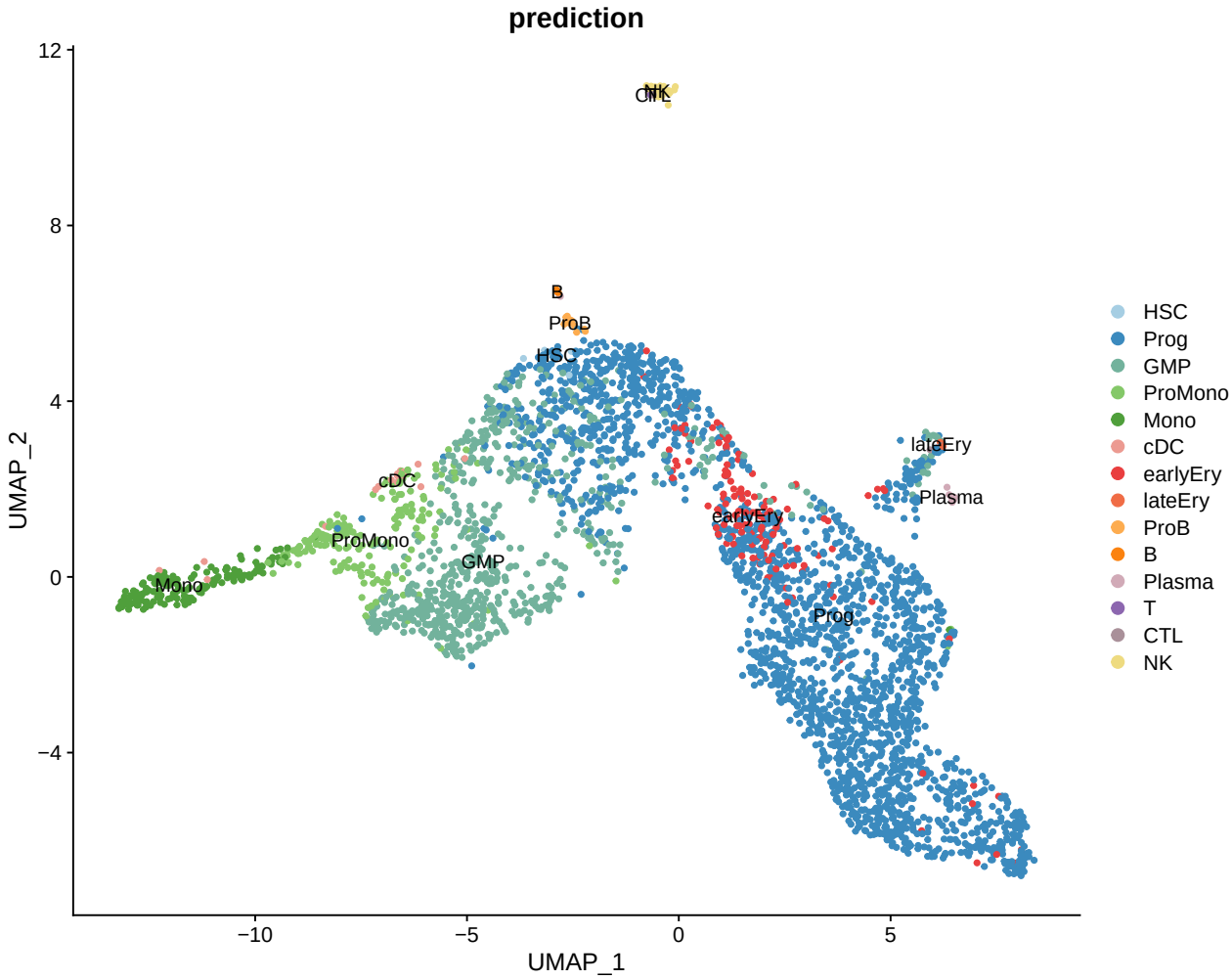


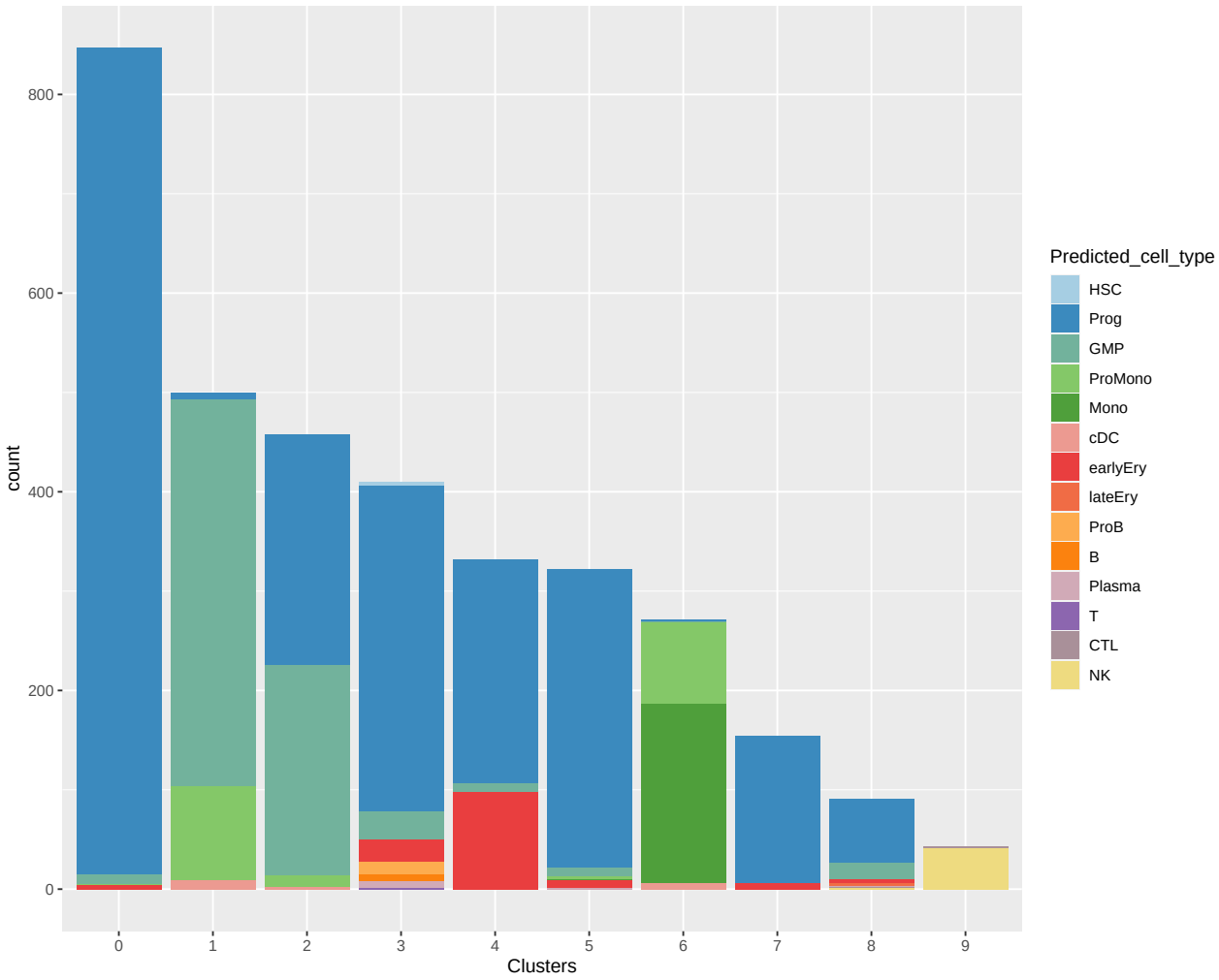
3. Predict the class of the cells using the markers and the expression of the BM cells form Van_Galen paper

```
## Performing PCA on the provided reference using 1821 features as input.
## Projecting cell embeddings
## Finding neighborhoods
## Finding anchors
##  Found 1128 anchors
## Filtering anchors
##  Retained 902 anchors
## Finding integration vectors
## Finding integration vector weights
## Predicting cell labels
##
##         HSC Prog  GMP ProMono Mono  cDC  pDC earlyEry lateEry ProB    B Plasma
##   CD34    4  920  299       38    0   12    0      122       0   12    0      1
##   CD38    0 1221  374      153  181    5    0       21       3    1    6      8
```

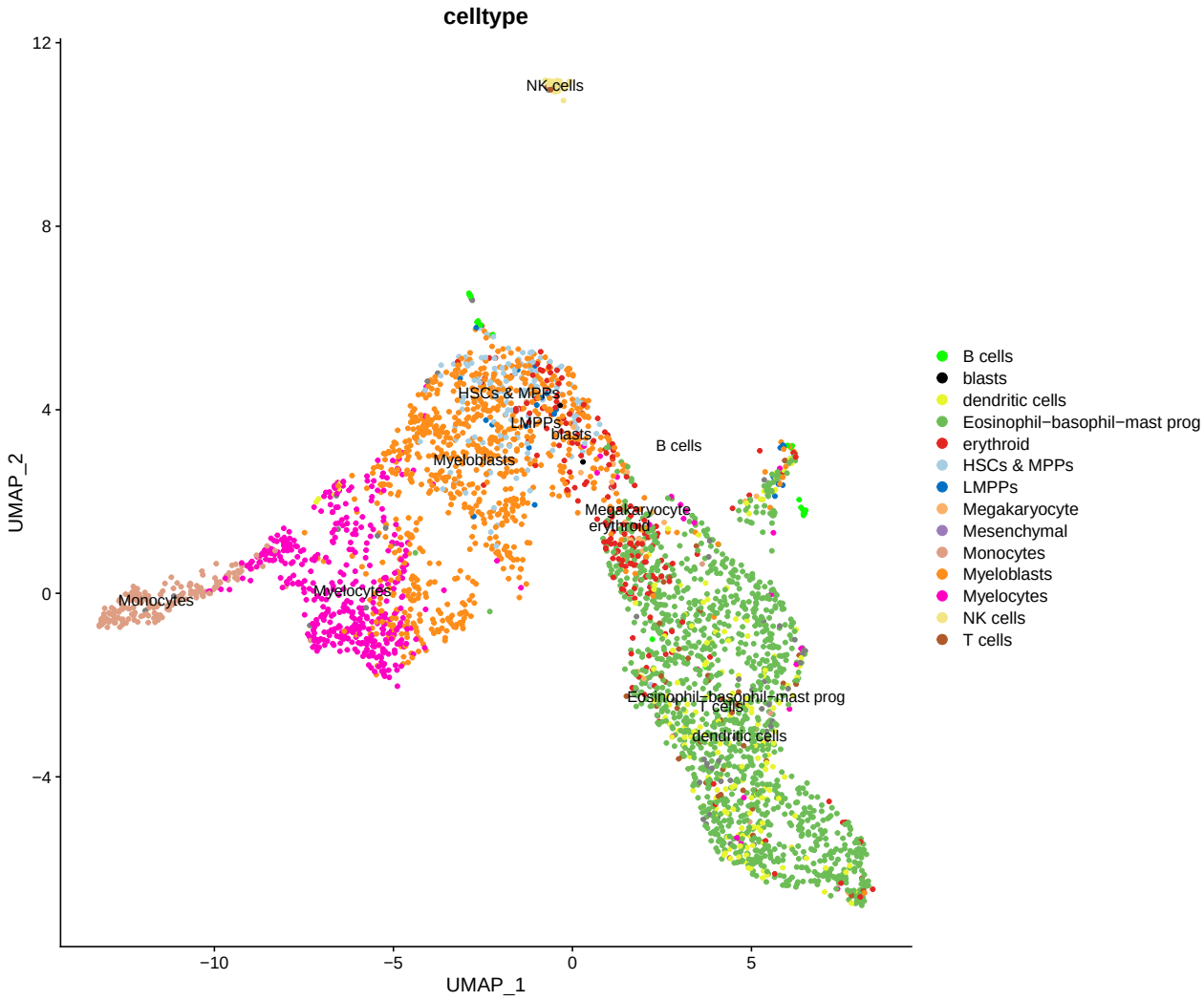
```
##
##          T  CTL   NK
##    CD34  0    0    0
##    CD38  1    3   42
```



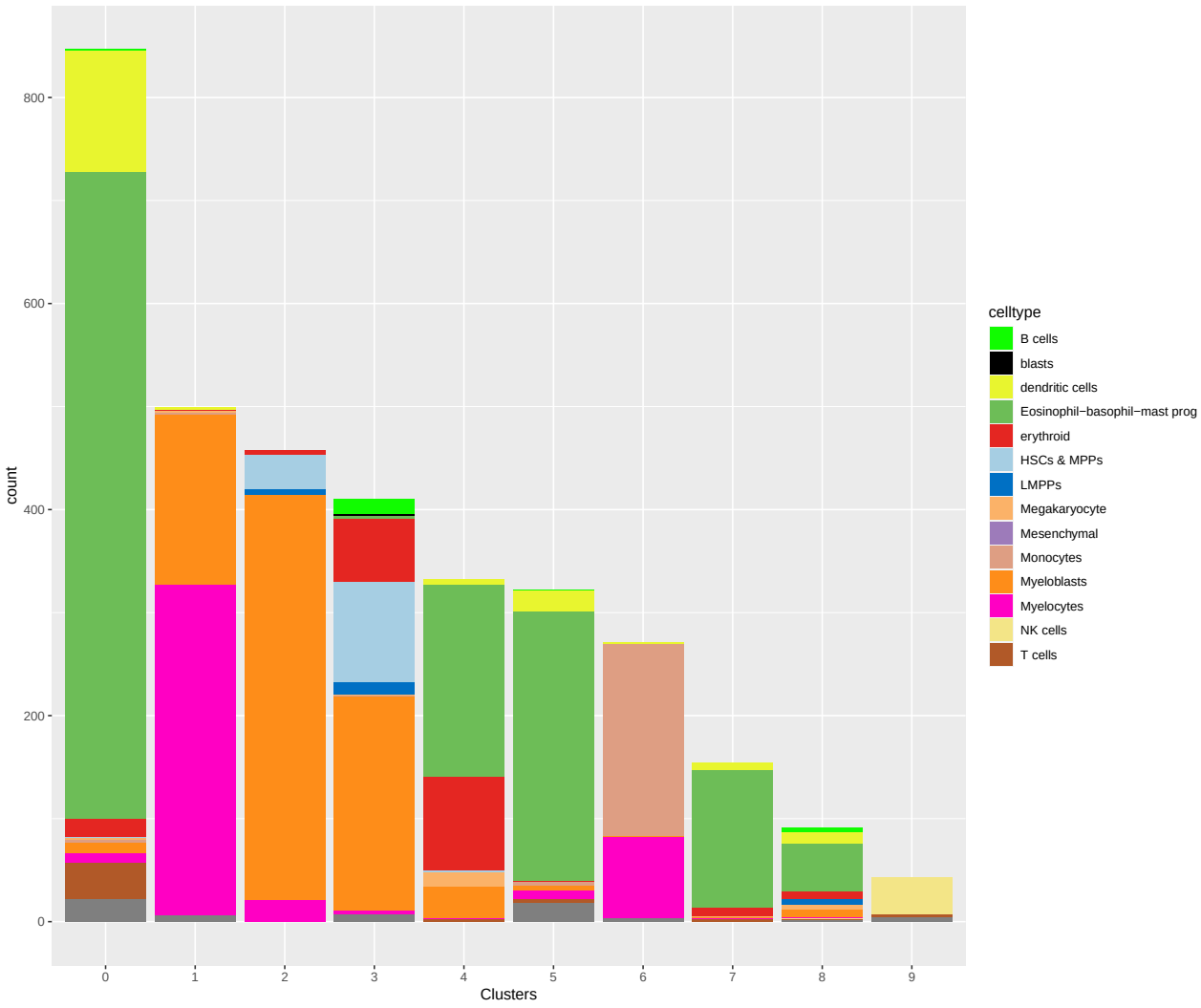

prediction
12
8
4
0
−4
UMAP_2
−10
−5
0
5
UMAP_1
NK
B
ProB
HSC
cDC
ProMono
GMP
Mono
earlyEry
lateEry
Plasma
Prog
HSC
Prog
GMP
ProMono
Mono
cDC
earlyEry
lateEry
ProB
B
Plasma
T
CTL
NK


count
800
600
400
200
0
0
1
2
3
4
5
6
7
8
9
Clusters
Predicted_cell_type
HSC
Prog
GMP
ProMono
Mono
cDC
earlyEry
lateEry
ProB
B
Plasma
T
CTL
NK

4. Project the predictions from Velten onto our UMAP




```
##
##                B cells                   blasts
##                     22                        2
##       dendritic cells Eosinophil-basophil-mast prog
##                    166                     1259
##           erythroid                  HSCs & MPPs
##                    192                      134
##                LMPPs                Megakaryocyte
##                     24                       22
##           Monocytes                  Myeloblasts
##                    194                      823
##           Myelocytes                  NK cells
##                    444                       37
##             T cells
##                     47
```



Cluster 2 appears as the one more enriched on LSC6.