AML9_Rx

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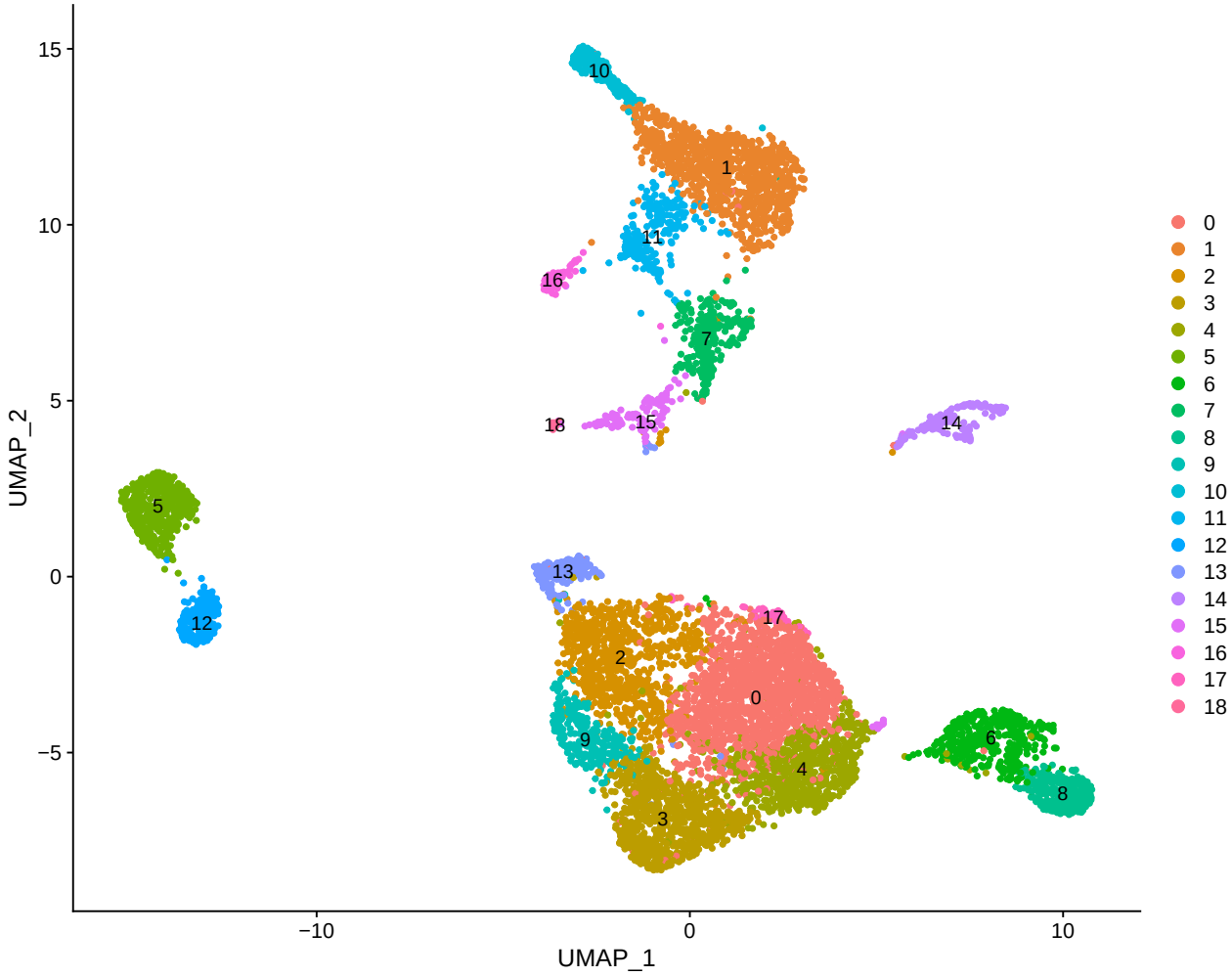
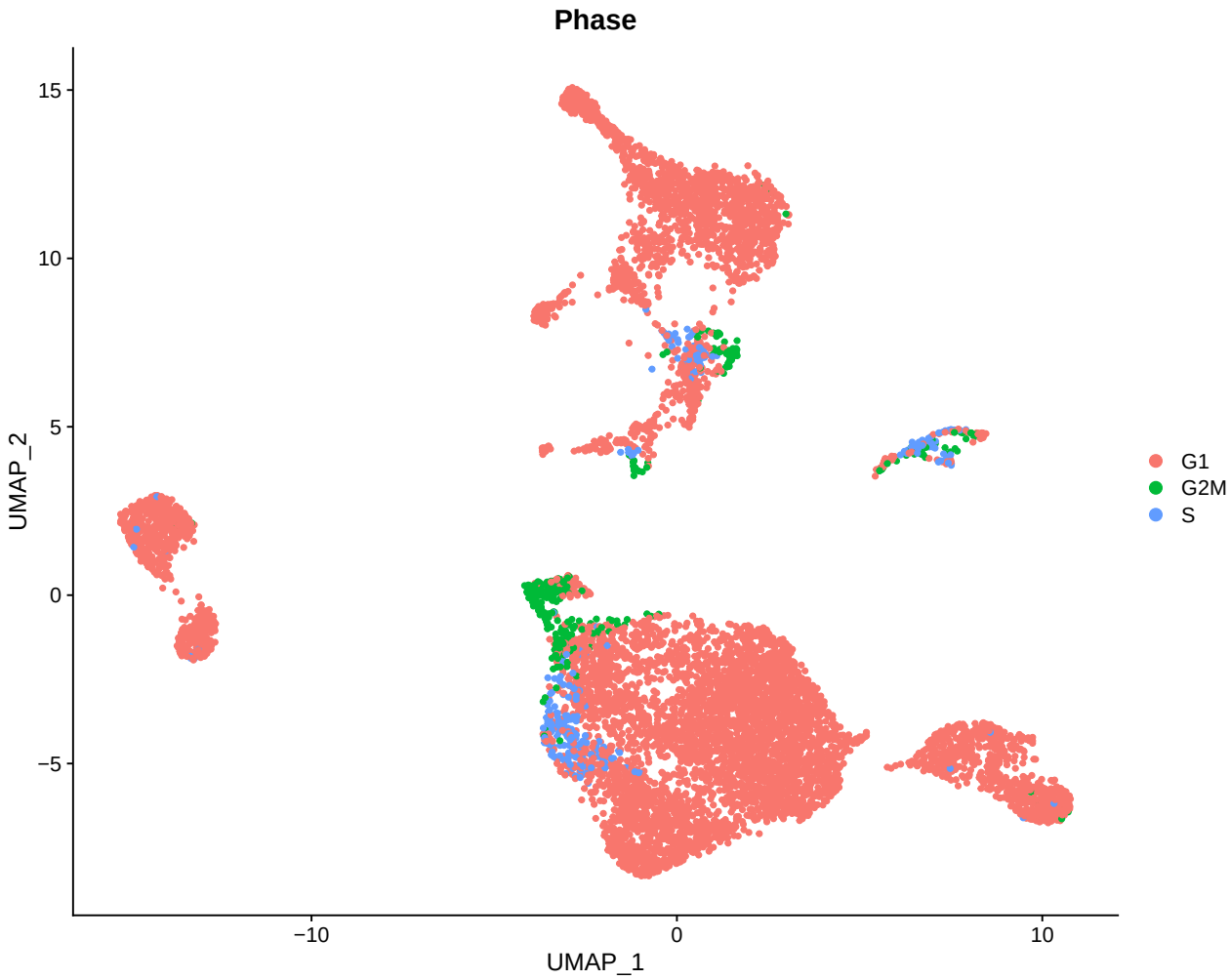
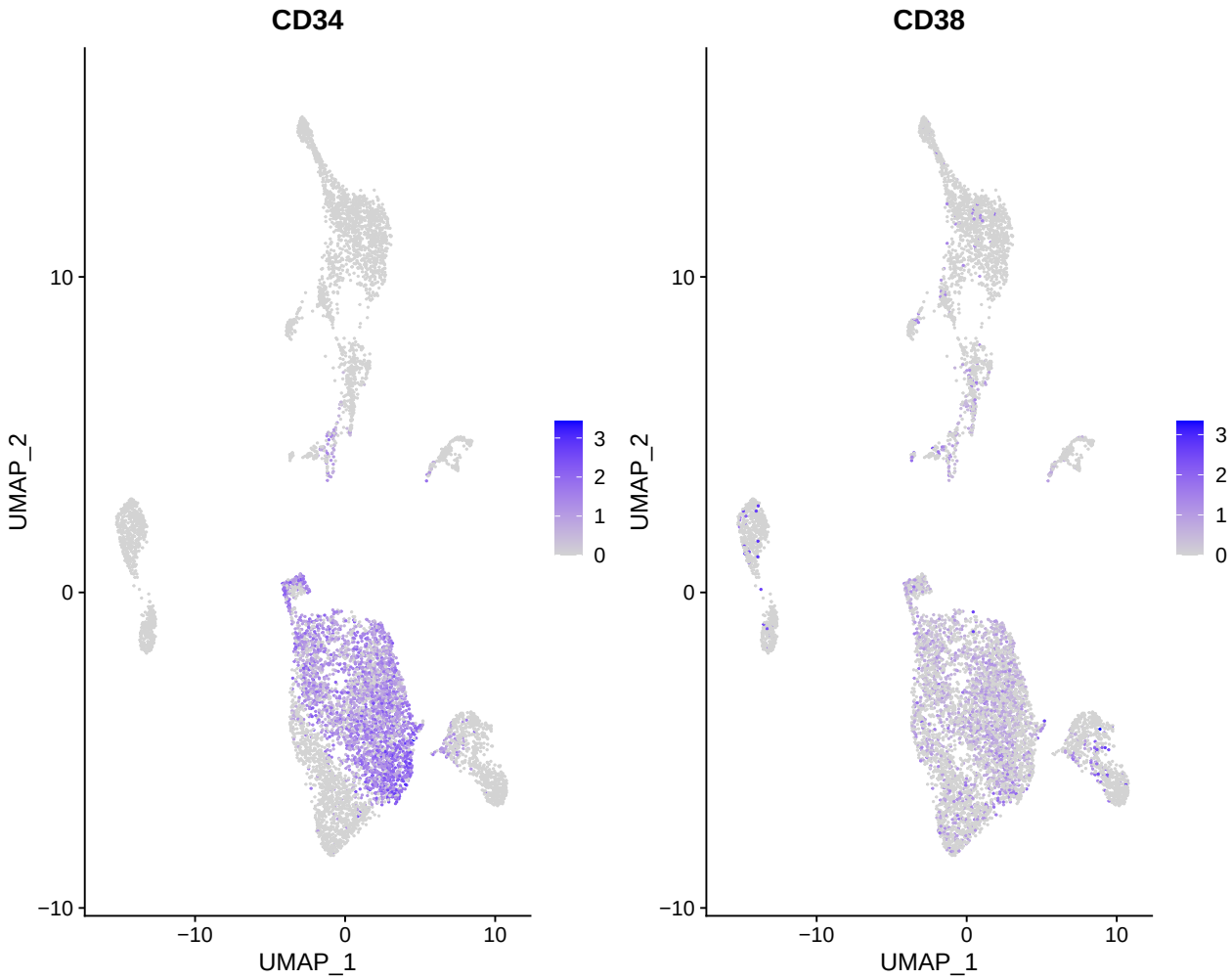
2022-02-09 10:27:43

Contents

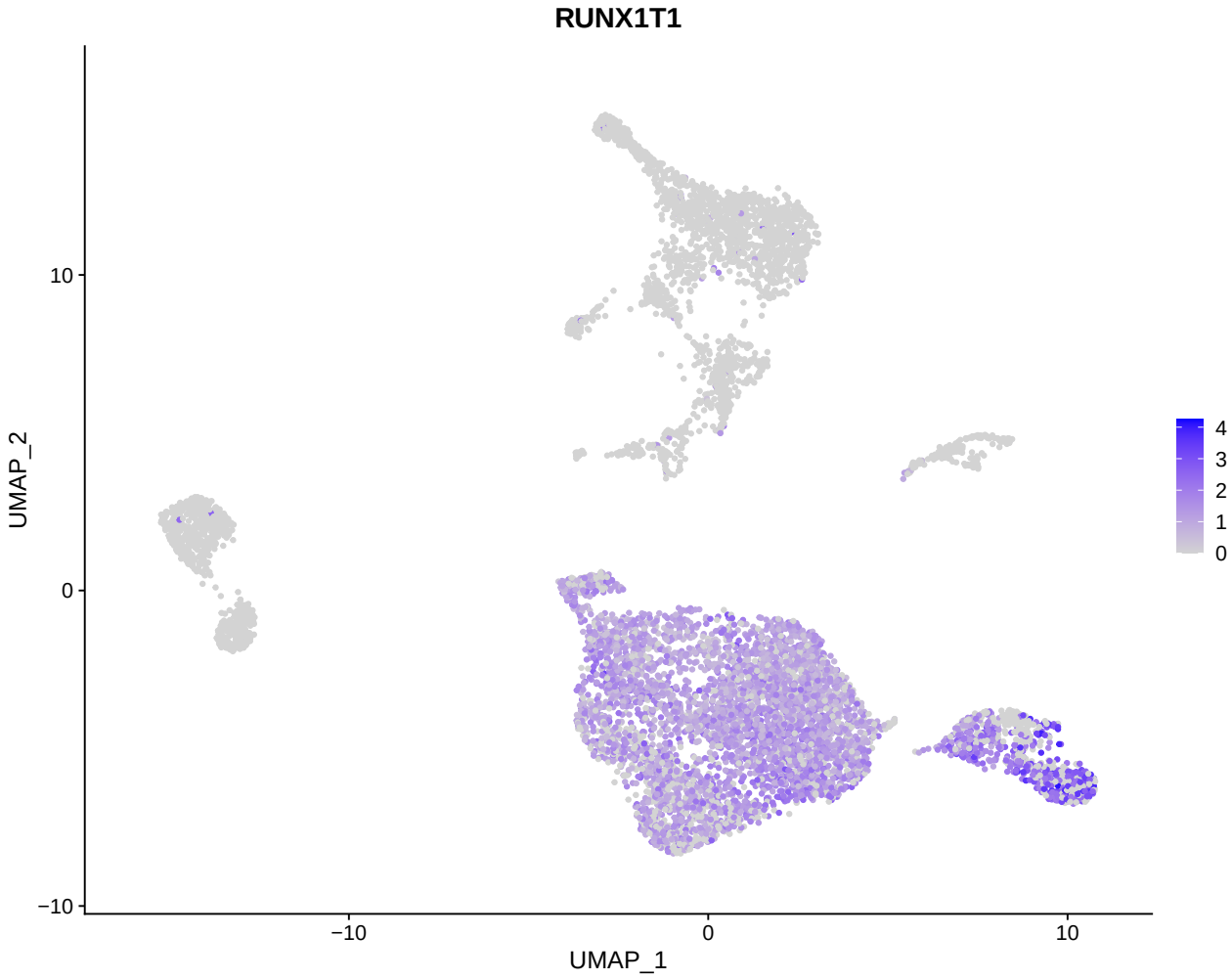
1. Put together both 34 and 38 libraries. Apply QC and dimensionality reduction.




Phase
15
10
5
0
−5
UMAP_2
−10
0
10
UMAP_1
G1
G2M
S

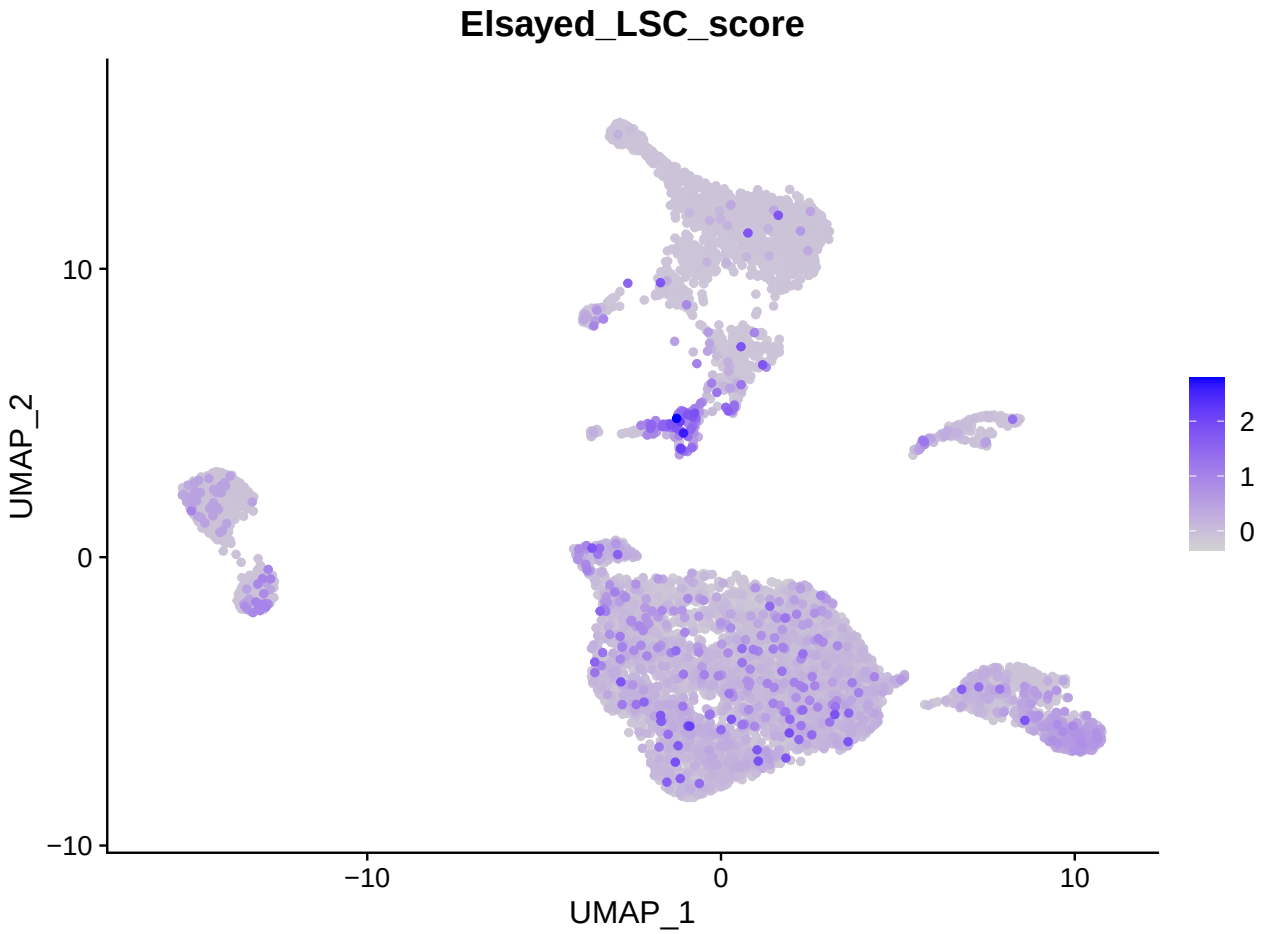


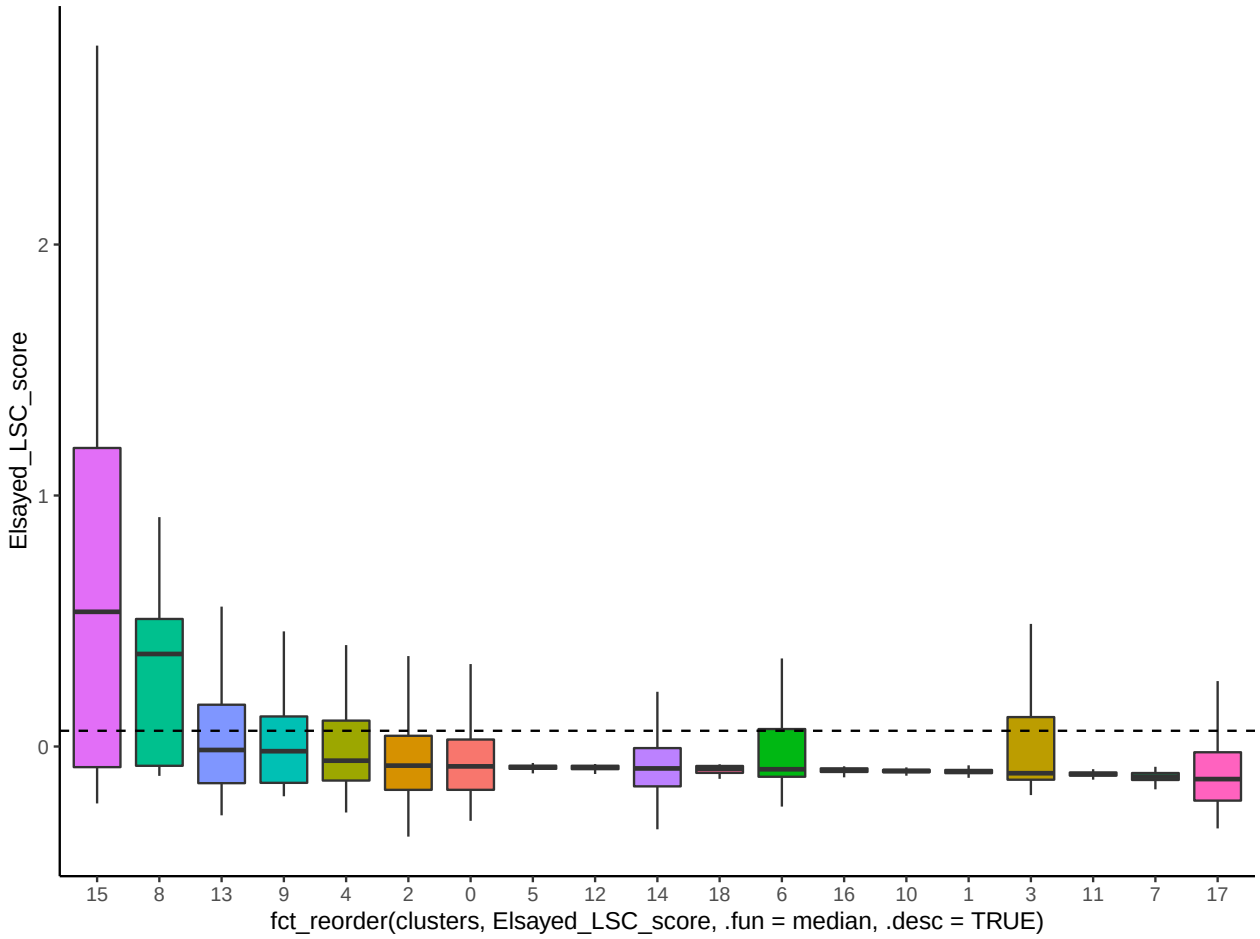

```
## Check for expression of malignant marker for t(8;21) RUNX1T1
```



2. Get the LSC6 score

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

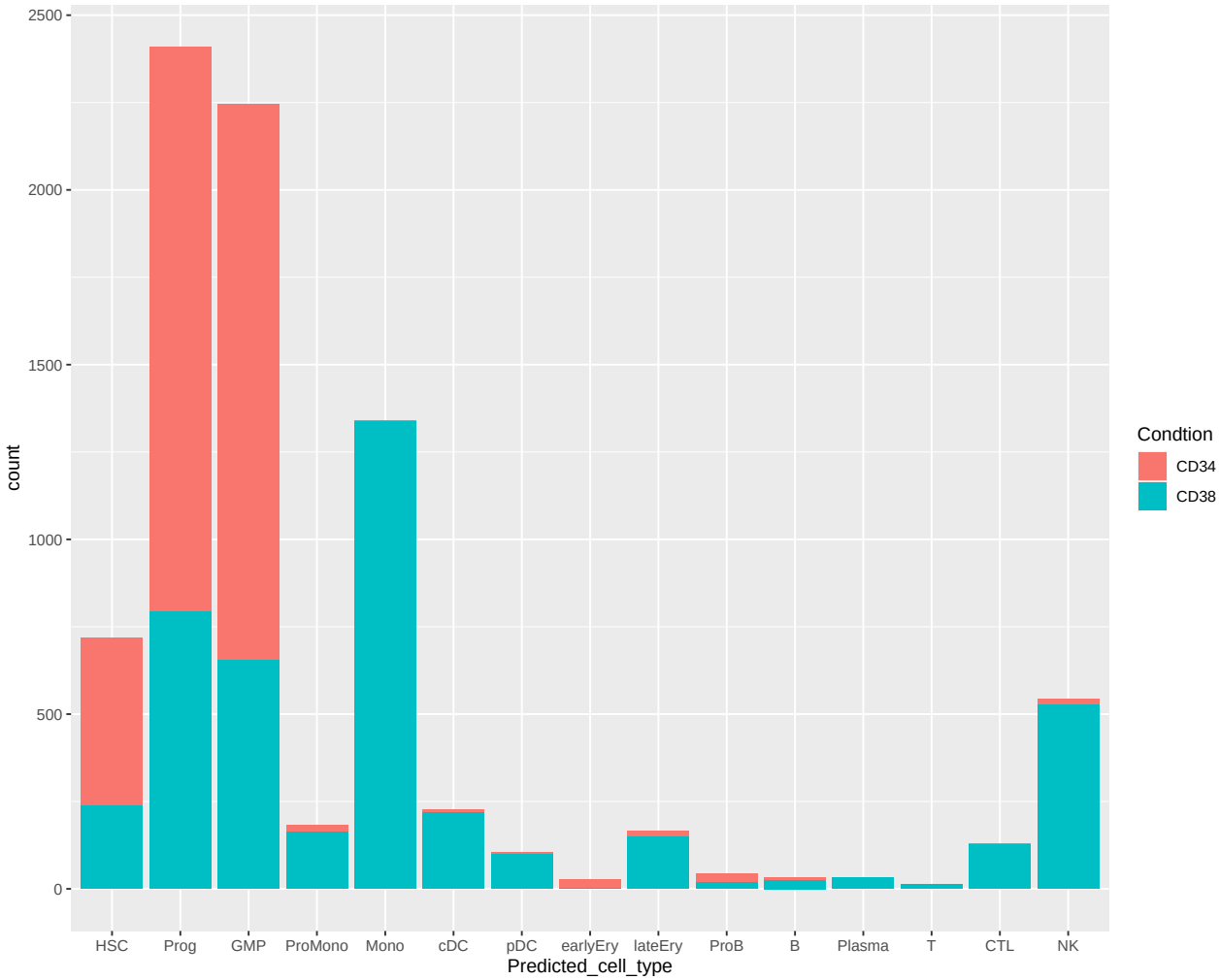

Elsayed_LSC_score
10
0
−10
UMAP_2
−10
0
10
UMAP_1
2
1
0

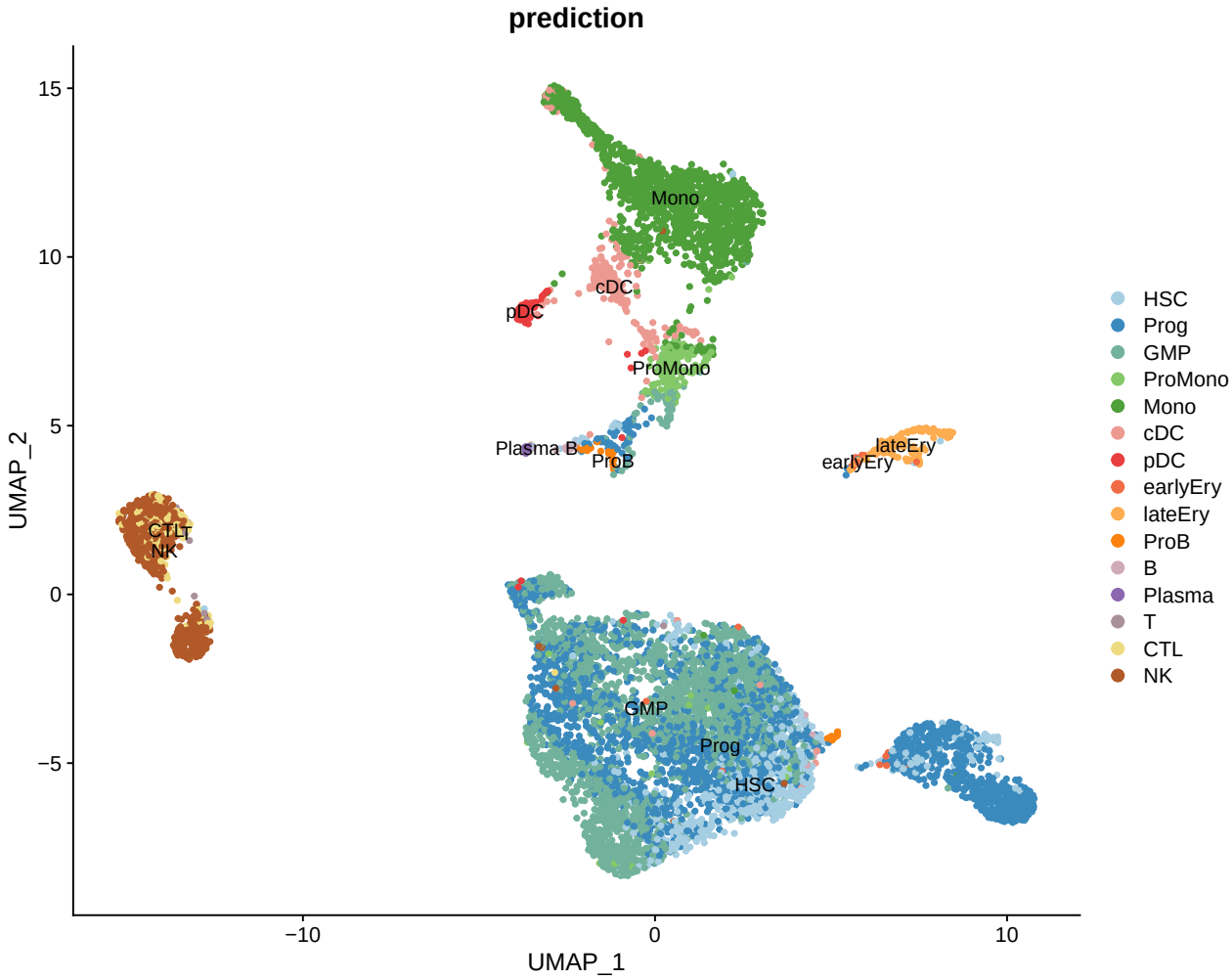


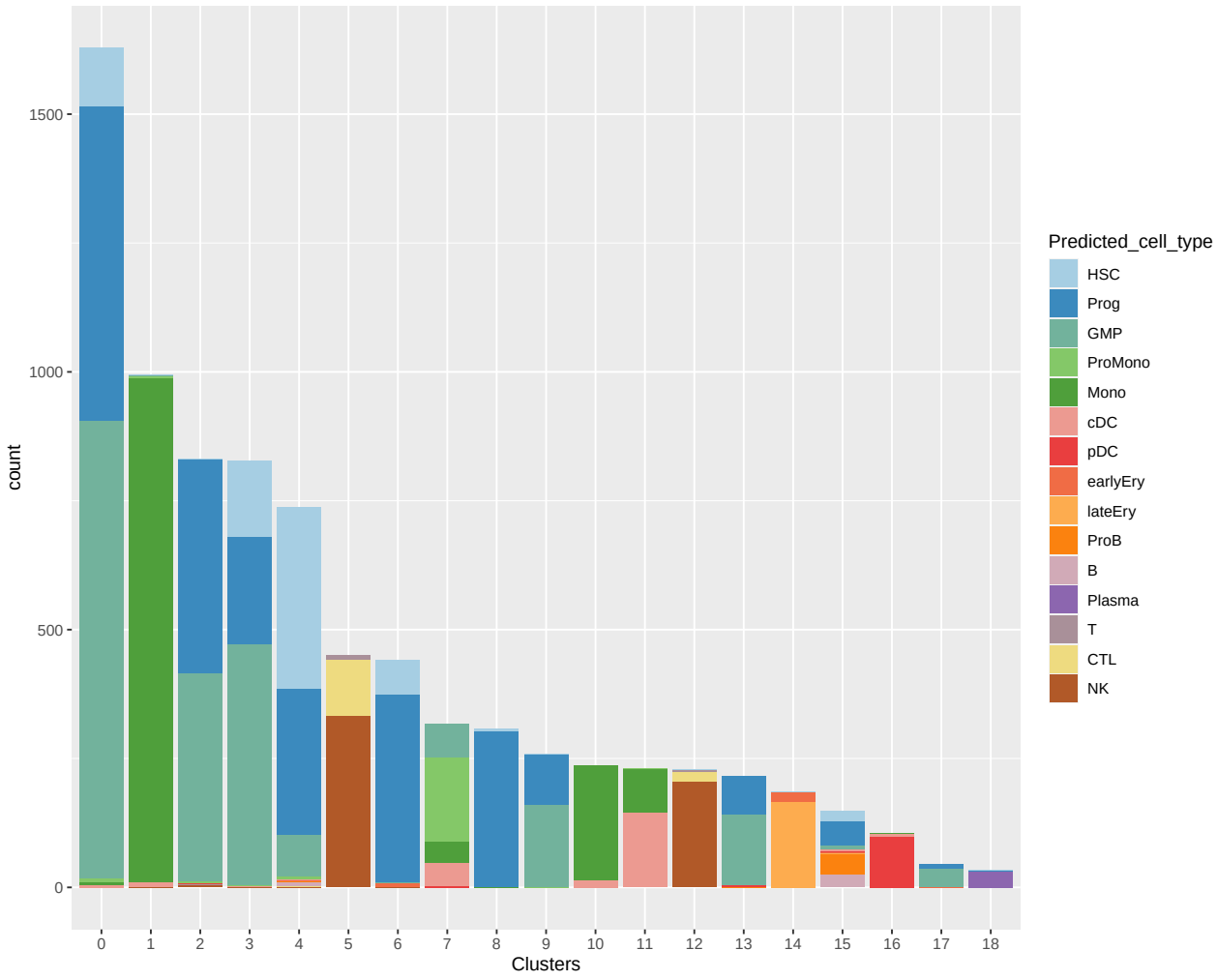
3. Predict the class of the cells using the markers and the expression of the BM cells form Van_Galen paper

```
## Performing PCA on the provided reference using 1821 features as input.
## Projecting cell embeddings
## Finding neighborhoods
## Finding anchors
##  Found 3841 anchors
## Filtering anchors
##  Retained 2763 anchors
## Finding integration vectors
## Finding integration vector weights
## Predicting cell labels
##
##         HSC Prog  GMP ProMono Mono  cDC  pDC earlyEry lateEry ProB    B Plasma
##   CD34  482 1618 1593      22    1    9    8       25      18   26    8      0
##   CD38  238  792  654     162 1338  218   98        2     149   18   25     31
```

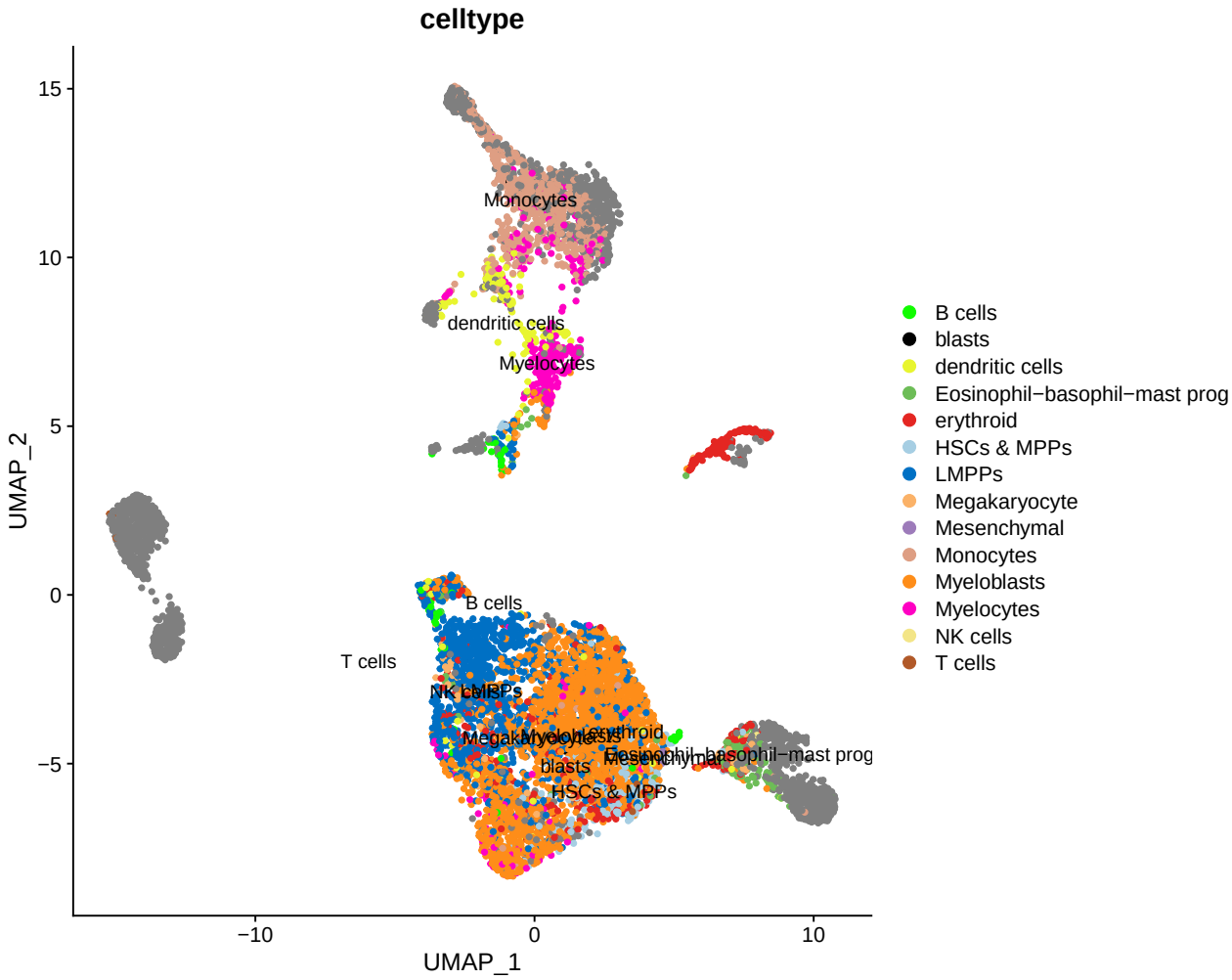
```
##
##              T  CTL   NK
##    CD34      1    5   16
##    CD38     13  126  527
```

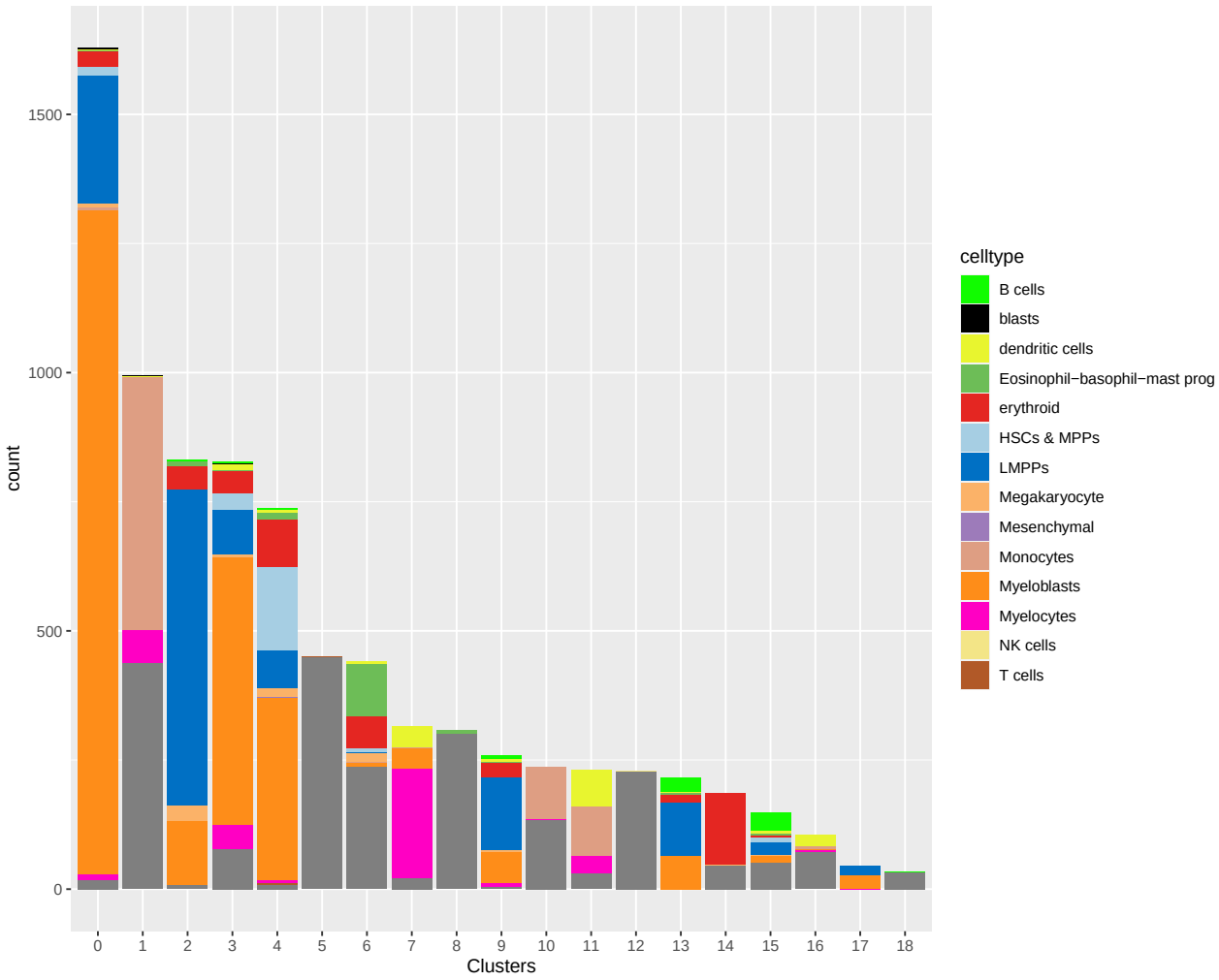



prediction
15
10
5
0
−5
UMAP_2
−10
0
10
UMAP_1
Mono
cDC
pDC
ProMono
Plasma B
ProB
earlyEry
lateEry
CTL
NK
GMP
Prog
HSC
HSC
Prog
GMP
ProMono
Mono
cDC
pDC
earlyEry
lateEry
ProB
B
Plasma
T
CTL
NK


count
1500
1000
500
0
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
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 15 seems to be healthy residual cells, non expressing tumoral marker RUNXiT1. Clusters 8, 13 and 9 they express RUNX1T1, but have not predicted any HSC from both in-silico predictions. Cluster 4, spite of would be under the threshold, is way more enriched in HSC predicted cells. In addition, this is the cluster that colocalize with cluster LSC 2 from the paired Dx. Therefore we would consider this cluster as the more likely enriched on LSC