

# AML6\_Rx

jtrincado

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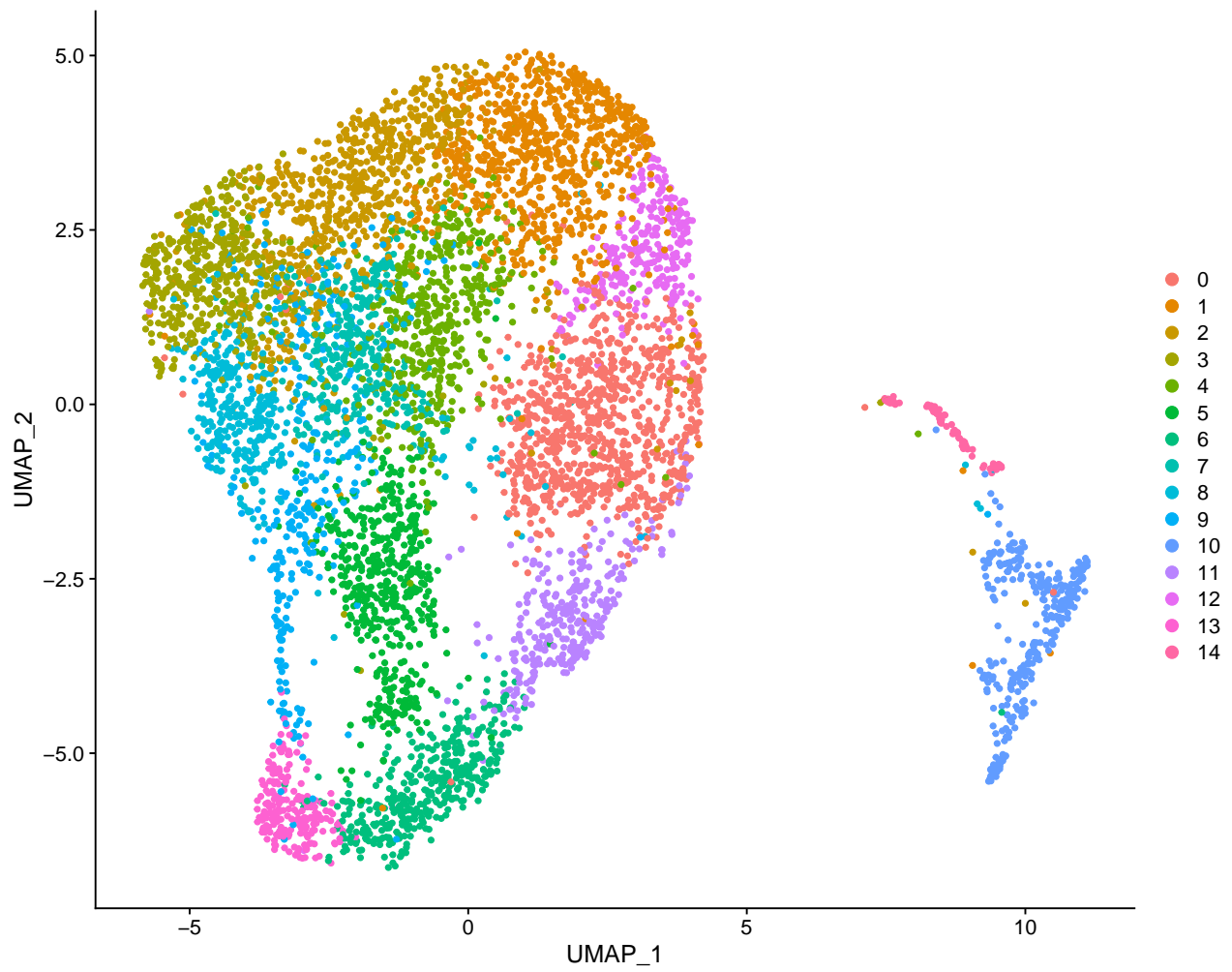
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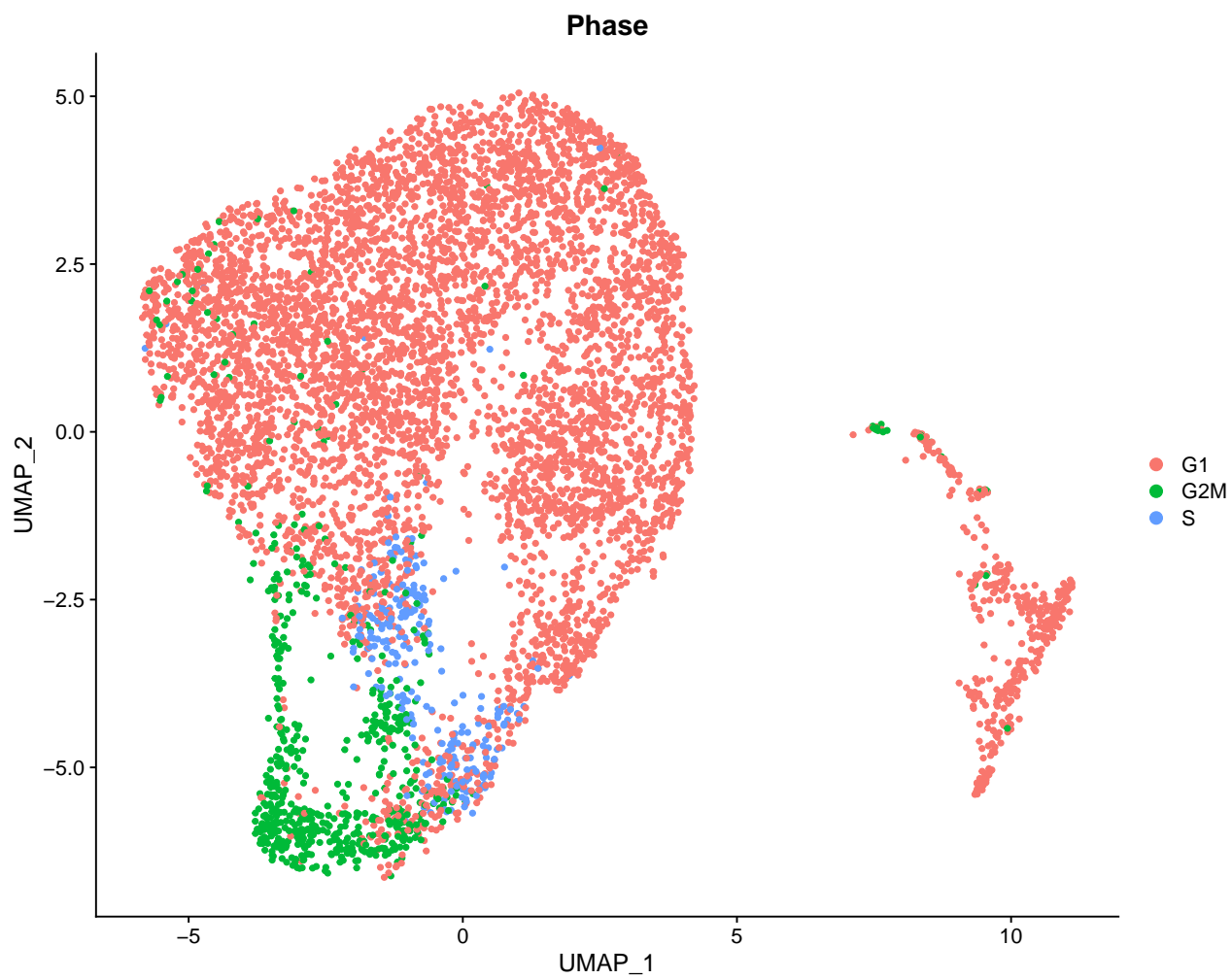
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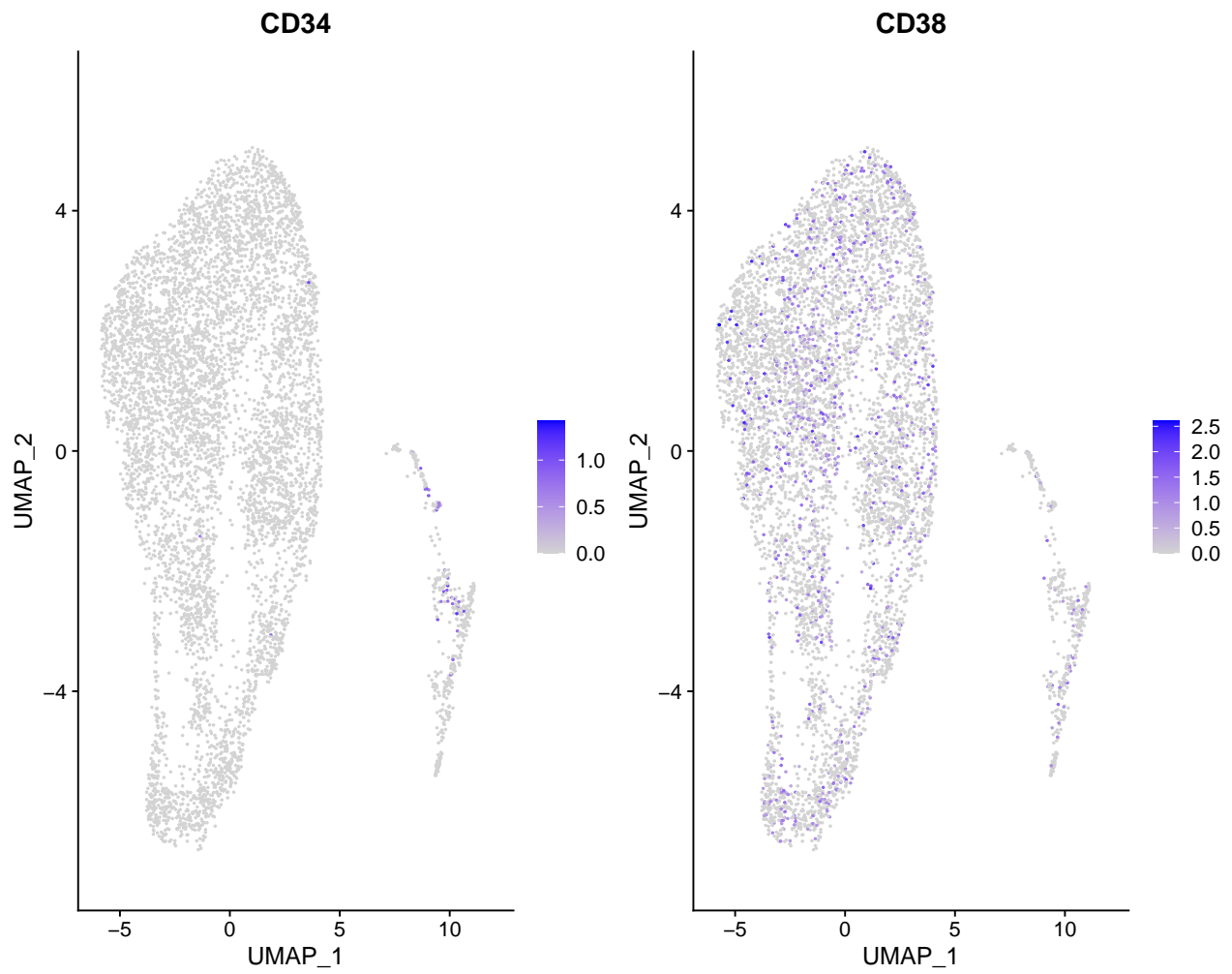
## 1. Put together both 34 and 38 libraries. Apply QC and dimensionality reduction.

```
## CD34_AAACCCAAGATGGTCG-1 CD34_AAACGCTCAACTCGTA-1 CD34_AAAGAACCAAATACGA-1
##                               12                               13                               0
## CD34_AAAGGATAGTGGTGAC-1 CD34_AAAGGATCAGCACAAG-1
##                               0                               0
## Levels: 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
```

```
## 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
```

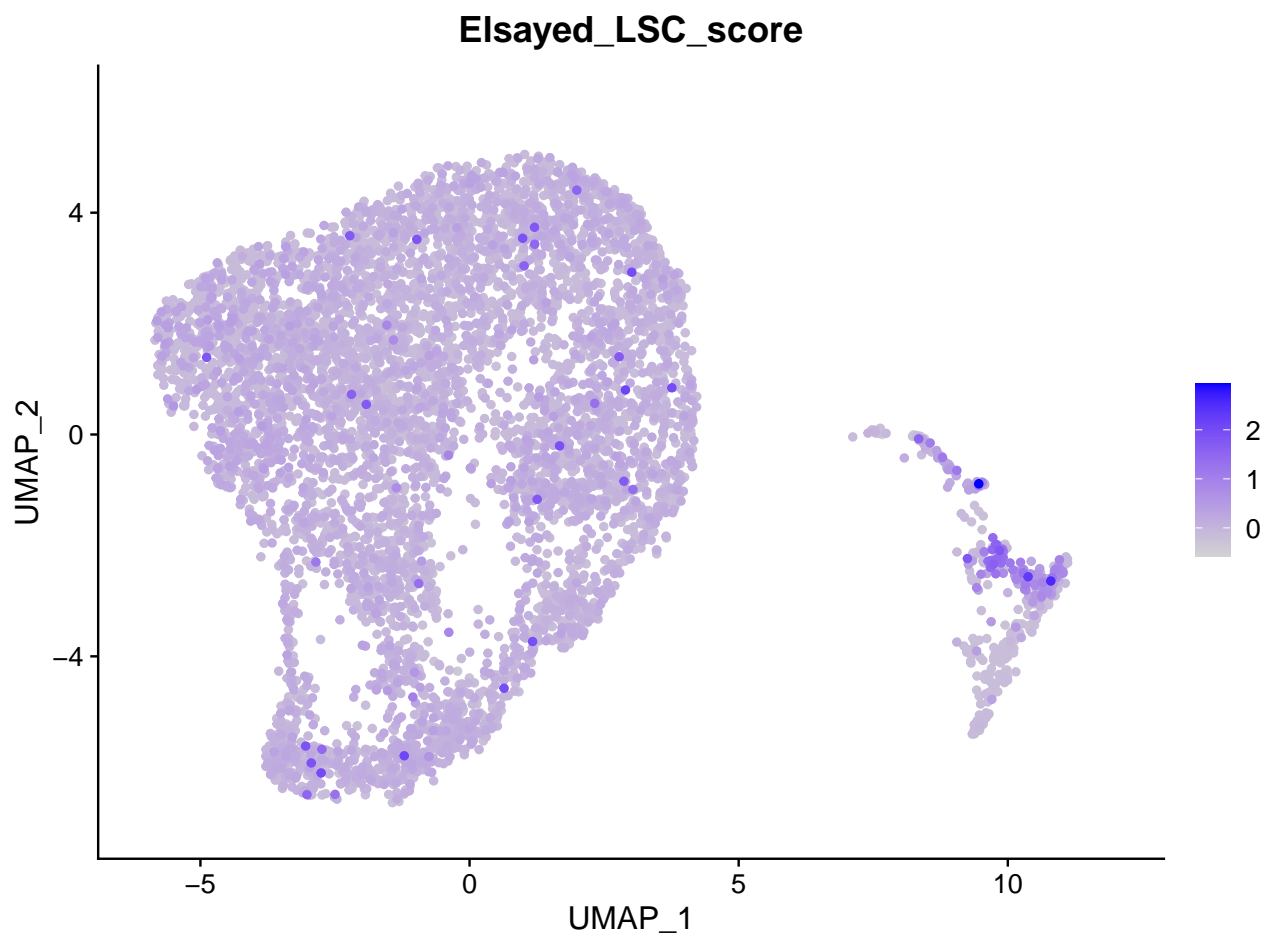


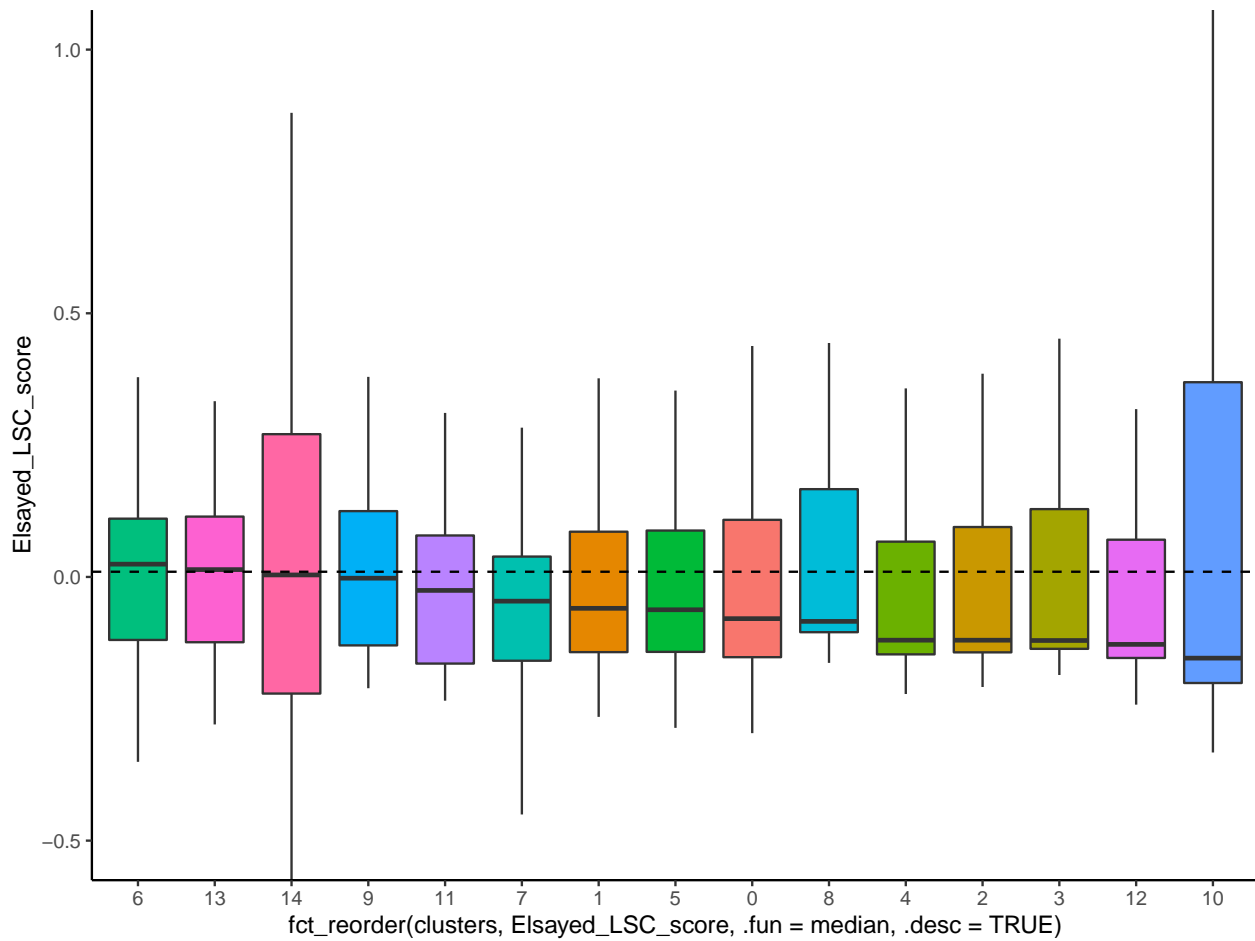




## 2. Get the LSC6 score

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

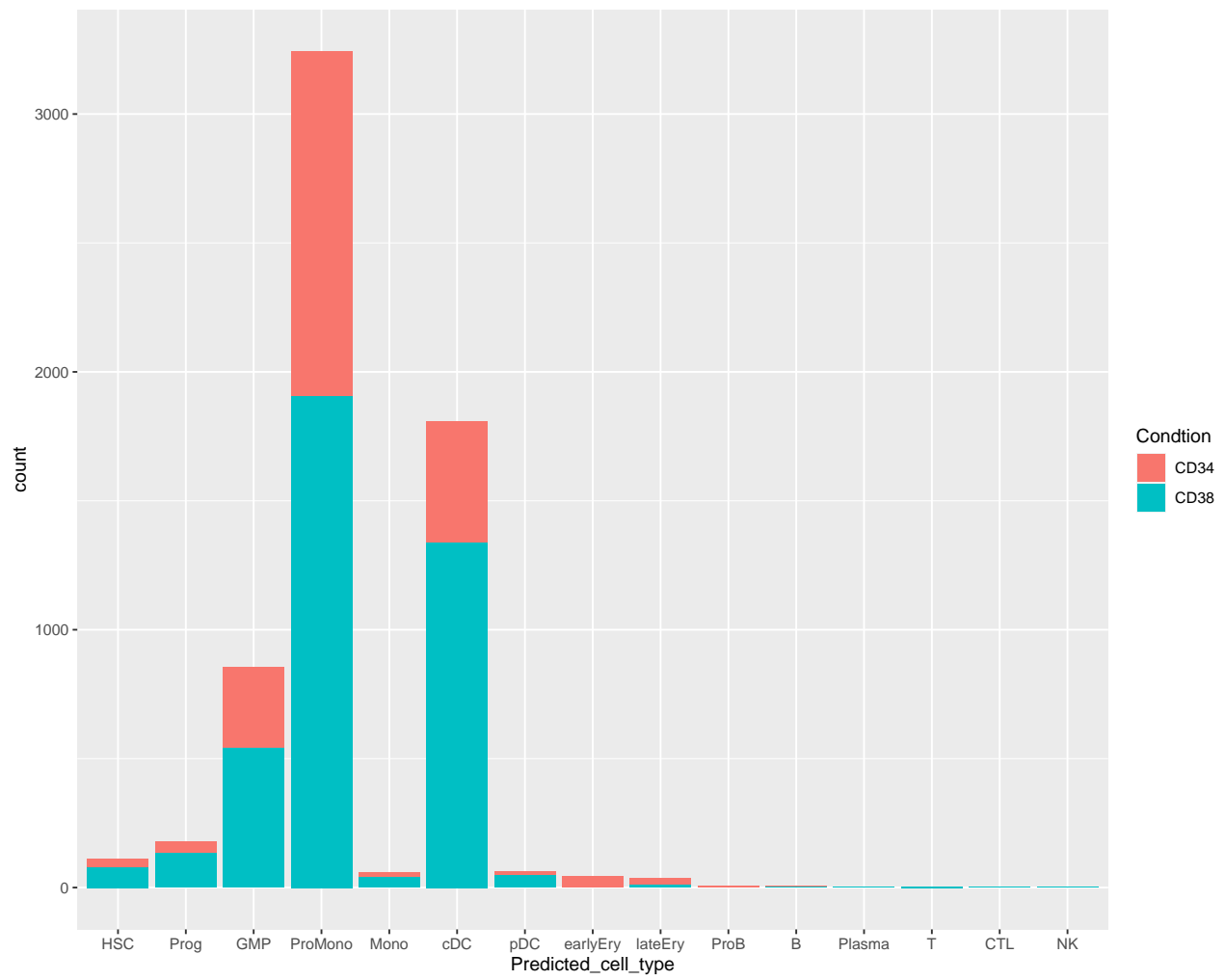


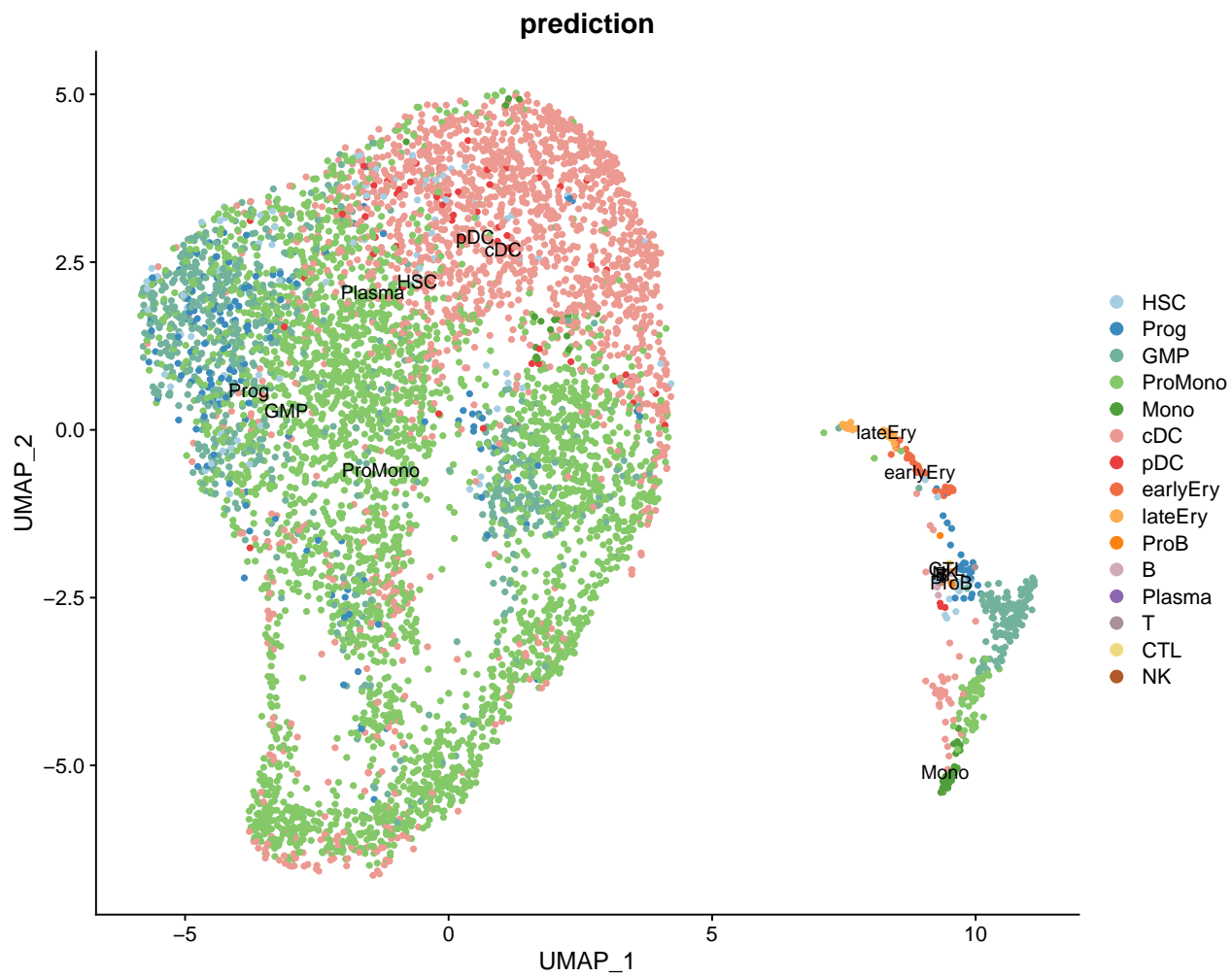


### 3. Predict the class of the cells using the markers and the expression of the BM cells form Van\_Galen paper

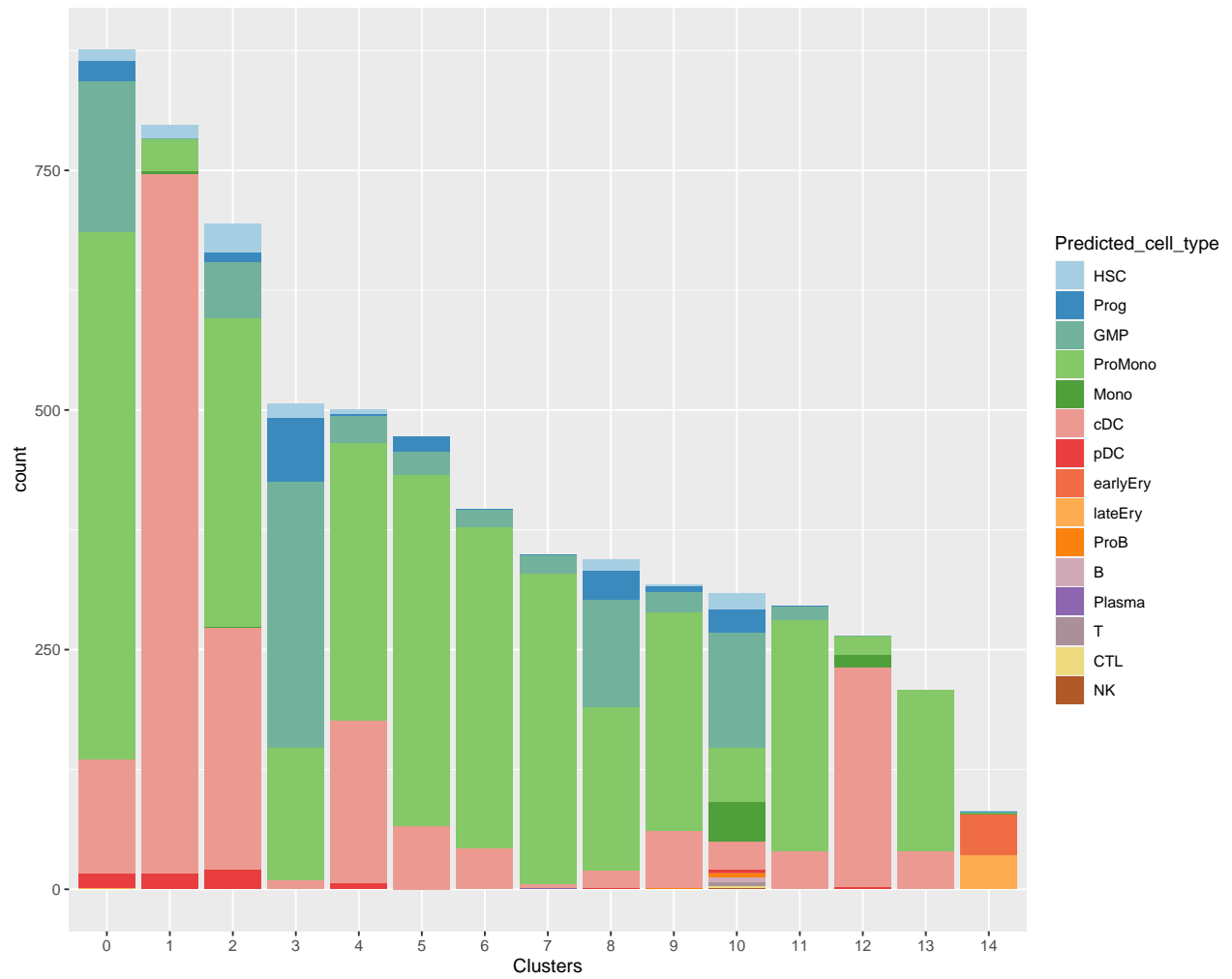
```
## Performing PCA on the provided reference using 1821 features as input.
## Projecting cell embeddings
## Finding neighborhoods
## Finding anchors
## Found 2373 anchors
## Filtering anchors
## Retained 1407 anchors
## Finding integration vectors
## Finding integration vector weights
## Predicting cell labels
##
##           HSC Prog  GMP ProMono Mono  cDC  pDC earlyEry lateEry ProB  B Plasma
##  CD34      30   45  313   1338   22  470   17      44      27   5    2      0
##  CD38      79  134  541   1906   38 1338   46       0       9    0    3      1
```

```
##
##      T   CTL   NK
## CD34   0     0     0
## CD38   4     2     1
```









#### 4. Project the predictions from Velten onto our UMAP

