

# AML4\_Rx

jtrincado

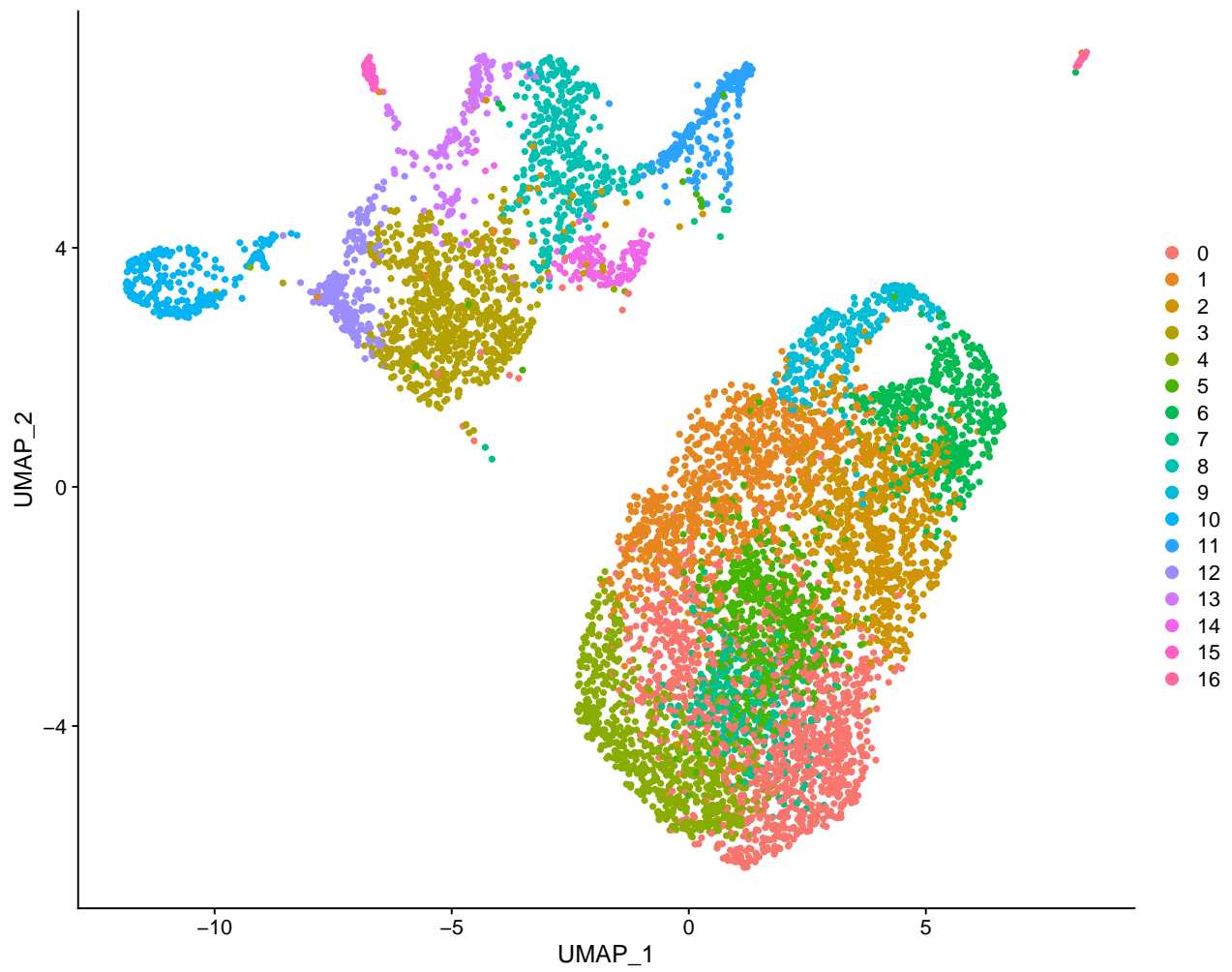
2022-02-08 16:22:59

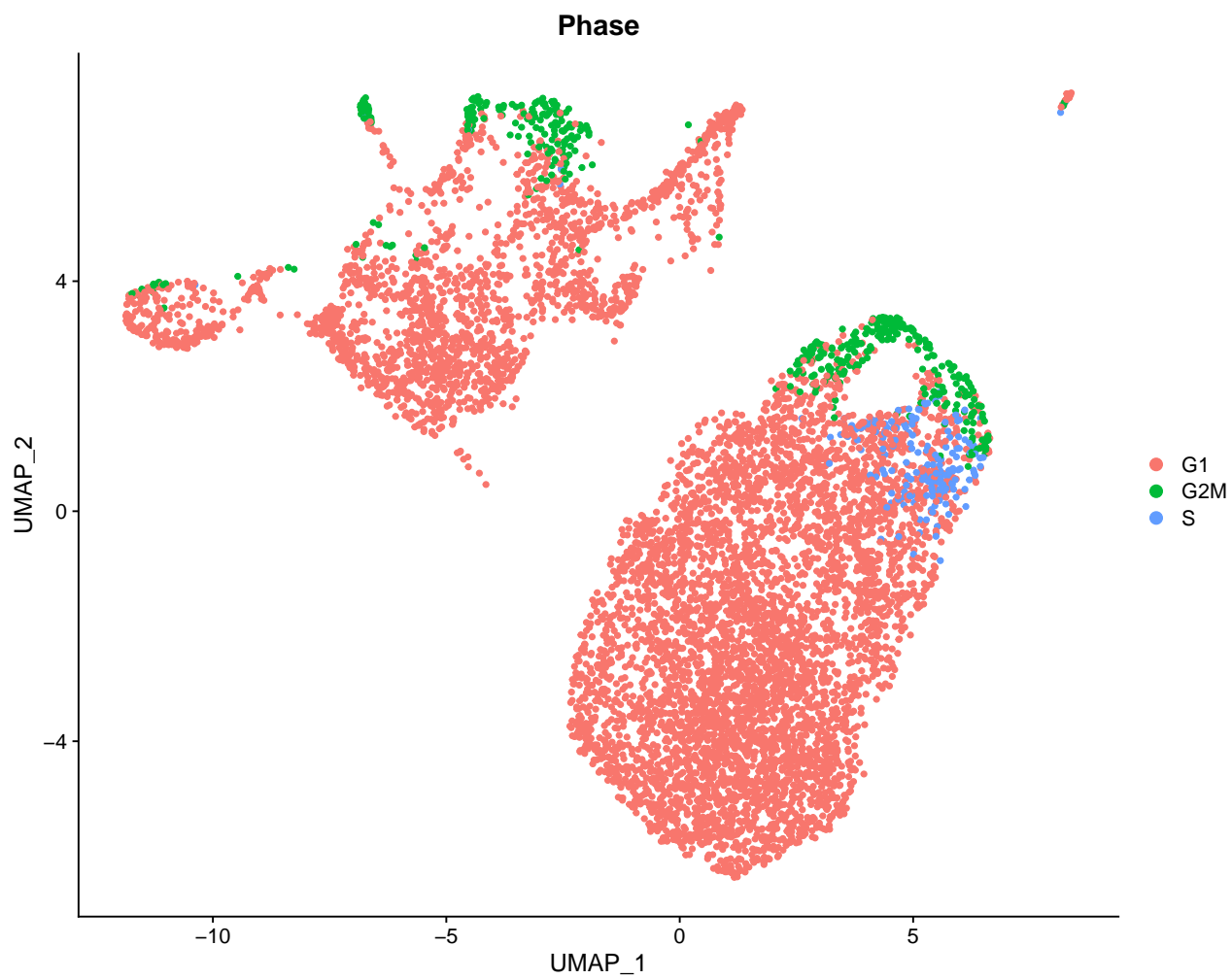
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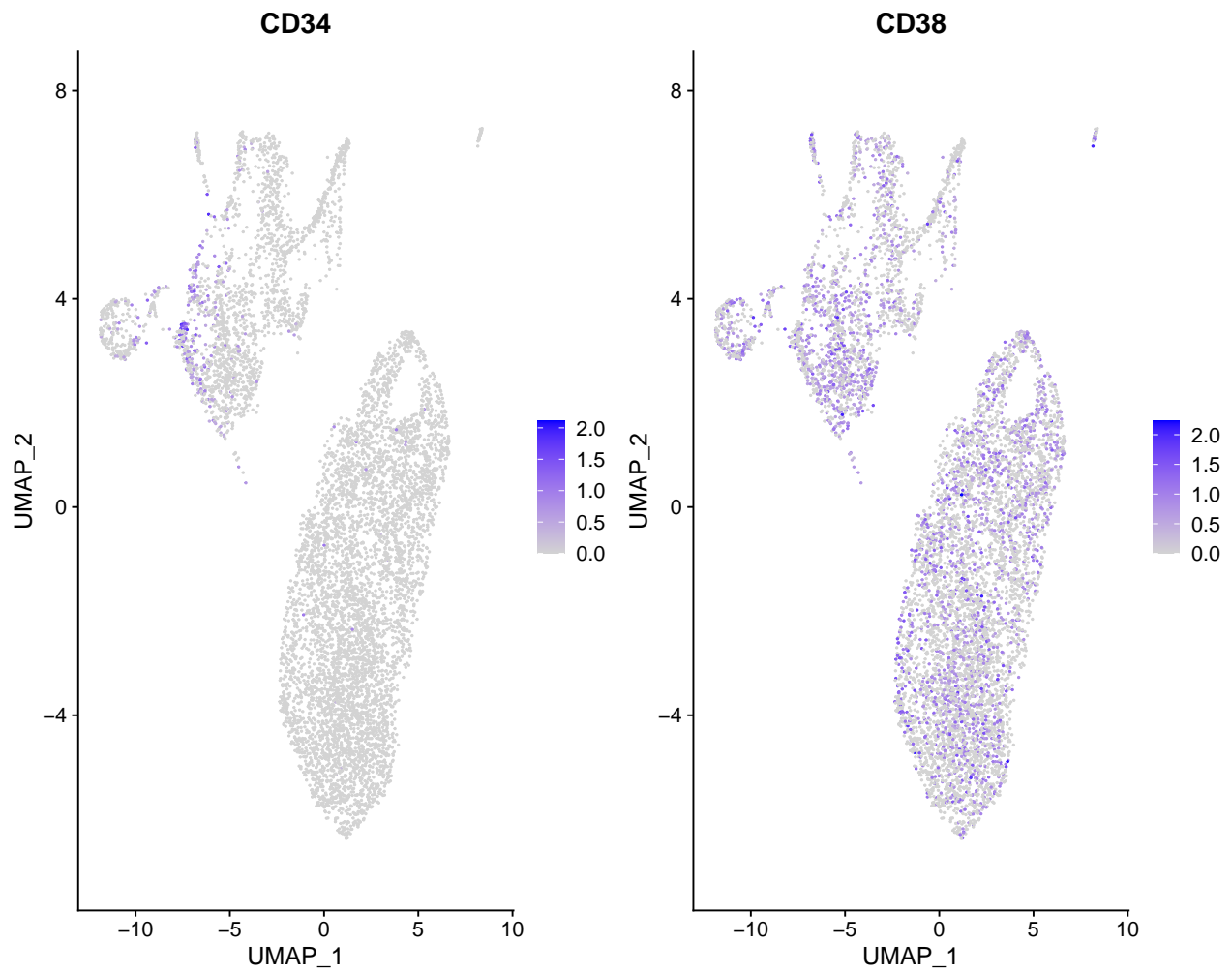
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## 1. Put together both 34 and 38 libraries. Apply QC and dimensionality reduction.

```
## 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
```

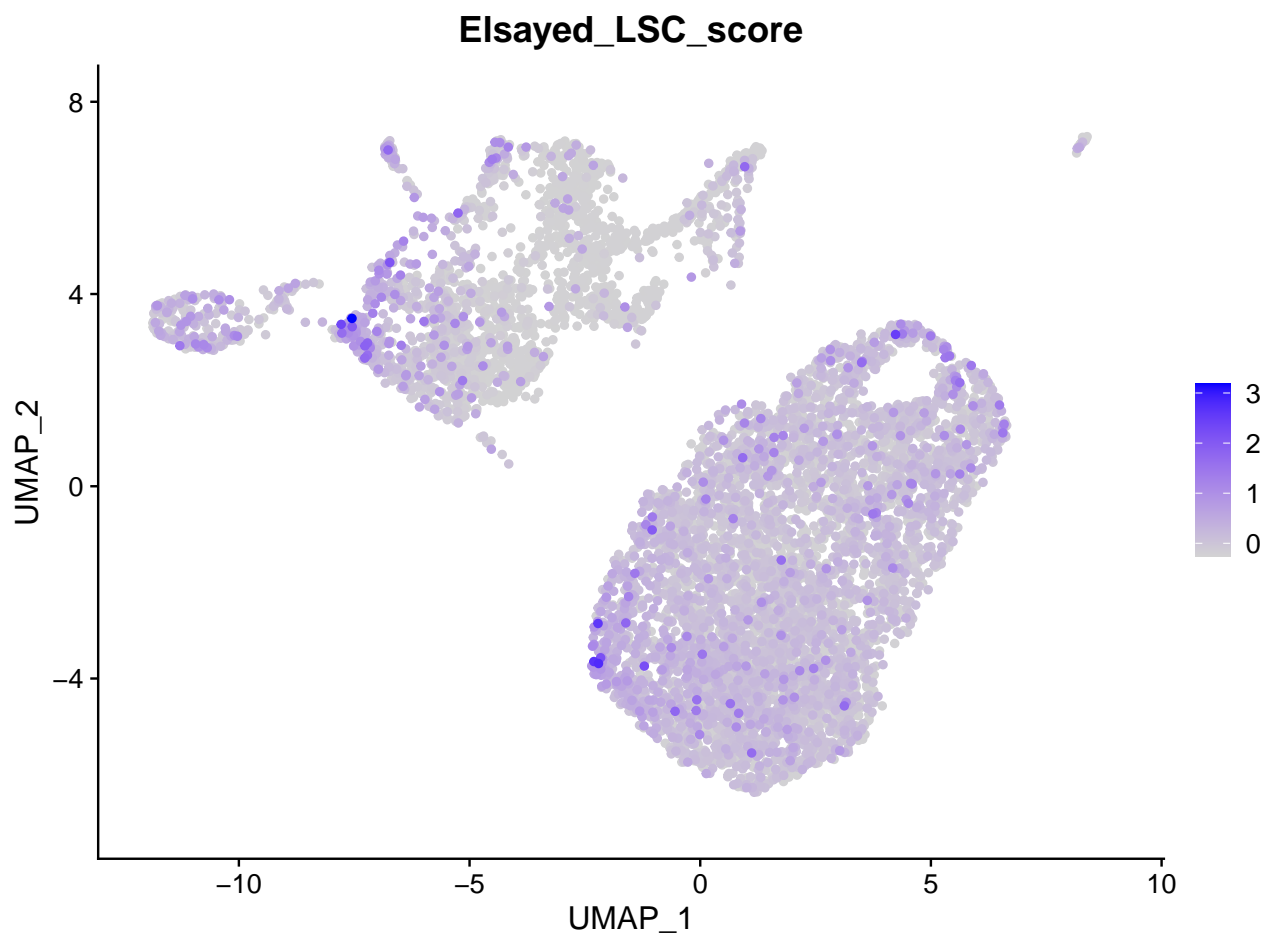


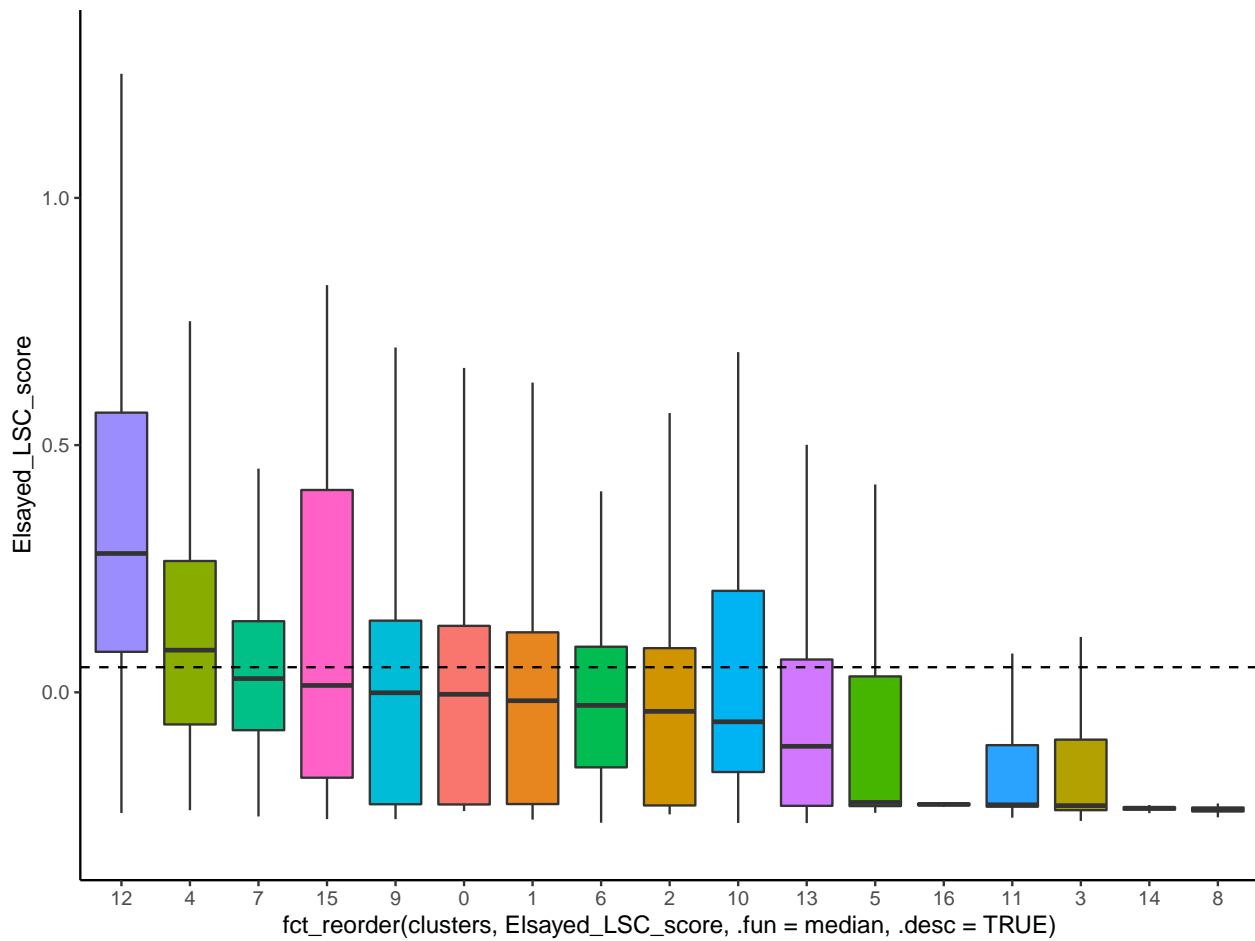




## 2. Get the LSC6 score

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

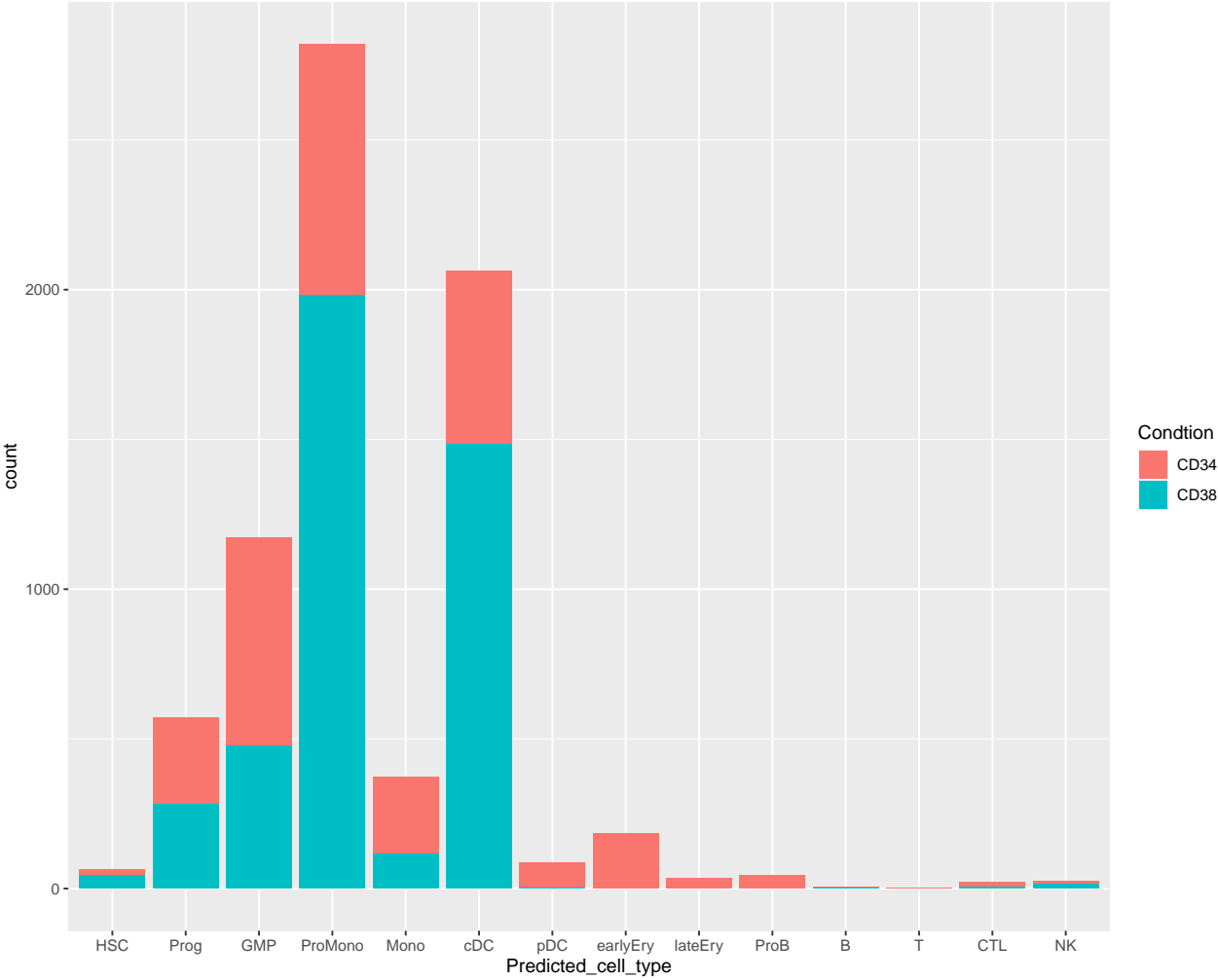


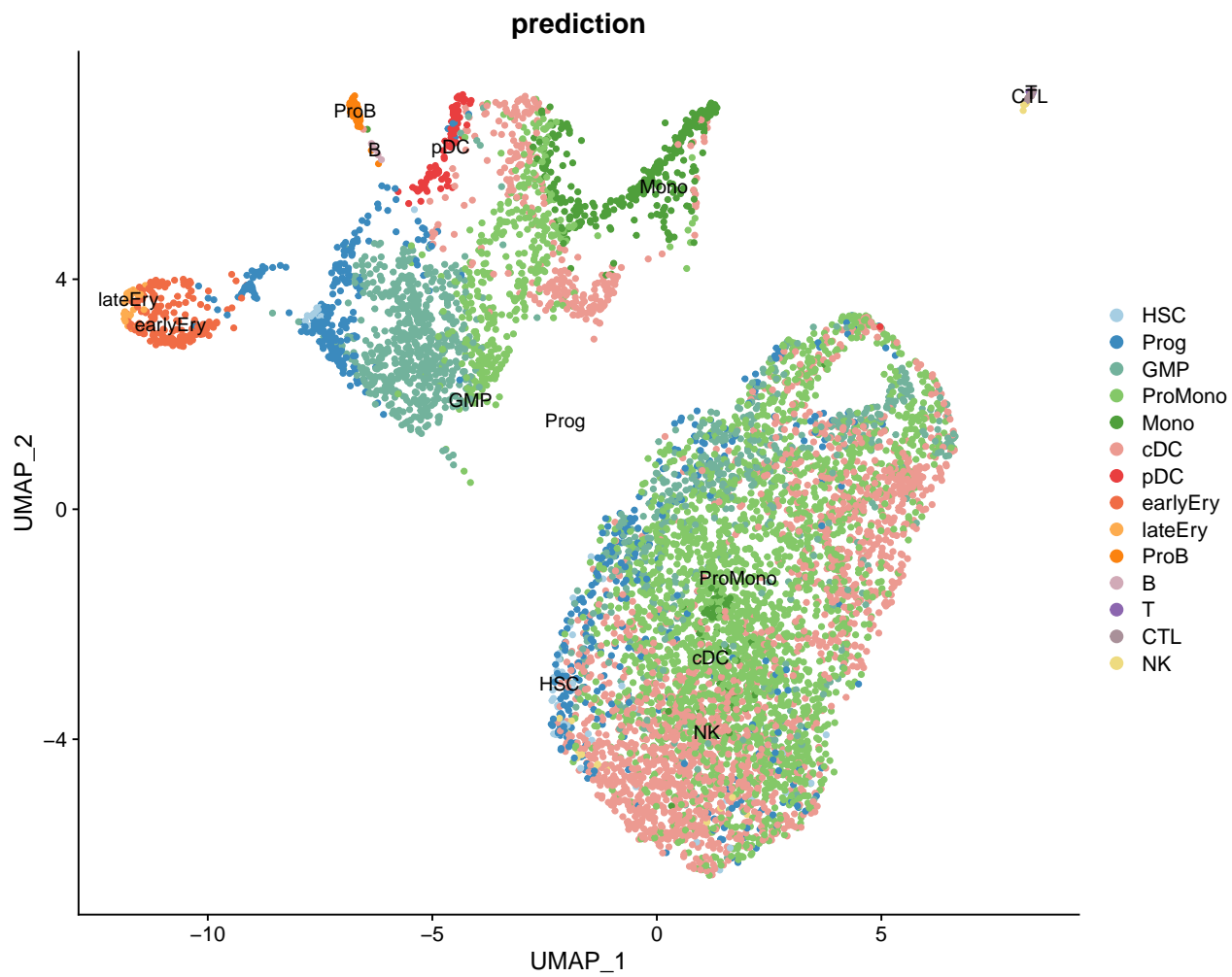


### 3. Predict the class of the cells using the markers and the expression of the BM cells form Van\_Galen paper

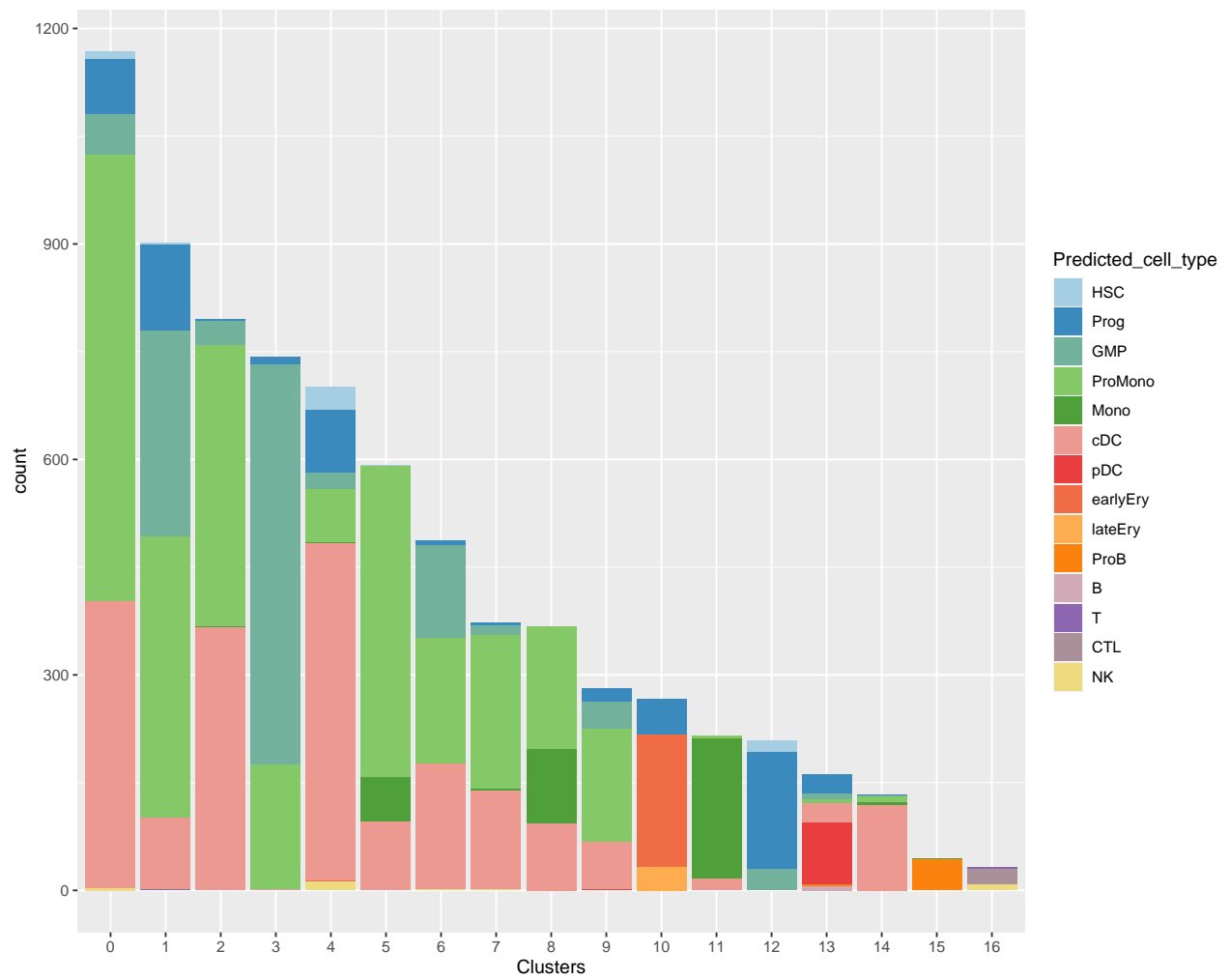
```
## Performing PCA on the provided reference using 1821 features as input.
## Projecting cell embeddings
## Finding neighborhoods
## Finding anchors
## Found 4073 anchors
## Filtering anchors
## Retained 3090 anchors
## Finding integration vectors
## Finding integration vector weights
## Predicting cell labels
##
##           HSC Prog  GMP ProMono Mono  cDC  pDC earlyEry lateEry ProB  B Plasma
##  CD34      21  289  698    840  257  579   87    185    33   45    3     0
##  CD38      43  282  475   1981  115 1485    1     0     0    0    3     0
```

##				
##		T	CTL	NK
##	CD34	3	16	9
##	CD38	0	6	16

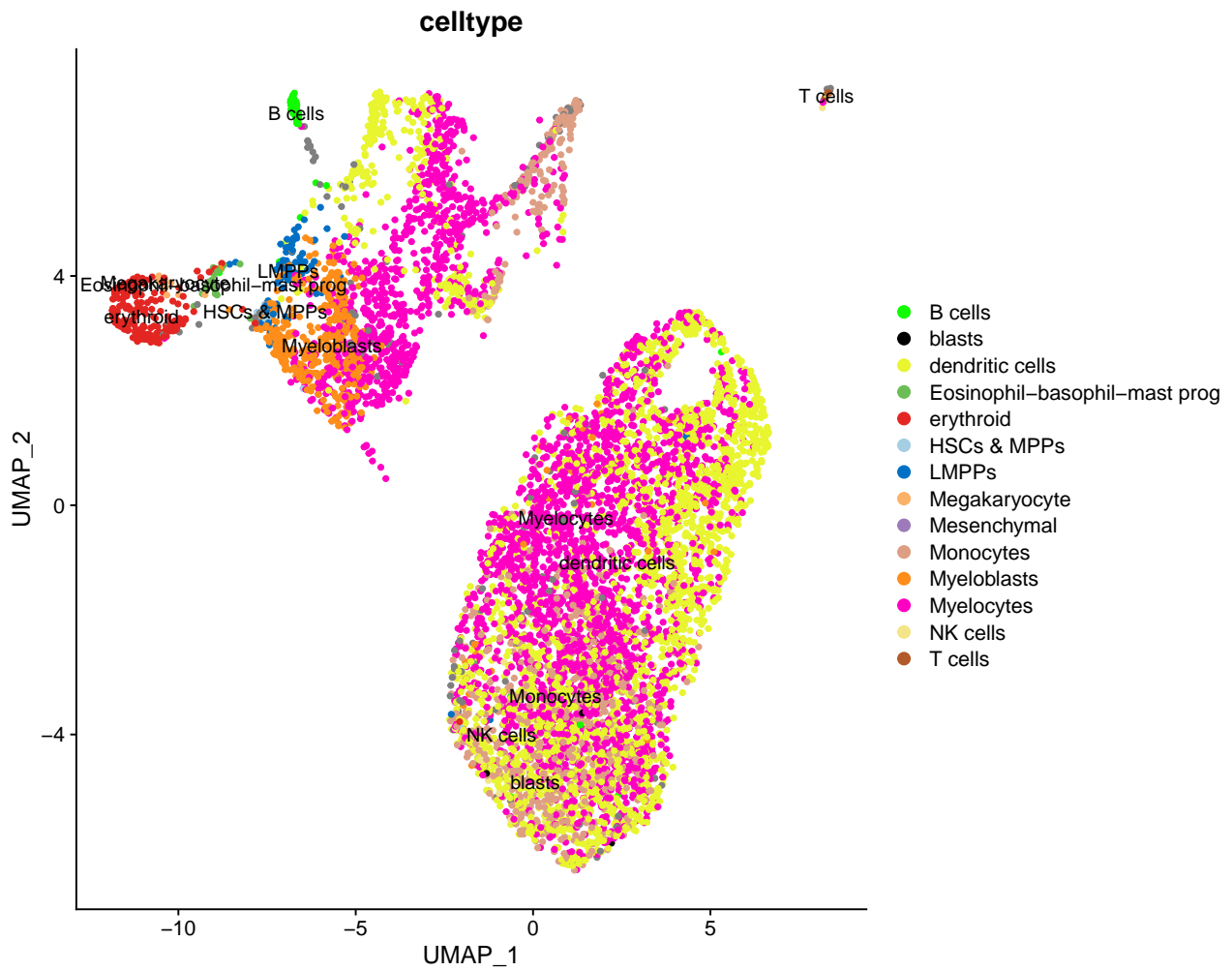


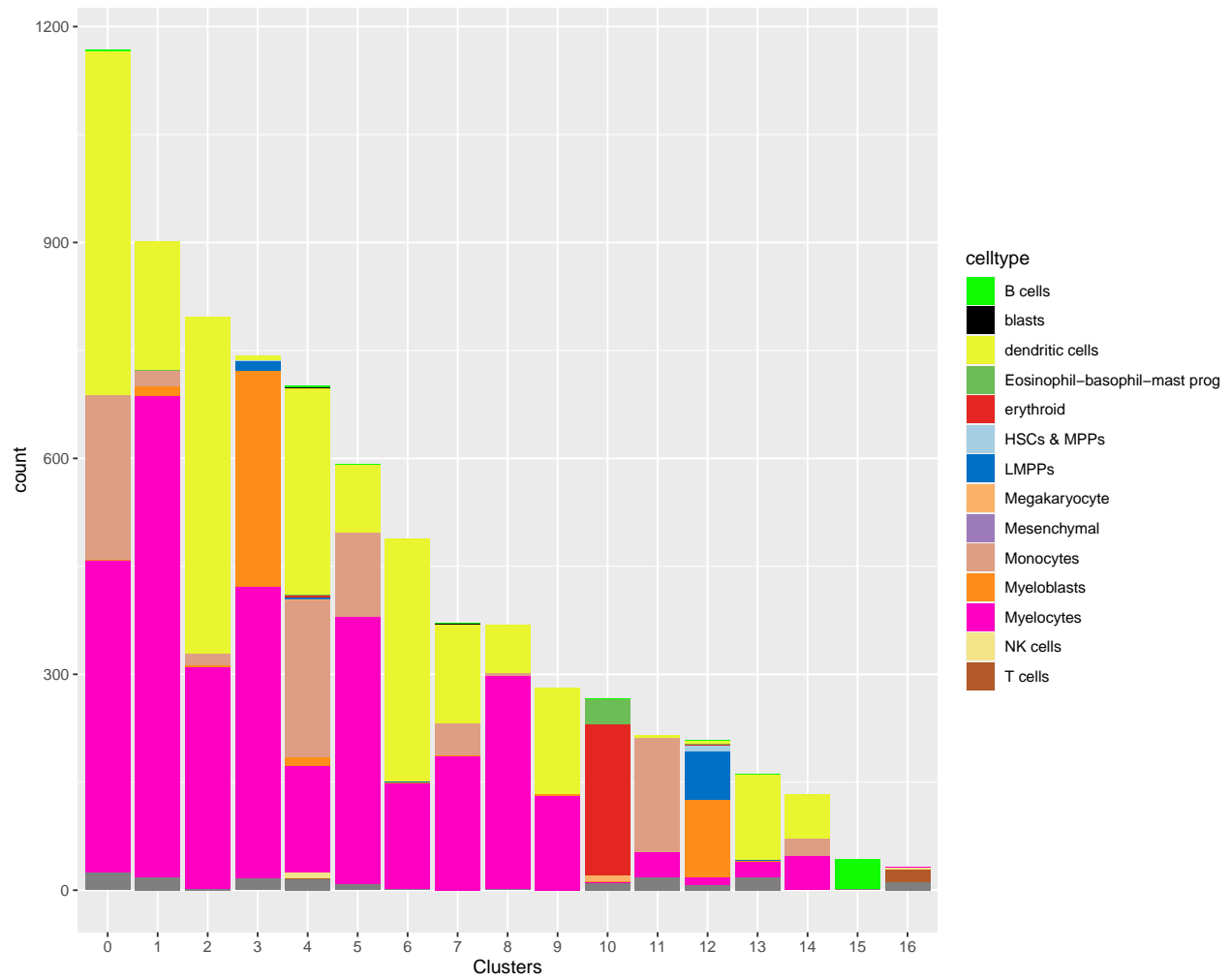






#### 4. Project the predictions from Velten onto our UMAP





Cluster 12 seems the one with greater LSC6 score. Cluster 4 is above the D10, but there are more HSC predicted on cluster 12