

AML8_Rx

jtrincado

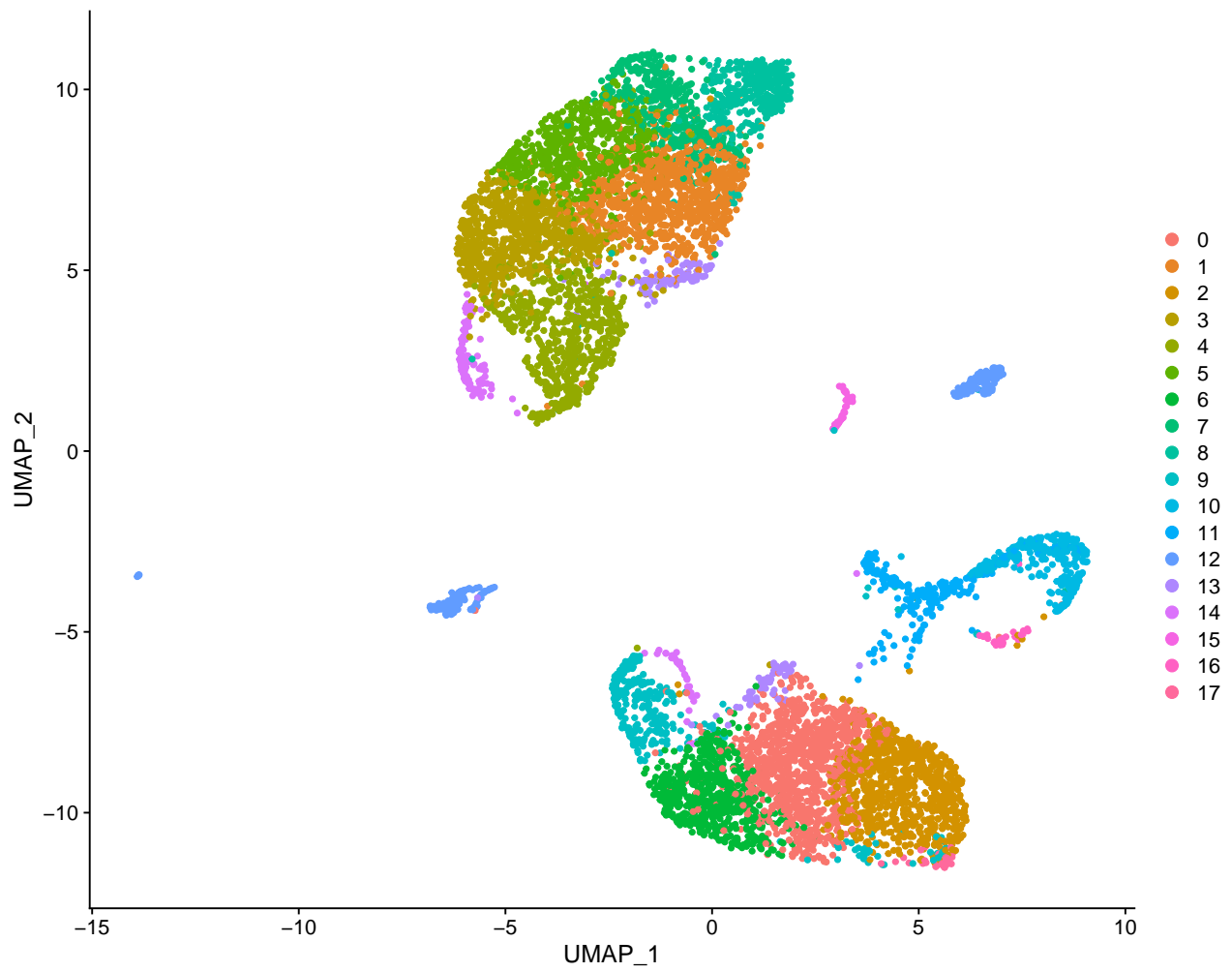
2022-02-09 10:02:45

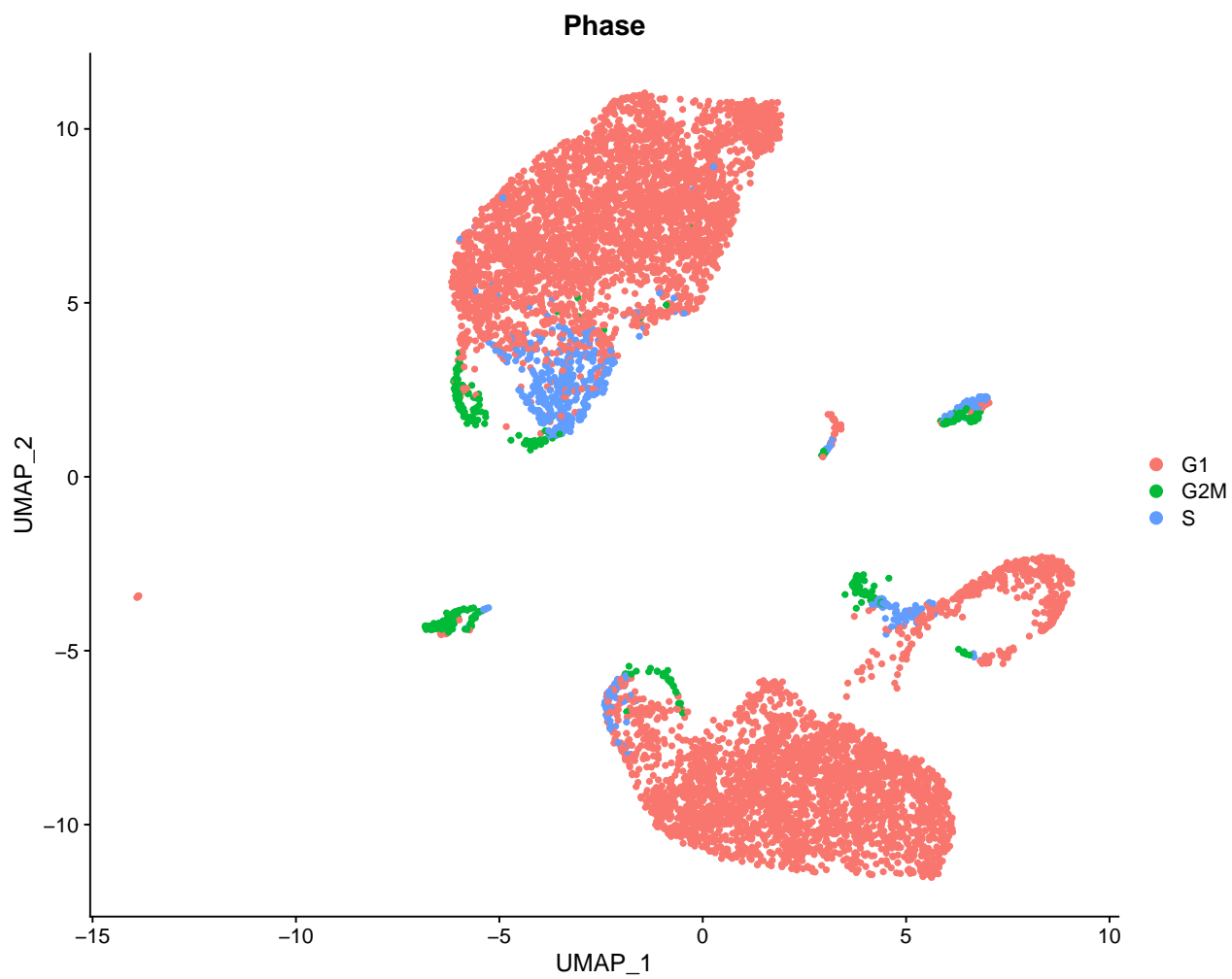
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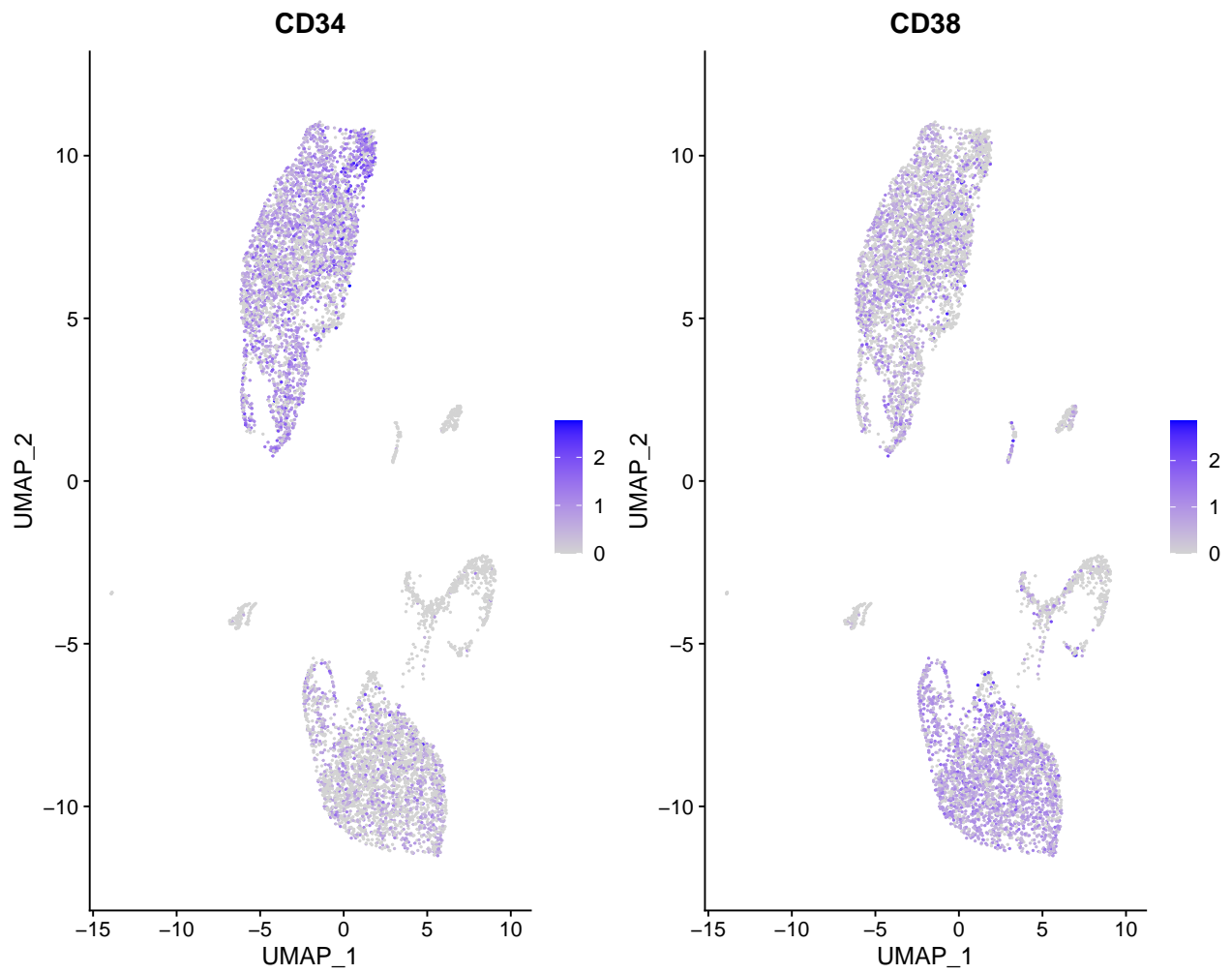
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1. Put together both 34 and 38 libraries. Apply QC and dimensionality reduction.

```
## 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
```

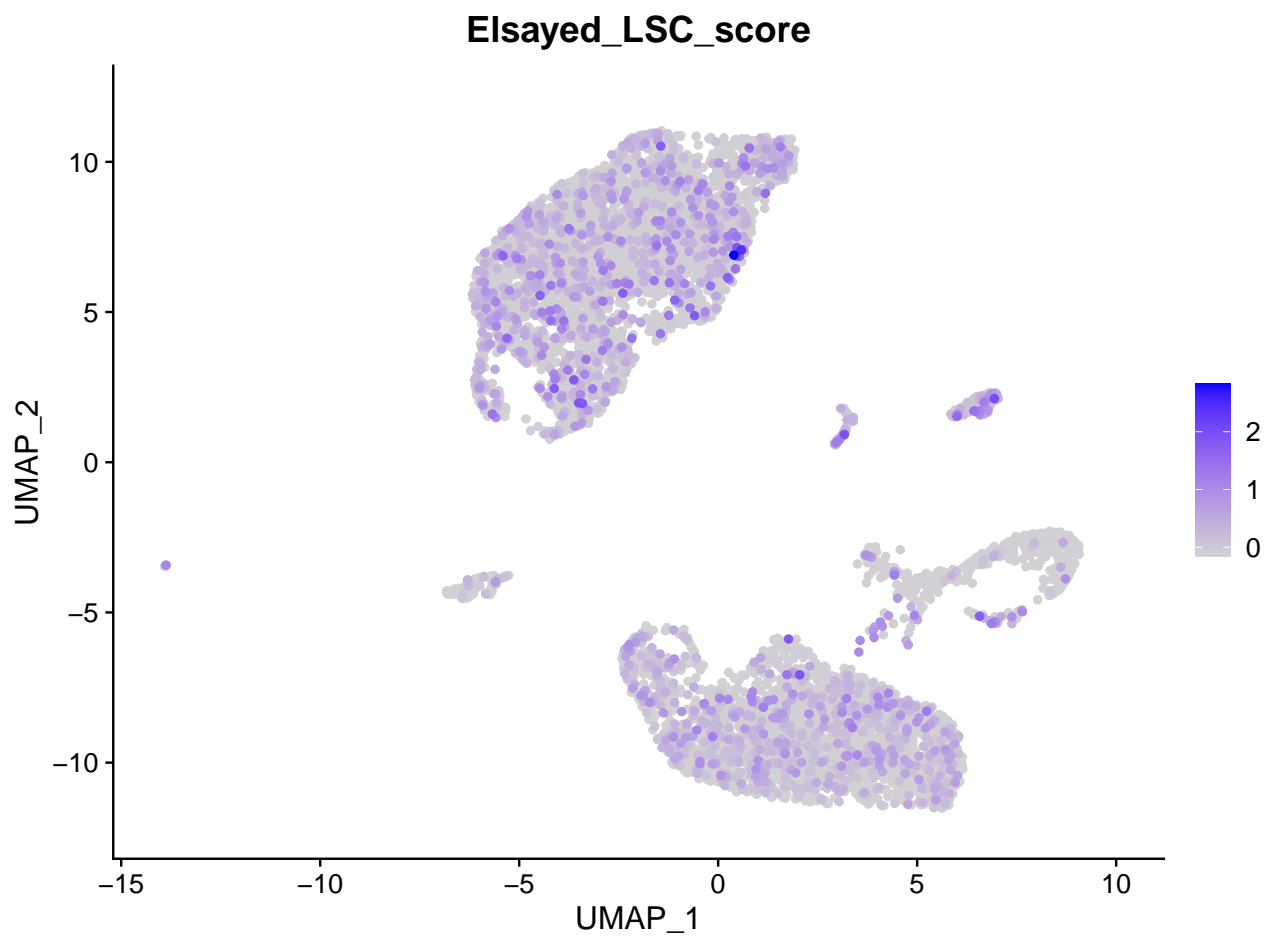


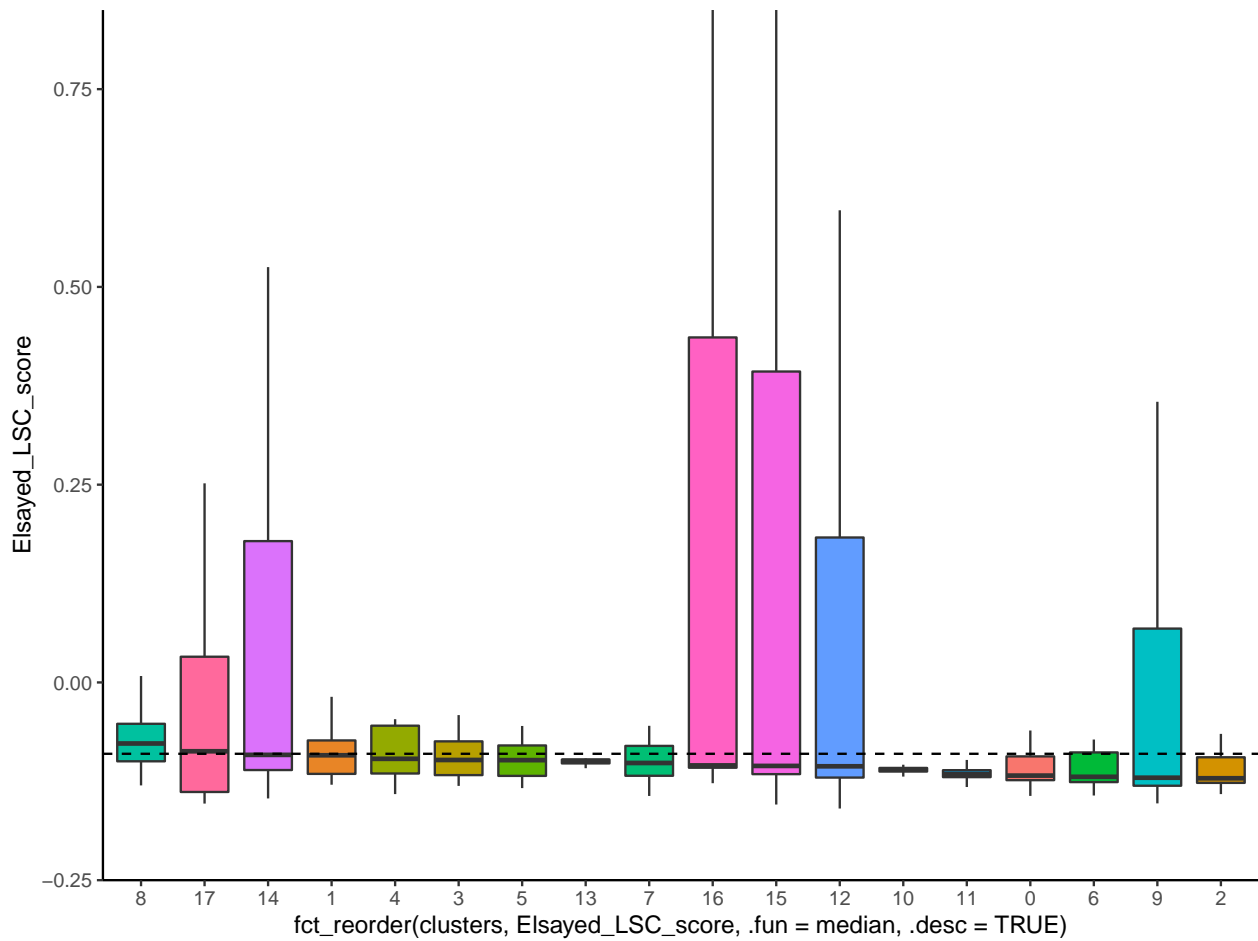




2. Get the LSC6 score

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

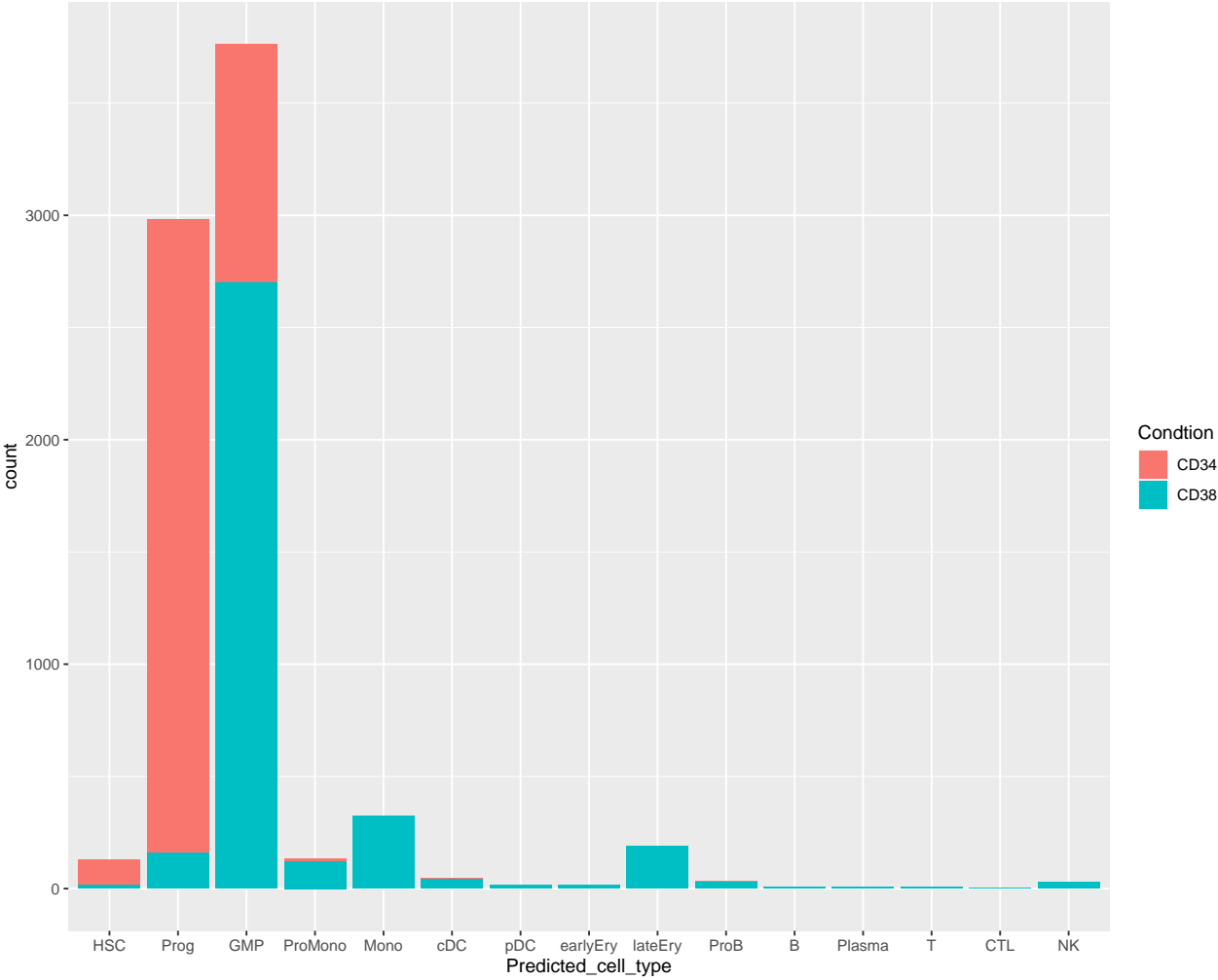


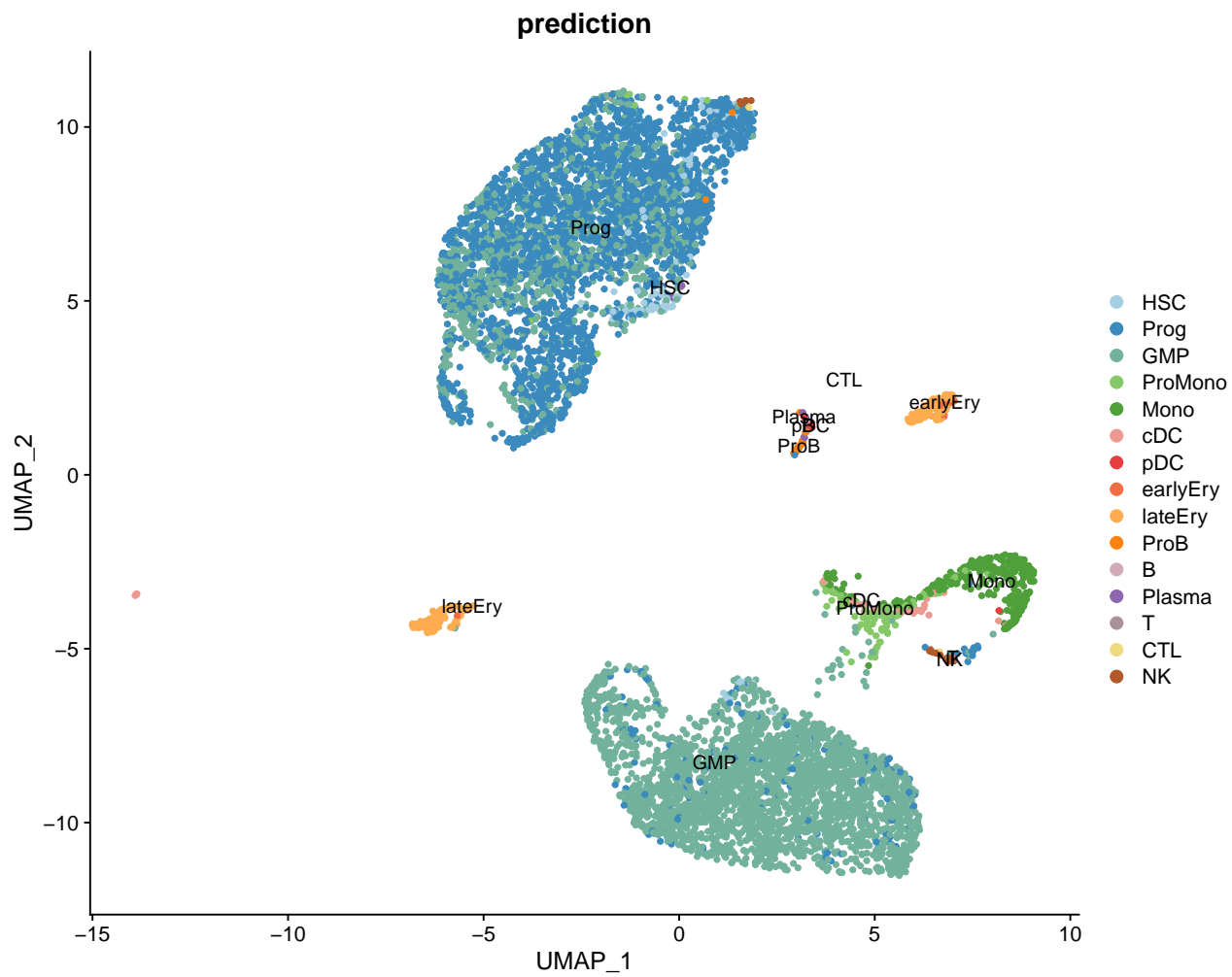


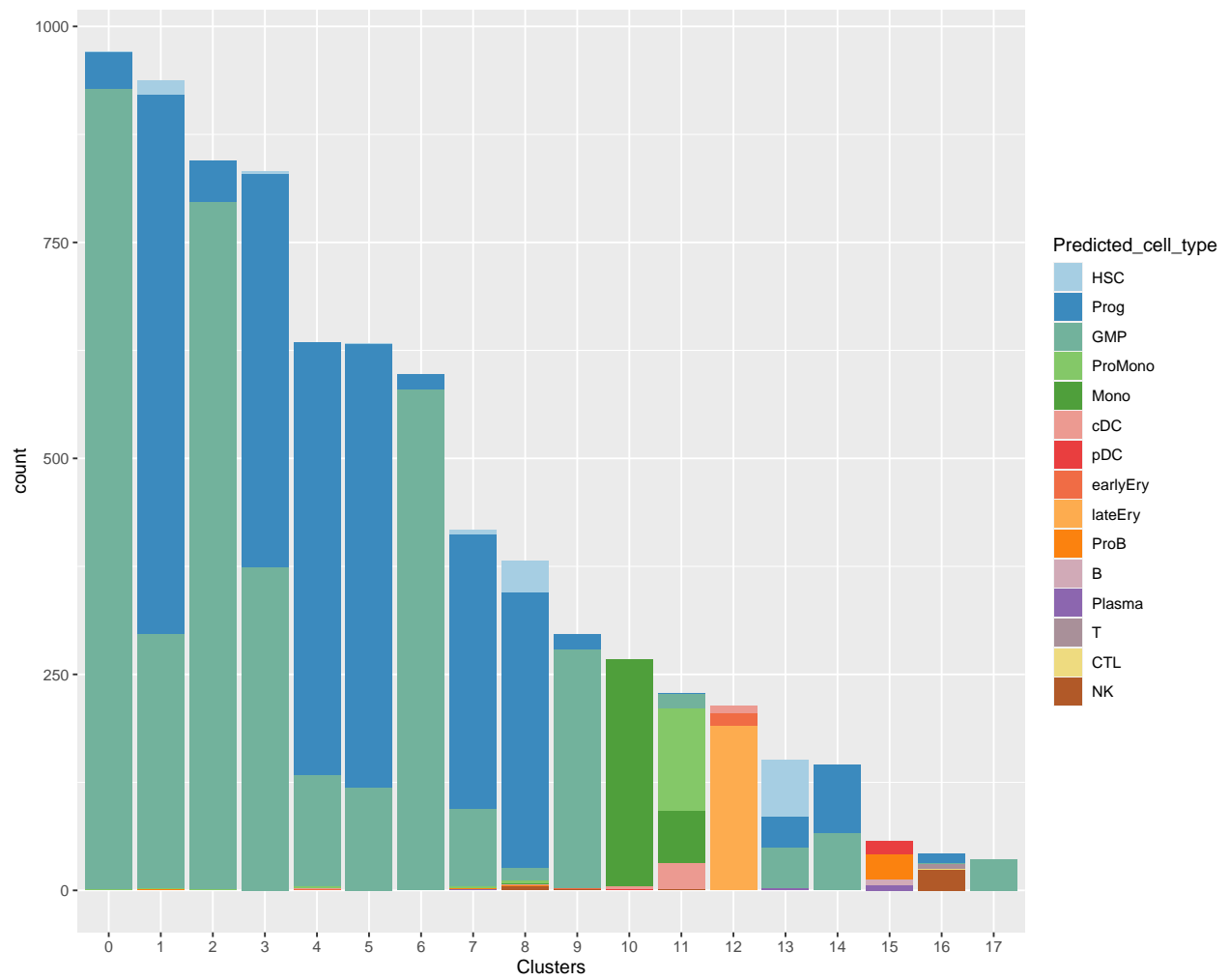
3. Predict the class of the cells using the markers and the expression of the BM cells form Van_Galen paper

```
## Performing PCA on the provided reference using 1821 features as input.
## Projecting cell embeddings
## Finding neighborhoods
## Finding anchors
## Found 3142 anchors
## Filtering anchors
## Retained 2243 anchors
## Finding integration vectors
## Finding integration vector weights
## Predicting cell labels
##
##           HSC Prog  GMP ProMono Mono  cDC  pDC earlyEry lateEry ProB  B Plasma
##  CD34   113 2826 1066      9    0    4    0      1      0    4    0    2
##  CD38    17  157 2698     122 323   42   16     17     190  29    6    7
```

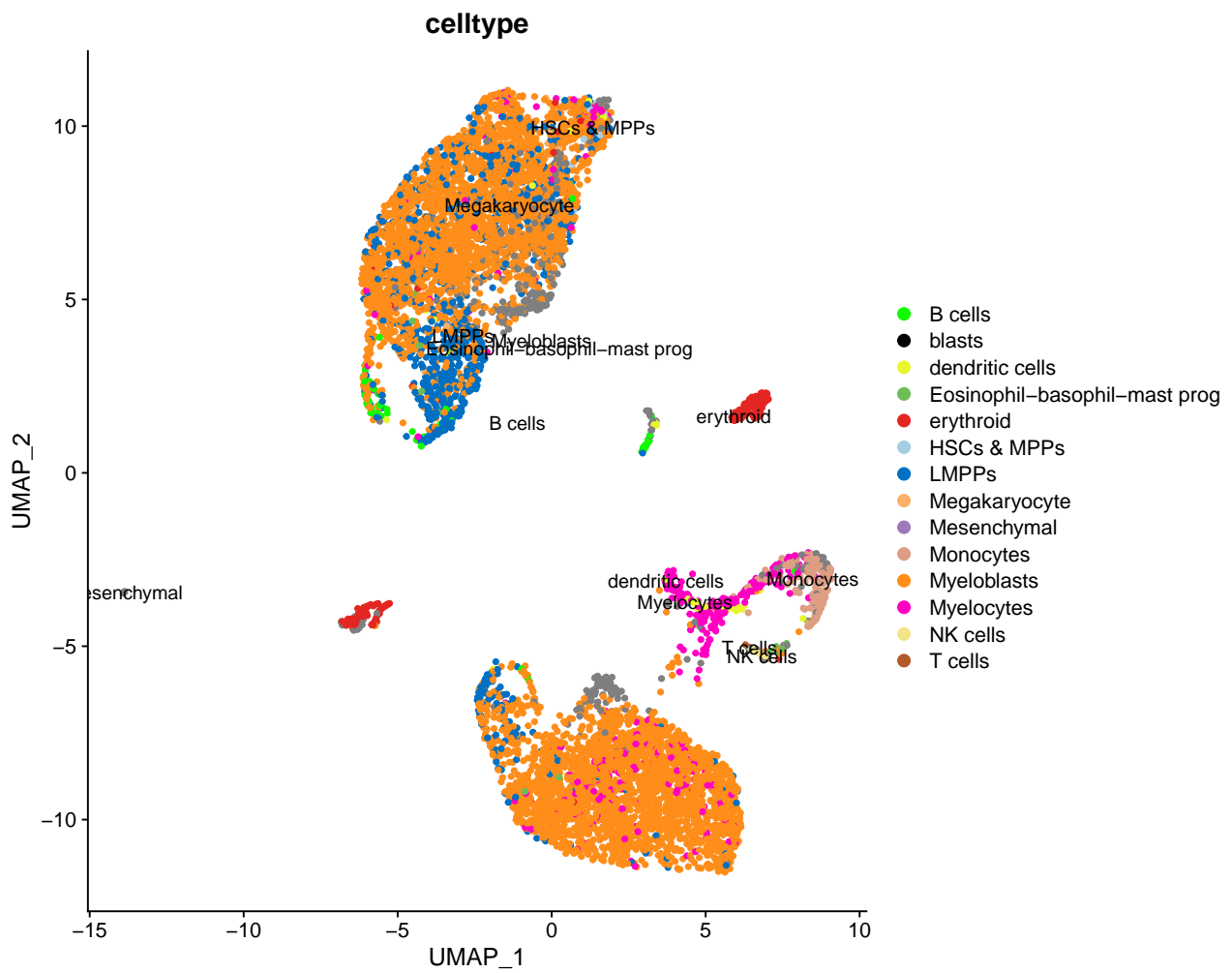
##		T	CTL	NK
##	CD34	0	1	0
##	CD38	5	1	30

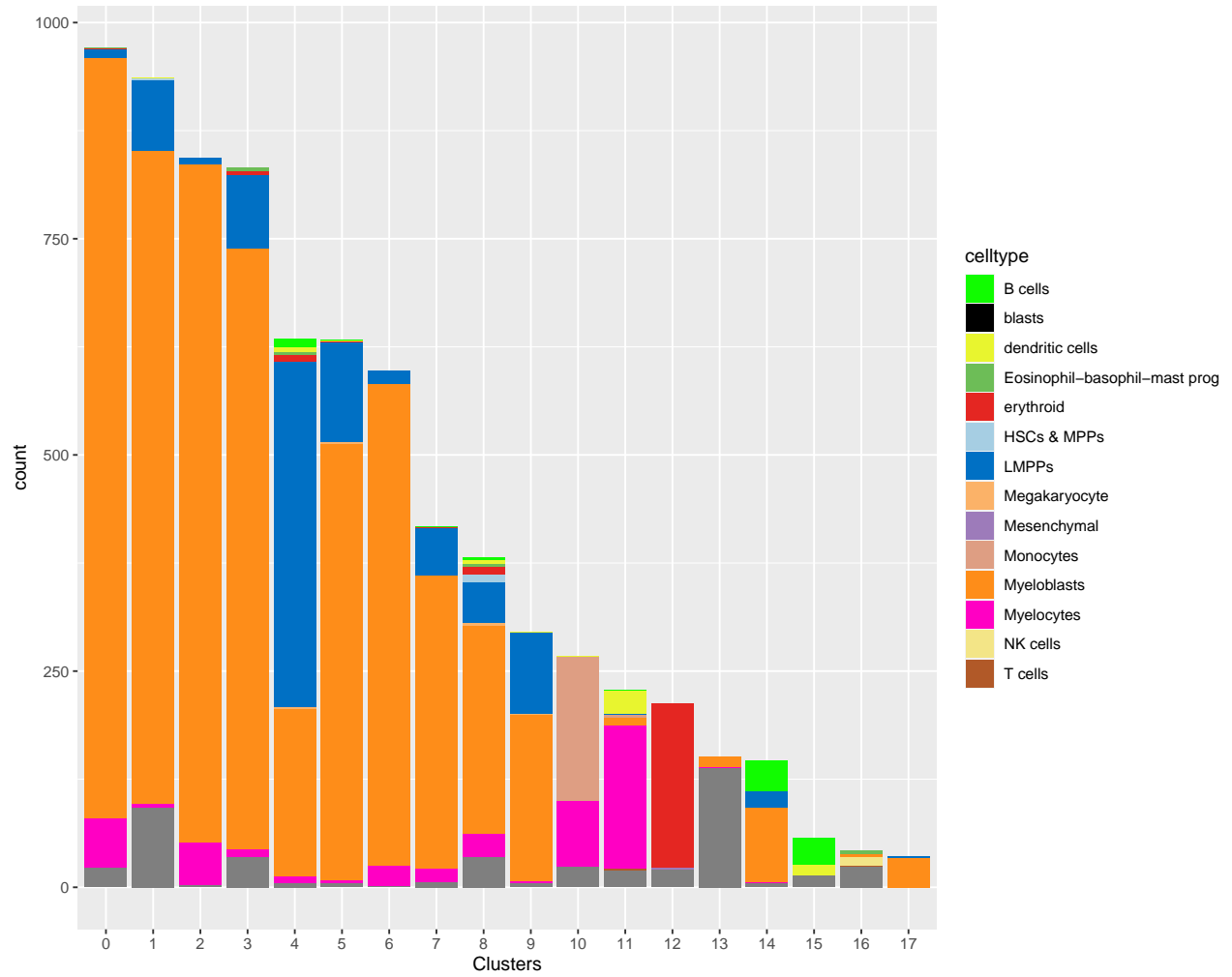






4. Project the predictions from Velten onto our UMAP





Cluster 8 seems the one with the highest LSC6 score. Cluster 17 also seems to be over the threshold, but there is not HSC predicted cells in the cluster. We propose cluster 8 as the one with LSC enrichment