

AML4_Dx

jtrincado

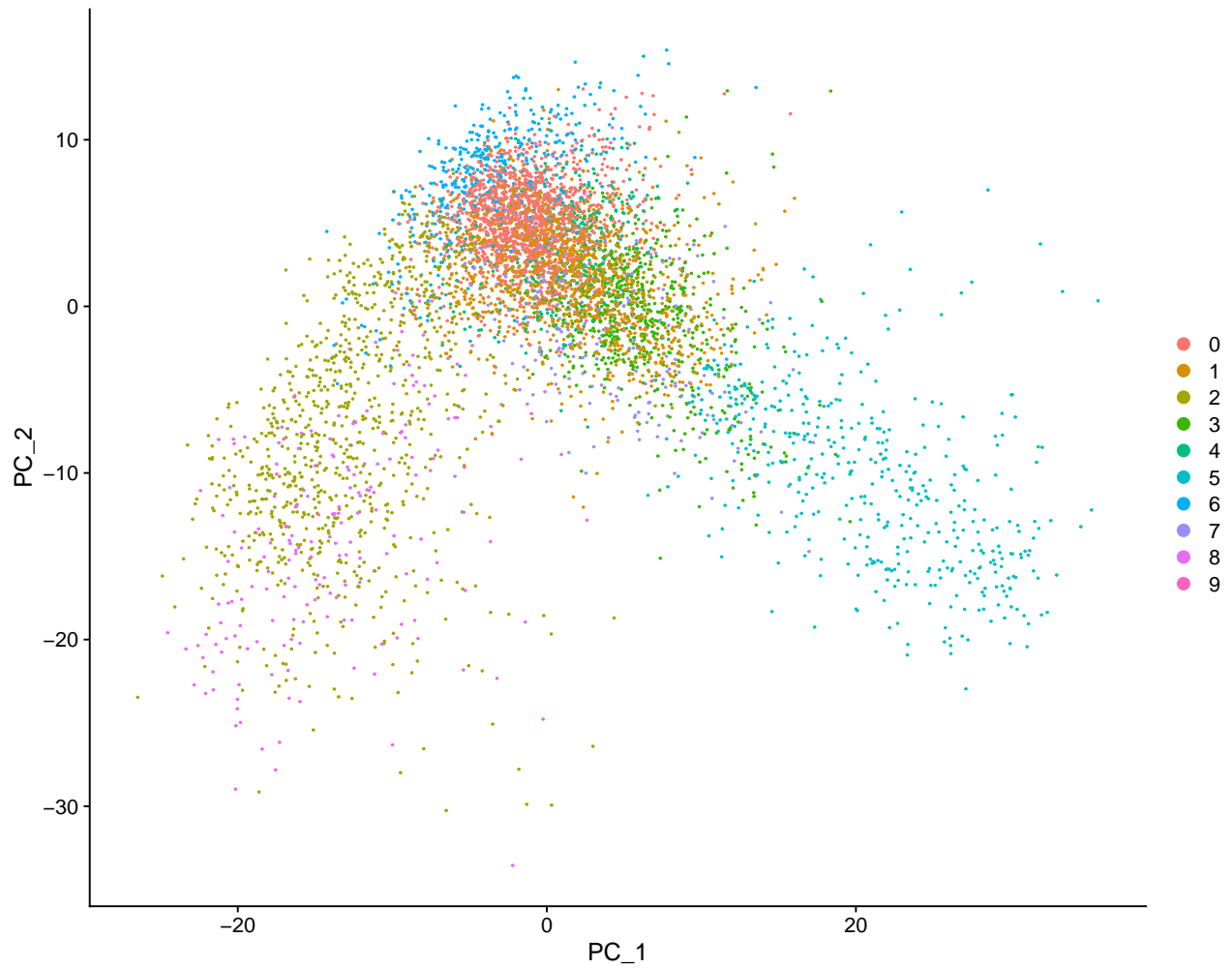
2022-02-08 15:43:12

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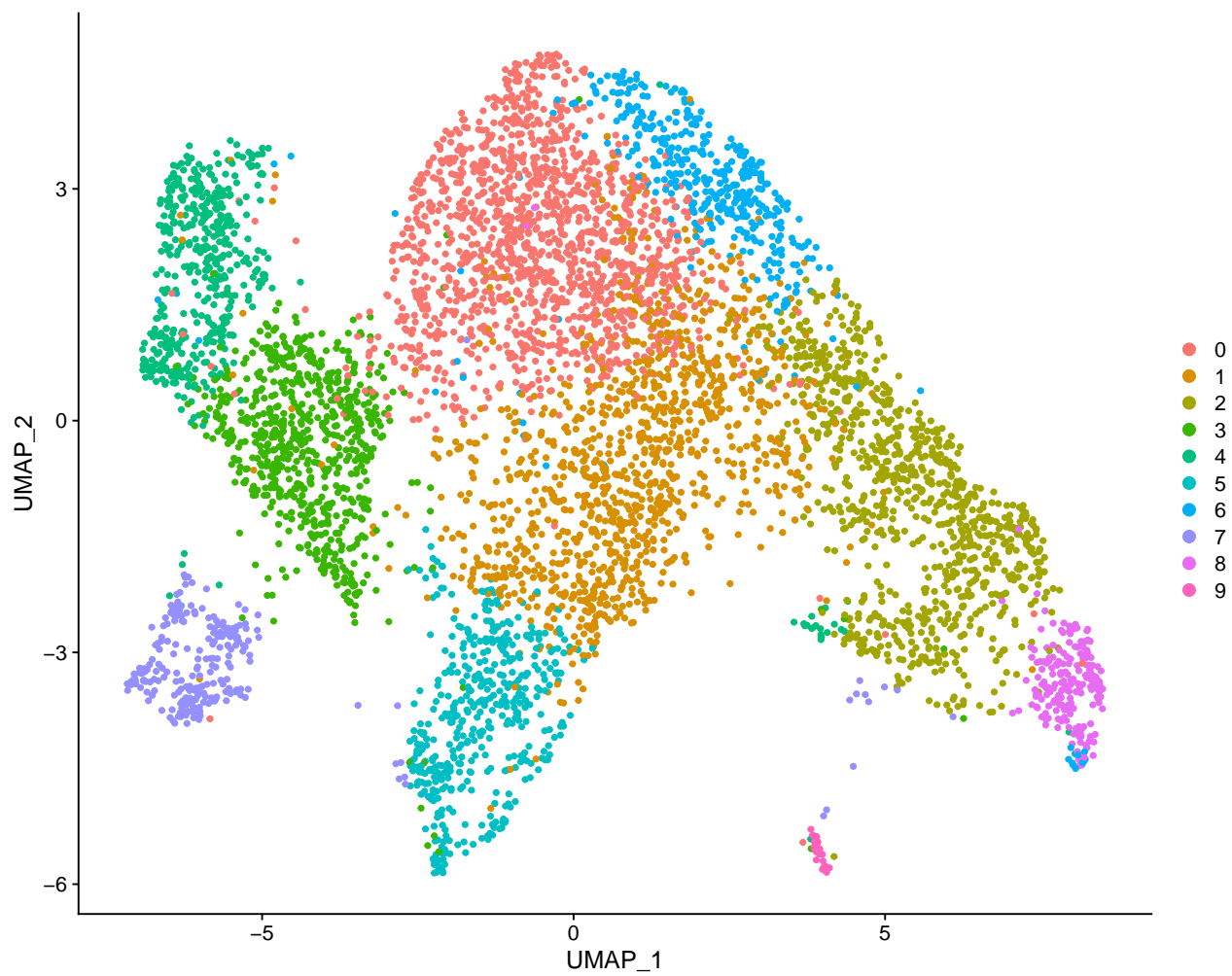
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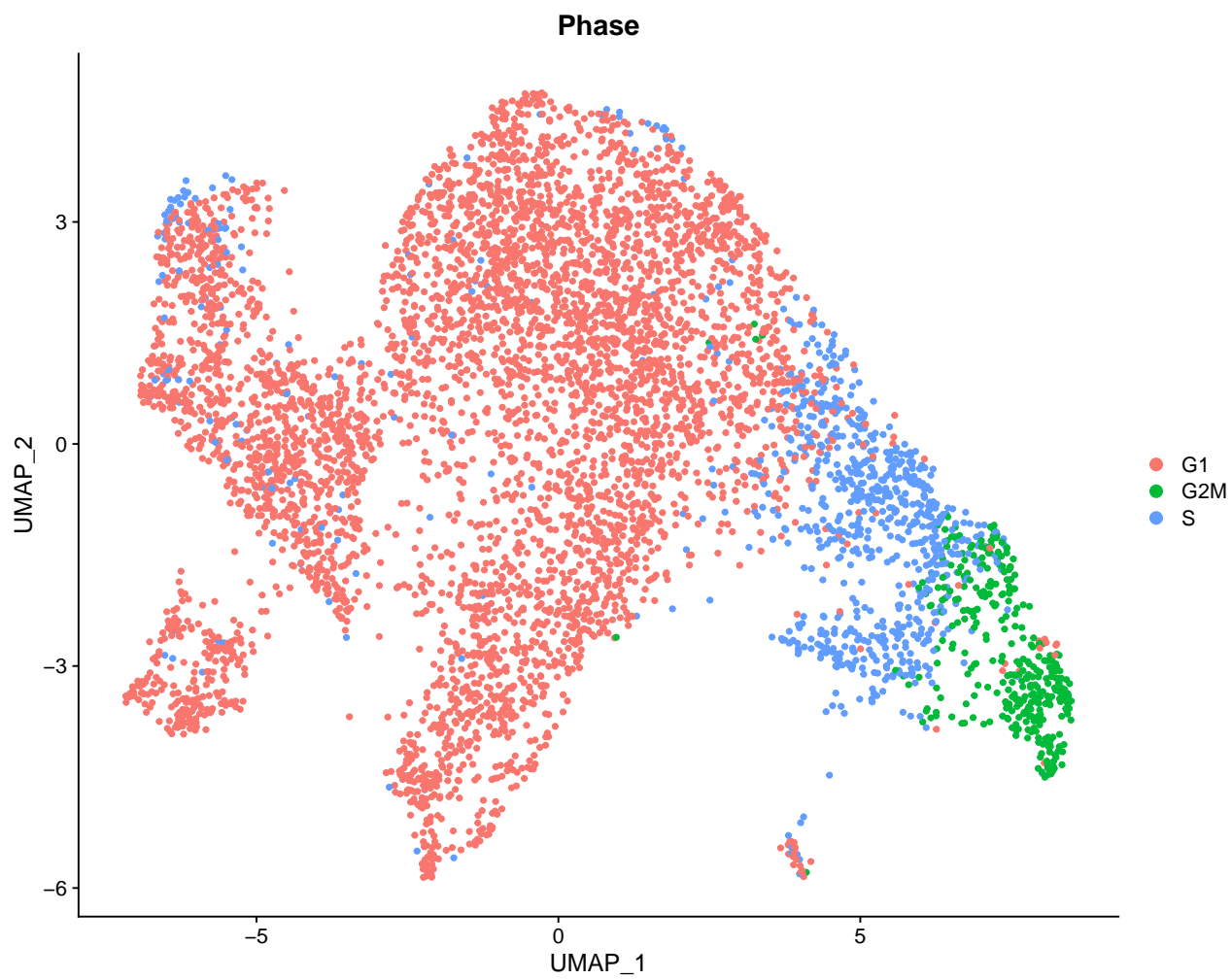
1. Put together both 34 and 38 libraries. Apply QC and dimensionality reduction.

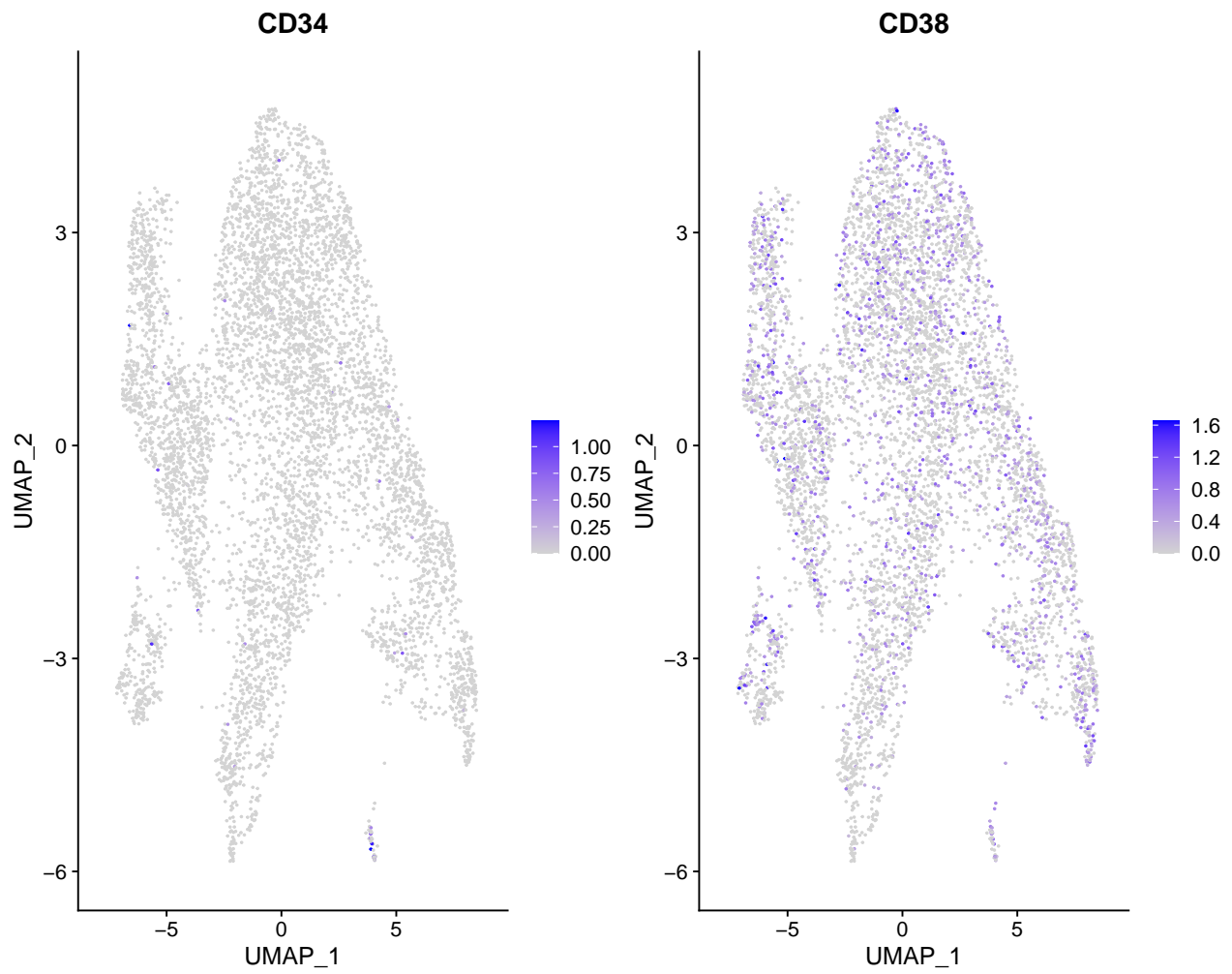
```
## Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck
##
## Number of nodes: 6060
## Number of edges: 202291
##
## Running Louvain algorithm...
## Maximum modularity in 10 random starts: 0.8474
## Number of communities: 10
## Elapsed time: 0 seconds
```



```
## 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
```

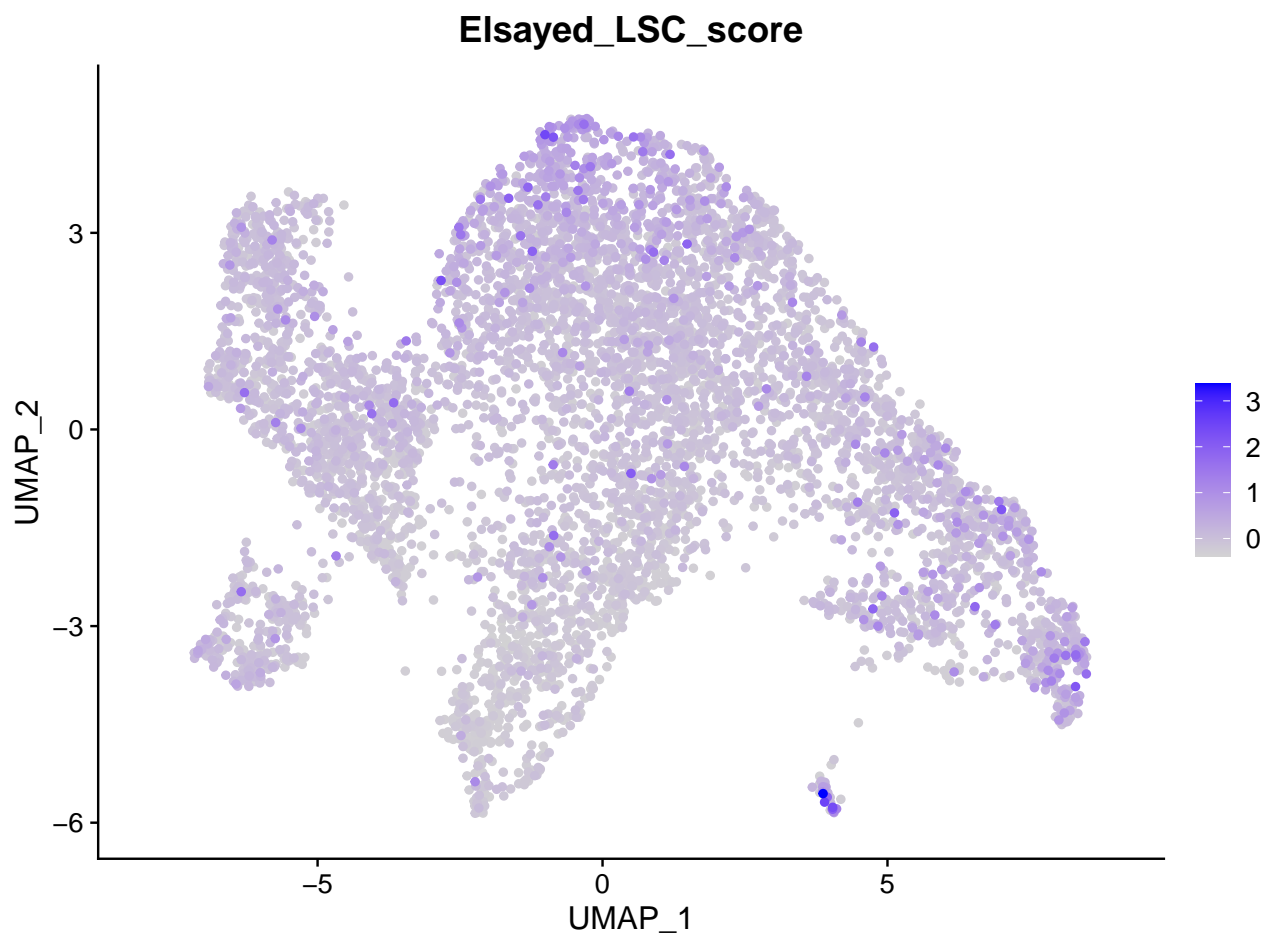


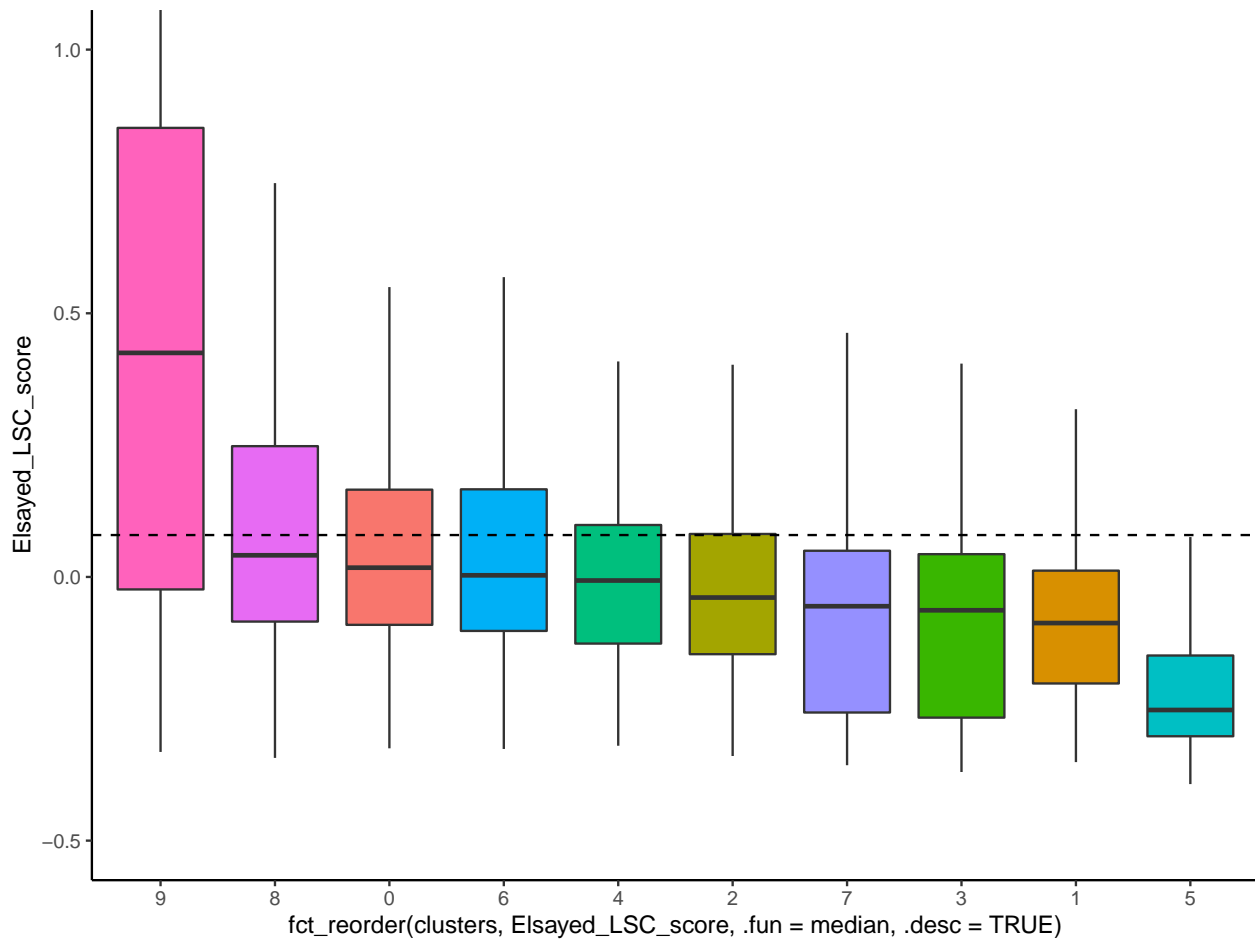




2. Get the LSC6 score

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

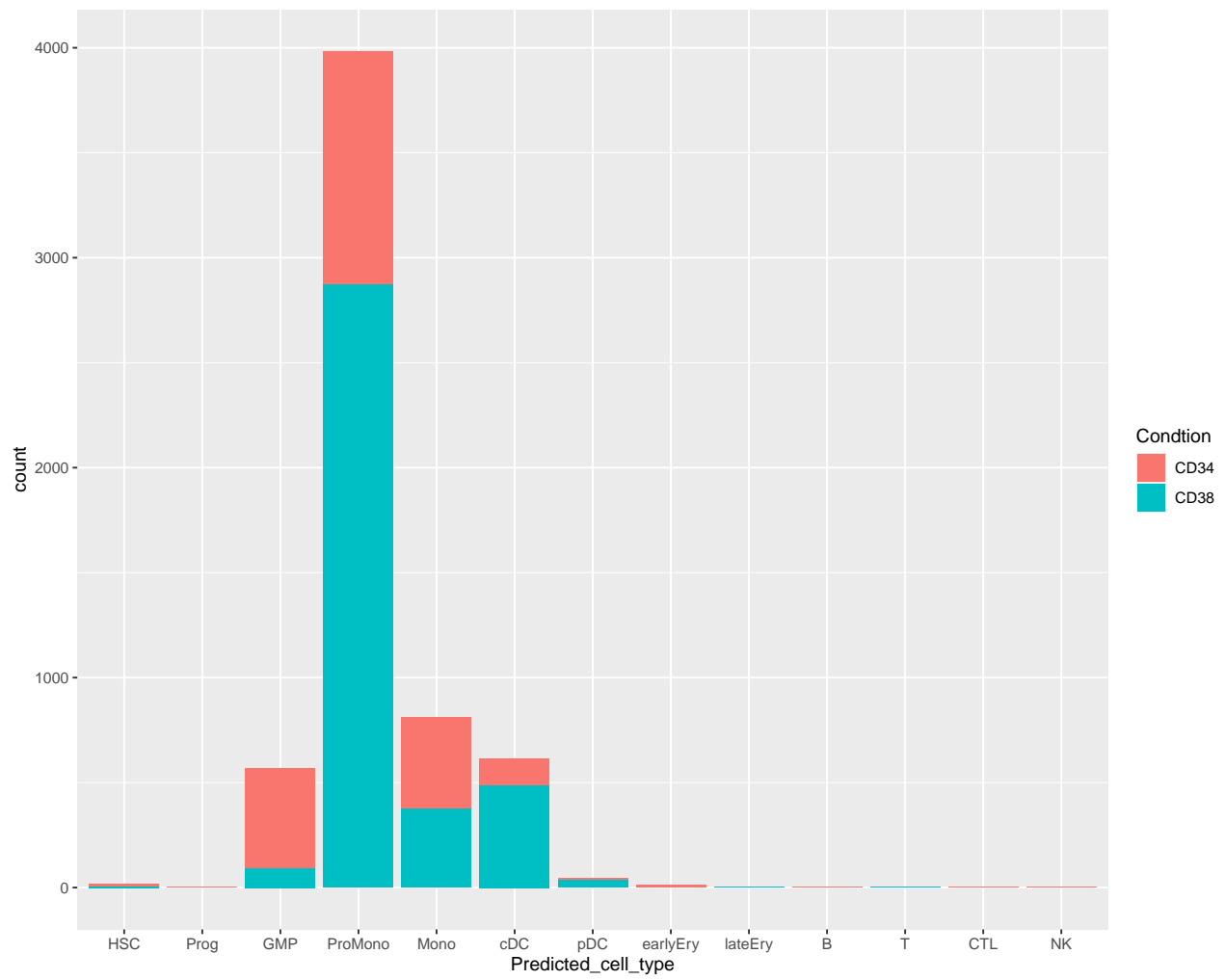


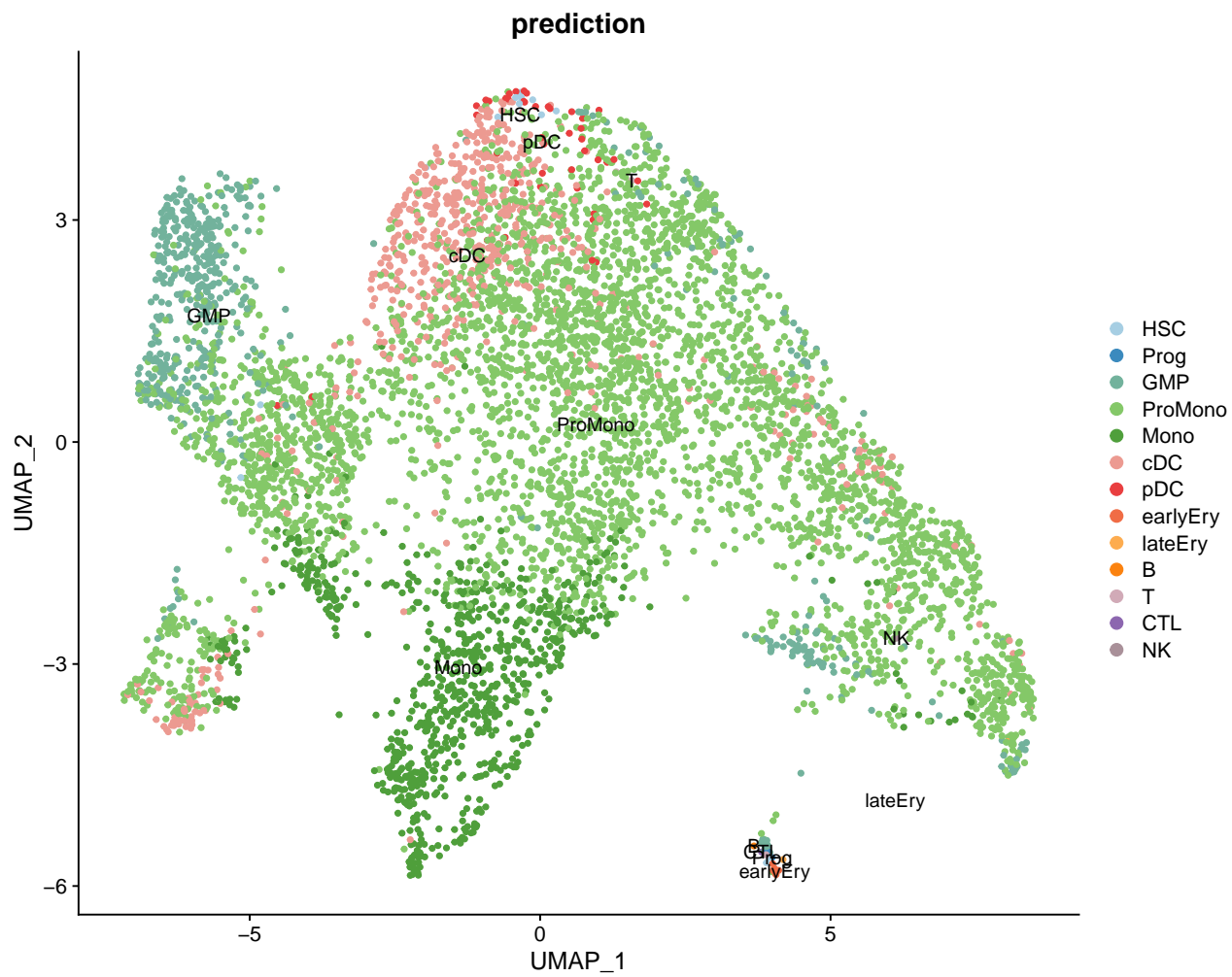


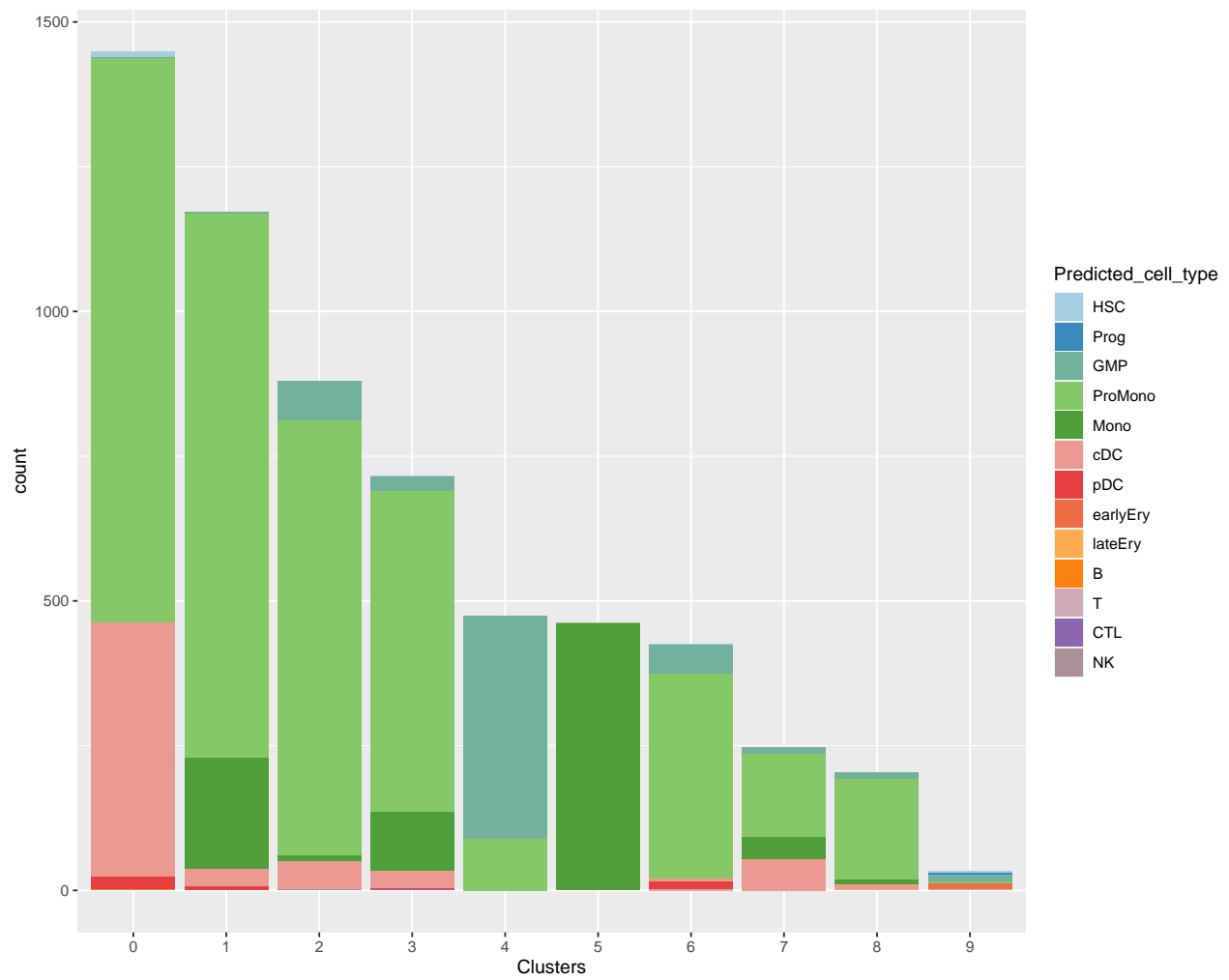
3. Predict the class of the cells using the markers and the expression of the BM cells form Van_Galen paper

```
## Performing PCA on the provided reference using 1821 features as input.
## Projecting cell embeddings
## Finding neighborhoods
## Finding anchors
## Found 1896 anchors
## Filtering anchors
## Retained 1082 anchors
## Finding integration vectors
## Finding integration vector weights
## Predicting cell labels
##
##           HSC Prog  GMP ProMono Mono  cDC  pDC earlyEry lateEry ProB  B Plasma
## CD34      10   3  477   1113  436  128   9      11      1   0    1      0
## CD38       5   0   92   2871  375  487  35      0      1   0    0      0
```

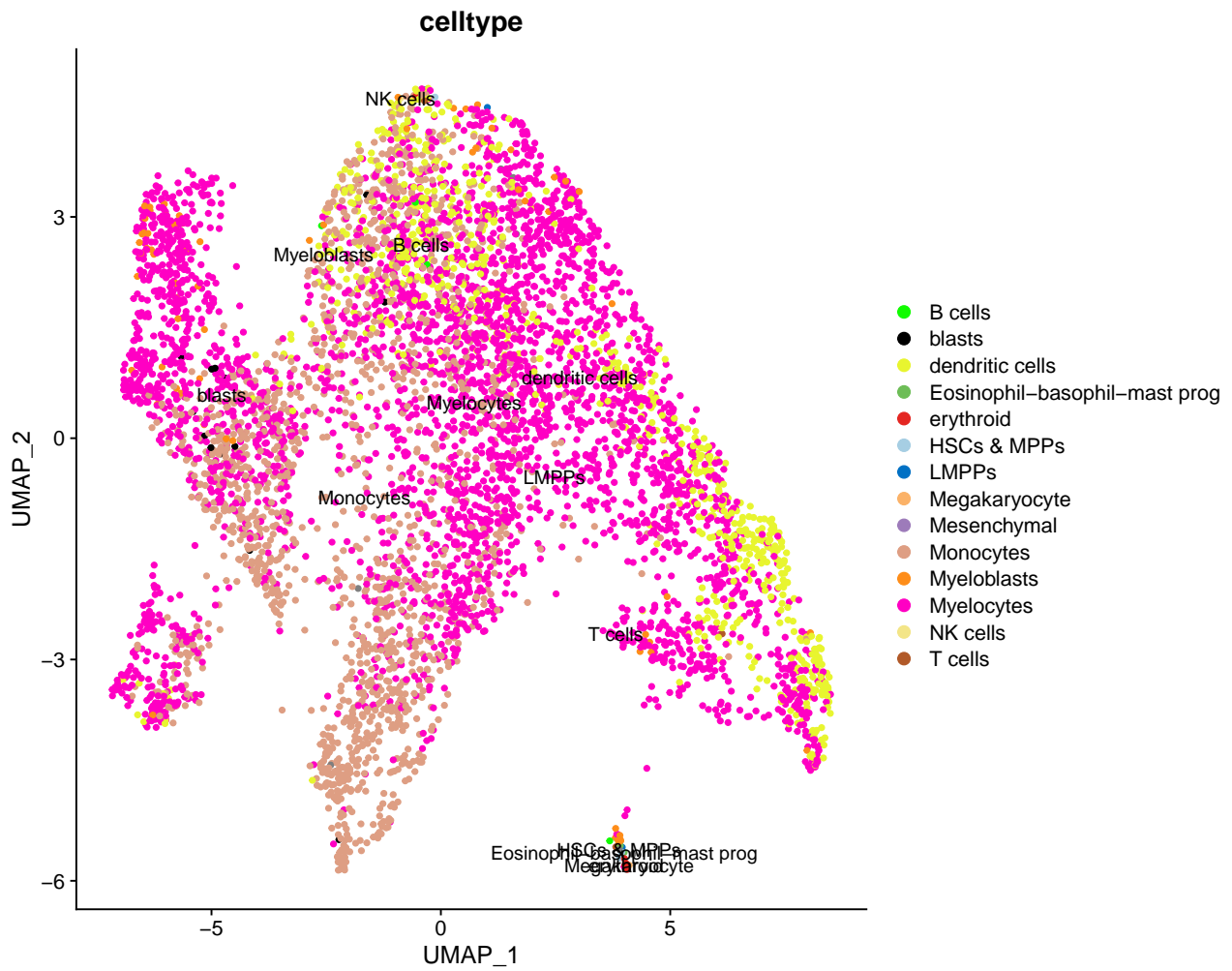
##		T	CTL	NK
##	CD34	1	1	1
##	CD38	2	0	0

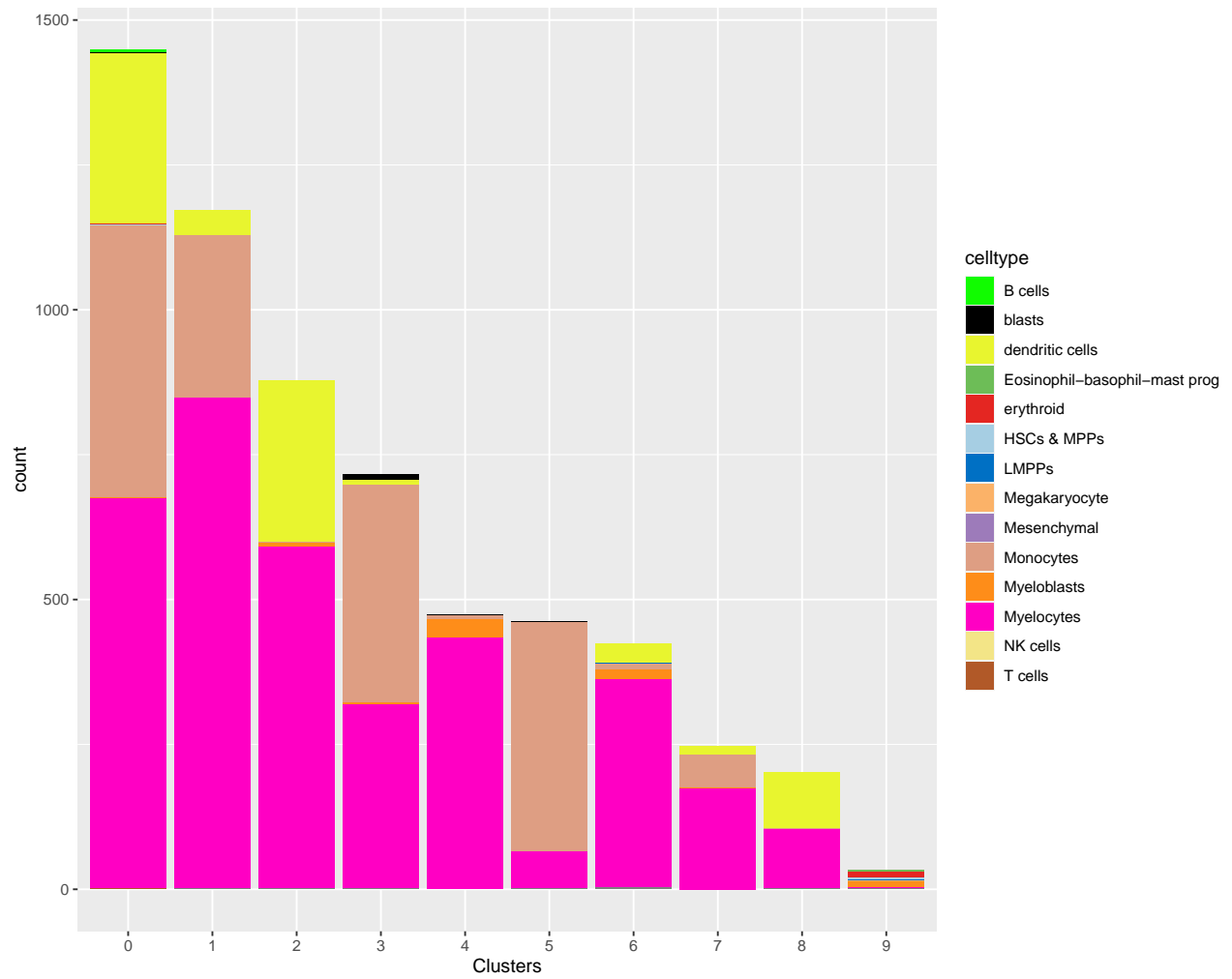






4. Project the predictions from Velten onto our UMAP





Cluster 9 seems the one with greater LSC6 score, spite of there isn't HSC-like predicted cells