

AML7_Rx

jtrincado

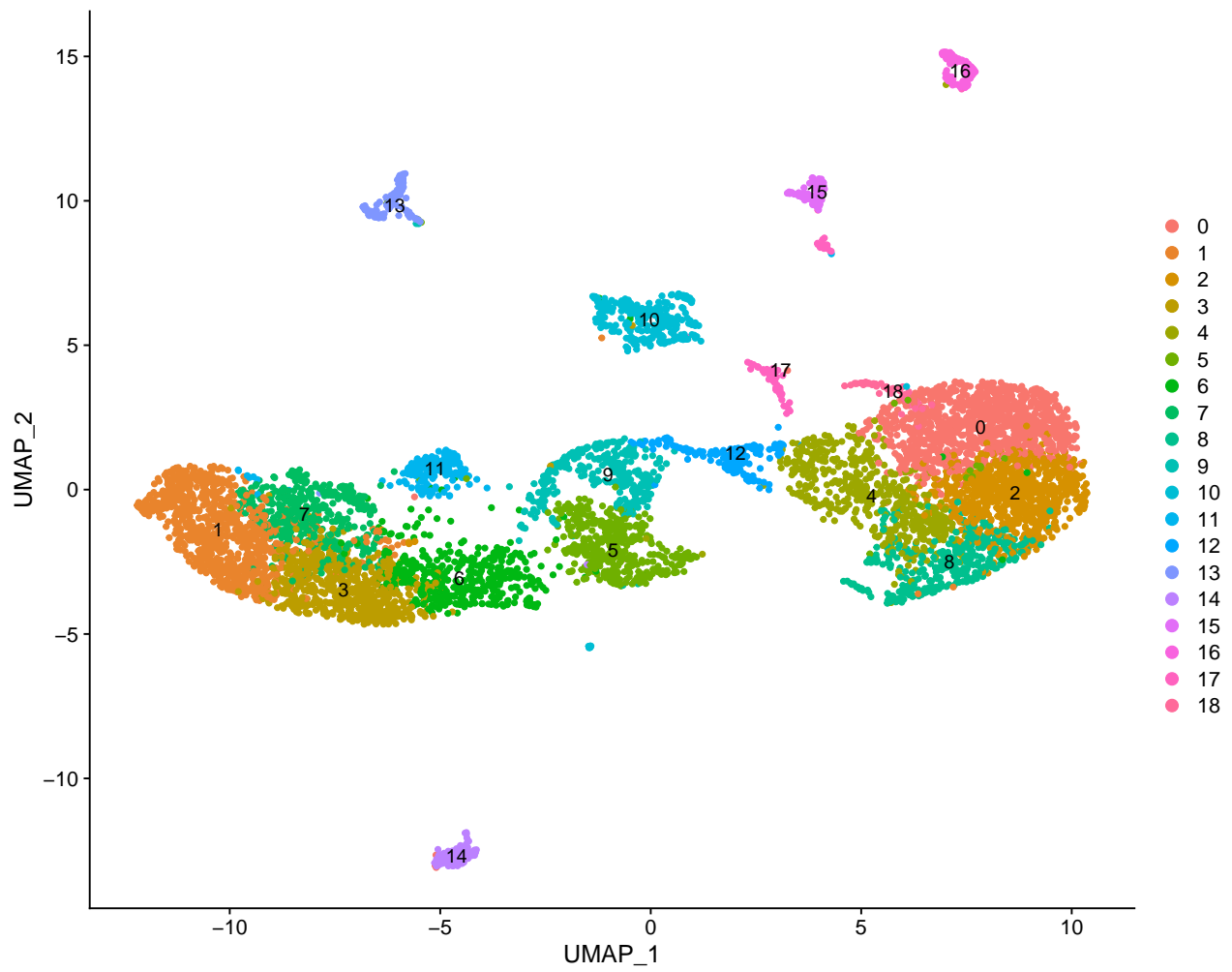
2022-02-09 12:32:52

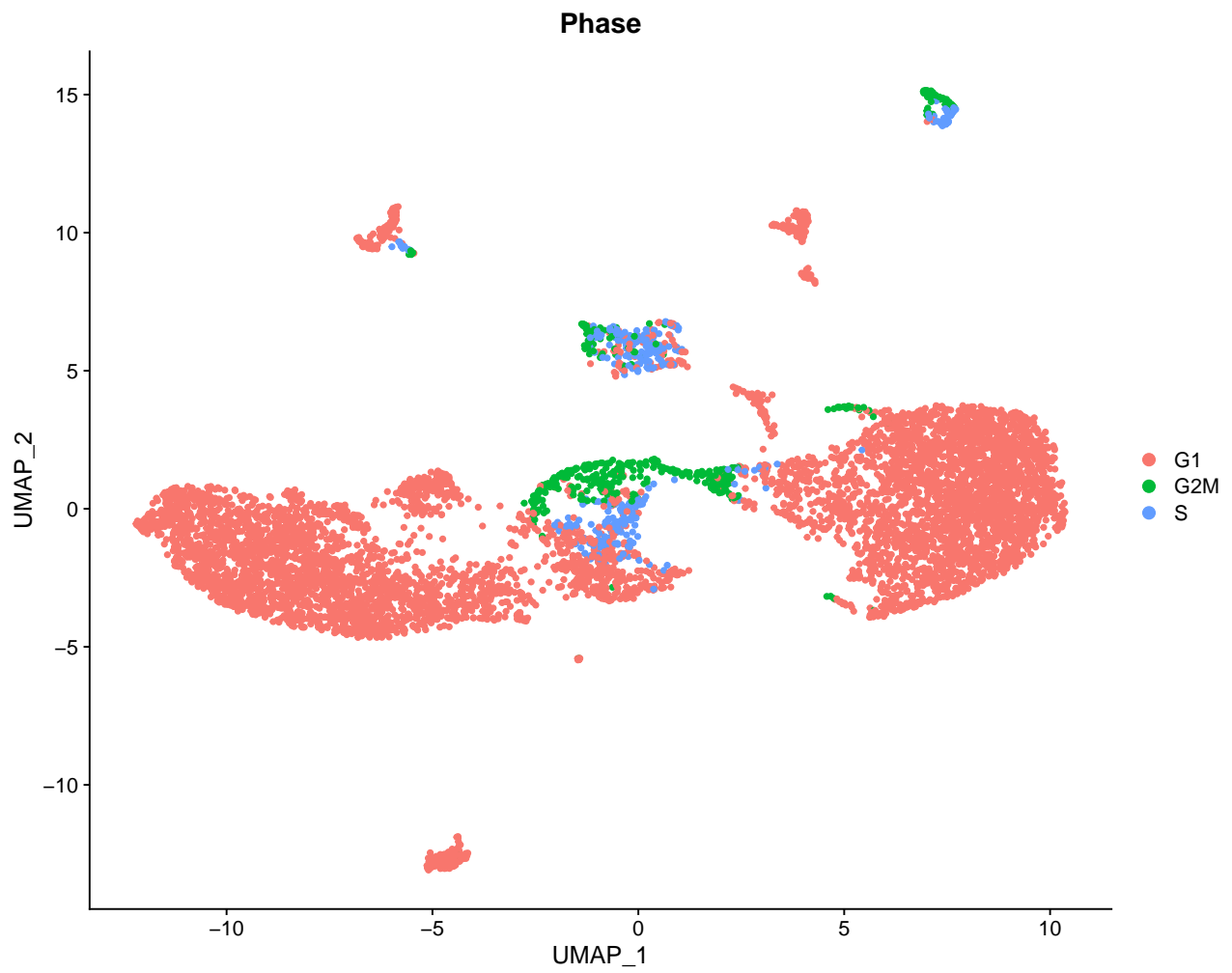
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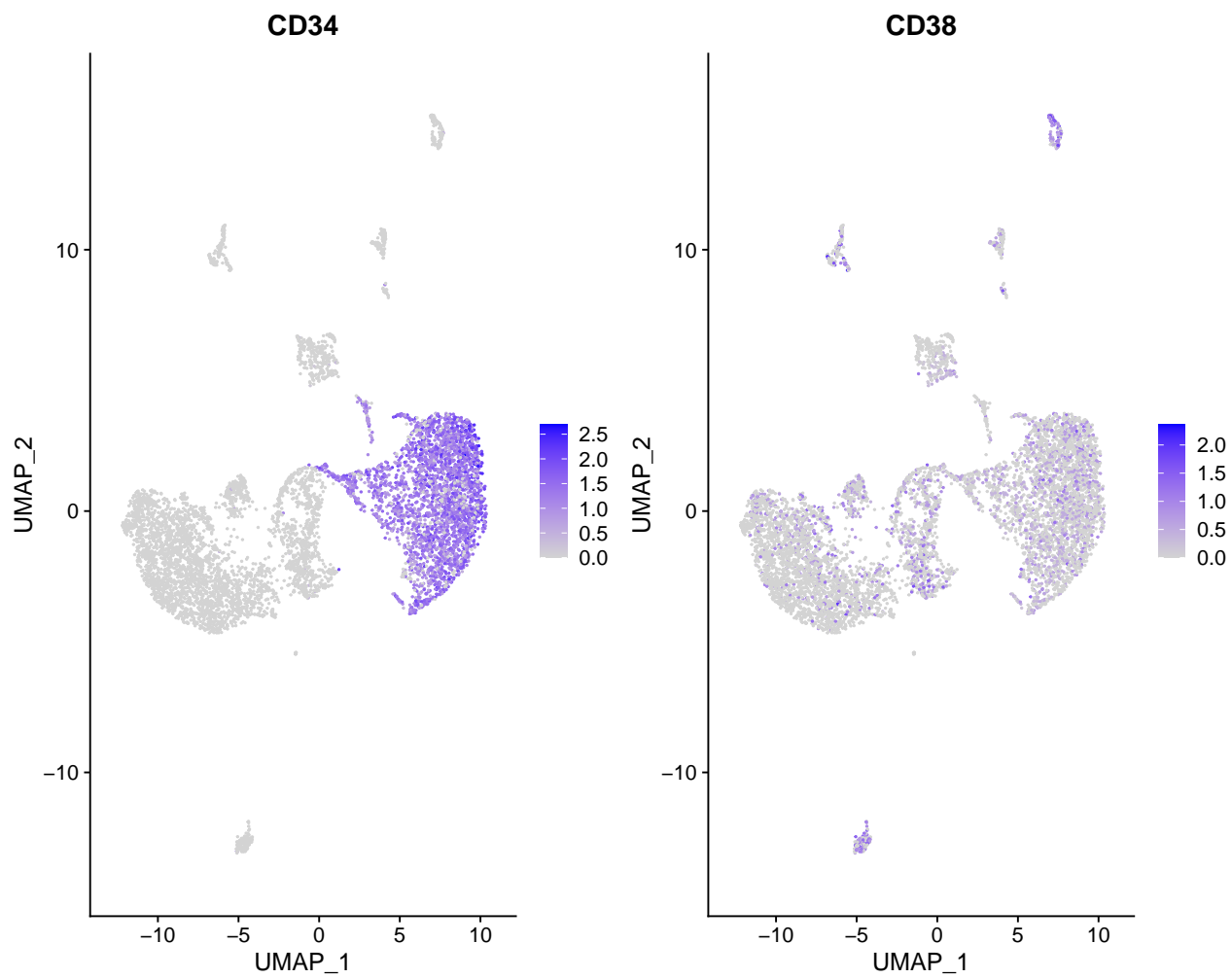
| | |
|--|----|
| 1. Put together both 34 and 38 libraries. Apply QC and dimensionality reduction. | 1 |
| 2. Get the LSC6 score | 5 |
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1. Put together both 34 and 38 libraries. Apply QC and dimensionality reduction.

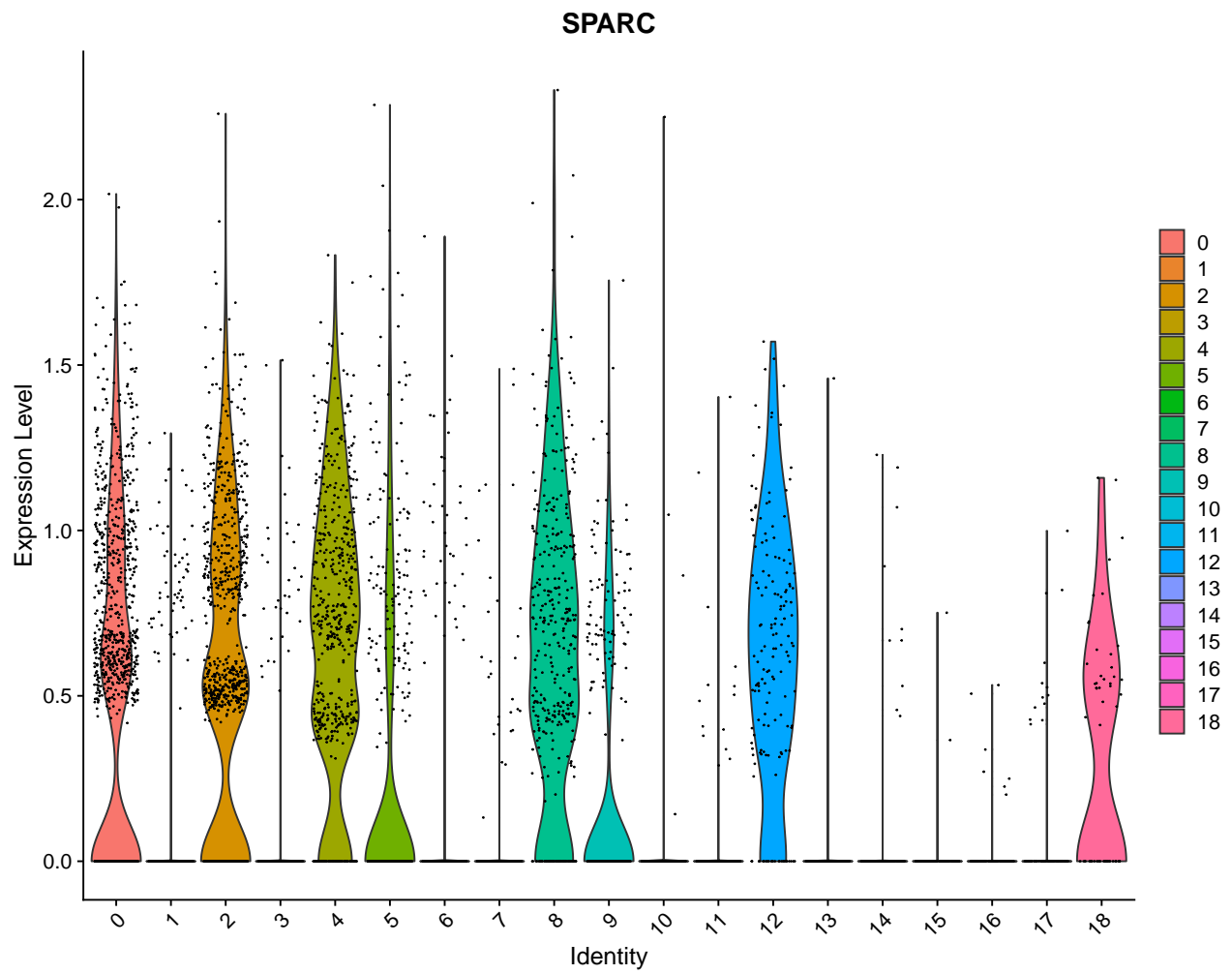
```
## Warning: The default method for RunUMAP has changed from calling Python UMAP via reticulate to the R  
## To use Python UMAP via reticulate, set umap.method to 'umap-learn' and metric to 'correlation'  
## This message will be shown once per session
```





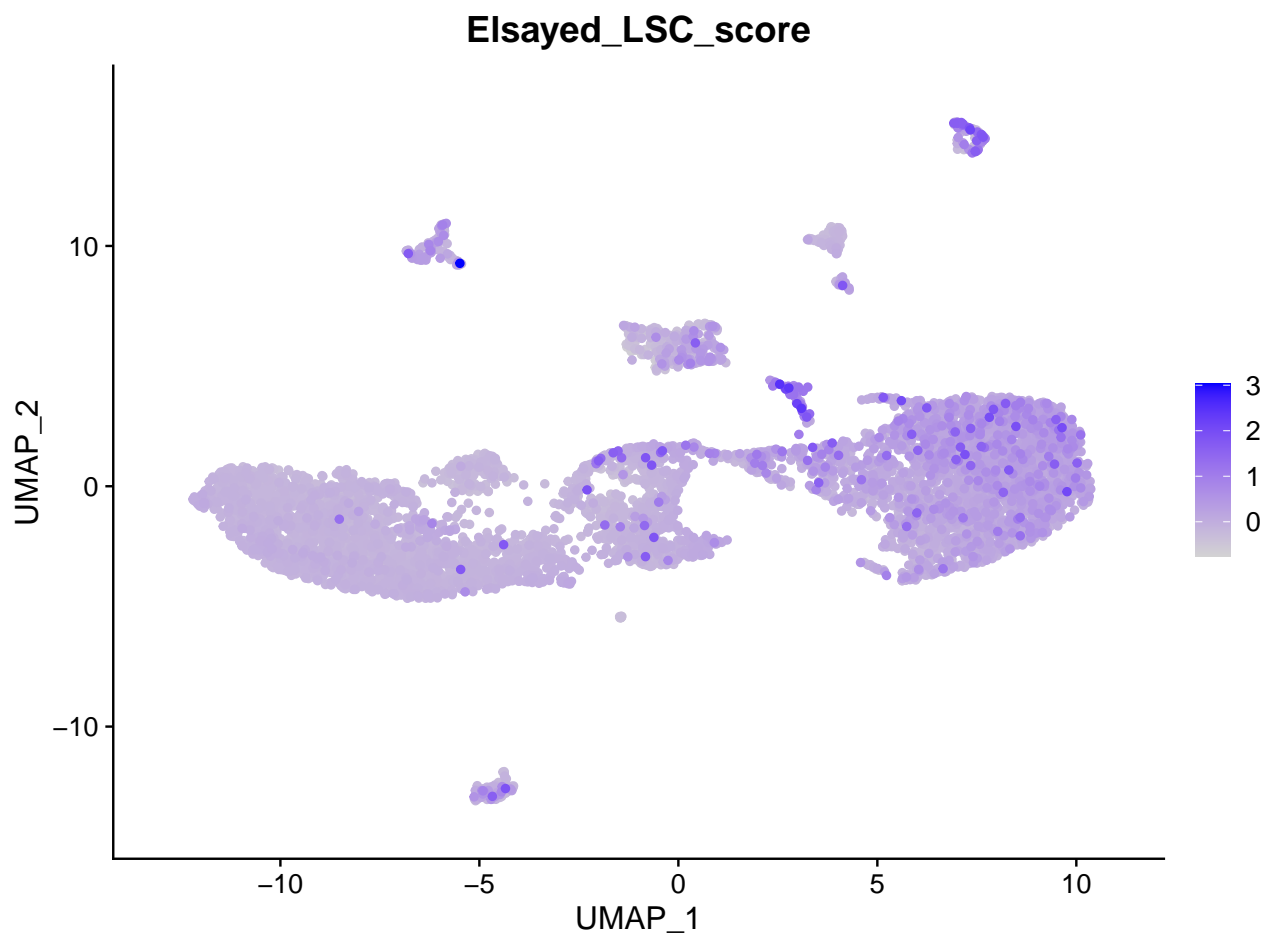


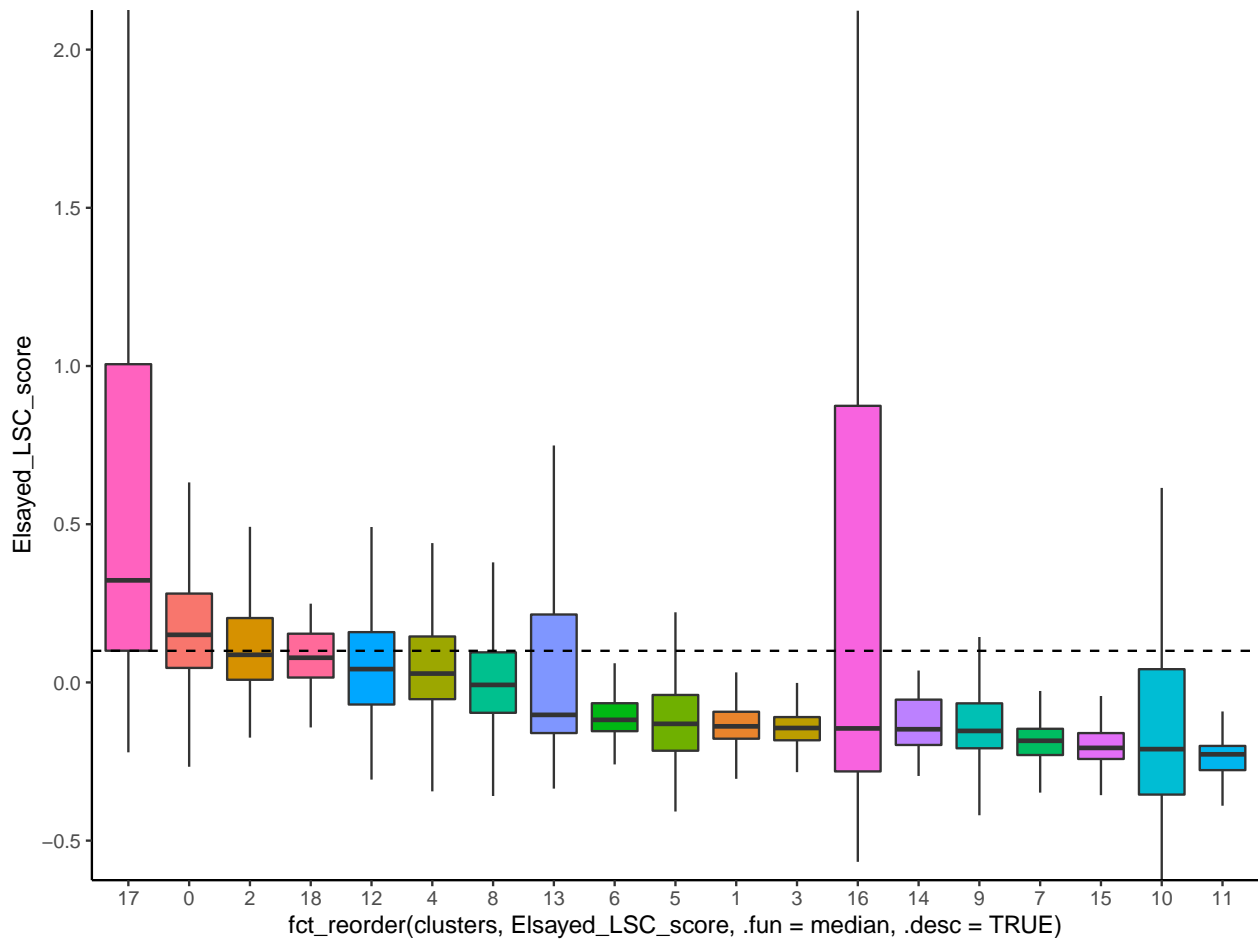
Check for expression of malignant marker for inv16 SPARC



2. Get the LSC6 score

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



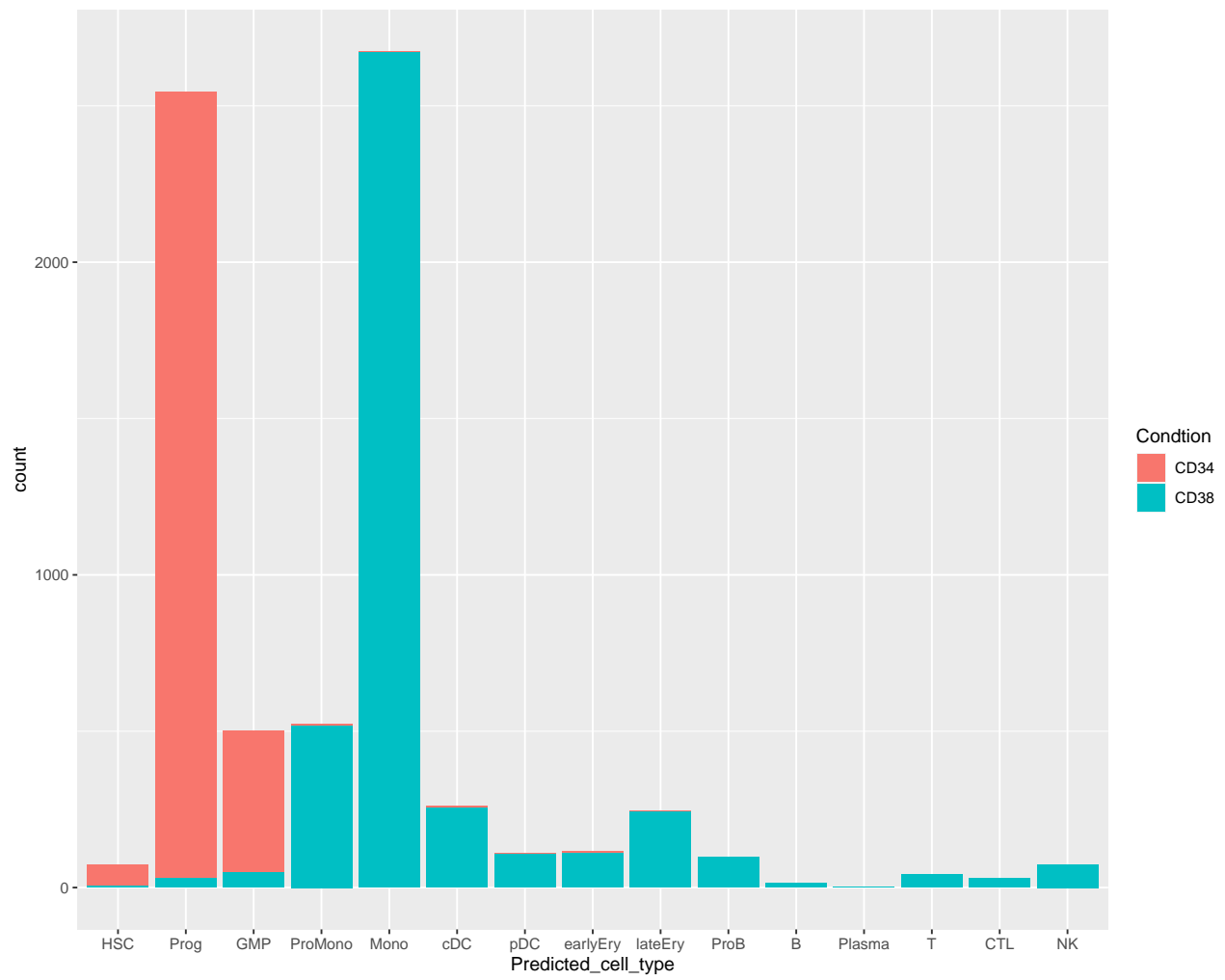


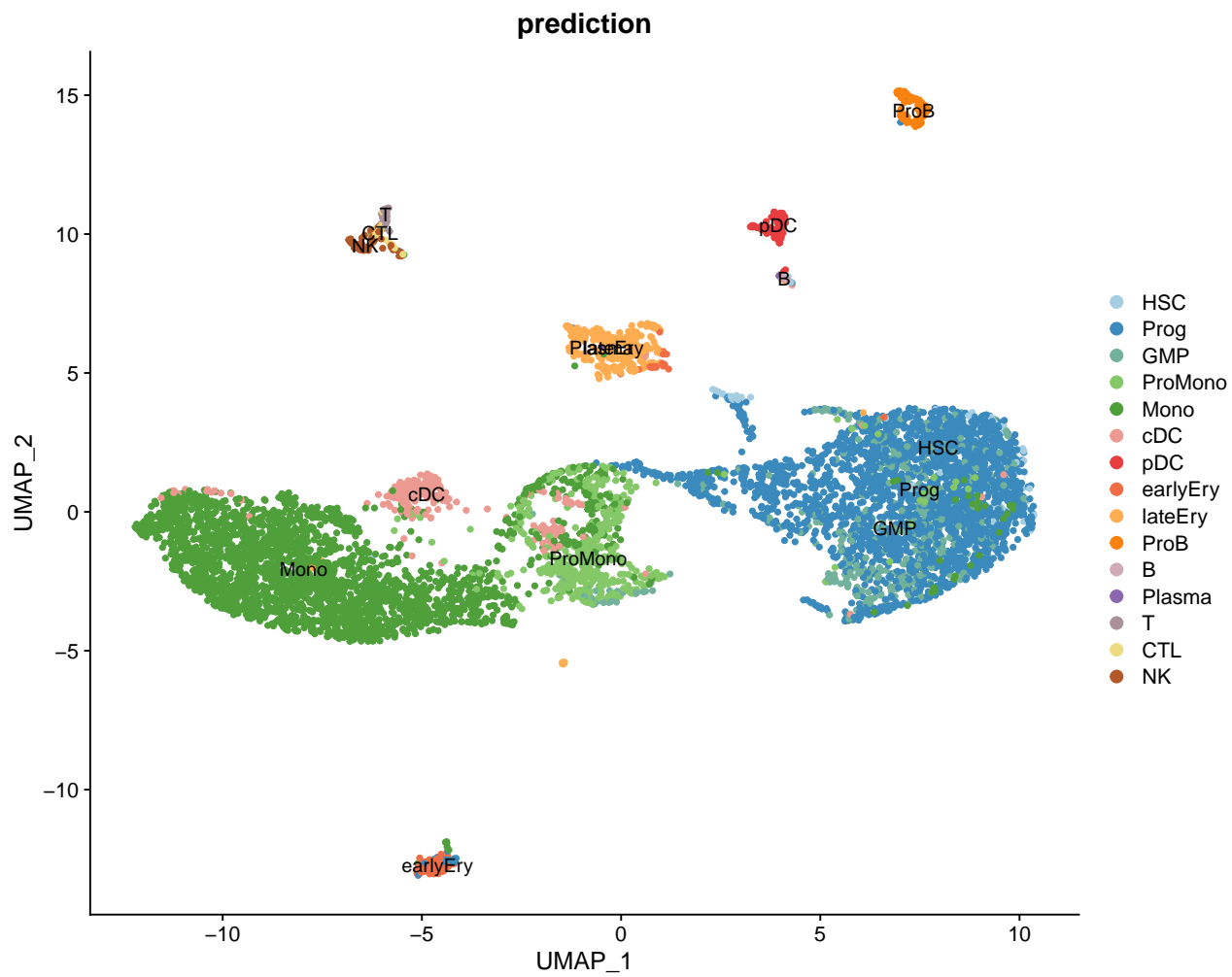
3. Predict the class of the cells using the markers and the expression of the BM cells form Van_Galen paper

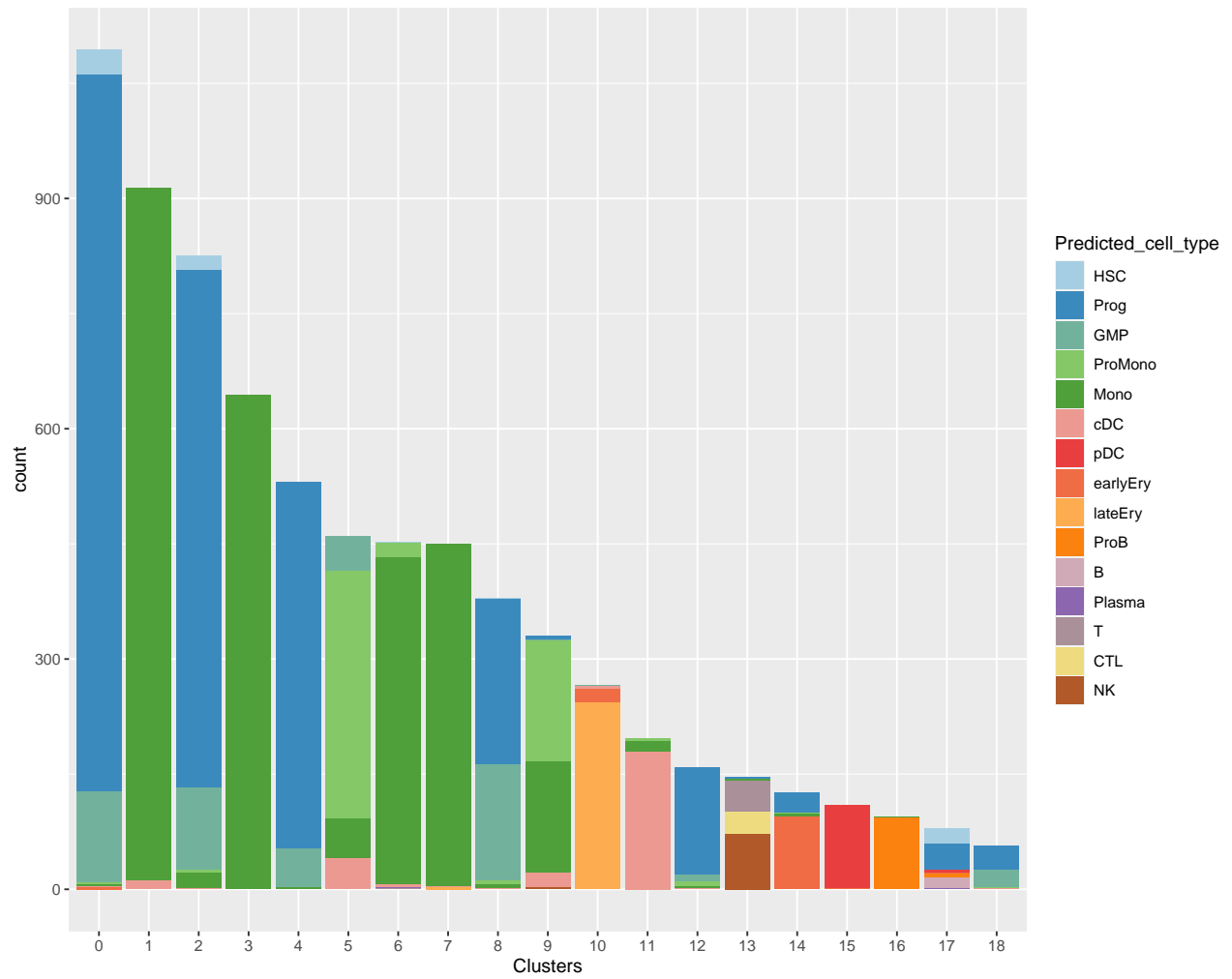
```
## Performing PCA on the provided reference using 1821 features as input.
## Projecting cell embeddings
## Finding neighborhoods
## Finding anchors
## Found 4361 anchors
## Filtering anchors
## Retained 3186 anchors
## Finding integration vectors
## Finding integration vector weights
## Predicting cell labels
##
```

| | HSC | Prog | GMP | ProMono | Mono | cDC | pDC | earlyEry | lateEry | ProB | B | Plasma |
|------|-----|------|-----|---------|------|-----|-----|----------|---------|------|----|--------|
| CD34 | 70 | 2515 | 456 | 6 | 5 | 7 | 6 | 8 | 5 | 0 | 0 | 0 |
| CD38 | 4 | 30 | 48 | 518 | 2670 | 254 | 106 | 109 | 241 | 98 | 15 | 3 |

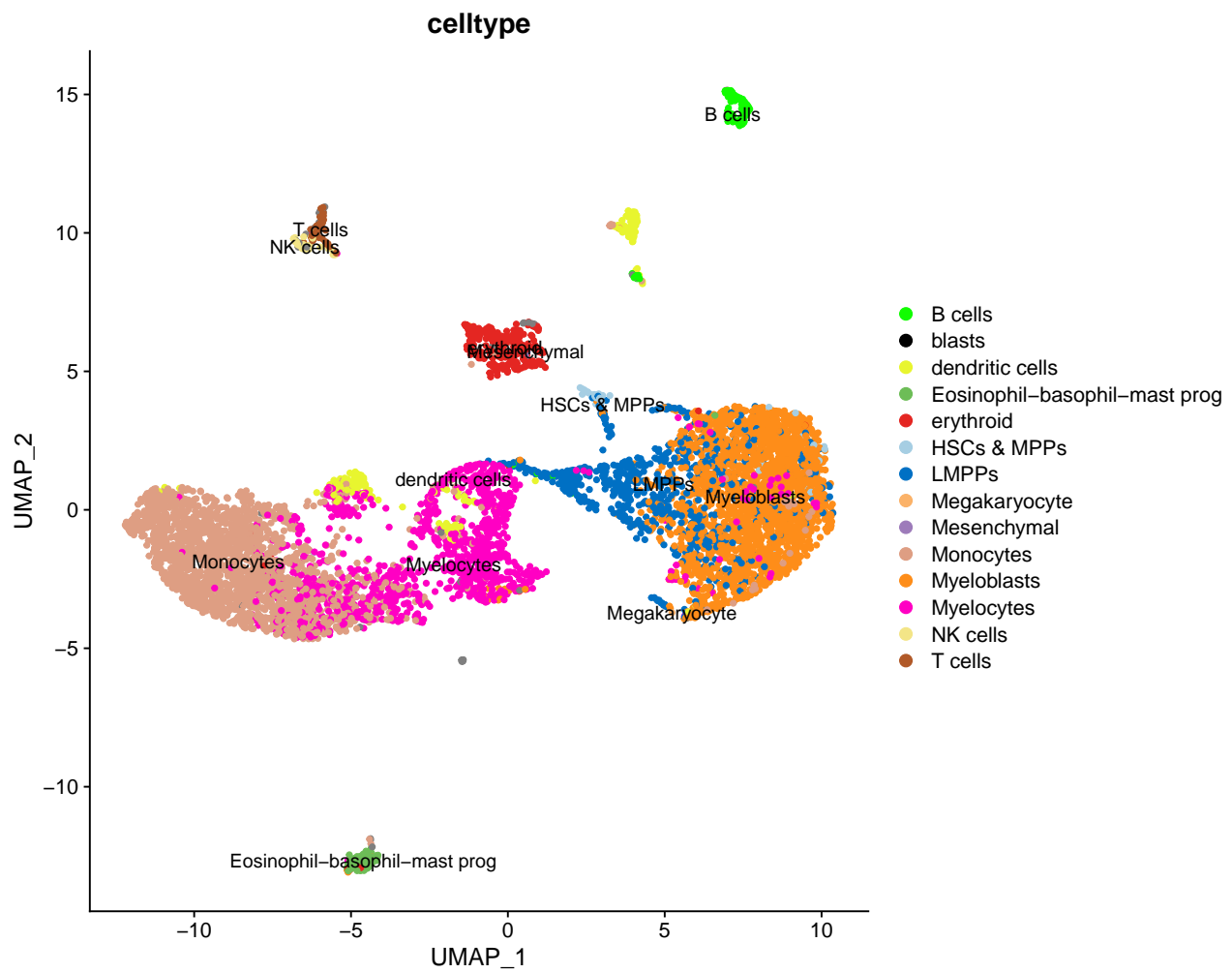
| | | | | |
|----|------|----|-----|----|
| ## | | T | CTL | NK |
| ## | CD34 | 0 | 0 | 0 |
| ## | CD38 | 41 | 29 | 74 |

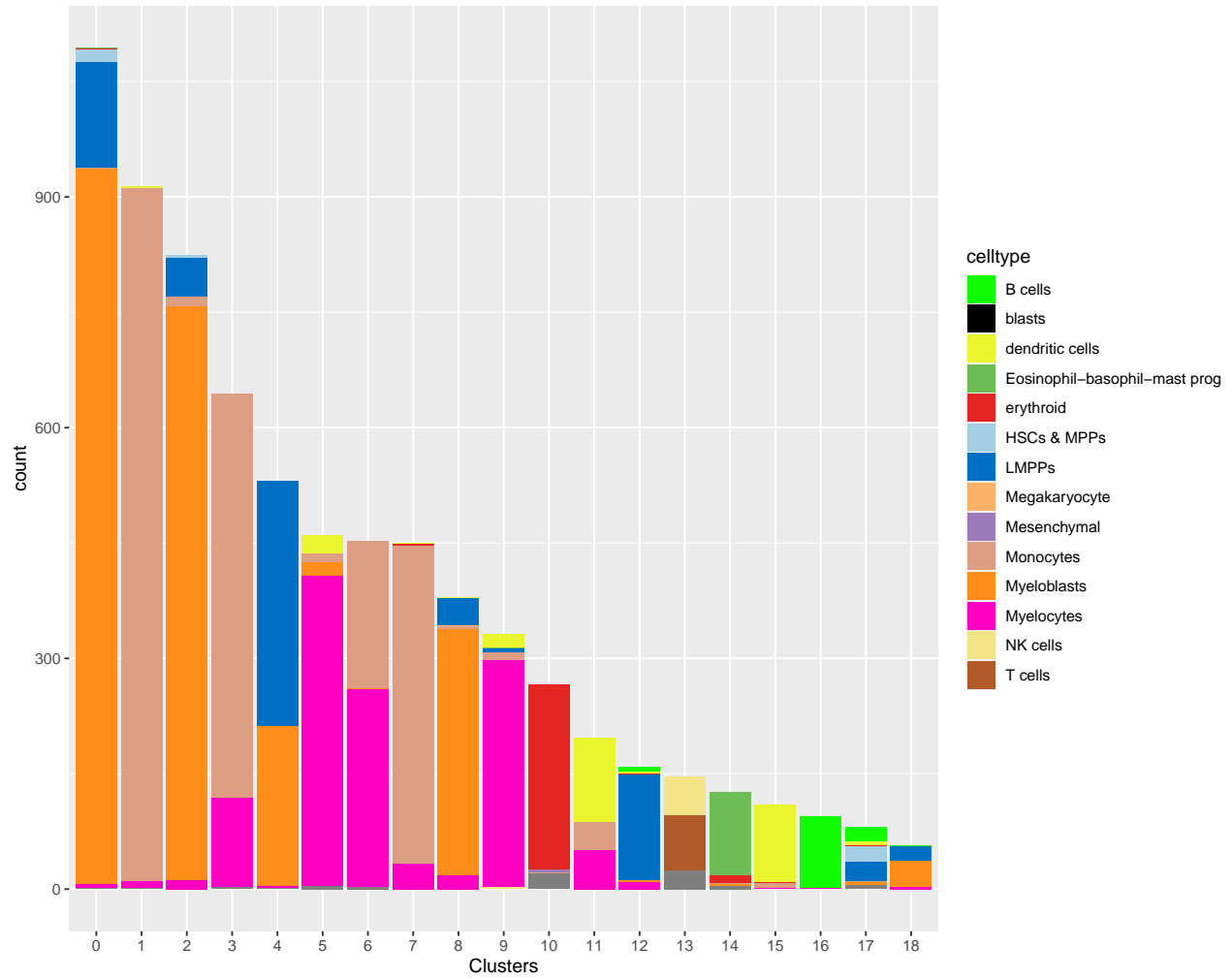






4. Project the predictions from Velten onto our UMAP





Cluster 17 and 0 are among the top according to LSC6 score and they bare a similar proportion of predicted HSCs. However, cluster 0 shows greater expression of malignant marker SPARC. This could suggest cluster 17 are healthy residual cells. In addition, cluster 0 is the one colocalizing with cluster 0 LSC from the paired Dx sample. Therefore, we propose cluster 0 as the one with LSC enrichment