AML6_Dx

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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
```

10
5
0
−5
UMAP_2
−5
0
5
UMAP_1
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14

Phase
10
5
0
−5
UMAP_2
−5
0
5
UMAP_1
G1
G2M
S

2. Get the LSC6 score

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

Elsayed_LSC_score
10
5
0
−5
UMAP_2
−5
0
5
UMAP_1
3
2
1
0
−1

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 2994 anchors

## Filtering anchors

##  Retained 1533 anchors

## Finding integration vectors

## Finding integration vector weights

## Predicting cell labels

##
##          HSC Prog  GMP ProMono Mono  cDC  pDC earlyEry lateEry ProB    B Plasma
##   CD34   134  332 2163    1629  992  145    2       73      17    0    5      0
##   CD38   107  298 2336    1597  238  198    0        0       0    0    0      0
```

```
##
##            T  CTL   NK
##    CD34   10    0    0
##    CD38    3    0    0
```

prediction
lateEry
earlyEry
pDC
B
T
GMP
HSC
ProMono
Prog
cDC
Mono
10
5
0
−5
UMAP_2
−5
0
5
UMAP_1
HSC
Prog
GMP
ProMono
Mono
cDC
pDC
earlyEry
lateEry
B
T

count
1500
1000
500
0
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Clusters
Predicted_cell_type
HSC
Prog
GMP
ProMono
Mono
cDC
pDC
earlyEry
lateEry
B
T

4. Project the predictions from Velten onto our UMAP

Cluster 11 seems the one with greater LSC6 score. Cluster 9 is also above D10, but cluster 11 seems to have a greater percentage of HSC predicted cells. We propose cluster 11 as the one with more LSC enrichment