

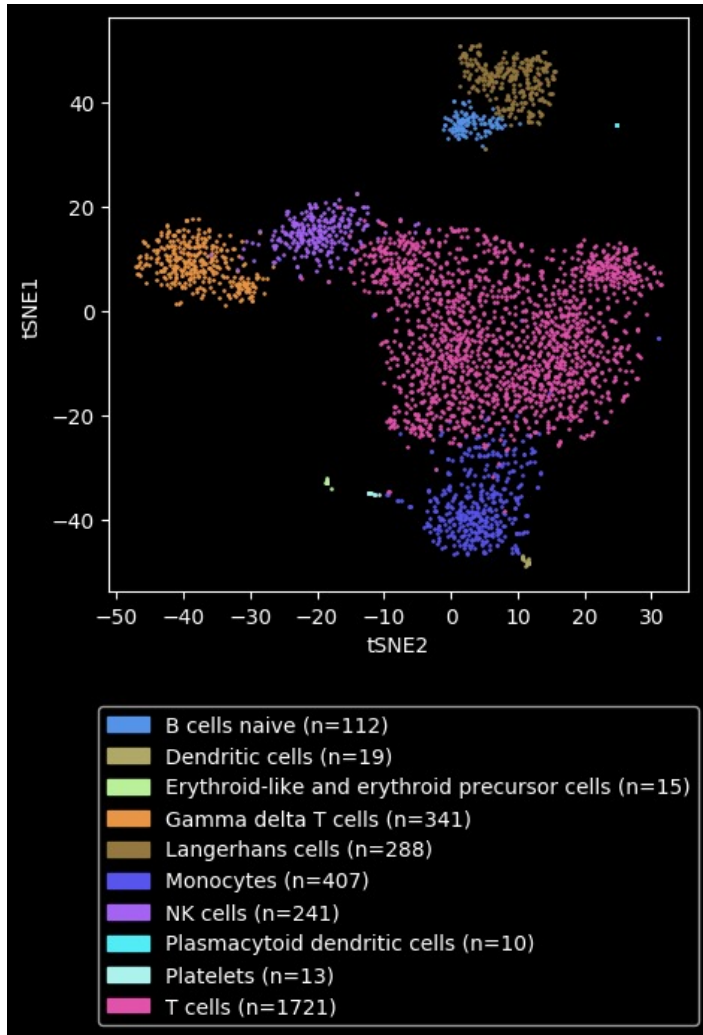
scRNA-SEQ ANALYSIS ON *HOMO SAPIENS* PERIPHERAL BLOOD MONONUCLEAR CELLS

BCG - GENOMICS AND TRANSCRIPTOMICS

A.A. 2023-2024

SABRINA PERVIN ABU

THE DATASET



- LINK TO PANGLAODB:
https://panglaodb.se/view_data.php?sra=SRA713577&srs=SRS3363004#google_vignette

- LINK TO THE ARTICLE: <https://pubmed.ncbi.nlm.nih.gov/32140464/> .

The study identified 13 clusters and 8 cell types (CD4+ T cells, CD14+ Monocytes, NK cells, B cells, CD8+ T cells, Megakaryocytes, FCGR3A + Monocytes, Dendritic cells).

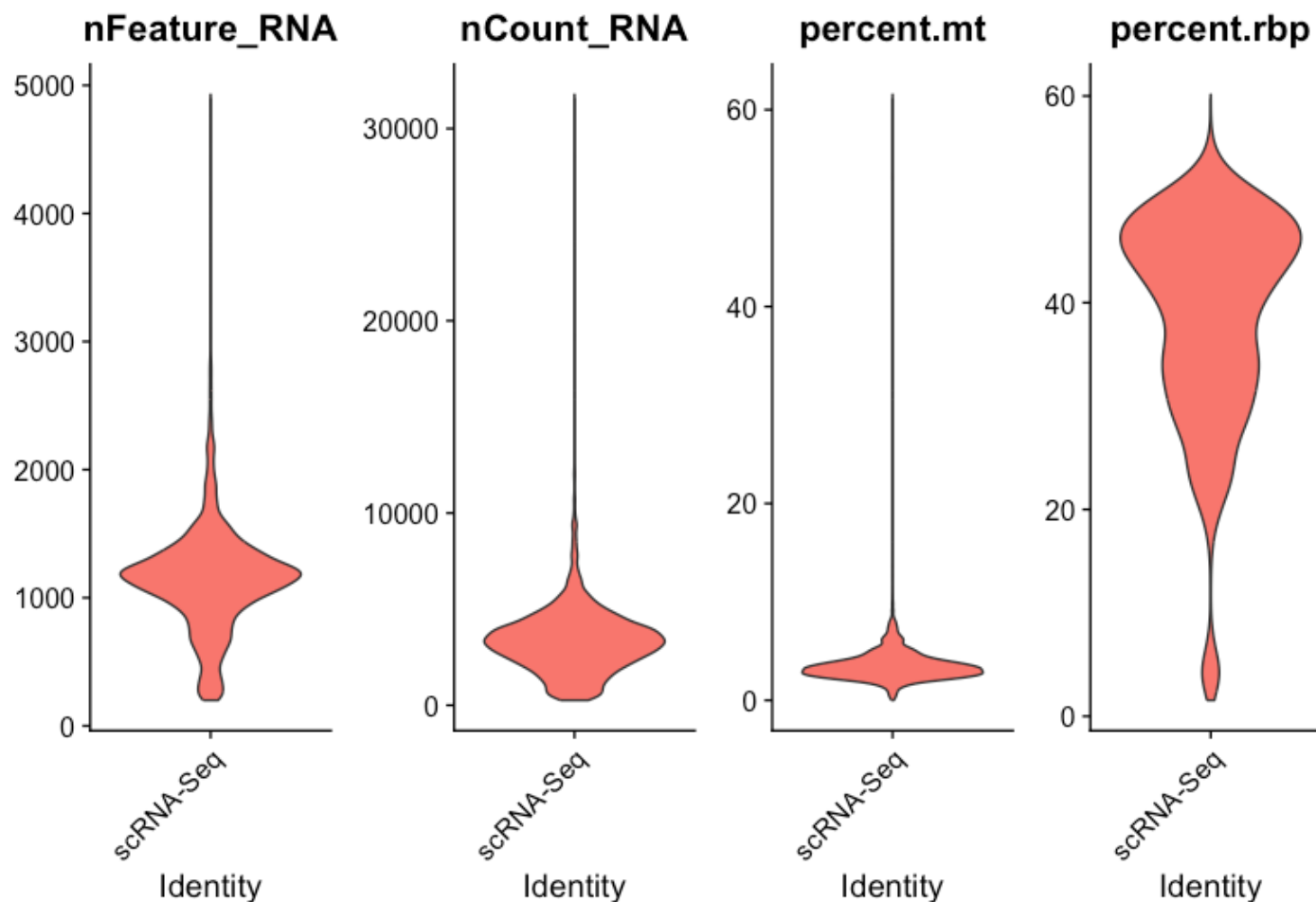
- SRA: SRA713577
- SRS: SRS3363004
- NUMBER OF CELLS: 3,334
- Peripheral blood mononuclear cells
Homo sapiens

QUALITY CONTROL

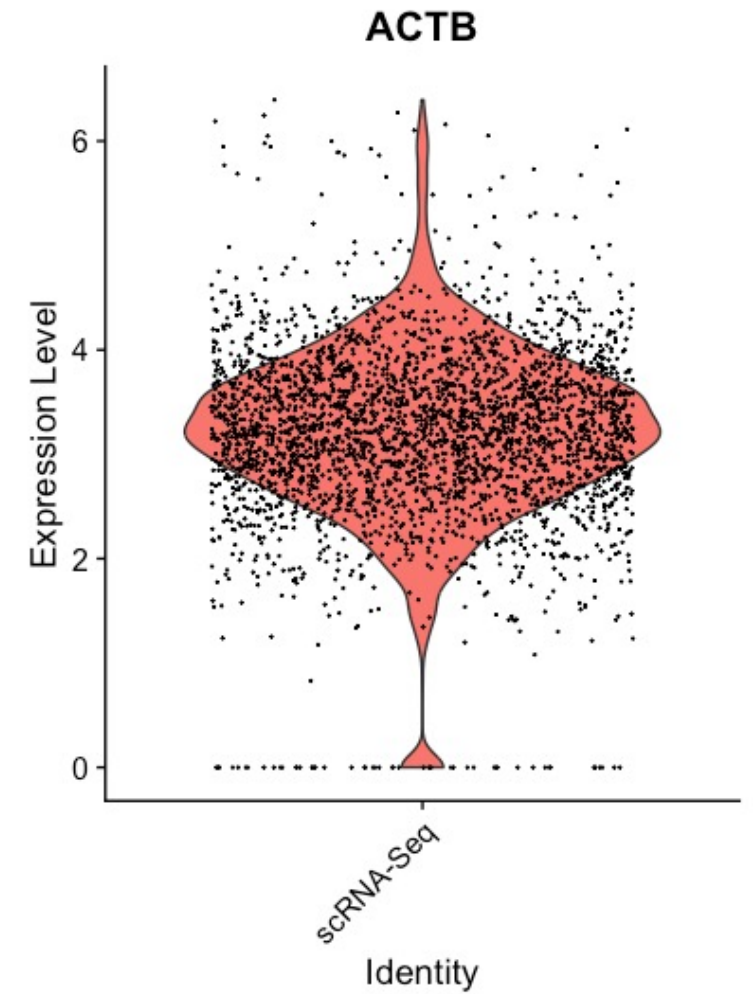
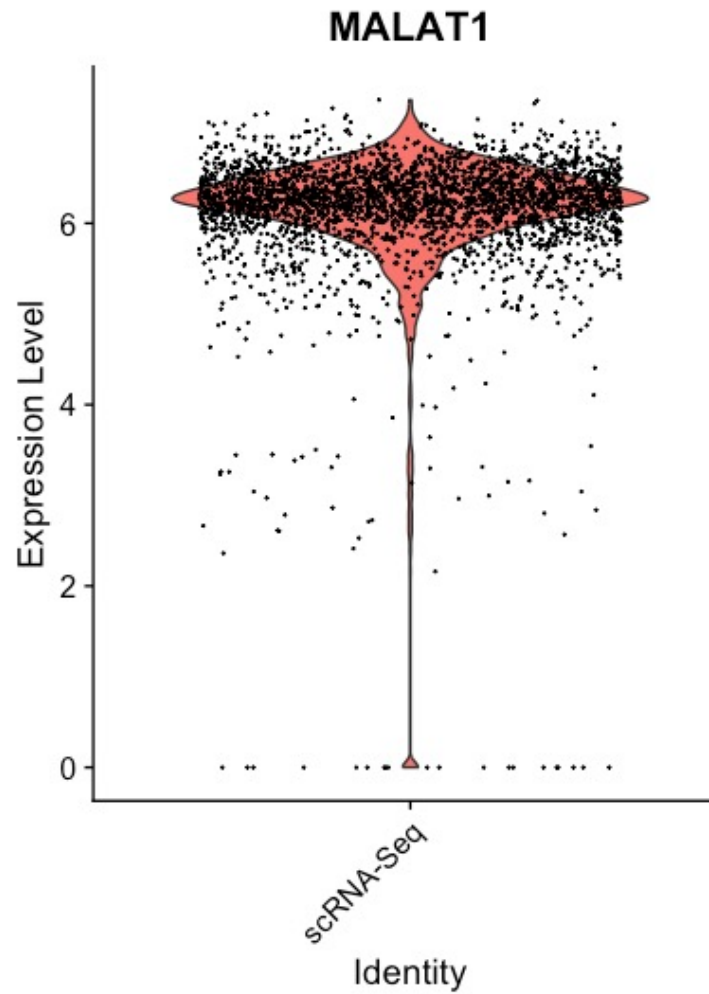
- nFeature_RNA shows the number of detected features per cell.
- nCount_RNA shows the count of RNA molecules detected.
- percent.mt indicates the percentage of mitochondrial gene expression.
- percent.rbp indicates the percentage of ribosomal gene expression.

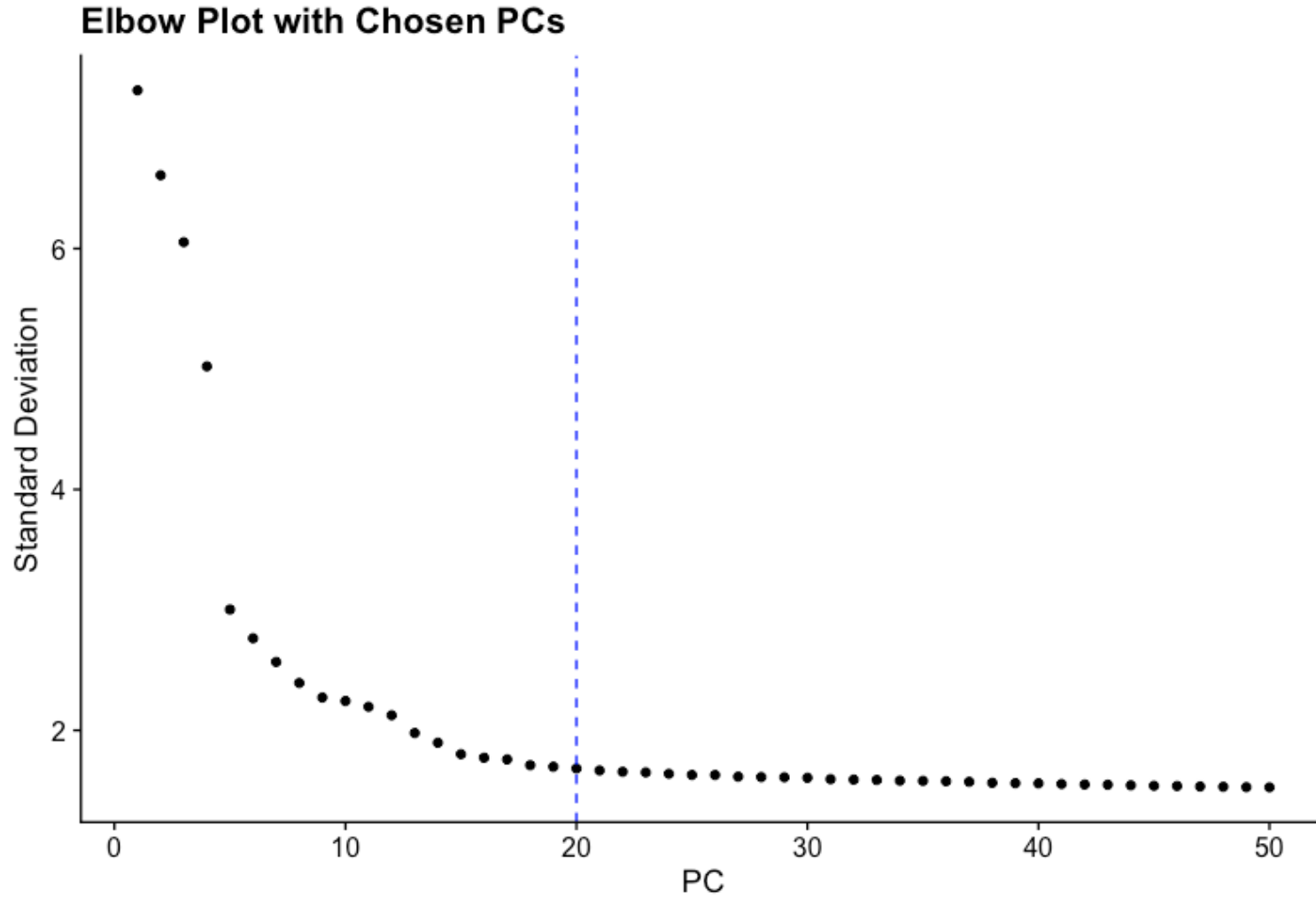
3568 samples → 3095 samples

- > 200 genes (possible empty droplets)
- < 2500 genes (possible doublets)
- < 5% mitochondrial gene content (cell might be under stress)



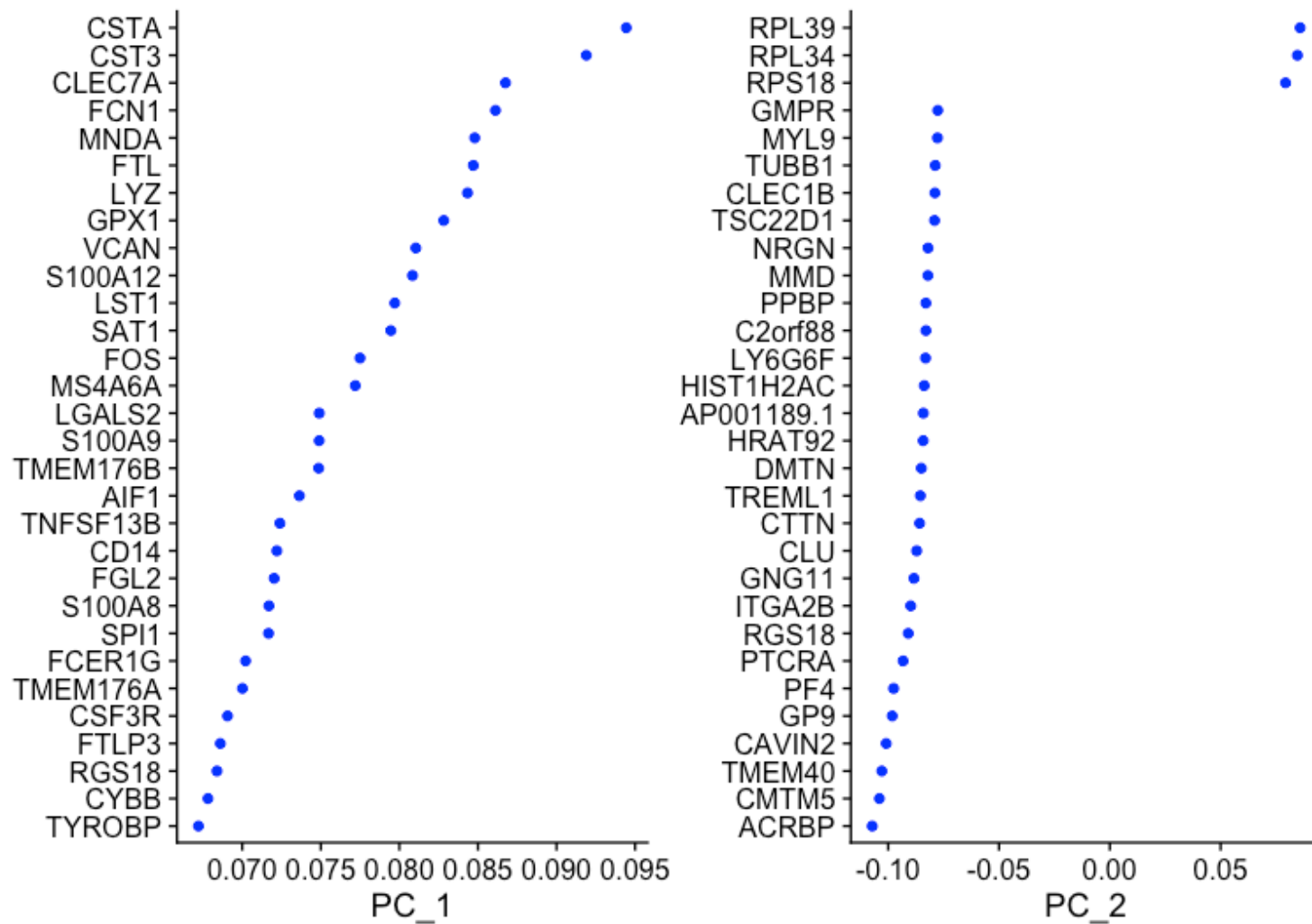
EXPRESSION OF UP-REGULATED GENE VS HOUSEKEEPING GENE





75% OF THE CUMULATIVE
VARIANCE IS EXPLAINED
BY THE FIRST 20 PCs

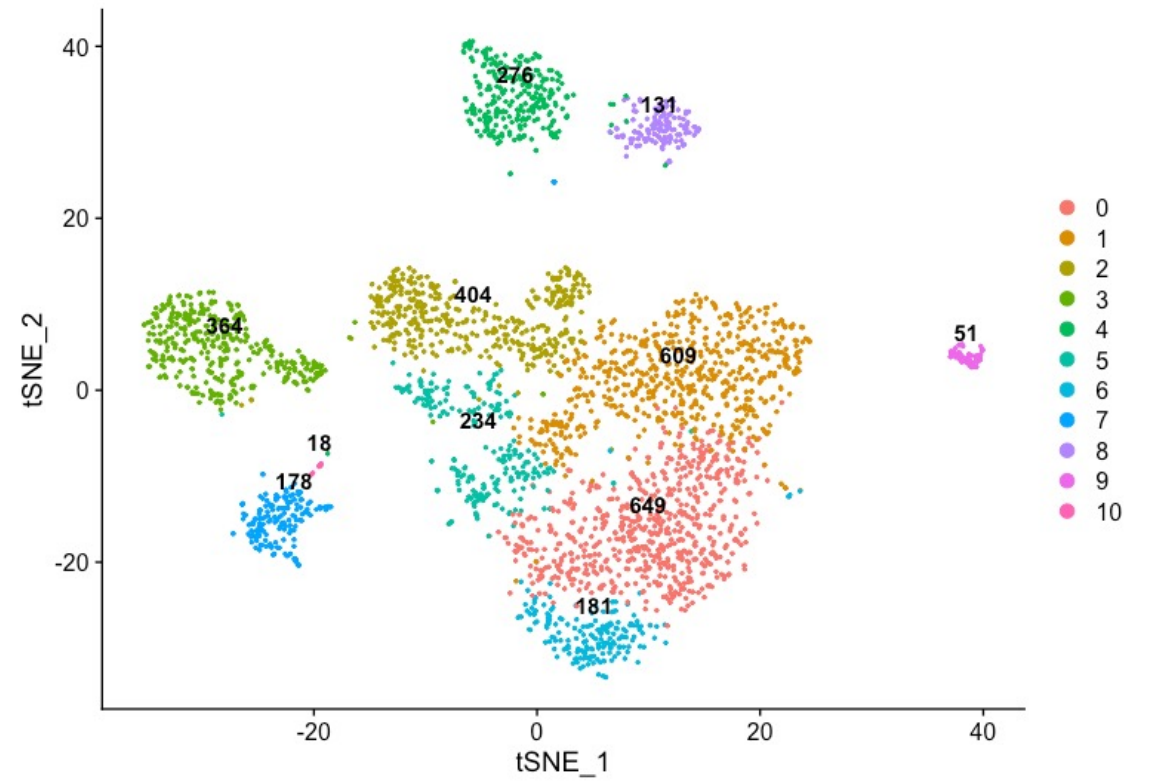
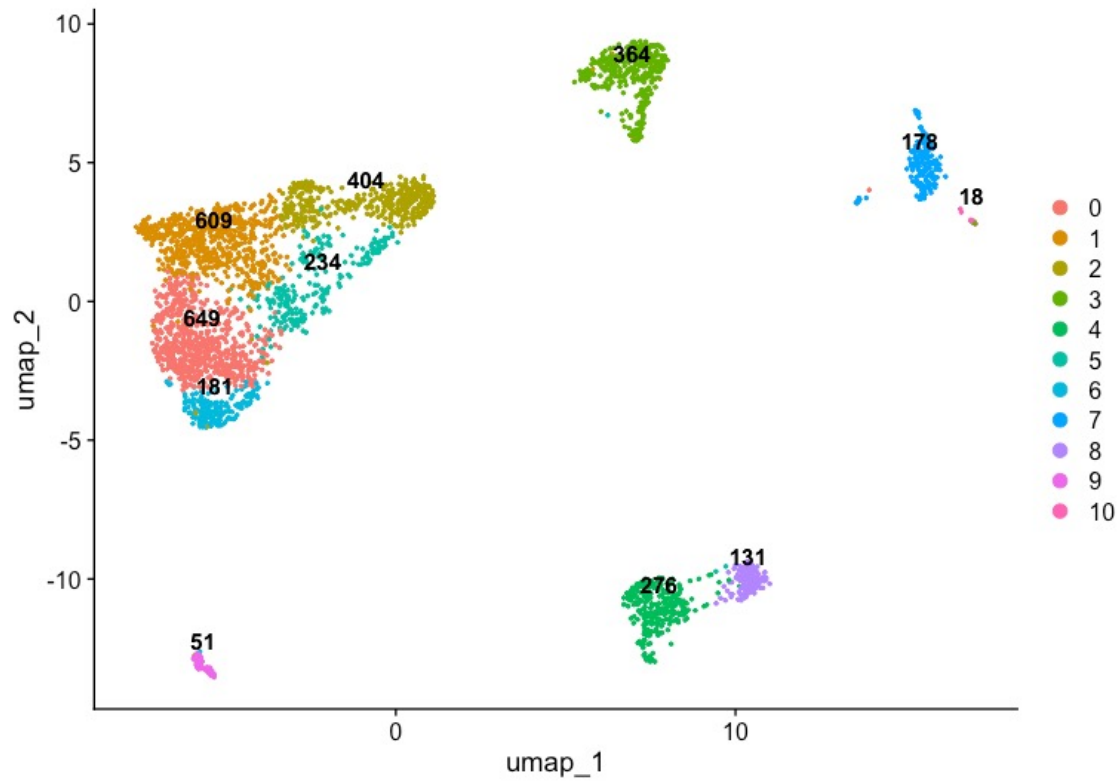
THE MOST VARIABLE GENES IN THE FIRST 2 PCs

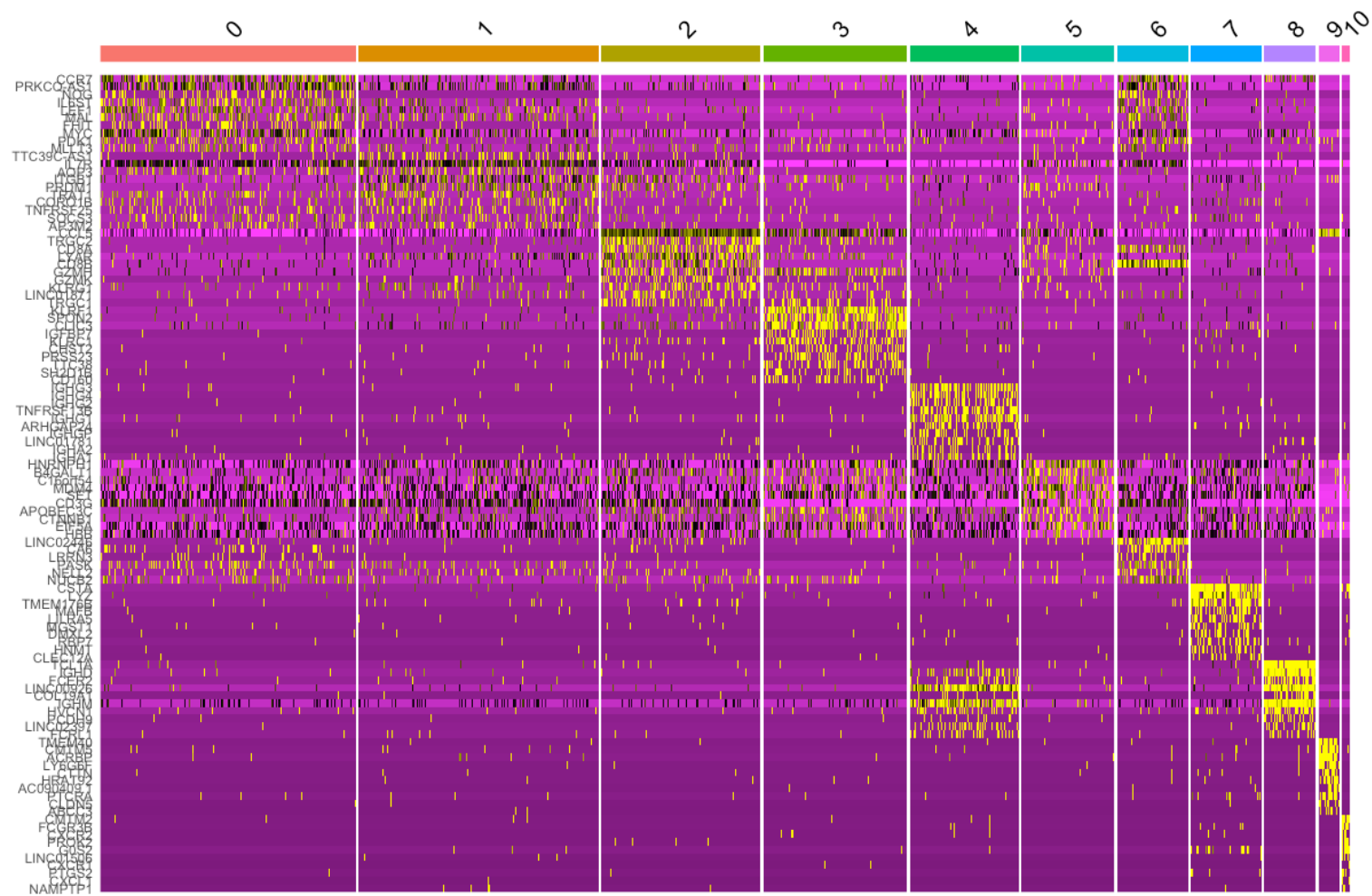


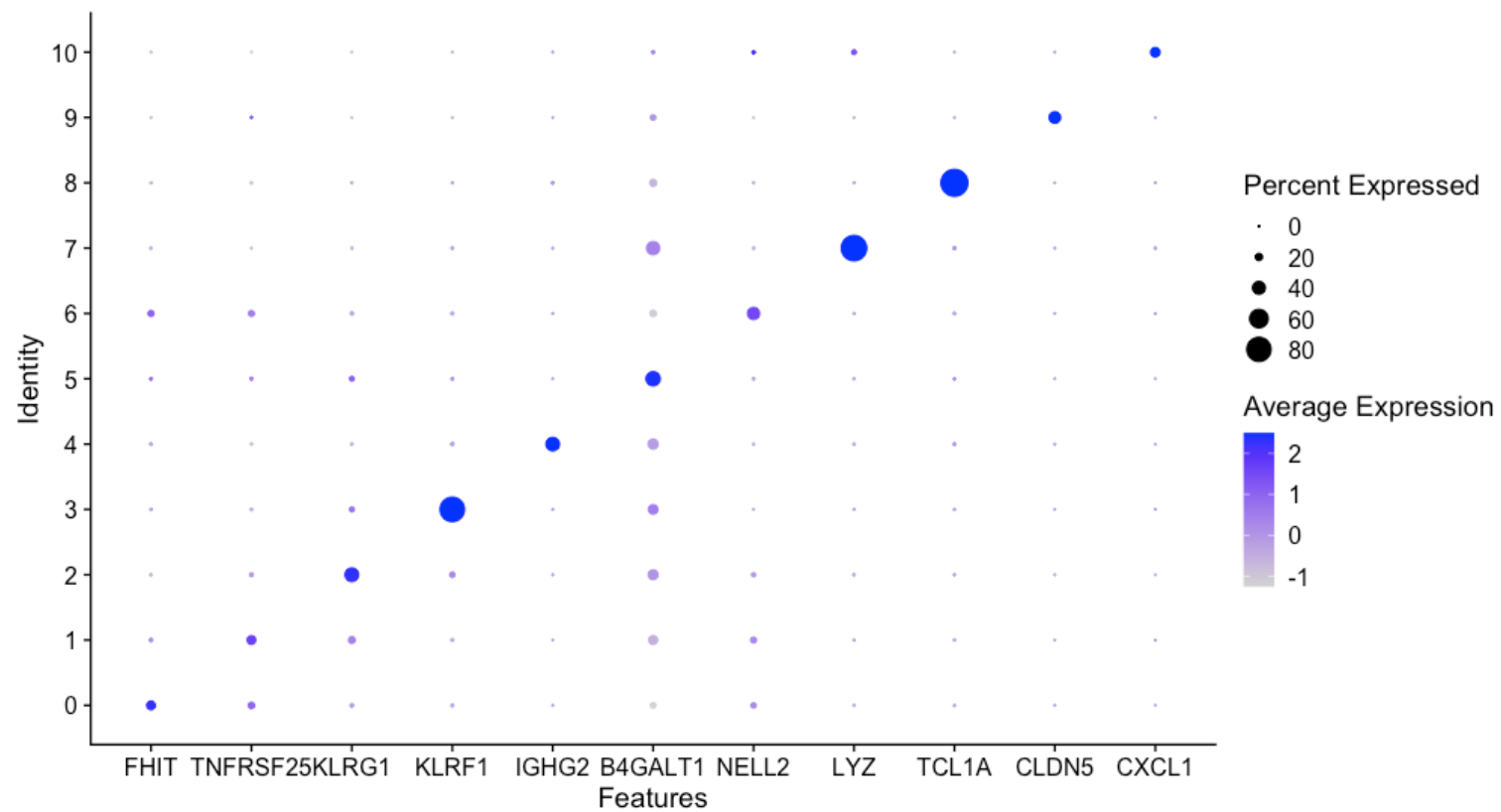
11 CLUSTERS



The 20 PCs are projected in a 2D plotting TSNE e UMAP

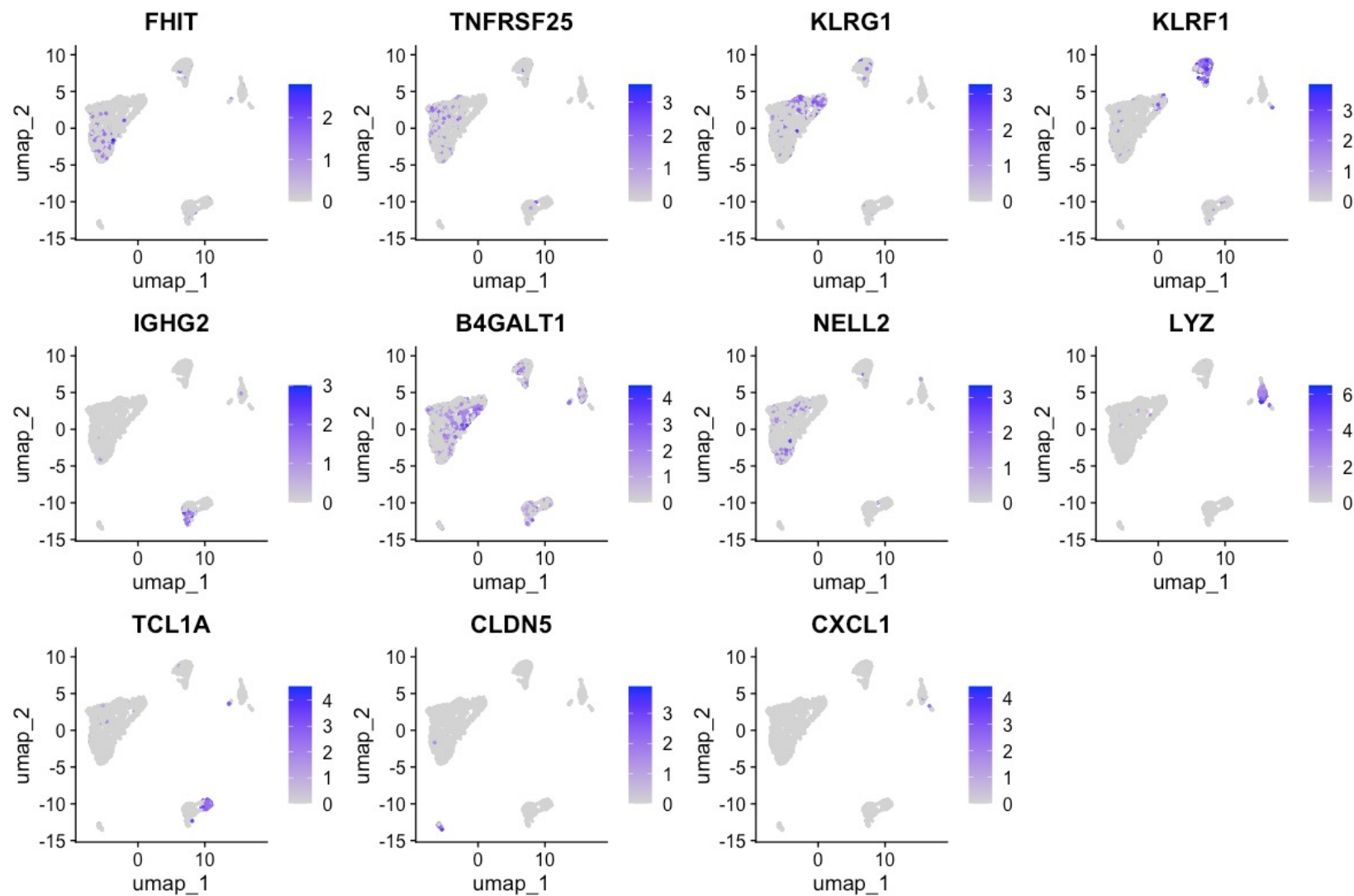






DOTPLOT

FEATURE PLOT



#CLUSTER 0: Oligodendrocytes

#CLUSTER 1: T-cells

#CLUSTER 2: Granulocytes

#CLUSTER 3: Nk-cells

#CLUSTER 4: B-cells

#CLUSTER 5: Monocytes

#CLUSTER 6: Excitatory neurons

#CLUSTER 7: Langerhans cells

#CLUSTER 8: Dendritic cells

#CLUSTER 9: Adipocytes

#CLUSTER 10: Basal respiratory cells

FINAL RESULTS

