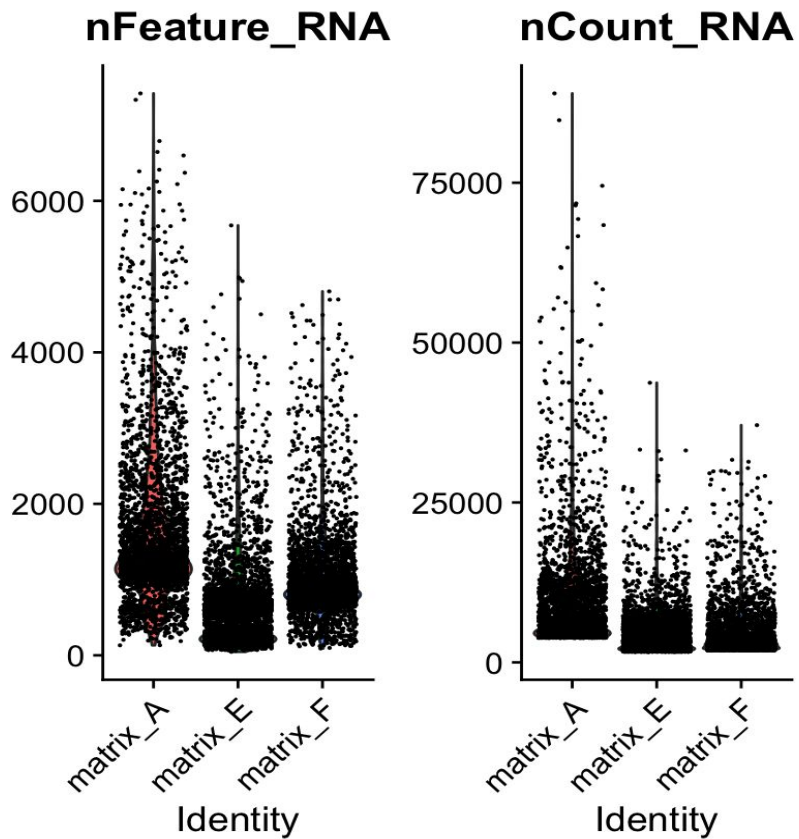


Single Cell RNA-Seq analyses on bone marrow data

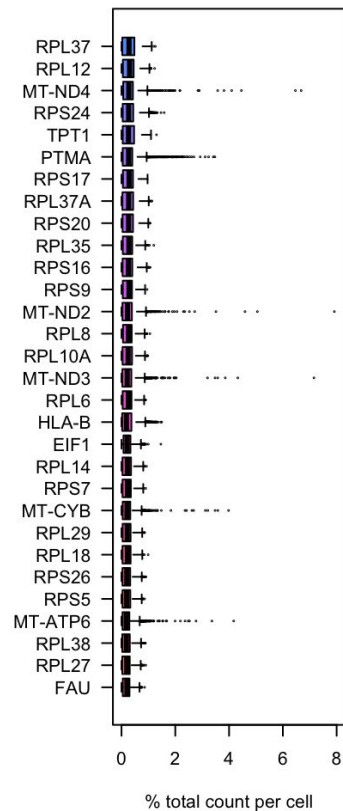
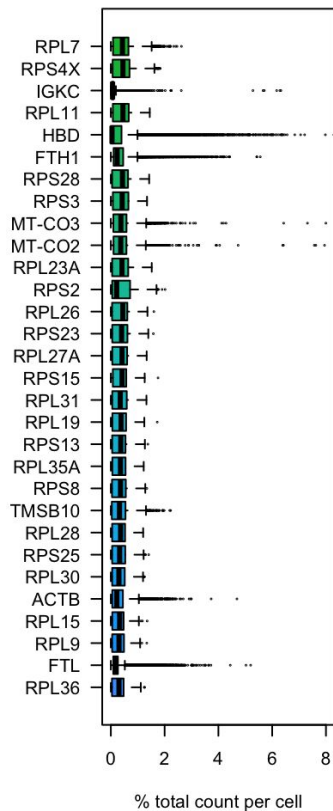
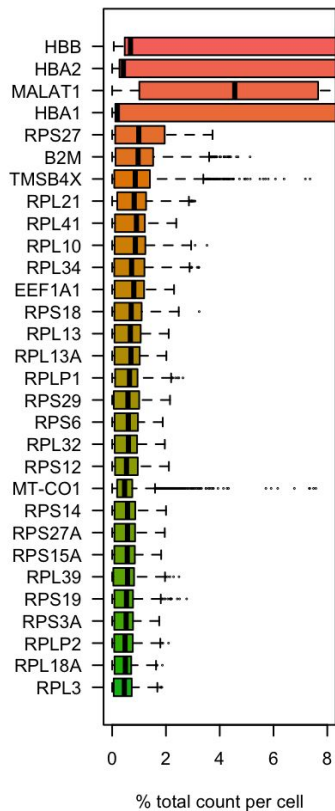
Main question: Which genes specifically drive the differentiation of Neutrophils?

Dominik Burri, Martina Troiani, Arianna Vallergera, Kristina Thumfart

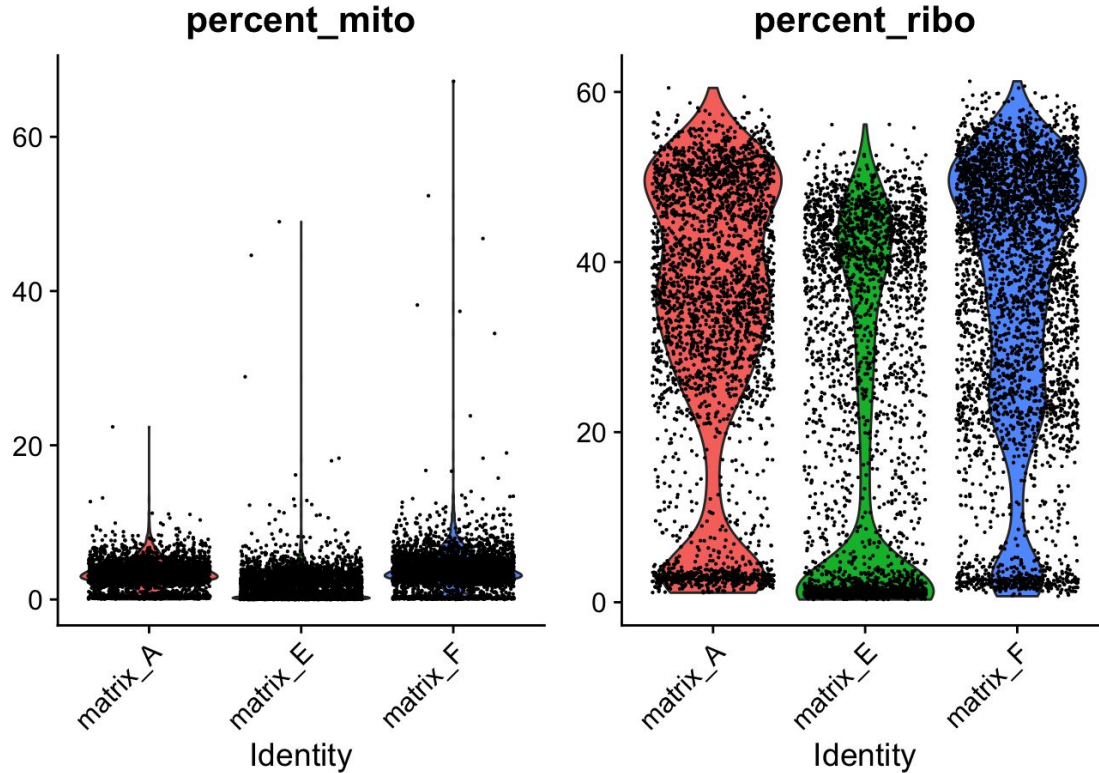
QC: nCounts/nFeatures



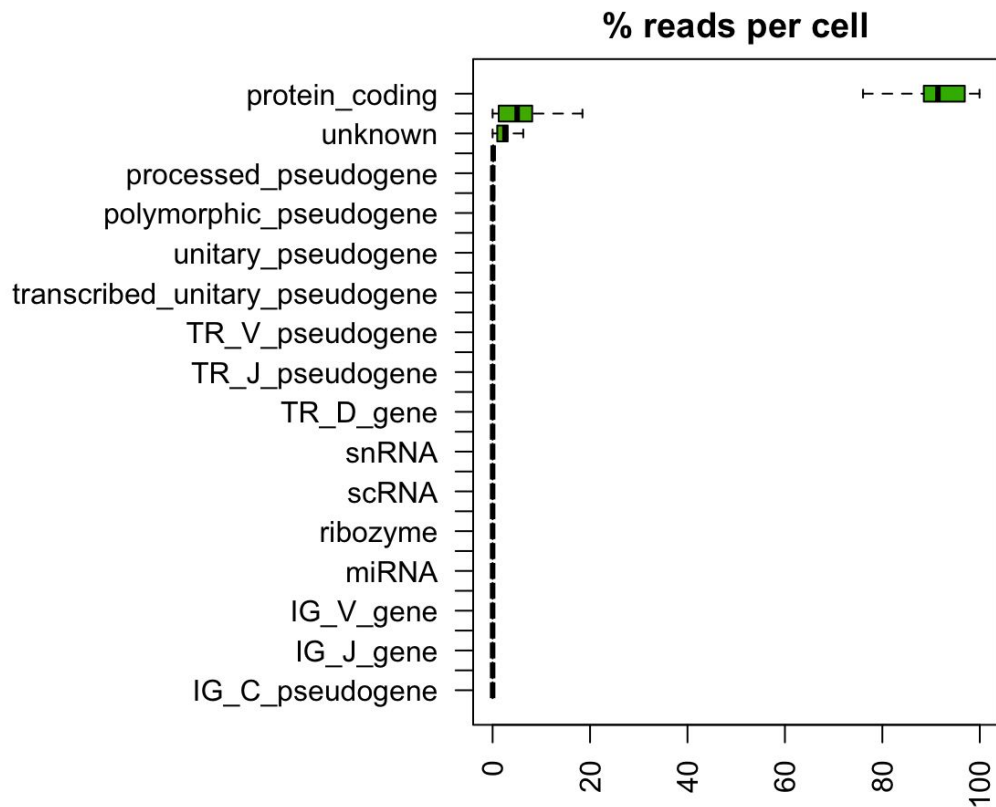
QC: Most expressed genes



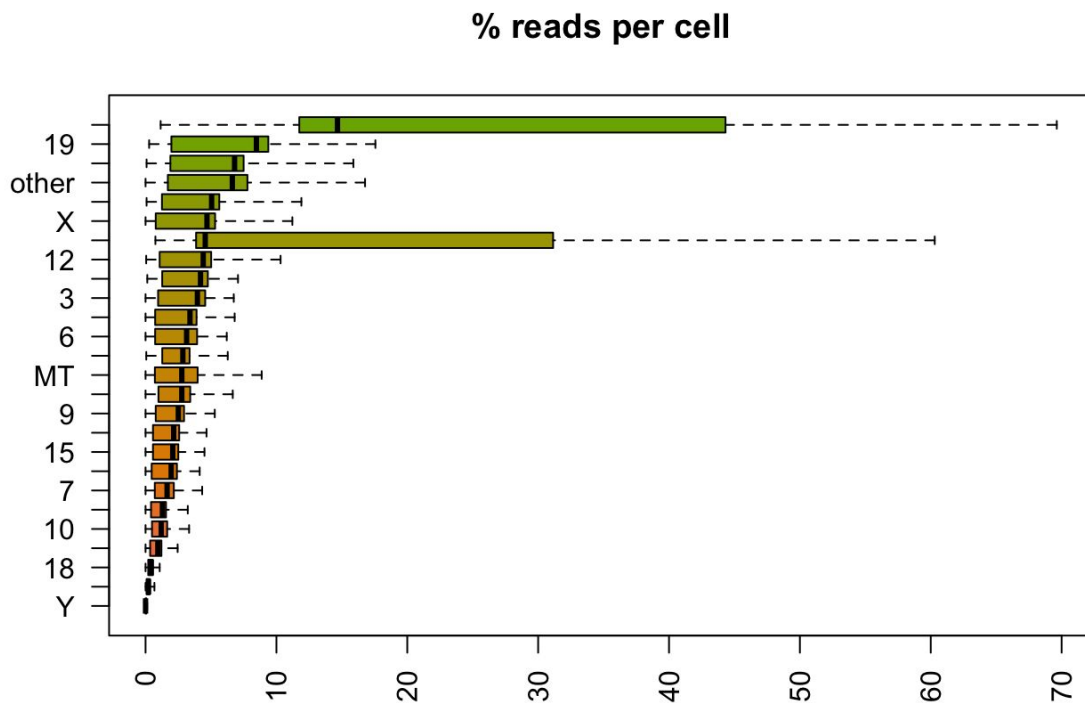
QC: mitochondrial and ribosomal gene %



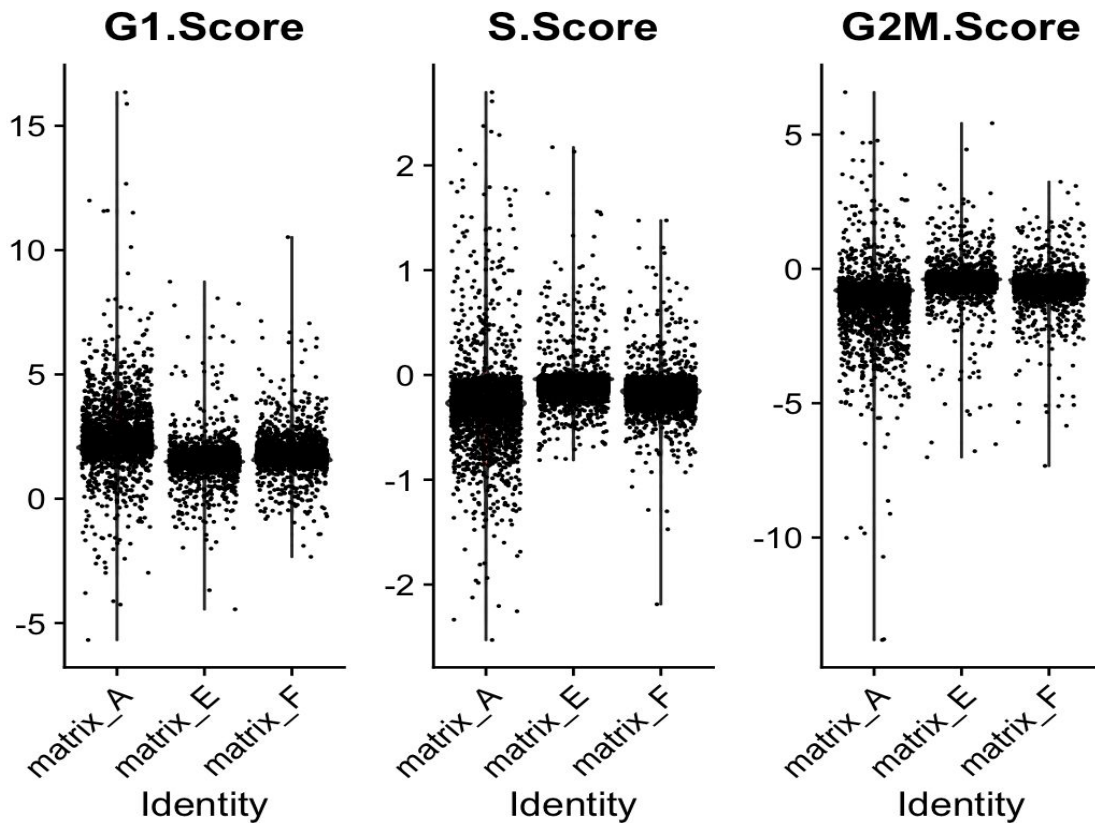
QC: biotype of genes



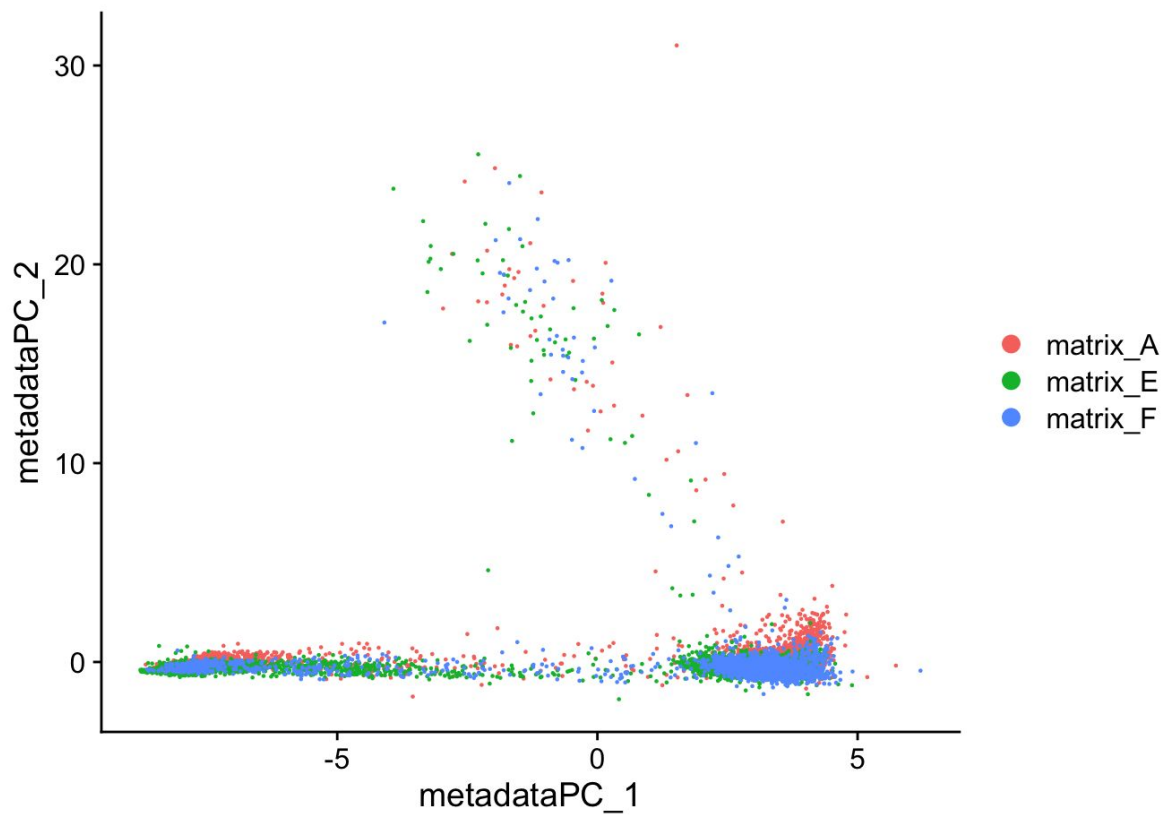
QC: chromosome location of genes



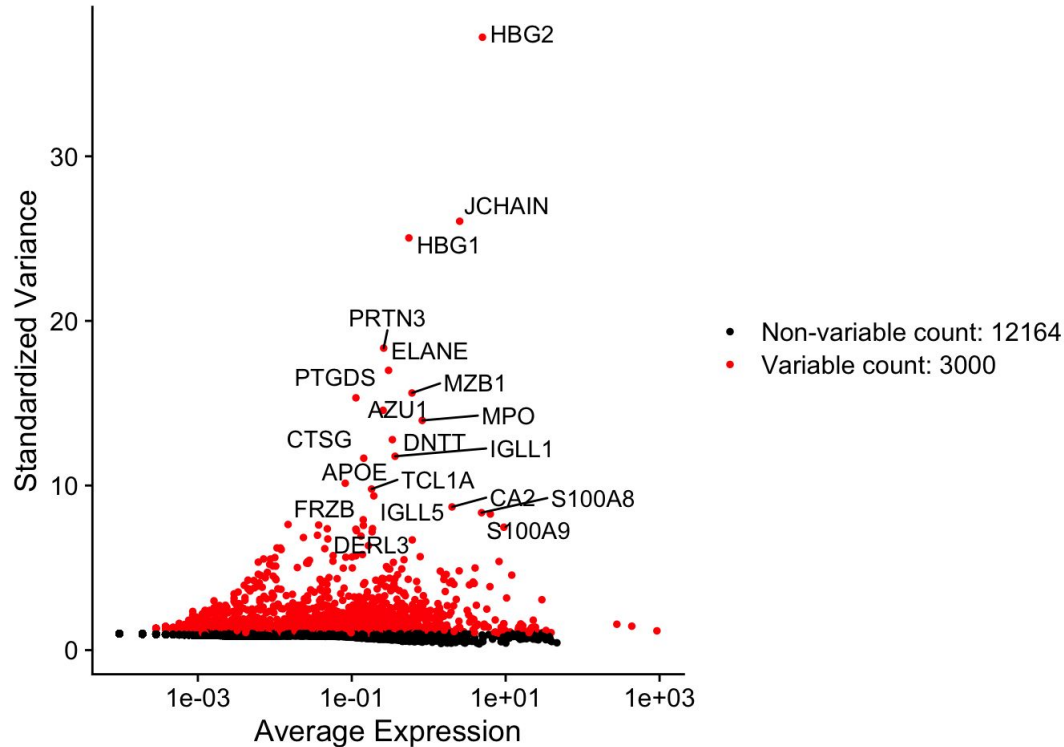
QC: Cell cycle comparison between samples



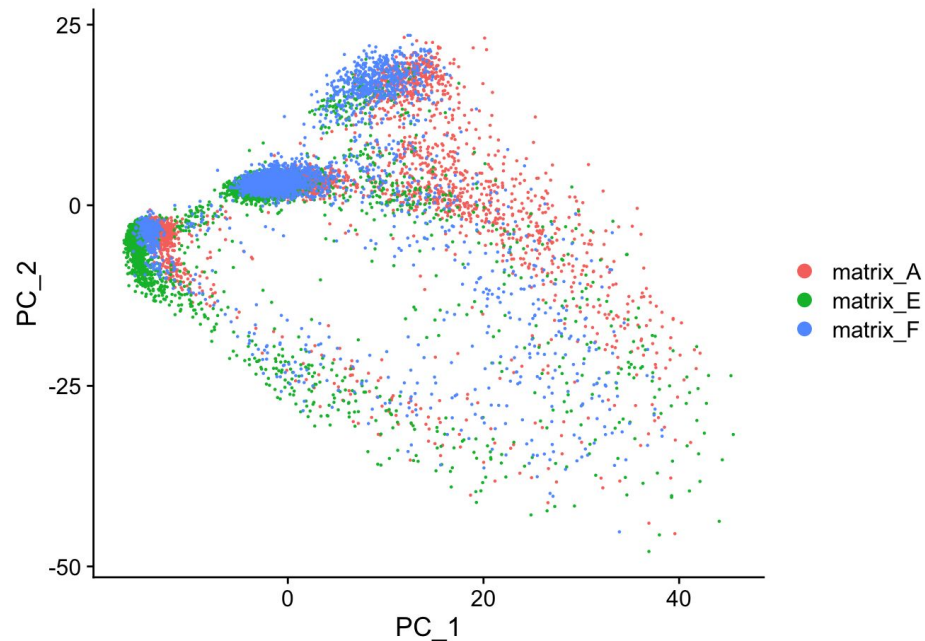
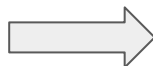
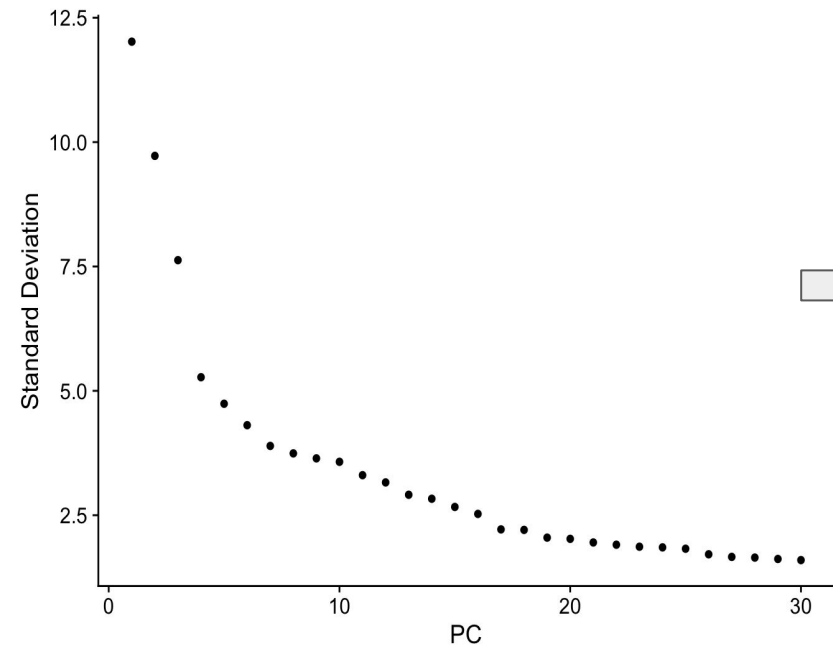
PCA on metadata



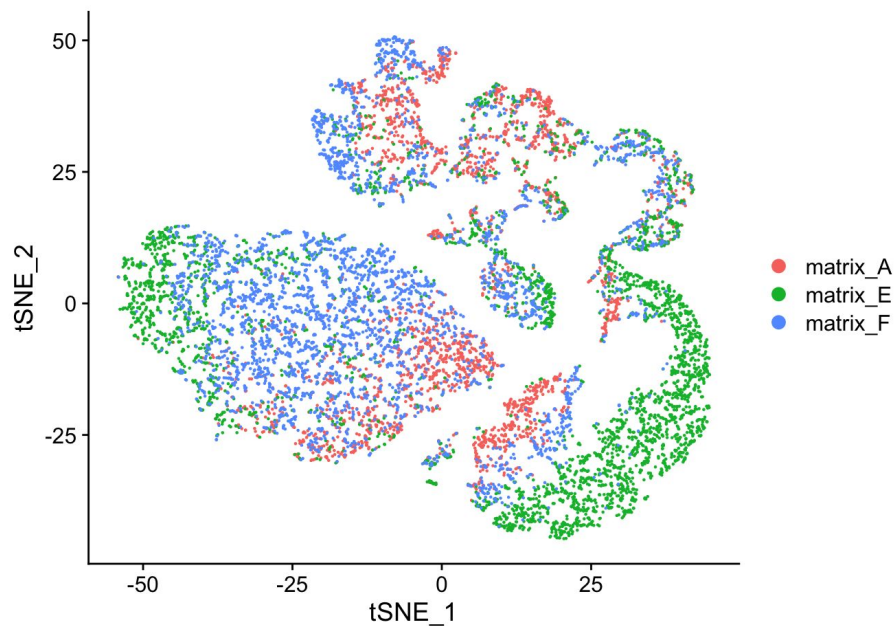
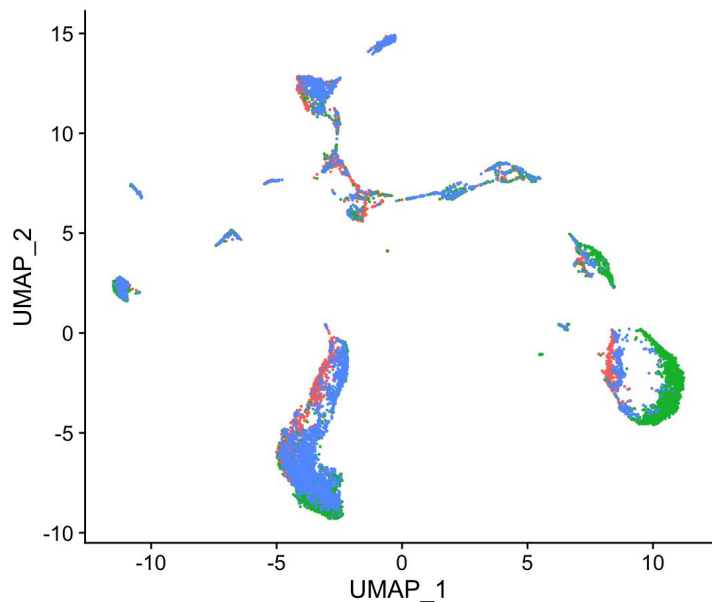
Feature Selection after Normalisation and Scaling



Data Visualisation - Elbow plot and PCA

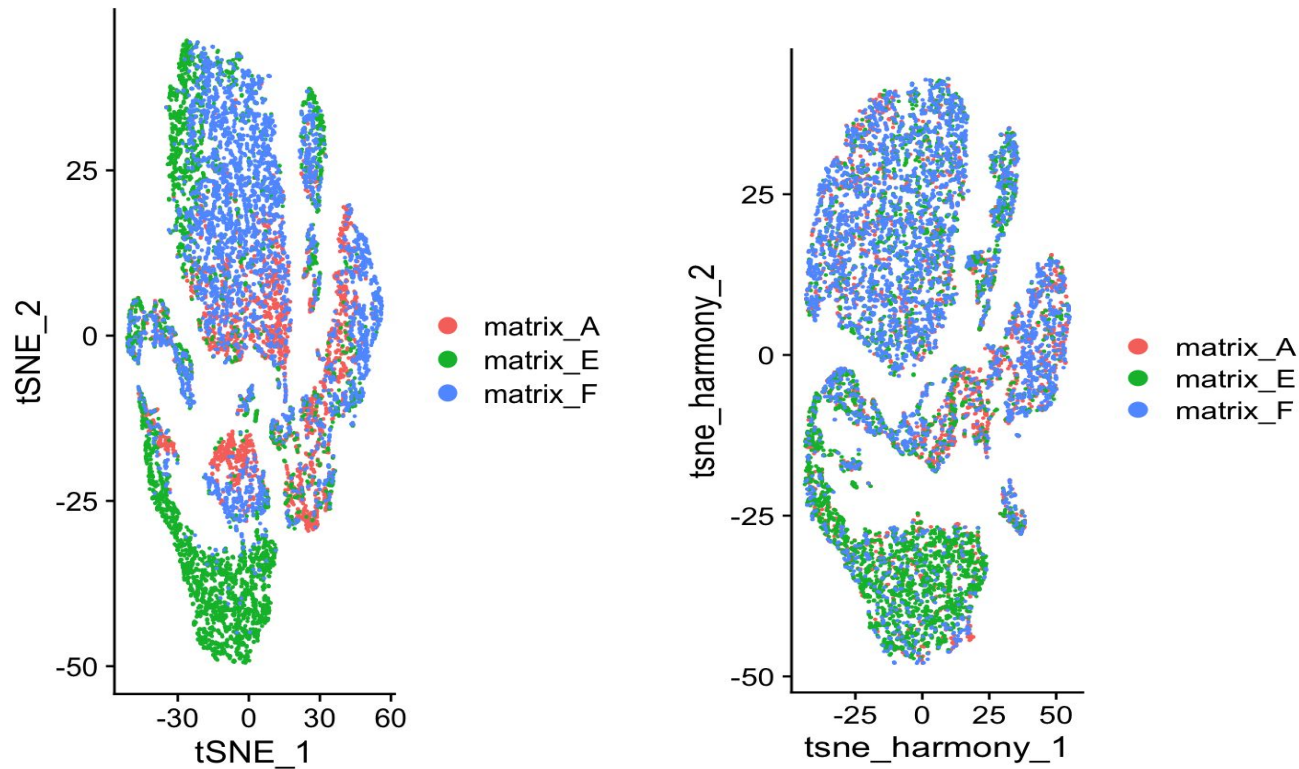


Data Visualisation - UMAP & tSNE

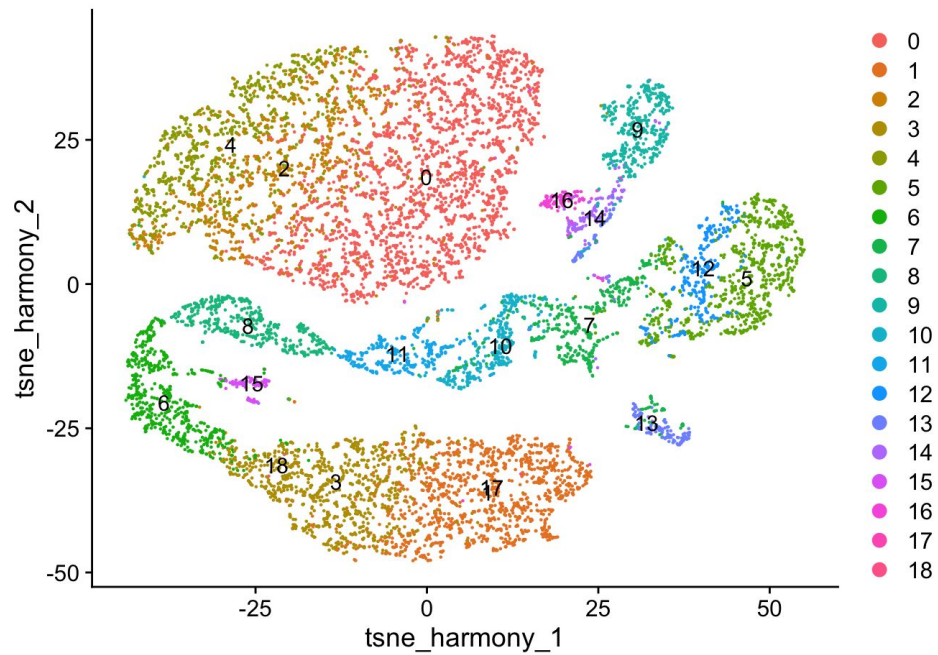
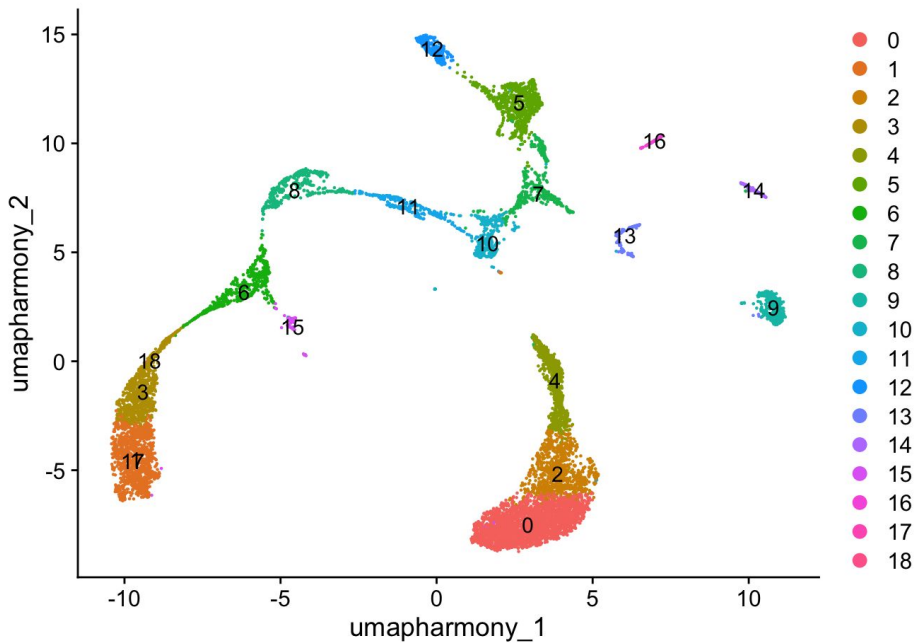


DATA INTEGRATION with harmony

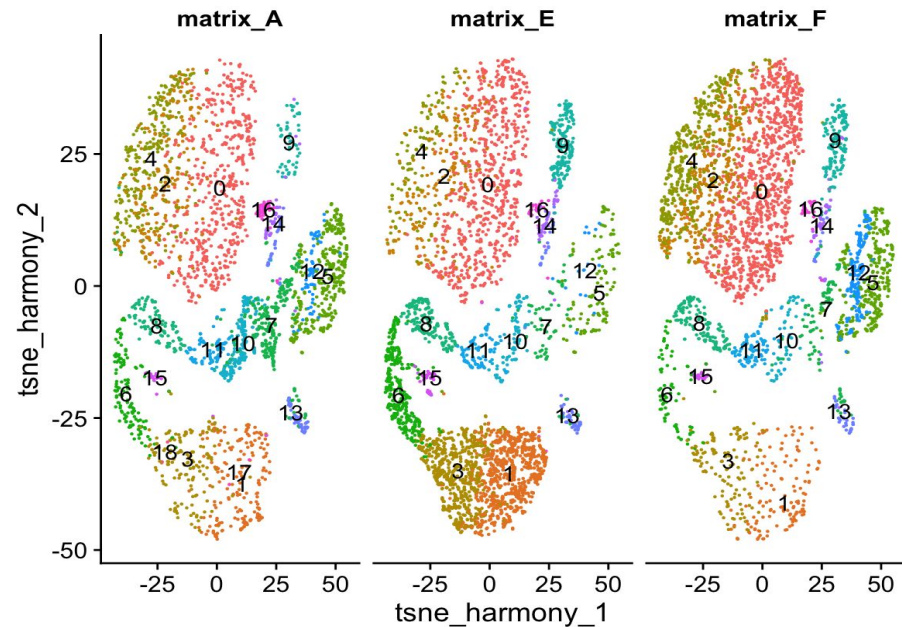
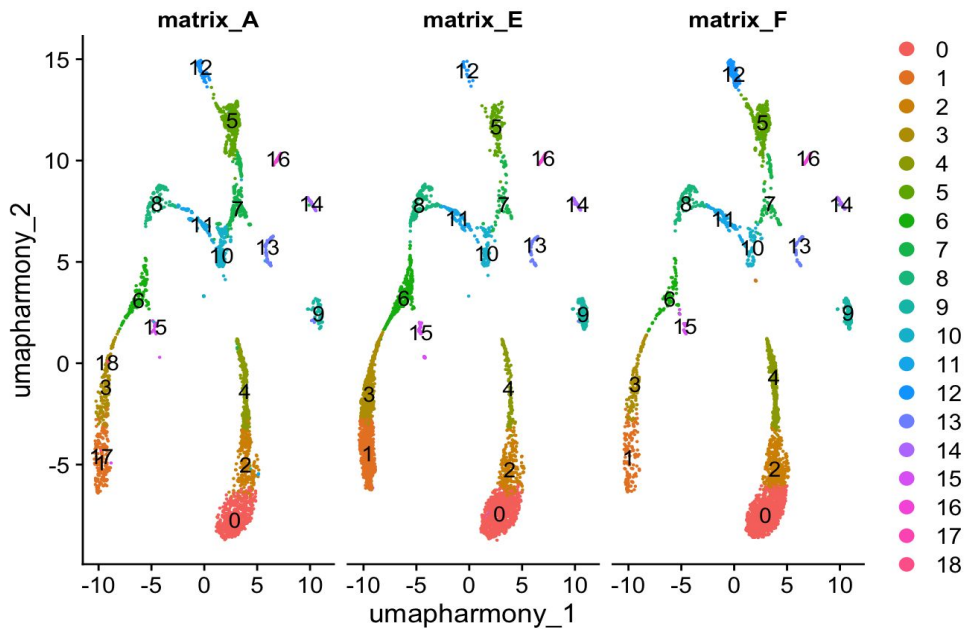
- data before and after integration



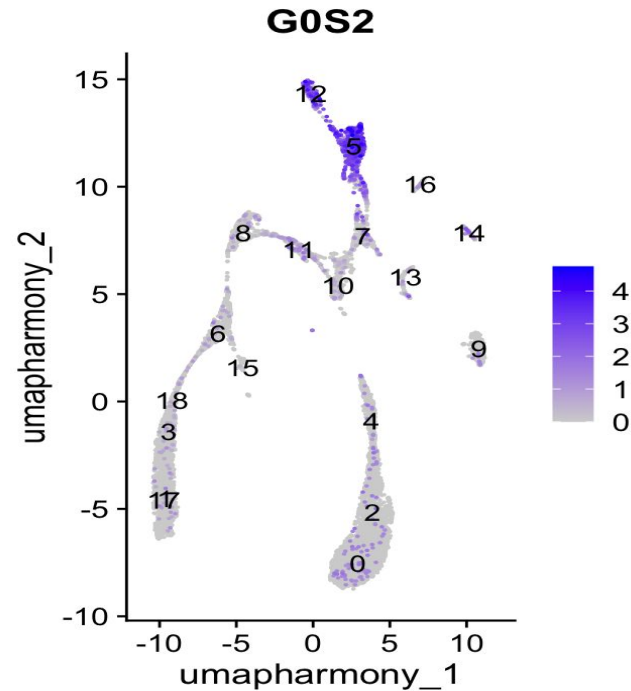
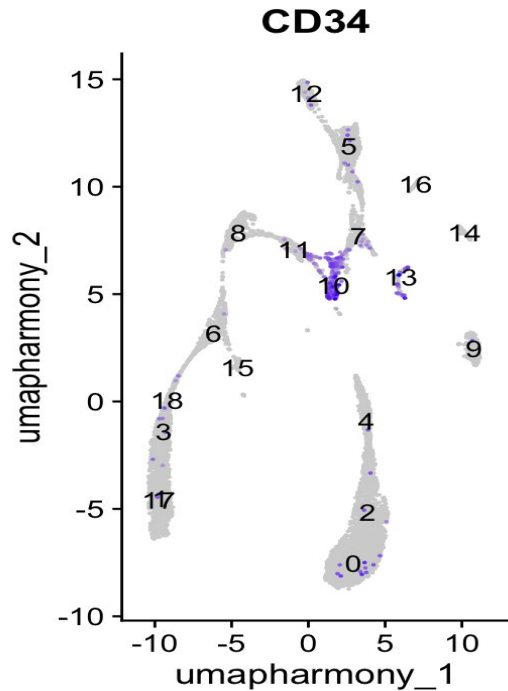
Cell clustering - UMAP & tSNE



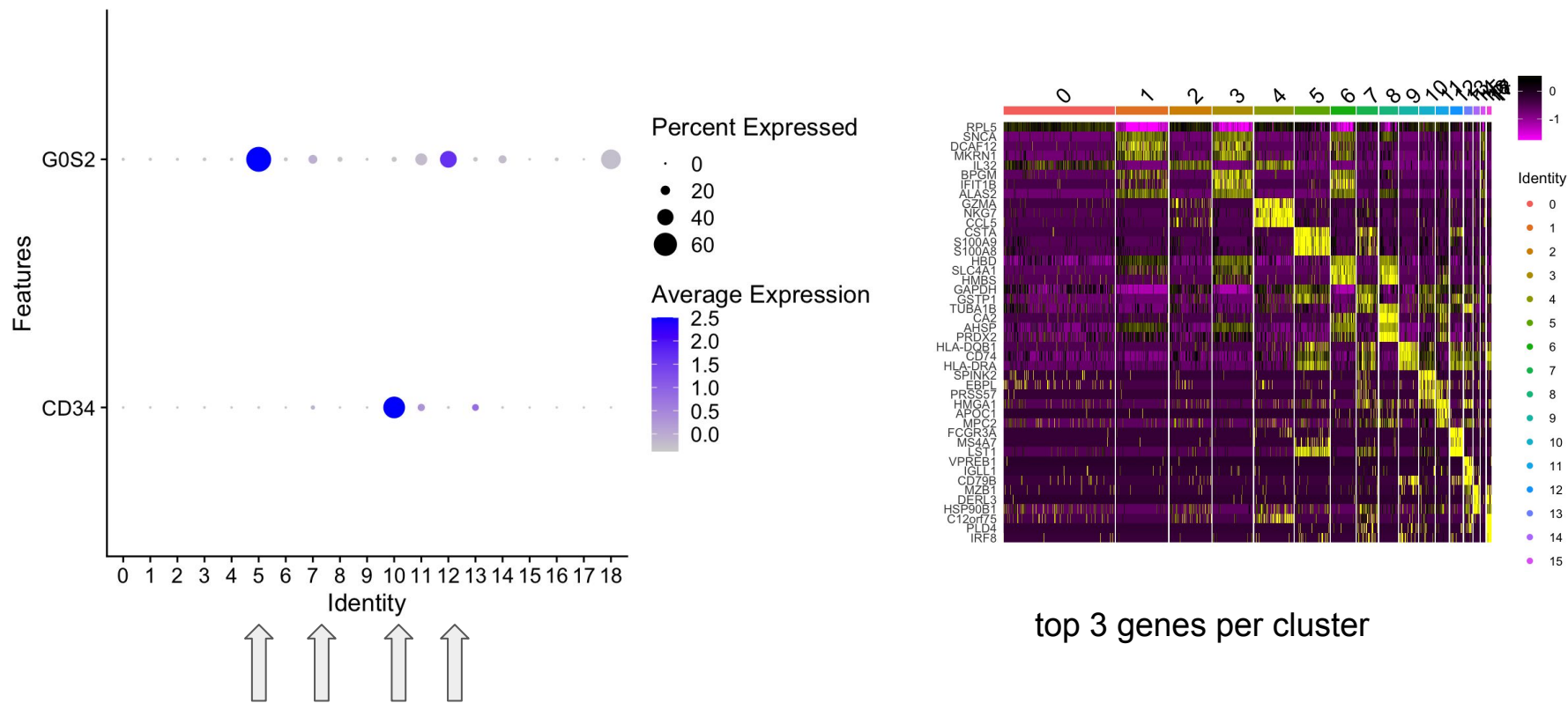
Cell clustering per sample



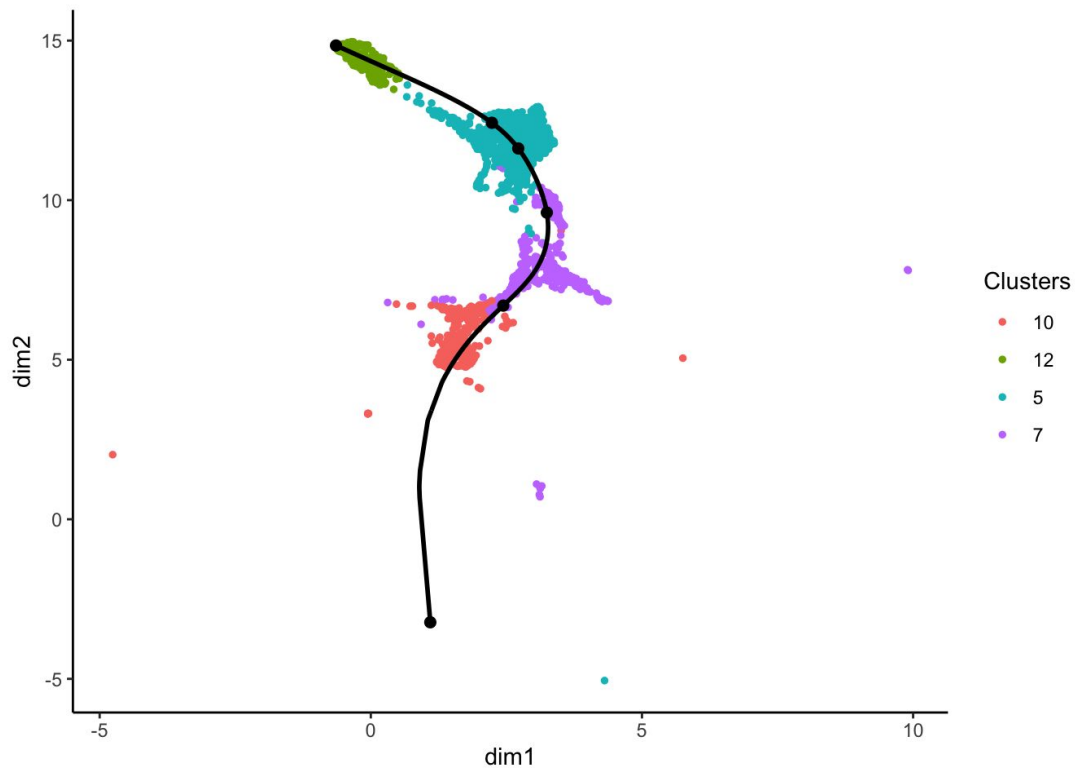
Differential expression: CD34 (progenitor marker) and G0S2 (mature neutrophil marker)



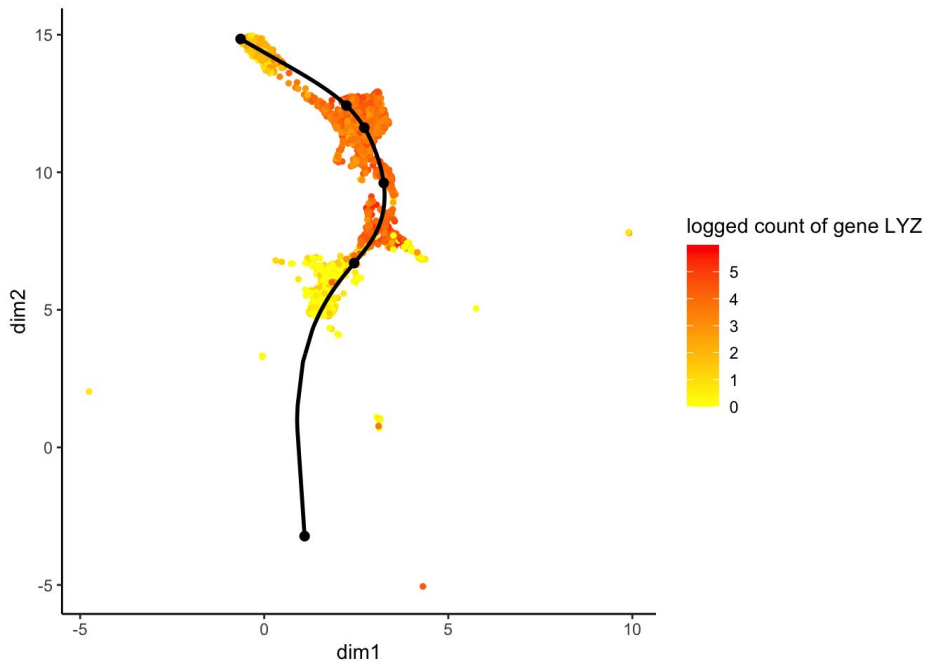
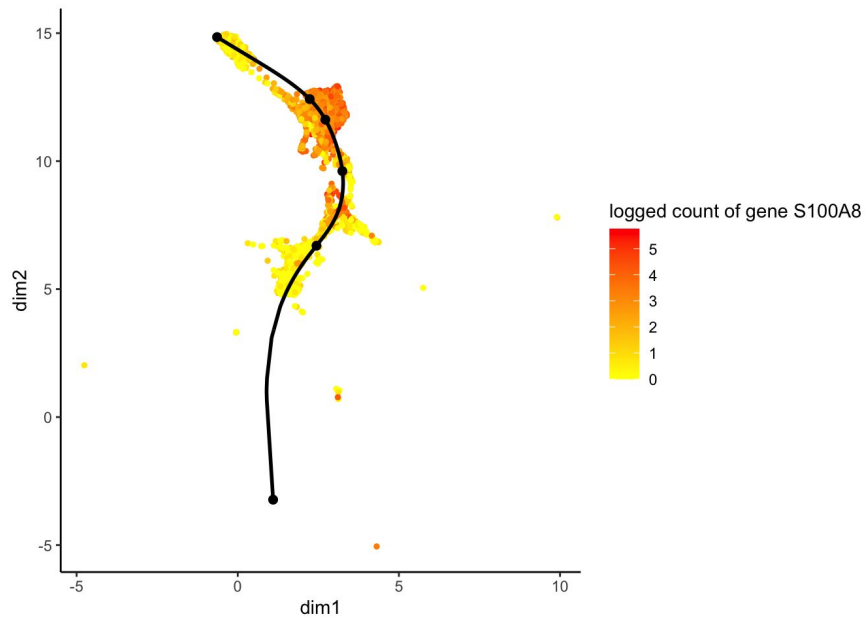
Selection of clusters using dotplot and heatmap



Trajectory inference (UMAP - harmony corrected)

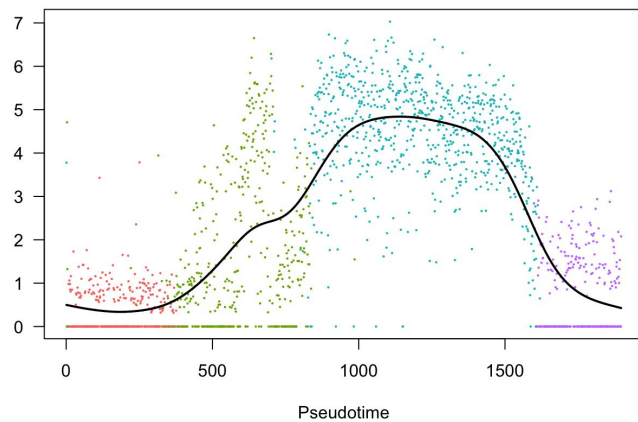


Trajectory inference (log-count of genes)

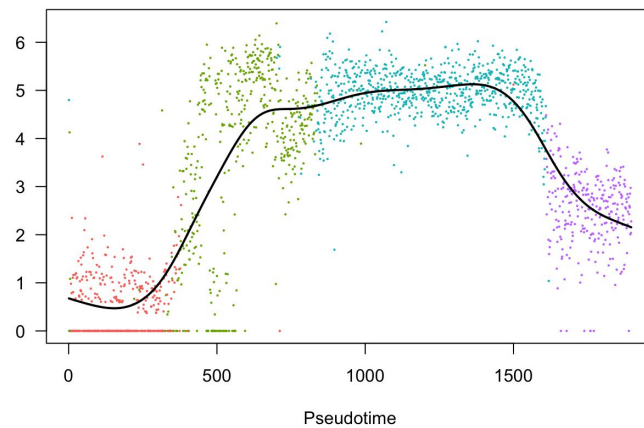


Trajectory inference (example gene in Pseudotime)

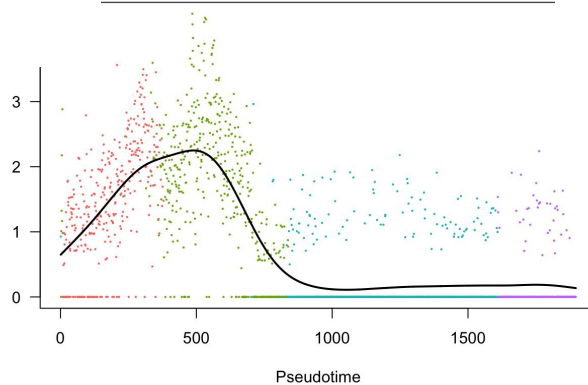
S100A8



LYZ



STMN1



Gene set enrichment

