

Group 5

Assignment on scRNA-seq Data Analysis

Snakemake Workflow Output Results

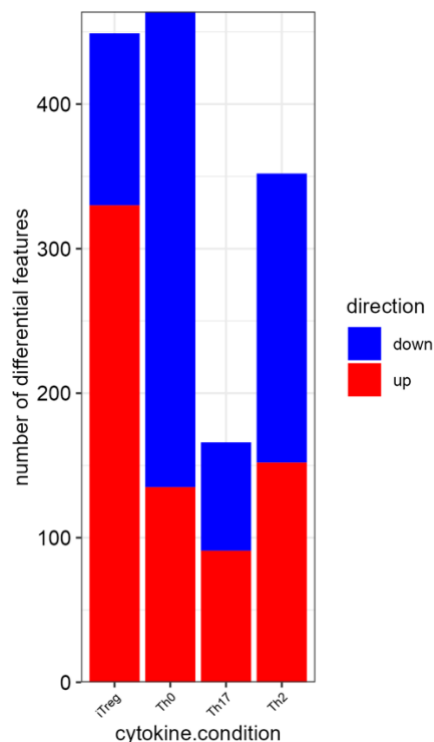
Group members

Ali Balbaid, Azari Bantan & Turki Sobahy

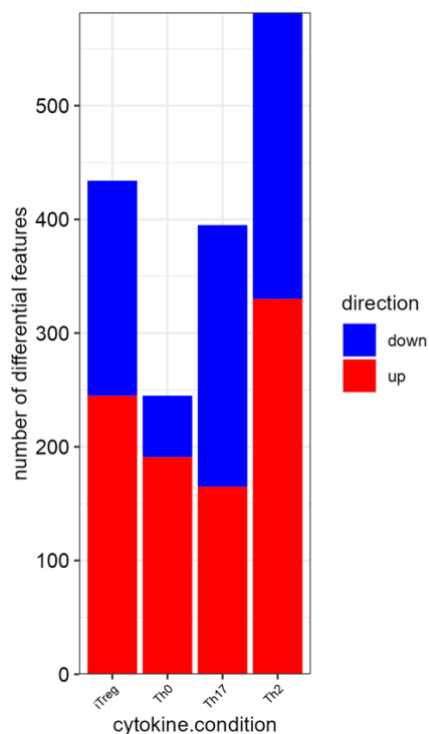
This report presents the output results from our version of the Snakemake workflow tailored for single-cell analysis, accessible at https://github.com/roblehmann/dea_seurat. This version is a fork and has been adapted in our own repository. It incorporates a pipeline that performs differential gene expression analysis and has been extended to include a new rule that generates a dot plot. This plot visualizes the top 10 marker genes for each cluster found in the 'cytokine.condition' column, and it does so for both naïve and memory T-cell types. The dataset is available at <https://doi.org/10.1038/s41467-020-15543-y>, from Gamez, et al. (2020) paper.

The number of differential features per cluster in A) memory and B) naïve T-cells.

A)

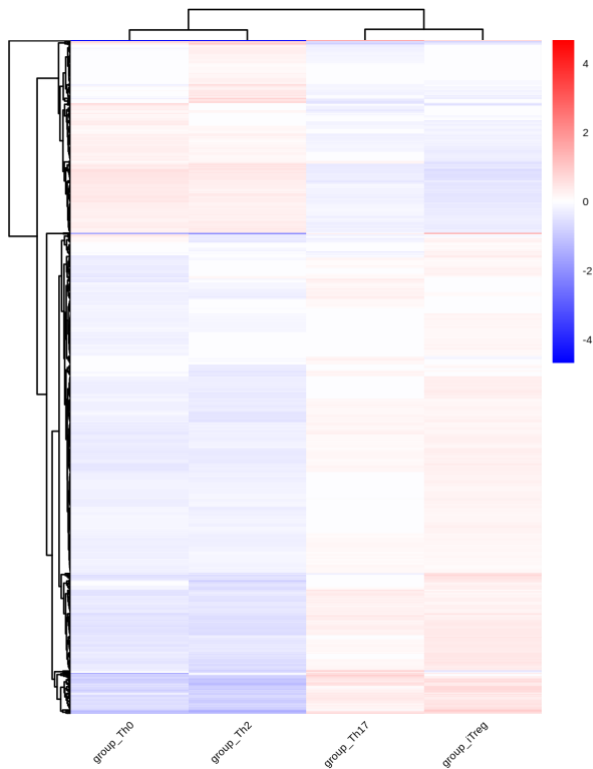


B)

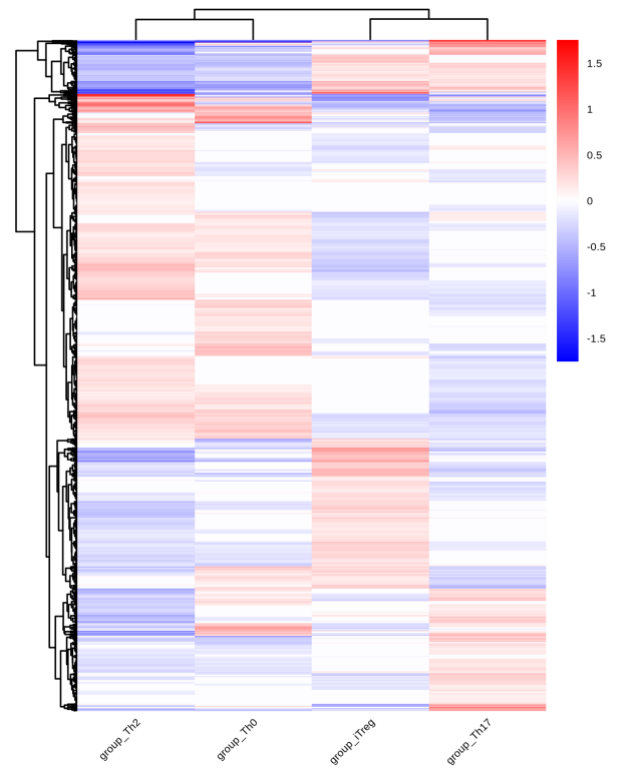


Heatmap of differentially expressed genes (lfc) per cluster in A) memory and B) naïve T-cells.

A)

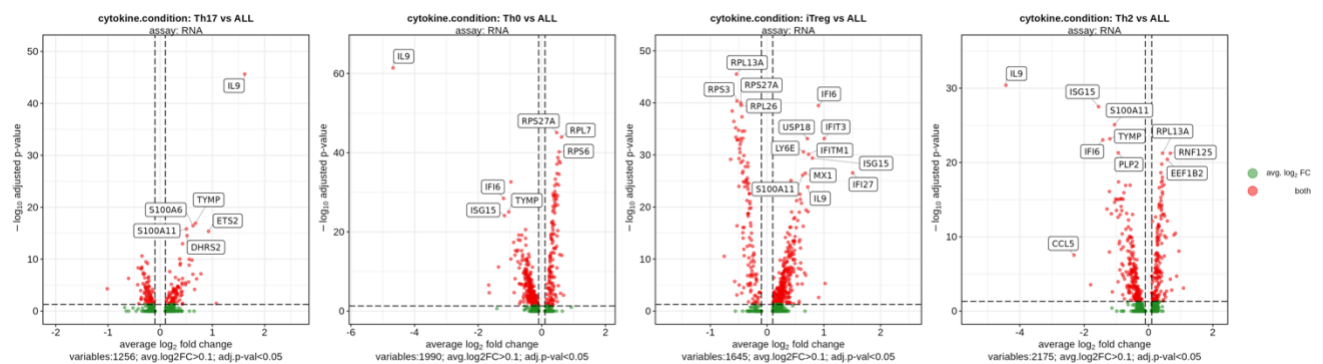


B)

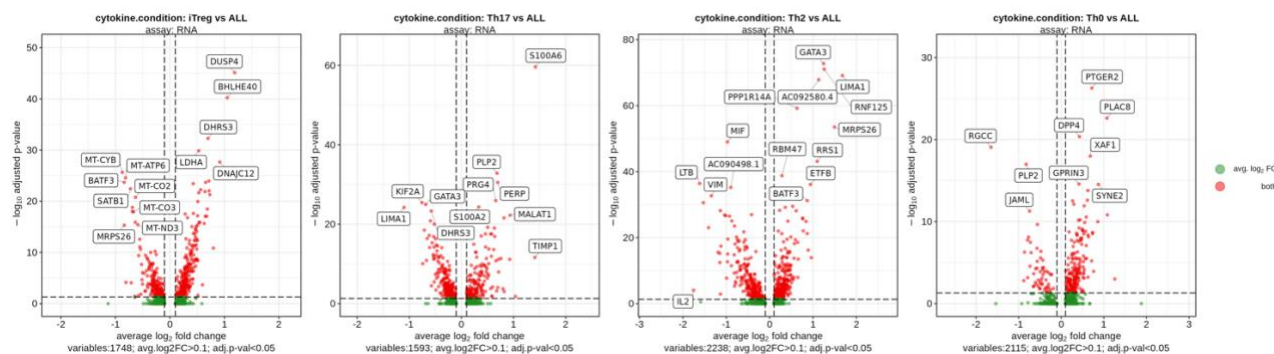


Volcano plot of differentially expressed genes per cluster in A) memory and B) naïve T-cells.

A)

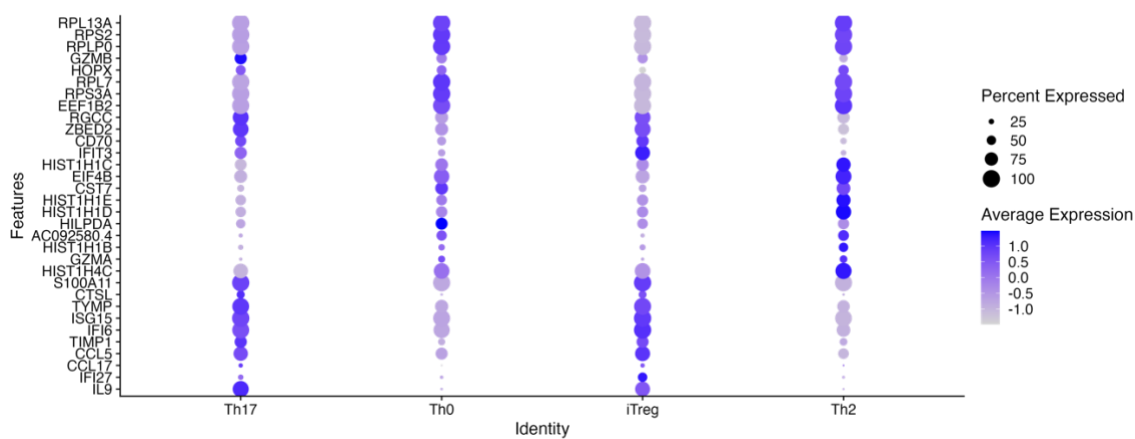


B)



Dot plot for the top 10 marker genes per cluster in A) memory and B) naïve T-cells.

A)



B)

