Title: Analysis of T Cell Response to Cytokine Stimulation

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Study Overview:

This research explores into the intricate dialogue among immune cells, focusing on how cytokines influence the evolution of naïve CD4+ T cells into specialized effector cells. Such transformation is crucial for orchestrating immune responses, with naïve CD4+ T cells differentiating into various T helper (Th) cell types under cytokine guidance.

Methodological Approach:

Our study utilizes single-cell RNA sequencing to unravel the differential gene expression patterns in human naïve and memory CD4+ T cells upon stimulation. We compared TCR/CD28-activated cells in the absence of cytokines (termed Th0) with cells exposed to cytokines, leading to the differentiation into Th2, Th17, and iTreg phenotypes.

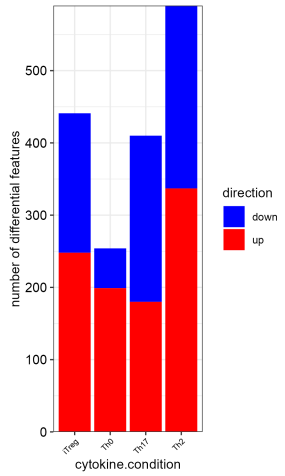
Key Findings:

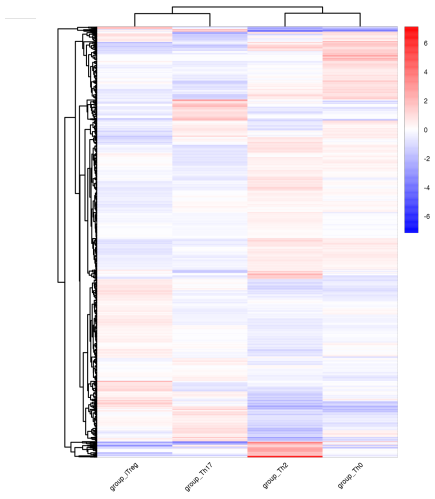
- **Gene Regulation Insights:**
  - **Naïve T Cells:** Significant upregulation and downregulation of genes were observed, identifying potential regulators like RGCC and DIXDC1 (upregulated) and XAF1 and PLAC8 (downregulated).
  - **Memory T Cells:** In this case, genes such as IL9 and TYMP showed upregulation, whereas RNF125 and RPL7 were downregulated.

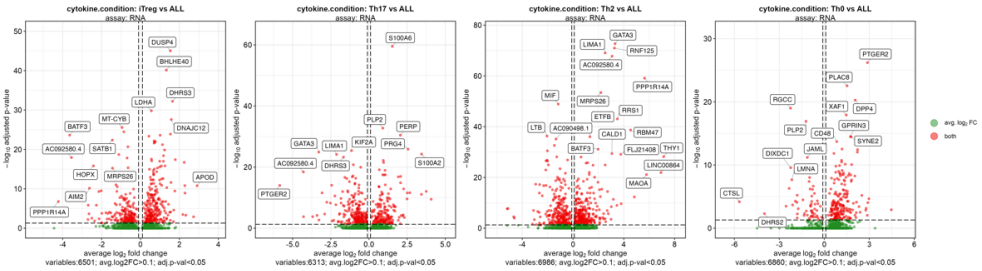
Visual Data Representation:

The study includes various graphical representations, barplot for the DE gene number, volcano plots and heatmaps, to visually depict the gene expression differences and highlight the clusters of genes with shared expression patterns across different T cell states

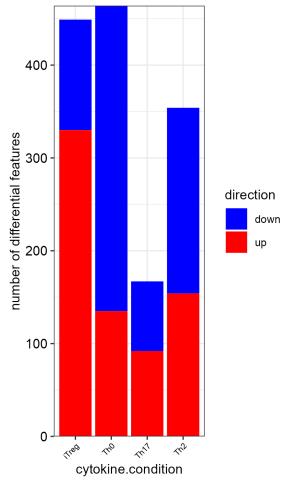
Naïve Tcells

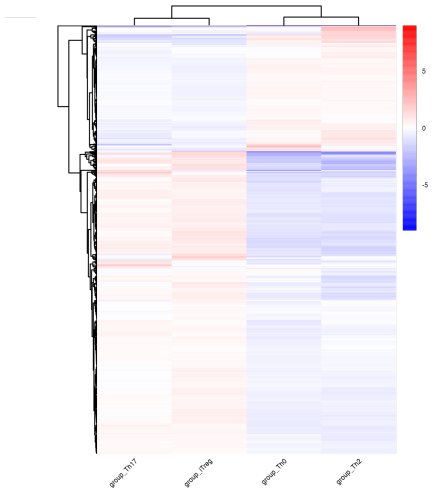


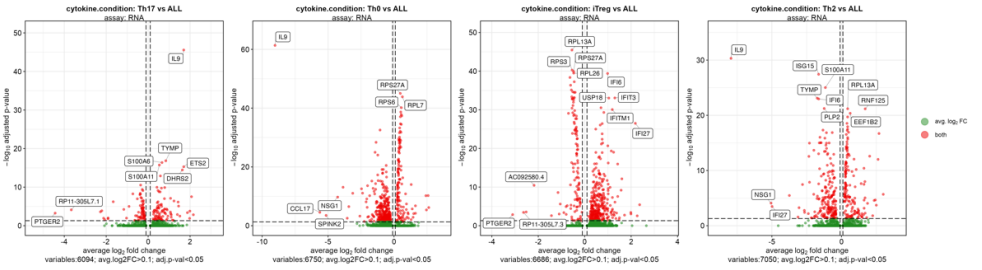




Memory Tcells







Add clustering with specified resolution to specified metadata column:

Group 4 assignment results in umap_res.R and umap_res.smk files where we compare a clustering using 0.6 resolution and add the column to our object metadata.

Conclusions:

Our analysis shows the complex transcriptional landscapes of naïve and memory T cell subsets, examining both overlapping and unique gene regulation mechanisms across T cell types. This investigation into differential gene expression offers a deeper understanding of T cell biology, paving the way for identifying novel therapeutic targets.