Group 3

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References

Cano-Gamez, E., Soskic, B., Roumeliotis, T.I. et al. Single-cell transcriptomics identifies an effectorness gradient shaping the response of CD4+ T cells to cytokines. Nat Commun 11, 1801 (2020). https://doi.org/10.1038/s41467-020-15543-y

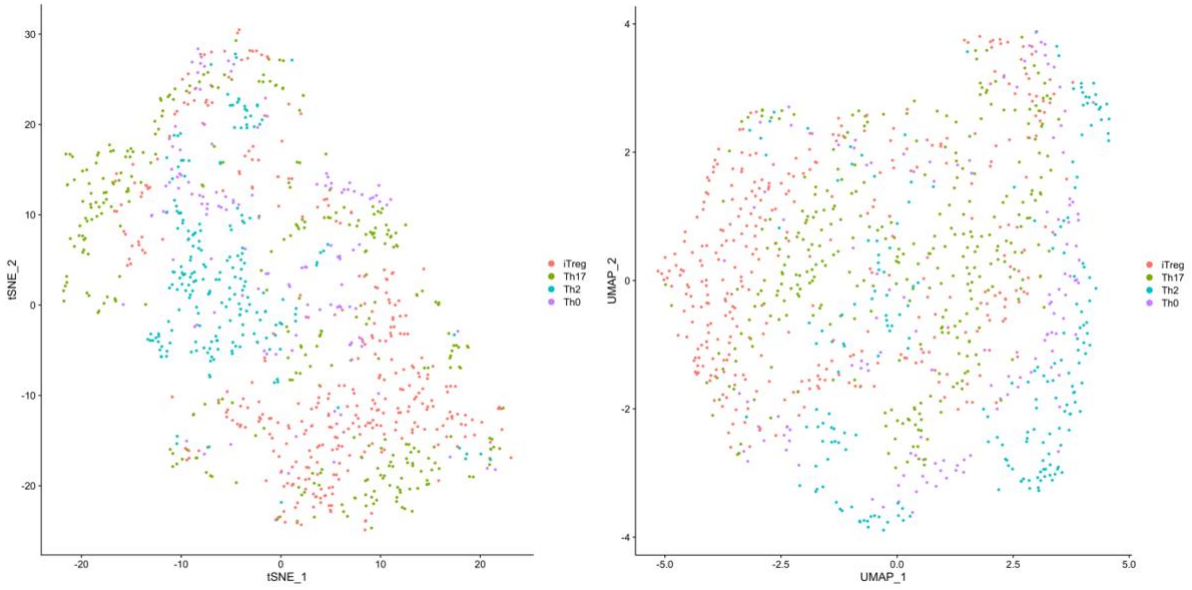
Differential Expression for naïve and memory cell datasets.

The communication between immune cells is mediated by cytokines, which promote the differentiation of cells into effector cell types. In particular, upon activation, naïve CD4+ T cells are polarized by cytokines into T helper (Th) phenotypes, including Th2, Th17 and iTreg. T helper cells in turn coordinate the downstream response of other immune cells.

In the analysis we investigated the effects of cytokines on human naïve and memory CD4+ T cells. We used single cell RNA-seq data to perform differential expression analysis between TCR/CD28-activated cells without cytokines stimulation (Th0) and four TCR/CD28-activated T helper phenotypes (Th2, Th17, and iTreg) stimulated in the presence of various cytokines.

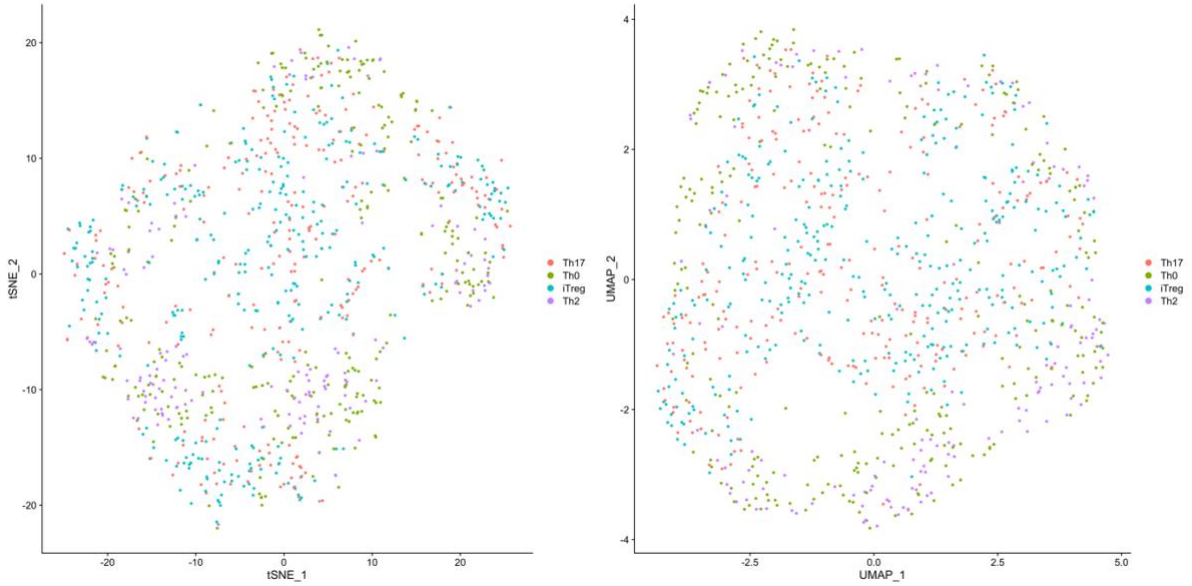
Datasets:

- Naïve T cells



The tSNE and UMAP plots display clustering of Naive T cells, suggesting heterogeneity in the cell population. The clusters do not strictly represent different Th phenotypes within the Naive T cells.

- Memory T cells

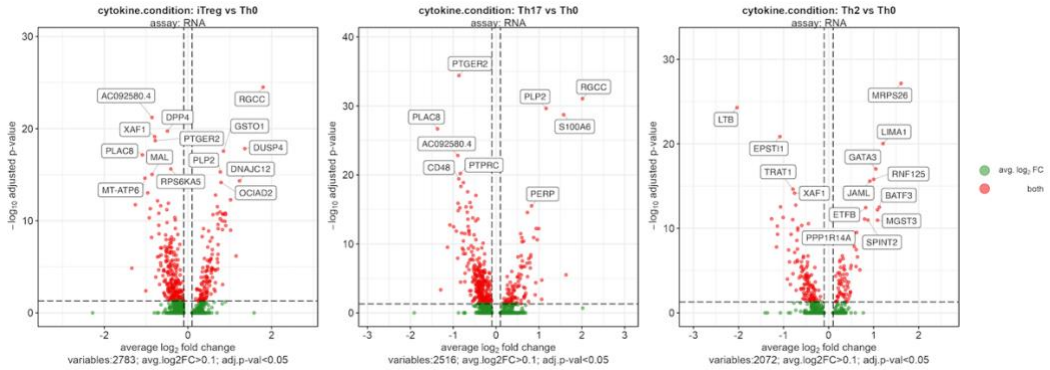


The tSNE and UMAP plots display clustering of Memory T cells, suggesting heterogeneity in the cell population. The clusters do not strictly represent different Th phenotypes within the Memory T cells.

Differential Expression results:

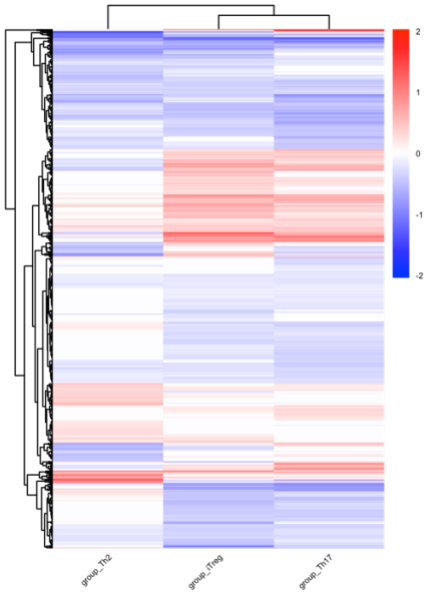
- Naïve T cells

1. Volvano plots of differential genes



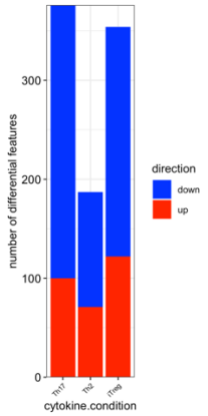
The volcano plots indicate several genes significantly upregulated or downregulated. The genes with the highest fold changes and statistical significance are potential key regulators of Naive T cell function. We can distinguish RGCC, PLP2 genes upregualted in both iTreg and Th17. XAF1 gene downregulated both in iTreg and Th2 as well as PLAC8, AC092580.4 genes downregulated both in iTreg and Th17.

2. Heatmap of differential features



We can distinguish several genes clusters that have a shared expression profile in Th17 and iTreg. A small cluster has genes that are upnregulated in comparison with Th0. And a few clusters of downregulated genes in comparison with Th0.

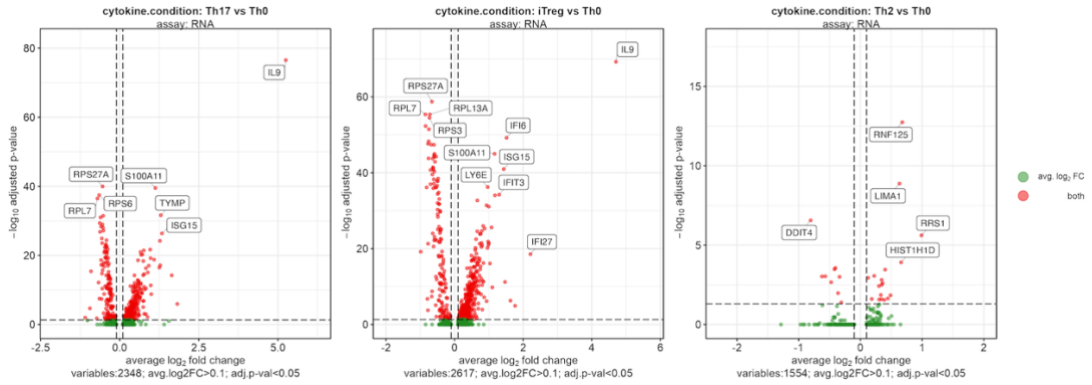
3. Number of genes



All of the Th phenotypes have aprox. 100 upregulated genes, however the number of downregulated genes is much higher for Th17 and iTreg.

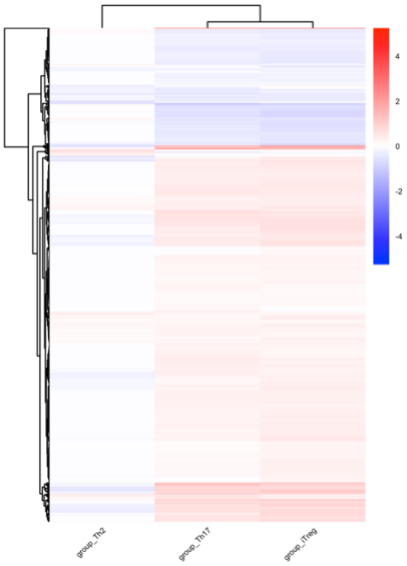
- Memory T cells

1. Volvano plots of differential genes



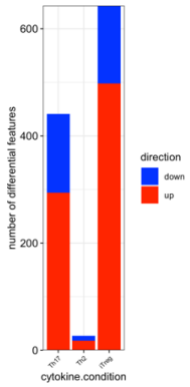
The volcano plots indicate several genes significantly upregulated or downregulated. The genes with the highest fold changes and statistical significance are potential key regulators of Memory T cell function. We can distinguish IL9, ISG15, S100A11 genes upregualted in both iTreg and Th17. RPS27A, RPL7 genes downregulated both in iTreg and Th17.

2. Heatmap of differential features



There are only a few differential genes between Th0 and Th2. We can distinguish two main genes clusters that have a shared expression profile in Th17 and iTreg. A small cluster has genes that are downregulated in comparison with Th0. And a big cluster of upregulated genes in comparison with Th0.

3. Number of genes



There are almost no differential genes between Th0 and Th2.

In summary, the analyses reveal complex transcriptional landscapes within Naive and Memory T cell populations, indicating both shared and distinct regulatory mechanisms across different T cell states. Further investigation into the genes identified as differentially expressed could provide valuable insights into T cell biology and potential therapeutic targets.