Single cell RNA - seq analysis for muscle samples

1. Results:

a. t-SNE :

In my analysis, the t-SNE plot (fig. 1)) closely aligns with the configuration observed in the reference paper. Specifically, the expected clustering of Endothelial Cells is evident, underscoring the reliability of the t-SNE analysis. Notably, T and B cells, alongside NK cells, exhibit close spatial affinity, reflecting their shared immune cell features. Furthermore, distinct separation is apparent among Satellite, LUM+FAP, and FBN1+FAP cells, delineating clear distinctions from both Endothelial and Immune cell groups. Importantly, the t-SNE plot unveils a distinct connection between Smooth Muscle Cells and Pericytes, akin to observations in the reference t-SNE plot. This congruence emphasizes the robustness of the t-SNE analysis in uncovering meaningful cellular relationships within the single-cell RNA sequencing dataset. The visualization details are derived from the t-SNE plot generated using sc.pl.tsne in Scanpy, with cell types indicated by color and a legend placed on data points for clarity.

Figure. 1: t-SNE plot

b. Heatmap:

In my analysis using sc.pl.heatmap in Scanpy, the heatmap (fig. 2) provides a visual representation of marker gene expression patterns (marker_genes_dict) across diverse cell types (groupby='cell_type'). The color map is specifically tailored to capture varying expression levels, employing a 'Reds' palette (cmap='Reds'). Both row and column hierarchical clustering are incorporated into the heatmap, as indicated by the presence of dendrograms (dendrogram=True). Adjusting the figure size to 12 by 8 inches (figsize=(12, 8)) enhances the clarity of the heatmap, offering a comprehensive depiction of gene expression across different cell types. It's important to note that the Y-axis dendrogram orientation in Python reflects the convention of placing variables along columns, differing from the X-axis dendrogram used in R. Despite this distinction, the heatmap closely aligns with the expression patterns observed in the reference paper.

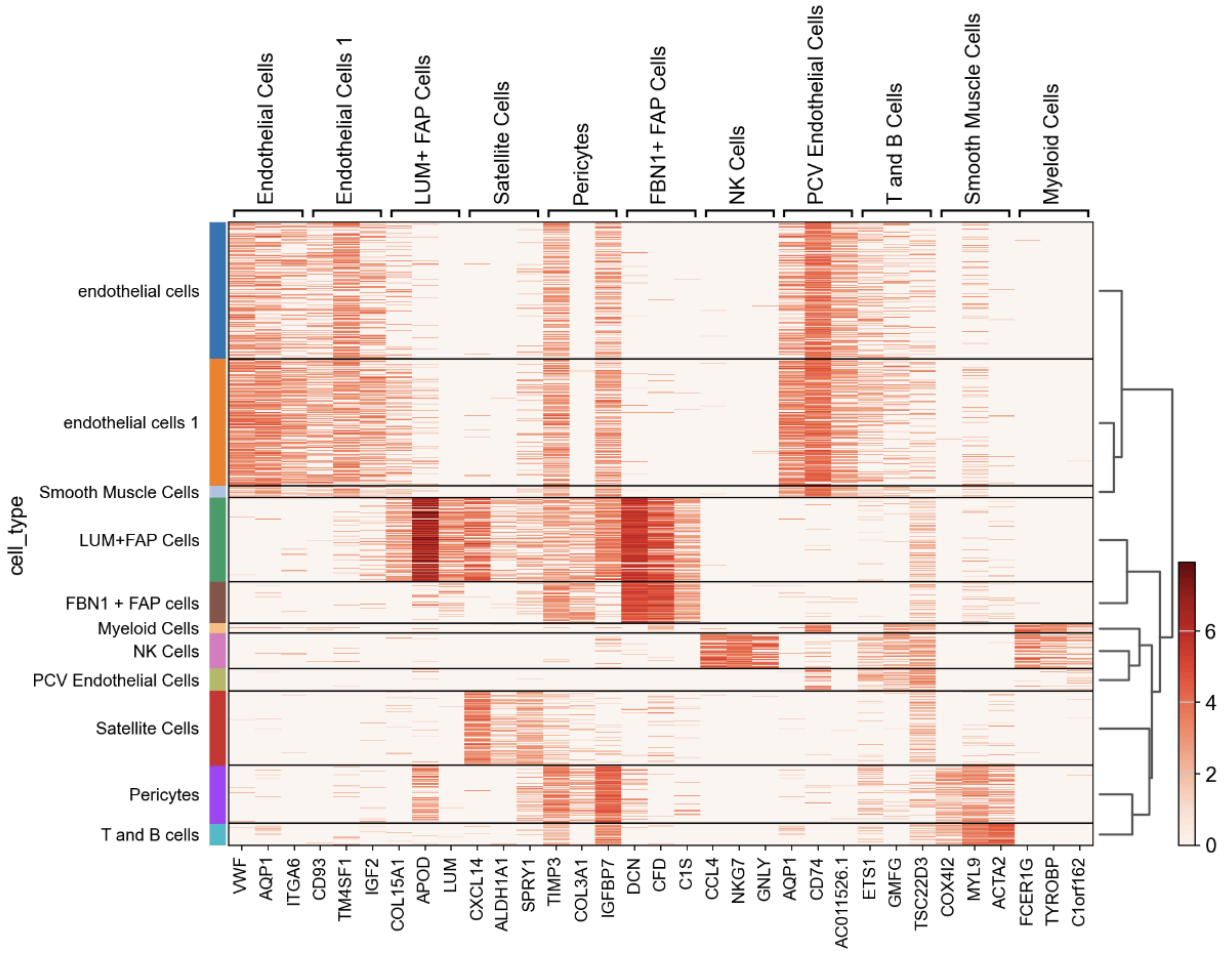

Figure. 2: Heatmap

2. References:

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2. Scanpy: Preprocessing and clustering 3k PBMCs https://scanpy-tutorials.readthedocs.io/en/latest/pbmc3k.html
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4. Seurat's guided clustering tutorial (Satija et al., 2015) https://satijalab.org/seurat/articles/pbmc3k_tutorial
5. anndata: Annotated data
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6. The scverse project provides a computational ecosystem for single-cell omics data analysis.
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