Single Cell Analysis of Tumors Expressing CD45 in Patients with HNSCC

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Abstract

Head and Neck Squamous Cell Carcinoma (HNSCC) is an aggressive form of cancer that is typically diagnosed at late stages which increases the risk of metastasis; in turn, limiting the treatment possibilities for patients with HNSCC. In this study 33 patient tumor samples that had positive and negative CD34 were analyzed; the primary objective was to determine the cell-type composition of these tumors. Furthermore, the secondary objective was to determine the differences in tumor compositions of male and female patients through gene expressions. Using single cell RNA sequencing (scRNAseq) cells were grouped in clusters to determine whether most of the tumors shared the same composition. By doing so it makes it possible to better understand biochemical pathways that enhance tumor growth in the tumor microenvironment (TME).

Background

Head and Neck Squamous Cell Carcinoma can be caused for a myriad of reasons. The treatment options for patients with HNSCC is typically very limited, patients that suffer form HNSCC typically have recurrences or their cancer metastasizes.

CD45+/- is an immune cell that is vital for the immune system while also regulating T-cell receptor signaling. CD45 can be indicative of tumor outcomes in HNSCC patients.

The GEO data was obtained from a previous research project did not go into much depth with the CD45 cells. It was decided to proceed with this data set because it had not been used for further analysis of positive and negative CD45.

Methodology

Data was obtained from the Gene Expression Omnibus (GEO); the specific data that we chose to analyze was GSE164690. More specifically the Single Cell data that had CD45+/- expression. Most of the analysis was done in R using the Seurat package. By doing so all of the different cell types found in each of the tumors were able to be clustered. This also allowed for the manipulation of the data in order to create visualizations that allowed for better understanding of HNSCC tumor compositions.
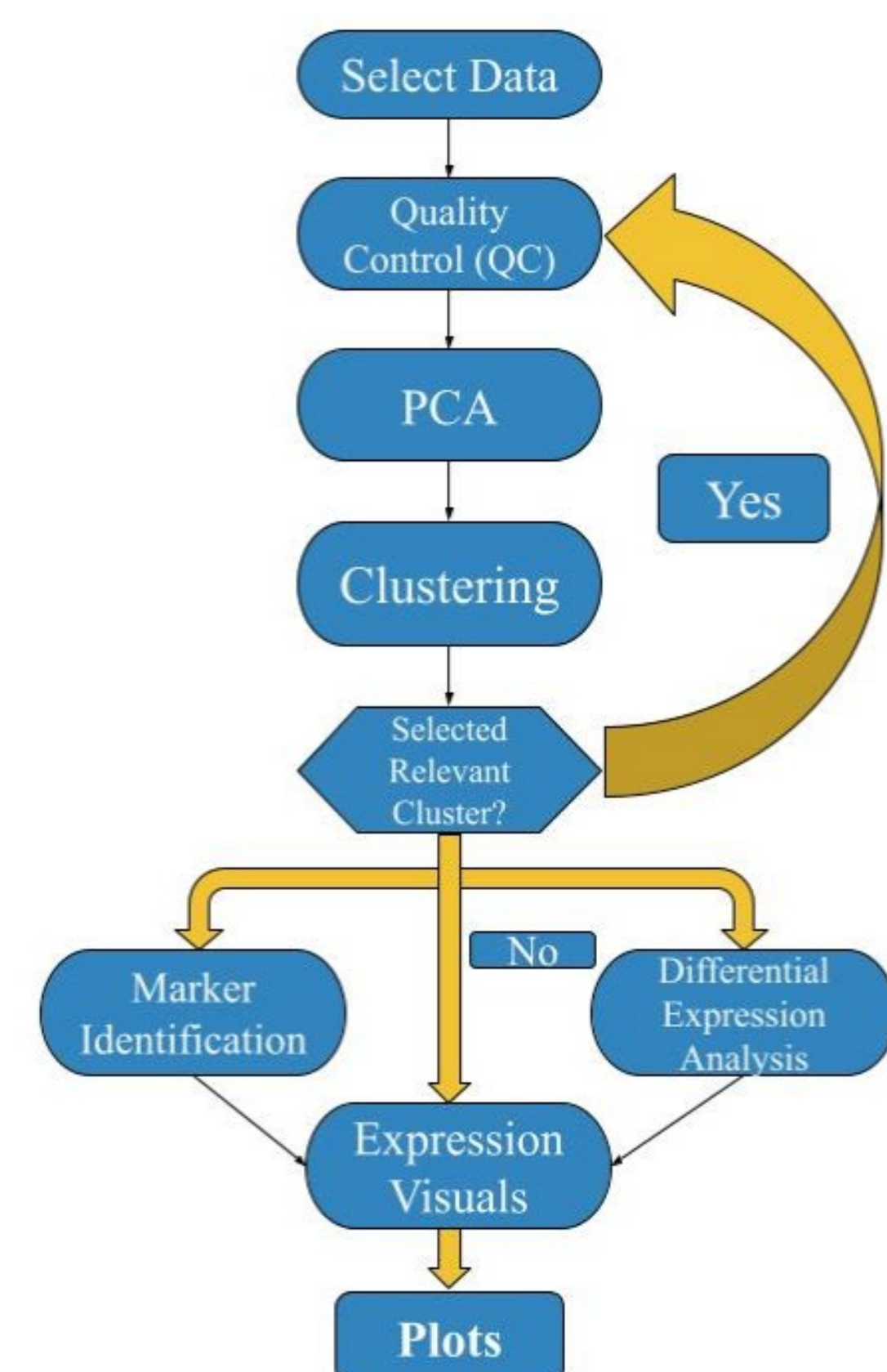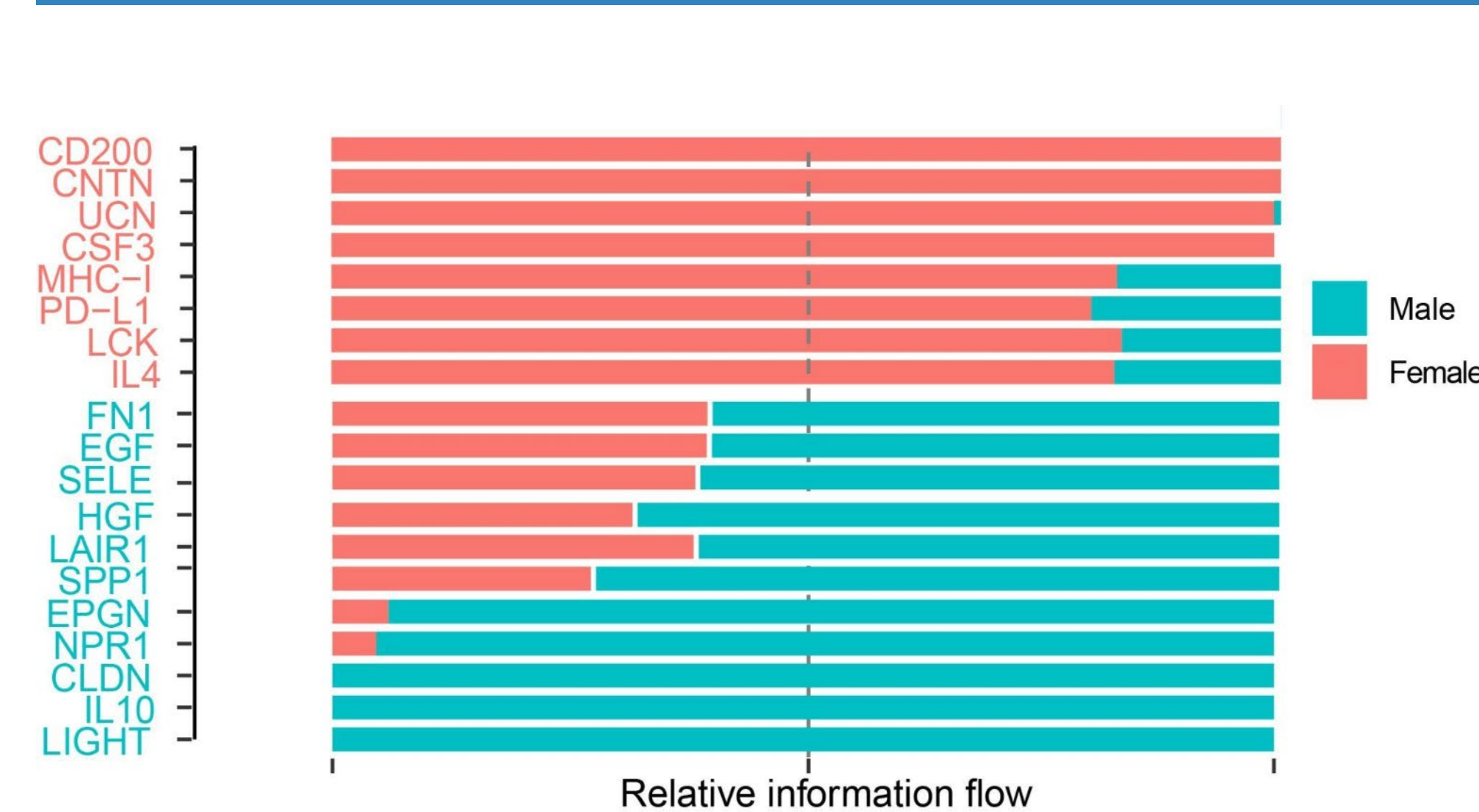
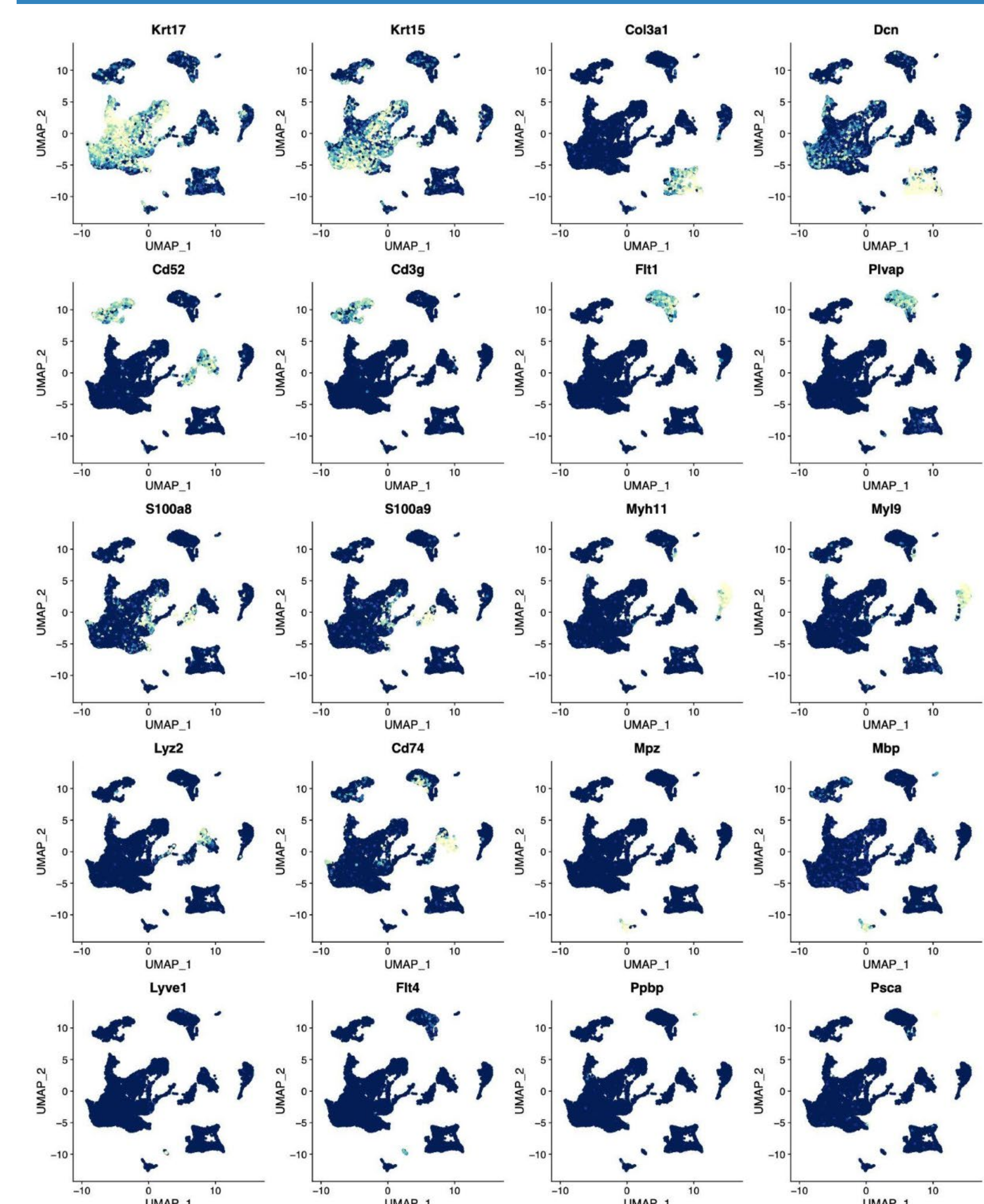## Results & Discussion

Figure 1
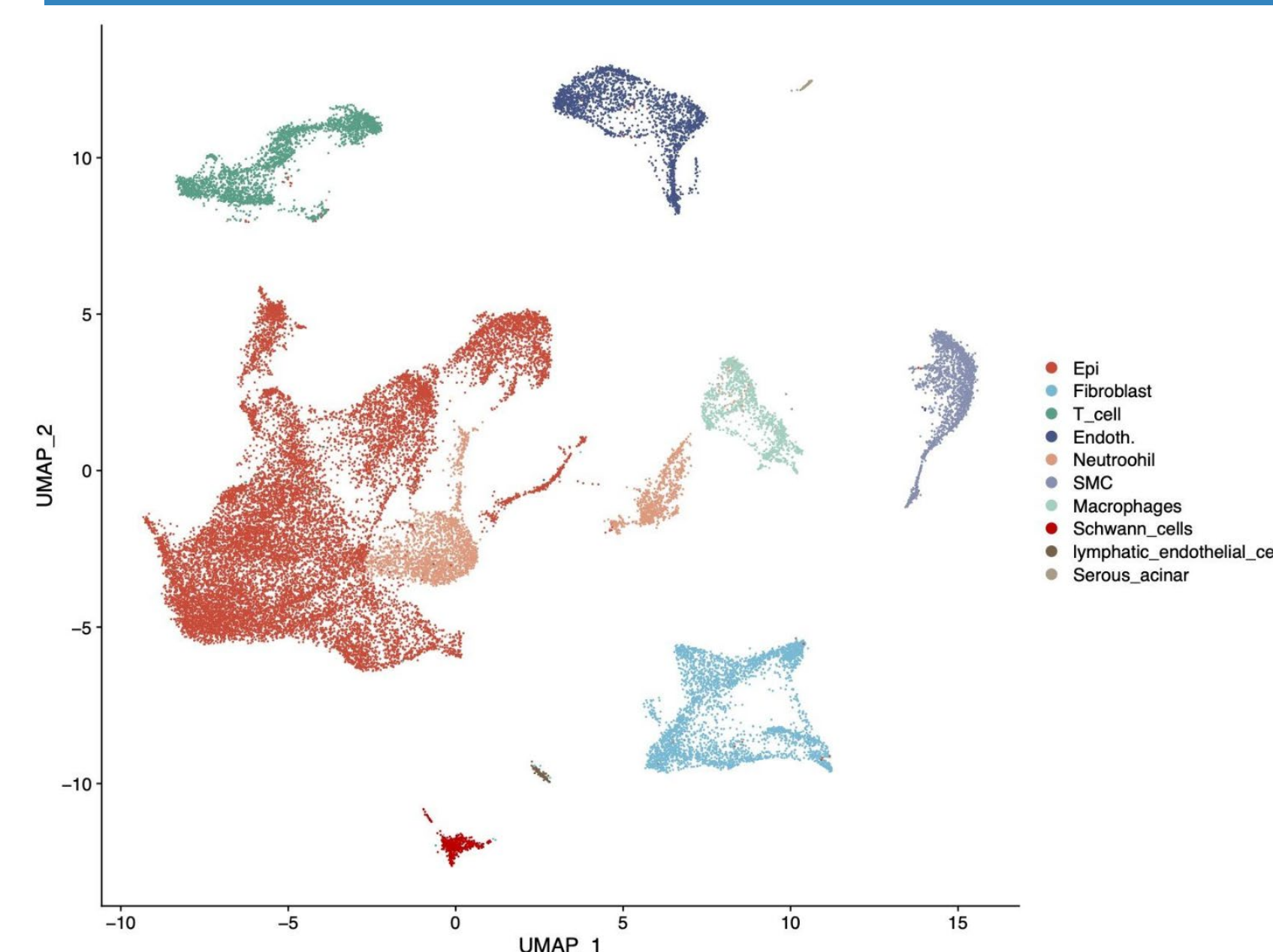
10 cell types clustered by color to show the similarities in the cell types.
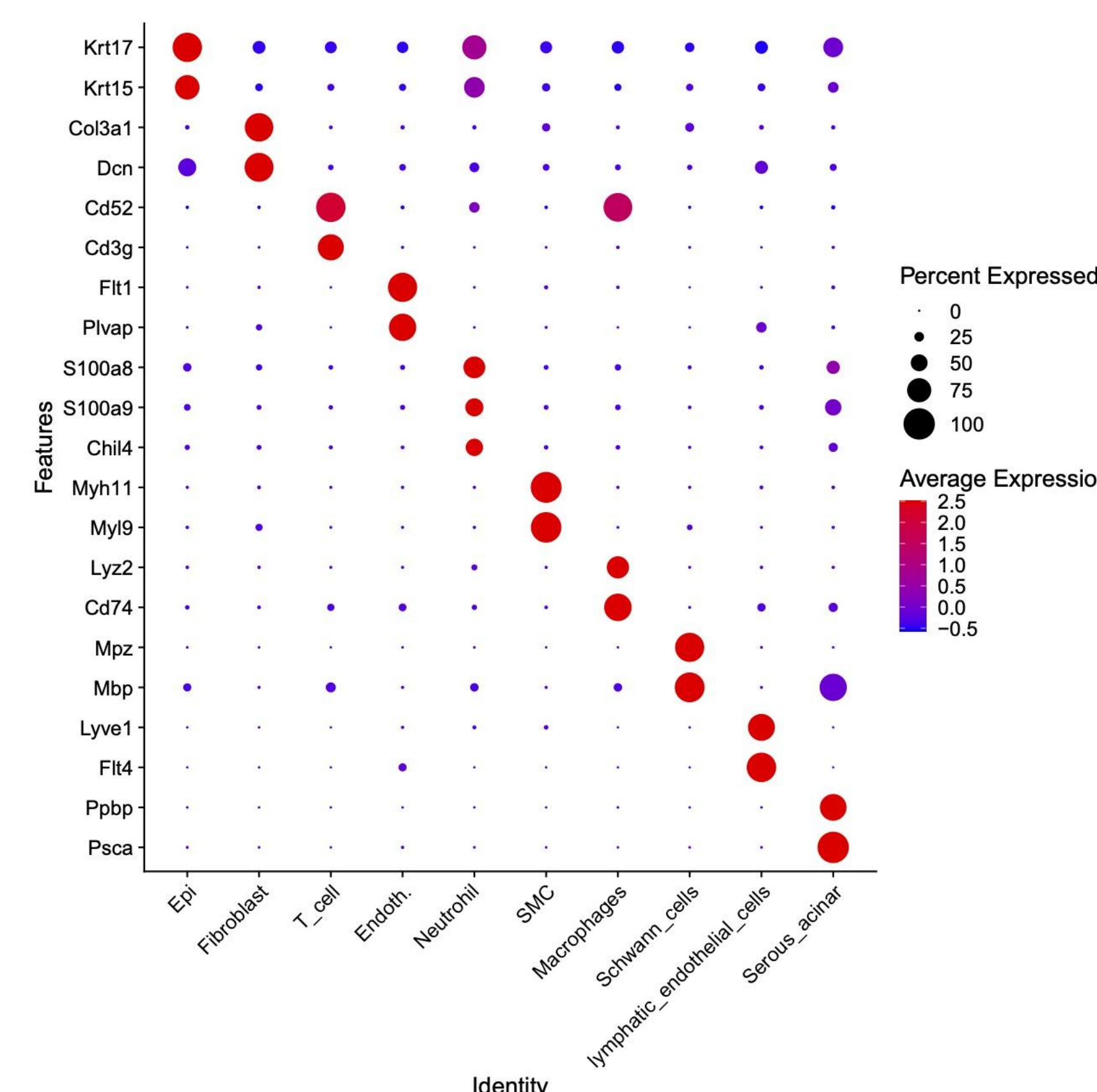
Figure 2

The following genes are associated with the female sex: CD200, CNTN, UCN, CSF3, MHC-1, PD-L1, LCK, IL4. Whereas these genes are associated with the male sex: FN1, EGF, SELE, HGF, LAIR1, SPP1, EPGN, NPR1, CLDN, IL10, LIGHT.

Figure 3

Shows where each gene is expressed in each cluster; this is cross referenced to Figure 1.

Figure 4

Displays a more mathematical visual representation of the relationship between the cell types and genes they are as follows: **Epi**: Krt17 (about 100%), Krt15 (about 75%), Dcn (about 50%), **Fibroblast**: Col3a1 (about 100%), Dcn (about 100%), **T cell**: Cd52 (about 100%), Cd3g (about 100%), **Endoth.**: Flt1 (about 100%), Plvap (about), **Neutrohil**: S100a8, S100a9, Chil4, Krt17, Krt15, **Smc**: Myh11, Myl9, **Macrophages**: Cd74, Lyz2, Cd52, **Schwan cells**: Mbp, Mpz, **Lymphatic endothelial cells**: Flt4, Lyve1, **Serous acinar**: Psca, Ppbp, Mbp, Krt17

Figure 5
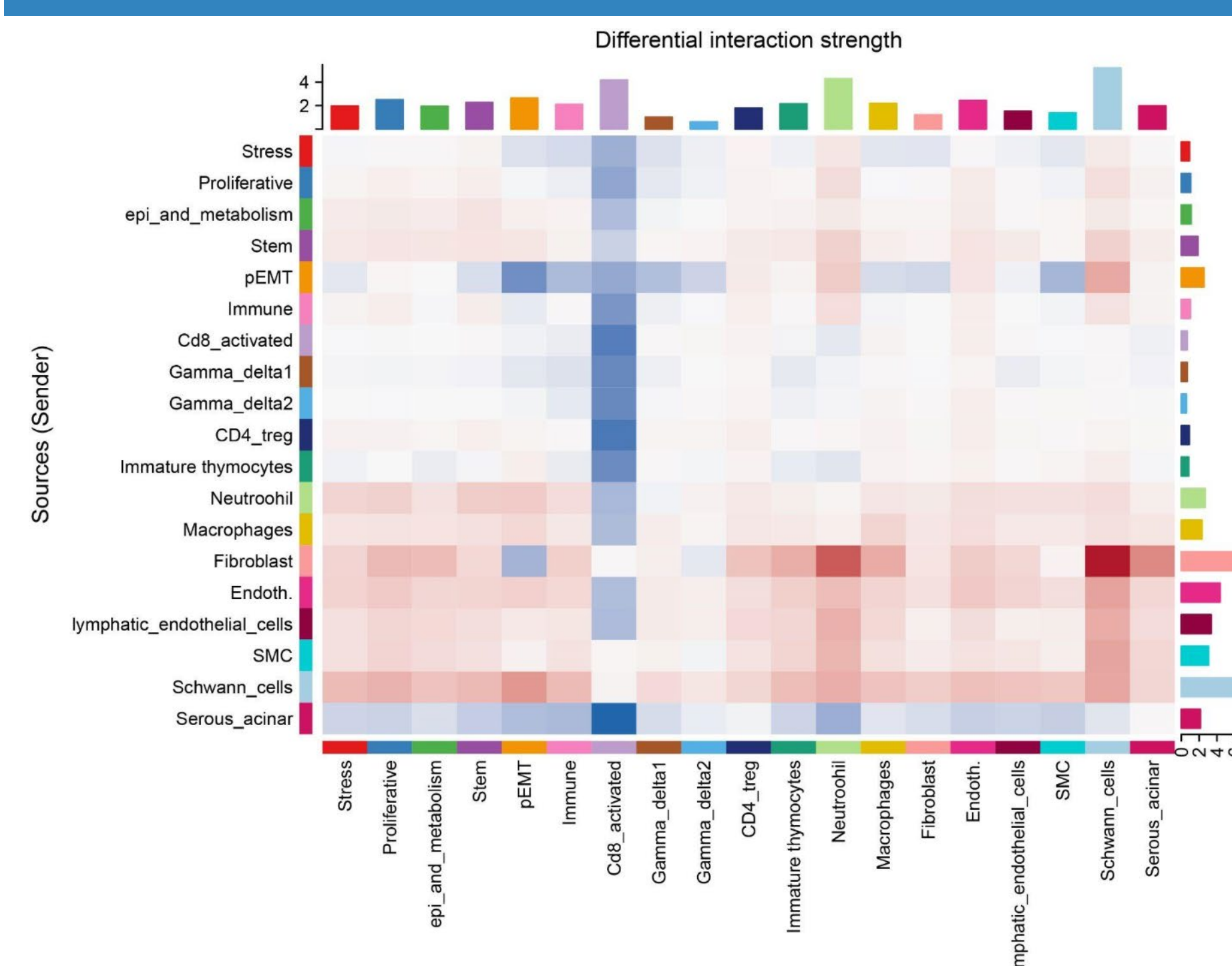
Cell interactions for Tumor Microenvironment (TME).

Future Work

With these results more individualized care for patients with tumors rather than more generalized methods is possible. In addition, the correlation between genes and sex; allows for the determination of sex of a sample through gene expression.

Conclusion

Targeting the biochemical pathways of the genes correlated with the cell types can minimize the tumors in the cell types. These findings also indicate that when these genes are expressed it is likely linked to the specific sex.