

Project: Spatial Omics Visualization - Diseased vs. Non-Diseased Kidney

Description

This repository contains an independent project to practice spatial data visualization in Python. Using publicly available spatial transcriptomics data, it compares the expression of specific cell types and marker genes in diseased and non-diseased kidney samples.

Note:

This project is purely for educational purposes and is not intended for publication. The aim is to develop skills in handling and visualizing spatial transcriptomics data.

Repository Contents

- **Kidney_Spacial_Omics.py:** Python script for analyzing and visualizing spatial transcriptomics data. The script includes:
 - Subsetting diseased and non-diseased samples.
 - Plotting cell type clusters.
 - Visualizing spatial expression of specific cell types and genes.
 - **Data Source:** The dataset is derived from the study:
<https://www.biorxiv.org/content/10.1101/2022.10.24.513598v2.full>
 - **GEO Accession:** [Series GSE211785](#)
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Steps to Reproduce

1. Data Preparation

- Download and preprocess the spatial transcriptomics data (e.g., .h5ad files) as outlined in the linked study.
- Save the data in the same directory as the script or update the file path in the script.

2. Run the Script

- Install required Python libraries: scanpy, matplotlib, and numpy.

- Update the sample_id in the script to switch between diseased and non-diseased samples.
- Execute the script to generate visualizations.

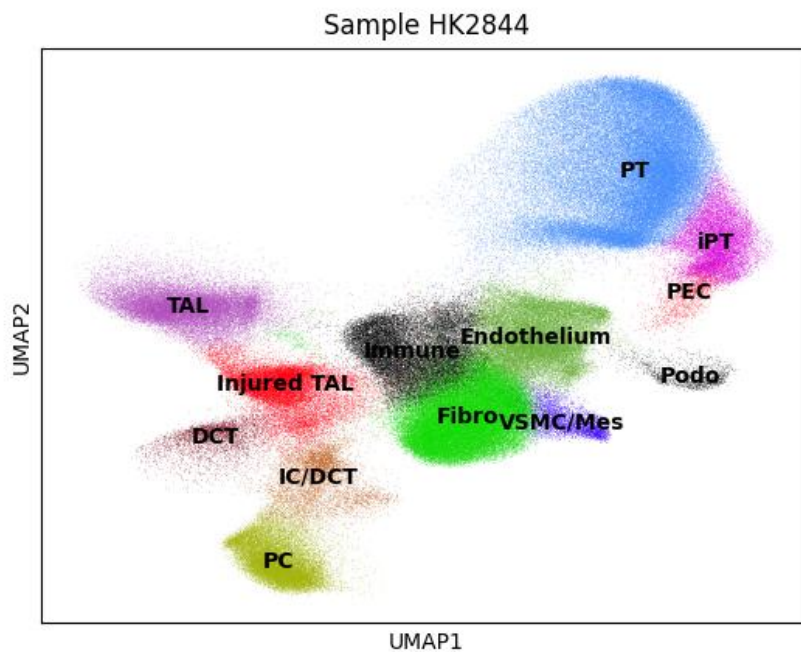
3. Visualizations

- **UMAP Clusters:** Visualize cell type clusters.
- **Marker Genes:** Plot top 10 expressed genes for each cell type.
- **Spatial Expression:** Show spatial distribution of specific cell types and marker genes in the tissue.

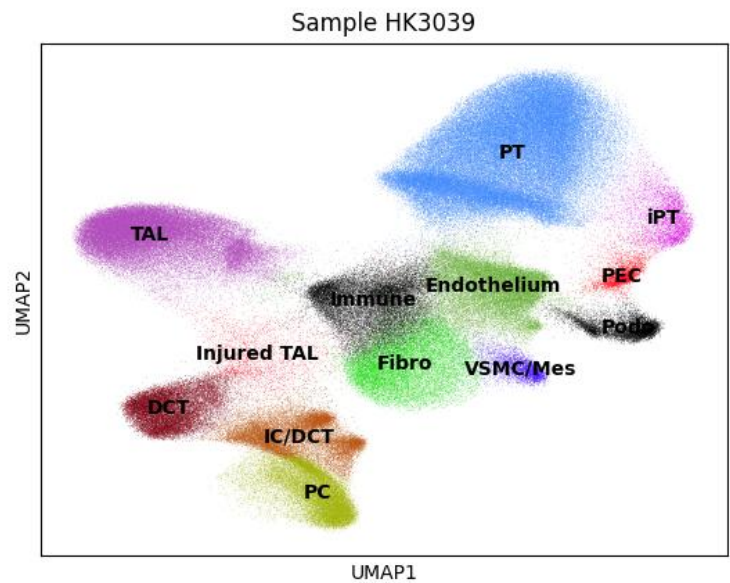
Visualization Examples

1. Cell Type Clustering

Diseased Sample (HK2844):

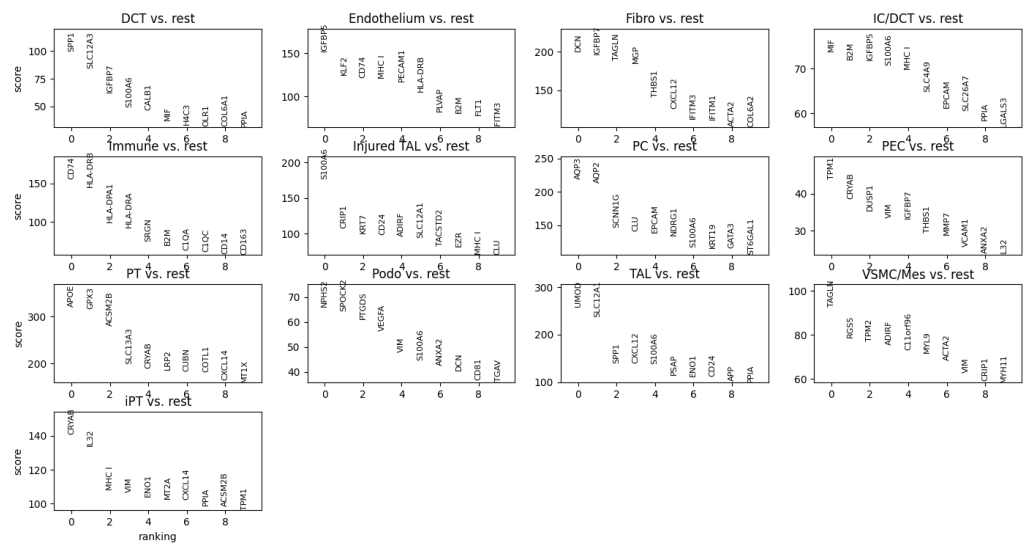


Healthy Sample (HK3039):

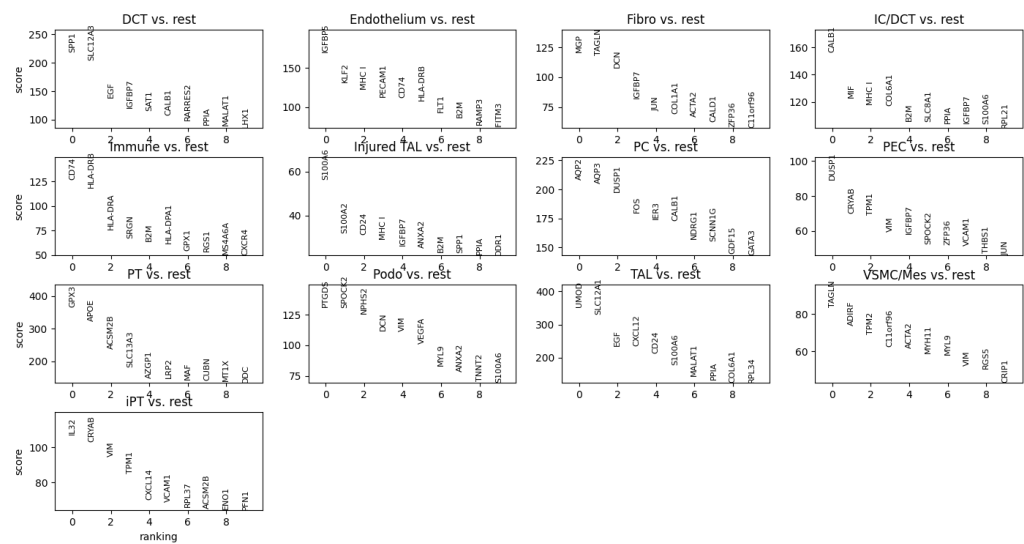


2. Marker Genes by Cell Type

Diseased Sample:

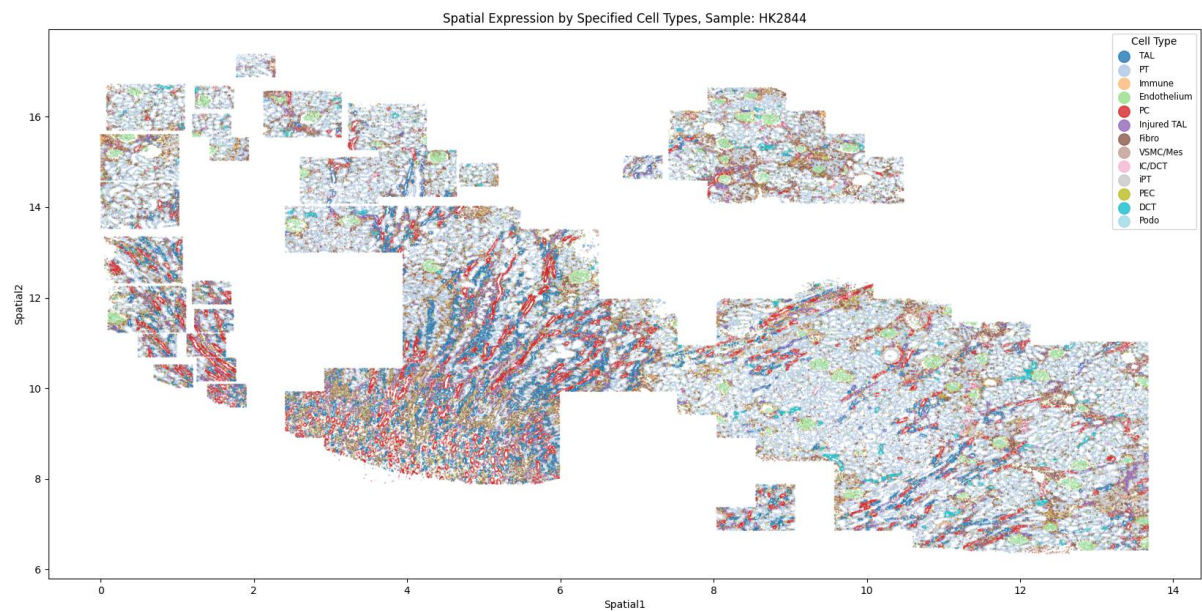


Healthy Sample:

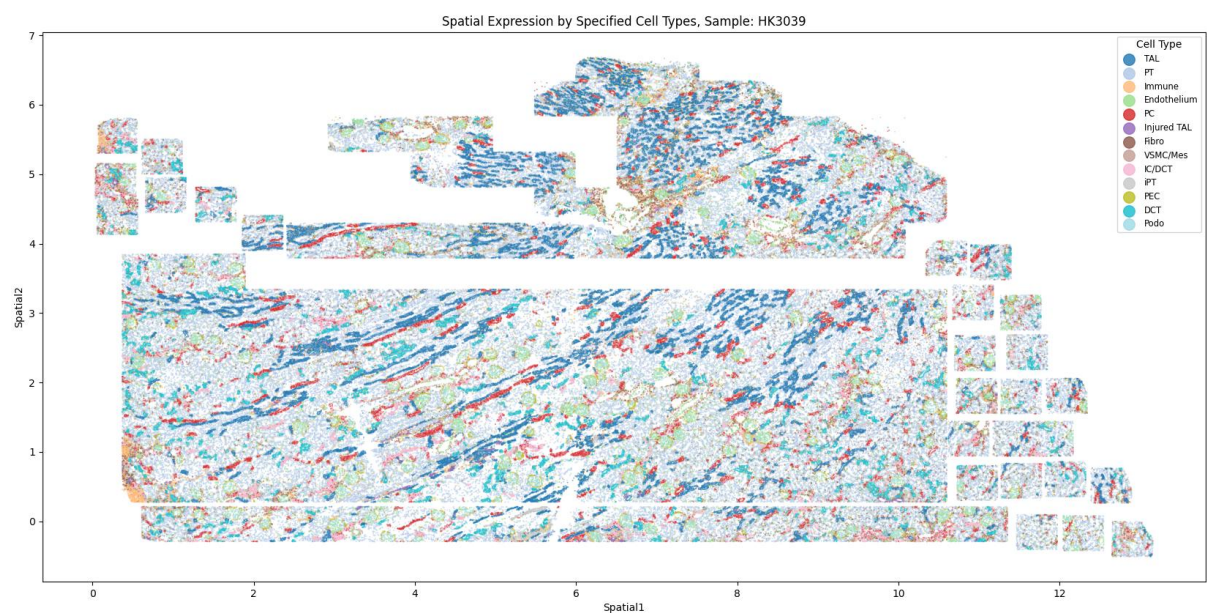


3. Spatial Expression of Cell Types

Diseased Sample:

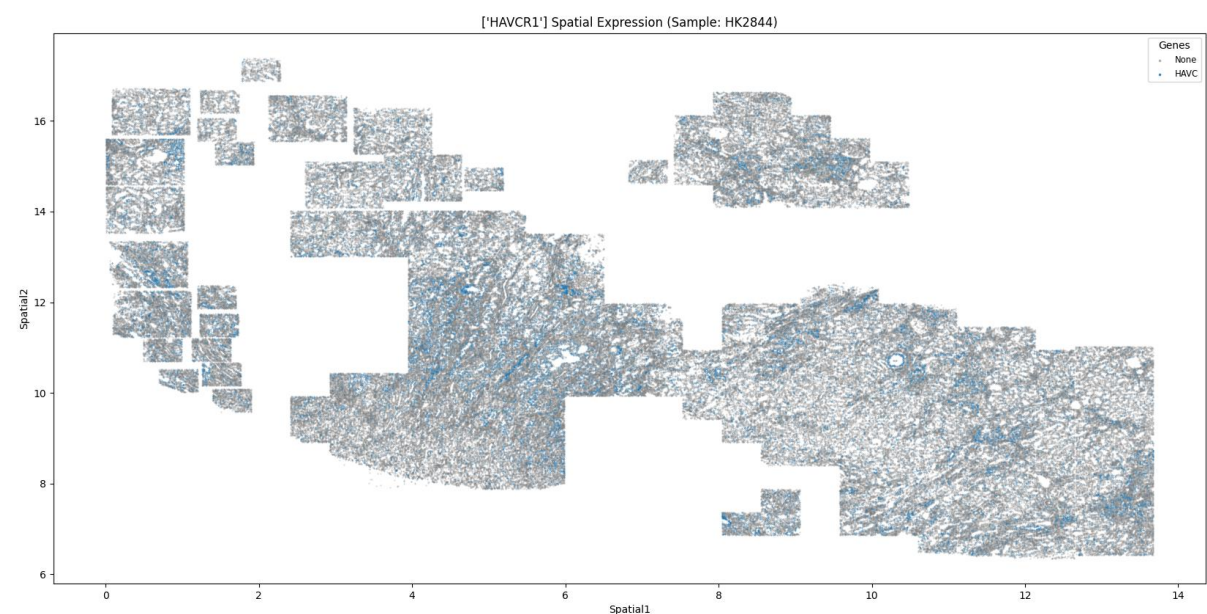


Healthy Sample:

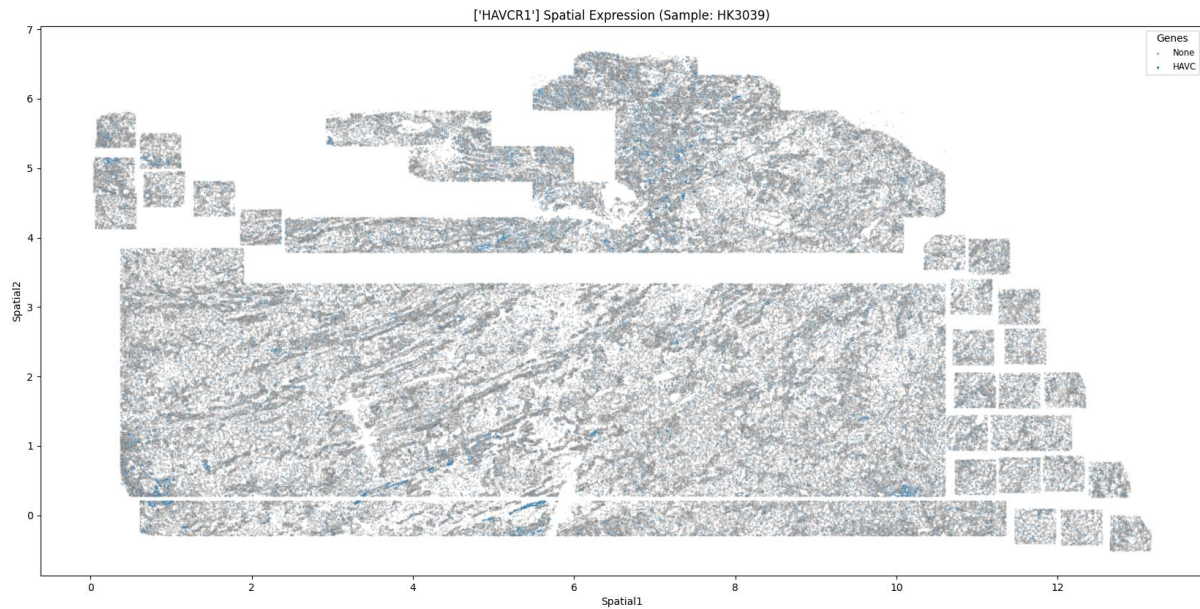


4. Spatial Expression of HAVCR1 Gene

Diseased Sample:



Healthy Sample:



Acknowledgments

This project is inspired by the study "Spatially resolved transcriptomics in the kidney" on BioRxiv. Special thanks to the authors for making the dataset publicly available.

Abedini, A., Levinsohn, J., Klötzer, K. A., Dumoulin, B., Ma, Z., Frederick, J., Dhillon, P., Balzer, M. S., Shrestha, R., Liu, H., Vitale, S., Devalaraja-Narashimha, K., Grandi, P., Bhattacharyya, T., Hu, E., Pullen, S. S., Boustany-Kari, C. M., Guarnieri, P., Karihaloo, A., ... Susztak, K. (2022). *Spatially Resolved Human Kidney Multi-Omics Single Cell Atlas Highlights the Key Role of the Fibrotic Microenvironment in Kidney Disease Progression*. <https://doi.org/10.1101/2022.10.24.513598>