

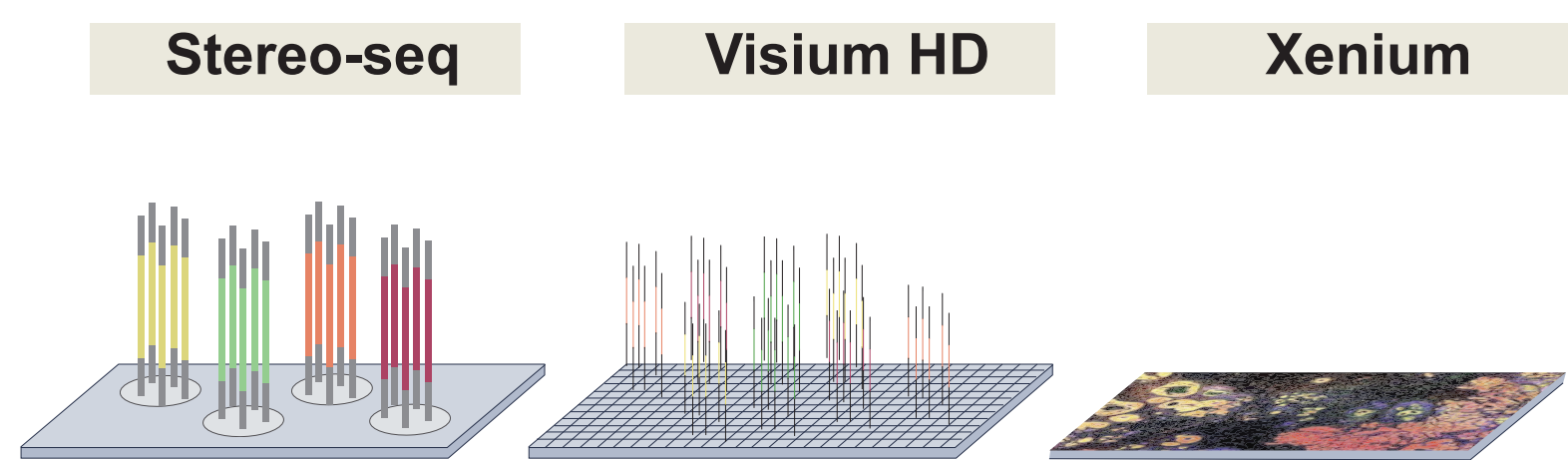
国际校区学生 POSTER DAY

HDSTdb: High Definition Spatial Transcriptomics Database

Yicheng Qi†, Yiru Chen†, Ruonan Tian, Ziwei Xue, Wanlu Liu*

Zhejiang University-University of Edinburgh Institute, Zhejiang University

Data Collection



Dataset from three sequencing platform were collected, standardized, and manually organized.

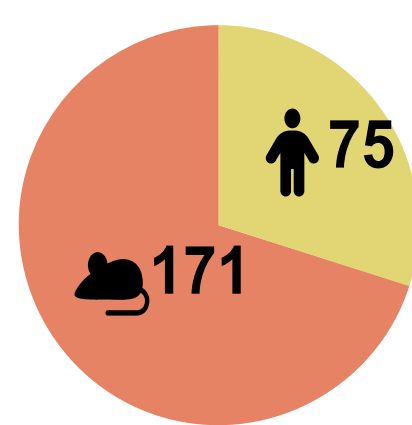
Total Projects

52

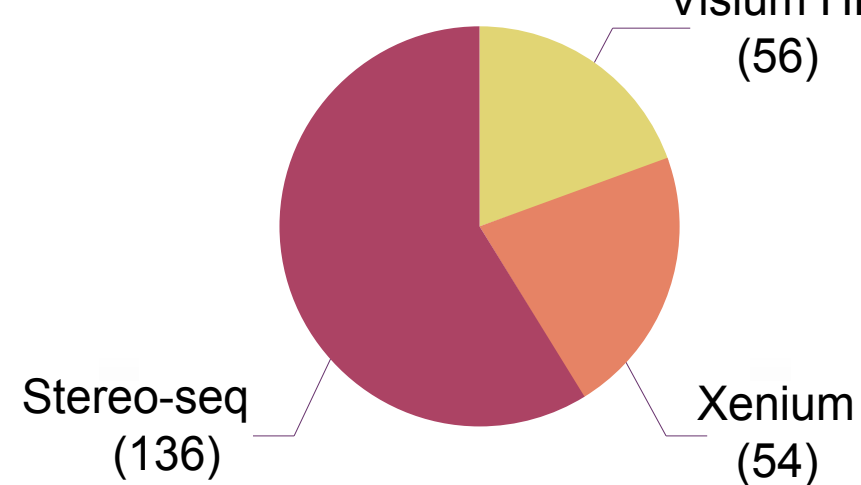
Total Samples

246

Species

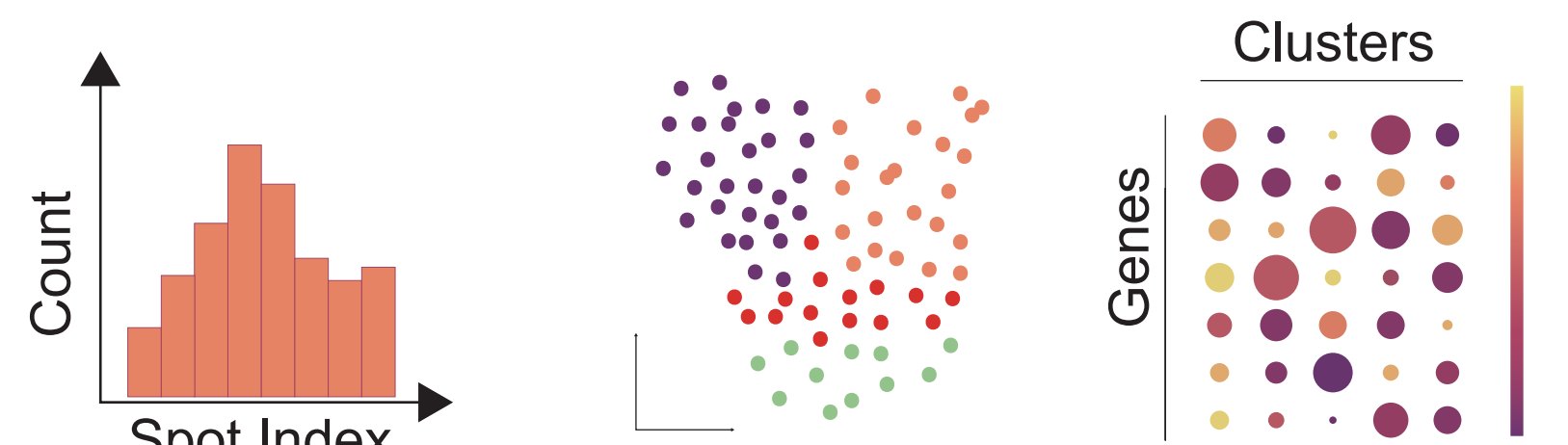


Sequencing Platforms



Advanced Analysis

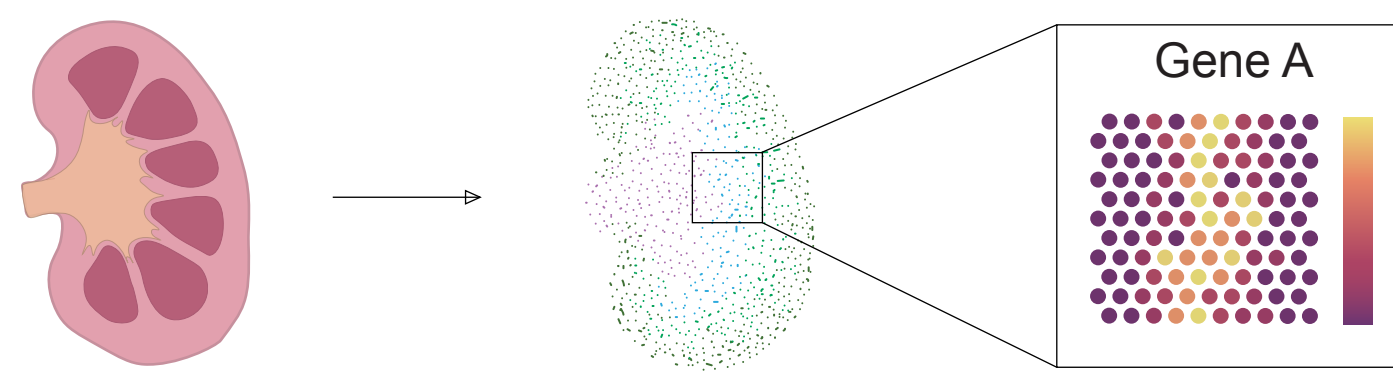
Quality Control Dimension Reduction Gene Expression



Comprehensive analysis, from quality control to further spatial gene analysis, like DEG calling, neighboring enrichment assessment.

Basic Visualization

Selected Sample Cluster Gene Expression



Clustering and visualization based on gene expression were conducted, along with a variety of features such as gene expression retrieval and manual annotation.

Tissues

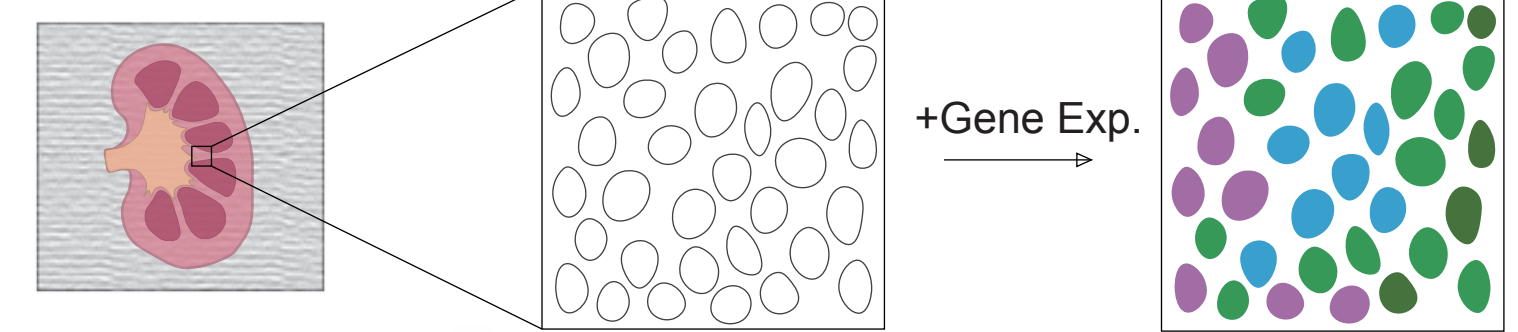
Liver: 76 (30.89%)
Embryo: 65 (26.42%)
Brain: 23 (9.35%)
...

Disease States

Healthy: 165 (67.07%)
Recovery: 12 (4.88%)
Colorectal Cancer: 11 (4.47%)
...

Cell Segmentation

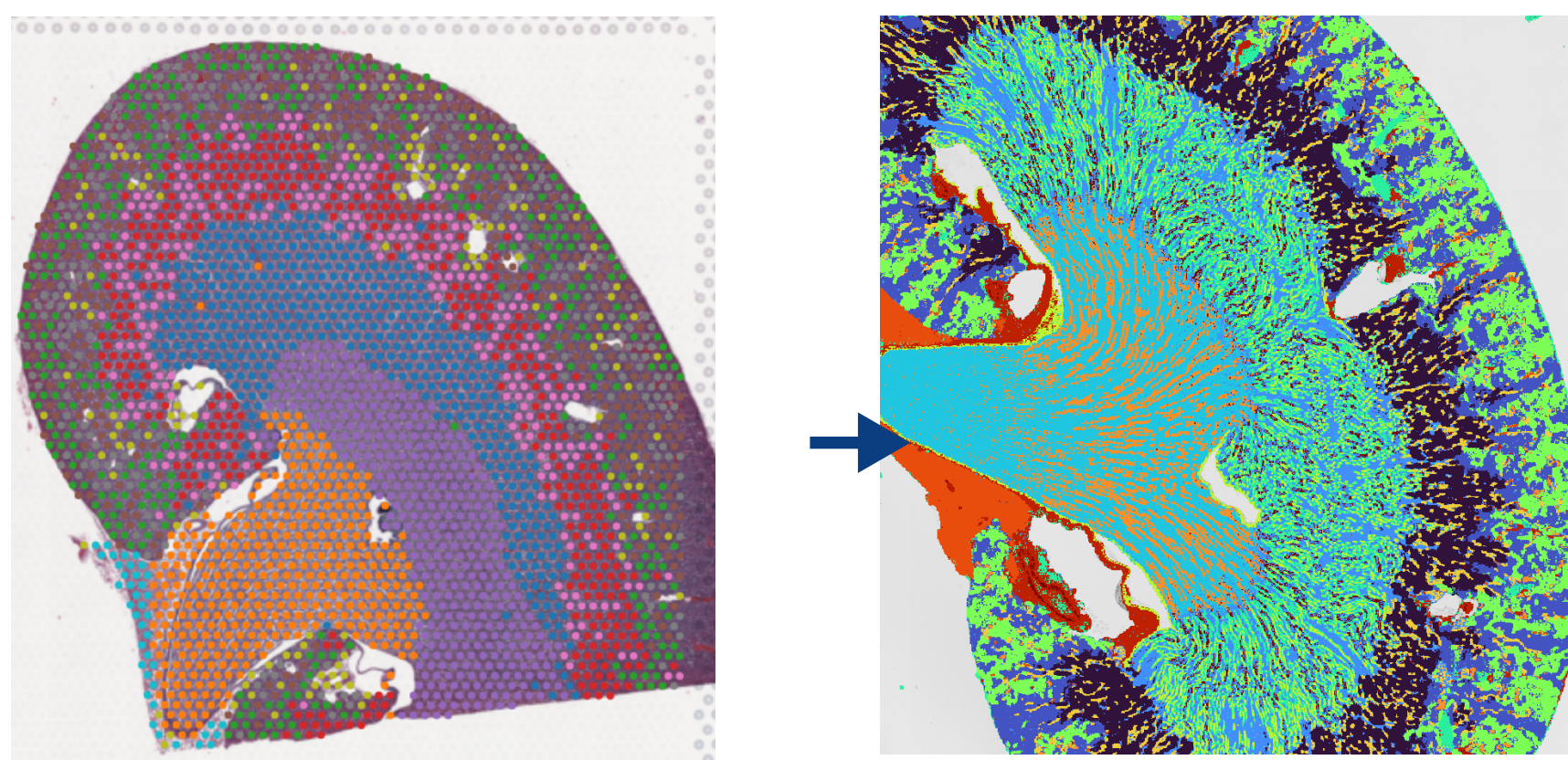
Histological Image Segmentation Cluster



The image-based cell or nucleus segmentation was performed first, followed by clustering and further analysis based on gene expression.

Introduction

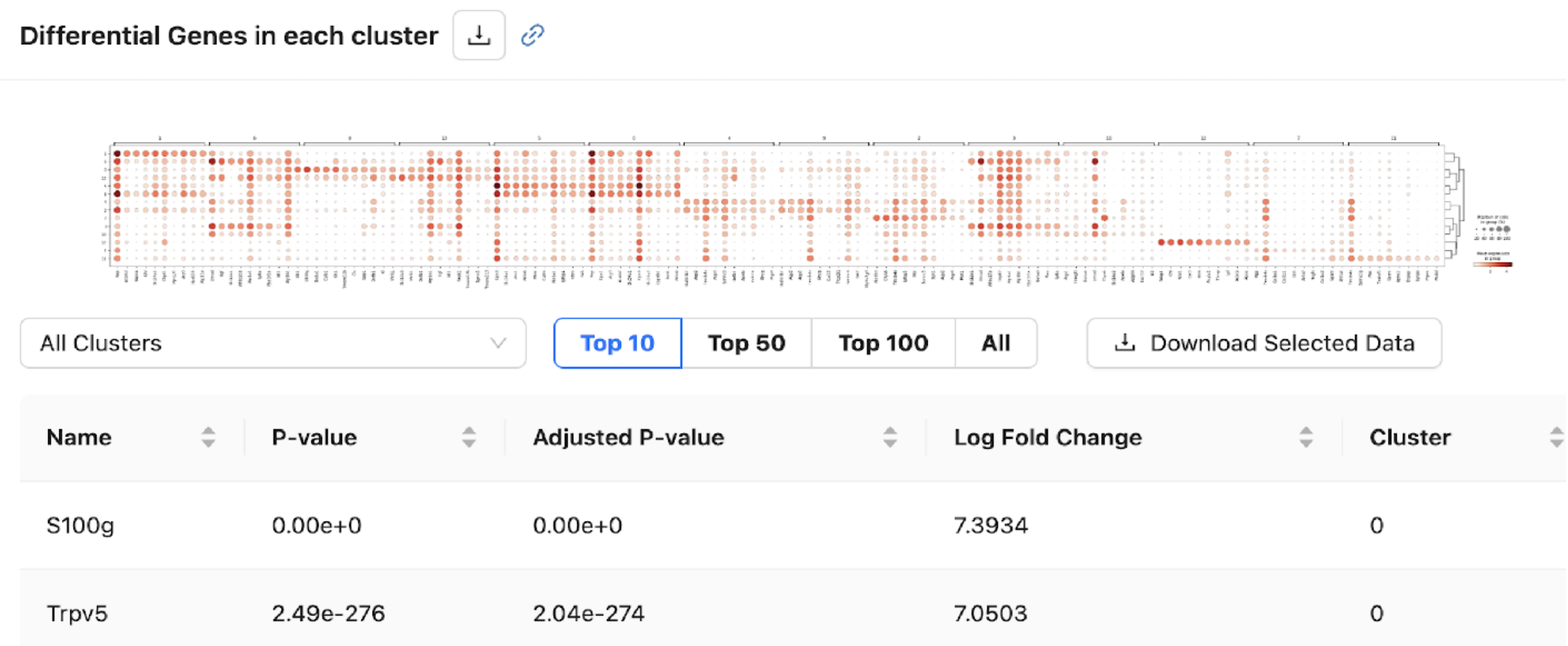
With the development of sequencing method of high resolution spatial transcriptomics (ST), current out-dated database designed for multi-cell ST data could not take the tasks for storage, visualization, and online analysis of sub-cellular or cellular level ST slices.



Previous
multi-cell level
10X Visium

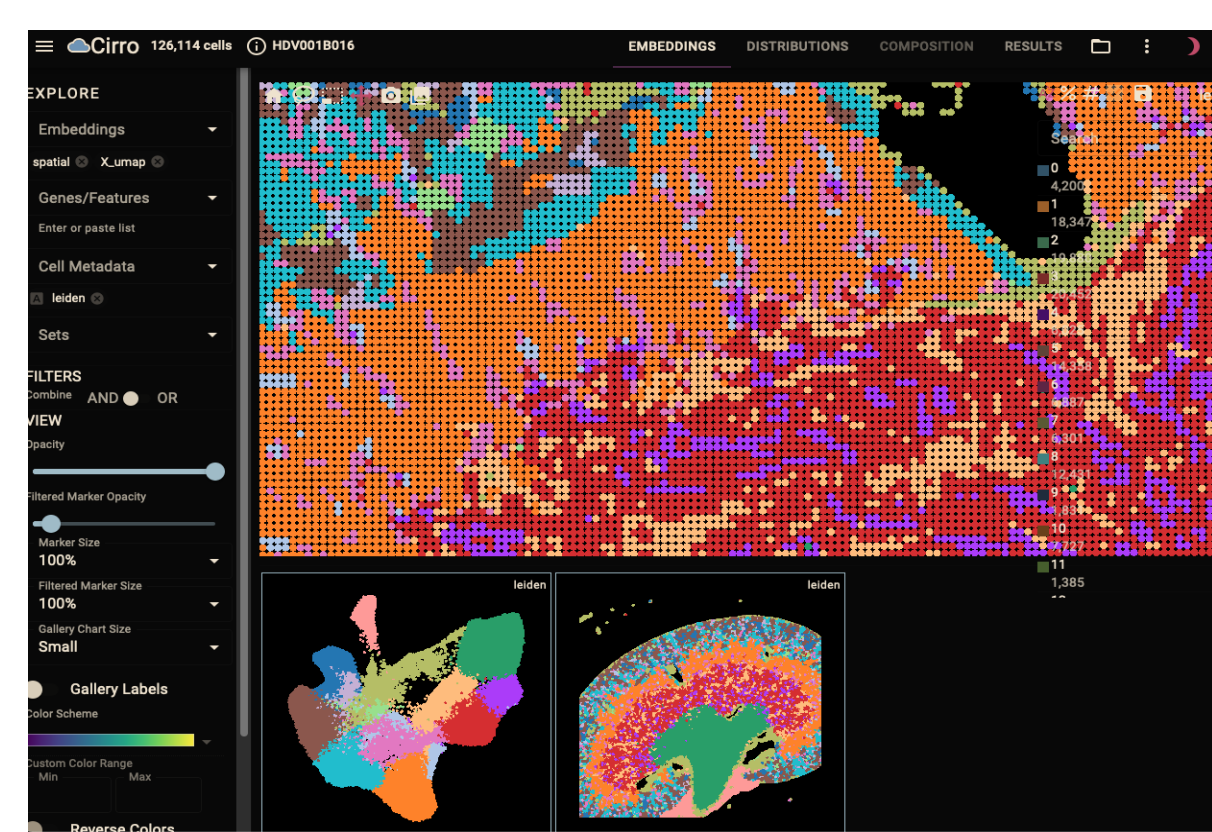
Advanced
sub-cellular level
Visium HD

Statistical Results

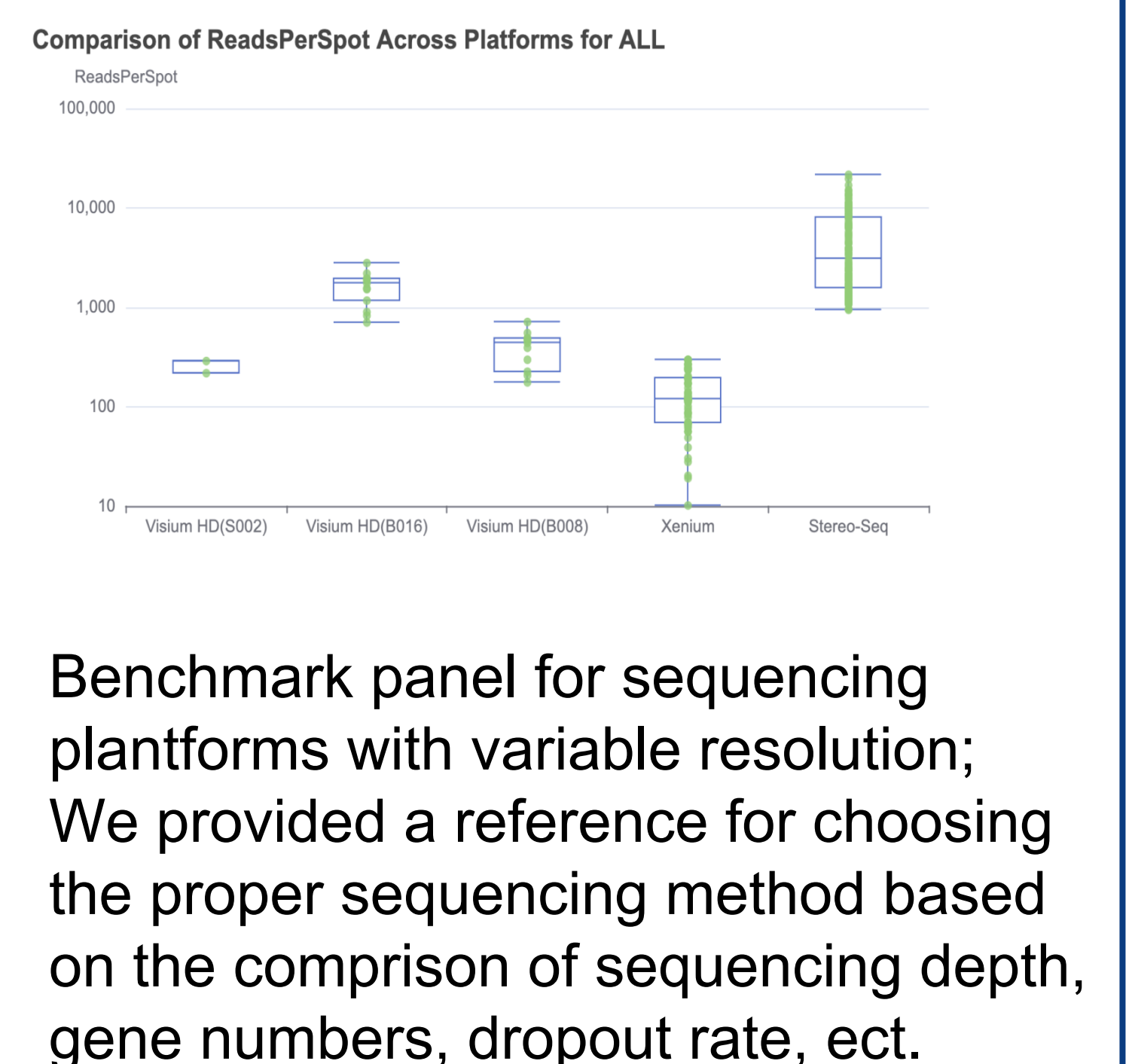


Advanced and comprehensive statistical results have been provided within every samples, including read count distribution, clustering (leiden) results, differential expression genes, ect.

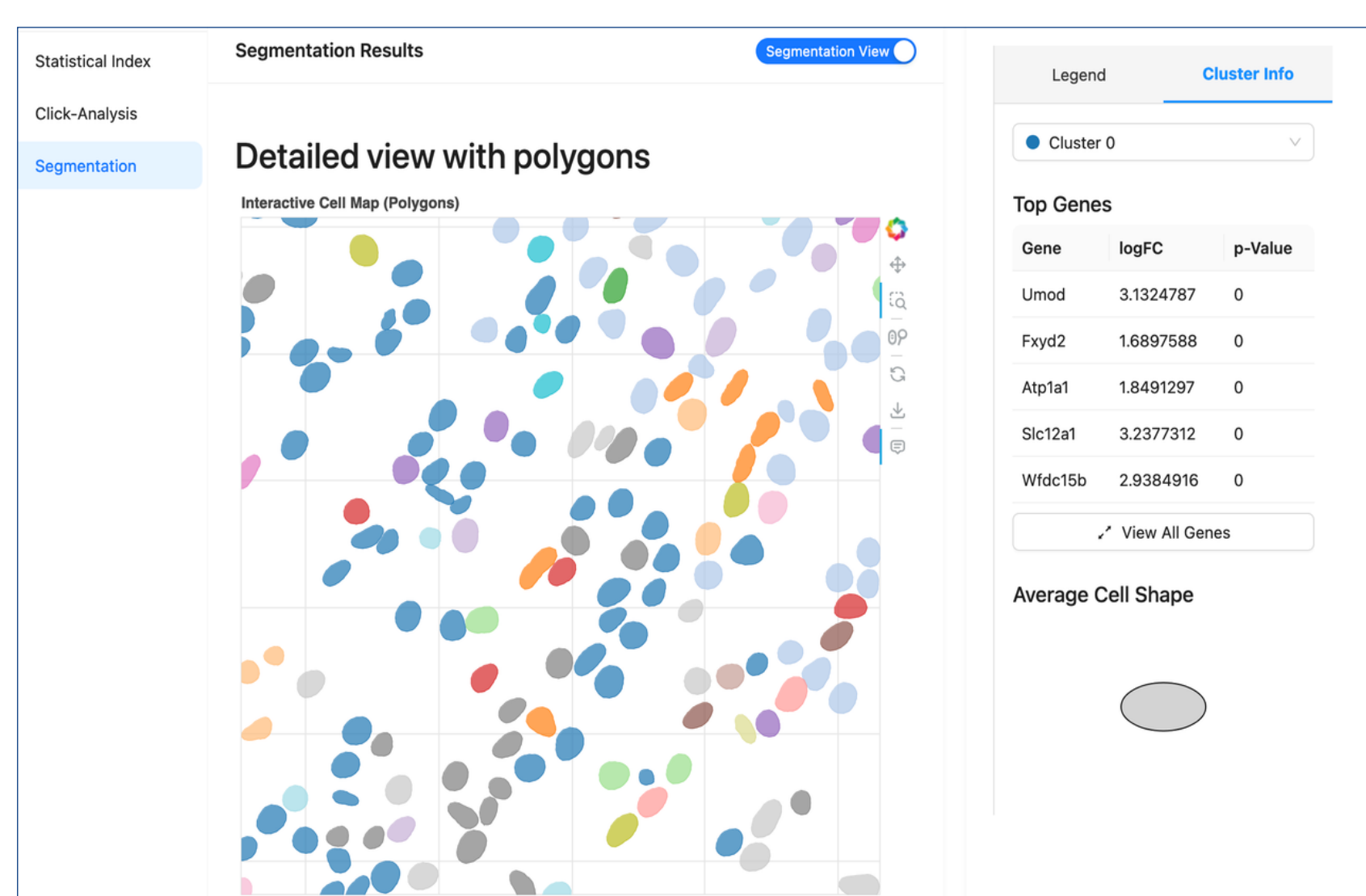
Online Analysis



User-friendly online analysis module integrated with Cirro; Users can annotate, change resolution of clustering, identifying marker genes by simple clicking.



Optimized Visualization



Optimized front-end technique for high-resolution visualization of cellular level segmentation; detailed shape and genetic information for cells.

Acknowledgements

The authors would like to thank all researchers who generated the datasets that are collected, analyzed, and displayed in our database.