

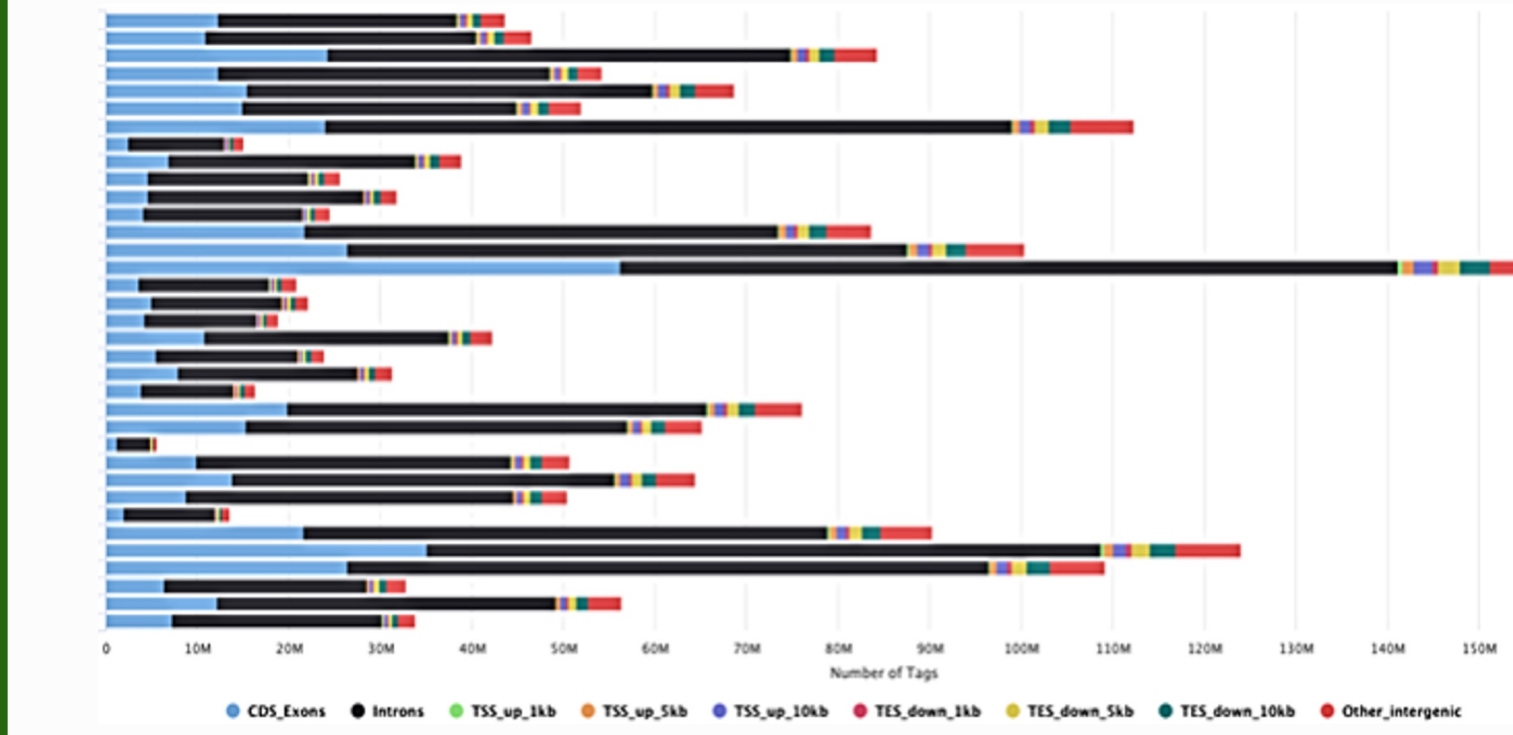
## U-BDS Services Overview

Provides reproducible, high-quality and cost-effective computational services, resources, and training with emphasis in the areas of genomics, transcriptomics, and systems biology. The services currently provided include:

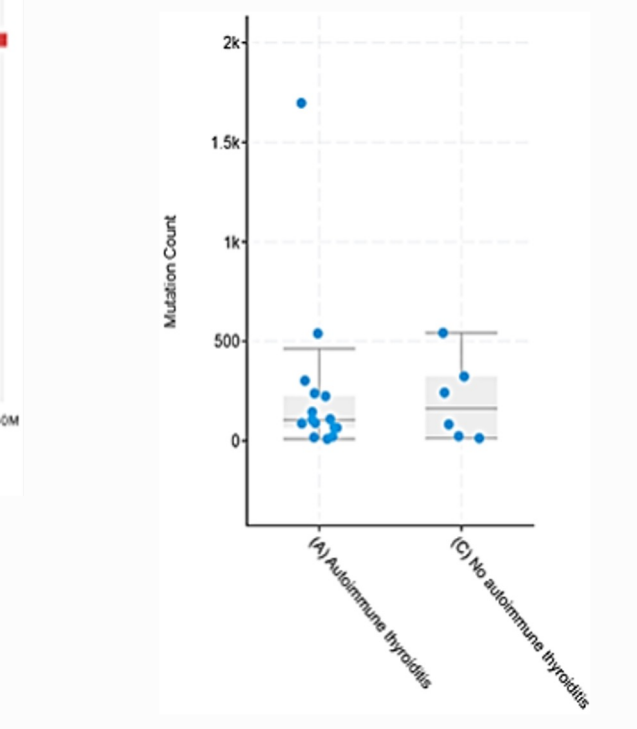
- **Genomics:** Exome and Whole Genome Sequencing analysis
- **Transcriptomics:** Bulk RNA-seq (whole-transcriptome, mRNA, and miRNA)
- **Single-cell/nuclei (sc/sn) omics:** RNA-seq, ATAC-seq, CITE-seq, multiome, cell hashing (multiplex) sequencing
- **Spatial Transcriptomics:** 10x Genomics (Visium and Xenium), NanoString GeoMx with plans to expand to CosMx
- **Support in method development:** pipeline development & custom projects overlapping with areas of U-BDS specialization
- **Web-app development:** R Shiny and Streamlit apps for interactive visualization of data
- **Support for writing manuscripts and grant applications:** budget justification, LoS, methods write-up, and supporting docs
- **Training:** workshops, guides, and weekly data science office hours (open to UAB) - Thursdays 1:30-2:00 pm
- **Other custom work:** develop reproducible research environments
- **Consultations:** 30 minutes to discuss study designs, analysis needs, grant application, and other technical details

## Genomics

### Cohort based variant classification/visualization

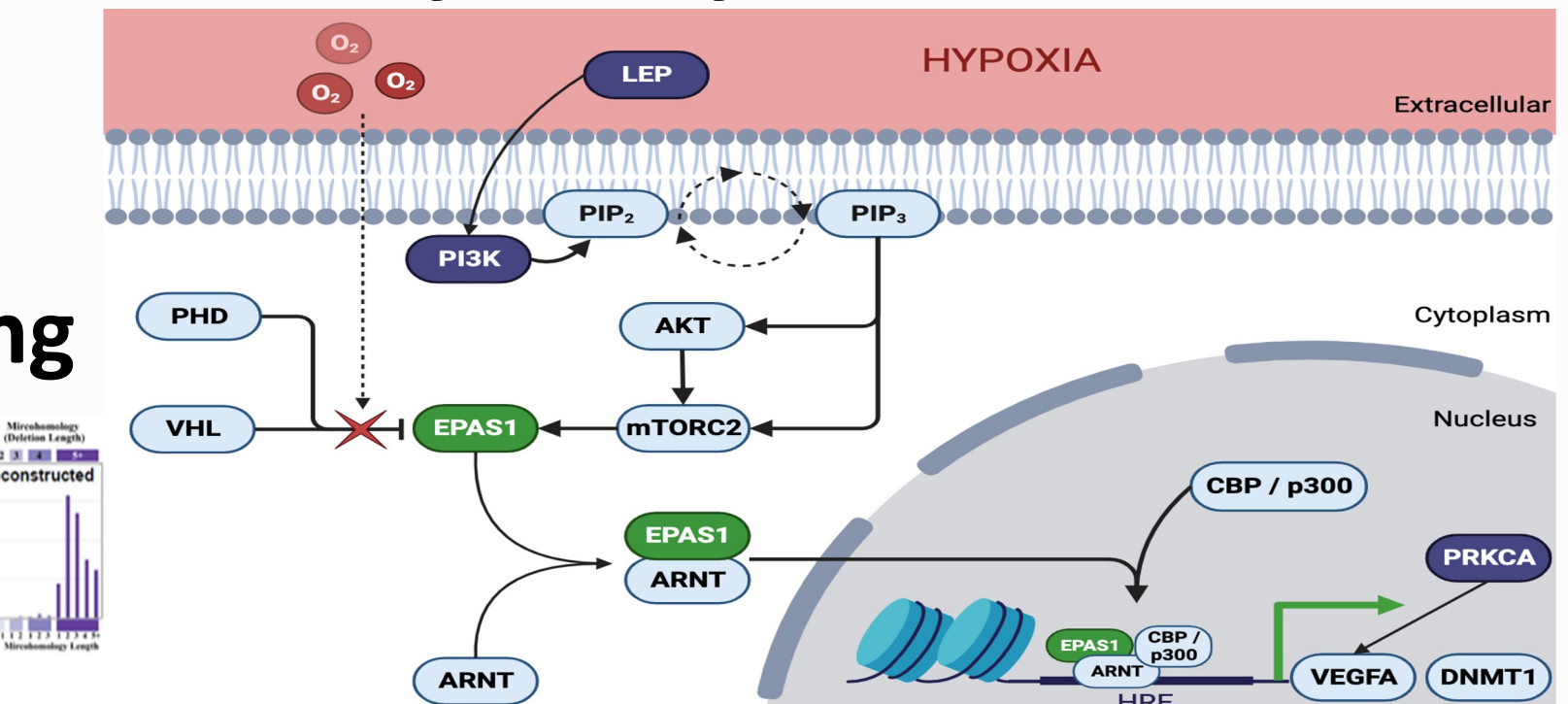


### G x P associations



WGS & WES based genomic analysis. Data QC, alignment, variant calling, functional impact analysis, and interpretation (small and structural variants and somatic and germline)

### Pathways analysis & visualization

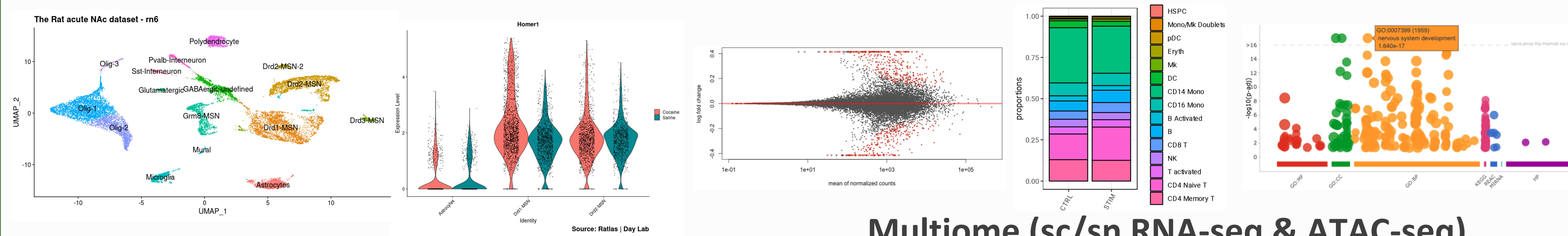


### Signature profiling

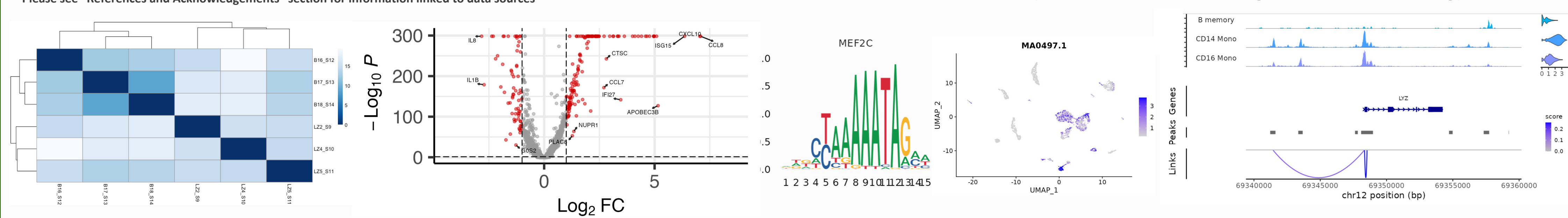


## Transcriptomics

Standard single-cell/nuclei analysis includes several layers of QC, dimensional reduction, data normalization, cell type identification, pseudobulk analysis, data visualization, among others



### Multime (sc/sn RNA-seq & ATAC-seq)



## Pipeline & App Development

- R and Python applications:
- R Shiny apps and Streamlit apps



- Pipelines:
- U-BDS supports nf-core pipelines, and develops custom pipelines with Nextflow
- Assistance in app hosting:
- Leverage UAB Research Computing (RC) resources with app hosting\*



\*U-BDS does not charge for app hosting in cloud.rc. We provide services for app development and aid users in app hosting only. Cloud.rc infrastructure is a RC resource and subject to RC policies and regulations.

## Training

- Weekly data science office hours
- Join #datascience Slack channel for more information: <https://join.slack.com/t/uablabs/signup>



- Online guide:
- [https://u-bds.github.io/training\\_guides](https://u-bds.github.io/training_guides)
- Includes training material for Docker, Singularity, nf-core pipelines

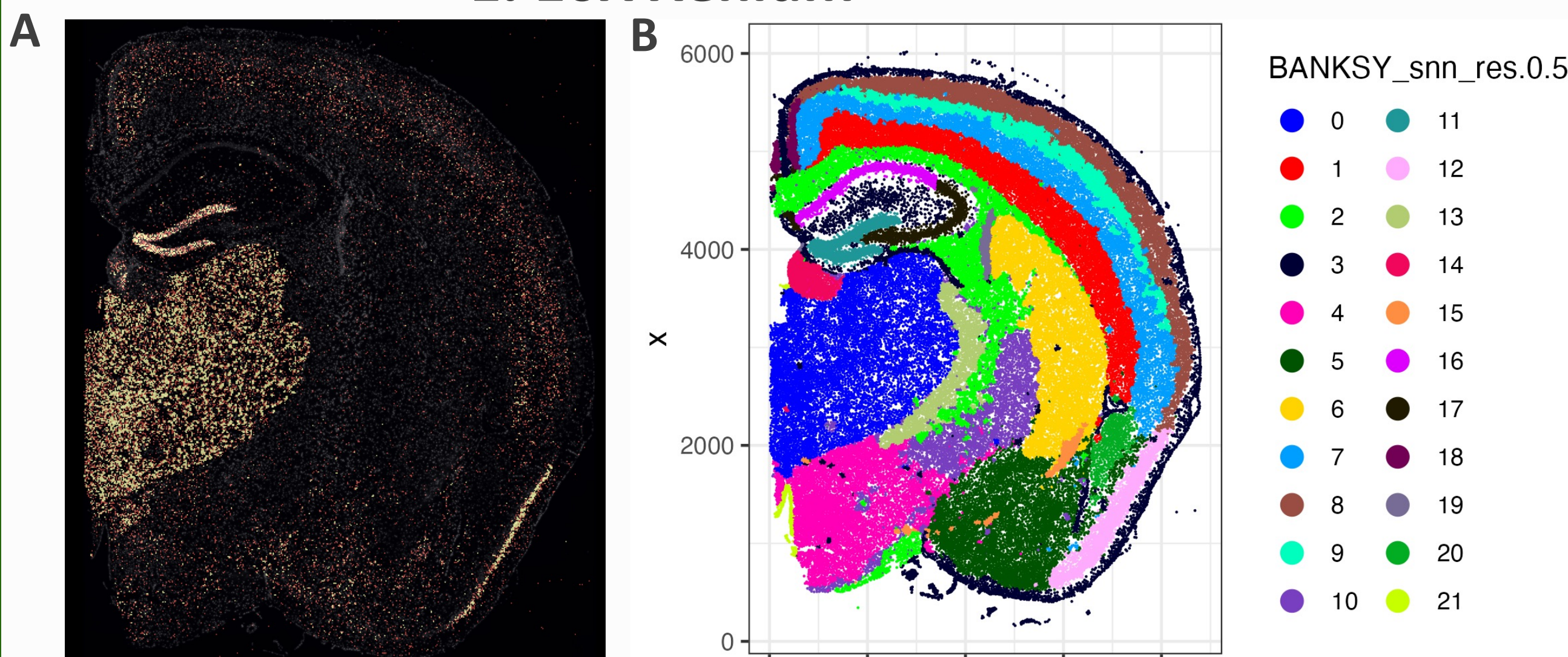


- Annual workshops
- Software Carpentry
- UNIX, Git, R, and Python
- Bulk RNA-seq
- Planned expansion for the future

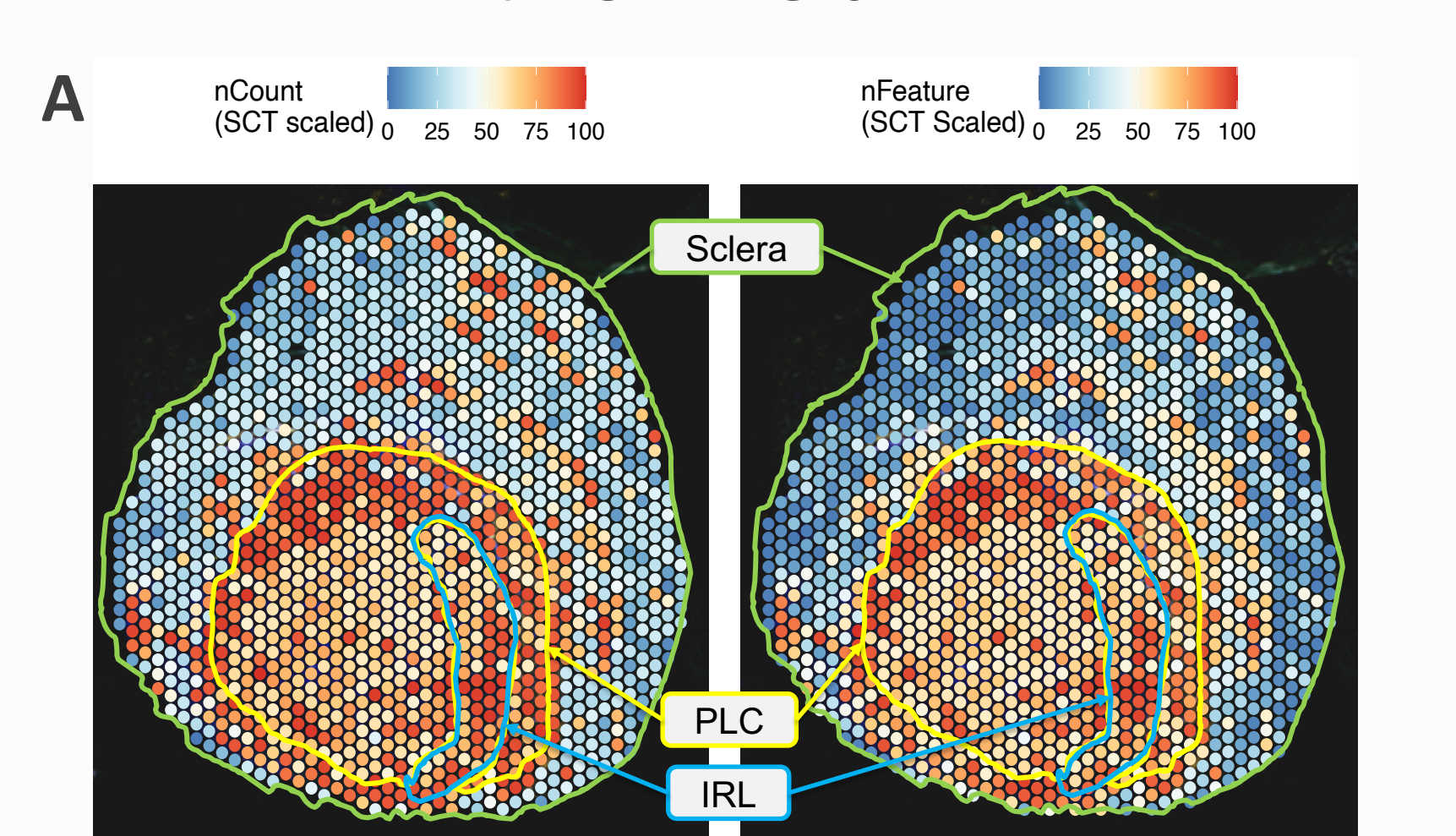


## Spatial Transcriptomics

### 1. 10X Xenium



### 2. 10X Visium



## How to Get Started

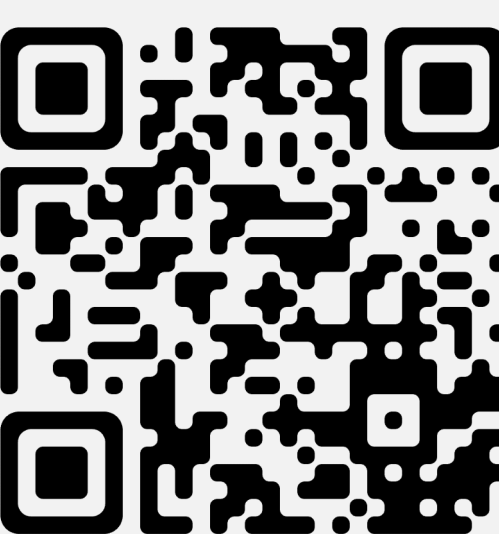
- Step 1** [Submit enquiry form](#)  
Submit an enquiry form from the U-BDS website
- Step 2** [Consultation](#)  
Upon review of the enquiry form, 30 minute consultation is scheduled to discuss project or grant application
- Step 3** [U-BDS documents](#)  
Generation of documents linked to enquiry. 1. Scope of Work (SOW) for projects detailing background, methods, milestones, deliverables, and quote or 2. grant support documents (due to demand, all document preparation costs \$75/hr)
- Step 4** [Start of project](#)  
Project is initiated following established core protocols and work detailed under the SOW or grant application.

## References & Acknowledgements

Jeremy Day Lab (PMID: 30863790 and Ratlas)  
 Alecia Gross Lab and Chris Girkin Lab (PMID: 39173459)  
 10X Multiome: Human PBMC (10k)  
 10X Xenium: Mouse Alzheimer's Disease over a time course  
 UAB Research Computing  
 Center for Computational Genomics and Data Science (CGDS)  
 Dr. Pallavi Iyer  
 UAB IRCP, and CIRC

## Contact Information

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1: 10X Xenium (in preparation for launch in 2025)

1A. *Ntng1* expression in the mouse brain with enrichment across expected anatomical areas (e.g.: hippocampal DG)  
 1B. BANKSY spatial clustering recovers tissue domains  
 1C. Cell type identification from 10X Xenium data (single-cell resolution)

2: 10X Visium (available)

Data shown is from the Alecia Gross and Chris Girkin laboratories in collaboration with U-BDS. The case study illustrates data derived from a brain dead organ donor, where the left eye was exposed to 30h of elevated intraocular pressure (IOP) vs control (right eye). A. Regions identified included the sclera, the posterior lamina cribrosa (PLC) and the immediate retro lamina (IRL). B. Proportion of spots within each anatomical segment and eye C. Illustrative example of one differential gene expression analysis from the study (in the PLC area).