UAB Biological Data Sciences (U-BDS) core provides extensive computational biology services to the UAB research community

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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), Bruker's 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) - <u>Thursdays 1:30-2:00 pm</u>
- **Other custom work:** develop reproducible research environments
- **Consultations:** 30 minutes to discuss study designs, analysis needs, grant application, and other technical details

Genomics

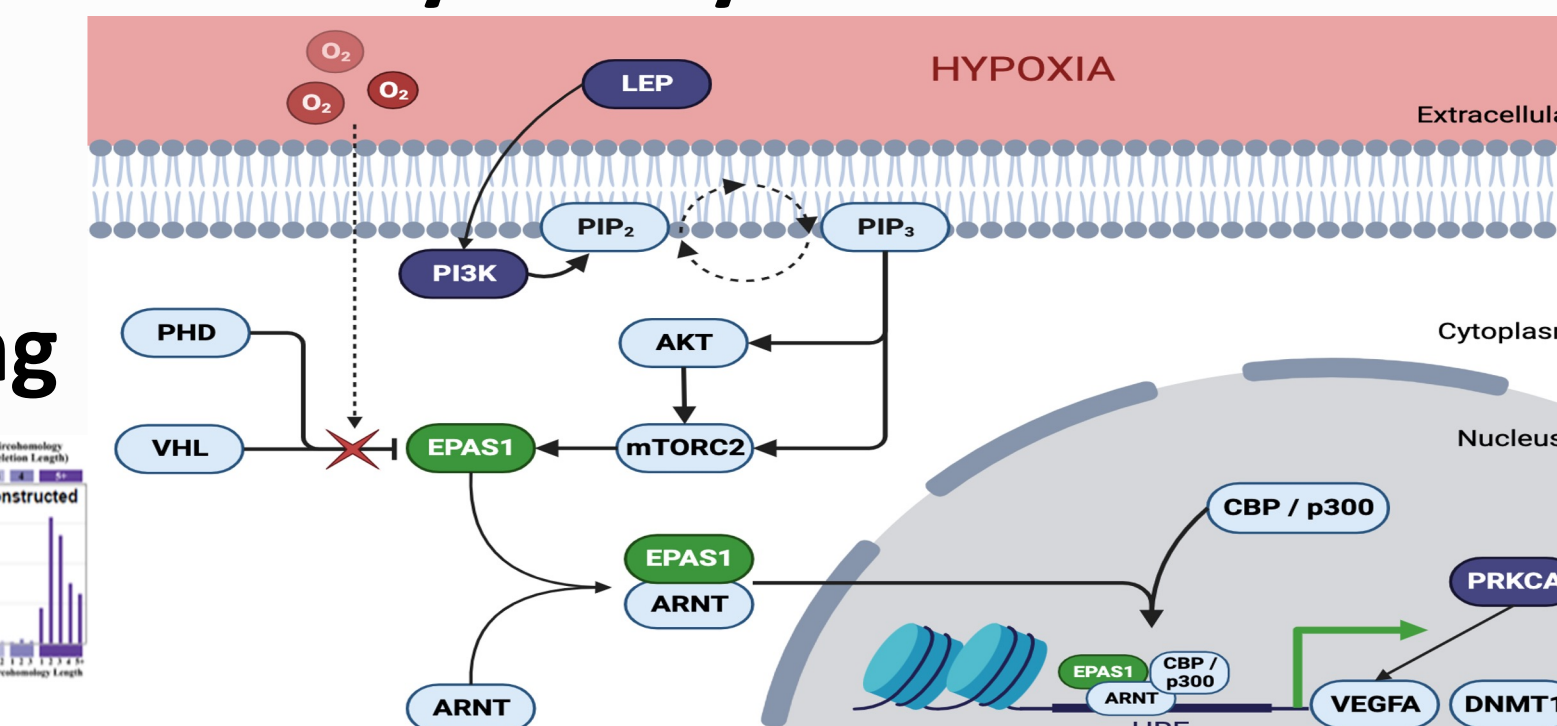**Cohort based variant classification/visualization**
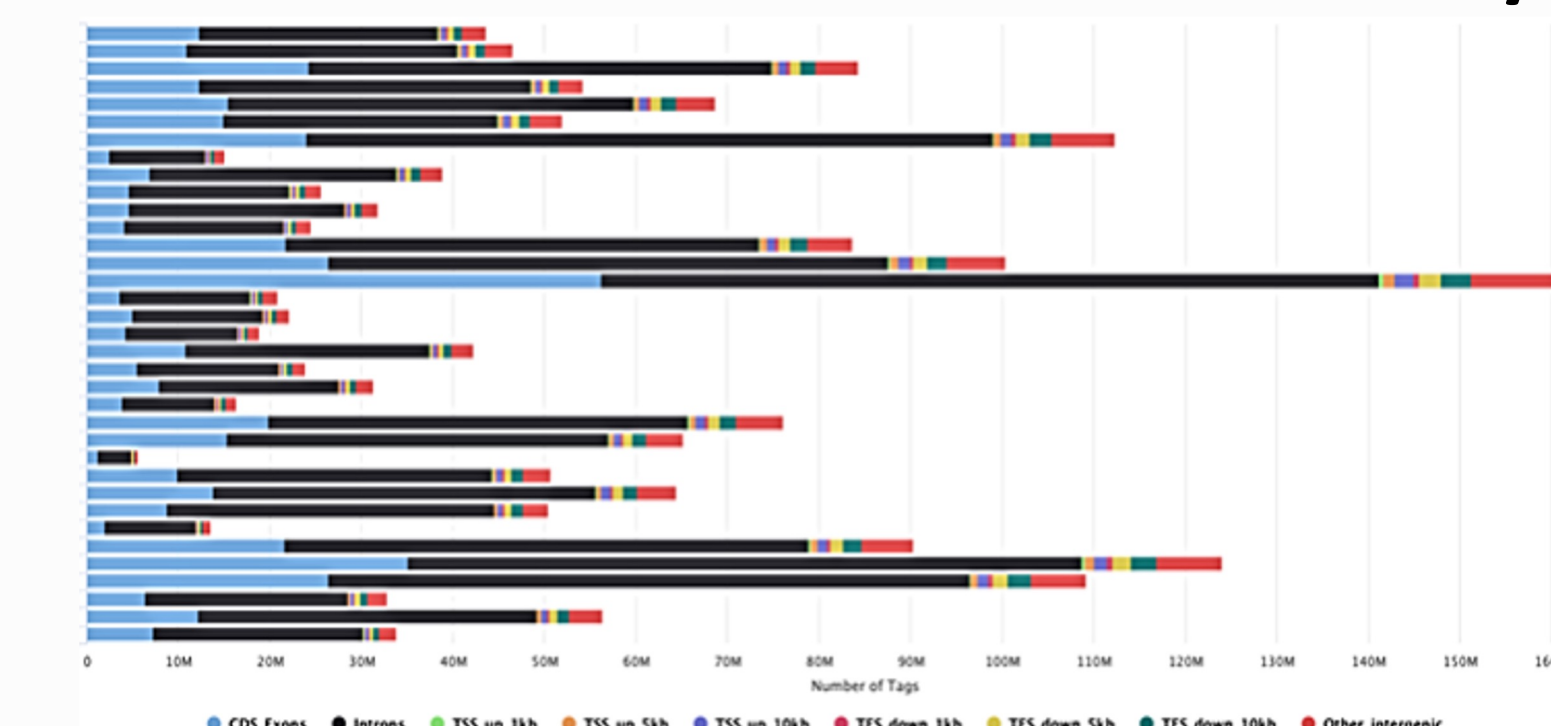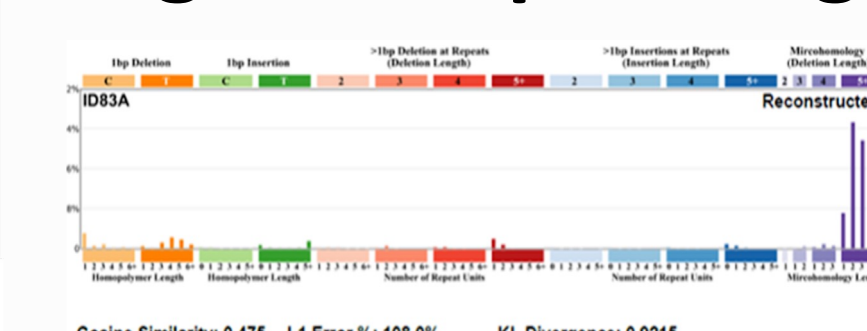

G x P associations
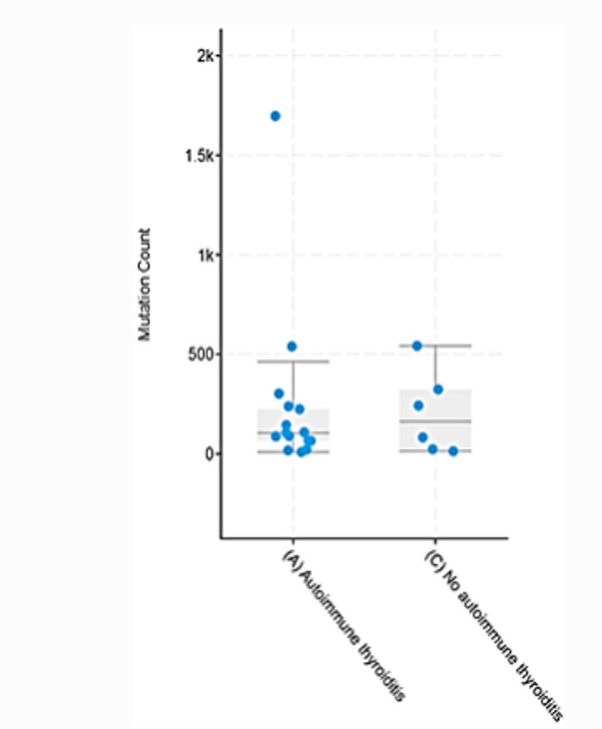
WGS & WES based genomic analysis. Data QC, alignment, variant calling, functional impact analysis, and interpretation (small and structural variants and somatic and germline)
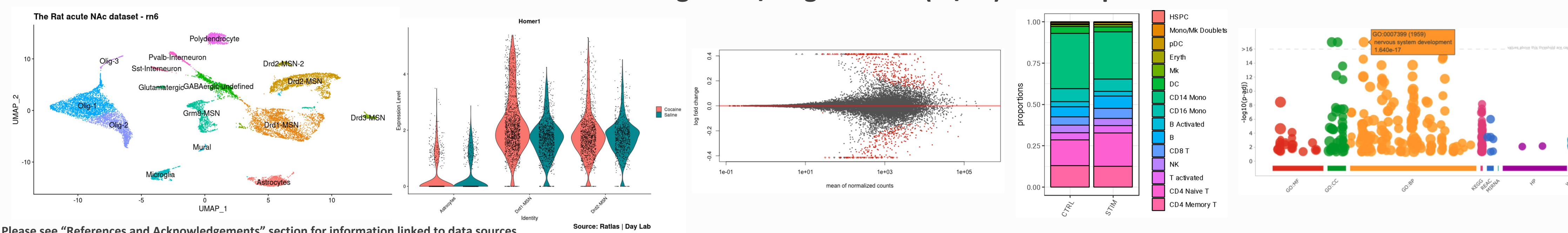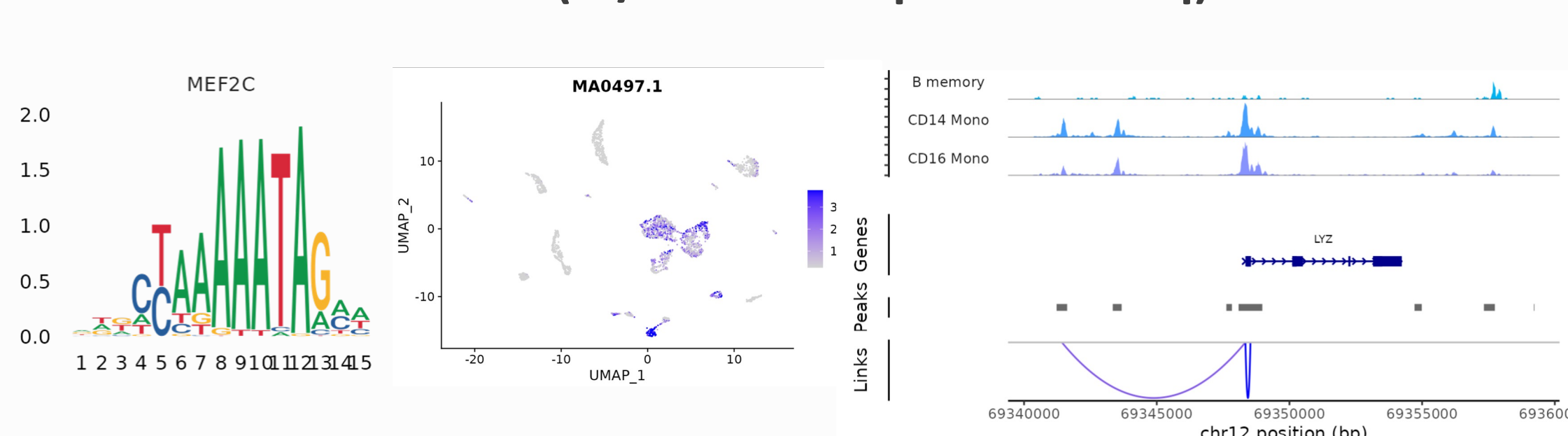
Signature profiling

Pathways analysis & visualization

Transcriptomics

Short–read single-cell/single-nuclei (sc/sn) RNA-seq

The Rat acute NAc dataset - rn6

Please see "References and Acknowledgements" section for information linked to data sources

Source: Ratlas | Day Lab

Multiome (sc/sn RNA-seq & ATAC-seq)

Long–read sc/sn RNA-seq

Oxford Nanopore

Gene–level 5' lung cancer DTCs   Transcript-level 5' lung cancer DTCs   Transcript-level darfish

Spatial Transcriptomics

1. 10X Xenium

PTS3

1: 10X Xenium

1A & 1B: Data shown is from Jeremy Day, Jasper Heinsbroek, Jamie Peters 10X Xenium Pilot experiment in collaboration with U-BDS

1A. BANKSY spatial clustering recovers tissue domains in the mouse brain

1B. UMAP of the identified spatial domains

1C & 1D: Data shown is from Jim George 10X Xenium Pilot experiment in collaboration with U-BDS

1C. Spatial overview of the Proximal Tubule Segment 3 (PTS3) cells

1D. Representative spatial plot and UMAPs of the identified spatial clusters across mouse kidney samples

2. 10X Visium

Proportions per eye

2: 10X Visium

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 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 region).

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.

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

Step 4 — **Start of project**
Project is initiated following established core protocols and work detailed under the SOW or grant application.

Training

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

- **Online guide:**
  - **https://u-bds.github.io/training_guides**
  - Includes training material for Docker, Singularity, nf-core pipelines
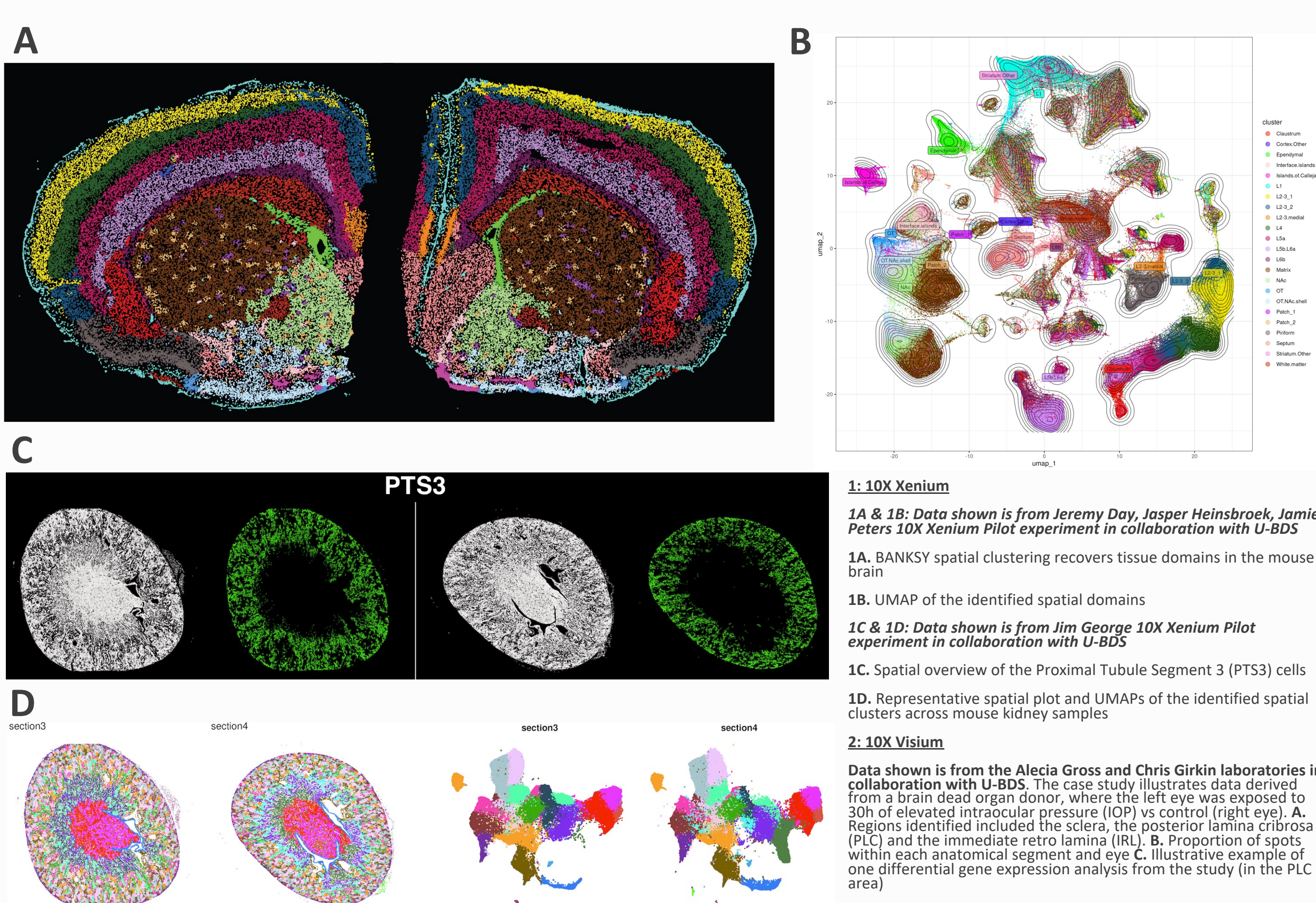
- **Annual workshops**
  - Software Carpentry
  - UNIX, Git, R, and Python
  - Bulk RNA-seq
  - Bioinformatics with nf-core
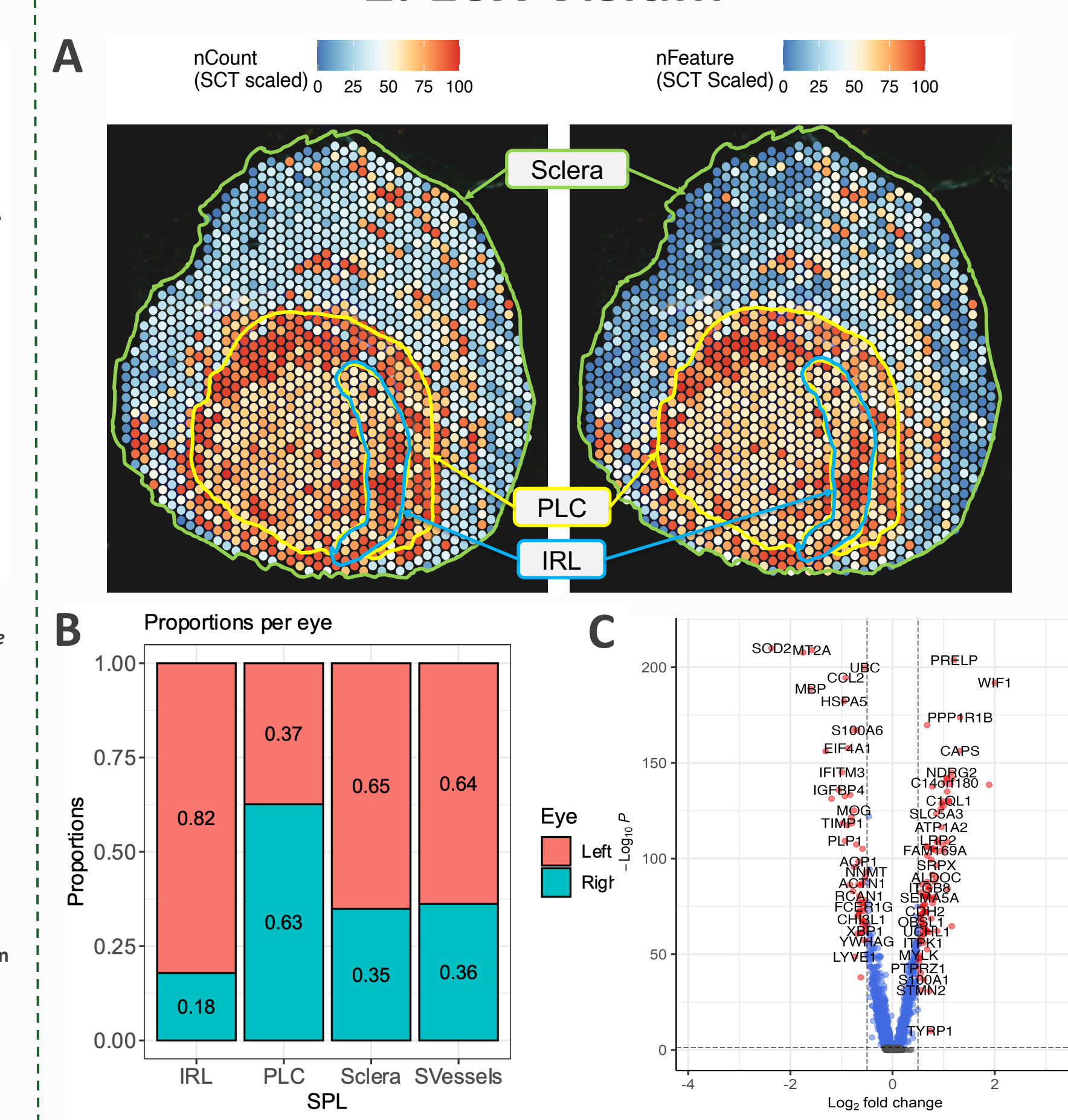 - Planned expansion for the future

References & Acknowledgements

Jeremy Day Lab (PMID: 30863790 and Ratlas)
Alecia Gross Lab and Chris Girkin Lab (PMID: 39173459)
Austyn Trull, Liz Worthey, Lara Ianov (PMID: 40905625)
10X Multiome: Human PBMC (10k)
10X Xenium Pilot Experiments: 1. Jeremy Day, Jasper Heinsbroek, Jamie Peters 2. Jim George
UAB Research Computing
Center for Computational Genomics and Data Science (CGDS)
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