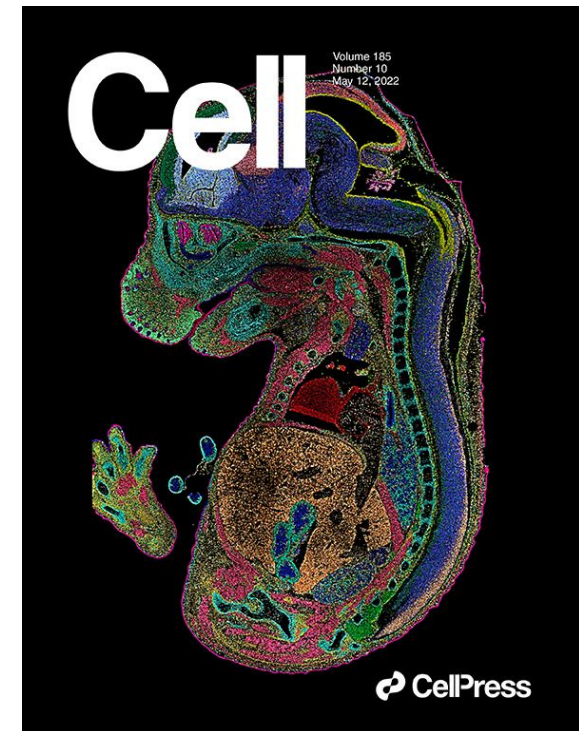- **The team:**
  - Ian Dirk Fichtner
  - Shashwat Sahay
  - Lotte Pollaris
- **Goal: Explore STEREO-SEQ**
  - New promising spatial technology [Chen et al. 2021] [Xia et al. 2022]
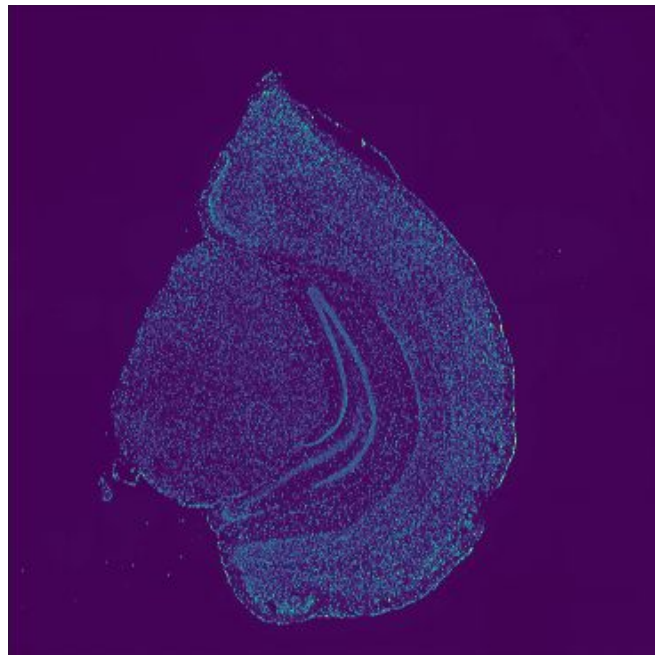 - Transcriptome-wide, sub-cellular spatially resolved data
- **Mid-hackathon status**
  - Curated some datasets
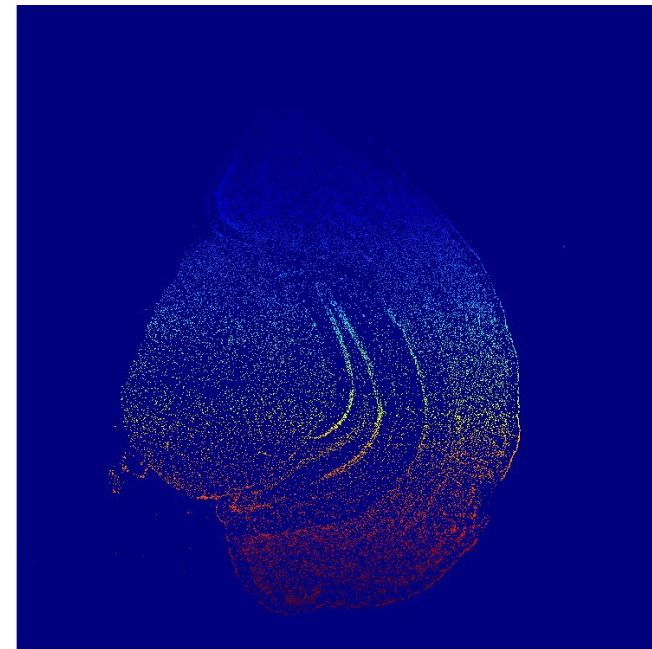 - Define data structures
  - Troubleshooting

- **Results**

  8119736 cells **x 22413** transcripts

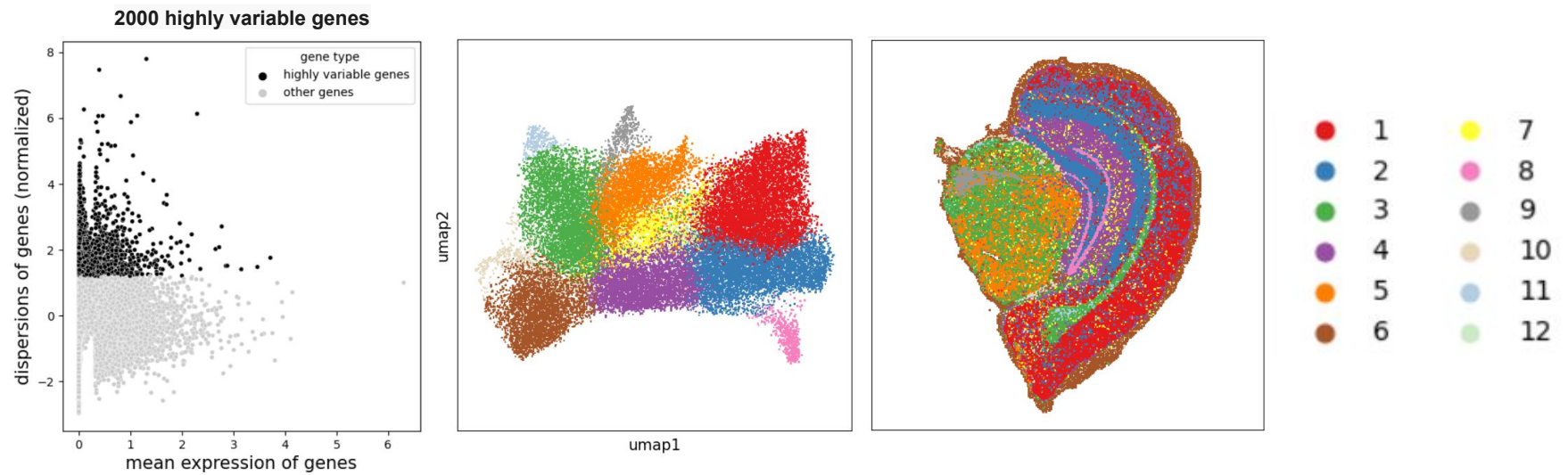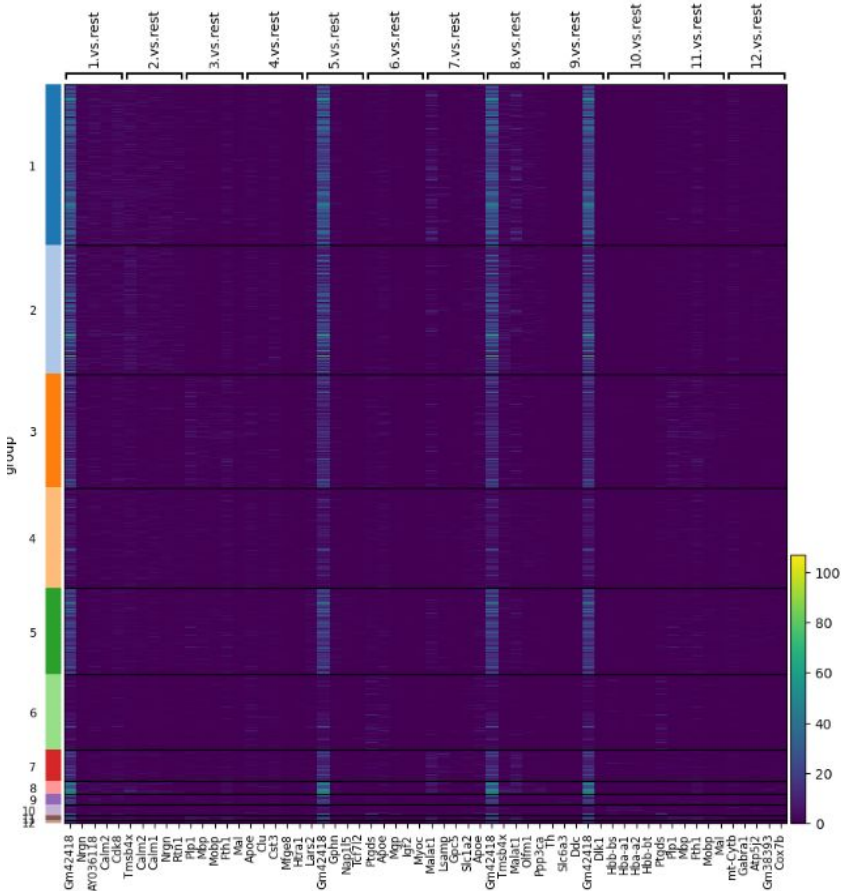Segmented Watershed

Project 6: #stereoseq

- **Results**

2000 highly variable genes

- **Results**

- **Outlook**

  - Set the groundwork for further downstream analysis

  - More segmentation methods

  - Allows for integration into `TXsim` pipeline

  - Evaluation of data quality

- **Challenges**

  - Segmentation methods are limited due to DAPI staining

  - Identification of cell boundaries with highly variable genes for segmentation is computationally challenging