St. Anna Kinderkrebsforschung
CHILDREN'S CANCER RESEARCH INSTITUTE

Interactive Seurat Visualisation using Vitessce and CellxGene

Internship presentation 22 February 2024

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Aims and Objectives

Visualisation method for Seurat objects that is:

1. Interactive
2. Web-based
3. Easily shareable
4. Able to display a variety of plot types / embeddings

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Visualisation method for Seurat objects that is:

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Intended Use:

1. Visual aid for publication (collaborators, readers etc)
2. Exploration of own data

Explored Tools

Tool	Web-based/shareable	Interactive	Range of Figures	User-friendly
Vitessce	✓	✓	✓	
CellxGene		✓	✓	✓
Loupe Desktop App		✓		✓
Single Cell Portal	✓	✓		
Automated Single Cell Analysis Portal	✓	✓		

CellxGene

CellxGene

- Requirements:
  - .h5ad file and pip install

CellxGene

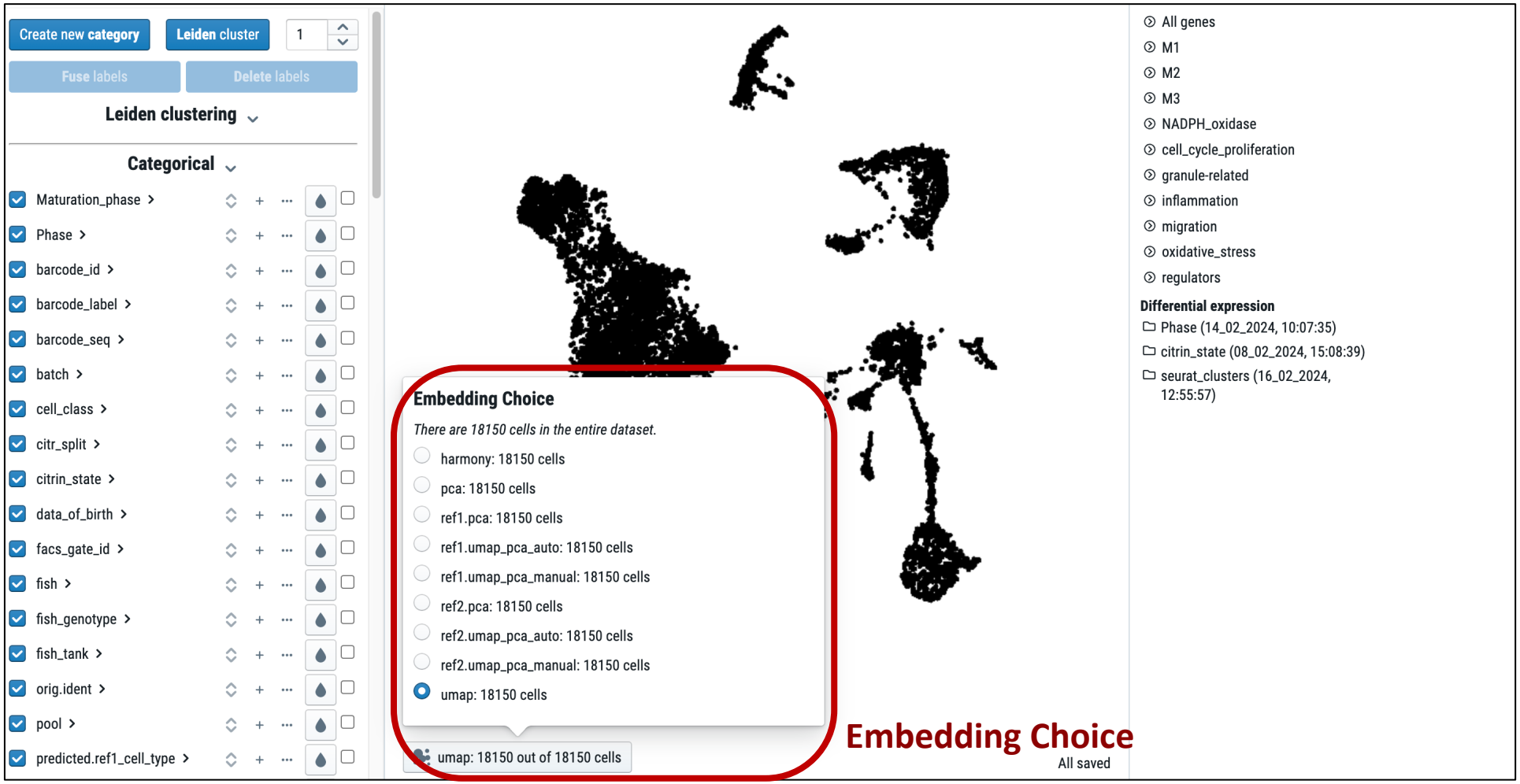
- Requirements:
  - .h5ad file

- Community Extensions:

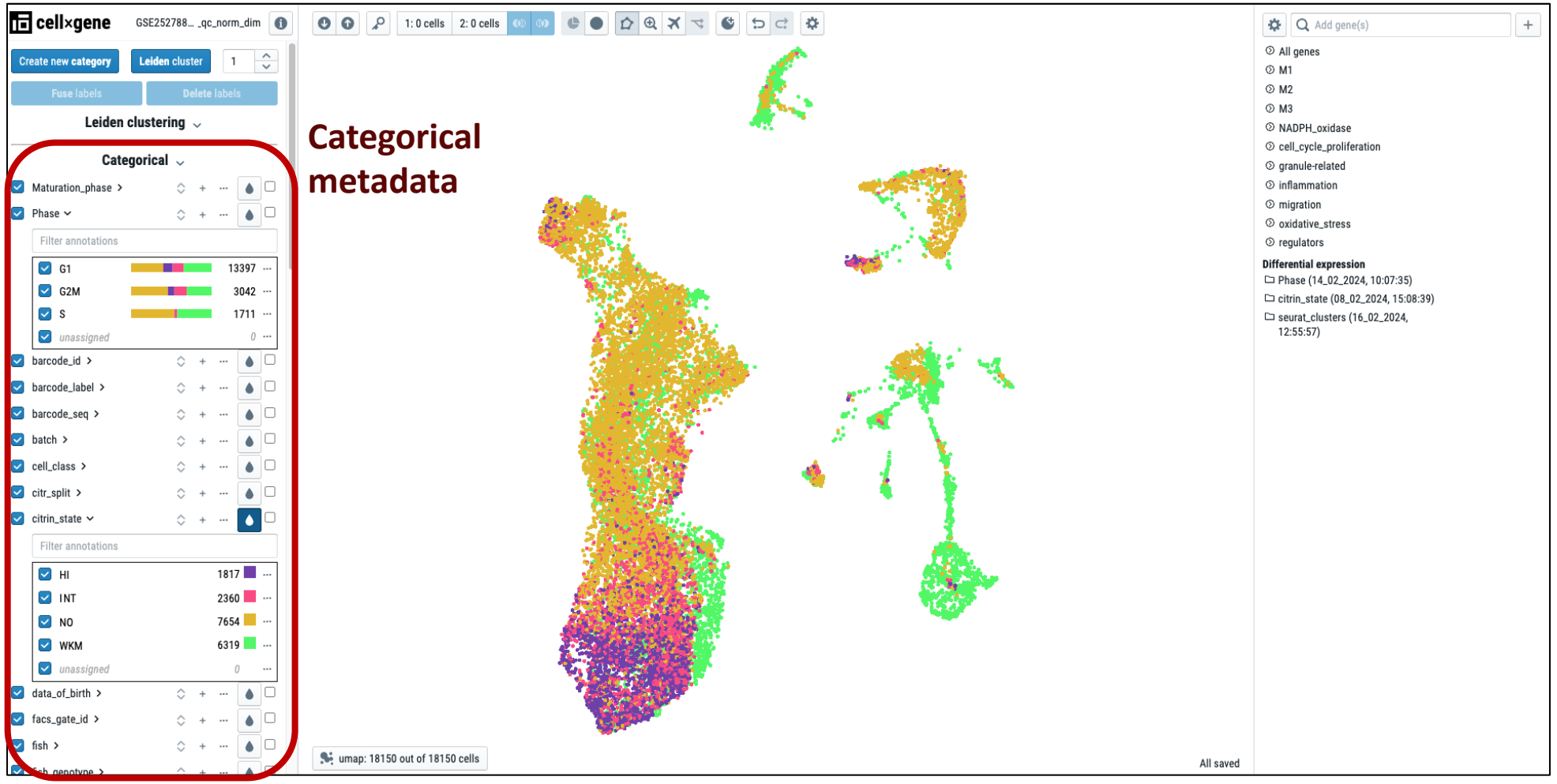
Explore CellxGene	**CellxGene Visualisation in Plugin**	**CellxGene Gateway**
Annotation, Exploration, data pre-processing	violin, stacked violin, stacked bar, heatmap, volcano, etc. plots	Multiple Datasets

Explore CellxGene (exCellxGene)

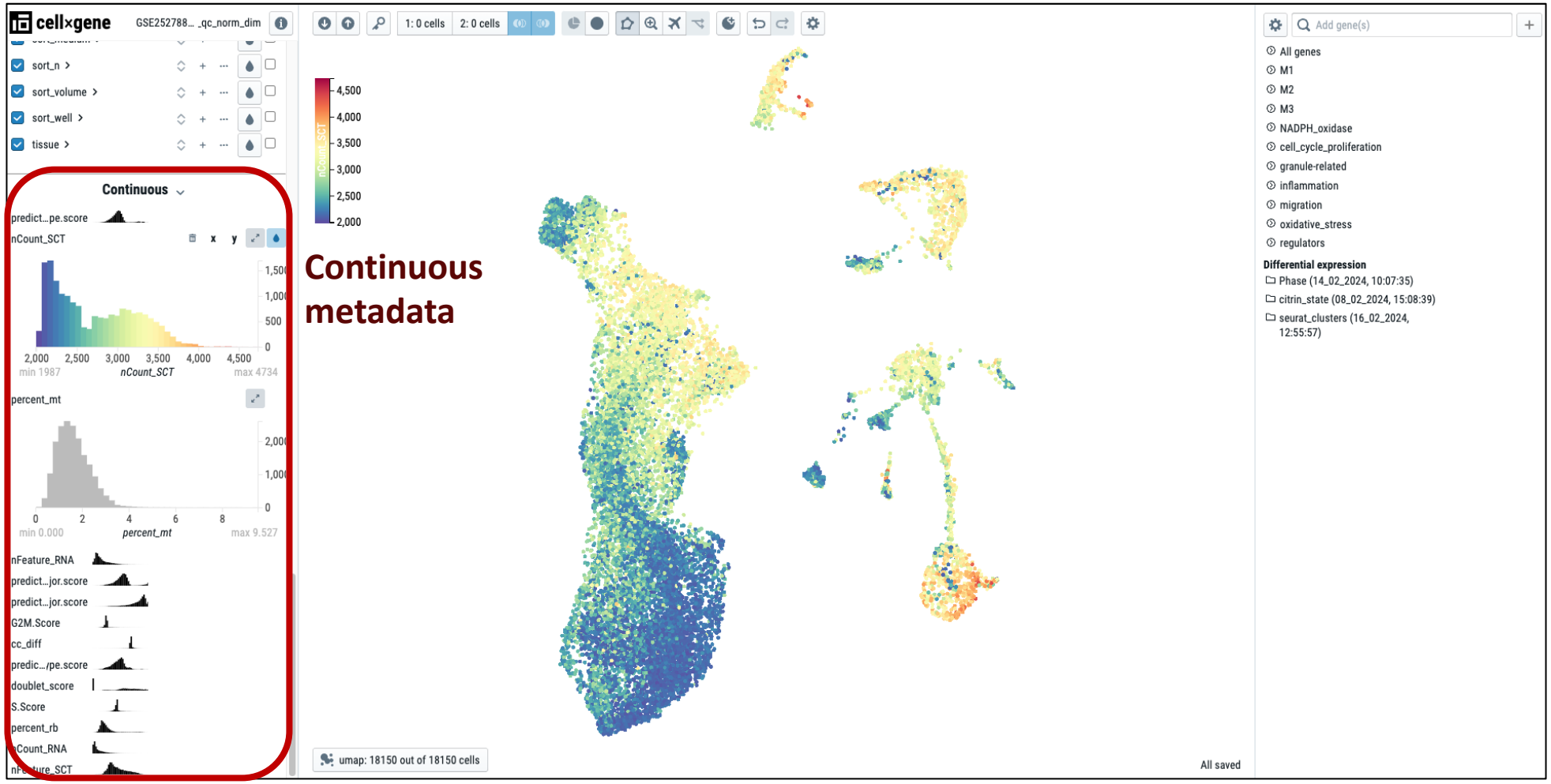
exCellxGene



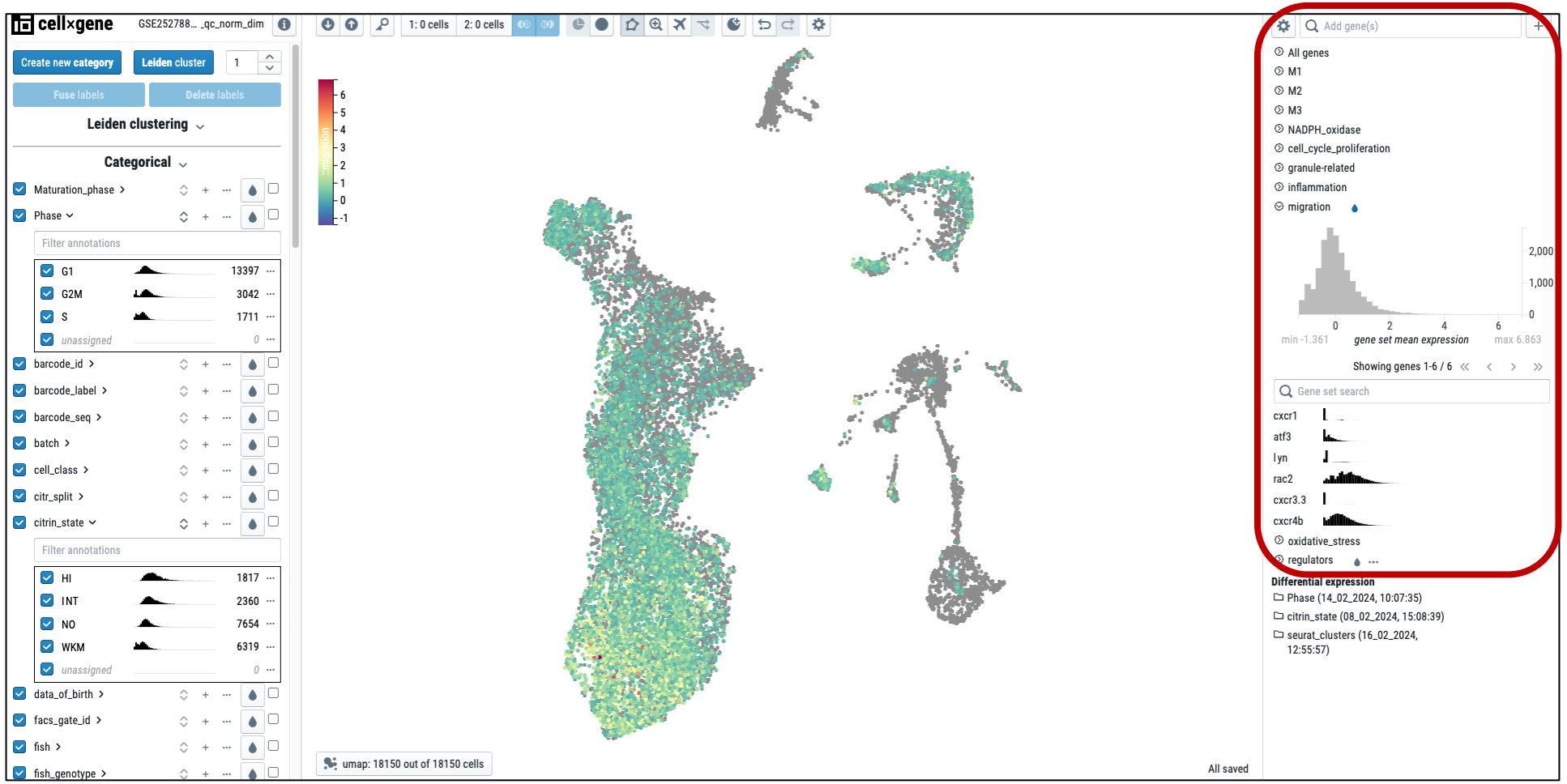
exCellxGene



exCellxGene

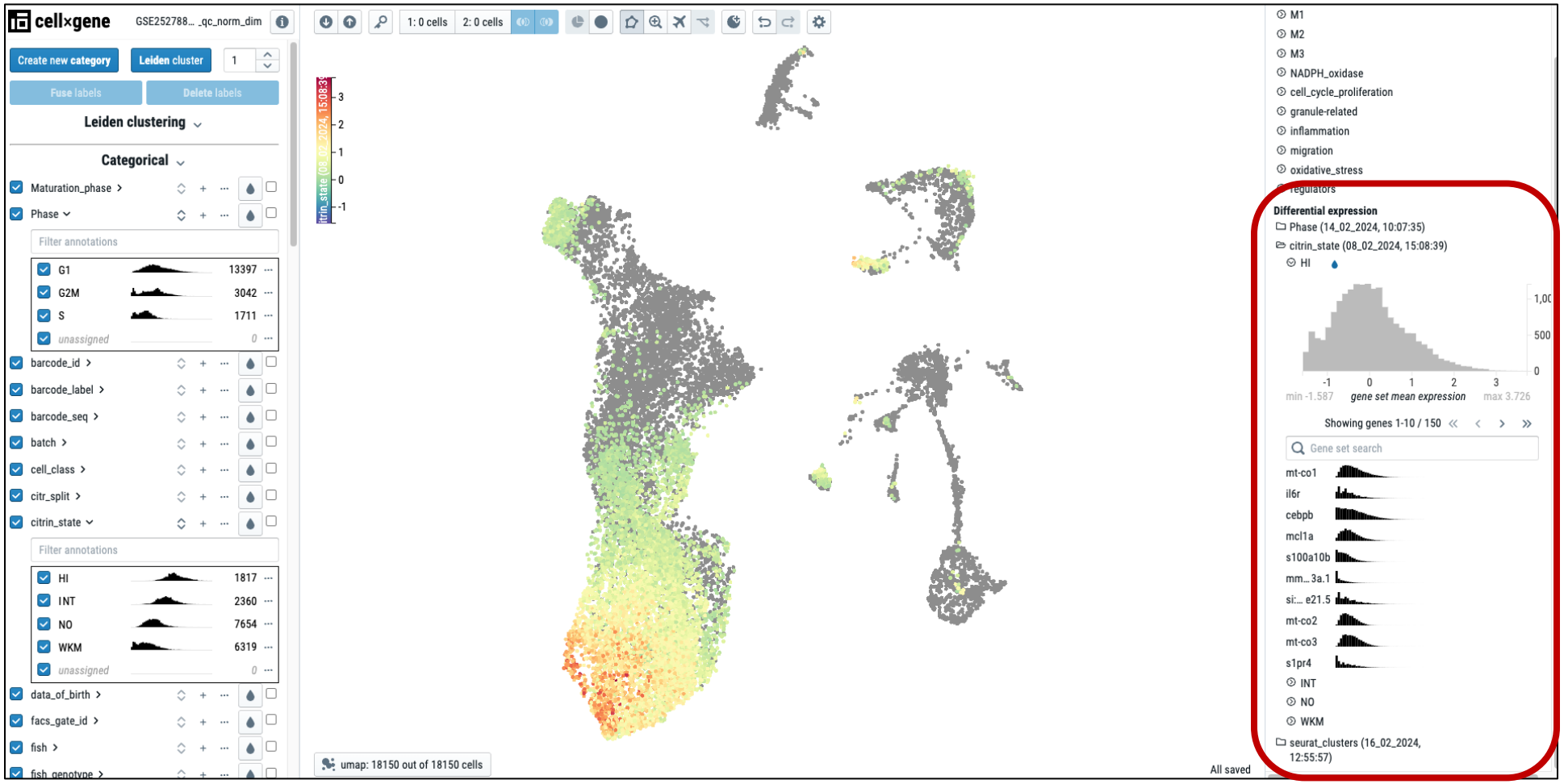


exCellxGene



Manually managed gene sets

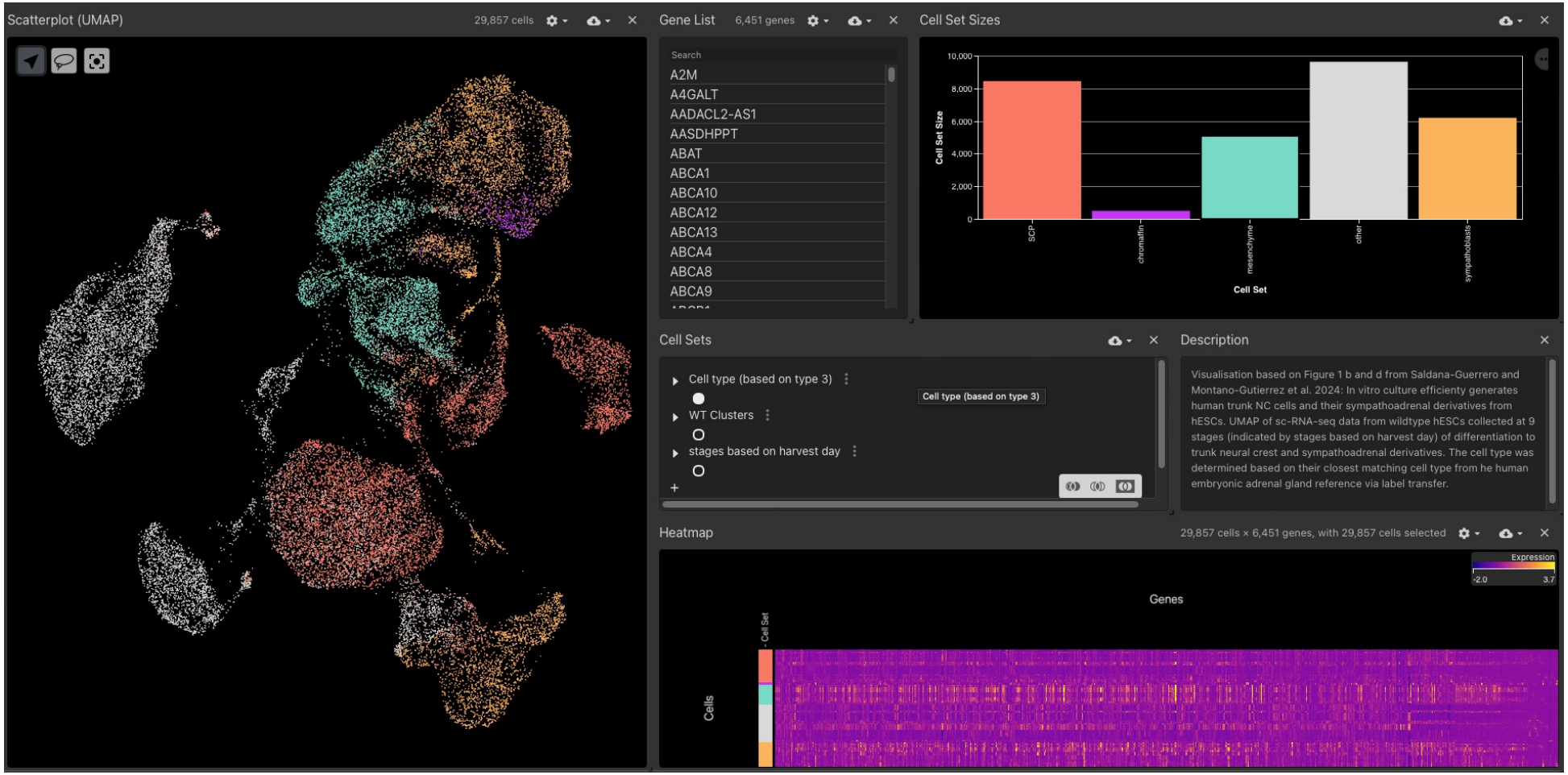
exCellxGene



Differentially expressed genes

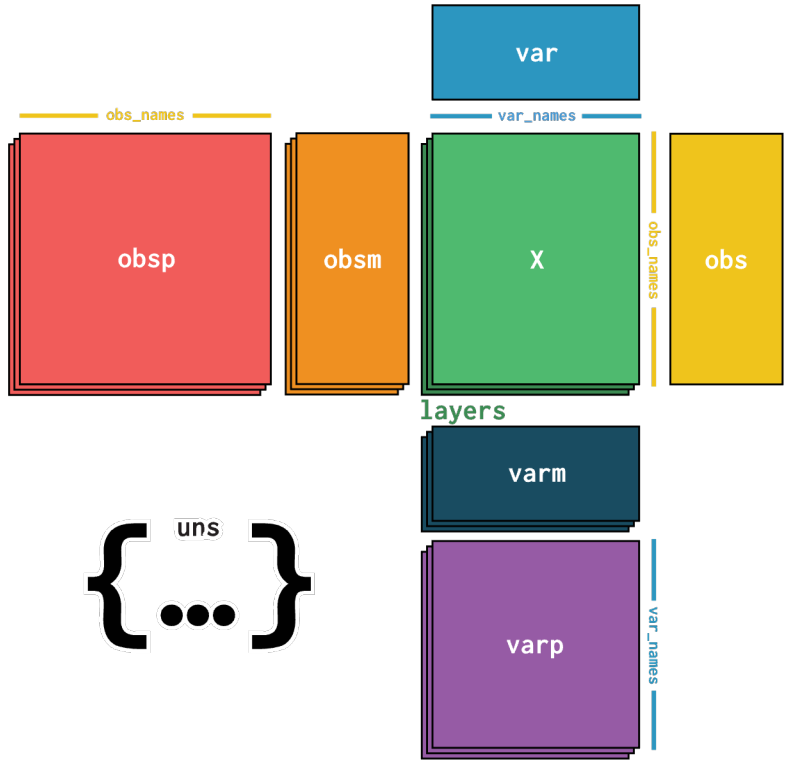
Vitessce

Widget / View types



Vitessce file requirement

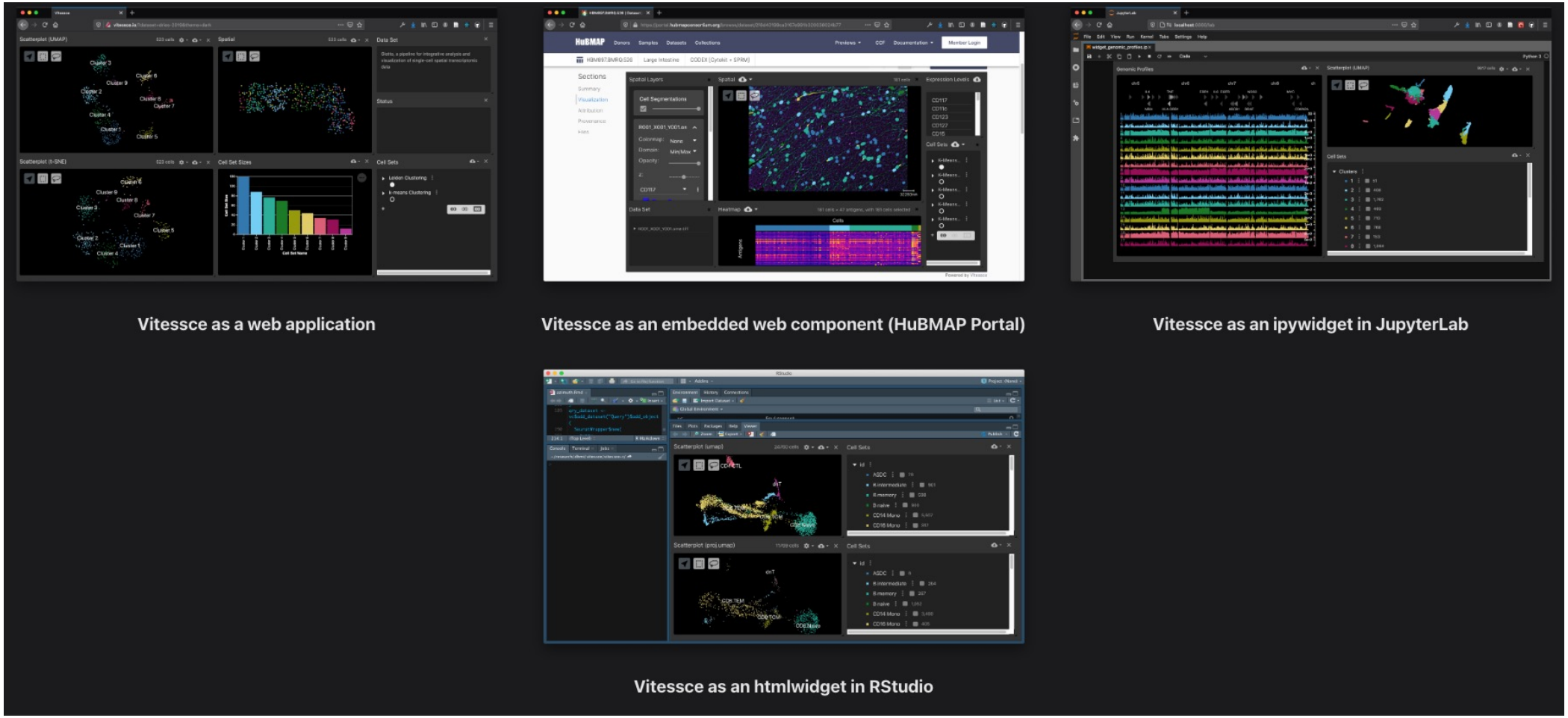
- Anndata-Zarr store



- Vitessce R and Python package to transform Seurat/.h5ad

```
adata_path <- file.path("data", "example", "example.h5ad.zarr")
vitessceAnalysisR::seurat_to_anndata_zarr(so, adatapath)
```

Vitessce Platforms



Vitessce Data Hosting

Locally	**Static Web Servers**
http-server	GitHub Pages, AWS S3 Buckets, Google Cloud
Not yet published data	Published and non-confidential data
Only shareable with file transfer	Shareable with unique vitessce.io url

Vitessce Config.JSON

The config specifies the:

1. Dataset
2. Visualisation types (widgets)
3. Linking widgets
4. Design (colours, layout)

```
{ "version": "1.0.16",
  "initStrategy": "auto"
  "name": "Zebrafish Neutrophil Figure 3",
  "description": ""Visualisation based on Fig. 3 from Kirchberger and Shoeb et al. 2024",

   "datasets": [{
      "uid": "A", "name": "My dataset",
      "files": [{
          "fileType": "anndata.zarr",
          "url": "https://esztersojtory.github.io/vitessce_data/zfish.h5ad.zarr",
          "options": {
            "obsEmbedding": [{...}],
            "obsSets": [{...},}],
            "obsFeatureMatrix": {...}}}]}],


   "coordinationSpace": {
    "dataset": { "A": "A"},
    "embeddingType": { "A": "UMAP"},
    "featureValueColormapRange": {"A": [0.15,0.23]},
    "obsSetColor": { "A": [ {"path": [], "color": [248, 225, 222 ]}]}},


   "layout": [
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        "embeddingType": "A",
        "featureValueColormapRange": "A",
        "obsSetColor": "A"},
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```
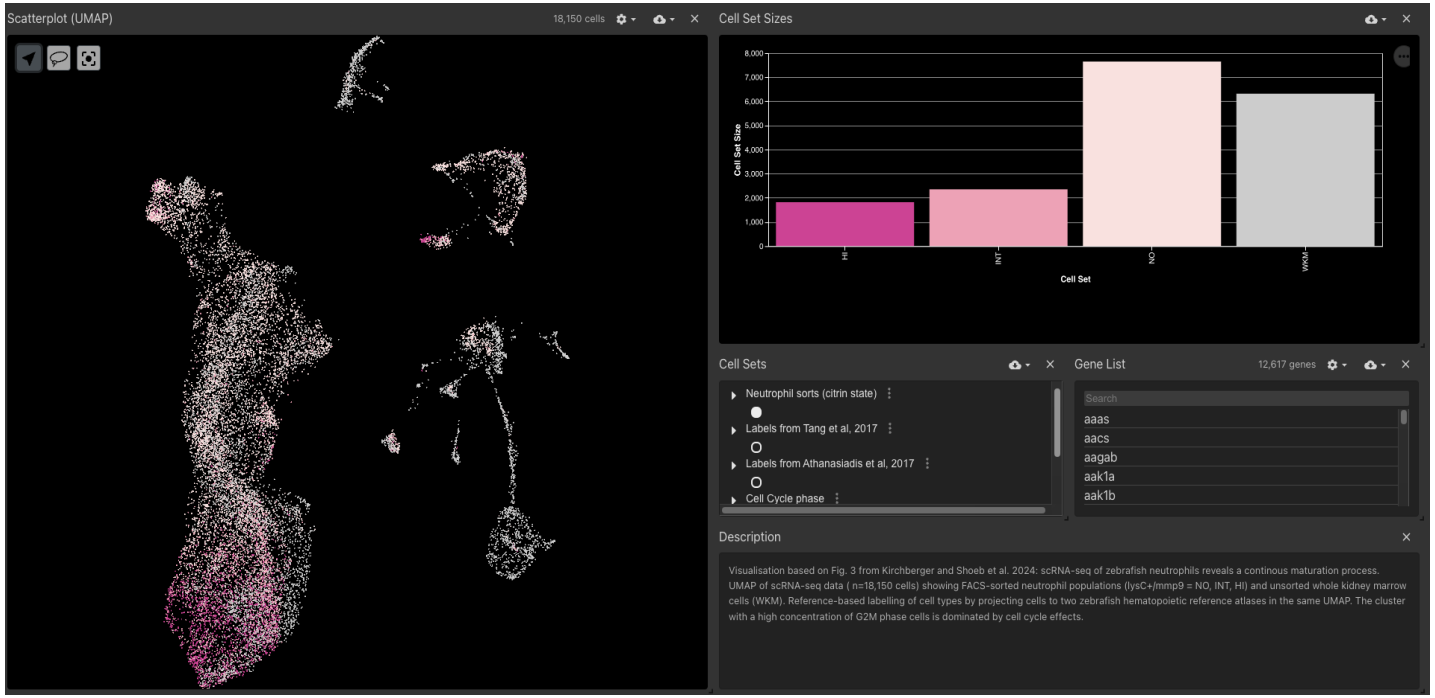
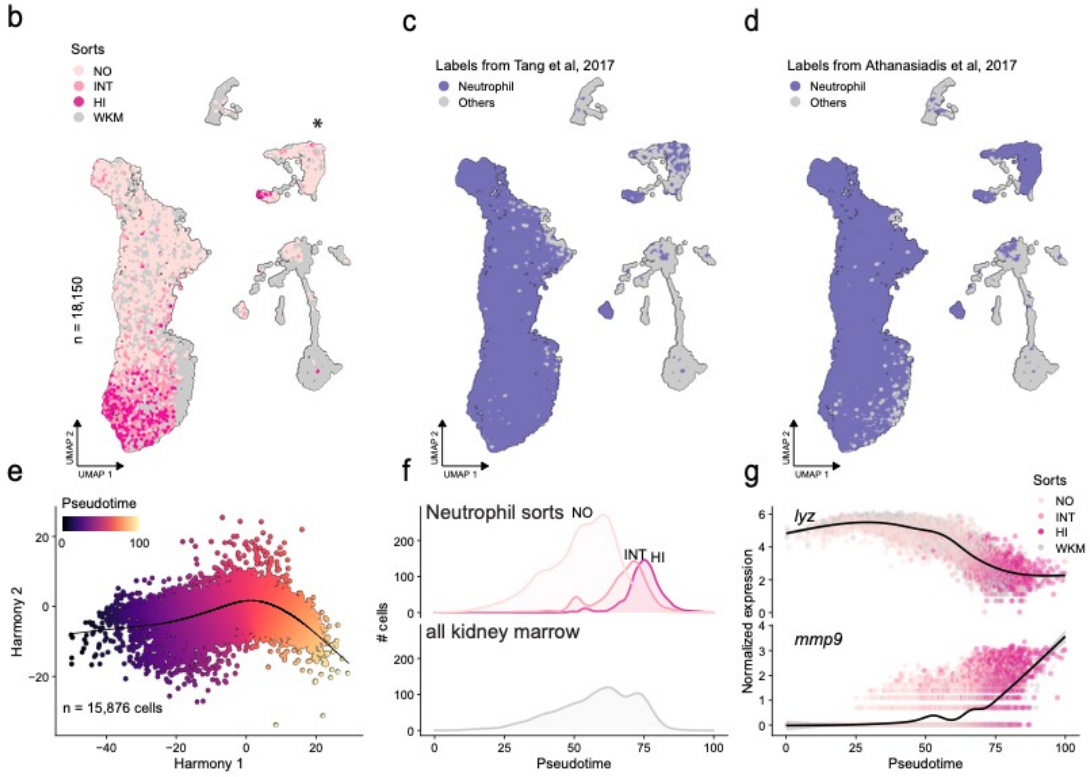
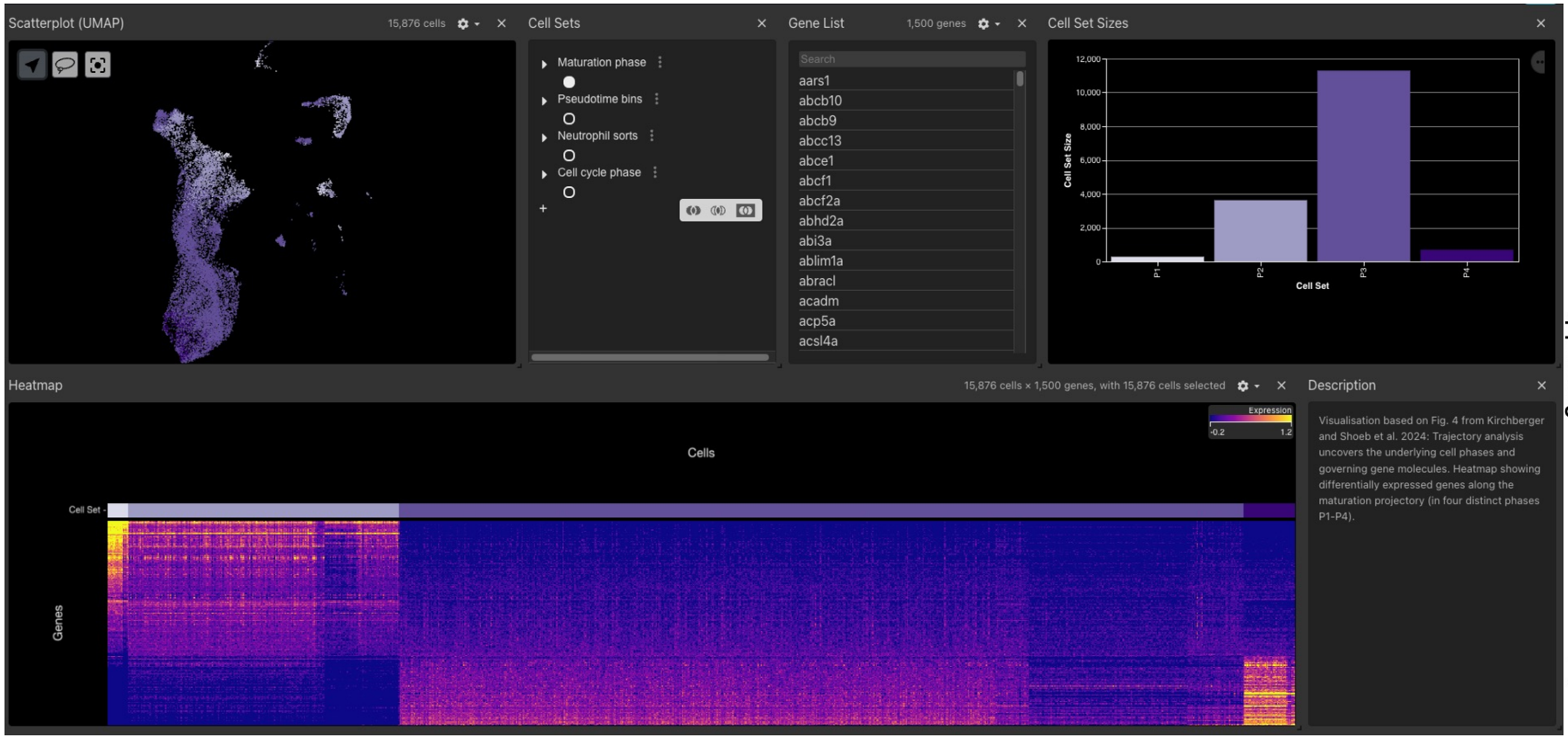

Applied Examples

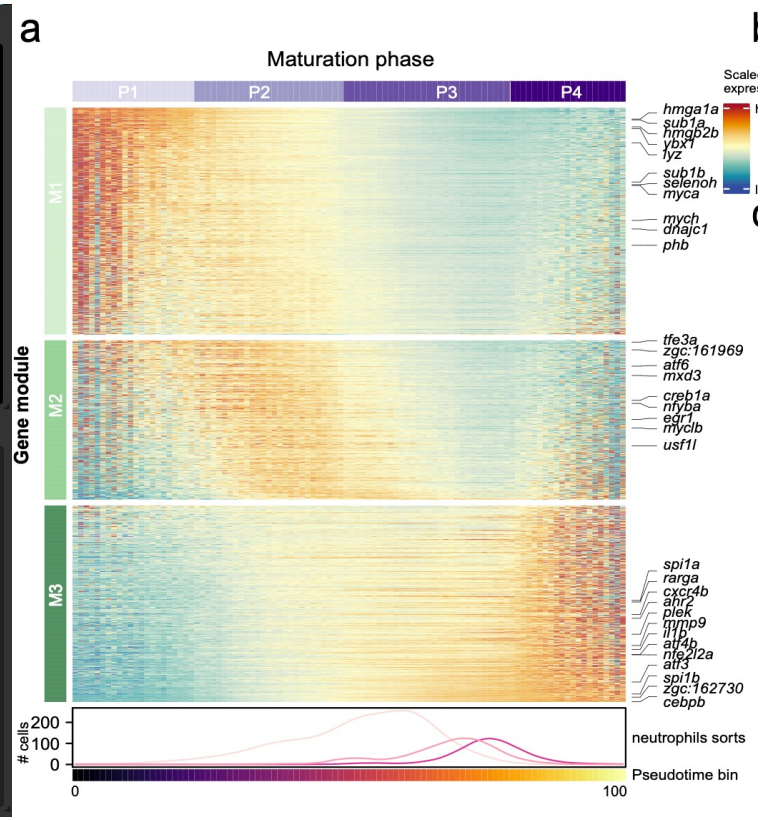
Mohamed’s zebrafish dataset (Fig 3)



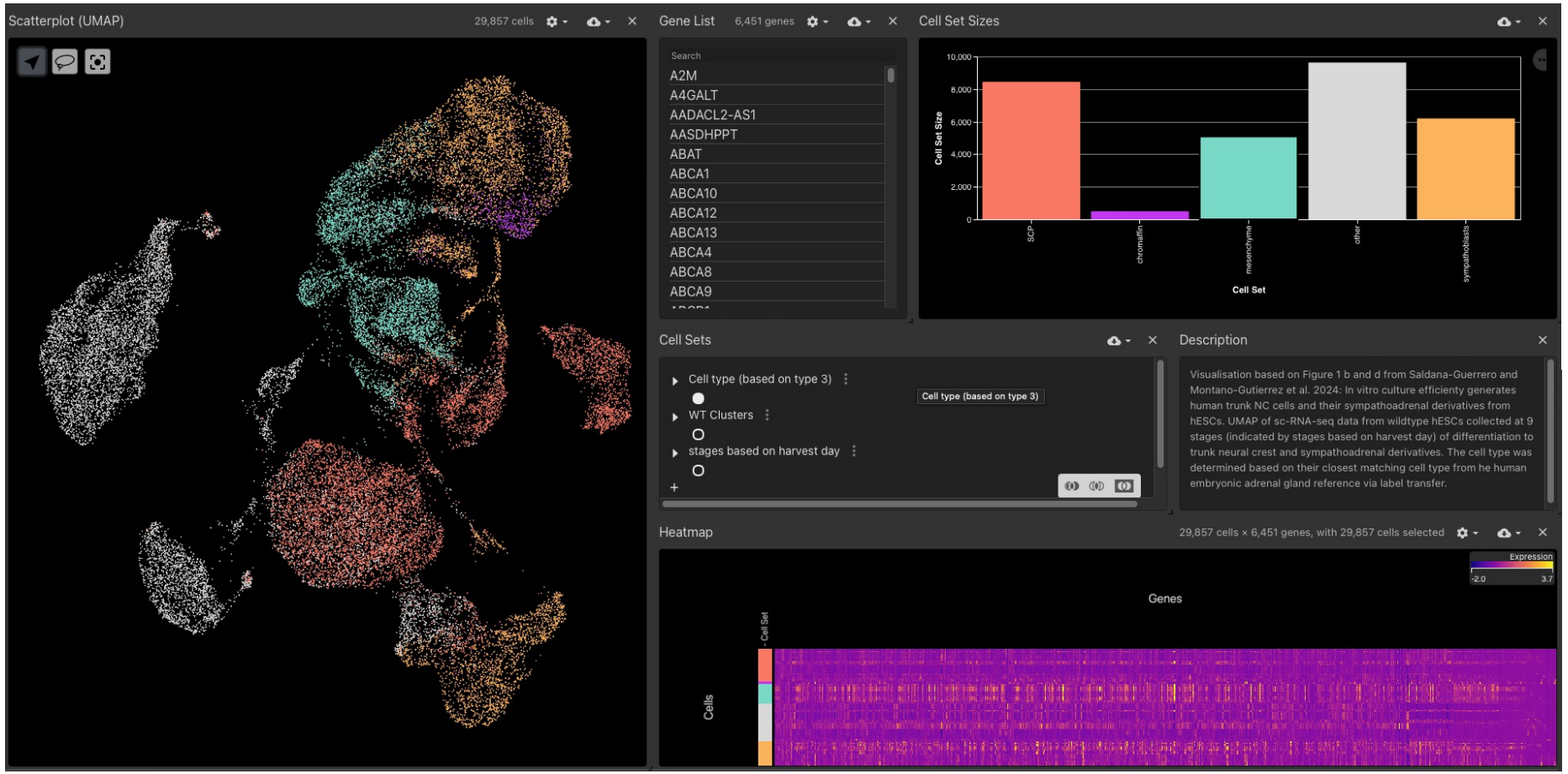


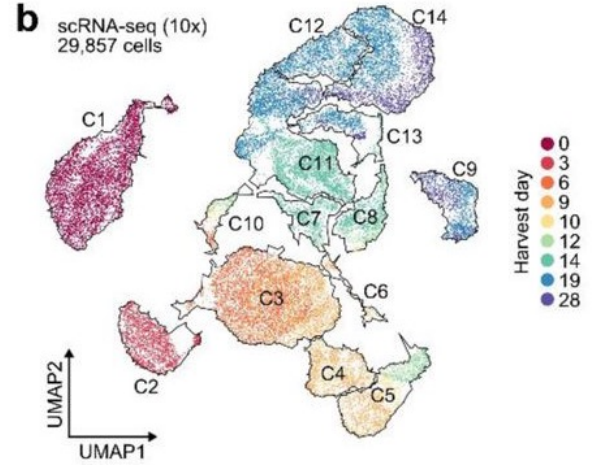
Mohamed's zebrafish dataset (Fig 4)

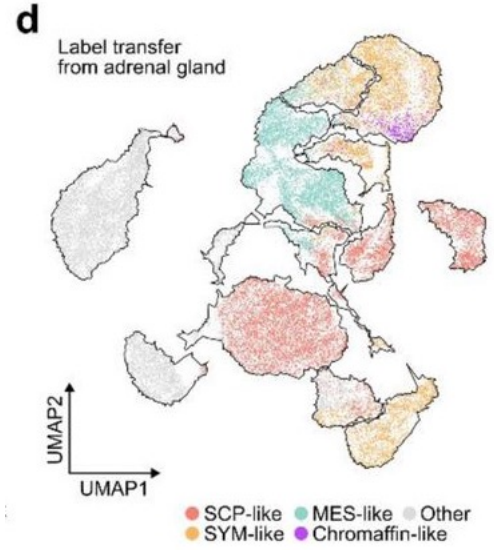




Luis' Wildtype Dataset







Demonstration

Thank you

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