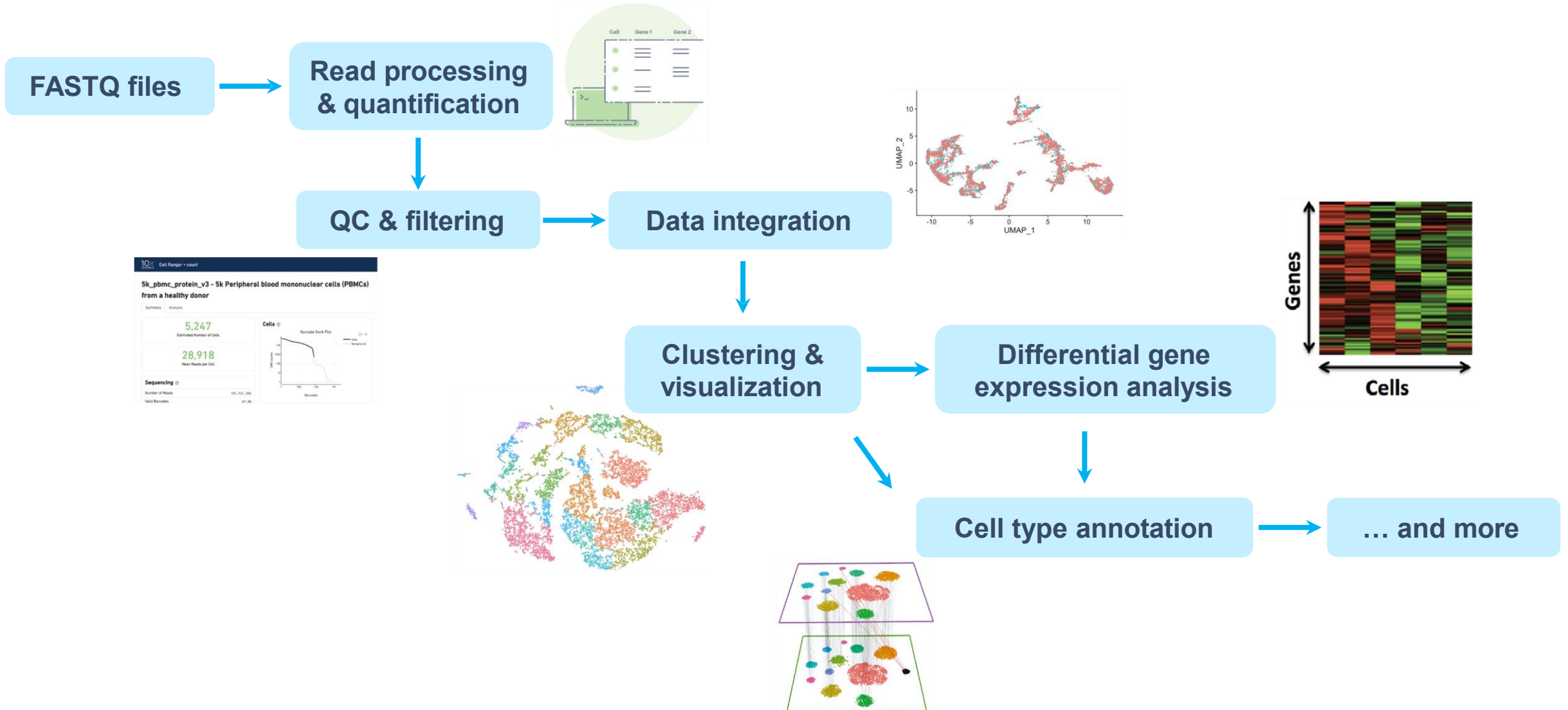
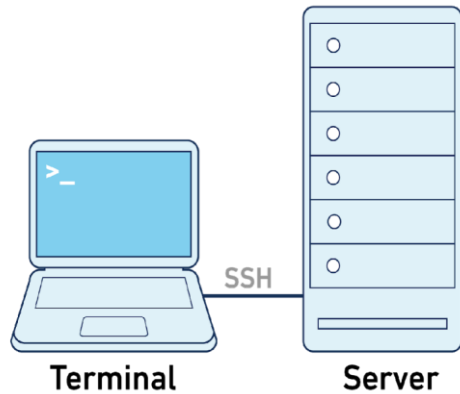


Online Processing of Sequencing Reads

Data analysis flow



Running Cell Ranger



On a Linux system

Required skills:

Understand the experimental design.

Comfortable running command line in the Linux environment.

Familiar with data management systems.

Know what to do if there are server issues.



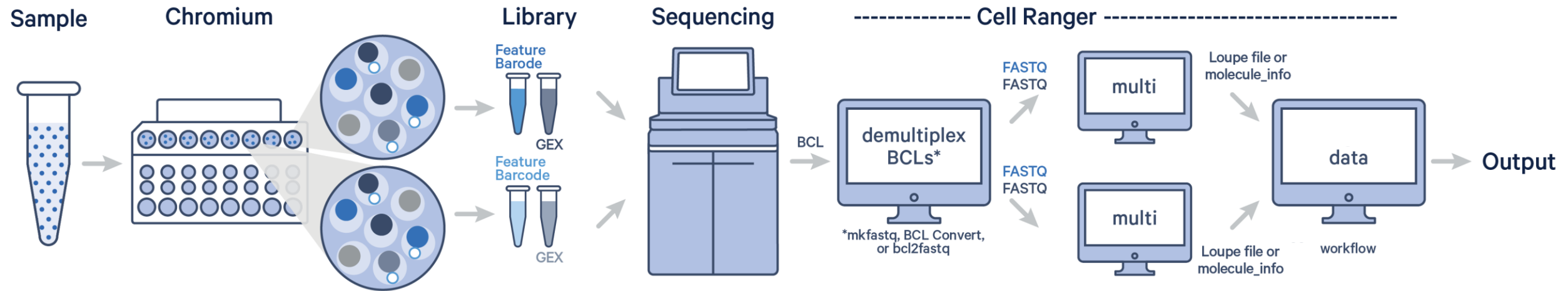
On 10x Cloud

Friendly user interface and simple data management.

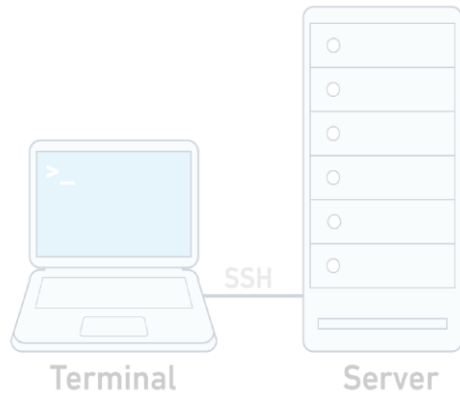
Required skill:

Understand the experimental design.

On a Linux system



Running Cell Ranger



On a Linux system

Required skills:

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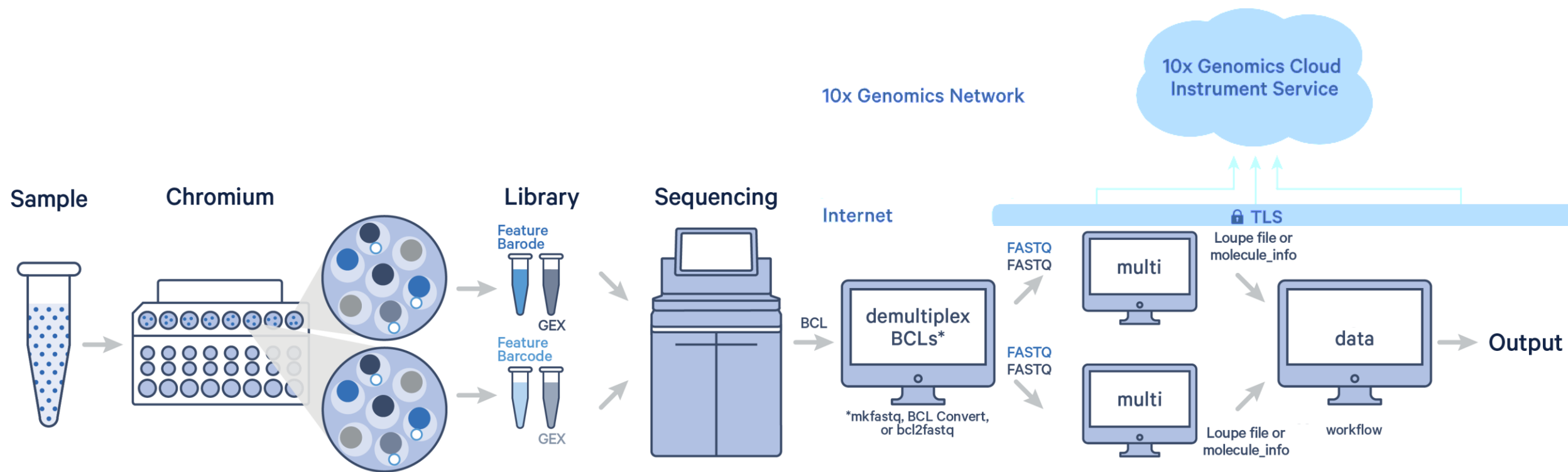


On 10x Cloud

Friendly user interface and simple data management.

Required skill:

Understand the experimental design.



Tools in the data analysis flow

10x
Cloud

Raw data processing from your web browser
Pipelines with user-interface friendly.

Quality
Assessment

web summary QC
Overview of Data quality

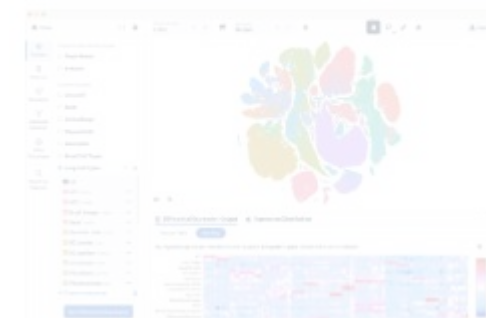
Loupe
Browser

Data exploration locally
Desktop tool for analysis and visualization

Cloud Analysis



Loupe Browser





10x Genomics Cloud

Interact with 10x Genomics Cloud platform



1. Upload your data (files)

Dev_26

Project ID: rn91vpfIlTyOiLDT5zO0UJQ

Input Files

Analyses

Upload Files

View analysis setup instructions

Apply library, feature, or image type to selected files

Create New Analysis

☐	Files	Library, Feature, or Image Type	Upload Date	Upload Path	Size	md5sum
☐	FASTQ E4_S1_L003 R1R2 Flowcell ID: 225VNGLT3	Next GEM Epi Multiome Gene Expression	2/18/2026	var/services/homes/bendezs/data/RAW/Development/scRNA/	29.18 GB	View all files
☐	FASTQ E5_S2_L003 R1R2 Flowcell ID: 225VNGLT3	Next GEM Epi Multiome Gene Expression	2/18/2026	var/services/homes/bendezs/data/RAW/Development/scRNA/	29.5 GB	View all files

Create a New Single Cell Multiome Gene Expression Only Analysis

This analysis uses the Cell Ranger pipeline to analyze only the Gene Expression data produced from the Chromium Next GEM Epi Multiome ATAC + Gene Expression product. For optimal data processing, we recommend to process both ATAC and Gene Expression data through Cell Ranger ARC. This will create an analysis using Cell Ranger count v9.0.1.

What you're analyzing

2 FASTQ sets

Collapse for less

E4_S1_L003

R1R2

Next GEM Epi Multiome Gene Expression

E5_S2_L003

R1R2

Next GEM Epi Multiome Gene Expression

Analysis settings

Pipeline

Cell Ranger Count v9.0.1

Analysis name *

GEX_Dev

A short name to help you identify this analysis.

Description (optional)

Enter a short description

Optionally add a description to help give context to the analysis. This will not affect your analysis.

Transcriptome reference *

Human (GRCh38) 2024-A

Select a Cell Ranger compatible transcriptome reference from the list above. To use a custom reference, upload one to your account and select it in the dropdown above.

Include intronic reads (optional)

☒

Count reads mapping to intronic regions

Including intronic reads, for both cellular and nuclei samples, could lead to higher sensitivity (higher UMI counts, more genes per cell) and less wasted sequencing. Learn more on our support site.

Generate BAM files *

☒

Generate BAM files as part of the analysis outputs

The BAM file could be useful for troubleshooting and downstream analysis. Turning this option off will reduce the time to run the analysis.

2. Choose the correct pipeline:
Fastq (GEX + ATAC)

Run Analysis

3. Wait

Analyses > **GEX_Dev**

GEX_Dev

Analysis ID: Q90sWIUrVTWWS1NoOofh5IA

Analysis Status Starting

Pipeline Cell Ranger Count v8.0.1

▶ [View all settings](#)

 **We'll email you when the analysis is complete.**

This could take several hours depending on the size of your data. Feel free to close this window or start another analysis in the meantime. Made a mistake? [Cancel analysis](#)

[Back to Project](#)

4. You can review your results

Dev_26

Project ID: rn91vpfllTyOiLDT5zO0UJQ

Input Files

Analyses

Upload Files

> Integrate Multiple Analyses

Integrate with Cell Ranger aggr

Integrate with SCTransform/Harmony

This pipeline can also be run by uploading modified Loupe files to your project

Analysis	Status	Process	Count v
GEX_Dev	Starting	3	

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Assessment

web summary QC
Overview of Data quality

Loupe
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Data exploration locally
Desktop tool for analysis and visualization

Cloud Analysis



web_summary.html

Tools in the data analysis flow

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Raw data processing from your web browser
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web_summary.html

Loupe Browser



Evercode v4 and Chromium



Trailmaker Pipeline module

[10x Cloud Analysis](#)

Trailmaker Insights module

[Loupe Browser](#)

Overview of Trailmaker Workflow

Fully integrated end-to-end workflow from FASTQ files to publishable figures

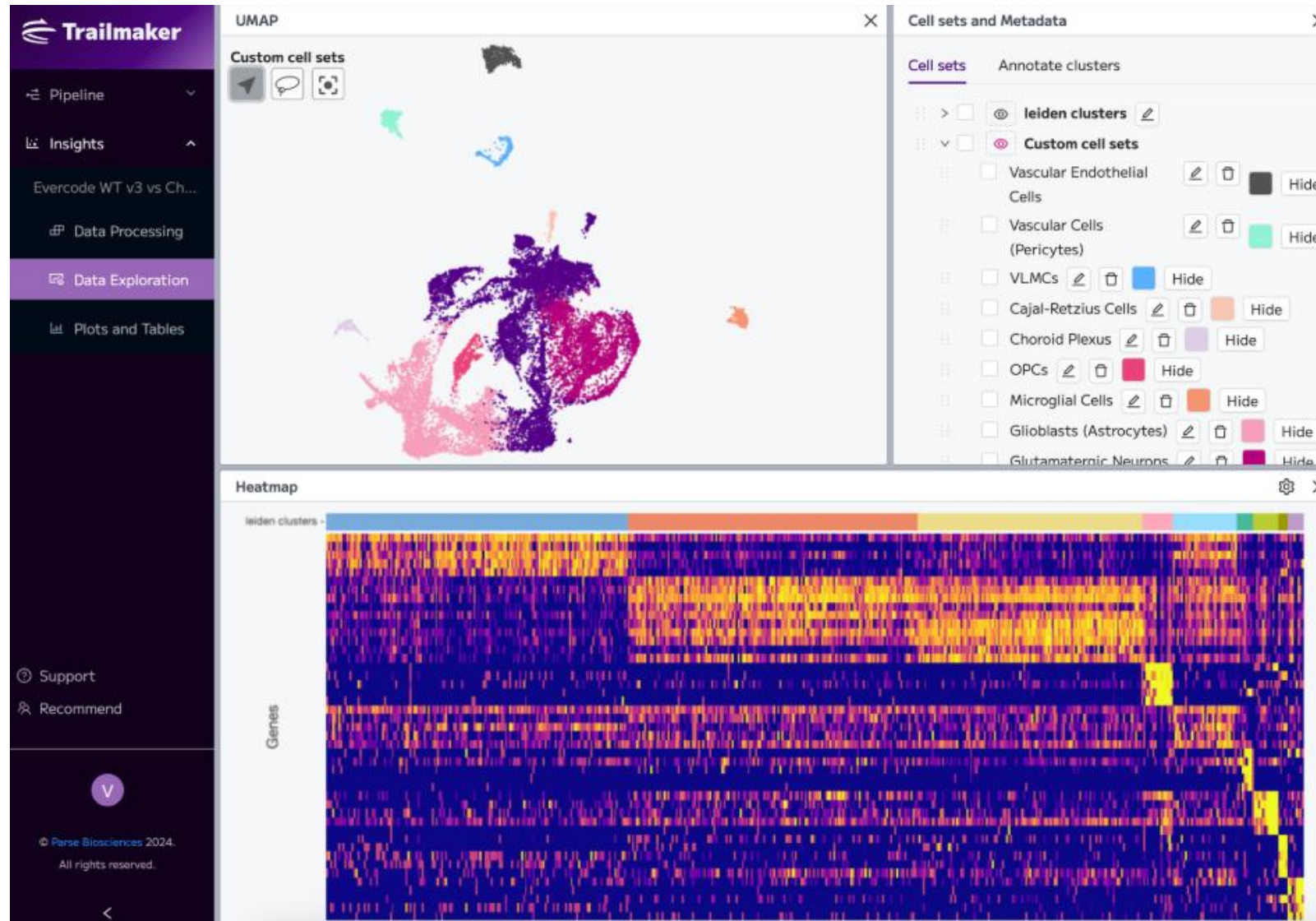
Trailmaker Pipeline Module (For raw FASTQ processing)



Trailmaker Insights Module (For exploration and visualization)



Trailmaker combines both roles inside one web platform



A software for scRNA-seq analysis.