

Loupe browser

Install the loupe browser

Currently using 9.0.0

<https://www.10xgenomics.com/support/software/loupe-browser/downloads>

Download the required files

Development: [atac_fragment [.tsv.gz](#) , cloupe file]

Development data link: [gdrive link](#)

Loupe Browser

v9.0.0

[Documentation & tutorials](#)[Public datasets](#)[Provide feedback](#)

Visium Image Alignment

Align your CytAssist Image or manually align fiducials for Space Ranger.

[Launch Visium Image Alignment](#)

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Now available: Loupe dataset aggregation in 10x Genomics Cloud Analysis

This new pipeline runs community developed algorithms SCTransform and Harmony for cross-experiment normalization, batch correction, and dataset integration. To get started, upload Loupe files to a Cloud Analysis project and create an analysis.

[Learn more](#)

1. Click on this button

Tutorial Files

Recent Files

[Clear Recent](#)[Open Loupe File](#)

Type

Name

Cell Count

Last Opened

2. Find your cloupe file

`kdr_t_development_e3_e7.cloupe`

1. Click on Projection Type

The screenshot displays a software interface for analyzing single-cell data. On the left, a sidebar contains navigation options: Home, Clusters, Features, Reanalyze, Advanced Selection, and Search for Features. The main panel shows a t-SNE plot of data points colored by cluster. A dropdown menu is open, showing the 'Projection type' as 'GEX t-SNE'. The menu lists several options: Pipeline-generated (ATAC t-SNE, ATAC UMAP, GEX t-SNE, GEX UMAP, Feature Plot), Imported, and 'loupe_projection_umap'. A red arrow points to the 'loupe_projection_umap' option. At the bottom, there are tabs for 'Feature Comparison Output', 'Expression/Accessibility Distribution', and 'Feature Linkage'.

Home

Clusters

Features

Reanalyze

Advanced Selection

Search for Features

Pipeline-generated groups

ATAC Graph-Based

ATAC K-Means

GEX Graph-Based

All

Cluster 1 (2433)

Cluster 2 (2407)

Cluster 3 (1693)

Cluster 4 (1498)

Cluster 5 (1380)

Cluster 6 (1356)

Cluster 7 (1156)

Cluster 8 (1086)

Cluster 9 (1052)

Cluster 10 (959)

Cluster 11 (859)

Cluster 12 (795)

Cluster 13 (790)

Cluster 14 (750)

Cluster 15 (629)

Cluster 16 (607)

GEX K-Means

Custom groups

LibraryID

seurat-stage

Projection type

GEX t-SNE

Pipeline-generated

ATAC t-SNE

ATAC UMAP

GEX t-SNE

GEX UMAP

Feature Plot

Imported

loupe_projection_umap

Split view

No Split

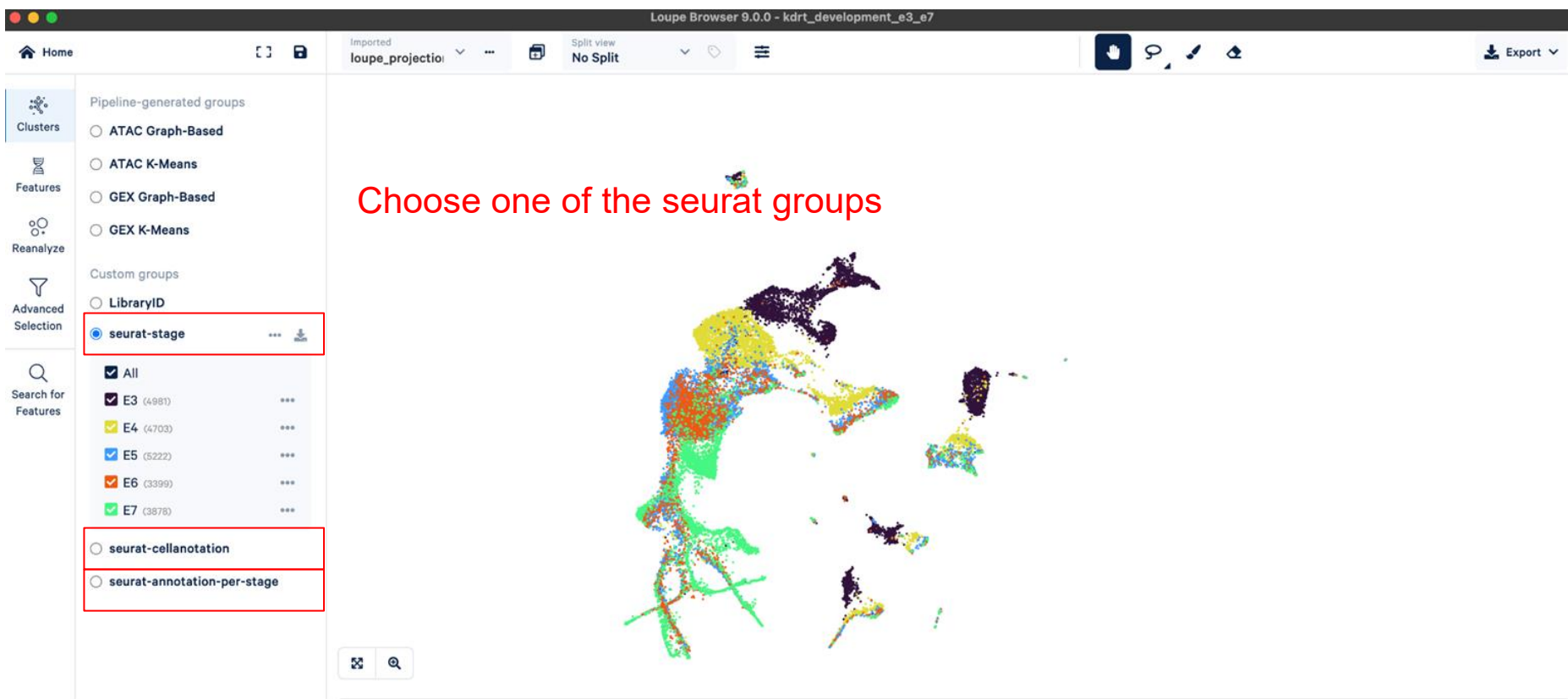
Export

Feature Comparison Output

Expression/Accessibility Distribution

Feature Linkage

2. Choose loupe_projection_umap



seurat-stage: E3,E4,E5,E6,E7

seurat-cellannotation: RPE, Lens, PCs, etc

seurat-annotation-per-stage: RPE_E3, RPE_E4, Lens_E3, etc

Gene Expression

Home

Clusters

Features

Reanalyze

Advanced Selection

Search for Features

Pipeline-generated groups

☐ ATAC Graph-Based

☐ ATAC K-Means

☐ GEX Graph-Based

☐ GEX K-Means

Custom groups

☐ LibraryID

☐ seurat-stage

☒ seurat-cellanotation

☒ All

☒ Amacrine (448)

☒ Bipolar (282)

☒ Blood (96)

☒ CM (2052)

☒ Cornea (731)

☒ Diencephalon (1152)

☒ Endothelial (252)

☒ Horizontal (438)

☒ Lens (847)

☒ Mesenchymal (2149)

☒ OS (215)

☒ PCs1 (937)

☒ PCs2 (1480)

☒ PCs3 (2828)

☒ PCs4 (2706)

☒ PCs5 (1728)

☐ seurat-annotation-per-stage

+ Create a new group

Run Feature Comparison

Imported loupe_projectio

Split view No Split

Export

1. Start with the Clusters Tab

2. Use the group you want to compare against



Feature Comparison Output

Expression/Accessibility Distribution

Feature Linkage

Violin Plots

To view violin plots of one or more features' expression distribution:

1. From the "Clusters" tab, select a group. This specifies the groups to compare gene expression distributions between (x-axis).

2. From the "Features" tab, select the feature(s) or feature group to display gene expression distribution for (y-axis).

3. (Optional) Change the "Scale value" for different UMI count visualization options.

4. View the violin plots of the selected feature(s) for the selected group in this panel.



Clusters



Features



Reanalyze

Advanced
SelectionSearch for
Features

Search genes/features

Genes of Interest

To begin exploring gene/feature expression, you can either search for a specific gene/feature, or upload a CSV file containing the features you're interested in.

3. Click on the 'Features' Tab

4. Add all the Genes of interest

Feature Comparison Output

Expression/Accessibility Distribution

Feature Linkage

Violin Plots

To view violin plots of one or more features' expression distribution:

1. From the "Clusters" tab, select a group. This specifies the groups to compare gene expression distributions between (x-axis).
2. From the "Features" tab, select the feature(s) or feature group to display gene expression distribution for (y-axis).
3. (Optional) Change the "Scale value" for different UMI count visualization options.
4. View the violin plots of the selected feature(s) for the selected group in this panel.

Search genes/features

Genes of Interest

Combine all below

OTX2

Gene
ENSGALG000100196
88

PAX6

Gene
ENSGALG000100236
42

RPE65

Gene
ENSGALG000100235
06

TYR

Gene
ENSGALG000100078
64

MITF

Gene
ENSGALG000100220
62

5. Choose your gene

6. LogNorm is good for scale value

7. Adjust the min/max if needed

Scale value

LogNorm

Log Normalized Exp - MITF

0.0 6.0

Filter barcodes

Save barcodes

5301 barcodes found

8. Violin plots will show on this Tab

Feature Comparison Output

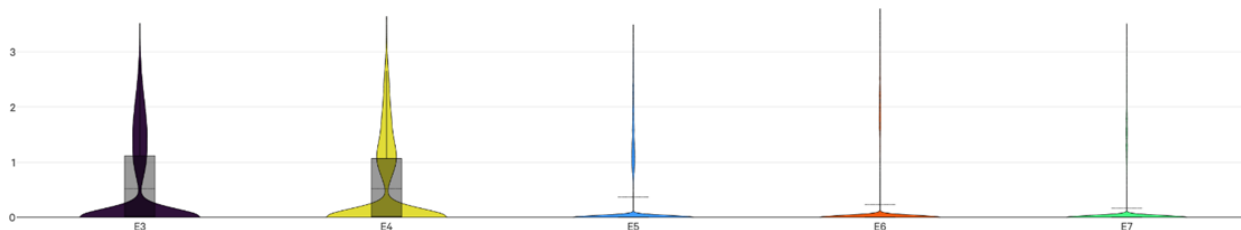
Expression/Accessibility Distribution

Feature Linkage

Violin Plots

Expression/accessibility distribution of MITF for the selected cluster group (seurat-stage) (only the barcodes in the current projection are included in the violin plot).

Log Normalized Exp - MITF (seurat-stage)



Differentially Expressed features

Loupe Browser 9.0.0 - kdr_t_development_e3_e7

Home [] [] Imported loupe_projectio Split view No Split Export

Clusters Pipeline-generated groups

- ☐ ATAC Graph-Based
- ☐ ATAC K-Means
- ☐ GEX Graph-Based
- ☐ GEX K-Means

Custom groups

- ☐ LibraryID
- ☒ **seurat-stage**

☒ All

☒ E3 (4981)

☒ E4 (4703)

☒ E5 (5222)

☒ E6 (3399)

☒ E7 (3878)

☐ seurat-cellnotation

☐ seurat-annotation-per-stage

+ Create a new group

Run Feature Comparison

1. Start with the Clusters Tab

2. Use the group you want to compare against

3. Run the Feature Comparison

Feature Comparison Output Expression/Accessibility Distribution Feature Linkage

Feature Table Heat Map

To perform an analysis to identify differentially expressed/accessible features:

1. From the "Clusters" tab, select the clusters that you wish to analyze.
2. Click on the "Run Feature Comparison" button at the bottom and choose how you want to compare the results.
3. View the output in this panel.

Home

Clusters

Features

Reanalyze

Advanced Selection

Search for Features

Pipeline-generated groups

ATAC Graph-Based

ATAC K-Means

GEX Graph-Based

GEX K-Means

Custom groups

LibraryID

seurat-stage

All

E3 (4981)

E4 (4703)

E5 (5222)

E6 (3399)

E7 (3878)

seurat-cellanotation

seurat-annotation-per-stage

+ Create a new group

Run Feature Comparison

Imported loupe_projectio

Split view No Split

Export

4. Choose the following options

Feature Comparison Settings

Compare all seleted clusters in seurat-stage:

To entire dataset

Feature type

Gene (GEX)

Start analysis

Feature Comparison Output

Feature TableHeat Map

5. Click on 'Start analysis'

To perform an analysis to identify differentially expressed/accessible features:

1. From the "Clusters" tab, select the clusters that you wish to analyze.

2. Click on the "Run Feature Comparison" button at the bottom and choose how you want to compare the results.

3. View the output in this panel.

Feature Comparison Settings



Compare all selected clusters in **seurat-stage**:

To entire dataset



To entire dataset

Find features that are differentially expressed/accessible in the selected cluster(s) against the entire dataset.

Between selected cluster(s) themselves

Find features that are differentially expressed/accessible between the selected cluster(s).

Across multiple samples

For the selected cell types, find features that are differentially expressed between samples in two experimental conditions using a pseudo-bulk calculation. Only applicable if the file contains multiple samples, and only gene expression data will be used in the calculation.

While the analysis runs, you can also review that there are also other options

Pipeline-generated groups

☐ ATAC Graph-Based☐ ATAC K-Means☐ GEX Graph-Based☐ GEX K-Means

Custom groups

☐ LibraryID☒ **seurat-stage**

...

☒ All☒ E3 (4981)

...

☒ E4 (4703)

...

☒ E5 (5222)

...

☒ E6 (3399)

...

☒ E7 (3878)

...

☐ seurat-cellnotation☐ seurat-annotation-per-stage

+ Create a new group



Run Feature Comparison

6. Click on this tab



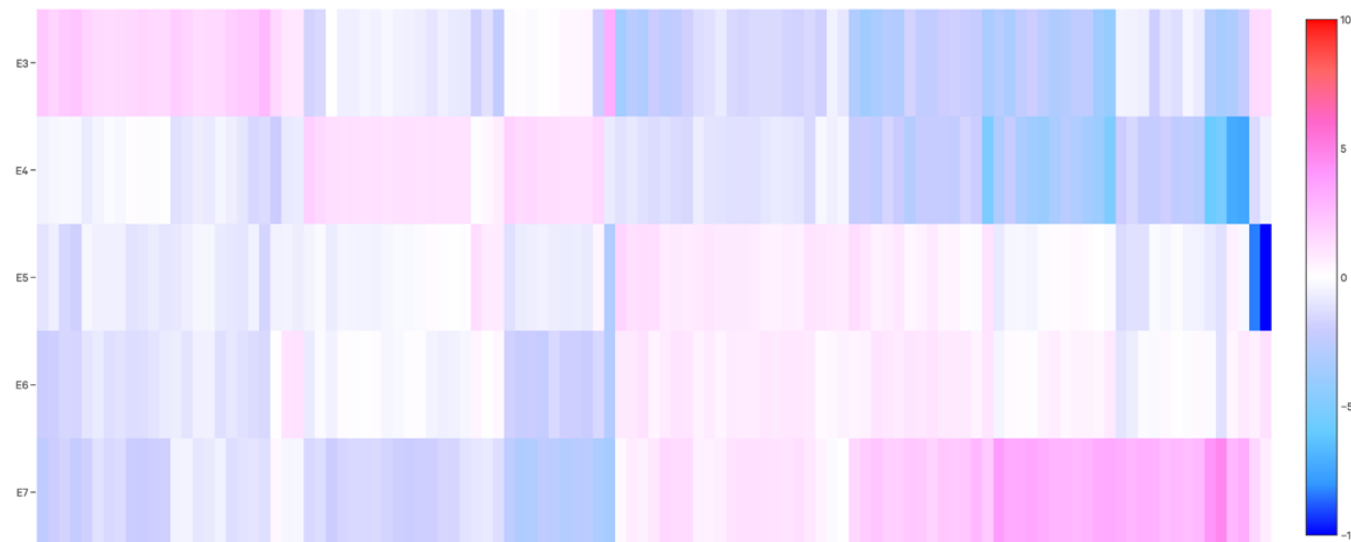
Feature Comparison Output

Expression/Accessibility Distribution

Feature Linkage

Feature Table

Heat Map

Up-regulated genes per selected cluster in group **seurat-stage**, compared to entire dataset (only the barcodes in the current projection are included in the Feature Comparison calculation).

7. Choose up/down regulated or other options

Heatmap Options

Filter features by

Up-regulated genes per selected cluster

☒ Hide genes with low average count

Grid features per cluster

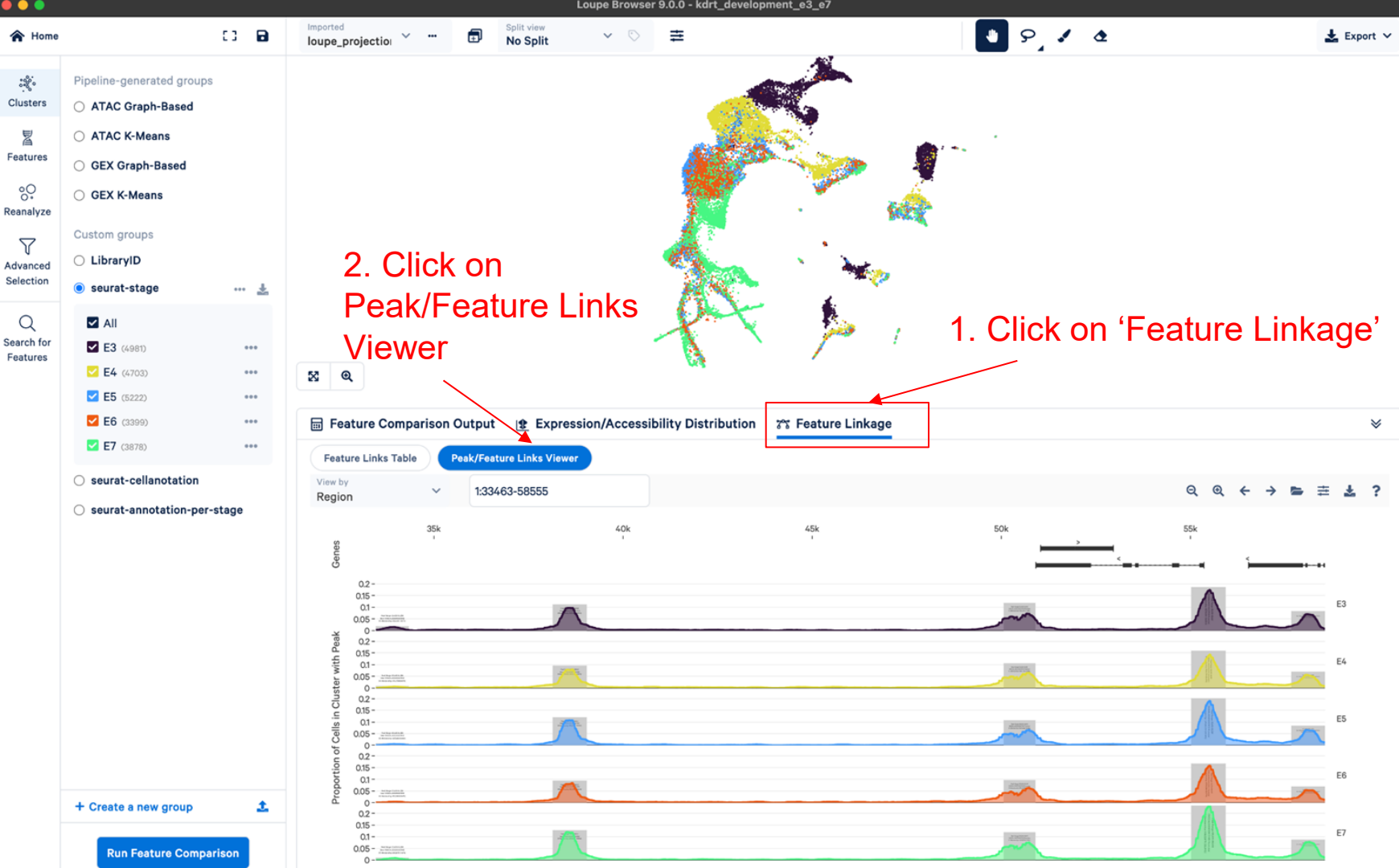
Auto



8. Download the graph as png

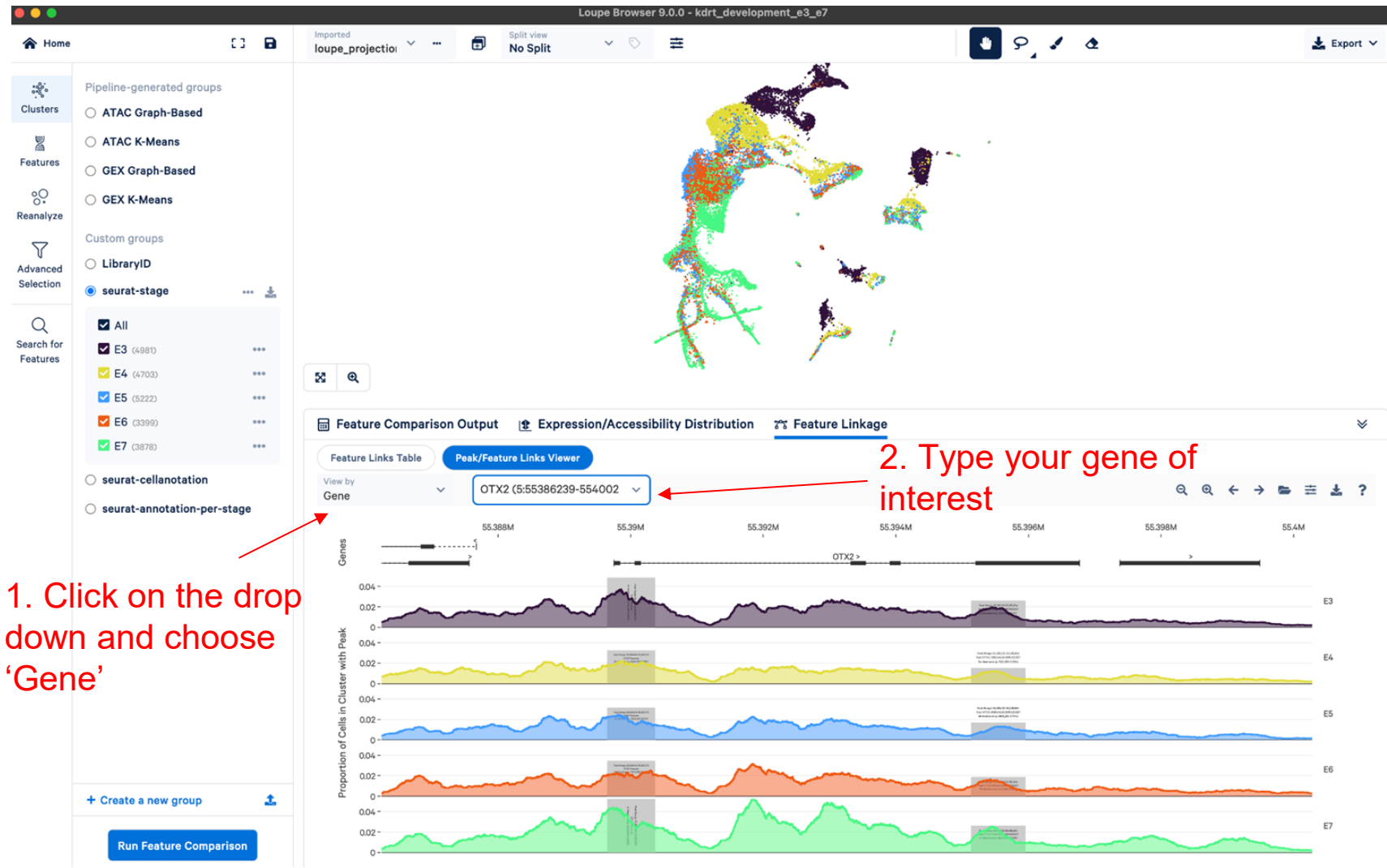


PEAKS AND LINKS



1. Click on the drop down and choose 'Gene'

2. Type your gene of interest



Loupe Browser 9.0.0 - kdr_t_development_e3_e7

Home

Imported loupe_projectio

Split view No Split

Export

Clusters

Pipeline-generated groups

- ATAC Graph-Based
- ATAC K-Means
- GEX Graph-Based
- GEX K-Means

Custom groups

- LibraryID
- seurat-stage

Search for Features

- All
- E3 (4981)
- E4 (4703)
- E5 (5222)
- E6 (3399)
- E7 (3878)

seurat-cellannotation

seurat-annotation-per-stage

+ Create a new group

Run Feature Comparison

3. Choose 'Load from file'

4. Type your gene of interest

2. Click on the folder icon and load the atac_fragment.tsv.gz file

1. Click on the drop down and choose 'Feature Links'

Feature Comparison Output

Expression/Accessibility Distribution

Feature Linkage

Feature Links Table

Peak/Feature Links Viewer

View by Feature Links

Search for a gene or peak...

Feature Links

Proportion of Cells in Cluster with Peak

Genes

E3

E4

E5

E6

E7

No Linked Features

Clusters

Pipeline-generated groups

- ☐ ATAC Graph-Based
- ☐ ATAC K-Means
- ☐ GEX Graph-Based
- ☐ GEX K-Means

Custom groups

- ☐ LibraryID
- ☒ **seurat-stage**

☒ All

☒ E3 (4981) ***

☒ E4 (4703) ***

☒ E5 (5222) ***

☒ E6 (3399) ***

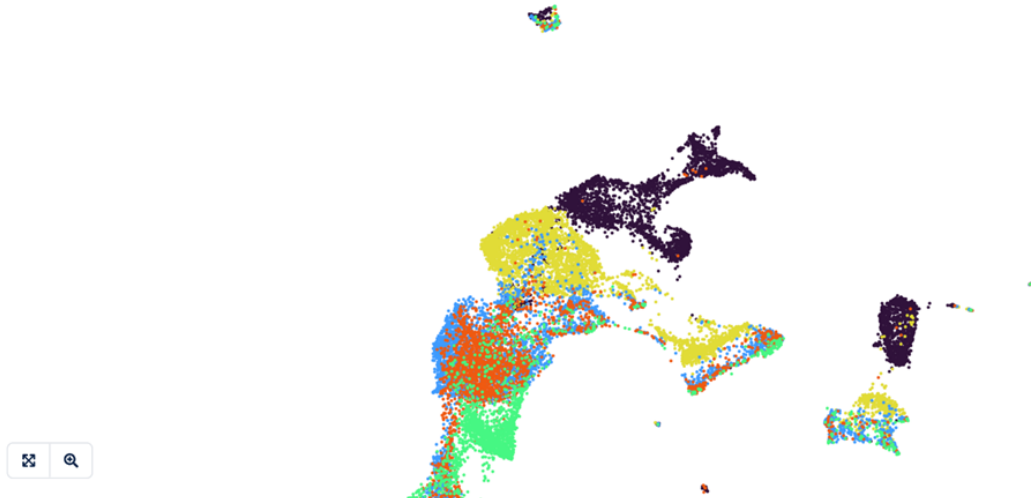
☒ E7 (3878) ***

☐ seurat-cellnotation

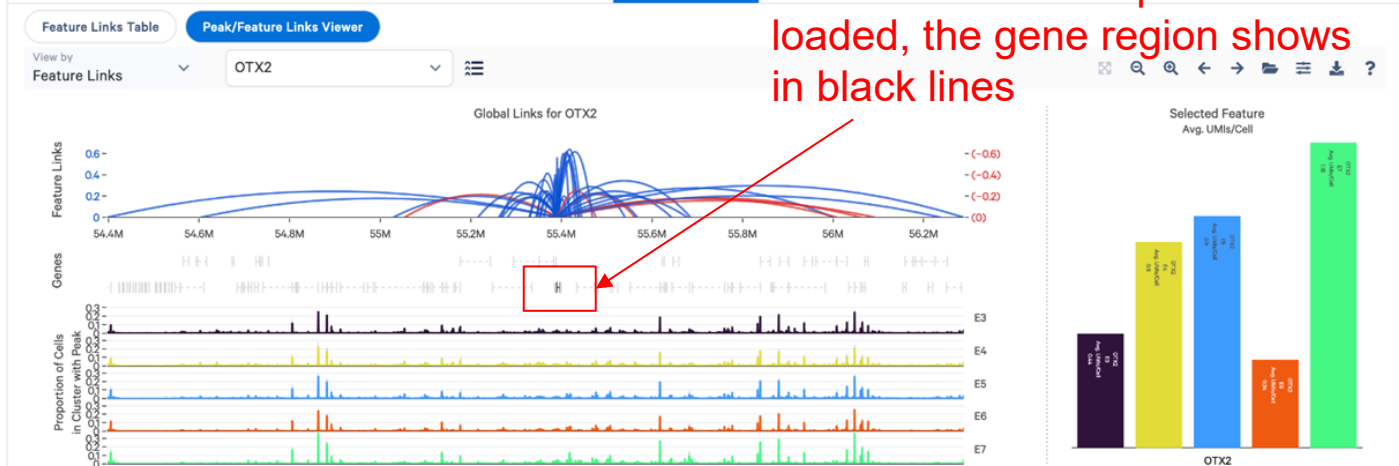
☐ seurat-annotation-per-stage

+ Create a new group

Run Feature Comparison



Feature Comparison Output Expression/Accessibility Distribution Feature Linkage



Clusters

Features

Reanalyze

Advanced Selection

Search for Features

Pipeline-generated groups

- ATAC Graph-Based
- ATAC K-Means
- GEX Graph-Based
- GEX K-Means

Custom groups

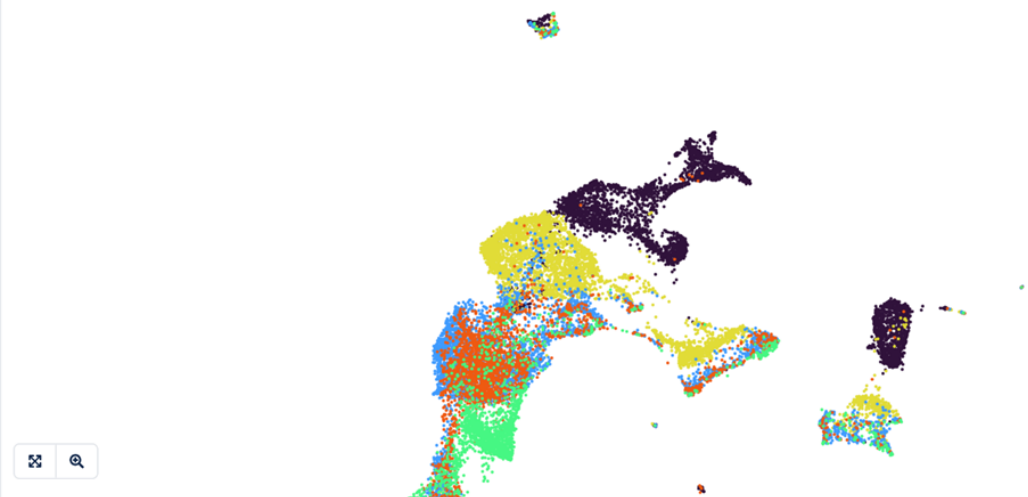
- LibraryID
- seurat-stage

- All
- E3 (4981)
- E4 (4703)
- E5 (5222)
- E6 (3399)
- E7 (3878)

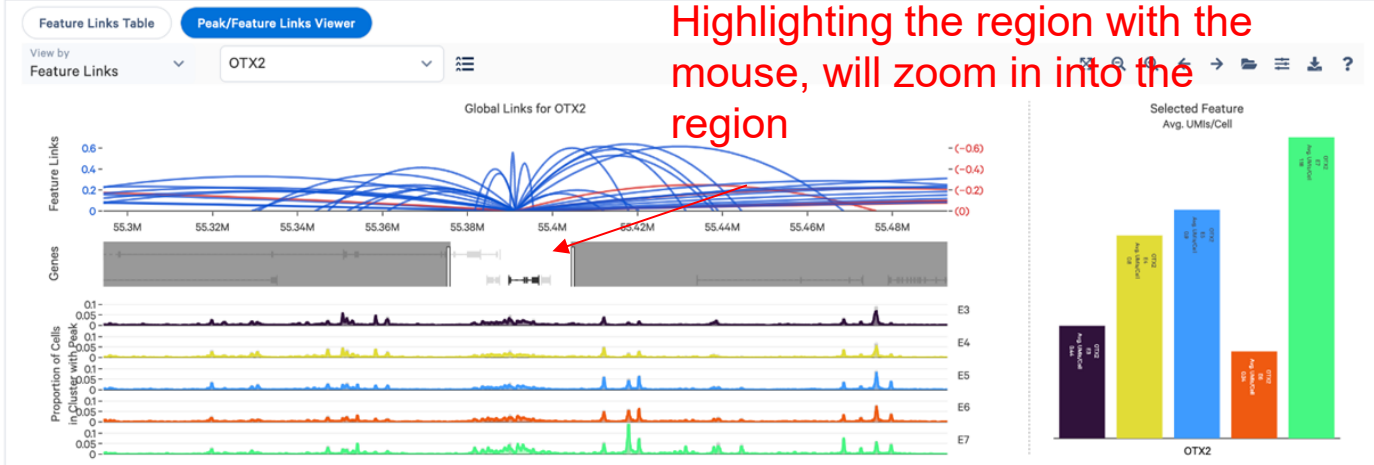
- seurat-cellannotation
- seurat-annotation-per-stage

+ Create a new group

Run Feature Comparison



Feature Comparison Output Expression/Accessibility Distribution Feature Linkage



you can see more details and use different options

