# How to use the CETA database

The **CETA** (**Comparative Eye Transcriptome Atlas**) database is an online resource that allows researchers to explore gene expression of the eyes of zebra finch, chicken, pigeon and anole lizards using spatial transcriptomics and the zebra finch retina in individual cell types using single-cell transcriptomics.

Below are practical guidelines for using the database.

### Accessing and navigating the Database

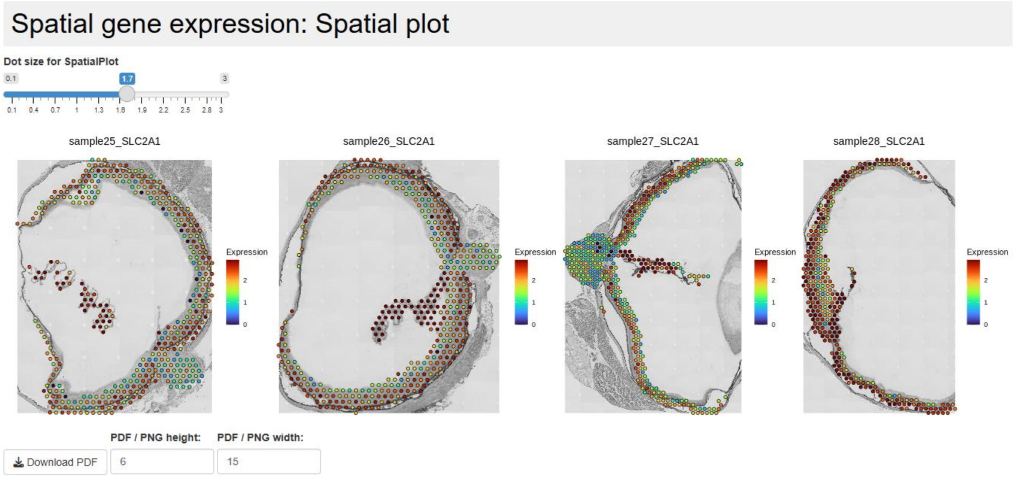
## How to Use The Spatial RNAseq Expression Tab

The Spatial RNAseq Expression tab in the ZeFIRST database provides detailed information on gene expression profiles across different regions of the zebra finch eye. Here’s a practical guide on how to use this feature effectively:

### Accessing Spatial RNAseq Expression Data

Select the Spatial RNAseq Expression Tab: Click the "Spatial RNAseq Expression" tab on the top navigation bar to open the Spatial gene expression interface.

1. **Spatial gene expression: Spatial plot**
    - Input Gene Symbol by typing the gene symbol of interest (e.g., "CA4") and click search.
    - Spatial Plot: a visual representation of the gene expression in a spatial context.
    - Adjust the dot size using the slider to change the visualization resolution.
    - Download the spatial plot as a PDF or PNG file by setting the desired dimensions and clicking the download buttons.



Spatial gene expression: Spatial plot

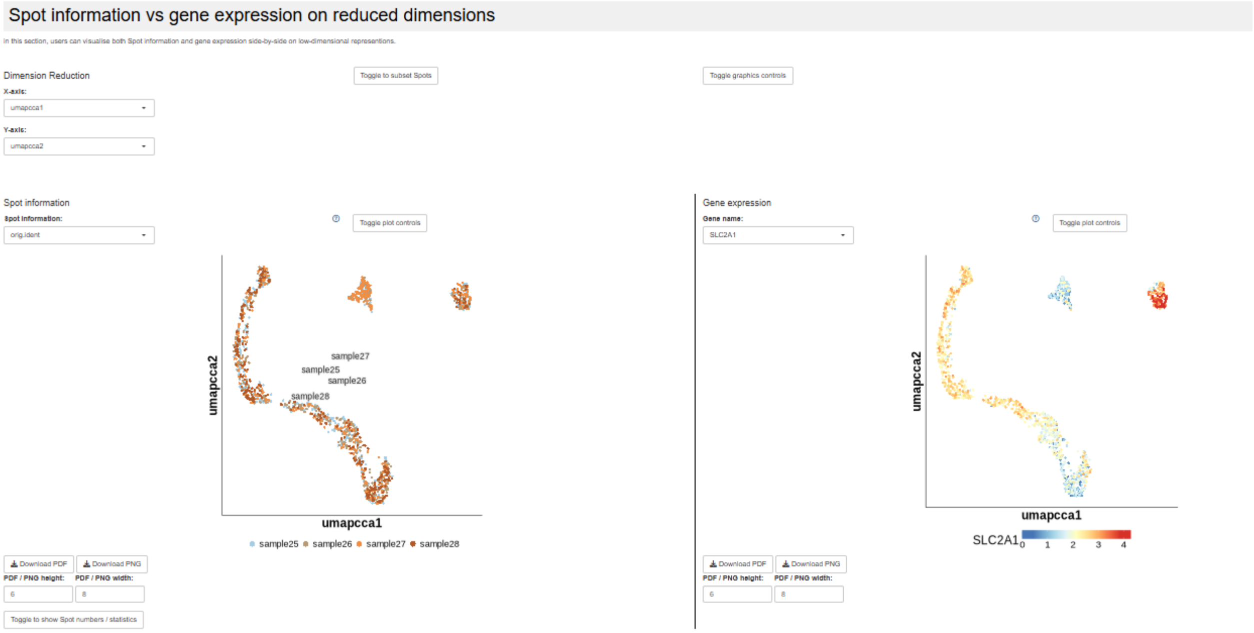
Dot size for SpatialPlot: 1.7

PDF / PNG height: 6

PDF / PNG width: 15

## 2. Spot information vs gene expression on reduced dimensions

- Dimension Reduction Plot: Visualization of Spot information and gene expression side-by-side on low-dimensional representations.
- Select the axes for dimension reduction (e.g., UMAP1 and UMAP2).
- Toggle between different spot information and gene expression views.
- Download the plots as PDF or PNG files.



Spot information vs gene expression on reduced dimensions

In this section, users can visualise both Spot information and gene expression side-by-side on low-dimensional representions.

Dimension Reduction

X-axis: umapcca1

Y-axis: umapcca2

Spot information

Spot information: orig.ident

PDF / PNG height: 6

PDF / PNG width: 8

Gene expression

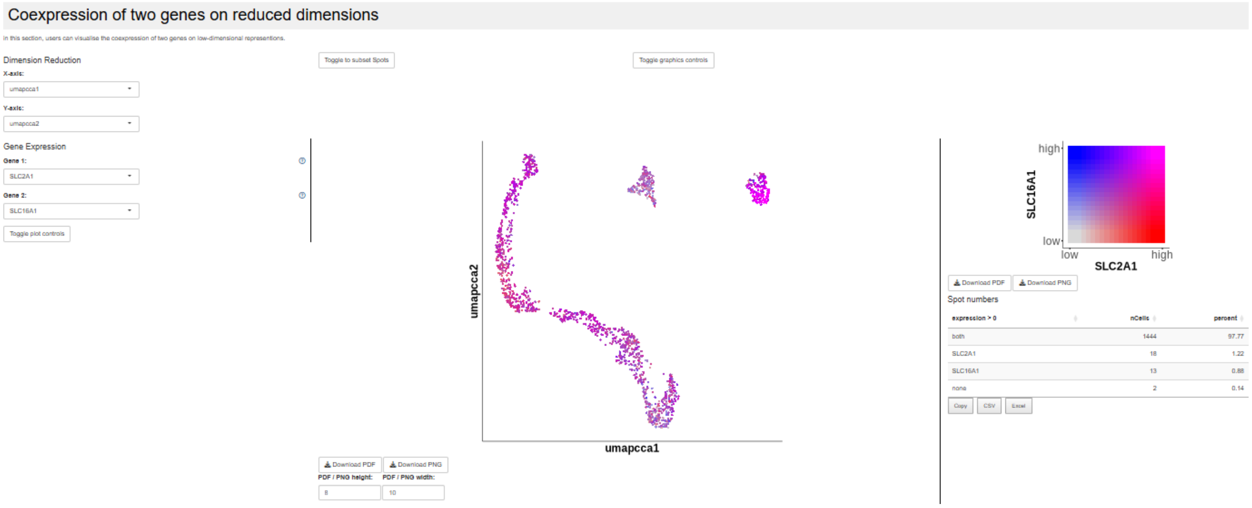
Gene name: SLC2A1

PDF / PNG height: 6

PDF / PNG width: 8

## 3. Co-expression of Two Genes

- Co-expression Plot: Co-expression of two genes on reduced dimensions.
- Select the genes to be analyzed (e.g., "CA4" and "SLC16A1").
- The plot shows the distribution of spots expressing both genes.
- Download the co-expression plot as a PDF or PNG file.



Coexpression of two genes on reduced dimensions

in this section, users can visualise the coexpression of two genes on low-dimensional representions.

Dimension Reduction

X-axis: umapcca1

Y-axis: umapcca2

Gene Expression

Gene 1: SLC2A1

Gene 2: SLC16A1

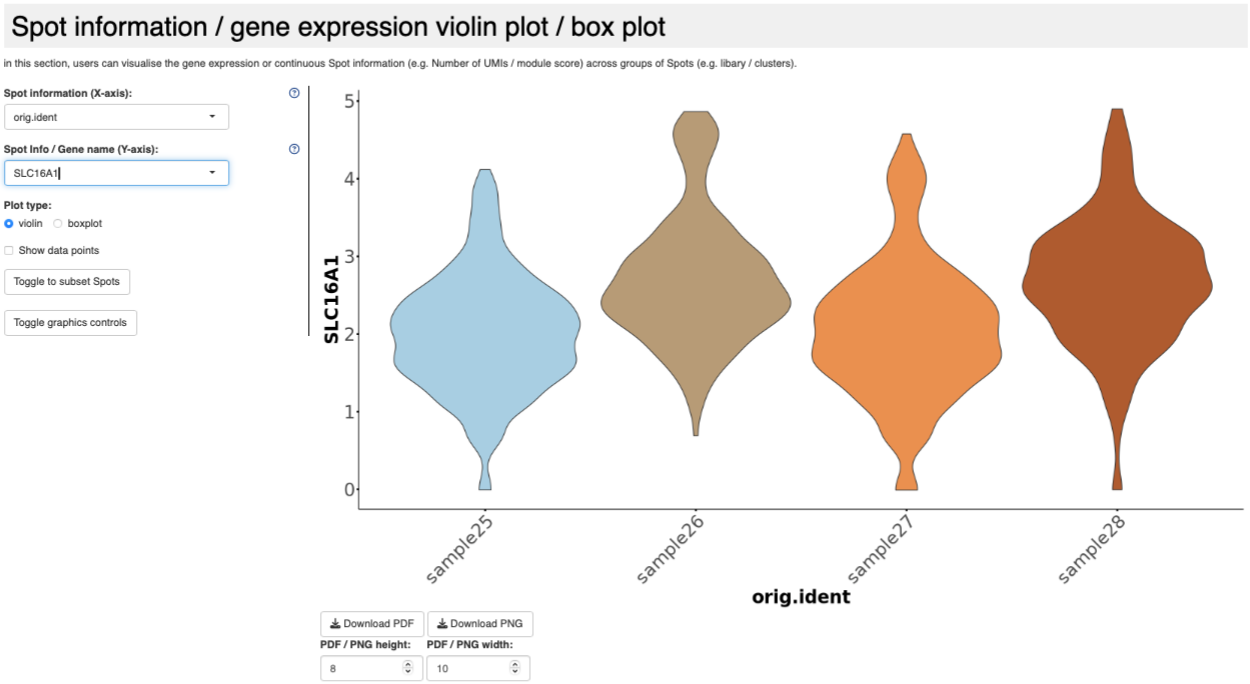
PDF / PNG height: 8

PDF / PNG width: 10

Spot numbers

| expression > 0 | nCells | percent |
|---|---|---|
| both | 1444 | 97.77 |
| SLC2A1 | 18 | 1.22 |
| SLC16A1 | 13 | 0.88 |
| none | 2 | 0.14 |

4. **Spot information / gene expression violin and box**
    - Violin and blox plots visualise spot information or gene expression across samples.
    - Select the X-axis and Y-axis parameters, and choose the plot type (violin or boxplot).
    - Toggle between showing data points and adjusting graphics controls.
    - Download the plots as PDF or PNG files.



Spot information / gene expression violin plot / box plot

in this section, users can visualise the gene expression or continuous Spot information (e.g. Number of UMIs / module score) across groups of Spots (e.g. libary / clusters).

**Spot information (X-axis):** orig.ident

**Spot Info / Gene name (Y-axis):** SLC16A1

**Plot type:** ● violin ○ boxplot

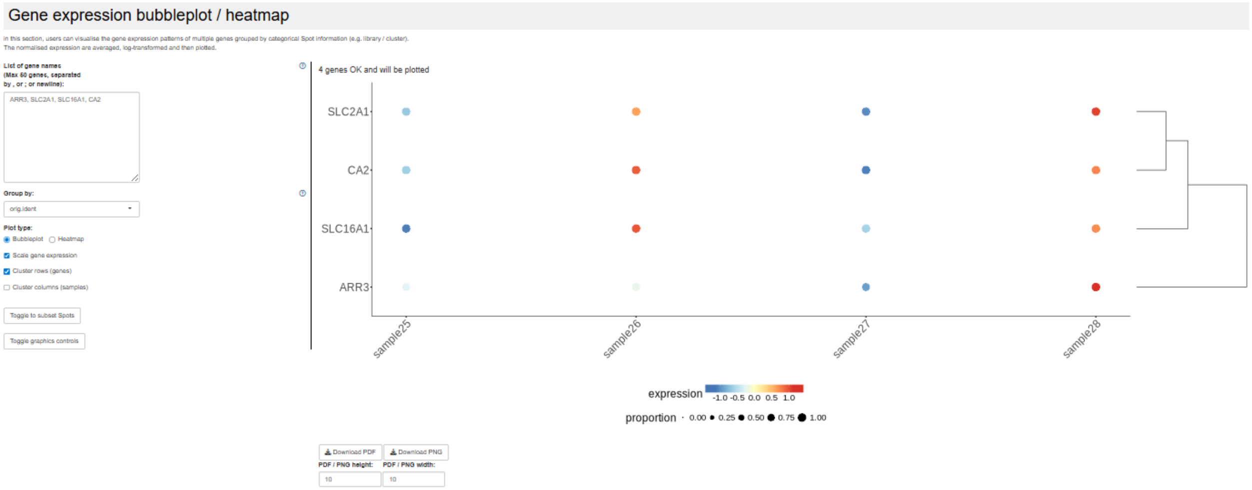
☐ Show data points

**PDF / PNG height:** 8

**PDF / PNG width:** 10

## 5. Gene Expression as Bubbleplots or Heatmaps

- This section allows you to visualize gene expression patterns of multiple genes across samples.
- Enter a list of gene names.
- Choose the plot type (bubbleplot or heatmap).
- Cluster rows (genes) and columns (samples) for better visualization.
- Download the plots as PDF or PNG files.



Gene expression bubbleplot / heatmap

In this section, users can visualise the gene expression patterns of multiple genes grouped by categorical Spot information (e.g. library / cluster).
The normalised expression are averaged, log-transformed and then plotted.

**List of gene names (Max 60 genes, separated by , or ; or newline):** ARR3, SLC2A1, SLC16A1, CA2

**Group by:** orig.ident

**Plot type:**
● Bubbleplot ○ Heatmap

☑ Scale gene expression

☑ Cluster rows (genes)

☐ Cluster columns (samples)

4 genes OK and will be plotted

**PDF / PNG height:** 10
**PDF / PNG width:** 10

# How to Use The scRNAseq Expression Tab

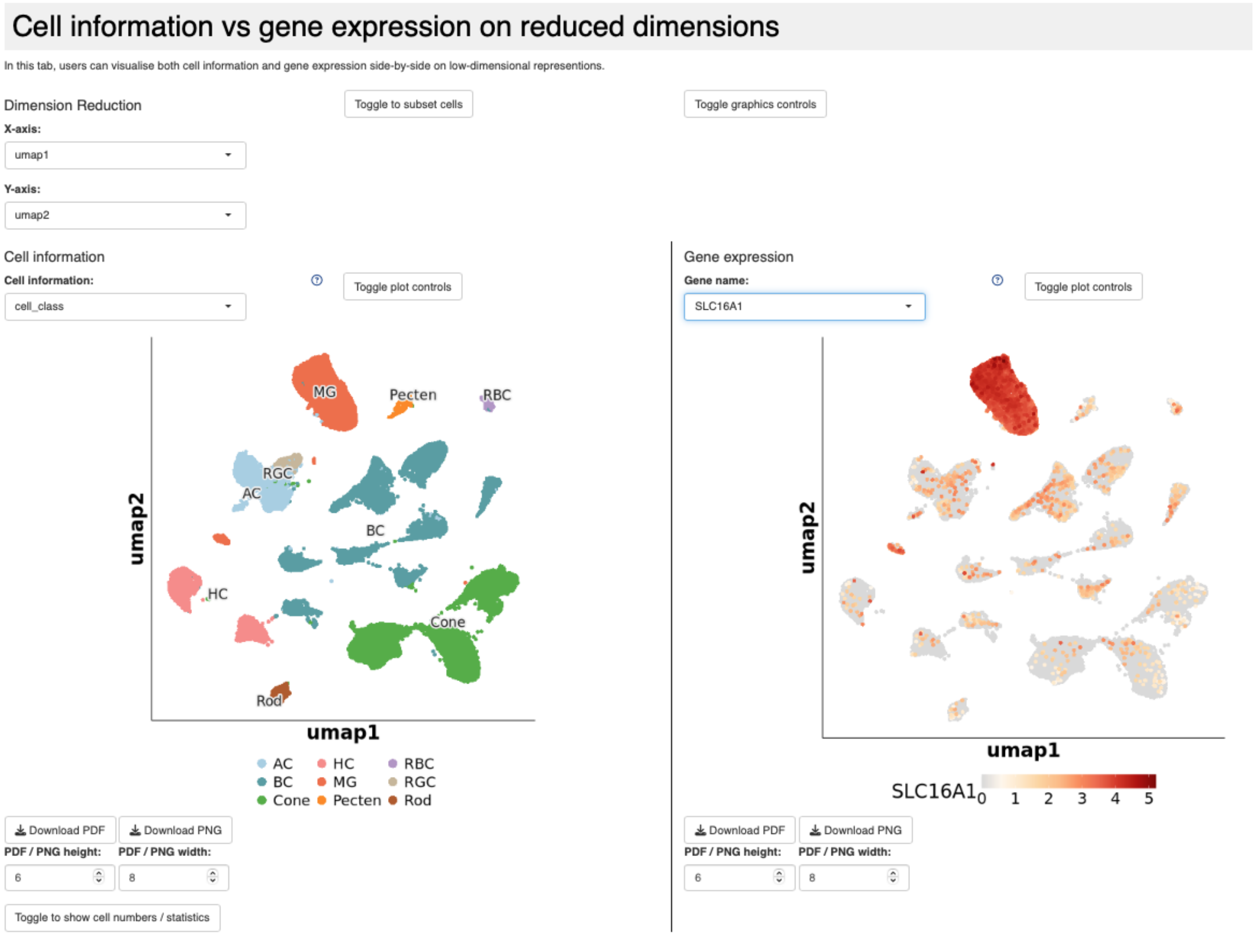
The scRNAseq Expression tab in the ZeFIRST database provides detailed information on gene expression profiles cell types in the zebra finch retina. Here's a practical guide on how to use this feature effectively:

## Accessing scRNAseq Expression Data

Select the scRNAseq Expression Tab: Click the "scRNAseq Expression" tab on the top navigation bar to open the single-cell gene expression interface.

### 1. Cell information vs gene expression on reduced dimensions

- Dimension Reduction Plot: Visualization of cell information and gene expression side-by-side on low-dimensional representations.
- Select the axes for dimension reduction (e.g., UMAP1 and UMAP2).
- Toggle between different cell information and gene expression views. Cell types are provided in the cell information "cell_class".
- Download the plots as PDF or PNG files.



Cell information vs gene expression on reduced dimensions

In this tab, users can visualise both cell information and gene expression side-by-side on low-dimensional representions.

Dimension Reduction

X-axis: umap1

Y-axis: umap2

Cell information

Cell information: cell_class

Gene expression

Gene name: SLC16A1

PDF / PNG height: 6

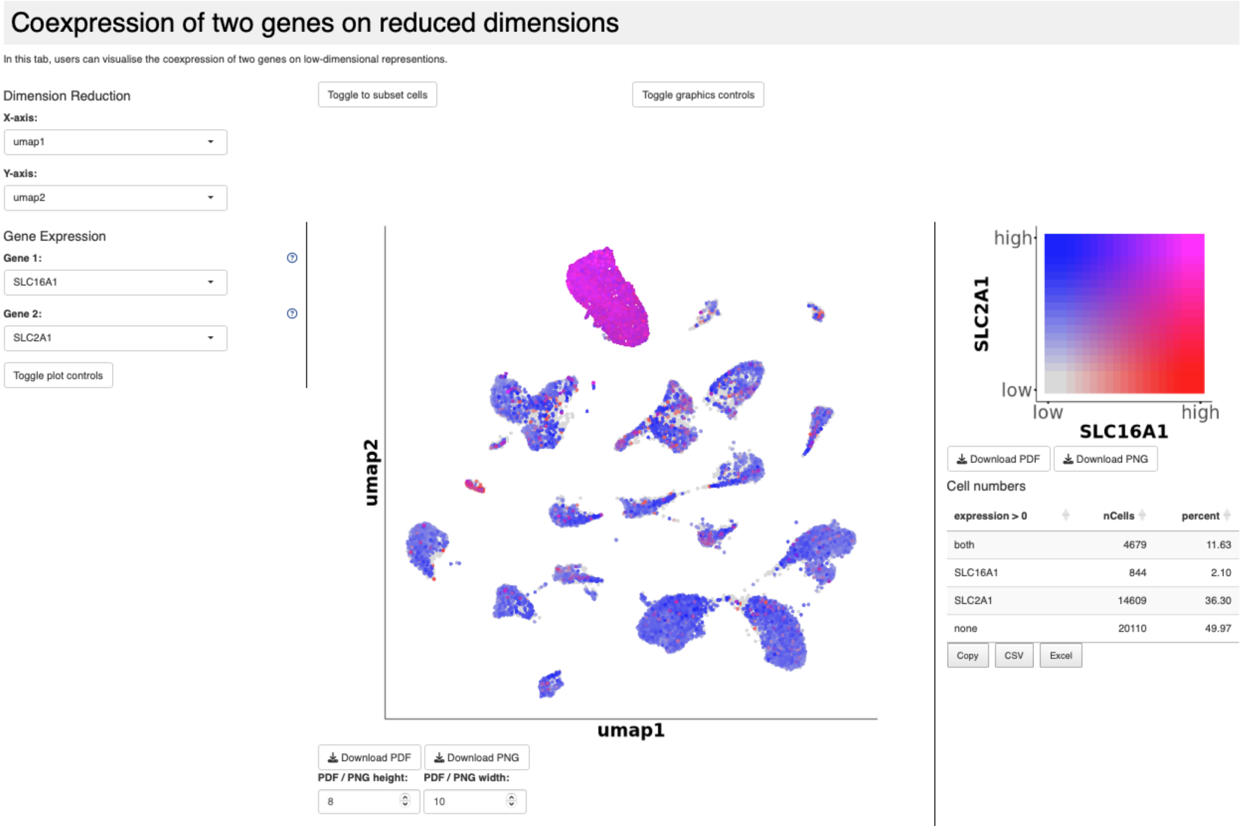
PDF / PNG width: 8

PDF / PNG height: 6

PDF / PNG width: 8

## 2. Co-expression of Two Genes

- Co-expression Plot: Co-expression of two genes on reduced dimensions.
- Select the genes to be analyzed (e.g., "SLC2A1" and "SLC16A1").
- The plot shows the distribution of spots expressing both genes.
- Download the co-expression plot as a PDF or PNG file.



Coexpression of two genes on reduced dimensions

In this tab, users can visualise the coexpression of two genes on low-dimensional representions.

Dimension Reduction

X-axis: umap1

Y-axis: umap2

Gene Expression

Gene 1: SLC16A1

Gene 2: SLC2A1

PDF / PNG height: 8

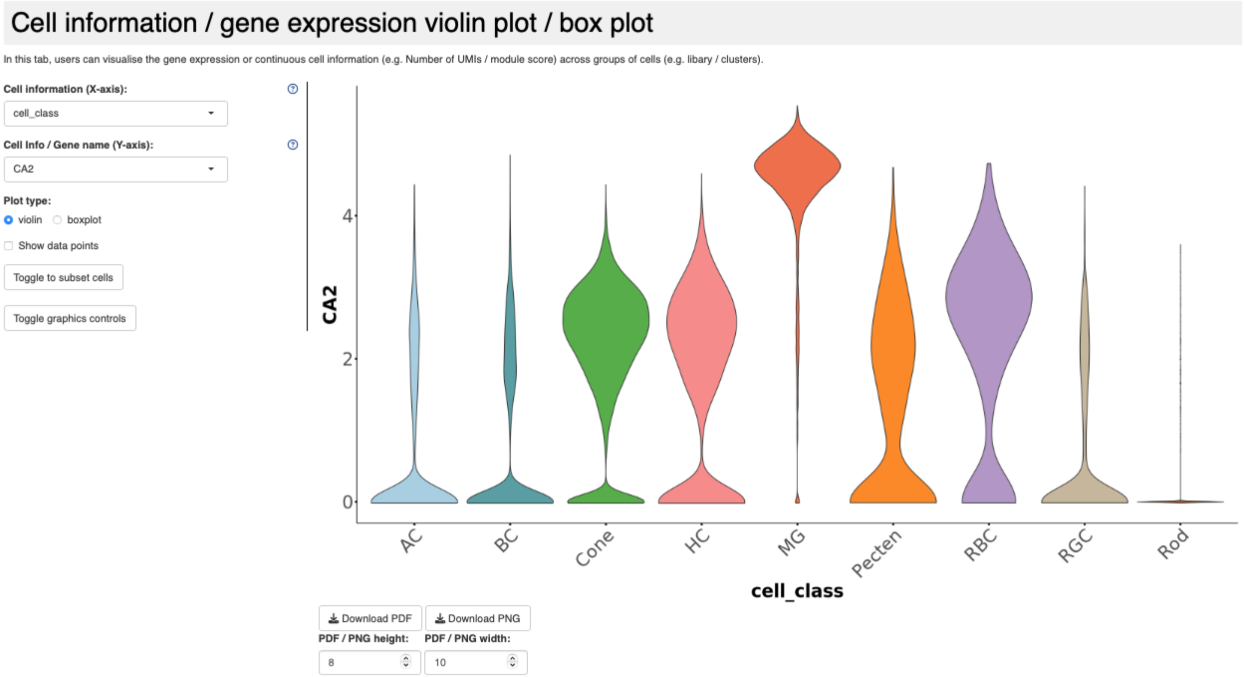
PDF / PNG width: 10

Cell numbers

| expression > 0 | nCells | percent |
|---|---|---|
| both | 4679 | 11.63 |
| SLC16A1 | 844 | 2.10 |
| SLC2A1 | 14609 | 36.30 |
| none | 20110 | 49.97 |

### 3. Cell information / gene expression violin and box

- Violin and blox plots provide a visualization of spot information or gene expression across samples or cell types.
- Select the X-axis and Y-axis parameters and choose the plot type (violin or boxplot).
- Toggle between showing data points and adjusting graphics controls.
- Download the plots as PDF or PNG files.



Cell information / gene expression violin plot / box plot

In this tab, users can visualise the gene expression or continuous cell information (e.g. Number of UMIs / module score) across groups of cells (e.g. libary / clusters).

**Cell information (X-axis):** cell_class

**Cell Info / Gene name (Y-axis):** CA2

**Plot type:** ● violin ○ boxplot

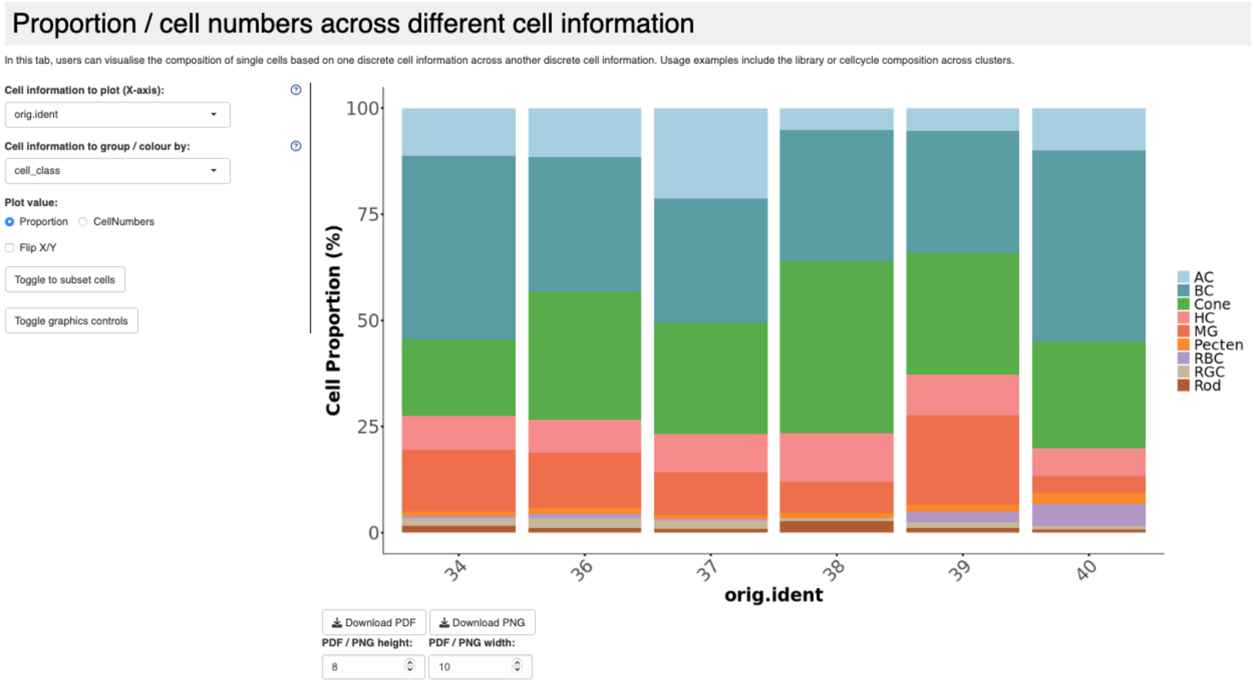
☐ Show data points

**PDF / PNG height:** 8

**PDF / PNG width:** 10

### 4. Proportion / cell numbers across cell types

- Stacked bar plot representing the proportion of cell types across samples
- Select the X-axis and Y-axis parameters and choose the plot values (proportion or absolute cell numbers).
- Download the plots as PDF or PNG files.



Proportion / cell numbers across different cell information

In this tab, users can visualise the composition of single cells based on one discrete cell information across another discrete cell information. Usage examples include the library or cellcycle composition across clusters.

Cell information to plot (X-axis): orig.ident

Cell information to group / colour by: cell_class

Plot value: ● Proportion ○ CellNumbers

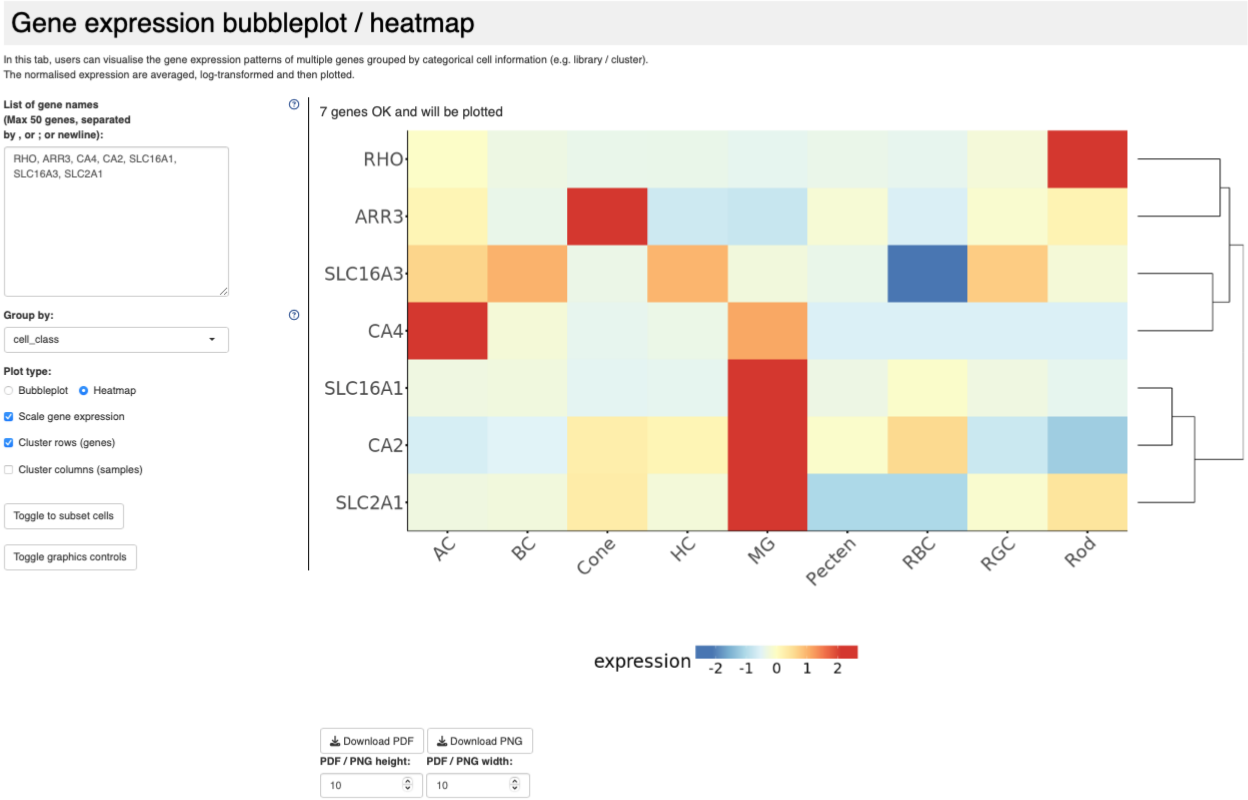
☐ Flip X/Y

PDF / PNG height: 8

PDF / PNG width: 10

## 5. Gene Expression as Bubbleplots or Heatmaps

- This section allows you to visualize gene expression patterns of multiple genes across samples.
- Enter a list of gene names.
- Choose the plot type (bubbleplot or heatmap).
- Cluster rows (genes) and columns (cell types) for better visualization.
- Download the plots as PDF or PNG files.



Gene expression bubbleplot / heatmap

In this tab, users can visualise the gene expression patterns of multiple genes grouped by categorical cell information (e.g. library / cluster).
The normalised expression are averaged, log-transformed and then plotted.

**List of gene names (Max 50 genes, separated by , or ; or newline):**

RHO, ARR3, CA4, CA2, SLC16A1, SLC16A3, SLC2A1

**Group by:** cell_class

**Plot type:** ○ Bubbleplot ● Heatmap

☑ Scale gene expression

☑ Cluster rows (genes)

☐ Cluster columns (samples)

7 genes OK and will be plotted

**PDF / PNG height:** 10

**PDF / PNG width:** 10