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# Main Panel



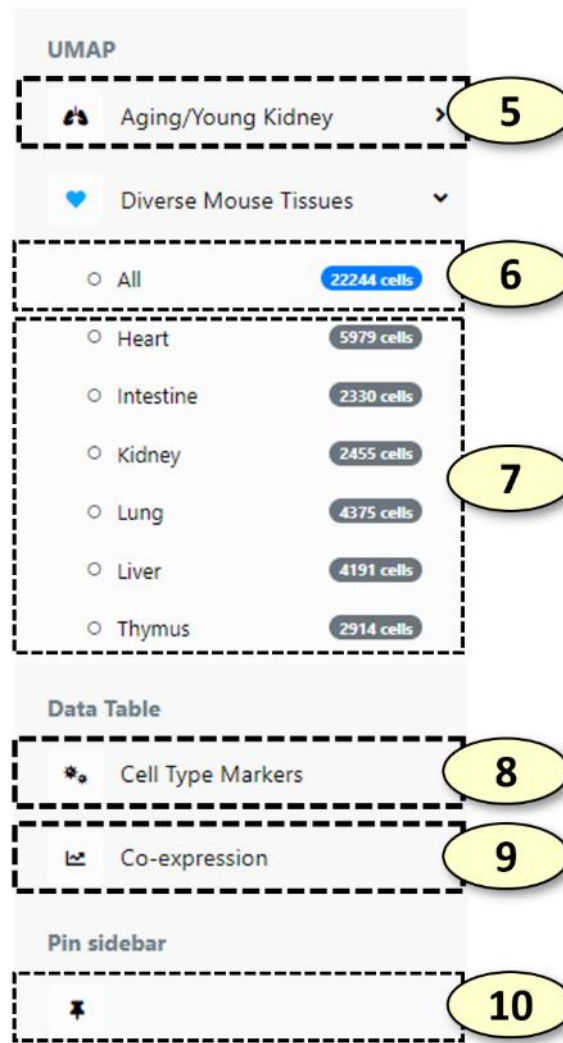
1. **[Capture]** Capture and save the current view as a PNG image file
2. **[Gene Search Box]** Users can explore single-cell gene expression patterns of each gene by typing a valid gene symbol in this gene search box.
  - The search box has an auto-completion feature that suggests a list of partially matched gene symbols to the user as a gene symbol is typed.
  - The summarized gene expression pattern of a gene is instantly visualized as it is being typed to aid more efficient exploration of our dataset without downloading additional data from the server.
  - Once an enter key is pressed, a tag representing the gene symbol (a gene symbol tag) is added to the gene search box. Next, a compressed data chunk containing an array of gene expression values of the gene symbol for the current subsampled (or all) cells is downloaded from our database, parsed in the user's web browser, and displayed on the web application.
  - Up to 200 genes can be simultaneously loaded in the web application by adding gene symbol tags in the gene search box one by one. A summarized gene expression pattern of each gene can be visualized by moving a mouse pointer over each gene symbol tag without downloading any additional data from our web database.
  - By clicking the 'X' symbol left to the gene symbol in each gene symbol tag, a gene symbol tag can be removed from the main gene search box. The removal of the gene symbol tag will lead to the removal of the single-cell-level gene expression values for the gene symbol from the memory, thus freeing unnecessary memory used by the web application
3. **[UMAP Plot for Cell Annotation]** Users can explore annotation labels of the cells on a UMAP graph. The type of annotation labels can be changed by selecting a different annotation in the selection tab located above the UMAP plot.
4. **[UMAP Plot for Gene Expression]** This UMAP graph will visualize normalized and log-transformed gene expression values of individual single cells using the UMAP coordinates of each cell.
  - Clicking a cell on either of the UMAP graphs will trigger downloading of the list of cell marker genes for the cluster to which the cell belongs, which will be subsequently visualized in the **[Cell Marker Panel]**. The

list of cell markers can be downloaded as a CSV file by clicking the 'Download' button located above the table displaying the marker gene list.



- Users can zoom in on a specific region of the UMAP plot by selecting the region when a magnifying glass symbol is active on the toolbar on the upper right side of the UMAP graph. The zoom level can be reset by double-clicking the plot background where no cells are present or clicking the "home" button at the plot toolbar.
- The two UMAP plots, the cell annotation and gene expression UMAP plots, will always display the same region of a graph, visualizing cell annotation labels and gene expression levels of the cells, respectively. The change of view of one UMAP plot will be automatically applied to that of the other UMAP plot.
- Additionally, users can change x-axis or y-axis values from UMAP coordinates to gene expression values of a gene of interest by (1) selecting the 'gene' option in the selection tab next to either the 'X' or 'Y' labels above the **[UMAP Plot for Gene Expression]** plot and (2) clicking the gene symbol tag in the gene search box. After the change of an axis, the axis label will be updated from 'UMAP-1' (or 'UMAP-2') to the gene symbol that has been selected to represent the axis. The axis can be changed back to the UMAP coordinates by selecting the 'UMAP-1' (or 'UMAP-2') option in the selection tab.

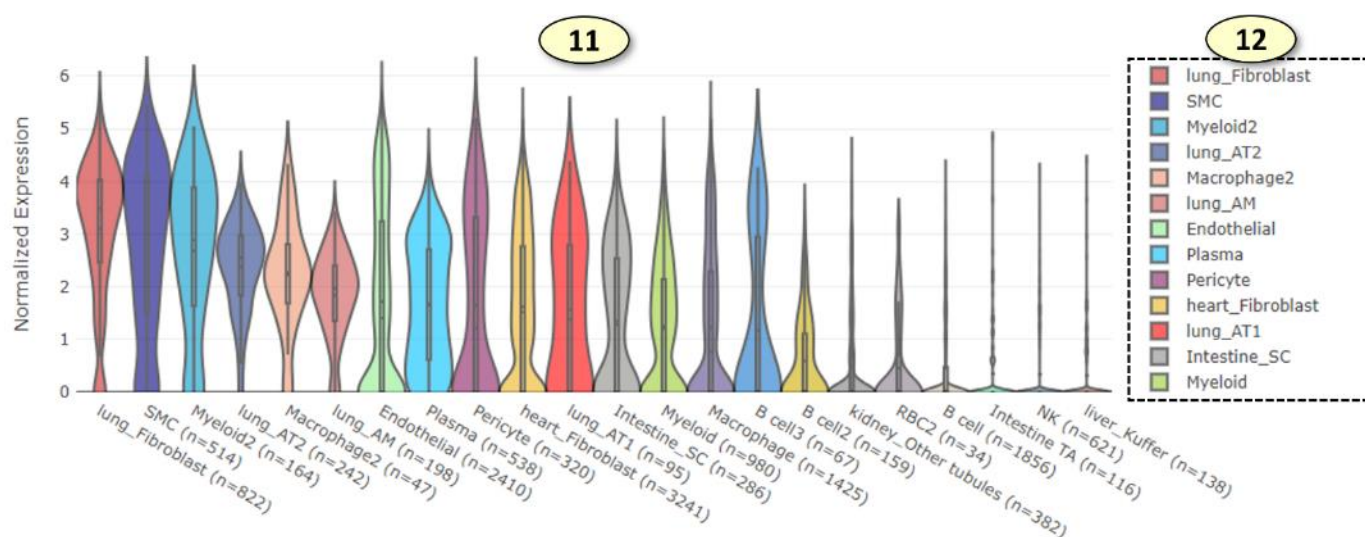
## Sidebar



5. **[Explore a dataset]** Click to see the samples (conditions) available for the dataset.
6. **[Load all cells of a dataset]** Load all cells of the dataset. The number of cells in the blue badge indicates the total number of cells in the dataset.
7. **[Load a subset of cells of a sample]** Load cells of a sample (or a condition). The number of cells in the grey badge indicates the total number of cells for the sample/condition.
  - Internally, when the user visualizes a gene, expression values of the gene are downloaded together, and changing a dataset or sample (without changing a gene) will not download the expression values of the gene redundantly (also, these expression values are cached, and up to expression values of 200 genes will be kept in the memory).
8. **[Cell type marker table]** Show/hide the cell marker table of the cell type of interest. The cell marker table is loaded when the user clicks a cell, which instructs the web application to download cell markers for the cell type of the clicked cell. The cell marker table can be downloaded by clicking the download button above the table.
9. **[Correlated gene table]** Show/hide the table of correlation results, which contains a list of genes whose expression values are correlated with the currently active gene for the current sample/condition/dataset. The table is loaded when the user loads a gene or changes the sample/condition/dataset, which instructs the web application to download a list of correlated genes for the cell type of the clicked cell. The cell marker table can be downloaded by clicking the download button above the table.
10. **[Sidebar control]** Maximize/minimize the sidebar, allowing more space to display the graphs.

- In mobile environments where the screen size is small, sidebar will collapse and will not appear at the left side of the application. In this case, clicking the green floating button at the top right of the application will show the sidebar again.

## Violin Plot



11. **[Violin plot]** For the cell types of the current sample/condition/dataset, expression values will be visualized as a violin plot and will be sorted by their average expression values, resulting in a cell type with the highest average expression values at the left side and a cell type with the lowest average expression values at the right side. The plot can be zoomed in by selecting a region to zoom through a click-and-drag action. The zoom level can be reset by clicking the plot background or clicking the "home" button at the plot toolbar.
12. **[Violin plot legend]** Violin plot of each cell type can be included/excluded from the plot by clicking its corresponding label in the plot legend.