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The Main Panel

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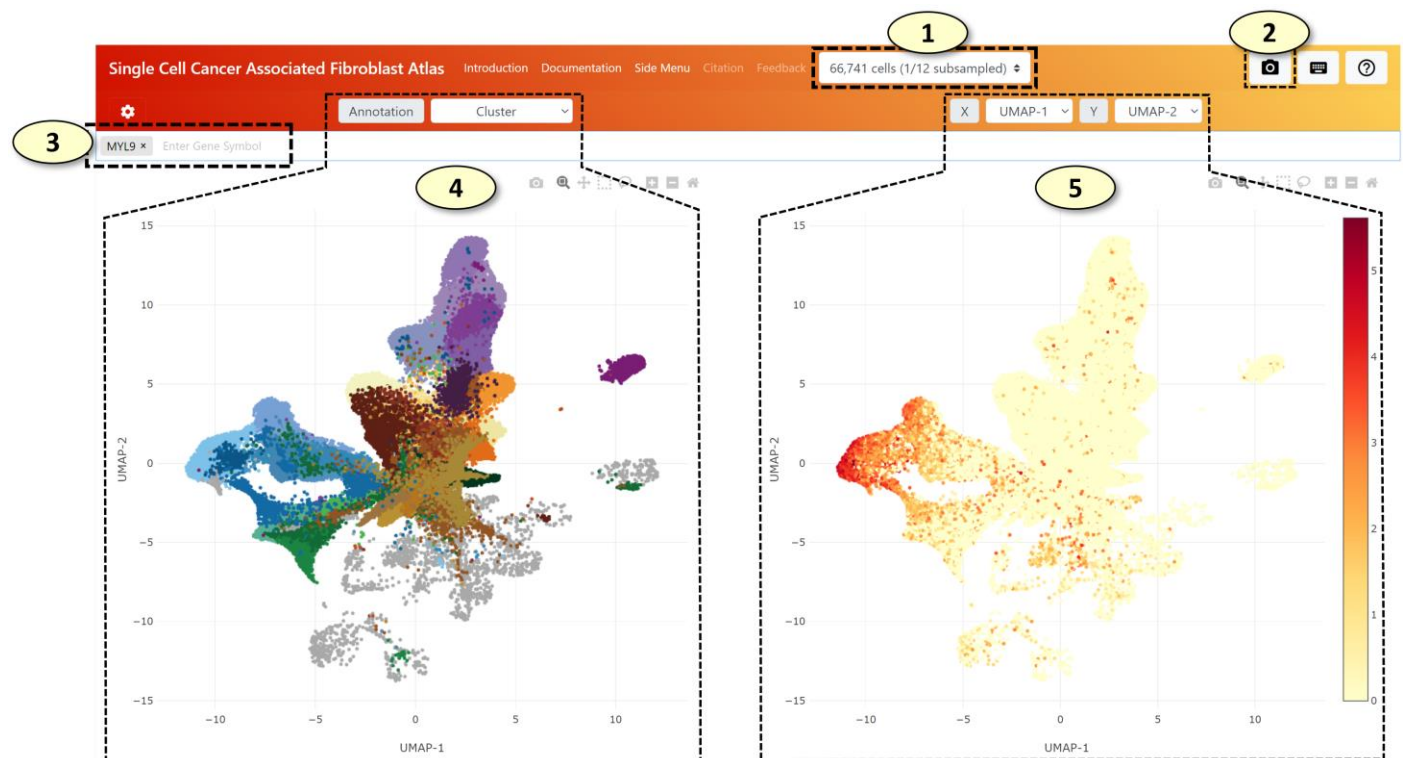
1. **[Select a Subsampling Level]** Select how many cells will be loaded on the web application.

    - Loading all cells (838,388 cells) from the dataset will require 1.7 GB of memory (a peak memory usage of 3.8 GB). Therefore, we recommend loading subsampled datasets on mobile browsers, while loading the full dataset only on the desktop.

2. **[Capture]** Capture and save the current view as a PNG image file

3. **[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.

    1) 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.

    2) 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.

    3) 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.

    4) 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.

    5) 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

4. **[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.

5. **[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 into a specific region of the UMAP plot by selecting the region when a magnifying glass symbol is active on the toolbar on the right upper side of the UMAP graph.

   ● 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.