

## RDS\_Vis\_1.1 User Guide

8/31/2023

This web app is designed for the visualization and exploration of single-cell RNA-seq data contained in Seurat objects. It currently comprises of six tabs, which can be found via the tabs on the navbar on the left hand side of the web page.

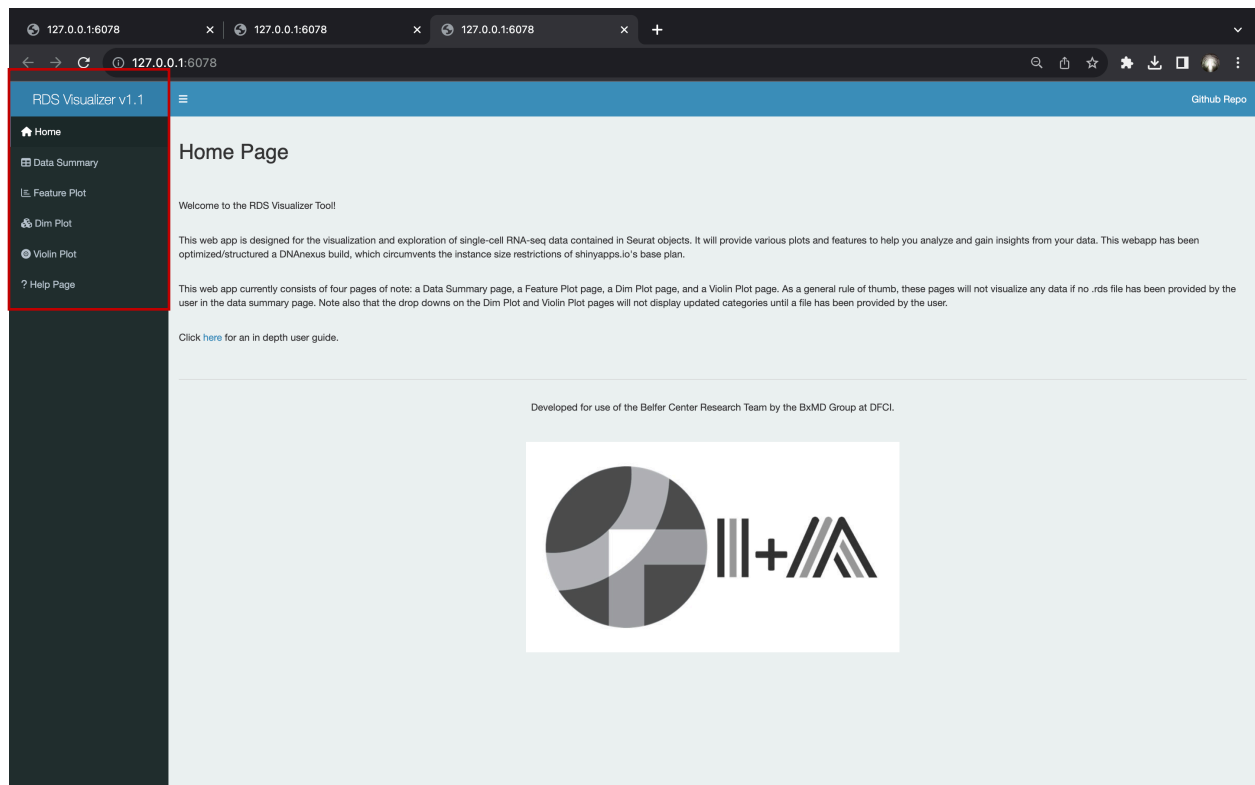


Fig 1. Navbar in red.

To get started, navigate to the Data Summary page and upload an .rds file. Upon completing the upload, the page will render a table summarizing the metadata for the uploaded Seurat file. The Metadata overview will only display the categorical columns of the metadata for the sake of visual parity. To inspect the entire object's metadata, users can click on the Metadata subtab.

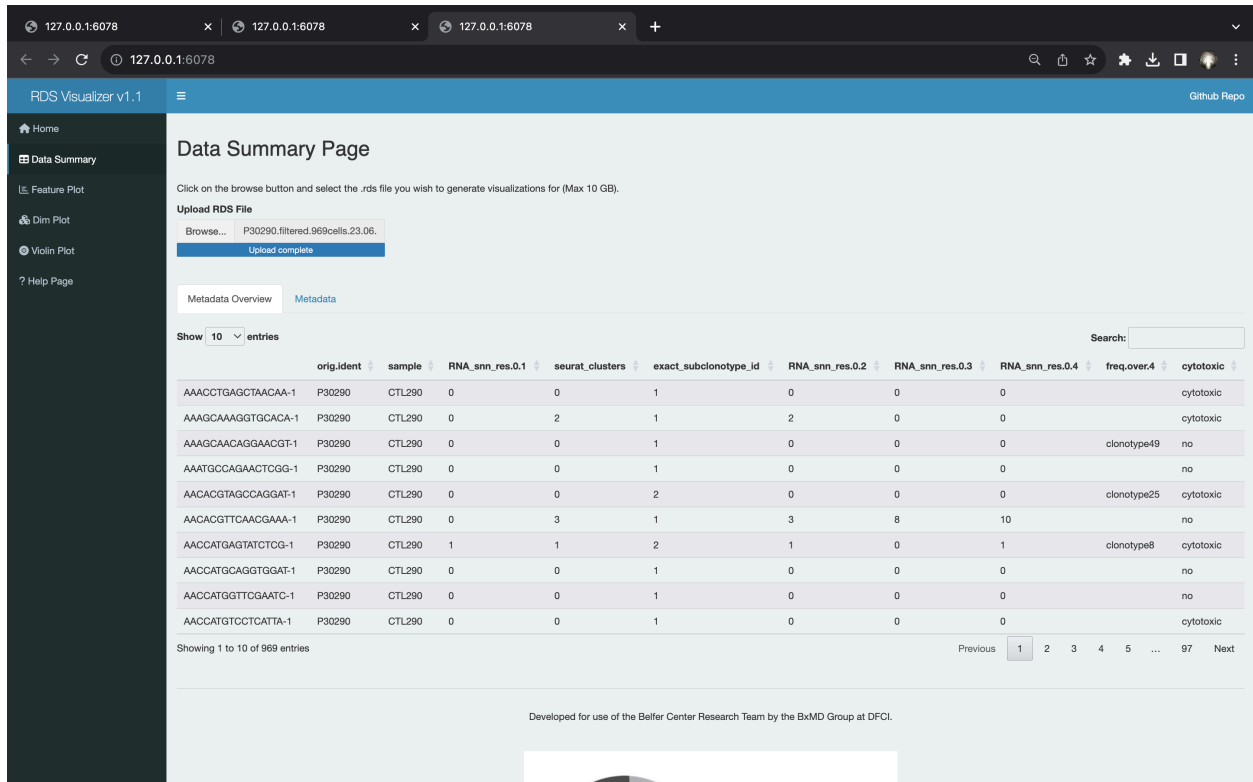


Fig 2. Data Summary page containing metadata of uploaded file after a successful upload.

From here, the user can navigate to one of three visualization pages: the Feature Plot page, the Dim Plot page, and the Violin Plot page.

Starting with the Feature Plot page, a list of ten sample genes should have rendered at the top of the page for preliminary exploration.

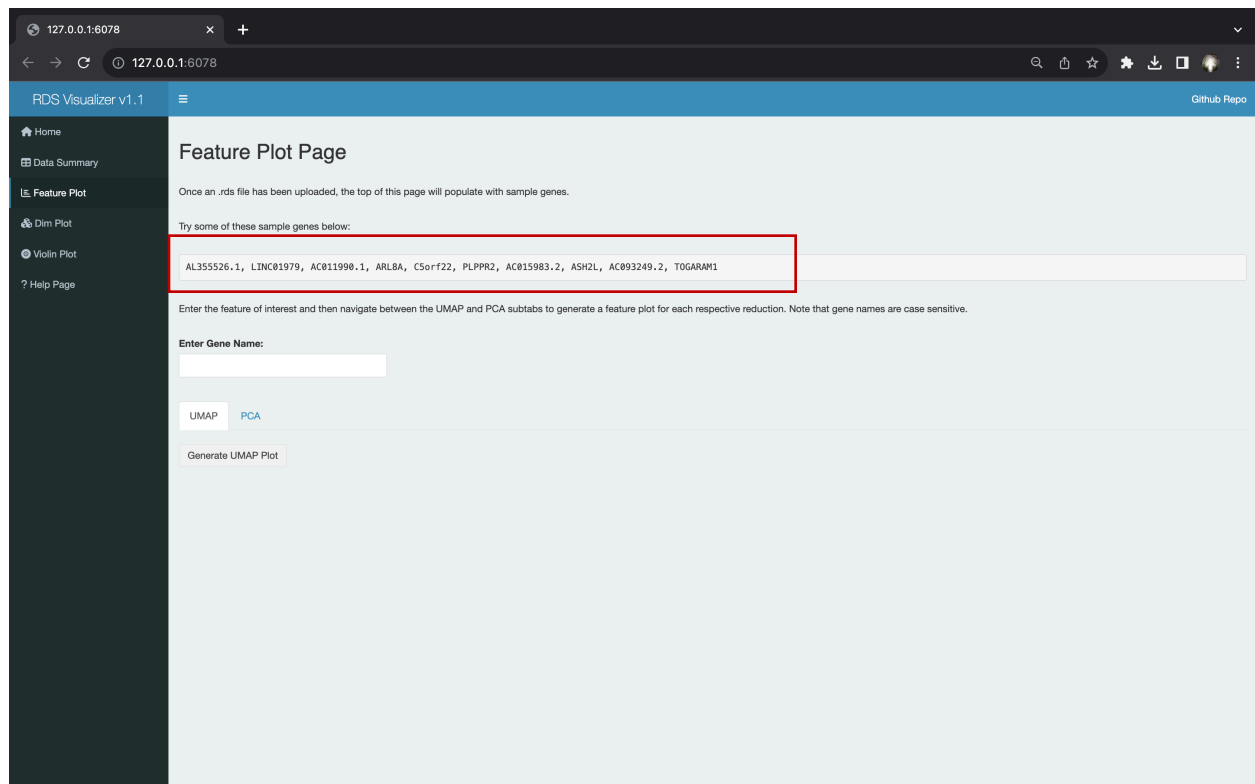


Fig 3. Sample genes that populate after a successful upload in red.

The user can input a gene or a list of genes into the search bar. Currently the webapp supports two reduction modes, UMAP and PCA. You can access these different options via the “UMAP” and “PCA” subtabs towards the middle of the page. After selecting the tab containing the preferred reduction, click on the plot button to render the Feature Plot of choice.

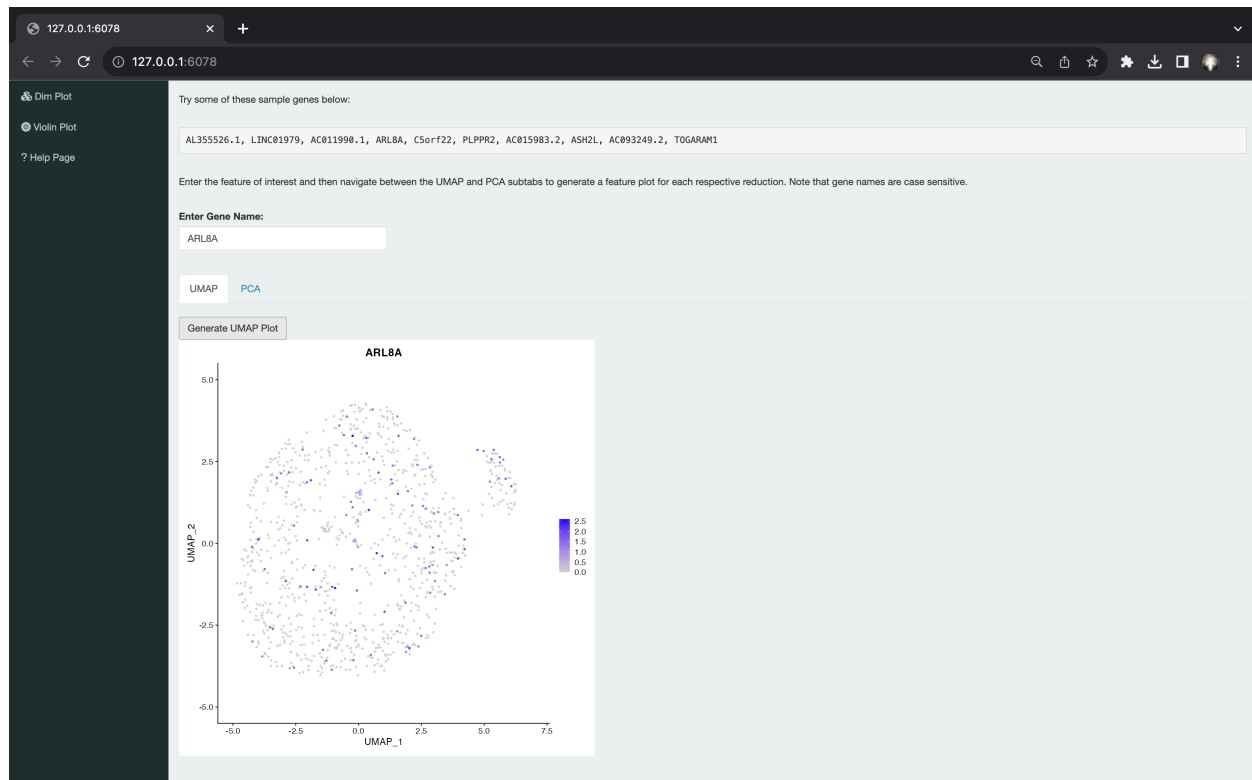


Fig 4. Result of inserting gene, selecting a reduction, and plotting.

While the gene search bar is not sensitive to leading and trailing spaces nor is it sensitive to trailing, it is case sensitive. It is best case to input gene(s) as a comma delimited list. If the user misinputs a gene or fails to check for upper/lowercase letters, the web app will inform the user of genes that are not able to be visualized.

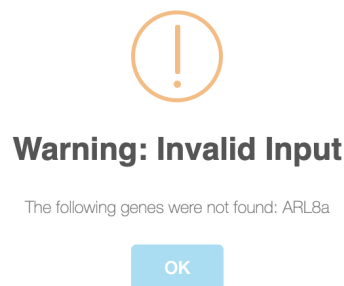


Fig 5. When inputting “ARL8a” instead of “ARL8A” user is notified that the gene is not contained in the uploaded .rds object.

As a side note, the `FeaturePlot()` function in Seurat does actually support the input and visualization of numeric columns from the metadata. However, in this build of the RDS Visualizer web app, the only currently accepted inputs are genes.

The next plot page is the Dim Plot page, which features a dropdown that will automatically update based on the categorical metadata columns in the uploaded Seurat file. Note that the categorical columns included are limited to those that have less than five levels.

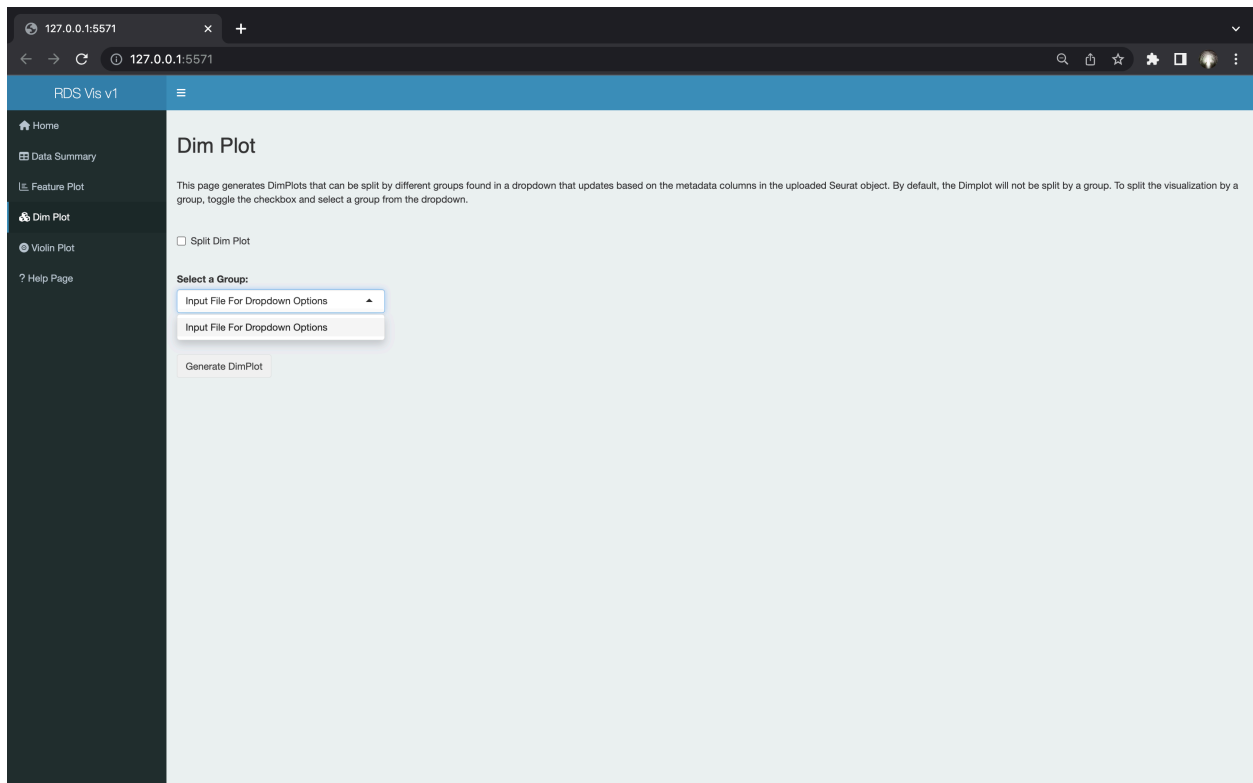


Fig 6. Dropdown menu prior to Seurat file upload.

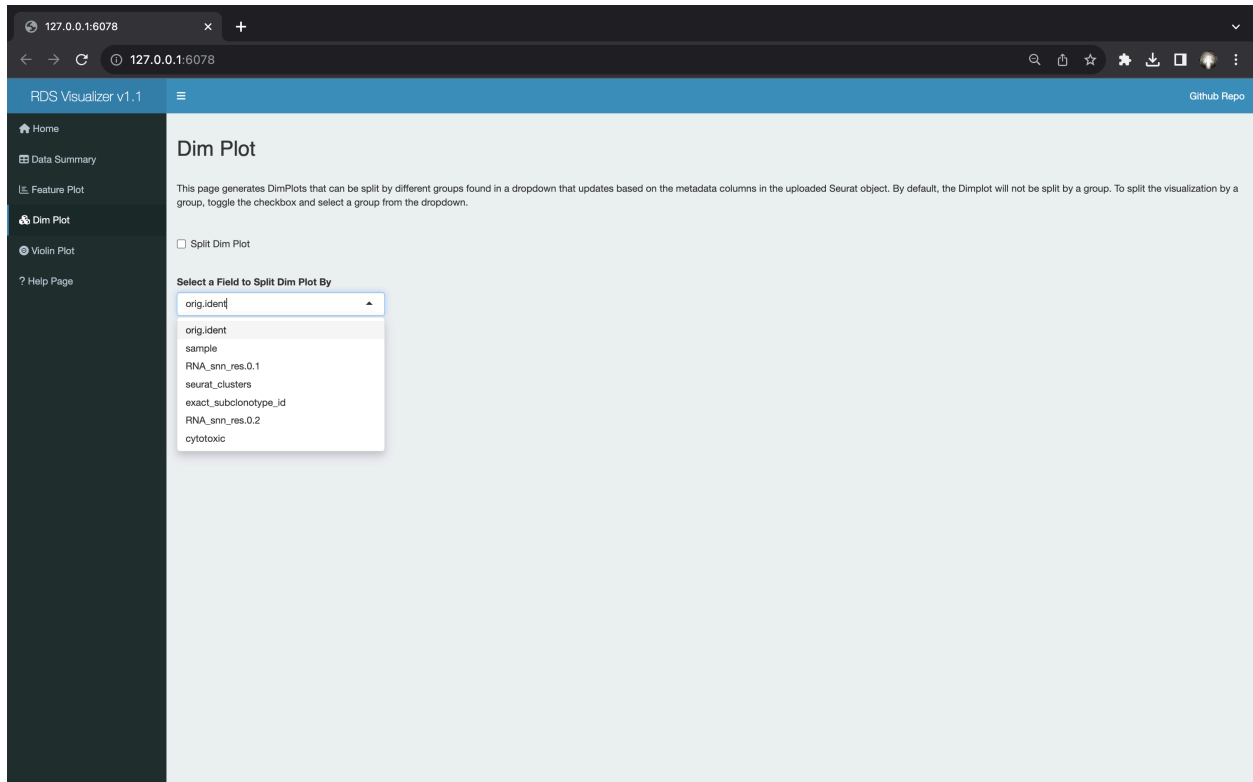


Fig 7. Dropdown menu after Seurat file upload.

After selecting a group from the dropdown and clicking the plotting button, the default view will be unsplit. To split the view by the same group you are grouping the data by, toggle the checkmark and re-click the plotting button.

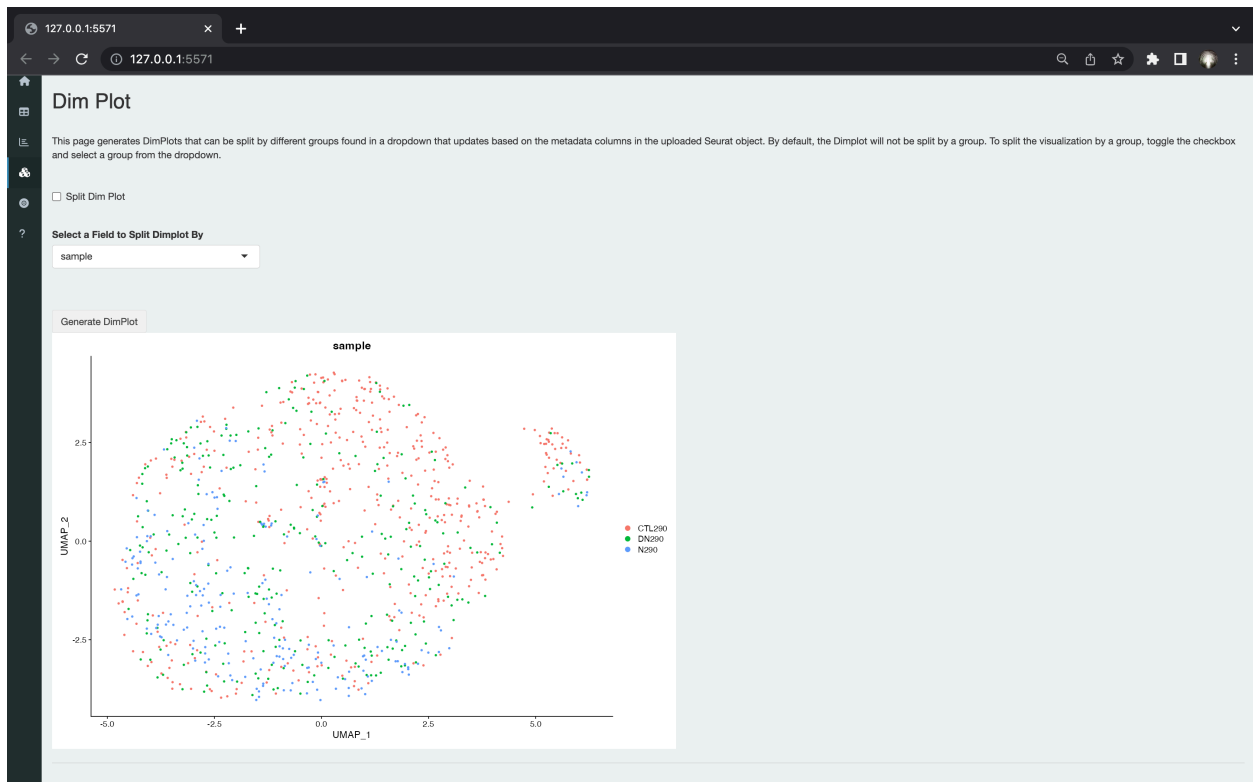


Fig 8. Unsplit Dim Plot view.

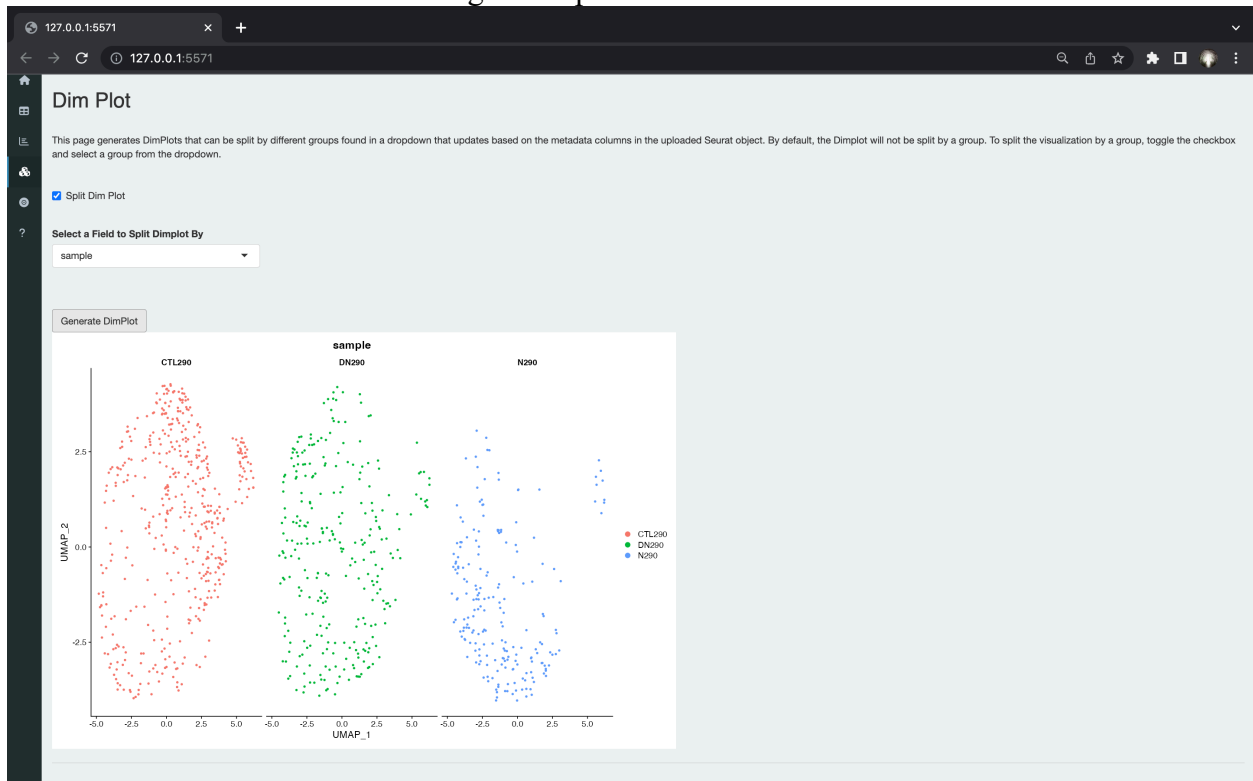


Fig 9. Split Dim Plot view. Note the checked “Split Dim Plot” button at the top of the page.

Lastly, there is the Violin Plot Page, which generates violin plots by combining elements of the Feature Plot and Dim Plot pages. Users can input a gene name in the same manner done in the Feature Plot Page. The behavior of the gene search bar is consistent with that of the Feature Plot page; comma delimited lists or single genes are acceptable inputs. The dropdown like in the Dim Plot Page auto-updates following the .rds file upload. The dropdown selection should be identical to that in the Dim Plot page. The default view is a split view there is not currently an unsplit view for this page.

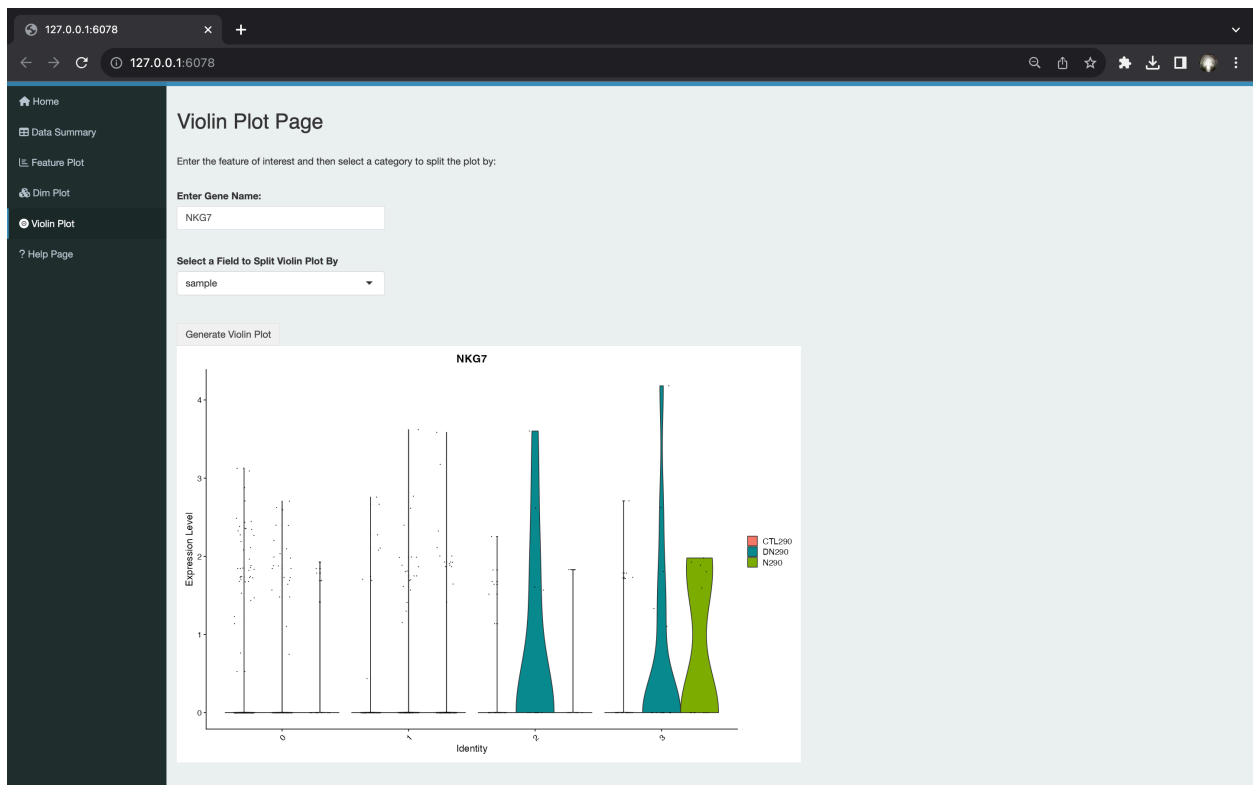


Fig 9. Split Violin Plot view.

Future features to be built out include a volcano plot!