Documentation

Data Clusters

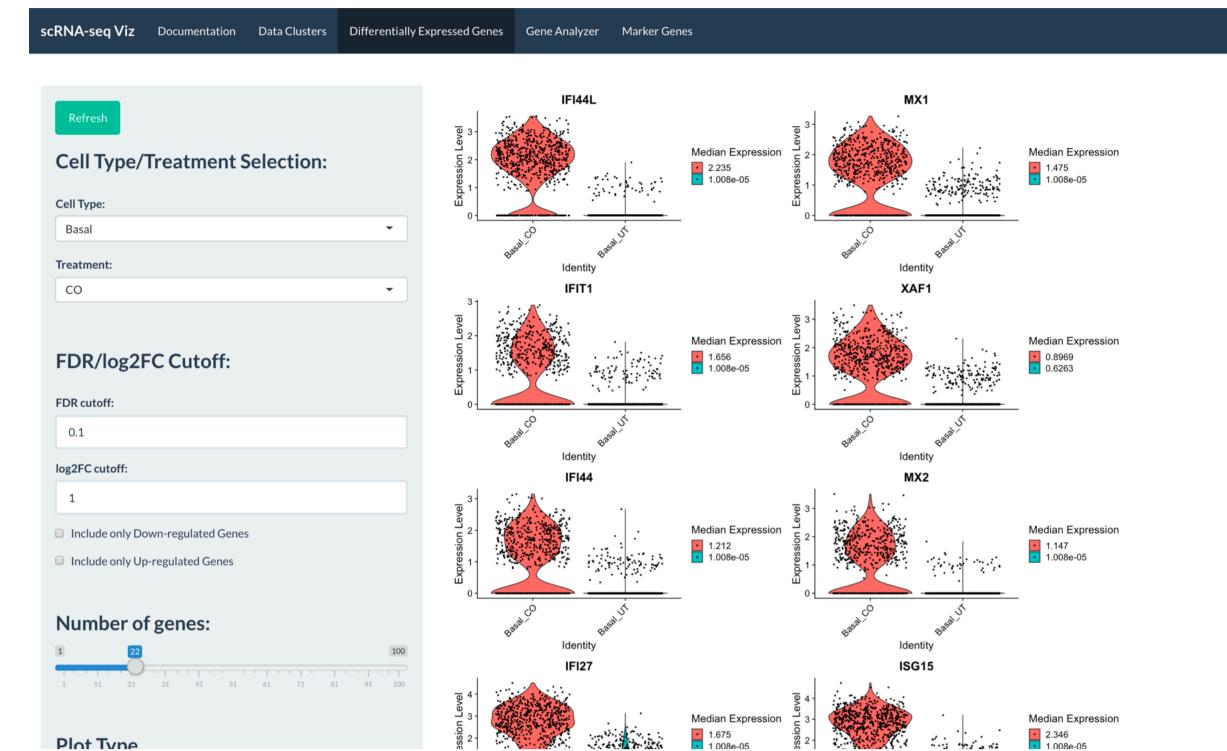
Explore various cell types with different dimension reductions or visualize our donors and treatments:

Options: scRNA-seq Viz Documentation Data Clusters Differentially Expressed Genes Gene Analyzer Reduction: UMAP **Group By:** cellType

- Dimension Reduction Type: [PCA, TSNE, UMAP]
- Group By:
 - Cell Types: This will color the graph based on the nine major cell types we classified.
 - RNA_snn_res.0.XX: This will color the graph based on groupings produced by Seurat at various resolutions. • A higher value of XX means that there is a higher resolution, and therefore more clusters or inferred groups of cell types.
 - Donor: This will color the graph based on our four donors. • Treatments: This will color the graph based on five treatments (including untreated).
 - Treatment vs. Celltype: This will color the graph based on celltypes under various treatments

Differentially Expressed Genes Explore the top N differentially expressed genes for various cell types and treatments:

Options:



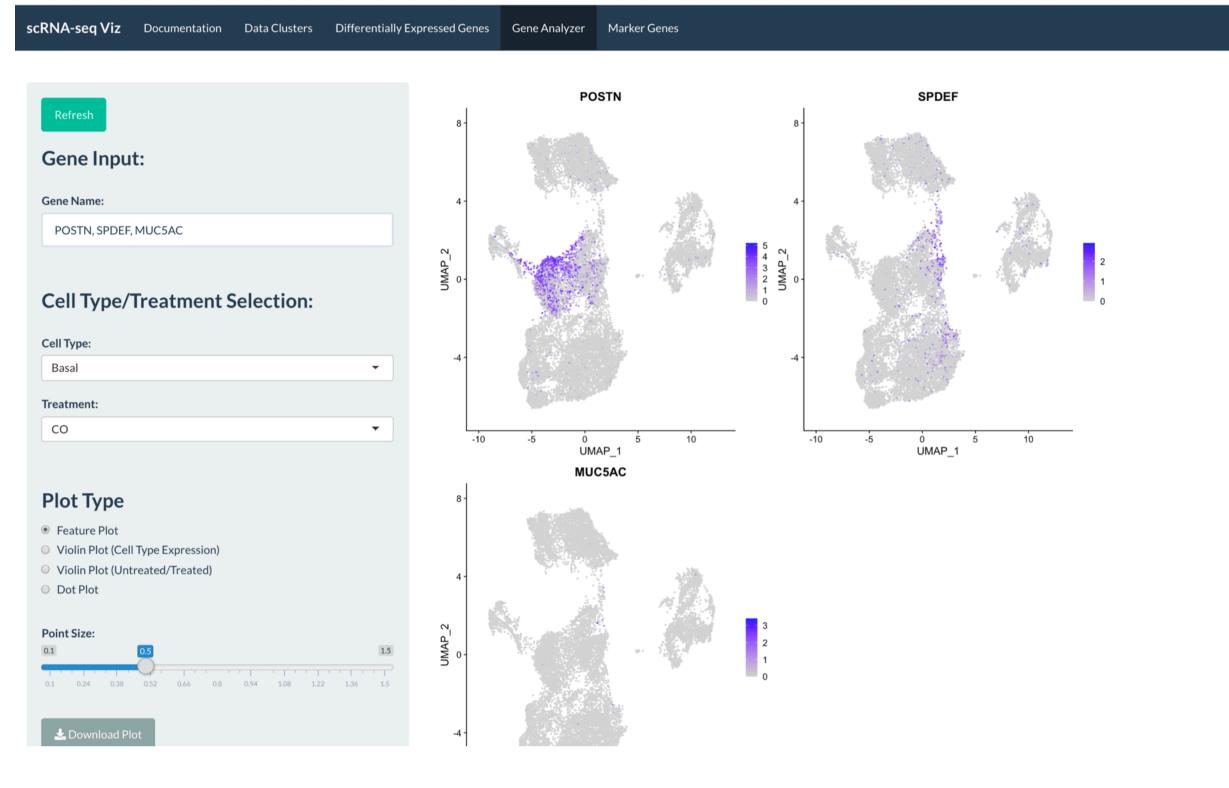
which cell type and treatment combinations you would like to look at • FDR/log2FC cutoff: These numerical values determine which how your top N genes are determined and filtered from the

• Cell Type/Treatment Selection: This drop-down menu (if your plot is a heatmap, the celltype menu is a checkbox list) allows you to select

- cellType/Treatment object
 - o Down-regulated genes are genes that have lower gene expression with respect to the untreated data. Initally, both down and upregulated genes are included. • The Include only Down-regulated Genes checkbox allows you view only down-regulated genes
- The Include only Up-regulated Genes checkbox allows you view only up-regulated genes • Number of Genes: This slider determnines how many genes you would like to view
- Plot Type: This selection determines whether you would like to view your genes as a FeaturePlot, ViolinPlot, Heatmap, or a DotPlot

Gene Analyzer Allow users to input interesting genes and visualize gene expression in various cell types and treatments:

Options:



• "HGNC" nomenclature genes and Gene symbols (i.e. not Ensemble ID etc.) are expected • Cell Type/Treatment Selection: This drop-down menu allows you to select which cell type and treatment you would like to look at • Plot Type: This selection determines whether you would like to view your genes as a FeaturePlot, ViolinPlot, or DotPlot

• Gene: This input bar allows you to input which genes you would like to look at. The required format is Gene1, Gene2, Gene3, ...

• If your plot type is a dotplot, see below for further documentation

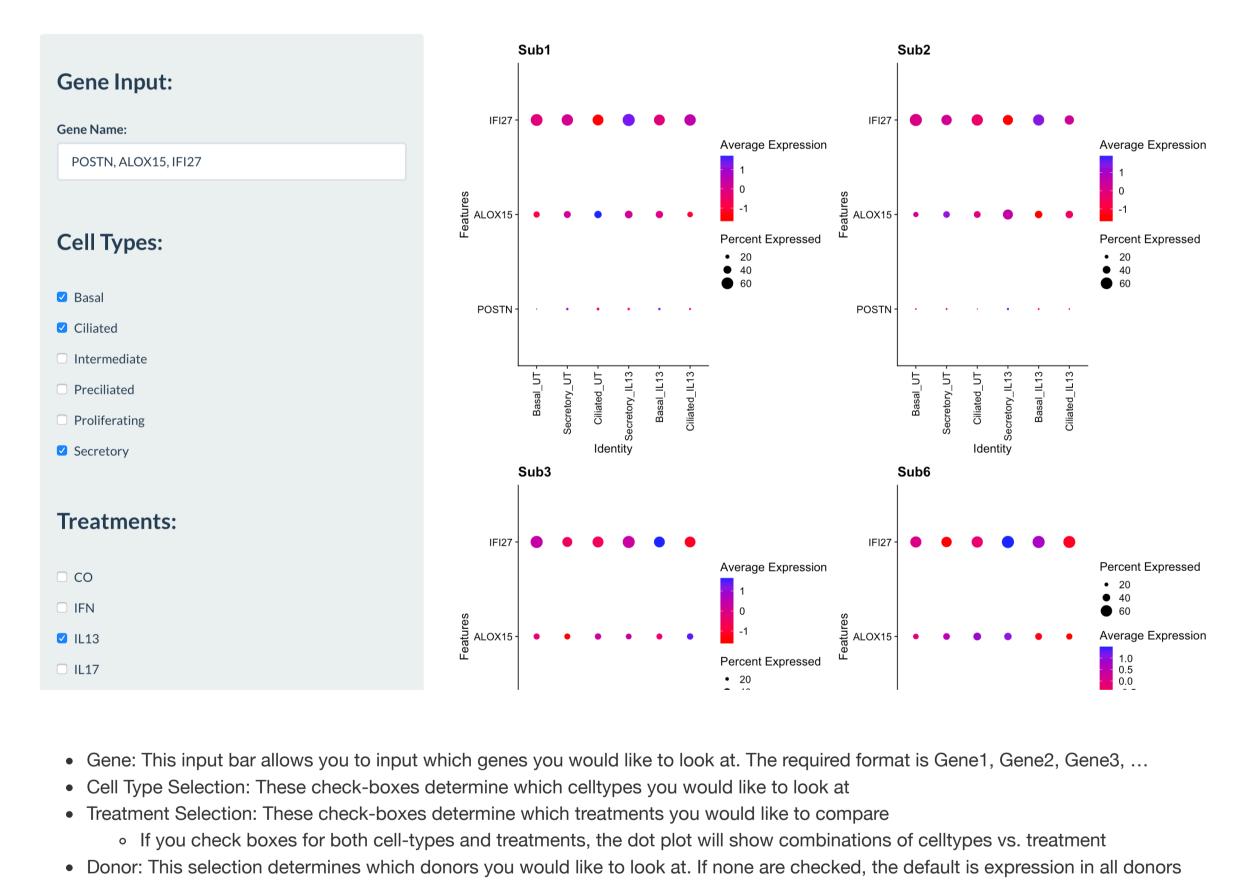
Option Under Gene Analyzer Tab: Allow users to input interesting genes and visualize how they vary under different cell types, treatments and donors using dot plots:

Options:

Dot Plot

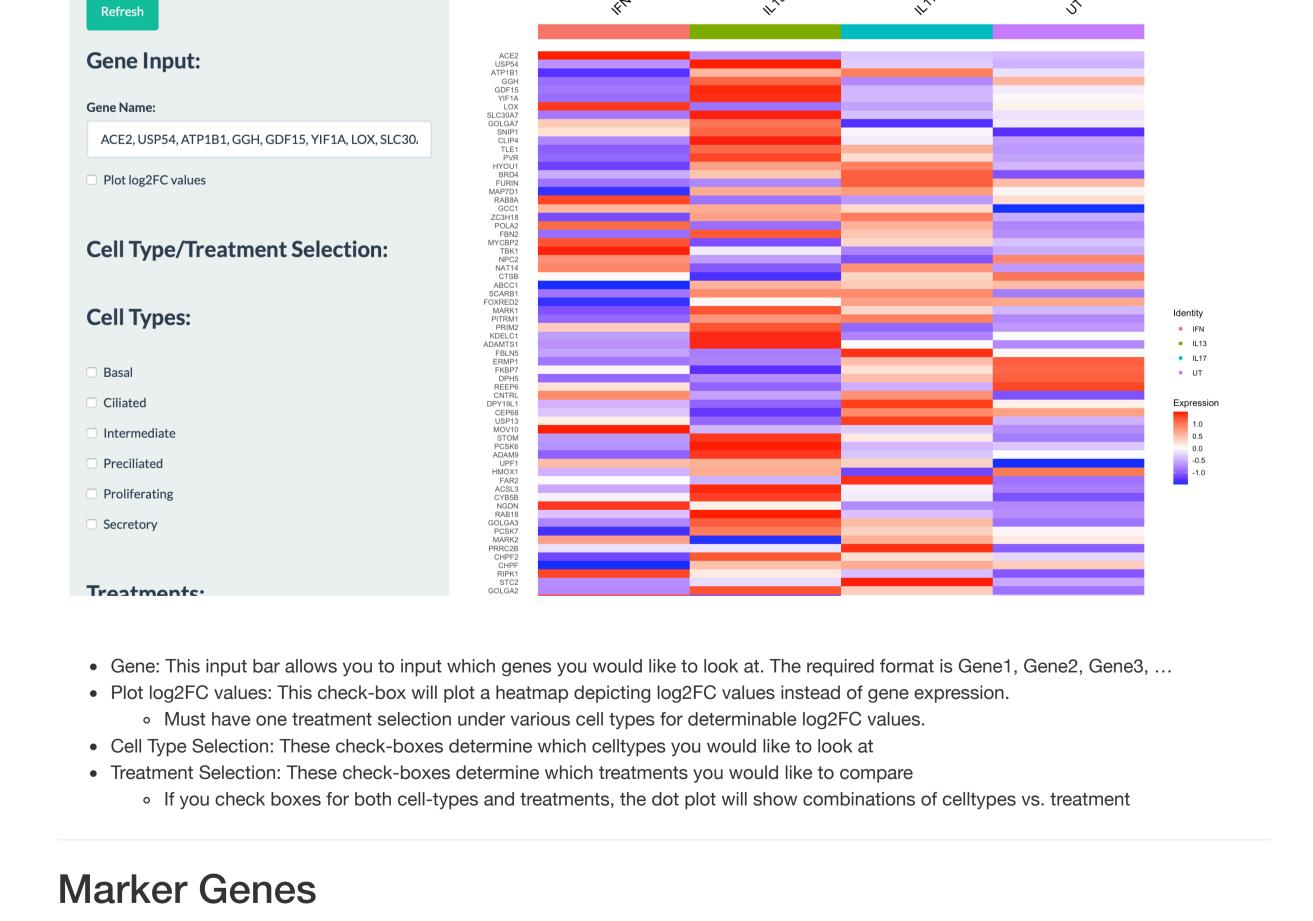
Options:

scRNA-seq Viz Documentation Data Clusters Differentially Expressed Genes Gene Analyzer



- Heatmap
- Option Under Gene Analyzer Tab: Allow users to input interesting genes and visualize how they vary under different cell types, treatments and donors using heatmaps:

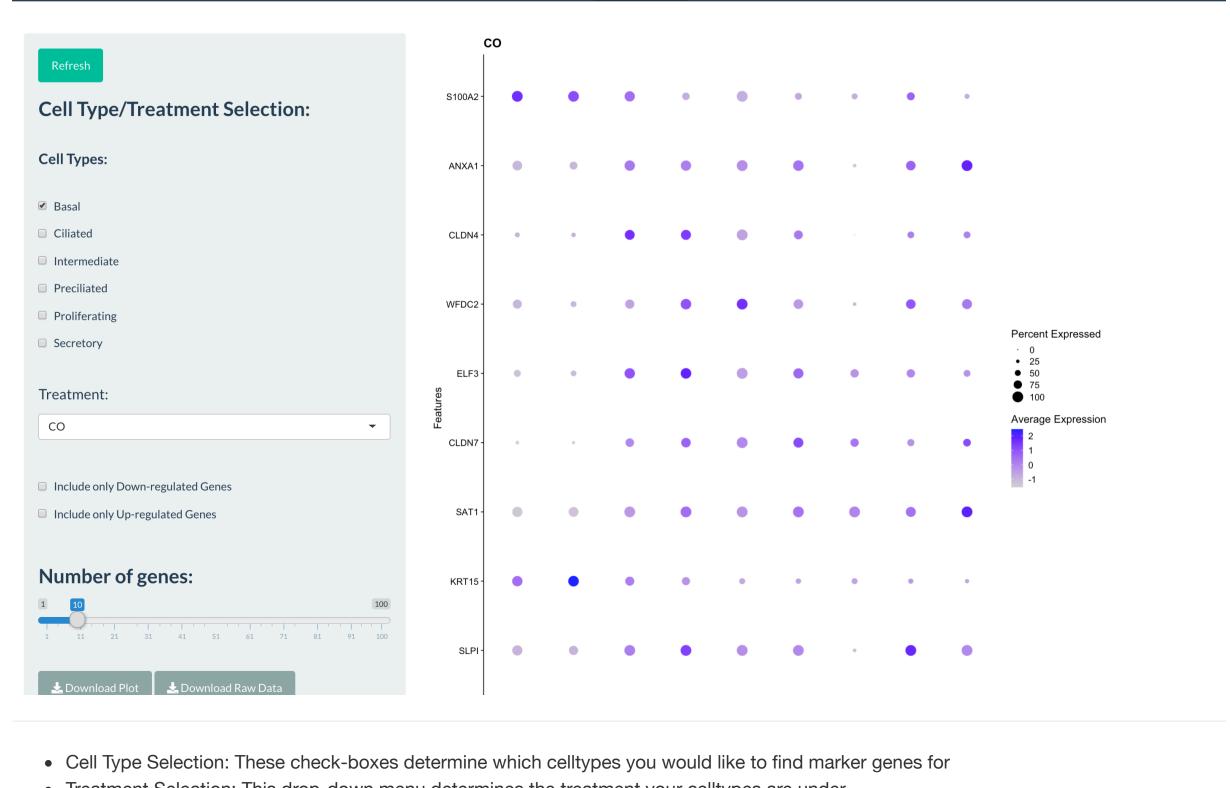
scRNA-seq Viz Documentation Data Clusters Differentially Expressed Genes Gene Analyzer Marker Genes



Options:

scRNA-seq Viz Documentation Data Clusters Differentially Expressed Genes Gene Analyzer Marker Genes

Allow users to identify top N marker genes for various cell types across other cell types under certain treatments



• Treatment Selection: This drop-down menu determines the treatment your celltypes are under

• Number of Genes: This slider determnines how many genes you would like to view