SeqGeq's Violin Plot Plugin - How To:

Violin plots are a popular way of illustrating expression patterns between genes of interest and across different populations or samples in single-cell RNA sequencing analyses. In SeqGeq this feature has been implemented as a plugin with some dependencies in R.

Installation

With regard to the R dependencies, this plugin has been tested in the R environment 3.4.2, and requires the path to R be specified in SeqGeq's Diagnostics preferences, as well as the ggplot2 package within R. This package can be installed in R simply by copy/pasting the following command there:

```
install.packages("ggplot2")
```

As with all plugins for SeqGeq you'll need the JAR file for the Violin plot plugin to be places in the plugins folder referenced within the Diagnostics preferences of SeqGeq.

Running the Plugin

Once the necessary dependencies have been put into place, users can select a population of interest from the Samples area of SeqGeq's workspace, click on the "Plugins" option within the Workspace tab of SeqGeq's workspace, and choose the Violin Plot plugin there:
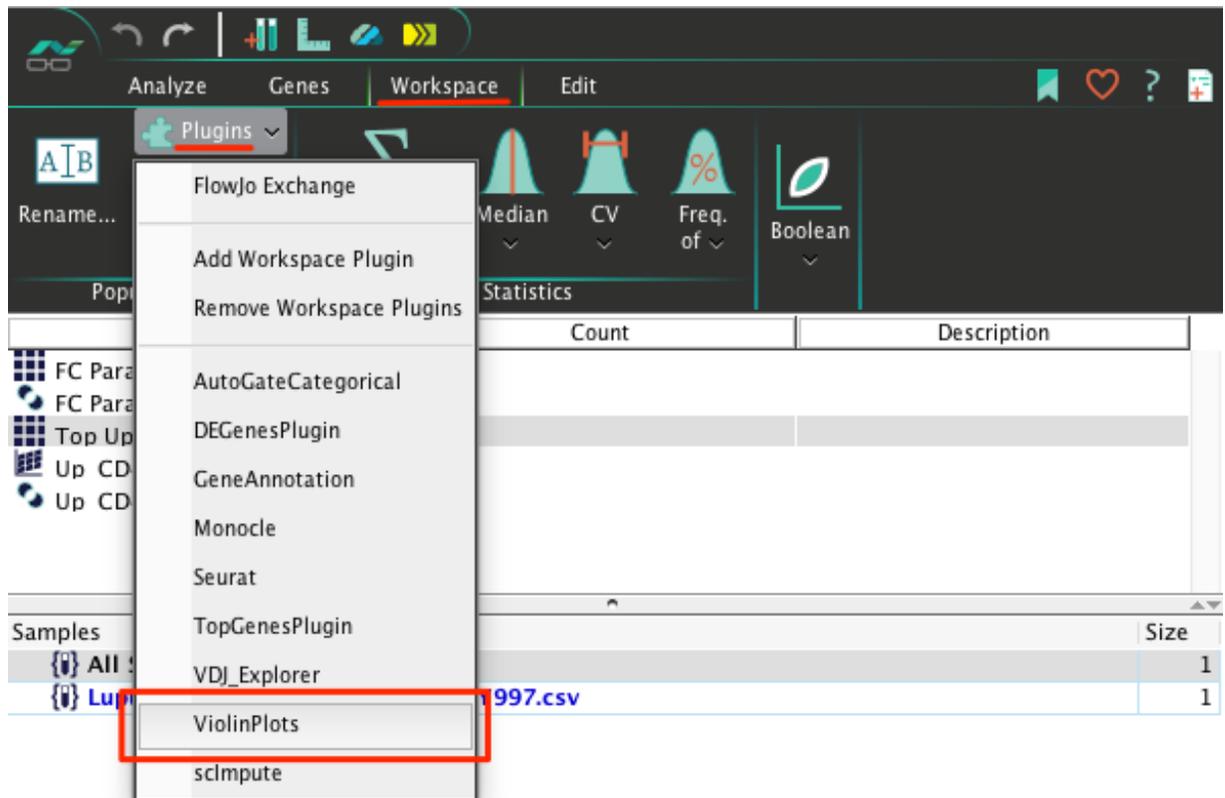
This will bring up a dialog in which researchers can select their genes of interest, as well as make adjustments to the violin plot settings:
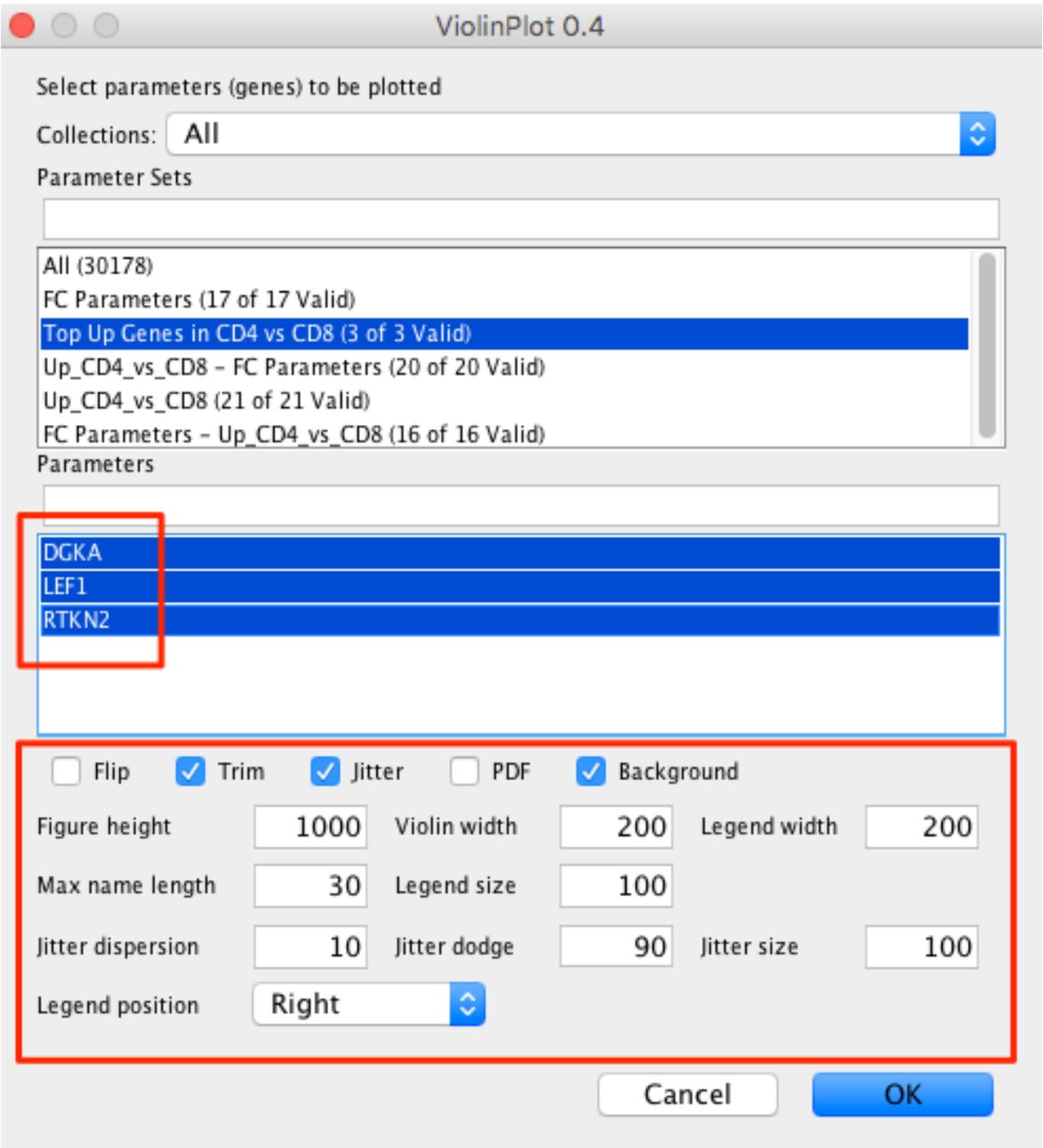
Doing so will generate a new node below the population selected which, when finished calculating, will prompt the user to drag that row from the workspace into their Layout Editor, in order to see the Violin plot displayed:
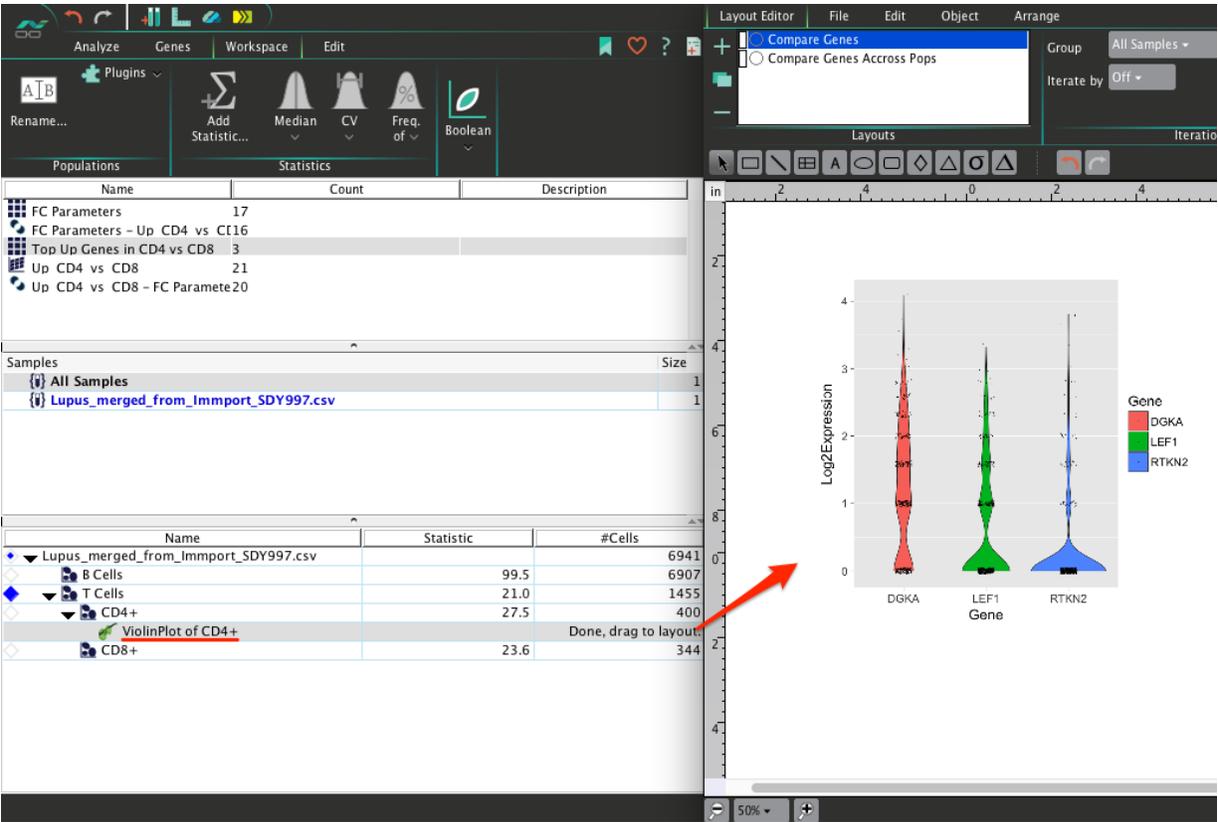
In order to compare genes from this initial Violin plot across numerous populations, simply drag the initial plugin node to the other populations of interest:
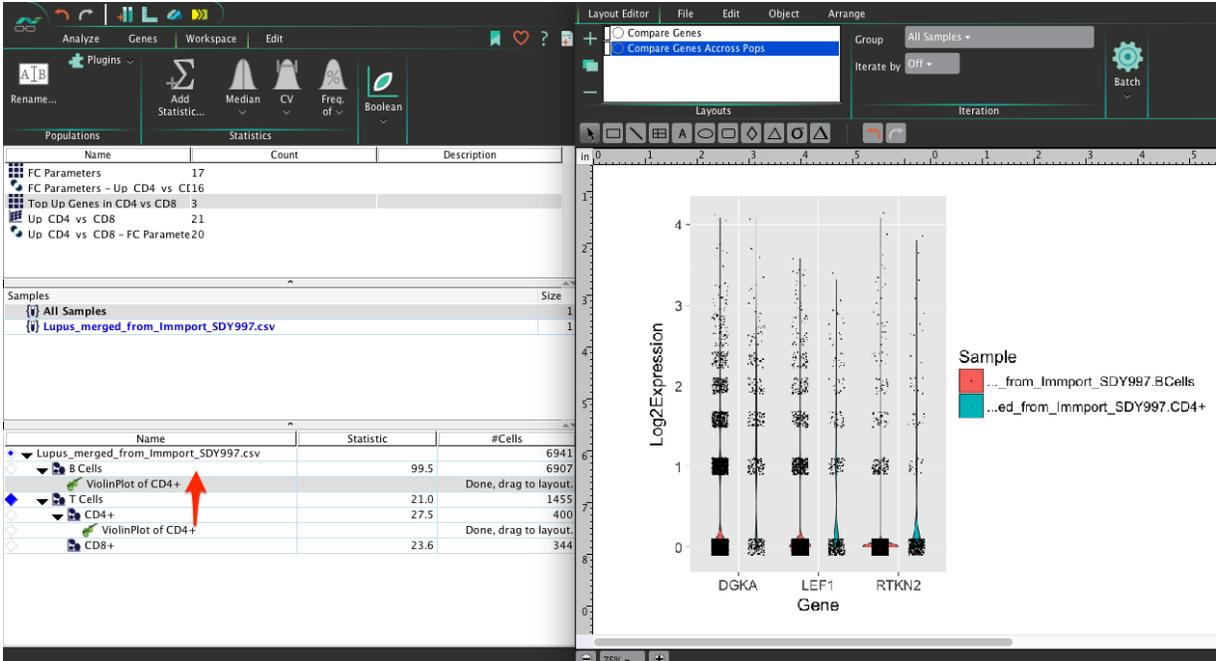
Help Resources

SeqGeq documentation is available at: docs.flowjo.com/seqgeq

For additional assistance with all things SeqGeq related, feel free to reach out for technical support: seqgeq@flowjo.com