SeqGeq's Violin Plot Plugin - How To:

Violin and box plots are popular ways of illustrating expression patterns between genes or proteins of interest and across different populations or samples. In FlowJo and SeqGeq these features have 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 FlowJo and/or 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 you'll need the JAR file for the Violin plot plugin to be placed in the appropriate plugins folder referenced within the Diagnostics preferences of FlowJo or SeqGeq.

Running the Plugin

Once the necessary dependencies have been put into place, users can select a population of interest in their workspace, click on the "Plugins" option within the Workspace tab, and choose the Violin Plot plugin there:
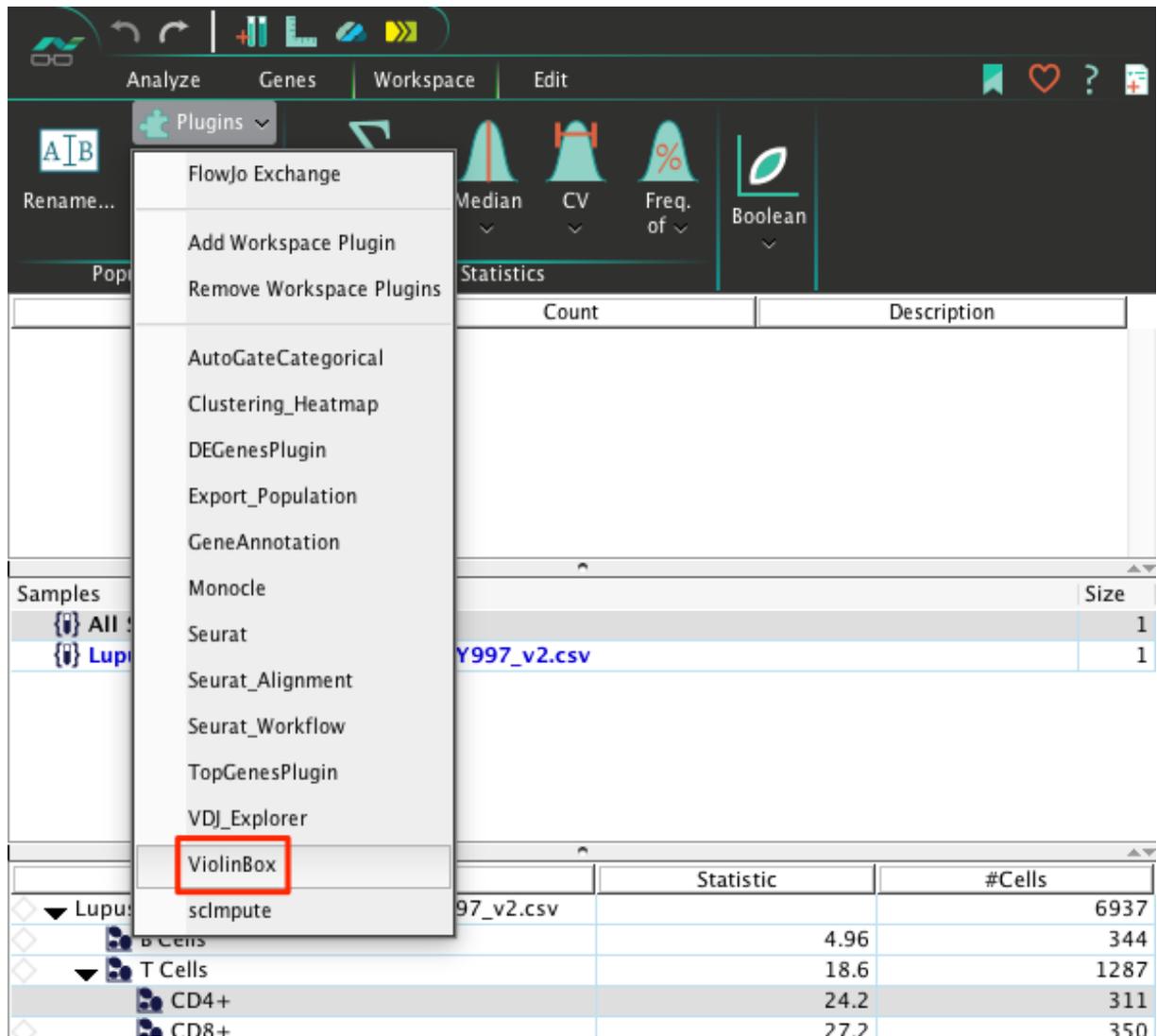
This will bring up a dialog in which researchers can select their parameters of interest, as well as make adjustments to the plot settings:

Clicking OK will calculate the plot selected, add a ViolinBox plugin node to the population selected, and create a new layout within SeqGeq's Layout Editor, in order to see the Violin plot displayed there:
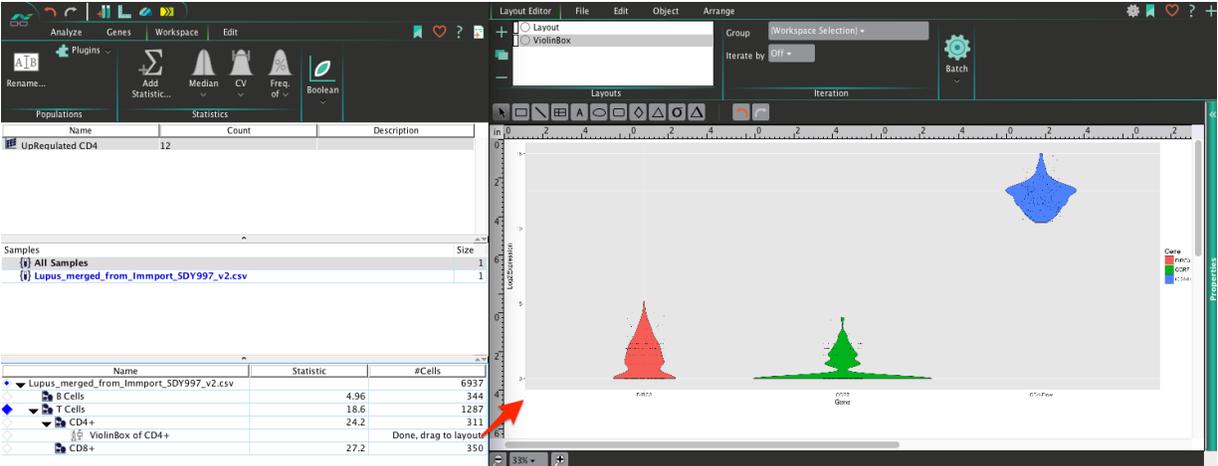
In order to compare genes from this initial Violin plot across numerous populations, simply drag the initial plugin node to the other populations of interest:
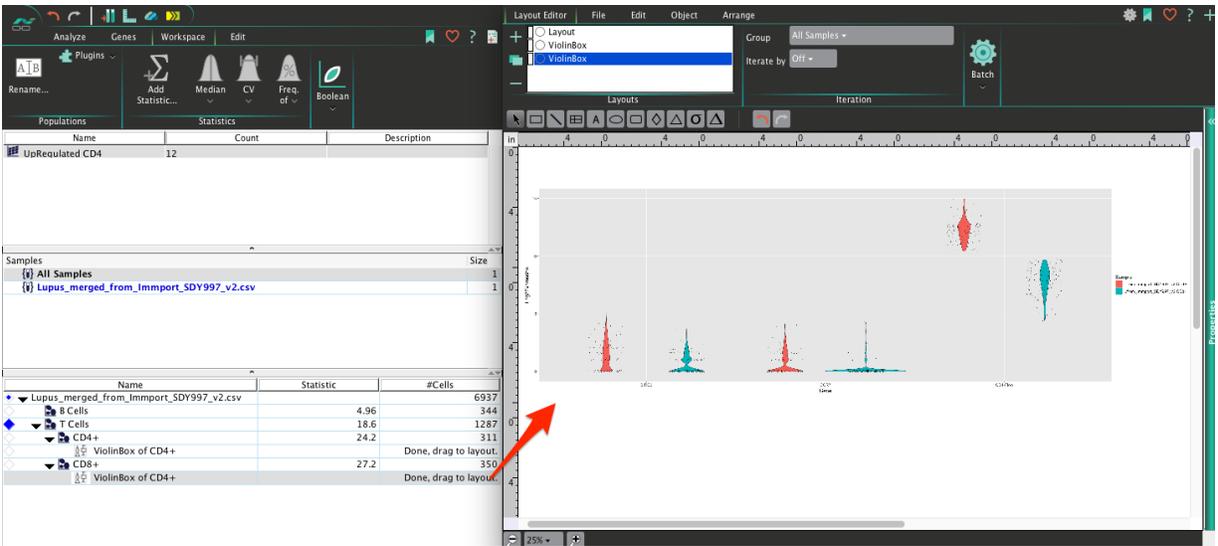
Help Resources

Documentation is available at:

docs.flowjo.com/d2
docs.flowjo.com/seqgeq

For additional assistance with all things single-cell analysis related, feel free to reach out for technical support: techsupport@flowjo.com or seqgeq@flowjo.com