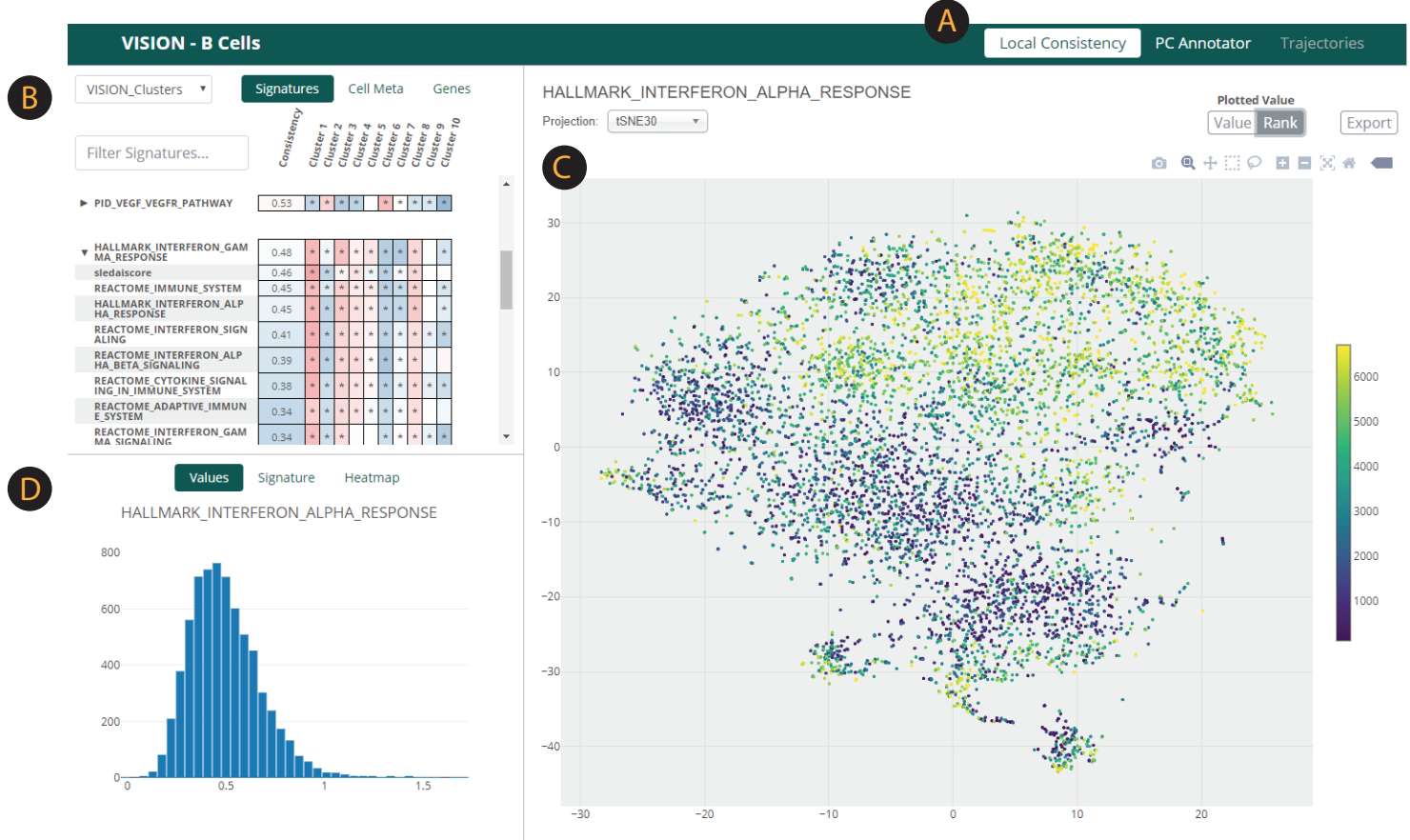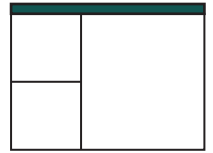# VISION Output Browser

Running the "viewResults" function on the analysis object launches a dynamic report in the user's web browser.
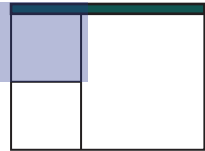
A) Select between the three main views. "Local Consistency" reports on signatures with high autocorrelation in the latent space. "PC Annotator" compares signatures with latent space principal components. "Trajectories" is available if a trajectory model was supplied and shows the results of signature autocorrelation within the trajectory model.

B) Change the plotted object. Choose between signatures, meta-data, and genes

C) Visualize signatures along with cells using 2-dimensional representations of the latent space

D) Extra information about the currently plotted object or selection

# Upper-Left Panel: Select Values to Visualize

Browse signatures for plotting

A) Signatures are grouped into collapsible rows based on signature value correlation

B) Search/Filter signatures

C) The first column ranks signatures by their C' value. High C' corresponds with high local autocorrelation. Click the value in this column to plot the signature.

D) The other columns show the result of a 1 vs. All differential signature test for the selected grouping variable. Hover over these values to see the significance and associated ROC AUC.

E) Switch the grouping variable for label-based 1 vs. all differential signature analysis.

Alternately, in the "Cell Meta" tab, meta-data can be visualized

The third tab allows for the selection of individual genes.

A) Search for genes and select for plotting

B) Recently selected genes are saved here for convenience. Click to re-select.

Scatter Plot Panel: Visualize Signatures
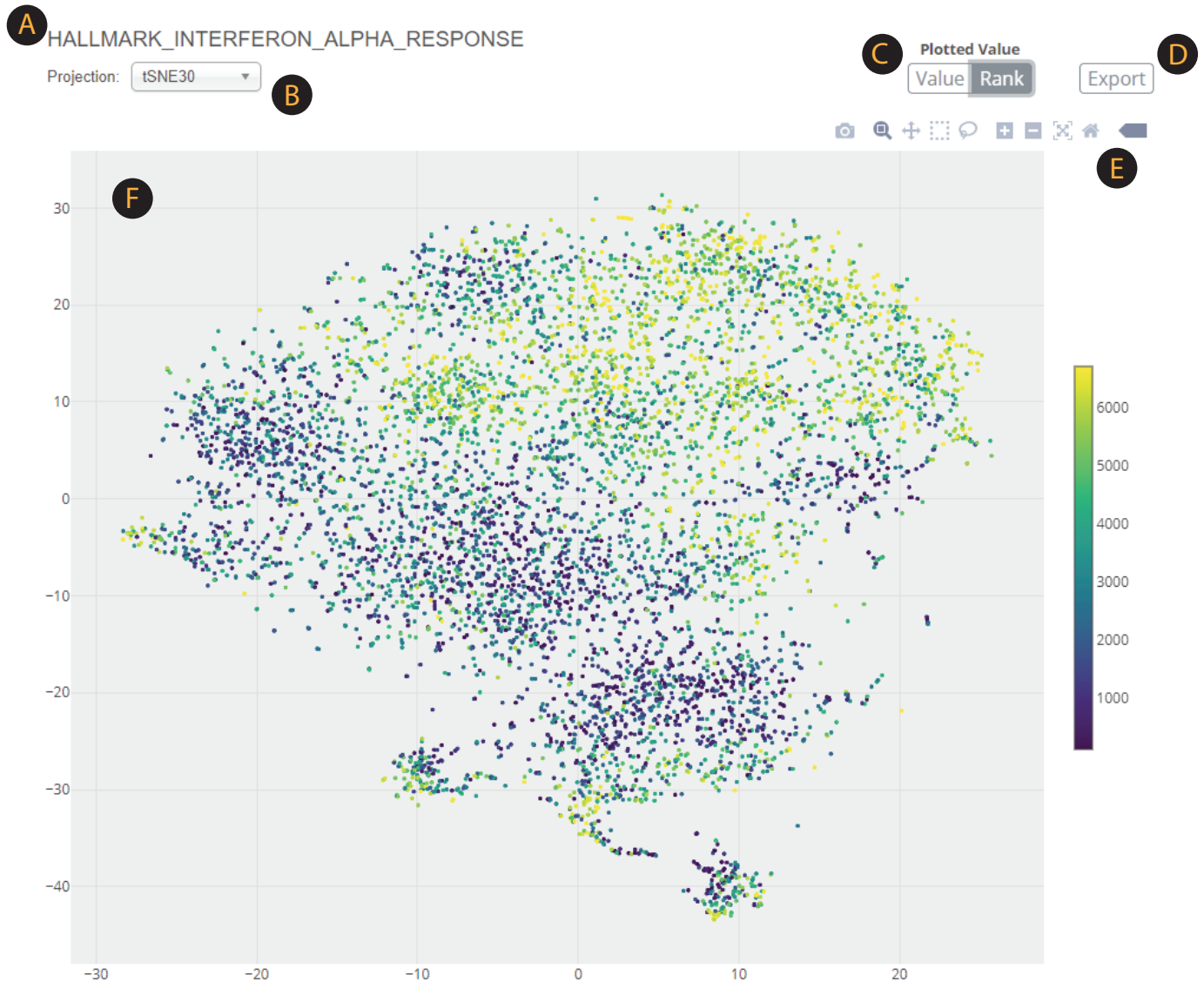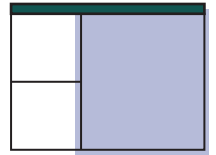
The scatter plot panel visualizes the currently selected variable (either signature scores, meta-data, or individual genes).
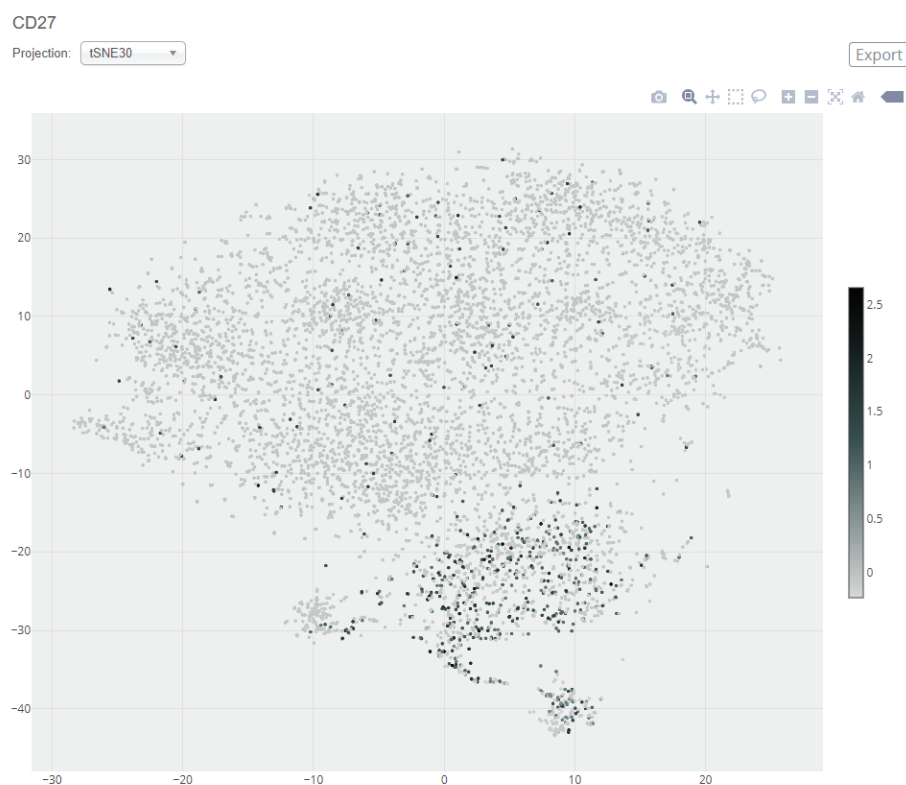
A) Name of currently plotted variable

B) Switch between 2D projections

C) Color based on values or value ranks

D) Download currently selected data as a CSV

E) Pan, Zoom, Select cells, and Save Plot as PNG

F) Plot area

Scatter Plot: Visualize Meta-Data/Genes

disease

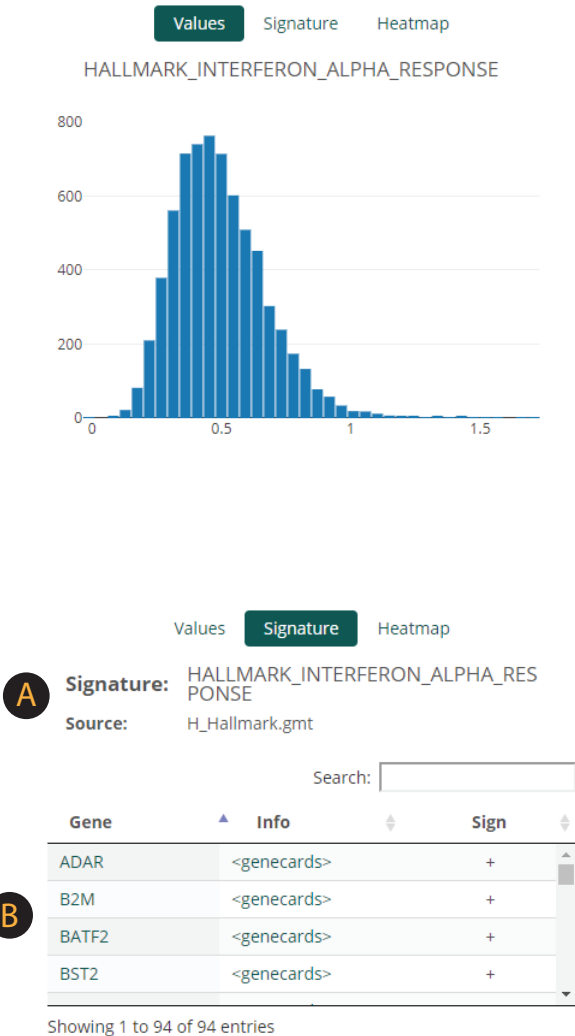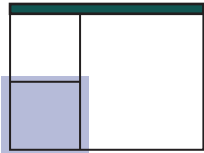Projection: [tSNE30 ▾]   [Export]
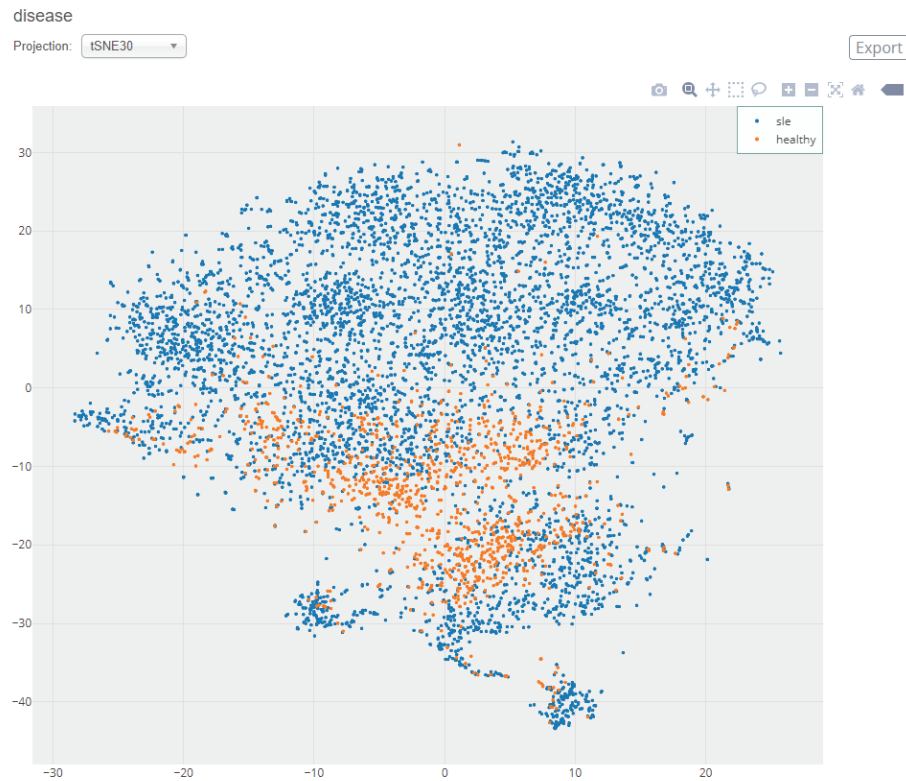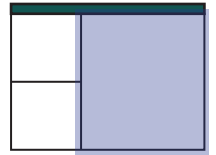
Meta-data may also be visualized

If the plotted variable is a discrete variable (such as cluster ID, stimulus, or disease state), the legend items can be clicked to select all cells within a group.

CD27

Projection: [tSNE30 ▾]   [Export]

Individual Gene Expression

Lower-Left Panel: Signature Info

The lower-left panel is used to display additional information about the currently plotted variable.

The "Values" tab shows a histogram of the value's distribution (here, signature scores) across the data set.

If the plotted item is a signature, the "Signature" tab shows additional information related to the signature.

A) Signature Name and Source (File Name)

B) Table of signature genes. Clicking gene symbol plots the selected gene. GeneCard links provided for convenience.


Additionally, if the plotted item is a signature, the heatmap tab visualizes gene expression within the signature genes.

A) Heatmap columns correspond with different values of the currently selected grouping variable (select in the upper-left panel)

B) Rows correspond to individual genes. Hover for gene name and z-score within the group. Clicking on a row plots the selected gene.
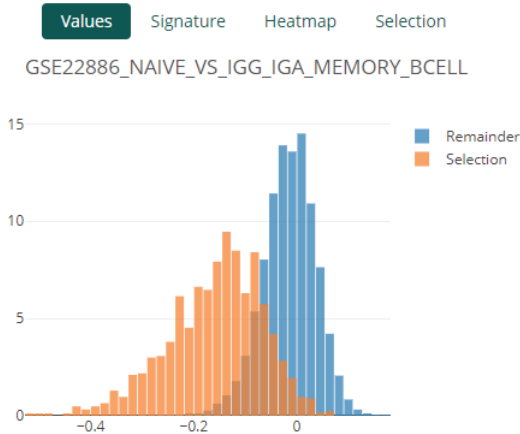
Lower-Left Panel: Selection Info
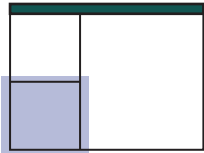
Clicking an individual cell in the scatter plot selects the cell. When a cell is selected, an extra tab is available in the lower-left panel with cell-specific info.

The cell ID as well as values for all cell-level meta-data are shown.

If a group of cells is selected, the "Values" tab shows the distribution of the selected cells in comparison to the rest of the cells.

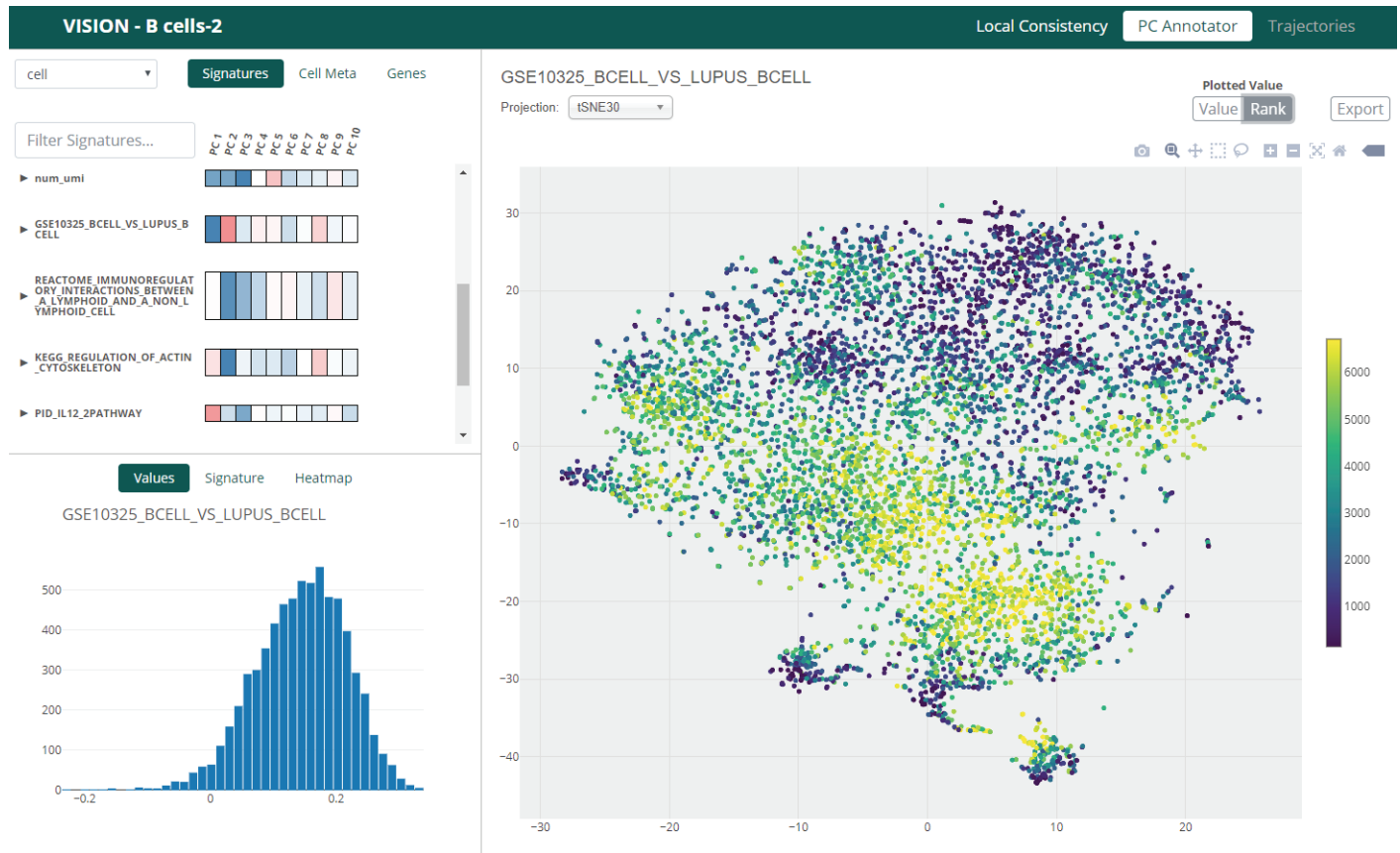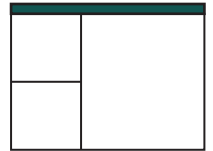Distributions are scaled within each group to sum to 100 (%)

Additionally, if a group of cells is selected, a "Selection" tab is available with meta-data information for the group.

For numerical meta-data, summary statistics are shown and for discrete meta-data, percentages within the group are listed.

Alternate View: PC Annotator

An alternate view is available by clicking "PC Annotator" in the top navigation bar.

In this view, signatures can be selected and sorted based on their correlation (Pearson's) with principal components of the latent space.

The upper-left panel colors (blue to red) are based on the Pearson's r (-1 to 1). Specific values are available by hovering over the cell and clicking the cell plots the signature.

Alternate View: Trajectories
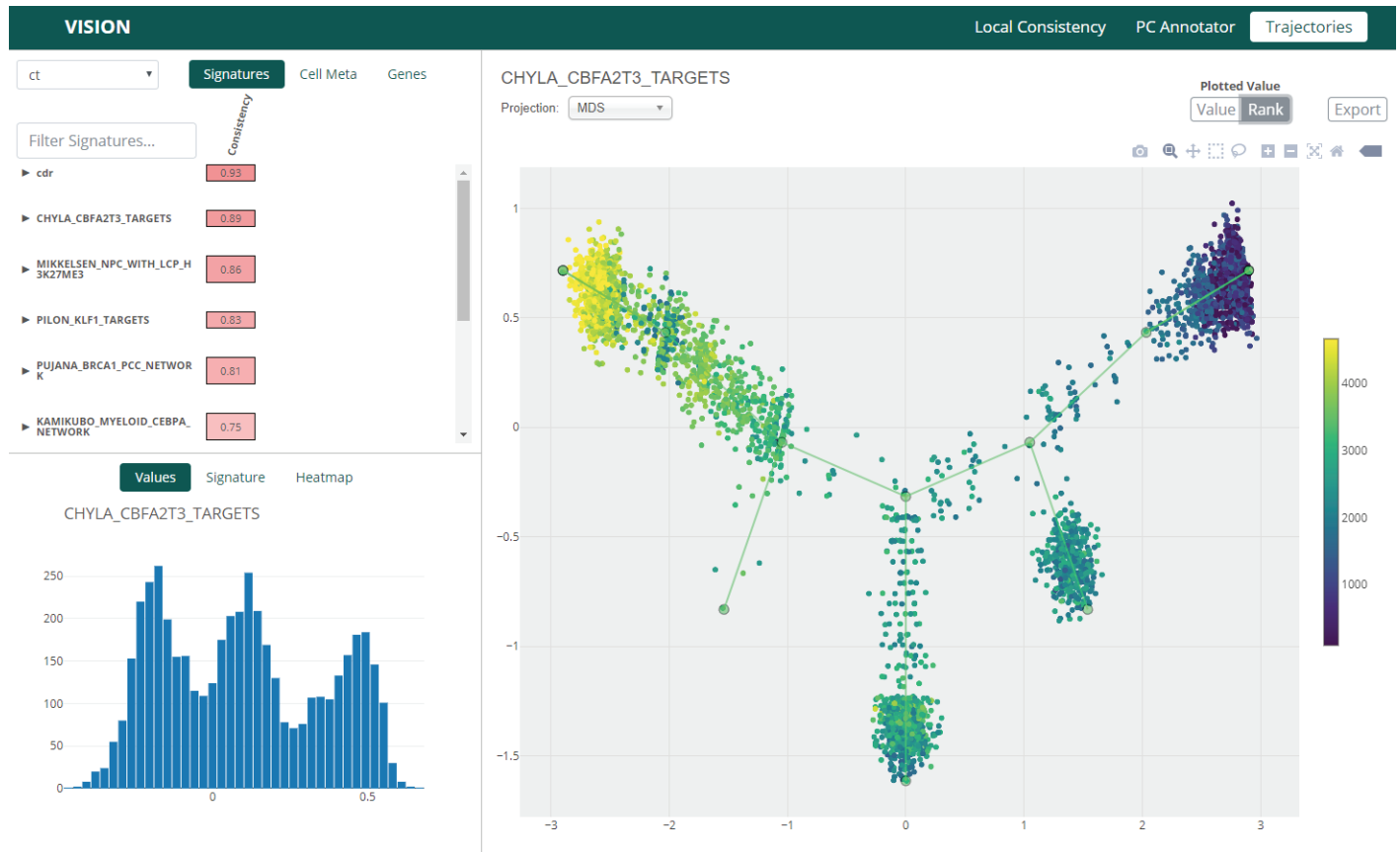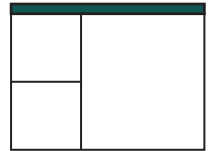
If a Trajectory model was supplied when creating the VISION object, the "Trajectory" view is available for selection in the top navigation bar.

In this view, instead of visualizing coordinates of 2d reductions of the latent space, the user can select between 2d reconstructions of the trajectory graph. Additionally, the graph itself is overlaid onto the plot.

Additionally, the shown signature local autocorrelation values in the upper-left are derived from a cell-cell KNN graph computed from the supplied trajectory model.