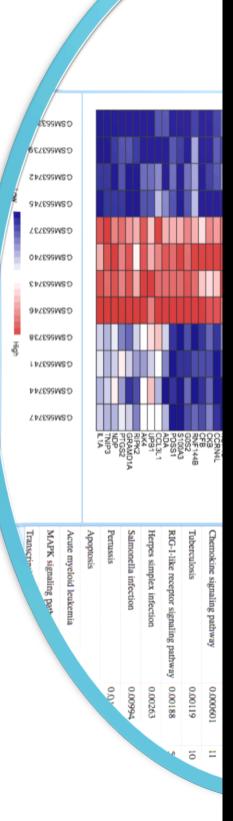
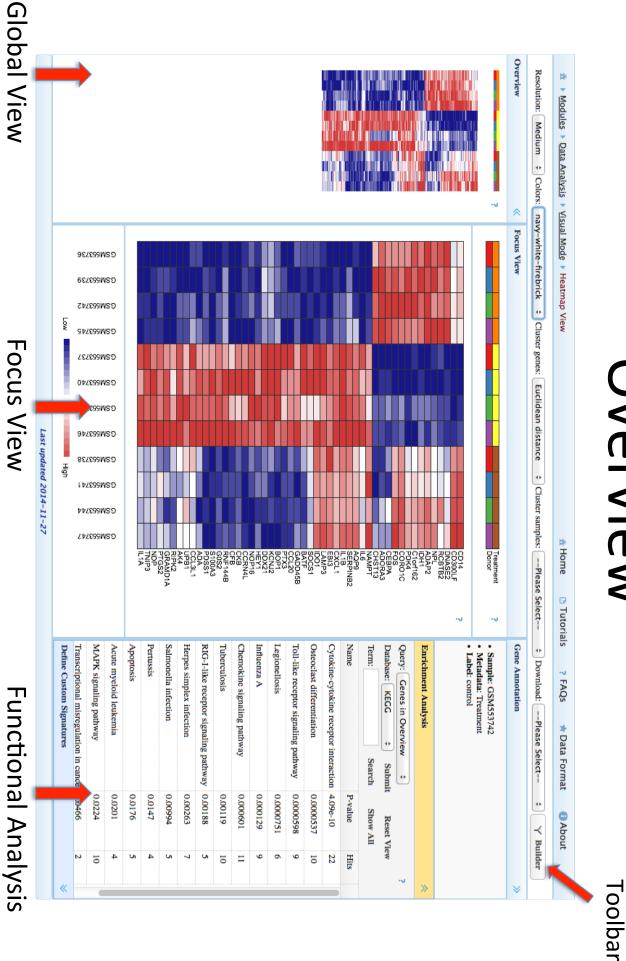


Visual Analytics with Heatmaps

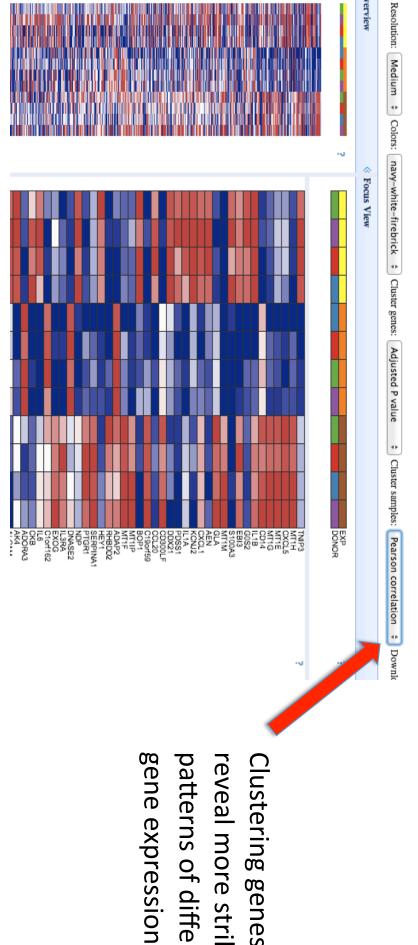


Overview





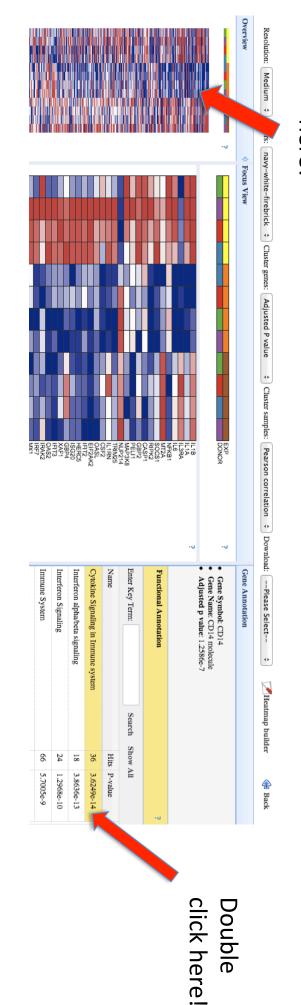
Explorer Mode: Cluster Genes



patterns of differential reveal more striking Clustering genes can

Explorer Mode: Focus View

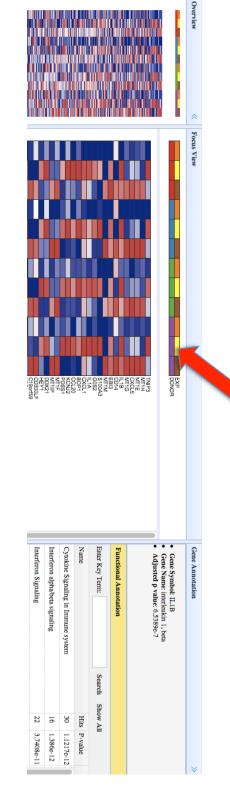
Drag-and-select here!



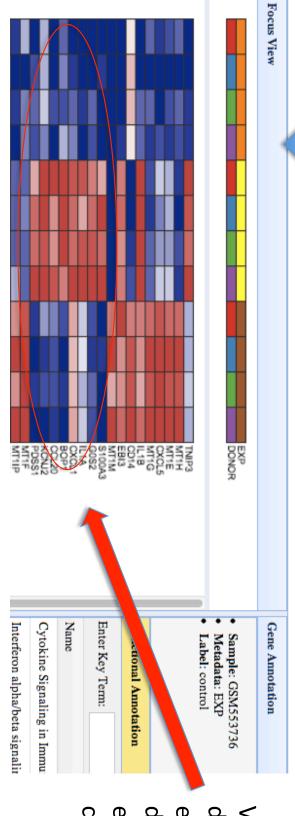
- Focus view shows current genes/metabolites of interest:
- Drag and select subsets of the global view to display in the focus VIew
- associated genes in the focus view Double click on a functional annotation name to display

Explorer Mode: Cluster Samples by Metadata

the samples by that metadata Click anywhere on the metadata row to order

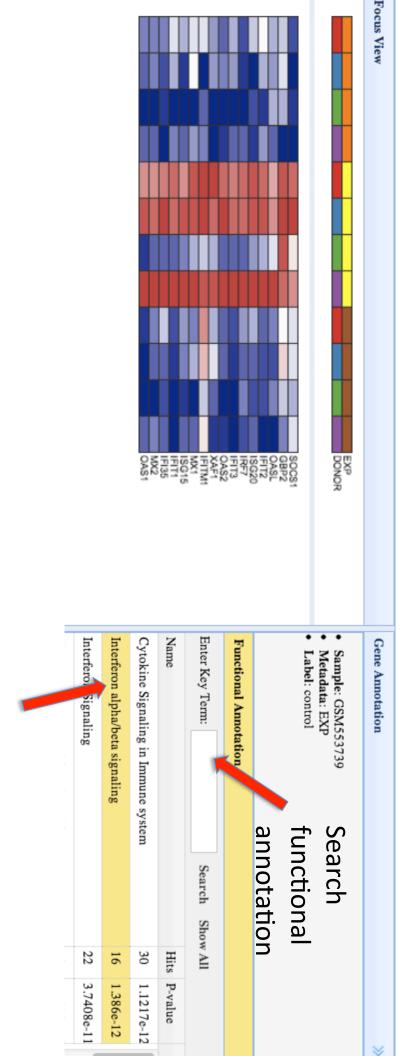


Experimental conditions (EXP) are ordered alphabetically



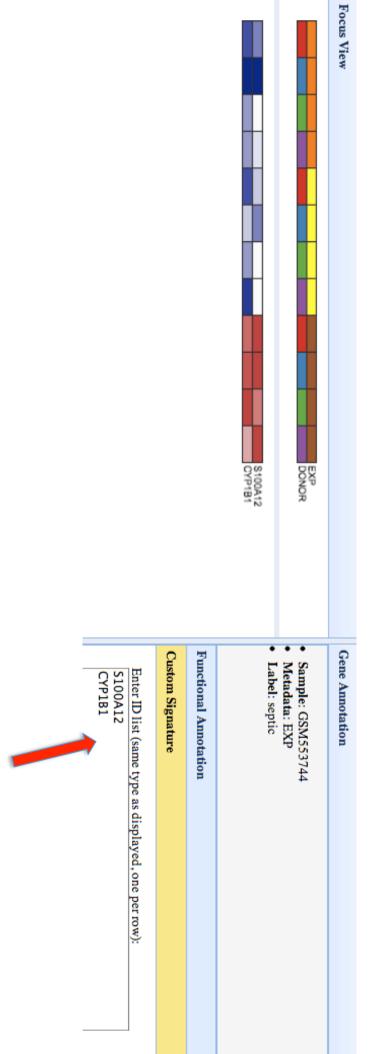
Visualize the differential gene expression between different experimental conditions

Explorer Mode: Visualize Predefined Functional Groups



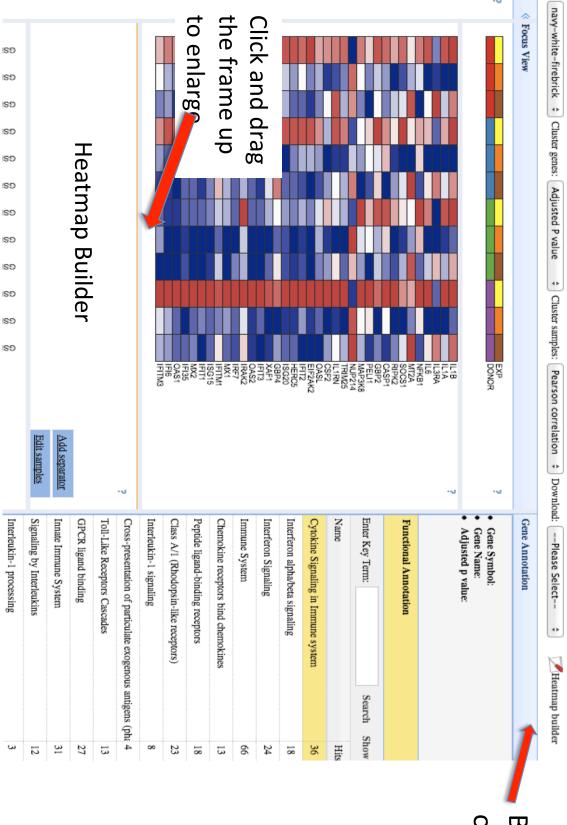
Double click to view differential expression of 16 genes associated with interferon alpha and beta signaling

Explorer Mode: Visualize a Custom Molecular Signature



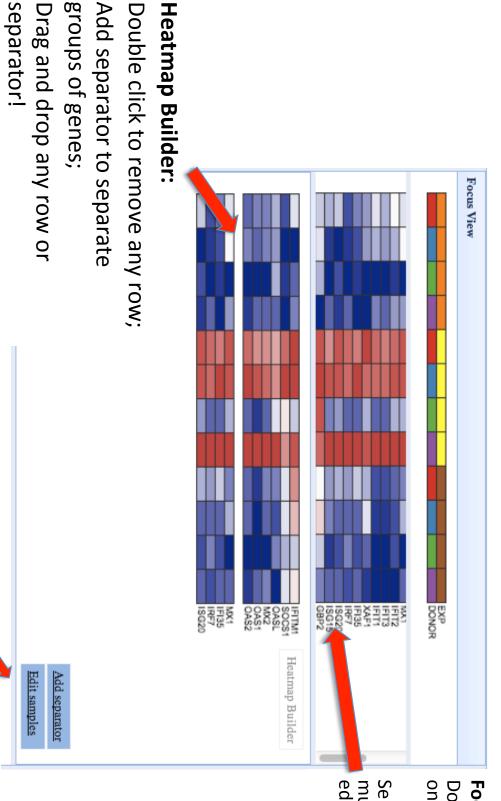
If you know which genes you are interested in, enter one or more in a list to display in the Focus View

Heatmap Builder



Build your own heatmap!

Build a Custom Heatmap



Focus View

on to add to editor Double click on any row

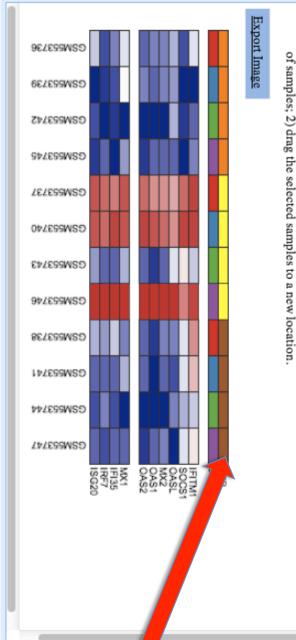
editor multiple rows to add to Select and drag to add

interest are selected and grouped, then click "Edit samples". If you want to edit samples, first make sure all genes of separator!

Edit Samples



- Remove a single sample: double clicking on the corresponding column;
- Rearrange a single sample: on the expression heatmap, drag-and-drop the sample to a specific location;
- Rearrange a batch of samples in two steps: 1) on the metadata heatmap, drag-and-select a consecutive list

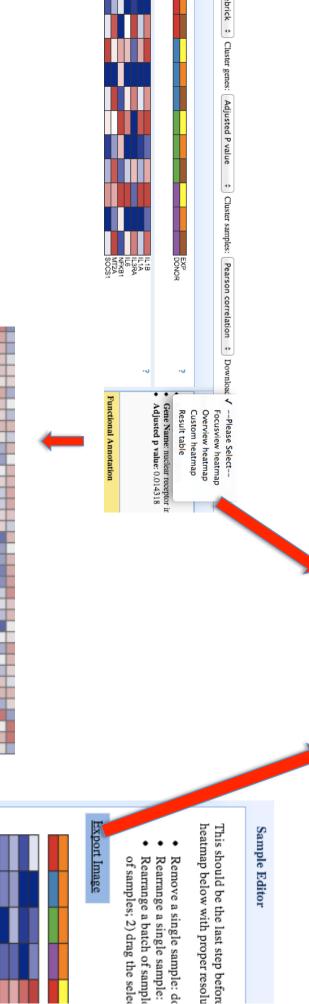


Final step before image export

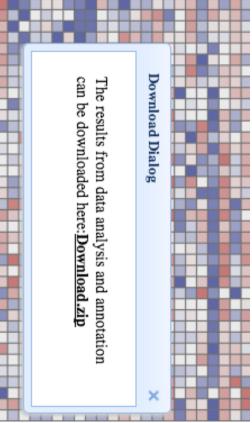
- Double click sample column to remove
- Drag and drop one or more samples to rearrange

Getting Images and Results

Many options for image export



Download result table as a zip file (significant genes and enriched functional groups)



GSM563736

GSW22333

GSW663742

GSM563745

=== END ===