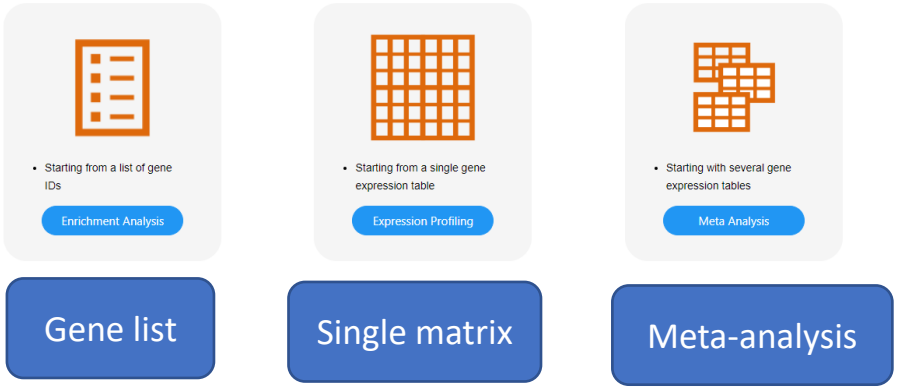
ExpressAnalyst - Tutorial
Starting from a list

-- Comprehensive platform for gene expression and meta-analysis

Intro to ExpressAnalyst

- Web platform for the analysis of gene expression data and meta-analysis
  - Previously part of NetworkAnalyst
- Designed for bench researchers rather than specialized bioinformaticians
- Integrates data processing, statistical analysis and data visualization to support:
  - Data comparisons
  - Biological interpretation
  - Hypothesis generation



Computer and browser requirements

- A modern web browser with JavaScript enabled
- Supported browsers include Chrome, Safari, Firefox, and Internet Explorer 9+
- For best performance and visualization, use:
    - Latest version of Google Chrome
    - A computer with at least 4GB of physical RAM
    - A 15-inch screen or bigger (larger is better)
- Browser must be WebGL enabled for 3D scatter visualization
- 50MB limit for data upload
    - ~300 samples for gene expression data with 20 000 genes

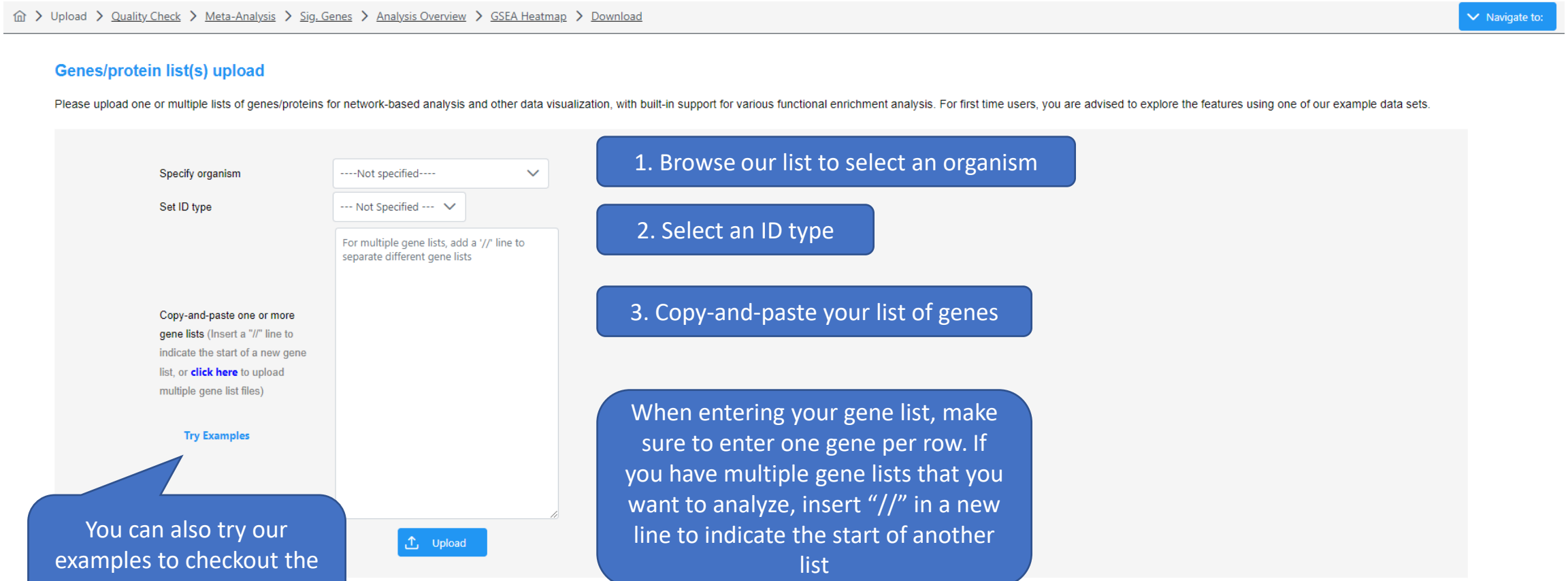
Goals for this tutorial

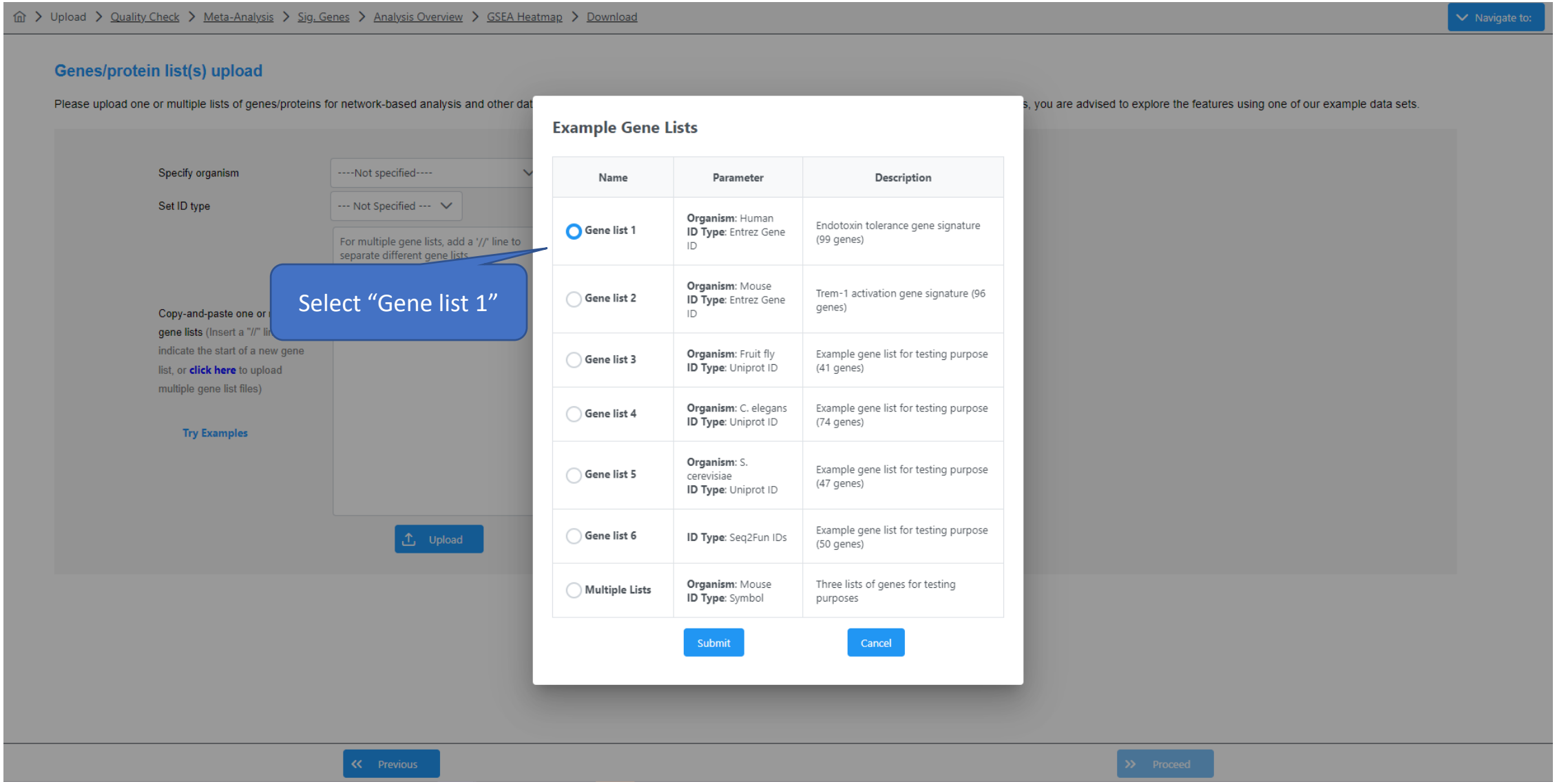
- Differential Expression (DE) analysis is the cornerstone of transcriptomics data analysis.

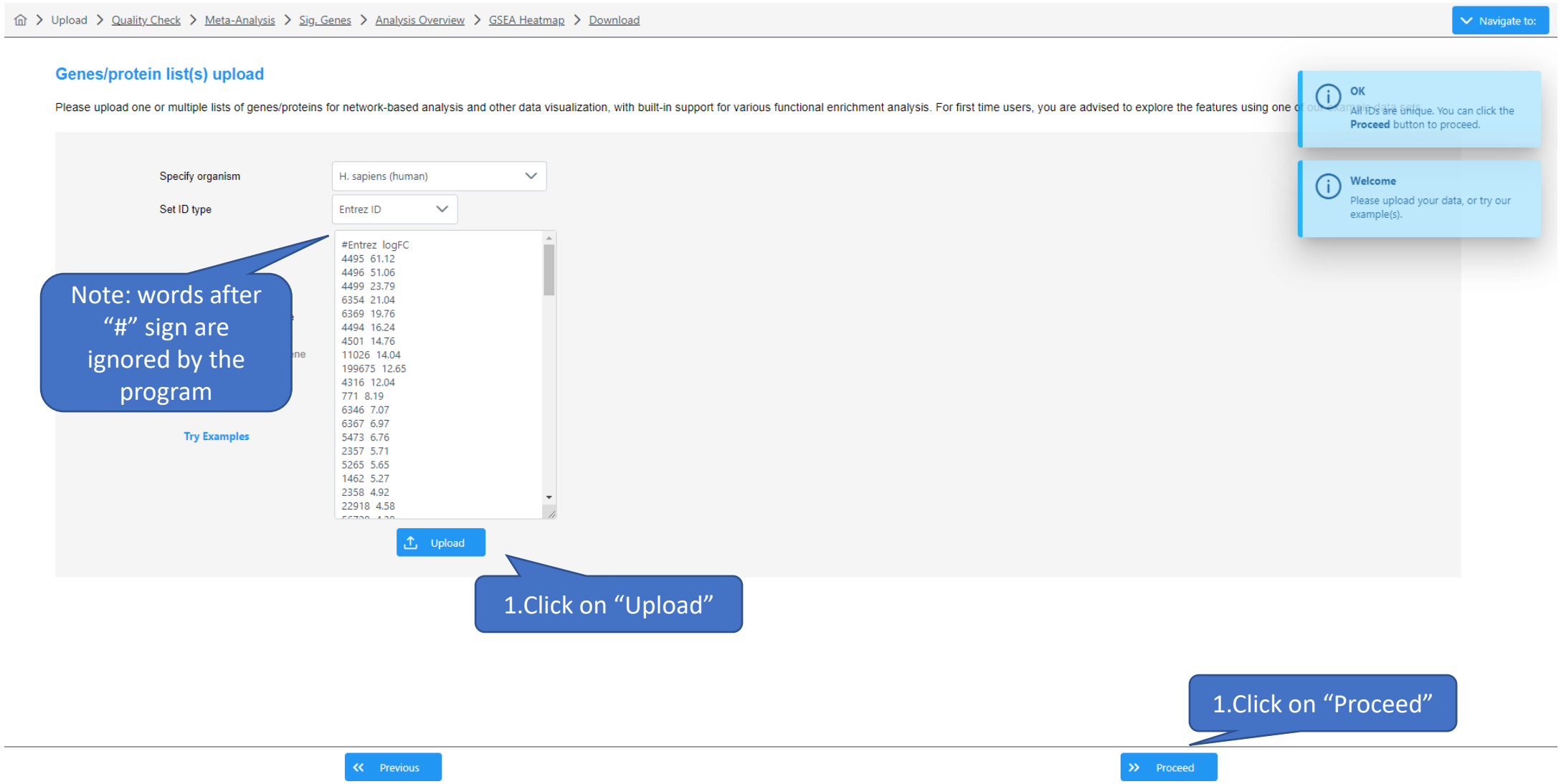
- Functional interpretation of the resulting DE genes is a key challenge.
  - There is also a lack of tools supporting the analysis of multiple gene lists (gene list meta-analysis)

- ExpressAnalyst introduces several visual analytics techniques to facilitate functional interpretation of DE genes and the analysis of multiple gene lists.

Data upload

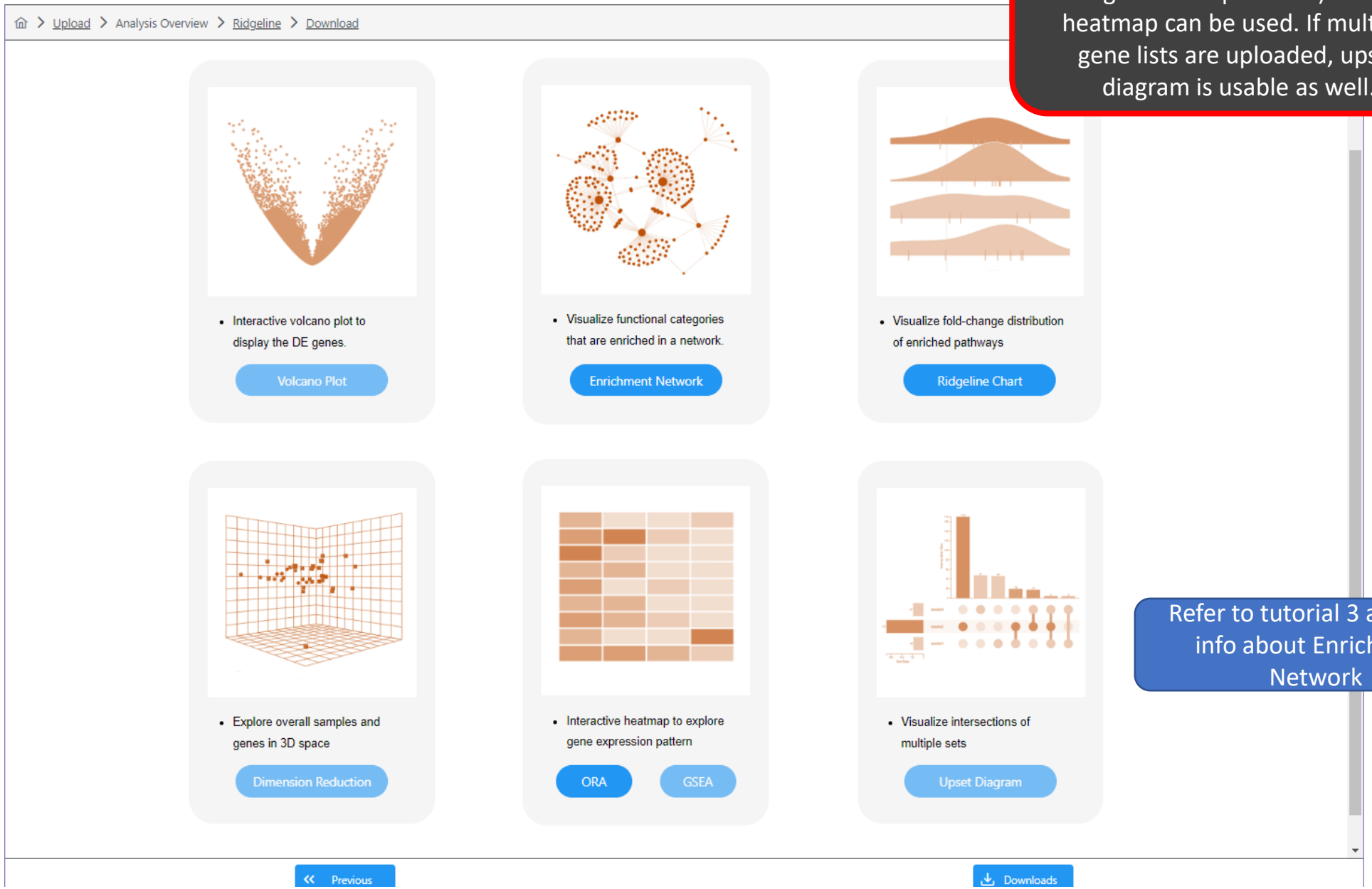

Upload
Quality Check
Meta-Analysis
Sig. Genes
Analysis Overview
GSEA Heatmap
Download
Navigate to:
Genes/protein list(s) upload
Please upload one or multiple lists of genes/proteins for network-based analysis and other data visualization, with built-in support for various functional enrichment analysis. For first time users, you are advised to explore the features using one of our example data sets.
Specify organism
----Not specified----
Set ID type
--- Not Specified ---
For multiple gene lists, add a '//' line to separate different gene lists
Copy-and-paste one or more gene lists (Insert a "//" line to indicate the start of a new gene list, or click here to upload multiple gene list files)
Try Examples
Upload
1. Browse our list to select an organism
2. Select an ID type
3. Copy-and-paste your list of genes
When entering your gene list, make sure to enter one gene per row. If you have multiple gene lists that you want to analyze, insert "//" in a new line to indicate the start of another list
You can also try our examples to checkout the features and have an idea of the data format
Previous
Proceed


Upload > Quality Check > Meta-Analysis > Sig. Genes > Analysis Overview > GSEA Heatmap > Download
Navigate to:
Genes/protein list(s) upload
Please upload one or multiple lists of genes/proteins for network-based analysis and other dat
s, you are advised to explore the features using one of our example data sets.
Specify organism
----Not specified----
Set ID type
--- Not Specified ---
For multiple gene lists, add a '//' line to separate different gene lists
Copy-and-paste one or
gene lists (Insert a "//" li
indicate the start of a new gene list, or click here to upload multiple gene list files)
Try Examples
Upload
Select “Gene list 1”
Example Gene Lists
Name
Parameter
Description
Gene list 1
Organism: Human
ID Type: Entrez Gene ID
Endotoxin tolerance gene signature (99 genes)
Gene list 2
Organism: Mouse
ID Type: Entrez Gene ID
Trem-1 activation gene signature (96 genes)
Gene list 3
Organism: Fruit fly
ID Type: Uniprot ID
Example gene list for testing purpose (41 genes)
Gene list 4
Organism: C. elegans
ID Type: Uniprot ID
Example gene list for testing purpose (74 genes)
Gene list 5
Organism: S. cerevisiae
ID Type: Uniprot ID
Example gene list for testing purpose (47 genes)
Gene list 6
ID Type: Seq2Fun IDs
Example gene list for testing purpose (50 genes)
Multiple Lists
Organism: Mouse
ID Type: Symbol
Three lists of genes for testing purposes
Submit
Cancel
Previous
Proceed


Upload > Quality Check > Meta-Analysis > Sig. Genes > Analysis Overview > GSEA Heatmap > Download
Navigate to:
Genes/protein list(s) upload
Please upload one or multiple lists of genes/proteins for network-based analysis and other data visualization, with built-in support for various functional enrichment analysis. For first time users, you are advised to explore the features using one
OK
All IDs are unique. You can click the Proceed button to proceed.
Welcome
Please upload your data, or try our example(s).
Specify organism
H. sapiens (human)
Set ID type
Entrez ID
#Entrez logFC
4495 61.12
4496 51.06
4499 23.79
6354 21.04
6369 19.76
4494 16.24
4501 14.76
11026 14.04
199675 12.65
4316 12.04
771 8.19
6346 7.07
6367 6.97
5473 6.76
2357 5.71
5265 5.65
1462 5.27
2358 4.92
22918 4.58
Try Examples
Upload
Note: words after "#" sign are ignored by the program
1.Click on "Upload"
1.Click on "Proceed"
Previous
Proceed

Visual analytics

For gene list input, only enrichment network, ridgeline chart (if fold change value is provided) and ORA heatmap can be used. If multiple gene lists are uploaded, upset diagram is usable as well.



Refer to tutorial 3 and 4 for info about Enrichment Network

Ridgeline diagram

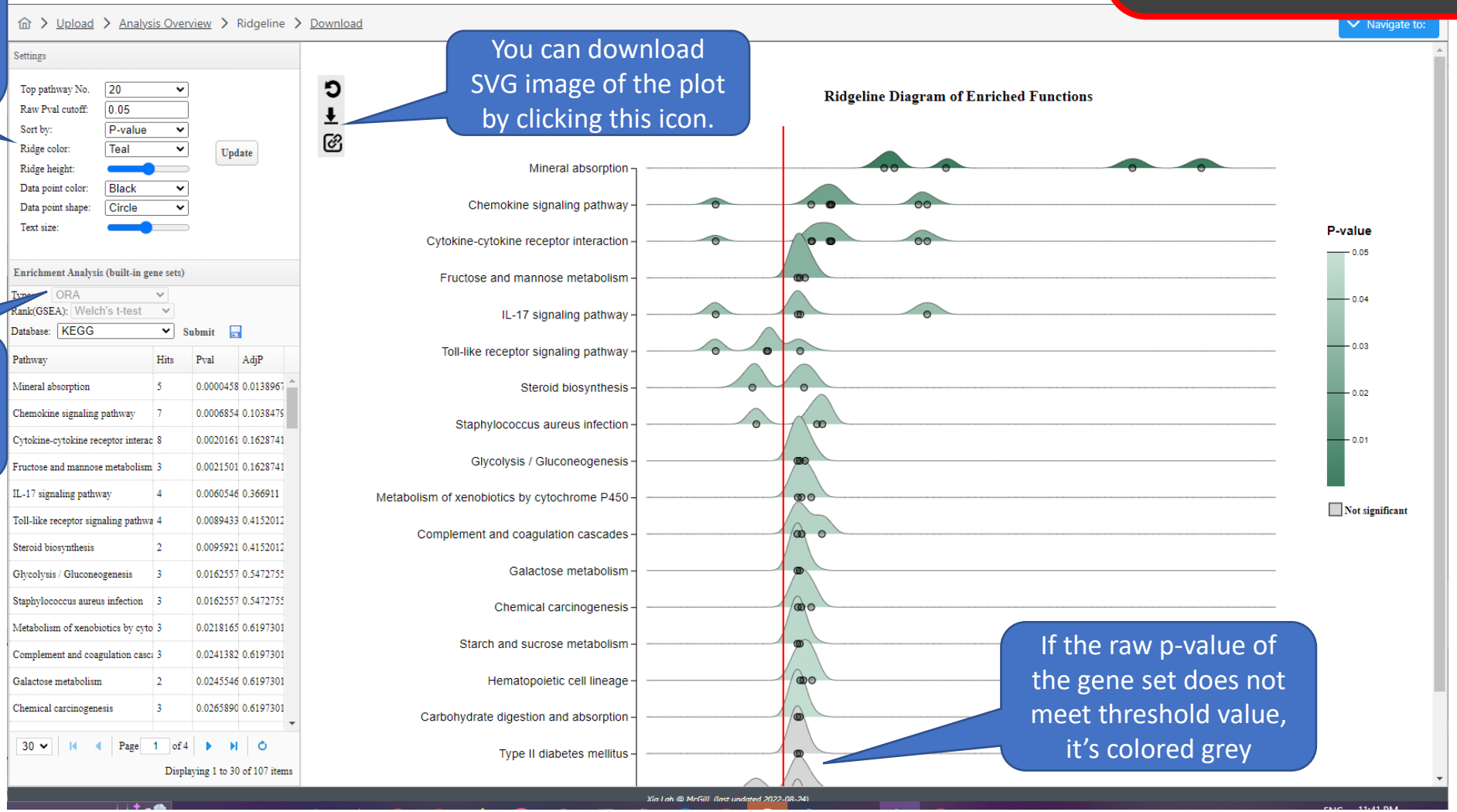
This analysis option is only available if fold change is provided in the gene list. It is useful for visualizing the overall fold-change distribution of the members of gene sets of interest.

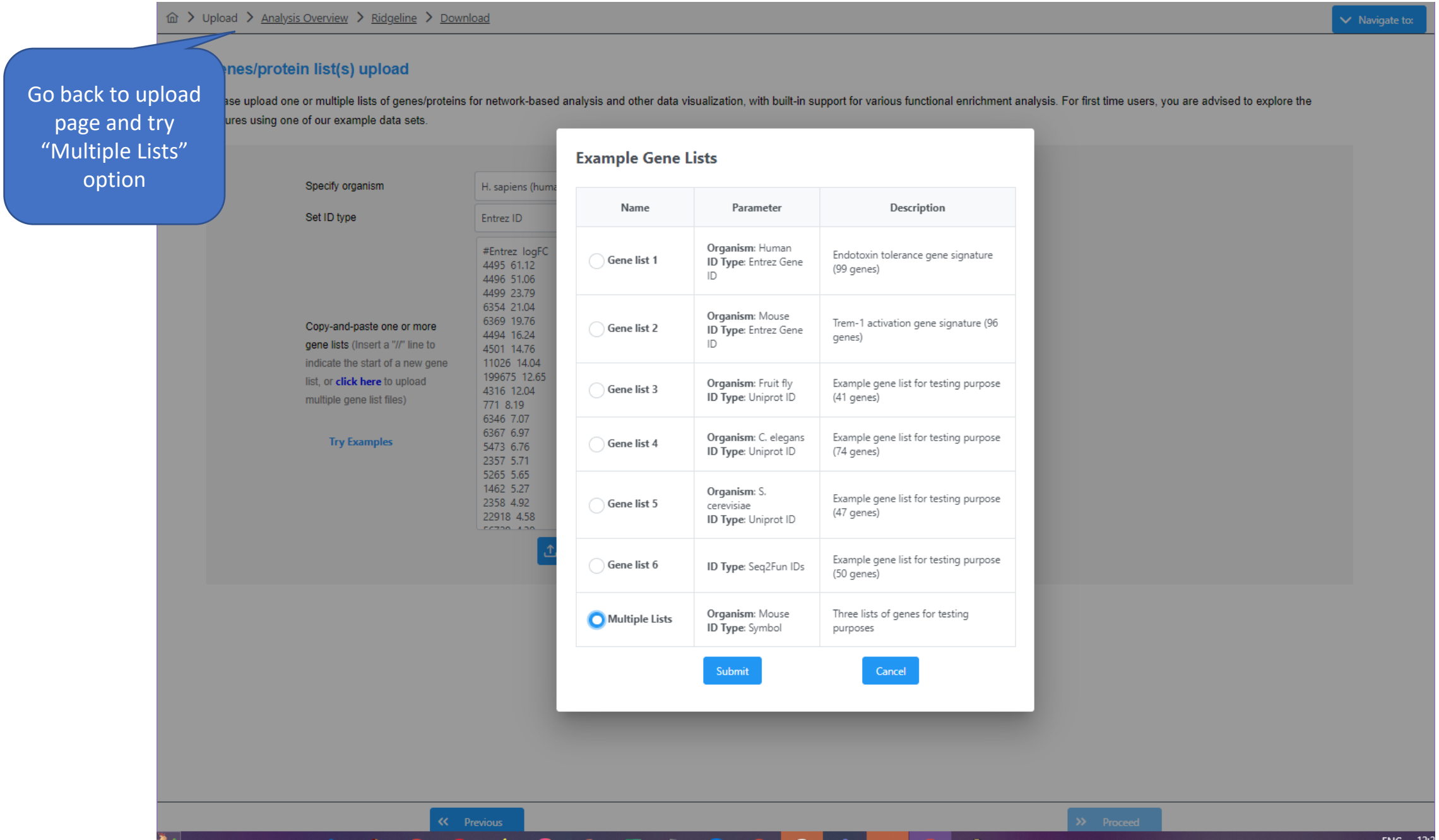
Settings panel is used to adjust ridgeline plot style and number of pathways disaplayed

GSEA option is only available when whole matrix is provided

You can download SVG image of the plot by clicking this icon.

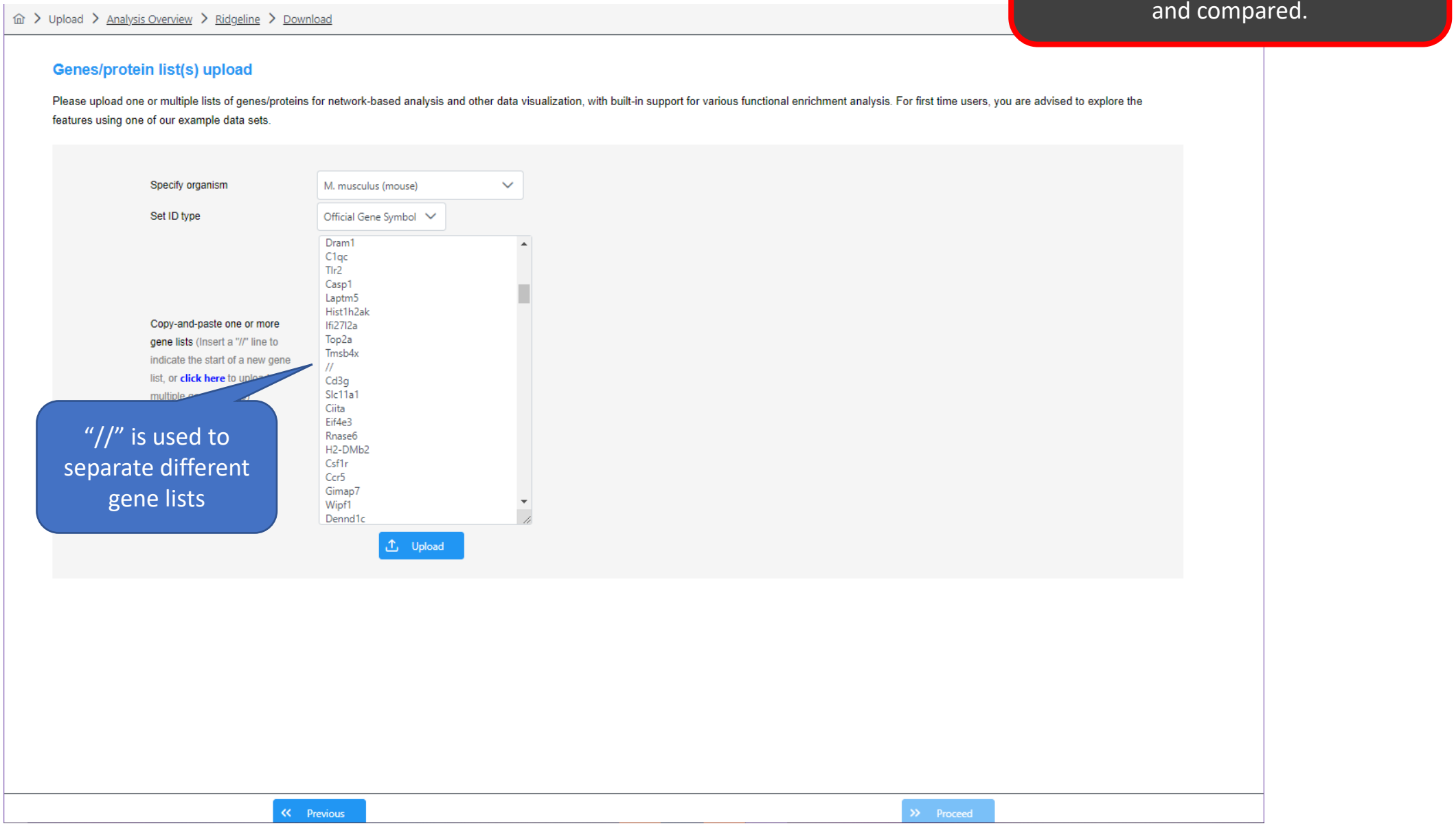
If the raw p-value of the gene set does not meet threshold value, it's colored grey





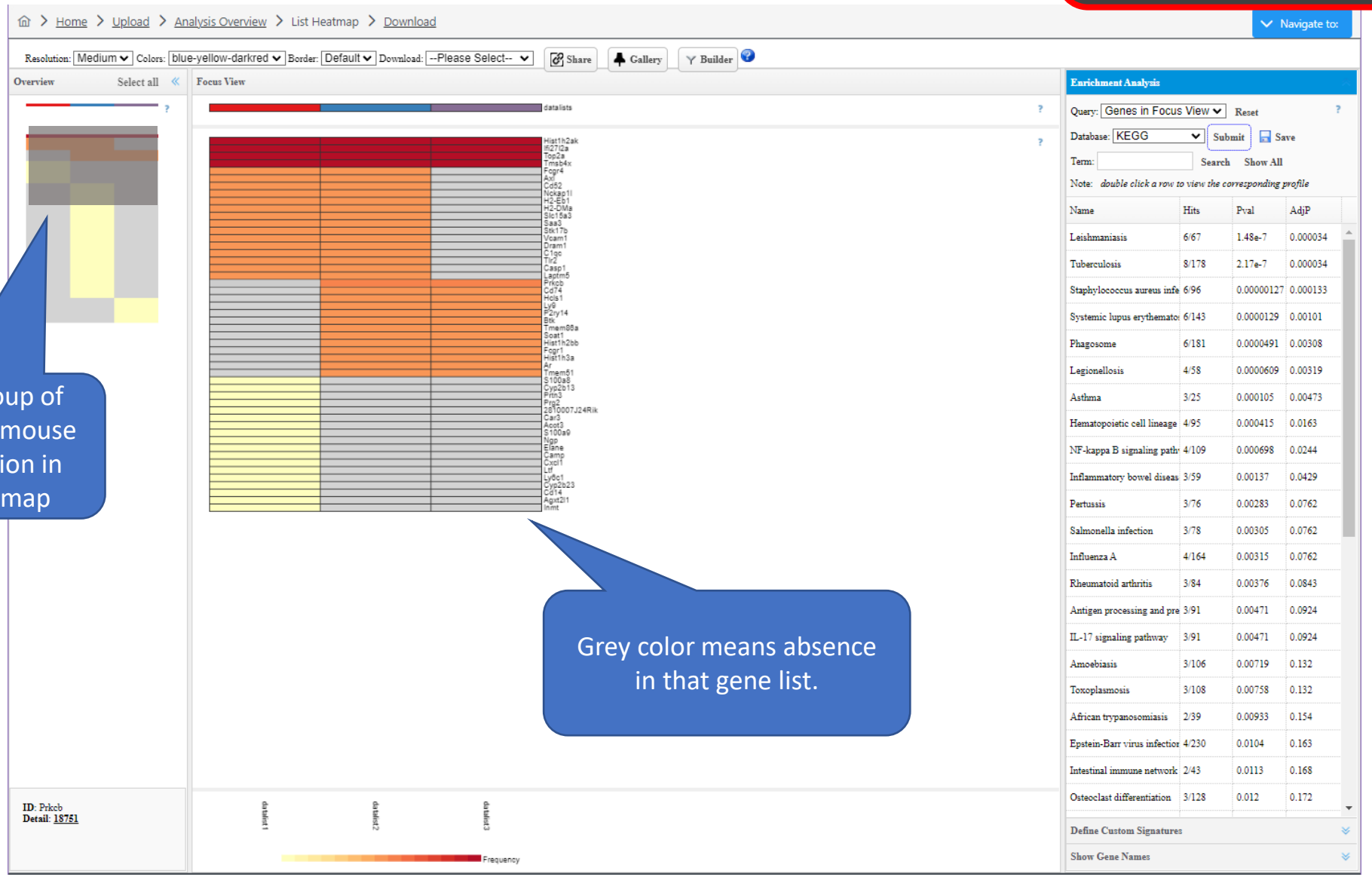
Go back to upload page and try “Multiple Lists” option

Multiple gene lists analysis is a type of meta-analysis where the DE genes of individual studies are integrated and compared.



ORA Heatmap

ORA heatmap is useful to visualize shared/unique genes across different datasets and perform enrichment analysis

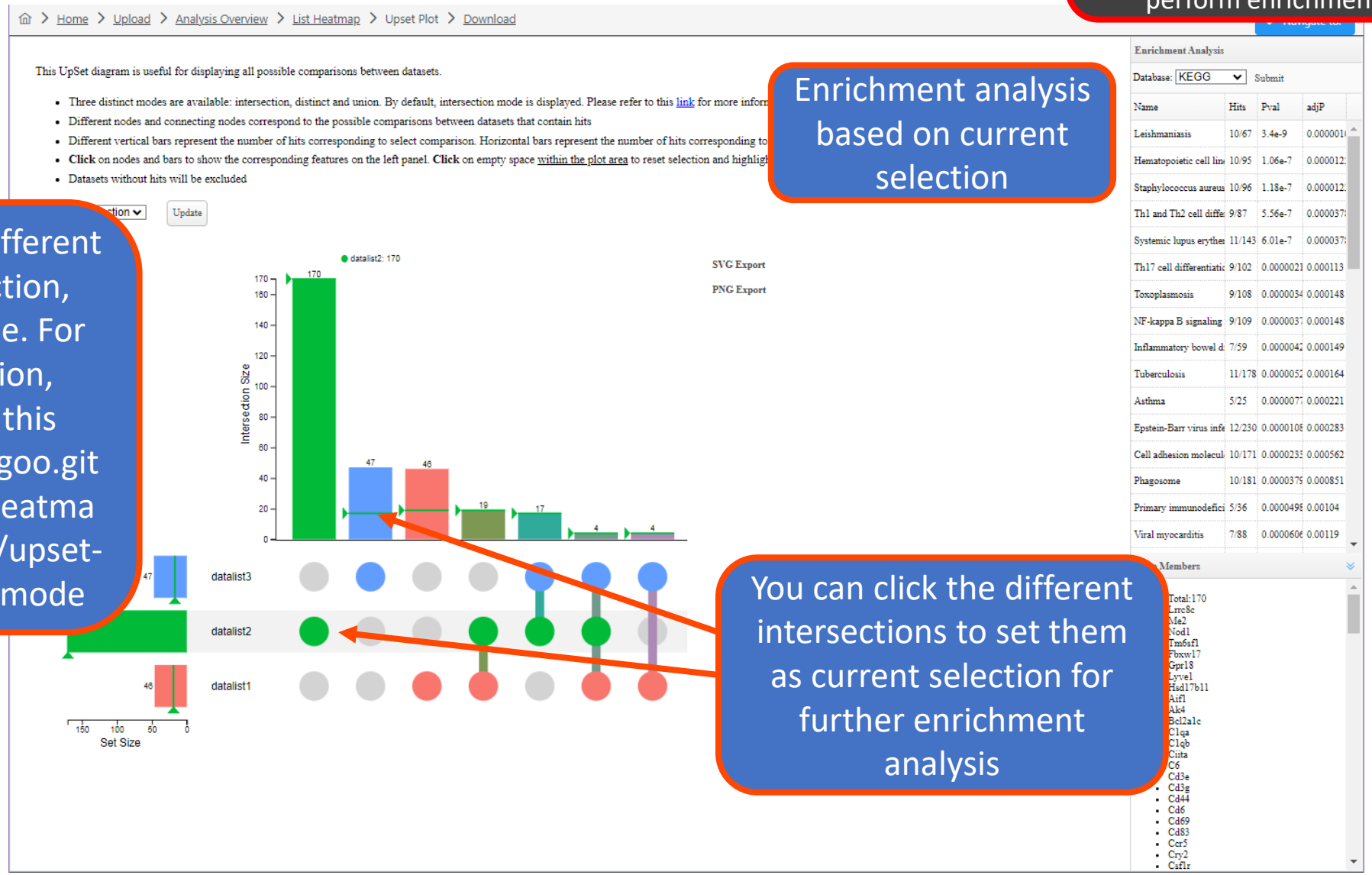


You can select a group of genes by using your mouse to drag select a region in the overview heatmap

Grey color means absence in that gene list.

Upset Diagram

Upset diagram is an alternative to venn diagram and our heatmap viewer, to visualize shared/unique genes across different datasets and perform enrichment analysis



There are three different modes: Intersection, Union and Unique. For more information, please refer to this link: https://jokergoo.github.io/ComplexHeatmap-reference/book/upset-plot.html#upset-mode

Enrichment analysis based on current selection

You can click the different intersections to set them as current selection for further enrichment analysis

The End

For more information, visit Tutorials, Resources

and Contact pages on www.expressanalyst.ca

Also visit our forum for FAQs on www.omicsforum.ca