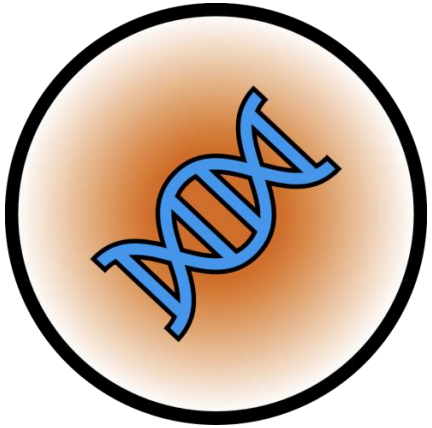
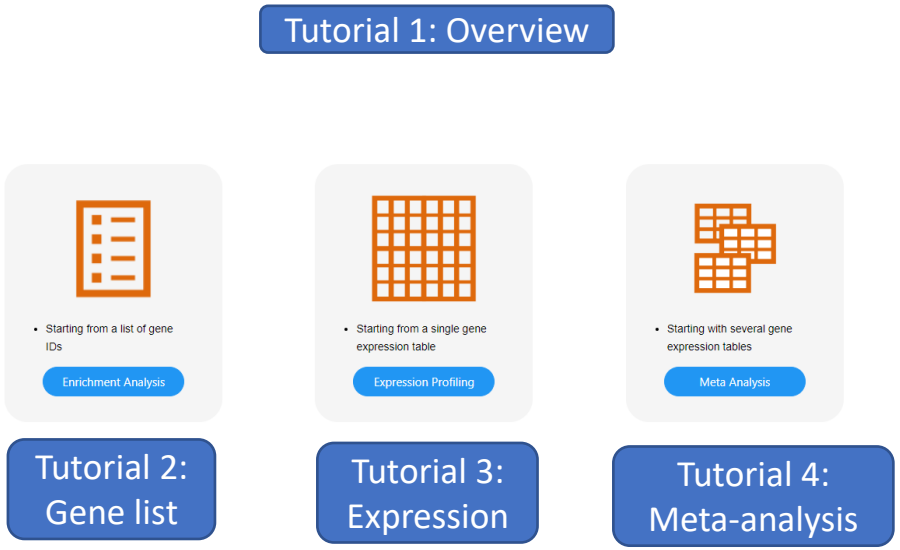
ExpressAnalyst: Tutorial 1 Overview

-- 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

NetworkAnalyst vs ExpressAnalyst

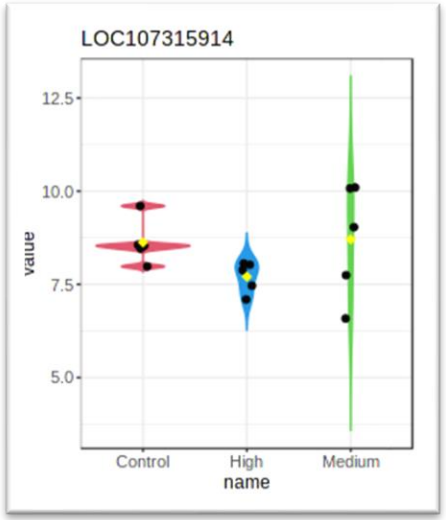
- Previous NetworkAnalyst platform has been divided into two distinct web tools.

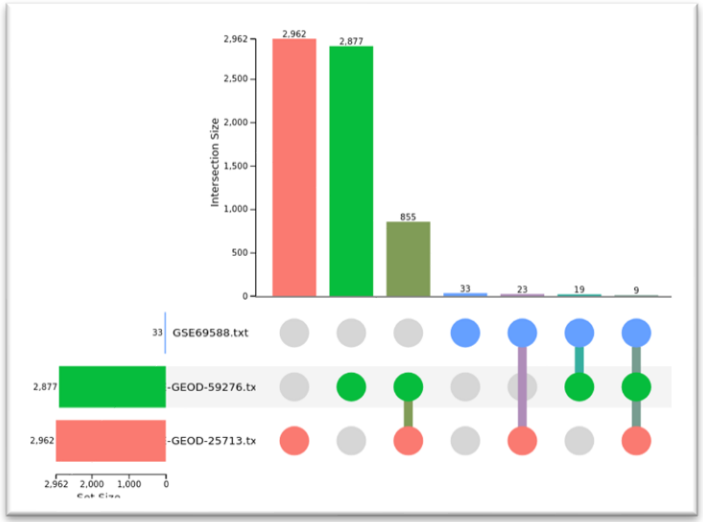
1. NetworkAnalyst is now dedicated to knowledge-driven network analysis using gene list as input.

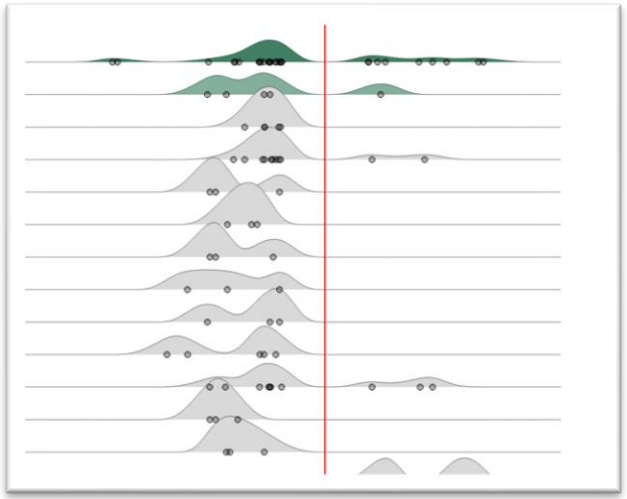
2. ExpressAnalyst focuses on gene expression profiling and meta-analysis.

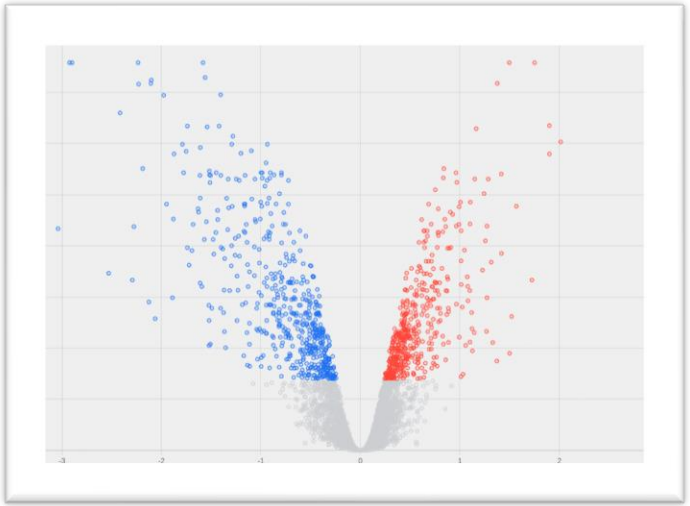
What's new?

- Ridgeline diagram to assess gene expression levels of enriched pathways
- UpSet diagram to visualize intersections of multiple datasets
- Revamped volcano plot, heatmap and 3D scatter plot visualization
- New interface





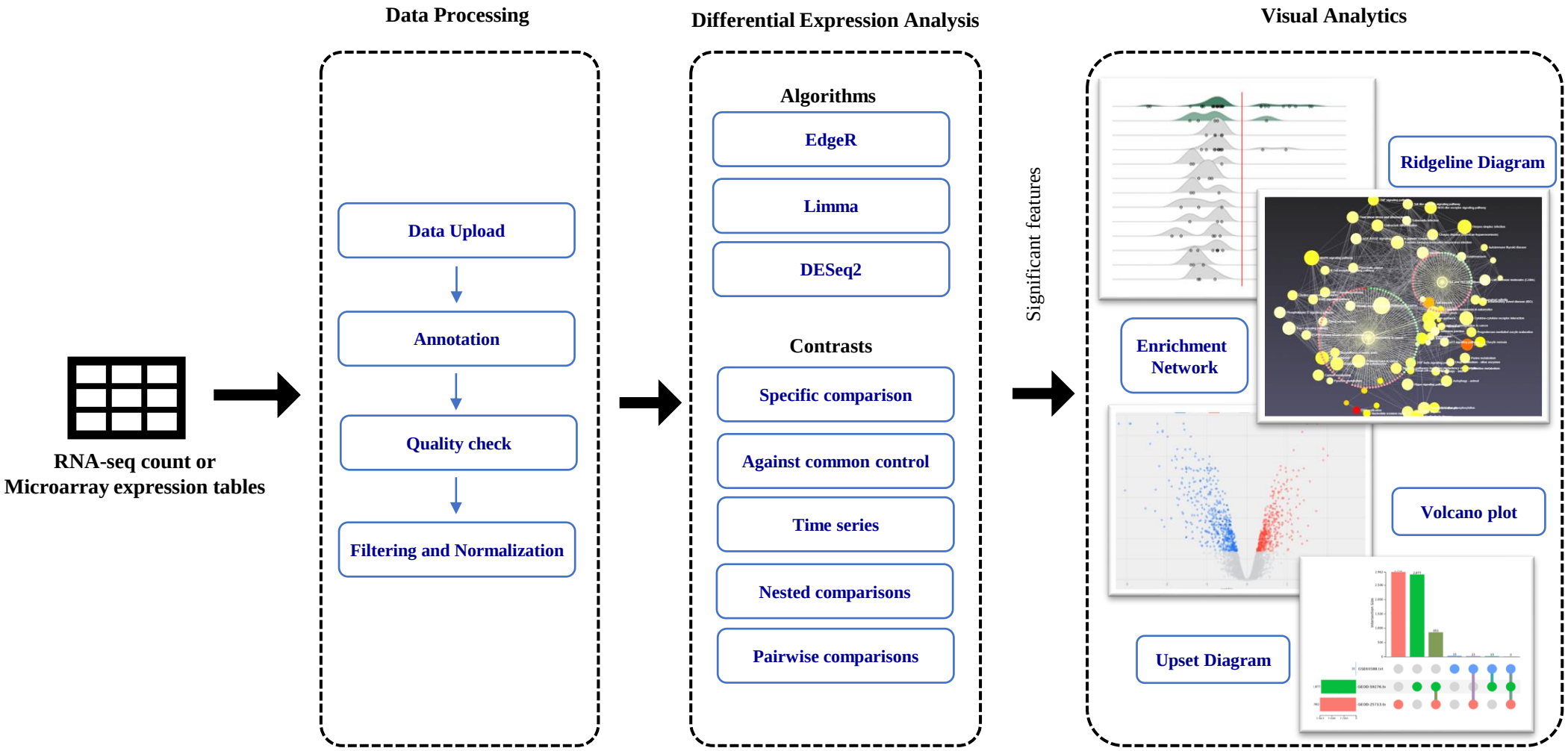




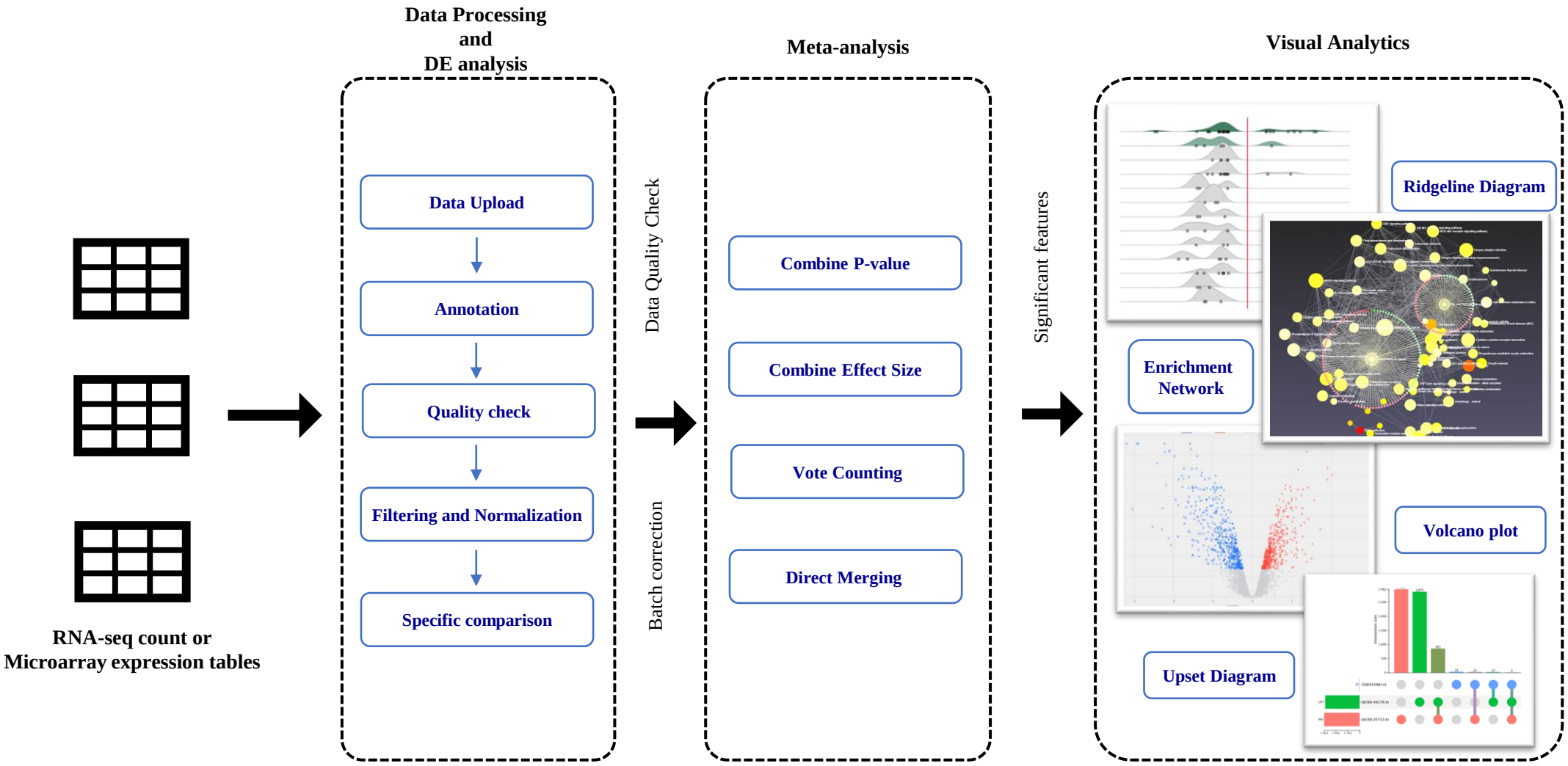
Overview

- Goal: To provide an integrative web-based framework for data processing, functional analysis and visualization of various forms of gene expression data.
  - Gene list(s)
  - Gene expression data matrix
  - Multiple gene expression data sets
- Overall approaches:
  - Advanced statistical methods coupled with interactive data visualization system.
- 50MB limit for data upload
  - ~300 samples for gene expression data with 20 000 genes

Gene expression workflow



Meta-analysis workflow



Functional profiling

- Overrepresentation analysis (ORA)
- Cut-off free functional enrichment analysis methods
  - Gene Set Enrichment Analysis (GSEA)
- Interactive volcano plot
- Advanced diagnostic plots for quality check purposes
- Dimension reduction: 3D PCA
- Intersection analysis (for multiple datasets)

Raw data processing using EcoOmicsAnalyst

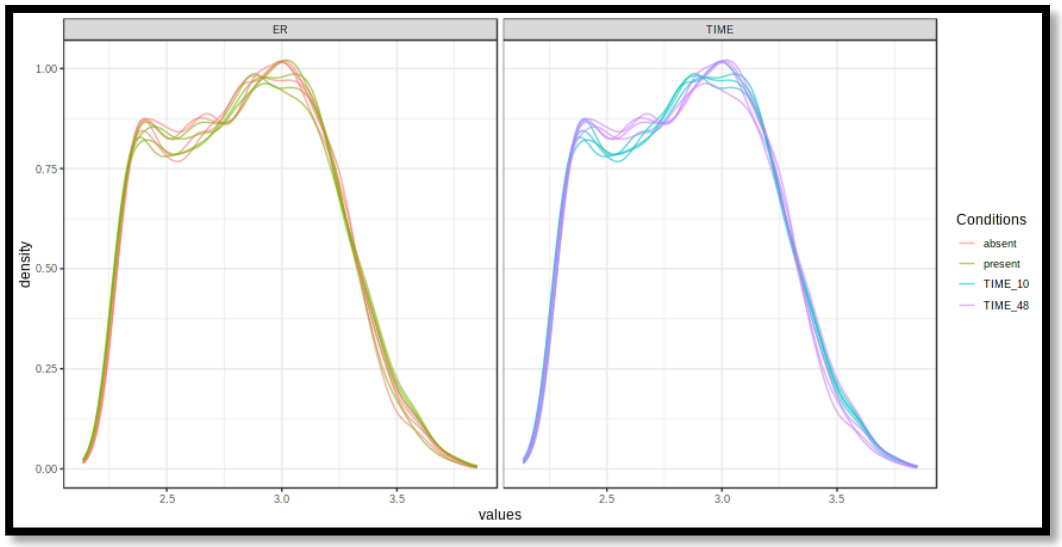
- ExpressAnalyst is dedicated for secondary and tertiary transcriptomics data analysis.

- For raw data processing please consider using EcoOmicsAnalyst.

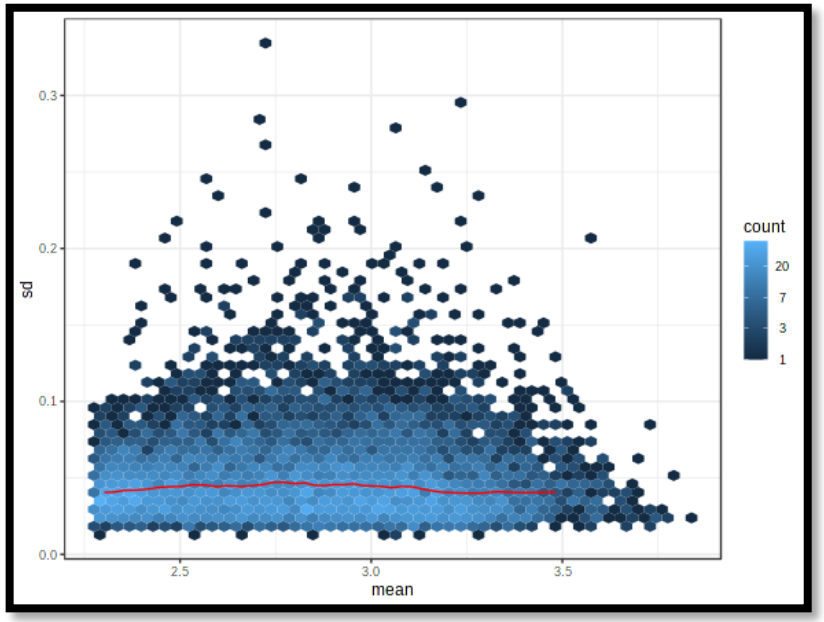
- Its objective is the conversion of RNAseq reads from **ANY** species to functionally annotated count tables (especially useful for non-model species)

Diagnostic plots

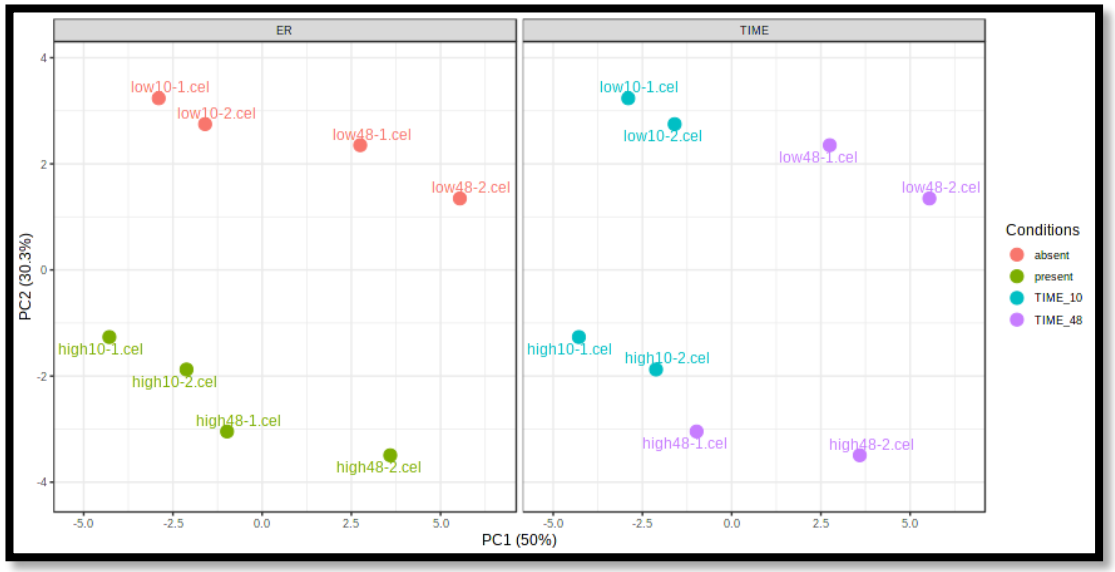
Density plot



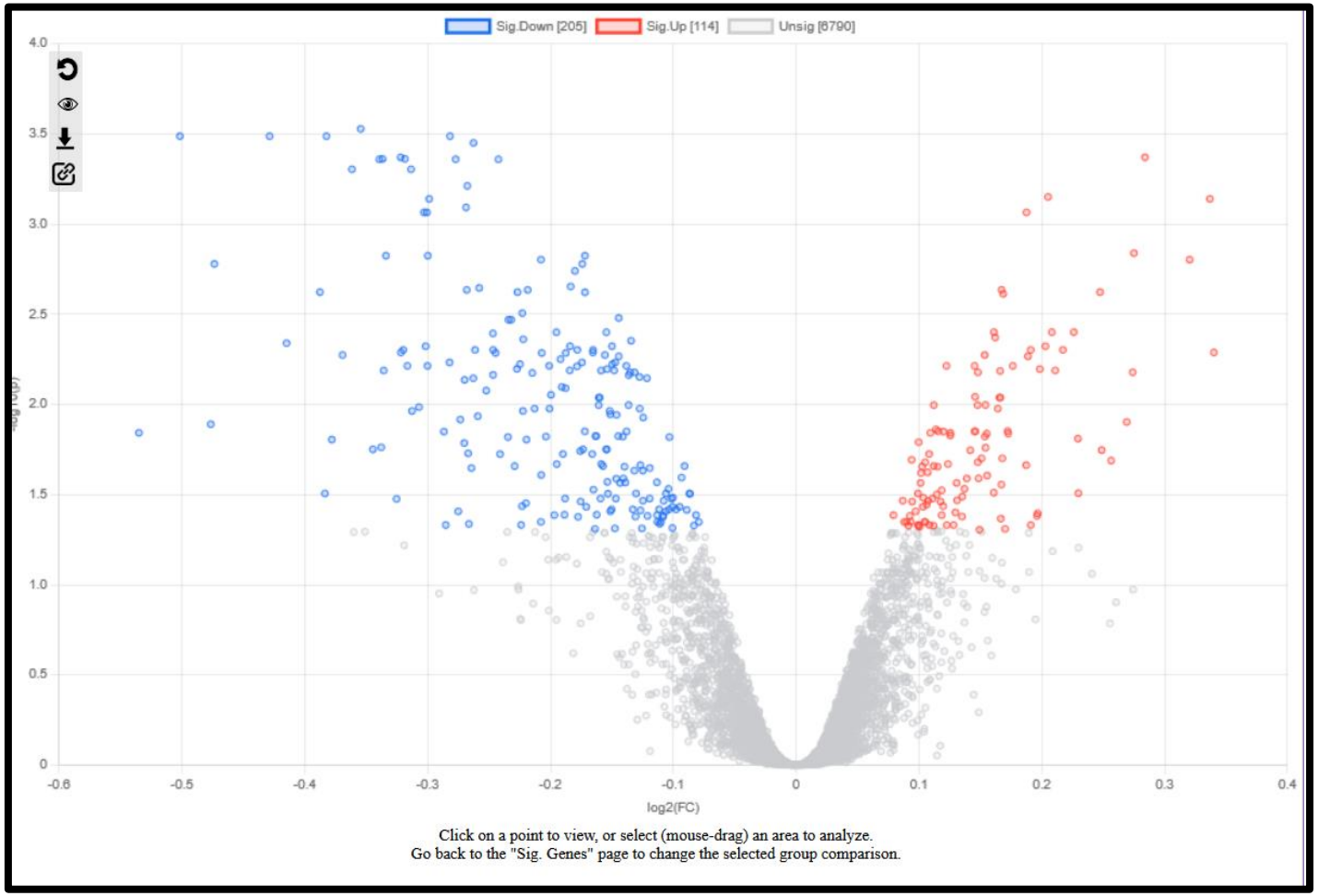
Mean Standard Deviation (MSD) plot



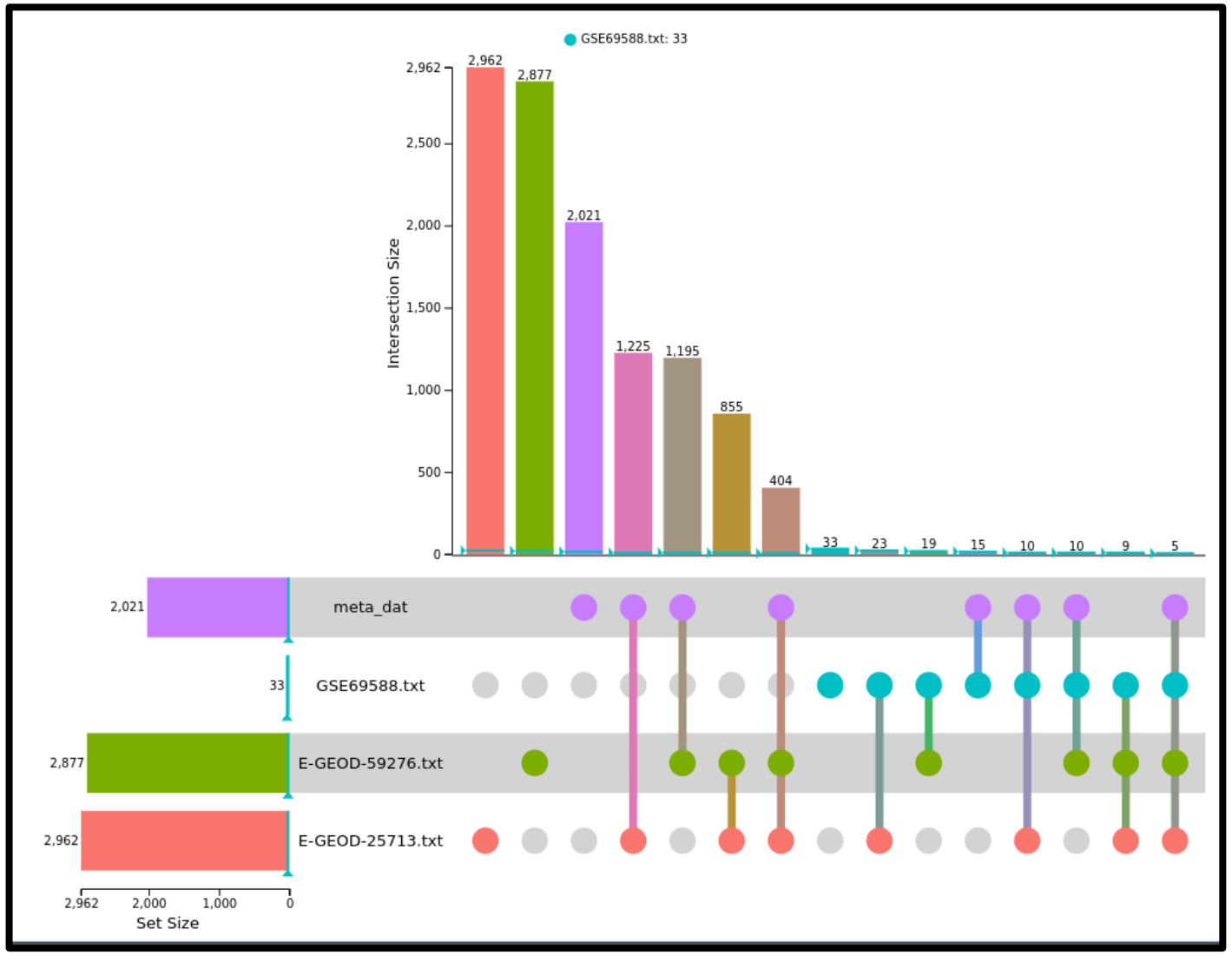
PCA plot



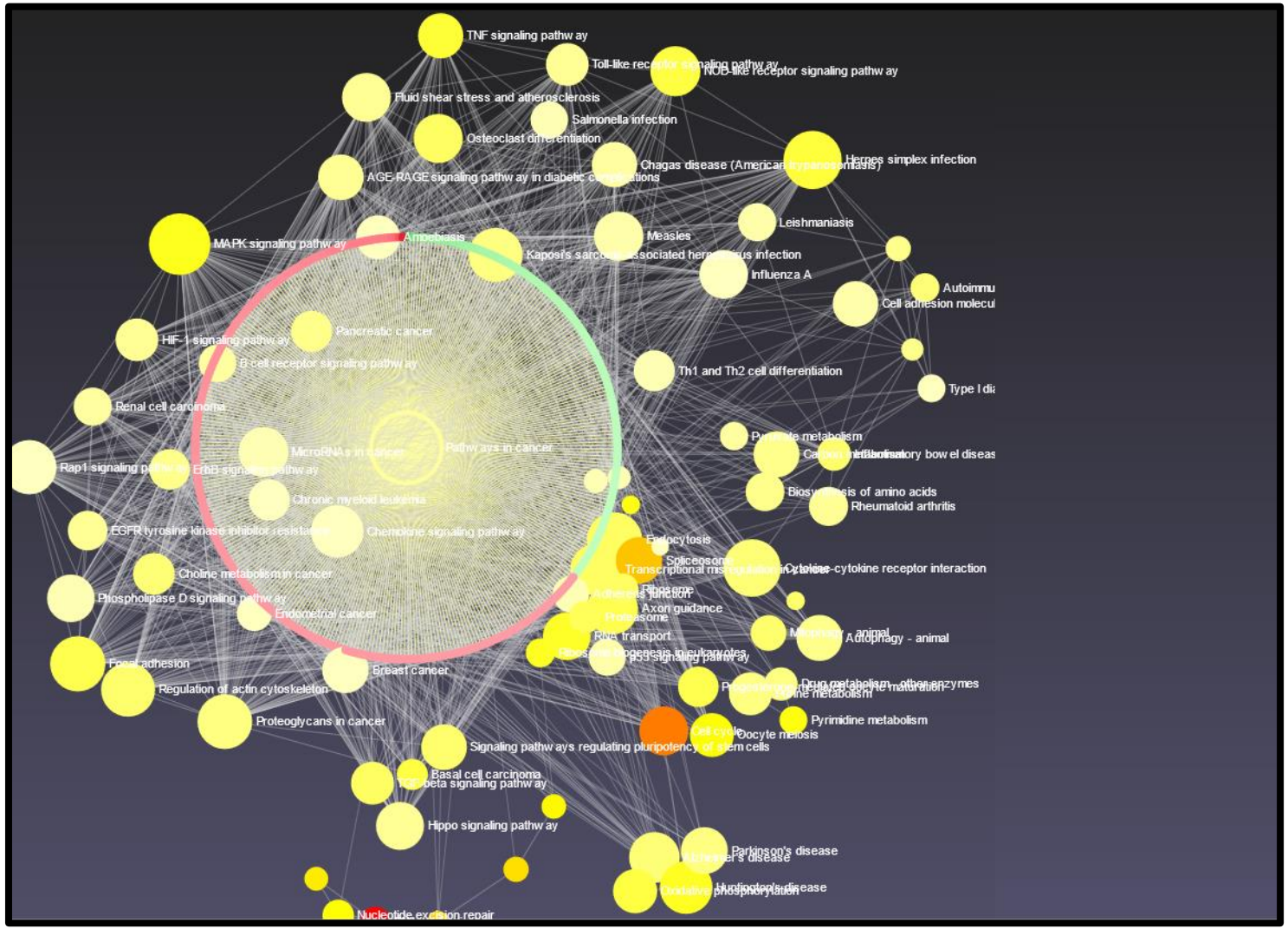
Interactive volcano plot



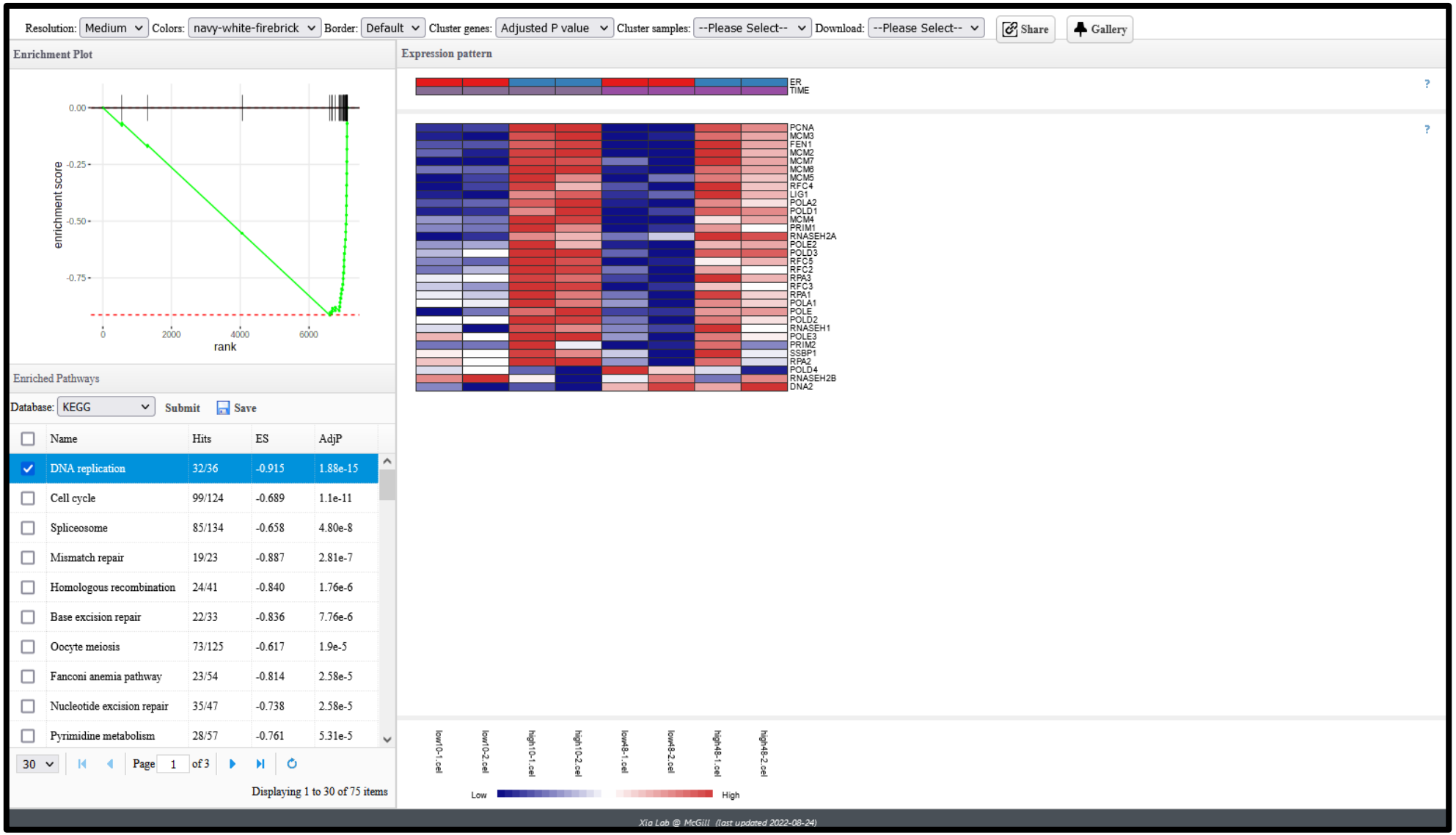
Upset diagram



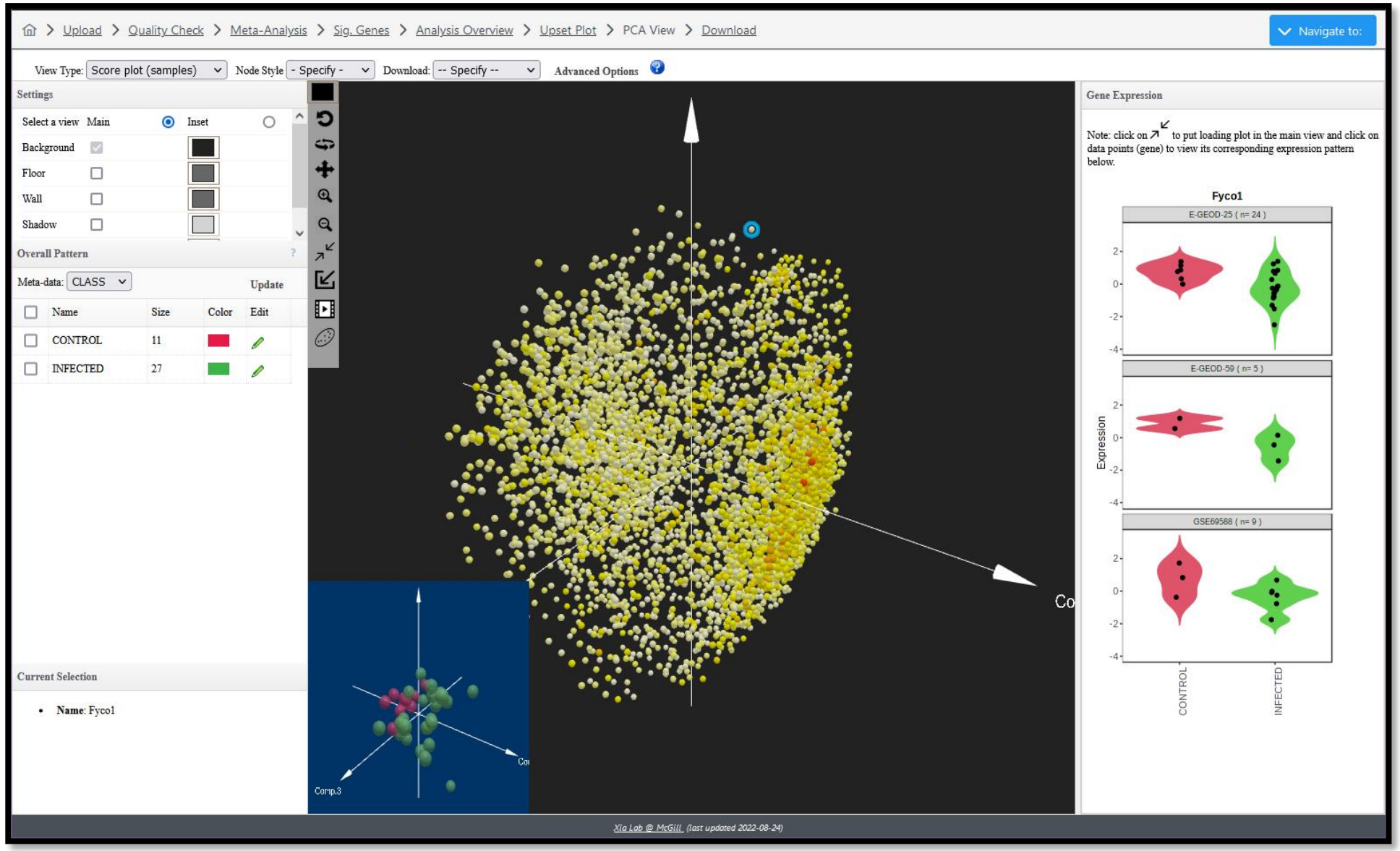
Enrichment Network



Interactive heatmap



Interactive scatter plot



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