



Banana Slug Analytics Platform

mRNA-Seq for Eukaryotes Analysis Results

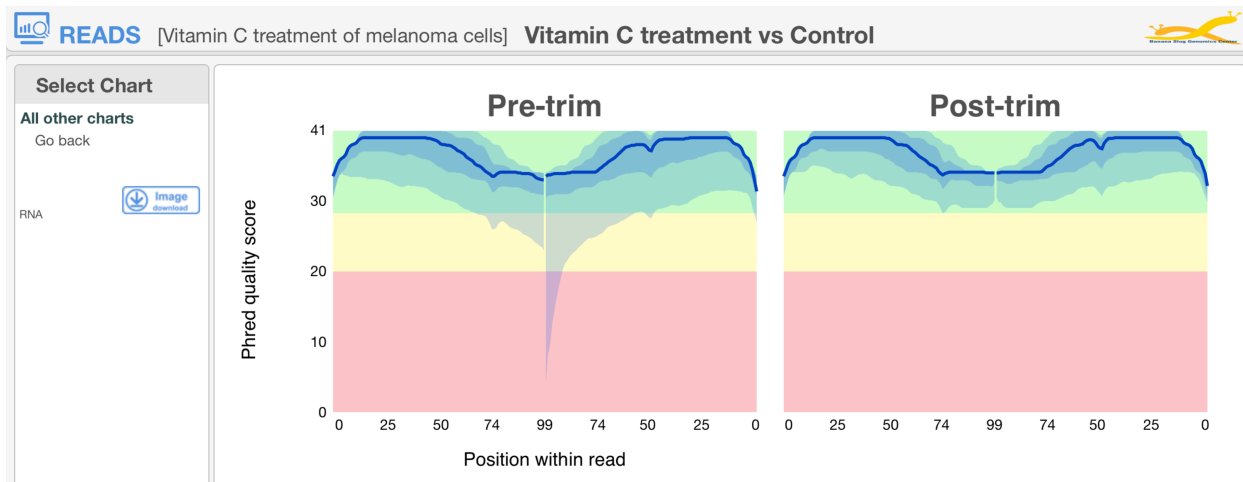
This document provides a guide to explore the mRNA-Seq for eukaryotes analysis results on the Banana Slug Analytics Platform. This should be expected to be used after the analysis has been performed.

At the HOME page of your account, select the project in the Projects panel on the left that has the analysis performed. Then click on the analysis listed under the Analyses panel on the right.

The TOOLS page will be opened with the results displaced in three groups: Quality Inspector, Differential Expression, and Gene Expression Visualizations. Users can also access the FILES page through the File Download link, the pipeline manifest used for the analysis, and the UCSC Genome Browser.

Quality Inspector

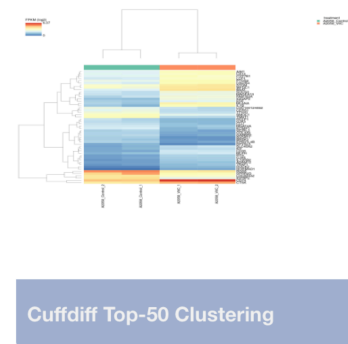
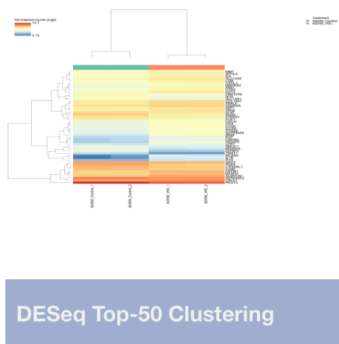
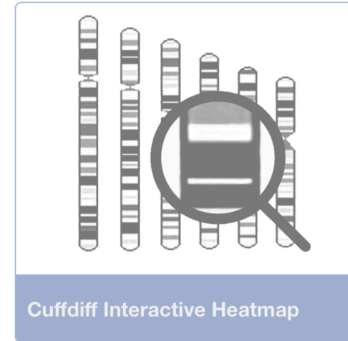
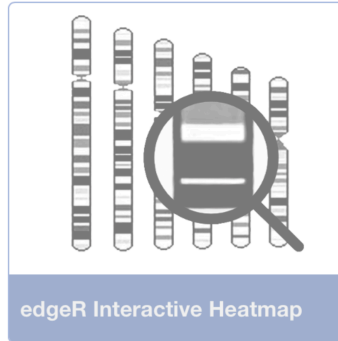
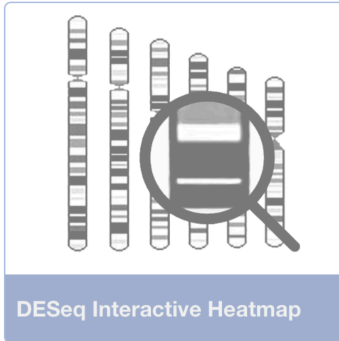
This tool allows users to explore the quality of the sequencing data for each sample. It includes the summary of read counts, the read mapping distribution at genes, the overall read coverage along transcripts, and the sequencing read quality before and after trimming.



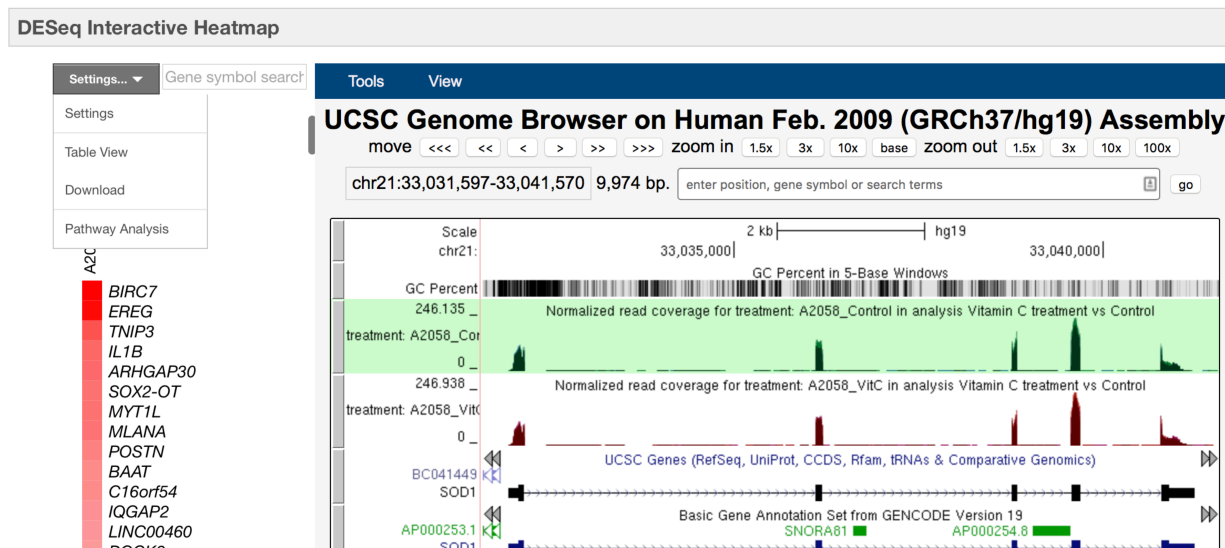
Differential Expression

Our analysis pipeline includes the use of DESeq, edgeR, and Cuffdiff for differential expression analysis. Users can explore the results by using the corresponding interactive heatmap. We also provide clustered heatmaps of the top 50 differentially expressed genes.

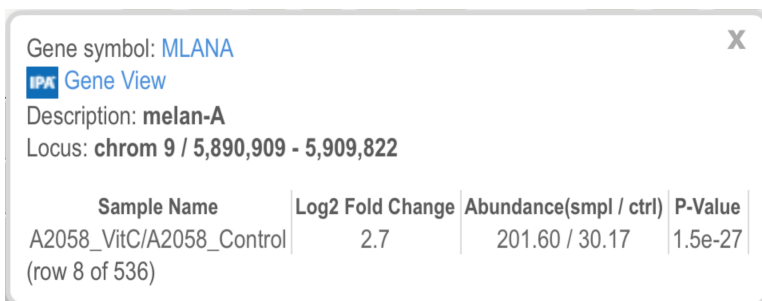
Differential Expression



Interactive Heatmap



Users can select the desired gene on the interactive heatmap to explore its expression profile and read coverage on the UCSC Genome Browser. By hovering a gene on the heatmap, the expression data including log2 fold change, abundance, and adjusted P-value will be displayed on a popup window.



To view the read coverage of a desired gene on the genome browser, click the gene on the heatmap and the corresponding genomic region will be shown.

The heatmap data can be displayed in a table format by selecting Table View under the Settings menu. User can also download the expression data in display by selecting the Download option. To change the display and filtering options of the heatmap, choose the Settings menu item.

Settings ✕

▼ Sample

ControlOrder

A2058_Control ⌵

Apply

▼ Sorting

Sort by: Hierarchical ⌵

Apply

▼ Filters

Filter	Using	Condition	Value	
P-Value	Minimum value in gene row ⌵	Less than or equal to ⌵	0.05	x
Add filter ⌵				Apply

▸ Colors

▸ Gene Lists

▸ Genome Browser

▼ Gene Information

Show Gene Symbols: On

Default Settings

By default, P-value < 0.05 is set as a filter to display data on the heatmap. If too few genes are shown, users can select to relax or remove the filter. Pairwise differential expression analysis is included. Users can select the appropriate sample as the control for comparison on the heatmap. Users can also upload a pre-determined gene list to be displayed on the heatmap.

For details on how to use the UCSC Genome Browser, please go to <https://genome.ucsc.edu/training/index.html>.

Gene Expression Visualizations

Our platform provides principal components analysis and sample correlation analysis in charts for visualization.

Gene Expression Visualizations

