



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.

Projects	New	Vitamin C treatment of melanoma cells		1	64	
aternal milk-derived miRNAs		Gustafson CB et al. Epigenetic reprogramming of		Analyses	Files	
tamin C treatment of melanoma	(melanoma cells by vitamin C treatment. Clin Epigenetics. 2015 7:51.		New Analysis	Upload File	
		Created Oct 2018 by admin				
		Analyses				
		Vitamin C treatment vs Control	ſ	Oct 16, 18		

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.

ipeline Type: mRNA-Seq for Differential Expression in Eukaryotes rganism: hg19 Platform: Illumina			Mapper: STAR		
Analysis Review Tools					
Quality Inspector	Diffe	rential Expression	Gene Expression Visualizations		

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.



Interactive Heatmap

DESeq Interactive Heatmap Gene symbol search Tools View Settinas UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly move <<< << > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x Table View chr21:33,031,597-33,041,570 9,974 bp. enter position, gene symbol or search terms 🗎 go Download Pathway Analysis 2 kb - ha19 Scale chr21: 33.035.000 33,040,000 220 GC Percent in 5-Base Windows BIRC7 246.135 EREG Normalized read coverage for treatment: A2058_Control in analysis Vitamin C treatment vs Control TNIP3 treatment: A2058_Cor IL1B 0_ ARHGAP30 246.938 _ Normalized read coverage for treatment: A2058_VitC in analysis Vitamin C treatment vs Control SOX2-OT MYT1L treatment: A2058_Vit(MLANA 0_ POSTN **M** UCSC Genes (RefSeq, UniProt, CCDS, Rfam, tRNAs & Comparative Genomics) D BC041449 K BAAT C16orf54 SOD1 IQGAP2 Basic Gene Annotation Set from GENCODE Version 19 SNORA81 ■ AP000254.5 AP000253.1 Ы LINC00460

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.

Gene symbol: MLANA			X			
IPA Gene View						
Description: melan-A						
Locus: chrom 9 / 5,890,909 - 5,909,822						
Sample Name	Log2 Fold Change	Abundance(smpl / ctrl)	P-Value			
A2058_VitC/A2058_Control	2.7	201.60 / 30.17	1.5e-27			
(row 8 of 536)						

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 ⁰				
 Sample 				
Control Order		A2058_Control		>
Sorting				Apply
Sort by:	Hierarchical 🗘			Apply
- Filters				
Filter	Using	Condition	Value	
P-Value	Minimum value in gene row	Less than or equal to	0.05	×
Add filter	1			Annie
▶ Colors				Арріу
▶ Gene Lists				
Genome Browser				
Gene Information				
Show Gene Symbols:			On	
			Defa	ault 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 <u>https://genome.ucsc.edu/training/index.html</u>.

Gene Expression Visualizations

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





