OmicsBox

Transcriptomics

Quality Control
Assembly
Quantification
Differential Expression

The OmicsBox Transcriptomics Module allows you to process RNA-seq data from raw reads up to the functional analysis in a flexible and intuitive way.

Quality Control

Use FastQC and Trimmomatic to perform the quality control of your samples, to filter reads and to remove low quality bases.

De-Novo Assembly

Assemble short reads with Trinity to create a de-novo transcriptome without a reference genome.

RNA-Seq Alignment

Alignment of RNA-seq data to your reference genome making use of STAR, an ultrafast universal RNA-seq aligner via the OmicsBox Cloud.

Quantify Expression

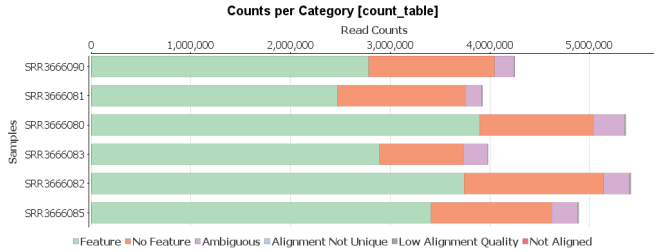
Quantify expression at gene or transcript level via HTSeq or RSEM and with or without a reference genome.

Differential Expression Analysis

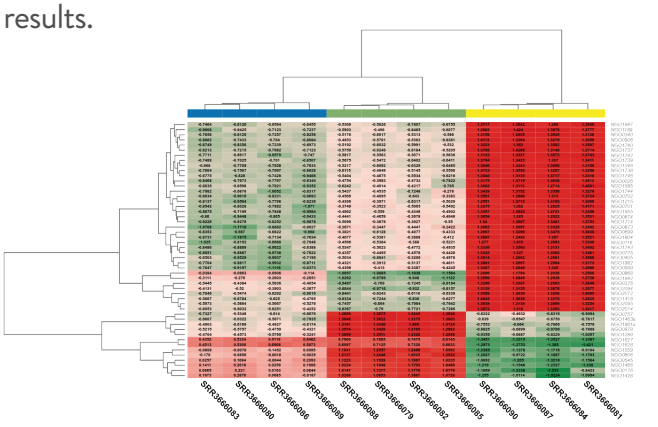
Detect differentially expressed genes between experimental conditions or over time with well-known and versatile statistical packages like NOISeq, edgeR or maSigPro. Rich visualizations help to interpret results.

Enrichment Analysis

By combining differential expression results with functional annotations, enrichment analysis allows to identify over- and under-represented biological functions.



Different statistical charts provide additional information about the assembly and quantification processes as well as a quality assessment of the results.



Interactive heatmaps help to intuitively check the differences and similarities between the expression values of the different genes and samples.

Nr	Tags	Name	FC	logFC	logCPM	P-Value	FDR
33	UP	NGO0873	9.89874	3.30724	5.70897	2.9411E-175	1.7121E-173
34	UP	NGO0702	6.96664	2.80046	8.47333	1.1717E-173	6.6202E-172
35	UP	NGO0701	8.92635	3.15807	7.72212	4.9597E-172	2.7222E-170
36	DOWN	NGO0606	-7.60586	-2.92711	6.92197	1.8017E-170	9.6143E-169
37	DOWN	NGO0757	-50.27895	-5.65188	5.25238	6.0946E-170	3.1643E-168
38	DOWN	NGO1463a	-6.27027	-2.64853	9.96006	8.4012E-170	4.2470E-168
39	UP	NGO1189	10.40901	3.37976	5.49797	8.4661E-166	4.1701E-164
40	DOWN	NGO0176	-39.04366	-5.28702	5.51934	1.1316E-165	5.4343E-164
41	DOWN	NGO0545	-5.79089	-2.53378	8.45118	6.8823E-165	3.2246E-163
42	UP	NGO0026	13.24887	3.7278	5.0641	3.5933E-164	1.6435E-162
43	DOWN	NGO1466	-4.98324	-2.31708	8.66767	1.1666E-158	5.2118E-157
44	UP	NGO0999	5.99829	2.58455	8.61918	2.6979E-156	1.1779E-154

Sort and filter the differential expression results and adjust the statistical criteria to review significant genes and combine them with functional information to gain biological insights.

BioBam Bioinformatics S.L.
Contact: sales@biobam.com
Support: support@biobam.com

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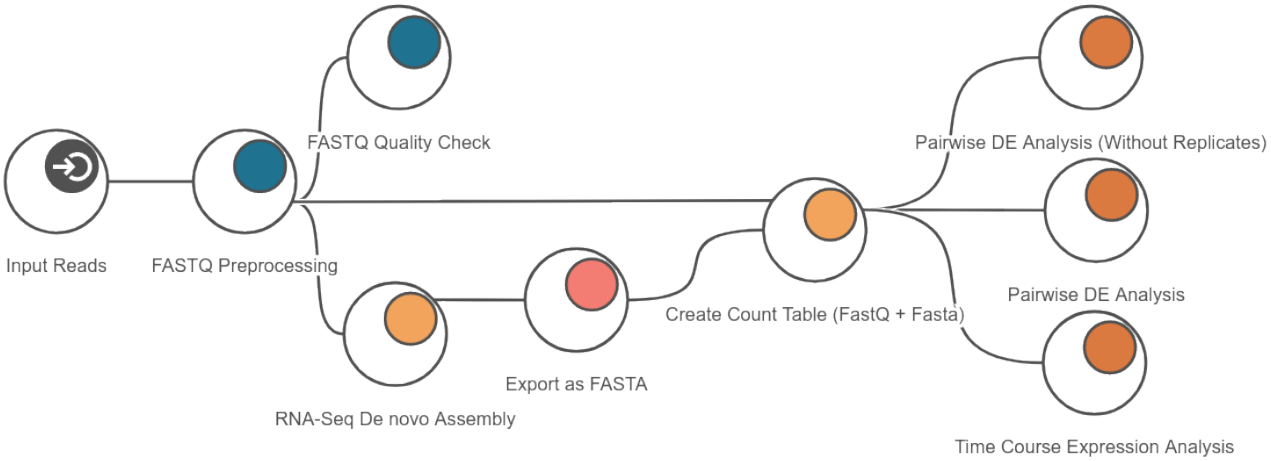
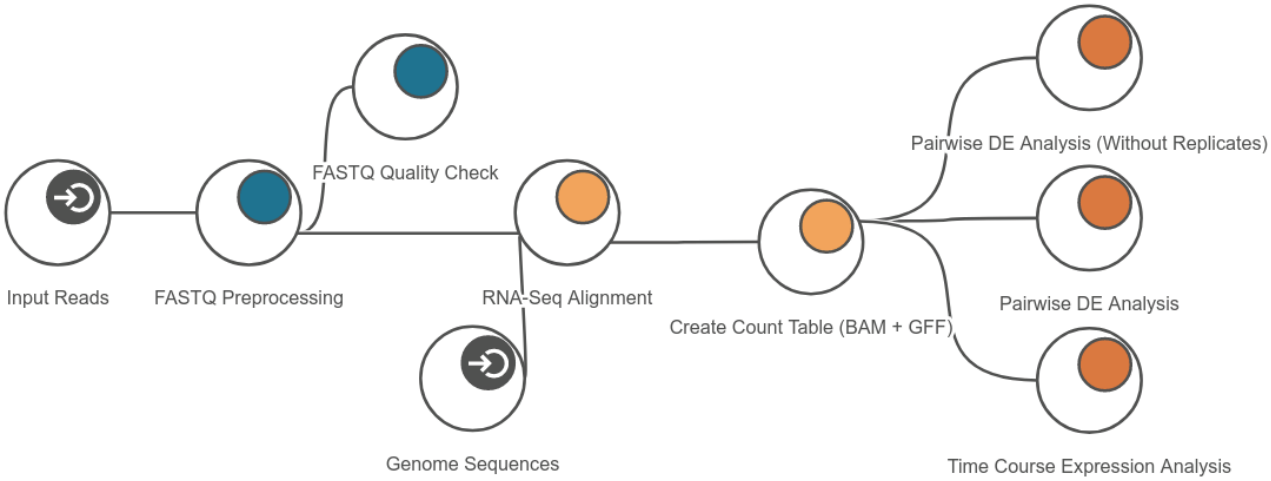


De-Novo Transcriptome Analysis

Generate your own reference transcriptome by assembling RNA-seq reads, estimate the expression value of each transcript sequence and perform differential expression analysis.



Reference-Based Transcriptome Analysis

This example workflow shows the analysis of an RNA-seq dataset with reference genome. After the quality control and the alignment, expression is quantified. The resulting count table can be used to detect differentially expressed genes.

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