# OmicsBox

The OmicsBox Transcriptomics Module allows you to process RNA-seq data froms 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.
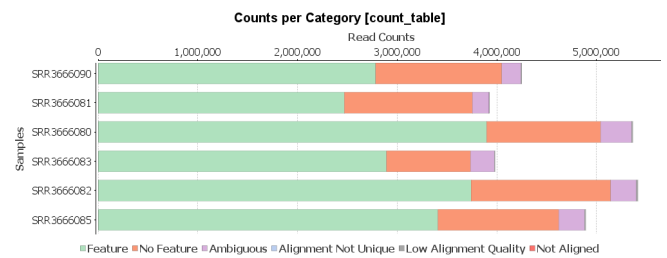
## Quantify Expression
Quantify expression at gene or transcript level via HTSeq or RSEM and with or without a reference genome.
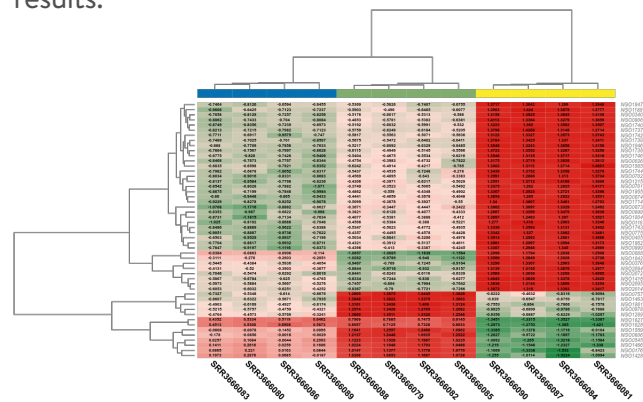
## Differential Expression Analysis
Detect differentially expressed genes between experimental conditions or over time with well-known and versatile statistical packages like NOISeq, edgeR or maSigPro. Rich visualizations help to interpret results.

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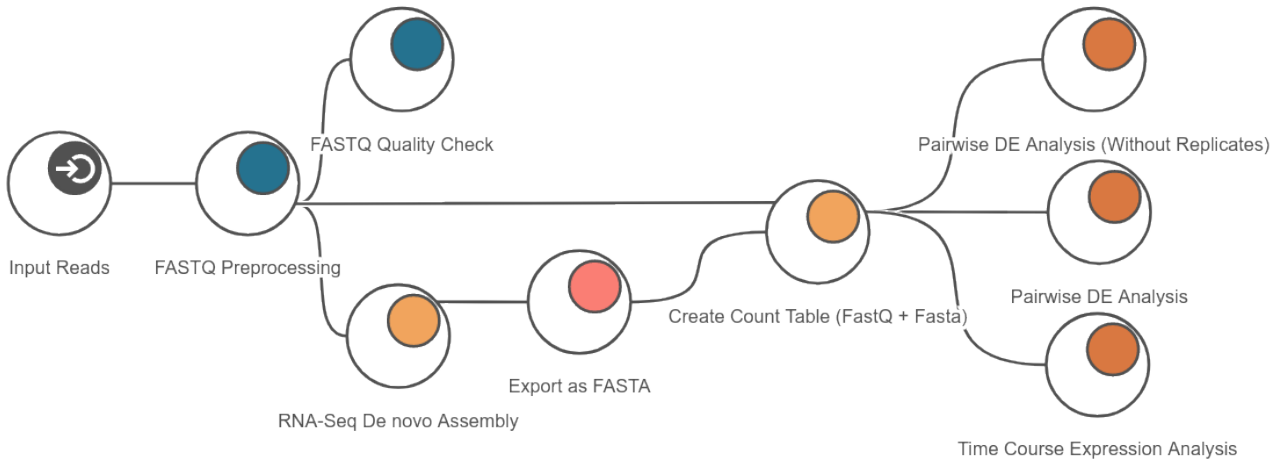


Counts per Category [count_table]

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.
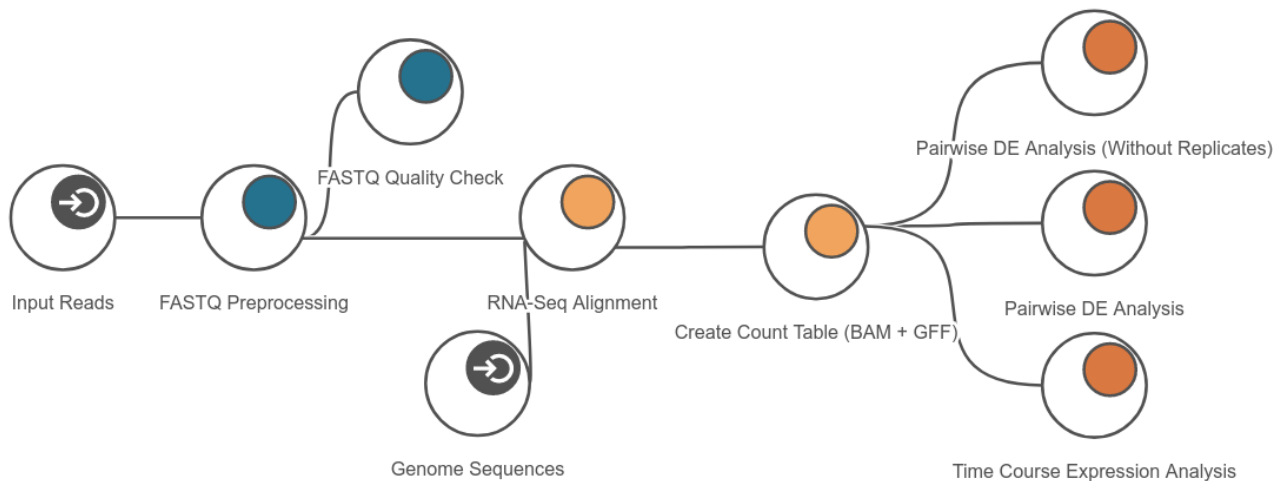
| Nr | Tags | Name | FC | logFC | logCPM | P-Value | FDR |
|---|---|---|---|---|---|---|---|
| 33 | UP | NGO0873 | 9.89874 | 3.30724 | 5.70897 | 2.9411E-175 | 1.7121E-173 |
| 34 | UP | NGO0702 | 6.96664 | 2.80046 | 8.47333 | 1.1717E-173 | 6.6202E-172 |
| 35 | UP | NGO0701 | 8.92635 | 3.15807 | 7.72212 | 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.

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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.