

QLUCORE® Omics Explorer & GENEVESTIGATOR®

Empowering biologists to analyze gene expression data on their own
From deep statistical analysis of single experiments to meta-profiling across hundred thousands of samples from public studies

Powerful and user-friendly tools for analysis and interpretation

The combination of Qlucore Omics Explorer and GENEVESTIGATOR allows users to easily analyze and interpret RNA-Seq experiments, both individually and in the light of publicly available expression data.

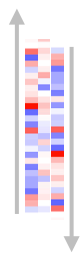


Qlucore Omics Explorer provides easy-to-use statistical tools and state of the art visualizations, empowering biologists to analyze their own and publicly available data sets, and quickly achieve high quality results and conclusions.



GENEVESTIGATOR provides powerful meta-analysis tools together with high quality curated public data, allowing biologists to comfortably explore expression data and interpret results in a data-driven manner.

Gene list analysis and integration: Use Cases



Find out more about the differentially expressed genes in your experiment

- What is the spatial expression pattern of the genes?
- Which other conditions regulate these genes, and how do they cluster?

Get further biological insights and meta-profiles, by bringing gene lists from Qlucore Omics Explorer into GENEVESTIGATOR.

Mark tissue-, cell type- or disease-specific genes in your data set

- What is the overlap between discriminating genes and tissue-specific genes?
- How are the samples clustering based on a certain disease?

Discover patterns in your data set by bringing gene lists from GENEVESTIGATOR into your data set in Qlucore Omics Explorer.