VUGENE

COMPREHENSIVE MULTI-OMICS EXPERTISE
Our team is experienced across the full spectrum of multi-omics research, ensuring a holistic understanding of biological systems.

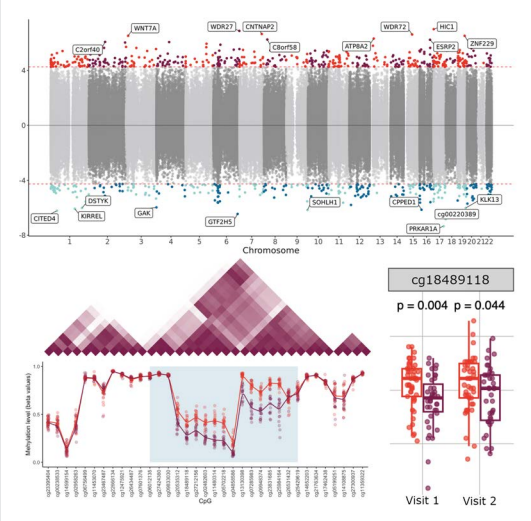
EPIGENOMICS
Investigation of DNA and chromatin modifications

TRANSCRIPTOMICS
Single-cell, spatial, and bulk tissue analysis

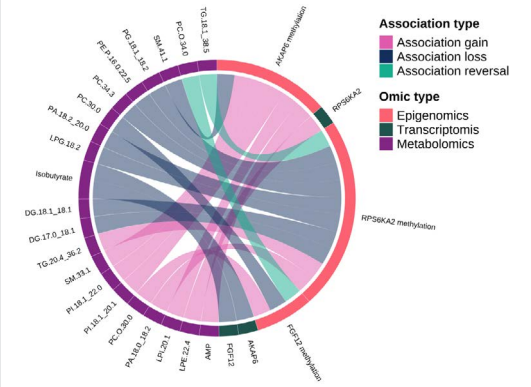
PROTEOMICS
Comprehensive protein profiling

METABOLOMICS
Targeted and untargeted analysis

HOLISTIC VIEW
From genome-wide landscapes, to point-level changes, we ensure a holistic and thorough understanding of biological systems.



MULTI-OMICS INTEGRATION
We provide deep biological insights by analyzing and integrating your data across multiple omics layers. Our intuitive visualizations translate this complexity into clear, actionable findings.



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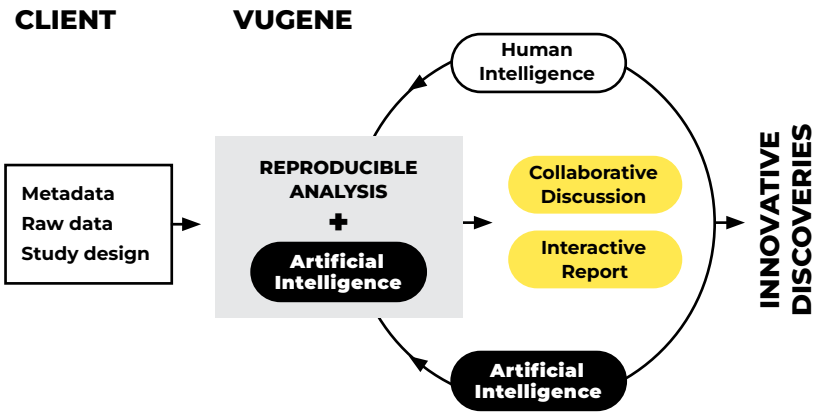
VUGENE specializes in multi-omics data analysis, empowering researchers to turn biological complexities into actionable knowledge.



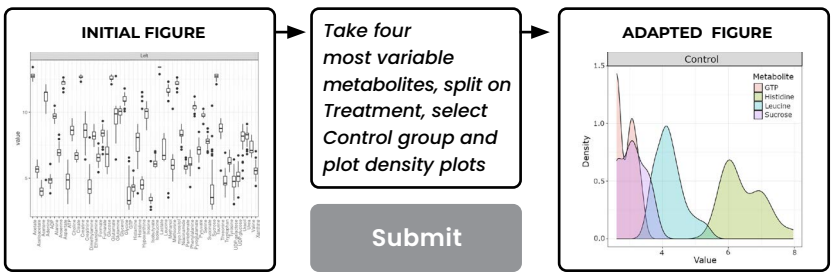
Fast, Reproducible, and Reliable Results
Our standardized workflows accelerate data analysis, delivering scalable and reliable results to move your research forward.

The Power of Human and Artificial Intelligence
We combine the best of both worlds. After initial AI-powered analysis, our team of experts personally reviews the results, adjusts parameters, and refines the output. This iterative process distills the most valuable findings and uncovers truly novel insights.

A Collaborative Process, Tailored to You
We believe in partnership. Throughout the project, we work closely with you, adapting our methods based on the discussions to ensure the results are perfectly tailored to your research goals.

Innovative Discoveries
Our multidisciplinary expertise, combined with AI-supported analysis, applies latest methods for rigorous screening of existing data and highlights truly novel findings within the results.

Interactive, AI-Assisted Service
Instantly customize figures, adjust parameters, and get help with interpretation using our bioinformatics agents – putting you in control of your data analysis.



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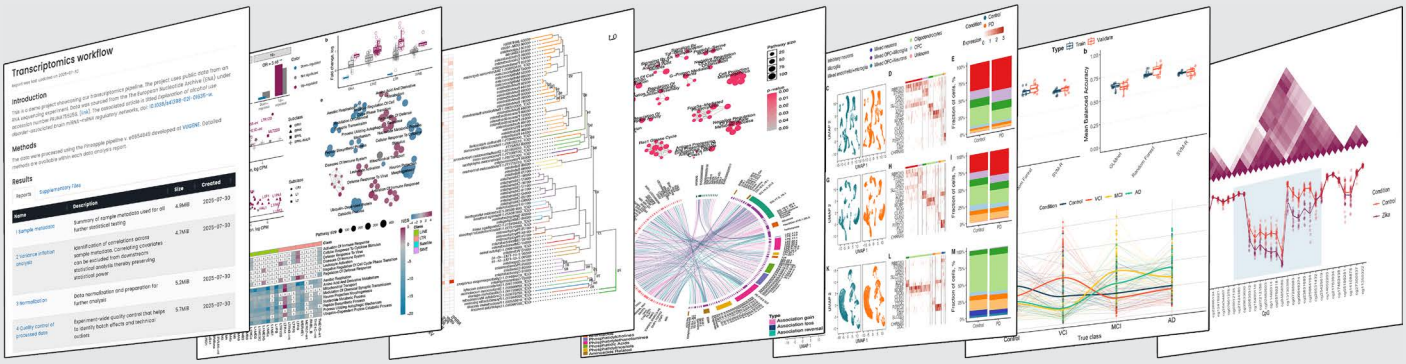
Clearer Insights. Better Science.

Transcriptomic Data Analysis

For studies using RNA-seq of bulk tissue samples



FROM DATA TO VALUE IN HOURS

Our AI-powered analysis automates each step, rapidly delivering results as an interactive web application that can be explored and shared across all stakeholders.

Identify Relevant Clinical Variables

Clinical information (e.g., age, sex, BMI, drug use) is used to identify the most relevant molecular changes. We compare AI-based predictions with supplied metadata to detect and correct labeling errors and select the minimal set of relevant clinical variables to preserve statistical power in subsequent steps.

Assess Quality

We perform quality control (QC) on each sample to identify library preparation problems and use a data-driven approach to detect samples that differ substantially from others in the experiment, ensuring more reliable downstream insights.

Normalize Across Samples

To reveal true biological variation, we detect and reduce subtle technical noise that can arise during sample processing. We normalize gene expression signals, filter out low-abundance transcripts, and adjust for known batch effects.

Find Differentially Expressed Genes

Depending on your experimental design and research question, we select the most appropriate, statistically rigorous approach. We account for technical and biological variability, including cellular heterogeneity, and automatically fit an appropriate linear regression model to each gene.

Pinpoint Affected Pathways

We perform gene set enrichment analysis (GSEA) across all major pathway databases, clustering similar pathways to explore how groups of genes act together, even when individual genes are not statistically significant.

Build Diagnostic Classifiers

We identify the minimal set of biomarkers that best differentiate sample groups. By evaluating multiple machine learning algorithms and cross-validation strategies, we assess classifier accuracy for potential diagnostic, prognostic, or treatment applications.

ADDITIONAL VALUE OUT-OF-THE-BOX

RNA-seq data contains a wealth of valuable information that often goes unexplored. To ensure you do not miss key insights, these analyses are included as part of our standard workflow.

Alternative Gene Splicing

Since many disorders are influenced by alternatively spliced gene transcripts, our workflow automatically identifies these genes and tests for statistically significant differences in splicing frequency across groups.

Investigate Drugs for Repurposing

Automated analysis of drug connectivity databases identifies compounds that may reverse the observed phenotype, uncovering new drug repurposing opportunities and highlighting candidates that could counteract disease signatures.

Microbial Abundance

Sequencing reads that do not map to the reference genome are assessed against bacterial and viral databases. Differential abundance analysis can identify potential contamination and characterize microbial species associated with your samples.

Get in touch to see how our intelligent analysis platform can redefine your multi-omics results

REQUEST A DEMO HERE

Clearer Insights. Better Science.