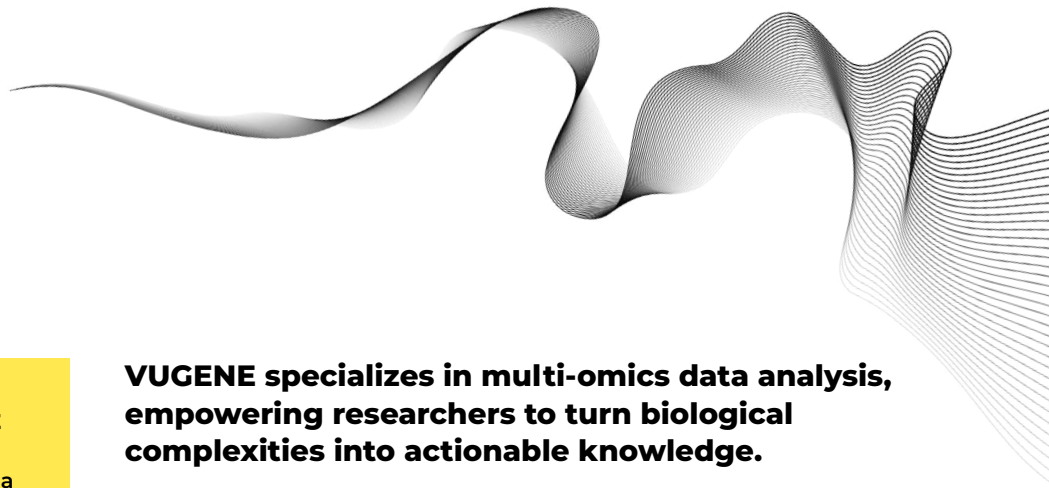




COMPREHENSIVE MULTI-OMICS EXPERTISE

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

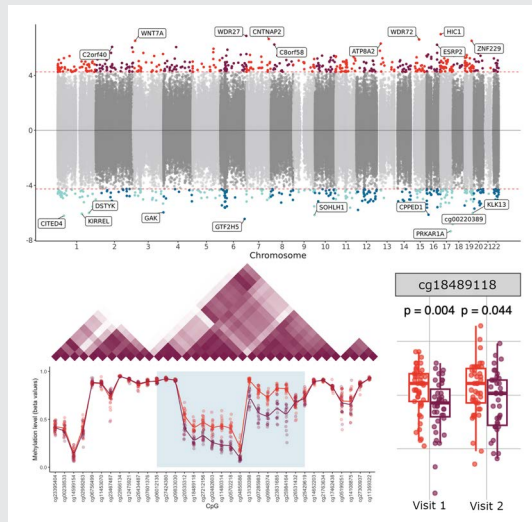
Comprehensive protein profiling

METABOLOMICS

Targeted and untargeted analysis

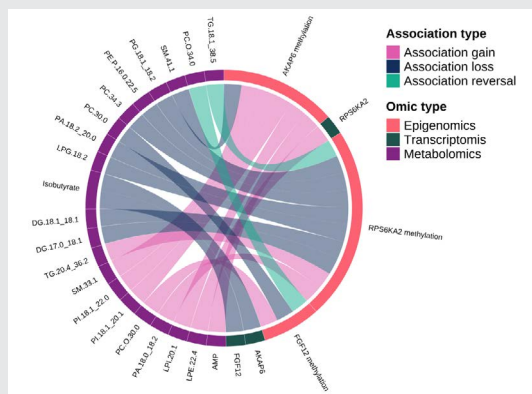
HOLISTIC VIEW

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



MULTI-OMICS INTEGRATION

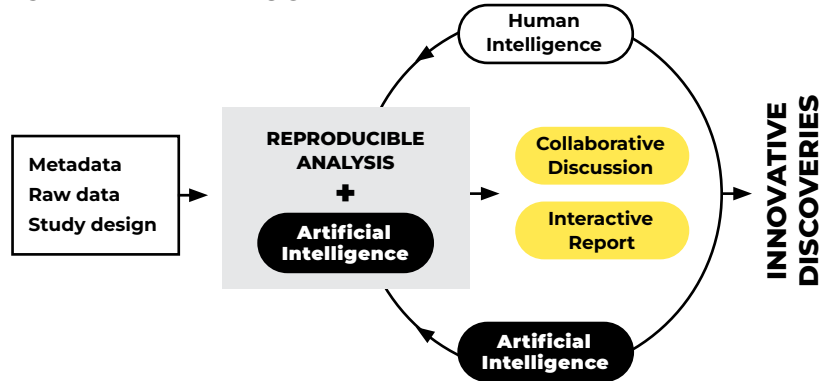
We provide deep biological insights by analyzing and integrating your data across multiple omics layers. Our intuitive visualizations translate this complexity into clear, actionable findings.



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

CLIENT

VUGENE



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

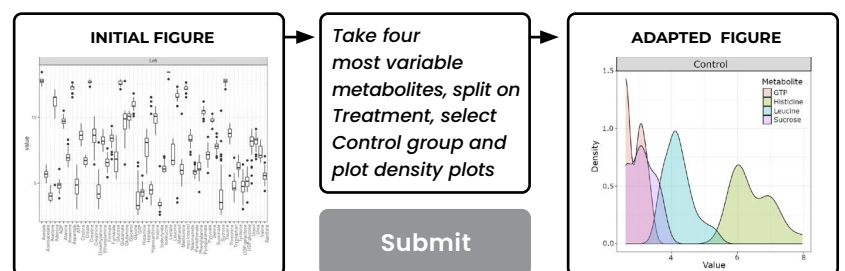
We believe in partnership. Throughout the project, we work closely with you, adapting our methods based on the discussions to ensure the results are perfectly tailored to your research goals.

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.

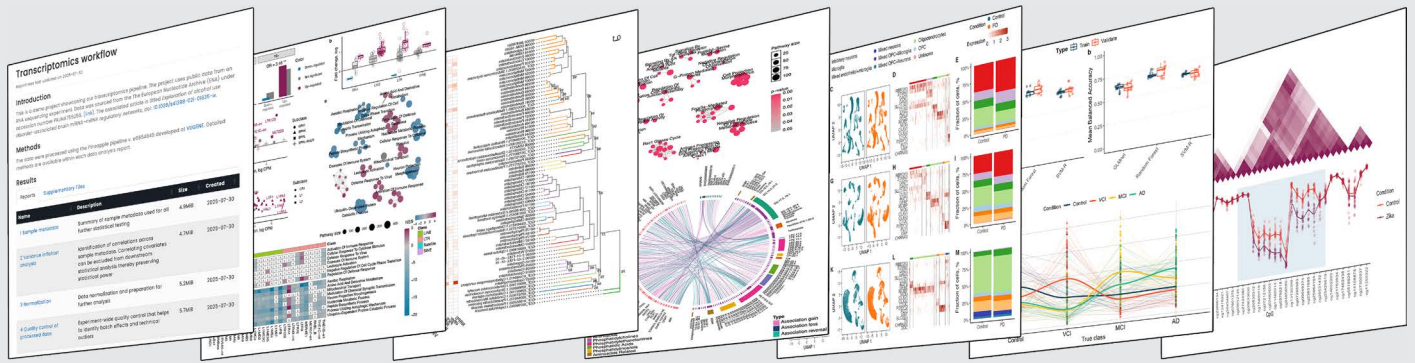


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**Clearer
Insights.
Better
Science.**



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

Robust quality control is crucial for reliable insights. Our pipeline automatically filters technical artifacts by assessing MultiQC reports, detecting doublets and empty droplets, and removing ambient, mitochondrial, and ribosomal RNA contamination.

Normalize Across Samples

Unexpected differences between cells and samples may arise due to subtle technical variability in sample processing. Our process eliminates this noise to reveal the underlying biology by standardizing gene expression across all cells, and adjusting for known batch effects. This is followed by a visual validation of the normalization using tSNE and UMAP plots.

Cell-Type Identification

Accurate cell population annotation is key for meaningful biological interpretation, cross-study comparisons, and robust downstream analysis. We use both reference-based and data-driven methods for the most accurate results.

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 in different cell populations, even when individual genes are not statistically significant.

ADDITIONAL VALUE OUT-OF-THE-BOX

Single cell and spatial transcriptomics 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.

Communication of Cell-Niches

Map the communication between cell niches. We pinpoint interactions between distinct cell populations by identifying the signaling pathways and ligand-receptor pairs that mediate intercellular communication. This analysis provides critical insights into cellular crosstalk and coordinated biological processes.

Spatially Variable Genes

Identify spatially variable genes by detecting differential expression prior to cell type annotation. This approach provides a comprehensive view of the average transcriptional response across the entire system.

Diagnostic Classifiers

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

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

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