

Connected Multiomics

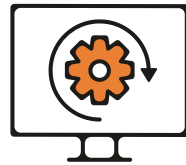
Powerful, intuitive, scalable multiomic analysis



Illumina Connected Multiomics is a cloud-based multiomic analysis solution that enables researchers to explore and analyze biological data at scale. The interactive graphical user interface makes analysis of large and complex data accessible without the need for advanced bioinformatics expertise. It delivers ease of use without sacrificing power. Take your study from sample preparation to data interpretation within the Illumina ecosystem and simplify how you approach multiomic analysis.



Unlock deeper biological insights

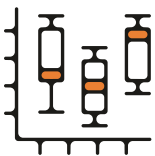


Intuitive and streamlined analysis



Scale your studies with ease

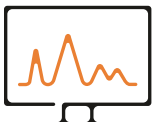
Confidently analyze multiomic data



Interactive visualizations
Information-rich and publication-ready visualizations



Data integration and streamlined workflows
Built to provide seamless multiomic workflows from assays to insights



Powerful statistical algorithms
Robust statistical methods for identifying key features

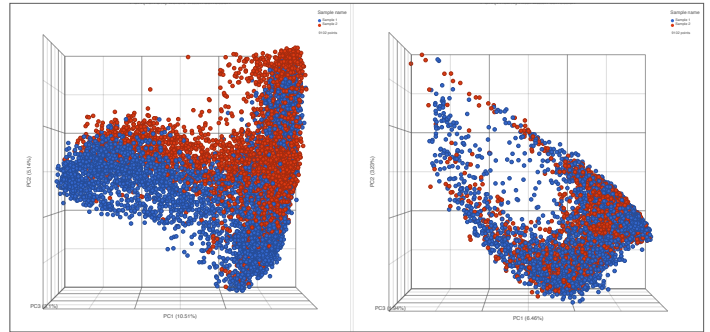


Security-first infrastructure
Built with industry standard security, privacy, and compliance standards in mind to help you maintain a trusted data environment

Interactive visualization



Proteomics - Synchronized views show highlighted cell types, gene ontology categories, and enrichment scores in interactive plots.



Batch effect - PCA showing before and after batch effect correction and how correction can help mitigate batch effects.

Designed to support multiple -omes and modalities



Bulk



Proteomics



Transcriptomics



Single-cell



Spatial



And more

Prepare libraries



Prepare libraries for single-cell, proteomics, spatial, etc.

Sequence



Sequence libraries using any Illumina sequencing platform

Analyze



Secondary analysis

Accurate and efficient analysis with DRAGEN

Interpret



Tertiary analysis

Explore and analyze multiomic data sets with interactive visualization and powerful statistics and tools

800.809.4566 toll-free (US) | +1.858.202.4566 tel
techsupport@illumina.com | www.illumina.com



Learn more



Request demo

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