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# Illumina Connected Multiomics

## Powerful, intuitive, scalable multiomic data analysis

Consolidate multiomic data analysis on a single platform to maximize insights and accelerate discoveries

Simplify interpretation from complex data sets without the need for advanced bioinformatics expertise

Obtain trusted results with powerful algorithms for data analysis and interactive visualizations

## Introduction

Multiomic analysis is a powerful multidisciplinary approach that combines data from multiple omes, including the proteome, transcriptome, epigenome, and genome, and integrates modalities, such as single-cell and spatial analyses, to provide a holistic view of complex biological systems. However, analyzing the large volumes of data generated in high-depth multiomic studies is computationally intensive. Integrating results and visualizing data from multiomic studies can present a significant bottleneck for labs.
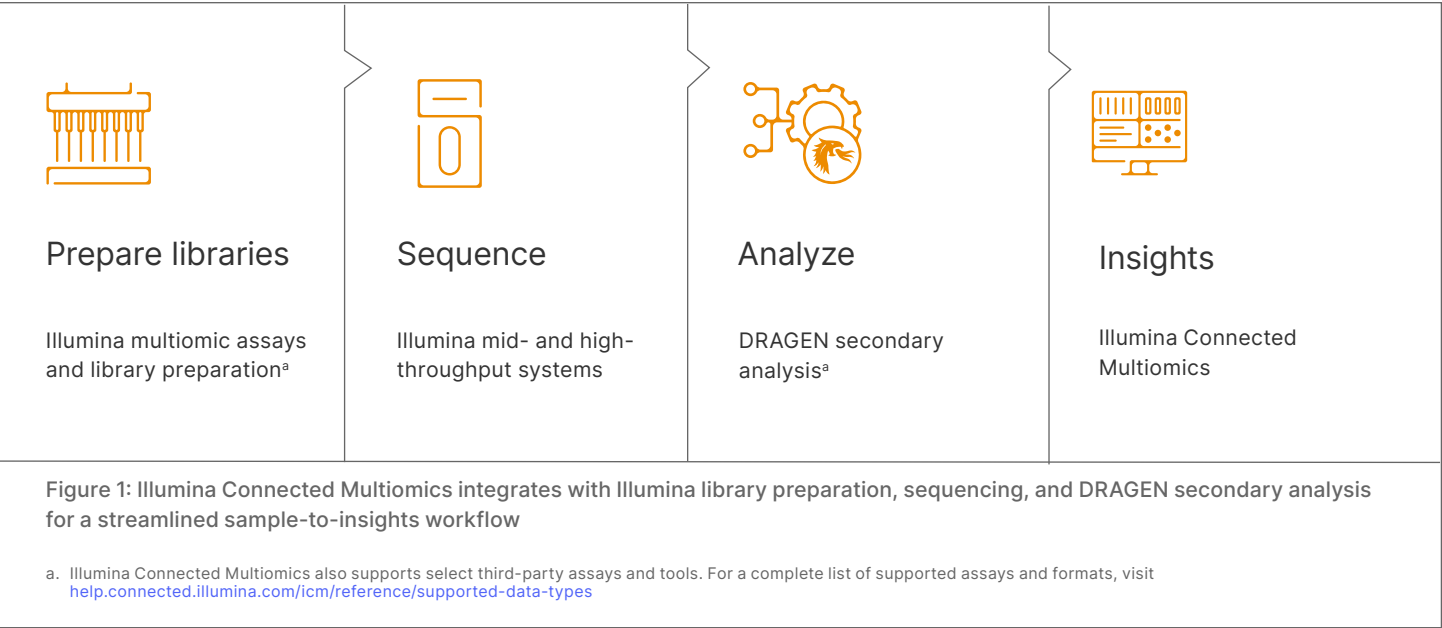
Illumina Connected Multiomics, an intuitive, scalable environment for analyzing and visualizing multiomic and multimodal data, overcomes these challenges. Built on established, industry-standard statistical algorithms, Illumina Connected Multiomics delivers high-quality results with rich, interactive visualizations that simplify data interpretation and accelerate discoveries. Integration with Illumina library preparation, sequencing, DRAGEN™ secondary analysis, and Correlation Engine omics knowledge bases streamlines operations from sample to insights (Figure 1). Illumina Connected Multiomics features an intuitive user interface with preconfigured and customizable workflows for key Illumina assays and select third-party assays. Researchers of all skill levels are empowered to explore their multiomic data easily and confidently.

## Intuitive interface

Illumina Connected Multiomics offers a comprehensive suite of genomic tools to enable multimodal analyses with workflows built to support emerging trends and advances in multiomics research. The software features a highly visual graphical user interface (Figure 2) designed for researchers of all skill levels to explore their multiomic data. Clear, actionable dialogs provide guidance through analysis and visualization, empowering users to perform data analysis with confidence. Additionally, Illumina Connected Multiomics provides access to advanced tools, customizable pipelines, and user controls for core laboratories and users with informatics expertise.

## Powerful multiomic analysis

Multiomic data analysis requires a suite of specialized tools designed to handle the complexity of integrating diverse biological data sets and extracting high-quality information from every sample. Illumina Connected Multiomics leverages analysis tools built using publicly available, industry-standard statistical algorithms and models to uncover patterns across omics layers so researchers can be confident in their results. Interactive visualization tools enable users to generate rich, publication-ready visuals and gain meaningful insights from large, multidimensional data sets.



| Prepare libraries | Sequence | Analyze | Insights |
| --- | --- | --- | --- |
| Illumina multiomic assays and library preparation[a] | Illumina mid- and high-throughput systems | DRAGEN secondary analysis[a] | Illumina Connected Multiomics |

Figure 1: Illumina Connected Multiomics integrates with Illumina library preparation, sequencing, and DRAGEN secondary analysis for a streamlined sample-to-insights workflow

a. Illumina Connected Multiomics also supports select third-party assays and tools. For a complete list of supported assays and formats, visit help.connected.illumina.com/icm/reference/supported-data-types

**Figure 2: Illumina Connected Multiomics interface**

The highly visual user interface empowers users of all skill levels to explore their multiomic data sets with confidence.

Illumina Connected Multiomics is versatile, enabling high-resolution data analysis across a range of multiomic applications,* including proteomics, transcriptomics, epigenomics, and genomics, and modalities, including single-cell and spatial transcriptomics. The software auto ingests output data files from DRAGEN analysis pipelines and supports the import of other commercially available platforms for maximum flexibility.

## Proteomics analysis

Illumina Connected Multiomics simplifies the analysis and visualization of complex high-throughput proteomic data. Following protein capture and library preparation using Illumina Protein Prep and sequencing on Illumina sequencing systems, the DRAGEN Protein Quantification pipeline performs secondary analysis, including protein counting and normalization, with quality control reporting. These outputs are further analyzed within Illumina Connected Multiomics, which enables sample filtering, dimensionality reduction, clustering, differential expression, and pathway analysis. Interactive 2D and 3D visualizations help researchers explore biological patterns and relationships across single-omic, multiomic, and multimodal data sets (Figure 3).

## Transcriptomics analysis

Illumina Connected Multiomics delivers comprehensive capabilities for transcriptomic data interpretation. After RNA extraction and library construction using Illumina RNA Prep, sequencing is performed on Illumina systems to generate raw reads. The DRAGEN RNA pipeline processes these reads through alignment, quantification, normalization, and rigorous quality checks. Once primary outputs are ready, Illumina Connected Multiomics provides advanced tools for refining data sets, applying dimensionality reduction, clustering samples, and identifying differentially expressed genes (Figure 4). Integrated pathway enrichment and interactive visual dashboards allow researchers to uncover functional relationships and biological trends across transcriptomic and multiomic contexts (Figure 4).

## Epigenomics analysis

Illumina Connected Multiomics enables the analysis of DNA methylation and genetic variation from a single sequencing run. Using Illumina 5-Base DNA Prep and the DRAGEN analysis pipeline, researchers can detect methylated cytosines alongside standard genomic variants, enabling deeper insights into gene regulation. Illumina Connected Multiomics gives users the ability to delve deeper into their methylation data with advanced analyses such as differentially methylated region (DMR) detection, gene set and pathway enrichment, principal component analysis (PCA), and unsupervised clustering (Figure 5). Visualization of sample-level QC metrics describing read mapping quality and CpG methylation calling makes it easier to filter out samples that fail to meet study criteria, ensuring that only high-quality data are used for downstream analysis. With Illumina Connected Multiomics, researchers can explore methylation changes across samples, annotate genomic regions, and link epigenetic modifications to biological functions to maximize insights from their genomic and epigenomic studies.

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* For a complete list of supported assays, visit
  help.connected.illumina.com/icm/reference/supported-data-types

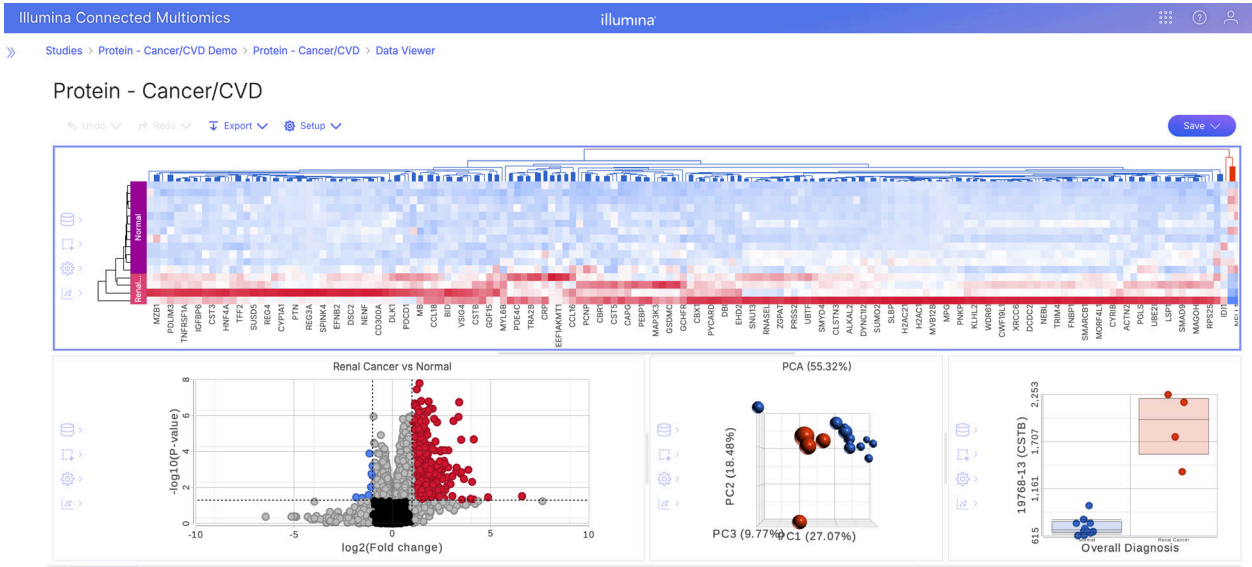For Research Use Only. Not for use in diagnostic procedures.

**Figure 3: Explore proteomic data at scale with powerful algorithms and visualizations**

Example of output from Illumina Connected Multiomics featuring (top) hierarchical clustering heat map identifying correlation between annotations and proteins, (bottom) volcano plots and PCA showing proteomic comparison between test and control samples.
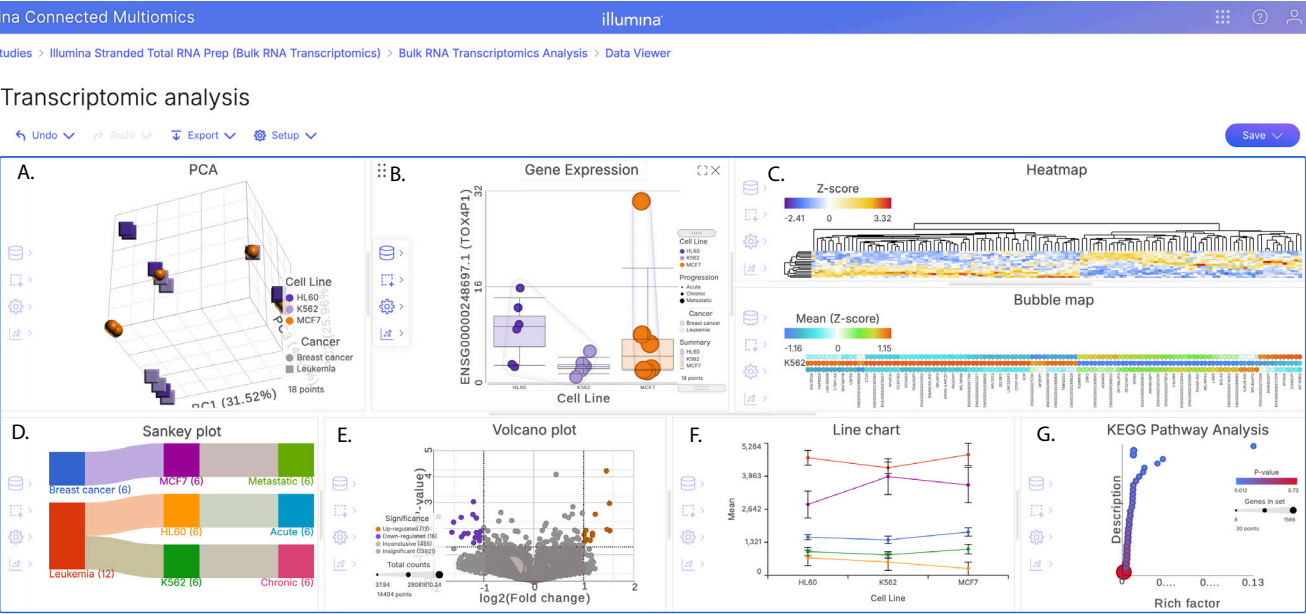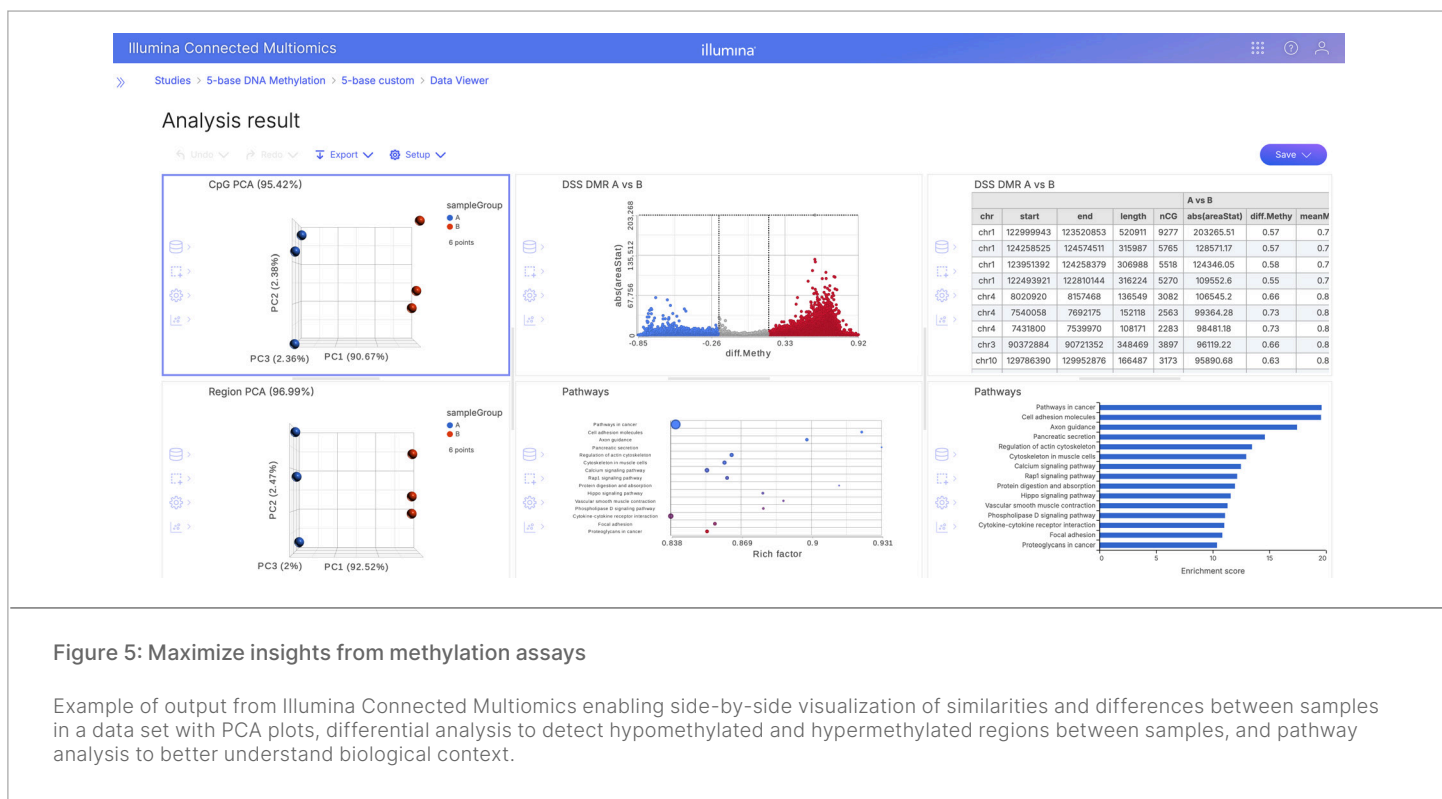


**Figure 4: Generate a comprehensive picture of the transcriptome with insightful visualizations in a user-friendly interface**

An example output from Illumina Connected Multiomics featuring (A) 3D PCA plot for each sample depicting dimension reduction colored by cell line and sized by cancer type, (B) box and whisker plot of gene expression across cell line, (C) heat map with hierarchial clustering showing gene relationships across samples and bubble map of mean gene values across cell lines, (D) Sankey plot depicting attribute relationships, (E) volcano plot showing the up and downregulation of genes, (F) line plot showing average gene expression across samples, and (H) pathway analysis to help interpret biology.

**Figure 5: Maximize insights from methylation assays**

Example of output from Illumina Connected Multiomics enabling side-by-side visualization of similarities and differences between samples in a data set with PCA plots, differential analysis to detect hypomethylated and hypermethylated regions between samples, and pathway analysis to better understand biological context.
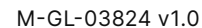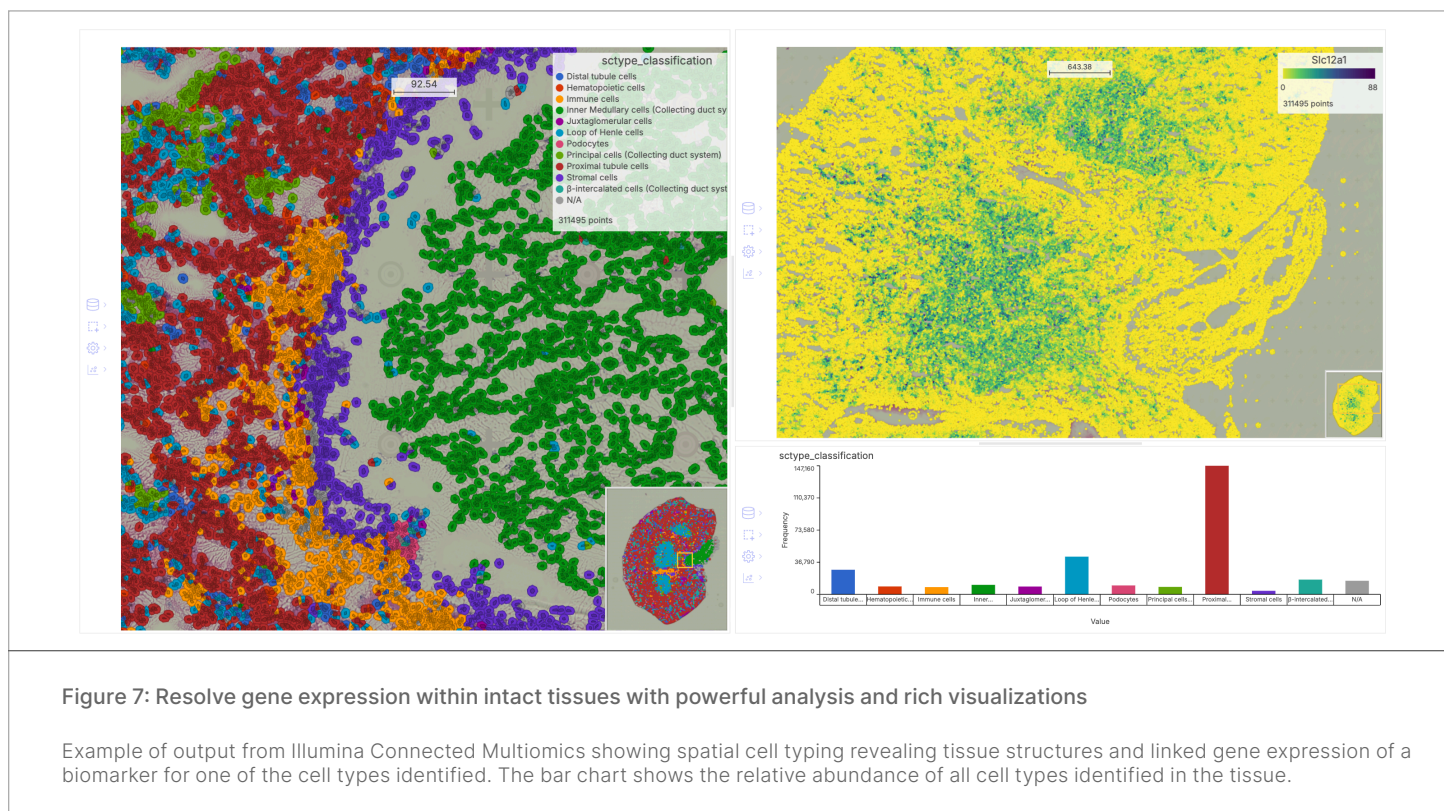
## Single-cell transcriptomics analysis

Analyzing single-cell transcriptomics data can be computationally intensive due to the high dimensionality, high volume, and technical and biological variability inherent to single-cell assays. Optimized for data generated using Illumina Single Cell 3′ RNA Prep and the DRAGEN Single Cell RNA pipeline, Illumina Connected Multiomics enables scalable analysis of up to a million cells, with tools for data quality control reporting, filtering, normalization, dimensionality reduction, clustering, cell classification, differential expression, and pathway analysis to maximize insights. Illumina Connected Multiomics gives users the ability to integrate data from select third-party single-cell RNA sequencing platforms and annotate results with phenotypic metadata for richer biological context. Researchers can explore multiple omics and modalities simultaneously using interactive 2D and 3D visualizations, with built-in tools to integrate cell populations for comparative analysis (Figure 6).

## Spatial transcriptomics analysis

With spatial transcriptomics, researchers can profile gene expression in intact tissues to reveal cellular behavior within the spatial context of complex tissues. Analyzing spatial transcriptomics data can be challenging due to the massive amounts of high-dimensional data that are generated when integrating outputs from sequencing and imaging modalities. Illumina Connected Multiomics enables spatial transcriptomics as part of a streamlined workflow that starts with Illumina spatial technology, followed by high-throughput sequencing, and secondary analysis with the DRAGEN Spatial Transcriptome pipeline, which aligns reads, maps spatial coordinates, segments cells via machine learning, and clusters data. The results are then explored interactively through Illumina Connected Multiomics. Specialized tools for differential expression analysis, automated cell typing, marker gene identification, and biological interpretation with publication-ready visualizations (Figure 7) empower researchers to uncover deeper insights into tissue structure and gene expression.

**Figure 6: Analyze multiple samples from single-cell RNA sequencing assays simultaneously with cutting-edge tools and visualizations**

Example of output from Illumina Connected Multiomics showing (A) PCA, UMAP projections, and cell typing visualized in 3D plots with synchronized bar graphs indicating highlighted cell types in all plots and differential expression between cell types to reveal potential biomarkers, (B) isolated or integrated view of cells enabling simultaneous exploration of multiple modalities within single-cell data sets, (C) interactive cell-level QC and cell filtering using UMI counts, detected genes, or mitochondrial and ribosomal counts.
UMAP, uniform manifold approximation and projection; UMI, unique molecular identifier.

**Figure 7: Resolve gene expression within intact tissues with powerful analysis and rich visualizations**

Example of output from Illumina Connected Multiomics showing spatial cell typing revealing tissue structures and linked gene expression of a biomarker for one of the cell types identified. The bar chart shows the relative abundance of all cell types identified in the tissue.

## Flexible, scalable workflows

Illumina Connected Multiomics is built to support both small-scale pilot experiments and large, multimodal studies. The platform is flexible, featuring both preconfigured and customizable workflows that streamline data import, aggregation, and annotation, enabling labs to curate comprehensive studies. Advanced informatics tools, scalable performance, and end-to-end workflows included in Illumina Connected Multiomics enhance operational efficiency within a security-first infrastructure designed to meet data privacy and compliance standards.

## Summary

Integrating findings from complementary modalities, including genomics, transcriptomics, epigenomics, and proteomics, into multiomic data sets provides a more comprehensive picture of cellular function. Illumina Connected Multiomics is an easy-to-use bioinformatics platform that streamlines the analysis of NGS and large-scale multiomics data in an intuitive visual user interface. Powerful statistical algorithms, information-rich visualizations, an interactive interface, and cutting-edge genomic tools empower researchers to analyze their data confidently, without the need for advanced informatics expertise.

**Learn more**  →

Illumina Connected Multiomics

DRAGEN secondary analysis

Ordering information

| Product | Catalog no. |
|---|---|
| Illumina Connected Multiomics Basic License | 20141940 |
| Illumina Connected Multiomics Professional License—Trial | 20141939 |
| Illumina Connected Multiomics Professional License—Annual | 20141942 |
| Illumina Connected Multiomics Professional License—Monthly | 20156707 |

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