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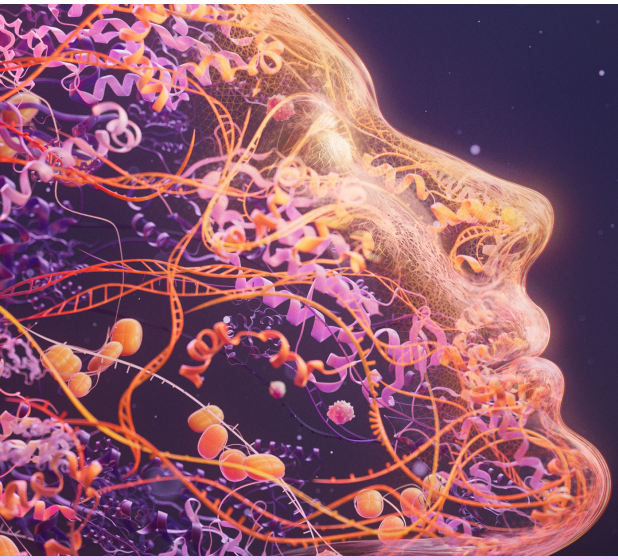


More insights from multiomic data

Understand the fundamentals of the data analysis workflow that combines genomic and transcriptomic sequencing data for comprehensive results

Easier-than-ever data analysis workflows for genomics and transcriptomics

Data analysis can be a complex and time-consuming part of multiomic research. Illumina multiomics data analysis solutions streamline workflows and simplify integrated genomic and transcriptomic analyses, enabling researchers to move more efficiently from sequencing data to biological insight.

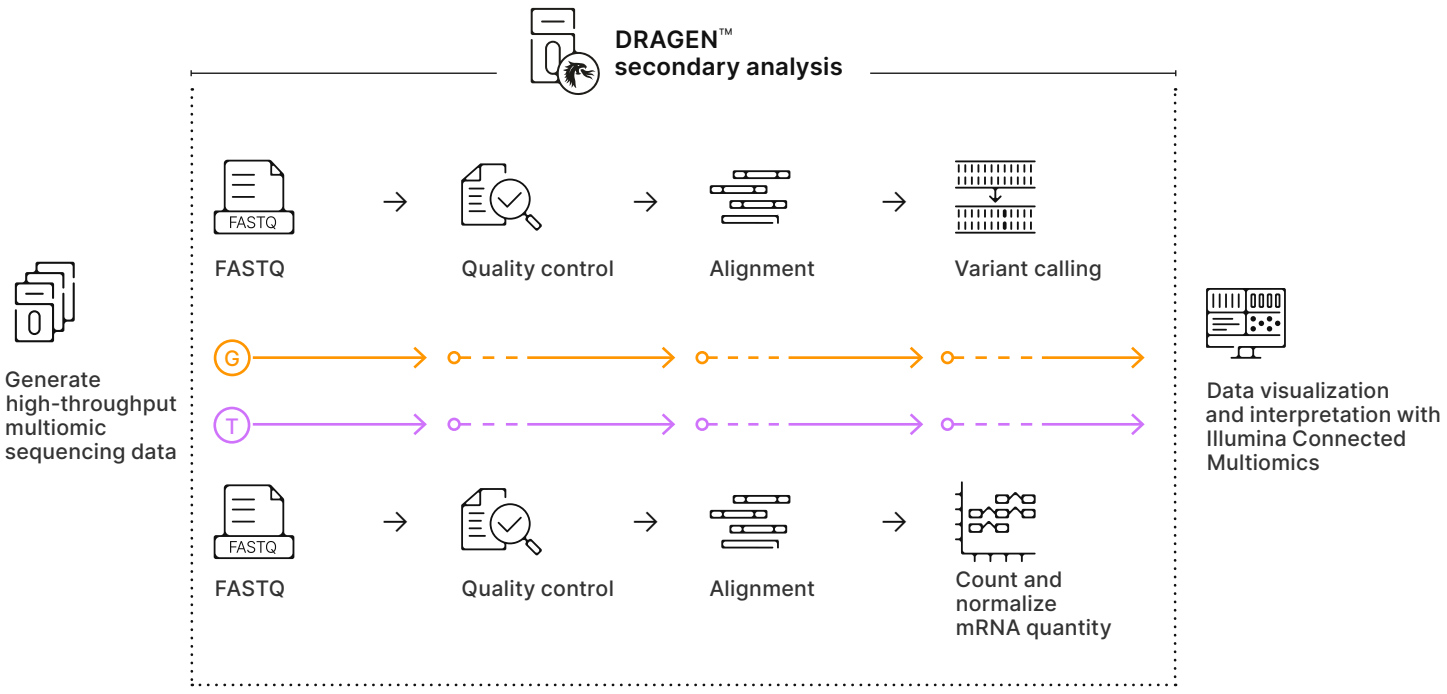


Figure 1: Multiomics analysis workflow for genomic and transcriptomic data

Multiomic workflows that integrate genomic and transcriptomic data involve several analytical steps that support the transition from raw sequencing data to biological insight. DRAGEN secondary analysis performs sequencing quality assessment, read alignment, sensitive and accurate variant calling, and RNA quantification with normalized expression outputs, to enable integrated genomic and transcriptomic interpretation. Illumina Connected Multiomics enables exploration and visualization of these multimodal data sets.

Simplified data interpretation delivers powerful multiomic insights

The strength of multiomics comes from the ability to interpret sequencing data across multiple molecular layers. Illumina Connected Multiomics provides fully integrated multiomic analysis with direct integration of outputs from DRAGEN secondary analysis. Using industry-standard statistical methods, the software generates clear, informative visualizations and delivers an end-to-end solution that scales to support large and small studies, simplifying multiomic analysis.

Learn more about Illumina Connected Multiomics

Request a demo →

Figure 2: Illumina Connected Multiomics makes it easy to create high-quality visualizations for clear data interpretation

In this example, integrated single-cell ATAC-Seq and proteomic analysis in Illumina Connected Multiomics highlights chromatin accessibility, cell-type clustering, differential features, and regulatory relationships across thousands of cells.

Illumina solutions empower multiomic methods

The integrated ecosystem, spanning multiomics library preparation, high-throughput sequencing, DRAGEN software powered by Illumina Genomic AI, and Illumina Connected Multiomics, powers end-to-end multiomic research workflows, delivering scalable, high-confidence insights from data generation through interpretation.

Library prep

Sequencing systems

Accurate variant calling and fast analysis

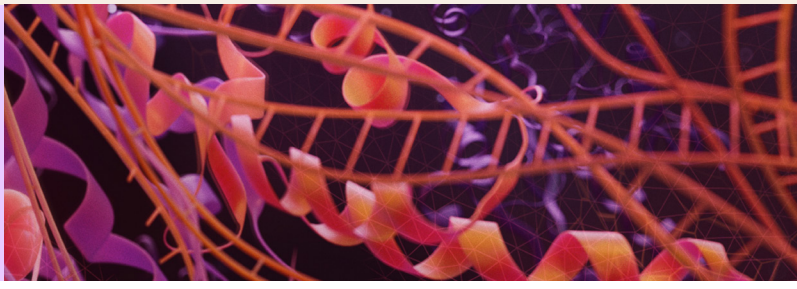
99.93% F1 score*
34 min analysis†

Deeper biological insights

* Illumina internal data on file, 2026, accuracy score calculated with DRAGEN v4.5 using benchmarking data from Precision FDA Truth Challenge v2. precision.fda.gov/challenges/10
† Process a 40× genome in ~34 min with all supported callers.

Start your Multiomics workflow today →

Explore our Multiomics data analysis workflow guide



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