Connected Multiomics

Transform 5-base DNA methylation data into biological understanding

Collaborate, discover, and amplify results

5-base DNA methylation studies can reveal thousands of epigenetic changes across the genome, but determining which signals are biologically meaningful and how they contribute to gene regulation can be challenging. Connected Multiomics helps researchers investigate methylation patterns, prioritize regions of interest, and place findings into biological context using curated knowledgebases.

Integrated environment

Unified environment for teams to collaborate on high-dimensional data with the same tools—no file transfers

Evidence-based reasoning

Evidence-based AI provides guidance, while curated knowledgebases contextualize findings to deepen research

Cumulative insights

Reproducible studies build on one another, enabling cumulative insights that maximize their collective impact

illumina®

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

© 2025 Illumina, Inc. All rights reserved. M-GL-03727

Connected workflow

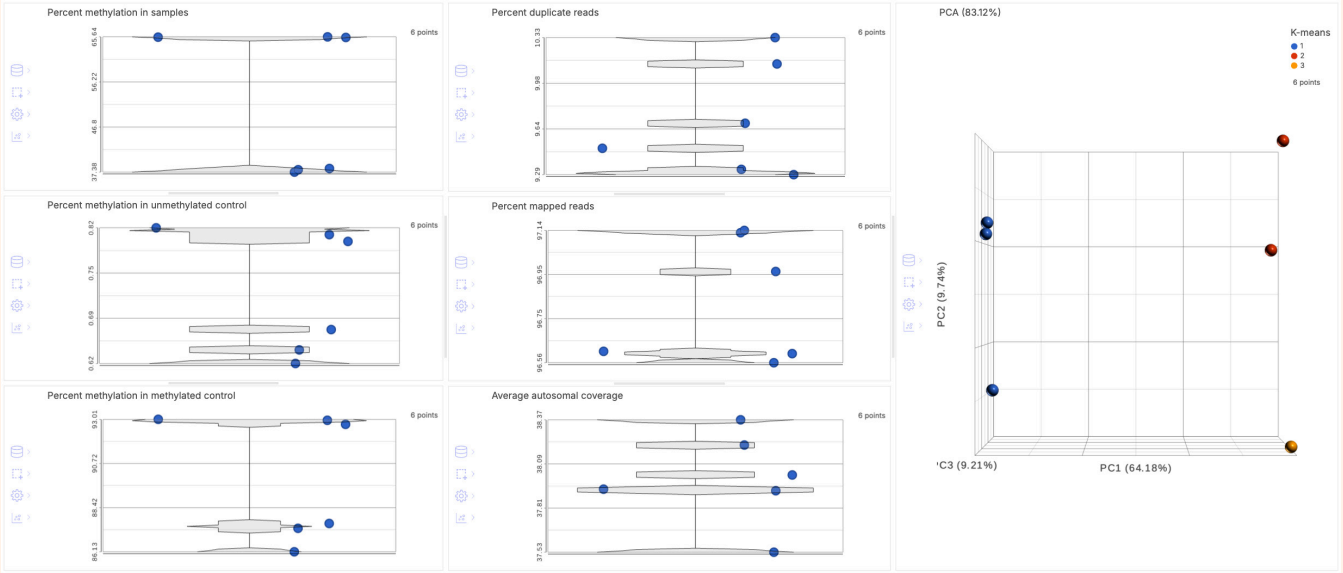
Connected Multiomics leverages DRAGEN™ 5-Base DNA pipeline outputs for biological exploration and interpretation. Researchers can investigate methylation patterns across samples, evaluate regional methylation changes, and explore relationships between epigenetic signals and gene regulation using interactive visualizations and validated analytical methods. Integrated access to curated knowledgebases supports biological interpretation and helps connect findings to biological pathways and processes.

Powerful analysis:

- Filter samples to ensure only high-confidence data feeds into downstream discovery
- Analyze differential methylation to pinpoint epigenetic drivers across conditions or phenotypes
- Generate and annotate regional methylation data to connect differentially methylated regions to functionally relevant genes
- Reduce data dimensionality to reveal epigenetic patterns and group samples
- Integrate methylation with DNA variants to uncover how genetic and epigenetic layers interact
- Interpret biological patterns to link methylation signatures to pathways and disease mechanisms

Prepare libraries	Sequence	Analyze	Exploratory analysis
Prepare samples using the Illumina 5-Base DNA Prep or 5-Base DNA Prep with Enrichment kits	Sequence libraries using Illumina mid and high throughput sequencers	Use DRAGEN 5-base for methylation aware alignment, methylation calling, SNV, CNV, SV, and assay QC	Use Illumina Connected Multiomics to prepare, explore, compare, and interpret 5-base DNA methylation data

Identify biologically meaningful methylation patterns



The left and middle columns show independent QC plots for sample methylation levels, control performance, duplicate reads, mapping rates, and autosomal coverage. The right column shows a PCA plot of methylation profiles, with the first three principal components explaining 83.1% of the total variance and revealing distinct sample clusters.

illumina®

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

Scan or click QR code to learn more