# illumina®

# Intuitive and powerful methylation analysis

## with Illumina Connected Multiomics



Illumina Connected Multiomics empowers researchers to intuitively analyze large-scale, complex gene regulation data, without requiring bioinformatics expertise. Seamlessly integrate methylation data with other omics and modalities to unlock deeper biological insights.

Leveraging robust and accurate Illumina DRAGEN™ analysis results, Connected Multiomics auto launches results directly in its interactive environment for biological exploration. The visual interface makes it easy to gain sample-level methylation insights, reduce data dimensions, cluster samples, detect and annotate biomarkers with meaningful methylation changes, and link changes to functional biological processes.
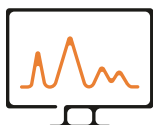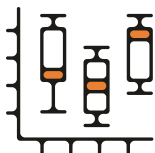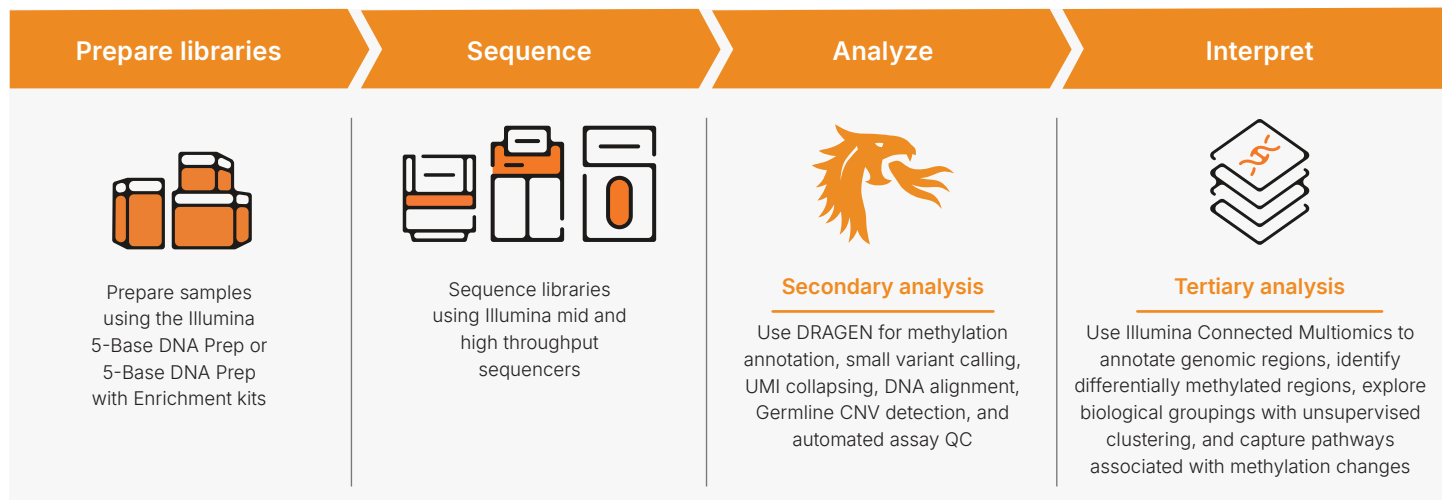
From sample preparation to data interpretation, the entire workflow is streamlined within the Illumina ecosystem. Simplify your methylation analysis and accelerate discovery.



**Unlock deeper biological insights**



**Streamline analysis with intuitive software**



**Scale your studies with ease**

## Confidently analyze multiomic data



**Interactive visualizations**
Explore methylation and variant annotation from a single sequencing run with information rich and publication ready visualizations



**Data Integration**
Attain results you can trust with robust statistical methods



**Multiomic and multimodal analysis**
Generate variant and methylation annotations from the same data reducing time, cost, and complexity, while enabling deeper biological interpretations without additional experiments



**Security-first infrastructure**
Protect the privacy of your data with industry-leading global and local security standards

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

A methylation workflow that integrates with the Illumina 5-base prep kits and sequencers to take biological studies from sample preparation to data interpretation.
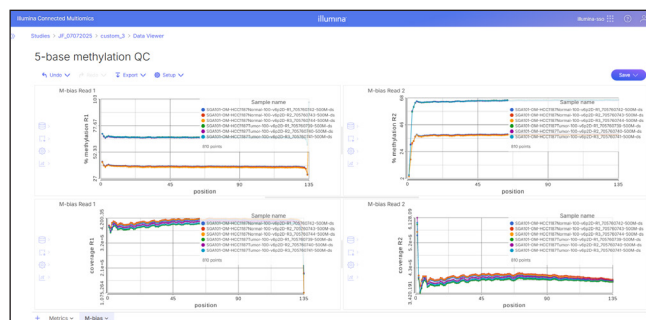
| Prepare libraries | Sequence | Analyze | Interpret |
|---|---|---|---|
| Prepare samples using the Illumina 5-Base DNA Prep or 5-Base DNA Prep with Enrichment kits | Sequence libraries using Illumina mid and high throughput sequencers | **Secondary analysis**<br>Use DRAGEN for methylation annotation, small variant calling, UMI collapsing, DNA alignment, Germline CNV detection, and automated assay QC | **Tertiary analysis**<br>Use Illumina Connected Multiomics to annotate genomic regions, identify differentially methylated regions, explore biological groupings with unsupervised clustering, and capture pathways associated with methylation changes |

## Bring your methylation data to life with interactive visualizations

Methylation QC metrics

M-bias

These plots are generated using the 5-base methylation QC task by extracting and plotting statistics in the secondary analysis output metric files. From the QC report, we visualize sample-level QC metrics that describe reads mapping quality and DNA methylation calling quality, for e.g., percentages of CpG methylation in the samples, in the unmethylated control, and in the methylated controls.

## Advanced features include:

- ✓ 5-base methylation QC report
- ✓ PCA and clustering
- ✓ Differential methylated regions (DMR) detection and annotation
- ✓ Gene set and pathway enrichment analysis

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

Learn more

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