

Streamlined methylation analysis with Illumina Connected Multiomics

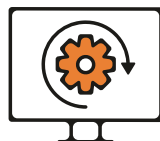
Powerful, intuitive, scalable multiomic analysis



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



Unlock deeper
biological insights



Intuitive and
streamlined analysis



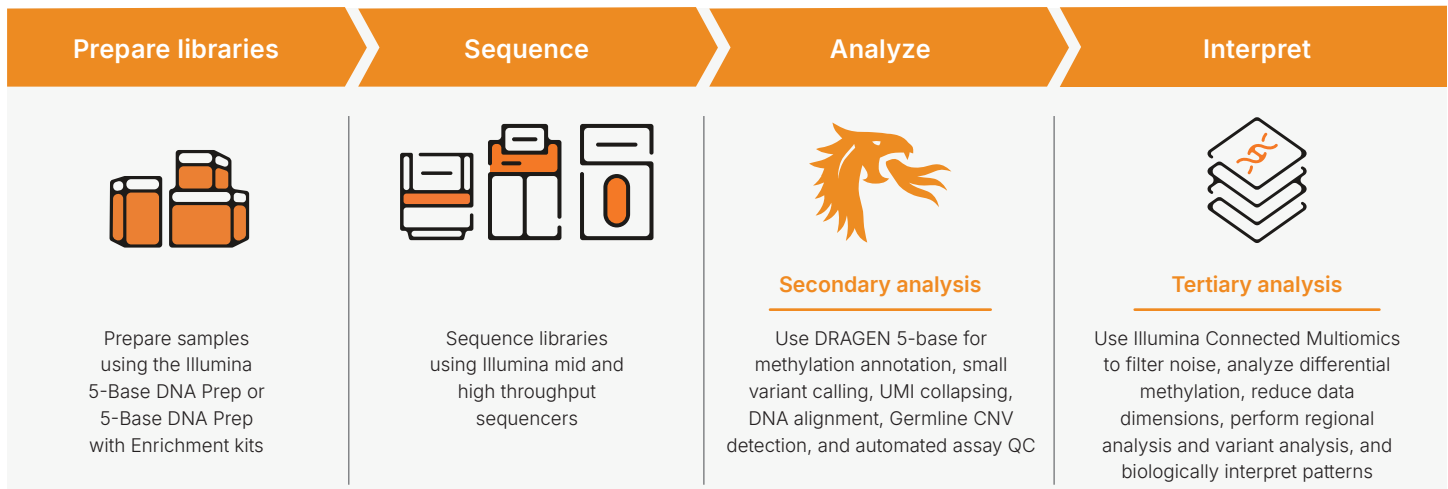
Scale
infrastructure

Connected workflow

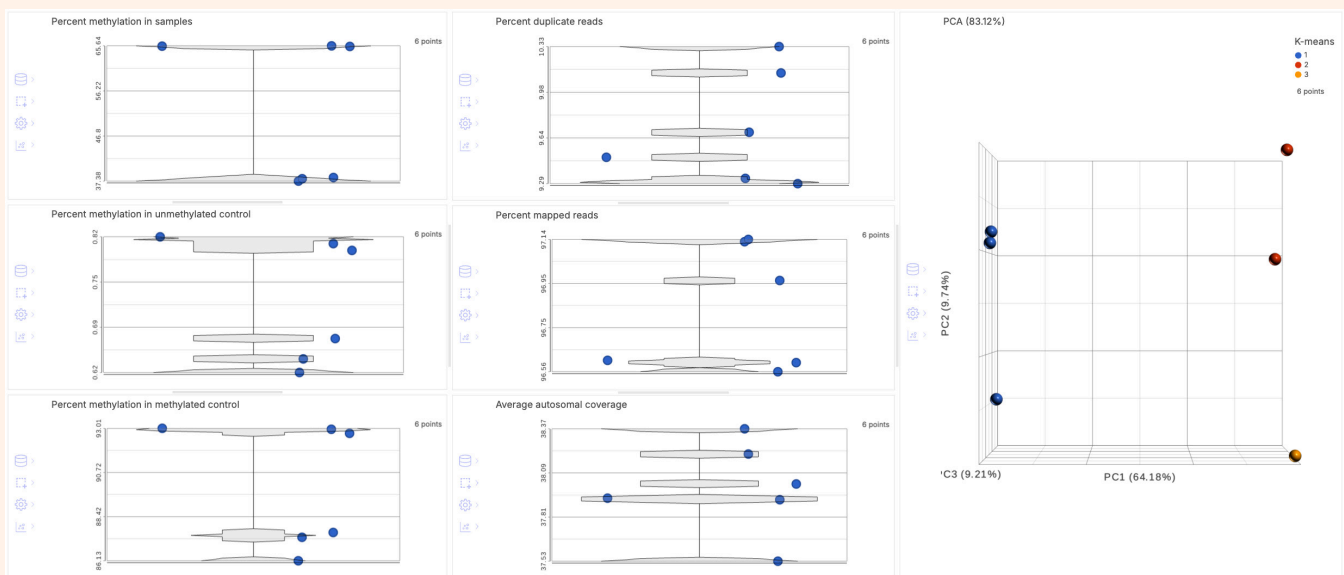
Optimized for Leveraging robust **DRAGEN™ 5-Base DNA pipeline** analysis results, Connected Multiomics enables you to perform biological exploration. The visual interface makes it easy to gain sample-level methylation insights, reduce data dimensions, cluster samples, detect and annotate biomarkers with meaningful methylation changes, and link changes to functional biological processes.

Advanced features include:

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



Bring your methylation studies to life with beautiful, interactive visualizations



Default pipeline outputs for 5-base analysis.

