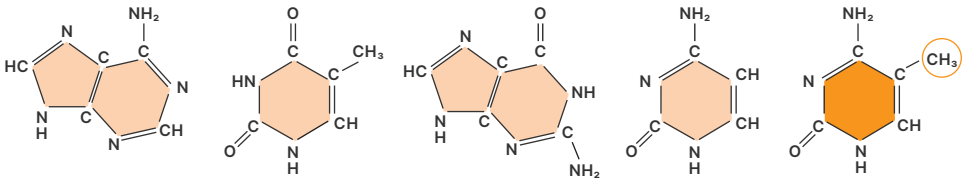
Illumina 5-base solution for methylation and variant detection

One assay. Dual insights.

Gain a comprehensive view of gene regulation with exceptional accuracy, simplicity, and scale. The Illumina 5-base solution is a fundamentally different approach to DNA methylation analysis. Novel chemistry and optimized algorithms enable simultaneous genomic and epigenomic discoveries in a single readout, with a streamlined workflow.

Genetic variation and methylation data in a single assay

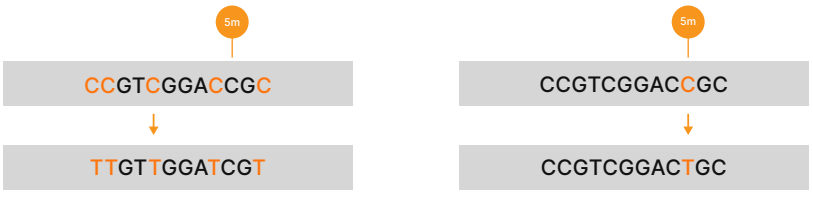
DNA is inherently multiomic, with modified bases that hold epigenetic information. The Illumina 5-base solution detects 5-methylcytosine (5mC) along with unmodified bases, A, T, G, and C, for multiomic insights.



Adenine A | Thymine T | Guanine G | Cytosine C | 5-Methylcytosine 5mC

Novel chemistry allows direct conversion of 5mC to T

Common methods for detecting DNA methylation use bisulfite or enzymes to convert unmethylated C to T. This reduces nucleotide diversity, making reads harder to align. Bisulfite treatment can also damage DNA, leaving data gaps. Illumina 5-base chemistry directly converts only 5mC to T in a simple, single step, which is nondamaging to DNA and retains library complexity.



Bisulfite or on-market enzymatic conversion

Illumina 5-base conversion

Advantages of the Illumina 5-base solution over other methylation detection methods

Metric	Bisulfite	On-market enzymatic	Illumina 5-base
DNA damage	High X	Medium X	Low √
Nucleotide diversity	Low X	Low X	High √
Workflow complexity	High X	High X	Low √
Methylation detection accuracy	High √	High √	High √
Variant detection accuracy	Low X	Low X	High √

Better efficiency

√ Advantages X Disadvantages

Streamline multiomic workflows

- Simple, single-step 5mC to T base conversion
- Easy library preparation completed in less than a day*

* For whole-genome workflow.

Make every read count

- Combined methylome and genome insights with high coverage uniformity
- Maximum sequencing output with greater mapping efficiency

Simplify data interpretation

- High-accuracy dual genomic and epigenomic annotations powered by DRAGEN™ analysis
- Easy-to-use, clear visualizations and analysis with Illumina Connected Multiomics

Streamlined library-to-analysis workflow from Illumina

Prepare samples

Compatible with multiple sample types, including cell-free DNA

Prepare libraries

Whole-genome sequencing or targeted enrichment†

Sequence

NovaSeq™ X Series or NextSeq™ 2000 System

Analyze

DRAGEN secondary analysis

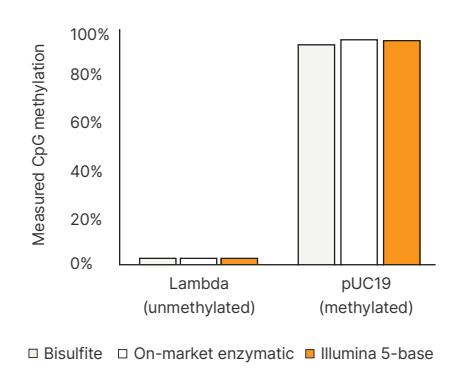
Insights

Illumina Connected Multiomics

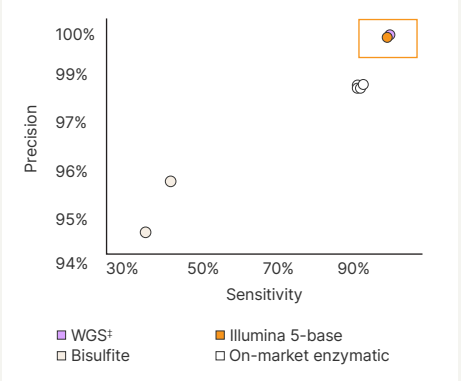
† Kits expected to launch H1 2026.

High-accuracy genome and methylome data in the same reads

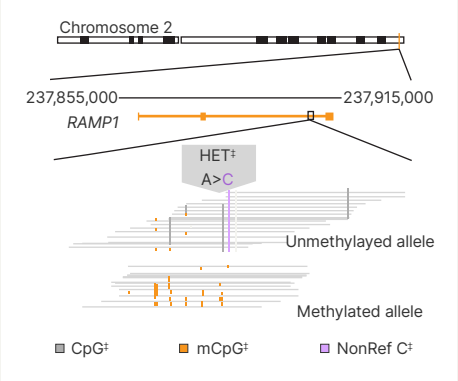
Methylation detection



Genetic variant detection



Together



High-accuracy methylation detection

Genome-wide accuracy of germline SNV‡ detection

Dual insights in the same reads

‡ WGS, whole-genome sequencing; SNV, single nucleotide variant; HET, heterozygous; CpG, cytosine-guanine dinucleotide; mCpG, methylated cytosine-guanine dinucleotide; NonRef C, non-reference cytosines.

Accessible multiomic discovery

The Illumina 5-base solution makes it easier to access multiomic insights and decipher the mechanisms of gene regulation. This richer context can help reveal biomarkers for cancer or genetic disease to accelerate disease research and therapeutic development efforts.

Learn more about the Illumina 5-base solution

illumina.com/5-base

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