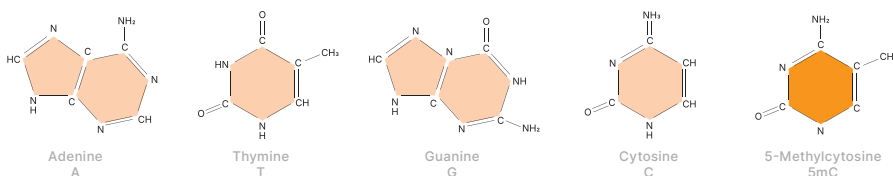


Dual insights. One easy assay.

Introducing a revolutionary solution to measure DNA methylation and genetic variation together, with exceptional accuracy, simplicity, and scale. Novel base conversion chemistry and powerful algorithms enable simultaneous genomic and epigenomic discovery in a single readout. Access a comprehensive view of gene regulation using a streamlined library-through-analysis solution from Illumina.

Genetic variation and methylation data in a single assay

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



Novel chemistry allows direct conversion of 5mC to T



Common methods for detecting DNA methylation use bisulfite or enzymes to convert unmethylated C to be read as T in sequencing data. This leads to libraries with low nucleotide diversity that are harder to align. The harsh conditions of bisulfite treatment damage DNA, leaving large gaps in genome data. Illumina 5-base chemistry directly converts only 5mC to T in a simple, single step, which is nondamaging to DNA and retains library complexity.

Accessible multiomic discovery

Comprehensive, accurate genome and methylome data in the same assay give richer context to help researchers decipher the sophisticated mechanisms of gene regulation and identify biomarkers. The Illumina 5-base solution makes multiomic insights more accessible to accelerate disease research and therapeutic development efforts.



Learn more about the Illumina innovation roadmap
illumina.com/innovation



Streamline your multiomic workflows

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



Make every read count

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



Easily interpret combined genome and methylome data

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

