

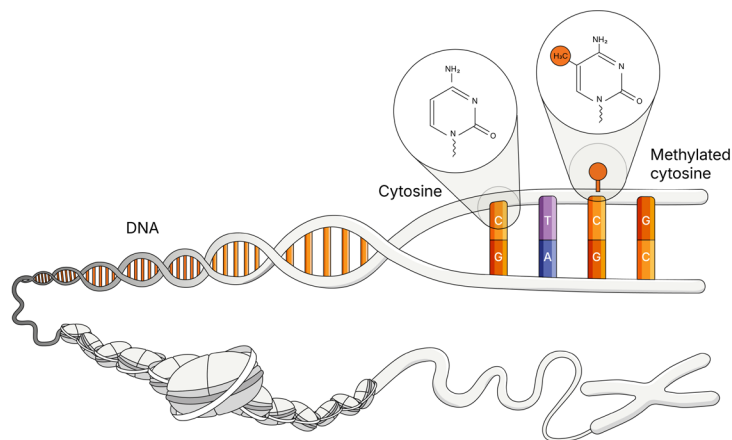
illumina 5-base solution

One assay. Dual insights. Integrated genomic and epigenomic analysis for advanced cancer research

Unlock genetic variants and DNA methylation patterns simultaneously—using a single, streamlined illumina 5-base assay.

Why it matters

Cancer biology is shaped by both genetic mutations and epigenetic regulation. Traditional single-omic approaches often miss this interplay. The illumina 5-base solution enables simultaneous detection of DNA variants and methylation patterns—delivering a more complete molecular understanding of cancer in one assay.



Key cancer research applications



Tumor classification & subtyping

Combined genetic and methylation data for improved tumor classification and to help enable predictive multiomic models; used in complex cancers like CNS*, sarcoma, and kidney, and supports prediction of tissue of origin in CUP.†



Comprehensive cancer profiling

Multi-cancer early detection applications that allow for mutations, methylation and fragmentomics in a single assay, resolving ambiguity inherent to single-omic approaches.



Cell-free DNA (cfDNA) analysis

Profiling circulating tumor DNA to support early detection, disease monitoring, and longitudinal studies, including emerging fragmentomic applications.



Epigenetic drivers of cancer

Revealing regulatory changes that drive tumor progression, without adding workflows or assays.



Accelerated biomarker discovery

Multiomic data enables faster discovery of novel therapeutic targets and disease biomarkers.



Faster publication timelines

Integrated workflows reduce complexity, streamline analysis, and shorten time-to-results.

* CNS, central nervous system (brain and spinal cord tumors).

† CUP, cancer of unknown primary (cancers where the origin site is not identified).

Key features of the Illumina 5-base solution

- **Dual insights, one workflow**
Simultaneously generate genomic and methylation data from the same sample, in a single library preparation, and in the same sequencing run—reducing workflow complexity and turnaround time.
- **Robust performance with challenging samples**
Validated with orthogonal methods, delivering confident single nucleotide variant (SNV) and methylation calls from low-input and low-quality samples.
- **Broad sample compatibility**
Supports fresh frozen tissue, cfDNA, genomic DNA (gDNA), and formalin-fixed, paraffin-embedded (FFPE)[‡] across a wide input range.
- **Cost-effective by design**
A single assay replaces multiple workflows—saving time, sequencing, and operational costs.
- **Fast turnaround**
Library prep and analysis completed in as little as 24–36 hours.[§]
- **Flexible research applications**
Available for whole-genome sequencing or targeted enrichment to focus on key cancer driver genes.
- **Integrated analysis & visualization**
DRAGEN™ secondary analysis with integrated visualization in Illumina Connected Multiomics—no advanced bioinformatics expertise required.

[‡] Application note demonstrating compatibility with FFPE available in H1 2026.
[§] For whole-genome kit.

Ready to advance your cancer research?

Learn more about the Illumina 5-base solution



Why Illumina 5-base for cancer research

High sensitivity to epigenetic change

Detect subtle methylation differences that contribute to tumor heterogeneity.

Built for translational research

Well-suited for disease classifiers, biomarker development, and multiomic discovery pipelines.

Tumor-normal pair analysis

Simultaneously compare somatic and germline variants alongside methylation profiles for comprehensive tumor characterization.

Optimized for limited samples

Extract maximum insight from scarce material—critical for rare tumors and minimal cfDNA inputs.

Easy workflow designed for operational efficiency

Minimal incremental sequencing required for methylation insights.

Seamlessly integrates with existing Illumina systems and software.

Illumina 5-base solution workflow

