CD Genomics
The Genomics Services Company

Illumina 5-base Sequencing Service

One assay for genome and methylome decision-making

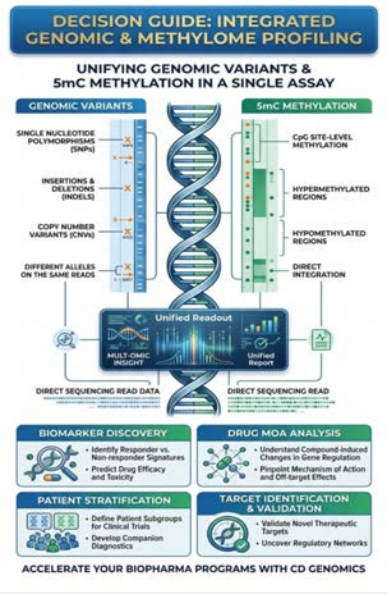
CD Genomics provides a single-assay 5-base sequencing workflow for integrated genomic and epigenomic insight.

Why teams choose this workflow

- Detction 5mc and SNVs in one assay
- Preserve DNA integrity and library complexity
- Improve mapping efficiency and coverage uniformity
- Support low-input and cfDNA-compatible projects

Best-fit use cases: oncology, biomarker discovery, genetic disease studies, and projects with limited or fragmented DNA.

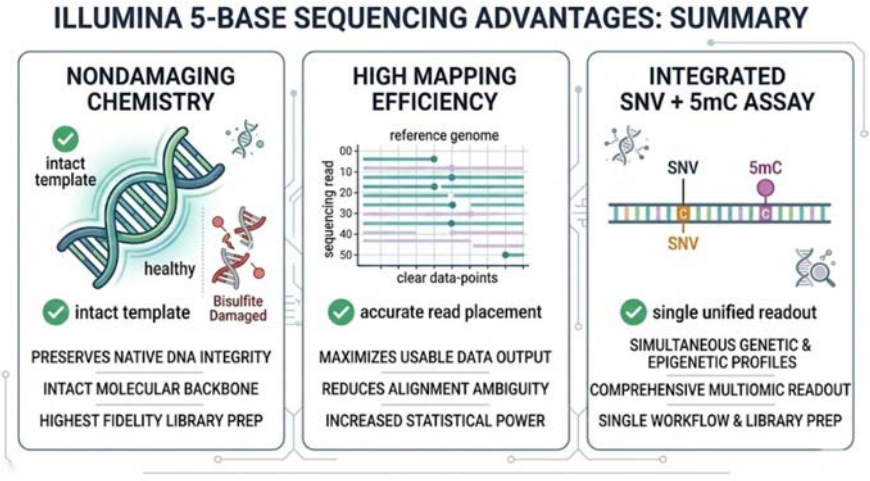
Request Quote



Integrated genomic and methylome profiling in a single assay.

Why this matters operationally

The 5-base approach reduces the typical trade-offs of conversion-heavy methylation workflows: nondamaging chemistry protects valuable samples, higher nucleotide diversity supports cleaner alignment, and a unified readout makes both SNV and 5mC analysis more actionable.



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A Better Decision Than Bisulfite-Only Thinking

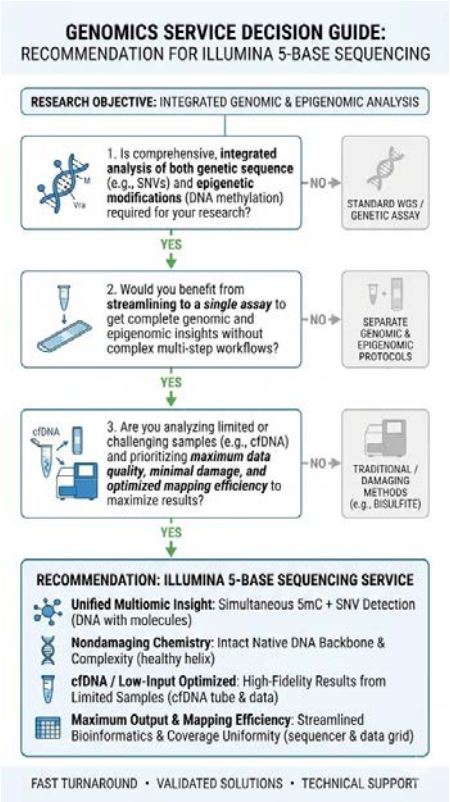
Use the comparison below to evaluate whether an integrated 5-base workflow is the stronger operational choice for your study.

Traditional bisulfite workflows answer part of the biological question, often at the cost of DNA damage, lower sequence complexity, and weaker support for variant analysis. For project owners, that means more uncertainty around data usability, interpretation, and sample risk.

Executive takeaway

If your team needs methylation insight without compromising variant interpretation, or if your samples cannot tolerate aggressive conversion workflows,

Decision metric	Bisulfite	Enzymatic	Illumina 5-base
DNA damage	High	Medium	Low
Nucleotide diversity	Low	Low	High
Workflow complexity	High	High	Low
Methylation detection	High	High	High
Variant detection	Low	Low	High

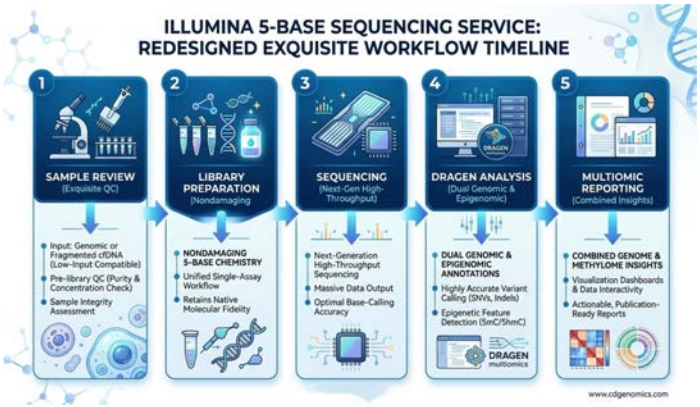


Decision path for integrated genomic and epigenomic study design.

From sample review to multiomic reporting

CD Genomics supports genome-wide and targeted enrichment study designs with a single-assay workflow from sample QC to sequencing, DRAGEN analysis, and integrated reporting.

Book a Call



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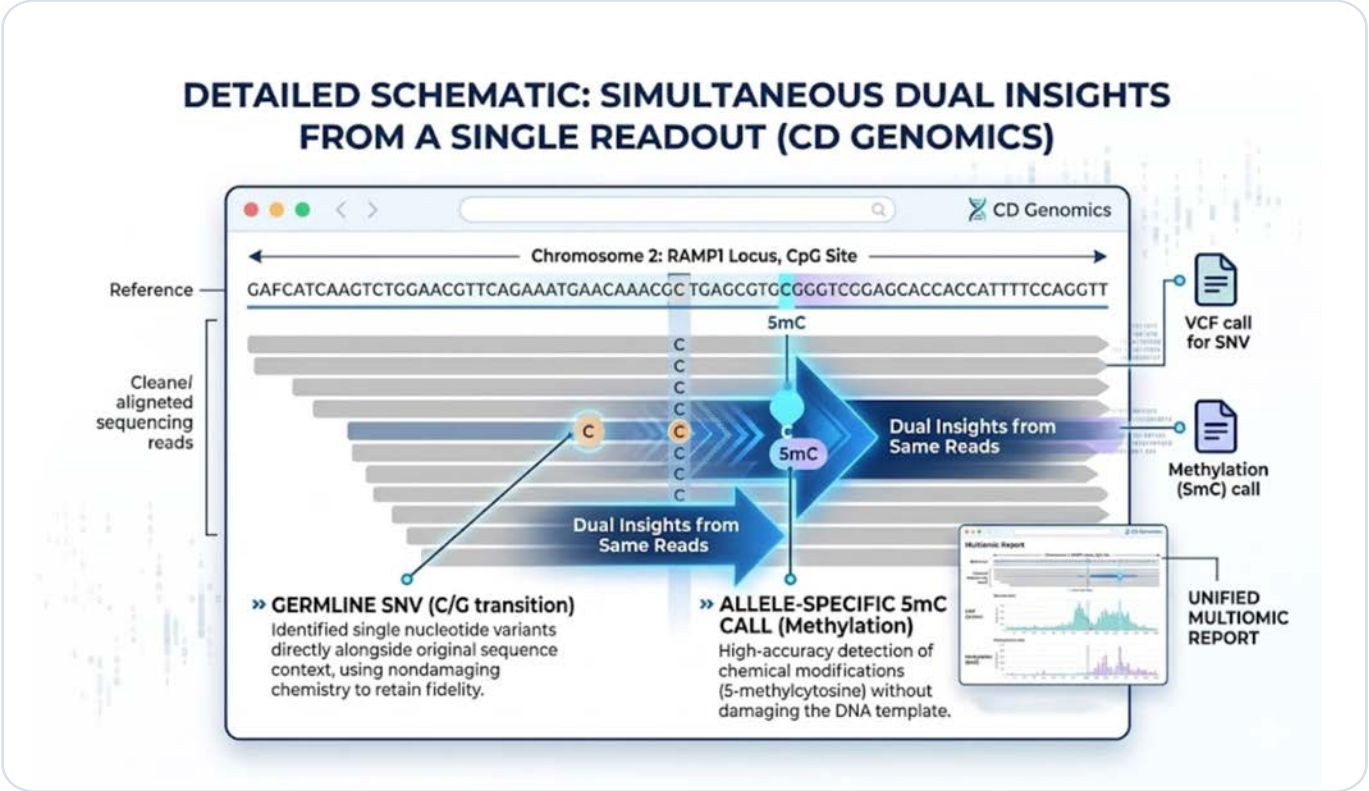
From Sample to Insight: What You Receive and How to Start

A concise project-launch page for scientists, BD teams, and translational program owners.



Standard deliverables

Dual insights from the same sequencing reads support direct interpretation of SNV context and allele-specific 5mC patterns.

- Raw FASTQ files
- QC reports
- BAM/CRAM alignment files
- Variant call files for SNVs and indels
- 5mC result outputs for downstream interpretation
- Structured files ready for reporting and review

What to prepare before launch

- Sample type and input amount (gDNA or cfDNA)
- Project objective: discovery, comparison, or validation
- Preferred scope: whole-genome or targeted enrichment
- Basic QC: concentration, purity, and fragment profile
- Internal decision points for study kickoff

Download Sample Submission Checklist

Contact CD Genomics for more information about project design and sample readiness.