

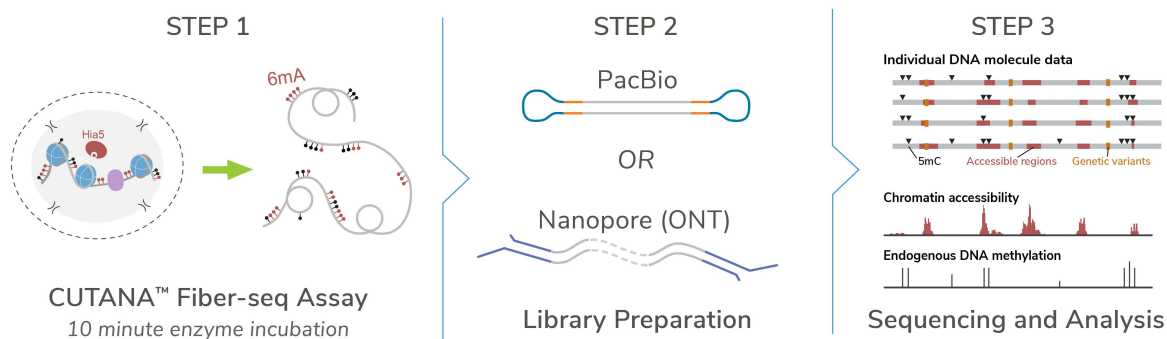
Comprehensive functional genomics meets long-read sequencing

CUTANA™ Fiber-seq is a groundbreaking platform that captures both genomic and epigenomic information in a **single long-read sequencing (LRS) assay**.

Fiber-seq **simultaneously profiles chromatin accessibility, DNA methylation, protein footprints, and genetic variants**, delivering unprecedented resolution of DNA sequence and chromatin features along individual DNA molecules.

Traditional multiomics often demands multiple assays, slowing research and consuming valuable resources. Because many of these approaches rely on short-read sequencing (SRS), they miss critical insights in complex genomic regions often tied to disease.

Fiber-seq uses a PCR-free, antibody-free workflow that simplifies experimental design



Nuclei are treated with CUTANA™ HiA5, an N6-methyladenine methyltransferase (6mA MTase) that methylates adenines within regions of accessible chromatin. Long-read sequencing data is analyzed to reveal multiomic information (e.g., chromatin accessibility, DNA methylation, genetic variants) at single-molecule level, which can also be aggregated for bulk analysis by genome or haplotype.

Fiber-seq detects open chromatin, DNA methylation, and protein footprints

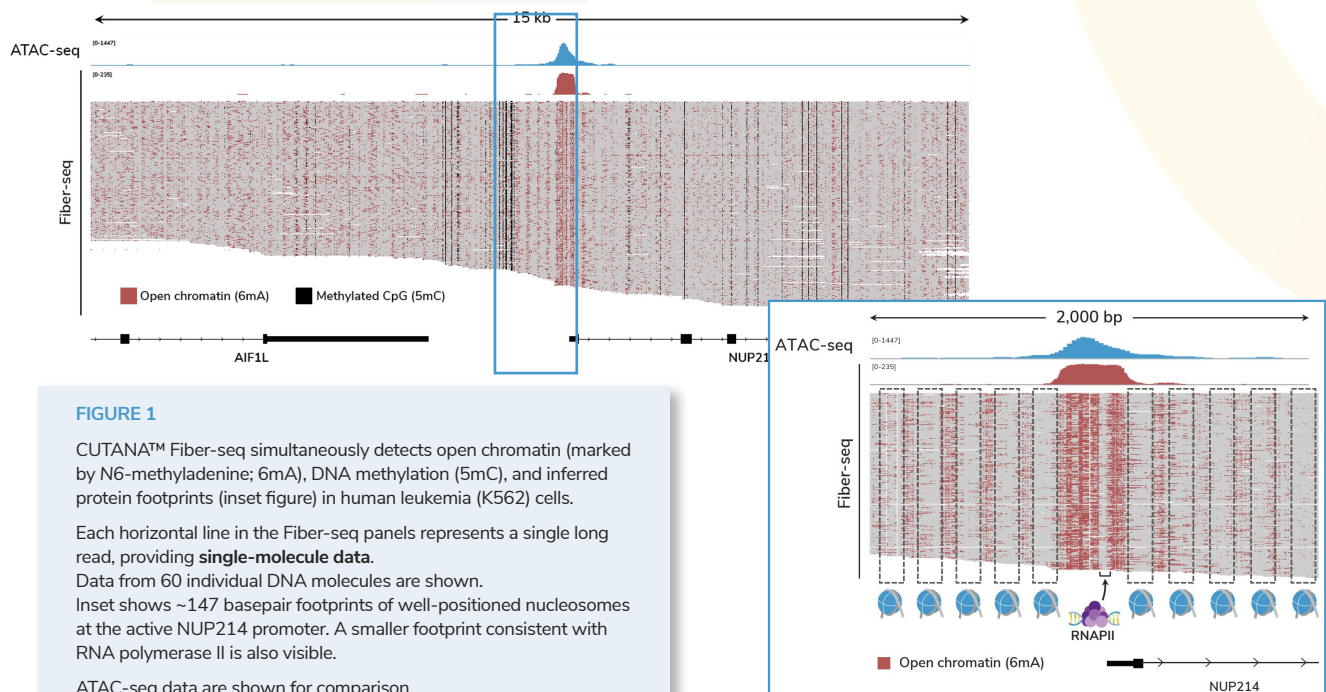


FIGURE 1

CUTANA™ Fiber-seq simultaneously detects open chromatin (marked by N6-methyladenine; 6mA), DNA methylation (5mC), and inferred protein footprints (inset figure) in human leukemia (K562) cells.

Each horizontal line in the Fiber-seq panels represents a single long read, providing **single-molecule data**.

Data from 60 individual DNA molecules are shown.

Inset shows ~147 basepair footprints of well-positioned nucleosomes at the active NUP214 promoter. A smaller footprint consistent with RNA polymerase II is also visible.

ATAC-seq data are shown for comparison.

Fiber-seq goes beyond ATAC-seq: uncover protein binding heterogeneity

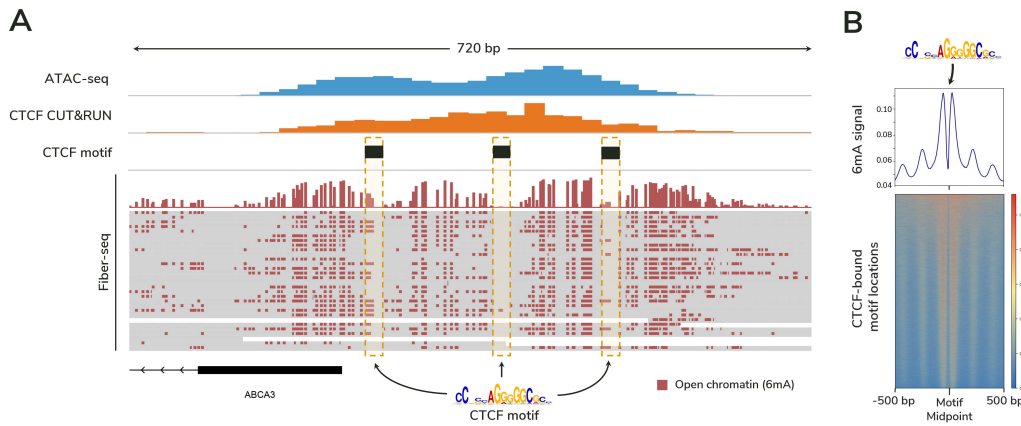


FIGURE 2

(A) Fiber-seq data from 30 individual DNA molecules are shown, with the top track displaying aggregate 6mA signal marking open chromatin. Each horizontal line below this track represents a single DNA molecule. Dotted boxes indicate CTCF motif regions. Because Fiber-seq provides single-molecule resolution, heterogeneity in protein binding across the cell population is revealed (the leftmost boxed region shows variable 6mA labeling, suggesting differential CTCF occupancy).

(B) Genome-wide 6mA signal demonstrates robust CTCF footprinting. Elevated 6mA levels flanking the motif midpoint reflect accessible DNA surrounding CTCF binding sites.

Fiber-seq: A single assay to simplify multiomic studies

	Fiber-seq	ATAC-seq	WGBS*	ChIP-seq
Multomics	✓	✗	✗	✗
Mapping resolution	Single-nucleotide	10-50 bp	Single-nucleotide	>150 bp
Data granularity	Profiles individual DNA molecules	Aggregated signal from bulk cell population	Aggregated signal from bulk cell population	Aggregated signal from bulk cell population
Protein footprinting	✓	✓ [†]	✗	✗
Native DNA methylation profiling	✓	✗	✗	✗
Sequencing platform	Long-read	Short-read	Short-read	Short-read

* WGBS = whole genome bisulfite sequencing
[†] ATAC-seq requires deep sequencing (>200M reads) for footprinting

Real-world applications of Fiber-seq

- Resolve rare disease**
 Link genetic variants to gene regulatory changes to uncover mechanisms of Mendelian disorders - PMID: [39880924](#)
- Profile brain epigenomics**
 Map cell-type-specific chromatin architecture in the human brain - PMID: [39631398](#)
- Unravel complex immunology**
 Identify haplotype-selective chromatin accessibility in immune cells - PMID: [40501892](#)
- Track transcriptional dynamics**
 Monitor RNA polymerase activity and its effects on chromatin structure - PMID: [39191261](#)
- Illuminate centromeres**
 Characterize conserved chromatin organization in repetitive centromeric regions - PMID: [40360747](#)
- Explore transposable elements**
 Reveal hidden regulatory elements in highly repetitive regions of the genome - PMID: [40147439](#)

Get Started with CUTANA™ Fiber-seq

	Catalog No.	Unit Size
CUTANA™ Fiber-seq Kit	14-2001-8rxn	8 reactions
	14-2001-24rxn	24 reactions
CUTANA™ Hia5 for Fiber-seq	15-1032-8rxn	8 reactions
	15-1032-24rxn	24 reactions
CUTANA™ Nuclei Extraction Buffer	21-1026	100 reactions

Prefer to have our experts run experiments for you?
 Explore our Fiber-seq Services for professional assay support and data delivery.

Visit epicypher.com/services/cutana-fiber-seq-assay-services/ or scan the QR code below.

