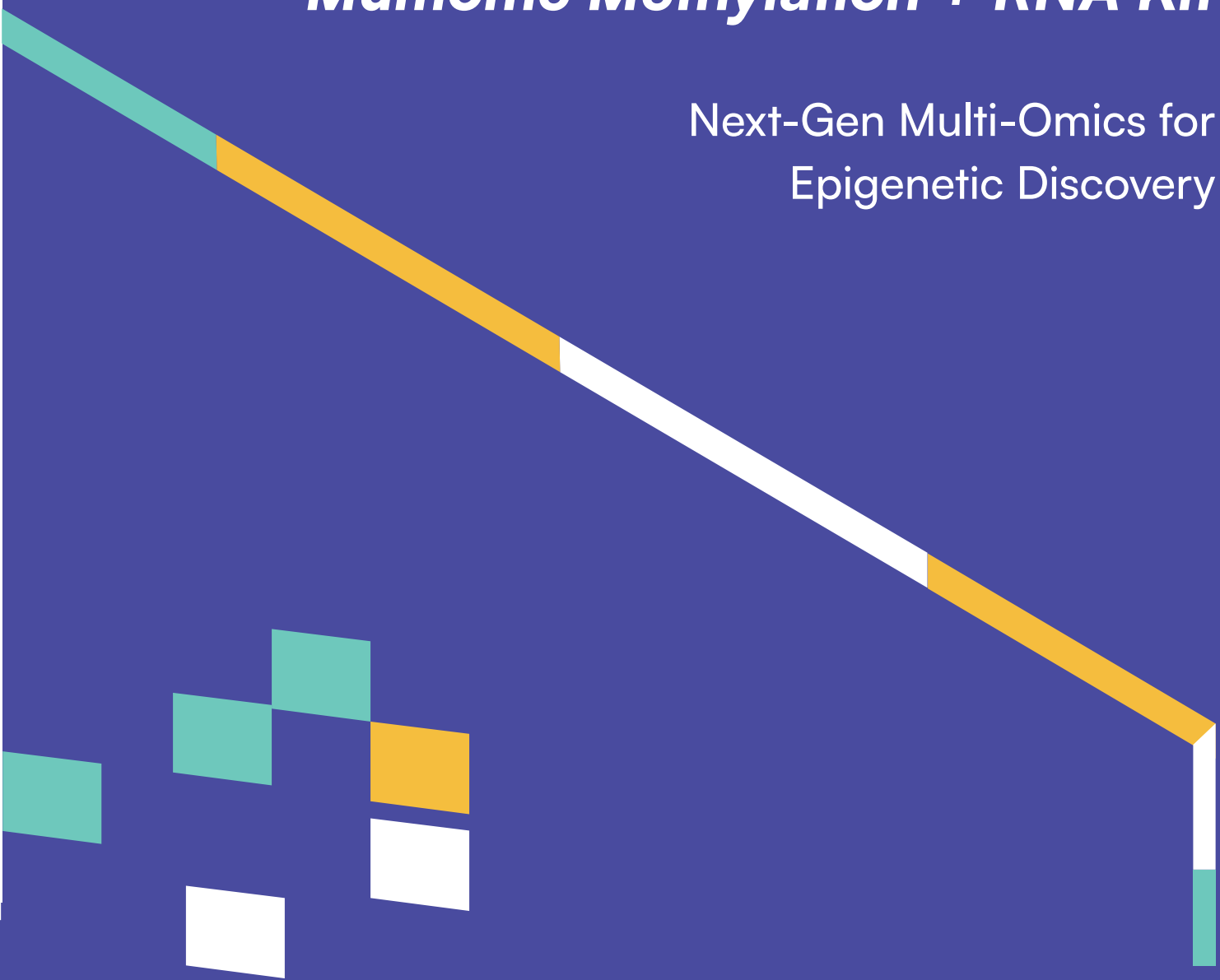
SEEKGENE

SeekOne™ DD Single-Cell Multiome Methylation + RNA Kit

Next-Gen Multi-Omics for
Epigenetic Discovery



Envision the Future

One Cell. Complete Profile.

Decode epigenetic regulation at single-base resolution.

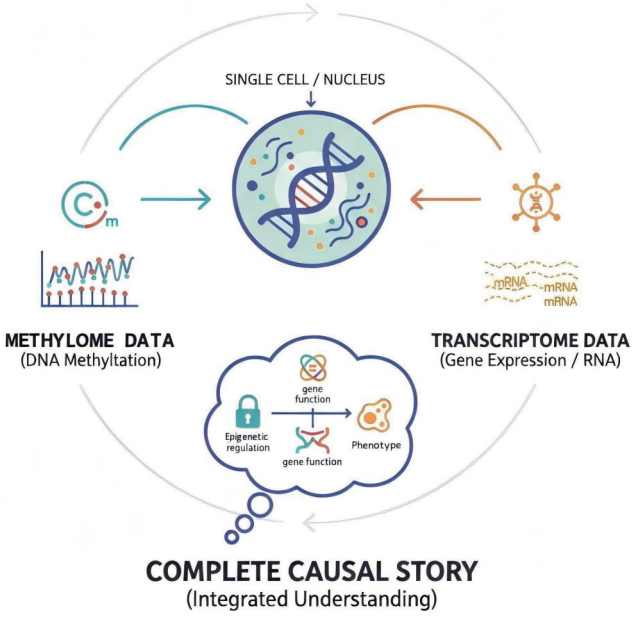
DNA methylation is a foundational layer of gene regulation. Yet most single-cell studies examine either the methylome or transcriptome alone.

Without true one-cell pairing:

01 Epigenetic—transcription linkage remains indirect

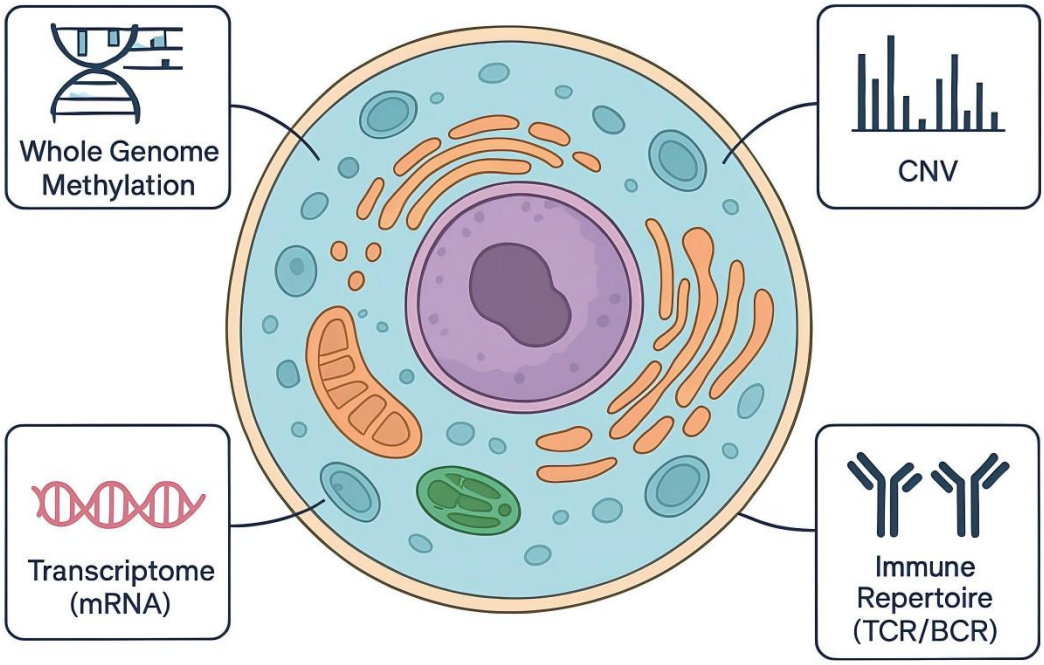
02 Cell identity inference lacks regulatory context

03 Mechanistic interpretation becomes speculative



SeekOne™ DD Single-Cell Multiome Methylation + RNA Kit (scMethyl + RNA) enables simultaneous, genome-wide DNA methylation and transcriptome profiling from the same single cell or nucleus, providing a unified regulatory landscape at single-base resolution.

One Cell, Complete Profile



True Single-Cell Multi-Omics Integration

Challenge

Bulk methylation masks cellular heterogeneity

Lack of direct methylation and transcription linkage

Sparse methylation data limits accurate clustering

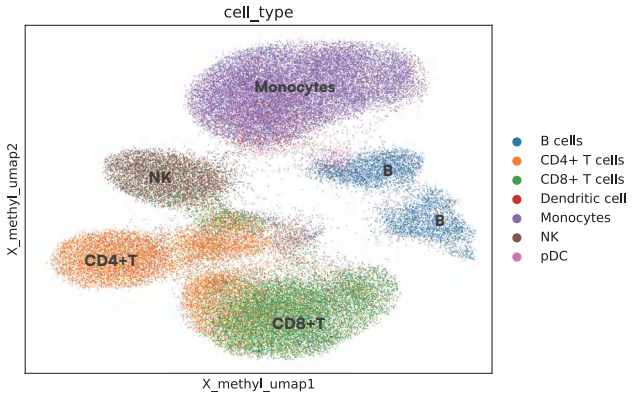
Our Solution

Droplet-based single-cell or single-nucleus encapsulation

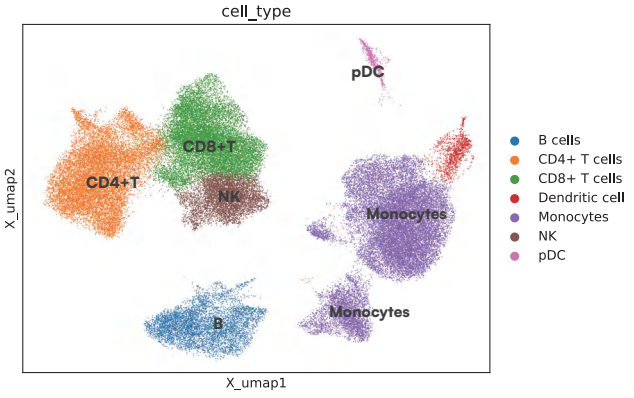
Simultaneous in-droplet methylation and RNA capture

RNA-assisted high-resolution cell annotation

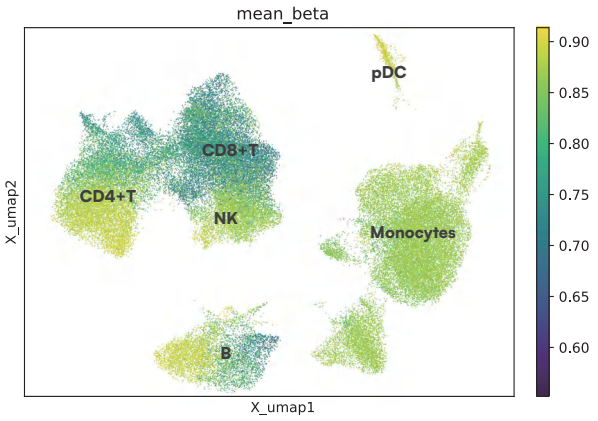
DNA Methylation and RNA Expression Reveal Distinct Cellular Landscapes



Methylation-basedclustering, annotated by mapping RNA-defined labels



RNA-based clustering & annotation



Methylation levels mapped onto the cell clusters

Methylation Mapping:

T and B cells exhibit significant global methylation differences even when RNA signatures are stable.

Scalable High Throughput

Challenge

Traditional single-cell methylation tech: ≤384 cells/run

Physical cell isolation increases sample loss and contamination

High per-cell cost limits large-scale studies

Our Solution

Flexible scale: 500—12,000 cells per run

No physical cell separation reduced sample loss

Automated in-droplet DNA/RNA reactions

Type	Method	Throughput
Multi-Omics	**SeekGene**	**500-12k cells**
Single methylation	scRRBS	96-384 cells
Single methylation	scWGBS	~96 cells
Single methylation	snmC-seq	384 cells
Single methylation	sci-MET	5k-10k cells
Single methylation	Cabernet	100-3k cells
Single methylation	SIMPLE-seq	1k-10k cells
Dual-Omics	scM&T-seq	96-384 cells
Dual-Omics	scMT-seq	50-100 cells
Triple-Omics	scTrio-seq	25-100 cells

Sample Type	Estimated Number of Cells	Mean Reads per Cell	Median Genes per Cell	Number of Reads	Valid Barcodes	Sequencing Saturation	Reads Mapped Confidently to Genome	Fraction Reads in Cells	Total Genes Detecte	Median UMI Counts per Cell
Human Prostate Cancer	14,867	24,632	1,212	366,204,415	94.62%	60.86%	91.32%	92.56%	33,633	2,267
Mouse Brain	12,305	29,637	2,053	364,695,404	89.23%	67.44%	93.23%	95.71%	26,447	6,039

Sample Type	Estimated Number of Cells	Number of Read Pairs	Valid Barcode Ratio	C-T Conversion	Reads Mapped Confidently to Genome	CpG Methylation Rate	CpG Coverage Rate	Total CPGs Detected	Genome Coverage Rate of Median Cell	CPGs of Median Cell	Read Pairs of Median Cell	Saturation of Median Cell	Fraction Reads in Cell
Human Prostate Cancer	14,867	1,363,656,959	94.02%	99.78%	84.24%	67.04%	95.94%	28,154,282	0.16%	61,161	38,514	21.11%	96.26%
Mouse Brain	12,305	1,751,872,086	95.49%	99.79%	76.50%	76.59%	96.59%	21,161,375	0.37%	96,995	79,331	22.87%	97.37%

Comprehensive CpG Detection & Genome Coverage

Challenge

Bisulfite conversion damages DNA and reduces complexity

Sparse CpG detection limits biological interpretation

Targeted approaches restrict genome-wide discovery

Our Solution

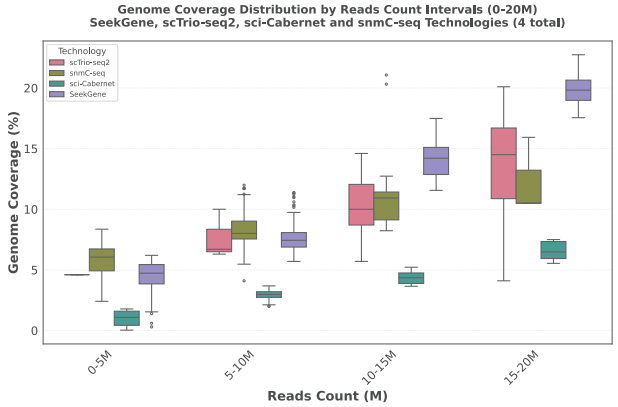
Bisulfite-free EM-seq chemistry preserves DNA integrity

High-efficiency Tn5 tagmentation

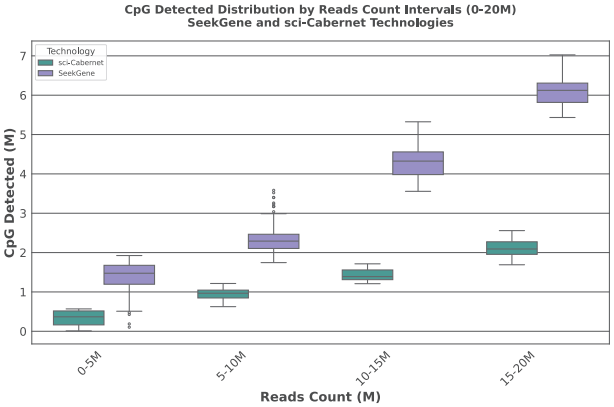
Unbiased genome-wide CpG detection

PBMC Performance

Transcriptome (RNA)		Epigenome (Methylation)		
Raw Bases	12 Gb	Raw Bases	**600 Gb**	**2.7 Tb**
Estimated Number of Cells	2,195	Estimated Number of Cells	2,195	2,195
Number of Read Pairs	38,863,818	Number of Read Pairs	2,078,504,886	9,041,245,927
Valid Barcode	93.50%	Valid Barcode Ratio	94.52%	94.37%
Reads Mapped to Genome	94.68%	Reads Mapped Confidently to Genome	80.47%	81.63%
Reads Mapped Confidently to Genome	92.22%	**CpG Coverage Rate**	**96.31%**	**97.38%**
Median Genes per Cell	1,076	**Total CpGs Detected**	**28,262,625**	**28,574,956**
Median UMI Counts per Cell	1,865	C-T Conversion	99.68%	99.86%
Mean Reads per Cell	17,705	CpG Methylation Rate	78.10%	77.9%
Total Genes Detected	22,897	**Genome Coverage Rate of Cell**	**1.46%**	**3.85%**
Sequencing Saturation	75.19%	**CPGs of Median Cell**	**519,263**	**1,421,188**
Fraction Reads in Cells	95.53%	Reads Pairs of Cell	376,263	1,616,695
/	/	Saturation of Median Cell	20.92%	49.56%
/	/	Fraction Reads in Cells	96.18%	96.15%



Genomecoverage distribution comparison



CpG detection distribution comparison

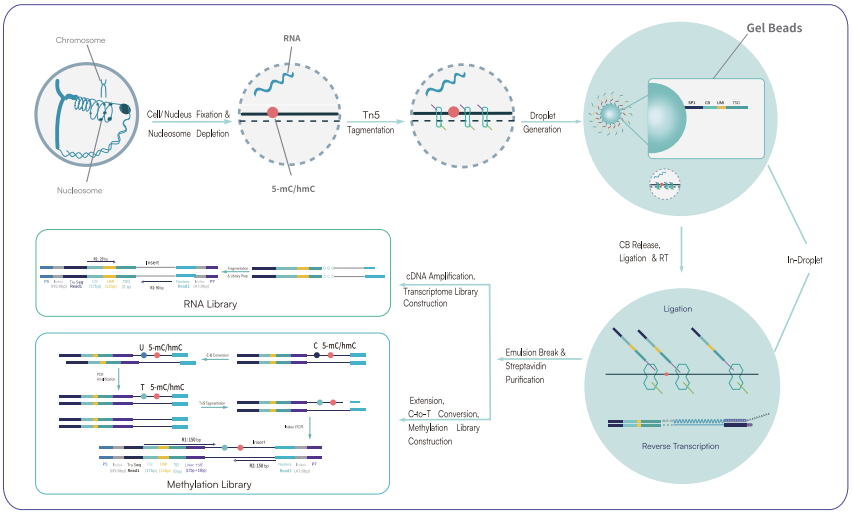
Streamlined Workflow & Integrated Bioinformatics

Streamlined 3-day end-to-end workflow (sample → library)

Standardized QC for both RNA and methylation libraries

SeekSoul™ integrated analysis pipeline (FASTQ → matrix)

Broad fresh/frozen sample support



Applications

These high-dimensional single-cell multi-omics data enable the simultaneous profiling of DNA methylation and transcriptome at single-cell resolution. They not only fill the gap in the association between epigenetics and gene expression and accurately reveal the regulatory rules underlying cellular heterogeneity, but also provide a complete causal basis from phenomenon to mechanism for scientific research in multiple fields, serving as a core pillar for unlocking the mysteries of epigenetic regulation.

Cancer Research

Developmental biology

Neuroscience

Immunology & chronic diseases

Product Name	Product Code	Specification
SeekOne™ DD Single-Cell Multiome Methylation + RNA Kit	K00901-08	8 tests

Ready to explore the multi-omics frontier?

Contact us to learn more.

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