BIOTECH INNOVATION AI/ML

ekei epigenetics

Research Platform

High resolution epigenetic sequencing at the lowest cost

Accelerate your fundamental research, large scale studies and AI algorithms training.

Introducing the ekei Epigenetics Research Platform

The ekei epigenetics research platform delivers the high-resolution data essential for breakthrough research, directly addressing the main barriers of high cost and limited data resolution.

Our proprietary wet-lab methods combined with high-throughput, high-coverage analysis overcome next-generation sequencing limitations, ensuring best-in-class epigenetic data for your projects.

The platform is optimized for flexibility and sensitivity. We support DNA analysis from diverse sources (blood, saliva, tissue, etc.) and excel with low input, enabling minimally invasive protocols and preserving precious samples. Beyond our core DNA methylation methods, protocol combinations acquire specific epigenetic factor data tailored to your unique goals.

Engineered for the AI era, ekei generates the robust, high-dimensional datasets required for modern machine learning. Empower your team to accelerate biomarker discovery, validate clinical outcomes, and deepen the understanding of complex processes like aging.
Whether your focus is anti-aging, disease therapeutics, drug discovery, or fundamental cell biology, ekei provides invaluable, high-confidence data for your next breakthrough.

Highlights

Whole Genome Sequencing

>25M unique CpG sites*

High-resolution Single Channel

Increased sensitivity for DMRs**

Best Samples Preservation

No harsh chemical reaction

* Minimum total count of CpG locations recorded based on experimental observations (N=20) and using latest T2TCHM13v.2 FASTA human reference genome. https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_009914755.1/

** While traditional techniques output quantified methylation information per CpG site, our platform captures single-channel information at each CpG site with increased sensitivity for highly or low methylated regions. With only 50M reads, it is possible to capture high-resolution information to highlight differentially methylated regions (DMRs) with strong confidence at a genome-wide scale.

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TARGET APPLICATIONS ANTI-AGEING · PHARMA · CELL BIOLOGY · AGRITECH

Advanced Features

✓ High-throughput sequencing of highly multiplexed libraries.

✓ Extensive genome coverage

✓ No harsh chemicals for DNA integrity preservation

✓ Analysis of methylation pattern in diverse genomic regions (promoters, enhancers, gene bodies, and intergenic spaces).

✓ CpH sites methylation detection.

✓ Robust detection at only ~50M reads, enabling significant cost saving compared to WGBS.

✓ Compatibility with various sample input (blood, bulk cells, tissues, saliva, buccal swabs).

✓ Customisable genomic annotation

✓ Possibility to add other epigenetic factors other than 5-mC (5-hmC, histone modification with CHIP-seq or with ATAC-seq).

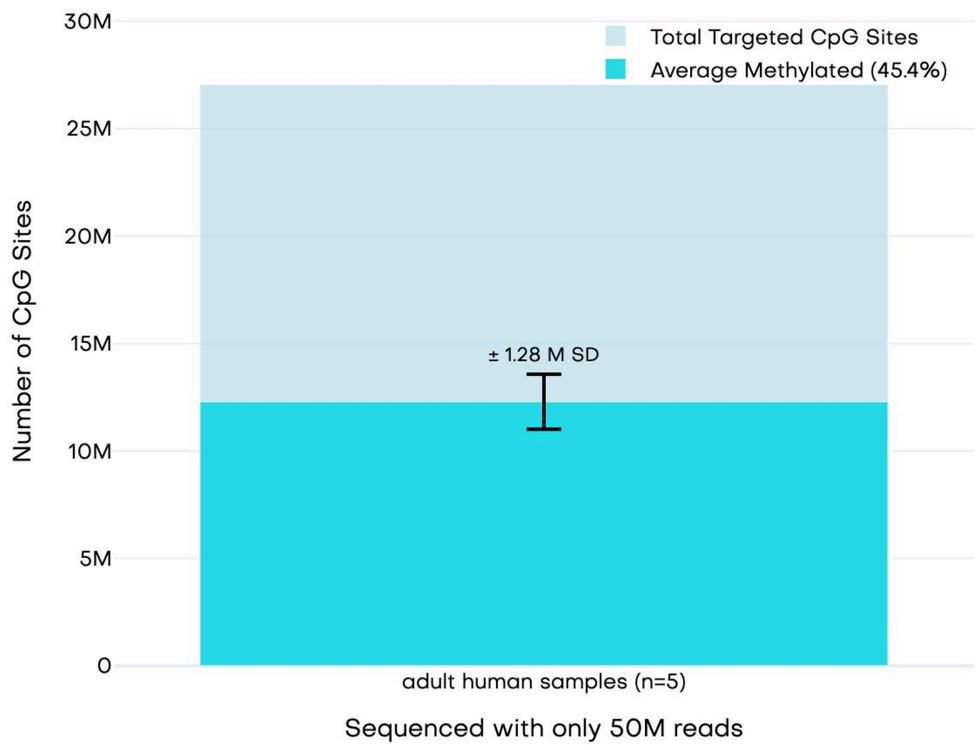
✓ Supports advanced bioinformatics.

✓ Secure data transfer methods

✓ Translation of discovery findings into cost-effective, targeted downstream assays for product development or clinical service integration

CpG Methylation Profile

(Standard Deviation based on 5 Samples)



Specifications

	EPIC	RRBS	WGBS	ekei
DNA coverage with CpGs targets	<1M	<5M	**34M***	**>25M****
DNA input quantity requirement	500ng	**100ng**	1000ng	**20ng**
Novel CpGs biomarkers discovery	✗	✗	✓	✓
Application for non-human DNA	✗	✗	✓	✓
High-throughput costs scaling	✗	✗	✗	✓
Low sequencing costs per CpG	✗	✗	✗	✓
No harsh chemical reaction	✗	✗	✗	✓

Collaboration Workflow

Consultation

We work with you to pinpoint how epigenetic data can accelerate your research, defining a clear path forward.

Design

Once objectives are set, we create tailored experiments to gather the most relevant data and ensure robust outcomes.

Sequencing

Using our proprietary methods, we sequence and process DNA methylation data, delivering high-resolution results.

Research

We turn these results into predictive algorithms and custom analytics to build your epigenetics strategy.

- Human DNA methylomes at base resolution show widespread epigenomic differences https://doi.org/10.1038/nature08514
- Reduced representation bisulfite sequencing for comparative high-resolution DNA methylation analysis https://doi.org/10.1093/nar/gki901
- A tiling resolution DNA microarray with complete coverage of the human genome https://doi.org/10.1038/ng1307

* 33,896,489 unique CpG sites were counted in the T2T-CHM13V2.0 human reference genome.
** Value based on experimental observations (N=20).

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