BIOTECH INNOVATION AI/ML

ekei epigenetics

Research Platform

Extremely low-cost, high-resolution epigenetics sequencing. Suited for fundamental research, large scale studies and AI algorithms training.

Introducing ekei epigenetics research platform, built on our innovative proprietary methods to revolutionise the adoption of epigenetics in various fields of research, pharmaceutical product development and clinical applications.

Epigenetics is a key element of life's adaptation potential. This dynamic layer of biological information adapts to life cycles, development phases, and responds to environmental factors and cellular stressors. In recent years, its study has revolutionised fields like longevity science, offering powerful ways to quantify biological ageing and providing critical insights into complex diseases, including cancer progression.

Today's main barrier to entry is the high cost and limited data resolution of epigenetic analysis. Our epigenetics platform is addressing these challenges by pushing the boundaries of the current next-generation sequencing solutions for high-throughput and high data coverage, coupled with our proprietary wet-lab methods to deliver best-in-class epigenetic data from various types of DNA samples.

Our platform is optimised for flexibility and sensitivity. We support DNA analysis from various sources, including blood, saliva, buccal swabs, bulk tissue and cellular secretomes. Our methods excel with low DNA input, enabling minimally invasive collection protocols and preserving precious sample material.

Since each project is unique, it may require information on various epigenetic factors in addition to the data from our core proprietary DNA methylation methods. Our platform allows for the combination of protocols to acquire the specific data needed, maximising the potential to achieve target goals.
Engineered for the era of artificial intelligence, ekei generates the robust, high-dimensional datasets essential for modern machine learning. Empower your research teams working in life science to accelerate the discovery of new biomarkers with greater confidence, to create tailored biotech products and therapeutics, to validate clinical trial outcomes more effectively and to deepen the understanding of ageing and to potentially reverse it.

If you are working on solutions for anti-ageing healthcare, cosmetics, complex diseases therapeutics, cancer biomarkers, pharmaceutical drug discovery, biobanks, fundamental cell biology or even agricultural biotechnology such as optimised crop breeding programs, our ekei epigenetics research platform will provide invaluable information for your research.

ekei

Highlights

Whole Genome

Our methods are able to sequence epigenetic information genome-wide, providing a considerable advantage over existing methods such as methylationEPIC arrays or RRBS. We are able to target over **25M** unique CpG sites* in the human genome, which includes up to **9.6M CpGs** in annotated gene locations as well as promoter and enhancer regions.

Cost-Efficiency

The core strength of our services lies in the use of novel proprietary lab methods that, when coupled with the most recent next-generation sequencing techniques, allow for maximum throughput and best data value at ultra-low cost. Using multiplexing, it is now possible to capture a wide human methylome for less than **30,000 JPY** in large studies.

High resolution single channel

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.

Best sample preservation

No chemically intense reaction, such as bisulfite conversion, is used on our platform; therefore, we guarantee the **best-in-class DNA sample preservation.**

Innovative, customizable platform

In most cases, our partners are looking for an **end-to-end solution** to guide them in their epigenetics adoption journey. We bring our expertise to consult on which ideas can be transformative, and together we design tailored protocols. We are also developing and running bioinformatics algorithms that will scavenge valuable information from the sequenced data. Once the discovery goals are achieved, we propose to develop ultra-focused epigenetic kits at orders of magnitude lower costs, tailored to look at discovered biomarkers to be implemented in our partners' product pipeline or clinical services.

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

ekei epigenetics

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

Features

- Supports high-throughput sequencing of highly multiplexed libraries, enabling cost-effective analysis of large sample cohorts.
- Provides extensive genome coverage for broad epigenetic insights by analysing more than half of the entire methylome.
- Avoids harsh chemical treatments like bisulfite conversion, minimising DNA degradation and preserving sample integrity.
- Enables analysis of methylation patterns in diverse genomic regions, including promoters, enhancers, gene bodies, and intergenic spaces.
- Detects methylation at CpH sites. Valuable for studying neurons, stem cells, plants, and other organisms with significant CpH methylation.
- Performs robust detection at only ~50 million reads for human sample (typically >10M mCpG sites identified), offering significant cost savings compared to deep WGBS. Sequencing depth is adjustable based on project goals.
- Accepts versatile sample input compatible with DNA extracted from various sources, including blood, bulk cells, tissues (e.g., skin), saliva, and buccal swabs. Please inquire regarding specific protocols for plasma/cfDNA.
- Allows customisable genomic annotation within specific genomic contexts by selecting annotations for promoters, enhancers, gene bodies, CpG islands, shores/shelves, and intergenic regions.
- Offers the option to add other epigenetic factors other than 5-mC, such as 5-hmC, histone modifications with CHIP-seq or with ATAC-seq.
- Supports advanced bioinformatics with flexible analysis pipelines, including customisable options for biomarker discovery and data delivery formatted for machine learning applications.
- Utilises secure data transfer methods tailored to client institutional requirements.
- Enables translation of discovery findings into cost-effective, targeted downstream assays suitable for product development or clinical service integration.

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.

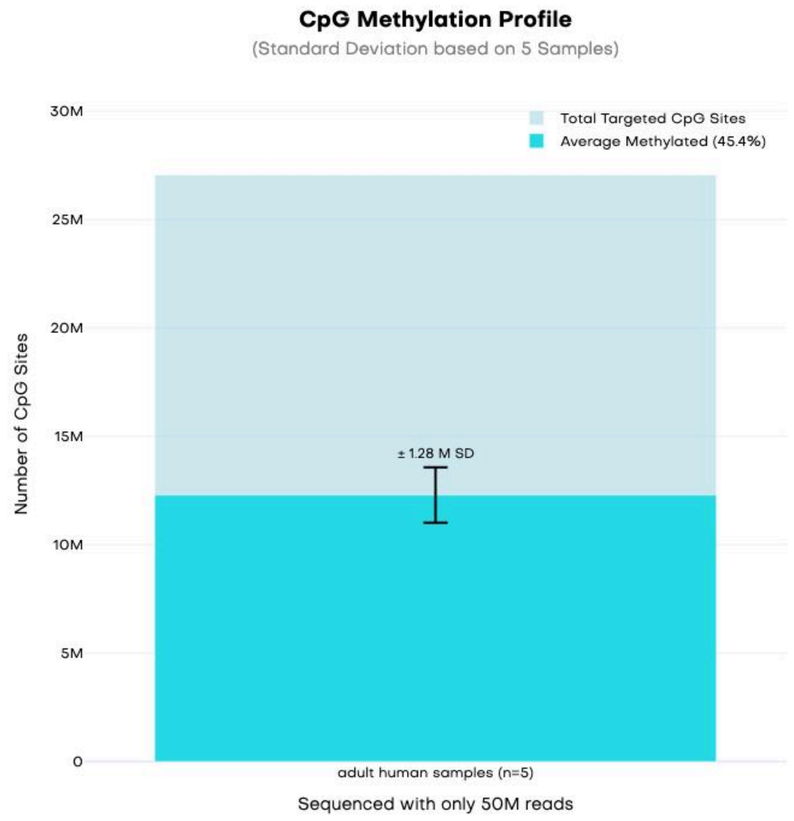
Sequencing

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.

Specifications



	EPIC	RRBS	WGBS	
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	✗	✗	✗	✓

- 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).