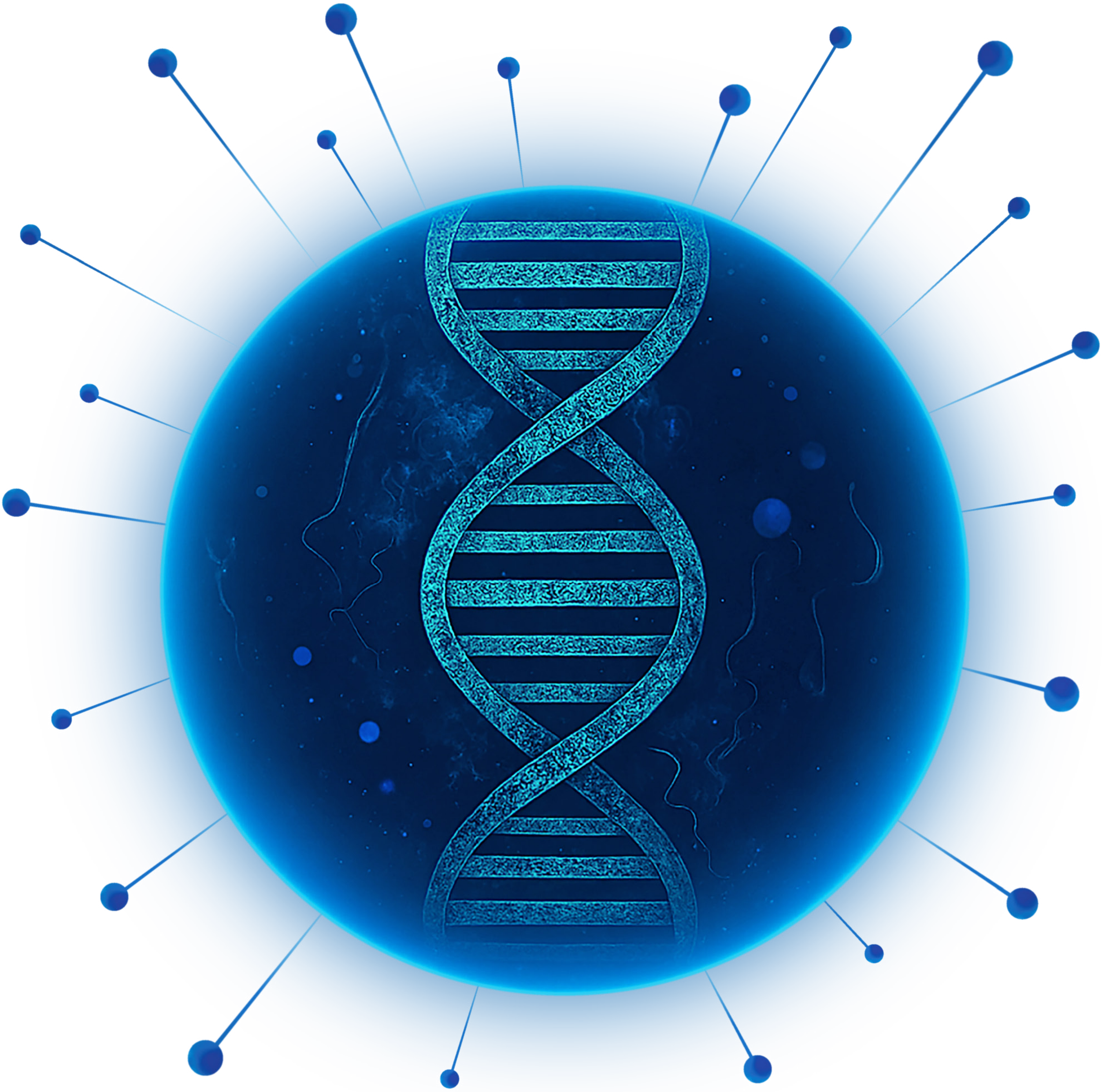
HIGH-THROUGHPUT | MULTIPLEXED | QUANTITATIVE

EpiFinder™

GenomePro



Epigenica

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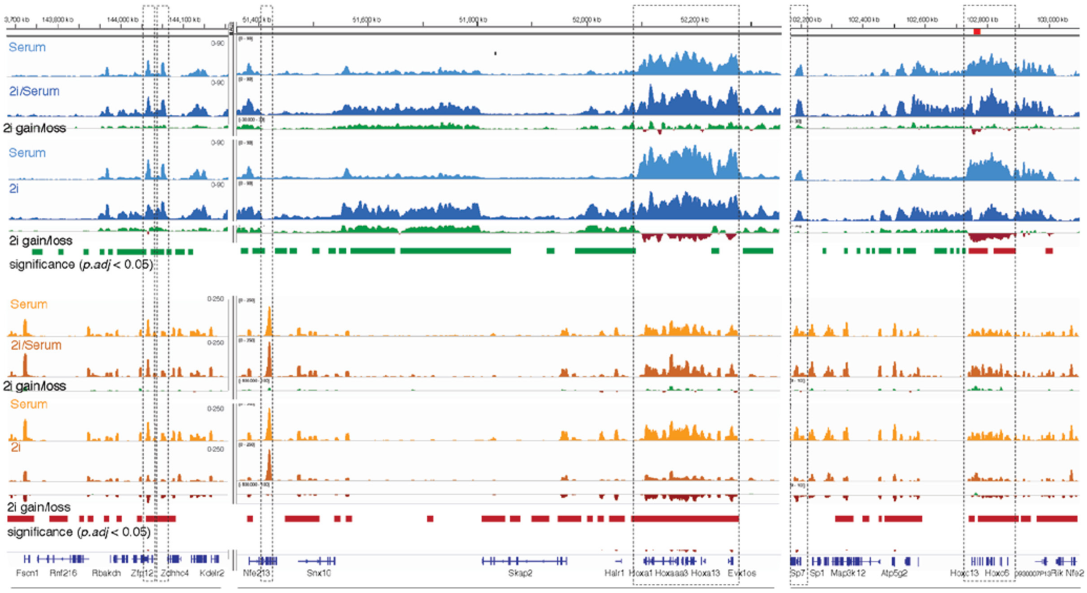
Elevate your epigenetic studies with EpiFinder™

Unlock the power of epigenetics with the EpiFinder™ platform, a ground-breaking innovation powered by our cutting-edge hmqChIP-seq technology. Discover a new era of multiplexed, quantitative, and high-throughput assays for histone post-translational modifications (hPTMs), DNA methylation (DNAme) and transcriptional factors (TFs). With EpiFinder™, you can now generate quantitative data at scale, faster, and more cost-efficiently than ever before. Our innovative approach provides comprehensive data-yield, enabling unparalleled insights into the intricate world of epigenetics. Our open-source analysis pipelines let you process and analyse EpiFinder™ data with ease.

Intrinsically quantitative ChIP-seq tracks

The pooled workflows of EpiFinder™ not only offer immense data yield, the data produced is also intrinsically quantitative, because samples are pooled early in the workflow. This not only removes all sample-to-sample variation typically observed in parallelised workflows, it also allows quantitative comparisons across all samples. Chromatin fragments carrying the target epitope (e.g. hPTMs) compete for the available antibody binding sites in each ChIP reaction, and the proportion of fragments captured in the ChIP reaction is directly proportional to the relative abundance of the hPTMs in each sample. Our analysis pipeline uses this information to scale the output tracks according to the true proportions, reliably and accurately identifying global and local quantitative differences across all conditions in the pool.



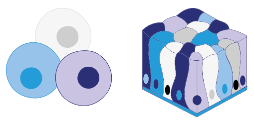
Example data exemplifies importance of quantitative ChIP-seq: Different pluripotent states of mouse embryonic stem cells were compared. Quantitative analysis reveals gains (green) and losses (red) between conditions, and statistical significance (green and red blocks) based on three replicates analysed of each state.

EpiFinder™
GenomePro

Tap into the full potential of our cutting-edge product with EpiFinder™ GenomePro, the ultimate solution designed for scientists seeking genome-wide, quantitative profiling across all your samples and replicates. The kit provides the reagents necessary to fragment and barcode up to 24 samples (e.g. 8 unique sample conditions in triplicates), starting with 0.5-1 million cells per replicate, and subsequently perform 8 ChIP reactions using antibodies of your choice.

The kit includes reagents and a detailed step-by-step protocol to generate sequencing-ready Illumina libraries, yielding up to 24 x 8 = 192 quantitative ChIP-seq tracks and corresponding Inputs, all from just 63,000 to 125,000 cells per final ChIP-seq track. The pooled workflow universally allows the quantitative comparison of signal and background, without the need for complex and expensive spike-in strategies. It also minimises sample-to-sample variation and reduces overall technical background. Overall, EpiFinder™ GenomePro boasts reduced background noise, increased specificity, and enhanced sensitivity while remaining a very cost-efficient solution.

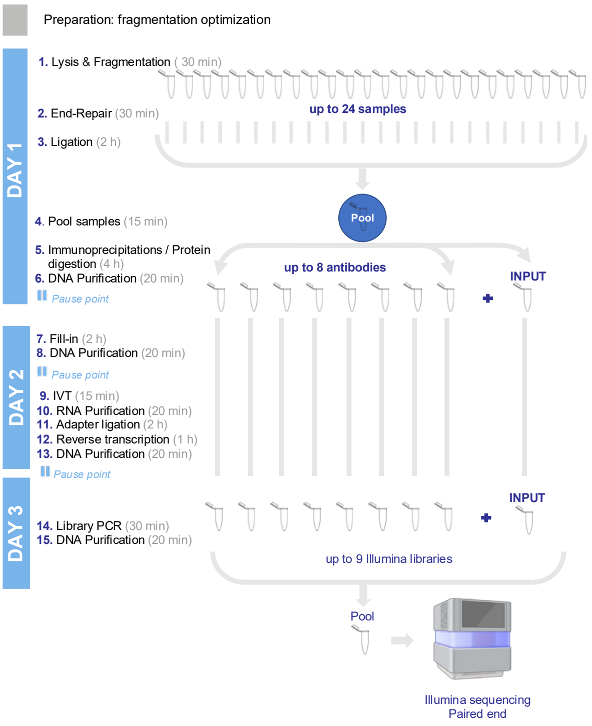
Cells or tissue



	EpiFinder™ GenomePro
Profiling method	Genome-wide
Sample type	Native & fixed cells or tissue
Conditions x targets	24 samples x 8 targets
Target	Histone PTMs, TFs, DNAme
Starting material per sample	500,000 - 1,000,000 cells
Sequencing depth	10 - 30 million reads/sample/IP

Workflow

The 3-day, ~14-hour hands-on time pooled workflow is accessible for all researchers, guided by our optimised protocol. It takes you through the whole process, including alternative steps needed for your chosen starting material. The kit comes with its own analysis pipeline, enabling an automated analysis workflow from FASTQ to demultiplexed and quantitative data (up to 192 genome-wide profiles), as well as various QC metrics and useful additional statistics.



Preparation: fragmentation optimization

DAY 1

1. Lysis & Fragmentation (30 min)
2. End-Repair (30 min)
3. Ligation (2 h)
4. Pool samples (15 min)
5. Immunoprecipitations / Protein digestion (4 h)
6. DNA Purification (20 min)

Pause point

DAY 2

7. Fill-in (2 h)
8. DNA Purification (20 min)

Pause point

9. IVT (15 min)
10. RNA Purification (20 min)
11. Adapter ligation (2 h)
12. Reverse transcription (1 h)
13. DNA Purification (20 min)

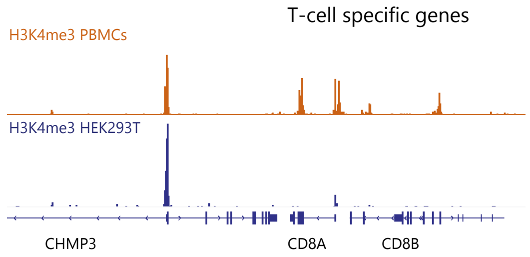
Pause point

DAY 3

14. Library PCR (30 min)
15. DNA Purification (20 min)

Choose your starting material

EpiFinder™ GenomePro has been validated with native and formaldehyde crosslinked cells (PBMCs, human cancer cell lines, mouse and human stems cells, etc...), as well as flash frozen tissues.



Quality controlled antibodies

Our commitment to excellence means we continually quality control antibodies, ensuring precision and reliability for your specific targets. The flexibility of the protocol also allows you to adapt other desired antibodies, using your routine practice.

Antibody recommendations for EpiFinderTM GenomePro

hPTM	Source	Company	Catalog #
H3K4me3	rb	Millipore	04-745
	rb	Active Motif	91263
H3K27me3	rb	Cell Signaling	9733
	rb	Absea	RC-5552
H3K9me3	rb	Absea	RC-6815
H3K36me3	rb	Active Motif	91265
H3K27ac	rb	Active Motif	91193
	rb	Absea	RC-5553
H3K9ac	rb	Active Motif	91104
	rb	Absea	KC244
H4K5ac	rb	Absea	RC5983
H3K4ac	rb	Absea	RC5990

DNA modification		Company	Catalog #
CpG methylation	MethylCollector™ MBD Capture Kit	Active Motif	55026

GenomePro Analysis Service

In addition to our convenient shipping kits, our experts can now support you by processing your samples directly in our lab. This service ensures high-quality data with a fast turnaround time, providing a seamless experience from sample submission to results.

Looking Ahead

GenomePro is our flagship solution today, delivering genome-wide, quantitative profiling at scale. Future extensions of our technology will open new opportunities in areas such as high-throughput global profiling and liquid biopsy analysis. These innovations will be designed to complement GenomePro and expand what's possible in epigenetic research.

Connect with our experts at support@epigenica.se to learn more about EpiFinder™ GenomePro and see how it can accelerate your discoveries and bring greater value to your research.

www.epigenica.se

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