EPIGENOMICS PROFILING SERVICES

- Chromatin analysis
- DNA methylation analysis
- RNA-seq analysis
Diagenode helps you uncover the mysteries of epigenetics
Integrative epigenomics analysis

DNA methylation analysis

- Reduced representation bisulfite sequencing (RRBS)
- Whole genome bisulfite sequencing analysis (WGBS)
- Genome-wide DNA methylation
- Differentially methylated region analysis

ChIP-seq/ChIP-qPCR analysis

- Histone modification ChIP-seq analysis
- Promoter analysis
- Enhancer analysis
- Transcription factor ChIP-seq analysis
- Customized NGS service
- Chromatin accessibility (ATAC-seq)

RNA-seq analysis

- Small RNA-sequencing
- mRNA analysis
- Whole transcriptome analysis
- Gene expression profiling
Expertise that you can trust

Our Epigenomics Profiling Services assure the sample preparation expertise and quality data that you seek. We provide epigenome-wide analyses for understanding epigenetic mechanisms, epigenetics-related drug discovery, epigenetic biomarker identification, and functional epigenomics.

Why Diagenode?

- **Expertise and trust**: Recognized epigenetics leader, official partner of BLUEPRINT, IHEC and FAANG
- **Innovative technology**: Utilization of the signature Bioruptor® sonication device for optimal chromatin and DNA shearing and the IP-Star® Automation device give reproducible and reliable optimization and results
- **Quality**: Multiple QC steps in all workflows and validated antibodies plus reagents deliver superior data

12 years of expertise and trust in epigenetics

- **End-to-end** epigenetics service and analysis
- **Collaborative** and customized project design
- Dedicated **in-house expert** for your project
- **Integrative** data analysis
- **Presentation-quality data** and graphs
Integrative epigenetics analysis

The promise of personalized medicine will be realized from an integrative approach to genetic and epigenetic testing. Epigenetic biomarkers open new avenues for early detection of diseases and the identification of therapeutic targets in diseases such as cancer. Our Epigenomic Profiling Services can help uncover the epigenetic mechanisms and epigenetic signature that are specific to a certain disease or tumor type, enhancing the personalized medicine approach.

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Chromatin analysis

Chromatin consists of DNA, histones and non-histone proteins. To form chromatin, DNA tightly wraps around histones. Generally, more highly condensed chromatin is less accessible to transcription factors and other DNA binding proteins, which has consequences for gene expression. Understanding the roles of histones and transcription factors is critical in understanding the regulation of gene expression.
Using ChIP-seq and ChIPmentation analysis, it is possible to profile histone modifications and transcription factor binding genome-wide to understand the regulation of gene expression in disease or in response to a drug treatment. Diagenode’s Epigenomic Profiling Services offer a wide variety of chromatin analysis options through ChIP-seq and ChIPmentation.
Chromatin analysis

ChIP-seq and ChIPmentation histone modifications on 10,000 cells

Post-translational modification of histones is implicated in the regulation of gene expression, necessitating the study of regulatory elements and their interacting proteins like active promoter and enhancer analysis. Profile genome-wide histone modifications by ChIP-seq analysis to understand transcriptional regulation.

- Active promoter: H3K4me3 enrichment
- Inactive promoter: H3K27me3 enrichment
- Enhancer: H3K4me1 and H3K27ac enrichment in regulatory regions
- Active gene body: H3K36me3

ChIP-seq

![ChIP-seq Enrichment Example](image)

*Enrichment at promoter and enhancer sites (red bars). ChIP-seq has been performed using chromatin from 10,000 K562 cells.*

ChIPmentation

![ChIPmentation Example](image)

*ChIPmentation has been performed using chromatin from 100,000, 10,000 and 5,000 K562 cells, and antibody targeting H3K4me3.*
Explore the effects of transcription factor binding through ChIP-seq analysis of a multitude of TFs including:

- CTCF: transcriptional and insulator activity
- p300/CBP: histone acetyltransferase
- Pol II, p53, and more
- Epigenetic writers, readers, erasers
- Nuclear receptors
- Tumor suppressor genes

ChIP-seq has been performed using chromatin from HeLa cells and the Diagenode ChIP-seq-grade HDAC1 (A), LSD1 (B) and p53 antibody (C)

Custom NGS services

- Low input libraries from picograms
- Specific analyses
- Complete customized project
DNA methylation analysis

The pattern of DNA methylation and histone modification(s) plays an essential role in maintaining cellular function. Abnormal DNA methylation – hypermethylation and hypomethylation – can result in adverse outcomes such as cancer or other disease. The quantification of 5-mC through genome-wide DNA methylation analysis can provide information for detection and prognosis of disease. Our DNA methylation analysis services include numerous bisulfite sequencing options for targeted or whole genome DNA methylation analysis across any species.

**Reduced representation bisulfite sequencing (RRBS)**

Unique licensed technology and optimized protocol that is more cost-effective than WGBS

- Inputs down to 100ng
- All vertebrates
- Single nucleotide resolution for cytosine methylation (5-mC)
- Epigenetic biomarker discovery
- FFPE and challenging samples

![Reduced representation bisulfite sequencing (RRBS)](image)

**Whole genome bisulfite sequencing (WGBS)**

- Genome-wide 5-mC: single nucleotide resolution
- Epigenetic biomarker discovery
- Methylation patterns of CpG, CHG, and CHH regions across the genome
- Epigenome-wide association studies (EWAS)
RNA-seq analysis

RNA sequencing uses next-generation sequencing (NGS) to uncover the presence and quantity of RNA for gene expression profiling across the transcriptome. Diagenode utilizes the unique capture and amplification by tailing and switching (CATS) methodology for generating RNA-seq libraries which is optimal for low or degraded inputs including those from liquid biopsies, FFPE, exosomes, serum, or plasma.

Small RNA and miRNA

- Post-transcriptional regulation of gene expression
- Novel transcripts and differentially-expressed small RNAs
- miRNAs involved in regulation of onco- and tumor-suppressor gene expression
- Differential miRNA expression

Messenger RNA (mRNA)

- Protein-coding RNA with specific poly A selection.
- Cancer-related mRNA signatures
- Aberrant mRNA translation in cancer pathogenesis
- Gene expression profiling and identification of differentially expressed genes (DEG)
- Epigenetic mechanism of gene expression (transcriptome plus H3K36me3 and H3K4me3 marks)
- Functional annotation of coding genes

Whole transcriptome and long non-coding RNA (LncRNA)

- Analysis of whole transcriptome and RNAs larger than 200nt with optional rRNA depletion
- Non-protein coding RNAs involved in chromatin remodeling & transcriptional/post-transcriptional regulation
Diagenode endeavors to provide pioneering solutions for epigenetics studies.

Please reach out to us for any other requests that may not have been highlighted in this brochure so that we can help with your exact needs.

Shop online in our EpiStore at www.diagenode.com