diagenode

Innovating Epigenetics Solutions

# Epigenomics Profiling Services

## Chromatin analysis

Histone modifications via ChIP-qPCR/ChIP-seq
Transcription factor binding via ChIP-qPCR/ChIP-seq
Chromatin accessibility (ATAC-seq)

## RNA sequencing and analysis

mRNA and small RNA sequencing
Low and difficult input RNA-seq
Whole transcriptome analysis and gene expression profiling

## DNA Methylation analysis

**Genome-wide:** Whole genome bisulfite-seq, EPIC array, RRBS, MeDIP/MeDIP-seq
**Targeted** DNA methylation assays
**DNA hydroxymethylation** analysis

## Bioinformatics data mining

Machine learning for enhanced analysis of complex data
Robust deep learning to uncover underlying biological significance of your data
Establish new biomarkers for disease diagnostics

| | Techniques | Standard analysis | Advanced analysis |
|---|---|---|---|
| Chromatin analysis | ·ChIP-seq (histones/TFs)<br>·ChIP-qPCR (histones/TFs) | · Read filtering and trimming<br>· Read mapping to the genome<br>· Peak calling | · Identification of differentially bound sites between groups of samples<br>· Genomic annotation<br>· Gene ontology enrichment<br>· Pathway enrichment<br>· Specific genomic region visualization |
| | · ATAC-seq | · Read filtering and trimming<br>· Read mapping to the genome<br>· Identification of open chromatin regions | · Differentially open chromatin region analysis<br>· Genomic annotation<br>· Nucleosome positioning<br>· Motif recognition<br>· Gene ontology enrichment<br>· Pathway enrichment |
| DNA methylation analysis | · RRBS<br>· WGBS | · Read filtering and trimming<br>· Read mapping to the genome<br>· Methylation calling | · CpG and region level differential methylation<br>· Genomic annotation<br>· Gene ontology enrichment<br>· Pathway enrichment |
| | · MeDIP/hMeDIP-seq | · Read filtering and trimming<br>· Read mapping to the genome<br>· Relative methylation quantification | · Differentially-methylated region identification<br>· Genomic annotation<br>· Gene ontology enrichment<br>· Pathway enrichment |
| | · EPIC arrays | · Raw β- values<br>· Data normalization<br>· Probe filtering<br>· Background correction | |
| | · Targeted analysis | · Read filtering and trimming<br>· Read mapping to the genome | · Differential methylation |
| RNA analysis | · RNA-seq | · Read filtering and trimming<br>· Read mapping to the genome or transcriptome<br>· Gene and transcript quantification | · Differentially-expressed gene identification<br>· Annotation<br>· Gene ontology enrichment<br>· Pathway enrichment |
| Data mining | · Probabilistic modeling<br>· Deep learning approaches<br>· Integrative analyses of different -omics datasets | · Feasibility phase - validation of the data set<br>· Training and testing<br>· Data mining analysis<br>· Interpretation of results | · Reporting<br>· Model validation<br>· Scientific support |



www.diagenode.com **Please contact us for more information**

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