diagenode

Innovating Epigenetics Solutions

Epigenomics Profiling Services

Chromatin analysis

Histone modifications via ChIP-qPCR/ChIP-seq on as low as 20,000 cells/ChIP
Transcription factor binding via ChIP-qPCR/ChIP-seq
Chromatin accessibility (bulk ATAC-seq and single cell ATAC-seq)

RNA sequencing and analysis

mRNA-seq and gene expression profiling
Small RNA-seq and miRNA-seq
Total RNA-seq and whole transcriptome analysis

DNA Methylation analysis

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

Bioinformatic analysis

Standard analysis including read filtering, mapping and peak calling/methylation calling
Advanced analysis including differential analyis, annotation, gene ontology, pathway analysis and other customized analysis
Data mining and machine learning

Consulting with our scientific experts

Get expert advice for the best design of your project
End to end and customized service

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

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

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