



Innovating Epigenetics Solutions

Epigenomics Profiling Services

Chromatin analysis

Histone modifications via
ChIP-qPCR/ChIP-seq

Transcription factors via
ChIP-qPCR/ChIP-seq

Chromatin accessibility
(ATAC-seq)

RNA-seq analysis

mRNA and small
RNA-sequencing

Low and difficult input RNA-seq

Analyses include whole transcriptome
analysis and gene expression
profiling

DNA methylation services

Genome-wide: Whole genome
bisulfite-seq, EPICArray, MeDIP/hMeDIP-seq

Reduced representation bisulfite sequencing

Targeted DNA methylation assays via
bisulfite pyrosequencing, amplicon
sequencing, or custom capture
probes

	Techniques	Standard analysis	Additional analysis
Chromatin analysis	<ul style="list-style-type: none"> ChIP-seq (histones/TFs) ChIP-qPCR (histones/TFs) 	<ul style="list-style-type: none"> Read filtering and trimming Read mapping to the genome Peak calling 	<ul style="list-style-type: none"> Identification of differentially bound sites between groups of samples Genomic annotation Gene ontology enrichment Pathway enrichment Visualizations of specific genomic regions
	<ul style="list-style-type: none"> ATAC-seq 	<ul style="list-style-type: none"> Read filtering and trimming Read mapping to the genome Identification of open chromatin regions 	<ul style="list-style-type: none"> Identification of differential open chromatin regions between groups of samples Genomic annotation Nucleosome positioning Motif recognition Gene ontology enrichment Pathway enrichment Visualizations
DNA methylation analysis	<ul style="list-style-type: none"> RRBS WGBS 	<ul style="list-style-type: none"> Read filtering and trimming Read mapping to the genome Methylation calling 	<ul style="list-style-type: none"> CpG and region level differential methylation Genomic annotation Gene ontology enrichment Pathway enrichment
	<ul style="list-style-type: none"> MeDIP/hMeDIP-seq 	<ul style="list-style-type: none"> Read filtering and trimming Read-mapping to the genome Relative methylation quantification 	<ul style="list-style-type: none"> Differential methylated regions Genomic annotation Gene ontology enrichment Pathway enrichment
	<ul style="list-style-type: none"> EPIC arrays 	<ul style="list-style-type: none"> Data normalization Probe filtering Background correction 	<ul style="list-style-type: none"> Gene ontology enrichment Pathway enrichment
	<ul style="list-style-type: none"> Targeted analysis via bisulfite pyrosequencing, amplicon sequencing or probe capture 	<ul style="list-style-type: none"> Pyrosequencing: pyrograms and methylation levels Targeted by NGS: Read filtering and trimming Read-mapping to the genome and methylation calling 	<ul style="list-style-type: none"> Differential methylation
RNA analysis	<ul style="list-style-type: none"> RNA-seq 	<ul style="list-style-type: none"> Read filtering and trimming Read-mapping to the genome or transcriptome Gene and transcript quantification 	<ul style="list-style-type: none"> Differentially-expressed genes Annotation Gene ontology Pathway analysis

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