DIAGENODE EPIGENOMICS PROFILING SERVICES

Bringing access to chromatin analysis closer to scientists

Introduction

Epigenetics is crucial for the regulation of gene expression and has broad relevance in biological processes like development, disease and response to the environment. While epigenetics research continues to push the boundaries of science, a number of technical and bioinformatics challenges often complicate studies and may be daunting for researchers. Our Epigenomics Profiling Services utilize our long history of expertise, making epigenetics research accessible to every researcher.

With our fully customizable Chromatin Profiling Services, we simplify your analyses of chromatin accessibility, histone modification profiling, and transcription factor binding sites across the genome. We pay particular attention to critical experimental steps, including but not limited to chromatin extraction and shearing, chromatin immunoprecipitation and library preparation, to ensure high-quality, interpretable data.

ChIP-seq Service
Histone modification and transcription factor

ChIP is a powerful tool to study the association of protein to DNA for analysis of epigenetics modifications, chromatin remodeling and regulation of gene expression by transcription factors. Our ChIP-seq service enables any scientist to access the highest quality ChIP-seq data with ready to publish figures.

Workflow

The complete workflow for ChIP-seq contains several critical steps: chromatin preparation and shearing, ChIP with ChIP-seq validated antibody, ChIP-seq library preparation, next-generation sequencing, and bioinformatics analysis.

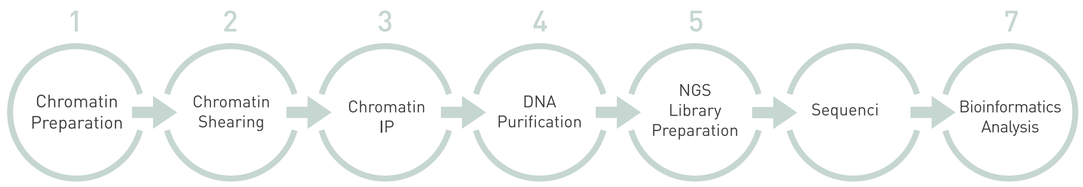


Figure 1
ChIP-seq workflow.

An efficient immunoprecipitation is key for a successful ChIP-seq experiment. Our team works together with the scientist and uses its chromatin shearing and ChIP optimization expertise to identify the protocol that best suits the research model.

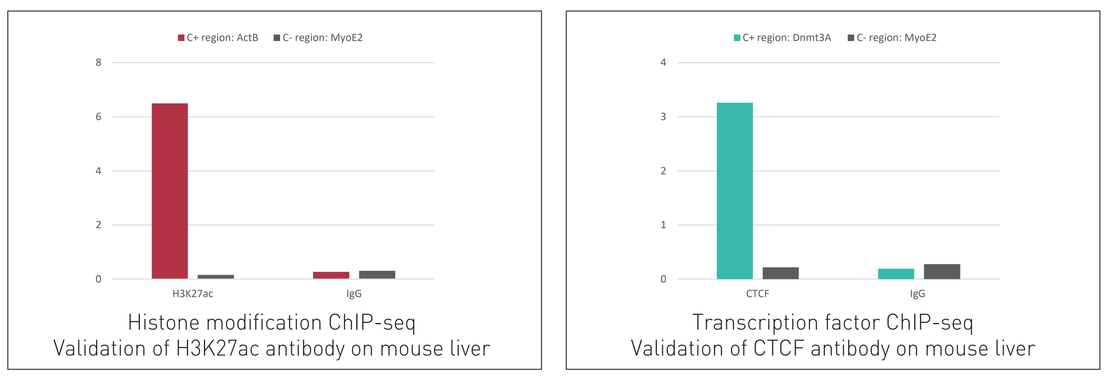


Figure 2
Antibody validation. Antibodies are validated by ChIP-seq before running the ChIP assay on the samples of interest.

Once the best ChIP conditions are validated, ChIP is performed on the samples of interest. Several quality controls are included in the process to ensure the quality of the libraries before Illumina® sequencing.

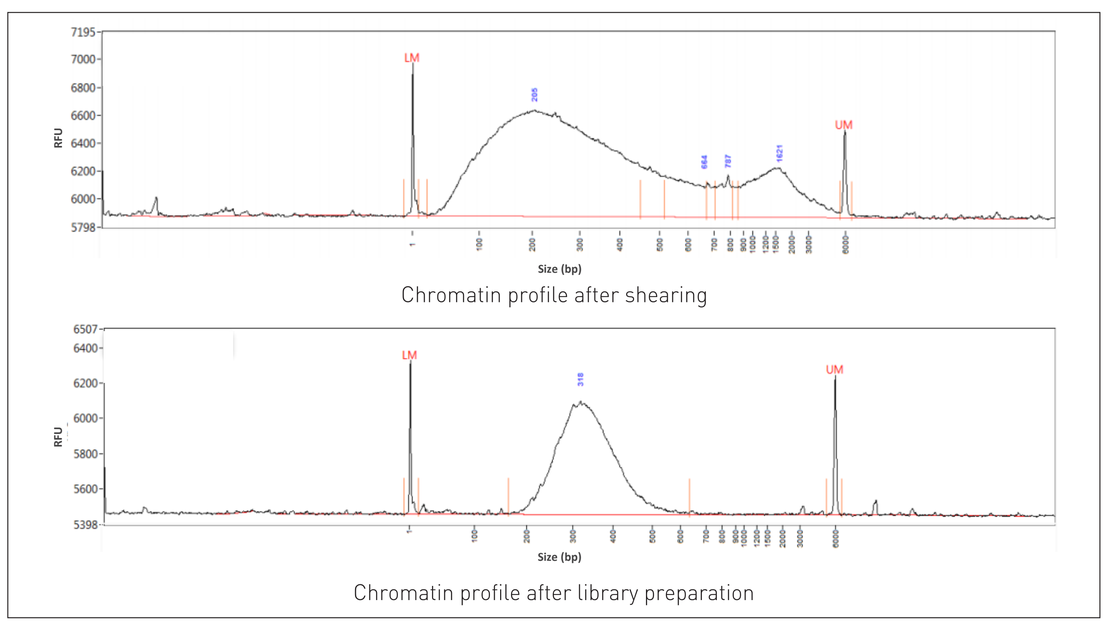
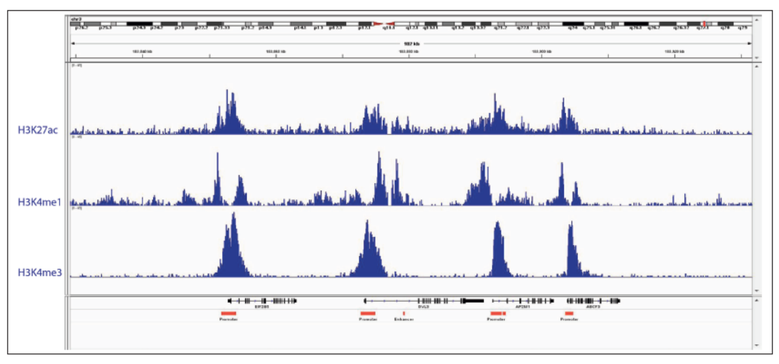


Figure 3
ChIP quality controls. Quality checks are performed along the ChIP-seq workflow.

Results

Our team expertise ensures the production of high quality data, even when dealing with low input libraries from picograms.



ChIP-Seq was performed using chromatin from 10,000 K562 cells and histone H3K27ac, H3K4me1, and H3K4me3 ChIP-seq grade antibodies (Diagenode).

Figure 4
Visualization of specific genomic regions. Reads enrichment at promoter and enhancer sites (red bars) are identified in a genome browser.

ATAC-seq Service
Standard and single-cell analysis

ATAC-seq is a sensitive tool to assess genome-wide chromatin accessibility. The technology is based on a hyperactive Tn5 transposase that simultaneously cuts open chromatin and ligates high-throughput sequencing adapters to these regions. Our ATAC-seq service enables any scientist to obtain genome-wide profiles of open and accessible regions of chromatin that are indicative of active regulatory regions.

Standard workflow

The complete workflow for ATAC-seq contains several critical steps: nuclei isolation, tagmentation, library preparation, next-generation sequencing, and bioinformatics analysis.

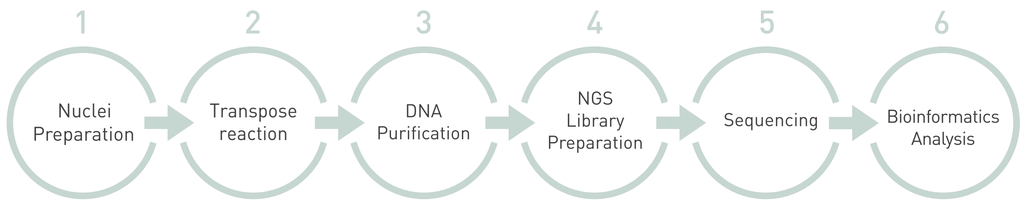


Figure 5
ATAC-seq workflow.

A pure nuclei preparation is key for a successful ATAC-seq experiment. Our team performs a first optimization step for every ATAC-seq project to ensure the best lysis condition for the samples of interest. Additionally, several quality controls are included in the process to ensure the quality of the libraries before Illumina® sequencing.

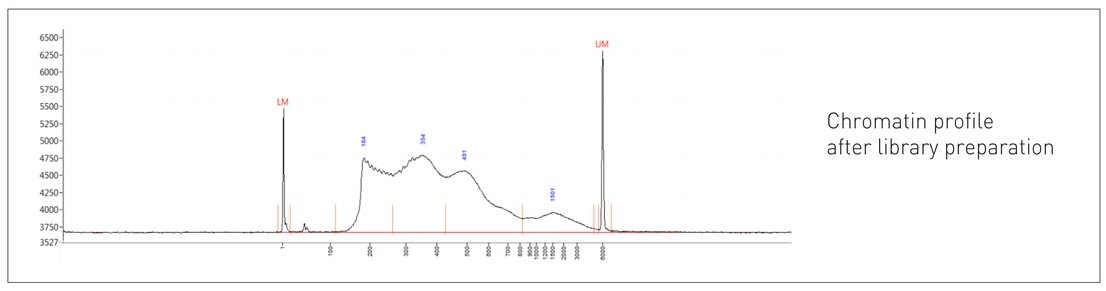


Figure 6
ATAC quality controls.

Results

Our bioinformatics team diligently optimizes pipelines to deliver biologically meaningful results within a short turnaround time. We work in close collaboration with scientists to fulfill specific analysis requirements.

For example, the affinity analysis is a robust, quantitative approach to assess for differentially open chromatin at consensus peaks. MA plots are a useful way of identifying differentially open chromatin regions.

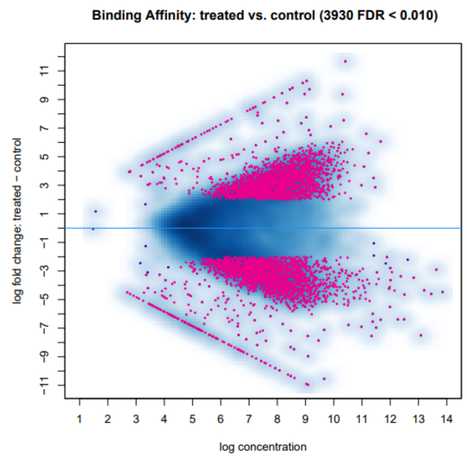


Figure 7
MA Plot. Treated versus control. Each point represents an open chromatin region. Differentially open chromatin regions with a log2 fold change equal or larger than 2 and a q-value < 0.01 are shown in red.

Single-cell analysis

Single-cell workflow

Our ATAC-seq service is now available for single-cell analysis. Our scATAC-seq service enables examination of genome-wide chromatin accessibility of thousands of cells in parallel, allowing examination of subpopulations of cells within a heterogenous population that would otherwise be lost in standard ATAC-seq.

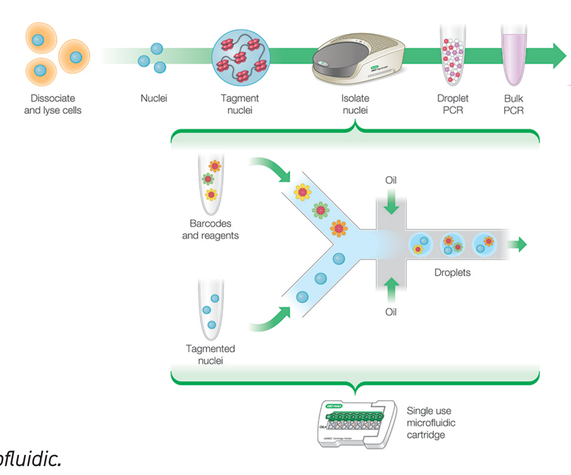


Figure 8
scATAC-seq protocol using droplet-based microfluidic.

Get high-resolution of cellular variability and system complexity

- Understand cell-to-cell heterogeneity
- Identify novel cell subpopulations
- Trace cell lineage
- Assess gene regulatory networks
- Discover novel biomarkers

Conclusion

Diagenode offers epigenomics services that you can trust for chromatin, DNA methylation, and RNA-seq analysis. Our team delivers the quality data you deserve for a wide range of epigenetics-related studies including discovery and biomarker identification projects.

Let's discuss your project

www.diagenode.com/en/categories/services