



Epigenome Sequencing

High-Throughput Gene Expression Regulation

Service Highlights

At SeqMatic, high-throughput epigenomic profiling of various aspects of chromatin architecture are analyzed with Illumina NovaSeq platforms. SeqMatic specializes in a variety of assays to analyze epigenetic modifications and the impact on gene regulation.

Comprehensive Services

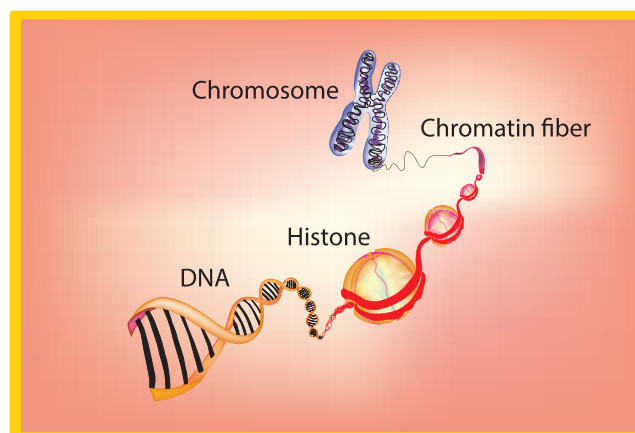
Available epigenomic analysis methods & solutions for epigenome profiling include:

- DNA methylation (bisulfite sequencing)
- Single-cell ATAC-Seq and Bulk ATAC-Seq for chromatin accessibility
- ChIP-Seq for examining transcription factor binding
- Multiome (ATAC-Seq and GEX) services available for integrated analyses

Our comprehensive services support research studies across diverse genome, transcriptome and epigenome applications for many organisms.

Features

- 10x Genomics Certified Service Provider
- Methyl-Seq - validated NEB protocols
- Scalability from few to hundreds of samples
- Expert pooling optimized by MiSeq Nano test run prior to deep sequencing
- Proprietary TailorMix PhiX control
- All projects are performed in a CLIA environment



Flexibility and Convenience

- Expert NGS Consultation
- Science-First Approach for Optimal Solutions
- White-Glove Services with Fast TAT

