CD Genomics
The Genomics Services Company

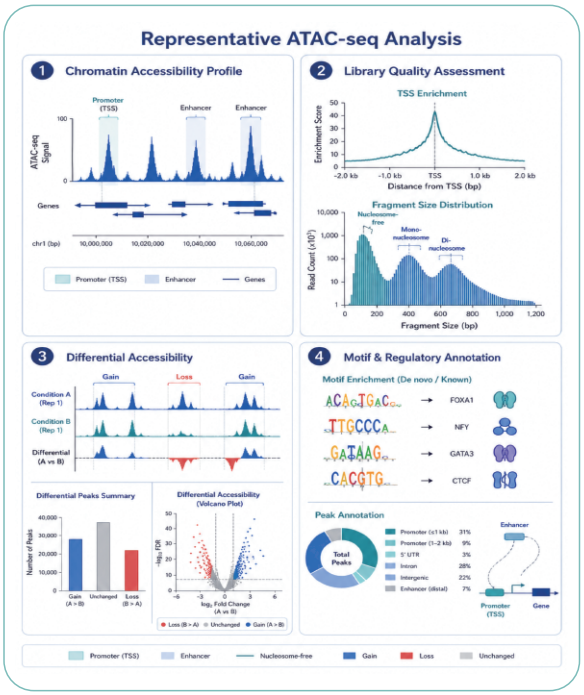
ATAC-seq: Chromatin Accessibility Profiling Service

CD Genomics provides ATAC-seq service to map genome-wide chromatin accessibility and uncover regulatory elements, transcription factor activity, and condition-specific epigenomic changes. In addition to bulk ATAC-seq, single-cell ATAC-seq and singlenucleus ATAC-seq options can support cell-typeresolved regulatory landscape analysis for heterogeneous or limited samples.

Open Chromatin Mapping | Regulatory Element Discovery | Differential Accessibility

Advantage Strip: Strategy-guided design· Sample-to-data QC · Differential accessibility · Motif analysis · Multi-omics interpretation

From nuclei preparation and library construction to peak calling, motif enrichment, and differential accessibility analysis, our ATAC-seq workflow helps researchers translate chromatin accessibility signals into biologically meaningful regulatory insights.



Service Scope

- Bulk, single-cell, and single-nucleus ATAC-seq for diverse study designs
- Genome-wide profiling of open chromatin and regulatory element landscapes
- Differential accessibility analysis across disease, development, treatment, or phenotype conditions

Why ATAC-seq Matters

- Captures accessible chromatin landscapes that reflect regulatory potential beyond gene expression alone.
- Helps identify accessible promoters, enhancers, and putative regulatory regions linked to transcriptional control
- Supports inference of transcription factor activity through motif enrichment and accessibility patterns.

Bioinformatics Deliverables

- QC summaries, peak sets, annotation, and differential accessibility results
- Motif enrichment, candidate TF interpretation, and visual outputs for reporting and follow-up

Analysis Snapshot

Analysis Module	What It Shows	Research Value
Peak Calling	Accessible chromatin regions	Identifies candidate regulatory elements
TSS Enrichment QC	Signal enrichment near promoters	Evaluates library quality
Differential Accessibility	Condition-specific open chromatin changes	Reveals regulatory remodeling
Peak Annotation	Genomic location of accessible regions	Links peaks to genes and features
Motif Enrichment	Overrepresented TF-binding motifs	Suggests candidate transcription factors
Multi-omics Integration	Accessibility linked with expression or epigenomic data	Supports mechanism-level interpretation