GENEWIZ®

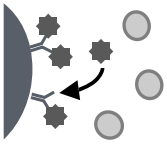
ATAC-SEQ

The Assay for Transposase-Accessible Chromatin using Sequencing (ATAC-Seq) employs a hyperactive form of Tn5 to efficiently label regions of open chromatin for analysis by next generation sequencing. A powerful tool for epigenetic analysis, ATAC-Seq can provide global mapping of nucleosome positions and identify active enhancer regions during development or pathogenesis.

ATAC-SEQ WORKFLOW

1. Sample Preparation

Isolate and freeze cells with protocol provided by GENEWIZ



2. Dead Cell Removal

If low viability, live cells are enriched using a magnetic bead-based approach

3. Nuclei Extraction & Library Preparation

Optimized ATAC assay produces robust signal from low inputs

4. Sequencing

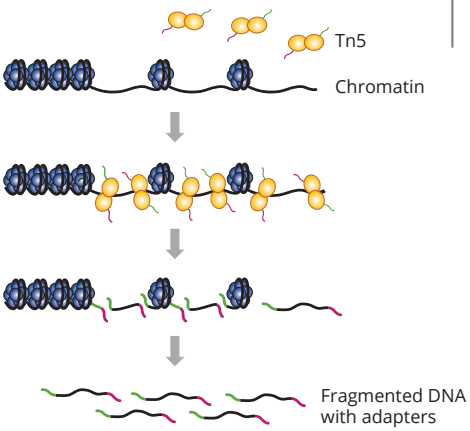
Guaranteed data quality exceeds Illumina® benchmarks

5. Bioinformatics

Alignment, peak calling, and multiomic data integration

See reverse for more information

GENEWIZ has developed a proprietary workflow for nuclei extraction and tagmentation-based library construction using cryopreserved cells as input material. Our optimized assay outperforms standard ATAC-Seq and other chromatin accessibility assays—such as FAIRE-Seq, MNase-Seq, and DNase-Seq.



FEATURES & BENEFITS

- **Convenient sample preparation –** freeze and store cells prior to submission; fresh cells or isolated nuclei are not required
- **Improved data quality –** higher signal-to-noise ratio compared to traditional ATAC-Seq
- **Flexible starting material –** submit as few as 50,000 cells; dead cell removal improves samples with low viability
- **Single-cell analysis** available using the 10x Genomics® Chromium™ platform

Solid science.
Superior service.

CONTACT GENEWIZ:
Ph.D. experts available to discuss your project:

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GENEWIZ®

MULTIOMIC SOLUTIONS
RNA-SEQ + ATAC-SEQ/CHIP-SEQ/WGBS

Next generation sequencing (NGS) data can now be integrated from independent NGS assays in a "multiomic" framework for unique insights into genomic and epigenomic regulatory systems. Most notably, transcriptional (e.g. RNA-Seq) data can be linked with epigenetic (e.g. ATAC-Seq) data to quantify how chromatin structure influences the regulation of gene expression.

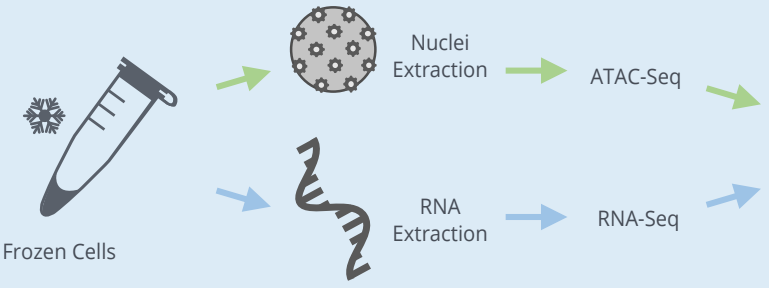
GENEWIZ MULTIOMIC BENEFITS

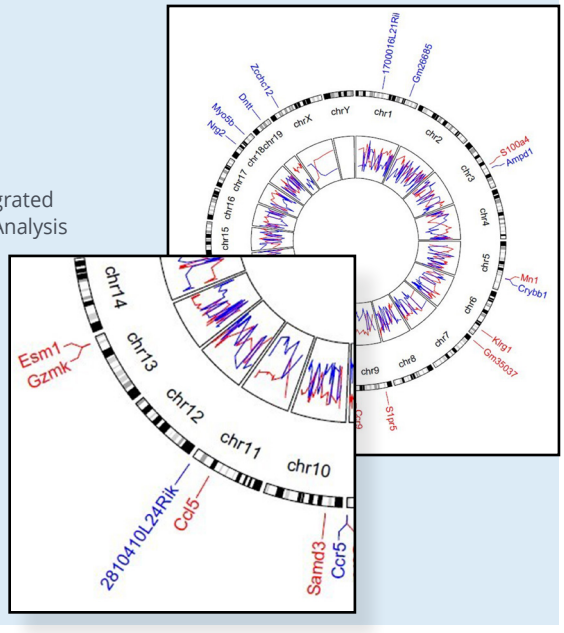
- ✔ Streamlined experimental design with sample splitting to reduce variability between assays
- ✔ Integrated data analysis provides greater insight into gene regulation
- ✔ Reduced cost and faster results from combined workflows
- ✔ Combine RNA-Seq with ATAC-Seq, ChIP-Seq, or whole genome bisulfite sequencing

THE GENEWIZ DIFFERENCE

- ✔ **Superior data quality** that exceeds Illumina® benchmarks
- ✔ **Dedicated Ph.D.-level support** throughout the entire project
- ✔ **Industry-leading turnaround time** with sequencing as fast as 1 week
- ✔ **Single-Cell ATAC-Seq + RNA-Seq available** using the 10x Genomics® Chromium™ platform

Example Workflow: ATAC-SEQ + RNA-SEQ





Our proprietary ATAC and RNA integration pipeline was used to analyze the differentiation of CD8 T cells. Chromatin accessibility was mapped in naïve (—) and effector cells (—) using ATAC-Seq. From RNA-Seq, down- and up-regulated genes were identified during the transition from naïve to effector cells. Overall, regions with strong differential gene expression showed corresponding differences in chromatin accessibility.

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