



Assay for Transposase-Accessible Chromatin with High Throughput Sequencing (ATAC-seq)

ATAC-seq is a high-throughput sequencing method for analysis of genome-wide chromatin accessibility, which is important for global epigenetic control of gene expression. Sequencing adapters are inserted into open chromatin regions by hyperactive Tn5 transposase. After PCR amplification, a sequencing library is constructed. All the open chromatin regions can be obtained under a specific space-time condition, not only limited to the binding sites of a transcription factor, or a certain histone modified region.

The Novogene Advantages

Extensive Experience

Over 100 projects successfully completed in 2019.

Data Guarantee

Strict quality control management ensures high-quality data.

Comprehensive Analysis

Our team of experienced scientists offer reliable analysis solutions to meet your project needs.

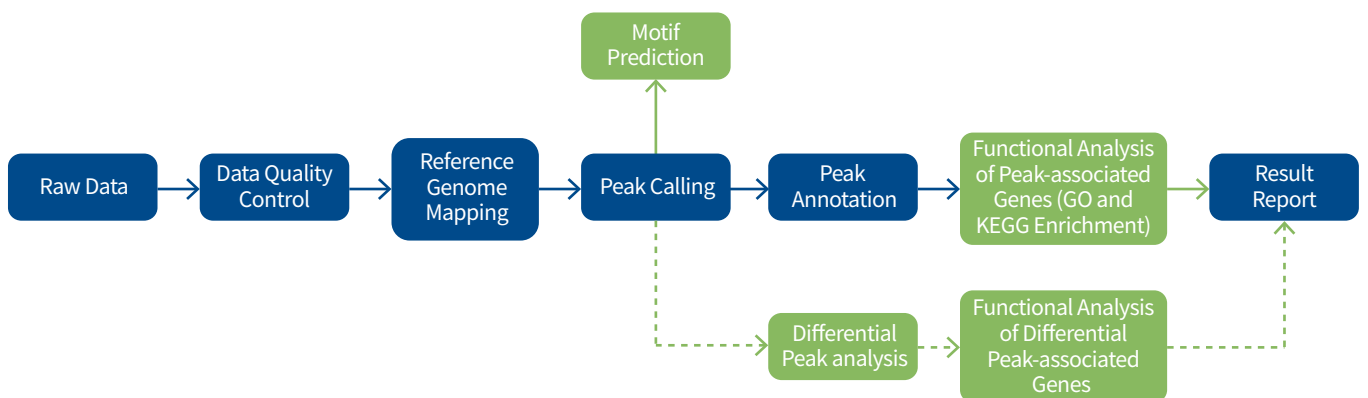
Project Workflow



Specifications

SAMPLE REQUIREMENTS	<p>Sample type: Tissues, live cells, or frozen cells</p> <p>Cell number: $\geq 1 \times 10^5$ cells, an accurate cell number is key to success of the experiment</p> <p>Tissue weight: ≥ 2 g fresh animal tissue</p>
SEQUENCING STRATEGY	<p>Library type: 100-500 bp insert cDNA library (depends on peak distribution)</p> <p>Sequencing platform: NovaSeq 6000</p> <p>Sequencing strategy: Paired-End 150 bp</p> <p>Recommended data output: 15 Gb raw data per sample</p>
TURNAROUND TIME	21 working days for 20 or fewer samples from verification of sample quality without data analysis

Analysis Pipeline



--> Only applicable for projects with comparable experimental groups.

Novogene Powered Publications

Year	Journal	Title
2019	<i>Cancer Research</i>	SET Domain-Containing Protein 4 Epigenetically Controls Breast Cancer Stem Cell Quiescence
2019	<i>Scientific Data</i>	Transcriptome and Chromatin Accessibility in Porcine Intestinal Epithelial Cells upon Zearalenone Exposure

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