

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

1. Sample Requirements

Sample Type	Required Amount	Viability
Cryopreserved Cells	≥ 500k cells	≥ 60%
Frozen Tissue	≥ 100mg (Recommended) ≥ 50mg (Min)	-

2. Sequencing Parameters

Sequencing Platform	Illumina NovaSeq 6000
Read Length	Paired-end 150 bp
Recommended Data Amount	9-15 Gb per sample
Data quality	Guaranteed ≥ 85% bases with Q30 or higher
Turnaround Time	21 working days if less than 48 samples without bioinformatic analysis

3. Data Analysis Contents

Standard analysis
Data quality control (Trim and filter; read length distribution, GC distribution, N ratio, clean reads)
Mapping onto reference genome (Mapping Quality Statistics, Distribution of the Reads, Sample Correlation Detection)
Fragment Size Prediction
Peak calling and peak distribution
Summits analysis
Motif analysis
Peak annotation (TSS, functional region, GO, KEGG)
Differential analysis



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