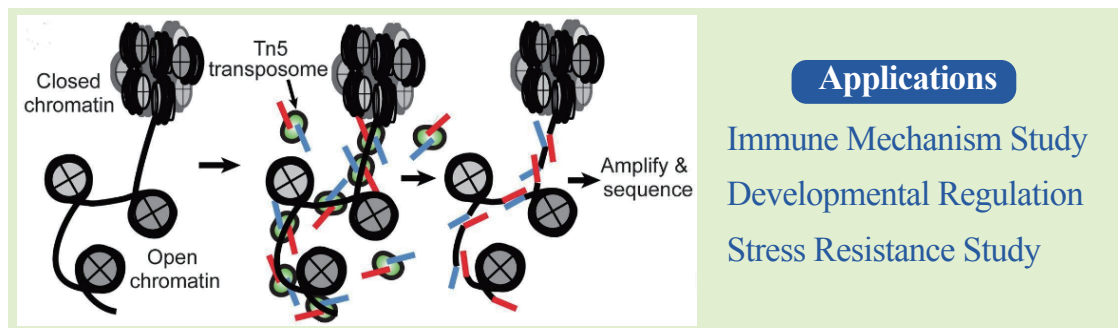
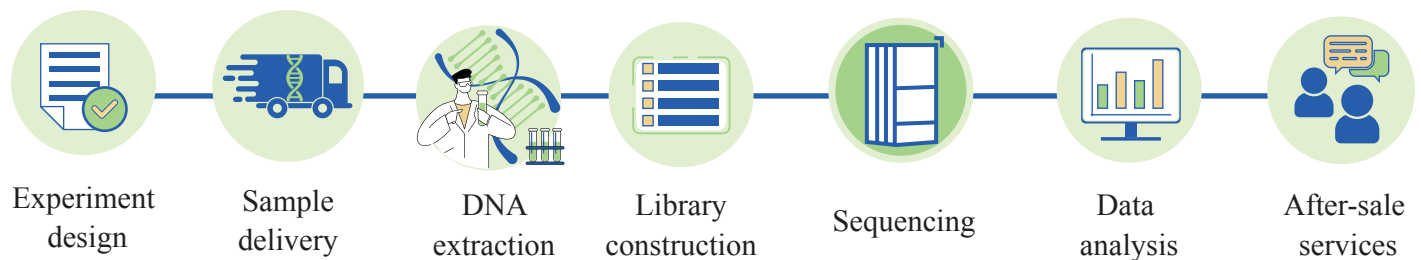


# Assay for Transposase Accessible Chromatin with high-throughput sequencing (ATAC-Seq)

Assay for Transposase Accessible Chromatin with high-throughput sequencing (ATAC-Seq) is a technique that utilizes high-throughput sequencing to study the accessibility of chromatin regions. It involves cutting open chromatin regions using a transposase enzyme, allowing identification of active regulatory sequences and potential transcription factor binding sites.



## Service Workflow



## Bioinformatics

### 1. Sequencing Data Quality Control

#### 2. Inner-sample Analysis

- » Data quality control
- » Peak calling and statistics
- » Distribution of mapped reads
- » Peak related genes and corresponding GO, KEGG annotation and enrichment analysis
- » Alignment with reference genome
- » Peak annotation (Gene functional element)
- » Motif analysis and transcription factor prediction

### 3. Inter-group Analysis

- » Sample correlation analysis
- » Differential peak identification
- » Motif of differential peaks
- » Differential peak related genes and corresponding GO, KEGG annotation and enrichment analysis

## Service Advantages

- High sensitivity: Low starting cell quantity is sufficient for library preparation and sequencing.
- Good experimental reproducibility: Technical replicates show excellent repeatability.
- Simultaneously reveal the genomic locations of open chromatin, DNA-binding proteins and transcription binding sites interactions.
- Comprehensive Analysis: Professional analysis pipeline to meet a variety of customized analysis needs.
- Extensive Experience: Hundreds of projects successfully completed so far, including animal and plant samples.
- BMKGENE has comprehensive workflow for multi-omics joint analysis.

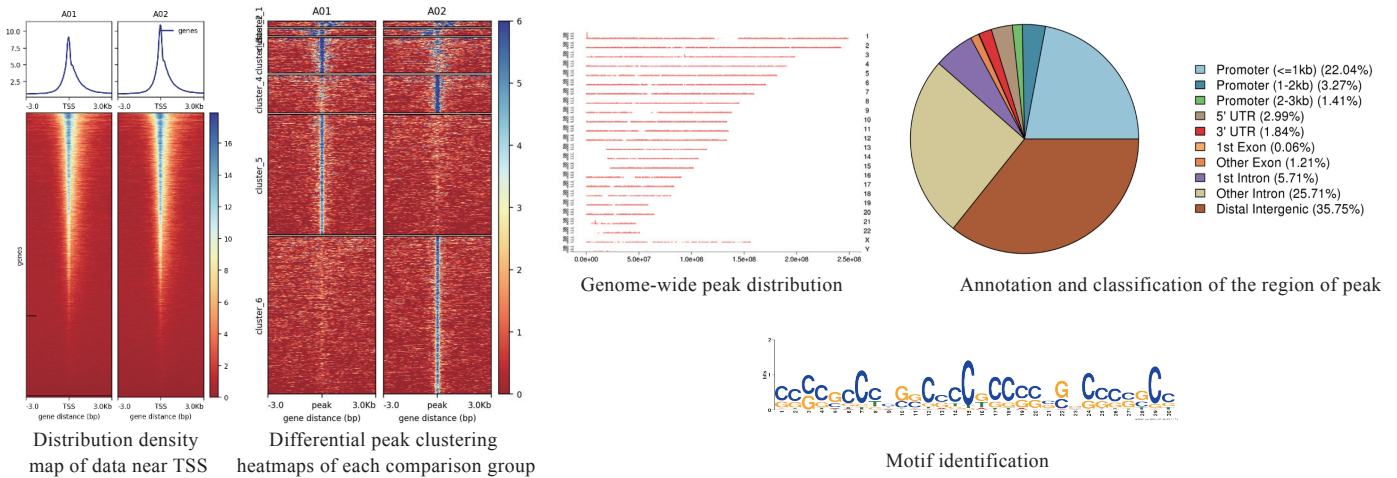
## Service Specifications

Library Type	Platform	Recommended data amount
ATAC-seq	Illumina PE150	≥ 50M reads

## Sample Requirements

Cells	Tissue	Blood
≥ 5x10 <sup>5</sup>	≥ 200 mg	≥ 2 mL

## Demo Results



## Featured Publications

Year	Journal	Title
2022	Horticulture Research	Telomere-to-telomere genome assembly of bitter melon ( <i>Momordica charantia</i> L. var. <i>abbreviata</i> Ser.) reveals fruit development, composition and ripening genetic characteristics



## Biomarker Technologies (BMKGENE) GmbH

BioZ, Johann-Krane Weg tech@bmkcloud.com  
 42, 48149 Münster, Germany www.bmkgene.com

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