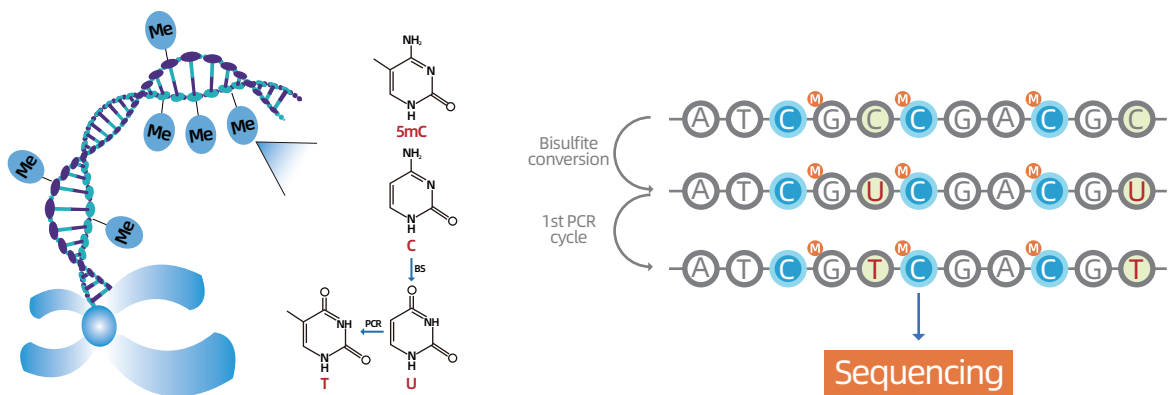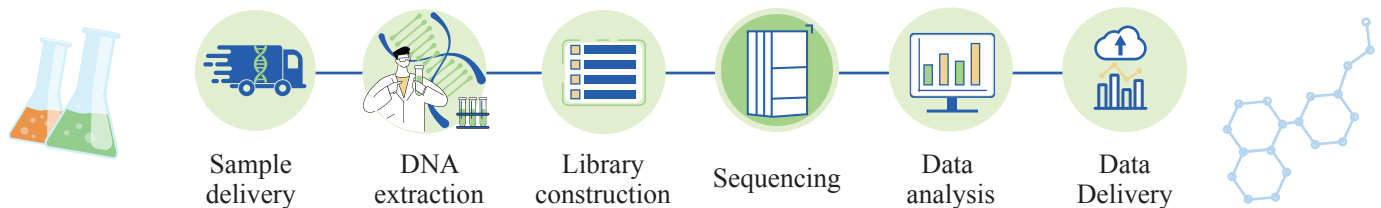# Whole Genome Bisulfite Sequencing (WGBS)

Whole-Genome Bisulfite Sequencing (WGBS) is considered the gold standard for DNA methylation studies. It invo -lves treating DNA with bisulfite, which converts unmethylated cytosines to uracils, followed by sequencing to dete -rmine methylation levels. WGBS offers a comprehensive and single-base resolution map of DNA methylation patt -erns across the entire genome.



## Service Workflow



Sample delivery → DNA extraction → Library construction → Sequencing → Data analysis → Data Delivery

## Bioinformation

**1. Sequencing Data Quality Control**

**2. Reference Genome Alignment**
- Statistics on reads mapping
- Sequencing depth and coverage of C sites

**3. Identification of DNA Met -hylation**
- Identification of DNA Methylation site
- Statistics on methylated sequence type (mCG, mCHG, mCHH)
- Distribution of methylated C sites
- Motif of methylated sites

**4. Genome-wide DNA Methy -lation Profile**
- Genome-wide mC density and distribution
- Methylation level of functional regions
- Methylation level at up- and down-stre -am regions
- CpG gene annotation

**5. Inter-group Differential Analysis**
- Identification of DMRs
- DMR annotation
- GO/KEGG enrichement analysis on DMR related genes

# Service Advantages ••••

» Gold standard for DNA methylation research.

» Provides a comprehensive and single-base resolution map of DNA methylation patterns across the entire genome.

» Enable the detection of allele-specific methylation.

» Demonstrates extensive expertise in WGBS across a diverse range of species.

» BMKGENE offers a mature and comprehensive analysis pipeline, allowing for the integrated analysis of WGBS with other omics data such as RNA-seq.
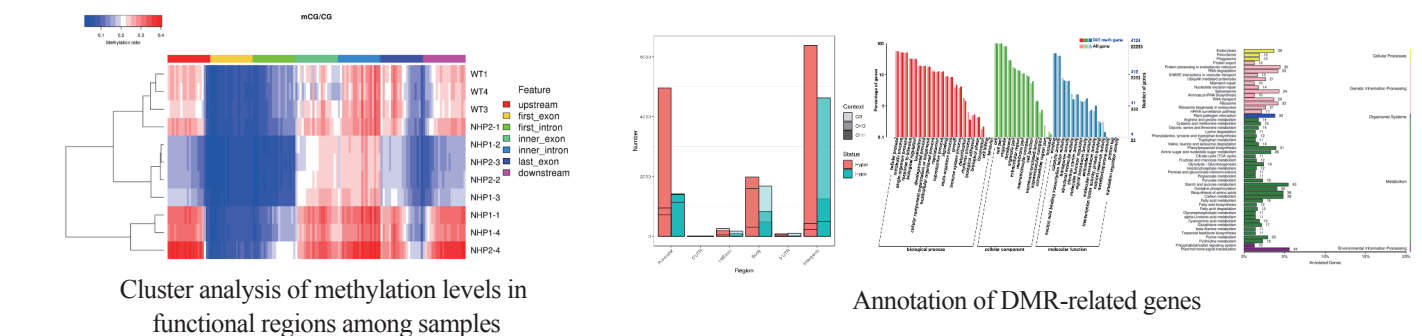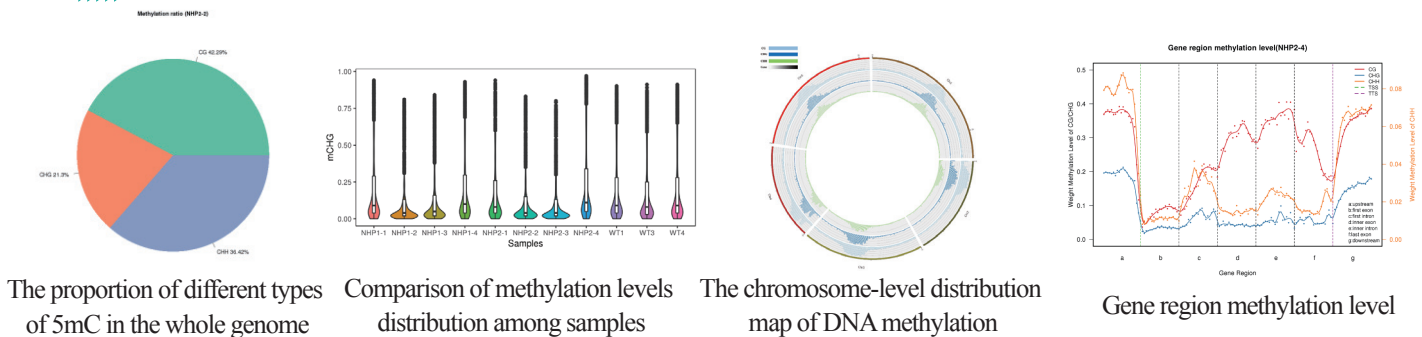
# Service Specifications ••••

| platform | Sequencing | Sample Delivery |
|---|---|---|
| Illumina | PE150 | 30X, three biological replicates, with high quality reference genome |

# Sample Requirements ••••

| Sample Type | Amount (µg) | Conc. (ng/µl) | Volume (µl) | Purity |
|---|---|---|---|---|
| gDNA | ≥ 2 | ≥ 20 | ≥ 20 | Limited degradation and contamination |

# Demo Results ••••

The proportion of different types of 5mC in the whole genome

Comparison of methylation levels distribution among samples

The chromosome-level distribution map of DNA methylation

Gene region methylation level

Cluster analysis of methylation levels in functional regions among samples

Annotation of DMR-related genes