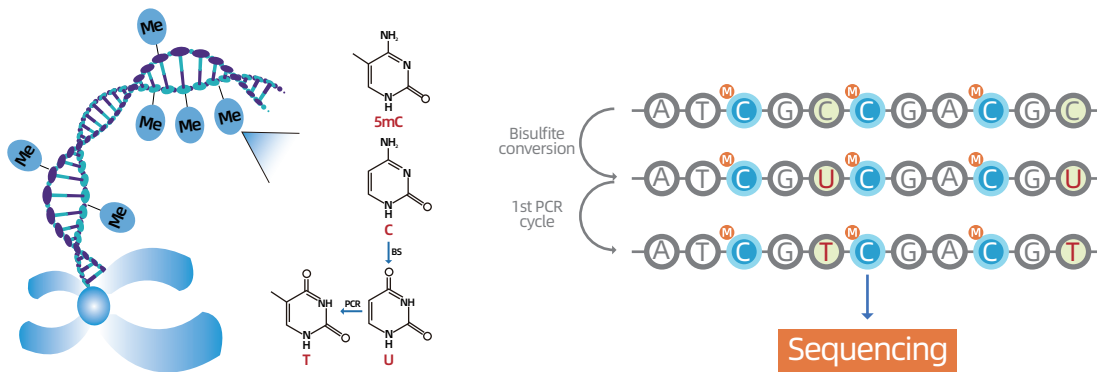
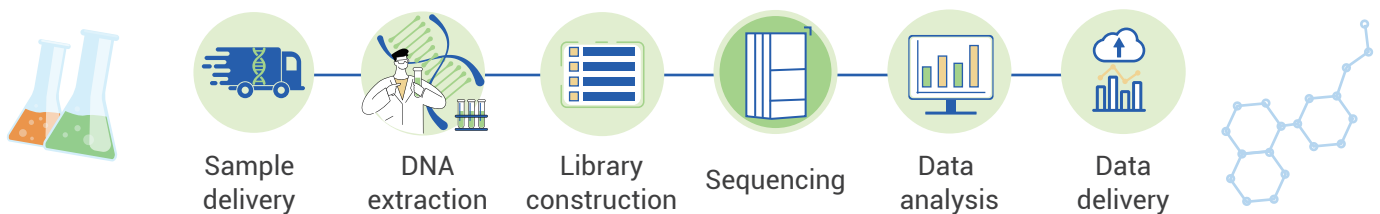


Whole Genome Bisulfite Sequencing (WGBS)

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



Service Workflow



Bioinformatics

- | | | | |
|--|---|---|--|
| 1. Data Quality Control | 3. Identification of DNA Methylation <ul style="list-style-type: none"> • 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 Methylation Profile <ul style="list-style-type: none"> • 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 <ul style="list-style-type: none"> • Identification of DMRs • DMR annotation • GO/KEGG enrichment analysis on DMR related genes |
| 2. Reference Genome Alignment <ul style="list-style-type: none"> • Statistics on reads mapping • Sequencing depth and coverage of C sites | | | |

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.
- 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.

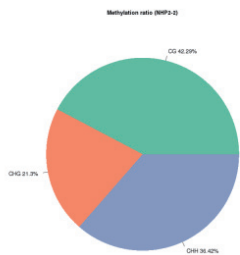
Service Specifications

Platform	Read Length	Sequencing Strategy
Illumina	PE150	30X, three biological replicates, with high quality reference genome

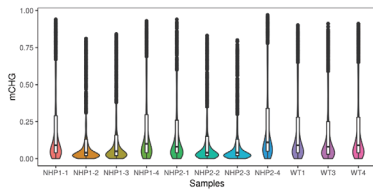
Sample Requirements

Sample Type	Amount (ng)	Conc. (ng/μL)	Volume (μL)	Quality
gDNA	≥ 400	≥ 5	≥ 20	No or limited degradation or contamination

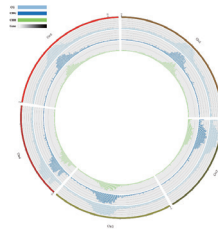
Demo Results



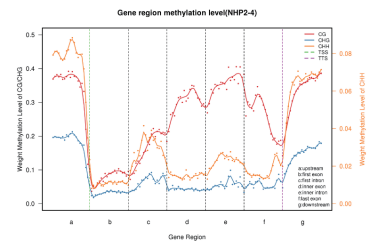
Proportion of different types of 5mC in the whole genome



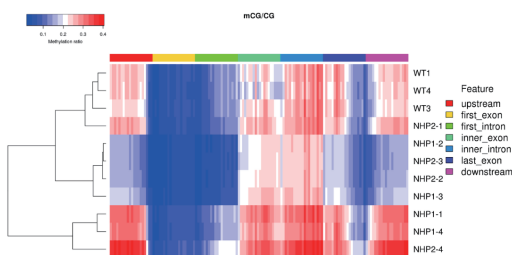
Comparison of methylation level distribution among samples



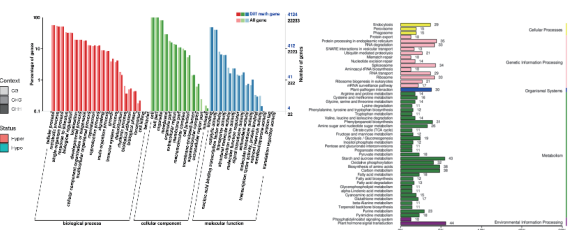
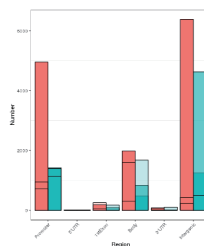
Chromosome-level distribution map of DNA methylation



Gene region methylation level



Cluster analysis of methylation levels in functional regions among samples



Annotation of DMR-related genes

Biomarker Technologies (BMKGENE)

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Global Locations

Germany United Kingdom United States China