Whole Genome Bisulfite Sequencing (Gene Methylation)

1. Sample Requirements

Sample Type	Required Amount	Volume	Concentration	Purity
Genomic DNA	⩾ 2.5 μg	⩾ 20 μL	⩾ 20 ng/μL	OD260/280=1.8-2.0; 0 < OD260/230 < 3; No degradation or contamination

Remark: This sample requirement is for reference only. If you have any questions, please consult your local sales or Novogene support for detailed information.

2. Sequencing Parameters

Platform	Illumina NovaSeq 6000
Read length	Paired-end 150
Sequencing depth	⩾ 30× coverage for the species with reference genome;
Data quality	Guaranteed ⩾ 80% bases with Q30 or higher

Remark: Detailed sequencing parameters can be consulted with your local sales or Novogene support.

3. Data Analysis Contents

Standard Analysis
Data quality control (filtering reads containing adapter or with low quality; Q20, Q30, error rate distribution, GC distribution, total bases)
Mapping onto reference genome (mapping rate, duplication rate, sequencing depth, reads coverage)
mCs detection, methylation level calculation
(1) Methylation level and frequency distribution in different sequence context (CG, CHG, CHH) (2) Methylation level and frequency distribution in different chromosomes (3) Methylation level and frequency distribution in different functional elements (promoter, 5'UTR, exon, intron, 3'UTR)
Differentially Methylated Site (DMS) detection
Differentially methylated regions (DMRs), Differentially Methylated Promoter (DMPs) detection and annotation
Function enrichment (Gene Ontology and KEGG Pathway) of DMR-associated genes and DMP-associated genes
Visualization of BS seq data

Remark: Detailed analysis contents can be consulted with your local sales or Novogene support.