

Whole Genome Bisulfite Sequencing

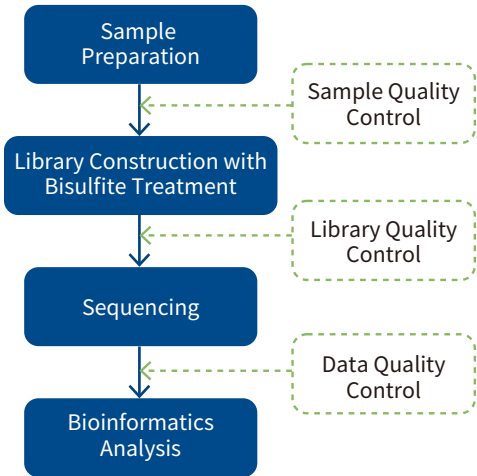
DNA methylation at the fifth position in cytosine (5-mC) has a fundamental influence on gene expression and cellular activity. Abnormal methylation patterns have been associated with several conditions and diseases, such as cancer. WGBS has become the gold standard for studying genome-wide methylation at single base resolution. Novogene offers comprehensive DNA methylation analysis, which is an increasingly widely-used application of NGS technology.

The Novogene Advantages

Novogene is a world leader in sequencing capacity using state of the art technology, including the latest Illumina NovaSeq platform.

- 1 Extensive Experience:**
Over 1000 projects successfully completed, and our data has been published in many noteworthy journals.
- 2 Unsurpassed Data Quality:**
We guarantee a sequencing quality score \geq Q30 for over 80% of the bases.
- 3 Comprehensive Data Analysis:**
We use widely accepted mainstream software, like Bismark, and a mature in-house pipeline for mapping, differentially methylated region (DMR) analysis, functional analysis and data visualization.

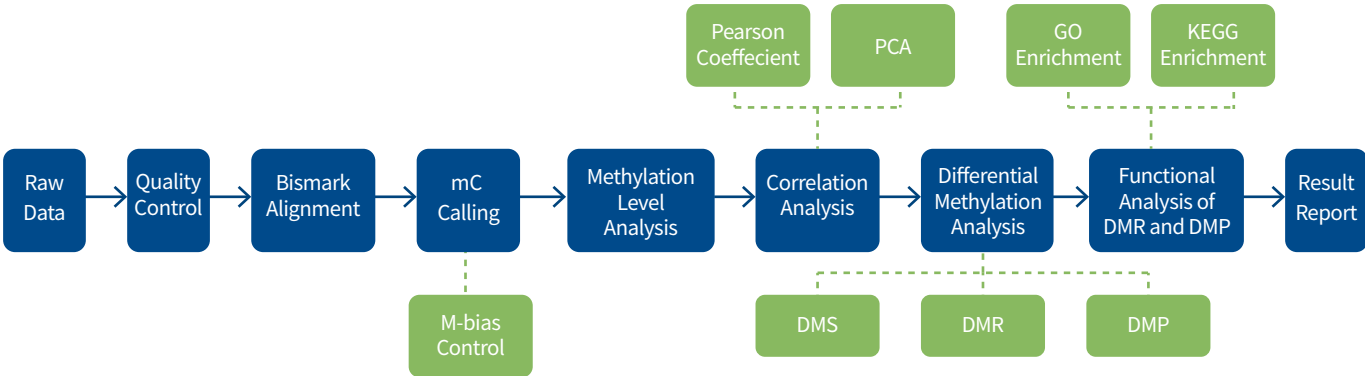
Project Workflow



WGBS Specifications

Sample Requirements	DNA amount: \geq 0.2 μ g. DNA concentration: \geq 5 ng/ μ l. Purity: OD260/280 = 1.8–2.0 without degradation, protein or RNA contamination.
Recommended Sequencing Depth	\geq 30 \times coverage
Data Quality Guarantee	Q30 \geq 80%. Bisulfite conversion rate \geq 99%.
Turnaround Time	34 working days for 20 or fewer samples from verification of sample quality without data analysis.

Analysis Pipeline



Novogene Powered Publications

Year	Journal	Title
2020	<i>Nature</i>	A Genomic and Epigenomic Atlas of Prostate
2018	<i>Plant Biotechnology Journal</i>	Single-Base Methylome Analysis Reveals Dynamic Epigenomic Differences Associated with Water Deficit in Apple
2017	<i>Bioinformatics</i>	Genome-wide Analysis of DNA Methylation Profiles in a Senescence-accelerated Mouse Prone 8 Brain using Whole-genome Bisulfite Sequencing
2016	<i>The Plant Cell</i>	Altered Transcription and Neofunctionalization of Duplicated Genes Rescue the Harmful Effects of a Chimeric Gene in Brassica napus
2014	<i>Genome Biology</i>	Whole-genome Analysis of 5-hydroxymethylcytosine and 5-methylcytosine at Base Resolution in the Human Brain

For Research Use Only. Exclusive for Clients in North and South America.



Follow us on LinkedIn