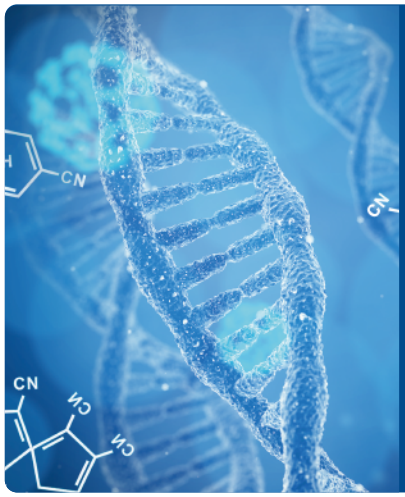
Novogene

RRBS

Reduced Representation Bisulfite Sequencing (RRBS)



DNA methylation research has always been a hot topic in disease research, and is closely related to gene expression and pheno- typic traits. RRBS is an accurate, efficient and economical method for DNA methylation research. Enrichment of promoter and CpG island regions by enzymatic cleavage (Msp I), combined with Bisulfite sequencing, provides high resolution DNA methylation detection.

WGBS, the current "gold standard " in detecting DNA methylation levels, is limited in its widespread use due to its higher cost. As a cost-effective methylation research method, RRBS has broad applications in large-scale clinical research.

Advantages of RRBS

Accuracy

The same as WGBS-Single base resolution

Repeatability

Suitable for differential analysis between multiple samples

Wider Range

Covers more than 5 million CpG sites across the genome

Cost Effective

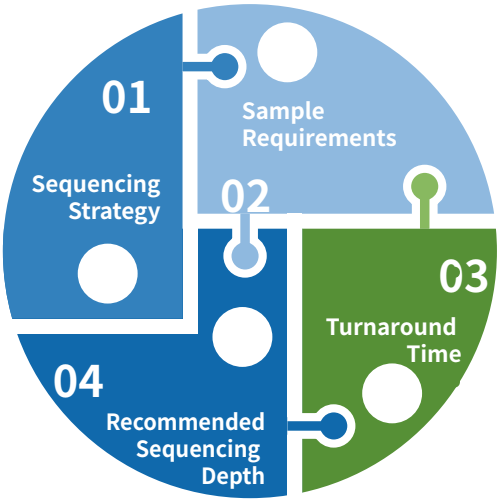
Provides the same coverage as WGBS with a lower data requirement, making this solution more cost-effective.

Project Workflow

RRBS Specifications

- 200-400-bp insert bisulfite treated DNA library.
- NovaSeq 6000 platform, paired-end 150 bp.

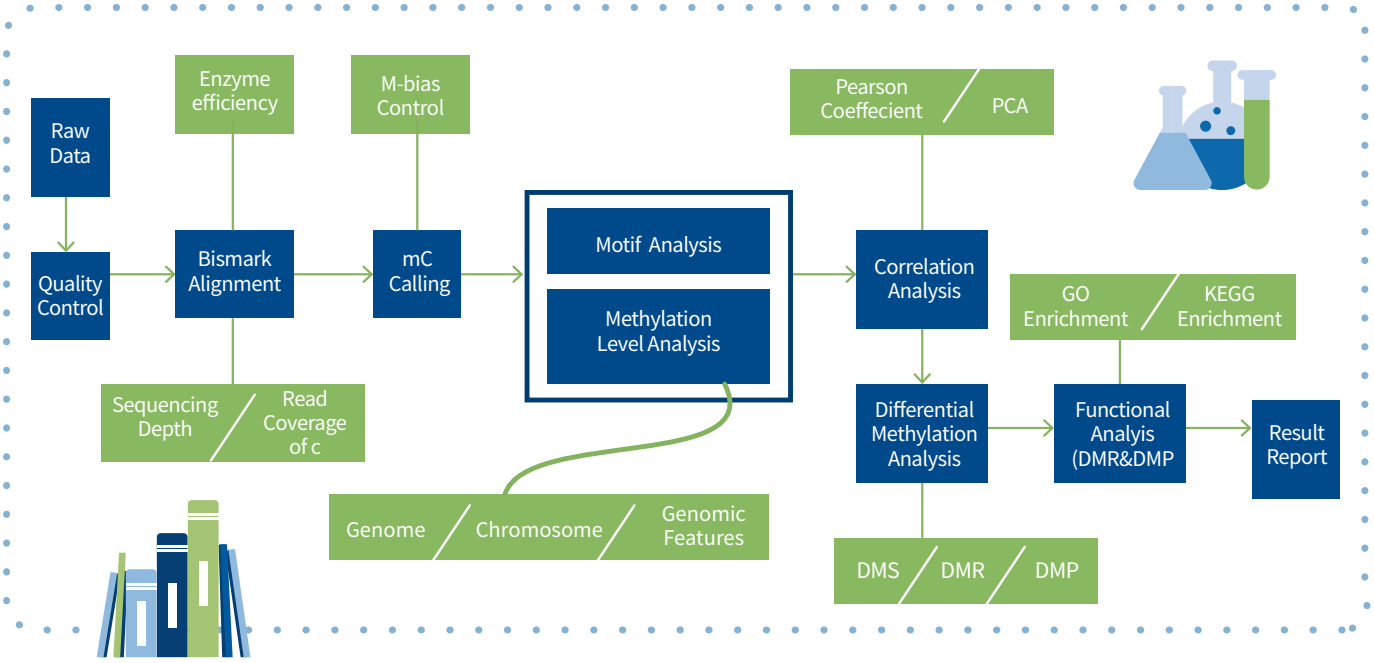
- 10 G/Sample recommended.



- DNA amount: ⩾ 1.5 μg.
- DNA concentration: ⩾ 20ng/μl.
- Purity: OD260/280 = 1.8–2.0 without degradation, protein or RNA contamination.

- 22 working days for 20 or fewer samples from verification of sample quality without data analysis.

Analysis Pipeline



Novogene Powered Publications

Year	Journal	Title
2019	*Journal of Agricultural and Food Chemistry*	Genome-Wide DNA Methylome and Transcriptome Analysis of Porcine Intestinal Epithelial Cellsupon Deoxynivalenol Exposure

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

Novogene Corporation Inc.

8801 Folsom Blvd #290, Sacramento, CA 95826

916-252-0068-383 inquiry_us@novogene.com en.novogene.com

Follow us on LinkedIn