DNBSEQ™ SERVICE OVERVIEW

Whole Genome Bisulfite Sequencing

Service Description

Methylation of DNA at the fifth position in cytosine (5-mC) is a stable epigenetic modification and plays an important role in many biological processes, including gene silencing, suppression of transposable elements, genomic imprinting and X chromosome inactivation. Detection and quantification of methylation are critical to understand gene expression and other processes subjected to epigenetic regulation.

Whole genome bisulfite sequencing (WGBS) is used to detect methylated cytosines by treating the DNA with sodium bisulfite before sequencing. WGBS has become the gold standard for studying genome-wide methylation at single base resolution.

Sequencing Service Specification

Our Whole Genome Bisulfite Sequencing Services are executed with DNBSEQ technology.

Sample preparation and services

- Library preparation, including bisulfite treatment
- 100 bp paired-end sequencing
- Clean data, standard and customized data analysis
- Available data storage and bioinformatics applications

Sequencing Quality Standard

- Guaranteed ≥90% of clean bases with quality score of Q20
- Guaranteed ≥99% bisulfite conversion rate
- Standard sequencing coverage ≥30X is recommended

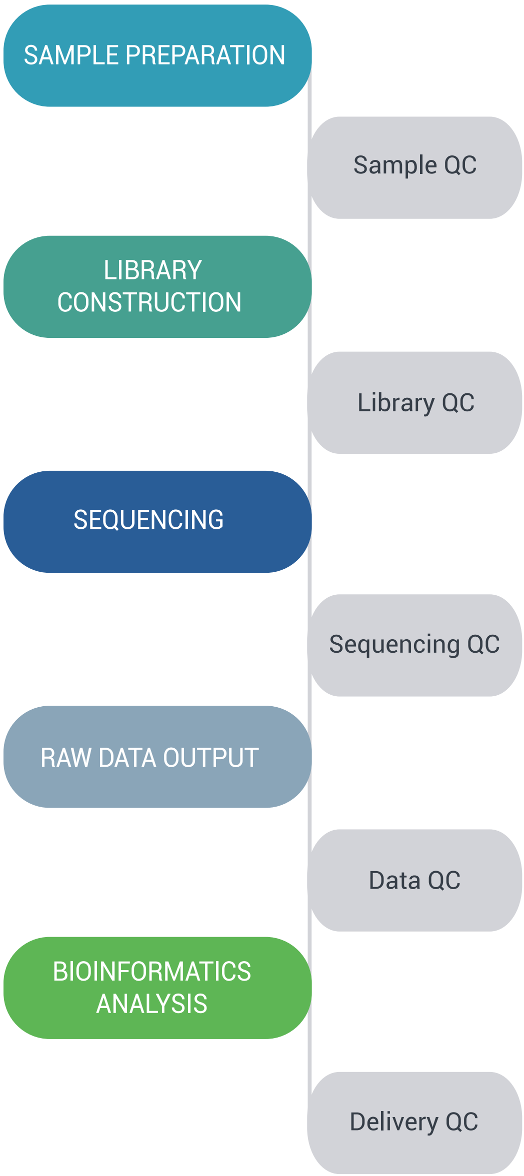
Turnaround Time

- Typical 26 working days from sample QC acceptance to filtered raw data availability
- Expedited services are available; contact Our specialist for details

Quality Data **Fast TAT** **Cost Effective**

Project Workflow

We care for your samples from the start through to the result reporting. Highly experienced laboratory professionals follow strict quality procedures to ensure the integrity of your results.



SAMPLE PREPARATION

Sample QC

LIBRARY CONSTRUCTION

Library QC

SEQUENCING

Sequencing QC

RAW DATA OUTPUT

Data QC

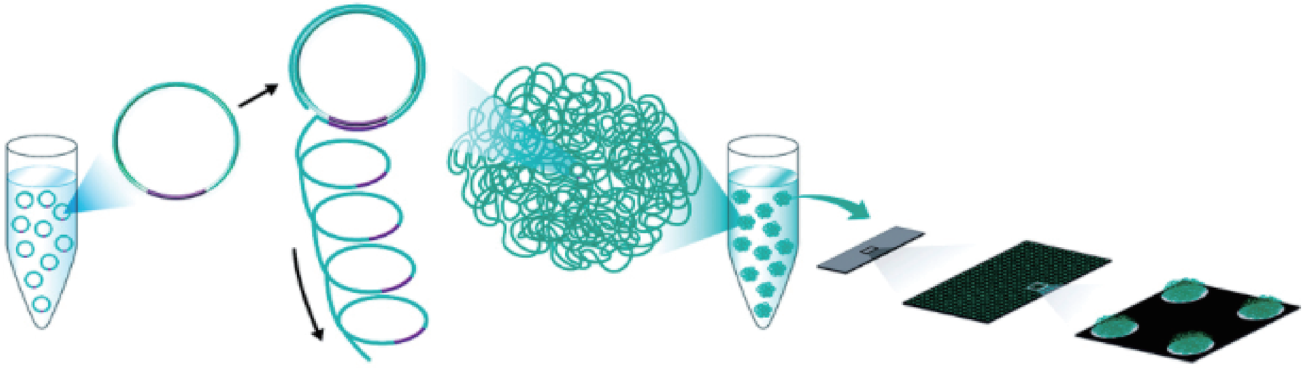
BIOINFORMATICS ANALYSIS

Delivery QC

DNBSEQ sequencing technology

DNBSEQ is an innovative high-throughput sequencing solution. The system is powered by combinatorial Probe-Anchor Synthesis (cPAS), linear isothermal Rolling-Circle Replication and DNA Nanoballs (DNB^{TM}) technology, followed by high-resolution digital imaging.

The combination of linear amplification and DNB technology reduces the error rate while enhancing the signal. The size of the DNB is controlled in such a way that only one DNB is bound per active site on the flow cell. This densely patterned array technology provides optimal sequencing accuracy and increases flow cell utilization.



Data Analysis

Besides clean data, we offer a range of standard and customized bioinformatics options for your whole genome bisulfite sequencing project.

Reports and output data flies are delivered in industry standard file formats: FASTQ, BAM, cout, .xls, .png

STANDARD ANALYSIS

- Data filtering
- Alignment
- Sequence depth and coverage analysis
- Calculation of methylation level
- Global trends of methylome
- Genome-wide methylation profiling
- Identification of differentially methylated regions (DMRs)

CUSTOMIZED ANALYSIS

Further customization of bioinformatics analysis to suit your unique project is available.
Please contact our technical representative for details.

Sample Requirements

We can process your gDNA,whole blood,cell line and fresh frozen tissue samples,with the following general requirements:

	DNA Amount and Concentration	Minimum Sample Volume
Regular Samples	Intact genomic DNA≥0.5 μg. Concentration ≥12.5 ng/μL	15 μL
Low Input Samples	Intact genomic DNA≥1 ng. Concentration≥0.5 ng/μL	15 μL

DNBSEQ Performance

The human standard sample NA12878 was used to validate DNBSEO WGBS. The PE100 sequencing data from DNBSEC was compared to the PE150 sequencing data from the N platform. Twodatasets of each platforms are included in the comparison. Both sequencing platforms shows high mapping rates in the range ofwith 82-86%, while the duplication rates of the DNBSEO platform are noticeable lower by around 10% (Figure 1). As a result the average data-using rate of DNBSEQ platform is 14.3% greater than that of N platform.

The GC-bias plot shows GC content has less impact on DNBSEQ platforms, whereas N platform prefers higher GC regions over the lower ones (Figure 2).

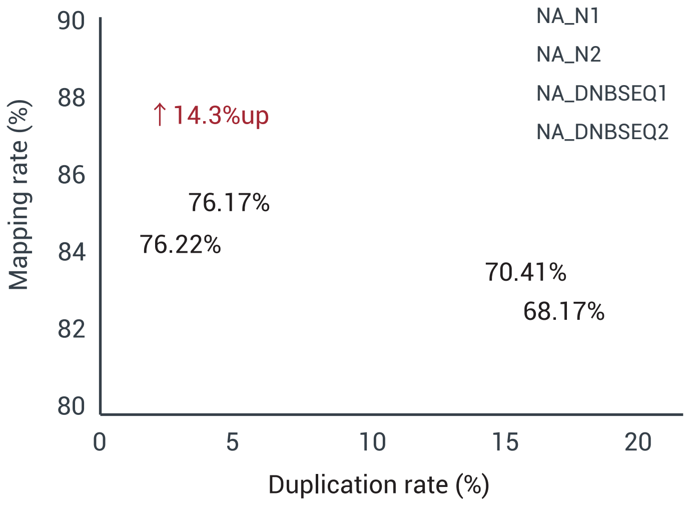


Figure 1. The mapping rate (Y axis), duplication rate (X axis), and data using rate (the size of the bubbles) of the four datasets. The data using rate in the bubbles refers to the proportion of valid reads (the duplicate removed mapped reads) data to the total filtered reads data.

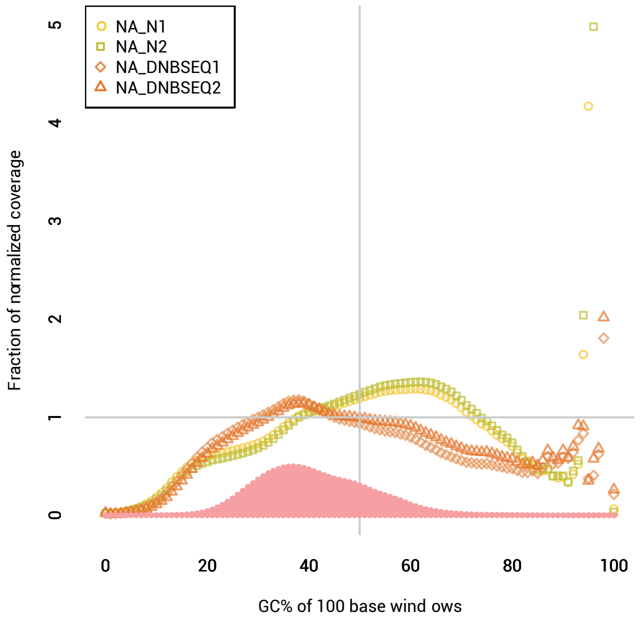


Figure 2. The GC-bias plot for the NA12878 genome. The yellow spots: GC composition distribution of the 2 datasets of N platform. The orange spots: GC composition distribution of the 2 DNBSEQ datasets.

To Learn More

If you have any questions or would like to discuss how our services can help you with your research, please don't hesitate to contact us at P_contact@innomics.com. We look forward to hearing from you!

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