

DNBSEQ™ SERVICE OVERVIEW

Metagenomic Sequencing



Service Description

Metagenomics studies of genetic material that is directly recovered from environmental samples, have benefitted greatly from advanced NGS technology as a method for the exploration of microbial biodiversity. Our metagenomics survey service applies whole genome shotgun sequencing of DNA isolated from environmental samples, with the advantages of high throughput and high coverage. It can provide information not only on species composition and abundance, but also on functional genes, gene differences between samples, metabolic pathways and gene resource mining for bioactive products.

Sequencing Service Specification

DNBSEQ Metagenomics Survey Sequencing services are executed with the DNBSEQ sequencing system.



Sequencing Service

- 150bp Paired-End sequencing
- Data output, standard and custom data analysis
- Available data storage and bioinformatics applications



Sequencing Quality Standard

- Guaranteed $\geq 80\%$ of bases with quality score $\geq Q30$

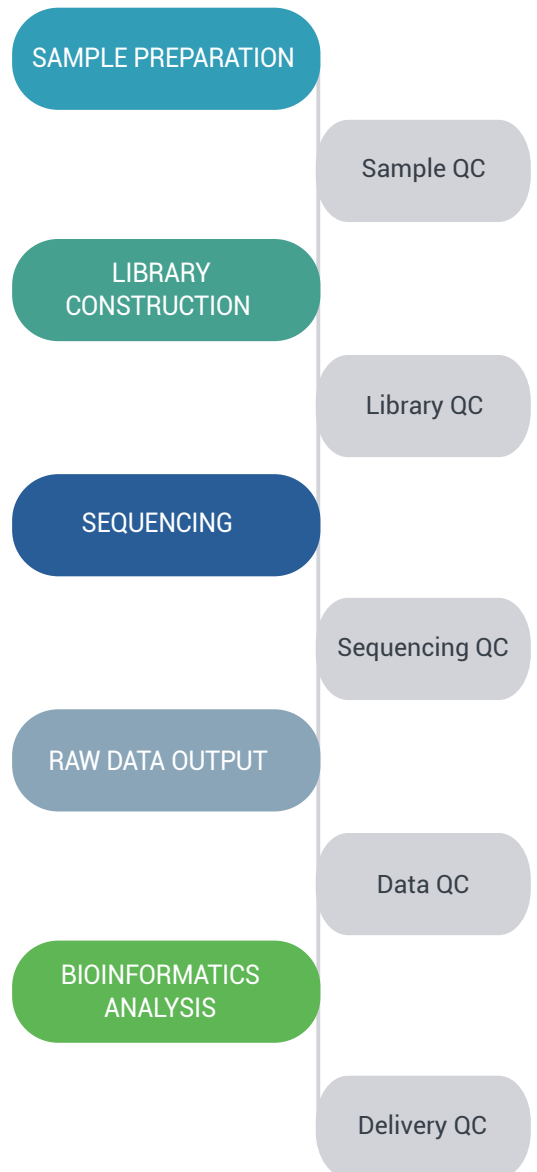


Turnaround Time

- Typical 18 working days from sample QC acceptance to filtered raw data availability
- Expedited services are available, contact us for details

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.

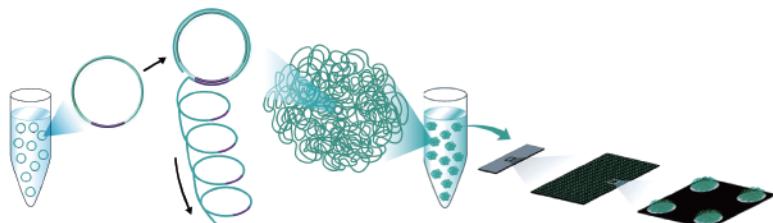


Quality Data Fast TAT Cost Effective



DNBSEQ Sequencing System

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™) 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 DNBSEQ flow cell. This densely patterned array technology provides optimal sequencing accuracy and increases flow cell utilization.

STANDARD ANALYSIS

- Data filtering
- Alignment
- Metagenomic *De Novo* assembly
- Non-redundant gene catalogue
- Prophage transposable element prediction
- Functional annotation based on KEGG, CAZy, eggNOG, CARD
- Species composition and diversity analysis
- Quantitative and differential analysis of gene abundance
- Principal component analysis

CUSTOMIZED ANALYSIS

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

SAMPLE REQUIREMENTS

We can process your extracted genomic DNA from a variety of environmental samples with the following general requirements:

SAMPLE	DNA AMOUNT AND CONCENTRATION	MINIMUM SAMPLE VOLUME
Regular	Intact genomic DNA ≥ 200ng concentration ≥ 8 ng/μL	15 μL

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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