

Metagenomic Survey

Service Description

Over 99% of natural microorganisms can not be isolated and cultured clonally. Traditional isolation and culture-dependent methods have limited the study of microorganisms in their natural environment. Metagenomic 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.

BGI's 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

BGI Metagenomic Survey Sequencing services are executed with the Illumina HiSeq sequencing system.



Sequencing Service

- 150bp Paired-End sequencing
- Raw Data, Standard and custom Data analysis
- Available Data storage and Bioinformatics applications



Sequencing Quality Standard

- Guaranteed $\geq 83\%$ of bases with quality score $\geq Q20$

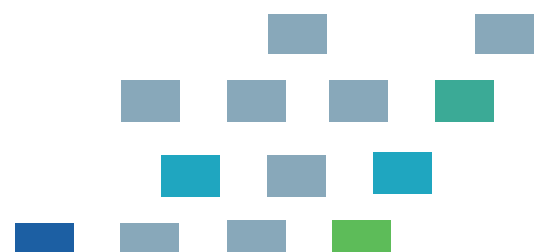
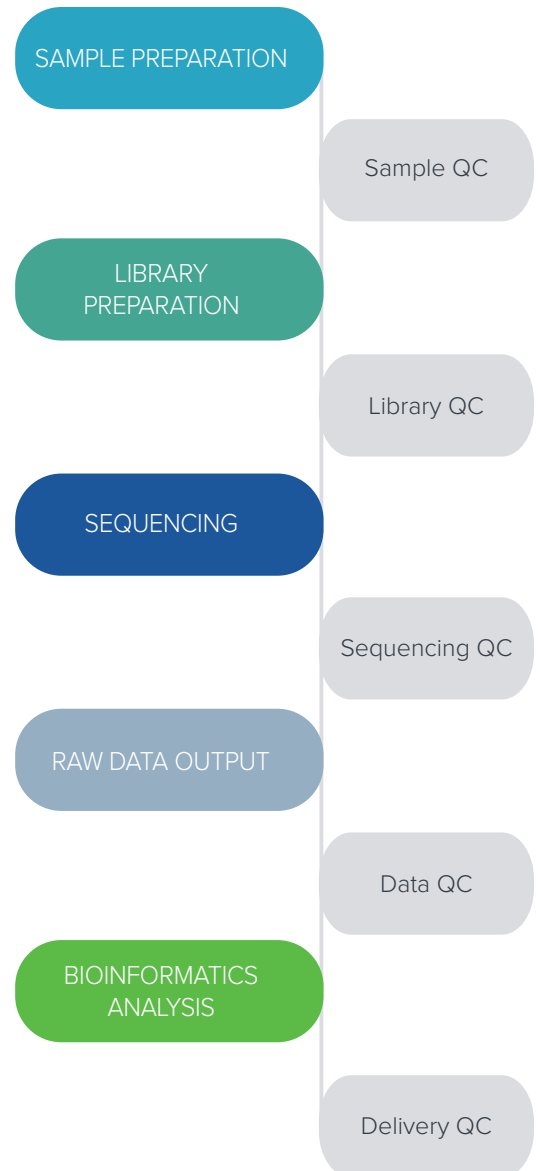


Turn Around Time

- Typical 40 working days after sample receipt for raw data delivery
- Expedited services are available, contact your local BGI specialist 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.



Data Analysis

Besides clean data output, BGI offers a range of standard and customized bioinformatics pipelines for your sequencing project.

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

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 your BGI technical representative

Sample Requirements

We can process your exacted 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 \geq 0.5 μ g, Concentration \geq 20 ng/ μ l | 15 μ l |
| Low Input | Intact genomic DNA \geq 200 ng, Concentration \geq 2.5 ng/ μ l | 15 μ l |
| Customised Low Input | Intact genomic DNA \geq 10 ng (even lower) | Depends on sample amount |

References

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2. Kristoffer F, Falk H, Trine N, et al. Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. *Nature* 528, 262–266 (10 December 2015) doi:10.1038/nature15766.
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4. Liu R, Hong J, Xu X. et al. Gut microbiome and serum metabolome alterations in obesity and after weight-loss intervention. *Nature medicine*. 2017. 23: 859–868. doi:10.1038/nm.4358

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Request Information or Quotation

Contact your BGI account representative for the most affordable rates in the industry, to discuss how we can meet your specific project requirements or for expert advice on experiment design, from sample to bioinformatics.

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