Service Description

Over 99% of natural microorganisms cannot 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 ≥ 83% of bases with quality score ≥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.

- **SAMPLE PREPARATION**
  - Sample QC

- **LIBRARY PREPARATION**
  - Library QC

- **SEQUENCING**
  - Sequencing QC

- **RAW DATA OUTPUT**
  - Data QC

- **BIOINFORMATICS ANALYSIS**
  - Delivery QC

- **Quality Data**
- **Fast TAT**
- **Cost Effective**
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:

<table>
<thead>
<tr>
<th>SAMPLE</th>
<th>DNA AMOUNT AND CONCENTRATION</th>
<th>MINIMUM SAMPLE VOLUME</th>
</tr>
</thead>
<tbody>
<tr>
<td>Regular</td>
<td>Intact genomic DNA ≥ 0.5µg, Concentration ≥ 20 ng/µl</td>
<td>15 µl</td>
</tr>
<tr>
<td>Low Input</td>
<td>Intact genomic DNA ≥ 200 ng, Concentration ≥ 2.5 ng/µl</td>
<td>15 µl</td>
</tr>
</tbody>
</table>

References