Service Description

Current short-read based Whole Genome Sequencing (WGS) is the most widely used method for identifying genome-wide aberrations such as point mutations with read length typically less than several hundred base pairs. This short-read based WGS approach is proven to be highly informative in terms of detection of point mutations, indels and copy number alterations. However, short-read sequencing often results in sequences with scaffolding gaps, bias due to high GC content, repeat sequences and mis-aligned sequences. To interrogate the human genome at a higher resolution with better quality, the standard NGS workflow is challenged, especially for complex Structural Variation (SV) discovery, due to insufficient read coverage at breakpoints and loss of long-range genomic contiguity.

Service Specification

- Co-barcoded LFR library preparation
- PE100 DNBseq™ sequencing
- Standard and customized bioinformatics analysis available
- Available data storage and bioinformatics applications
- CAP/CLIA laboratory services available

Sequencing Quality Standard

- Guaranteed ≥80% of bases with quality score of ≥Q30

Turnaround Time

- 40 working days from sample QC acceptance to filtered raw data availability
- Expedited services are available, contact your local BGI specialist for details

Project Workflow

We care for your samples from the start 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

BIOMINFORMATICS ANALYSIS

Delivery QC
Technology

BGI's Innovative Single Tube Long Fragment Read (stLFR) technology produces reads longer than 10 kb with high consensus accuracy, uniform coverage and superior SV detection capability, while maintaining reproducibility and consistency. With a small amount of input HMW genomic DNA (as low as 1 ng, approximately 300 genomic equivalents), added to a single tube containing 30 million barcoded beads, where the gDNA molecules are barcoded and subjected to random priming and polymerase amplification. Co-barcoded DNA fragments are then released followed by a modified library preparation process. The resulting libraries undergo DNA Nanoball (DNB™) generation and DNBSeq sequencing. BGI's proprietary computational algorithm uses the barcodes to assemble sequencing reads to the original HMW DNA molecule, enabling the construction of contiguous segments of phased variants.

Long Fragment Read WGS for superior SV detection

Compared with conventional WGS services, stLFR-based Long Fragment Read WGS (lfrWGS) delivers less bias, higher coverage, higher reproducibility and near-complete genomic information. It significantly improves structural variants detection while maintaining the same excellent sensitivity for SNP, Indel and CNV detection. lfrWGS does not have the high error rate problem and high cost of long read sequencing platforms from Pacific Biosciences and Oxford Nanopore but provides a means to detect many of the complex genomic variants including SV by computationally maintaining the genomic contiguity.

DNBseq Sequencing Technology

DNBseq is an innovative high-throughput sequencing solution, developed by BGI's Complete Genomics subsidiary. 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 flow cell. This densely patterned array technology provides optimal sequencing accuracy and increases flow cell utilization.
Data Analysis

In addition to clean data output, BGI offers a range of standard and customized bioinformatics pipelines for your human WGS project. Reports and output data files are delivered in industry standard FASTQ, BAM, Excel formats with publication-ready tables and figures.

**STANDARD BIOINFORMATICS ANALYSIS**

- Filtering
- Alignment
- SNP calling and annotation
- SNP validation and comparison
- SNP functionality and conservation prediction
- SNP Statistics per functional element
- InDel calling and annotation
- InDel validation and comparison
- InDel statistics per functional element
- CNV calling and annotation
- SV calling and annotation
- Phasing

**CUSTOM ANALYSIS**

Further customization of Bioinformatics analysis to suit your unique project is available: Please contact your BGI technical representative.

Application example

This figure below shows a case study in which IfrWGS (upper panels) successfully sequenced and identified the culprit of the SMN1 gene (left panels) whose mutations are responsible for the genetic disorder Spinal Muscular Dystrophy (SMA). The highly homologous counterpart SMN2 gene (right panels) often interferes with the result from regular WGS (lower panels) by mis-representing the sequencing and mapping results, making this case impossible to resolve. IfrWGS enables analysis of genomic areas that are inaccessible by regular WGS.

![Graphical representation of data analysis results](image-url)
Sample Requirements

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

<table>
<thead>
<tr>
<th></th>
<th>Amount (concentration)</th>
<th>Storage condition</th>
<th>Shipping</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genomic DNA*</td>
<td>&gt;300ng (≥1ng/μl)</td>
<td>-80°C, avoiding freeze-thaw cycles</td>
<td>Dry ice</td>
</tr>
<tr>
<td>Whole Blood</td>
<td>≥1ml</td>
<td>-80°C in EDTA anticoagulant tube, avoiding freeze-thaw cycles, no blood clotting</td>
<td>Dry ice</td>
</tr>
<tr>
<td>Fresh Frozen Tissue</td>
<td>≥50mg</td>
<td>-80°C, avoiding freeze-thaw cycles</td>
<td>Dry ice</td>
</tr>
<tr>
<td>Cell pellets</td>
<td>≥5x10⁹ cells</td>
<td>-80°C, avoiding freeze-thaw cycles</td>
<td>Dry ice</td>
</tr>
</tbody>
</table>

*For genomic DNA samples, the minimum DNA fragment size should be higher than 23kb. We recommend QIAGEN MagAttract HMW DNA Kit (Cat No.10: 67563) for DNA extraction.

Publications


Request Information or Quotation

Contact your BGI account representative for the most affordable rates in the industry and 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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