Service Description

Transcriptome sequencing is used to reveal the presence, quantity and structure of RNA in a biological sample under specific conditions. Compared to hybridization-based RNA quantification methods such as microarray analysis, sequencing-based transcriptome detection can quantify gene expression with low background, high accuracy and high levels of reproducibility within a large dynamic range. In addition, transcriptome sequencing does not require an existing genome sequence and can detect mutations/SNPs, splice variants and fusion genes that can not be obtained by microarrays.

BGI also provides Whole Transcriptome sequencing, which provides sequencing information for both mRNA and Long non-coding RNA (lncRNA). Whole Transcriptome Sequencing can identify novel IncRNAs besides detection and quantification of known IncRNAs.

Sequencing Service Specification

BGI transcriptome sequencing services are executed with the Illumina HiSeq 4000 sequencing system.

- Multiple choices for mRNA enrichment and rRNA removal kits
- Regular and strand-specific transcriptome library
- 100bp and 150bp paired-end sequencing options available
- Raw data and bioinformatics analysis are available in standard file formats
- Advanced and custom bioinformatics data analysis
- Cloud-based data storage and delivery system
- ≥30 Million reads per sample recommended

Turn Around Time

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

Locations

BGI’s sequencing services are available from a variety of BGI service laboratory locations, including:

- Copenhagen, Denmark
- Philadelphia, USA
- Hong Kong, China

BGI also has a network of laboratories across mainland China.
Data Analysis

In addition to raw data output, BGI offers a range of standard and customized bioinformatics pipelines for your Transcriptome sequencing project. Reports and output data files are delivered in industry standard file formats: FASTQ, BAM, FPKM calculation and Excel.

STANDARD ANALYSIS

- Filtering
- Alignment
- Quantitative expression profiles
- Detection of differentially expressed genes
- Spliced transcript analysis
- Fusion gene analysis
- SNP and Indel detection
- RNA editing analysis
- Gene ontology analysis
- Pathway enrichment analysis
- Hierarchical clustering analysis

- Additionally, for Whole Transcriptome Sequencing: IncRNA analysis included

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 total RNA, blood, cell line, FFPE, fresh frozen tissue and single cell samples from a variety of species, with the following general requirements:

<table>
<thead>
<tr>
<th>Sample Type</th>
<th>Species</th>
<th>Amount</th>
<th>Concentration (ng/µl)</th>
<th>RIN Value</th>
<th>OD 260/280</th>
<th>OD 260/230</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total RNA</td>
<td>Human/Animal</td>
<td>≥200ng</td>
<td>≥20</td>
<td>RIN≥7.0</td>
<td>28S/18S≥1.0</td>
<td>28S/18S≥1.0</td>
</tr>
<tr>
<td></td>
<td>Fungi</td>
<td>≥1ug</td>
<td>≥40</td>
<td>RIN≥6.5</td>
<td>28S/18S≥1.0</td>
<td>28S/18S≥1.0</td>
</tr>
<tr>
<td></td>
<td>Plant</td>
<td>≥200ng</td>
<td>≥20</td>
<td>RIN≥6.0</td>
<td>28S/18S≥1.0</td>
<td>28S/18S≥1.0</td>
</tr>
<tr>
<td></td>
<td>Prokaryotes</td>
<td>≥1ug</td>
<td>≥40</td>
<td>RIN≥7.0</td>
<td>23S/16S≥1.0</td>
<td>23S/16S≥1.0</td>
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<tr>
<td></td>
<td>Insect</td>
<td>≥200ng</td>
<td>≥20</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
</tr>
</tbody>
</table>

For BGI’s scientific publications relating to RNA-Seq (Transcriptome) Sequencing, sample shipping instructions or sample submission forms, please visit our website.

www.bgi.com