BGISEQ SERVICE OVERVIEW

RNA-Seq (Transcriptome) Sequencing

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, splice variants and fusion genes that can not be detected by microarrays.

Sequencing Service Specification

BGI transcriptome sequencing services are executed with the BGISEQ sequencing system, featuring cPAS and DNA Nanoballs (DNB™) technology for superior data quality.

Sample Preparation and Services

- Multiple choices for mRNA enrichment and rRNA removal kits
- Stranded and non-stranded sequencing is available
- 100bp paired-end sequencing
- ≥30 Million reads per sample recommended
- Raw data and bioinformatics analysis are available in standard file formats
- Advanced and custom bioinformatics data analysis
- Cloud-based data storage and delivery system

Sequencing Quality Standard

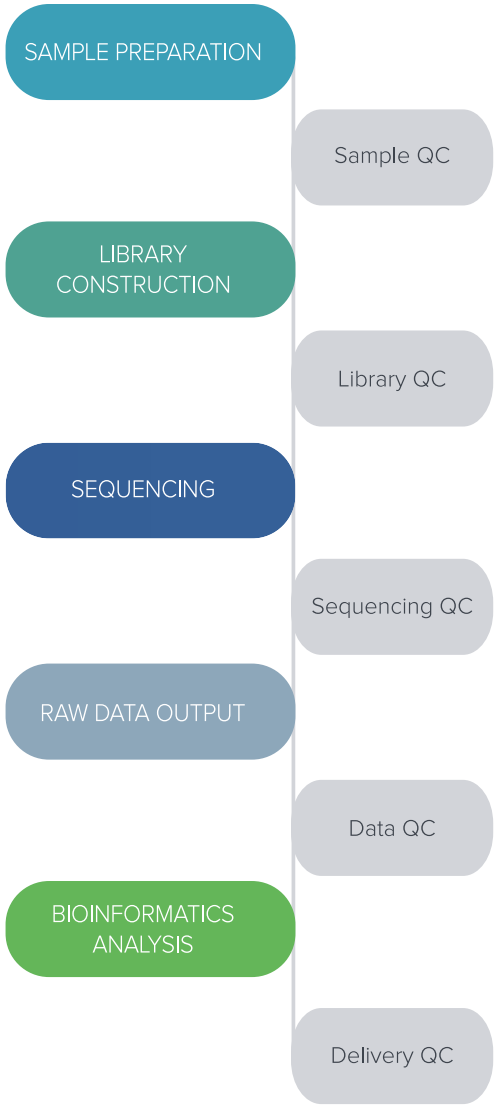
- Guaranteed ≥80% of bases with quality score of ≥Q30

Turnaround Time

- Typical 30 working days from sample QC acceptance to filtered raw data availability
- Expedited service are available, contact your local BGI specialist for details

Project Workflow

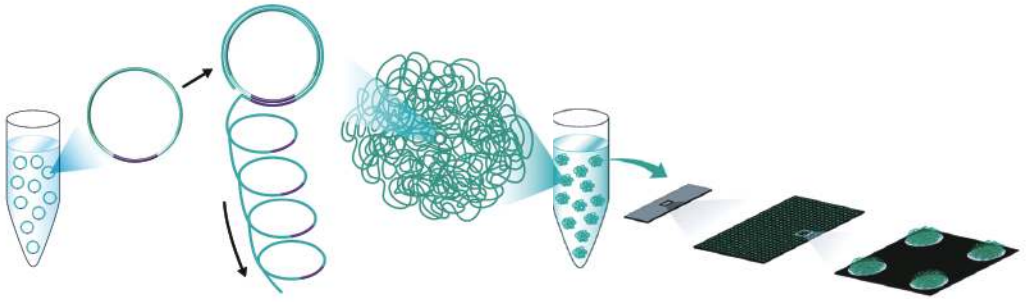
We care for your samples from the start through to the result reporting. Highly experienced laboratory professionals follow strict quality procedures to ensure the integrity of your results.



BGISEQ Sequencing System

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



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 and Excel.

Standard Analysis

- Quantitative expression profiles
- Alternative splicing analysis
- Fusion gene analysis
- SNP and Indel detection
- Time series analysis
- Gene ontology analysis
- Pathway enrichment analysis
- Hierarchical clustering analysis
- Protein-Protein Interaction (PPI) analysis
- Fungal pathogenic gene annotation (For fungi)
- Plant disease resistance genes annotation (For plant)

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 tissues and single cell samples from a variety of species, with the following general requirements:

Sample Type	Species	Amount	Concentration (ng/μL)	RIN/RQN Value	28S/18S
Total RNA	Human	≥200ng	≥20	≥7.0	≥1.0
	Mouse/Rat	≥200ng	≥20	≥7.0	≥1.0
	Insect	≥1μg	≥40	N/A	N/A
	Other Animals	≥1μg	≥40	≥7.0	≥1.0
	Plant /Fungi	≥1μg	≥40	≥6.5	≥1.0

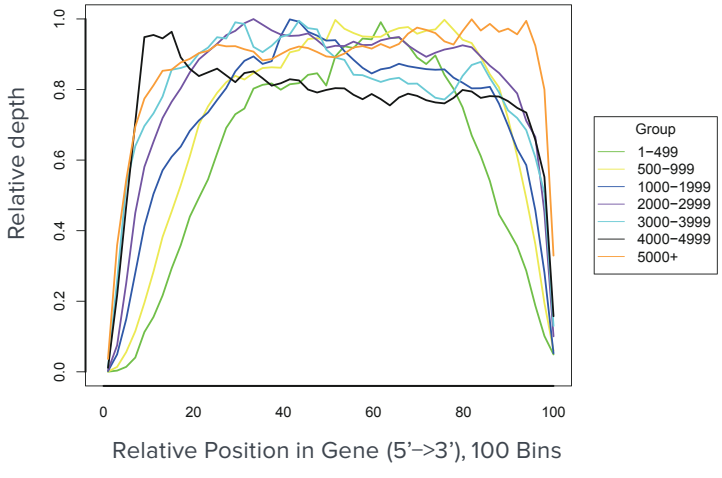
Sample Type (For Human Samples)	FFPE	Whole Blood	Cell Line	Tissue
Requirement	≥5 slides ≥5 μm slice per slide	≥1mL	≥$2*10^5$ cells	≥30mg

Low-input transcriptome sequencing is available.

BGISEQ Transcriptome Sequencing Performance

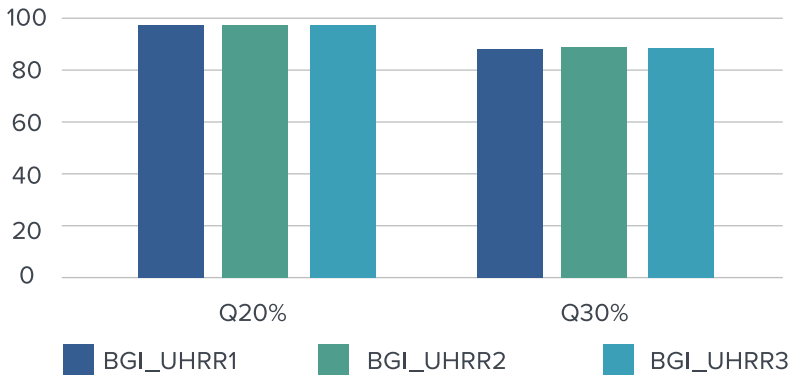
3 Sequencing libraries were prepared from the Universal Human Reference RNA (UHRR) sample using BGI library preparation kits and sequenced using the BGISEQ system with paired-end 100bp read length to generate 50 million reads per library. Evaluation of data quality, transcripts coverage, mapping rate and qPCR correlation performance, shows that the BGISEQ system provides excellent RNA sequencing data for your RNA research.

Reads Distribution Performance



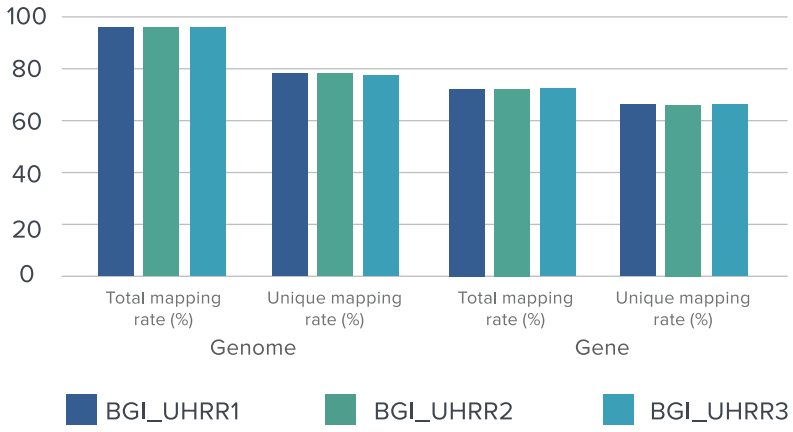
› Reads distribution of BGISEQ transcriptome sequencing: There is an even distribution of reads from 5' end to 3' end for different length transcripts.

Sequencing Data Quality



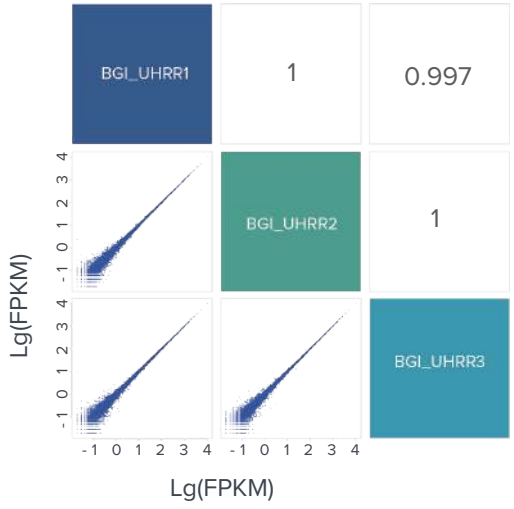
- Data quality of BGISEQ transcriptome sequencing: Q20 is higher than 95% and the Q30 is higher than 88% using paired-end 100bp sequencing.

Mapping Performance



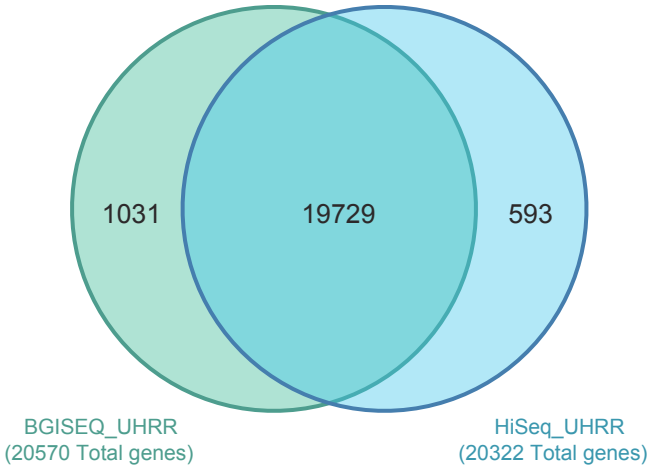
- Mapping performance of BGISEQ transcriptome sequencing: The unique genome mapping rate is higher than 70% and the unique gene mapping rate is higher than 60%.

Reproducibility Performance



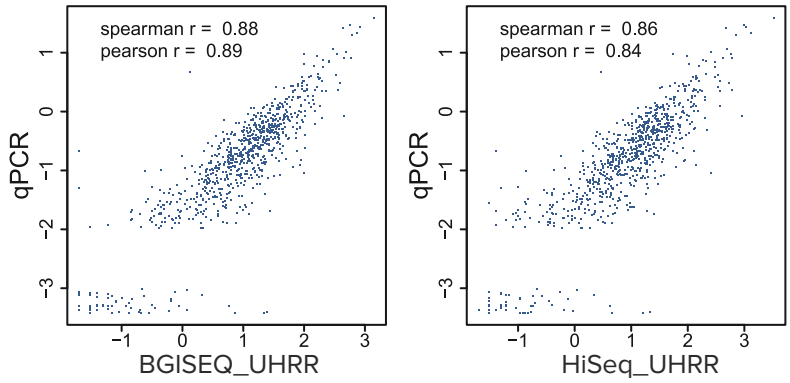
- Reproducibility of BGISEQ transcriptome sequencing: The gene expression level detected by three technical replicates are highly consistent (Spearman coefficient values >0.997).

Gene Detection Performance



- Gene detection performance of BGISEQ transcriptome sequencing: More than 96% of the genes are detected on both BGISEQ and HiSeq 4000 platforms with 50 million paired-end reads.

qPCR Correlation Performance



- qPCR correlation performance of BGISEQ transcriptome sequencing: The gene expression level detected by BGISEQ, HiSeq 4000 and qPCR are consistent.

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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For BGISEQ Transcriptome Sequencing sample shipping instructions or sample submission forms, please visit our website.

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We Sequence, You Discover