DNBSEQ™ SERVICE OVERVIEW
RNA Sequencing (Transcriptome)

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 cannot be detected by microarrays.

Sequencing Service Specification

BGI transcriptome sequencing services are executed with the DNBSEQ™ sequencing technology, 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 sequencing
· 100bp and 150bp paired-end sequencing options available
· ≥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

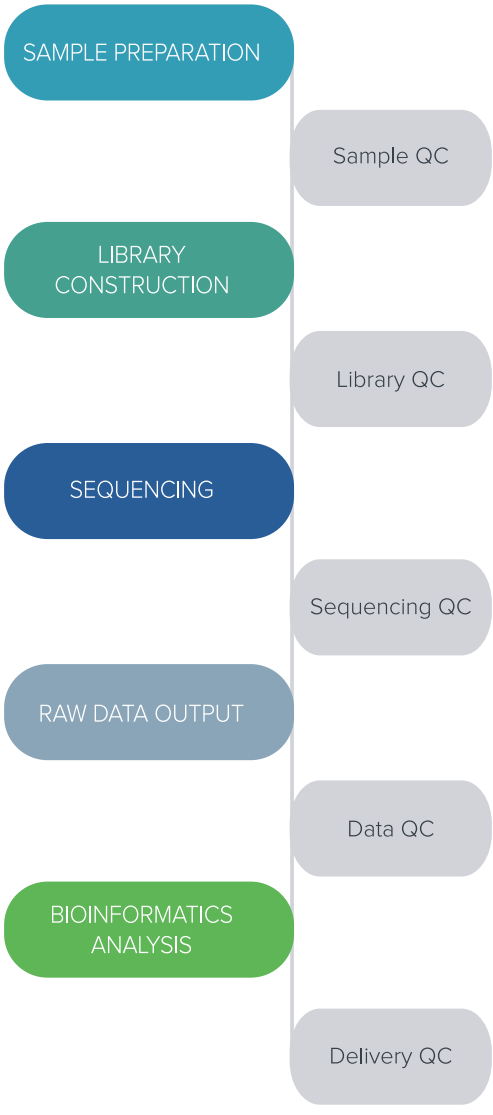
· Guaranteed ≥80% of bases with quality score of ≥Q30

Turnaround Time

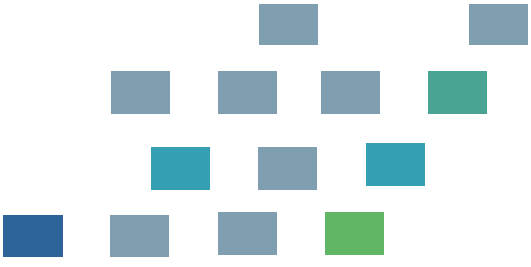
· Typical 18 working days from sample QC acceptance to filtered raw data availability
· Expedited service are available, contact your local BGI specialist for details

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.

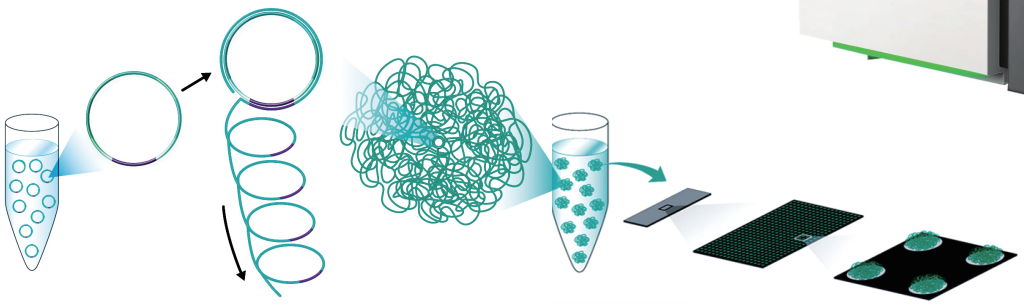


Quality Data Fast TAT Cost Effective



DNBSEQ™ Sequencing System

DNBSEQ™ 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 DNBSEQ™ flow cell. This densely patterned array technology provides optimal sequencing accuracy and increases flow cell utilization.

Data Analysis

In addition to 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
- Time series analysis
- Pathway enrichment analysis
- Hierarchical clustering analysis
- Protein-Protein Interaction (PPI) analysis
- Gene ontology analysis

Data Visualisation and Customized Analysis with the Dr. Tom System

- Interactive data visualization tools for Expression Analysis, Gene Set Enrichment Analysis, Association Analysis and More.
- Access world-leading Databases for Powerful Data Mining
- AI-based Literature Retrieval for Easy Referencing

Further customization of Bioinformatics analysis to suit your unique project isavailable: 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:

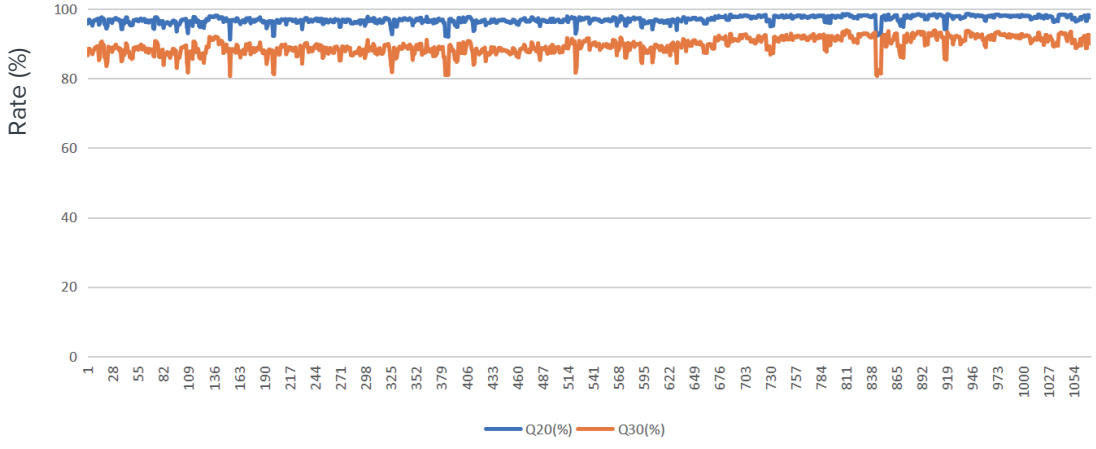
Sample	Species	Amount	Concentration (ng/μL)	RIN/RQN Value	28S/18S	DV_{200}
Total RNA	Human/mouse/rat (non-whole blood)	≥200ng	≥10	≥7	≥1.0	N/A
	Human (whole blood)	≥500ng	≥40	≥7	≥1.0	N/A
	Human (FFPE)	≥200ng	≥70	≥2	N/A	≥30%
	Insect	≥1μg	≥40	N/A	N/A	N/A
	Other Animals	≥1μg	≥40	≥7	≥1.0	N/A
	Plant	≥1μg	≥40	≥6	≥1.0	N/A
	Fungi	≥1μg	≥40	≥6.5	≥1.0	N/A

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.

Stable and High-Quality Data Performance

1,072 samples were randomly selected from over 10,000 samples that were sequenced at BGI's laboratory over a period of 6 months. The data output and data quality remained stable over that period. The average Q20 and Q30 scores were 97% and 89.5% respectively.

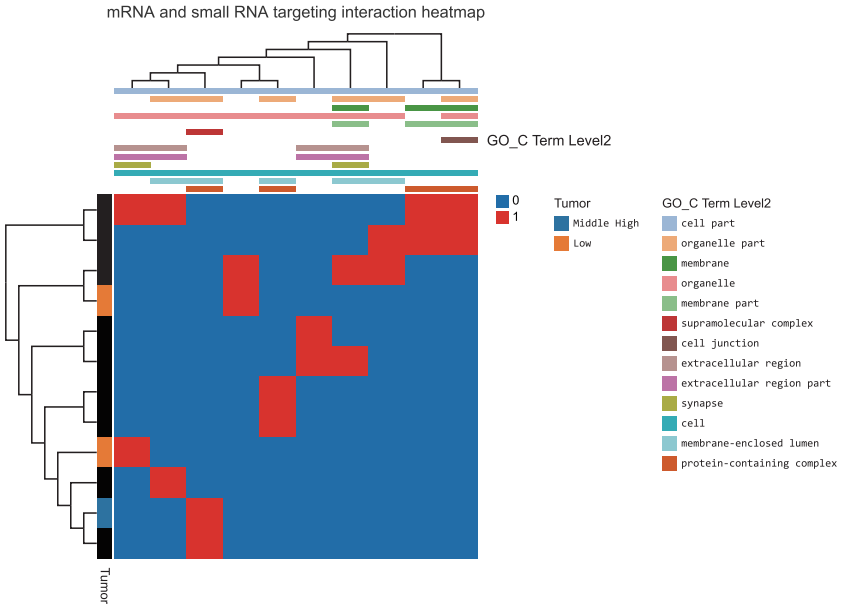


Stable data quality scores from our DNBSEQ™ production line

Core Capabilities of Dr.Tom system

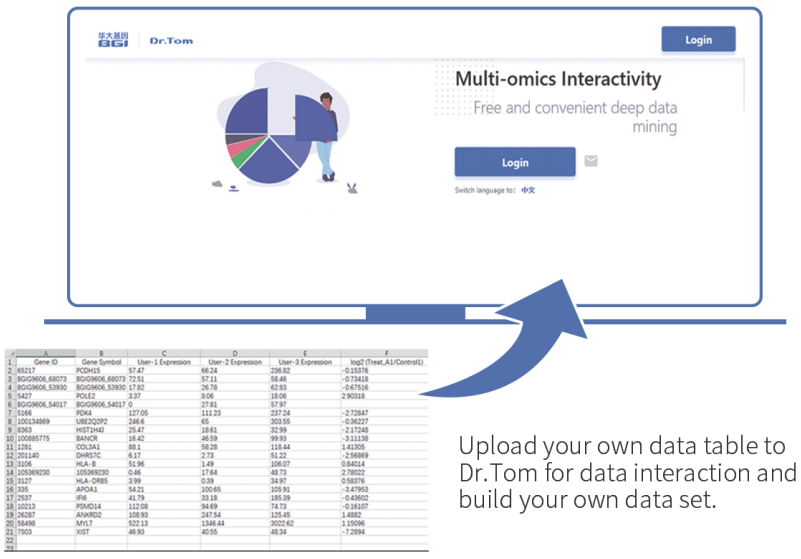
Association Analysis

With a simple click Dr.Tom lets users detect RNA association with target genes, based on their interaction relationship (such as PPI, Target, Co-expression, ceRNA, GGI and RNAplex), or based on the position relationship (such as upstream and downstream position).



Custom Datasets

Customers can upload their own gene expression data, using tool boxes for graphing and visualization, and construct their own gene annotation database for enrichment, clustering and multi-omics association analysis.



Upload your own data table to Dr.Tom for data interaction and build your own data set.

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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Published Oct 2020.

All Services and Solutions are for research use only.

DNBSEQ™ Services are executed in our service laboratories in China.

We Sequence, You Discover