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 splice variants and fusion genes that cannot be detected by microarrays.

Sequencing Specification

Our 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 library
- 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

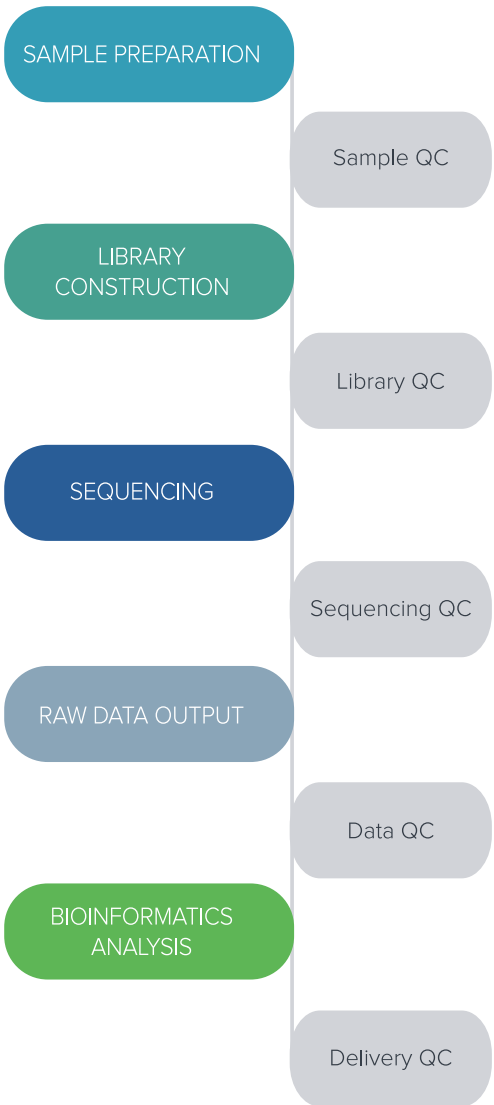
Turn Around Time

- Typical 18 working days from sample QC acceptance to filtered raw data availability
- Expedited service are available, contact our specialist for details

Quality Data | Fast TAT | Cost Effective

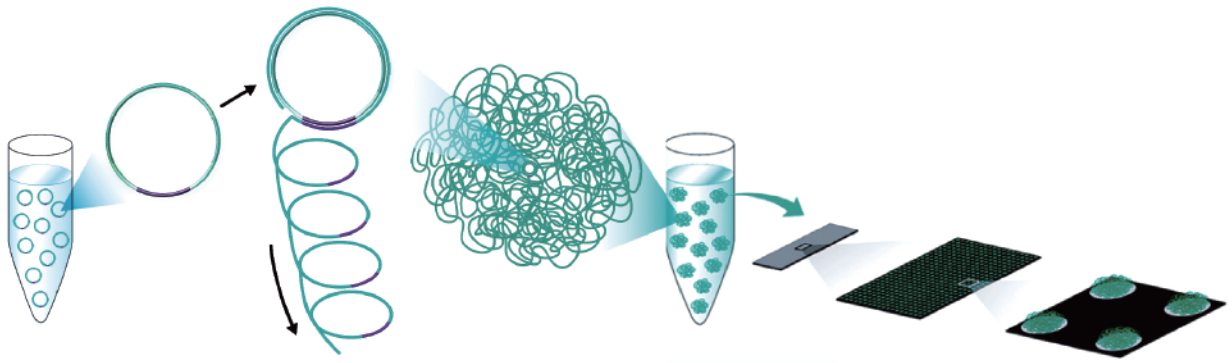
Project Workflow

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.



DNBSEQ™ technology:

DNBSEQ™ sequencing technology combines the power of DNA Nanoballs (DNB™), PCR-free Rolling Circle Replication, Patterned Nano Arrays and cPAS to deliver a new level of data clarity and affordability. The combination of linear amplification and DNB™ technology reduces the error rate while enhancing the signal, resulting in real advantages.



Highly accurate base calling.
Much lower duplication rates for more usable data.
Virtually no index mis-assignment for high throughput without loss of sample integrity.

Data Analysis

In addition to data output, we offer 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

- Gene expression analysis
- Alternative splicing analysis
- Fusion gene analysis
- Time series analysis
- Pathway enrichment analysis
- Hierarchical clustering analysis
- Protein-Protein Interaction (PPI) analysis
- Gene ontology analysis

Data Visualization 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 is available: Please contact our 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:

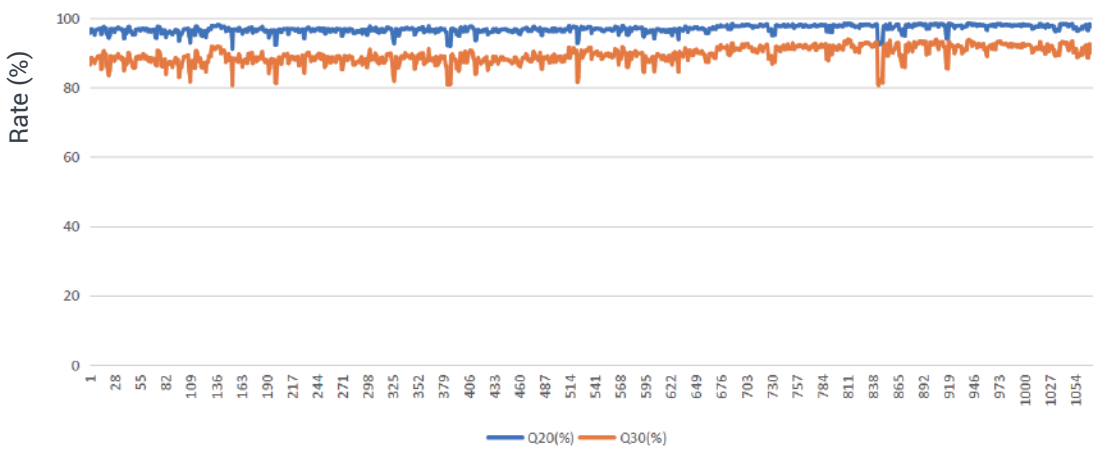
Sample	Species	Amount	Concentration (ng/μL)	RIN/RQN Value	28S/18S	DV_{200}
Total RNA	Human/mouse/rat (non-whole blood)	≥200ng	≥10	≥7	≥1.0	N/A
	Human (whole blood)	≥500ng	≥40	≥7	≥1.0	N/A
	Human (FFPE)	≥200ng	≥70	≥2	N/A	≥30%
	Insect	≥400ng	≥10	N/A	N/A	N/A
	Other Animals	≥400ng	≥10	≥7	≥1.0	N/A
	Plant	≥400ng	≥10	≥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 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.

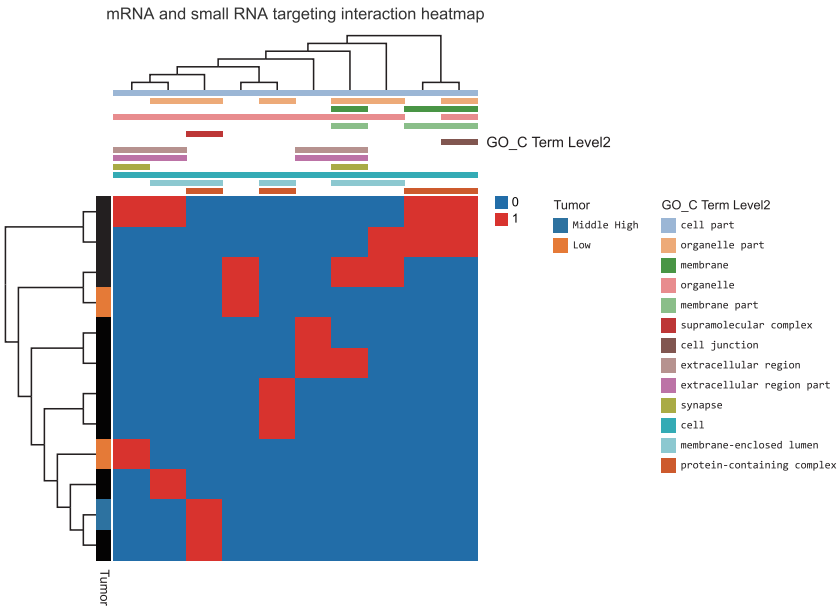


Stable data quality scores from our DNBSEQ™ production line

Core Capabilities of Dr.Tom system

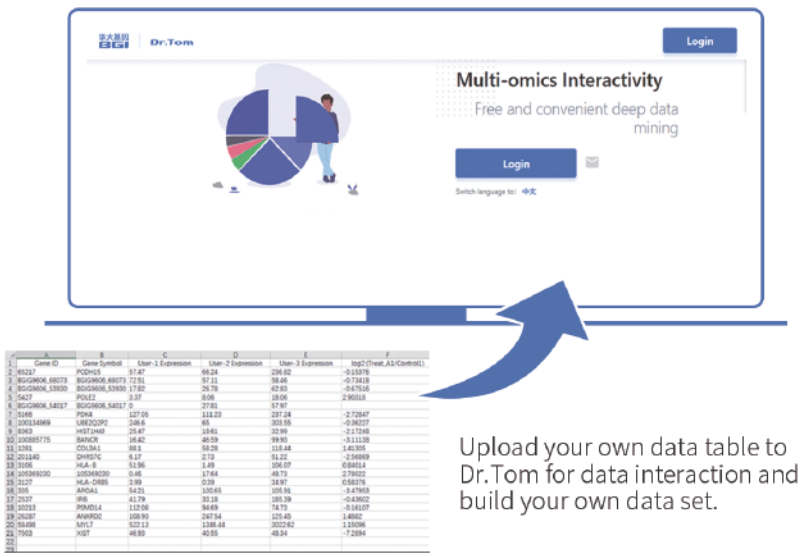
Association Analysis

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.



To Learn more

If you have any questions or would like to discuss how our services can help you with your research, please don't hesitate to contact us at P_contact@innomics.com. We look forward to hearing from you!

Innomics Inc.
750 N. Pastoria Ave
Sunnyvale, CA 94085
USA

www.innomics.com