# DNBSEQ™ SERVICE OVERVIEW

# Long Non-coding RNA Sequencing

## Service Description

Long non-coding RNAs (lncRNAs) are a large class of transcribed RNA molecules with a length of more than 200 nucleotides that do not encode proteins. lncRNAs are thought to encompass nearly 30,000 different transcripts in humans, hence lncRNA transcripts account for the major part of the non-coding transcriptome.
lncRNA discovery is still at an early stage and only a small proportion of lncRNAs have so far been investigated. Although we can start to classify different types of lncRNA functions, we are still far from being able to predict the function of new lncRNAs.

We offer expression profiling as one way to uncover the function of lncRNA. Identifying lncRNAs that are differentially expressed during development or in particular situations can shed light on their potential functions. Alternatively, looking for lncRNAs and protein-coding genes whose expression is correlated, can indicate co-regulation or related functions.

## Sequencing Service Specification

DNBSEQ™ Long non-coding RNA Sequencing services are executed with the DNBSEQ™ Technology Platform, with the benefit of lower cost and faster turnaround time.

- Paired-end 100 bp
- Strand specific library with rRNA removal
- Data and bioinformatics analysis are available in standard file formats
- Advanced RNA data visualization and data mining with Dr.Tom system

Sequencing Quality Standard

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

Turnaround Time

- Typical 27 working days from sample QC acceptance to filtered data availability
- Expedited services are available, contact our specialist for details

Quality Data    Fast TAT    Cost Effective

## Project Workflow

We care for your project from the receipt of samples through to the reporting of results. 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
DATA OUTPUT
Data QC
BIOINFORMATICS ANALYSIS
Delivery QC

## Data Analysis

In addition to data output, we offer a range of standard and customized bioinformatics pipelines for your Long non-coding RNA sequencing project. Reports and output data files are delivered in industry standard file formats: FASTQ, BAM and Excel.

### STANDARD ANALYSIS

- Identification of mRNA and LncRNA
- Quantification and differential expression analysis
- Gene ontology analysis and pathway enrichment analysis

### DR.TOM SYSTEM ANALYSIS

- Transcription factor prediction (For AnimalTFDB/PlantTFDB)
- GSEA Analysis
- Rfam、Pfam、Reactome、COG、EggNOG and InterPro annotation
- miRNA-mRNA interaction, lncRNA-mRNA interaction analysis
- Protein-Protein Interaction (PPI) analysis
- Co-expression Interaction Network Analysis
- Custom dataset table upload

## Sample Requirements

We can process your total RNA, blood, cell line, FFPE, fresh frozen tissues samples from a variety of species, with the following general requirements.
Purity: OD260/280 ≥ 2.0, OD260/230 ≥ 2.0, without degradation and DNA contamination

| Species | RNA Amount and Concentration | Quantitative Result |
|---|---|---|
| Human, mouse and rat | Total RNA ≥200ng | RIN≥7.0 |
| | Concentration ≥20ng/μl | 28S/18S≥1.0 |

## 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!

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