

NEXT GENERATION SEQUENCING

RNA-Seq Technical Specifications

GENEWIZ RNA SEQUENCING SERVICES

Standard
RNA-Seq

Strand-
Specific
RNA-Seq

Small
RNA-Seq

Ultra-Low
Input
RNA-Seq

Single-Cell
RNA-Seq*

Iso-Seq*

Digital
Spatial
Profiling*

*Not covered here. See genewiz.com for more details.

RNA SEQUENCING WORKFLOW

1



Experimental Design

Define objectives and design assay accordingly

2



Sample Preparation

Extract and purify input RNA

3



Library Preparation

Enrichment, cDNA synthesis, and adapter ligation

4



Sequencing

Sequence libraries using NGS platforms

5



Data Analysis

Trim, filter, and map reads; perform advanced analysis

6



Project Delivery

Receive data files and post-delivery support

1 Experimental Design

GENEWIZ provides resources to help you find the best NGS solution and experimental design for your project.



Interactive NGS Solution Selection Tool:
genewiz.com/ngs



Contact us for a **free technical consultation** with a Ph.D.-level scientist

2 Sample Preparation

Sample Type*	Minimum Amount †	Recommended Amount
Total RNA ‡	500 ng (standard) 10 pg (ultra-low)	2 µg
Eukaryotic cell pellet	10 ⁴ cells (standard) 1 cell (ultra-low)	10 ⁶ cells
Prokaryotic cell pellet	10 ⁶ cells	10 ⁸ cells
Frozen tissue	2 mg	10 mg
FFPE	2 slides	4 slides

*Other sample types accepted. View [Sample Submission Guidelines](#) for details.

†Please inquire about submitting lower inputs.

‡Contact us about GENEWIZ's RNA Stabilization Tubes to ship RNA samples at ambient temperature.

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3 Library Preparation

RNA-Seq Service	Target RNA	RNA Selection Method
Standard & Strand-Specific	mRNA (eukaryotic)	Poly(A) selection
	mRNA + lncRNA	rRNA depletion
Small	Small RNA (miRNA, siRNA, piRNA)	Size fractionation with adapter ligation to 5' phosphate
Ultra-Low Input	mRNA (eukaryotic)	Poly(A) selection with enrichment for full-length transcripts

4 Sequencing

Platform	Illumina® NovaSeq™ or HiSeq®
Configuration	2x150 bp
Depth	Customizable to your project needs*
Data Quality	Guaranteed ≥80% bases with Q30 or higher

*Generally, we recommend 5-10 million read pairs per sample for small genomes (e.g. bacteria) and 20-30 million read pairs per sample for large genomes (e.g. human, mouse). Medium genomes often depend on the project, but 15-20 million read pairs per sample is typically sufficient. For *de novo* transcriptome assembly projects, we recommend 100 million read pairs per sample.

5 Data Analysis

RNA-Seq Service	Standard Analysis Package	Additional Analysis Options
Standard Strand-Specific Ultra-Low Input	<ul style="list-style-type: none"> Trimming Mapping Differential gene expression 	<ul style="list-style-type: none"> Gene fusion discovery RNA SNP/INDEL detection Novel transcript discovery <i>De novo</i> transcriptome assembly
Small	<ul style="list-style-type: none"> Trimming Mapping Differential gene expression Small RNA discovery 	

6 Project Delivery

Data Delivery Options



SFTP



Customer
Cloud
Account



External
Hard
Drive
(US Only)

Deliverables for All Projects

- Sample quality control report
- Raw data (FASTQ files)

Optional Deliverables

- Aligned data (BAM file)
- Hit counts (TXT file)
- DGE results (CSV file)
- GO enrichment analysis (CSV file)
- Differential splicing analysis (DEXSeq report)
- De-multiplexed, aggregated Picard BAM file with summary metrics