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	• Trimming • Mapping • Differential gene expression	• Gene fusion discovery • RNA SNP/INDEL detection • Novel transcript discovery • *De novo* transcriptome assembly
Small	• 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	Optional Deliverables
• Sample quality control report • Raw data (FASTQ files)	• 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

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