

RNA-Seq Technical Specifications

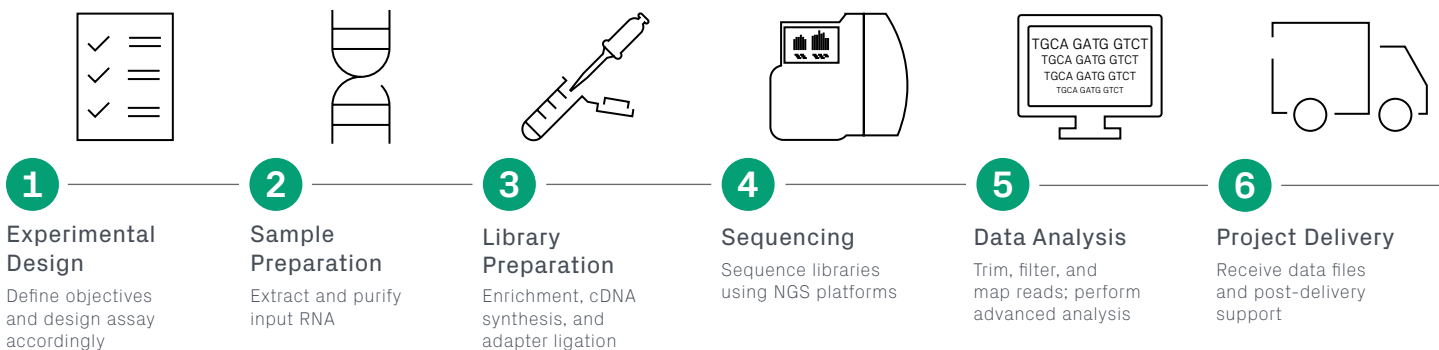


GENEWIZ RNA Sequencing Services

- 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

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 	

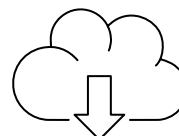
6 Project Delivery

Deliverables for All Projects	Optional Deliverables
<ul style="list-style-type: none"> Sample quality control report Raw data (FASTQ files) 	<ul style="list-style-type: none"> 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

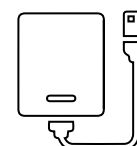
DATA DELIVERY OPTIONS



SFTP



Customer Cloud Account



External Hard Drive
(US Only)

