

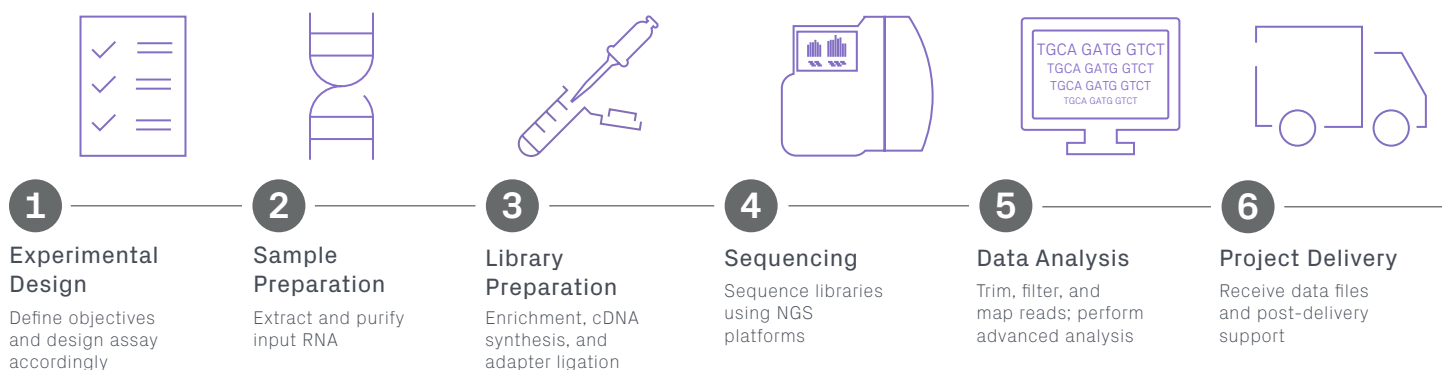
# RNA-Seq Technical Specifications

## Azenta Life Sciences 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](http://genewiz.com) for more details.

## RNA Sequencing Workflow



### 1 Experimental Design

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



Interactive NGS Solution Selection  
Tool: [genewiz.com/ngs](http://genewiz.com/ngs)



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

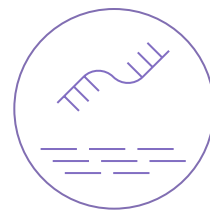
### 2 Sample Preparation

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

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

<sup>†</sup>Please inquire about submitting lower inputs.

<sup>‡</sup>Contact us about Azenta Life Sciences' RNA Stabilization Tubes to ship RNA samples at ambient temperature.



# RNA-Seq Technical Specifications

## 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"> <li>Trimming</li> <li>Mapping</li> <li>Differential gene expression</li> </ul>	<ul style="list-style-type: none"> <li>Gene fusion discovery</li> <li>RNA SNP/INDEL detection</li> <li>Novel transcript discovery</li> <li><i>De novo</i> transcriptome assembly</li> </ul>
Small	<ul style="list-style-type: none"> <li>Trimming</li> <li>Mapping</li> <li>Differential gene expression</li> <li>Small RNA</li> </ul>	

## 6 Project Delivery

### Data Delivery Options



SFTP



Customer  
Cloud  
Account



External  
Hard Drive  
(US Only)

Deliverables for All Projects	Optional Deliverables
<ul style="list-style-type: none"> <li>Sample quality control report</li> <li>Raw data (FASTQ files)</li> </ul>	<ul style="list-style-type: none"> <li>Aligned data (BAM file)</li> <li>Hit counts (TXT file)</li> <li>DGE results (CSV file)</li> <li>GO enrichment analysis (CSV file)</li> <li>Differential splicing analysis (DEXSeq report)</li> <li>De-multiplexed, aggregated Picard BAM file with summary metrics</li> </ul>



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