

RNA Sequencing



Admera Health offers a full suite of RNA sequencing solutions designed to meet the needs of researchers across academia, biotech, pharmaceutical, animal health, and more. Our CAP-accredited, CLIA-certified laboratory delivers high-quality data with fast turnaround times and expert bioinformatics.

Sample Types Accepted

FFPE

Total RNA

Blood

Fresh frozen tissue

Fresh Cells*

Preserved Cells*

Cell Pellet*

**Inquire for more details*

Bulk RNA-seq (+ circRNA-seq)

Quantify protein-coding gene expression, reveal mRNA splicing, study alternative polyadenylation, and evaluate non-coding RNA regulation across the transcriptome.

Bioinformatics include: Trimming & QC · STAR mapping · HTSeq Count · Picard QC · Normalization · DE analysis (MA-plot, PCA, heatmaps, volcano plots) · GO/KEGG functional enrichment
CircRNA-seq: circRNA detection + circular & linear comparison

Long-read RNA-seq (Iso-Seq)

Sequence full-length transcripts for characterizing isoforms, resolving alternative splicing and fusion transcripts, and discovering novel isoforms.

Bioinformatics include: Cluster full-length isoforms · map isoforms to genome · classify transcripts · gene & isoform expression comparison* · GSEA* · GO/KEGG enrichment* · splicing variant analysis*

High-throughput RNA-seq

Low-cost, scalable, automation-compatible workflows using RNA barcoding & multiplexing.

Accelerate drug discovery and large-scale comparative studies with 3' Tag-seq delivering high-throughput data with fewer sequencing reads at reduced cost. Flexible input from cells or RNA with up to 384-sample multiplexing per run.

Available Platforms

DRUG-Seq

BRB-seq

Smartseq 3' DE

Quantseq

*Supports RNA or cell input · up to 384-sample pooling
2M–5M reads/sample · >9K–12K genes detected.
Contact us to select the right platform for your study*

Small RNA-seq

Profile microRNAs, piRNAs, siRNAs, and other small non-coding RNAs. Quantify regulatory smRNA populations.

- Novel small RNA detection
- miRNA discovery & quantification

Bioinformatics include: Quantify miRNA, piRNA, snoRNA, snRNA, + DE analysis

Metatranscriptomics

Profile gene expression across entire microbial communities. Understand active metabolic pathways and microbial interactions in complex matrices.

Bioinformatics include: Trimming & QC · STAR mapping · HTSeq Count · Picard QC · Normalization · DE analysis (MA-plot, PCA, heatmaps, volcano plots) · GO/KEGG functional enrichment



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 908-222-0533

RNA Sequencing

CLIA/CAP Laboratory

We operate in a CLIA-certified, CAP-accredited environment, ensuring all project receive exceptional care and meet rigorous quality standards

Fast Turnaround

Typical RNA-seq turnaround time is 10-15 business days. Expedited services are available upon request.

Expertise with less-than optimal samples

Extensive experience and optimized workflows for low input samples (as low as 10ng)

Expert Bioinformatics

From standard analysis to custom pipelines, our bioinformaticians deliver interpretable, publication-ready results

Our Optimized RNA-seq Workflow



1. Sample submission

Ship samples on dry ice or room temperature to our site in South Plainfield, NJ



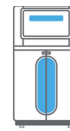
2. RNA Extraction & QC

RNA is extracted and assessed for adequate RNA integrity & purity



3. Library Preparation

Wide range of technologies with optimized protocols for your assay type



4. Sequencing Customizable depth

Sequencing options spanning short and long reads: Illumina, PacBio, and others



5. Data Analysis Standard or Custom

Data QC
FASTQ files
Custom analyses

Comparison Guide

Service	RNA Input Recommendation	Coverage	Best For
Total RNA-seq	10ng-1ug	All RNA types	Comprehensive profiling
mRNA-seq	10ng-1ug	Coding mRNA	Gene expression, DEG
smRNA/miRNA-seq	20ng-1ug	smRNA: 20-200nt, miRNA: 18-32nt	Regulatory RNA discovery
Iso-seq	500ng-2ug	Full-length	Isoform characterization
High-Throughput Gene Expression	1ng-120ng	Coding mRNA	Large cohort studies
Metatranscriptomics	100ng-1ug	Community-wide	Microbial expression



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