

A 3D rendering of a cell and a DNA double helix. The cell is a large, textured sphere with a smaller, more detailed sphere attached to its surface. A DNA double helix is shown extending from the cell. The background is a dark green gradient.

miCORE mRNA Sequencing

Comprehensive Service Completed in Under 5 Weeks

Comprehensive Service Package

From top-notch isolation to library preparation, sequencing, and in-depth analysis — we have you fully covered. Not only that: We can ensure the entire service package is completed in under 5 weeks.

Cost-effective and Flexible Pricing

You are in control : You get to choose the starting and concluding steps, while we offer highly competitive fixed rates tailored to your needs.

Experience Exceptional Customer Satisfaction

Our quality, speed, and outstanding customer service ensure exceptional levels of customer satisfaction.

Overview miCORE mRNA Sequencing

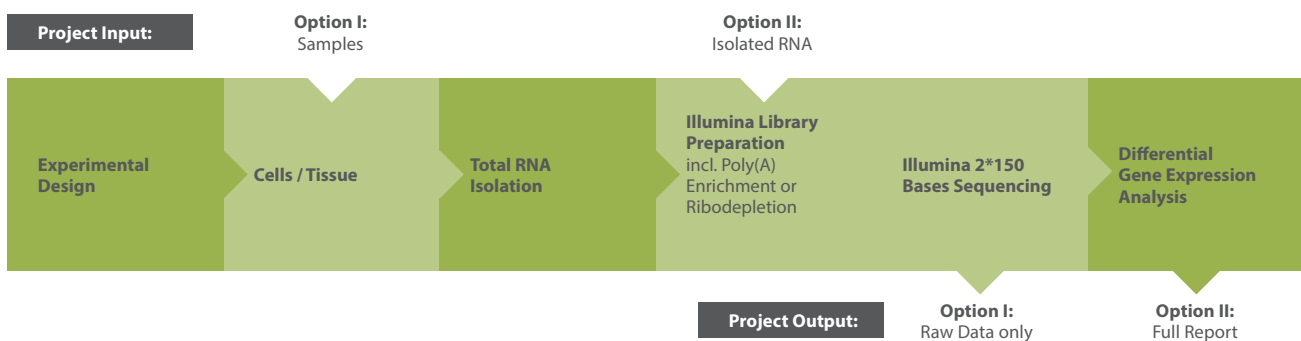
Explore the power of mRNA sequencing with Microsynth's miCORE mRNA Sequencing service. This transformative transcriptomics technique leverages the power of next-generation sequencing (NGS) to precisely quantify sequenced

molecules, opening the door to hypothesis-free analysis.

Discover new isoforms, alternative splice sites, rare transcripts, gene fusions, and underlying mechanisms in a single experiment. Choose our state-of-the-art bioinformatics analysis

module to uncover expression profiles, pathways, and gene networks for thoughtful causal studies. Microsynth's miCORE mRNA Sequencing service is designed to support your research with precision and efficiency.

Workflow and Service Description



RNA Isolation: Outsource the RNA isolation to Microsynth. We have considerable expertise when it comes to challenging samples and we've got a standard pricing structure in place for many cell and tissue sample types.

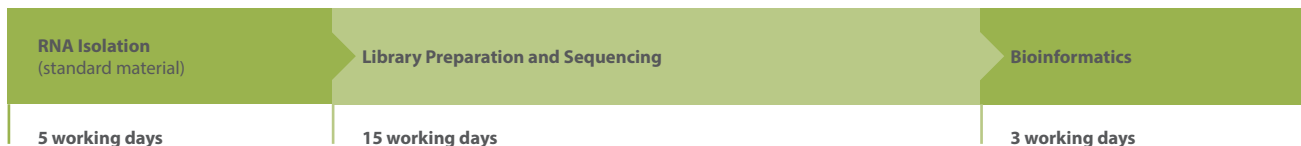
Library Preparation: The library preparation includes QC of total RNA samples, poly(A) enrichment or ribodepletion, cDNA synthesis, and Illumina Library preparation using indexes for multiplexing as well as equimolar pooling

according to library quantification measurements.

Sequencing: Experience the ease of sequencing with our convenient per-sample data packages. From 5 million read pairs (5 million forward reads + 5 million reverse reads) per individual for bacterial samples to the recommended 30 million read pairs for mammalian poly(A) enriched libraries, you can optimize your research potential.

Bioinformatics: Bioinformatics for mRNA sequencing includes differential gene expression, pathway enrichment, and alternative splicing analysis. Results include heat maps of expression patterns and top up-regulated and down-regulated genes, log fold changes, their significance, enriched pathway plots, as well as differential exon usage.

Timeline



We also offer an express service option for an additional fee to expedite the sequencing of your samples.

miCORE mRNA Sequencing Products

Laboratory:

20011 – 14 RNA isolation for mRNA Sequencing (Cells, Tissue, Bacteria, Yeast)

30006 Illumina Stranded RNA Library (Poly(A) enrichment)

30007 Illumina Stranded RNA Library (Ribodepletion)

30705 Illumina Sequencing (5 Mio Read Pairs, 2*150 bp)

Bioinformatics Analysis:

30111 Differential Gene Expression Analysis

30202 Comparative Statistics