



NEGEDIA Digital mRNAseq

Code NGD0010R

Code NGD0011R

NEGEDIA Digital mRNAseq is a technology that accurately measures gene expression. It is based on isolating the 3' end of polyadenylated transcripts, but it does not require Poly(A) enrichment or rRNA depletion. Digital mRNAseq is an attractive solution to perform comparative gene expression analysis on many samples with an efficient, reproducible, and economical approach. The method is ideal for every range of RNA quality (FFPE, degraded RNA).

AVAILABLE OPTIONS

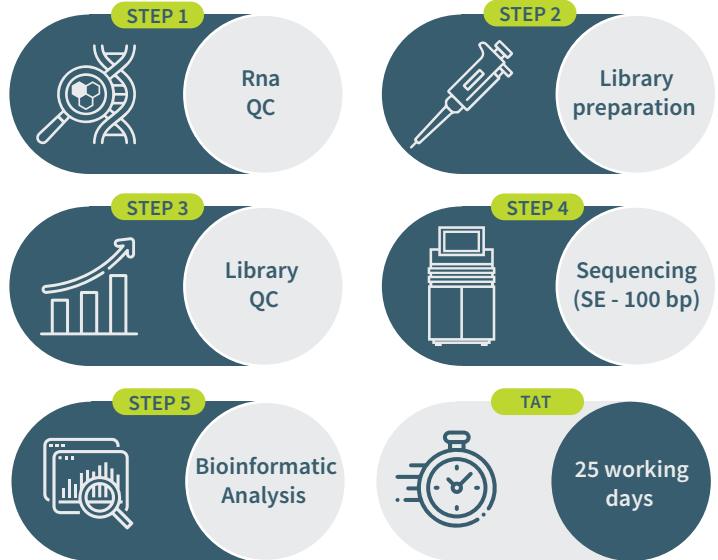
Digital mRNAseq Research Grade (NGD0010R)

Estimated output per sample is ≈ **4 million reads**.
The output is ideal for differential expression, GO pathway analysis and experimental confirmations.

Digital mRNAseq Clinical Grade (NGD0011R)

Estimated output per sample is ≈ **8 million reads**.
This service is designed with strict standards and precision, making it ideal for analyzing clinical samples in research studies. The workflow is optimized for molecular pathology samples, including FFPE.

OUR SERVICE INCLUDES



STARTING MATERIALS

For best results with low quality samples, we strongly recommend Digital RNAseq - Clinical Grade (NGD0011R).

SERVICE CODE

NGD0010R (tissues, cells, blood)

NGD0011R (degraded samples, FFPE, liquid biopsies)

STARTING MATERIAL

500 ng for Qubit quantified RNA (10 µl / concentration 50 ng/µl)

QUALITY REQUIREMENTS

- Medium quality RNA
- OD 260/280 1.9-2.1 and an OD 260/230 2.0-2.2
- RNA should have an RNA Integrity Number (RIN) > 7 (RIN < 7 is acceptable)
- Dissolved in RNase, DNase and protease free high molecular grade water

STORAGE & SHIPPING

- Storage: - 80 °C
- Shipping: on dry ice unless RNA is precipitated in ethanol
- Samples have to be sent in 1.5 ml snap cap tubes.

For low quantity or quality RNA please contact our Customer Service at service@negedia.com



APPLICATION NOTES

Ideal for low quality samples: Negedia Digital mRNA-seq is a powerful tool for analyzing the cellular transcriptome profile with a wide range of applications, including:

- **Quantitative profiling of transcripts** across different tissues or samples under various conditions and treatments.
- Study of **developmental mechanisms** and **drug resistance** through tissue-specific or time-resolved gene expression analysis.
- **Omics analysis** in combination with genomic data.
- **Investigation** of **pathogenic mechanisms** and clinical subtypes for clinical diagnosis.

EXPERIMENT DESIGN SUGGESTIONS:

For optimal results, submit at least 4 biological replicates. If high variability is expected, is highly recommended to increase the number beyond 4 per condition.

BIOINFORMATICS ANALYSIS

II LEVEL ANALYSIS (INCLUDED IN NGD0010R NGD0011R)



- FastQ files
- Mapped reads (BAM files)
- Raw counts per gene (csv file)
- Quality report

III LEVEL ANALYSIS (INCLUDED IN NGD0010R NGD0011R):



- Gene expression (DEGs) and Pathways analyses:
 - Quality plots (Density plot, PCA, correlation cluster)
 - DEGs Volcano plots, heatmaps
 - DEGs lists (csv files)

DISCOVER
OUR INTERACTIVE
REPORT



SCAN THE
QR CODE

NEGEDIA® is a cutting-edge NGS laboratory built on the Telethon Foundation's 30 years of expertise in rare genetic disease research. We are committed to making genomics accessible across the Life Sciences, providing high-precision sequencing and bioinformatics solutions for both research and clinical applications.

➤ **Clinical Services:** Supporting laboratories, clinics, and hospitals in leveraging NGS for clinical research and diagnostic advancements.

➤ **Research Services:** Assisting research institutes and universities at every stage, from experimental planning to advanced bioinformatics analysis.

For more information or to discuss a project, contact us at info@negedia.com

GENOMICS AND BEYOND

UNI EN ISO 9001:2015

