

Non-coding RNA and Epitranscriptomic Solutions

| GlycoRNA Arrays **NEW !**

Cover Y-RNA/Y-RNA fragment, tRNA, tiRNA&tRF, pre-miRNA, miRNA & more

| Downstream-of-Gene Transcript (DoG RNA) Arrays **NEW !**

Profile DoG RNAs and all their target RNA types simultaneously

| R-loop Profiling **NEW !**

Profile the lncRNA/mRNA/circRNA organized R-loops in gene regulation by DRIPc-seq

| Circular RNA Arrays

Accurately profile circular RNAs by highly specific circular junction probe design

| LncRNA Arrays

Overcome the limitations of RNA-seq for lncRNAs often at low abundance

| Small RNA Arrays

Accurately profile miRNA, pre-miRNA, tRNA, tsRNA, and snoRNA simultaneously

| Epitranscriptomic Arrays

Quantify the percentage of m6A modifications at the transcript specific level

| m6A Single Nucleotide Arrays

Locate and quantify the exact m6A site at single nucleotide resolution

| Small RNA Modification Arrays **NEW !**

Quantify o8G/m7G/m6A/Ψ/m5C in miRNAs, pre-miRNAs & tsRNAs



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The New Vortex Mixer

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- Quickly vortex tubes with just one touch

The Vortex Mixer is ideally suited for assay protocols that require gentle mixing, all the way up to resuspensions that require vigorous vortexing. Find out more at usascientific.com/vortex_mixer.



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Who we are

Cellecta Inc., a trusted provider of genomic products and services, has successfully collaborated with the world's leading pharma, biotech, government, and academic institutions since 2006. Our recognized expertise in viral vector production, functional screening, cell engineering and multiplex qRT-PCR has given rise to a portfolio of offerings useful for loss-of-function and gain-of-function phenotypic screening, cell barcoding, targeted RNA-Seq and adaptive immune receptor profiling, and more.

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July 10-12 | Montreal, QC, Canada

18TH AACR CONFERENCE ON THE SCIENCE OF CANCER HEALTH DISPARITIES IN RACIAL/ETHNIC MINORITIES AND THE MEDICALLY UNDERSERVED

September 18-21 | Baltimore, MD

ADVANCES IN OVARIAN CANCER RESEARCH

September 19-21 | Denver, CO

MECHANISMS OF CANCER IMMUNITY AND CANCER-RELATED AUTOIMMUNITY

September 24-27 | Montreal, QC, Canada

ADVANCES IN PEDIATRIC CANCER RESEARCH

September 25-28 | Boston, MA

ADVANCES IN PANCREATIC CANCER RESEARCH

September 28-October 1 | Boston, MA

AACR-NCI-EORTC INTERNATIONAL CONFERENCE ON MOLECULAR TARGETS AND CANCER THERAPEUTICS

October 22-26 | Boston, MA

AACR-KCA JOINT CONFERENCE ON PRECISION MEDICINE IN CANCER

November 13-14, 2025 | Busan, Korea

CANCER EVOLUTION

December 4-6 | Albuquerque, NM

SAN ANTONIO BREAST CANCER SYMPOSIUM

December 9-12 | San Antonio, TX

THE RISE IN EARLY ONSET CANCERS – KNOWLEDGE GAPS AND RESEARCH OPPORTUNITIES

December 10-13 | Montreal, QC, Canada

FUSION-POSITIVE CANCERS

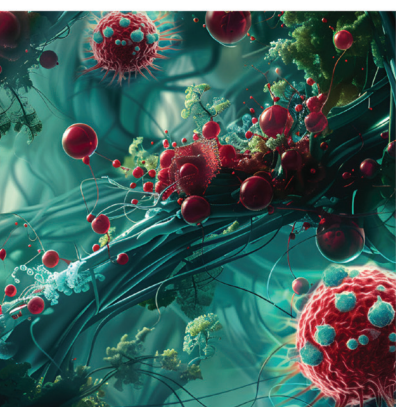
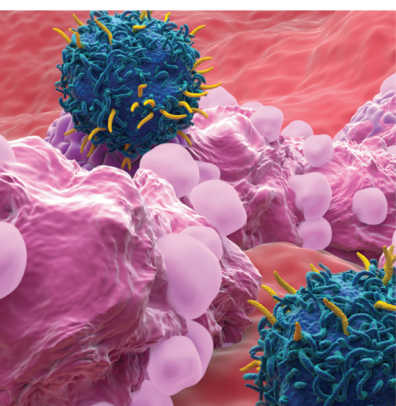
January 13-15, 2026 | Philadelphia, PA

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Figure 1 | Comparison of CORALL and conventional whole transcriptome RNA-Seq library preparation workflows

Transcriptome-wide Evaluation of siRNA Activity with CORALL

RNA-Seq is a method of choice to evaluate the functional consequences of the treatment with RNA therapeutics such as siRNAs. Lexogen's CORALL was used to prepare libraries for whole transcriptome RNA-Seq, aiming to **confirm the anticancer activity of siRNAs against oncogenes in cervical cancer cells**¹.

In another study, siRNAs were designed to serve as anti-COVID-19 therapeutic, targeting mRNAs of factors driving pulmonary fibrosis associated with a poor prognosis of COVID-19. Here, CORALL was successfully used to **evaluate the impact of antifibrotic siRNA therapeutics on a transcriptome-wide level**².

References

¹ Gu *et al.*, 2021, *NAR* (23): 1172-1190, doi: 10.1016/j.omtn.2021.01.018

² Ahn *et al.*, 2022 *Sci. Rep.* (11): 19161, doi: 10.1038/s41598-021-98708-z



Key Benefits:

- Fragmentation-free RNA-Seq library prep with superior end-to-end coverage and true start site representation to cover all bases.
- Built-in UMIs for highly accurate expression analysis of coding and non-coding transcripts.
- Easily scalable automation-friendly workflow.



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