



Evaluate the Activity of RNA Therapeutics with CORALL RNA-Seq V2

Get the best sequencing results for demanding applications with **CORALL RNA-Seq V2**. Add extra-confidence with built-in Unique Molecular Identifiers (UMIs) and process any sample type and quality with ease in only 6 steps: from sample to sequencing-ready library in less than one day.



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.



Interested to learn more?

Check the product page for more information on our website!