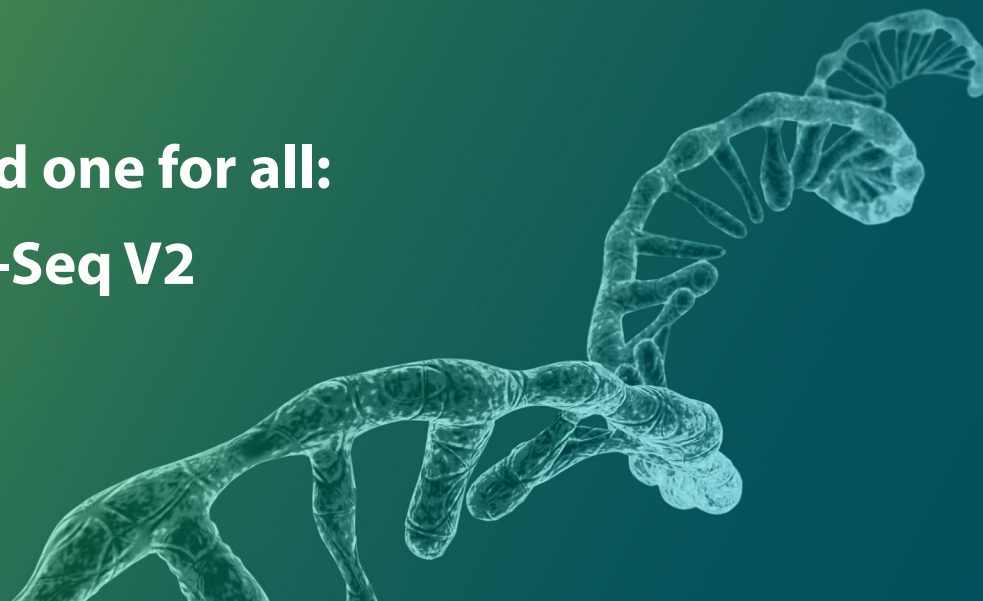


All-in-one and one for all: CORALL RNA-Seq V2



Get the best sequencing results for all sample types and qualities with CORALL RNA-Seq V2 - Lexogen's fast and flexible whole transcriptome RNA-Seq Library Prep Kit.

NEW! Enhance your whole transcriptome sequencing (WTS) workflow and cost-effectiveness by generating the optimal insert size required for your application! Two distinct library generation chemistries allow fragmentation bias-free library generation and size selection.



NEW! Fragmentation-free insert size adjustment.

Standard library size (~ 350 bp) provides a perfect fit for gene expression analysis. Long library size (~ 550 bp) is the ideal choice for demanding applications such as alternative splicing, isoform analysis, and fusion detection.



Ideal for challenging samples, degraded RNA, and FFPE material.

The robust and fragmentation-free protocol with built-in UMIs make this kit the ideal choice for library preparation from all sample types and RNA qualities.



Excellent performance on low input RNA.

CORALL's flexible input range (1 ng - 1000 ng) is the perfect fit for processing precious samples with limiting material. The sensitive protocol delivers reproducible, high-quality data from as low as 1 ng input RNA.



Fast, flexible, and fragmentation-free library prep in just 4.5 hours.

CORALL RNA-Seq V2 only requires 6 steps, saving valuable time and allowing the preparation of sequencing-ready-libraries in a single day.

For more information, visit our website [lexogen.com](https://www.lexogen.com) or contact us at sales@lexogen.com

Fast and flexible library prep in only 4.5 hours

In contrast to conventional WTS RNA-Seq, CORALL library preparation requires only 6 steps and can be completed in 4.5 hours (Fig. 1). CORALL does not require RNA fragmentation and is thus perfectly suited for processing of degraded or FFPE RNA.

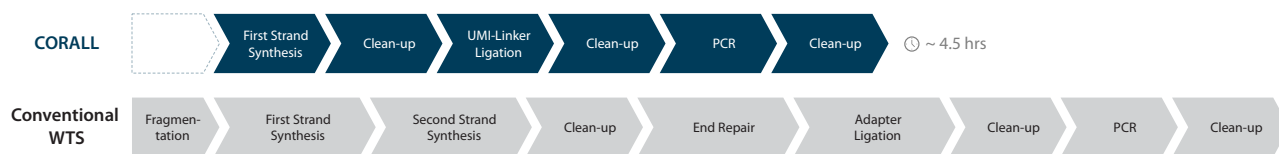


Figure 1 | Comparison of CORALL and conventional WTS RNA-Seq library preparation workflows.

Excellent performance on low input RNA

The complete CORALL RNA-Seq V2 workflow is highly reproducible (Fig. 2) and delivers high-quality RNA-Seq data even for low input samples down to 1 ng total RNA (prior to poly(A) selection or ribo-depletion).

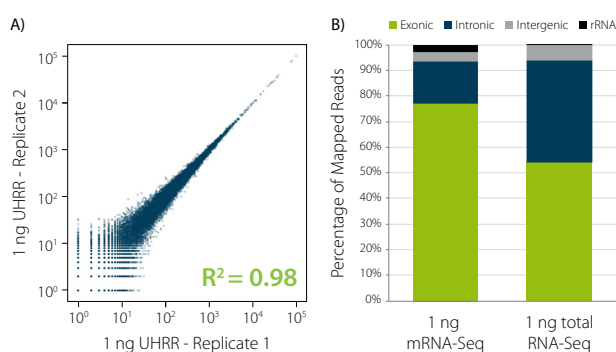


Figure 2 | Exceptional performance on low input RNA. A) Excellent correlation for replicates of 1 ng Universal Human Reference RNA (UHRR) processed with CORALL mRNA-Seq V2. B) Read distribution for 1 ng input RNA for CORALL mRNA-Seq V2 and CORALL Total RNA-Seq V2 with RiboCop rRNA depletion.

Wide input range and exceptional sensitivity

CORALL mRNA-Seq V2 displays exceptional gene discovery rates across the widest input range and is highly sensitive even for input as low as 1 ng total RNA prior to mRNA enrichment (Fig. 3).

Exceptional performance on FFPE samples

CORALL Total RNA-Seq V2 with RiboCop rRNA depletion is ideal for processing degraded and compromised samples, including FFPE material (Fig. 4).

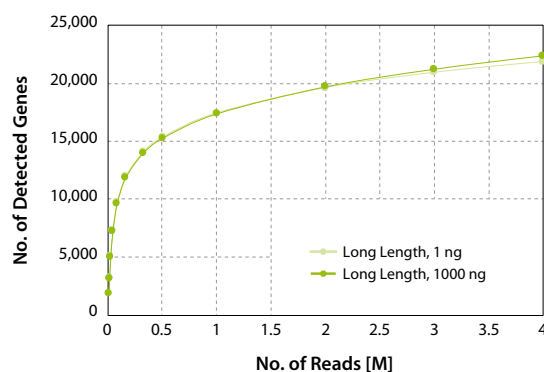


Figure 3 | Gene discovery rates. CORALL mRNA-Seq libraries with long inserts were prepared from 1000 ng and 1 ng UHRR. The number of detected genes was plotted against the total number of uniquely mapping exonic reads.

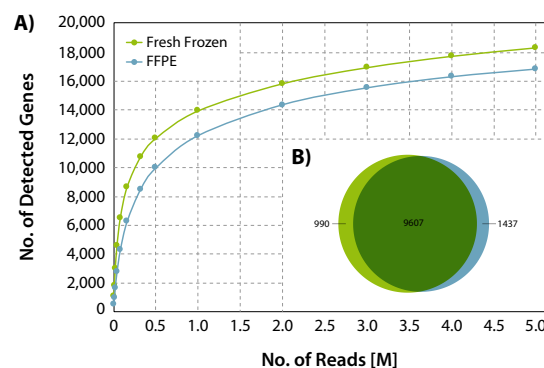


Figure 4 | Gene discovery rates for fresh frozen (FF) and FFPE derived human liver RNA. A) Gene detection rates. The number of detected genes is plotted against the total number of reads mapping uniquely to exons. B) Overlap of detected genes at normalized expression levels >5 CPM (for uniquely mapping reads).

CORALL RNA-Seq V2

Lexogen's fast and flexible library prep kit with exceptional performance for challenging samples.

- **NEW!** CORALL RNA-Seq V2 enables preparation of longer libraries for isoform and fusion detection, alternative splicing and more.
- The fragmentation-free protocol complete with RiboCop rRNA depletion is the ideal choice for degraded and FFPE RNA.
- CORALL's time-saving and easy workflow enables processing from sample to sequencing-ready library in less than one day.
- CORALL RNA-Seq V2 supports the widest input range (1 ng - 1000 ng) with excellent sensitivity for low input RNA.

Ordering Information

Cat. №	Product Name	Kit sizes
171 - 176	CORALL RNA-Seq V2 Library Prep Kit with UDIs (Set A1, A2, A3, A4, B1, or A1 - A4)	24, 96, 384
177 - 182	CORALL mRNA-Seq V2 Library Prep Kit with UDIs (Set A1, A2, A3, A4, B1, or A1 - A4)	96, 384
183 - 184	RiboCop HMR V2 and CORALL Total RNA-Seq V2 Library Prep Kit with UDIs (A1 or B1)	24, 96
185 - 186	RiboCop HMR+Globin and CORALL Total RNA-Seq V2 Library Prep Kit with UDIs (A1 or B1)	24, 96

For more information and additional resources, please visit our website.

