Covaris®
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Overcome the Challenges with Degraded RNA

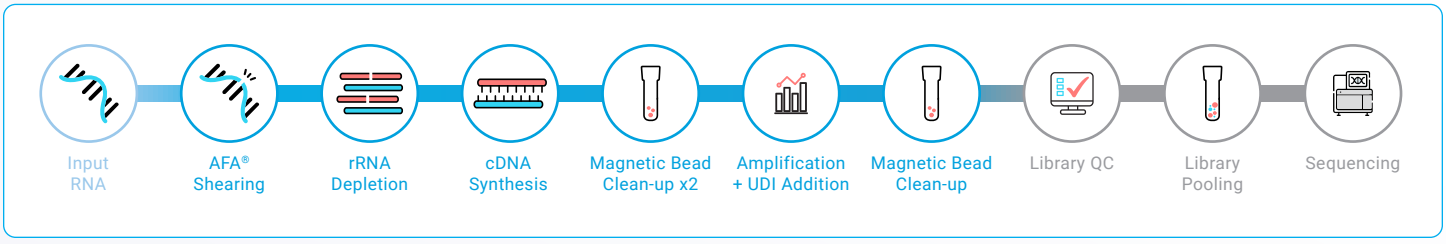
truCOVER® Total RNA Library Prep Kit

Covaris truCOVER Total RNA Library Prep integrates the proven accuracy and reliability of our industry-leading Adaptive Focused Acoustics® (AFA®) nucleic acid shearing with an optimized workflow from sample to sequencing. The result? Higher quality data, faster turnaround, and greater efficiency for your RNA-Seq applications.

Designed specifically for generating strand-specific libraries from Total RNA isolated from a variety of sources, including FFPE.

- High precision in detection of gene fusions and alternative splicing events at lower sequencing depths
- Seamlessly integrates with Covaris truXTRAC® FFPE SMART Solutions for an end-to-end optimized workflow from sample extraction up to sequencing for FFPE
- Captures consistenly higher proportion of exonic reads (30–40%) across all tested samples, maximizing high data available for differential gene expression (DGE)
- Optimized RNA library prep workflow leveraging AFA-driven fragmentation to ensure reproducibility & enhanced library diversity
- Consistent performance with the most challenging samples, using RNA with DV_{200} scores as low as 30%
- Robust depletion, resulting in >99% elimination of cytoplasmic and mitochondrial rRNA
- Broad range of input material: 10–500 ng, enabling maxium recovery, zero waste, and wide utilization
- Unique Covaris Bead Purification Reagent ensures efficient elimination of primer/adapter dimers
- Fast, 4 hour workflow with minimal hands-on time making it very automation friendly
- Supports efficient, high-quality data generation with reduced waste, enabling stronger ROI, and more confident downstream analyses

truCOVER Total RNA Library Prep Kit Workflow



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Get ready for efficient and effective library prep.

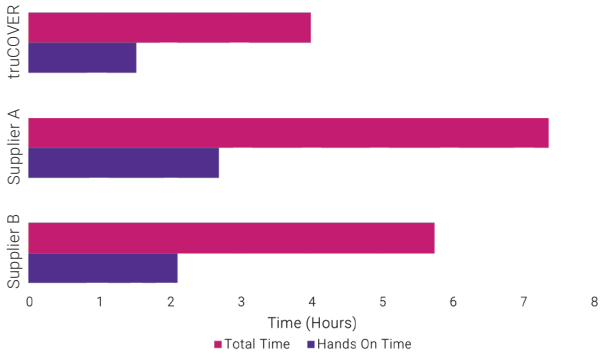
Request more information at www2.covaris.com/Total_RNA

Simplified Workflow Reduces Turnaround Time by up to 40%

truCOVER Total RNA Library Prep integrates fragmentation and strand-specific library construction into a simplified, streamlined workflow with significantly reduced hands-on time.

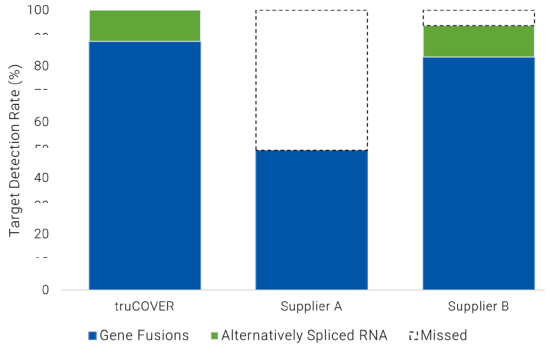
truCOVER Total RNA Library Prep (~4 hrs)	Supplier A (~7 hrs)	Supplier B (~6 hrs)
Input RNA	Input RNA	Input RNA
AFA® Shearing	rRNA Depletion	1st & 2nd Strand cDNA Synthesis
rRNA Depletion	Fragmentation	Amplification
1st & 2nd Strand cDNA Synthesis	1st Strand Synthesis	1st Magnetic Bead Clean-up
1st Magnetic Bead Clean-up	2nd Strand Synthesis	2nd Magnetic Bead Clean-up
2nd Magnetic Bead Clean-up	A-Tailing	Depletion Preparation
Amplification + UDI Addition	Adapter Ligation	rRNA Depletion
3rd Magnetic Bead Clean-up	1st Magnetic Bead Clean-up	Amplification
	Amplification	3rd Magnetic Bead Clean-up
	2nd Magnetic Bead Clean-up	4th Magnetic Bead Clean-up

Workflow Time Requirements



By utilizing a single-enzyme, single-incubation step for cDNA synthesis and optimizing magnetic bead clean-ups, the protocol reduces total workflow time to approximately 4 hours.

Precision of Structural Variants Detection



truCOVER detected all gene fusions and alternatively spliced RNAs in the Seraseq® FFPE Tumor Fusion RNA Reference Material, at a depth of only 25M reads (typical kits require 50M+ reads).

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