

Twist RNA Sequencing Workflows Solutions

Flexible tools to measure known transcripts and capture unknown biology

KEY BENEFITS

Complete RNA sequencing workflows

- Targeted RNA Sequencing or Whole Transcriptome kits
- Compatible with Twist UMI, UDI and standard and fast hybridization reagents
- Enrich for relevant transcripts with the RNA Exome or custom RNA panels
- Available 16 and 96 sample configurations

Save time and sequencing reads

- Perform RNA Library Preparation in less than 5 hours
- Deplete rRNA & hemoglobin from Total RNA
- Automation friendly reagents and streamlined protocols

Elevated performance

- Build high quality stranded RNA Sequencing libraries
- Total RNA Input from 1 ng to 1,000 ng
- Compatible with low quality, degraded RNA from FFPE

Twist Bioscience delivers comprehensive RNA library preparation solutions that save time and sequencing cost while optimizing for performance in any workflow. While typical RNA library prep kits can be laborious and expensive, Twist offers targeted and unbiased workflows that reduce time at the bench and integrate with our current set of NGS reagents including our target enrichment kits. Each workflow delivers high quality libraries ready for sequencing on a sequencing platform from a wide range of inputs and sample types including translation research samples.

TARGETED RNA SEQUENCING

Sequence only RNA transcripts that matter to your research by combining Twist RNA Library Prep, Twist Target Enrichment, and our purpose-built panels with our exon-aware design algorithm. Whether utilizing Twist RNA Exome or a Twist-designed custom panel, Twist delivers cost-effective targeted sequencing libraries for any type of research. The targeted sequencing workflow can increase the sensitivity and power of your NGS studies by enriching for targeted transcript and enabling the ability to scale up the number of samples sequenced.

WHOLE TRANSCRIPTOME SEQUENCING

Study the complete RNA transcriptome by combining our Twist RNA Library Prep with Twist rRNA & Globin Depletion kit. Twist depletion removes highly expressed ribosomal RNA and hemoglobin from human, mouse, and rat species. The whole transcriptome workflow enables unbiased gene expression analysis and the ability to discover new transcripts and isoforms in interesting tissues and samples.*

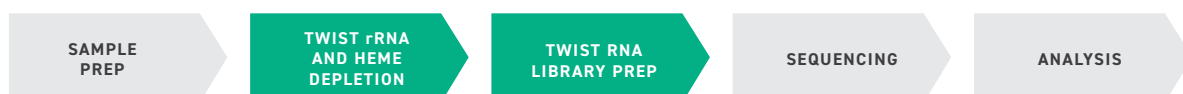
Complete Workflows for RNA Library Preparation

Twist's RNA products offer a complete NGS solution that produces uniform sequencing libraries for RNA sequencing. The end-to-end workflows achieve this by combining streamlined and effective library preparation kits, high quality unique dual indices (UDI), unique molecular identifiers (UMI), optimized target enrichment, and proprietary exon-aware panel design algorithm.

Twist Targeted Sequencing Workflow

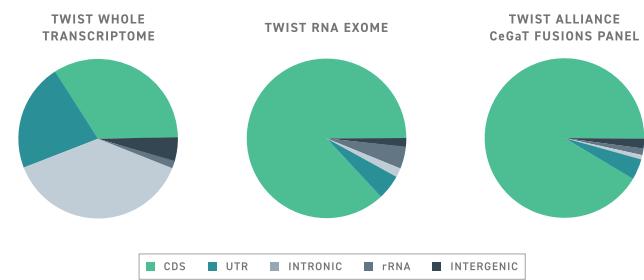


Twist Whole Transcriptome Sequencing Workflow

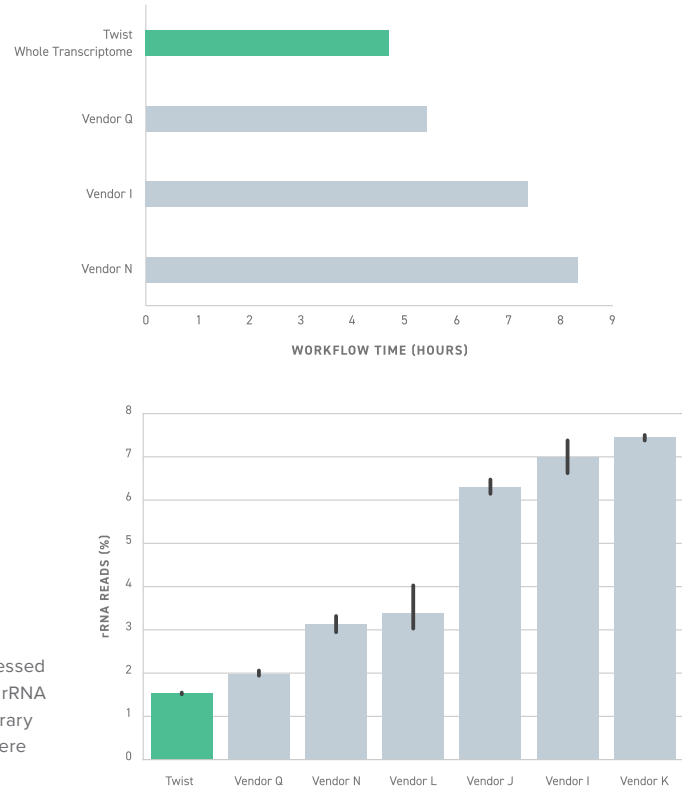


More reads with less bench time

With the Twist RNA Library Prep users can build RNA libraries for sequencing in less than 5 hours. Twist rRNA & Globin Depletion Kit effectively removes unwanted high expressing targets. Alternatively, Twist target enrichment workflow positively selects for important transcripts and leaves out these read-consuming high expressors.



Twist RNA workflow saves time and reads. Twist and competitor workflows were all processed with 100 ng of Universal Human Reference (UHR) RNA with their respective protocols. For rRNA depletion comparison, vendor depletion kits were used in combination with Twist RNA Library Prep. Workflow time includes everything from start to finish of the protocol. All samples were sequenced on an Illumina NextSeq 550 and downsampled to 10M reads.



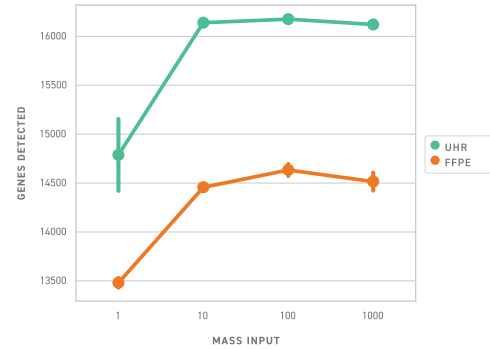
Better performance for important samples

Experimental outcomes often hinge on the availability and quality of samples. It is important to have a kit that handles a range of mass and degradation states. The Twist RNA Library prep accepts input from 1 ng to 1,000 ng allowing for a wide range of experimental designs for both target enrichment and whole transcriptome workflows. Furthermore, the whole transcriptome workflow delivers reads across the whole transcript and enables the assignment of each read to the originating DNA strand.

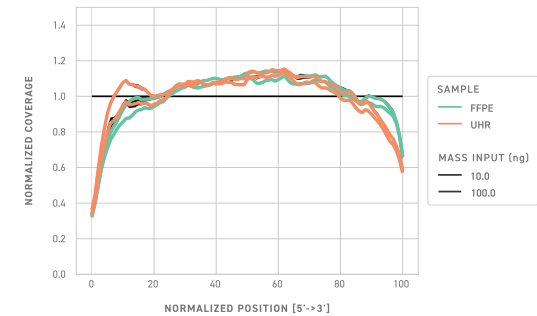
RNA SOURCE (100 NG)	RNA %	ESTIMATED LIBRARY COMPLEXITY*	UMI DUPLICATE READS %	INCORRECT STRAND READS %	PF BASES %	USABLE BASES % (EXONIC + UTR)
UHR	1.53	57,135,794	1.72	1.82	99.68	55.67
FFPE	3.41	62,555,013	2.38	2.20	99.53	50.14

QC metrics for 100 ng samples.

Build high quality libraries to sequences across transcripts and the transcriptome. Whole transcriptome libraries from UHR and and formalin-fixed paraffin-embedded (FFPE) RNA (RIN=3.3, DV200=66%) were generated with the Twist RNA Library Prep kit samples were sequenced on an Illumina NextSeq 550 and downsampled to 10M reads.



Number of genes detect at different input amounts.



Average coverage of the top 1,000 expressed genes.

LEARN MORE
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ORDERING INFORMATION

- 107060:** Twist RNA Library Prep Kit, 16 Samples
- 107061:** Twist RNA Library Prep Kit, 96 Samples
- 107147:** Twist RNA Library Prep with Depletion, 16 Samples
- 107148:** Twist RNA Library Prep with Depletion, 96 Samples