Twist RNA Exome

Target the transcriptome and discover more biology

KEY BENEFITS

Designed for human transcriptome

- Target 35.8Mb bases, 19,708 genes and 63,215 isoforms
- Design built with Gencode and RefSeq databases
- Greater than 1.8 fold enrichment over whole transcriptome

Target enrichment for RNA

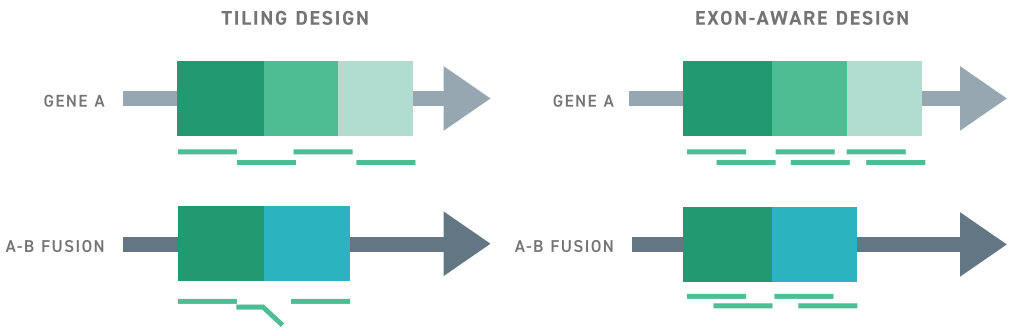
- Exon-aware probe designs for protein coding regions, fusions and isoforms
- Fewer reads per sample for higher throughput
- Enriches for intact transcripts even from small amount of degraded RNA (eg. FFPE)

Routine RNA sequencing of human samples for translational research has provided critical insights into the pathology of human diseases. Differential gene expression is a powerful tool to identify the pathways driving disease mechanism and progression. Furthermore, isoforms and fusion genes can identify important changes in the protein expression and cellular function that have a major impact on disease. Unfortunately, clinical samples are often extracted from formalin-fixed paraffin-embedded (FFPE) samples. The fixation process is often inconsistent across samples and can severely degrade RNA, interfering with accurate gene quantification and isoform detection.

The Twist RNA Exome with Twist RNA Library Prep and Twist Target Enrichment provides a reliable method of generating transcriptome sequencing data from RNA extracted from a variety of sources including FFPE. RNA Exome increases the signal while requiring fewer sequencing reads. This enables the detection of low expressing targets that are critical for an accurate picture of the transcriptional state of the cell. The Twist RNA Exome requires less sequencing reads than other methods to detect the same number of genes. This enables our users to allocate reads to more samples or detect more with the samples on hand. Finally, the RNA Exome's exon-aware design approach leaves open the ability to detect isoforms and junctions that may otherwise get lost. This complete sequencing solution can produce highly complex and uniform sequencing reads for RNA sequencing analysis of the transcriptome.

Exon-aware design

Each target enrichment application has a unique set of design requirements. RNA splicing presents unique challenges when tiling target capture probes across exonic regions. Twist panel design experts have devised a unique exon-aware design strategy that takes splicing into account. Typical capture probes would be tiled across junctions, such as undetected isoforms, or fusion genes. In exon-aware tiling, our designs avoid placing probes over exon-exon boundaries, to not inadvertently bias against novel transcripts.

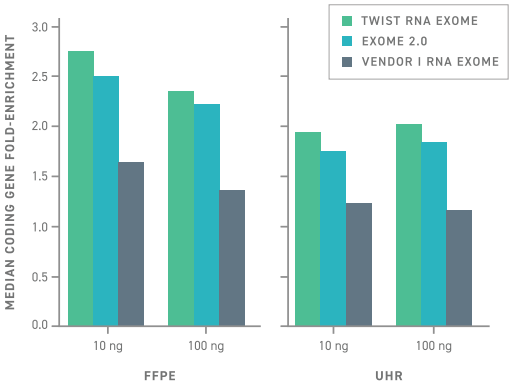


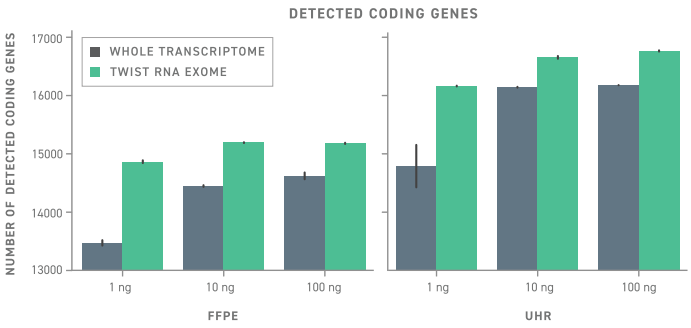
Panel designs built for the transcriptomes. Exon-aware design overcomes the isoform bias introduced by typical tiling approaches.

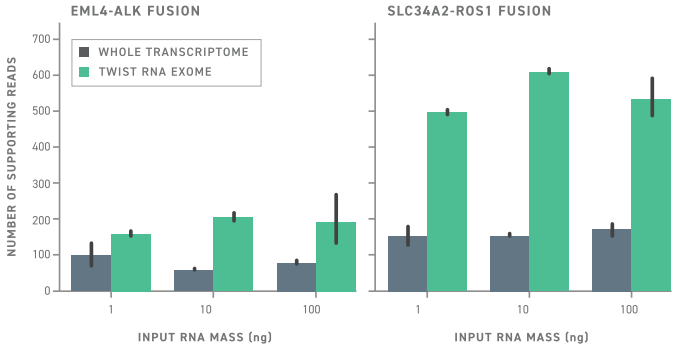
For Research Use Only. Not for use in diagnostic procedures

Detect more genes with fewer reads

The Twist RNA Exome panel enriches transcripts across the transcriptome regardless of their magnitude of expression. Overall enrichment with the exon-aware design strategy is substantially improved over a conventional tiling design and delivers a measurable increase in signal over whole transcriptome sequencing with the same number of reads. This leads to a substantial increase in the number of detected coding genes with both FFPE and Universal Human Reference (UHR) RNA. Importantly, this impacts the ability to detect low expressing and rare transcripts such as RNA gene fusions.





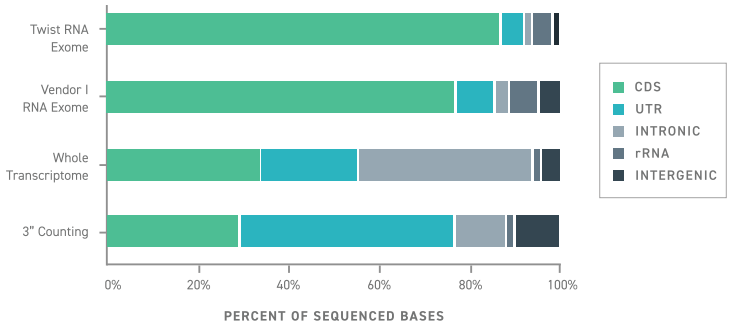


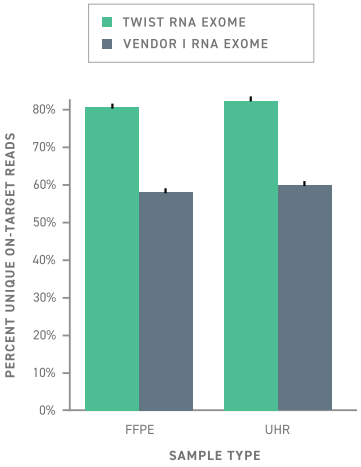
Twist RNA Exome can detect more targets with fewer reads. All libraries were prepared with the Twist RNA Library Prep and enriched with Twist Standard Hybridization Reagent Kit v2. All samples were sequenced on an Illumina NextSeq 550 and downsampled to 10M reads.*

Top right: The median coding gene fold-enrichment over whole transcript was measured for each exome.
Bottom left: The number of genes detected for RNA Exome and whole transcriptome workflows were compared for FFPE and UHR RNA at difference input amounts.
Bottom right: Cell-line-derived FFPE standard material that contained well-defined fusion events was used to assess the ability to enrich RNA gene fusion.

More reads for important targets

The Twist RNA Library Prep coupled with the Twist Standard Hybridization Reagent Kit v2 delivers significant advantages for sequencing transcriptome with the RNA Exome. The Twist RNA Exome has a higher on-target rate with more of the reads aligning to protein coding sequencing (CDS). Approximately 80% of reads are unique and in coding sequences, while competitor RNA exome is approximately 60% For a sample sequence of 20 million reads, this translates into 16 million unique reads and from coding regions versus 12 million.





Twist RNA Exome delivers more valuable reads. 100 ng of FFPE or UHR RNA was processed with hybridization and library prep kits from the respective vendor. All samples were sequenced on an Illumina NextSeq 550 and downsampled to 10M reads.*

** Data on file 2022.*

LEARN MORE

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ORDERING INFORMATION

107143: RNA Exome 2 Reactions
107144: RNA Exome 12 Reactions
107146: RNA Exome 96 Reactions