TWIST BIOSCIENCE

More reads isn't the answer

Detect more genes, identify critical fusions, and cut sequencing costs with Twist RNA Exome, engineered for smarter enrichment.

>80%
Reads on-target
(vs ~60% competitor)

40%
Less sequencing cost
vs. Whole Transcriptome

2.4x
Enrichment on
FFPE samples

Why Twist RNA Exome outperforms whole transcriptome sequencing

EFFICIENCY

Detect more with less

- Whole transcriptomic sequencing detects ~15,000 genes from 10M reads, RNA exome detects just as many genes with only 6M reads.
- ~80% of unique on-target reads vs. ~60% from leading competitors' transcriptome enrichment.
- This translates to 40% fewer sequencing reads needed for equivalent data — a direct cost saving per sample.

**Same data.
40% more samples per run.**

PERFORMANCE

Rescue your most challenging samples

- FFPE samples show >2.4× enrichment with RNA Exome vs. whole transcriptome.
- Twist RNA Library Prep includes an optional FFPE repair module to boost RT to first-strand yield.
- Recover data from precious degraded samples critical in clinical research and translational oncology workflows.

Unbiased enrichment of degraded FFPE.

PRECISION

Find fusions others miss

- "Exon-Aware" design positions probes within exons — not across junctions — enabling capture of both known and novel gene fusions and Novel Splice Variants.
- RNA Exome delivers more fusion-supporting reads than whole transcriptome with the same number of total reads.
- Can detect fusions in FFPE even at low input down to 1 ng.

Enhance fusion detection from challenging low input samples.

	ON-TARGET READS	READS REQUIRED TO DETECT 15,000 GENES IN REFERENCE DNA	READS IN CODING SEQUENCING	GENE EXPRESSION PROFILE	FUSION DETECTION
WTS	~35%	10M	36%	Yes	Lower sensitivity
RNA EXOME	**~80% of reads on coding sequences**	**6M**	**85%**	**Yes**	**Higher sensitivity, with more fusion supporting reads**

Source: Twist Bioscience internal data

Learn more at **twistbioscience.com/ngs** or contact us at **sales@twistbioscience.com**

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