

QIAseq Targeted RNAscan Panels

Applying digital RNA sequencing to scan for known and novel fusion genes

Products

Product Details

Resources

Products

QIAseq Targeted RNAscan Panels are intended for molecular biology applications. These products are not intended for the diagnosis, prevention, or treatment of a disease.



QIAseq Targeted RNAscan HC Panel (12)

Cat no. / ID. 333612

Kit containing ALL reagents (except indexes) for targeted Fusion sequencing; fixed panel for 12 samples; more than 100 fusions

[Copy order details](#)

\$2,510.00

[Configure at GeneGlobe](#)



QIAseq Targeted RNAscan HC Panel (96)

Cat no. / ID. 333615

Kit containing ALL reagents (except indexes) for targeted Fusion sequencing; fixed panel for 96 samples; more than 100 fusions

[Copy order details](#)

\$13,942.00

[Configure at GeneGlobe](#)

QIAseq Targeted RNAscan Panel (12)

Cat no. / ID. 333602

Kit containing ALL reagents (except indexes) for targeted Fusion sequencing; fixed panel for 12 samples; less than 100 fusions

 [Copy order details](#)

\$1,675.00

 [Configure at GeneGlobe](#)

QIAseq Targeted RNAscan Panel (96)

Cat no. / ID. 333605

Kit containing ALL reagents (except indexes) for targeted Fusion sequencing; fixed panel for 96 samples; less than 100 fusions

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\$9,758.00

 [Configure at GeneGlobe](#)

Features

- Accurate quantification of a large number of fusion genes
- Identify new fusion gene partners, no prior knowledge of breakpoint needed
- Works with low-quality RNA, including RNA from FFPE and liquid biopsy
- Requires low RNA input, as low as 15 ng of un-enriched RNA
- Automation-friendly

Product Details

The QIAseq Targeted RNAscan Panels are a complete Sample to Insight solution that applies the molecular barcode-based digital RNA sequencing strategy to quantify known and new fusion genes. Digital RNA sequencing is a unique approach in which genes are tagged with molecular barcodes before amplification, overcoming the issues of PCR duplicates and library bias. In addition, the unique single primer extension approach allows the detection of new fusion gene partners. The proprietary data-analysis pipeline enables highly confident calls of low-abundance fusion transcripts and novel fusion gene identification.

Each QIAseq Targeted RNAscan Panel contains all the necessary components to construct libraries from enriched targets. The panels are platform-agnostic and will work on both Illumina and Ion Torrent instruments. The primer design is based on single primer extension, in which each target is enriched by one target-specific primer and one universal primer – a strategy that reduces the amount of required primers. All primers required for a panel are pooled into an individual primer pool to reduce panel handling and the number of pools required for enrichment and library construction. Platform-specific indexes, which are contained in a separate box, allow multiplexing of up to 384 samples per sequencing run.

Performance

- Accuracy: Innovative digital sequencing (incorporating molecular barcodes) eliminates PCR duplication and amplification bias to confidently detect known and novel fusions.
- Specificity: The unique combination of our proprietary primer design algorithm and rigorous testing of every primer assay guarantees high specificity and accurate results.

- **Content:** The QIAseq targeted RNAscan panels offer a high degree of flexibility in content and sample multiplexing. Several cataloged panels have been developed for a wide range of applications. One can also build a custom panel for specific content, or to extend the contents of an existing cataloged panel. Up to 384 samples can be multiplexed using the QIAseq indexes.
- **Flexibility:** Because the QIAseq targeted RNAscan panels use single primer extension, primers can be designed to detect known fusions based on characterized breakpoints or to discover novel fusions.

Principle

PCR duplicates are a major issue in targeted RNA sequencing for gene fusion detection, since – through PCR amplification – they turn unique RNA molecules into identical RNA molecules that cannot be distinguished from each other. This, in turn, results in the inability to confidently detect gene fusions. To overcome the issue of PCR duplicates, the QIAseq targeted RNAscan panels use digital sequencing by incorporating molecular barcodes into the starting RNA material before any amplification takes place – thereby preserving the uniqueness of the starting RNA molecules and overcoming the issues of not only PCR duplicates and amplification bias.

Procedure

The entire workflow of the QIAseq Targeted RNAscan Panels – from extracted RNA to sequencing-ready libraries – can be completed in 9 hours. Extracted RNA is converted to cDNA, targets are molecularly barcoded and enriched, and libraries are constructed. Sequencing files can be fed into the QIAseq pipeline – a cloud-based data analysis pipeline – which will filter, map and align reads, as well as count unique molecular barcodes associated with targeted regions and call fusions. This data can then be fed into QCI for interpretation.

Applications

The QIAseq Targeted RNAscan Panels can be used to detect known and novel gene fusions from a wide range of sample types for numerous applications.

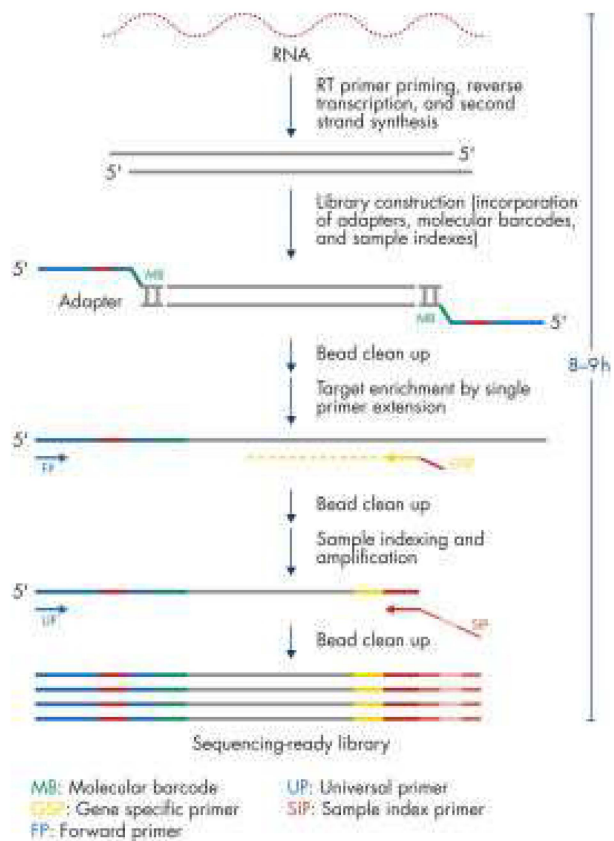
Sample types:

- FFPE
- Fresh or frozen tissue
- Cell lines

Applications:

- Detection of known gene fusions based on well-characterized breakpoints
- Discovery of novel gene fusions using exon- or gene-based primer designs

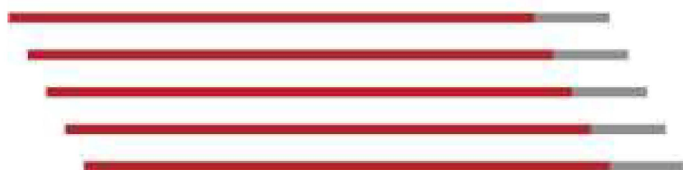
Supporting data and figures



Workflow

Isolated RNA, as low as 20 ng, is converted to cDNA. This is followed by the library construction step, in which IL-N7 adapters, molecular barcodes, and sample indexes are incorporated into DNA fragments generated in the previous step. Library fragments now serve as templates for target enrichment using single primer extension. In this step, targets are enriched using a single gene-specific primer and a universal forward primer. The final step is library amplification and sample indexing (for dual indexing) using the IL-S5 sample index primer and a universal primer.

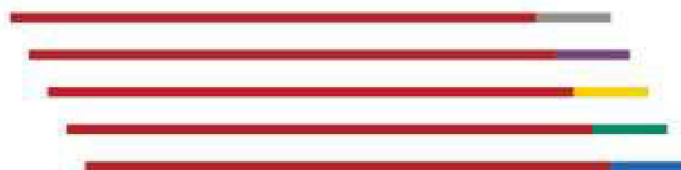
5 replicates of 1 transcript



All 5 reads have
the same MT

Counted as 1

5 unique transcripts of a gene



5 sequencing reads have
5 different MT

Counted as 5



Workflow

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Resources

Kit Handbooks (1)



QIAseq Targeted RNAscan Panels Handbook

EN▼ PDF (787KB)

Scientific Posters (1)



Explore the RNA Universe!

EN▼ PDF (1MB)

Safety Data Sheets (1)



Safety Data Sheets

EN▼

Brochures & Guides (1)

