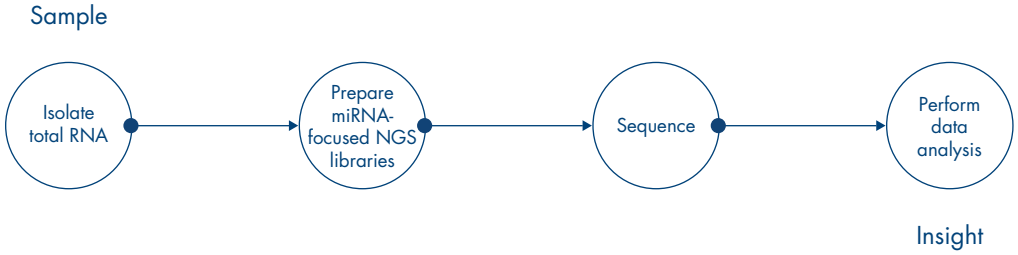
Product Profile

QIAseq™ miRNA Library Kit

Unparallelled miRNA-focused sequencing for accurate digital quantification

The QIAseq miRNA Library Kit provides:

- Proprietary sequencing technology that maximizes miRNA mapped reads by all but eliminating adapter dimers and other contaminating RNA. Multiplex more samples per sequencing run!
- No more gels! From sample to sequencer in hours with a painless bead-based workflow.
- Starting from 1 ng of total RNA: Go from Biofluids, low input samples, FFPE and any tissue.
- Unique Molecular Indices(UMI) enable accurate, digital quantification: Count the unique miRNA molecules in your sample, don't sample your reads!



The QIAseq miRNA Library Kit is a true Sample to Insight® solution for miRNA quantitation and novel miRNA discovery using next generation sequencing(NGS). The QIASeq miRNA kit is a completely gel-free kit, with enhanced miRNA yields to maximize mapped miRNA reads. Optimized reaction chemistry enables robust, miRNA-specific libraries while minimizing reaction biases and eliminating adapter dimers, delivering the most accurate quantification for true miRNA expression.

Free and unbiased: Free from gels, unbiased quantification with UMIs

Thus far, miRNA sequencing has been fraught with challenges. Library preparation is suboptimal, often relying on a tedious gel purification to isolate a miRNA-specific library. When sequenced, loss of reads occurs due to library prep artifacts (adapter dimers) and contaminating RNA (such as rRNA). QIAGEN technology eliminates most adapter dimers and contaminating RNAs are significantly reduced with enhanced and optimized chemistry. Collectively, the QIAseq miRNA Library Kit gives you a robust library, freed from gels, adapter dimers and unwanted RNA signals. Now, the total workflow can be accomplished in less than one day, rapidly taking you from sample to sequencer.

NGS power, qPCR accuracy

The power of NGS enables faster and more cost effective experiments as samples can be prepped and run without the need to pool samples or reduce sample numbers because of cost. qPCR experiments are limited in their targeting, and prep and experimentation can take weeks for a large project. Because most miRNA NGS experiments are focused on miRNA expression, the QIAseq miRNA Library Kit is the solution to bring qPCR-quality quantitation with NGS power. QIAseq miRNA enables you to generate a miRNA-specific library with substantially reduced side-products (Figure 1). Get to your data in a matter of days, even when performing a large project.

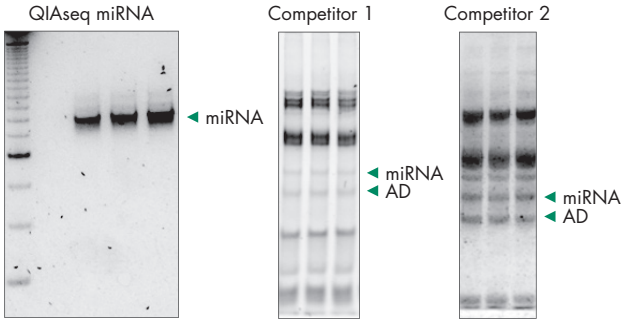


Figure 1. Adapter dimers (AD) and contaminating RNA steal your reads during miRNA sequencing experiments. While gels can be used to eliminate adapter dimers and contaminating RNA, there is still a possibility for high prevalence in sequencing reads even after gel excision. On the above left, QIAseq miRNA shows a robust miRNA library with no adapter dimers or contaminating RNA after the basic protocol that includes a bead-based purification. Compared to libraries generated with competitor kits (prior to a required tedious gel excision), the QIAseq-derived miRNA library is much more robust and devoid of adapter dimers and contaminating RNAs.

From sample to sequencer in under a day

The QIAseq miRNA Library kit not only improves sequencing performance, but gives you more time for other experiments. A huge issue with miRNA sequencing workflows has been the need for gel-based size selection. Prepping, running and then excising the correct band from the gel takes time and can add at least a day to time critical experiments. Using a bead-based selection, the amount of time needed is reduced to hours not days (Figure 2).

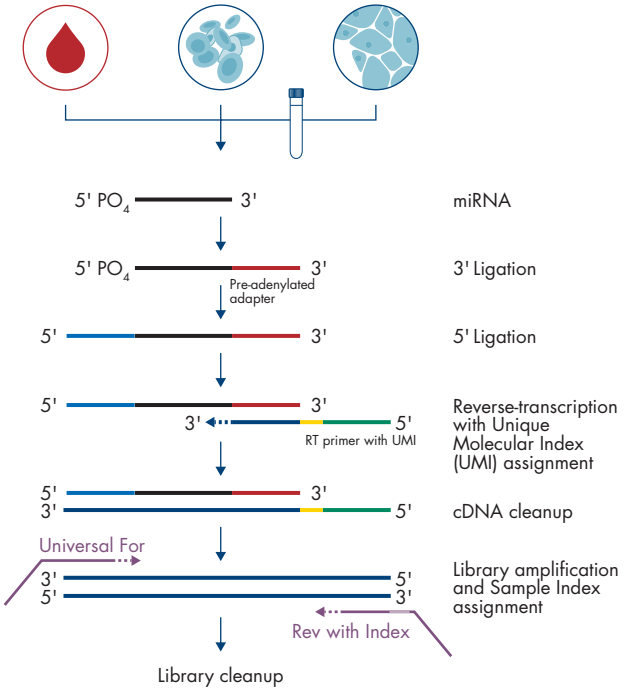


Figure 2. Under a day prep. Starting with total RNA isolated from any sample, the entire QIAseq miRNA Library Kit workflow can be completed in 7 hours. Unique Molecular Indices are attached during the RT reaction. Thus any library amplification and sequencing biases can be accounted for.

Start from the lowest input samples

Liquid biopsy research has shown that miRNA are key biomarkers for a host of conditions that can be measured through biofluids such as serum or plasma, urine and CSF among others. In addition, miRNA are found in exosomes and preserved well in FFPE because of their small, but powerful, size. QIASeq miRNA Library Kit is the solution for low sample amounts and large studies. Sample size minimums for miRNA can be restrictive, but QIAseq miRNA experiments can start with as little as 5ng of total RNA. This can unlock studies based on limited amounts of fluid, tissue or cells.

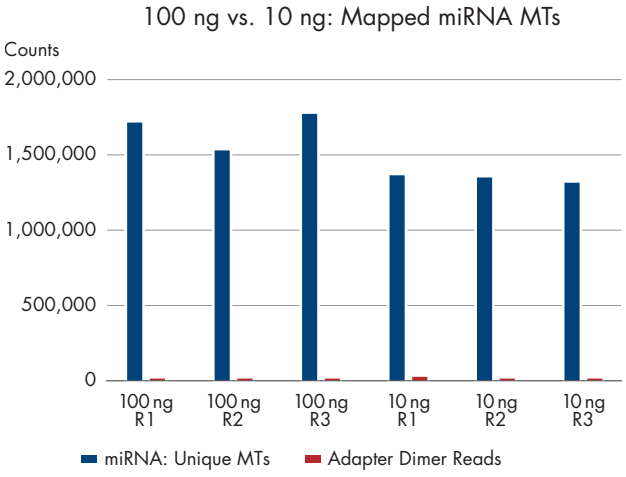


Figure 3 (Right): Optimized to map miRNA. By quantifying the unique molecular indecies, improve your quantification and differential expression data. UMIs are attached early in the workflow, ensuring that bias from library amplification and sequencing is minimized. In addition, adapter dimers account for only a small percentage of reads in comparison to mapped reads, even with the gel-free, bead-based purification.

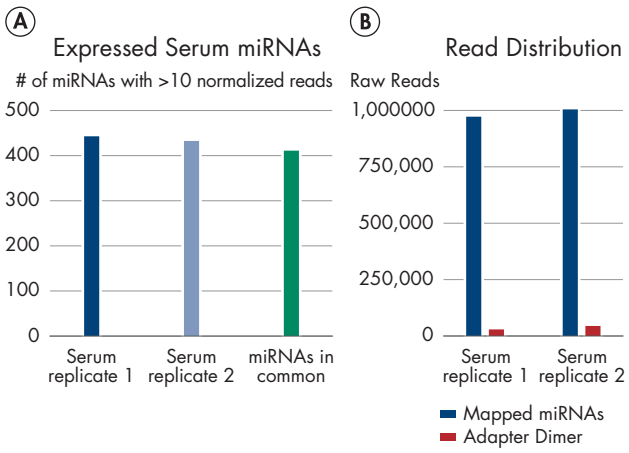


Figure 4 (Left): Enhanced yields from biofluids such as serum. Graph A shows robust detection of miRNA from serum samples. Graph B shows mapped reads compared to adapter dimers in serum samples. QIAseq miRNA still shows superior mapping of miRNAs even with limited samples.

Unbiased miRNA Quantification with UMIs

NGS offers tremendous power and scalability, with the caveat that library amplification and sequencing biases may occur. These biases can significantly affect quantitation numbers and requires quantification of raw reads versus the actual biological molecules. To combat this, the QIAseq miRNA NGS Kit attaches unique molecular indices to each miRNA molecule early in the prep process, significantly reducing bias and batching affects. The indexes are sequenced as part of the normal read; and then through the GeneGlobe Data Analysis Center, they are identified and counted, enabling accurate differential or absolute quantification (Figure 5).

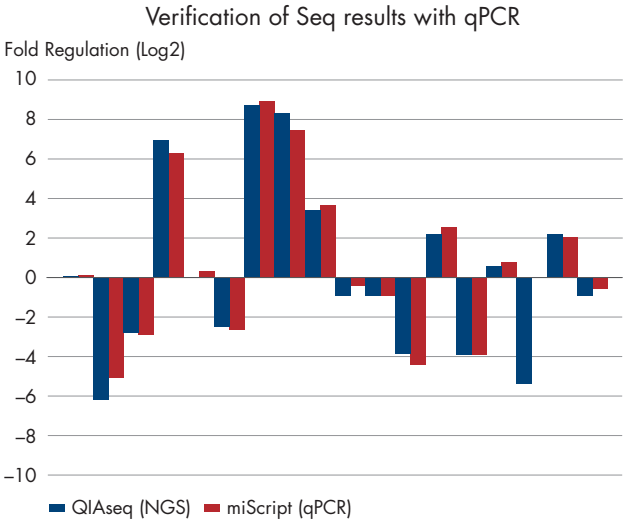


Figure 5 (above): QIAseq miRNA data results provide high correlation when validated with qPCR. By quantifying molecular tags, bias from PCR and clustering is reduced. This produces data capable of post sequencing validation with qPCR assays.

Any species, every miRNome

With the QIAseq miRNA Library Kit, the whole miRNome profile of any species can be discovered. Sequence information can be analyzed, both primary and secondary, through the Gene Globe Data Analysis Center. Starting with a fastq file, miRNA are mapped to all known species as well as identifying novel miRNA. QIAseq miRNA truly enables novel biomarker discovery from any species.

Ordering Information

Product	Contents	Cat. no.
QIAseq miRNA Library Kit (12)	Contains reagents and primers necessary for library generation of 12 samples on Illumina platforms	331502
QIAseq miRNA Library Kit (96)	Contains reagents and primers necessary for library generation of 96 samples on Illumina platforms	331505
QIAseq miRNA NGS 12 Index IL (12)	Sequencing adapters, primers and indexes compatible with Illumina platforms. 12 indexes for 12 samples	331592
QIAseq miRNA NGS 48 Index IL (96)	Sequencing adapters, primers and indexes compatible with Illumina platforms. Two 48 indexes for 96 samples	331595

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at **www.qiagen.com** or can be requested from QIAGEN Technical Services or your local distributor.