Product Profile

QIAseq® miRNA Library Kit

Build RNA-seq libraries for miRNA, piRNA and other16–40-mer RNAs

The QIAseq miRNA Library Kit provides:

- Maximum miRNA mapped reads using an LNA®-enhanced sequencing technology
- miRNA-specific libraries free from adapter dimers and contaminating RNA
- A gel-free workflow to go from sample to sequencer in hours
- Sample input flexibility – start from as little as 1 ng of input RNA and a variety of samples
- Unique molecular indices (UMIs) for accurate, digital quantification

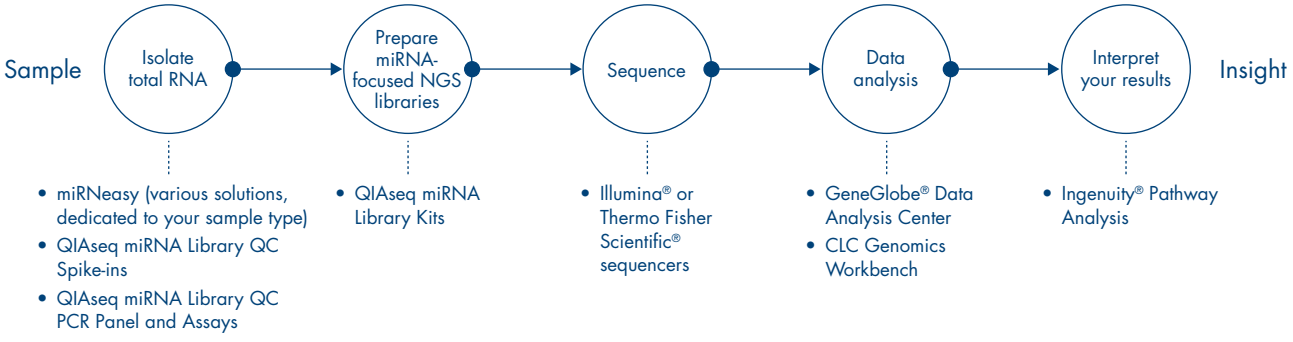
The QIAseq miRNA Library Kit is a true Sample to Insight® solution for miRNA quantitation and novel miRNA discovery using next-generation sequencing (NGS). Its gel-free workflow and enhanced miRNA yields maximize mapped miRNA reads. Optimized reaction chemistry enables robust, miRNA-specific libraries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

Free from gels and contaminants

miRNA sequencing is fraught with challenges. Library preparation is suboptimal, often relying on a tedious gel purification to isolate a miRNA-specific library. When sequenced, read loss occurs due to library prep artifacts (adapter dimers) and contaminating RNA (such as rRNA). The QIAseq miRNA Library Kit has a gel-free, bead-based workflow, and its enhanced and optimized chemistry eliminates most adapter dimers and contaminating RNA.

NGS power, qPCR accuracy

NGS enables faster and more cost-effective experiments, as samples can be prepared and run without sample pooling or reducing sample numbers. qPCR experiments, on the other hand, are limited in their targeting, and prep and experimentation can take weeks to complete. The QIAseq miRNA Library Kit combines qPCR-quality quantitation with NGS power, as most miRNA NGS experiments are focused on miRNA expression. The kit generates miRNA-specific libraries with substantially reduced artifacts (Figure 1). ▷



Get your data in a matter of days, even while handling large sample numbers.

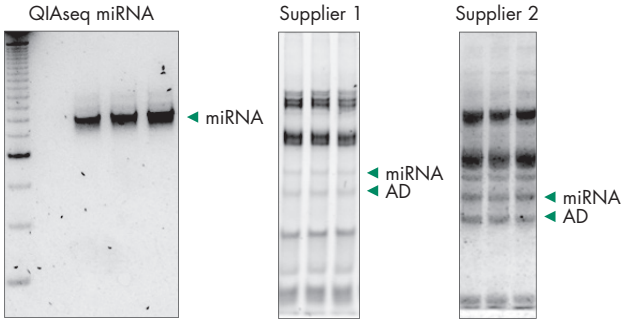


Figure 1. Adapter dimers (AD) and contaminating RNA steal your reads during miRNA sequencing experiments. Adapter dimers and contaminating RNA can remain in your sample even after gel excision. Compared to libraries generated with kits from other suppliers (before a tedious and mandatory, gel excision), the QIAseq-derived miRNA library (which relies on a gel-free, bead-based purification) 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 also saves your time. miRNA sequencing workflows usually involve a gel-based size selection step. Preparation, running and excising the correct band from the gel takes time and can add at least a day. The QIAseq miRNA Library Kit uses bead-based selection, which reduces the time needed for the entire workflow to just a few hours (Figure 2).

Start from the lowest input samples

miRNAs are key biomarkers for a host of conditions that can be measured through biofluids such as serum or plasma, urine and CSF among others. miRNAs are also found in exosomes and are preserved well in FFPE samples due to their small size. Sample size minimums for miRNA can be restrictive, but with the QIAseq Kit, you can start with as little as 1 ng of total RNA. This can unlock studies based on limited amounts of fluid, tissue or cells.

Dedicated quality control along the miRNA sequencing workflow is crucial for low-abundance RNA samples such as liquid biopsies and exosomes. QIAGEN's portfolio of qPCR assays and panels (complete with spike-ins) help assess sample quality using qPCR and NGS performance using spike-ins.

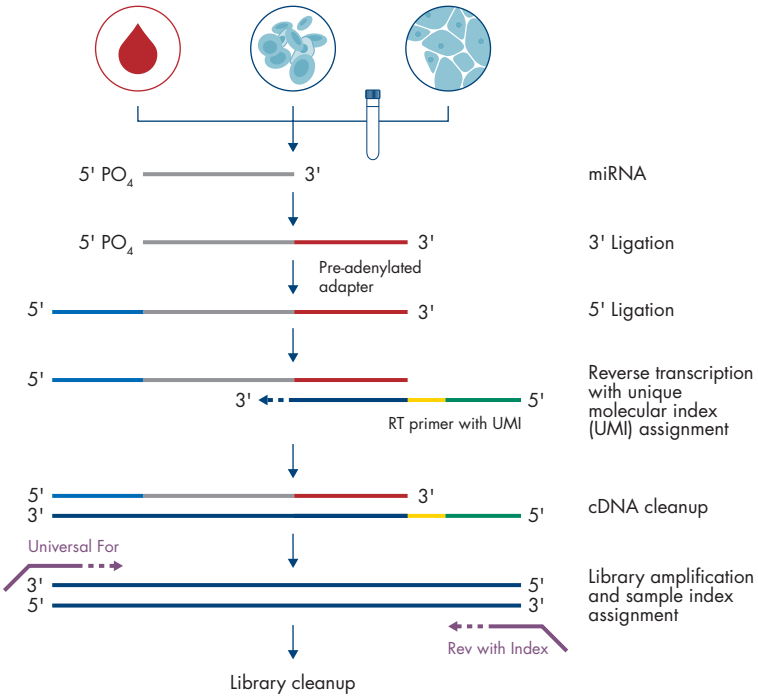


Figure 2. Library prep in less than a day. The entire QIAseq miRNA Library Kit workflow can be completed in 7 hours, starting with total RNA isolated from any sample. UMIs attached during the reverse-transcription reaction help minimize bias associated with library amplification and sequencing bias.

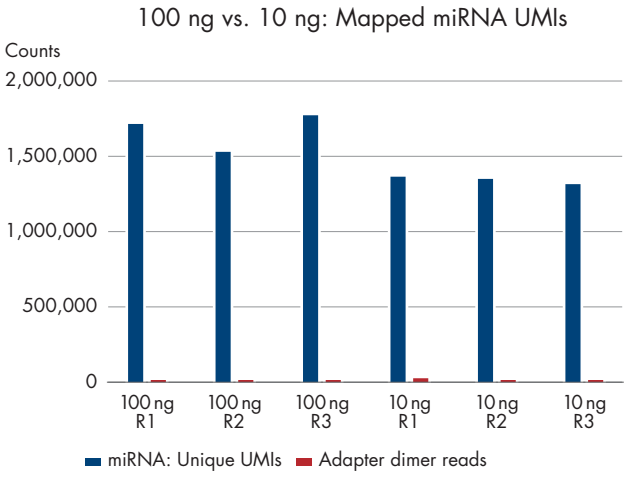


Figure 3. Optimized to map miRNA. Quantifying UMIs can improve quantification and differential expression data. UMIs are attached early in the workflow, ensuring that bias as a result of library amplification and sequencing is minimized. Due to the gel-free, bead-based purification, adapter dimers account for only a small percentage of reads.

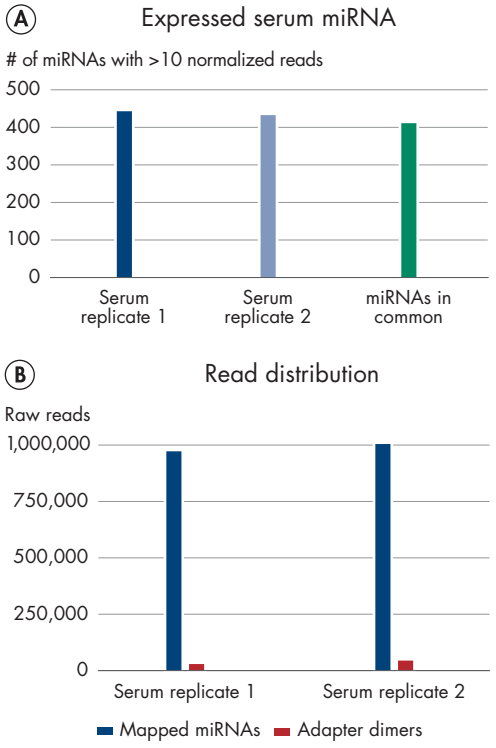


Figure 4. Enhanced yields from biofluids such as serum, and even with limited sample numbers. Graph A shows robust detection of miRNA from serum samples, and graph B shows mapped reads compared to adapter dimers in serum samples; both sets of data obtained using the QIAseq miRNA Library Kit.

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, which means reads do not reflect the actual amount of miRNA present in the sample. To combat this, the QIAseq miRNA Library Kit attaches unique molecular indices to each miRNA molecule early in the workflow, significantly reducing bias and batching effects. UMIs are sequenced as part of the normal read enabling accurate differential or absolute quantification (Figure 5).

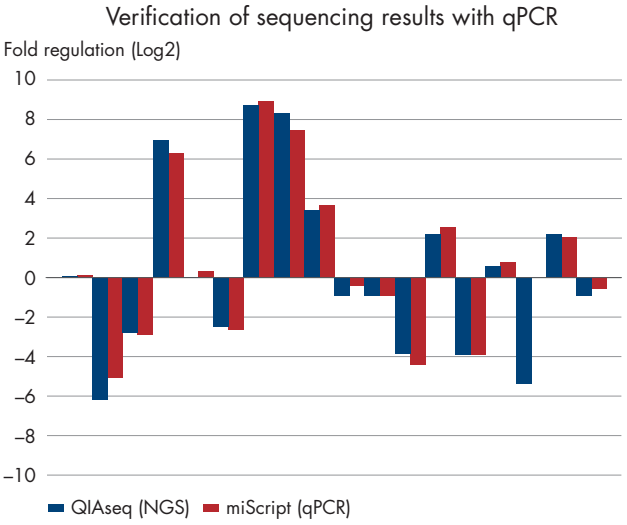


Figure 5. The QIAseq NGS data correlates with qPCR data. By quantifying UMIs, biases from PCR and clustering are reduced.

Any species, every miRNome

With the QIAseq miRNA Library Kit, the whole miRNome profile of any species can be discovered. Sequence information – both primary and secondary – can be analyzed using the GeneGlobe Data Analysis Center or the CLC Genomics Workbench. Starting with a FASTQ file, miRNA are mapped to all known species; novel miRNAs are identified by mapping reads to the entire miRBase database. The QIAseq miRNA Library Kit 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 indices compatible with Illumina platforms; 12 indices for 12 samples	331592
QIAseq miRNA NGS 48 Index IL (96)	Sequencing adapters, primers and indices compatible with Illumina platforms; two 48 indices for 96 samples	331595
QIAseq miRNA NGS 96 Index IL (96)	Sequencing adapters, primers and indices compatible with Illumina platforms; 96 indices for 96 samples (pre-plated in 96-well plate for ease of use)	331565
QIAseq miRNA NGS 48 Index TF (96)	Sequencing adapters, primers and indices compatible with Thermo Fisher platforms; two 48 indices for 96 samples	331585
QIAseq miRNA NGS 12 Index TF (12)	Sequencing adapters, primers and indices compatible with Thermo Fisher platforms; 12 indices for 12 samples	331582
QIAseq miRNA Library QC qPCR Panel Kit (48)	Includes 52 RNA spike-ins, 10x RT enzyme mix, 5x reaction buffer, 10x RT primer mix, UniSp6 RNA spike-in template, ready-to-use PCR Panel in 96- or 384-well plate(s), nuclease-free water	331541
QIAseq miRNA Library QC qPCR Assay Kit	Includes 52 RNA Spike-ins, 10x RT Enzyme Mix, 5x Reaction Buffer, 10x RT Primer Mix, UniSp6 RNA Spike-in template and qPCR assays for 103a-3p, 191-5p, UniSp6, 451a, 23a-3p, 30c-5p, UniSp-100 and UniSp-101	331551
QIAseq miRNA Library QC Spike-ins	52 QIAseq miRNA Library QC Spike-ins, sufficient for up to 500 samples; nuclease-free water	331535
CLC Genomics Workbench	A comprehensive package for the analysis and visualization of NGS data; user-friendly, high-performing software, scalable to enterprise solutions and easy upload to IPA	832000
Ingenuity Pathway Analysis	All-in-one software for scientists to understand the biological meaning of 'omics data; accesses a knowledge base of millions of biological relationships	830018 (1-year license)

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.