

Product Profile

QIAseq Ultralow Input Library Kit

For maximizing the quality of Illumina®-compatible NGS libraries from all DNA samples, including those with damaged or extremely limited quantities of DNA

During next-generation sequencing (NGS) library preparation it is essential to capture as much of a sample's unique genomic information as possible for sensitive variant calling and accurate sequence motif detection. However, this can prove challenging, especially when the starting material contains damaged or extremely limited quantities of DNA. Examples of NGS sample types with these issues are formalin-fixed, paraffin-embedded (FFPE) tissues, ancient DNA, ChIP DNA, and fine needle aspirate (FNA) and laser capture microdissection (LCM) tumor biopsies. Circulating cell-free DNA (cfDNA) from liquid biopsies can present the additional challenge of very low post-isolation concentrations. Applying standard library preparation chemistries to such damaged or limited DNA samples can give rise to quality problems that limit the utility of the data generated: low library yield, low conversion rates or a high percentage of reads derived from adapter dimer molecules.

The QIAseq Ultralow Input Library Kit incorporates new, ultra-efficient end-repair and ligation chemistries into a complete and streamlined solution capable of generating high-quality libraries from any DNA sample, even such damaged or limited types. The chemistry can handle a wide range of input, from 10 pg to 100 ng fragmented DNA. The libraries generated are suitable for multiple applications, including whole genome sequencing and hybrid capture. What's more, the possibility to automate the workflow means it is possible to run it quickly and with high confidence.

Benefits of the QIAseq Ultralow Input Library Kit:

- Flexible protocol for input amounts as low as 10 pg and as high as 100 ng
- Highly efficient end-repair and ligation to maximize performance from limited or damaged DNA
- Compatible with a wide range of sample types, including FFPE, ChIP, ancient and cell-free DNA
- Automation-friendly dual-barcoded adapter plate included in the 96-reaction kit

High-quality library generation from the lowest possible DNA input amounts

Most common solutions for NGS library prep still require inputs of 10–100 ng DNA to generate a high-quality library, especially for the large genomes of most mammalian and plant species (Figure 1). The chemistry of such products also exhibits a drop-off in performance when the input is below 1 ng DNA, with library yields and conversion rates dropping rapidly while the percentage of adapter dimer reads rises dramatically.

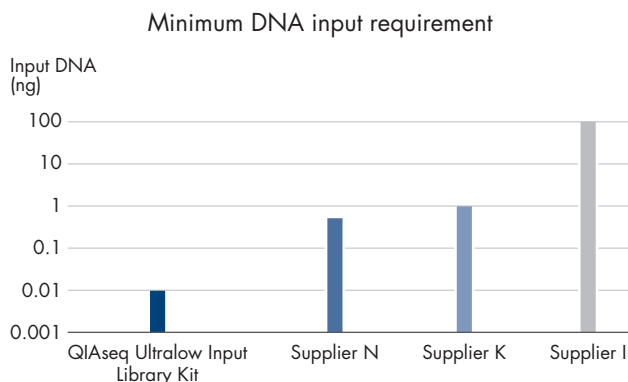


Figure 1. Minimum DNA input requirements for a selection of currently available library preparation products. The 10 pg minimum input for QIAseq Ultralow Input Library Kit is at least 50-fold lower than that for any other leading library preparation chemistry.

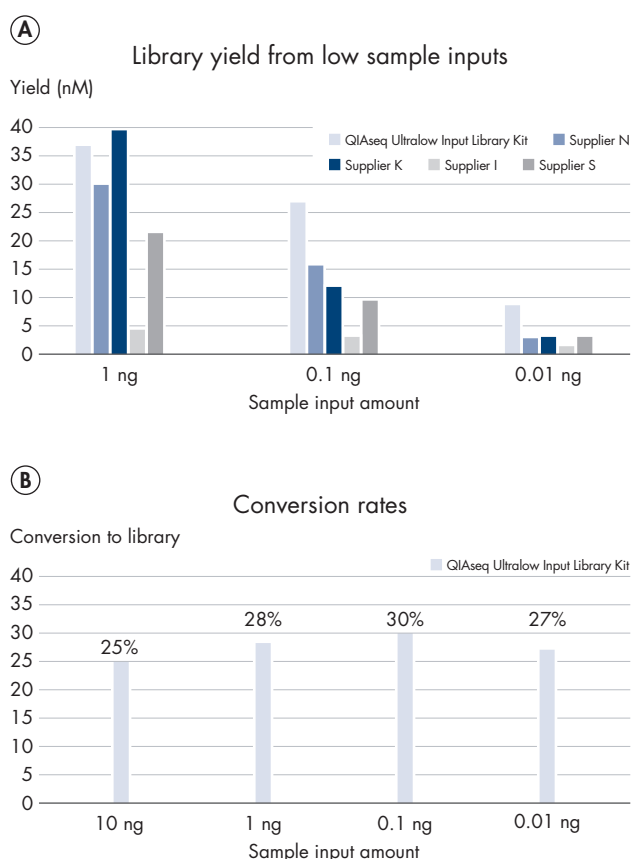


Figure 2. Higher yields and consistent conversion rates across a range of sample inputs and dilutions. **A** Library yields from low sample inputs with a selection of currently available library preparation products. The QIAseq Ultralow Input Library Kit gives higher total library yields than kits from other suppliers with sample inputs below 1 ng DNA. **B** The QIAseq Ultralow Input Library Kit chemistry offers a consistent conversion rate of genomic information to adapter-ligated library molecules across a 1000-fold dilution range, from 10 pg to 10 ng DNA.

The novel, highly efficient enzymes and protocols of the QIAseq Ultralow Input Library Kit eliminate these issues, enabling library generation from even sub-nanogram samples, while also retaining the flexibility to process samples with up to 100 ng input DNA (Figure 2A). A consistently high conversion rate is obtained across this wide range of DNA inputs (Figure 2B). High-volume end-repair and adapter ligation reactions are also suitable for samples such as circulating cfDNA that may be too dilute for success with other methods.

In addition, when compared to kits from other suppliers, the QIAseq Ultralow Input Library Kit generates libraries with a significantly lower rate of reads mapped to adapter dimers, even at the lowest input amount of 10–100 pg DNA (Figure 3).

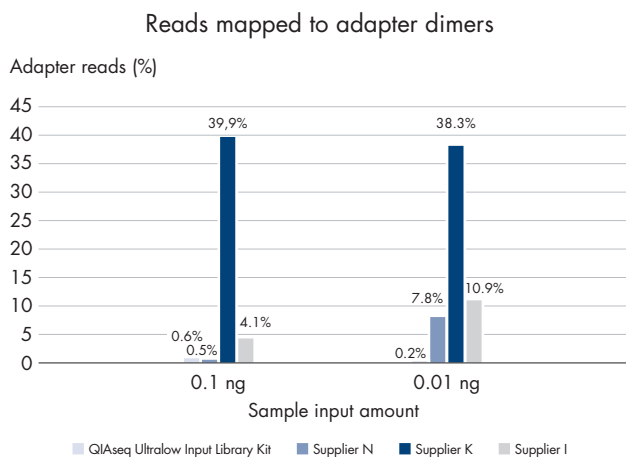
Robust results for a wide range of sequencing applications

The QIAseq Ultralow Input Library Kit was designed with the most challenging samples in mind: those where the starting material is limited or diluted, such as circulating cfDNA and DNA from FNA and LCM biopsies, or damaged, such as FFPE DNA, ancient DNA samples and CHIP DNA. It has been demonstrated to generate high-quality libraries free from adapter dimers with as little as 100 pg circulating cfDNA or FFPE DNA with consistently high yields and conversion rates (Figure 4).

Flexible workflow for low- and high-throughput library prep

Designed to start from enzymatically, chemically, mechanically or naturally fragmented double-stranded DNA, the QIAseq Ultralow Input Library Kit uses an optimized end-polishing reaction and the novel Ultralow Input Ligation formulation along with QIAGEN's proprietary HiFi PCR Master Mix (Figure 5) to maximize the conversion rate of sample DNA into an NGS-ready library while evenly amplifying both high and low G/C genomic regions.

The 96-reaction kit includes dual-barcoded adapters that are compatible with all Illumina sequencers. They come in a foil-sealed 96-well plate for ease of automation and reduced risk of cross-contamination. While adapters are not included in the 12-reaction size kit, two sets of 12-plex adapters, each with a single six-nucleotide barcode, can be ordered separately (cat. no. 180985 and 180986).



Enable new genomic insights from limited or damaged DNA samples

Genomic research requires simple but robust solutions that enable genomic insights at scale from the full range of DNA samples, from 100 ng of high-quality genomic DNA to previously inaccessible samples, such as DNA from fine needle aspirates (FNA), laser capture microdissection (LCM), liquid biopsies and archival FFPE DNA. The QIAseq Ultralow Input Library Kit meets the requirements of this wide range of sample types, making it the definitive library preparation solution to yield high-quality, Illumina sequencer-ready libraries from even the most challenging samples.

Figure 3. Rate of read mapping to adapter dimers. The QIAseq Ultralow Input Library Kit gives lower adapter dimer read mapping than other commercially available kits.

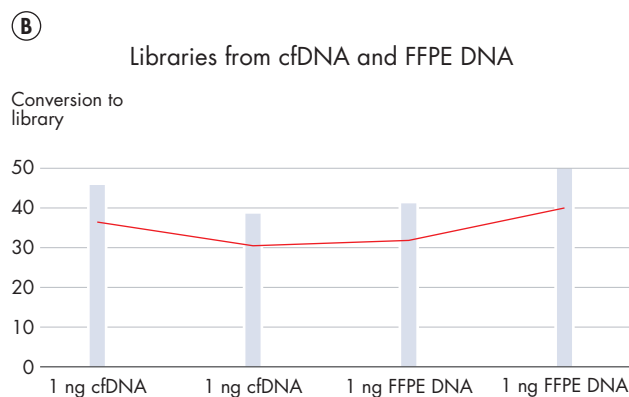
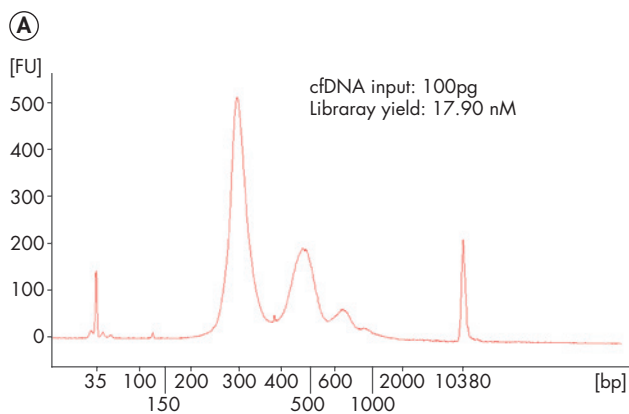


Figure 4. The QIAseq Ultralow Input Library Kit generates appropriate-quality libraries from samples of circulating cfDNA and FFPE DNA. **A** Library free from adapter dimers generated from 100 pg circulating cfDNA. **B** Consistently high yield and conversion rate generated from 1 ng samples of circulating cfDNA or FFPE DNA.

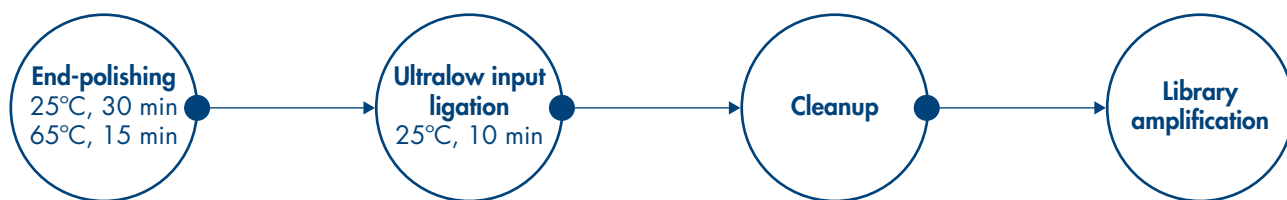


Figure 5. The QIAseq Ultralow Input Library Kit workflow

Ordering Information

Product	Contents	Cat. no.
QIAseq Ultralow Input Library Kit (96)	For 96 reactions: Buffers and reagents for Ultralow Input End Polishing, Ultralow Input Ligation, and HiFi library amplification. Includes 96-plex Adapter Plate with individually pierceable foil sealed wells. For use with Illumina instruments.	180495
QIAseq Ultralow Input Library Kit (12)	For 12 reactions: Buffers and reagents for Ultralow Input End Polishing, Ultralow Input Ligation, and HiFi library amplification. 12-plex adapters sold separately. For use with Illumina instruments.	180492

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.

For more information on this versatile library prep, visit www.qiagen.com/QIAseq-ULI

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