

sparQ DNA Frag & Library Prep Kit

Integrated enzymatic fragmentation and library prep with unrivaled speed and performance

FEATURES & BENEFITS:

- High quality libraries in 2.5 hours from 1 ng – 1 µg of input DNA
- Tunable and reproducible fragmentation size range
- Simple, convenient 2-step workflow with minimal hands-on time
- Novel chemistry and high-fidelity amplification minimizing bias
- Superior sequence coverage uniformity and low duplication rate

DESCRIPTION:

The sparQ DNA Frag & Library Prep Kit is optimized for enzymatic fragmentation of DNA and streamlined construction of high quality libraries for sequencing on Illumina® NGS platforms. The simple, convenient 2-step workflow can be completed in 2.5 hours with minimal hands-on time and accommodates DNA input amounts from 1 ng to 1 µg.

Quantabio's engineered DNA frag and polishing enzymes work in concert to generate fragment sizes that are tunable and reproducible based on reaction time. The DNA fragmentation and polishing reactions are combined in a single step to generate 5'-phosphorylated and 3'-dA-tailed fragments. This minimizes over fragmentation while greatly simplifies the library prep workflow. Subsequent high efficiency ligation of adapters is performed in the same tube without an intervening cleanup step. If library amplification is required, the HiFi PCR Master Mix and Primer Mix ensure even amplification with minimal bias.

This kit is compatible with single-indexed, or dual-indexed Y-shaped adapters routinely used in library construction.

Streamlined workflow (1 ng – 1 µg input DNA)

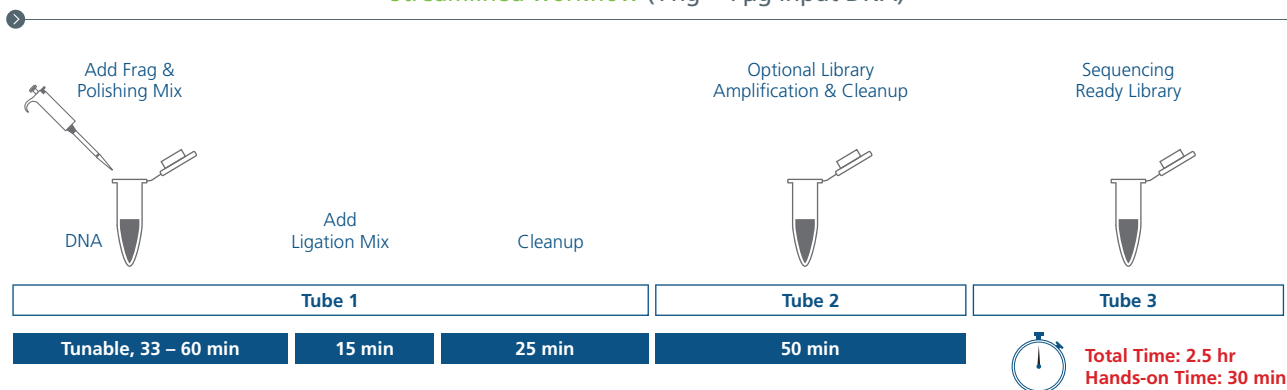


Figure 1 The streamlined workflow utilizes a proprietary enzyme mix that combines fragmentation and DNA polishing in a single step to simplify library construction. High efficiency adapter ligation and cleanup are performed in the same tube, followed by an optional amplification step using HiFi PCR Master Mix and Primer Mix.

Tunable & reproducible fragmentation

The sparQ DNA Frag & Library Prep kit is designed to produce consistent and reproducible fragments that are tunable to application-specific sizes. The fragmentation profile closely resembles Covaris mechanical shearing. Flexible input DNA amounts ranging from 1 ng – 1 µg can be accommodated. The single-tube enzyme mix fragments DNA and then automatically proceeds to the DNA polishing reaction, thus minimizing potential over fragmentation. Guidelines of incubation time and expected size based on input amount are provided below.

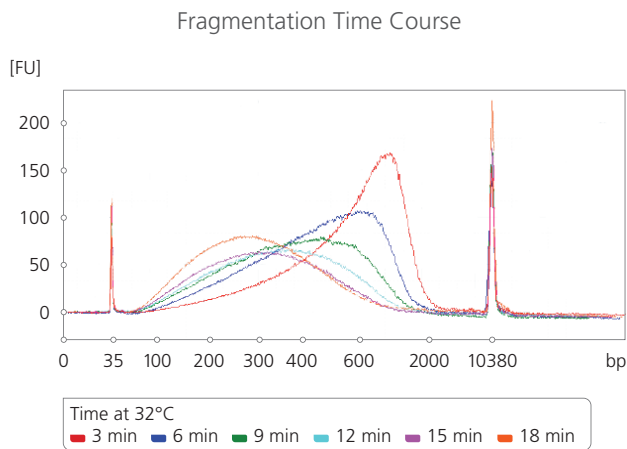


Figure 2 sparQ DNA Frag & Library Prep Kit is tunable to the desired fragment size. 100 ng Human gDNA was subjected to fragmentation with a series of incubation time points (3 – 18 min). After fragmentation, DNA samples were purified and then visualized using an Agilent High Sensitivity DNA Kit.

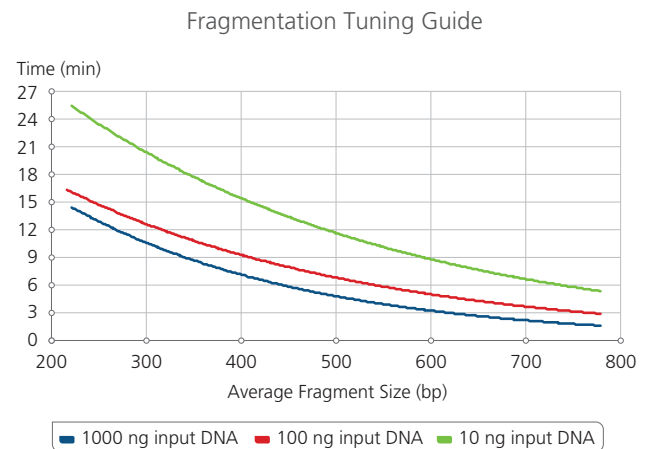


Figure 3 Guidelines for tuning fragmentation size. If input DNA falls between values displayed on the graph, an estimate can be used for optimizing fragmentation times.

Superior library prep efficiency and yields

The novel and optimized chemistry used in the sparQ DNA Frag & Library Prep Kit coupled with proprietary enzyme mix lead to better sensitivity and higher library yields. PCR-free workflows are enabled for 100 ng of input DNA. For applications requiring amplification, the HiFi PCR Master Mix and Primer Mix allow researchers to achieve target concentration with very few cycles thereby reducing PCR-derived artifacts. Ultimately, precious samples can be saved for additional applications when necessary.

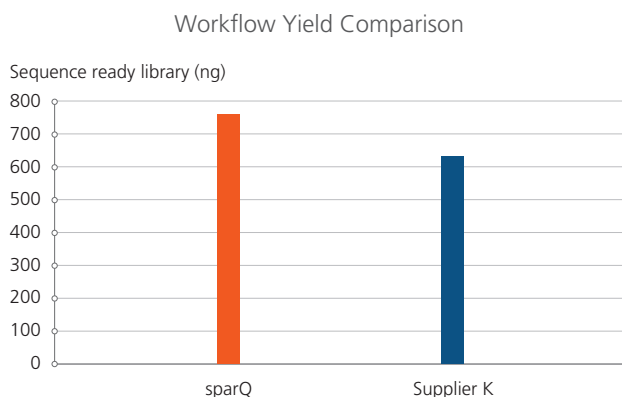


Figure 4 sparQ DNA Frag & Library Prep Kit shows significantly higher NGS library preparation efficiency. Libraries with 300 bp average DNA fragments from 100 ng of gDNA Coriell NA12878 were prepared using sparQ DNA Frag & Library Prep Kit and a commercial kit from Supplier K. Manufacturers' manuals were carefully followed. Amplified libraries (5 PCR cycles) were quantified by Qubit fluorometric quantitation method.

Uniform coverage across a wide GC-spectrum

The sparQ chemistry enables high quality library construction with even coverage across a board GC-spectrum including challenging GC- and AT-rich regions. Reproducible and uniform genome coverage is achieved independent of input DNA amounts, comparable to coverage obtained by mechanical shearing workflows.

The sparQ DNA Frag & Library Prep Kit ensures similar total coverage depth for the majority of genomic targets, thus reducing the need for additional sequencing, resulting in less sequencing per sample and lower total sequencing costs.

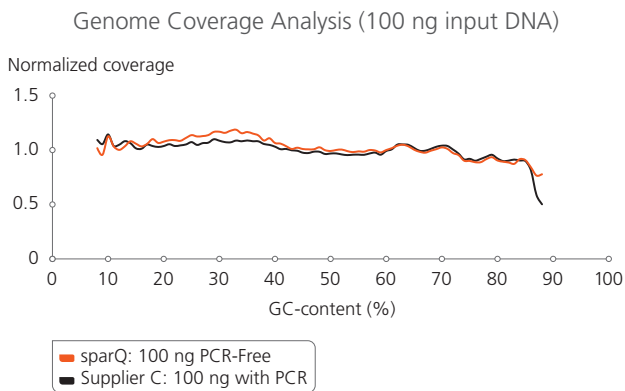
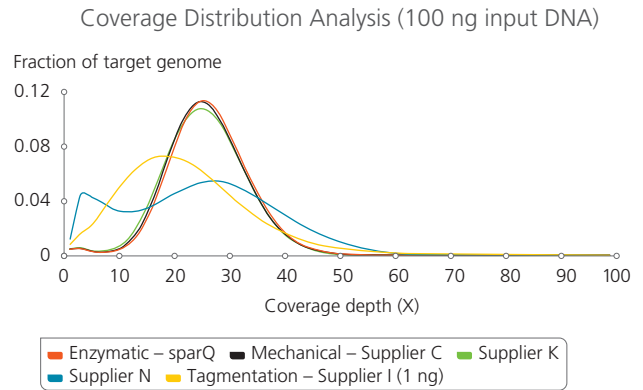
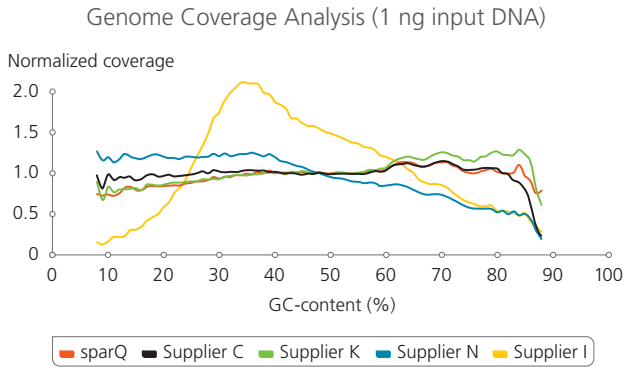


Figure 5 Library prepared using sparQ DNA Frag & Library Prep Kit resulted in uniform coverage across the wide range of GC-content. Libraries were prepared using different DNA fragmentation and library preparation kits with 1 ng or 100 ng of microbial gDNA followed by sequencing on Illumina MiSeq. 2 million reads from each tested library were down-sampled and analyzed. Coverage uniformity against GC-content resulting from different DNA fragmentation and library preparation kits were compared by plotting normalized coverage for a wide GC-content. Libraries prepared using PCR-free workflow of sparQ DNA Frag & Library Prep Kit with 100 ng of microbial genomic DNA shows similar high performance as a typical amplified library prepared by mechanical shearing method.

High quality sequencing metrics with low duplication rates

Excellent sequencing metrics – high mapping percentage and low duplication artifacts – are achieved with the sparQ DNA Frag & Library Prep Kit, ensuring the greatest return on sequencing investments.

	Fragmentation	1 ng input DNA		100 ng input DNA	
		Mapped reads	Duplication	Mapped reads	Duplication
sparQ	Enzymatic	91.9%	0.07%	94.5%	0.04%
Supplier K	Enzymatic	92.4%	0.08%	93.5%	0.03%
Supplier I	Tagmentation	93.8%	0.28%	–	–
Supplier C	Mechanical	93.0%	0.09%	93.6%	0.03%

sparQ DNA Frag & Library Prep Kit generates high quality DNA libraries with minimal duplication artifacts. Libraries were prepared with 1 ng and 100 ng of microbial genomic DNA, amplified for 12 and 6 cycles respectively, and subsequently sequenced on Illumina MiSeq. Each library was down-sampled to 2 million reads (150 bp paired-end reads) and aligned to a reference genome with only unique alignments reported.

ORDER INFO

Product Name	Quantabio Catalog Number	Size
sparQ DNA Frag & Library Prep Kit - 24	95194-024	24 rxns
sparQ DNA Frag & Library Prep Kit - 96	95194-096	96 rxns
sparQ DNA Library Prep Kit - 24	95191-024	24 rxns
sparQ DNA Library Prep Kit - 96	95191-096	96 rxns
Related Products		
sparQ HiFi PCR Master Mix	95192-050	50 rxns (1 x 1.25 ml)
sparQ HiFi PCR Master Mix	95192-250	250 rxns (5 x 1.25 ml)
sparQ PureMag Beads - 5 ml	95196-005	5 ml
sparQ PureMag Beads - 60 ml	95196-060	60 ml
sparQ PureMag Beads - 450 ml	95196-450	450 ml
sparQ Fast Library Quant Kit (for Q) - 50 R	95197-050	50 rxns
sparQ Fast Library Quant Kit (for Q) - 500 R	95197-500	500 rxns
PerfeCta® NGS Quantification Kit - Illumina - 500 R	95154-500	500 x 20 µl rxns
PerfeCta NGS Quantification Kit - Illumina, ROX - 500 R	95155-500	500 x 20 µl rxns
PerfeCta NGS Quantification Kit - Illumina, Low ROX - 500 R	95156-500	500 x 20 µl rxns

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