

sparQ DNA Library Prep Kit

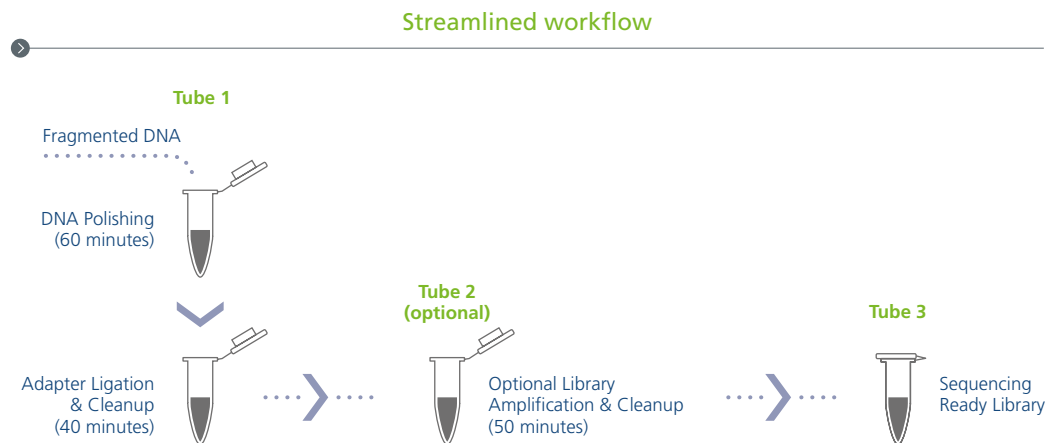
Prepare for sequencing success with the highest quality library

FEATURES & BENEFITS:

- Simplified 2-step protocol speeds sample prep to under 3 hours and minimizes sample loss from transfer steps
- Increased library yields enable the construction of low input DNA sample from 250 pg
- Minimized bias improves coverage across difficult to sequence regions ensuring optimal results and reduced coverage gaps
- PCR-free workflows enabled from 100 ng input DNA
- Improved overall sequencing workflow economics

DESCRIPTION:

An optimized kit for the rapid construction of DNA libraries from fragmented double-stranded DNA for sequencing on Illumina® NGS platforms. DNA polishing reactions are combined in a single step to convert fragmented DNA into 5'-phosphorylated and 3'-dA-tailed DNA fragments suitable for direct ligation of sequencing adapters without the need for an intervening cleanup saving valuable time and bead purification expense. The HiFi PCR Master Mix and Primer Mix allows for the optional, unbiased amplification of fragments with appropriate adapters ligated to both ends. The kit is compatible with input amounts from 250 pg to 1 µg DNA and multiple sample types.

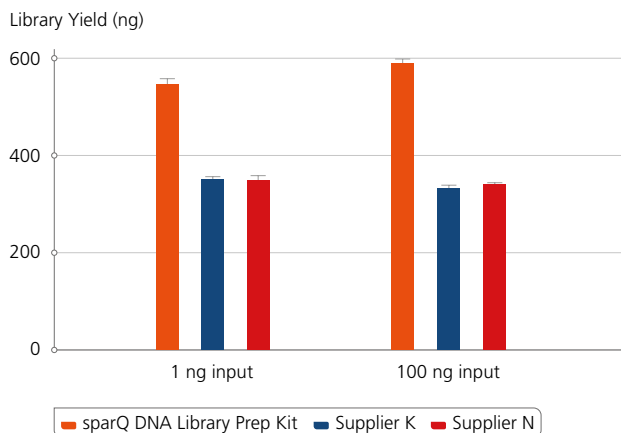


The streamlined workflow can be completed in under 3 hours with minimal hands-on time. A single tube is used for DNA polishing, ligation, and cleanup. A second tube is used for workflows requiring PCR amplification and a final tube receives the sequencing-ready library.

Maximize library yields and increase sequenceable molecules

Critical first steps in library preparation depends heavily on the efficiency and sensitivity of the enzymes involved in DNA polishing and adapter ligation steps. The sparQ enzymes have been engineered, optimized, and selected for superior performance. The proprietary cocktail of enzymes is formulated to generate the highest yield and quality of adapter-ligated libraries over a broad range of input DNA down to as little as 250 pg enabling successful library construction for challenging samples and PCR-free workflows where input DNA is ≥ 100 ng.

Library Yield Analysis

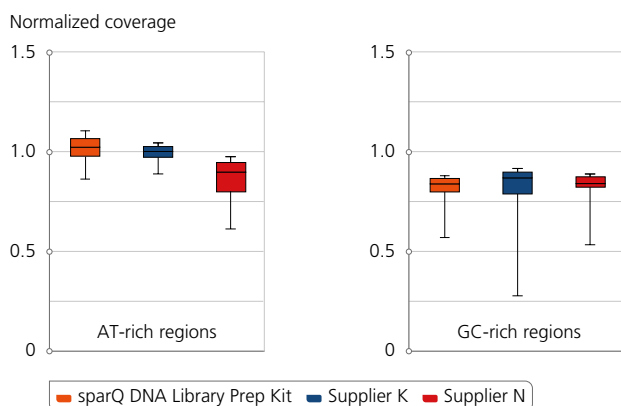


1.1 sparQ DNA Library Prep Kit produces high quality libraries from a broad range of DNA inputs with significantly higher yields. Libraries were prepared with Covaris-sheared DNA (250 bp average size) using kit manufacturers' instructions. Amplified libraries (6 amplification cycles for 100 ng input DNA and 13 amplification cycles for 1 ng input DNA) were quantified with Qubit fluorometric quantitation method.

Minimize bias and gaps in sample genome coverage

The highly efficient library prep reduces the bias resulting in the superior quality you need and expect, to minimize coverage gaps especially for challenging regions like GC- and AT-rich sequences. For applications requiring amplification, the high fidelity master mix is formulated to increase library yield reducing the number of cycles required to create a sequence-ready library thereby reducing additional PCR-derived artifacts.

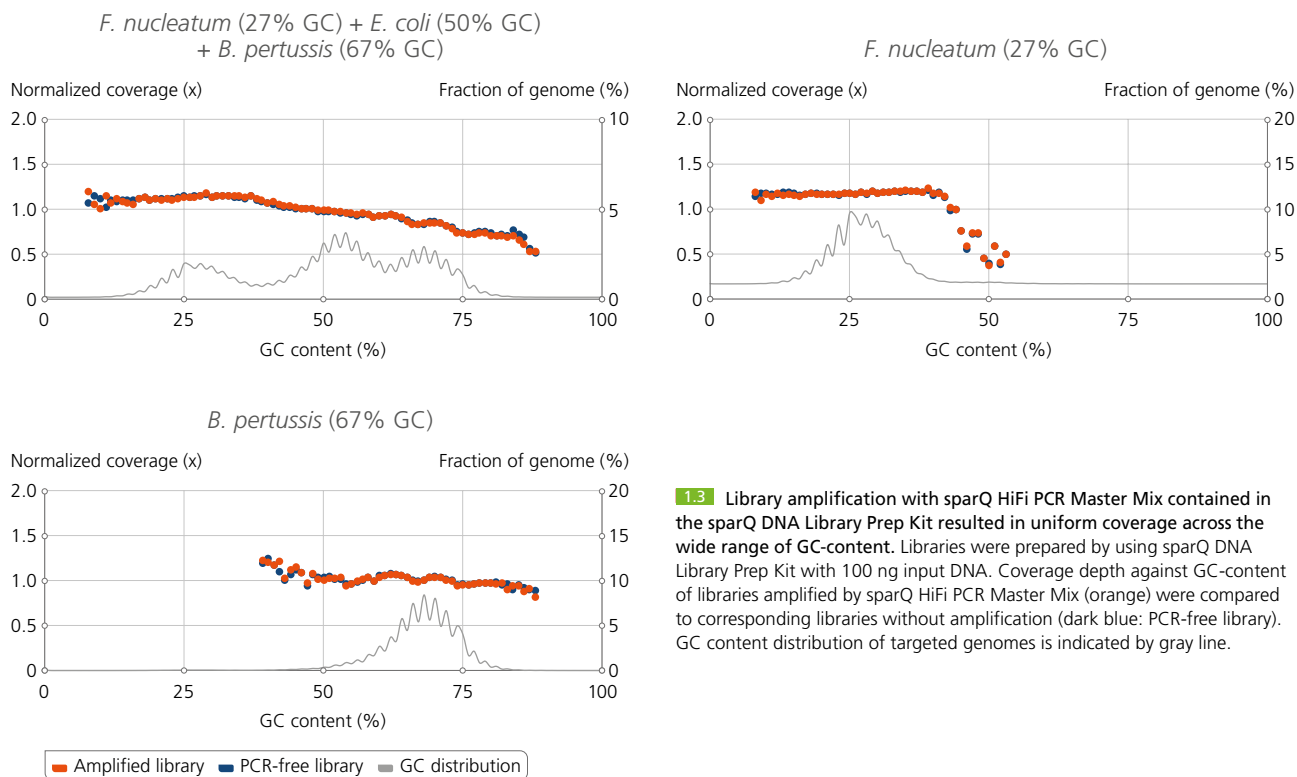
Coverage across Challenging Regions



1.2 Amplified libraries were prepared from 100 ng of microbial genomic DNA and subsequently sequenced on Illumina MiSeq. 2 million reads from each tested library were down-sampled and analyzed. Coverage uniformity for different library preparation kits were compared by plotting normalized coverage for both extreme AT-rich regions (8%-20% GC-content) and GC-rich regions (75%-88% GC-content).

Create amplified libraries with PCR-free results

Comparison of library preparation performed with sparQ DNA Library Prep Kit matches PCR-free workflows. Low amplification bias enables better coverage uniformity resulting in greater sequencing depth or multiplexing capabilities.



1.3 Library amplification with sparQ HiFi PCR Master Mix contained in the sparQ DNA Library Prep Kit resulted in uniform coverage across the wide range of GC-content. Libraries were prepared by using sparQ DNA Library Prep Kit with 100 ng input DNA. Coverage depth against GC-content of libraries amplified by sparQ HiFi PCR Master Mix (orange) were compared to corresponding libraries without amplification (dark blue: PCR-free library). GC content distribution of targeted genomes is indicated by gray line.

Improve Sequencing Results and Economics

High library conversion efficiency maintains a comprehensive view of your sample genome. Whether using an amplified or PCR-free workflow, sparQ DNA library prep produces industry leading sequencing results as determined by the high number of reads mapping back to the reference genome with minimal duplication rates. Outcomes optimize your sequencing results and workflow economics.

	Library Amplification	1 ng input DNA		100 ng input DNA	
		Mapped reads	Duplication	Mapped reads	Duplication
sparQ	with Amplification	94.3%	0.07%	95.5%	0.04%
Supplier K		95.0%	0.09%	95.6%	0.04%
Supplier N		94.9%	0.07%	95.4%	0.03%
sparQ	PCR-Free			95.6%	0.03%
Supplier K				95.3%	0.02%
Supplier N				95.1%	0.02%

sparQ DNA Library Prep Kit generates high quality DNA libraries with minimal duplication rates. Libraries were prepared with 1 ng and 100 ng of microbial genomic DNA 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 Library Prep Kit - 24	95191-024	24 rxns
sparQ DNA Library Prep Kit - 96	95191-096	96 rxns
sparQ Adapter Barcode Set A	95193-A96	12 single index barcodes for 96 rxns
sparQ Adapter Barcode Set B	95193-B96	12 single index barcodes for 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)
PerfeCtra® NGS Quantification Kit - Illumina - 500 R	95154-500	500 x 20 µl rxns
PerfeCtra NGS Quantification Kit - Illumina, ROX - 500 R	95155-500	500 x 20 µl rxns
PerfeCtra NGS Quantification Kit - Illumina, Low ROX - 500 R	95156-500	500 x 20 µl rxns

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