

sparQ NGS Product Guide

- Streamlined workflows
- Higher yields
- Superior coverage
- Wide input range



sparQ RNA-Seq HMR Kit

Ultra FAST RNA library prep with integrated rRNA & globin depletion

FEATURES & BENEFITS:

- High quality directional RNA library prep in 4.5 hours
- Simple workflow with 3 reaction tubes, 9 steps and 10 components
- Increased yield by up to 3x*
- Improved results for samples with limited quantity and/or poor quality RNA

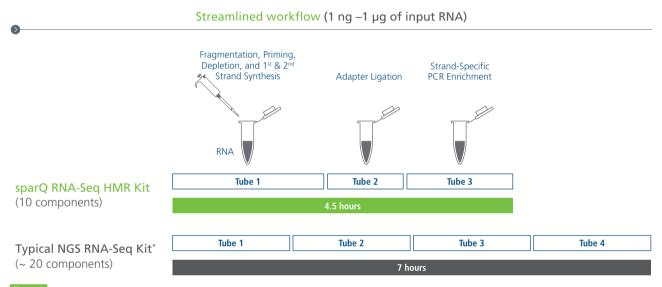
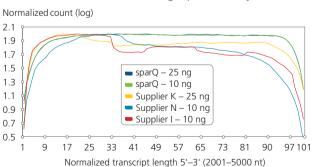


Figure 1 sparQ RNA-Seq HMR Kit workflow is simplified to 3 reaction tubes, 9 steps and 10 components. rRNA and globin mRNA removal is integrated with the RNA fragmentation and priming step, enabling faster time to result, less hands-on time and fewer pipetting steps.



Better Overall Coverage Uniformity

Figure 2 Uniform 3' transcript coverage. sparQ RNA-Seq HMR Kit was uniquely able to retain uniform 3' coverage for FFPE RNA, a feature that will help correctly identify full-length genes in low quality samples. For UHR RNA, all RNA-seq kits showed comparable uniformity.

* compared to typical NGS RNA-seq kits with ribo-globin depletion

Increased Unique Transcript Identification

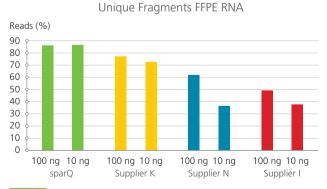


Figure 3 Comparison of Unique Fragments. The sparQ RNA-Seq HMR Kit consistently demonstrated higher rates of unique fragments indicating the highest library diversity regardless of RNA input quantity and sample type, which will enable more accurate quantification of low-level or rare transcripts and better transcript quantification.

FFPE RNA, Limiting Input Quantity

sparQ mRNA-Seq Kit

Ultra-sensitive mRNA library prep workflow with efficient poly(A) capture

FEATURES & BENEFITS:

- Highly sensitive mRNA detection with input as low as 5 ng of total RNA
- Reproducible transcript profiling
- High quality directional RNA library prep with streamlined workflow of 4.75 hours
- Efficient isolation of mRNA allowing detection of most coding genes

DESCRIPTION:

sparQ mRNA-Seq Kit enables efficient preparation of stranded mRNA-seq libraries for Illumina[®] NGS platforms. The streamlined workflow reduces hands-on time and allows sample to sequencing in a single day. High-quality, reliable mRNA-seq libraries are delivered with consistency and reduced bias from as little as 5 ng and up to 1 µg of total RNA.

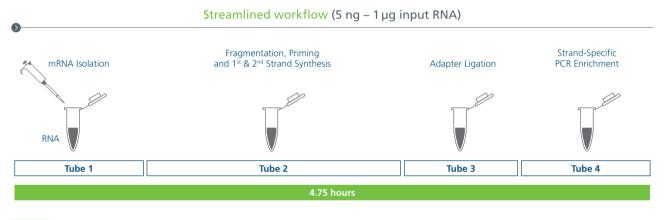
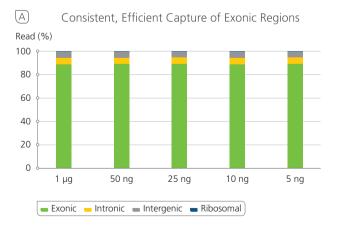
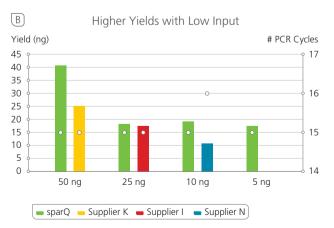


Figure 4 sparQ mRNA-Seq Kit workflow delivers a simple workflow with a rapid protocol that allows for sample to sequencing in a single day.





Quantabio

Figure 5 sparQ mRNA-Seq Kit is highly sensitive. High quality libraries are generated across broad range of input amounts, down to 5 ng. sparQ mRNA-Seq libraries were compared against suggested minimum input amounts of other suppliers. A Consistently high proportion of protein coding reads and low rRNA reads (<1%) was achieved for efficient poly(A) mRNA isolation. B Higher library yield was observed with consistent number of PCR cycles regardless of input total RNA amount.

DNA Library Preparation

sparQ DNA Frag & Library Prep Kit

Rapid DNA library prep with integrated enzymatic fragmentation

1 DNA Frag and Polishing

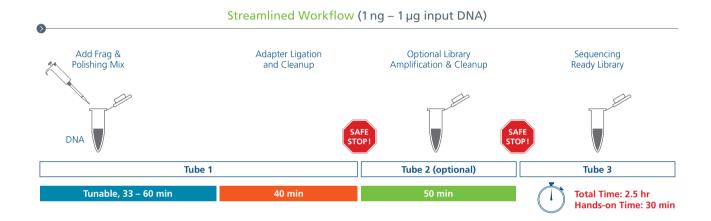
- One-step, tunable fragmentation size ranges for varying inputs
- Minimal fragmentation bias (comparable to mechanical shearing)

2 Adapter Ligation

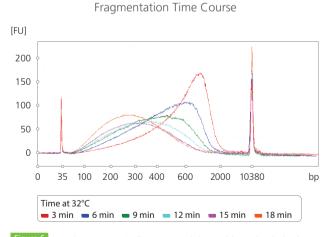
- Streamlined workflow-proceed in same tube
- High efficiency ligation validated with various adapter types

3 PCR Amplification (optional)

- Superior HiFi amplification efficiency and uniform coverage
- Simple PCR master mix format



Tunable & Reproducible Fragmentation



Maximize Coverage Uniformity

Genome Coverage Analysis (1 ng input DNA)

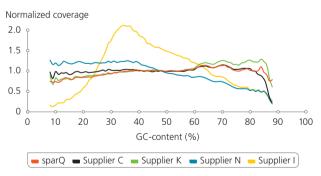


Figure 6 sparQ DNA Frag & Library Prep Kit is tunable to the desired fragment size. 100 ng human gDNA was subjected to fragmentation with a series of incubation time points (3 – 18 min). After fragmentation, DNA samples were purified and then visualized using an Agilent High Sensitivity DNA Kit.

Figure 7 Library prepared using sparQ DNA Frag & Library Prep Kit resulted in uniform coverage across a wide range of GC-content. Libraries were prepared using different DNA fragmentation and library preparation kits with 1 ng of microbial genomic DNA followed by sequencing on Illumina MiSeq.

sparQ DNA Library Prep Kit

Streamlined, versatile single-tube solution for high quality library prep

1 DNA Polishing

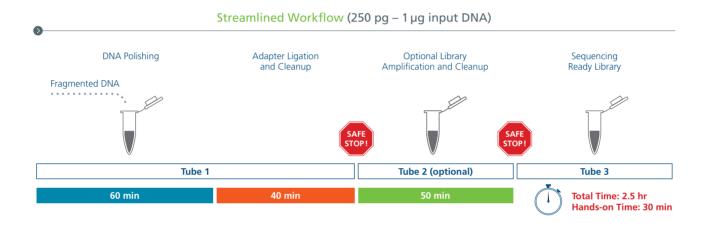
- Combined DNA end-repair and dA-tailing
- Wide DNA input range
- Input sheared DNA, FFPE DNA, cfDNA or amplicons

2 Adapter Ligation

- Streamlined workflow-proceed in same tube
- High efficiency ligation validated with various adapter types

3 PCR Amplification (optional)

- Superior HiFi amplification efficiency and uniform coverage
- Simple PCR master mix format



Superior Coverage Uniformity

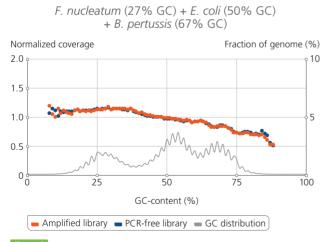


Figure 8 Consistent coverage over a broad range of GC-content with sparQ HiFi PCR Master Mix. Libraries amplified by sparQ HiFi PCR Master Mix (red) provide uniform GC coverage, similar to corresponding libraries without PCR (blue). Consistent Library Prep Efficiency

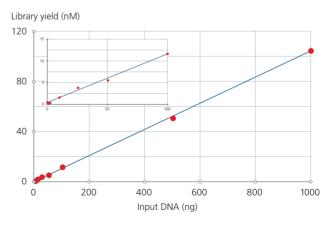


Figure 9 sparQ DNA Library Prep Kit resulted in consistent library prep efficiency across a broad range of sample inputs. Libraries were prepared from Covaris-sheared human genomic DNA with sparQ DNA Library Prep Kit without library amplification. Preamplified libraries were quantified with qPCR-based method.

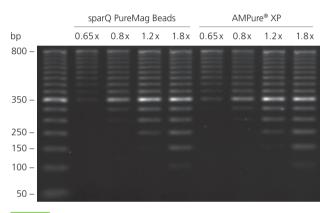


sparQ PureMag Beads

Fast, reliable nucleic acid purification & size selection for NGS workflows

FEATURES AND BENEFITS:

- High recovery of DNA and RNA fragments greater than 100 bp
- Efficient removal of unwanted reaction byproducts
- Consistent single or double-sided size selection



Efficient Recovery of DNA

Figure 10 sparQ PureMag Beads show equivalent performance to AMPure XP for DNA purification. 50 bp DNA ladder was purified with sparQ PureMag Beads and AMPure XP at different beads to DNA ratios and analyzed on 2% agarose gel.

- Seamless integration into existing NGS workflows and automation friendly
- Can be stored at 4°C for up to 2 years and RT for 6 months

Equivalent Size Selection to SPRIselect®

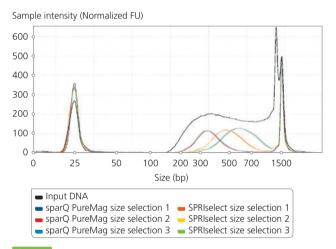


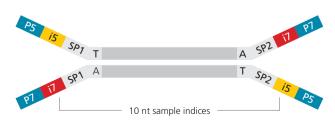
Figure 11 sparQ PureMag Beads show equivalent performance to SPRIselect for size selection. Fragmented DNA was size selected using different beadsto-sample ratios to select for fragment ranges: (1) 250-500 bp, (2) 450-600 bp or (3) 500-800 bp, using either sparQ PureMag Beads or SPRIselect. Peaks at 25 and 1500 bp represent low and high MW markers.

sparQ UDI Adapters

FEATURES AND BENEFITS:

- Flexible pooling: multiplex up to 96 samples per sequencing run
- Improved performance prevents index hopping and enhances demultiplexing accuracy
- Multiple applications including whole genome sequencing (with amplification or PCR-free), target enrichment, whole transcriptome sequencing and many more

Dual-Indexed Barcoded Adapters for Multiplexing up to 96 Samples on Illumina Instruments



repliQa HiFi ToughMix

High-fidelity, high-efficiency library amplification

FEATURES AND BENEFITS:

- Fidelity of >90x wild type Taq
- Tough Tested tolerant to a wide range of PCR inhibitors
- Extreme Speed up to 3x faster PCR results with extension rates as fast as 1 kb/ sec*
- Superior Sensitivity higher yields from lower inputs as little as 2 pg
- Long Range amplify +24 kb gDNA, +40 kb DNA
- * For fragments less than 1 kb in size.

Low bias for AT and GC rich Genomes

Sum of (LCI enzyme-LCI PCRfree) / LCI PCRfree for each of 4 test genomes

4 genome score

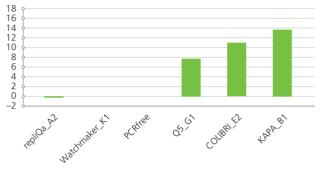


Figure 12 Multi-genome average low coverage index (fraction of genome covered at < 50 % mean coverage) ranking taking the sum of the LCI (low coverage index) values for all four genomes compared to that obtained from PCR free data. Four genomes analyzed covered both AT- and GC-rich genomes as well as more balanced GC content species: *B. pertussis, E. coli, C. dificile,* and *P. falciparum.* Figure modified from Identifying the best PCR enzyme for library amplification in NGS, Quail *et al.*

sparQ Universal Library Quant Kit

Fastest qPCR-based library quantification in 40 minutes

FEATURES & BENEFITS:

- 50% shorter run time than typical cycling protocols
- Accurate and reliable quantification of Illumina[®] NGS libraries
- Exceptional quantitative sensitivity and reproducibility
- Stabilized, ready-to-use DNA standards for convenient use

Equivalent Performance to Kapa Library Quantification Kit

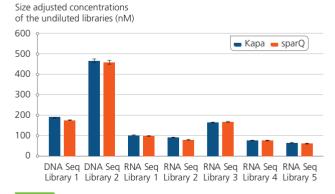
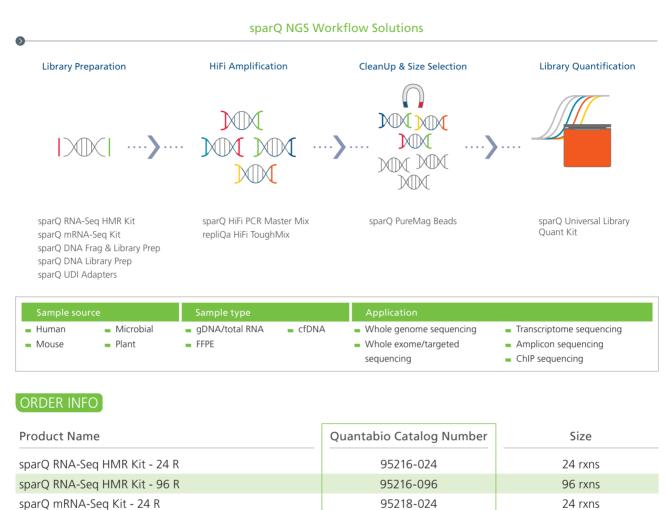


Figure 13 Diverse libraries quantified using both sparQ Universal Library Quant Kit and Kapa[™] Library Quantification Kit were highly comparable. Seven libraries (2 DNA, 5 RNA) were prepared and each quantified according to each manufacturer's cycling protocol.



Ignite a sparQ in your NGS workflows



95218-096

95194-024

95194-096

95191-024 95191-096

95200-025

95200-100

952005100

95192-050

95192-250

95196-005

95196-060

95196-450

95210-100

95210-500

95211-096

MK-SF-0043 REV 04 sparQ NGS Product Guide 0125



96 rxns

24 rxns

96 rxns

24 rxns

96 rxns

25 rxns

100 rxns

500 rxns

50 rxns (1 x 1.25 ml)

250 rxns (5 x 1.25 ml)

5 ml

60 ml

450 ml

100 rxns

500 rxns

1-96 UDI Adapters

sparQ mRNA-Seg Kit - 96 R

sparQ DNA Frag & Library Prep Kit - 24

sparQ DNA Frag & Library Prep Kit - 96

sparQ DNA Library Prep Kit - 24

sparQ DNA Library Prep Kit - 96

repliQa HiFi ToughMix - 25

repliQa HiFi ToughMix - 100

repliQa HiFi ToughMix - 500

sparQ HiFi PCR Master Mix

sparQ HiFi PCR Master Mix sparQ PureMag Beads - 5 ml

sparQ PureMag Beads - 60 ml

sparQ PureMag Beads - 450 ml

sparQ UDI Adapters (1-96)

sparQ Universal Library Quant Kit - 100 R

sparQ Universal Library Quant Kit - 500 R