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 5x*
- Improved results for samples with limited quantity and/or poor quality RNA

DESCRIPTION:

sparQ RNA-Seq HMR Kit simultaneously depletes rRNA and globin mRNA while generating stranded RNA-seq libraries for Illumina® NGS platforms in 4.5 hours. In a single step and tube, RNA fragmentation and depletion of abundant ribosomal and globin transcripts (human, mouse, and rat) are integrated. The proprietary, highly optimized enzymes and streamlined workflow generate high quality, directional transcriptome NGS libraries from either intact or degraded RNA samples, with key improvements for low input and FFPE samples.

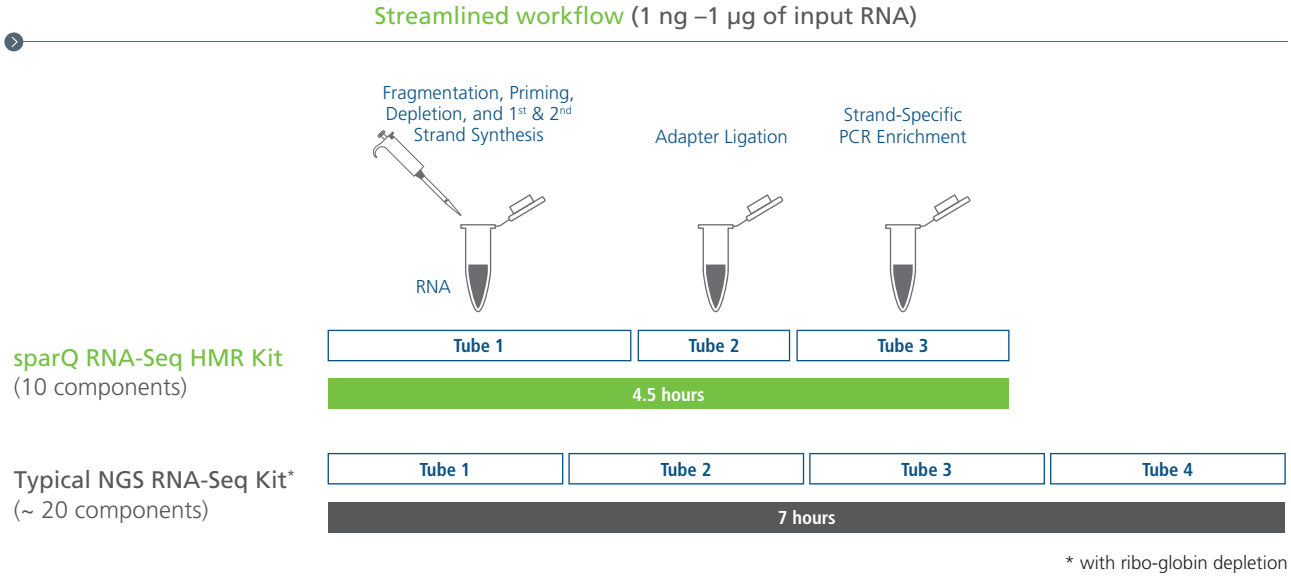

Figure 1 **sparQ RNA-Seq HMR Kit workflow is simplified to 3 reaction tubes, 9 steps and 10 components.** rRNA and globin mRNA removal is integrated with the RNA fragmentation and priming step, enabling faster time to result, less hands-on time and fewer pipetting steps.

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

Efficient removal of rRNA and globin mRNA

sparQ RNA-Seq HMR Kit generates high quality libraries that efficiently capture transcripts of interest by retaining high percentage of coding regions while leaving minimal amount of rRNA and globin mRNA. Consistent results were observed regardless of sample quantity and quality. The simplified workflow of the kit features seamless integration of ribo-globin depletion, RNA fragmentation and priming into a single step for less handling of RNA samples.

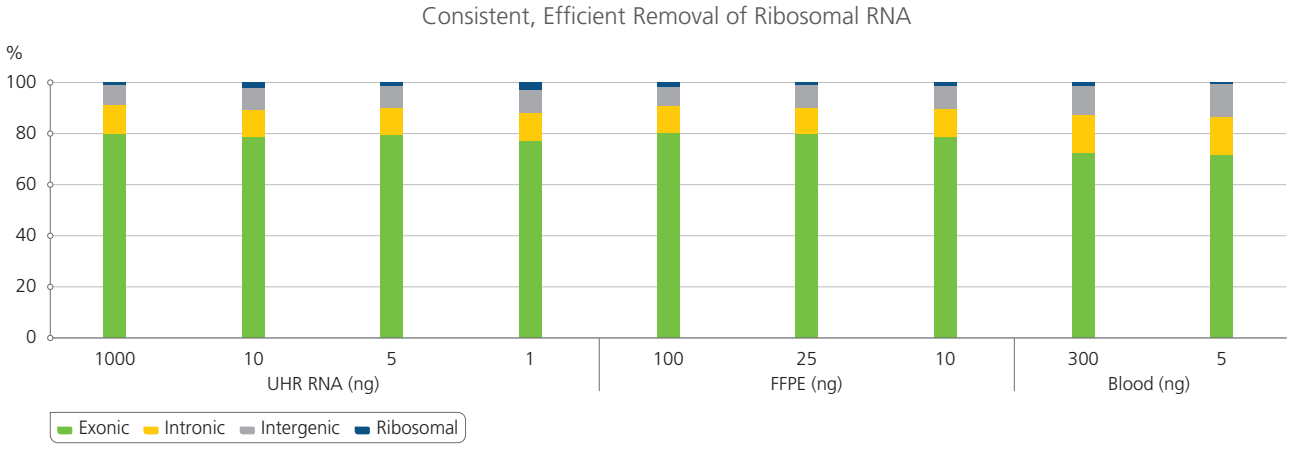

Figure 2 **High proportion of reads mapped to protein coding regions.** Libraries were prepared from various sample types at varying input amounts, then sequenced. Reads were mapped to the human transcriptome RNA biotypes. Libraries prepared with sparQ RNA-Seq HMR Kit showed the highest proportion of protein coding reads, when compared with other supplier kits, and very low rRNA reads (0–5%).

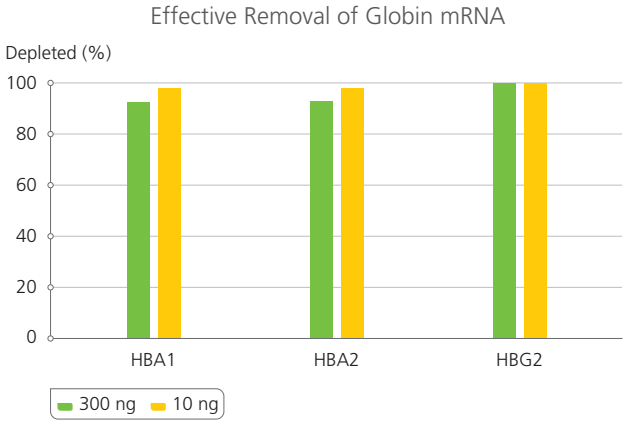

Figure 3 **Consistent, high percentage of globin mRNA depletion.** sparQ RNA-Seq HMR libraries were generated with 300 ng and 10 ng input of blood samples according to the standard protocol, then compared against a library generated without globin mRNA depletion at 300 ng input. Globin mRNA HBA1, HBA2 and HBG2 levels were measured using TPM (transcripts per million) count calculated with CLC Genomic Workbench 20.0.4. Abundant globin mRNA was efficiently depleted, allowing for data focused on mRNA and other RNA biotypes of high interest.

Improved results for low input and degraded samples

sparQ RNA-Seq HMR Kit prepares libraries that consistently show high yield, high uniformity and increased unique transcript identification from either intact or degraded samples. The proprietary, highly optimized enzymes support key improvements for low input and degraded samples.

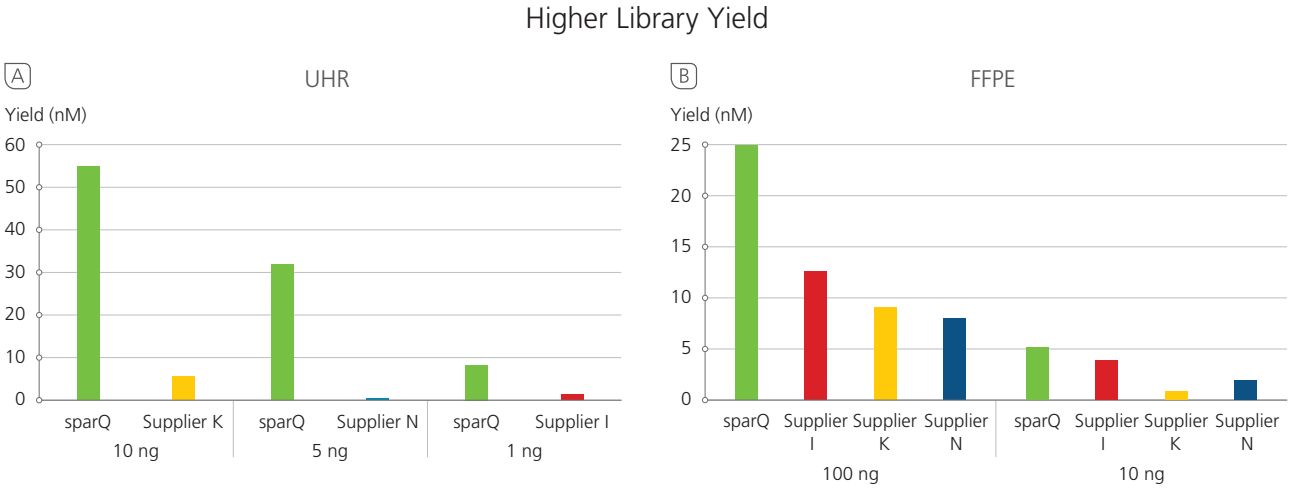

Figure 4 **Higher library yield observed with sparQ RNA-Seq HMR Kit for low input and degraded input RNA.** Comparable library yields were obtained with each kit using 1 µg of Universal Human Reference (UHR) RNA. For low input quantities of UHR RNA, the lowest recommended RNA input amount for each kit was used. A The sparQ RNA-Seq HMR Kit generated consistently higher yields at low UHR RNA inputs and B higher yields with low quality FFPE RNA (RIN 3.5) for both input amounts.

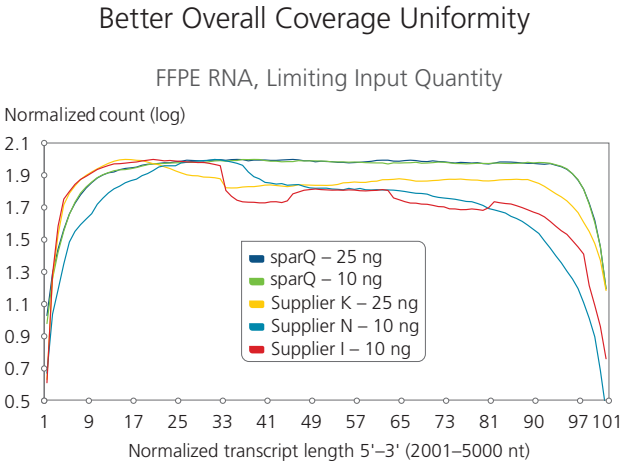

Figure 5 **Uniform 3' transcript coverage.** sparQ RNA-Seq HMR Kit was uniquely able to retain uniform 3' coverage for FFPE RNA, a feature that will help correctly identify full-length genes in low quality samples. For UHR RNA, all RNA-seq kits showed comparable uniformity.

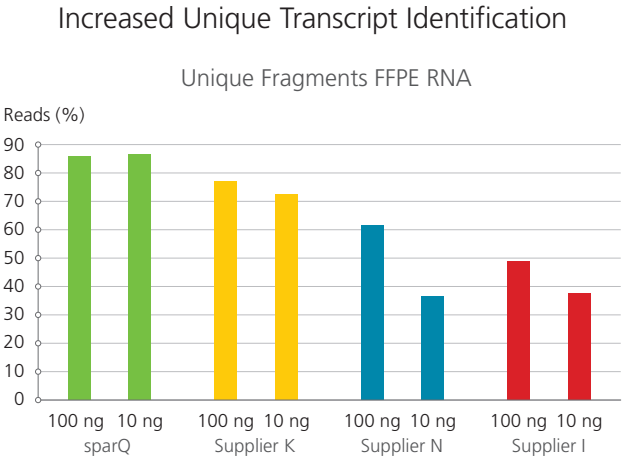

Figure 6 **Comparison of Unique Fragments.** The sparQ RNA-Seq HMR Kit consistently demonstrated higher rates of unique fragments indicating the highest library diversity regardless of RNA input quantity and sample type, which will enable more accurate quantification of low-level or rare transcripts and better transcript quantification.

Excellent data concordance

Reproducible results are achieved between high and low input amounts for various sample types.

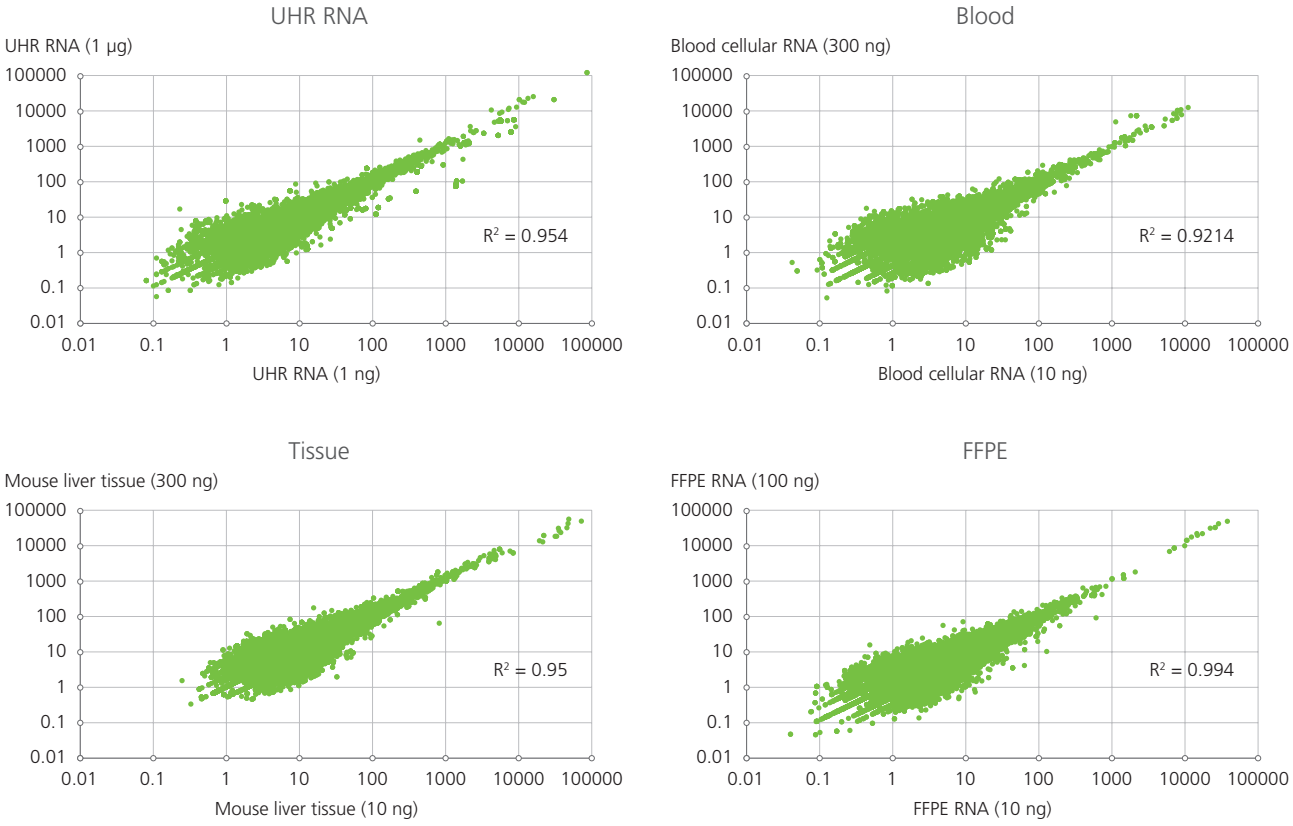

Figure 7 **High data concordance between high vs. low RNA input amounts of various sample types was achieved.** The libraries were sequenced on the Illumina® NextSeq550 instrument at 2 x 100 bp. The sequenced reads were analyzed by aligning the reads to the reference genome of each sample accordingly using the CLC Genomics Workbench 20.0.4 software (Qiagen®).

ORDER INFO

Product Name	Quantabio Catalog Number	Size
sparQ RNA-Seq HMR Kit - 24 R	95216-024	24 rxns
sparQ RNA-Seq HMR Kit - 96 R	95216-096	96 rxns
Related Products		
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 UDI Adapters (1-96)	95211-096	1–96
sparQ Universal Library Quant Kit - 100 R	95210-100	100 rxns
sparQ Universal Library Quant Kit - 500 R	95210-500	500 rxns
Extracta Plus RNA - 10 R	95214-010	10 rxns
Extracta Plus RNA - 50 R	95214-050	50 rxns