Quantabio

Product Information	
sparQ RNA-Seq HMR Kit	
Part Number	95216-008
Number of Reactions	8 Reactions
Storage Temperature	-25°C to -15°C
Lot Number	77502060
Expiration Date	2024-07-28

Component Part Numbers:

1126260 Frag Prime RG Depletion Mix
1126263 1st Strand Enzyme Mix
1126266 2nd Strand Buffer
1126269 2nd Strand Enzyme Mix
1126272 Rapid Ligation Buffer (5X)
1126275 T4 DNA Ligase
1126278 HiFi Plus Master Mix (2X)
1126281 Primer Mix
1129848 Bead Booster
1126284 UDI Dilution Buffer

Product Specifications	
95216	
Assay	Library Functional Assay
Specification	Functional

Quality Control Analysis and Specifications:

Library Prep Functional Assay: Quality of the sparQ RNA-Seq HMR Kit is tested functionally by preparation of a cDNA library from high quality reference total RNA. The differences in library yield and profile among different lots must be within 15%. Sequencing of the amplified cDNA library must yield mapped reads >90%.

Enzyme components were tested prior to assembly and free of contaminating endonucleases and exonucleases. Enzyme purity was >95% as determined by SDS-PAGE and negligible *E. coli* genomic DNA contamination was confirmed by qPCR.

Limitations of Use

Quantabio and UltraPlex, qScript, GelTrack, ToughMix, PerfeCTa, and FastMix are registered trademarks of QIAGEN Beverly, LLC. Applied Biosystems, StepOne, StepOnePlus and ROX are trademarks of Thermo Fisher Scientific and or its subsidiaries. Please contact QIAGEN-Beverly for more information.

This product was developed, manufactured, and sold for in vitro use only. The product is not suitable for administration to humans or animals. SDS sheets relevant to this product are available upon request.

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Product Description:

sparQ RNA-Seq HMR Kit simultaneously depletes rRNA and globin mRNA while generating stranded RNA-seq libraries 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.