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.

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

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.