

| Product Information         |   |
|-----------------------------|---|
| sparQ DNA Library Prep Kits |   |
| Part Number                 | 95191-024   |
| Number of Reactions         | 24 Reactions  |
| Storage Temperature         | -25°C to -15°C                                      |
| Lot Number                  | 66169235  |
| Reference Number            | 090920, 080920, 82101620, 082020, 080720, 275754821 |
| Expiration Date             | 09/30/2022  |

**Product Description:**

The sparQ DNA Library Prep Kit provides components for the rapid construction of DNA libraries from fragmented double-stranded DNA for sequencing on Illumina® NGS platforms. The streamlined workflow can be completed in under 3 hours with minimal hands-on time. The 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. The 2X HiFi PCR Master Mix and Primer Mix allow the optional, unbiased amplification of fragments with appropriate adapters ligated to both ends. The kit is compatible with multiple sample types and facilitates efficient and consistent library construction from a wide range of input amounts from 0.25 ng to 1000 ng DNA.

**Components:**

- 84514 DNA Polishing Enzyme Mix, 0.240mL
- 84516 DNA Polishing Buffer, 0.120mL
- 84518 DNA Ligase, 0.240mL
- 84520 DNA Ligation Buffer, 0.480mL
- 84522 HiFi PCR Master Mix (2X), 0.600mL
- 84524 Primer Mix, 0.072mL

| Product Specifications |                          |
|------------------------|--------------------------|
| 95191                  |                          |
| Assay                  | Library Functional Assay |
| Specification          | Functional               |

**Quality Control Analysis and Specifications:**

**Library Prep Functional Assay:** Quality of the sparQ DNA Library Prep Kit is tested functionally by preparation of a DNA library from bacterial genomic DNA with GC-content of 10-80%. The differences in library yield and profile among different lots must be within 15%. Sequencing of the amplified library must yield mapped reads >90% and normalized coverage between 0.7 and 1.3 across the full GC spectrum.

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.

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