



sparQ PureMag Beads

Cat. No.	95196-005	Size:	5 mL
	95196-060		60 mL
	95196-450		450 mL

Store at 2°C to 8°C

Description

sparQ PureMag Beads uses reversible nucleic acid-binding properties of magnetic beads for fast and efficient nucleic acid purification. It is an ideal choice for reaction cleanup during NGS library preparation to remove primers, primer-dimers, unincorporated nucleotides, salts, adapters and adapter-dimers. This product can also be used for DNA size selection and provides consistent size range by simply manipulating the beads to sample ratio. Compatible with both manual and automated purification of nucleic acids, sparQ PureMag Beads can substitute other similar products with little or no change to the existing protocol or the instrument setting.

Instrument Compatibility

This product is compatible with automation platforms.

Storage and Stability

Store the product in a constant temperature refrigerator at 2°C to 8°C upon receipt. Please do not freeze.

For lot specific expiry date, refer to package label, Certificate of Analysis or Product Specification Form.

Additional reagents and materials that are not supplied

- Magnetic separation device
- Vortexer
- Pipettors
- Freshly-prepared 80% ethanol
- Elution Buffer (10 mM Tris pH 8.0), TE Buffer, or nuclease-free water

General Guidelines

Use good laboratory practices to minimize cross-contamination of nucleic acid products.

Always use PCR tubes, microfuge tubes, and pipette tips that are certified sterile, DNase- and RNase-free.

Before You Begin

Equilibrate the sparQ PureMag Beads to room temperature (RT) prior to use.

Fully resuspend the beads in homogenous form before use.

Always prepare fresh 80% ethanol prior to use.

Protocol

1. Reaction Cleanup in NGS Workflows

There are several sample purification steps in NGS library preparation workflow, including post adapter ligation and library amplification. sparQ PureMag Beads can be used in all those steps. We have demonstrated that the sparQ PureMag Beads can be directly used to replace AMPure® XP beads when using any of Quanta Bioscience sparQ DNA library preparation kits, and no protocol change, or additional optimization is required. Below are examples of how to use sparQ PureMag Beads for each purification step involved during library preparation using sparQ kits.

A. Removal of Divalent Cations and EDTA from Input Nucleic Acid

Input DNA for the fragmentation reaction should be in water, 10 mM Tris, buffer EB, or LoTE (0.1X TE). If the DNA was dissolved in 1X TE or the concentration of cations and chelators is not known, we strongly recommend purifying the DNA per instructions below.

1. If DNA is in a volume of less than 50 µl, adjust the volume to 50 µl with nuclease-free water.
2. Equilibrate the sparQ PureMag Beads to RT for at least 20 min.
3. Add 90 µl of thoroughly vortexed and equilibrated beads to the reaction for a ratio of 1.8X and mix well by pipetting. If DNA is in a volume greater than 50 µl, scale the volume of the beads appropriately such that the ratio of beads to DNA is 1.8X.
4. Incubate the mixture for 5 min at RT. Pellet the beads on a magnetic stand for 2-4 min and carefully discard the supernatant without disturbing the beads.
5. Wash the beads with 200 µl of 80% ethanol. Pellet the beads on the magnetic stand and discard the supernatant. Repeat the wash once.
6. Air-dry the beads on the magnetic stand for 5 min or until the beads are dry.
7. Thoroughly resuspend the dried beads in 45 µl of 10 mM Tris-HCl, pH 8.0 and incubate for 2 min at RT. Pellet the beads on the magnetic stand and carefully transfer 42.5 µl of supernatant into a new tube.
8. Determine the concentration of the purified DNA using Qubit, PicoGreen or other methods.

B. Reaction Cleanup after Adapter Ligation

The optimal beads to DNA sample ratio for DNA fragments in the >150 bp size range is 0.8X. Conditions may differ if the desired DNA size range is different.

1. Equilibrate the sparQ PureMag Beads to RT.
2. Vortex the beads thoroughly and add 80 µl (0.8X) to reaction tube. Mix well by pipetting.
3. Incubate the mixture for 5 min at RT. Pellet the beads on a magnetic stand (e.g., DynaMag®) and carefully discard the supernatant.
4. Wash the beads with 200 µl of the freshly-prepared 80% ethanol. Pellet the beads on the magnetic stand and discard the supernatant. Repeat the wash once.
5. Air-dry the beads on the magnetic stand for 5 - 10 min or until the beads are dry. Over-drying of beads may result in lower DNA recovery.
6. Resuspend the dried beads in 25.5 µl of 10 mM Tris-HCl, pH 8.0 and incubate for 2 min at RT. Pellet the beads on the magnetic stand. Carefully transfer 23.5 µl of supernatant into a new tube. The sample can be stored at -20°C if not proceeding immediately to library amplification or other downstream processes.

C. Post PCR-Amplification Cleanup

1. Equilibrate the sparQ PureMag beads to RT.
2. Thoroughly vortex the beads slurry and add 50 μ l (1X) to the PCR reaction. Mix well by pipetting.
3. Incubate the mixture for 5 min at RT. Pellet the beads on a magnetic stand (e.g., DynaMag[®]) and carefully discard the supernatant.
4. Wash the beads with 200 μ l of 80% ethanol. Pellet the beads on the magnetic stand and discard the supernatant. Repeat the wash once.
5. Air-dry the beads on the magnetic stand for 5 min or until the beads are dry. Over-drying of beads may result in lower DNA recovery.
6. Resuspend the dried beads in 32.5 μ l of 10 mM Tris-HCl, pH 8.0 and incubate for 2 min at RT. Pellet the beads on the magnetic stand. Carefully transfer 30 μ l of supernatant into a new tube. The sample can be stored at -20°C if not proceeding immediately to library quantification or other downstream processes.

2. Size Selection in NGS library Preparation

Depending on the specific application, size selection may be required to ensure the DNA insert size falls into a certain range. Size selection can be implemented in different steps, such as after DNA fragmentation, post-ligation cleanup, or after library amplification. Because the reaction buffer, especially the ligation buffer, can greatly influence the size selection range, it is recommended to perform size selection after an initial purification using the sparQ PureMag Beads (see section 1A-1C for detailed instruction). If size selection without initial purification is preferred, the exact amount of beads used needs to be determined empirically.

The following protocol and guidelines are based on double-sided size selection of fragmented DNA without Y-shaped adapters attached. Additional optimization is required if using adapter ligated DNA or post-PCR DNA. The size range reflects the final fragment size, so if calculating the insert size, please take into account that the adapter size and configuration both have a significant impact on the size of the fragment appearing on the Bioanalyzer or other size differentiation and detection instruments. Example below shows the double-sided size selection of DNA sample in a 50 μ l volume, and the targeted size selection range of 200-400 bp (centered around 300 bp: Figure 1)

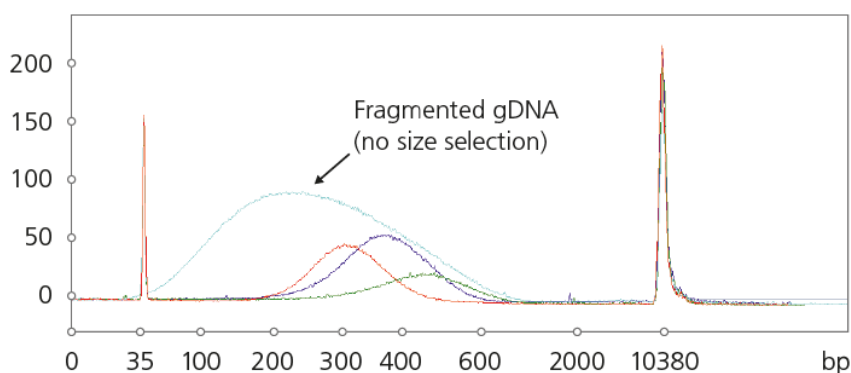
1. Equilibrate the sparQ PureMag Beads to RT for at least 20 min.
2. Thoroughly resuspend the beads.
3. Vortex the beads and add 35 μ l (0.7X) to reaction tube. Mix well by pipetting.
4. Incubate the mixture for 5 min at RT. Pellet the beads on the magnetic stand until the liquid is clear. Do not discard supernatant.
5. Transfer all supernatant to a new tube. Be careful not to carry any beads into the new tube.
6. Add 10 μ l of new beads into the tube contains the supernatant and mix thoroughly by vortexing or pipetting up and down several time with Pipette set at 100 μ l. To ensure the accurate amount of beads is added, take extra caution during pipetting and mixing as the solution can be viscous to handle.
7. Pellet the beads on the magnetic stand. Carefully discard the supernatant after the liquid is clear.
8. Keep the tube on the magnetic stand and wash the beads with 200 μ l of the freshly-prepared 80% ethanol.
9. Pellet the beads on the magnetic stand and discard the supernatant. Repeat the wash once.
10. Air-dry the beads on the magnetic stand for 5 min or until the beads are dry. Over-drying of beads may result in lower DNA recovery.
11. Resuspend the dried beads in desired volume of 10 mM Tris-HCl, pH 8.0 or water and incubate for 2 min at RT. Pellet the beads on the magnetic stand. Carefully transfer the eluent into a new tube.

Table 1. General guideline for double-sided size selection of various size-range of DNA fragments

	Final DNA fragment size range		
	200-400 bp	250-500 bp	300-700 bp
1 st bind beads amount	35 μ l	30 μ l	25 μ l
2 nd bind additional beads amount	10 μ l	10 μ l	10 μ l

The volume of beads added was calculated based on starting DNA in 50 μ l of Tris buffer or water.

Normalized RFU



sparQ PureMag Beads DNA Ratio	Targeted size range (bp)	Peak average (bp)
0.7x, 0.9x	200-400	301
0.6x, 0.8x	250-500	377
0.5x, 0.7x	300-700	464

Figure 1. Example of genomic DNA fragment before (bright blue) and after double-sided size selection in the range of 200-700 bp.

Quality Control

All kit components are subjected to quality control, including DNA recovery assay, DNA size selection assay (specific size range), RNA Recovery Assay, and PCR Inhibition Assay.

Limited Label Licenses

Use of this product signifies the agreement of any purchaser or user of the product to the following terms:

1. The product may be used solely in accordance with the protocols provided with the product and this manual and for use with components contained in the kit only. QIAGEN Beverly, Inc. grants no license under any of its intellectual property to use or incorporate the enclosed components of this kit with any components not included within this kit except as described in the protocols provided with the product, this manual, and additional protocols available at www.quantabio.com. Some of these additional protocols have been provided by Quantabio product users. These protocols have not been thoroughly tested or optimized by QIAGEN Beverly, Inc.. QIAGEN Beverly, Inc. neither guarantees them nor warrants that they do not infringe the rights of third-parties.
2. Other than expressly stated licenses, QIAGEN Beverly, Inc. makes no warranty that this kit and/or its use(s) do not infringe the rights of third-parties.
3. This kit and its components are licensed for one-time use and may not be reused, refurbished, or resold.
4. QIAGEN Beverly, Inc. specifically disclaims any other licenses, expressed or implied other than those expressly stated.
5. The purchaser and user of the kit agree not to take or permit anyone else to take any steps that could lead to or facilitate any acts prohibited above. QIAGEN Beverly, Inc. may enforce the prohibitions of this Limited License Agreement in any Court, and shall recover all its investigative and Court costs, including attorney fees, in any action to enforce this Limited License Agreement or any of its intellectual property rights relating to the kit and/or its components.

©2018 QIAGEN Beverly Inc. 100 Cummings Center Suite 407J Beverly, MA 01915

Quantabio brand products are manufactured by QIAGEN, Beverly Inc.

Intended for molecular biology applications. This product is not intended for the diagnosis, prevention or treatment of a disease.



Related NGS Products Sold Separately

sparQ DNA Frag & Library Prep Kit

Cat. No.	95194-024	Size:	24 reactions
	95194-096		96 reactions

sparQ DNA Library Prep Kit

Cat. No.	95191-024	Size:	24 reactions
	95191-096		96 reactions

sparQ Adapter Barcodes Set A

Cat. No.	95193-A96	Size:	96 reactions
----------	-----------	-------	--------------

sparQ Adapter Barcodes Set B

Cat. No.	95193-B96	Size:	96 reactions
----------	-----------	-------	--------------

sparQ HiFi PCR Master Mix

Cat. No.	95192-050	Size:	50 reactions
	95192-250		250 reactions

The sparQ HiFi PCR Master Mix is a high efficiency, high-fidelity, and low bias PCR master mix for NGS workflows requiring DNA library amplification prior to sequencing. The included primer mix allows amplification of DNA libraries flanked by adapters containing the P5 and P7 Illumina® flow cell sequences.

PerfeCTa NGS Quantification Kit – Illumina

Cat. No.	95154-500	Size:	500 reactions
----------	-----------	-------	---------------

PerfeCTa NGS Quantification Kit – Illumina, ROX

Cat. No.	95155-500	Size:	500 reactions
----------	-----------	-------	---------------

PerfeCTa NGS Quantification Kit – Illumina, Low ROX

Cat. No.	95156-500	Size:	500 reactions
----------	-----------	-------	---------------

The PerfeCTa NGS Quantification Kits use real-time PCR to enable accurate quantification of DNA Libraries compatible with sequencing on Illumina NGS platforms. The included stabilized pre-diluted standards and pre-qualified primer set ensures reproducible and precise results.

Trademarks

AMPure® XP is a registered trademark of Beckman Coulter, DynaMag™, is a trademark of Thermo Fisher Scientific and its subsidiaries unless otherwise specified, Illumina is a registered trademark of Illumina, Inc., PerfeCTa® is a registered trademark of QIAGEN Beverly, Inc.