NGS Clean and Select Beads
Product Handling Guide

Shipping: Ambient temperature

Catalog number: MDX041

Batch No.: See vial

Store at 4 °C to 8°C

meridian BIOSCIENCE™

Storage and stability:
NGS Clean and Select Beads is shipped at ambient temperature. On arrival store at 4 °C to 8°C for optimum stability. Do not freeze as this will damage the beads.

Expiry:
When stored under the recommended conditions and handled correctly, full activity of the kit is retained until the expiry date on the outer box label.

Safety precautions:
Read and understand the SDS (Safety Data Sheets) before handling the reagents. Hardcopies of the SDS will be provided with the first shipment, thereafter they will be available upon request.

Quality control:
Meridian operates under ISO 13485 Quality Management System. NGS Clean and Select Beads and its components are extensively tested for nuclease contamination and absence of nucleic acid contamination.

Notes:
For research or further manufactured use only.

Description

NGS Clean and Select Beads is an efficient NGS library preparation clean-up and selection system based on paramagnetic beads. It is designed for the removal of salts, primers and dNTPs and size selection of DNA fragments that can be used directly for downstream applications. The protocol can be used manually or adapted for liquid handling workstations.

Kit components

Table 1

Component
NGS Clean and Select Beads

Users Guidelines

Allow JetSeq Clean beads to equilibrate at room temperature. Vortex the JetSeq Clean beads reagent thoroughly to fully resuspend the magnetic beads prior to usage.

Determine the NGS Clean and Select Beads volume required for each step as follows:
Volume of Sample x Recommended Beads Ratio = Volume of NGS Clean and Select Beads.

For example, 65 µL of sample and 0.8x ratio is required, 65 (µL) x 0.8 = 52 µL of beads is needed.

Sample Clean-Up

Use a 0.8x Beads Ratio to determine the volume of NGS Clean and Select Beads, add it to the sample.

Go to the wash protocol.

Left-Sided Size Selection

The size range of DNA fragments recovered with left-sided size selection is dependent on the ratio (volume) of NGS Clean and Select Beads added to the sample.

Table 2 is a guideline to the ratio of beads to add; however it is recommended to optimize the bead:sample volumetric ratio.

Table 2

Fragments to be selected	Recommended beads:sample ratio
>100 bp	0.8x
>120 bp	0.6x
>150 bp	0.5x
>180 bp	0.4x
>250 bp	0.3x
>400 bp	0.2x

Go to the wash protocol.

Double Sided Size Selection

Table 3 is a guideline for the purification of NGS libraries however it is recommended to optimize the bead:sample volumetric ratio if libraries are prepared using different manufacturer reagents.

Table 3

Fragment Size	First cut ratio	Second cut ratio
250-300 bp	0.4x	0.3x
300-350 bp	0.4x	0.2x
350-400 bp	0.3x	0.2x
400-500 bp	0.2x	0.2x
600-700 bp	0.2x	0.1x

1. Perform the first cut by adding the required volume of beads to the sample. Pipette up and down at least 10 times. Incubate at room temperature for 5 minutes.
2. Place the plate on a magnetic stand to separate the beads.
3. Aspirate and transfer the clear supernatant to clean plate. Do not discard supernatant! Discard the beads containing unwanted large fragments.
4. Perform the second cut by adding appropriate volume of homogenous beads the supernatant.

Go to the wash protocol.

Wash protocol

1. Pipette up and down at least 10 times. Incubate at room temperature for 5 minutes.
2. Place the plate on a magnetic stand to separate the beads.
3. Aspirate and discard the cleared supernatant, avoiding the beads.
4. Add 30 µL 70% ethanol and incubate at room temperature for 1 minute.
5. Aspirate and discard the cleared supernatant. Repeat the ethanol wash step.
6. Leave the plate on the magnetic stand for 3 minutes to air dry the beads. Remove any residue liquid with a pipette.
7. Note: Residual ethanol may interfere with downstream applications. Do not over-dry the beads as this will decrease yield. The bead pellet is dry when the appearance of the surface changes from shiny to matt.
8. Elute the sample in an appropriate volume of Elution Buffer (10mM Tris -HCl pH 8.0) or molecular biology grade water. Mix well by pipetting up and down 10 times or vortex for 30 seconds.
9. Incubate at room temperature for 2-3 minutes.
10. Place the plate onto a magnetic stand to separate the beads and transfer the cleared supernatant containing cleaned-up DNA to a new plate.
11. Use the eluted material for the desired downstream applications or store it at the conditions recommended by the specific protocol followed.

Technical Support

For any technical enquiries, please contact our Technical Support team via email at: mbi.tech@meridianlifescience.com

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