

Hieff NGS™ UCF.ME DNA Selection Beads

Product description

Hieff NGS™ UCF.ME DNA Selection Beads are prepared based on the SPRI (Solid Phase Reverse Immobilization) principle and is applicable for DNA purification and size selection during the preparation of next generation sequencing (NGS) libraries. Hieff NGS™ UCF.ME DNA Selection Beads are compatible with various of DNA and RNA library prep kits. This product is manufactured in an ultra-clean facility with a high level of cleanliness and can be used for DNA purification step during pathogen detection processes.

Specifications

Cat.No.	17266ES03 / 17266ES08 / 17266ES56 / 17266ES75
Size	1 mL / 5 mL / 60 mL / 450 mL

Components

Components No.	Name	17266ES03	17266ES08	17266ES56	17266ES75
17266	UCF.ME DNA Selection Beads	1 mL	5 mL	60 mL	450 mL

Storage

This product should be stored at 2~8°C for 18 months.

Notes

1. For your safety and health, please wear a lab coat and disposable gloves during operation.
2. Magnetic beads must be equilibrated at room temperature for at least 30 minutes before use.
3. Prepare 80% ethanol fresh before use, as stored ethanol will affect recovery efficiency.
4. When performing size selection, the initial sample volume must be $\geq 100 \mu\text{L}$. If the volume is insufficient, supplement with ultrapure water. Small sample volumes may result in increased pipetting errors, which can affect the accuracy of size selection.
5. This product is for research use only!

Instructions

Preparation

Take the magnetic beads out of the refrigerator and equilibrate at room temperature for at least 30 minutes. Prepare 80% ethanol.

Size selection

The size selection procedure is shown in Figure 1, and the specific steps are as follows.

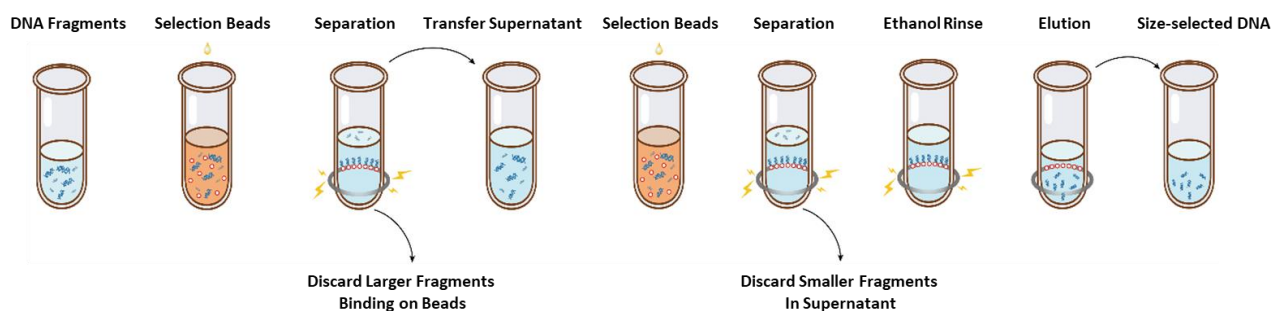


Figure 1 The Operation Flowchart of Size Selection

1. Vortex or gently invert the magnetic beads to ensure thorough mixing.
2. As required, refer to Table 1 and add the first round of sorting magnetic beads to the DNA solution. Vortex to mix or pipette up and down 10 times to mix.
3. Incubate at room temperature for 5 minutes.
4. Briefly centrifuge the tube and place it in a magnetic rack. Once the solution has cleared (approximately 5 minutes), carefully transfer the supernatant to a clean centrifuge tube.

[Note]: When transferring the supernatant, leave about 2 μL of liquid at the bottom of the tube. Do not aspirate the entire supernatant to avoid collecting magnetic beads, which may affect the sorting efficiency.

Example: For an initial volume of 100 μL , with a 0.8 $\times$ ratio for the first round, add 80 μL of magnetic beads. It is recommended to aspirate 178 μL of supernatant.

5. Refer to Table 1 and add the second round of sorting magnetic beads to the supernatant.
6. Vortex to mix or pipette up and down 10 times to mix, and incubate at room temperature for 5 minutes.
7. Briefly centrifuge the tube and place it in a magnetic rack. Once the solution has cleared (approximately 5 minutes), carefully remove the supernatant.
8. Keep the centrifuge tube in the magnetic rack, add 200 μL of freshly prepared 80% ethanol to wash the magnetic beads, and incubate at room temperature for 30 seconds. Carefully remove the supernatant.
9. Repeat step 8.
10. Keep the centrifuge tube in the magnetic rack, open the cap, and dry the magnetic beads until slight cracking is observed (approximately 5 minutes).

[Note]: Do not allow the beads to dry for too long. Over-drying the magnetic beads will affect the purification efficiency.

11. Remove the centrifuge tube from the magnetic rack and add an appropriate amount of ddH₂O ($\geq 20 \mu\text{L}$). Vortex or gently pipette to mix thoroughly and incubate at room temperature for 5 minutes.
12. Briefly centrifuge the tube and place it in the magnetic rack to separate the magnetic beads from the liquid. Once the solution has cleared (approximately 5 minutes), carefully aspirate the supernatant into a clean tube. The sorting process is now complete.

Reference conditions for DNA size selection

The calf thymus DNA was fragmented by sonication to prepare smear fragments of 100-1000 bp, and double-round sorting was performed according to Table 1. The results were analyzed using the Agilent 2100 Bioanalyzer (Figure 2).

Table 1. Recommended condition for DNA size selection

Length of DNA fragment	250-350 bp	320-420 bp	450-550 bp	550-700 bp	700-900 bp	800-1000 bp
First-round ratio(Beads:DNA)	0.80×	0.70×	0.60×	0.55×	0.50×	0.45×
Second-round ratio(Beads:DNA)	0.20×	0.20×	0.20×	0.15×	0.15×	0.15×

[Note]: The "x" in the table represents the sample DNA volume. For example, if the library insert fragment length is 250 bp and the sample DNA volume is 100 μ L, the volume of magnetic beads used for the first round of sorting would be $0.80 \times 100 \mu\text{L} = 80 \mu\text{L}$; the volume of magnetic beads used for the second round of sorting would be $0.20 \times 100 \mu\text{L} = 20 \mu\text{L}$.

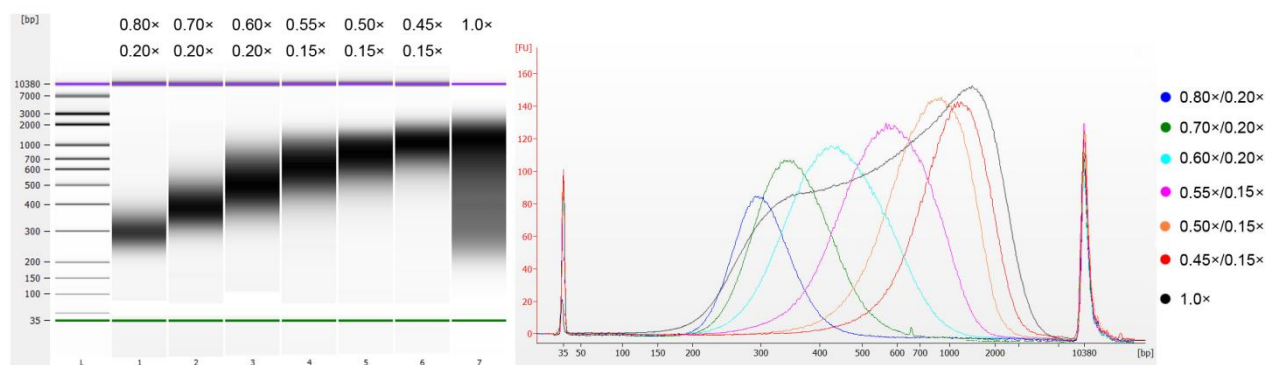


Figure 2. Agilent 2100 high sensitivity DNA chip electropherogram