QIAseq® Beads for high-quality DNA purification with NGS library size selection

Elevate your next-generation sequencing (NGS) research with our magnetic bead solution. QIAseq Beads remove adapter dimers and other unwanted components for purification with high efficiency to ensure the success of your NGS projects. Here's what you can expect with QIAseq Beads:

- Efficient and precise library-size selection
- High-quality libraries
- Cost effective
- Automation compatible

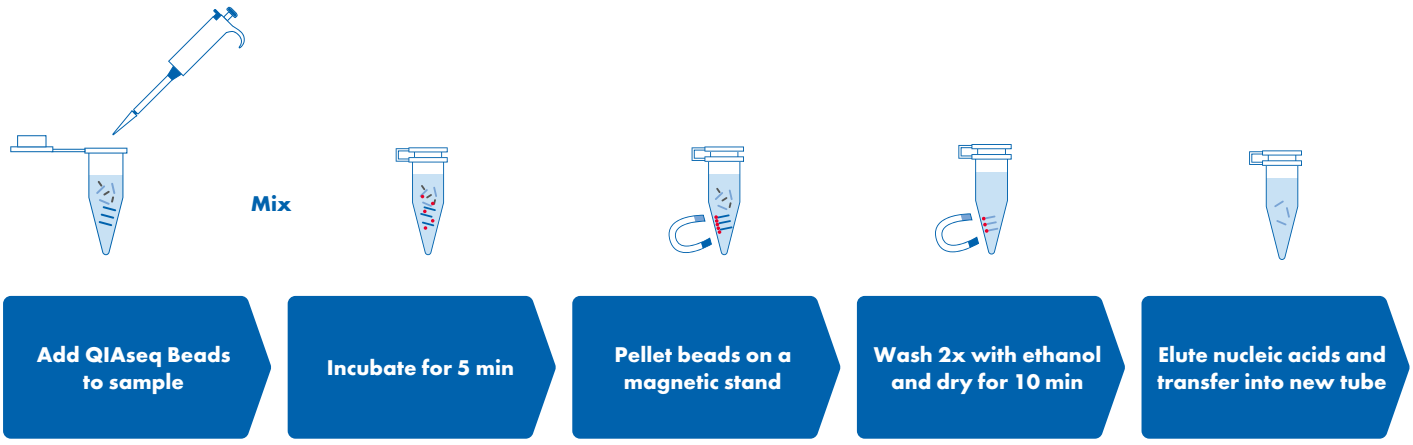

Figure 1. QIAseq Beads size-selection workflow.
QIAseq beads are used for automated or manual purification of PCR products and fragmented DNA. The workflow provides efficient and precise size selection for NGS libraries. The high-quality purified DNA contributes to high-quality NGS data.

Higher bead ratio for cleanup with QIAseq Beads

	Bead ratio	
Round of cleanup	**QIAseq Beads**	**Competitor A**
First, after ligation	0.8x	0.8x
Second, after ligation	1.1x	1.0x
Third, after library amplification	1.2x	1.0x

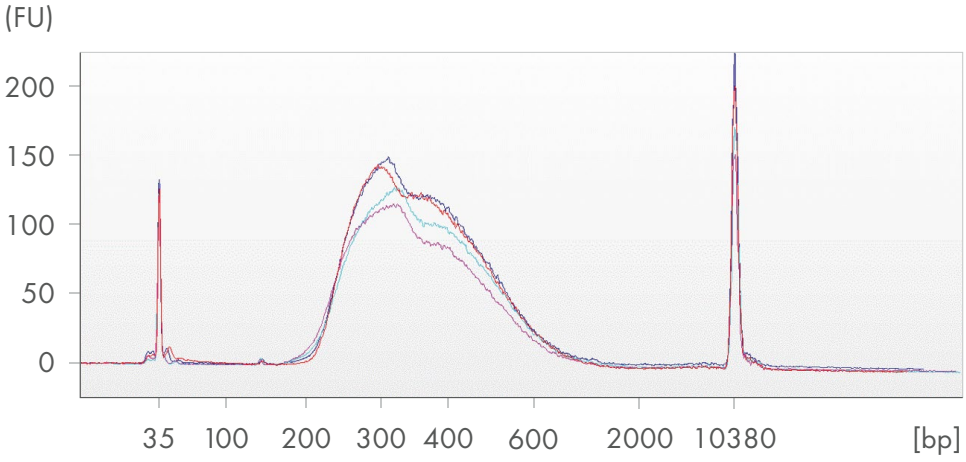

Figure 2. QIAseq beads result in high library purity, high yield and expected library size distribution even at low inputs.
Fifty picograms of genomic DNA was used as starting input and samples were prepared using a QIAseq FX library kit using either QIAseq Beads (blue and red) or Competitor A beads (pink and turquoise). The subsequent libraries were analyzed to determine library size and purity.

Figure 3. Effect of bead-to-DNA ratio in aqueous solution on fragment recovery.
To determine the effect of varying bead-to-DNA ratios on DNA fragment size selection, DNA size ladder was diluted in water to a total volume of 50 µL and incubated with various volumes of QIAseq Beads from 25 µL (0.5x) to 75 µL (1.5x). After DNA binding for 5 minutes at room temperature, the tubes were placed on a magnetic stand for another 5 minutes until the solution cleared. Next, the supernatant was discarded and the beads were washed twice with 200 µL 80% ethanol. After the final ethanol wash, the supernatant was removed and the magnetic beads were dried completely. The pellet was eluted in 6 µL Buffer EB. An aliquot (1 µL) was analyzed on an Agilent BioAnalyzer high sensitivity chip along with unpurified size ladder (reference ladder). **(A)** Fragment quantification. **(B)** Percentage distribution of fragments compared to reference.

Ordering Information

Product	Cat. no.
QIAseq Beads (10 mL)	333923
QIAseq Beads (55 mL)	333903
QIAseq Beads (400 mL)	333927

Learn more about QIAseq Beads for efficient and precise size-selection of DNA fragments for NGS library preparation at **www.digitalinsights.qiagen.com/ipa**