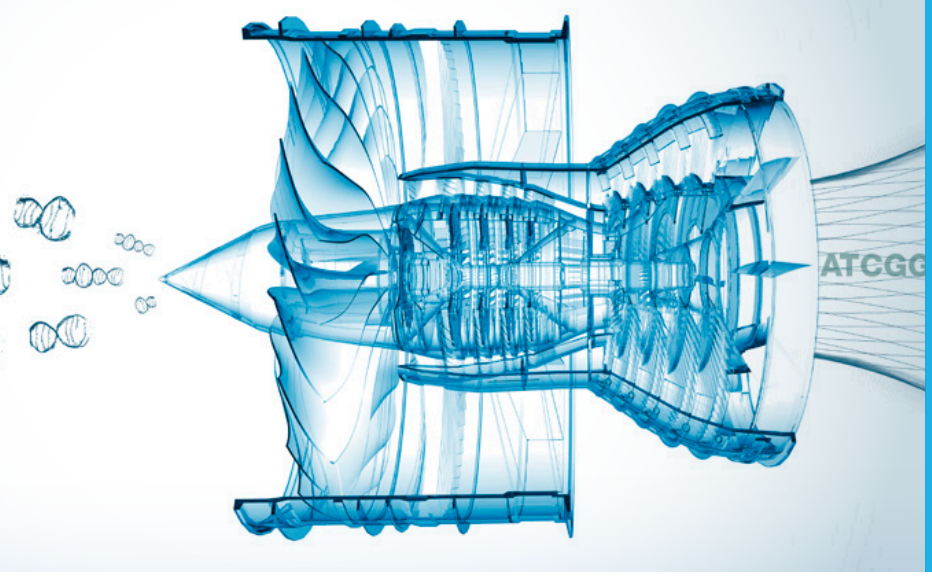


JetSeq™ Clean

Powering NGS

JetSeq™ Clean enables reaction clean-up, as well as a single- or double-sided size selection of libraries following the fragmentation, ligation and PCR steps in the next generation sequencing (NGS) library preparation workflow.

- **Precise:** consistent bead diameter for highly-reproducible selection of the user-defined fragment size range
- **Efficient:** excellent recovery of fragments greater than 100 bp and efficient removal of all contaminants
- **Flexible:** highly effective clean-up from all types of fragmentation, ligation and PCR reactions
- **Fast:** eliminates centrifugation or filtration steps for fast manual processing and simple integration with automated liquid handling platforms
- **Robust:** bead composition specifically developed to withstand the rigours of the NGS workflow

JetSeq™ Clean is a NGS library preparation clean-up system based on paramagnetic bead technology, manufactured under nuclease-free conditions. It is designed for efficient purification of nucleic acid fragments in the next generation sequencing workflow. JetSeq Clean provides maximum flexibility allowing for left-, right- or double-sided size selection. JetSeq Clean removes salts, primers, primer-dimers and dNTPs, while library fragments are selectively bound to the magnetic particles based on their size. Purified library fragments are eluted from the magnetic particles using water or a low salt buffer and can be used directly for all downstream NGS applications. The protocol can be performed manually, or adapted to liquid handling workstations (e.g. Agilent, Beckman, Caliper, Eppendorf, Hamilton, PerkinElmer and Tecan) using 96- or 384-well formats.

APPLICATIONS

JetSeq Clean is perfectly-suited to the following applications:

- NGS library preparation
- Sanger sequencing
- PCR
- Recovery from enzymatic reactions

HIGH RECOVERY

JetSeq Clean is designed for highly-efficient and robust library fragment clean-up from a variety of enzymatic reactions including fragmentation, end-repair, A-tailing, adapter ligation and PCR (Fig. 1). The kit utilizes high binding capacity paramagnetic bead technology that binds and purifies library fragments, removing inhibitors, sequencing adapters, primer-dimers, unincorporated nucleotides, enzymes and salts. Library fragments can then be quickly and easily recovered without the need for centrifugation or vacuum filtration steps. This purification procedure can therefore be easily incorporated onto automated liquid handling platforms equipped with magnetic plates in both 96- and 384-well formats.

JetSeq Clean recovers both single stranded and double stranded nucleic acid fragments greater than 100 bp consistency and highly-reproducibly in a ready-to-use format for downstream NGS applications.

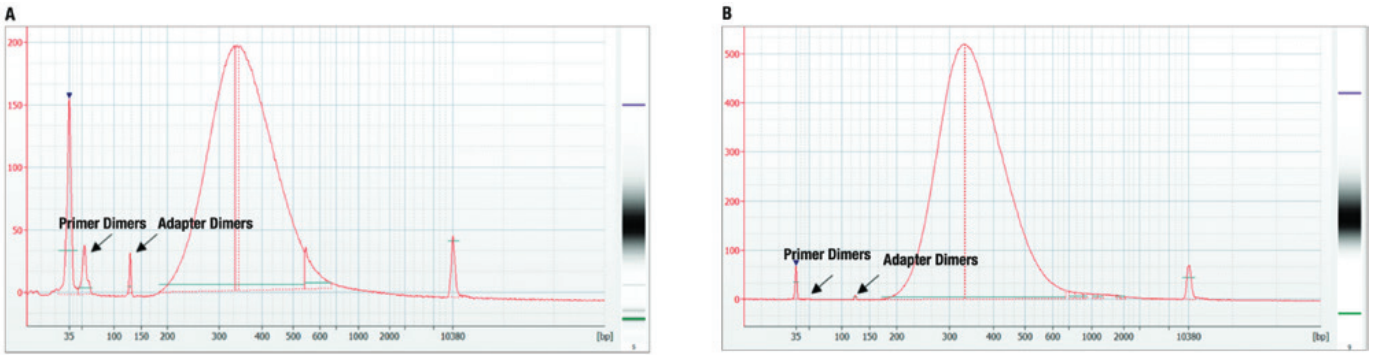
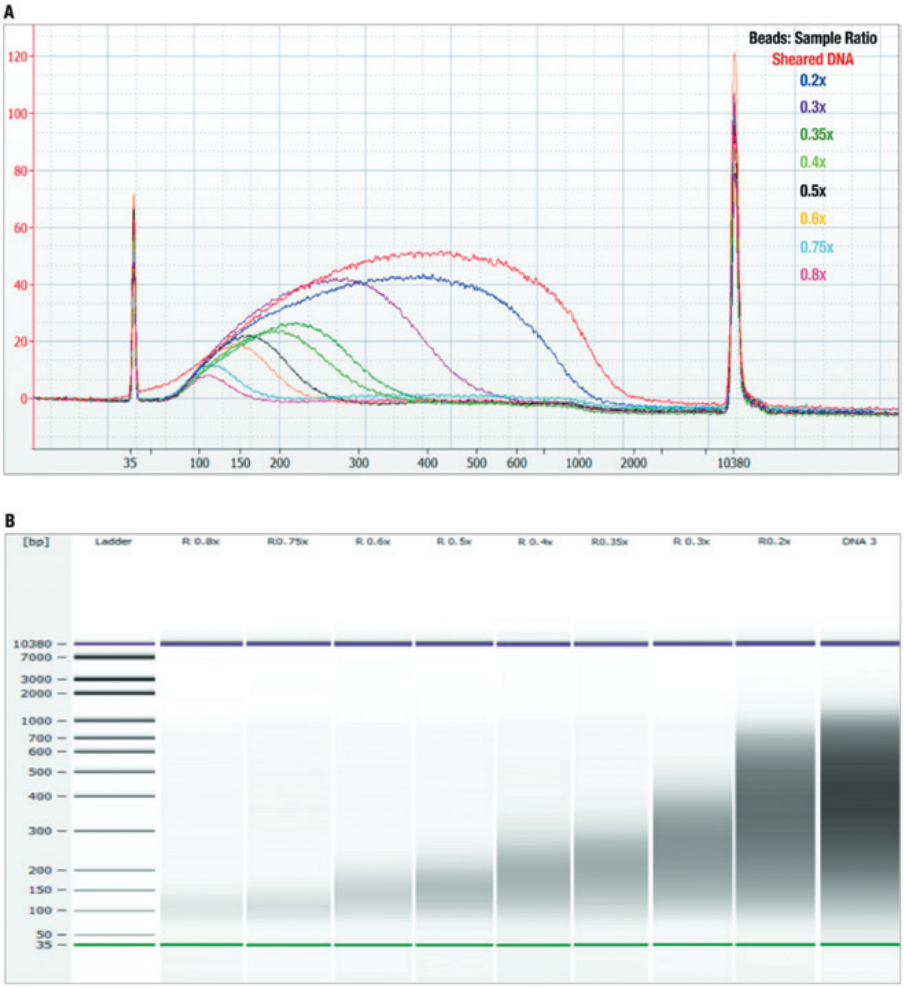


Fig. 1 Removal of PCR contaminants by JetSeq Clean bead purification
(A) Electropherogram and virtual gel view showing the library size profile, including the presence of unincorporated adapters and PCR primers prior to the bead clean-up step.
(B) Bead clean-up of the same library using the JetSeq Clean at 1.2X bead:DNA ratio (vol:vol) to remove these low molecular weight products.

SIZE SELECTION

JetSeq Clean selectively binds nucleic acid fragments based on the volume ratio of bead suspension and sample. Increasing the volume ratio favors the binding of shorter fragments to the beads. This can be used for single-side size selection (left or right), with the exclusion of smaller or larger sized fragments (Fig. 2), or for double-sided size selection, where two successive purification steps are performed to first exclude larger fragments above the target size range and then smaller fragments below the target size range (Fig. 3).

Right Selection



Left Selection

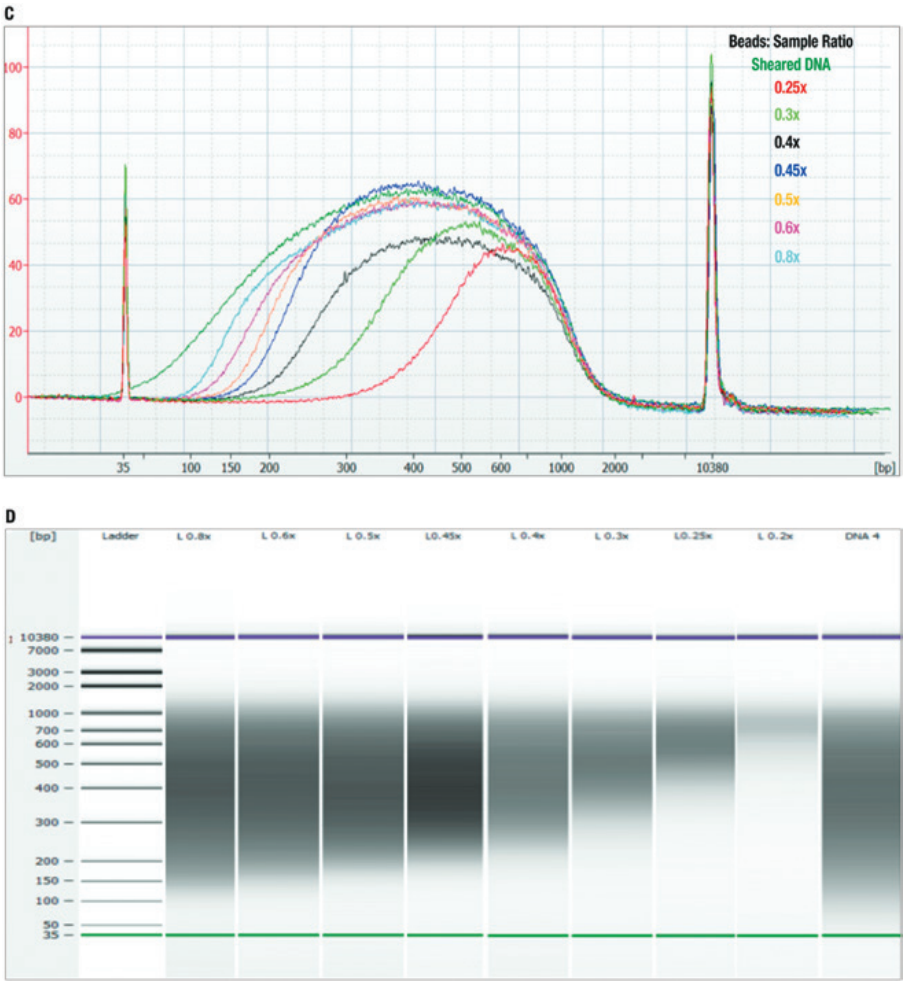


Fig. 2 DNA size distribution after single-side size selection
For right or left side size selection, the fragmented sample is mixed with JetSeq Clean to a range of sample to bead ratios to either recover fragments above a lower size limit, or below an upper size limit, respectively. The peak electropherogram view (A,C) and the virtual gel view (B,D) results illustrate the precision of JetSeq Clean in selection of a specific, user-defined range of fragments for NGS.

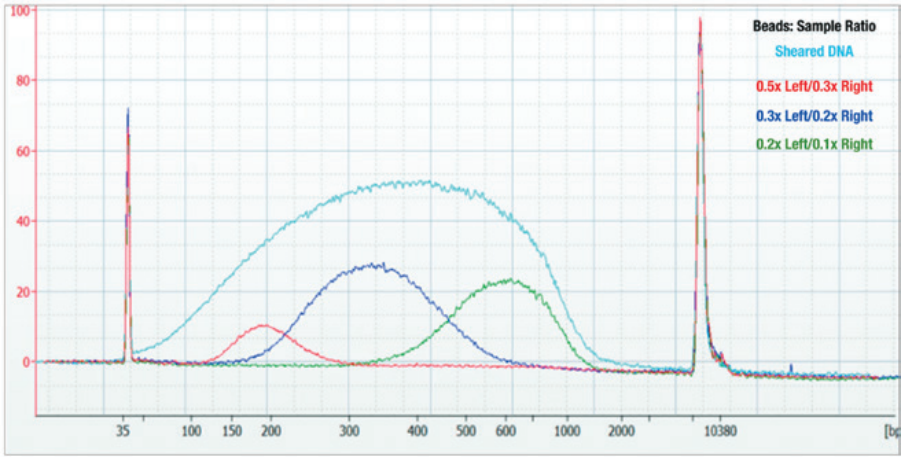
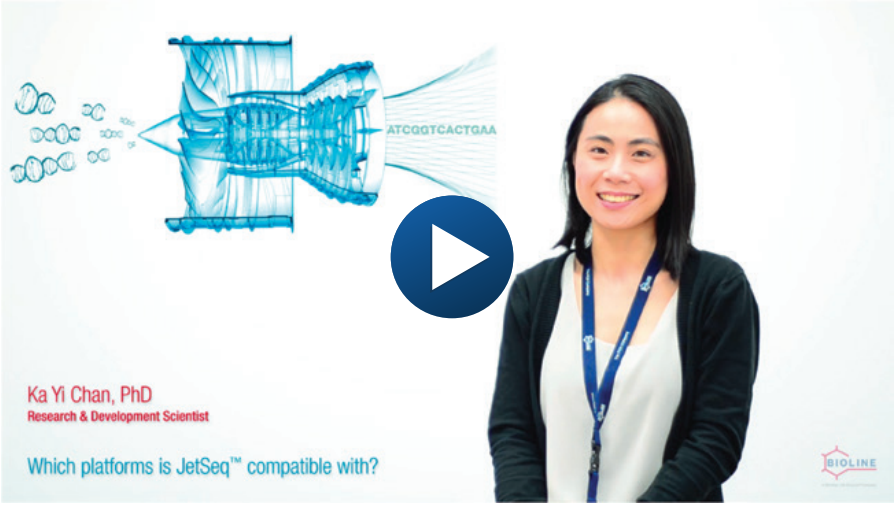


Fig. 3 Size distribution after double-side size selection
For double-side size selection, supernatant from a right-side selection step, which excludes the largest library fragments, is then re-purified using a different ratio of beads, according to the left side size selection protocol to exclude the smallest library fragments. The results illustrate that precise adjustment of the size selection parameters allows JetSeq Clean to recover a highly-specific range of library fragments and remove unwanted reaction components.



Watch JetSeq™ Library Preparation Kits
Our Research & Development Scientist, Ka Yi Chan discusses our JetSeq Library Preparation Kits; which includes the JetSeq ER & Ligation Kit and the JetSeq Flex DNA Library Preparation Kit.

Subscribe and Watch the full video on our YouTube channel > **Bioline: Meridian Bioscience**

Related Products

Products	Size	Cat. #
JetSeq™ Flex DNA Library Preparation Kit (PCR Amplified Libraries)	96 Reactions	BIO-68027
JetSeq™ ER & Ligation Kit (PCR-Free Libraries)	96 Reactions	BIO-68026
JetSeq™ Hi-ROX Library Quantification Kit	500 Reactions	BIO-68028
JetSeq™ Lo-ROX Library Quantification Kit	500 Reactions	BIO-68029
ISOLATE II Genomic DNA Kit	50 Preps	BIO-52066

Ordering Information

JetSeq™ Clean	Size	Cat. #
JetSeq Clean	50 mL	BIO-68031
	500 mL	BIO-68032

Contact information:

Global
E: info@meridianlifescience.com
Toll free: +1 800 327 6299

Australia
E: info.au@meridianlifescience.com
Tel: +61 (0)2 9209 4180

Connect with us:

bioline.com/jetseq

meridian BIOSCIENCE®
LIFE DISCOVERED. LIFE DIAGNOSED.

ISO 13485 Certified

08/20