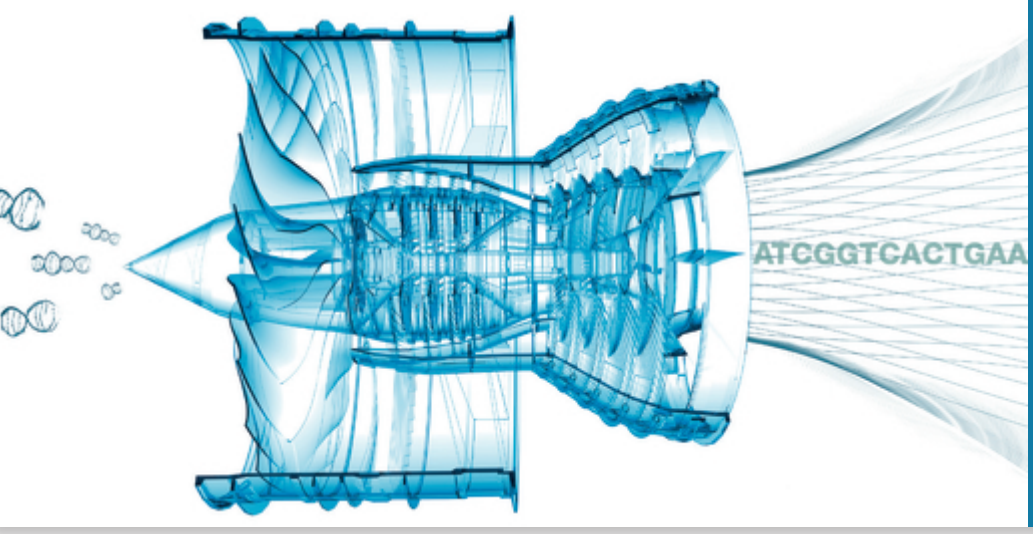

JetSeq™ DNA Library Preparation Kit

Powering NGS

- **Low input:** end-repair, A-tailing and ligation combined in the same tube, thereby eliminating cleanup steps and improving sample yield
- **Improved confidence:** simpler protocol with fewer steps for reduced risk of sample loss and offering greater peace-of-mind
- **Increased speed:** library preparation in less than 3 hours for reduced time to results and increased sample throughput
- **Highly efficient:** reaction buffer pre-optimized to provide maximum reaction efficiency and highest conversion rates
- **Improved quality:** reliable library preparation from even very challenging samples, providing maximum coverage
- **Maximum convenience:** sequencing adaptors, enabling indexing of up to 16 samples, already included in the kit

The JetSeq™ DNA Library Preparation Kit is designed to generate high-quality next generation sequencing (NGS) libraries suitable for sequencing on Illumina® instruments.

The success of next-generation sequencing is partly dependent upon the precise and accurate processing of the input DNA. High-quality library preparation from sheared DNA requires efficient processing during a series of molecular biology reactions and good recovery during the intermediate purification steps.

FASTER LIBRARY CONSTRUCTION

By combining end repair, A-tailing and ligation in a single tube, the JetSeq™ DNA Library Preparation Kit protocol offers a faster turnaround time (Fig. 1), with minimal manual effort, thereby enabling complete library construction in less than 3 hours. The elimination of purification steps minimizes sample loss, while optimization of the JetSeq buffer system ensures high-yield of sequence-ready libraries.

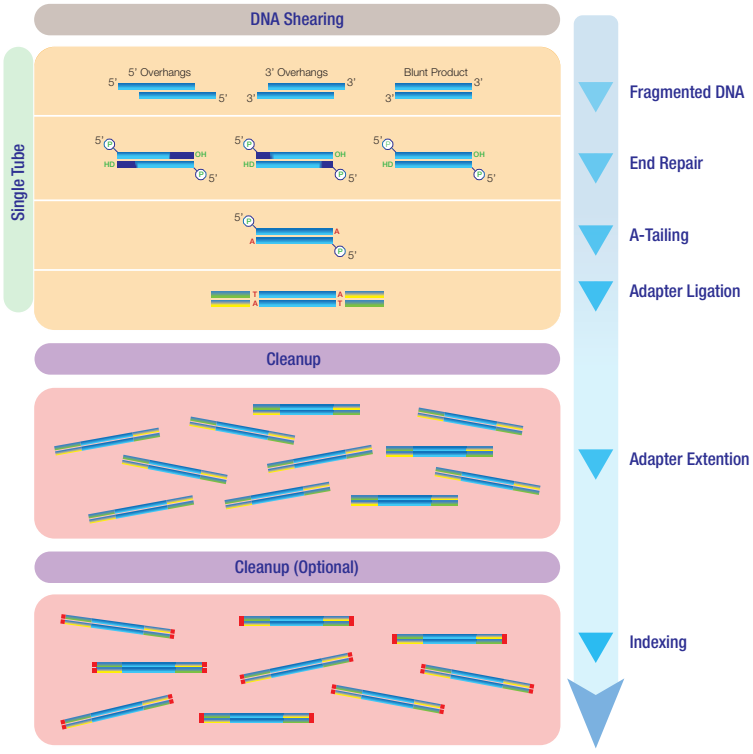

Fig. 1 Quality score across all bases
The JetSeq DNA Library Preparation Kit protocol incorporates fewer steps. This simpler, shorter protocol reduces both hands-on time and the total time required for preparation of library DNA.

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HIGH LIBRARY QUALITY AND YIELD

The JetSeq DNA Library Preparation Kit contains all of the enzymes and buffers necessary for end repair, A-tailing, ligation and amplification in convenient, optimized master mix formulations, as well as 16 barcoded adapters that can be used for single or multiplex reads.

Library adapter ligation efficiency

Ligation efficiency strongly influences library diversity and quality. The JetSeq Kit is highly efficient at converting DNA into an adapter-ligated library, resulting in higher sequence coverage. The kit contains all of the enzymes and buffers necessary for highly-efficient conversion of the input DNA to a sequenceable, adapter-ligated library (Fig. 2).

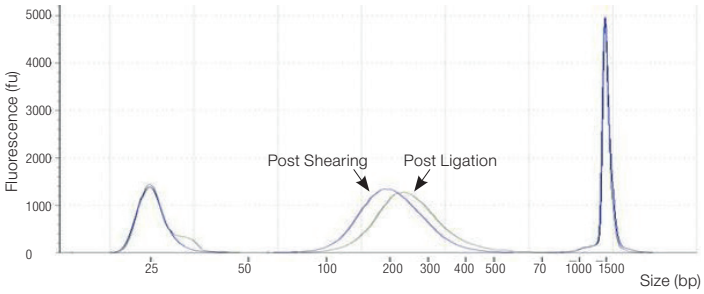

Fig. 2 Ligation efficiency
An example of a DNA library prepared using the JetSeq DNA Library Preparation Kit. Input DNA (~200 bp) was ligated to the adaptors and cleaned using AMPure beads. The concentration of pre-ligated and post-ligated DNA was then normalized, then run on a Bioanalyzer 2100. The electropherogram shows the increase in fragment size due to the addition of the adaptors to both ends of the target fragments and the absence of un-ligated adapters that are likely to decrease the efficiency of library amplification and/or sequencing.

REDUCED AMPLIFICATION BIAS

The GC content plays an important role in the efficiency of fragments to pass through each step of the sample preparation and sequencing workflow. Differences in the percentage of GC in fragments can result in these fragments becoming relatively enriched or depleted, leading to misleading sequence data and NGS results. This means that more sequencing per sample is needed, so that a minimum level of coverage in a region of interest is achieved.

Sequence bias

The JetSeq DNA Library Preparation Kit uses a highly efficient polymerase, together with an optimized buffer formulation to ensure uniform amplification of all genomic regions including those that contain highly variable GC content, thereby reducing bias and ensuring even coverage in subsequent sequencing reactions.

HIGH-QUALITY LIBRARY CONSTRUCTION

Sequence coverage

Sequencing coverage describes the average number of reads that align to, or cover, known reference bases and determines whether variant discovery can be made with a certain degree of confidence at particular base positions. High-performance enzymes in the JetSeq Kit deliver exceptional sequence quality scores even 150 bases into the read (Fig. 3), giving greater coverage and reducing the possibility of sequencing gaps.

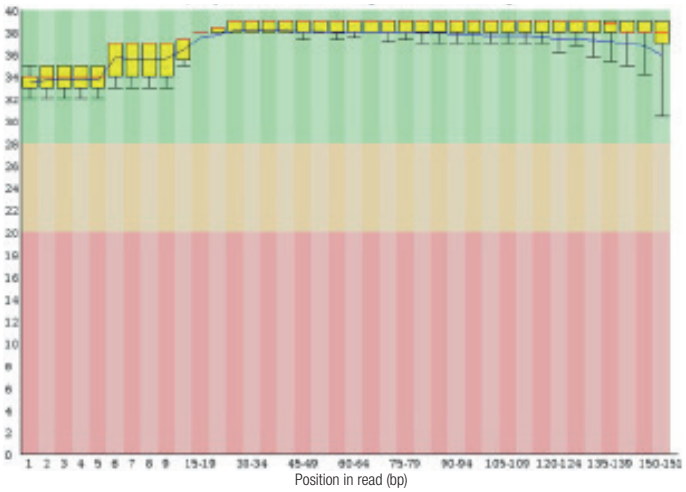

Fig. 3 Quality score across all bases
The median per base quality score was high (greater than 30 giving a base call accuracy of 99.9%) for all bases, including up to 150 bases into the read. This reduces the requirement for post-acquisition bioinformatics (e.g. read size reduction to remove poor quality sequence), giving complete confidence in the data.

Ordering Information

JetSeq™ DNA Library Preparation Kit	Size	Cat. #
JetSeq DNA Library Preparation Kit	16 Reactions	BIO-68025

Please contact us for institutional pricing, special price quotations and availability of bulk pack sizes.

PSGBL1115V1

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