LOTUS DNA LIBRARY PREP KIT

One kit. Flexible workflow. Endless applications.

Get the uniform sample coverage you need without relying on expensive equipment

Regain valuable time with a fast simple workflow

Create application-specific NGS libraries by adding IDT adapters and xGen products for target capture

The Lotus DNA Library Prep Kit enables streamlined preparation of high-quality next generation sequencing (NGS) libraries from double-stranded DNA. The kit uses enzymatic fragmentation to generate libraries suitable for PCR-free, PCR-amplified, and targeted sequencing applications on Illumina platforms.The kit combines a single-tube reaction for fragmentation, end repair, and dA tailing with ligation and bead-based purification steps, thereby reducing sample handling and overall library preparation time to approximately 2 hours (Figure 1). This kit is also compatible with a range of DNA inputs (1–250 ng) with low bias for uniform sequence coverage (Figure 2).

This modular kit allows you to customize your library for your application. For example:

- Fragment size—incubation times are used to control fragmentation size
- Adapters and indexing strategy—ligation is used to attach P5 and P7 adapters (not included in kit) using standard TA-library construction. Customize with full-length or stubby adapters, and use any sample indexing strategy you choose.
- Flexible workflow—PCR is optional, depending on your adapter or sample input requirements.

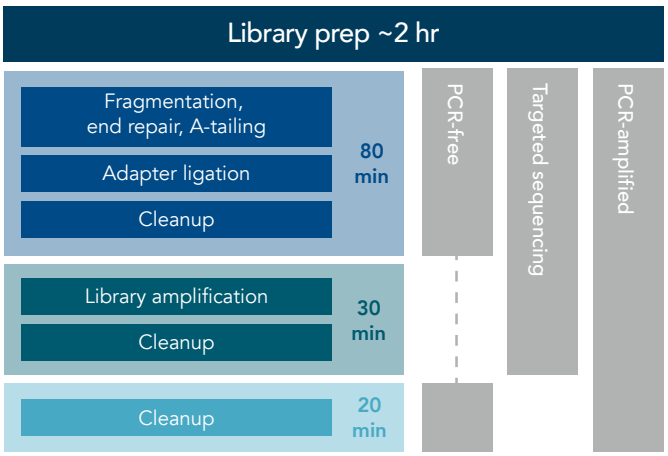

Figure 1. Lotus DNA Library Prep workflow. Our easy enzymatic method takes you from sample to sequencing while eliminating the need for acoustic shearing methods that require instrumentation and extra time.

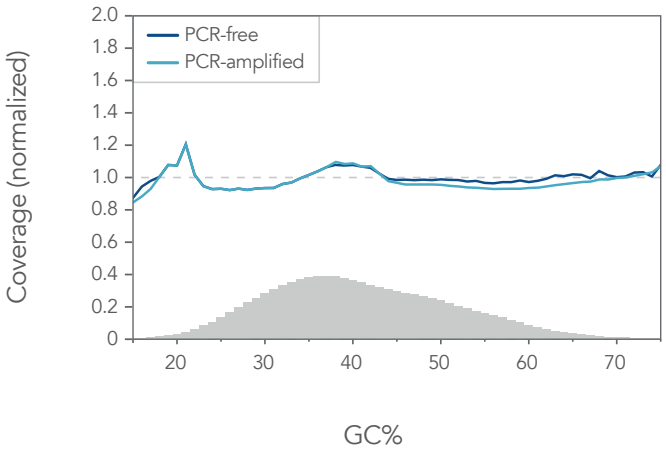

Figure 2. Uniform GC coverage and low bias from PCR-free and PCR-amplified libraries. Shown are normalized coverage of each Lotus library (dark and light blue lines), the expected normalized coverage of 1.0 (dotted line), and the number of 100 bp windows at each GC% (histogram).

SUPERIOR PERFORMANCE IN APPLICATIONS SUCH AS METAGENOMICS AND TARGETED SEQUENCING

The Lotus DNA Library Prep Kit is well-suited for a wide variety of applications. When tested with metagenomic samples, representation of an artificial microbial community was consistent across a range of inputs (Figure 3). IDT adapters and xGen Lockdown Probes and Panels are manufactured using stringent, proprietary methods that are critical for producing high-quality oligonucleotides for NGS applications. When these adapters and hybridization capture probes are used with the Lotus Kit for targeted sequencing, results show consistent, highly uniform, sequence coverage (Figure 4).

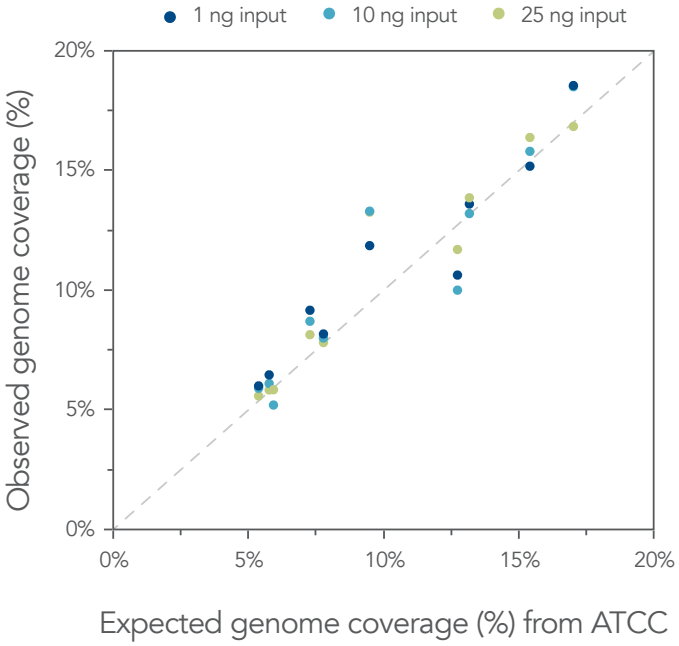

Figure 3. Variability in GC content, size of genomes, and input amount do not influence results in a metagenomics analysis. Libraries were prepared using the Lotus kit, MSA-1000™ microbiome standard (ATCC, an artificial microbial community of 10 strains; input amounts were 1, 10, and 25 ng), full-length adapters, and PCR amplification with P5 and P7 primers.

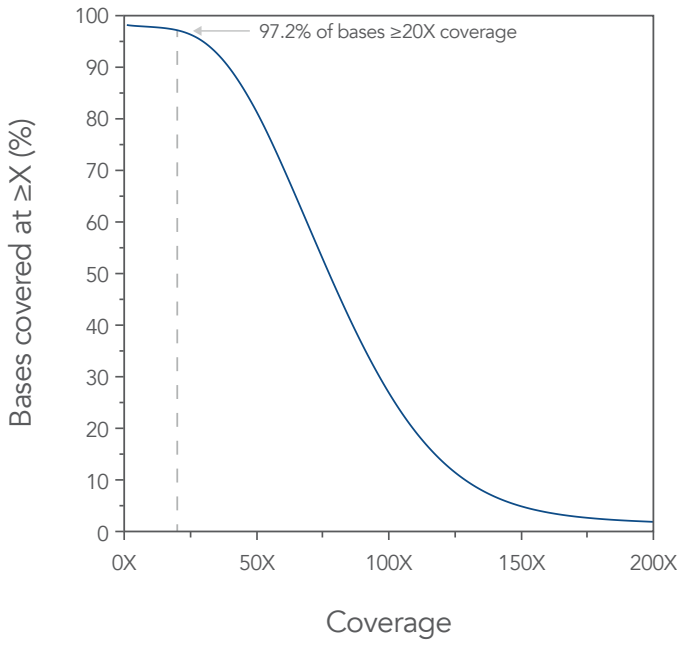

Figure 4. Highly uniform sequence coverage with the xGen Exome Research Panel v2 leads to lower sequencing costs. 12 Lotus DNA libraries were created from 100 ng of human genomic DNA (Coriell) using xGen Stubby Adapter and UDI Primer Pairs and were enriched in a single 12-plex capture using the xGen Exome Research Panel v2. The enriched libraries were sequenced (2 x 100) on a NextSeq® instrument (Illumina) and subsampled to 5 Gb. The data shows the mean coverage for the 12 libraries and indicates deep, uniform coverage with a flanked on-target rate of 94.7%, mean target coverage of 64.5X, and a duplication rate of 3.3% (calculated with Picard).

ORDERING INFORMATION

Product	Size	Catalog #
Lotus DNA Library Prep Kit	16 rxn	10001073
	96 rxn	10001074
	96 rxn	10005153
(Recommended) IDT adapters	Varies	www.idtdna.com/NGS-adapters
(Optional) IDT hybridization capture probes and reagents	Varies	www.idtdna.com/xGen

> FOR MORE INFORMATION, VISIT **WWW.IDTDNA.COM/LOTUS**

For Research Use Only. Not for use in diagnostic procedures.

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