

xGen™ METHYL-SEQ DNA LIBRARY PREPARATION KIT

Comprehensive methylome coverage from low-input research samples



Comprehensive sample representation



High multiplex capability



Low bias library preparation from low input amounts

The xGen Methyl-Seq Library Prep Kit utilizes Adaptase™ technology that efficiently captures bisulfite-converted ssDNA molecules into library molecules for epigenetic research studies. The resultant libraries represent uniform and comprehensive genome coverage.

APPLICATIONS

- Whole genome bisulfite sequencing (WGBS)
- Targeted sequencing with hybridization capture enrichment and reduced-representative bisulfite sequencing (RRBS)
- Genome-wide methylation identification using cfDNA
- Bisulfite-converted DNA enriched by methylated DNA immunoprecipitation (MeDIP), chromatin immunoprecipitation (ChIP), etc.

SAMPLE TYPES

- Genomic DNA
- Formalin-fixed, paraffin-embedded (FFPE)
- Circulating, cell-free DNA (cfDNA)
- Fresh and frozen tissue

2-HOUR WORKFLOW FOR BISULFITE-CONVERTED SAMPLES

The xGen Methyl-Seq DNA Library Prep Kit workflow maximizes DNA recovery through a post-bisulfite library preparation, utilizing an efficient adapter attachment that is compatible with single-stranded, bisulfite-converted DNA (**Figure 1**). Library complexity from this kit is significantly greater than those from methods that perform bisulfite conversion after library construction. Importantly, the template-independent adapter attachment chemistry of the xGen Methyl-Seq DNA Library Prep Kit provides a more complete, less biased library as observed from comprehensive methylome coverage by WGBS.

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

> WWW.IDTDNA.COM

Adaptase technology

- 17 minutes

Extension

- 8 minutes

Ligation

- 15 minutes

Indexing PCR

- Time varies

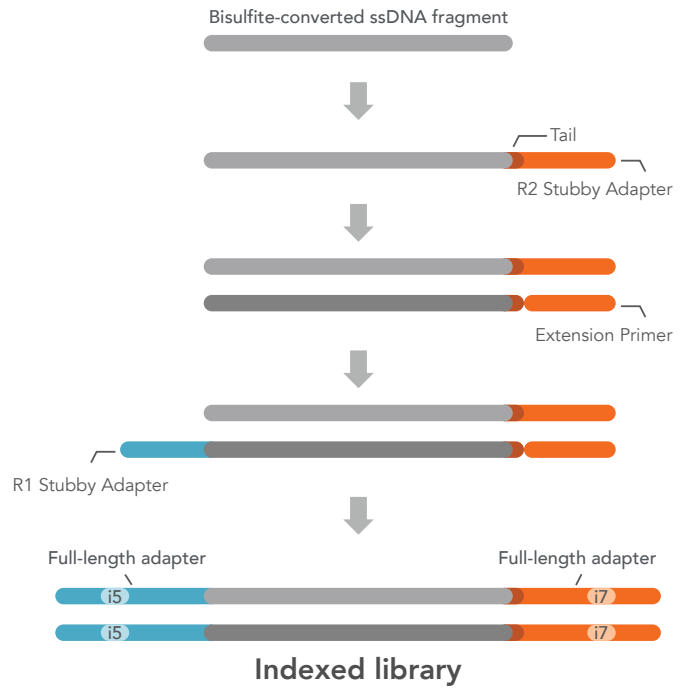
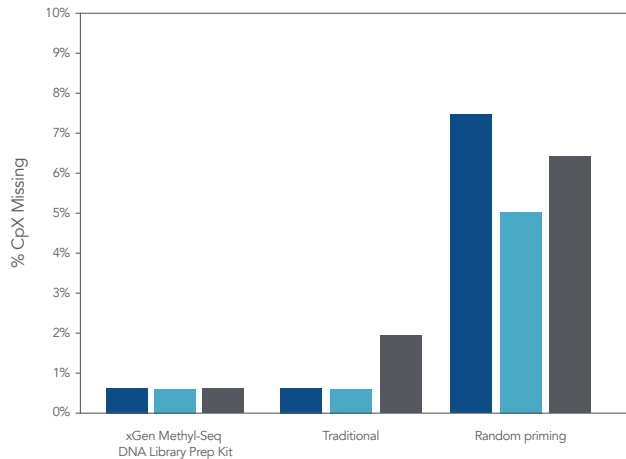


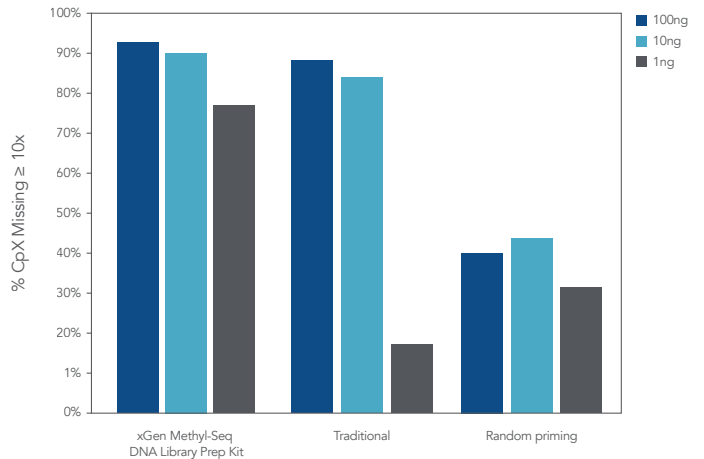
Figure 1. The xGen Methyl-Seq DNA Library Prep Kit workflow constructs libraries from single-stranded, bisulfite-converted DNA fragments. The Adaptase step simultaneously performs end repair, tailing, and ligation of the R2 Stubby Adapter to the 3' end of each fragment. The extension step produces a uracil-free strand, while the ligation step adds R1 Stubby Adapter to the new uracil-free strand. Indexing PCR increases library yield and incorporates full-length adapters with sample-specific index sequences.

COMPREHENSIVE COVERAGE FROM 1 NG OF INPUT DNA

(A) CpX sites uncovered



(B) CpX Sites covered $\geq 10X$



(A) At all three sample inputs (100 ng, 10 ng, and 1 ng) ($n = 2$), the xGen Methyl-Seq Library Prep Kit and the traditional bisulfite library prep method leave a minimal amount of CpX (CpG + CpH) sites uncovered. However, the random priming method exhibits at least 4% of CpX sites missing at every input amount tested. **(B)** The percentage of CpX sites covered at least 10X is greater than 90% for the xGen Methyl-Seq DNA Library Prep Kit at 100 ng but decreases to approximately 75% at 1 ng. The traditional bisulfite library prep method covers greater than 80% of CpX sites at least 10X for 100 ng and 10 ng inputs, but this coverage diminishes greatly at 1 ng. The random priming method exhibits poor coverage of CpX sites at each input, with the percentage of CpX sites covered at least 10X at about 40% for all inputs.

> FOR MORE INFORMATION, VISIT WWW.IDTDNA.COM/METHYL-SEQ

For Research Use Only. Not for diagnostic procedures. Unless otherwise agreed to in writing, IDT does not intend these products to be used in clinical applications and does not warrant their fitness or suitability for any clinical diagnostic use. Purchaser is solely responsible for all decisions regarding the use of these products and any associated regulatory or legal obligations.

© 2022 Integrated DNA Technologies, Inc. All rights reserved. xGen is a trademark of Integrated DNA Technologies, Inc., and is registered in the USA. Normalase and Adaptase are trademarks of Integrated DNA Technologies, Inc. All other marks are the property of their respective owners. For specific trademark and licensing information, see www.idtdna.com/trademarks.

Doc ID: RUO22-1251_001 08/22