xGen™ DNA EZ v2–Early Access

Reliable library prep, batch after batch: Consistent performance for your next generation sequencing (NGS) workflow

- Consistent performance
- Equivalent performance to mechanical shearing
- Low artifact rate
- PCR-Free Option

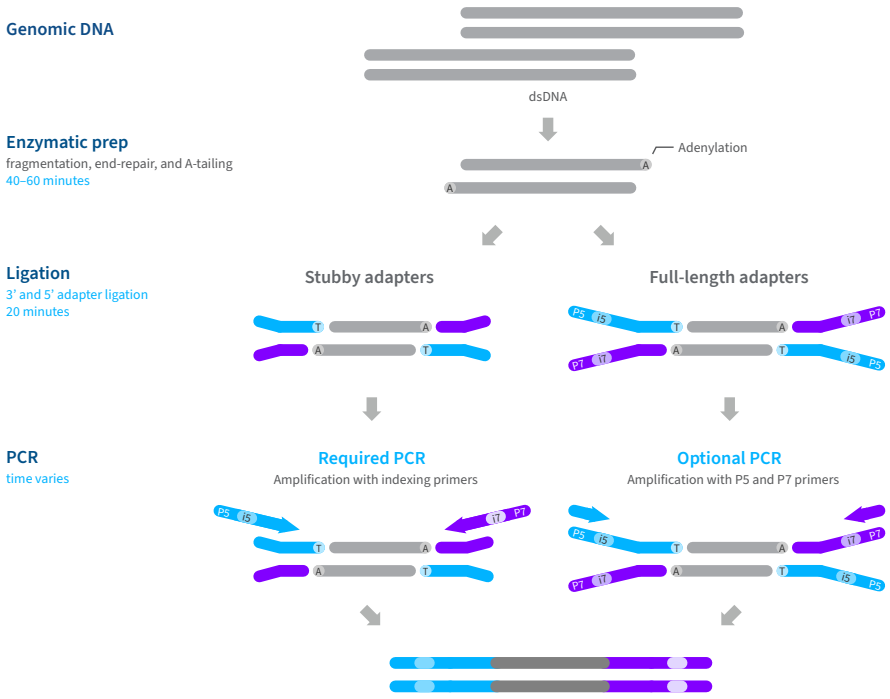
Your workflow, optimized for reliable results

Achieve reliable results without the guesswork. The xGen DNA Library Prep EZ v2 Kit is designed to deliver consistent workflow performance—batch after batch, user to user—so you can focus on generating high-quality sequencing data instead of troubleshooting variability. With a streamlined workflow and robust chemistry, this next-generation solution helps you save time, reduce errors, and gain confidence in every library prep.

• **Consistent Results Across Batches and Users** – Eliminate variability and reduce time spent adjusting fragmentation settings. Enjoy predictable performance every time.

• **Minimize Artifacts for Cleaner Data** – Achieve ultra-low artifact rates comparable to mechanical shearing, ensuring high-quality sequencing results.

• **Bias-Free, PCR-Free Options** – Achieve fragmentation performance equivalent to mechanical shearing while enabling PCR-free workflows that deliver more uniform coverage, reduce duplication rates, and minimize indels for superior sequencing accuracy.



The next generation of our trusted performer is here! The xGen DNA EZ Library Prep v2 Kit delivers unmatched versatility, supporting a wide range of input amounts and applications. Whether you prefer PCR or PCR-Free workflows, this kit is your reliable choice for streamlined, cost-effective sequencing.

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

idtdna.com

IDT™ INTEGRATED DNA TECHNOLOGIES

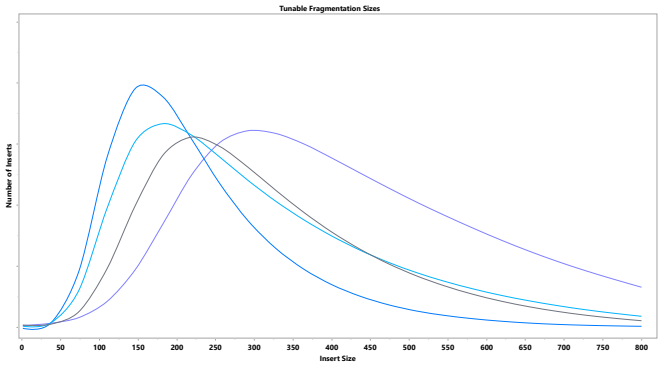
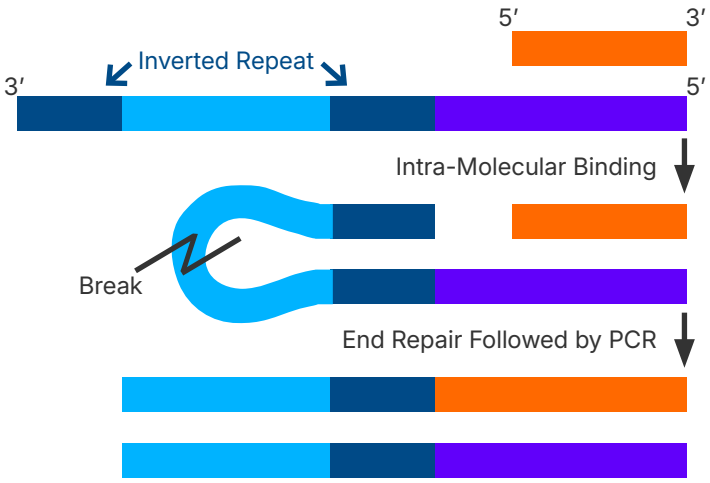


Figure 1. Tunable Fragmentation sizes generated by xGen EZ v2. Coriell DNA was used as the input into the xGen EZ v2 protocol with enzymatic shear times of 10 to 30 minutes. This resulted in insert sizes that varied from approximately 200 base pair (bp) to 400 bp. The resulting libraries were sequenced on a NextSeq 2000 with a P2 XLEAP flowcell. This demonstrates the ability for a single enzymatic fragmentation mix to generate different insert sizes with different reaction times.

FADE artifacts have been shown to impact variant calling by increasing false positives. Some enzymatic activity exposes inverted repeats and enables intramolecular binding, which can cause material from both strands to be combined into single strand.

High chimeras can negatively impact alignment, can masquerade as fusions or structural variants (inversions, translocations), consume more memory in BFX pipelines and increase the need for advanced algorithms to identify chimeric reads.



Gregory et al. NAR Genom Bioinform. 2020

Low Artifact Rate (Chimera, FADE) enables high-confidence variant calls and more accurate data while shortening turn around time.

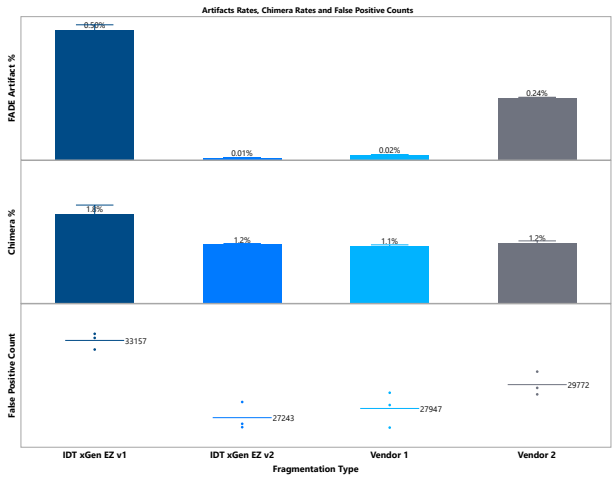


Figure 2. Artifact rates, Chimera rates, and false positive counts. Coriell DNA (25 ng, NA12878) was used as input into xGen EZ v1, xGen EZ v2, and two kits readily available from non-IDT vendors. The DNA was enzymatically sheared to 350 bp in accordance with the particular kit's protocol. The resulting libraries were subjected to targeting using the Standard 2000 hyb panel (IDT). 350 ng of library was used for a 17 hour hybridization for all libraries. The resulting targeted libraries (n = 3) were sequenced on a NextSeq2000 with a P3 XLEAP flow cell and the resulting data was downsampled to 20 M reads per library for analysis. The % FADE artifacts and % chimeras observed for each library type

Minimal fragmentation bias batch to batch and across users, equivalent to Covaris shearing, resulting in more uniform coverage and higher confidence in sequencing results.

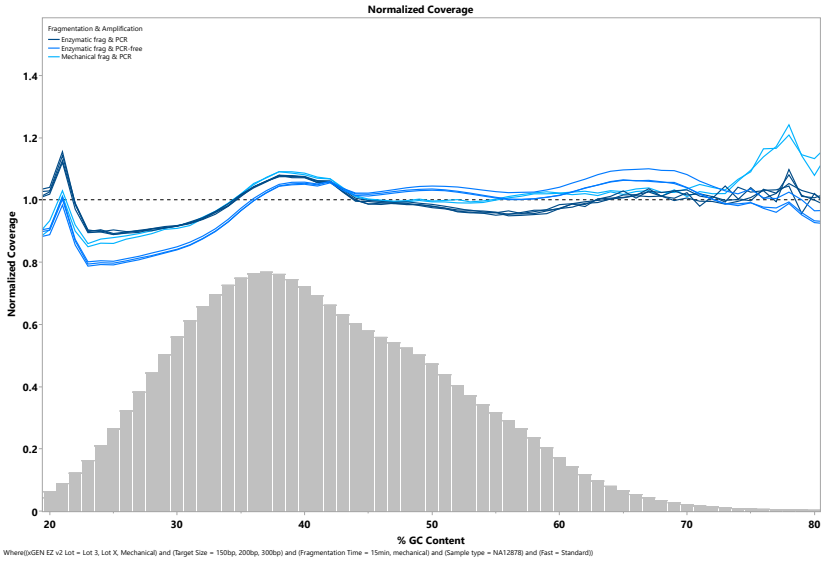


Figure 3. Genomic coverage for the xGen EZ v2 kit. This figure shows the genomic coverage for Coriell DNA (NA12878) for xGen EZ v2 with from either the PCR or PCR-free workflows and the xGen cfDNA and FFPE library prep kit with mechanical shearing. For PCR-free, 250 ng of DNA input was converted to library according to the xGen EZ v2 PCR-free protocol and sheared to 300 bp. The resulting libraries (n = 3) were sequenced on a NextSeq 2000 with a P4 XLEAP flow cell and downsampled to 340 M reads. For PCR, 100 ng of DNA input was converted to library according to the xGen EZ v2 with PCR protocol and sheared to 350 bp. The resulting libraries (n = 4) were sequenced on a NextSeq 2000 with a P2 XLEAP flow cell and downsampled to 2 M reads. For mechanically sheared libraries, 50 ng of DNA input was sheared to 150 bp and subjected to the xGen cfDNA and FFPE library prep kit with PCR amplification. The resulting libraries (n = 3) were sequenced on a NextSeq 2000 with a P2 flowcell and downsampled to 14 M reads. The resulting genomic coverage from 20-80% GC is shown here.

Consistency across batches, target sizes, input amounts, and users, resulting in more uniform coverage and higher confidence in sequencing results.

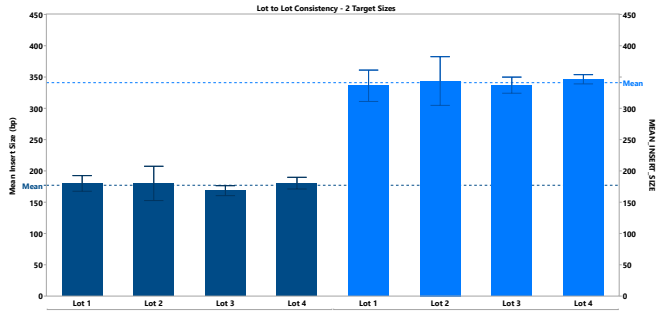
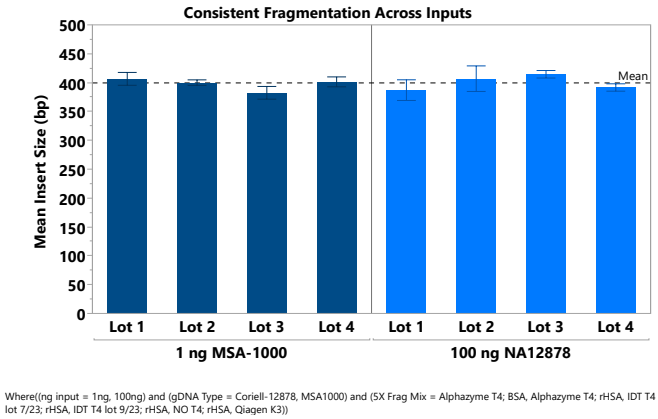


Figure 4. Lot to Lot consistency with four separate lots of enzymatic fragmentation mix at 200 bp and 350 bp shear sizes. One ng of Coriell DNA (NA12878) was used as input into the xGen EZ v2 protocol. The protocol was followed as written with enzymatic shear times of 22 minutes for 200 bp and 10 minutes for 350 bp. Four replicates were performed for each lot and each size. The resulting NGS libraries were sequenced on a NextSeq2000 with a P2 XLEAP flow cell and the resulting data was downsampled to 40 M reads per library (n = 4) for analysis. The mean insert size was determined and shown above. The four independent lots showed excellent consistency in library size at both 200 and 350 bp, indicating the ability to consistently create enzymatic fragmentation mixes.



Where((ng input = 1ng, 100ng) and (gDNA Type = Coriell-12878, MSA1000) and (5X Frag Mix = Alphazyme T4; BSA, Alphazyme T4; rHSA, IDT T4 lot 7/23; rHSA, IDT T4 lot 9/23; rHSA, NO T4; rHSA, Qiagen K3))

Figure 5. Consistent Fragmentation across inputs and DNA types. Both one ng of a bacterial genome mix (MSA-1000) and 100 ng of Coriell DNA (NA12878) was used as input into the xGen EZ v2 protocol and sheared to 350 bp using a 12 minute shear time. Four independent lots of fragmentation mix were used. The PCR cycles used were those recommended by the xGen EZ v2 protocol, specifically 9 cycles for 1 ng input and 3 cycles for 100 ng input. The resulting libraries (n = 4) were sequenced on a NextSeq2000 with a P2 XLEAP flow cell and the resulting data was downsampled to 20 M reads per library (MSA-1000) or 3-6 M reads per library (Coriell) for analysis. The mean insert size is shown here. Mean insert size across the different inputs is extremely consistent, with a 399.6 bp mean size observed for the 1 ng input and a 399.9 bp mean size observed for the 100 ng input. This demonstrates the consistency of the xGen EZ v2 fragmentation mix at varying input amounts and types.

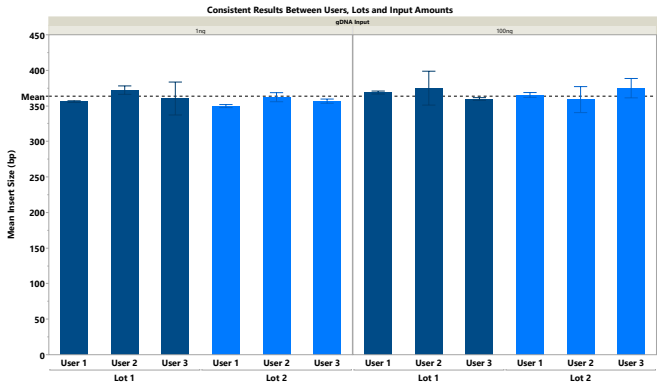


Figure 6. User consistency with xGen EZ v2. Mean insert sizes were generated using two independent lots of fragmentation mix in the xGen EZ v2 workflow with three different users. The users targeted 350 bp by shearing for 10 minutes. Two inputs, 1 ng and 100 ng, were also included in this experiment. The resulting libraries (n = 4 minimum per condition) were sequenced on a NextSeq 2000 with a P3 XLEAP flowcell and downsampled to 20 M reads. Excellent size consistency was observed between lots, users, and input amounts.

Specifications

Feature	Detail
Sample Types	Fresh frozen tissue, gDNA, PCR amplicons, high quality FFPE*
Input range	0.1-1000 ng
Adapters	Stubby adapter included, to support PCR+ workflows, indexing primers sold separately Full-length adapters sold separately
Sequencer system compatibility	Illumina sequencing instruments, Ultima Genomics UG100, Element Biosciences AVITI, DNBSEQ sequencer

Ordering information

Catalog #	Product	Price
10029335	xGen DNA Library Prep EZ v2 (EAP), 96 rxn*	$1,137.50

**Early Access kit configuration supports both PCR +/- workflows*

For more information, visit **go.idtdna.com/NGSearlyaccess**