MosaiX™ Library Prep Kit

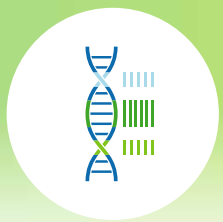
High-Complexity DNA Library Preparation

Early Access

Whole Genome Sequencing

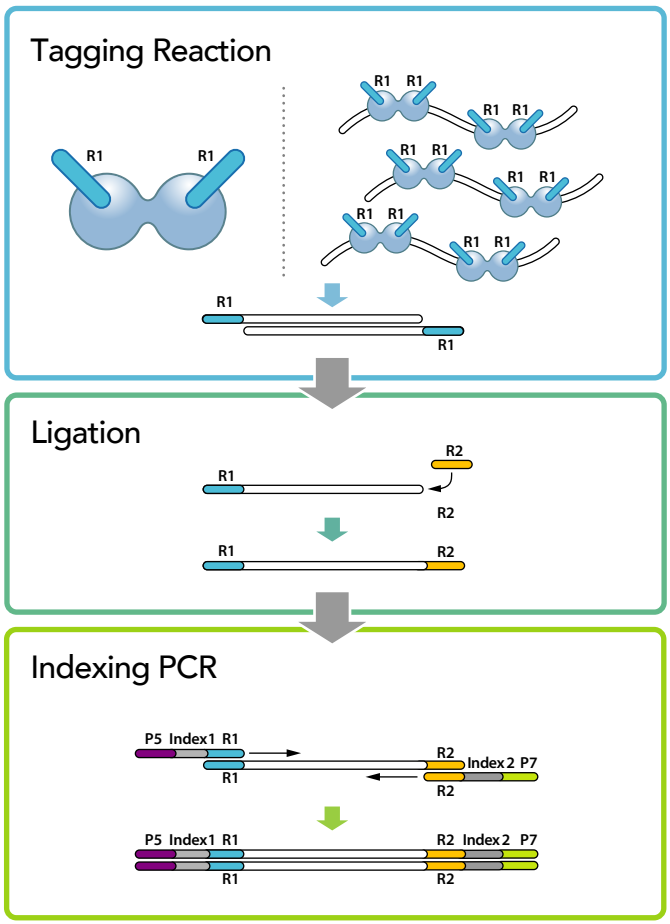
Low Pass Genome Sequencing

Whole Exome Sequencing



Targeted Hybrid Sequencing

The simplicity of tagmentation, the library complexity of ligation



seqWell directional tagmentation with TnX™ …complexity made simple

No need to choose between ease-of-use, library complexity or cost-efficiency. With MosaiX you can have all three.

- Uniform sequence coverage with low duplication rate
- High degree of flexibility: DNA input, batch size, index strategy, and buffer tolerance
- Streamlined workflow provides time and labor savings
- Significant cost and consumables savings

Figure 1: DNA is fragmented and 5′ Read 1 (R1) adapters added via tagmentation using TnX, followed by 3' ligation of Read 2 (R2) adapters. P5 and P7 indexes are added via PCR.

seqWell

MosaiX™ Library Prep Kit

seqWell Directional Tagmentation: 90-minute Workflow

MosaiX library prep generates high-complexity libraries with an automation-friendly workflow powered by TnX , the next-generation transposase engineered for reduced insertion bias, increased enzyme activity, and enhanced inhibitor tolerance. TnX simplifies fragmentation by eliminating the need for time-consuming DNA shearing or digestion while providing improved uniformity of coverage compared to alternative library prep methods.

Streamlined, Scalable Workflow

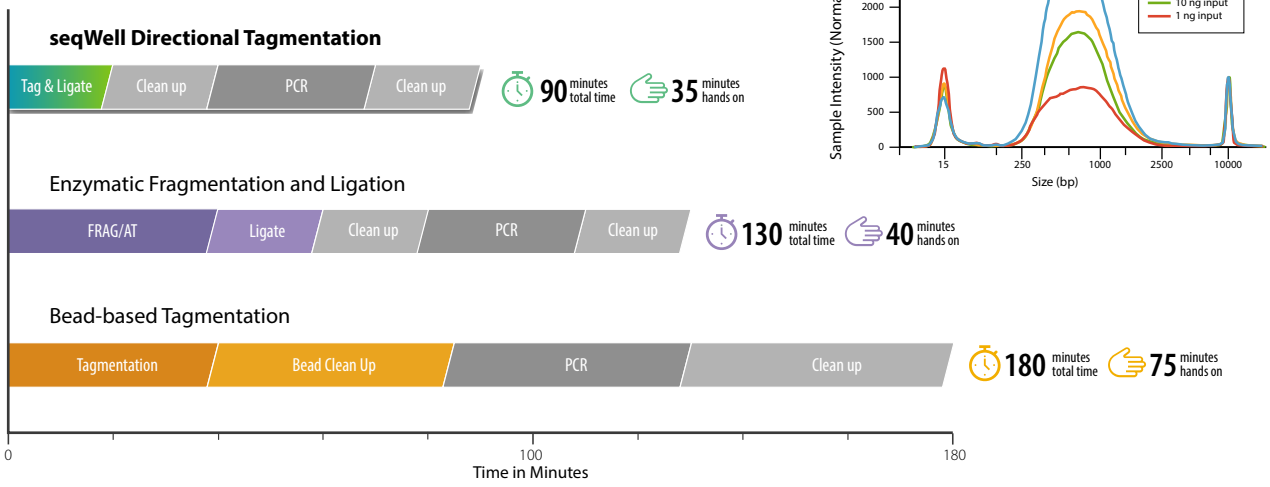


Figure 2: Times for technology workflows are based on manufacturers' standard protocols. During seqWell directional tagmentation, the tagging and ligation reactions occur sequentially with in the same well. Following bead clean up, P5 and P7 indexes are added via PCR. **Inset** – Following PCR, libraries prepared from 1-50 ng of human genomic DNA (NA12878) using MosaiX were diluted 1:10 and run on a TapeStation D5000 HS kit for fragment sizing. Mean fragment sizes (with adapter) of ~650 – 850 bp were seen independent of DNA starting concentration.

Reduced Insertion Bias and Improved Inhibitor Tolerance

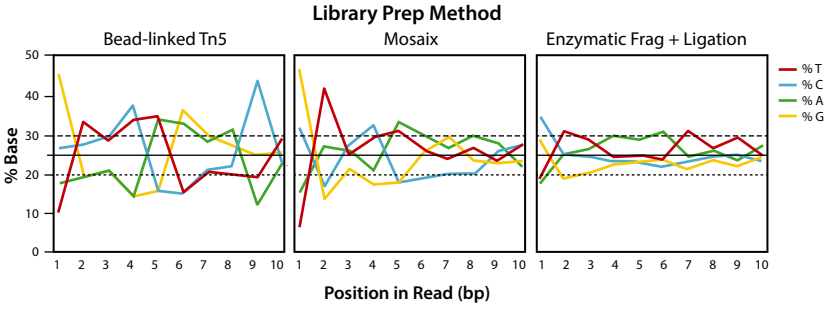


Figure 3: Read start base bias for bead-linked tagmentation (Tn5), MosaiX (TnX), and enzymatic fragmentation are shown. Reduced bias of TnX versus Tn5 is observed with a profile similar to that of enzymatic fragmentation.

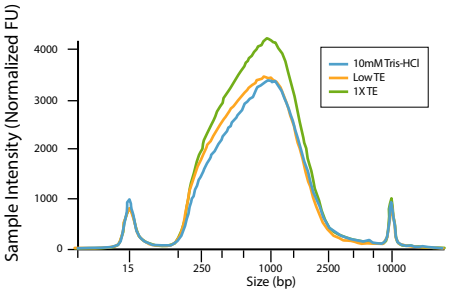
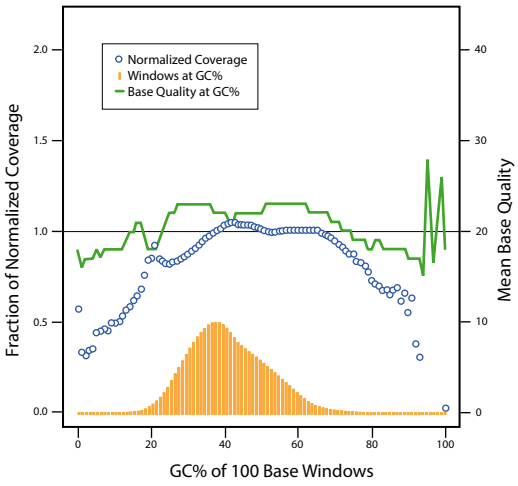


Figure 4: MosaiX fragmentation profiles are unaffected by EDTA allowing DNA dilution in a variety of buffers.

MosaiX™ Library Prep Kit

High-complexity Libraries Using 50% Shorter Workflow

Superior Performance & Scalability - Whole Genome Sequencing (WGS)



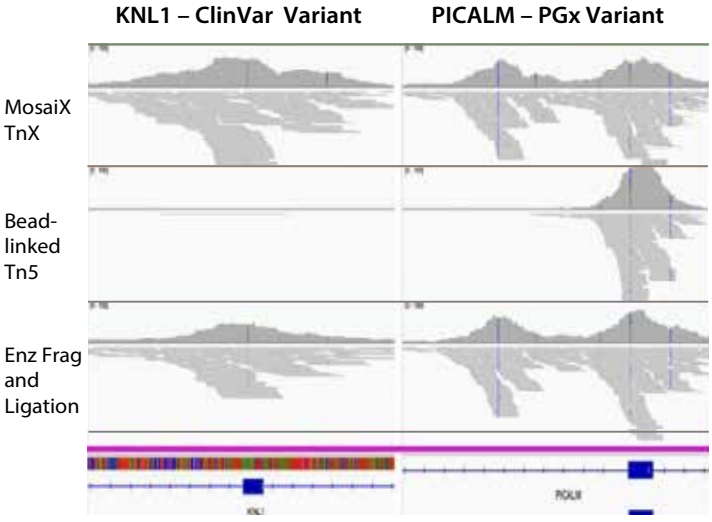
MosaiX library prep led to superior WGS sequence data compared to a competitor tagmentation method, including higher mean coverage, lower duplication rate and larger estimated library size (complexity). It's streamlined workflow provides the speed and scalability to support WGS efforts of any size.

Library Prep Method	Mean Coverage (X)	% Bases ≥20X	Duplication (%)	Estimated Library Size
MosaiX	27.4	84%	10%	3,374,667,137
Bead-linked Tn5	23.9	80%	14%	2,871,092,622

Figure 5: Libraries were generated from 50 ng of NA12878 DNA (Genome in a Bottle) using MosaiX (seqWell) or a competitor tagmentation-based kit following manufacturers' standard protocols. Libraries were sequenced on a NovaSeq™ X Plus, data down sampled to 105 Gb, and sequences aligned to hg38. A normalized coverage plot including mean base quality for MosaiX libraries shows the reduced GC bias of TnX.

Find Those Critical Exome Targets with TnX

Improved Variant Detection - Whole Exome Sequencing (WES)



No need to sacrifice variant calling quality to scale up your WES projects. TnX transposase can access difficult regions that Tn5 cannot, leading to less target drop outs compared to competitor transposase methods.

Library Prep Method	Duplication (%)	HS Library Size	% Zero Cvg
MosaiX	4.2%	285,255,870	0.69%
Bead-linked Tn5	7.9%	167,531,020	0.82%
Enz. Frag & Ligation	6.0%	201,223,608	0.68%

Figure 6: Libraries were generated using MosaiX, competitor bead-linked tagmentation, or competitor enzymatic fragmentation and ligation from 50 ng of NA12878 DNA (Genome in a Bottle). Libraries underwent target capture using Twist's Exome 2.0 panel and sequenced on a NextSeq™ 2000. Data were down sampled to 6 Gb each and aligned to Twist exome capture targets on hg38.

seqWell

"I have been really impressed with the **outstanding performance** of MosaiX library prep...

...(which) **reliably resulted** in libraries with **high complexity and uniform coverage** that provided for more **precise sequencing data.**

All this was achieved using an extremely **efficient workflow**."

Massimo Delledonne, PhD
Professor of Genetics,
University of Verona, Italy

MosaiX Library Prep Specifications (Early Access)

Sample Input Types	Genomic DNA
DNA Input Range	1 - 50 ng*
Buffer Compatibility	DNA diluted in 10mM Tris-HCl, 1X TE, Low TE, or Water
Total Library Prep Time	90 minutes (35 minutes hands-on time)
Mean Output Fragment Size** *Fragment sizes as measured by TapeStation (including adapters)*	• WGS protocol (recommended 0.7x bead clean up): 850 bp ± 15% • Target capture protocol (recommended 0.8x bead clean up): 700 bp ± 15%
Indexing Strategy	• Any tagmentation-compatible indexing or custom primers can be used • 24 or 96 UDI primers will be provided with early access
Supported Paired Reads (clusters/sample)	≥400 million
Reactions per kit	24 or 96
Sequencer Compatibility	• All Illumina sequencing platforms • Compatible with Complete Genomics platforms or Element Biosciences AVITI™ using conversion kits for Illumina libraries

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