

seqWell

# **NGS DNA Library Preparation**

## Get your data faster with seqWell's library prep workflows

#### Better Transposase | Better Libraries | Better NGS

Accelerate your NGS workflows with a truly multiplexed library preparation solution engineered for speed, consistency and scalability. seqWell's advanced tagmentation-based technology enables the rapid generation of high-quality libraries from hundreds to thousands of samples, dramatically reducing time to data.

At the heart of this solution is TnX, seqWell's next-generation transposase, which delivers superior coverage uniformity, higher library yields and greater complexity. The streamlined, plate-based workflow minimizes hands-on time and simplifies sample handling, allowing for seamless integration into your existing lab processes. Effortlessly multiplex thousands of samples with built-in normalization that ensures reliable, reproducible results every time.

Designed to scale with your research, this solution supports a wide range of applications - from synthetic biology and targeted amplicon sequencing to both low- and high-depth whole-genome sequencing of human, plant, animal, and microbial samples. See reverse side for the seqWell Kit Comparison Guide.

### www.biocat.com/seqwell



- Streamlined workflows
- High level of multiplexing
- Automation-friendly
- Increased throughput
- Improved data uniformity

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## seqWell Kit Comparison Guide

Product	ExpressPlex <sup>™</sup> 2.0	purePlex™	plexWell™	MosaiX™	LongPlex™
Primary Applications	Plasmid and amplicon sequencing	<ul> <li>Low frequency variants in plasmids and ampli- cons</li> <li>Microbial/small ge- nome WGS</li> <li>Low coverage human/ large genome WGS</li> <li>Metagenomic sequen- cing</li> </ul>	<ul> <li>Low frequency variants in plasmids and ampli- cons</li> <li>Microbial/small ge- nome WGS</li> <li>Low coverage human/ large genome WGS</li> </ul>	<ul> <li>Human whole genome sequencing (WGS)</li> <li>Human whole exome sequencing (WES)</li> <li>Human germ line target capture panels</li> <li>Plant &amp; animal WGS and target capture panels</li> </ul>	<ul> <li>Long read sequencing</li> <li>Microbial/small genome WGS</li> <li>Targeted hybrid capture</li> <li>Metagenomic sequencing</li> <li>Low pass, large genome</li> </ul>
Transposase Enzyme	TnX	Hyperactive Tn5	Hyperactive Tn5	TnX	Hyperactive Tn5
Sample Types	Amplicons (>350 bp), Plasmids	Amplicons (>500 bp), Plasmids, Genomic DNA	Amplicons (>500 bp), Plasmids, Genomic DNA	Genomic DNA	Genomic DNA
Total Prep Time (hands-on time)	100 min (30 min)	155 min (45 min)	190 min (55 min)	90 min (35 min)	105-225 min* (40 min)
Input Mass	1 - 40 ng	5 - 50 ng (based on batch size)	3 - 30 ng, 5 - 25 ng 10 ng average	50 - 100 ng	150 - 500 ng
Indexing Method	CDI	UDI	CDI	Any tagmentation- compatible indexing or custom primers	UDI
Batch Range	8-96 or 348*	8-24	96	1-96	1-24*
Total Samples	96 / 384 / custom	96	96 / 384	24 / 96	96
Number of Available Unique Index Combina- tions	up to 6144	384	96 / 2304	N/A	96
Paired-End Reads (Clusters) per Sample Supported	≤4 million	≤20 million	≤4 million, ≤20 million	≥400 million	N/A
Sequencing Platform	Illumina	Illumina	Illumina	Illumina	PacBio

\*Depending on the protocol