

# seqWell Product Comparison Guide



Product	ExpressPlex™ 2.0 Library Prep Kit	ExpressPlex™ Plus Library Prep Kit (Coming soon)	AgriPrep™ Library Prep Kit	MosaiX™ Library Prep Kit	LongPlex™ Multiplexing Kit
Primary Applications	<ul style="list-style-type: none"> <li>Plasmid and amplicon sequencing</li> </ul>	<ul style="list-style-type: none"> <li>Microbial/small genome WGS</li> <li>Metagenomic sequencing</li> <li>Low-pass coverage of large genomes (up to 5X human coverage)</li> </ul>	<ul style="list-style-type: none"> <li>Genotyping-by-sequencing (GBS)</li> <li>Low-pass sequencing</li> <li>Skim sequencing</li> </ul>	<ul style="list-style-type: none"> <li>Human whole genome sequencing (WGS)</li> <li>Human whole exome sequencing (WES)</li> <li>Human germline target capture panels</li> <li>Plant &amp; animal WGS and target capture panels</li> </ul>	<ul style="list-style-type: none"> <li>Long-read sequencing</li> <li>Plasmid sequencing</li> <li>Microbial/small genome WGS</li> <li>Targeted hybrid capture</li> <li>Matagenomic sequencing</li> <li>Low-pass, large genome</li> </ul>
Transposase Enzyme	TnX™	TnX™	TnX™	TnX™	Hyperactive Tn5
Sample Types	Amplicons (>350 bp), plasmids, colony PCR, RCA	Genomic DNA	Plant & animal genomic DNA	Genomic DNA	Genomic DNA
Total Prep Time (hands on time)	100 min (30 min)	100 min (30 min)	100 min (30 min)	90 min (35 min)	105-225 min* (40 min)
Input Mass	1-40 ng	<ul style="list-style-type: none"> <li>10-200 ng working range</li> <li>20-100 ng normalization range</li> </ul>	<ul style="list-style-type: none"> <li>10-200 ng working range</li> <li>20-100 ng normalization range</li> </ul>	50-100 ng	150-500 ng
Indexing Method	CDI	CDI	CDI	Any tagmentation-compatible indexing or custom primers	UDI
Batch Range	8-96 or 384*	8-96	8-96	1-96	1-24*
Number of Samples/Kits	96/384/custom	96	96	24/96	96
Number of Available Unique Index Combinations	Up to 6144	Up to 1536	<ul style="list-style-type: none"> <li>Up to 1536 off-the-shelf</li> <li>Up to 3072 via custom ordering</li> </ul>	N/A	96
Paired-End Reads (Clusters) per Sample Supported	≤2 million	≤50 million	≤50 million	≥400 million	N/A

\*depending on the protocol

# seqWell Tagify™ Reagent Comparison Guide



Reagents	Tagify i5 UMI	Tagify Custom
Primary Applications	Gene editing on/off-target analysis assays	<ul style="list-style-type: none"> <li>• Gene editing on/off-target analysis assays</li> <li>• Chromatin accessibility assays</li> <li>• Any application requiring DNA fragmentation &amp; tagging</li> </ul>
Transposase Enzyme	Hyperactive Tn5	TnX or Hyperactive Tn5
Sample Types	Genomic DNA	Genomic DNA
Barcoding Strategy	Up to 24 unique: <ul style="list-style-type: none"> <li>• 10 bp i5 barcode</li> <li>• 10 bp UMI sequence</li> </ul>	Custom <ul style="list-style-type: none"> <li>• i5/i7</li> <li>• Universal adapters</li> <li>• Customer-specified oligo</li> <li>• UMI, UDI, CDI</li> </ul>
Reactions/Kit	<ul style="list-style-type: none"> <li>• 1 or 4 sets of Tagify i5 UMI 24 stamped in 96-well microtiter plate</li> <li>• Custom dispense</li> </ul>	N/A
DNA Input Recommended	50 ng	Dependent on customer application
Standard Dispense Volume/Well	3 µl or 4 µl in 96-well microtiter plate	Custom dispense in tube or plate (10 µl minimum volume)
Output Fragment Range	800-2000 bp (using region mode with a range of 200-7500 bp)	Fragment range designed to meet customer needs