

seqWell Product Comparison Guide



Product	ExpressPlex™ 2.0 Library Prep Kit	ExpressPlex™ Plus Library Prep Kit <i>(Coming soon)</i>	AgriPrep™ Library Prep Kit	MosaiX™ Library Prep Kit	LongPlex™ Multiplexing Kit
Primary Applications	<ul style="list-style-type: none"> Plasmid and amplicon sequencing 	<ul style="list-style-type: none"> Microbial/small genome WGS Metagenomic sequencing 	<ul style="list-style-type: none"> Genotyping-by-sequencing (GBS) Low-pass sequencing: up to 5x human Skim sequencing Targeted hybrid capture 	<ul style="list-style-type: none"> Human whole genome & whole exome sequencing Targeted hybrid capture Plant & animal WGS Microbial & metagenomic sequencing 	<ul style="list-style-type: none"> Long-read sequencing Plasmid sequencing Microbial/small genome WGS & metagenomics Targeted hybrid capture Low-pass, large genome
Transposase Enzyme	TnX™	TnX™	TnX™	TnX™	Hyperactive Tn5
Sample Types	Amplicons (>350 bp), plasmids, colony PCR, RCA	Microbial genomic DNA	Plant, animal & human genomic DNA	Genomic DNA	Genomic DNA & plasmids
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)
DNA Input Concentration	<ul style="list-style-type: none"> 0.25-10 ng/μl working range 1.25-10 ng/μl normalization range 	<ul style="list-style-type: none"> 1.25-12.5 ng/μl working range 2.5-12.5 ng/μl normalization range 	<ul style="list-style-type: none"> 2.5-50 ng/μl working range 5-25 ng/μl normalization range 	0.25-4 ng/μl	10-33.3 ng/μl*
DNA Input Total Mass	<ul style="list-style-type: none"> 1-40 ng* working range 5-40 ng* normalization range 	<ul style="list-style-type: none"> 5-50 ng working range 10-50 ng normalization range 	<ul style="list-style-type: none"> 10-200 ng working range 20-100 ng normalization range 	1-40 ng	150-500 ng*
Indexing Method	CDI	CDI	CDI	Any tagmentation-compatible indexing or custom primers	UDI
Sample Batch Range	8-96 or 384*	8-96	8-96	1-96	1-24 or 8-24*
Number of Samples/Kits	96/384/custom	96/384/custom	96/384/custom	24/96	96
Number of Available Unique Index Combinations	Up to 6144	Up to 1536	<ul style="list-style-type: none"> Up to 1536 off-the-shelf Up to 3072 via custom ordering 	96	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 TnX Universal Adapters	Tagify Custom
Primary Applications	Gene editing on/off-target analysis assays	NGS assays relying on Illumina-compatible adapters	<ul style="list-style-type: none"> • Gene editing on/off-target analysis assays • Chromatin accessibility assays • Any application requiring DNA fragmentation & tagging
Transposase Enzyme	Hyperactive Tn5	TnX	TnX or Hyperactive Tn5
Sample Types	Various forms of DNA	Various forms of DNA	Various forms of DNA
Barcoding Strategy	Up to 24 unique: <ul style="list-style-type: none"> • 10 bp i5 barcode • 10 bp UMI sequence 	Equimolar Illumina-compatible P5 & P7 universal adapters	Custom <ul style="list-style-type: none"> • i5/i7 • Universal adapters • Customer-specified oligo • UMI, UDI, CDI
Reagent Size	<ul style="list-style-type: none"> • 1 or 4 sets of Tagify i5 UMI 24 stamped in 96-well microtiter plate • Custom dispense 	<ul style="list-style-type: none"> • 50 µl at 0.2 U/µl • 200 µl at 0.2 U/µl 	N/A
DNA Input Recommended	50 ng	Dependent on customer application	Dependent on customer application
Standard Dispense Volume/Format	3 µl or 4 µl/well in 96-well microtiter plate	50 µl or 200 µl/vial	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)	650 - 850 bp	Fragment range designed to meet customer needs