

	plexWell 96	plexWell 384	plexWell Plus 24	plexWell WGS24	plexWell Kit Comments
Method	Sequential Transposition	Sequential Transposition	Sequential Transposition	Sequential Transposition	Normalized iterative barcoding
Sample Type	Amplicons, Plasmids, Genomic DNA, cDNA	Amplicons, Plasmids, Genomic DNA, cDNA	Amplicons, Plasmids, Genomic DNA, cDNA	Genomic DNA	FFPE samples or amplicons/short fragments < 200 bp are not applicable
DNA Input Required	3-30 ng	3-30 ng	3-30 ng	300 ng	Input Totals per Sample
Format	1 x 96	4 x 96	Multiplex in increments of 8, 16 or 24	1x24	Kit configurations were specifically designed to create flexible multiplexing
Number of Unique Index Combinations	96	384	96	24	Indexes are pre-aliquoted in 96 well plates
Application	Synthetic construct sequencing (amplicons, plasmids, etc), low-pass whole genome sequencing, whole small genome sequencing (<20Mb), scRNA-seq, Metagomics/Microbiome Screening	Synthetic construct sequencing (amplicons, plasmids, etc), low-pass whole genome sequencing, whole small genome sequencing (<20Mb), scRNA-seq, Metagomics/Microbiome Screening	Synthetic construct sequencing (amplicons, plasmids, etc), low-pass whole genome sequencing, whole small genome sequencing (<20Mb), scRNA-seq, Metagomics/Microbiome Screening	Complex Whole Genome (>20 Mb) for high coverage sequencing	Targeted hybridization, targeted panels and exomes are not validated yet.
Supported Data Output/Sample	<= 1.5 Gbp per sample	<= 1.5 Gbp per sample	<= 1.5 Gbp per sample	validated up to 120 Gbp per sample	Supports Variable Data Output/Sample - depends on sample type, coverage and available sequencer
Average output fragment size	400 bp	400 bp	400 bp	550 bp	Tunable and plexWell generates larger, uniform average insert size compared to other kits.
Number of PCR cycles	12	12	12	4	
Sequencer compatibility	MiSeq, NextSeq 500, NovaSeq 6000, iSeq, all HiSeq - all compatible with appropriate final library sizing	MiSeq, NextSeq 500, NovaSeq 6000, iSeq, all HiSeq - all compatible with appropriate final library sizing	MiSeq, NextSeq 500, NovaSeq 6000, iSeq, all HiSeq - all compatible with appropriate final library sizing	HiSeq, NovaSeq 6000	