

	plexWell 96	plexWell 384	plexWell Plus 24	plexWell LP 384	plexWell WGS24	Kit comments
Method	Sequential transposition	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	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	5 – 25 ng	200 ng	Input totals per sample
Format	1 x 96	4 x 96	Multiplex in increments of 8, 16, or 24	4 x 96	1 x 24	Kit configurations were specifically designed to create flexible multiplexing
Number of unique index combinations	96	Up to 1,152	96	Up to 1,152	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 (<20 Mb), scRNA-seq, Metagomics/Microbiome screening	Synthetic construct sequencing (amplicons, plasmids, etc.), Low-pass whole genome sequencing, Whole small genome sequencing (<20 Mb), scRNA-seq, Metagomics/Microbiome screening	Synthetic construct sequencing (amplicons, plasmids, etc.), Low-pass whole genome sequencing, Whole small genome sequencing (<20 Mb), scRNA-seq, Metagomics/Microbiome screening	Synthetic construct sequencing (amplicons, plasmids, etc.), Low-pass whole genome sequencing, Whole small genome sequencing (<50 Mb), scRNA-seq, Metagomics/Microbiome screening	Complex whole genome (>20 Mb) for high-coverage sequencing	Targeted hybridization, targeted panels, and exomes are not yet validated
Supported paired reads (clusters)/sample	≤4 million	≤4 million	≤4 million	≤10 million	≤400 million	
Output fragment range*	400 – 1,200 bp	400 – 1,200 bp	400 – 1,200 bp	400 – 1,200 bp	500 – 1,000 bp	Tunable and plexWell generates larger, uniform average insert size compared to other kits
Number of PCR cycles	12	12	12	8	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	MiSeq, NextSeq 500, NovaSeq 6000, iSeq, all HiSeq—all compatible with appropriate final library sizing	HiSeq, NovaSeq 6000	

\*Average fragment size will be dependent on SPRI cleanup parameters used.