

	plexWell™ 96	plexWell™ 384	plexWell™ Plus 24	plexWell™ LP 384	purePlex™ DNA Library Prep	plexWell™ WGS24
Method	Sequential transposition	Sequential transposition	Sequential transposition	Sequential transposition	Sequential transposition	Sequential transposition
Sample type	Amplicons, Plasmids, Genomic DNA, cDNA	Amplicons, Plasmids, Genomic DNA, cDNA	Amplicons, Plasmids, Genomic DNA, cDNA	Genomic DNA	Amplicons, Plasmids, Genomic DNA, cDNA	Genomic DNA
Reactions per kit	96	384	96	384	96	24
DNA input required	3 – 30 ng	3 – 30 ng	3 – 30 ng	5 – 25 ng	5 - 50 ng	200 ng
Format	1 x 96	4 x 96	Multiplex in increments of 8, 16, or 24	4 x 96	Up to 96-plex Allows flexible batching anywhere from 1-96	1 x 24
Indexing Method	CDI	CDI	CDI	CDI	UDI	CDI
Number of unique index combinations	96	2,304	96	2,304	96	24
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	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
Supported paired reads (clusters)/sample	≤4 million	≤4 million	≤4 million	≤20 million	≤ 20 million	≤400 million
Output fragment range*	400 – 1,200 bp	400 – 1,200 bp	400 – 1,200 bp	400 – 1,200 bp	400 - 1200 bp	500 – 1,000 bp
Number of PCR cycles	12	12	12	8	8	4
Sequencer compatibility	plexWell and purePlex libraries are compatible with all Illumina sequencing platforms.					

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