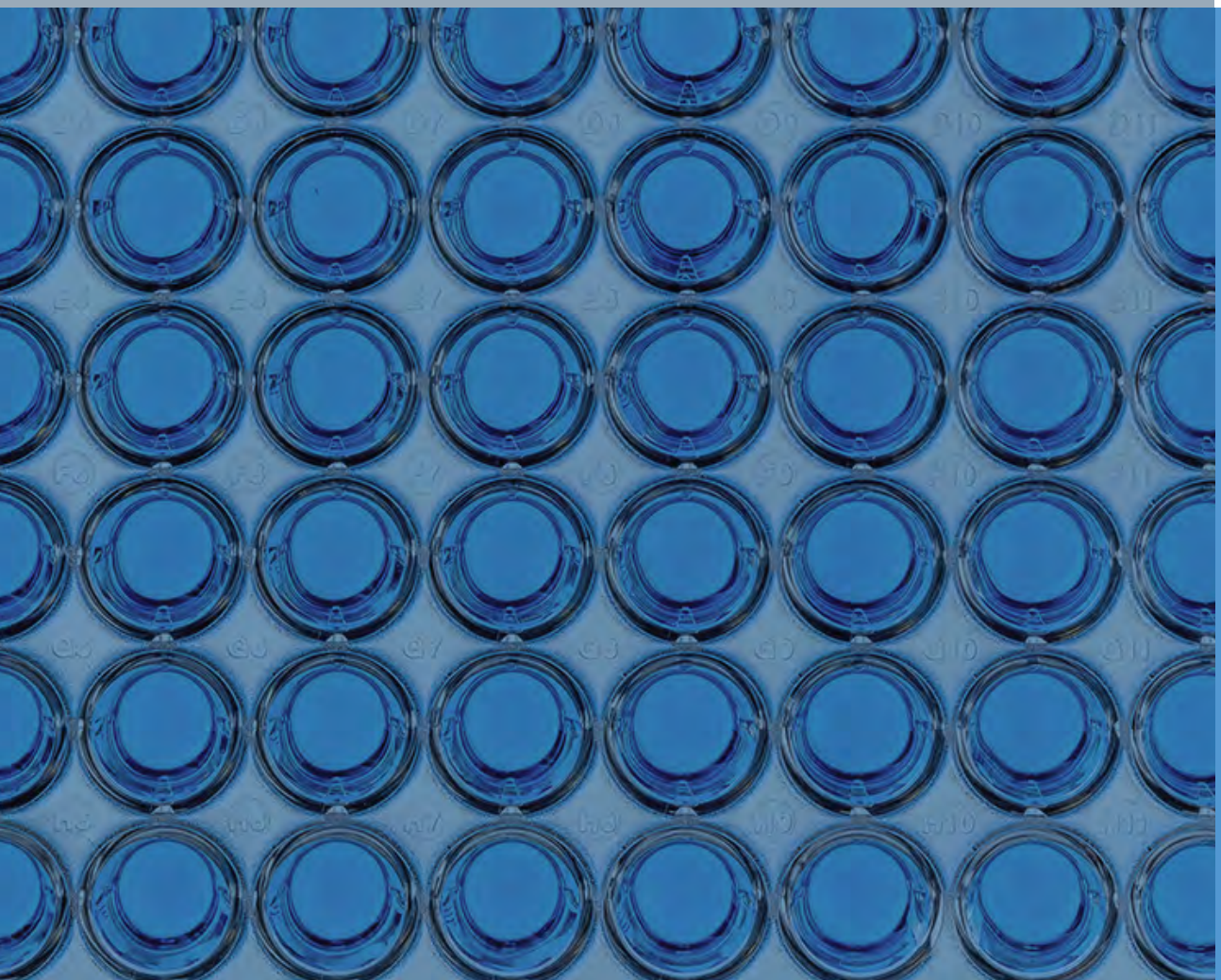
purePlex™ DNA Library Prep Kit

Featuring speed, batch flexibility, and data confidence with UDIs.

seqWell's core technology is a true multiplexing library prep system for making normalized NGS libraries quickly and easily from large numbers of samples.



purePlex™ DNA Library Prep Kit

Featuring speed, batch flexibility, and data confidence with UDIs.

Principal Features

Fast, flexible workflow with no requirement for full plate processing

Auto-normalization reduces QC burden, improves data consistency

Early pooling for easier sample handling

Reduced GC bias compared to other transposase-based methods

Accurate sample identification

Multiple index sets available

Application Strengths

Low-pass whole genome sequencing

Whole small genome sequencing (<50 Mb)

Metagenomics/Microbiome screening scRNA-seq

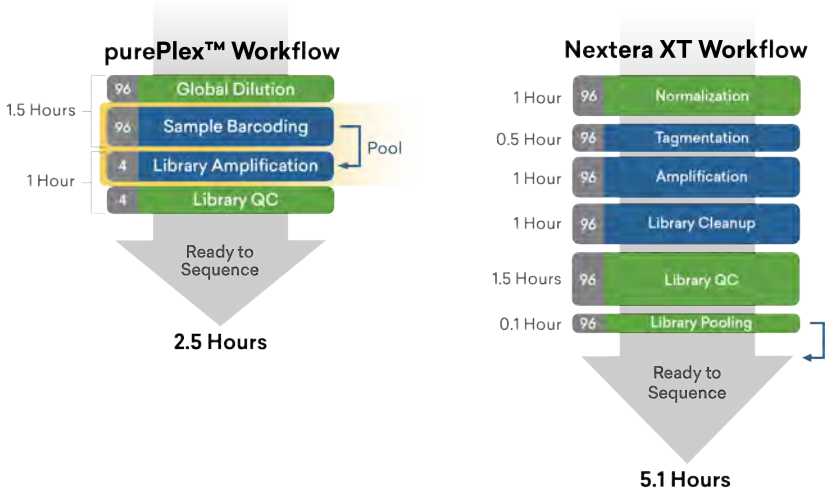
Synthetic construct sequencing (amplicons, plasmids, etc.)

Reduces labor costs and QC burden

The purePlex DNA Library Prep Kit leverages our patented Tn5 transposase-based chemistry where simple molecular tagging steps add dual indexes early on in the library prep process, enabling pooling of samples prior to any bead cleanups or amplification steps.

A distinct advantage of the purePlex workflow is the elimination of individual sample and library normalization which reduces the QC and labor costs compared to traditional UDI workflows.

From samples to loading sequencer in less than a day's work



2.5-hour workflow for preparing 96 samples
45 min. hands-on time

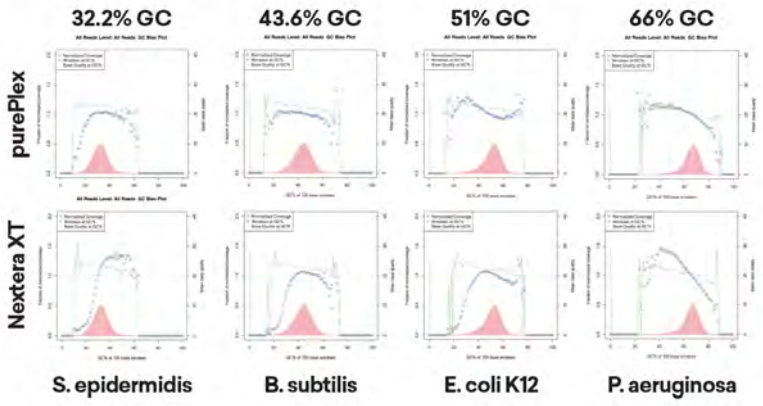
Save money and the planet through using less plastic

"With our streamlined workflow, you can save more than 50% in plastics per sample compared to Nextera XT, based on our estimates. And that results in savings of $7 or more per plate."

– Maura Costello, Team Leader, R&D, seqWell

Robust performance for all GC contents

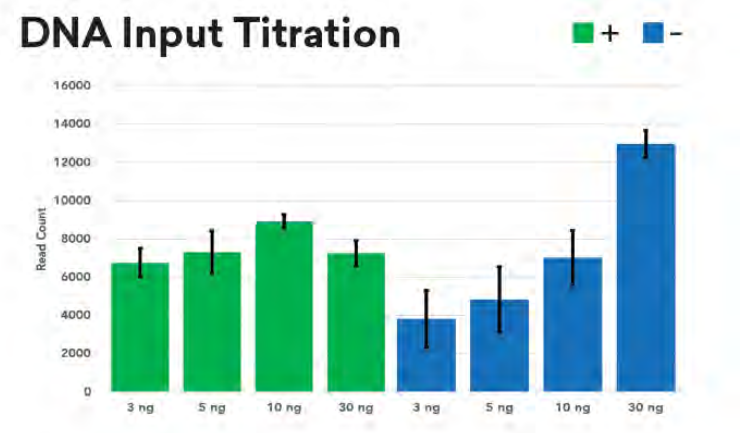
GC bias plots demonstrate purePlex has more even coverage across high and low GC regions compared to Nextera XT.



Auto-Normalization of Read Depth

Samples were normalized to inputs of 3, 5, 10, and 30 ng then underwent purePlex library prep with (+) and without (–) normalization reagent.

Read counts for each sample are equal, regardless of input, when normalization reagent is used. In contrast, without normalization reagent, sample read count scales with input.



Specifications

purePlex™ DNA Library Prep Kit

Catalog #301067 and #301068

Specifications	Description
Sample Type	Genomic DNA, cDNA, amplicons, plasmids
DNA Input Range	5-50 ng
Number of Unique Index Combinations	192 (more in development)
Supported Paired Reads (Clusters/Sample)	≤ 20 million
Output Fragment Range	400 – 1,200 bp
Applications	Low-pass whole genome sequencing, Whole small genome sequencing (<50 Mb), scRNA-seq, Metagenomics/ Metagenomics/Microbiome screening Synthetic construct sequencing (ampicons, plasmids, etc.)
Reactions per Kit	96

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