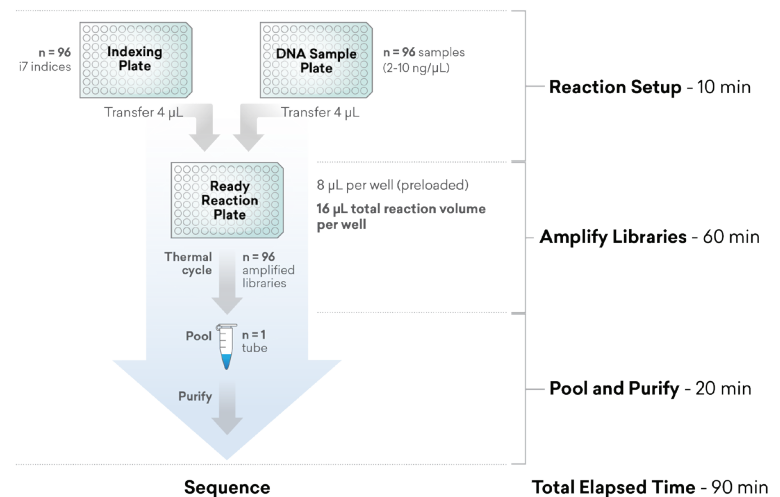


ExpressPlex™ Library Prep Kit

Designed for rapid turnaround of plasmid, amplicon, or synthetic construct sequencing, the ExpressPlex™ Library Prep Kit[†] is the fastest high-throughput preparation method available.*

- 90-minute library prep with ~30-minute hands-on time (for 96 samples)
- Built-in read count and insert size normalization
- Flexible batch sizes, combinatorial dual indexing
- High multiplexing capabilities
- Designed to support automation and flexible reaction volumes

*Based on total time to prepare 96 samples

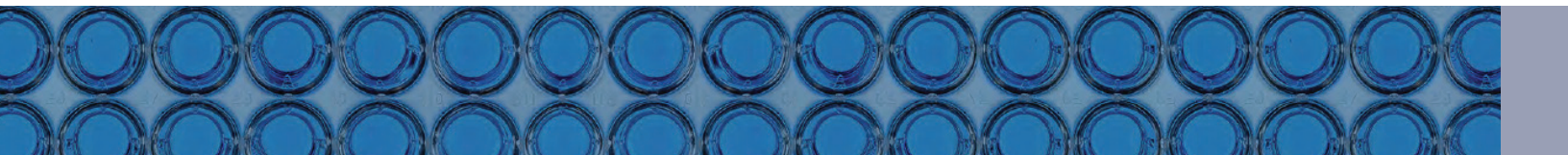


The simplicity of the ExpressPlex workflow makes it uniquely well-suited for manual, automated, and ultra high-throughput library prep from plasmids and PCR products.

Spend your time on data and results, not pipetting! ExpressPlex users can:

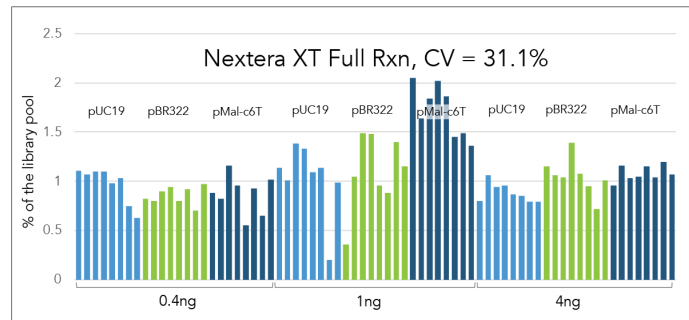
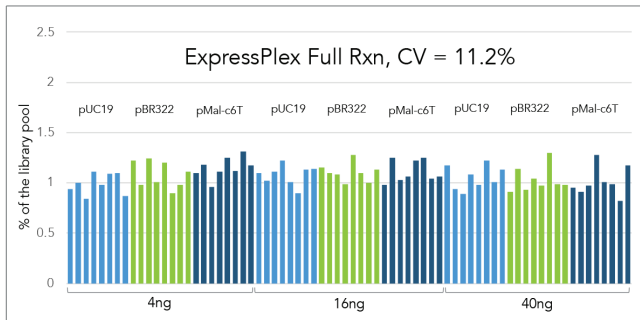
- Go from extracted samples to libraries on the sequencer in $\leq \frac{1}{2}$ a day
- Easily automate your protocol
- Multiplex up to 1,536 samples
- Reduce labor while increasing efficiency
- Decrease chance for errors via minimal handling steps
- Save significant time, cost, and plastics versus other protocols

[†]Patents Pending • For Research Purposes Only – Not for Diagnostic Use

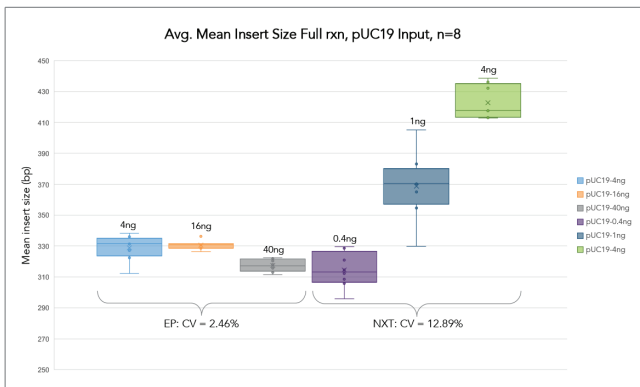
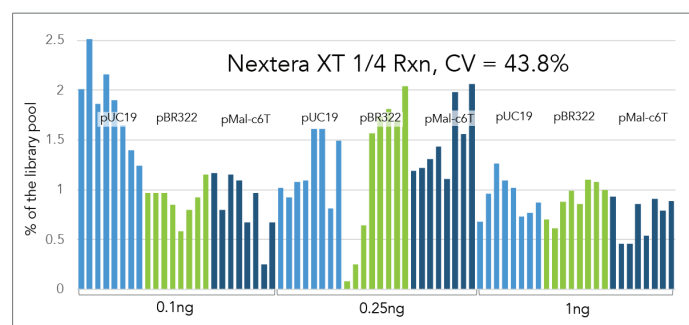


Auto-Normalization of Read Count and Insert Size

ExpressPlex demonstrates significantly higher levels of normalization compared to competitors, enabling a simplified workflow where individual normalization is no longer required to achieve more consistent read-depths across samples. Insert sizes are consistently conserved across a broad range of inputs.



Libraries were prepared from three different reference plasmids of varying sizes across a 10-fold input range at full reaction volume for ExpressPlex (16 μ L) and Nextera XT (50 μ L), as well as at $\frac{1}{4}$ miniaturized reaction volume for Nextera XT. For each method, inputs ranged from 4-40ng for ExpressPlex (standard input is 16ng) and 0.4 - 4ng for Nextera XT (standard input is 1ng). Inputs were scaled appropriately for $\frac{1}{4}$ reactions.



Libraries from pUC19 plasmid DNA were simultaneously prepared at 3 different input amounts (n=8 each input amount). ExpressPlex demonstrated greater consistency in average insert size across a 10-fold range. In each case, the standard input for both kits (16ng for ExpressPlex, 1ng for Nextera XT) was also included as a mid-range data point.

Interested in ExpressPlex? Contact seqWell today!



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