

ExpressPlex™ 2.0

Workflow simplicity
TnX performance

One Step NGS Library Prep



Engineered for rapid, cost-effective, high-throughput NGS library prep



Simple workflow

- One-step tagmentation & amplification
- Pre-plated, ready-reaction plates containing mastermix
- Up to 80% reduction in consumables usage



Uniform coverage

- TnX next-generation transposase
- Reduced bias
- Increased library complexity



Auto-Normalization

- Built-in total read output & insert size normalization
- Enables 40-fold range of DNA input
- Streamlined sample pooling



Scalable

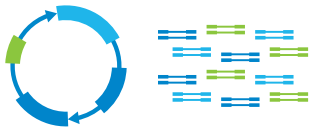
- Massive multiplexing – up to 6144 barcodes
- Automation-friendly
- Easily miniaturized



Rapid

- Sample-to-sequencer in < 2 hours
- 100-minute workflow
- < 30 minutes hands-on time

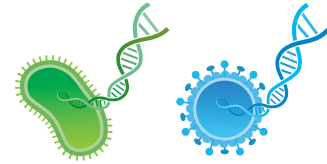
Applications



Plasmid & amplicon sequencing



Synthetic construct screening



Small genome sequencing

Better transposase

Better libraries

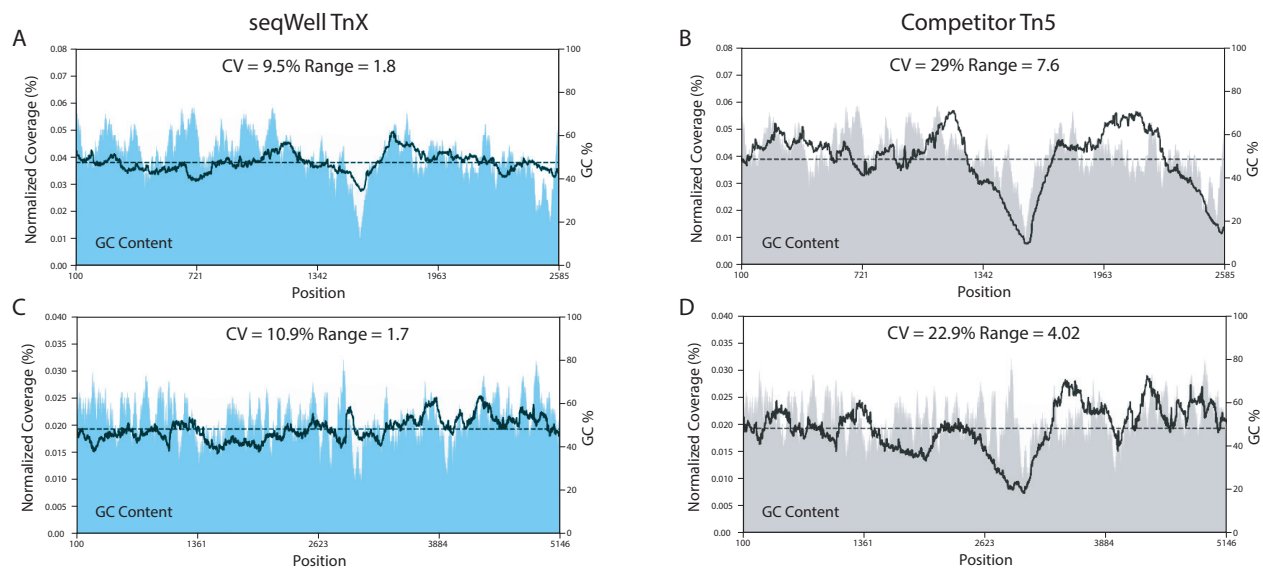
Better NGS

TnX: Reduced bias, improved uniformity of coverage

TnX, seqWell's next-generation transposase, was developed using fit-for-purpose engineering that targeted improvements in 3 key enzyme attributes: activity, insertion bias and robustness. These improved attributes translate into robust workflows and enhanced sequencing performance.

- Improved GC bias profiles
- Fewer gaps in regions of interest
- Increased library complexity
- Workflow simplicity and flexibility

TnX Outperforms the Competition

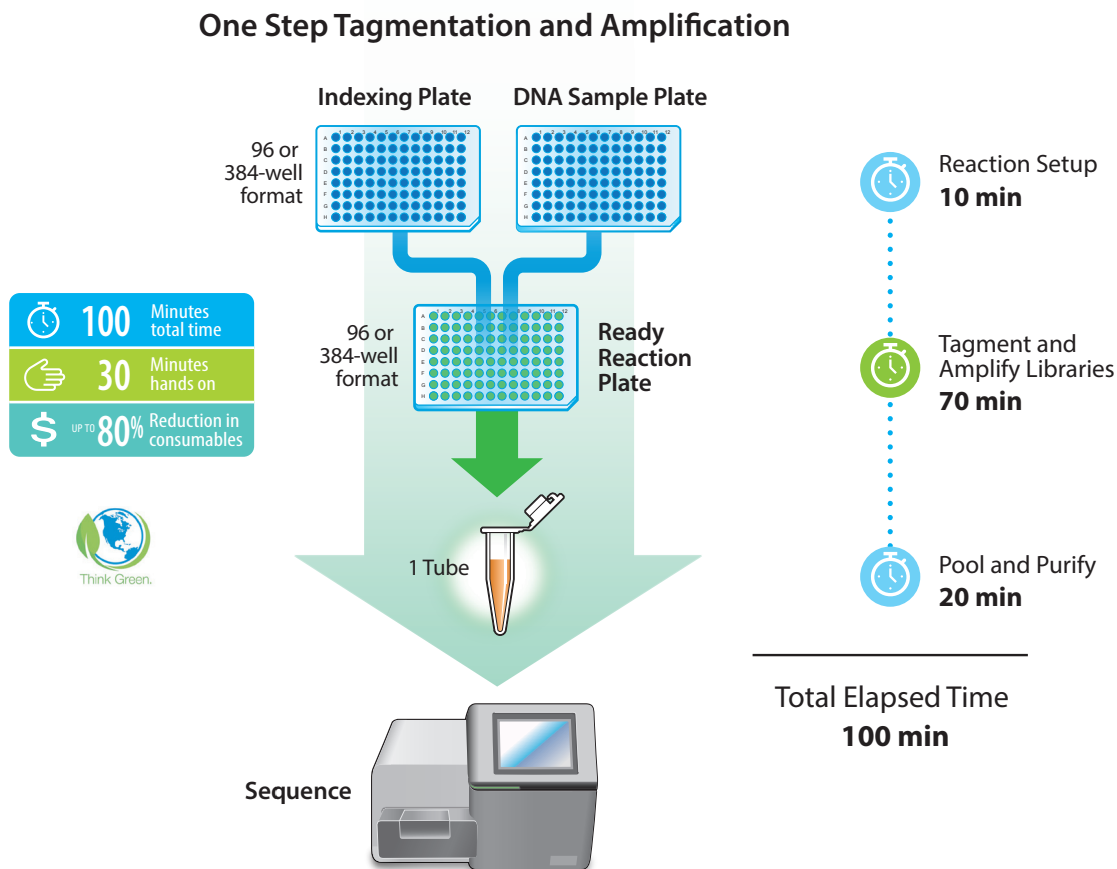


Library preparation for pUC19 (A & B) and pMal-c67(C & D) was performed using the ExpressPlex 2.0 kit (TnX) or a competitor kit (hyperactive Tn5) using standard manufacturers' protocols and sequenced on an Illumina MiSeq. TnX produced better uniformity of coverage with significantly lower CVs.

ExpressPlex™ 2.0

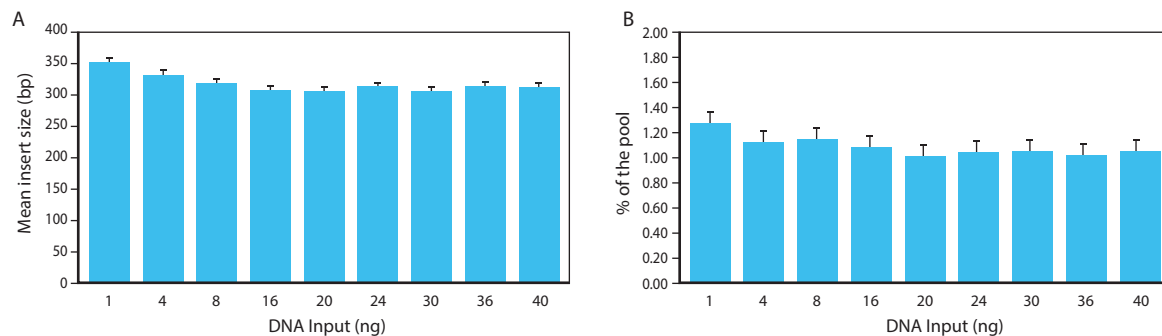


A library prep workflow like no other



Simplified workflow through auto-normalization

Read Depth and Mean Insert Size Uniformity



Normalization of individual samples is no longer required to achieve consistent read-depths and mean insert sizes. Libraries were generated from a range of pUC19 DNA input (1 – 40 ng). Read count normalization (A) with a CV of 12.7% and mean insert size (B) with a CV of 5% were observed for 18 samples spanning a 40-fold range of pUC19 DNA input.

Don't let library prep be your bottleneck

ExpressPlex 2.0

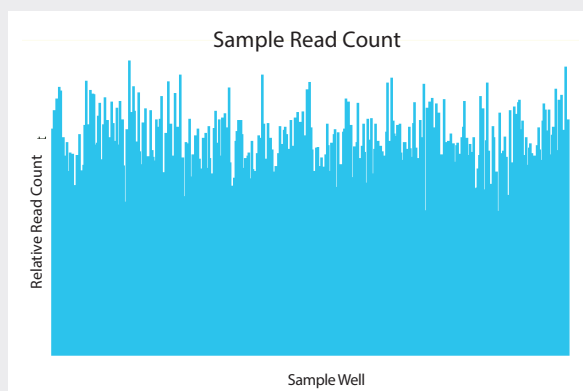
Harness ExpressPlex miniaturization, multiplexing, and automation compatibility to turn your benchtop sequencer into a cost-effective sequencing factory. Streamline your end-to-end workflow further by eliminating plasmid purification using colony PCR or rolling circle amplification (RCA).

- Colony-to-sequence data in <24 hours
- Up to 6144 unique indexes
- 96-, 384- and bulk reagent formats available



Automation Guide

Automation in action: Beckman Coulter Echo 525



Automation allows miniaturization down to 3 μ L reactions. Reactions were set up with a control pUC19 plasmid on the Beckman Coulter Echo 525 instrument, with sequential transfers of DNA sample (750 nL), Indexing Reagent (750 nL), and Ready Reaction Mix (1500 nL). The resulting 384-well plate was thermocycled, individual wells pooled into a single tube, purified by SPRI bead technology, and sequenced. The CV of read counts was < 14% with no failed wells or anomalies. When downsampled to 2,000 read pairs per sample, all plasmids were successfully assembled and circularized.

ExpressPlex™ 2.0



Specifications

| | |
|-------------------------------------|---|
| Sample Input Types | Purified plasmid DNA, RCA-amplified DNA, colony PCR amplicons, amplicons >350 bp, microbial genomic DNA |
| Kit Formats | 96-well, 384-well or custom dispense |
| DNA Input Recommended | 96-well format: <ul style="list-style-type: none"> • 1 - 40 ng for plasmid & amplicon sequencing • 1 - 40 ng for microbial WGS 384-well format: <ul style="list-style-type: none"> • 0.5 – 20 ng for plasmid & amplicon sequencing |
| Number of Unique Index Combinations | Up to 6144 combinatorial dual indexes (CDIs) |
| Batch Size | <ul style="list-style-type: none"> • 8-96 samples (96-well format) • 384 samples (384-well format) |
| Output Fragment Range* | 400 – 1,200bp |
| Number of PCR Cycles | <ul style="list-style-type: none"> • 12 cycles for plasmids • 15 cycles for amplicons • 12 cycles for microbial WGS |
| Sequencer Compatibility | <ul style="list-style-type: none"> • All Illumina sequencing platforms • Compatible with Complete Genomics platforms or Element Biosciences AVITI™ using conversion kits for Illumina libraries |

* Fragment size will depend on magnetic bead cleanup ratios used.

Ordering Information

| Catalog Number | Format | Number of Plates | Index Set* |
|----------------|---------------------------------|------------------|------------|
| 301170 | 96-well | 1 | Any Index |
| 301176 | 96-well | 4 | Set 1000 |
| 301177 | 96-well | 4 | Set 2000 |
| 301178 | 96-well | 4 | Set 3000 |
| 301179 | 96-well | 4 | Set 4000 |
| 301152 | 384-well | 1 | Any index |
| 301159 | 384-well | 4 | Any index |
| Inquire | Bulk or custom reagent dispense | | |

* All kits supplied with unique combinatorial dual indexes



66 Cherry Hill Drive, Beverly, MA 019151
(855) SEQWELL (737-9355)

© 2025 seqWell Inc. All rights reserved.

For Research Use Only. Not for use in diagnostic procedures. seqWell, the seqWell logo, TrnX and ExpressPlex are trademarks of seqWell, Inc. All product names and trademarks are the property of their respective owners.

ExpressPlex™ 2.0