plexWell™ Technology
Library Preparation Simplified

seqWell

Discover the Benefits and Features of "True Multiplexing"

plexWell's unique sequential barcoding allows the creation of balanced library pools without the need for sample or library normalization. The simplified 3-hour workflow allows for efficient paralleled multiplexing of 10s to 1000s of samples in a single sequencing run without sacrificing library quality.

**Precision Multiplexing**

Scalable Workflow

Integrated Normalization

Precision Multiplexing with plexWell

Uniform Depth of Coverage and Insert Size on More Samples

plexWell technology yields balanced multiplexed libraries containing highly uniform insert size distributions and sample read counts.

Read Count Normalization
96-plex Read Output % Across Variable Input

Compression of Input DNA Range
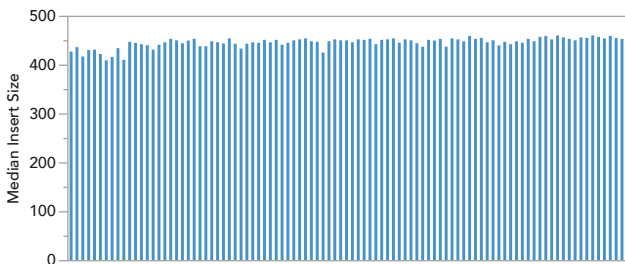
>90% of input samples at 0.5% or higher output representation; >80% of input samples within 4-fold output range; 1.5 log normalization effect within support input range (100-fold input range reduced to 2.5 output range). E. coli library preparation with plexwell gives consistently longer median inserts , maximizing the per read usable data. Insert sizes are consistent over a range of inputs.
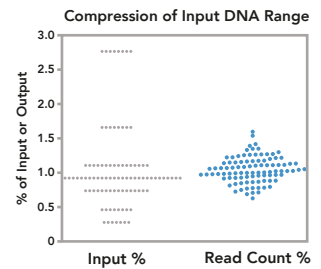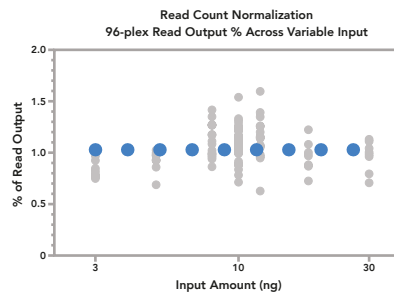
Minimal Bias for Diverse Applications

Microbial Genome

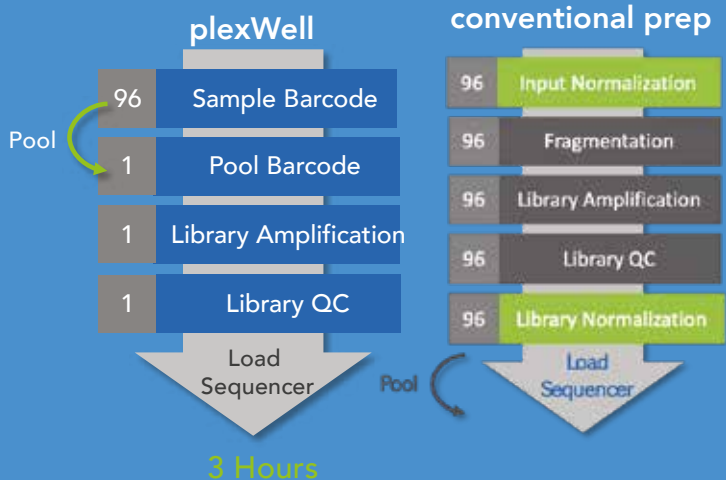Mammalian Genome
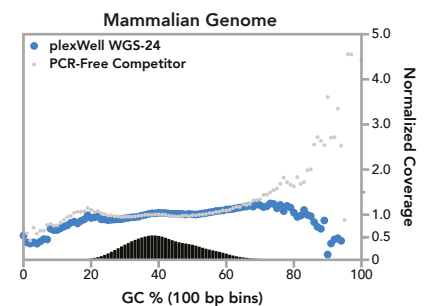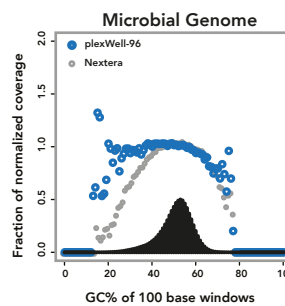
plexWell Applications:

- Small & Large Whole Genomes
- Microbial Genomes
- Amplicons & Plasmids
- Low-Pass Plant/Animal/Human
- BAC/Fosmid/Cosmids
- RNAseq
- 16s or ITS

sopachem life sciences
innovations for better science

Simple and Scalable Workflows

plexWell

96	Sample Barcode
1	Pool Barcode
1	Library Amplification
1	Library QC

Pool

Load Sequencer

3 Hours

conventional prep

96	Input Normalization
96	Fragmentation
96	Library Amplification
96	Library QC
96	Library Normalization

Load Sequencer

Pool

- 3 hours total time from samples to sequencer loading
- No quantification of sample DNA
- Eliminate library normalization
- Multiplex thousands of samples in a day
- No upfront or additional equipment cost

Normalizing Iterative Barcoding Technology

input amount — Sample Barcoding — Sample Pooling — Pool Barcoding & Amplification

High / Medium / Low
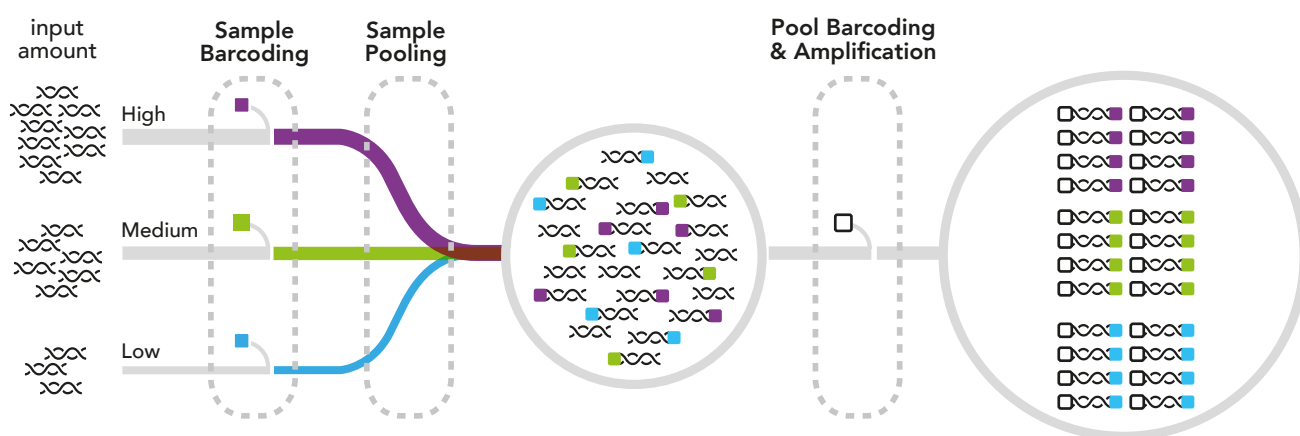
Sample Barcoding
Multiple input samples are tagged with limiting quantities of sample-specific, barcodes containing P7-adapters.

Pool Barcoding
Tagged samples are pooled into a single tube and undergo plate barcoding using excess P5-adapters.

Normalized Library
Following final library amplification and QC, the auto-normalized library is ready for sequencing.

% of Sample in Multiplexed Library (192 Samples)

Competitor — plexWell
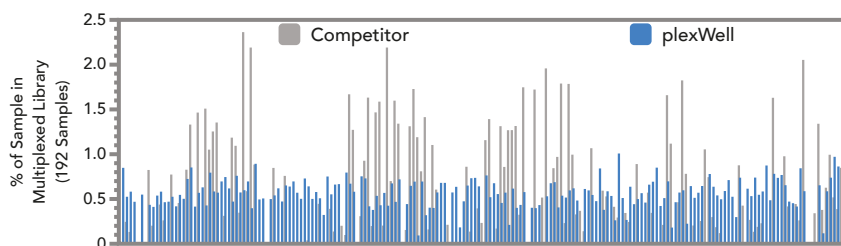
plexWell achieves a significantly better level of multiplexing uniformity for highly multiplexed sequencing applications. At left, sequencing results obtained for sequencing 192 samples of amplified single-cell cDNA with plexWell (blue) and Competitor reagents (gray). Input DNA for Competitor was pre-normalized, whereas plexWell library was made from un-normalized amplified cDNA. Read count variation for plexWell showed 27% C.V. versus 71% for Competitor.

Time and Cost Savings for Multiplexed Sequencing Applications

35 Minutes Hands-on Time

3000 Samples Per 8 Hour Day

as low as €7 Per Sample

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Ready to integrate plexWell™ technology into your NGS workflow?
Contact your local distributor Sopachem to learn more

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www.seqwell.com