seqWell

AgriPrep™

powered by ***ExpressPlex***

Bred for NGS workflow simplicity and throughput

Harvest actionable insights using scalable, genome-wide sequence exploration

Improvements in imputation software and decreasing sequencing costs have increased the reliance on low-coverage whole genome sequencing (lcWGS) within agrigenomics. However, when scaled to the population level, many NGS library prep methods fall short on throughput and affordability.

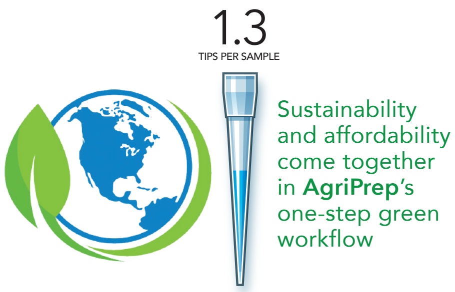
AgriPrep is powered by seqWell's next-generation TnX™ transposase and their proprietary one-step ExpressPlex™ workflow to support ultra-high-throughput plant & animal low-pass WGS & SKIM-sequencing approaches.

Simple workflow
- One-step tagmentation & amplification
- Auto-normalization
- Early sample pooling
- Easy to train

Scalable
- Automation-friendly
- Up to 3072 indexes
- Available in bulk reagent format

Affordable
- Up to 95% reduction in consumables
- Significant labor savings
- Easily miniaturized

Don't let library prep be a bottleneck



Unmatched 100-minute workflow

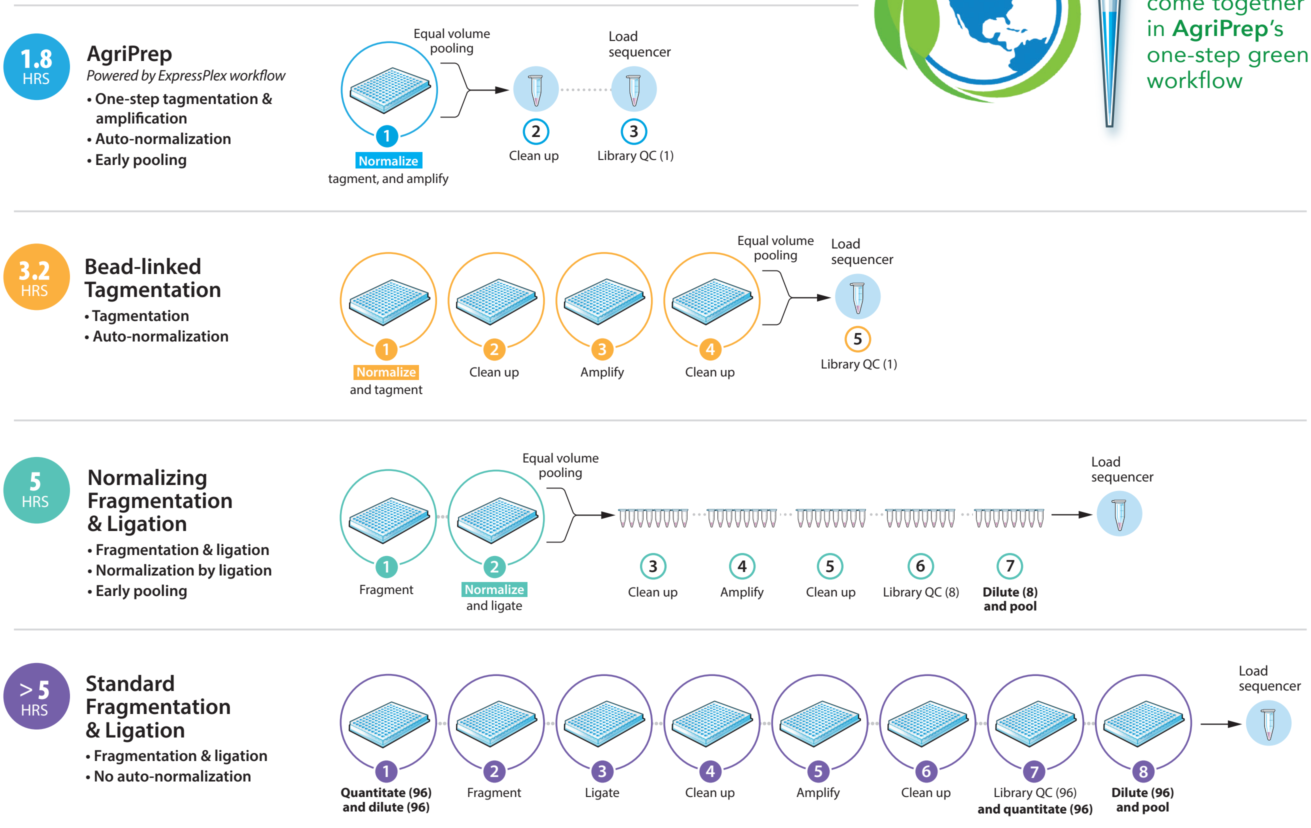
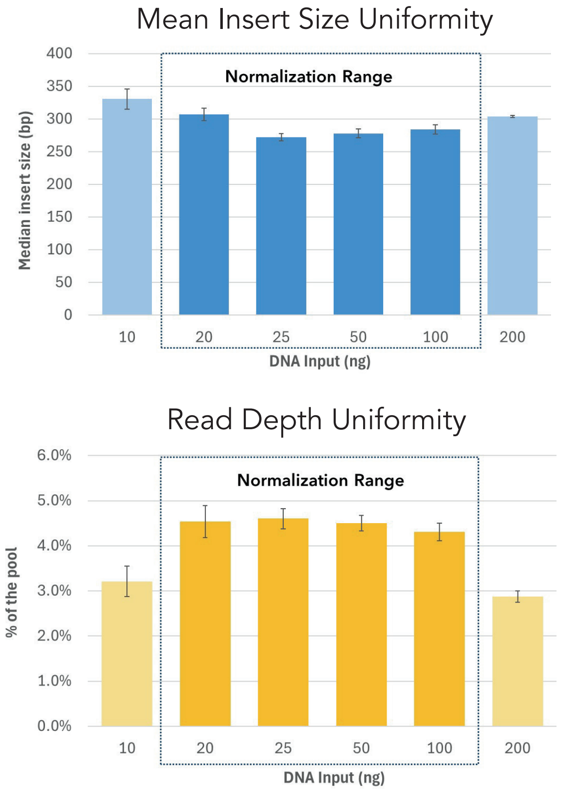


Figure 1. AgriPrep and competitor workflows derived from standard publicly available protocols.

Auto-normalization maintains quality and provides cost efficiencies



Auto-normalization of mean insert size and read depth eliminates the need to individually quantify and dilute samples ensuring uniform coverage for all your critical samples.

Additional benefits include:

- Rapid protocol for higher laboratory throughput
- Labor and consumables cost savings
- Lower sequencing costs to meet coverage requirements for all samples
- Fewer opportunities for contamination or errors

Figure 2: A 24-plex library pool was generated from 10 - 200 ng of Barley genomic DNA using AgriPrep and sequenced on an Illumina MiSeq™ i100 system. AgriPrep has a working range of 10 to 200 ng of DNA input, with auto-normalization of both mean insert size and read depth from 20 to 100 ng. (A) Mean insert size across the total working range (CV = 8.6%) and normalization range (CV = 6.9%). (B) Read depth across the total working range (CV = 17.5%) and normalization range (CV = 10.5%)

Extracting economic value through genome-wide discovery

Samples	Genome size (Gb)	Genome description	Average mean coverage	Mean insert size (bp)	Duplication rate
Barley *(Hordeum vulgare)*	5.3	Repeat-rich	0.54	459	1.7%
Soybean *(Glycine max)*	1.1	Moderately-repetitive	0.75	415	0.9%
Rice *(Oryza sativa)*	0.4	Low-repeat	0.57	438	0.7%

Discover new insights to drive more informed decision-making using the scale, affordability and flexibility of low coverage WGS at a fraction of the cost of high-depth sequencing.

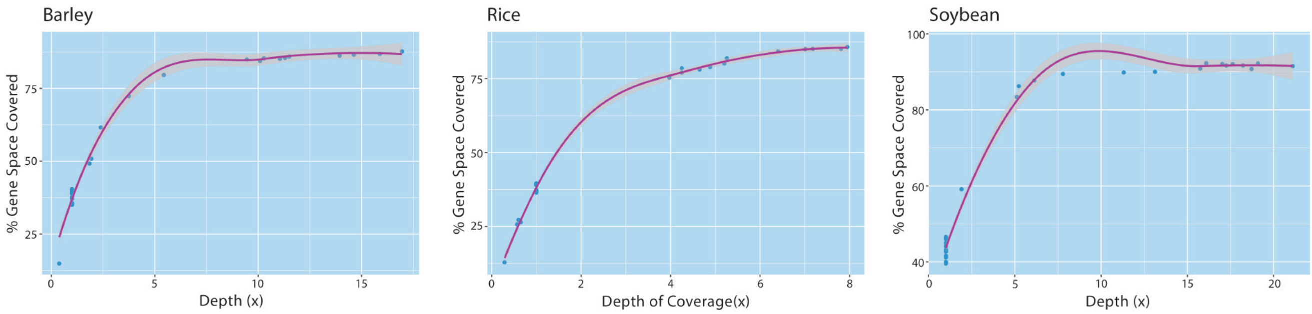


Figure 3: The % gene space covered by depth sequenced (X) is shown for samples from Barley, Rice, and Soybean prepared with AgriPrep and sequenced to various depths.

Specifications

Primary Sequencing Applications	• Genotyping-by-sequencing (GBS) • Low-pass sequencing • SKIM-seq
Sample Types	Plant or animal genomic DNA
Transposase	TnX - next generation transposase
Kit Formats	• 96-well • Custom dispense
Total Libray Prep Time: Extracted DNA to Sequence-ready Library	100 minutes (30 minutes hands-on time)
DNA Input: Working Range	10-200 ng
DNA Input: Normalization Range	20-100 ng
Number of Unique Index Combinations	• Up to 1536 combinatorial dual indexes (CDIs): off-the-shelf • Up to 3072 CDIs: via custom ordering
Batch Range	8-96 samples

Ordering Information

Catalog Number	Format	Number of Plates	Index Set*
301737	96-well	1	Any Index
301721	96-well	4	Set 1000
301722	96-well	4	Set 2000
301723	96-well	4	Set 3000
301724	96-well	4	Set 4000
301729	96-well	4	Any index
Inquire	Bulk or custom reagent dispense		

* All kits supplied with unique combinatorial dual indexes

seqWell
66 Cherry Hill Drive, Beverly, MA 01915
(855) SEQWELL (737-9355)

AgriPrep™
powered by ExpressPlex