Data Quality at the Core

Seamless Solutions from Sample Prep to Data Acquisition for Plant Genomics Workflows

PLANT GENOMICS

ACCELERATING *answers*

BECKMAN COULTER
Life Sciences

Advancing Plant Genomics through Reliable Lab Automation Solutions and High-Quality Reagents

Since 1986, Beckman Coulter Life Sciences has been providing tools for plant and animal research, beginning with the groundbreaking Biomek 1000 automated workstation. Today, thanks in part to our experience and expertise in lab automation and reagents, we're helping researchers accelerate answers in:

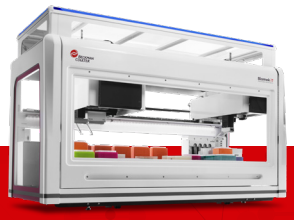
- Plant breeding & selection
- Crop yield
- Biomarker development
- Pest and disease resistance
- Trait discovery

In this era of machine learning (ML) and artificial intelligence (AI), the role of lab automation solutions and high-quality reagents is paramount in plant genomics. AI and ML models require high-quality, well-characterized datasets for accurate predictions and training. By combining our robust lab automation and reagent solutions, you can generate the reproducible data needed for these training sets. With these models unlocked, you'll then be able to accelerate crop improvements and drive toward sustainable agriculture.

The Plant Genomic Workflows That We Automate

- Nucleic Acid Extractions
- Assay Miniaturization – Miniaturized NGS, NanoGBS
- CRISPR/CAS-9
- Genotyping by Sequencing (GBS)
- Transcriptome Sequencing
- Quantitative PCR Evaluation
- Nucleic Acid Quantification and QC
- Nucleic Acid Cleanup
- Whole Genome Sequencing (WGS)
- Epigenetic Studies
- High-Throughput PCR Setup
- NGS Library Preparation

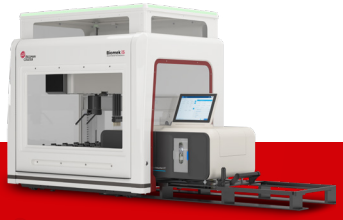
The Solutions That Make It Happen



Biomek Automated Workstations

Echo Acoustic Liquid Handlers

Biomek Echo One Workstation



Integrated Workstations

Automated Liquid Handling Software

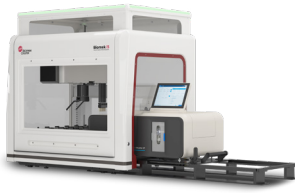
High-Throughput Genomic Reagent Solutions
(AMPure XP, SPRIselect, CosMCPrep, DNAdvance)

Tips

Empowering Plant Genomics Through Automation

Our lab automation solutions streamline and optimize critical processes such as sample preparation, reliable data tracking and seamless integration with other analytical instruments. By reducing human error, increasing throughput and improving data quality, you can extract meaningful insights from your genomic data. With this data, you can develop targeted breeding strategies and address challenges related to resource scarcity, disease susceptibility and environmental stressors.



What Sets Our Liquid Handlers Apart

Accuracy, Precision and Reproducibility

- The Span-8 pipettor on Biomek Automated Workstations enables low-volume transfers of 0.5 µL with inaccuracy of less than 0.12% and CV* less than 4.58%, and high-volume transfers of 900 µL with inaccuracy of less than 0.102 % and **CV* less than 0.392%**.
- For the low-volume transfer of 0.5 µL using the 384 Multichannel Head, the mean transfer volume for each individual head was less than 0.38% for inaccuracy and CV* was less than 5.06%. The 96 Multichannel Head transferred a high volume of 950 µL with inaccuracy of 0.1% and **CV* less than 0.28%**.
- Echo Acoustic Liquid Handler allows for precise, contact-free acoustic transfers in **volumes as small as 2.5 nL**.
- The Echo 650 Series can lower assay replicate requirements through increased assay precision.

Throughput

- Large deck capacity and on-deck device utilization.
- Selective tip feature of the multichannel head provides flexibility for both low- and high-throughput applications.
- Echo Acoustic Liquid Handler allows for fast any-well-to-any-well transfers, enabling previously **hours-long** DNA/RNA normalization, barcoding, and pooling of libraries down to **minutes-scale**.

Scalable and Modular

- Our experts have integrated **300+** different third-party devices from **over 60 manufacturers** to transform our liquid handlers into advanced lab automation solutions.

Sustainable and Cost-Reducing

- Echo Acoustic Liquid Handlers:
  - Decrease plasticware costs by **75% per year** through reduced reaction volumes.
  - Reduce dependency on single-use plastic pipette tip with tip-less and contact-free automated liquid handling.
  - Enables reuse of Echo-qualified plates, which helps minimize plastic waste.
- Biomek Automated Workstations:
  - Biomek software enables **tip reuse** for reduced plastic tip usage.
  - Biomek tips and consumables are recyclable polypropylene code #5.
  - Eligible for recycling through trade-up programs**
- Partnership with Polycarbin to drive sustainability through closed-loop recycling solutions and low-carbon lab products***

Scan the QR code to learn more about our reagents through selected research publications

Case Study

NanoGBS: A Miniaturized Procedure for High-Throughput Plant Genotyping-by-Sequencing Library Preparation

Experimental Setup

- GBS libraries were constructed for a set of 96 **soybean** samples using StdGBS and NanoGBS methods.
- To minimize pipetting errors and ensure a reproducible reaction, minimum transfer volumes were fixed to 5 µL in StdGBS. In contrast, a fast, accurate, uniform, and precise tipless liquid transfer—on a nanoliter scale—was achieved in NanoGBS using ADE technology (Echo Acoustic Liquid Handler).

Results

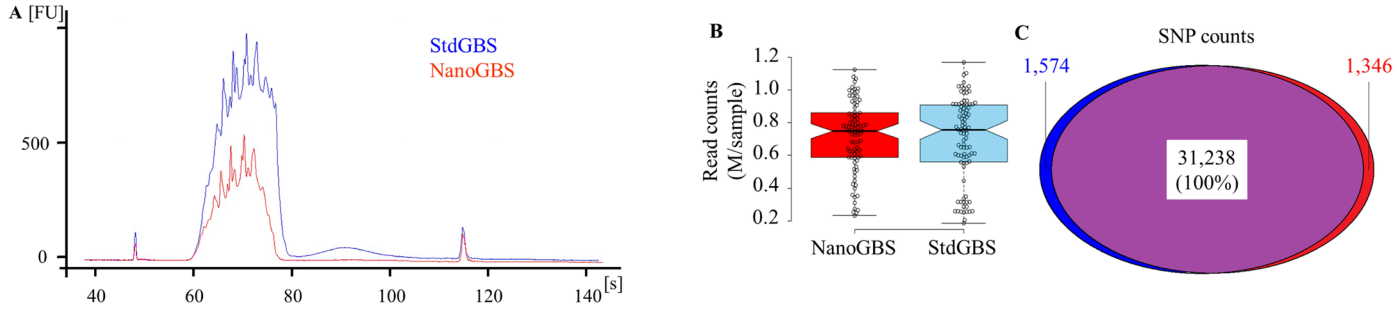


Figure 1
Comparison of results obtained from standard genotyping-by-sequencing (StdGBS) vs. NanoGBS pooled libraries for a set of 96 soybean samples. **(A)** Quality of DNA library pools using a Bioanalyzer. **(B)** Distribution of reads per sample after demultiplexing. **(C)** Number of SNPs and overlap between SNP catalogues derived from StdGBS vs. NanoGBS libraries. The level of agreement between SNPs called with these methods presented in percentage.

GBS library prep. (µL)	StdGBS	NanoGBS
DNA	10.0	1.0
RE-digestion Mix*	20.0	2.0
Ligation Mix	15.0	1.5
Adapter†	5.0	0.5
Total	**50.0**	**5.0**
Dead volume‡ (µL)	5.0	1.0
Pooling (µL/sample)	5.0	5.0

*RE: restriction enzyme.
†Includes sample-specific barcodes.
‡Pipetting margin and/or residual volume that cannot be used.

Table 1. Amount of reagents used for preparation of a genotyping-by-sequencing (GBS) library based on standard GBS (StdGBS) and NanoGBS methods.

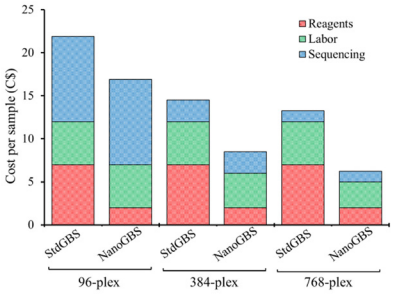
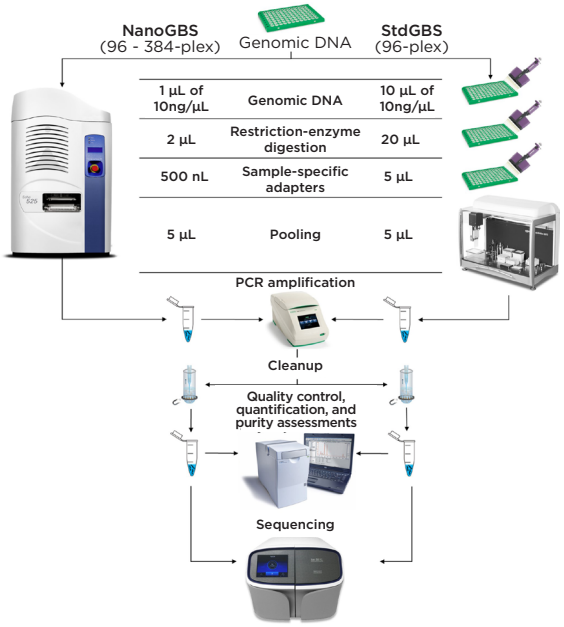


Figure 2. Detailed estimation of cost of genotyping-by-sequencing (GBS) genotyping per sample using standard GBS (StdGBS) vs. NanoGBS methods in three different multiplexing conditions.

Library		1	96-plex	Total
Type of Plastic		Recyclable	Non-recyclable	
Amount of Used Plastic (gr)	StdGBS	63	59	122
	NanoGBS	0	14	14
Reduction %		100	76	89

Table 3. Estimated amount of disposable plastic usage in one 96-plex genotyping-by-sequencing (GBS) experiment using standard GBS (StdGBS) and NanoGBS methods.

Workflow



Conclusions

NanoGBS using Echo 525 Acoustic Liquid Handler:

- Reduced the volume of reagents used by 90%
- Reduced genotyping cost by 70%
- Reduced plastic used by 90%
- Reduced handling time by 75%

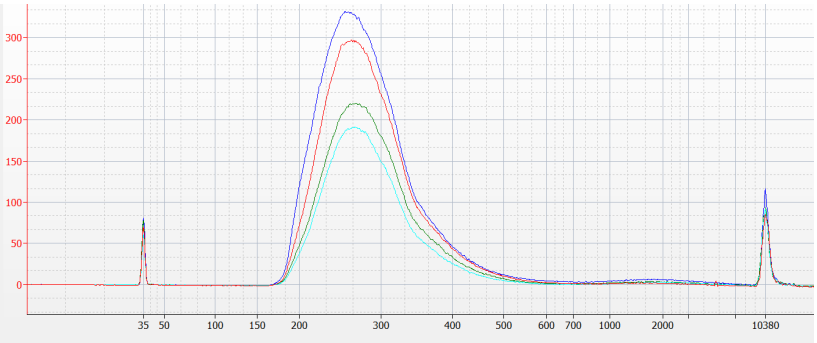
Case Study

Miniaturized, fully automated NEBNext Direct® Genotyping Solution using the Biomek i7 Hybrid Automated Workstation in conjunction with the Echo 525 Acoustic Liquid Handler for marker-assisted breeding

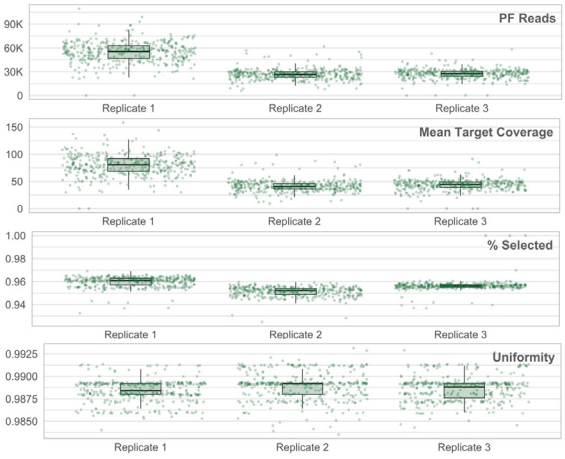
Experimental Setup

- The method was conducted using the NEBNext Direct® Genotyping Solution with 25 ng **tomato** DNA input per sample in a 384-plex distributed over four 96-well-plates, using 96 pre-capture sample indexes and one post-capture pool index per 96-well plate.
- The Echo 525 Acoustic Liquid Handler was used for miniaturization of the fragmentation and end prep as well as the 5' Adapter Ligation with Sample Indexing steps by a factor of 4x.
- Subsequent steps of the workflow were performed on the Biomek i7 Hybrid Automated Workstation.

Results



Electropherograms of final libraries from replicate 3 assessed with an Agilent Bioanalyzer High Sensitivity DNA chip.



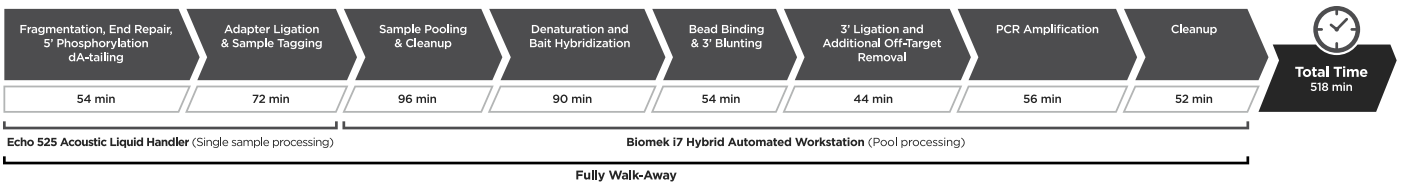
Box plot showing the number of reads passing Illumina's filter for each of the 384 samples per replicate as measured by the Picard Alignment Summary Metrics tool. Sequencing on an Illumina MiSeq yielded counts between 21,114-109,577 with an average of 54,992.78 (Replicate 1) and 6,106-61,930 with an average of 27,085.95 (Replicates 2 and 3).

Box plot showing the mean target coverage for each of the 384 samples per replicate as calculated by the Picard HS Metrics tool. Analysis of sequencing data from the Illumina MiSeq showed a mean target coverage between 30-158.34 with an average of 80.14 (Replicate 1) and 9.40-98.74 with an average of 42.80 (Replicates 2 and 3).

Box plot showing the percentage of bases located on or near a target for each of the 384 samples per replicate calculated by the Picard HS Metrics tool. Analysis of sequencing data from the Illumina MiSeq showed percent selected is >92.49% across all samples. Two dropouts in Replicate 1 and four in Replicate 3 are not shown for scaling purposes.

Box plot showing the sequencing uniformity for each of the 384 samples per replicate as calculated by the Picard HS Metrics tool. Uniformity is defined as the percentage of targets with coverage greater than 20% of the mean target coverage. Analysis of the sequencing data highlights the uniformity of >98.36% across all samples. Two dropouts in Replicate 1 and four in Replicate 3 are not shown for scaling purposes.

Workflow



Conclusions

- Integration of the Echo 525 Acoustic Liquid Handler enables the miniaturization of the single sample processing steps by a factor of 4x, reducing the operational costs through reduction of plastic consumables.
- Miniaturization and automation of the NEBNext Direct® Genotyping Solution generates consistent data to address the high-throughput demands of marker-assisted plant breeding applications.

Genomic Reagents That Enable Real Discoveries

Our nucleic acid cleanup and extraction reagents—powered by SPRI technology and widely known as the science behind the AMPure XP reagent—deliver accurate and reproducible results. These automation-ready bead-based reagents use paramagentic beads to bind nucleic acids enabling you to obtain high-quality genomic data.

Our genomic reagents are the gold standard in nucleic acid purification and cleanup technology. They've helped generate research in over 20,000 scientific publications and are suggested for use in over 200 library preparation kits, including kits from trusted sequencing companies like Illumina©, Oxford Nanopore Technologies, and Pacific Biosciences (PacBio), among others.

What Sets Our Genomic Reagents Apart

High-Performance Chemistries

- Ideal for nucleic acid extraction, DNA/ RNA from cells, tissue, blood and even challenging formalin-fixed, paraffin-embedded (FFPE) samples.
- SPRI technology enables our chemistries to deliver high-performance isolation, purification and cleanup protocols supporting workflows such as Genotyping-by-Sequencing (GBS), next-generation sequencing (NGS), transcriptome sequencing, nucleic acid quantification and QC, and quantitative PCR to name a few.

Versatile and Customizable

- Researchers have had successful extractions from small to large (HMW) nucleic acids from various sources as well as from a variety of different organisms, extracting both DNA and RNA from a single sample. You can use our chemistries with manual and/or fully automated methods on your choice of platforms, for optimum performance, flexibility and scalability.

Sustainability

- Renewable, recyclable paper is used for void fill in packaging.

Scan the QR code to learn more about our reagents through selected research publications

Cleanup, Purification, and Size Selection Reagents

SPRI Bead-Based Nucleic Acid Cleanup and Size Selection Reagents		Input Material	Output	Applications
	**AMPure XP** Maximizing recovery, consistency, and speed to facilitate the entire NGS workflow, AMPure XP reagent meets the stringent needs of today's genomic applications and minimizes the risk of losing important genetic information. It's the gold standard in bead-based, next-generation sequencing cleanup—in fact, it's suggested in over 200 library preparation kits.	PCR Products, Fragmented DNA	DNA	• PCR Purification • NGS Cleanup
	**SPRIselect** Suggested in over 40 library preparation kits, SPRIselect reagent gives you more flexibility and control, enabling reproducible and customizable size selection with minimal lot-to-lot variance. Stable at room temperature.	PCR Products, Fragmented DNA	Size Selected DNA	• PCR Purification • NGS Cleanup • DNA/RNA Size Selection
	**CosMCPrep** CosMCPrep reagent offers a single protocol for the purification of a variety of template types, including low-copy plasmids, high-copy plasmids, fosmids, BACs and cosmids.	Bacterial Culture	Plasmid DNA	• Plasmid Purification • Sanger Sequencing‡

Genomic Extraction Chemistries

SPRI Bead-Based Nucleic Acid Extraction Reagents		Input Material	Output	Applications
	**DNAdvance** Compatible with a variety of downstream analysis tools, DNAdvance reagent consistently delivers superior recovery of nucleic acids and purification of high-quality DNA.	Tissues, Swabs	DNA	• PCR‡ • qPCR‡ • SNP Genotyping‡ • NGS‡

Scan the QR code to learn more about our reagents through selected research publications

*The Artel Multichannel Verification System (MVS®) is routinely used to verify accuracy and precision in volume transfers across liquid handlers. It is a NIST (National Institute of Standards and Technology) traceable system. The Artel company has successfully shown low-volume pipetting with calibrating techniques by adjusting offsets and slopes.
**This trade-up program is ONLY available in North America
*** This partnership is ONLY available in North America
‡ Examples of downstream uses for isolated nucleic acids.

The Biomek Automated Workstations and Echo Liquid Handlers are not intended or validated for use in the diagnosis of disease or other conditions.

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Life Sciences

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For Beckman Coulter's worldwide office locations and phone numbers, please visit Contact Us at **beckman.com**

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