

Collect. Spin. Load.

Direct processing of **PAXgene® Blood ccfDNA Tubes** on the QIASymphony SP



Custom primary tube handling protocols available for the **PAXgene Blood ccfDNA Tube** along with the **QIASymphony PAXgene Blood ccfDNA Kit**.

- ❖ Eliminate plasma transfer.
 - Reduce risk of sample mixup.
 - Minimize risk of blood exposure.
- ❖ Save time.
- ❖ Minimize costs and waste.



For Research Use Only.
Not for use in diagnostic procedures.

Explore more at www.preanalytix.com

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 **PreAnalytiX**

A QIAGEN / BD Company



More data. One reaction.

Totally on-target assay design. The most intelligent targeted sequencing assay design ever. With comprehensive coverage of critical hotspot SNVs, contiguous tiled regions in coding sequences, and intron-exon boundaries in a revolutionary fast, simple, single-tube workflow, characterization and screening of your targets of interest is finally within reach. And on-target.

**Accel-Amplicon™
Custom NGS Panels**

Swift
BIOSCIENCES™

swiftbiosci.com

iontorrent



One tube. Many answers.

Ion AmpliSeq technology helps you get the most from your precious samples in a single NGS run

From inherited disease and cancer research to animal health studies, Ion AmpliSeq™ targeted next-generation sequencing (NGS) panels, combined with Ion Torrent™ systems, enable reliable, scalable analysis of many genes and important biomarkers, including SNPs, indels, and fusions—all with one panel, in just one NGS run.



See how Ion AmpliSeq technology can work for you at thermofisher.com/ampliseq

ThermoFisher
SCIENTIFIC

High Efficiency Chemically Modified Synthetic sgRNA for CRISPR

Essential for CRISPR Editing
in Primary, Stem Cells,
Therapeutic Applications
and Challenging Cell Lines.



Visit Us @ **ASHG 2017**

Booth 507

Reduce Library Prep Costs

100-Fold

Echo® Liquid Handlers enable library preparation in low microliter volumes for a range of sequencing methods. Dramatically reduce reagent costs, conserve samples, and eliminate steps – all while improving library quality.

Echo acoustic liquid handling allows...

- ▶ 100-fold reduction of library prep reaction volumes
- ▶ 30-fold reduction of sample pooling turnaround time
- ▶ Increased sample throughput
- ▶ Automation of workflow to easily prepare thousands of samples
- ▶ Improved accuracy of results

Comparison of Liquid Handling Methods*

	Manual Pipetting	Echo® Liquid Handler
Amount of DNA	50 ng	0.06 – 2.0 ng
DNA volume (Rxn)	25 µL	200 nL
Library prep volume (Rxn)	25 µL	300 nL
Total volume	50 µL	0.5 µL
Reactions per kit	96	9600
Cost per reaction	\$72.91	\$0.73

For more information, visit www.labcyte.com/sequencing.

* Low-Cost, High-Throughput Sequencing of DNA Assemblies Using a Highly Multiplexed Nextera Process. Shapland et al. ACS Synth. Biol., 2015

LABCYTE ™
The Future of Science is Sound

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AACR

American Association
for Cancer Research®

ANNUAL MEETING

2018 ★ CHICAGO



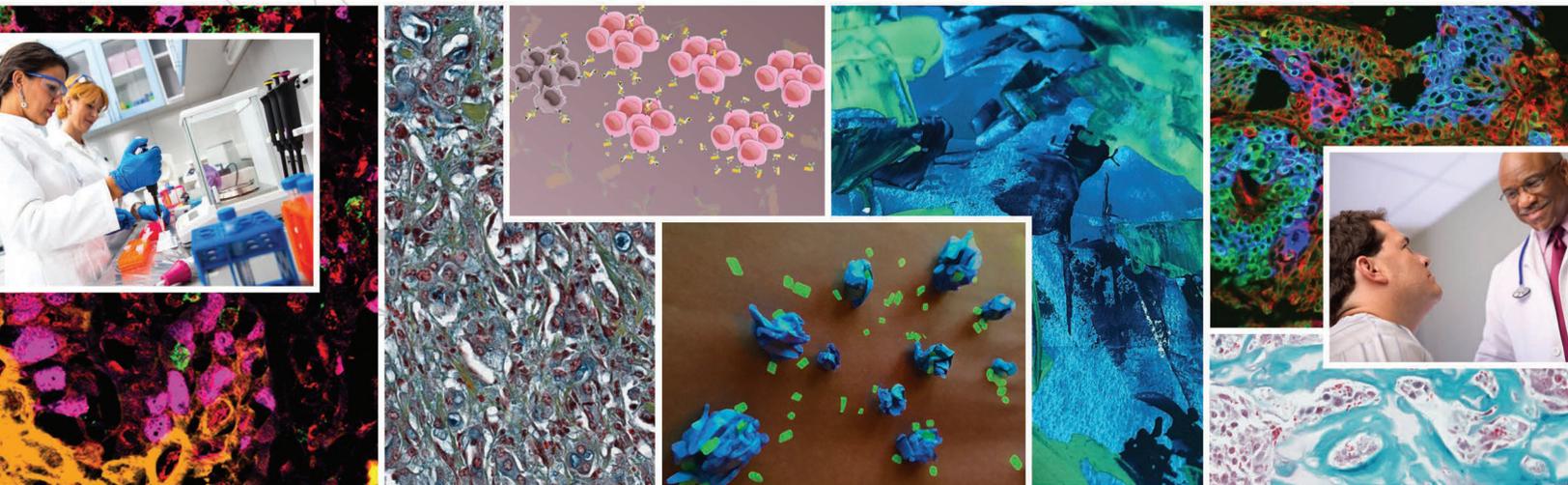
APRIL 14-18, 2018 • MCCORMICK PLACE NORTH/SOUTH • CHICAGO, ILLINOIS • AACR.ORG • #AACR18

DRIVING ————— ★
**INNOVATIVE
CANCER SCIENCE**
TO PATIENT CARE ————— ★

Join us in Chicago, for the latest innovative and inspiring cancer research from around the world...

THE AACR ANNUAL MEETING 2018!

The AACR Annual Meeting highlights the work of the best minds in cancer research and medicine from institutions all over the world. This meeting presents the many scientific discoveries across the breadth of cancer research – from population science and prevention, to cancer biology, translational, and clinical studies; to survivorship and advocacy. You will form new collaborations and learn how to apply exciting new concepts, tools, and techniques to your research. This year's program, with the theme of "Driving Innovative Cancer Science to Patient Care," will be a comprehensive, cutting-edge scientific event that you will not want to miss!



Submit your abstract by Friday, December 1, 2017

Register and save by December 15, 2017

Become a Member! Join the AACR and receive a discount on registration.

We look forward to seeing you in Chicago!

Agarose for Molecular Biology

Besta™ LE Agarose, Multi-purpose

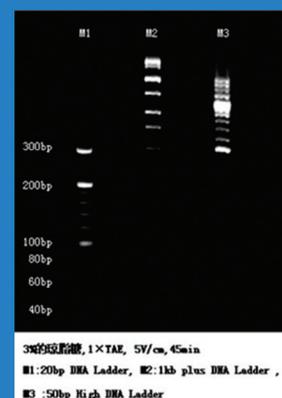
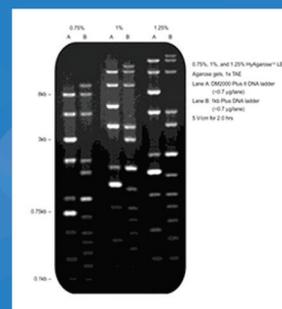
Besta™ LE Agarose is a low EEO, multi-purpose, standard melting point agarose that yields high resolution sharp DNA bands with high clarity and low background. Its optimized gel strength enhances ease of gel processing and handling.

Besta™ LM Agarose

Besta™ LM Agarose is a Low Melting and gelling point agarose producing gels with great sieving properties and higher clarity when compared with standard agarose. Besta™ LM Agarose is ideal for in-gel manipulations which can be performed without prior extraction of the DNA from the gel slice.

Besta™ HR Agarose

Besta™ HR Agarose is a PCR grade, intermediate melting point agarose that efficiently separates small DNA fragments between 20 and 800 bp in length and yields ultra-high resolution with high clarity and low background. It is suitable for the analysis of AFLP's (Amplified Fragment Length Polymorphisms), STR's (Short Tandem Repeats) and tetra-nucleotide repeats.



Quantify multiple pathogens in water.



RPA has enabled researchers in Germany to develop an automated DNA amplification and chemiluminescence microarray platform that can simultaneously identify and quantify multiple viral and bacterial contaminants in water.

Hear more about this and other amazing innovations:
twistdx.co.uk/water

RPA. It really works.
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Long story short: Bionano reveals more.

Long- and short-read NGS data identifies smaller DNA mutations, but lacks critical information around genome structure.

Bionano genome mapping fills in what's missing from sequencing-based data providing unmatched structural variation discovery and analysis for structural variations ranging from 1,000 bp to megabase pairs in length.

99% sensitivity for large homozygous insertions and deletions*

87% sensitivity for large heterozygous insertions and deletions*

98% sensitivity for translocations*

98% sensitivity for inversions**



bionano[®]
GENOMICS

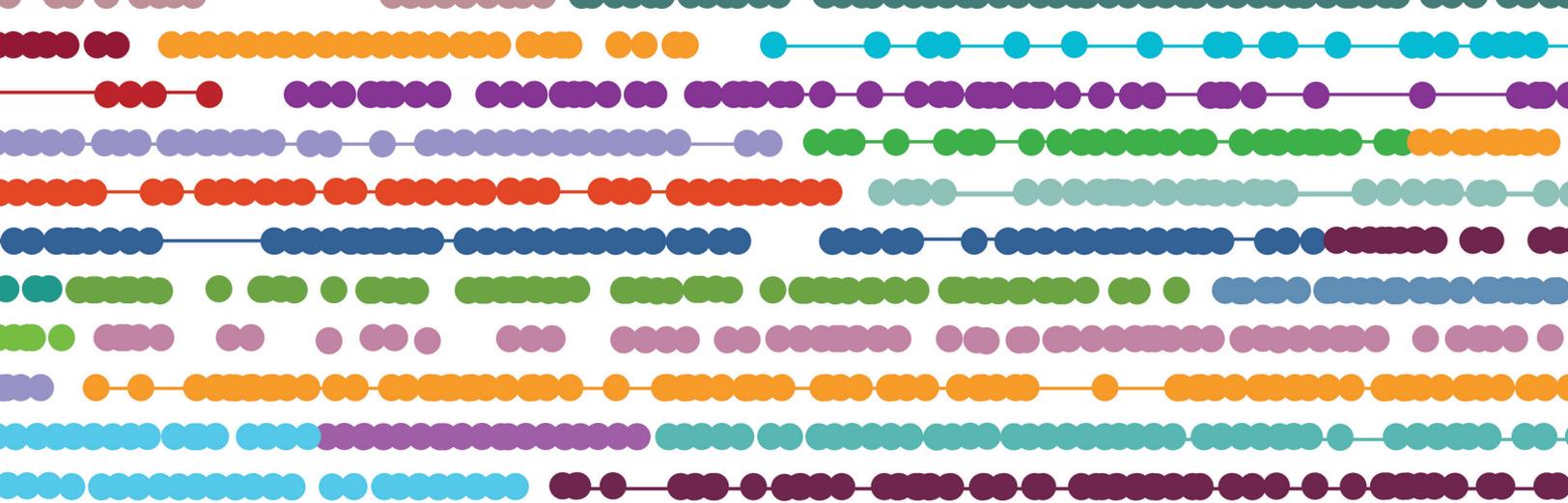
Put the power of Bionano data to work in your research.

Learn more at bionanogenomics.com

*Bionano Genomics. (2016). Bionano Genomics' Next-Generation Mapping Identifies Large Structural Variants in Cancer and Genetic Disorders [White paper]. http://bionanogenomics.com/wp-content/uploads/2017/02/Bionano_Human-Structural-Variations-White-Paper.pdf

**Bionano Genomics. (2017). Bionano Genomics Announces Inversion Detection Algorithms With Unmatched Sensitivity [Press release]. <https://bionanogenomics.com/wp-content/uploads/2017/09/Press-Release-Bionano-Genomics-Announces-Inversion-Detection-Algorithms-With-Unmatched-Sensitivity.pdf>

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- Resolve haplotype information, fully characterize complex structural variants, and improve access to medically relevant genes

- Future-proof your genomes with affordable *de novo* assembly for reference-free variant calling

- Getting data does not have to be complicated with our simple solutions, automatable workflows, low sample input, and easy-to-use software

Find what's missing.



Go beyond the current short-read technology. Use the Chromium™ System to obtain long-range information through the power of Linked-Reads for a single, comprehensive solution.

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