

# JUST RIGHT FOR GENOMICS

## ROOTED IN GENOMIC RESEARCH, DEVELOPED FOR THE FUTURE.

By simultaneously quantifying and qualifying nucleic acid samples in parallel, the Fragment Analyzer™ is transforming sample prep analysis for the world's leading genomic research institutions. Automate genomic QC for an array of applications, including total and degraded RNA isolations, genomic DNA extractions and NGS library preparations—giving you better results in less time, with less effort.



More at [AATI-US.COM](http://AATI-US.COM)

*Transforming NGS  
Library Prep Applications*

# *Discover More from Your Liquid Biopsy Samples*

## Accel-Amplicon™ Panels

### **A Proven All-in-One Amplicon Solution**

- Delivering 1% somatic mutation detection from 10 ng of DNA
- Simple single-tube, 2-hour workflow

## Accel-NGS® 2S Hyb DNA Library Kit

### **Highest Library Diversity, Lowest Inputs**

- Enabling whole exome sequencing from 25 ng of DNA
- Compatible with all hybridization enrichment panels



**Swift**  
BIOSCIENCES™  
[www.swiftbiosci.com](http://www.swiftbiosci.com)

# The S is for Simplicity

The new Ion S5™ System.  
Targeted sequencing has  
never been simpler.

Simple library prep tools, cartridge-based reagents and automated data analysis have reduced DNA-to-data hands-on time to less than 45 minutes. So you'll spend less time doing routine molecular biology, and more time informing time-sensitive decisions.



#### Ion AmpliSeq™ technology

As little as 1 ng low-quality DNA  
sample input for library prep



#### Cartridge-based reagents

Less than 15 minutes of  
sequencing setup time



#### 2.5 to 4 hours of run time

Fastest run time of any  
benchtop sequencer

Watch the Ion S5 System in action at  
[thermofisher.com/ionS5](http://thermofisher.com/ionS5)

**ThermoFisher**  
SCIENTIFIC

## Bulk M-MLV and RNasin at competitive prices

### ⊙ M-MLV (H-) Reverse Transcriptase US\$1.5 per KU for more than 1,000 KU

- H minus Moloney Murine Leukemia Virus (M-MLV) Reverse Transcriptase is a recombinant M-MLV reverse transcriptase. RNase H activity has been eliminated by a point mutation in the RNase H domain of M-MLV RTase, ensuring high yields.
- Deficient RNase H activity to reduce RNA template degradation during the first-strand cDNA synthesis.
- cDNA up to 12 kb.

### ⊙ RNasin (RNase inhibitor) US\$6.7 per KU for more than 100 KU

RNasin is a ribonuclease inhibitor extracted from human placenta with a molecular weight 51 kDa. It inhibits the activity of RNase by specifically binding up to RNase with a non-covalent bond. RNasin, free of RNase or Nickase, can maintain its activity at pH from 5 to 8, and the highest one at pH7.8.

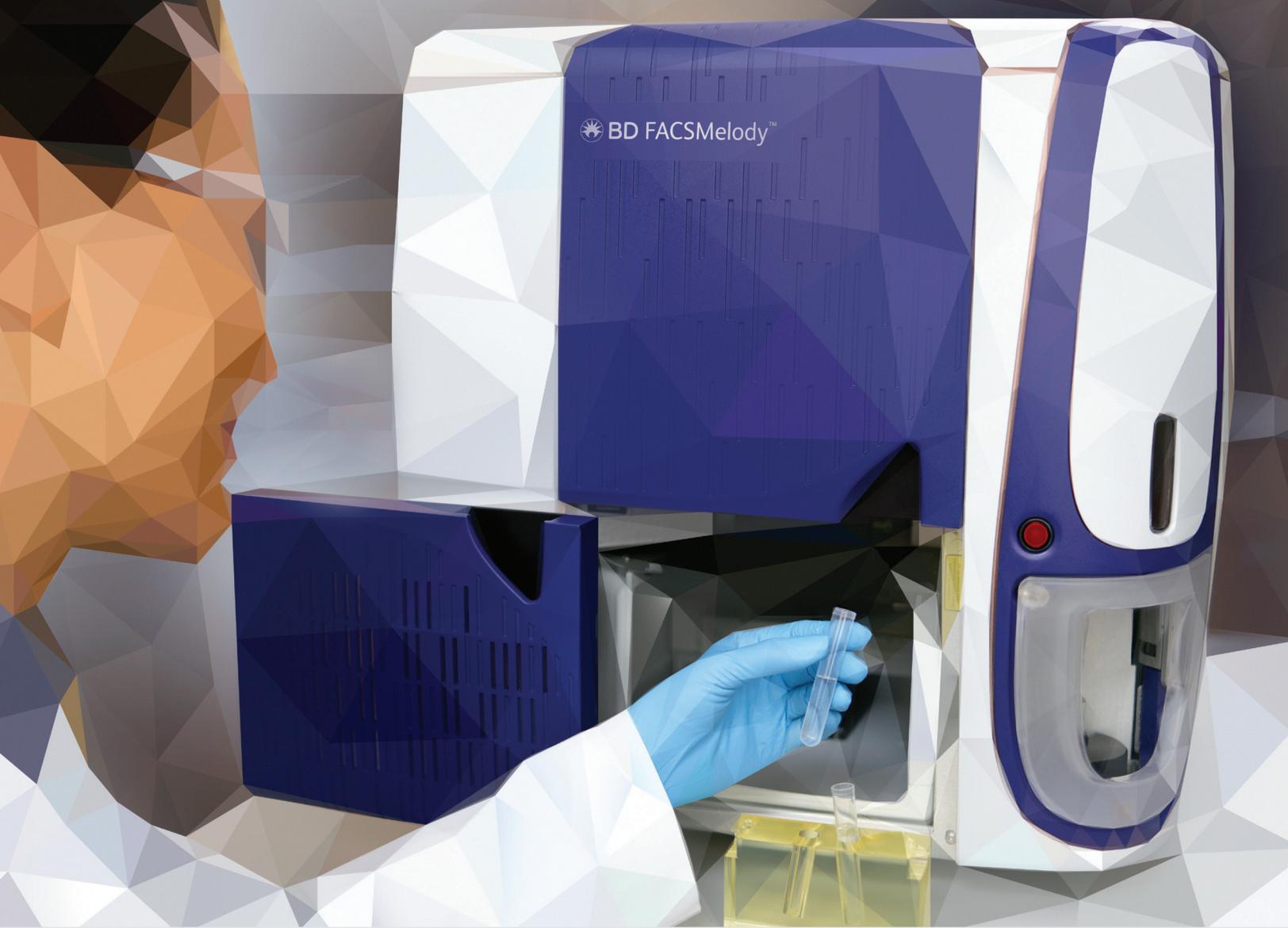
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# THE DIFFERENCE OF **ONE** SIMPLE SORT

**ONE RESEARCHER, ONE SORTER, ONE CELL, MANY DISCOVERIES.** BD is dedicated to developing easy-to-use cell sorting technologies that simplify accurate and reliable flow cytometry. The **BD FACSMelody™** cell sorter introduces a powerful combination of high performance, reproducible results and automated ease of use from a brand whose integrated flow cytometry portfolio and rigorous standards you can trust. BD FACSMelody is an affordable cell sorter that requires minimal training making it an ideal solution to advance your research. Its software guides the operator through every step, with a system sort readiness of less than 17 minutes for optimal timeliness. Designed to improve efficiency and throughput, it comes with the full suite of BD service and support to help you maximize your investment. Learn more about the one cell sorter that is easy to learn, to use and to maintain. Discover the difference one company can make. **Discover the new BD.**

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# AACR

American Association  
for Cancer Research

# ANNUAL MEETING

2017

WASHINGTON, DC

RESEARCH  
**PROPELLING**  
CANCER  
**PREVENTION**  
AND  
**CURES**

April 1-5, 2017 • Walter E. Washington Convention Center • Washington, DC

AACR.org • #AACR17



## Join us in Washington, DC

for the latest innovative and inspiring cancer research from around the world...  
the AACR Annual Meeting 2017!

You won't want to miss this five-day, comprehensive program offering world-class opportunities to learn, collaborate, and share not only the progress made in cancer research, but also the promise of what is to come. This new era of cancer discovery is unprecedented with respect to rapidly emerging cancer science and new and effective molecularly targeted therapies.

The best and brightest researchers in the world will attend this meeting that covers every aspect of cancer – from molecular biology, clinical studies, epidemiology, and prevention to survivorship. And you'll want to be among them.

**Submit your late-breaking abstract by  
THURSDAY, JANUARY 12.**

**Register and save by  
JANUARY 29.**

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

**110**  
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# AACR

American Association  
for Cancer Research

**We look forward to seeing you in Washington, DC!**

# Introducing novoWorx™, a Genome Data Management and Analytics platform

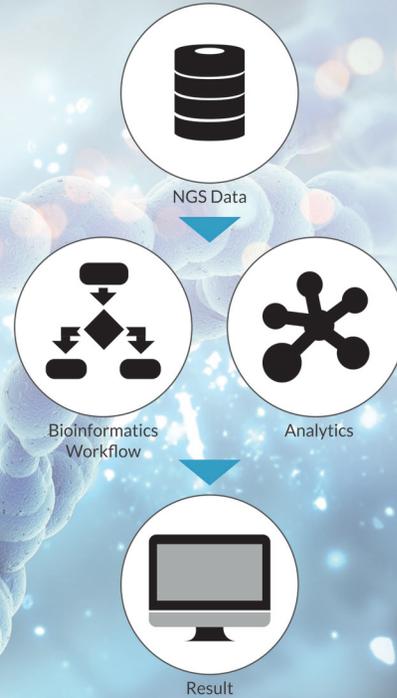
A comprehensive multi proprietary platform to accelerate your research by using sophisticated, fully automated solutions powered by the latest technologies.

## Why novoWorx™?

- The only commercially available tool to offer embedded novoAlign™ and novoSort™ programs for high-throughput bioinformatics analysis.
- A modular system for delivering canned genomics pipelines.
- Process large datasets consisting of multiple samples without programming knowledge.
- Generates all the outputs in standard formats required for downstream/tertiary analysis by other systems.

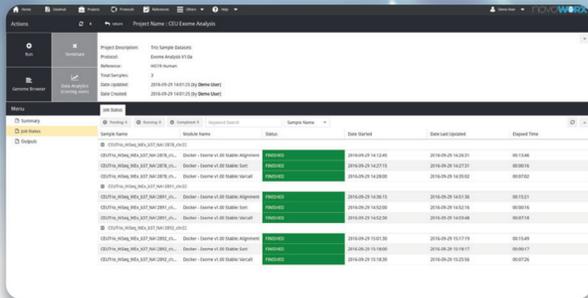
## Features

- Web-enabled and secure interface with access control.
- Drag and drop files into the interface.
- Supports multiple samples run from a single click, no coding required to loop through large sample collection sets.
- Integrated genome browser.
- Cluster-aware (SGE support) and monitor all running, pending and completed jobs.
- Result file downloads.
- Browse all files as reactive tables and figures.



Information on pipelines and analytics tools are available on the website.

**CONTACT US FOR A DEMO TODAY!**



Streamlined, user-friendly interface for easy navigation



Ready to use downloadable results

Requirement	Minimum	Recommended
<b>CPU</b>	Dual Core 1.8 GHZ	Octa Core 3.2 GHZ
<b>Memory</b>	4 GB DDR2	16 GB DDR3
<b>Storage space</b>	5 GB for installation media 15 GB post installation* 100 GB free space**	5 GB for installation media 15 GB post installation* 100 GB free space**
<b>Network</b>	500Kb/s download speed	1 Mb/s download speed
<b>Virtual Machine Environment</b>	Any Virtual Machine Environment capable of importing OVA files	Oracle VirtualBox (recommended) or VMware

\*only takes into account the OVA installation media.  
\*\*post installation file size.

	Files	Size
novoWorx™ (Required)	novoWorx Databases HG19 Reference files	2 GB 18 GB

Free trial download available, visit us at [www.novocraft.com](http://www.novocraft.com) to request for your trial license today



## Open up a new horizon in gene expression analysis!

The **QuantSeq 3' mRNA-Seq Library Prep** has been specifically developed for gene expression analysis with RNA-Seq. It is the best alternative to microarrays in this application.

- ✓ Genome-wide analysis of gene expression
- ✓ Just 2 hours of hands-on time
- ✓ Simplified data analysis
- ✓ Sequencing of up to 96 samples in one lane
- ✓ Down to 100 pg of total RNA input
- ✓ Suitable for low-quality RNA
- ✓ From USD 19.80/prep



Contact us at [info@lexogen.com](mailto:info@lexogen.com) if you need more information or would like to test QuantSeq.

Echo® Acoustic LIQUID HANDLING  
for SYNTHETIC BIOLOGY

## Reduce DNA Assembly and QC Costs **100-Fold**

Echo® Liquid Handlers use acoustic energy to transfer DNA oligos and reagents, allowing the reduction of DNA assembly and NGS library preparation reaction volumes. Dramatically reduce reagent costs, save samples, and eliminate steps - all while improving the quality and throughput of synthetic genes.

**100-fold reduction of Gibson or Golden Gate assembly reaction volumes**

**100-fold reduction of NGS library preparation volumes**

**Increased assembly and QC throughput**

**Automation to easily process thousands of assemblies**

### COMPARISON OF LIQUID HANDLING METHODS

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

For more information, visit [www.labcyte.com/synbio](http://www.labcyte.com/synbio).

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# WE MAKE DATA USEFUL. YOU MAKE THE DISCOVERIES.

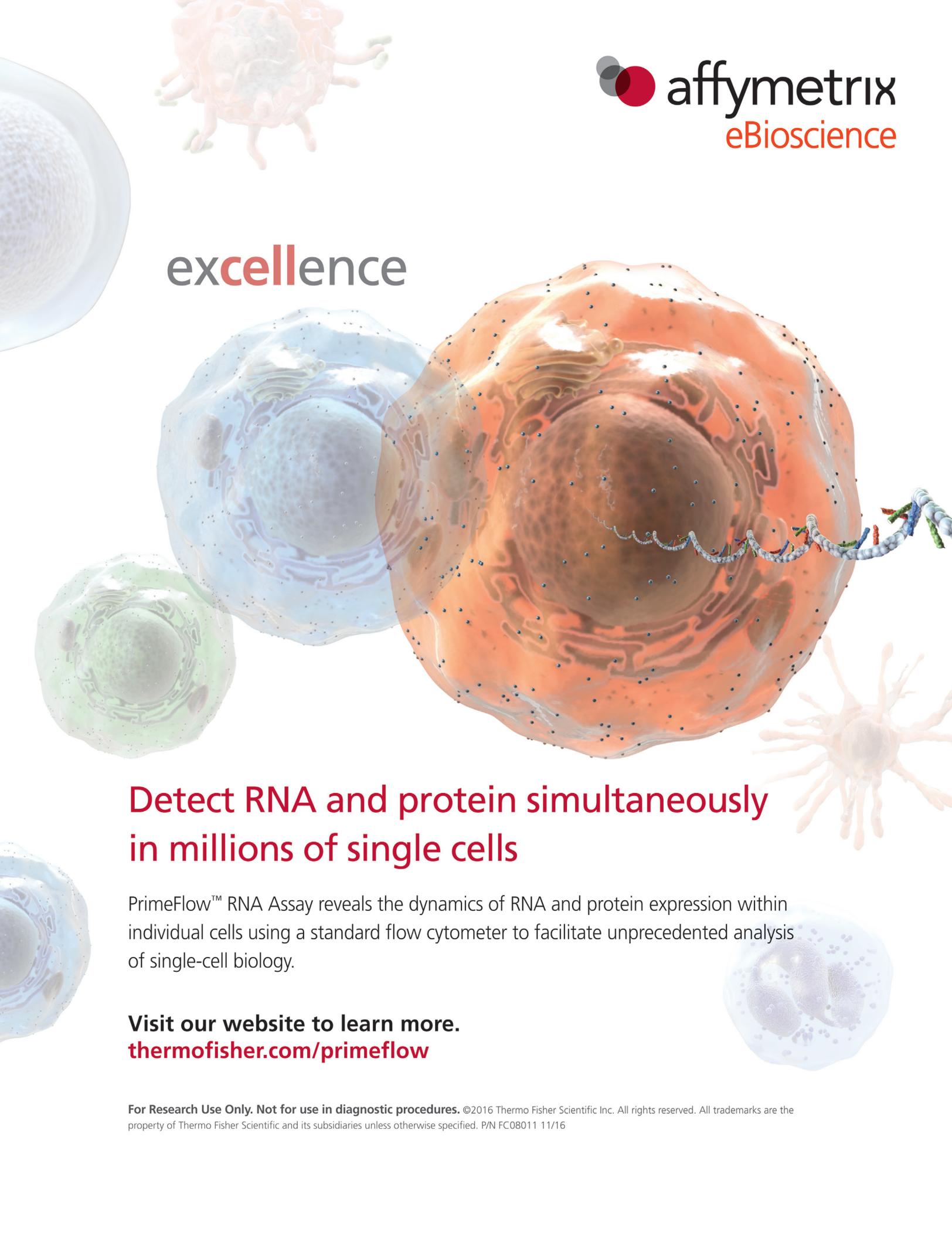
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Our bioinformaticians make The Cancer Genome Atlas (TCGA) data usable. More than a petabyte of multidimensional cancer genomic data from 11,328 patients, 140 metadata fields, and over 200 tools and workflows — all ready for immediate analysis in the cloud.



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## Detect RNA and protein simultaneously in millions of single cells

PrimeFlow™ RNA Assay reveals the dynamics of RNA and protein expression within individual cells using a standard flow cytometer to facilitate unprecedented analysis of single-cell biology.

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