The Maize Genome:

Ripe with Promise

Interest in the genetics of maize began in the early 1900s when geneticists began to document the many varieties and explore the implications of genetic crosses. Understanding the maize genome will enable geneticists to develop new and improved maize varieties that are more nutritious or can withstand harsher environments.

In this special poster, presented in conjunction with the first publication of the full maize genome sequence, we trace the history of modern maize from its beginnings as a wild grass called teosinte, to what is today one of the most productive and widespread crops in the world.

The Maize Genome Poster is available for download at:
www.sciencemag.org/products/posters/maize_poster.pdf

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The SOLiD™ 3 Plus System

The right answer, the first time. The SOLiD™ 3 Plus System enables unsurpassed accuracy and throughput to translate your discoveries into biologically relevant information.

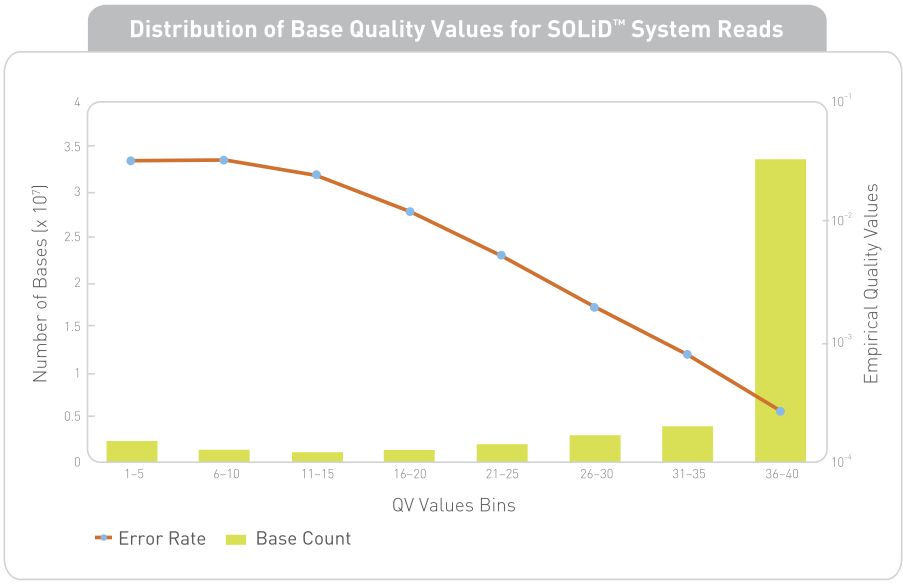


Figure 1. Distribution of bases and their empirical quality values from SOLiD™ System Sequencing.

SOLiD™ 3 Plus System Specifications	
Throughput	60+ GB of mappable sequence or 1 billion reads per run with SOLiD™ 3 Opti reagents
Library Type	• Mate-paired libraries (insert sizes between 600 bp to 10 kb) • Fragment libraries
Starting Material Type	DNA or cDNA isolated from blood or single cells, RNA, BAC, plasmids, fosmids, tissue (high tumor load), and PCR products
Amount of Starting Material	Required input of starting material varies by application • 10 ng to 5 µg for fragment library • 5 µg to 20 µg for mate-paired library
Slide Configuration	Individual samples: 1 to 8 per flowcell Multiplexed samples: up to 256 per run
Flowcells	2 independent flowcells
System Accuracy	Greater than 99.94% accuracy due to 2 base encoding
Consensus Base Accuracy	Greater than 99.999% accuracy at 15x coverage
Base Quality	Greater than 80% of bases at >QV30
Multiplexing	16 barcodes currently available
Analysis	• SAM format exports • Powerful computer cluster for large-scale application analysis • Customizable application analysis with new bioinformatics analysis framework for flexible data review

System Attributes

Highest number of bases greater than QV30

The SOLiD™ 3 Plus System enables the superior accuracy and sensitivity to detect biological variation. The innate error-checking capabilities within 2 base encoding result in highly accurate base sequence; a significant number of bases have quality values greater that 30 (Figure 1). This attribute translates to less coverage required for variant detection, yields fewer false positives, and facilitates a corresponding reduction in validation for project time and cost savings.

Cost-effective research without costly upgrades

The SOLiD™ 3 Plus System generates 60+ GB of mappable sequence or greater than 1 billion reads per run. This level of throughput enables large-scale resequencing and tag-based experiments to be completed more efficiently and rapidly than ever before. The SOLiD™ 3 Plus System's intrinsic open slide format and flexible bead densities facilitate increases in throughput without major system modifications.

Streamlined analysis and data management

The SOLiD™ 3 Plus System supports standard Sequence Alignment Map (SAM) format with base calls and associated quality values. Experience the benefits of the higher accuracy enabled by 2 base encoding and of the flexibility to export to standard downstream analysis tools. Advanced software solutions reduce analysis time through a 20–40% reduction in data footprint and real-time data export.

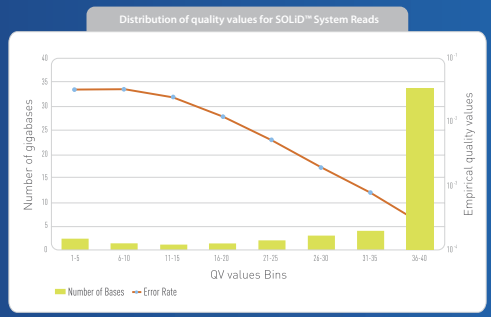
Can Your Next Gen Sequencer Tell The Difference?

Have confidence in your sequencing results with the new SOLiD™ 3 Plus System.

- Superior accuracy and sensitivity for variant discovery with less coverage
- Increased throughput and lower running costs
- Standard base sequence format with the quality of color space

The SOLiD™ 3 Plus System. The right answer, the first time.

For data demonstrating the superior accuracy of the SOLiD™ 3 Plus System go to **www.appliedbiosystems.com/solidaccuracy**



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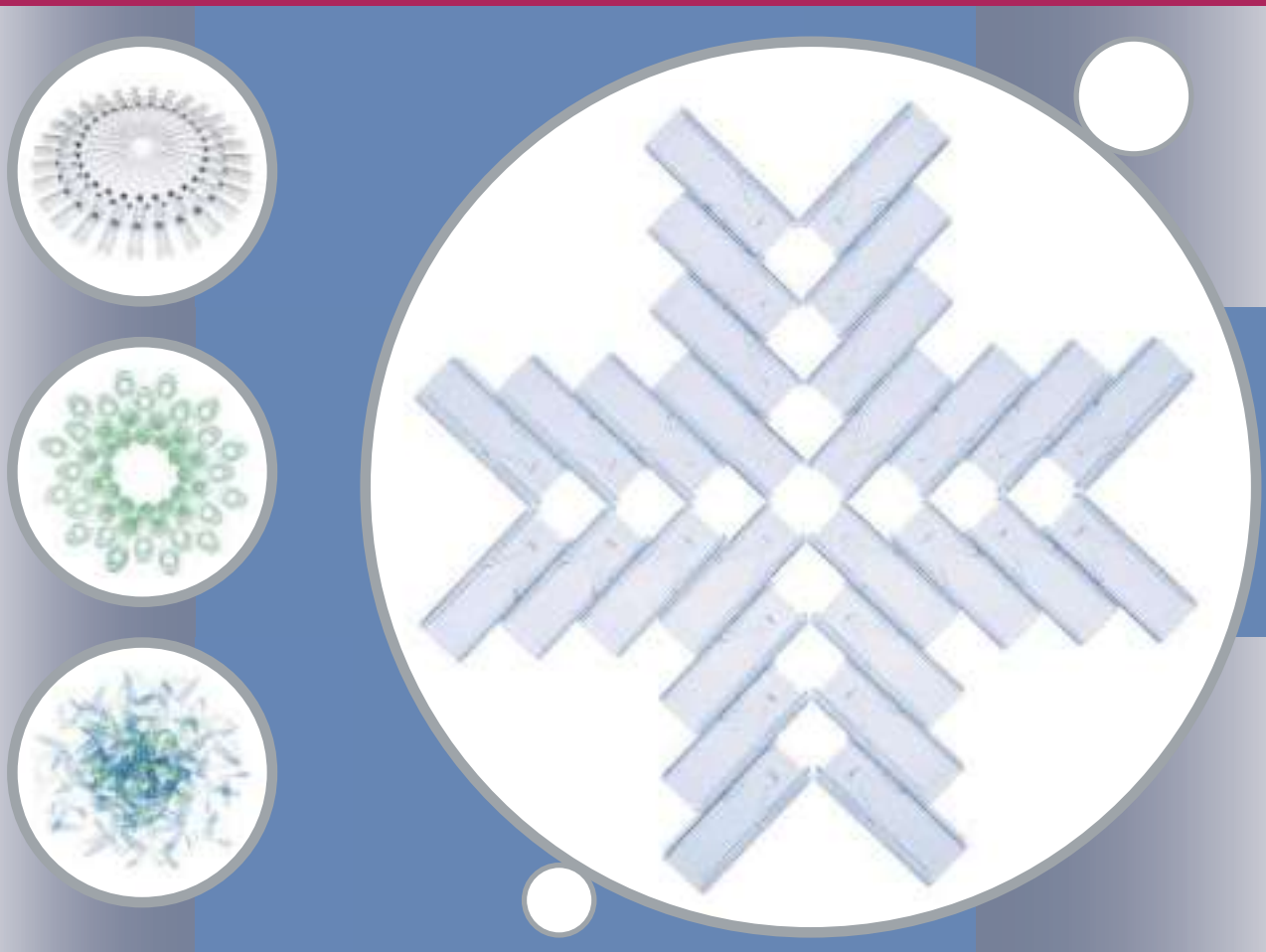

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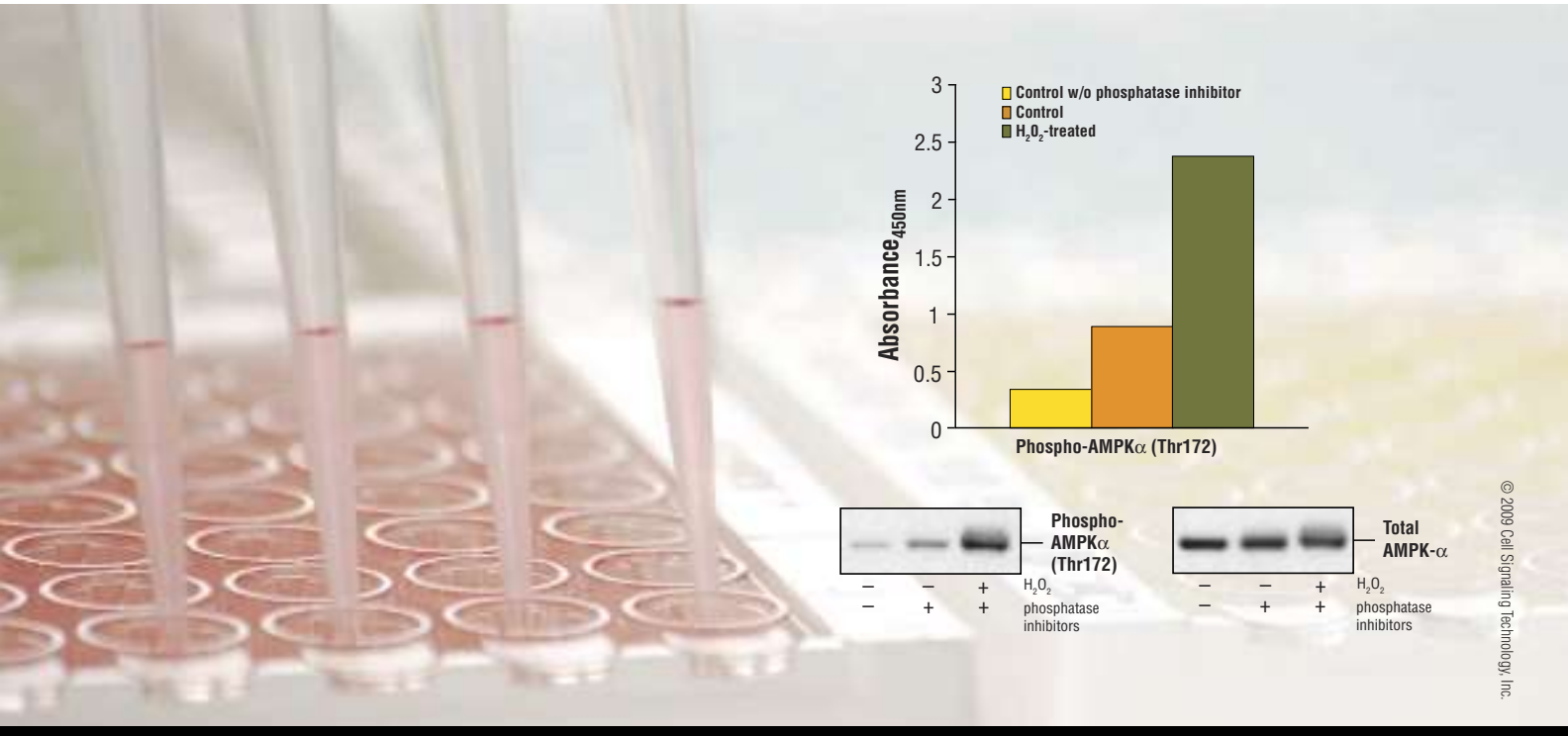

PathScan® Sandwich ELISA Kits & Antibody Pairs

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Above: *Treatment of C2C12 cells with H_2O_2 stimulates phosphorylation of AMPKα at Thr172, detected by the* ***PathScan® Phospho-AMPKα (Thr172) Sandwich ELISA Kit #7959****. The absorbance readings at 450 nm are shown in the top figure, while the corresponding western blots using Phospho-AMPKα (Thr172) (D79.5E) XP™ Rabbit mAb #4188 (left panel) or AMPKα (23A3) Rabbit mAb #2603 (right panel) are shown in the bottom figure.*

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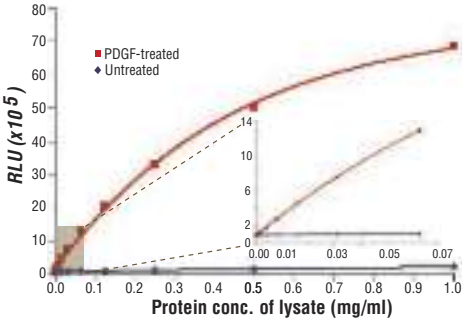

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