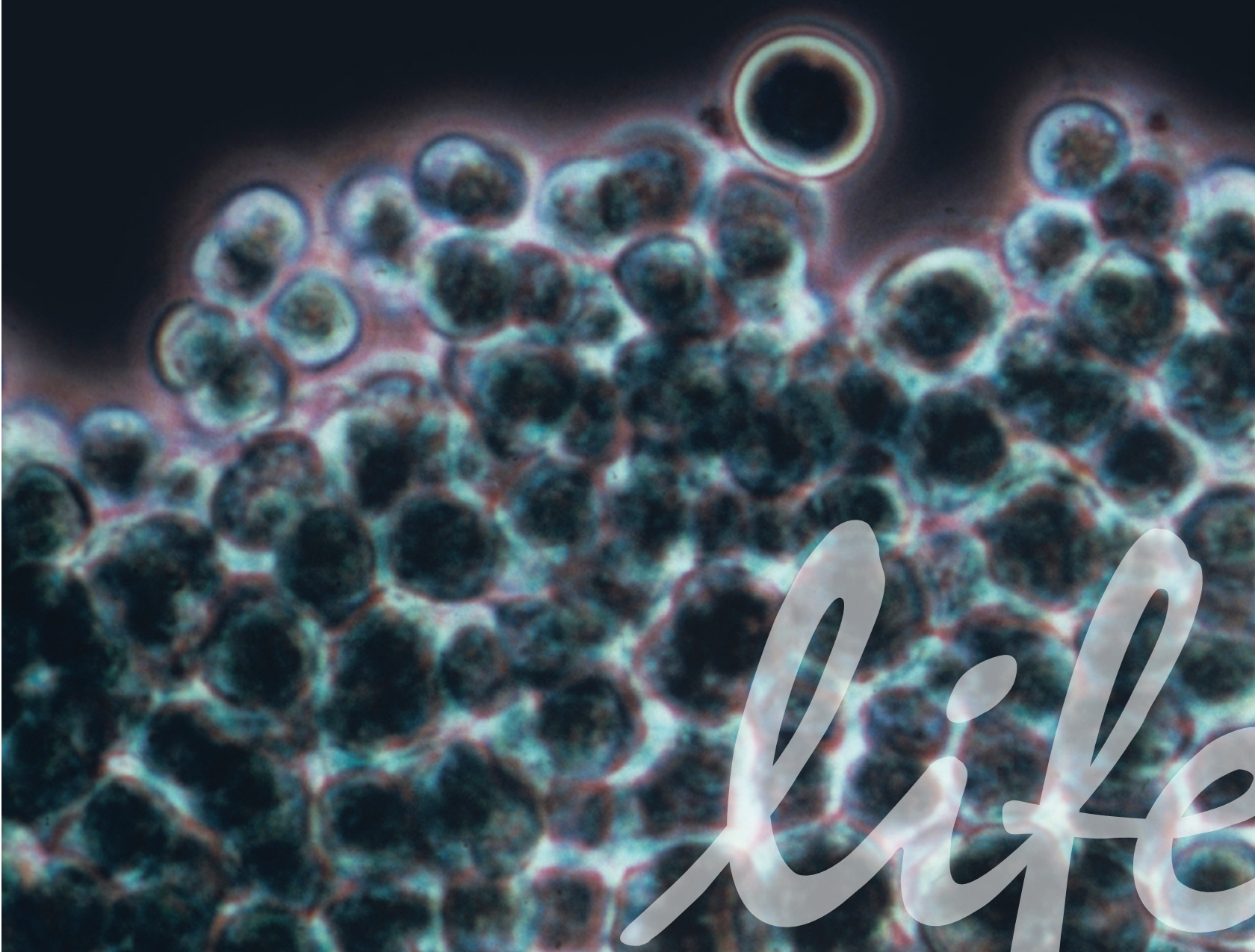
applied biosystems
part of life technologies

SOLiD™
SYSTEM SEQUENCING

See the Difference

Discover the Quality Genome

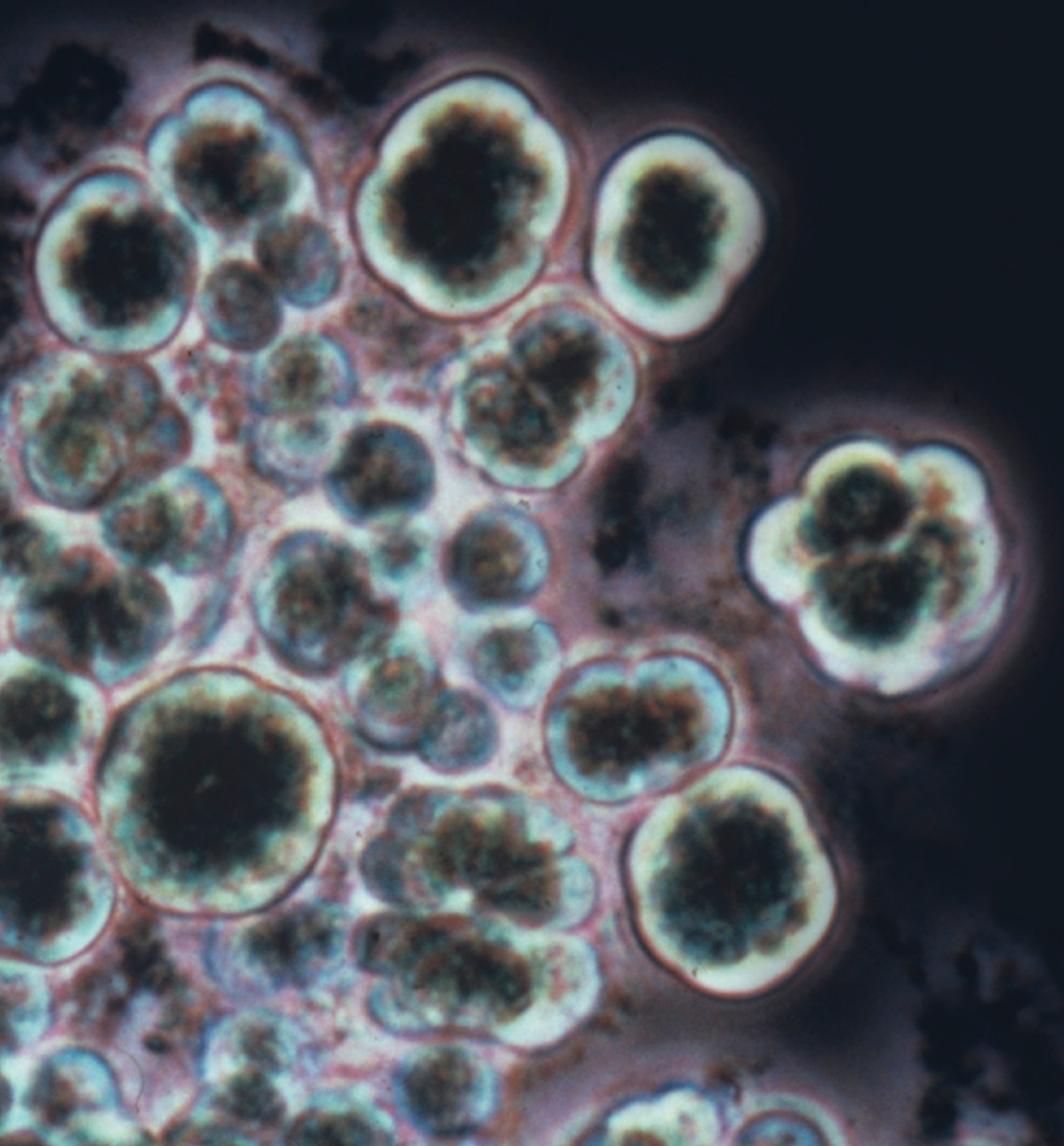


See the Difference

With a commitment to your peace of mind, Life Technologies provides a portfolio of robust and scalable next-generation sequencing systems. Based on innovative ligation-based chemistry, the SOLiD™ Portfolio empowers scientists with the accuracy, throughput, and cost to support your research—today and tomorrow.

Discover the SOLiD™ Portfolio:

- Unrivaled accuracy
- Scalable platform
- Automated workflows
- Easy-to-use application-specific kits
- Integrated data analysis solutions
- Comprehensive support



See the Quality Genome

As researchers strive to translate genomic data into biologically relevant knowledge, the quality and cost of generating that data becomes increasingly important. The Quality Genome is a combination of accuracy and throughput that enables research studies to be conducted more cost-effectively than ever before.

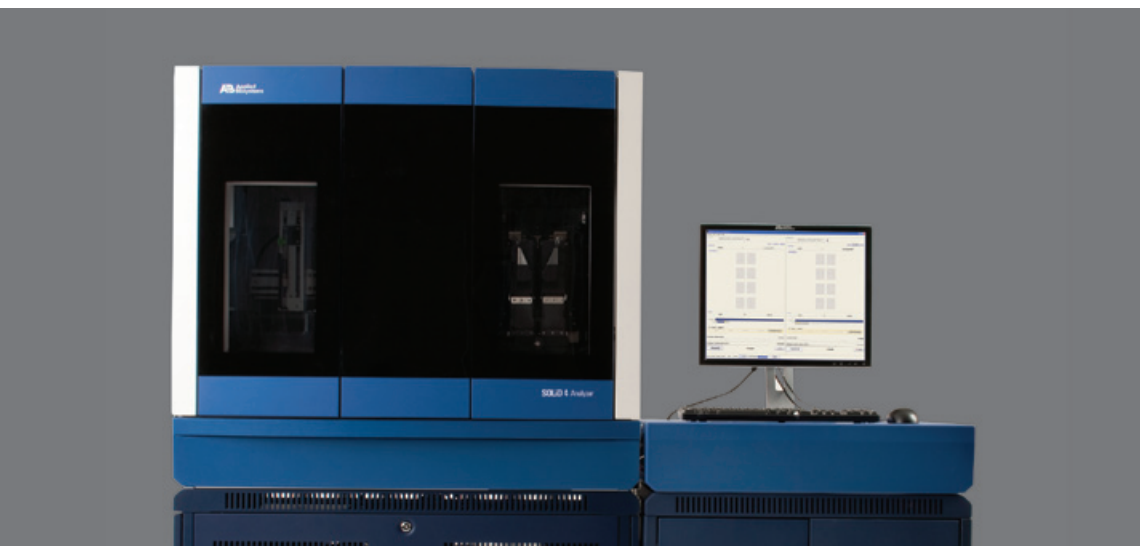
$$\text{Quality Genome}^{TM} = \frac{\text{Accuracy x Throughput}}{\text{Cost}}$$

See more and spend less with the Quality Genome:

As low as $3K per 30X coverage of the genome with SOLiD™ 4*hq**

- Discover rare, causative variants at lower coverage
- Detect variants in pooled or heterogeneous samples
- Reduce false positive rates and downstream validation costs
- Run more samples as larger projects become more cost-effective

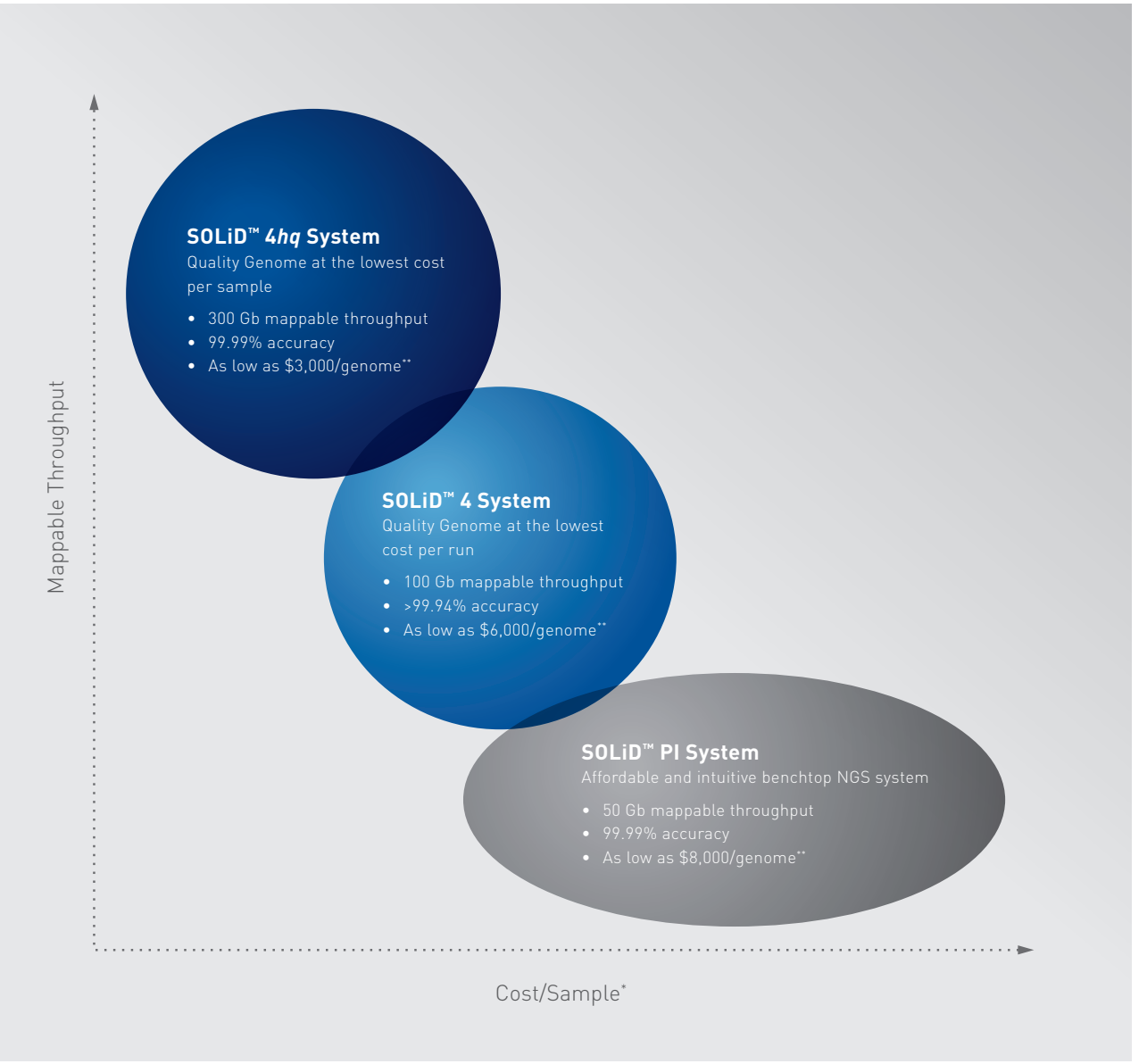
* Costs reflect approximate US list prices at optimal running efficiencies



See More Mappable Throughput

Life Technologies provides a portfolio of next-generation systems to fit with your throughput and cost needs. Have confidence in your results and discover the peace of mind brought to you by the Quality Genome.

The SOLiD™ Platform



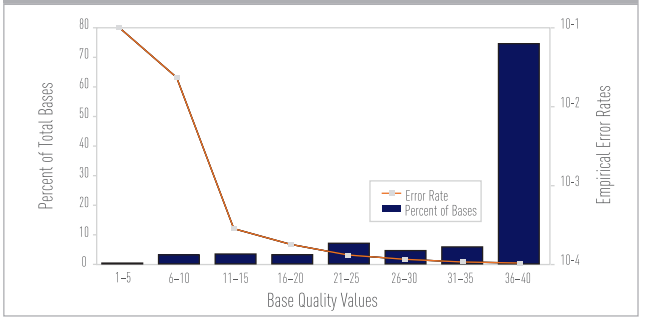
* Costs reflect approximate US list prices at optimal running efficiencies

** Cost per genome represents sequencing of the human genome at 30X coverage

See Unrivaled Accuracy

Accuracy drives the Quality Genome by providing the sensitivity to detect more variation with less coverage.

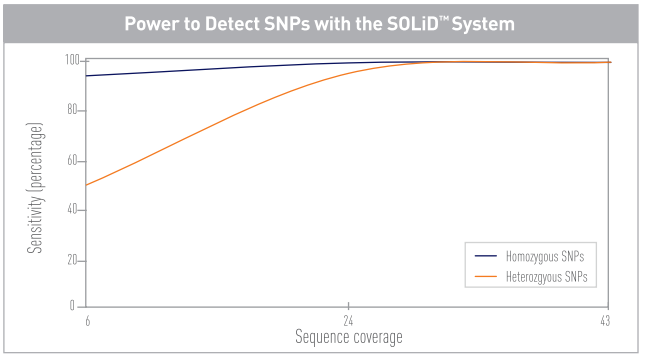
Distribution of Base Quality Values for SOLiD™ System Reads



Greater than 80% of bases higher than QV 30

The SOLiD™ System automatically reports quality values for each base. The base quality values demonstrate high correlation with empirically-generated error rates.

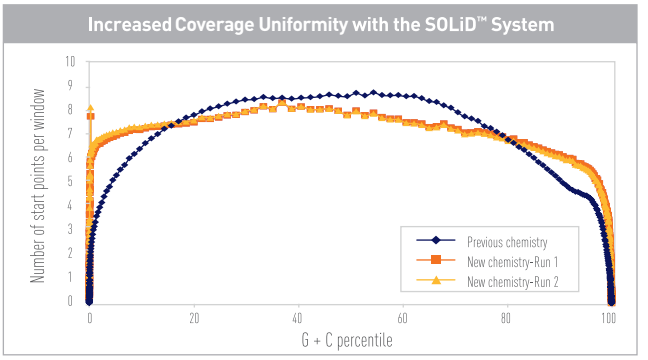
Power to Detect SNPs with the SOLiD™ System



High Sensitivity and Specificity For SNP Detection

Evaluation of SOLiD™ System SNP calling accuracy at various sequencing coverage levels as compared to 7X Sanger sequencing and SNP genotyping data for HuRef DNA reveals the SOLiD™ System's aptitude for genome-wide comprehensive SNP detection.

Increased Coverage Uniformity with the SOLiD™ System



Uniform sequence coverage with SOLiD™ System Chemistry

Enhancements to the SOLiD™ System's chemistry continue to increase the performance and data quality. The unique coverage is shown as a function of G+C percentile for previous sequencing chemistry and replicate runs of the new Total Precision (ToP) chemistry.

The SOLiD™ System's advantage in detecting variation at lower coverage has been demonstrated in numerous publications.[1]

[1] **Selected Publications**

Clark MJ et al. (2010) U87MG Decoded: The Genomic Sequence of a Cytogenetically Aberrant Human Cancer Cell Line. *PLoS Genetics*, 6 (1): e1000832 DOI: 10.1371/journal.pgen.1000832.

Rubin C-J et al. (2010) Whole-genome resequencing reveals loci under selection during chicken domesticationNature 464, 587-591.

McKernan KJ et al. (2009) Sequence and structural variation in a human genome uncovered by short-read, massively parallel ligation sequencing using two base encoding. *Genome Research* 19:1527–1541.

For a complete list of publications supporting the accuracy of the SOLiD™ System, visit **www.appliedbiosystems.com/solidaccuracy**.

See the Scalability

The SOLiD™ System combines unmatched scalability and sample multiplexing for more cost-effective per-sample analysis.

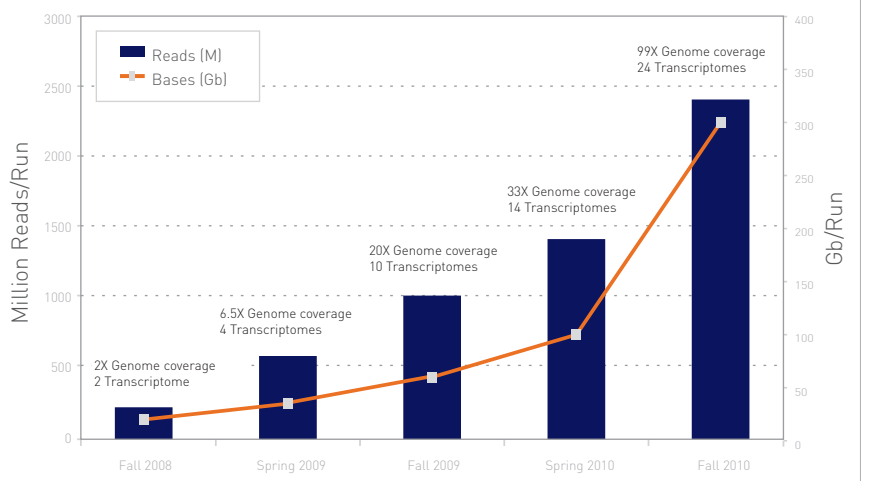
Lower Cost Experiments		
Application	**Cost/Sample***	
	SOLiD™ 4 System	SOLiD™ 4*hq* System
Genome	$6000	$3000
Exome	$300	$160
Transcriptome	$150	$120
ChIP-Seq	$150	$80

* Costs represent approximate US list prices at optimal running efficiencies

Unmatched scalability with an open slide format and flexible bead densities enable increased throughput on the same system with modest optimizations.

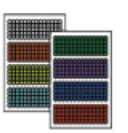
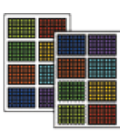
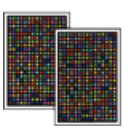
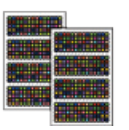
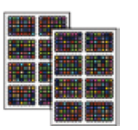
With more mappable reads per run, the SOLiD™ System allows researchers the power to analyze more samples in a single run and provides more uniform coverage across the genome. The scalability of the SOLiD™ System provides more high-quality reads without compromising data accuracy as occurs with increased read lengths.

SOLiD™ System: Throughput Advances



Maximum flexibility with two independent flowcells and flexible slide segmentation, enabling users to run multiple independent experiments on the SOLiD™ System.

Sample multiplexing with up to 96 barcodes, facilitating additional flexibility and dramatically reducing the cost per sample.

	Unsegmented Full Slide	Quad	Octet
Individual Samples	 2 samples/run	 8 samples/run	 16 samples/run
Multiplexed Samples (96 barcodes)	 ⩽96 samples/slide x 2 slides/run ⩽192 samples/run	 ⩽96 samples/segment ⩽4 segments/slide x 2 slides/run ⩽768 samples/run	 ⩽96 samples/segment ⩽8 segments/slide x 2 slides/run ⩽1,536 samples/run

See Automated Workflows

Increased ease of use and reduction in hands-on time improve reproducibility and lower cost per experiment.

Workflow Automation

The new SOLiD™ EZ Bead™ System provides an automated solution for reproducible templated bead preparation with less than 1 hour of hands-on time. The system modularity and quality control checkpoints provide greater experimental control. Additional support for multiplexed libraries helps further maximize time and cost savings.

Benefits of automation with the SOLiD™ EZ Bead™ System include:

- 80% reduction in hands-on time
- Increased reproducibility
- Multiplexed library support, which facilitates maximum time and cost savings
- Modularity to fit individual throughput and lab needs
- Quality control checkpoints throughout the workflow for greater experimental control

The SOLiD™ EZ Bead™ System

SOLiD™ EZ Bead™ Emulsifier

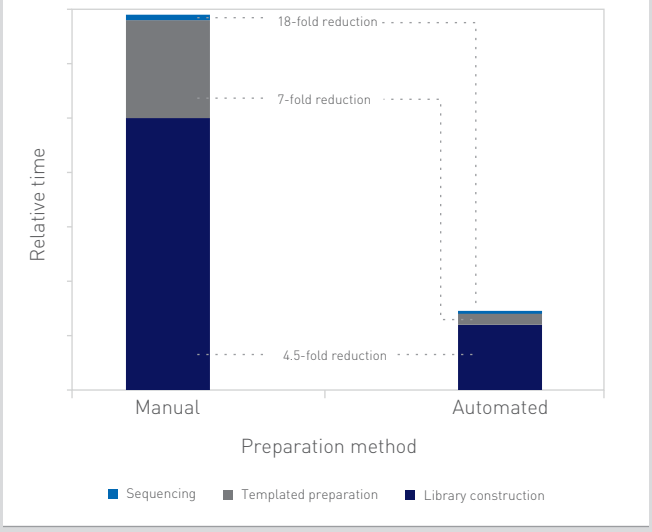
SOLiD™ EZ Bead™ Amplifier

SOLiD™ EZ Bead™ Enricher

Library Prep Automation

An automated method for preparing and purifying multiple fragment libraries is now available. In combination with SOLiD™ barcoding kits and the SOLiD™ EZ Bead™ System, automated liquid handling system protocols help ease the burden of processing multiple samples.

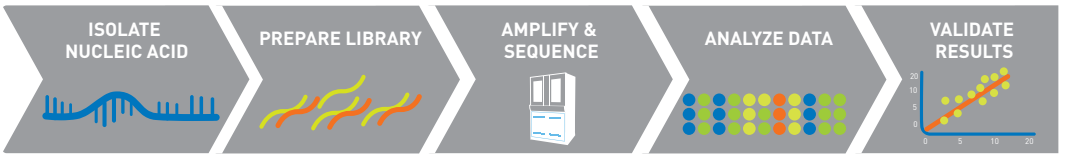
Total time Savings with Automation for 24 samples



See End-to-End Applications

Life Technologies takes you from sample to results with complete solutions for a variety of applications.

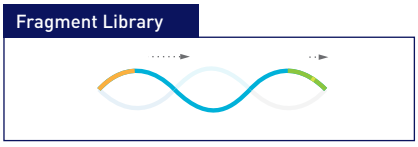
The SOLiD™ Platform Enables End-to-End Workflows

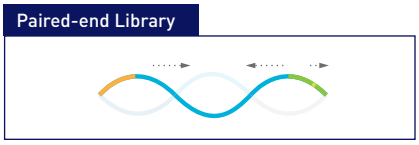


de novo					
Resequencing					
Transcriptome					
RNA-Seq					
SAGE™					
ChIP-Seq					
Methylation					
	Easy-to-use sample prep	Optimized library prep kits	Higher-accuracy sequencing	Push-button analysis pipelines	Gold-standard validation systems

Robust, easy-to-use kits are available for all library types—fragment, mate-pair, and now paired-end. With new paired-end capabilities, you can detect novel nucleotide alterations, SNPs, CNVs, splice variations, and fusion transcripts with less DNA than ever before. Intelligent barcode strategy for fragment and paired-end libraries ensures accurate assignment without the introduction of bias.

Library Types for Every Application

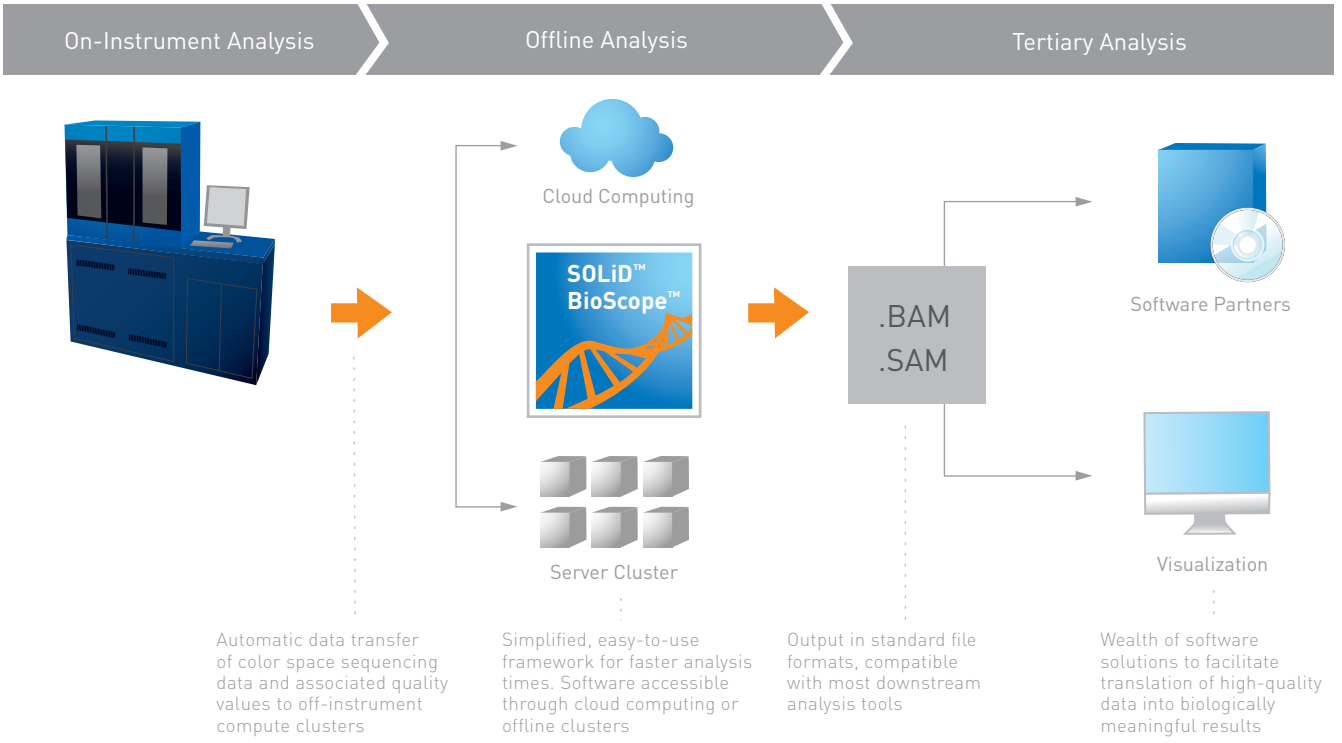




See Powerful Bioinformatics

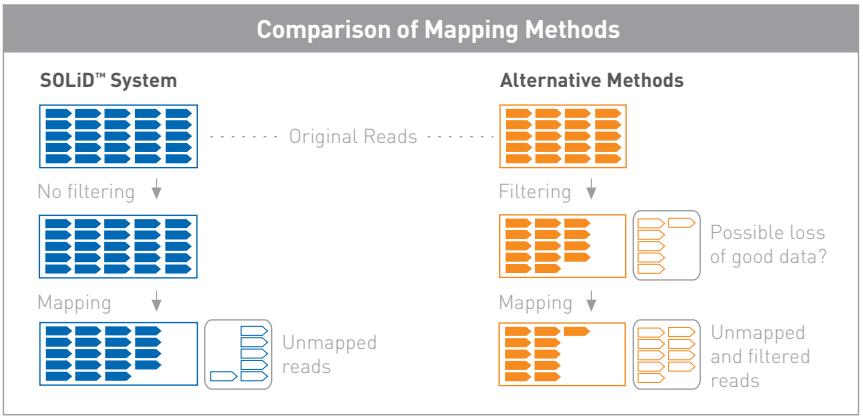
The SOLiD™ System continues to expand its ecosystem of easy-to-use, end-to-end software solutions. The flexible open platform allows you to perform downstream data analysis with your favorite third-party academic or commercial analysis package.

SOLiD™ System Data Analysis Workflow



See More Mapped Data

The SOLiD™ System enables more total mapped reads to give more sensitivity and enhanced flexibility during your data analysis steps. With more mappable reads, you will have the peace of mind that all relevant data are available to you for analysis.



See the Community of Support

With more than 2,000 field personnel, Life Technologies has the most extensive network of dedicated Field Application Specialists and Service Engineers to work with you, so that you can feel confident that we will be there when and where you need us most.

SOLiD™ Sales Field Application Specialists
- System and component experts
- Application knowledge and experience
- Guidance to the right platforms and reagents
- Experimental design and support

SOLiD™ Bioinformatics Specialists
- Computer science, IT, and bioinformatics expertise
- Data preparation and analysis

SOLiD™ Field Service Engineers
- Technical engineering system knowledge
- Installation
- Repairs and maintenance

SOLiD™ Global Training Facilities
- Regional Centers of Excellence
- System and chemistry training
- Bioinformatics training
- Sample preparation training

The SOLiD™ Community

Created to give you broader access to advanced sequencing technologies, this network is a self-governing, worldwide community offering public spaces for anyone interested in next-generation sequencing, as well as private spaces for SOLiD™ System users.

Register at **solid.community.appliedbiosystems.com** to start sharing information with your colleagues and to learn the latest news within the SOLiD™ Community.

New SOLiD™ Systems			
Specifications	SOLiD™ 4 System	SOLiD™ 4*hq* System*	SOLiD™ PI System*
Mappable Throughput/ Run**	Up to 100 Gb	Up to 300 Gb	Up to 50 Gb
System Accuracy	99.94%	99.99%	99.99%
Cost/Genome***	As low as $6,000	As low as $3,000	As low as $8,000
Read Length	• Fragment: 50 bp • Mate-pair: 2 x 50 bp • Paired-end: 50 x 25 bp	• Fragment: 75 bp • Mate-pair: 2 x 75 bp • Paired-end: 75 x 35 bp	• Fragment: 75 bp • Mate-pair: 2 x 75 bp • Paired-end: 75 x 35 bp
Multiplexing	• 48 RNA barcodes • 96 DNA barcodes	• 96 RNA barcodes • 96 DNA barcodes	• 96 RNA barcodes • 96 DNA barcodes
Run Time	• 3 days for 35 bp • 11 days for 50 x 25 bp • 12 days for 2 x 50 bp	• 3 days for 35 bp • 12 days for 75 x 35 bp • 14 days for 2 x 75 bp	• 1 day for 35 bp

* These systems are under development and the specifications are subject to change.
** Expected throughput.
*** Costs reflect approximate US list prices at optimal running efficiencies. Cost per genome represents sequencing of the human genome at 30X coverage. Regional pricing may vary.

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