



discover what comes from  
**accuracy**

Discover the 5500 Series SOLiD™ Sequencers

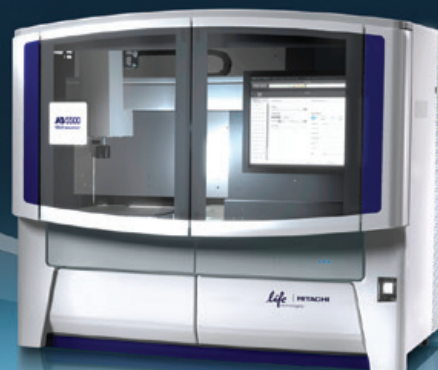
# what does your research demand?

The sequencing of the human genome marked a turning point in history. Today, it's no longer just a question of sequencing genomes—it's about translating that information into knowledge. But that process presents its own set of challenges:

"I want to **accurately** characterize all the variations in my sample using a single platform, including SNPs, copy number, structural variants, gene regulation, and expression."

"I'm looking for a next-generation sequencing technology so I can stay competitive, but it needs to be **practical for my lab**, like Sanger sequencing."

"I need a technology that is **cost-effective** on a per-sample basis regardless of the project size."



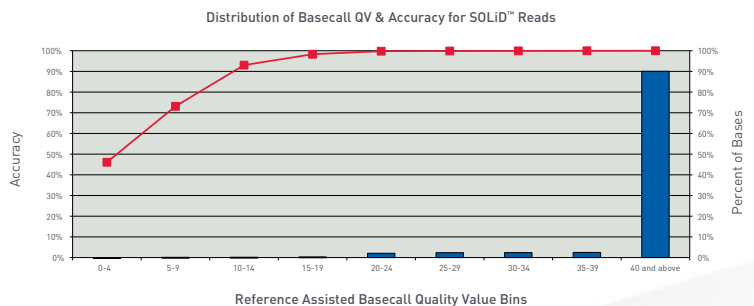
# the answers are here

Building on a powerful legacy of engineering excellence, the new 5500 Series SOLiD™ Sequencers move your research closer to the discovery of biologically relevant outcomes with unrivaled accuracy, flexibility, and ease of use.

“I **need** to understand the impact of tumor subpopulations on disease progression.”

## accuracy...the simple answer

- Up to 99.99% accuracy using the Exact Call Chemistry (ECC) module allows for mutation detection at lower coverage
- Quality values  $\geq 40$  for up to 90% of mapped bases result in stronger consensus sequence
- More mapped reads provide increased sensitivity and dynamic range
- Higher raw read accuracy with ECC for reference-free analysis enables *de novo* assembly

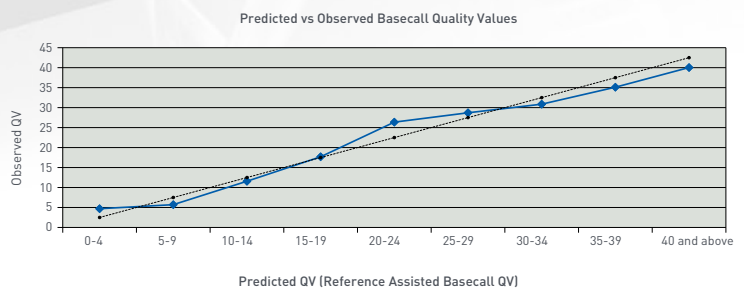


Data is based on 5 Million 50 bp reads of *Escherichia coli* DH10B sequenced with Exact Call Chemistry

## when higher coverage isn't enough

- Detect somatic subpopulations—discover variants down to 1% of your population with up to 99.99% accuracy
- Detect with less coverage—identify variants present in 5% of your sample with  $\frac{1}{3}$  the sequence coverage needed, with 99.0% accuracy

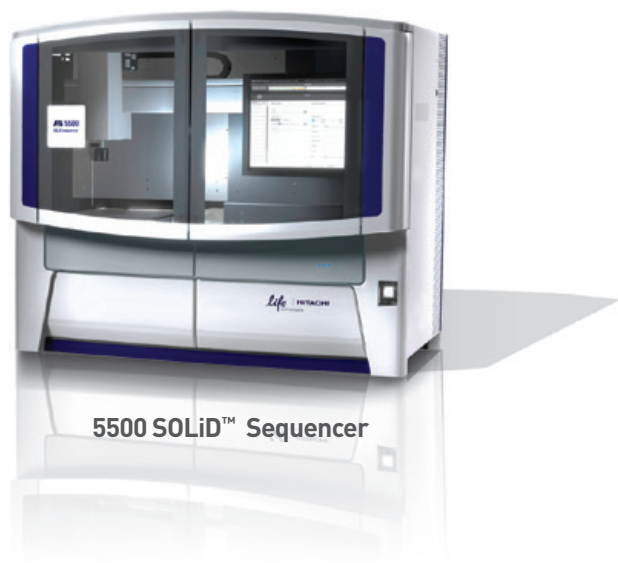
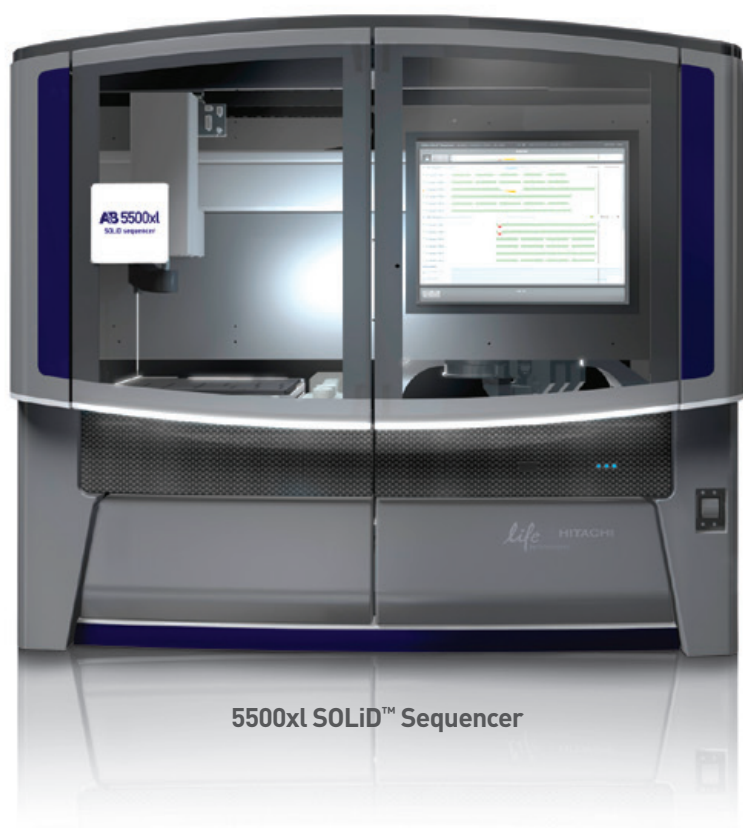
For more information, go to [www.appliedbiosystems.com/solidaccuracy](http://www.appliedbiosystems.com/solidaccuracy)



Data is based on 5 Million 50 bp reads of *Escherichia coli* DH10B sequenced with Exact Call Chemistry. Predicted QV is the value assigned by the algorithm. Observed QV is the empirically measured quality after mapping reads to the reference sequence.

# instrumental to your success

Whether it's the 5500xl SOLiD™ Sequencer for rapid, cost-effective, large genomic studies or the 5500 SOLiD™ Sequencer for efficient, economical, smaller-scale investigations, you have the benefit of a robust, user-friendly, and remarkably accurate sequencing technology that satisfies the needs—and exceeds the expectations—for confident and consistent answers across a wide range of applications.



“I **want** the robustness and ease of use of the 3500 Genetic Analyzer, and the throughput of the SOLiD™ System.”

# what will you find with the 5500 Series SOLiD™ Sequencers?



## **exactly** what you're looking for

- Benchtop instrument and user-friendly control software simplify sequencing
- 1-2 configurable microfluidic FlowChips with 6 independent lanes each enable flexibility
- Embedded sequencing controls maximize data quality and performance
- Flexible system configuration allows multiple applications in a single run
- Reduction of data footprint by 60% allows for faster data transfer and analysis
- Pay-per-use reagents provide cost-effective consumable usage
- Application-specific kits offer ease of use
- 96 barcodes for sample multiplexing in DNA and RNA applications afford cost-effective runs

# committed to your research from sample to result

- Automated, reproducible, templated bead preparation with typically less than 1 hour of hands-on time
- Optimized sample prep kits for RNA-Seq, ChIP-Seq, exome resequencing, and DNA methylation
- Robust, easy-to-use kits for all library types, including fragment, mate-pair, and paired-end
- Reference-free analysis with Exact Call Chemistry Module
- Intelligent barcode/multiplexing strategy for fragment and paired-end libraries, permitting accurate assignment without introducing bias
- Suite of software solutions to help meet your resource and infrastructure needs



“I **want** easy, robust sample prep kits and push-button analytical software.”

# flexible and nimble to support your experimental needs

- Microfluidic FlowChip allows cost-effective processing for every available application
- 6 independent lanes per FlowChip support multiple experiment types in a single run
- Flexibility to run a single lane or a full FlowChip saves time and cost with pay-per-use reagents
- Rapid run times expedite analysis of single or multiple samples
- Library support for 96 barcodes gives maximum efficiency and economy
- Ability to disable individual lanes minimizes reagent usage when needed

2 Exome Samples<sup>1</sup>  
(75 bp x 35 bp)

2 mRNA Profiles<sup>2</sup> (75 bp)

24 ChIP-Seq Samples<sup>3</sup>  
(35 bp)

24 microRNA Samples<sup>4</sup>  
(35 bp)

1 Structural Variation/  
Inversion Experiment<sup>5</sup>  
(60 bp x 60 bp)

2 Methylation Samples<sup>6</sup>  
(enriched) (75 bp)

All calculations assume optimal running efficiencies and the following coverage:

1. ~100x coverage of human exome
2. ~100M reads per sample
3. ~5M reads per sample
4. ~5M reads per sample
5. ~4x coverage of human genome
6. ~60M reads per sample

“I **want** the flexibility to run a single sample in one day without paying for the whole run.”

# a 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 you can be confident that we will be there when and where you need us most.

## **SOLiD™ Sales and 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**

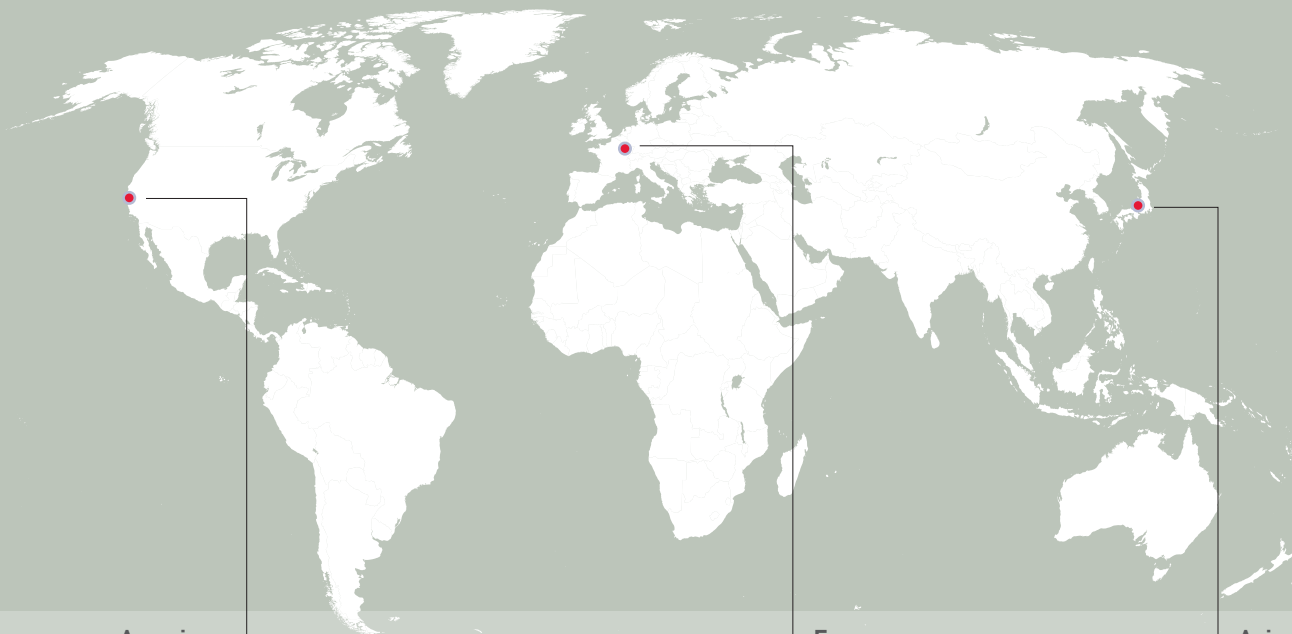
- Computer science, IT, and bioinformatics expertise
- Data preparation and analysis

## **SOLiD™ Field Service Engineers**

- Technical engineering system knowledge
- Installation
- Repairs and maintenance

## **SOLiD™ Global Training Facilities**

- Application support centers
- System and chemistry training
- Bioinformatics training
- Sample preparation training



### **Americas**

350 Field Sales and Application Specialists  
120 Direct  
300 Field Service  
210 Supply Chain Global Support

### **Europe**

330 Field Sales and Application Specialists  
270 Field Service  
150 Supply Chain

### **Asia-Pacific**

200 Field Sales and Application Specialists  
200 Field Service  
40 Supply Chain

## **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](http://solid.community.appliedbiosystems.com) to start sharing information with your colleagues and learn the latest news within the SOLiD™ Community.

# the 5500 Series SOLiD™ Sequencers you asked—we answered



# what does your lab demand?

	<b>5500 SOLiD™ Sequencer with microbeads</b>	<b>5500xl SOLiD™ Sequencer with microbeads</b>	<b>5500xl SOLiD™ Sequencer with nanobeads</b>
<b>System accuracy<sup>1</sup></b>	up to 99.99%	up to 99.99%	up to 99.99%
<b>Typical throughput/day<sup>2</sup></b>	10–15 Gb/day	20–30 Gb/day	30–45 Gb/day
<b>Samples/run<sup>3</sup></b>	<ul style="list-style-type: none"> <li>• 1 genome</li> <li>• 12 exomes</li> <li>• 6 transcriptomes</li> </ul>	<ul style="list-style-type: none"> <li>• 2 genomes</li> <li>• 24 exomes</li> <li>• 12 transcriptomes</li> </ul>	<ul style="list-style-type: none"> <li>• 3 genomes</li> <li>• 40 exomes</li> <li>• 20 transcriptomes</li> </ul>
<b>Independent lanes</b>	1–6	1–12	1–12
<b>Typical run time</b>	<ul style="list-style-type: none"> <li>• 1 day for 35 bp (1 lane)</li> <li>• 7 days for 60 bp x 60 bp (6 lanes)</li> <li>• 7 days for 75 bp x 35 bp (6 lanes)</li> </ul>	<ul style="list-style-type: none"> <li>• 1 day for 35 bp (1 lane)</li> <li>• 7 days for 60 bp x 60 bp (12 lanes)</li> <li>• 7 days for 75 bp x 35 bp (12 lanes)</li> </ul>	<ul style="list-style-type: none"> <li>• 1 day for 35 bp (1 lane)</li> <li>• 7 days for 60 bp x 60 bp (12 lanes)</li> <li>• 7 days for 75 bp x 35 bp (12 lanes)</li> </ul>
<b>Typical throughput/run<sup>4</sup></b>	90 Gb	180 Gb	300 Gb
<b>Read length</b>	<ul style="list-style-type: none"> <li>• MP: 60 bp x 60 bp</li> <li>• PE: 75 bp x 35 bp</li> <li>• Fragment: 75 bp</li> </ul>	<ul style="list-style-type: none"> <li>• MP: 60 bp x 60 bp</li> <li>• PE: 75 bp x 35 bp</li> <li>• Fragment: 75 bp</li> </ul>	<ul style="list-style-type: none"> <li>• MP: 60 bp x 60 bp</li> <li>• PE: 75 bp x 35 bp</li> <li>• Fragment: 75 bp</li> </ul>
<b>Multiplexing</b>	96 for RNA and DNA	96 for RNA and DNA	96 for RNA and DNA

1. Calculated using Exact Call Chemistry Module on sequencing control beads, reference-free.

2. Range calculated from optimized run efficiencies of PE and MP runs.

3. Genomes/run assumes mate-pair sequencing at 30x coverage of the human genome.

Exomes/run assumes PE sequencing at 100-150x coverage across human exome.

Whole Transcriptome calculated using PE sequencing at 100M reads per sample.

4. Calculated from optimized run efficiencies of a high-density MP run.

Life Technologies offers a breadth of products DNA | RNA | protein | cell culture | instruments  
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