

## Genomic Services

**Leverage the expertise and capabilities of Solexa's Genomics Services group to rapidly and cost-effectively complete your research projects.**

Rely on Solexa's Genomics Services group to design and complete your projects in record time at costs unmatched by other technology. With years of experience delivering high quality service, Solexa's Genomic Services group offers a range of capabilities from consultation on experimental design, to sample handling and preparation, to data analysis and bioinformatics consultation. Solexa's range of services enables you to tailor the proper combination to best meet your research needs. The combination of a proven track record of executing on high value projects plus a team of seasoned professionals, makes access to Solexa's sequencing-by-synthesis technology convenient and affordable.

For more information or to discuss your particular research needs, please contact Solexa's Genomic Services at 510-670-9300 or [services@solexa.com](mailto:services@solexa.com)

## Services and Applications

### Services

- Consultation with experimental design
- Sample preparation and quality control
- Sequencing
- Data analysis and bioinformatics consultation

### Applications

- Whole genome sequencing
- Candidate region or gene sequencing
- Digital expression profiling
- Small RNA analysis

\* If your specific application does not appear on the list, please contact our Genomic Services group - we can work with you to design the appropriate protocols and processes to handle your application.

## About Solexa

Solexa, Inc. (NASDAQ: SLXA) is developing and commercializing a new genetic analysis instrument system based on our novel Clonal Single Molecule Array™ technology and proprietary reversible terminator chemistry. This new platform, the Solexa Genome Analysis System, is being designed to offer a powerful new approach to some of today's most important genetic analysis applications, including:

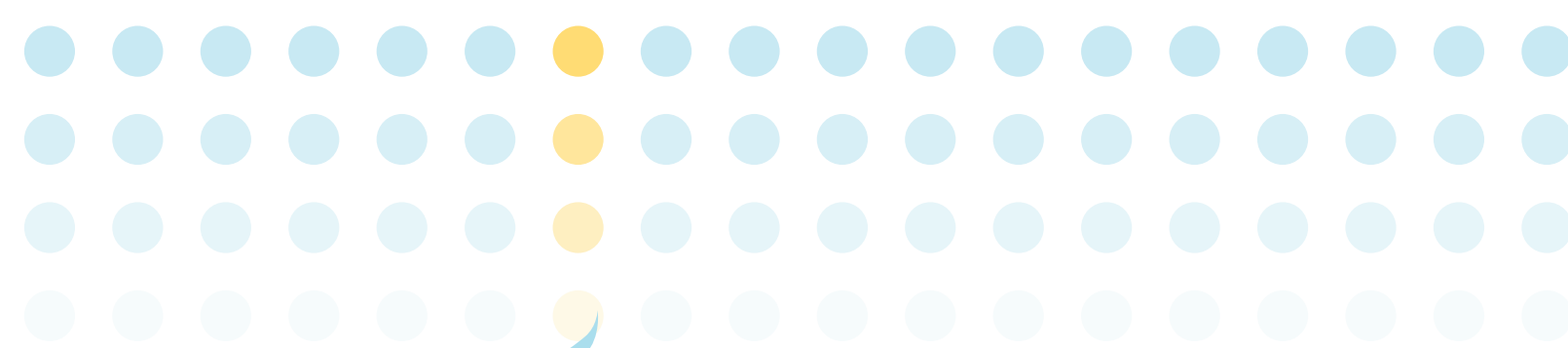
- Whole genome and candidate region sequencing
- Digital expression profiling
- Small RNA identification and quantification
- Hybridization array data validation

To learn more about Solexa, our technology, and our products, please visit [www.solexa.com](http://www.solexa.com) or email us at [info@solexa.com](mailto:info@solexa.com)

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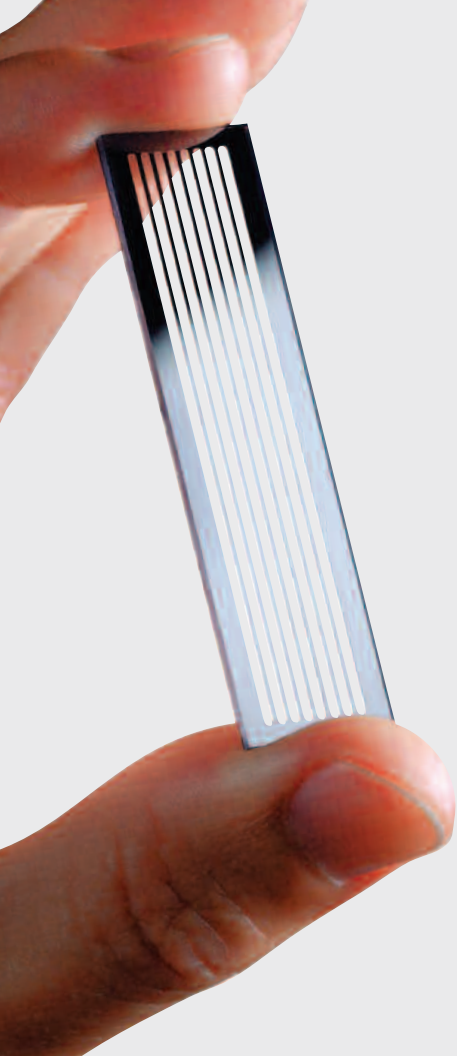
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Advancing genetic analysis  
one billion bases at a time.™



Solexa Genome Analysis System



## Solexa Genome Analysis System

The Solexa Genome Analysis System is a groundbreaking new platform for genetic analysis and functional genomics. Dramatically improving speed and reducing costs, it is suitable for a range of applications including whole genome and candidate region sequencing, expression profiling, and small RNA identification and quantitation. Leveraging proprietary reversible terminators and Clonal Single Molecule Array™ technology, the Solexa Genome Analysis System has the potential to generate upwards of one billion bases of data per single run, and in the process transform the way many experiments are devised and carried out.

The Solexa Genome Analysis System is an integrated platform comprised of the Solexa 1G Analyzer, the Solexa Cluster Station, dedicated reagents and consumables, and complete suite of Data Collection and Application Analysis software.



### The Flow Cell

The flow cell is an 8-channel glass and silicon-based substrate in which clusters are generated and the sequencing reaction is performed. Each of the 8 channels are individually addressable, so researchers can interrogate anywhere from 1-8 distinct samples per flow cell. Within each channel of the flow cell, millions of primers act as capture mechanisms for the fragmented DNA or cDNA. This simple and elegant approach leads to a device density that significantly exceeds that of other platforms that rely on photolithography, mechanical spotting, or positioning of beads into wells to achieve their density. Each channel of the flow cell is capable of yielding up to 5 million distinct clusters and generating over 125Mb of sequence data. The flow cell's format versatility allows researchers to tailor the use of the device to the specific needs of their applications and utilize the platform for a variety of interrogations.

## Sequencing

The Solexa Genome Analysis System is ideal for genome-scale as well as targeted sequencing projects. This platform has the potential to allow researchers to sequence a human genome for under \$100,000 and in a matter of weeks, a feat that would mark a dramatic improvement over the capabilities offered by existing technologies. Sequencing-By-Synthesis using proprietary reversible terminators allows the Solexa Genome Analysis System to provide a high degree of sequencing accuracy even through homopolymeric regions, which will allow researchers to sequence complex genomes rapidly and economically. The versatile format of the flow cell also allows researchers to tailor the system to meet the specific needs of their application. With the potential to generate over 125Mb of sequence data per channel, the Solexa Genome Analysis System provides researchers with the opportunity to sequence multiple bacterial genomes in a single instrument run, thus achieving even greater efficiency and throughput.

## Expression Profiling

The Solexa Genome Analysis System can generate sequence based (i.e., *digital*) genome-wide expression profiles of any transcript, from any gene, in any species without the need for *a priori* knowledge of the species' transcriptome. The Solexa Genome Analysis System will enable researchers to generate this digital data at costs comparable to existing technologies that generate analog measurements of expression changes. Furthermore, since Solexa's approach to measuring expression changes involves sequencing up to 5 million tags derived from a sample, researchers can have greater confidence in their measurements, particularly that of lower expression genes.

**No prior knowledge of transcripts required:** Ideal for analyzing organisms with poorly annotated genomes as well as for discovery of novel transcripts in well-annotated genomes.

**Genome-wide validation of hybridization array data:** Validate array data at whole genome scale for less cost than conventional Real Time or Northern Blot techniques.

**Discovery and analysis of small RNA:** Unbiased representation of small RNAs allows analysis of micro-RNAs and archived samples.

## Benefits

### Unparalleled data density

Analyze up to 40M distinct clusters per flow cell

### Lowest cost per genome

Sequence a human genome for under \$100,000

### Highest throughput

Generate up to 1Gb of data per run

### Accuracy and confidence

Obtain accurate sequence data, even through homopolymers

### Application versatility

Perform a range of genetic analysis applications all on one platform

## Applications

### Whole genome sequencing

Sequence a human genome in weeks not years

### Candidate region sequencing

Economically sequence focused regions across hundreds to thousands of samples

### Gene expression profiling

Generate digital (i.e., sequence-based) data at costs comparable to analog data methods

### Small RNA discovery and analysis

Gain the most complete view of small RNA<sup>1</sup> across a wide range of species


### Genome annotation

Rapidly and economically sequence transcribed regions of genomes

<sup>1</sup>Lu, C., et al. Science. 2005 Sep 2; 309(5740): 1567-9.

## System Workflow: Simple, robust, and highly automated

**1. Sample Preparation**



**Duration:** 7 hours

- Shear genomic DNA
- Repair ends
- Ligate adapters


**2. Cluster Generation**



**Duration:** < 4 hours

- Place reagents onto Cluster Station
- Place flow cell onto Cluster Station
- Add samples
- Press "start" button

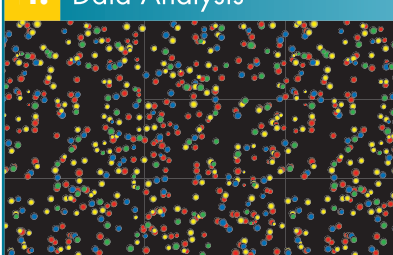
**3. Sequencing-by-Synthesis**



**Duration:** 48-72 hours\*

- Place reagents onto the Solexa 1G Genetic Analyzer
- Place flow cell onto the Solexa 1G Genetic Analyzer
- Press "start" button

**4. Data Analysis**



**Duration:** ~8 hours

- Start automated analysis:
  - Image processing
  - Base calling
- Transfer data to automated analysis pipeline for secondary analysis

\* Duration of the run depends on the desired number of sequencing cycles; complete walk-away automation

