HiScan™SQ System

Two proven technologies, one powerful platform

HiScanSQ Highlights

- **Designed for Flexibility**
  The resolution of next-generation sequencing and the high-throughput processing of arrays enable a wide breadth of applications
- **Proven Performance**
  The most successful, trusted sequencing and array technologies available ensure the highest data quality
- **One Streamlined Solution**
  Minimized instrument hands-on time through a number of cutting-edge user interface features, automating and streamlining experiment setup and processing procedures

Introduction

The HiScanSQ system (Figure 1) integrates the power and resolution of next-generation sequencing with the high-throughput capacity of genotyping, gene expression, and methylation arrays, delivering unprecedented flexibility for experimental design. The instrument features two distinct components, the HiScan Reader and the SQ Module. The HiScan Reader functions as a high-speed, precision imaging scanner for Illumina sequencing and microarray-based analyses. The SQ Module is a reagent handling fluidics device needed to perform Illumina next-generation sequencing.

The integration of sequencing and microarray-based experiments offers unlimited possibilities for genomic research. Together, these complementary technologies provide a powerful approach to genetic discovery and validation, enabling researchers to take any course of study and ask virtually any question of the genome, transcriptome, or epigenome. HiScanSQ allows researchers to:

- Identify target SNPs from sequencing experiments to design iSelect® custom genotyping panels for any species and any study
- Leverage targeted resequencing as the ultimate follow up to genome-wide association studies (GWAS) for any species
- Transition between array-based and sequencing-based gene expression analysis
- Combine the coverage of the Infinium HumanMethylation450 BeadChip with mRNA-seq for a comprehensive, integrated analysis of genome-wide gene expression and methylation

TruSeq Technology

The TruSeq family of reagents represents the latest advancement of Illumina's sequencing by synthesis (SBS) technology. Permeating the entire chemistry workflow, from sample preparation through DNA sequencing, TruSeq underlies Illumina sequencing and empowers it to deliver the industry's most accurate genomic data for a broad range of applications.

Figure 1: The HiScanSQ System

The HiScanSQ system includes two separate components: the HiScan Reader (left) and the SQ Module (right). The HiScan Reader is a high-performance scanner, capable of analyzing next-generation sequencing flow cells and Illumina BeadArray products. The SQ module is an advanced fluidics device for SBS reagent handling.

SBS chemistry enables massively parallel sequencing of millions of fragments using a proprietary reversible terminator-based method that detects single bases as they are incorporated into growing DNA strands. A fluorescently-labeled terminator is imaged as each dNTP is added and then cleaved to allow incorporation of the next base. Since all four reversible terminator-bound dNTPs are present during each sequencing cycle, natural competition minimizes incorporation bias. Base calls are made directly from signal intensity measurements during each cycle, which greatly reduces raw error rates compared to other technologies. The end result is highly accurate base-by-base sequencing that eliminates sequence-context specific errors, enabling robust base calling across the genome, including repetitive sequence regions and within homopolymers.

TruSeq technology delivers the most accurate human genome at any level of coverage, with the highest yield of error free reads and fewest gaps, giving researchers the highest confidence in their data integrity to draw sound biological conclusions.

Easiest Sequencing Workflow

The Illumina sequencing workflow is based on three simple steps: libraries are prepared from virtually any nucleic acid sample, amplified to produce clonal clusters, and sequenced using massively parallel synthesis. Library preparation can be performed using Illumina's simplified TruSeq sample prep kits or Nextera's Illumina sequencer-compatible DNA Sample Prep Kits. Cluster generation occurs on the cBot automated cluster generation system, where hands-on time is less than ten minutes, compared to more than six hours of hands-on effort for emulsion PCR methods. The process of creating sequencing templates is complete in about four hours per flow cell. Pre-configured sequencing reagents are dropped in the instrument reagent racks prior to the start of the run.

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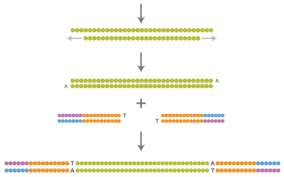
Figure 2: Next-Generation Sequencing Simplified



Library Preparation
~2 h [15 min hands-on (Nextera)]
< 6 h [< 3 h hands-on (TruSeq)]

Cluster Generation
~5 h (<10 min hands-on)

Sequencing by Synthesis
~1.5 to 8.5 days

CASAVA
2 days (30 min hands-on)

The industry's simplest sequencing workflow, from standardized library preparation kits, to automated cluster generation, to streamlined sequencing and real-time data analysis.

BeadArray Technology

Microarrays are making greater contributions in a growing number of fields, especially human disease research and trait studies for many agriculturally important species. Illumina's BeadArray products provide powerful array-based solutions for genotyping, gene expression profiling, and methylation analyses. The proven GoldenGate® and Infinium® Genotyping assays offer the industry's best data quality and have catalyzed many revolutionary discoveries in disease research. The DASL® and DirectHyb Assays enable highly accurate genome-wide expression profiling from a range of sample types. HiScanSQ provides high-precision array scanning of the BeadChips associated with these assays. The instrument delivers high signal-to-noise ratios, low limits of detection, and a broad dynamic range to provide superior results for a diverse number of applications.

The HiScan Reader is capable of sub-micron resolution using high-performance lasers, optics, and detection systems (Table 3). The result is dramatically reduced scan times, even on the highest density BeadChips (Table 4), while maintaining exceptionally high data quality and reproducibility.

Diverse Applications

HiScanSQ enables numerous array- and sequencing-based applications (Table 5). The high-performance reader supports a number of proven array-based genotyping, gene expression profiling, and methylation assays. The combination of both short and long-insert paired-end sequencing, coupled with 2 × 100 bp read lengths and powerful TruSeq chemistry greatly expands the range of sequencing experiments. Low input requirements for both technologies enable a number of applications where sample is limited. The HiScanSQ also offers researchers the ability to pause a sequencing run to scan arrays, supporting more efficient lab management and experimental flexibility. With integrated sequencing and array technology, HiScanSQ opens up a world of new possibilities.

Figure 3: HiScanSQ Innovative Design Features

The touch screen user interface facilitates step-by-step setup and provides real-time reporting

The combo drawer contains dual compartments for easy array and flow cell loading

Pre-configured, plug-and-play reagents are ready for up to 200 sequencing cycles

Internal paired-end fluidics allows for seamless second-read sequencing

Innovative engineering and human interaction design features provide a simplified user experience and minimize hands-on time.

Convenient Modular Design

HiScanSQ's unique design allows researchers to modularly build out the system so that it can be customized to meet evolving research needs. Labs that begin with sequencing can add arrays at any time by purchasing a convenient product option kit that includes all the small lab equipment needed to process Illumina BeadArray assays. For labs that start with array-based experiments using the standalone HiScan Reader, the SQ Module, and cBot cluster generation system can be easily added to enable next-generation sequencing. The compact SQ Module provides all the components necessary to perform Illumina's SBS chemistry, including an integrated paired-end fluidics system for seamless second-read sequencing. With such convenient modular design, HiScanSQ provides the flexibility to take on any course of research, easily adapting to keep pace with changing demands.

Labs that want to optimize sample throughput for array-based studies can add the AutoLoader2.x and liquid handling robots to automate sample loading and preparation, maximizing the number of samples that can be processed in a given time frame. The Illumina Laboratory Information Management System (LIMS) lets researchers efficiently manage sample tracking for array projects, minimizing sample handling errors and streamlining large projects.

Streamlined Data Analysis

The analysis software and hardware included with HiScanSQ contributes to an end-to-end approach that enables researchers to rapidly move from raw data acquisition to publishable, biologically meaningful results. Illumina's GenomeStudio® data analysis software provides simplified, graphical analysis and interaction with DNA and RNA data. This comprehensive software package includes analytical tools for both sequencing and array-based experiments in an intuitive user environment. Illumina also partners with a number of third-party vendors who offer powerful tools that streamline and expand data analysis.

Table 1: HiScanSQ Sequencing Performance Parameters

Read Length	Run Time	Output
1 × 35 bp	~1.5 days	23–26 Gb
2 × 50 bp	~4.5 days	67–75 Gb
2 × 100 bp	~8.5 days	135–150 Gb
Reads	Up to 750 million clusters passing filter, and up to 1.5 billion paired-end reads	
Throughput	Up to 17.5 Gb per day for a 2 × 100 bp run	
Performance	Greater than 85% bases higher than Q30 at 2 × 50 bp* Greater than 80% bases higher than Q30 at 2 × 100 bp*	

*Install specifications for HiScanSQ sequencers with an Illumina PhiX library and cluster densities between 610 – 678K/mm^2 that pass filtering on a HiScanSQ system using TruSeq v3 Cluster and SBS kits for HiSeq. Performance may vary based on sample quality, cluster density, and other experimental factors. Paired 100 bp runs may vary in the range of 80 to 90% of bases above Q30 and paired 50 bp runs typically vary in the range of 85 to 95% bases above Q30 based on the above factors.

Table 2: HiScanSQ Sequencing Application Examples

	Exome Sequencing	Targeted Resequencing	mRNA-Seq (Discovery)	mRNA-Seq (Profiling)	ChIP-Seq	Small Genome Sequencing
Example	62 Mb Exome 75× coverage	5 Mb region > 75× coverage†	60 M* reads per sample	Avg. 7 M reads per sample	Avg. 90 M reads per sample	4 Mb bacterium > 50× coverage
Read Length	2 × 100 bp	2 × 75 bp	2 × 75 bp	1 × 50 bp	1 × 35 bp	2 × 50 bp
Samples per Run	24	96	48	96	8	96
Run Time	~8.5 days	~6.5 days	~6.5 days	~2.5 days	~1.5 days	~4.5 days

***** Double the reads for paired-end runs

† Using the Illumina TruSeq Exome Enrichment Kit

Table 3: HiScan Reader Performance Parameters

	Performance Specification
Lasers	A two-laser system with wavelengths at 532 and 660 nm
Optical System	Time Delayed Integration (TDI) line scanning and two CCD sensors for high-resolution performance and fast data rate
Scanner Resolution	0.375 micron spatial resolution with dual-channel collection

Table 4: HiScan Reader Array Scan Times

BeadChip	Scan Time (per sample)	Manual Loading (samples/week)*	Automated Loading (samples/week)†
HumanOmni2.5-8	6.5 minutes	364	1,088
HumanOmniExpress	3.7 minutes	576	1,728
HumanOmni Express‡	6 minutes	384	1,152
HumanCytoSNP-12	1.8 minutes	576	1,728
iSelect® HD	1 minutes	1,152	3,456
Universal-32§	0.3 minutes	1,440	1,440

*Assuming 8-hour day, 5-day week, single HiScan

†Assuming 24-hour automated scanning, single HiScan, Autoloader 2.x, and liquid handling automation

‡Scan times based on content selection

§ For GoldenGate Indexing™ assay

Table 5: Diverse Array and Sequencing Applications

Research Areas	BeadArray Applications	Sequencing Applications
Whole-Genome Analysis	Whole-Genome Genotyping, FFPE Sample Analysis	Whole-Genome Discovery
Copy Number Variation (CNV)	CNV Analysis	CNV Discovery
Targeted Genome Analysis	Custom and Focused Genotyping	Exome Sequencing, Targeted Resequencing
Gene Regulation and Epigenetic Analysis	Whole-Genome DNA Methylation Profiling	ChIP-Seq, Small RNA Analysis, Methylation Discovery and Analysis
Gene Expression	Whole-Genome Expression Profiling, FFPE Sample Analysis	Transcriptome Discovery, Profiling
Cytogenetics	Cytogenetic Analysis	Digital Karyotyping

Site Requirements

Operating Environment	
Temperature	22°C ± 3°C
Humidity	Non-condensing 20%–80%
Altitude	Less than 2,000 m (6,500 ft)
Air Quality	Pollution degree rating of II
Ventilation	Maximum of 4,000 BTU/h
System Power Requirements with Monitor and PC	
Power	100–240V AC 50/60Hz, 20A, 1500W
HiScan Reader Physical Specifications	
Width	28.3 in (71.9 cm)
Height	29.3 in (74.5 cm)
Depth	27.5 in (69.8 cm)
Weight	300 lbs (136 kg)
SQ Module Physical Specifications	
Width	23.1 in (58.7 cm)
Height	28.6 in (73.9 cm)
Depth	23.2 in (58.9 cm)
Weight	194 lbs (88 kg)

For primary sequencing data analysis, Illumina's HiSeq Control Software (HCS) offers real-time analysis processing that automatically produces image intensities and quality-scored base calls directly on the instrument computer for alignment to a reference sequence and subsequent analysis. For secondary analysis, Consensus Assessment of Sequence and Variation (CASAVA) software allows for rapid alignment, counting, and variant discovery. Secondary data analysis software can be installed on an existing IT infrastructure. A Pipeline analysis server is available for customers requiring a ready-to-use solution. IlluminaCompute provides a turn-key computing infrastructure to rapidly scale the rate of sequence analysis.

Summary

HiScanSQ is the first instrument to offer integrated next-generation sequencing and microarray analysis. The combination of these complementary technologies enables an unmatched range of applications and superior flexibility for experimental design. A convenient modular design allows researchers to build the system to evolve with their research needs. With HiScanSQ, unlocking answers from the genome, epigenome, and transcriptome is only an array or flow cell away.

HiScanSQ Kits and Accessories

Product	Catalog No.
HiScanSQ System	SY-201-2001
HiScan Reader	SY-103-1001
SQ Module	SY-101-2001
cBot Clonal Amplification System	SY-301-2002
AutoLoader2.x Single (Dual)	SY-202-1001 (1002)
AutoLoader2.x Dual	SY-202-1002
Pipeline Analysis Server	SE-301-1003
GoldenGate Product Option Kit, 110V (220V)	SE-101-1001 (1002)
Gene Expression (IVT) Product Option Kit, 110V (220V)	SE-101-1003 (1004)
Universal Starter Kit, 110V (220V)	SE-101-1005 (1006)
Infinium Genotyping LIMS Server System, 110V (220V)	WG-15-103 (104)
GoldenGate Genotyping LIMS Standalone Server, 110V (220V)	SC-35-101 (102)
GoldenGate Genotyping LIMS Upgrade, 110V (220V)	SC-35-103 (104)
GoldenGate Genotyping and Infinium Automation, Post-Amplification LIMS-ready, 110V (220V)	SC-30-403 (404)
GoldenGate Genotyping and Infinium Automation, Post-Amplification, 110V (220V)	SC-30-401 (402)

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