

iScanSQ

The first integrated next-generation sequencing and array-based system, enabling the broadest set of genomic, epigenomic, and transcriptomic analysis applications.

NEXT-GENERATION SEQUENCING: A RESEARCH TOOL FOR ANY LAB

iScanSQ (Figure 1) is the first system to integrate the high-throughput capability of genotyping and gene expression arrays with the flexibility and resolution of sequencing. The SQ Module is an add-on device that enables sequencing by synthesis technology on the iScan System, Illumina's state-of-the-art imaging scanner. With the SQ Module, labs that have traditionally run microarray assays now have a convenient and economical gateway to the power of next-generation sequencing.

Illumina's next-generation sequencing technology has made genome-scale sequencing routine for labs of any size. Researchers have embraced the broad range of applications it enables, and are publishing at an unprecedented rate¹.

ISCANSQ HIGHLIGHTS

- **Integrated:** Efficiently combine array and sequencing technologies to enable an unmatched range of applications
- **Flexible:** Easily transition between array and sequencing assays for any experimental design
- **Cost-Effective:** Conveniently and economically add next-generation sequencing capabilities to your research
- **High-Quality:** Reliably generate the highest raw read accuracy and maximal output of perfect reads

Array and Sequencing Integration

Unlimited possibilities stem from the integration of microarray and sequencing experiments. The synergistic application of these complementary technologies provides a powerful approach to genetic discovery and validation.

- Leverage targeted resequencing as the ultimate follow-on to genome-wide association studies (GWAS).
- Transition between array-based and sequencing-based gene expression analysis.
- Validate array-based expression and splice variant data.
- Identify target SNPs from sequencing experiments to design iSelect® custom genotyping panels for any species and any study.

Diverse Sequencing Applications

The power of Illumina sequencing technology, combined with the flexibility for paired-end reads, multiplexing, and customizable read lengths, opens up a world of new applications (Table 1).

- Resequence small genomes or targeted genomic regions.
- Gain a deeper understanding of the transcriptome with mRNA-Seq.
- Discover and profile miRNA expression.
- Characterize genome-wide DNA-protein interaction sites with ChIP-Seq.

Any lab currently running an iScan System can now expand its capability to maximize the utility of their

FIGURE 1: ISCANSQ ENABLES AN UNMATCHED RANGE OF APPLICATIONS



iScanSQ combines the iScan System (left) with the SQ Module (right) to integrate array and sequencing technology in a single system.

investment, and have greater control over experiments and scheduling. Labs with only occasional needs for sequencing can avoid the expense of separate lab space and personnel.

FAST, SIMPLE, AUTOMATED

iScanSQ provides a streamlined workflow that allows researchers to generate meaningful data quickly and efficiently. Illumina Sequencing technology provides an easy-to-use protocol that does not require emulsion PCR. This allows for a self-contained system that minimizes handling errors and contamination concerns, eliminating the need for robotics or clean rooms.

PERFORMANCE

The iScan System is the industry's highest performance array scanner. Its superior lasers, optics, and detection systems provide sub-micron

TABLE 1: ISCAN SQ APPLICATION EXAMPLES

	SMALL GENOME SEQUENCING	TARGETED RESEQUENCING	mRNA-SEQ (DISCOVERY)	mRNA-SEQ (PROFILING)	CHIP-SEQ	SMALL RNA SEQUENCING
Example	5 Mb bacterium, 30× coverage	5 Mb region, 30× coverage	40M* reads per sample	Avg. 5M reads per sample	Avg. 15 million read per sample	2.5M reads per sample
Read Length	2 × 50 bp	2 × 50 bp	2 × 75 bp	1 × 75 bp	1 × 50 bp	1 × 35 bp
Samples per Run	96	8	4	24	8	48
Run Time	≤ 6.5 days	≤ 6.5 days	≤ 9.5 days	≤ 5.5 days	≤ 3.5 days	≤ 2.5 days

* Double the reads for paired-end runs

resolution and unmatched speed. The addition of the SQ Module to an iScan System provides the optimal performance and data quality expected by Illumina customers for both array-based and sequencing applications (Table 2).

DATA ANALYSIS

The analysis software and hardware included with iScan SQ contribute to an end-to-end sequencing approach that enables researchers to rapidly move from raw data acquisition to publishable, biologically meaningful results. Illumina's Sequencing Control Software (SCS) offers real-time analysis processing that automatically produces image intensities and quality-scored base calls directly on the instrument computer. These reads can be aligned to a reference sequence and analyzed using the Pipeline analysis software. In combination with the Consensus Assessment of Sequence and Variation (CASAVA) software, GenomeStudio® data analysis software provides intuitive, graphical analysis and interaction with DNA and RNA data.

TABLE 2: ISCAN SQ PERFORMANCE

ISCAN SQ FOR SEQUENCING

Data Generation	> 20 Gb of high-quality data per paired-end flow cell, with > 70% of bases above Q30
Sequencing Run Times	<ul style="list-style-type: none"> • 2.5 days for a 36-bp single-read sequencing run • 5 days for a 2 × 36-bp paired-read sequencing run • 6.5 days for a 2 × 50-bp paired-read sequencing run • 9.5 days for a 2 × 75-bp paired-read sequencing run
Daily Throughput	Minimum of 2.1 Gb of high-quality filtered bases per day
Samples per Flow Cell	1–12 samples per flow cell-lane (8–96 samples per flow cell)
Read Accuracy	<ul style="list-style-type: none"> • Raw Read Accuracy of > 98.5% • Consensus Read Accuracy of > 99.9% at ≤ 3× coverage
Cluster Density	• 133–200 million clusters per flow cell
Applications	• Small genome sequencing, targeted resequencing, mRNA and small RNA sequencing, and CHIP sequencing

ISCAN SQ FOR BEADARRAY

Substrate Compatibility	Infinium® HD, iSelect HD BeadChips, GoldenGate® Universal BeadChips
Applications	GWAS, copy number variation analysis (CNV), focused genotyping, custom genotyping, gene expression profiling, and methylation profiling

SQ MODULE

To perform sequencing using the iScan System, a SQ Module, cBot Cluster Generation System, and data analysis tools are required (Table 3). The SQ Module enables single-read and paired-end sequencing by synthesis technology. cBot generates clonal clusters of template molecules that will be sequenced on the surface of an eight-channel flow cell. Sequencing chemistry and image acquisition occur while the flow cell is in the iScan Reader. The *Illumina Sequencing Technology Spotlight*² provides more information about the sequencing chemistry and workflow.

Comprehensive installation and training is included with every iScanSQ purchase. Following installation by a Field Service Engineer, extensive on-site training is performed by an Illumina Field Applications Scientist. Ongoing technical support is provided by Illumina Technical Support Scientists.

Both the iScan System and SQ Module are benchtop instruments designed to fit easily in typical laboratories (Table 4).

TABLE 3: HARDWARE REQUIREMENTS FOR PAIRED-END OR SINGLE-READ SEQUENCING

COMPONENTS

- iScan System
- SQ Module*
- cBot Cluster Generation System
- Data Processing Tools

*The SQ Module will be available in early 2010.

TABLE 4: PHYSICAL SPECIFICATIONS

SQ MODULE

Width	61 cm (24 in)
Height	76 cm (30 in)
Depth	71 cm (28 in)
Weight	50 kg (110 lb)

SUMMARY

iScanSQ enables seamless integration of sequencing-based experiments with array-based assays. As the only such integrated system, it makes an expanded range of genetic analysis applications available to any lab.

ORDERING INFORMATION

PRODUCT	DESCRIPTION	CATALOG NO.
SQ Module*	The SQ Module enables sequencing applications to be performed on the iScan System. The module includes fluidics system required for next-generation sequencing using sequencing-by-synthesis technology.	SY-101-2001
iScan System	The iScan System includes an iScan Reader, computer workstation, air isolation table, data acquisition and analysis software, installation, training, and a one-year warranty.	SY-101-1001
cBot	cBot is a stand-alone, software controlled system for the automated generation of clonal clusters from single DNA molecules on flow cells.	SY-301-2002

*The SQ Module will be available in early 2010.

REFERENCES

- (1) <http://www.illumina.com/publications/overview.ilmn>
- (2) http://www.illumina.com/Documents/products/techspotlights/techspotlight_sequencing.pdf

ADDITIONAL INFORMATION

Visit our website or contact us at the address below for more information about Illumina genetic analysis systems and sequencing applications.

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