

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/mm² 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 75x coverage | 5 Mb region > 75x coverage [†] | 60 M* reads per sample | Avg. 7 M reads per sample | Avg. 90 M reads per sample | 4 Mb bacterium > 50x 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

