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HiSeqTM 2000 Sequencing System

Performance specifications

Instrument Configuration

CE marked and ETL listed instrument (HiSeq 2000 only)

Computer and touch screen display

Installation setup and accessories

Data collection and analysis software

Instrument Control Computer

Base Unit: 2x Intel Xeon X5560 2.8 GHz CPU

Memory: 48 GB RAM

Hard Drive: 4x 1.0 TB 7200 RPM SATA

Operating System: Windows Vista *Note: Computer specifications will be regularly upgraded. Contact your local account manager for current configuration.

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

For Indoor Use Only

Laser

532 nm, 660 nm, 700–840 nm, 650 nm (barcode reader)

Dimensions

W×D×H: 118.6 cm × 76.0 cm × 94.0 cm

(46.7 in × 30.0 in × 37.0 in)

Weight: 221.4 kg (488 lbs)

Crated Weight: 312 kg (688 lbs)

Power Requirements

100–240V AC 50/60Hz, 20A, 1500W

A region-specific uninterruptible power supply comes with the HiSeq 2000 instrument.

HiSeq 2000 Performance Parameters

HiSeq 2000 Performance Parameters*

Read Length	Run Time	Output
1 × 35 bp	~1.5 days	26–35 Gb
2 × 50 bp	~4 days	75–100 Gb
2 × 100 bp	~8 days	150–200 Gb

*Sequencing output generated with a PhiX library and cluster densities between 260,000–347,000 clusters/mm2 that pass filtering on a HiSeq 2000.

Throughput

Up to 25 Gb per day for a 2 × 100 bp run.

Reads

Up to one billion clusters passing filter, and up to two billion paired end reads.

Performance

HiSeq 2000 provides the greatest yield of perfect reads and bases greater than Q30:

- Greater than 90% bases higher than Q30 at 2 × 50 bp**
- Greater than 85% bases higher than Q30 at 2 × 100 bp**

**Human genome at supported cluster densities

HiSeq 2000 Kits and Accessories

HiSeq 2000 System Specifications With Monitor and PC: Catalog No. SY-401-1001

Application	Catalog No.
HiSeq 2000 Sequencing System	SY-401-1001
cBot Clonal Amplification System	SY-301-2002
Paired-End DNA Sample Prep Kit	PE-102-1001
Genomic DNA Sample Prep Kit	FC-102-1001
HiSeq Paired-End Cluster Generation Kit	PE-401-1001
HiSeq Single-Read Cluster Generation Kit	GD-401-1001
HiSeq Sequencing Kit (200 cycles)	FC-401-1001
HiSeq Sequencing Kit (50 cycles)	FC-401-1002

Innovative design features make HiSeq 2000 the easiest-to-use next- generation sequencing system. Flow cells are loaded on the vacuum-controlled loading dock. Pre-configured, plug-and-play reagents sufficient for up to 200 cycles drop into racks in the machine's chiller compartment, requiring only two minutes of hands-on time. A simple touch screen user interface, including on-screen, step-by-step instructions with embedded multimedia help, simplifies run setup. Real-time progress indicators provide at-a-glance status, and remote monitoring allows a single user to check progress on multiple systems from any browser or internet-enabled phone.

HiSeq 2000 can be operated in single or dual flow cell mode, offering unmatched experimental flexibility and instrument scalability. Independently-operable flow cells allow applications requiring different read lengths to run simultaneously. Leveraging Illumina's proven and widely-adopted, reversible terminator-based sequencing by synthesis chemistry in combination with innovative engineering, HiSeq 2000 delivers the industry's highest sequencing output and fastest data generation rate. Human interaction design features and the easiest sequencing workflow set a new standard for simplicity and user experience. With unmatched cost-effectiveness, HiSeq 2000 is the first commercially available sequencer to enable researchers to obtain ~30× coverage of two human genomes in a single run for under $10,000 (USD)* per sample.

Unprecedented Output

HiSeq 2000 makes it possible for individual labs to take on the largest and most complex sequencing studies at the lowest cost. With cutting-edge scanning and imaging technology, clusters on both surfaces of the flow cell can be sequenced.

HiSeq 2000 Highlights

- High Accuracy and Unprecedented Output: Generate up to 200 Gb per run with the highest yield of data greater than Q30, 2 × 100 bp read length, up to 25 Gb per day, two billion paired-end reads per run.

- Breakthrough User Experience: Easily set up runs with simplified library prep, automated clonal amplification, pre-configured, plug-and-play reagents, simple flow cell loading, touch screen-enabled user interface, and integrated paired-end fluidics.
- Unmatched Cost-Effectiveness: Unrivalled output and ease of use provide the lowest overall operating cost. Sequence two human genomes at greater than 30× coverage in 8 days. Process 200 gene expression samples in a single run at a per sample price less than microarrays.

Illumina's HiSeq 2000 sequencing system enables individual labs to take on larger and more complex studies, including routine human genome sequencing.

Flow cells are easy to load on the vacuum- controlled loading dock with feedback LED switch.

Touch screen user interface facilitates step-by-step run setup. Simply enter read length, single- or paired-end read, and indexing information on-screen.

Internal paired-end fluidics eliminate need for a separate second- read module.

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

Optical modules with dual-surface flow cell imaging and time-delay integration scanning allow highest output and fastest data rate.

TruSeq Chemistry

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

SBS technology 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.

Powered by TruSeq chemistry, Illumina sequencing delivers the most accurate human genome at any level of coverage. The highest yield of error free reads and most base calls above Q30 provide researchers the highest confidence in their data integrity to draw sound biological conclusions.

Easiest Sequencing Workflow

The 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. With HiSeq 2000, library preparation is performed using simplified 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. For sequencing, either one or two flow cells can be loaded on HiSeq 2000, enabling different experimental conditions to be run simultaneously. Pre-configured sequencing reagents are dropped in the instrument reagent racks prior to the start of the run.

Streamlined Data Analysis Solution

Accompanying the unprecedented sequencing output of HiSeq 2000 is a data analysis solution for transforming billions of bases of raw sequencing data into publishable, biologically meaningful results. HiSeq Control Software offers real-time analysis processing that automatically produces image intensities and quality-scored base calls on the instrument computer for alignment to a reference sequence and subsequent analysis. In combination with the Consensus Assessment of Sequence and Variation (CASAVA) software, GenomeStudio® data analysis software provides intuitive, graphical analysis. The optional IlluminaCompute system is available as a comprehensive and scalable computing architecture for genomic data processing and analysis. IlluminaCompute is an individually configured, pre-packaged data analysis solution consisting of scalable processing, scale-out storage, and comprehensive support for installation, training, and maintenance.

Accelerate your research with HiSeq 2000

HiSeq 2000 redefines the trajectory of sequencing by combining innovative engineering with proven sequencing by synthesis chemistry to set new standards for output, simplicity, and cost-effectiveness. With HiSeq 2000, the ability to process larger numbers of samples and to decode larger and more complex genomes means that virtually any sequencing project is now within reach.