illumina®

HiSeq™ Sequencing Systems

Redefining the trajectory of sequencing.

HiSeq System Highlights

- **High Accuracy and Unprecedented Output:** Generate up to 600 Gb per run with the highest yield of data greater than Q30.
- **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 with the industry's simplest sequencing workflow provide the lowest overall operating cost.
- **Flexibility:** HiSeq 1000 offers broader access to HiSeq technology, providing an easy upgrade path to the HiSeq 2000 as sequencing needs change.

Sequence at a Scale Never Before Possible

HiSeq Sequencing Systems combine Illumina's proven and widely-adopted, reversible terminator-based sequencing by synthesis (SBS) chemistry with innovative engineering. Comprised of the HiSeq 2000 (Figure 1) and HiSeq 1000 systems, this high-performance sequencing family combines human interaction design features and the easiest sequencing workflow, setting a new standard for simplicity and user experience.

The HiSeq 2000 sequencing system delivers the industry's highest sequencing output and fastest data generation rate. With the industry's simplest sequencing workflow and unmatched cost effectiveness, HiSeq 2000 has lowered the cost of whole-human genome sequencing to unrivaled levels.

Offering the same outstanding user experience and cost per data output (Gb), the HiSeq 1000 enables researchers to access HiSeq performance, with a built-in upgrade path should sequencing throughput needs change.

Unprecedented Output

HiSeq Systems make it possible for individual labs to take on the largest and most complex sequencing studies at a lower cost. With cutting-edge scanning and imaging technology, clusters on both surfaces of the flow cell can be sequenced, dramatically increasing the number of reads, sequence output, and data generation rate. The ultra-high output and speed of the two flow cell HiSeq 2000 makes it possible to sequence > 5 human genomes at ~30× coverage simultaneously, up to 192 gene expression samples or 100 exome samples in a single run. The HiSeq 1000 System is an exceptionally powerful tool for researchers who do not require the throughput of a HiSeq 2000. It enables researchers to sequence > 2 human genomes at ~30× coverage or 96 gene expression samples in one run.

Breakthrough User Experience

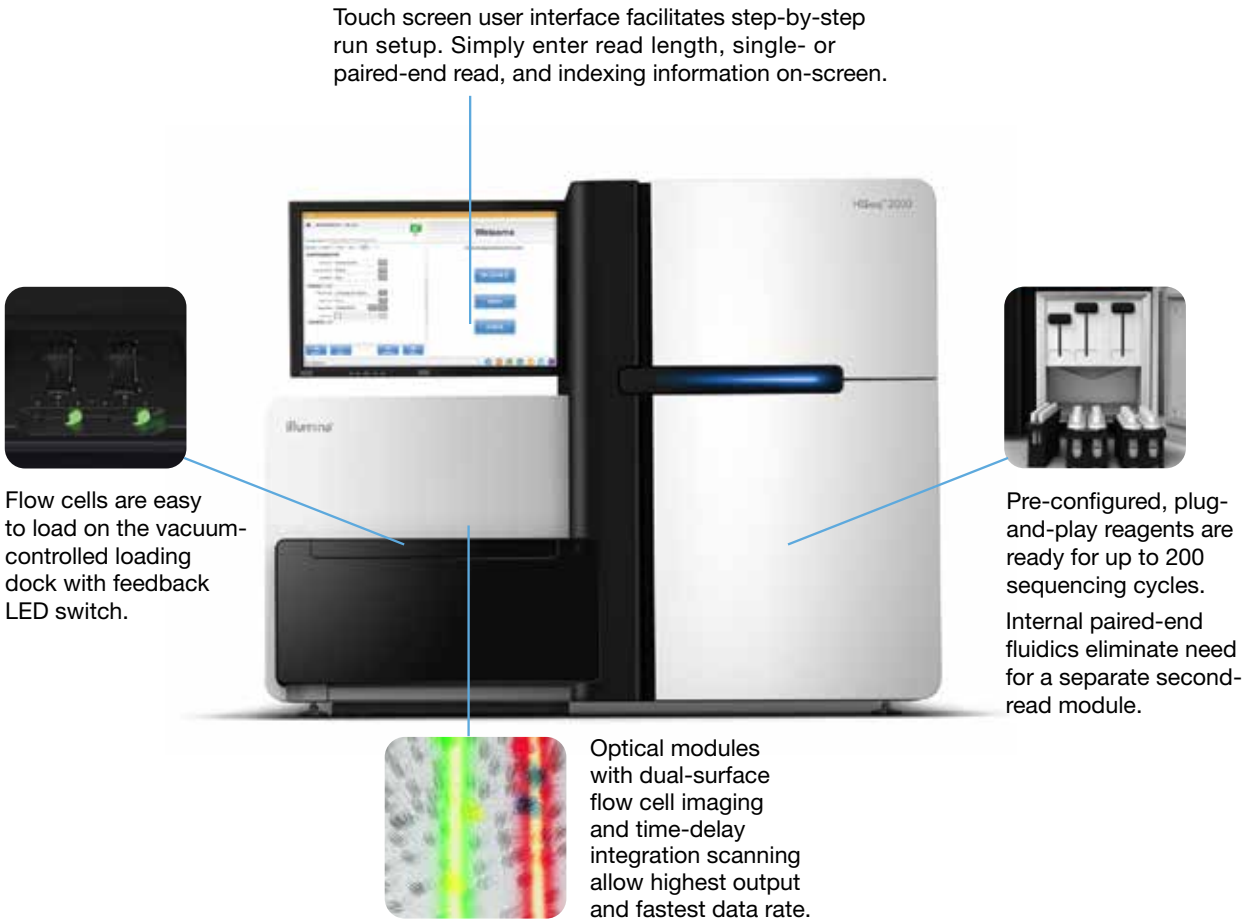
Innovative design features make HiSeq Systems the easiest-to-use next-generation sequencing systems (Figure 2). Flow cells are loaded on the vacuum-controlled loading dock. Pre-configured, plug-and-play reagents sufficient for up to 200 cycles plus indexing, drop into racks in the machine's chiller compartment, 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. Its independently-operable flow cells allow applications requiring different read lengths to run simultaneously. The single flow cell HiSeq 1000 delivers the same user experience and output per flow cell, and can be easily upgraded to the dual flow cell HiSeq 2000 to meet growing research needs.

Figure 1: HiSeq 2000 System

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

Figure 2: HiSeq 2000 Innovative Design Features



HiSeq Systems redefine the trajectory of sequencing. Innovative engineering and human interaction design features provide a breakthrough user experience and unmatched cost-effectiveness.

Figure 3: Next-Generation Sequencing Simplified

Library Preparation	Cluster Generation	Sequencing by Synthesis	CASAVA
~2 h [15 min hands-on (Nextera)] < 6 h [< 3 h hands-on (TruSeq)]	~5 h (<10 min hands-on)	~1.5 to 11 days	2 days (30 min hands-on)

From simplified library preparation kits and automated cluster generation, to streamlined sequencing by synthesis and complete data analysis, Illumina HiSeq sequencing systems offer the industry's simplest next-generation sequencing workflow.

TruSeq™ Chemistry

The TruSeq family of reagents represents the latest advancement of Illumina's SBS technology. Permeating the entire chemistry workflow, from library 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.

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 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 library prep kits or Nextera's Illumina sequencer-compatible DNA Library 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 and HiSeq 1000 is Illumina's 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.

Installation and Support

Comprehensive installation and training is included with every HiSeq System purchase, along with on-going technical support, maintenance and service. Illumina's industry-leading support is available in North America, Europe, and Asia.

Easy Upgrade Path

HiSeq 1000 provides another entry point into the world of HiSeq high-performance sequencing, providing the scalability needed to accomodate expanding sequencing needs. HiSeq 1000 instrument upgrades are performed on-site, quickly transforming the system to a HiSeq 2000 to deliver the industry's highest sequencing output and fastest data generation rate.

HiSeq System Information

HiSeq System Performance Parameters

Parameters	Single Flow Cell (HiSeq 2000 or 1000)*		Dual Flow Cell (HiSeq 2000 only)	
Read Length	Run Time	Output	Run Time	Output
1 × 35 bp	~1.5 days	47–52 Gb	~2 days	95–105 Gb
2 × 50 bp	~4.5 days	135–150 Gb	~5.5 days	270–300 Gb
2 × 100 bp	~8.5 days	270–300 Gb	~11 days	540–600 Gb
Reads	Up to 1.5 billion clusters passing filter, and up to 3 billion paired-end reads		Up to 3 billion clusters passing filter, and up to 6 billion paired-end reads.	
Throughput	Up to 35 Gb per day for a 2 × 100 bp run		Up to 55 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†			

*HiSeq 2000 can be run as a single flow cell or dual flow cell system.

†Install specifications for HiSeq sequencers with an Illumina PhiX library and cluster densities between 610 – 678 K/mm² that pass filtering on a HiSeq 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.

HiSeq System Specifications with Monitor and PC

Instrument Configuration
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, 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
Illumina provides a region-specific uninterruptible power supply for all HiSeq instruments.

Product Safety
CE marked and ETL listed instrument

HiSeq Systems and Accessories

	Catalog No.
HiSeq 2000 Sequencing System	SY-401-1001
HiSeq 1000 Sequencing System	SY-405-1001
HiSeq 1000 to HiSeq 2000 Upgrade	SY-405-1002
cBot Clonal Amplification System	SY-301-2002

Accelerate Your Research with HiSeq Systems

HiSeq Systems redefine the trajectory of sequencing by combining innovative engineering with proven SBS chemistry to set new standards for output, simplicity, and cost-effectiveness. With the HiSeq 2000 and HiSeq 1000, 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.

Learn More

For more information about HiSeq 2000, HiSeq 1000, and Illumina sequencing, visit www.illumina.com/systems.

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