

HiSeq[®] 1500/2500 Sequencing Systems

The world's most powerful sequencer, now faster and more flexible than ever.

HiSeq System Highlights

- Unprecedented Flexibility**
 Choose between rapid-run and high-output modes, offering scalable output from ~10 to 600 Gb for a broad range of applications and sample sizes
- Incredible Speed and Throughput**
 Complete projects in record time with the highest daily throughput of any sequencing system
- Exceptional Data Quality**
 Build confidence in your results with the most widely adopted and proven Illumina SBS chemistry
- Complete End-to-End Sequencing Solutions**
 Use streamlined sample prep, automated paired-end sequencing, and the BaseSpace[®] App Store for a flexible and fully integrated sequencing solution

Incredible Speed and Throughput

Rapid-run mode is a revolutionary addition to the design of the HiSeq System that leverages reduced cycle times and onboard cluster generation to significantly accelerate run times. In rapid-run mode you can complete fully automated clustering and sequencing for short read applications in a single business day or whole-genome sequencing applications in just over a day with paired-end 100 bp reads. With data throughput greater than 100 Gb, a human genome can be sequenced at greater than 30x coverage in about a day (Figure 2). Rapid turnaround time coupled with superior data quality is critical where quick and accurate answers are needed. The accelerated run times of rapid-run mode and the ability to process approximately 600 million sequencing templates in parallel deliver the highest daily throughput of any sequencing system currently available.

Exceptional Data Quality

High data quality is ensured by leveraging the industry's most widely adopted sequencing by synthesis (SBS) chemistry. SBS technology on the HiSeq 1500/2500 Systems utilizes a proprietary reversible terminator-based method that detects single bases as they are incorporated into growing DNA strands. Since all four reversible, terminator-bound dNTPs are present during each sequencing cycle, natural competition minimizes incorporation bias and greatly reduces raw error rates compared to other technologies. The end result is highly accurate base-by-base sequencing that virtually eliminates

Introduction

The HiSeq 1500/2500 Systems are the latest additions to the world's most highly adopted next-generation sequencing platform. HiSeq 1500/2500 Systems build on the same core architecture as the revolutionary HiSeq 2000 System with integrated advances such as onboard cluster generation and a rapid-run mode that enable the fastest walk-away workflows (Figure 1).

Unprecedented Flexibility

The HiSeq 2500 System is the first Illumina sequencing system to feature two run modes—rapid-run and high-output run mode—for one or two flow cells simultaneously, enabling a flexible and scalable platform. Rapid-run mode provides quick results, efficient processing of a limited number of samples, and longer paired-end 150 base pair reads, which allow greater depth of coverage and improved assembly for *de novo* applications. High-output mode is perfect for larger studies with more samples or when the greatest depth of coverage is required. High-output mode allows batch processing of ~5x more samples than rapid-mode and enables completion of large projects with the fewest runs possible.

Multiple HiSeq 2500 configurations allow tunable output from ~10 Gb or ~300 million single-end reads in seven hours to 600 Gb or six billion paired-end reads in 11 days depending on application needs or project deadlines. Efficient sample batching has never been easier, and turnaround times have never been faster. HiSeq 1500 shares these dual run modes, with support for a single flow cell rather than two flow cells. The HiSeq 1500/2500 Systems empower your lab with unprecedented flexibility to support the broadest range of applications and study sizes.

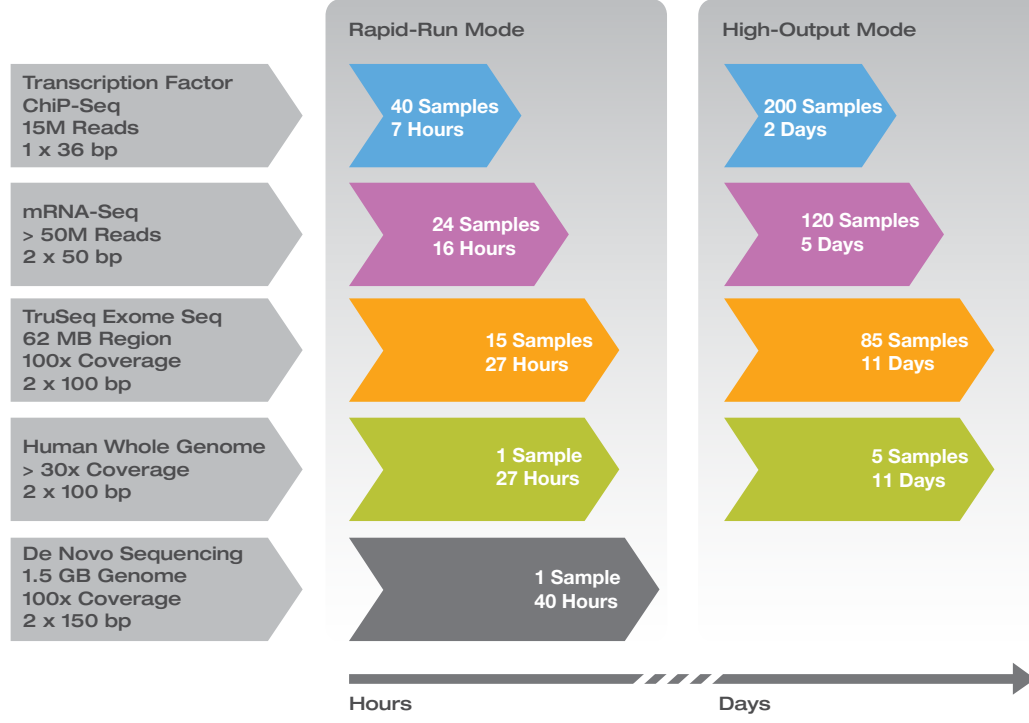
Figure 1: The HiSeq 2500 System



The HiSeq 2500 System is the only high-throughput sequencing system that combines scalability from ~10–600 Gb of total output with flexible run modes to support multiple applications and superior turnaround times.

HiSeq 1500/2500 System Information

Figure 2: Unprecedented Flexibility for Multiple Applications



With two run modes and the ability to process one or two flow cells simultaneously, the HiSeq 2500 supports a broad range of applications and study sizes. Values in this figure are examples based on system performance capabilities using two flow cells. Variation can be expected due to cluster density, sample quality, and other experimental factors. Run times are approximate and include onboard cluster generation and sequencing for rapid-run mode and sequencing only for high-output mode. Indexing run times are not included.

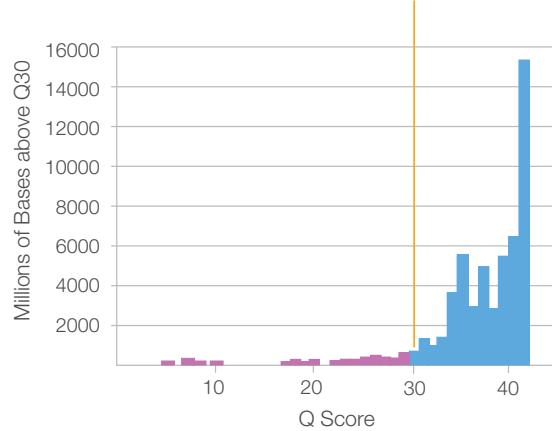
sequence-context-specific errors, even within repetitive sequence regions and homopolymers. Illumina sequencing delivers the most accurate human genome at any level of coverage, the highest yield of error-free reads, and the highest percentage of base calls above Q30 in the industry (Figure 3).

Superior Data Analysis and Storage Solutions

New developments in Illumina bioinformatics include improved data compression, faster sequence alignment algorithms, and a set of plug-and-play data computing and storage solutions.

HiSeq 1500/2500 software reduces data volume by more than 50% without compromising data quality. This allows output rates to double without needing to double data storage capacity. HiSeq 1500/2500 software also enables a live connection to BaseSpace®, a cloud-based environment for sequence alignment, data analysis, and expandable data storage. Uploading data to BaseSpace occurs in real-time and is generally finished within minutes of run completion. No additional charges are incurred for data upload, data alignment, or variant calling in BaseSpace. Researchers can collaborate through the BaseSpace cloud by sharing results instantly and securely with anyone around the world.

Figure 3: Reads vs. Q Score in Rapid-Run Mode



Quality scores for a human genome 2 x 101 base pair run on a HiSeq 2500 System in rapid-run mode. This example shows 92% of bases sequenced above Q30.

HiSeq System Performance Parameters

Read Length	High-Output Run Mode*			Rapid-Run Mode*		
	Dual Flow Cell (HiSeq 2500 only)	Single Flow Cell (HiSeq 1500 or 2500)	Dual Flow Cell Run Time	Dual Flow Cell (HiSeq 2500 only)	Single Flow Cell (HiSeq 1500 or 2500)	Dual Flow Cell Run Time
1 x 36	95–105 Gb	47–52 Gb	2 days	18–22 Gb	9–11 Gb	7 hours
2 x 50	270–300 Gb	135–150 Gb	5.5 days	50–60 Gb	25–30 Gb	16 hours
2 x 100	540–600 Gb	270–300 Gb	11 days	100–120 Gb	50–60 Gb	27 hours
2 x 150	N/A	N/A	N/A	150–180 Gb	75–90 Gb	40 hours
Reads Passing Filter	Up to 3 billion single reads or 6 billion paired-end reads	Up to 1.5 billion single reads or 3 billion paired-end reads		Up to 600 million single reads or 1.2 billion paired-end reads	Up to 300 million single reads or 600 million paired-end reads	
Quality	≥ 85% of bases above Q30 at 2 x 50 bp ≥ 80% of bases above Q30 at 2 x 100 bp			≥ 85% of bases above Q30 at 2 x 50 bp ≥ 80% of bases above Q30 at 2 x 100 bp ≥ 75% of bases above Q30 at 2 x 150 bp		

* Install specifications based on Illumina PhiX control library at supported cluster densities (between 610–678 K clusters/mm² passing filter using TruSeq v3 or 700–820 clusters/mm² passing filter using TruSeq Rapid kits. Run times for rapid-run mode correspond to onboard cluster generation (1.5 hours) and sequencing; for high-output mode, run times correspond to sequencing only. Performance may vary based on sample quality, cluster density, and other experimental factors. HiSeq 2000 instruments prior to serial number 700895 will run slightly slower in rapid-run mode when upgraded.

BaseSpace also offers Illumina Sequence Analysis and Comparison software (iSAAC™)—the fastest aligner available today. With a 4–6x increase in speed, iSAAC software can align a 30x genome to a reference in just a few hours. The alignment can be performed in BaseSpace at no cost or using affordable, commodity computing hardware. iSAAC software is simple and easy to use for biologists, yet flexible enough for bioinformaticians to access and modify the open source code. Additional tools and software will be offered through the BaseSpace App Store, which will offer a combination of commercially available, free-ware, and user-developed applications.

Researchers can also use IlluminaCompute™, a set of plug-and-play computing and storage solutions for sequencing data. IlluminaCompute features industry-leading technology from our partners Dell and EMC Isilon, installation and maintenance from Illumina Customer Solutions, and a preconfigured software suite for data processing, alignment, and variant detection. With IlluminaCompute, labs can become fully operational in weeks rather than months, even without pre-existing IT infrastructure.

Installation, Training, and Support

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

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 E5-2630 2.3 GHz CPU
 Memory: 64 GB RAM
 Hard Drive: 8 x 1.0 TB 3.5" Enterprise SATA (2 OS - RAID1 drives, 6 data RAID 5 drives)
 Operating System: Microsoft Windows 7

Note: Configurations apply to newly manufactured HiSeq 1500/2500. For HiSeq 1500/2500 upgrades, see HiSeq 1000/2000 data sheet for specifications. 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 2000 m (6500 ft)
 Air Quality: Pollution degree rating of II
 Ventilation: Maximum of 4000 BTU/h
 For Indoor Use Only

Laser

532 nm, 660 nm, 650 nm (barcode reader)

Dimensions

WxDxH: 118.6 cm x 76.0 cm x 94.0 cm (46.7 in x 30.0 in x 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

