HiSeq X™ Series of Sequencing Systems

Maximum throughput and lowest cost for population-scale whole-genome sequencing.

Highlights

- **$1000 Genome Is a Reality**
  HiSeq X Ten System is the first and only platform to break the $1000 barrier human whole-genome sequencing
- **Population- and Production-Scale Whole-Genome Sequencing**
  HiSeq X Ten System delivers > 18,000 human genomes per year; HiSeq X Five System delivers > 9000 human genomes per year
- **Proven Performance**
  Take advantage of industry-leading data quality with the highly accurate Illumina sequencing by synthesis technology
- **Species Expansion**
  Now enabling cost-effective whole-genome sequencing of nonhuman species with unrivaled throughput

Introduction

Through continuous innovation, Illumina has broken down barriers in human genome sequencing by increasing data throughput at an astounding rate, more than doubling each year, while dramatically reducing the price to sequence a human genome. Illumina technology enabled sequencing of the first genome at 30× coverage, the first cancer genome, and the first genome in a single day.[1-3] Now, Illumina technology is helping researchers reach another milestone—the $1000 human genome. The HiSeq X Ten System, a set of 10 HiSeq X instruments, is the first and only platform to deliver a $1000 human genome, generating tens of thousands of high-quality, high-coverage genome sequences (Figure 1). With its ultrahigh throughput and unprecedented low price per genome, the HiSeq X Ten System makes population-scale whole-genome sequencing (WGS) a reality (Table 1).

For laboratories wanting to take advantage of the power of the HiSeq X Ten System for production-scale sequencing, Illumina offers the HiSeq X Five System. Requiring a lower level of initial capital investment, the HiSeq X Five System provides accurate, accessible WGS for thousands of samples per year at a slightly higher, yet still affordable, price per human genome (Table 1). Laboratories that start with the HiSeq X Five System and then increase their capacity to 10 or more instruments can realize the throughput of the HiSeq X Ten System and the $1000 human genome.

Table 1: HiSeq X System Sequencing Capacity

	HiSeq X Ten System	HiSeq X Five System
Minimum Number of Instruments	10	5
Annual Genome Capacity	> 18,000	> 9000
Price per 30× Genome	< $1000	< $1500

When operating at scale, HiSeq X Ten and HiSeq X Five Systems generate a staggering level of throughput, sequencing thousands of genomes per year.

Nonhuman Species Expansion

HiSeq X Systems can now apply population-scale sequencing to nonhuman species. The HiSeq X System delivers high coverage in various areas, including agriculture and model organism research in the pharmaceutical industry. By providing ultra-high–throughput and an unprecedented price point per genome, the HiSeq X System provides customers with an opportunity to reshape the economics and scale of whole-genome sequencing beyond the human species.

HiSeq X Ten System—Maximum Throughput, Lowest Cost Population-Scale WGS

The HiSeq X Ten System is the first sequencing platform to break the $1000 barrier for 30× coverage of a human genome. When used at scale, the HiSeq X Ten delivers a $1000 human genome, inclusive of instrument depreciation, sequencing consumables, DNA extraction, library preparation, and estimated labor for a typical high-throughput genomics laboratory.

Figure 1: The HiSeq X Ten System—The HiSeq X Ten System is a suite of 10 individual HiSeq X instruments.

For Research Use Only. Not for use in diagnostic procedures.

Purpose-Built for Population-Scale Genome Sequencing

Designed and optimized for population-scale WGS, the 10 instruments of a HiSeq X Ten System generate a staggering level of throughput for processing tens of thousands of samples. Now, researchers can analyze human and nonhuman genomes at an unprecedented scale and advance the study of cancer and complex diseases at a record pace.

HiSeq X Five System—Maximum Throughout, Production-Scale WGS

With a lower initial capital investment, but higher price per genome, the HiSeq X Five System provides access to HiSeq X patterned flow cell technology and production-scale WGS at a cost and scale appropriate for large genome centers. The HiSeq X Five System consists of 5 individual HiSeq X instruments that, when operating at scale, have the capacity to sequence > 9000 human genomes a year. This level of throughput allows researchers to complete large WGS projects rapidly, in their own labs.

Innovative Technology, Proven Performance

The HiSeq X Ten and HiSeq X Five Systems use proven Illumina sequencing by synthesis (SBS) chemistry, the most widely adopted next-generation sequencing technology. This chemistry ensures industry-leading data quality and gives researchers the utmost confidence in their results (Table 2). Building on this powerful foundation, the HiSeq X Series incorporates a new patterned flow cell technology to generate massive throughput. Patterned flow cells contain billions of nanowells at fixed locations, a design that provides even cluster spacing and uniform feature size to deliver extremely high cluster density (Figure 2). A proprietary clustering method, exclusion amplification, ensures that only a single DNA template binds and forms a cluster within a single well, resulting in high well occupancy and maximum data output.

Integrated, End-to-End Solution

Systems in the HiSeq X Series are available separately or as part of Illumina SeqLab, an integrated solution that includes laboratory best practices from sample preparation to variant detection (Figure 3).

Superior Library Preparation

To achieve exceptional genome coverage for accurate, comprehensive variant calling, the HiSeq X Ten and HiSeq X Five Systems support 2 library prep kits. The TruSeq® DNA PCR-Free Library Prep Kit provides a fast, gel-free protocol for preparing WGS libraries with superior coverage of areas that are traditionally difficult to sequence, such as high GC-rich regions, promoters, and repetitive content. PCR-free preparation reduces library bias and gaps, resulting in unsurpassed data quality for detecting the greatest number of variants. The TruSeq Nano DNA Library Prep Kit allows for efficient sequencing of samples with as little as 100 ng DNA. The enhanced workflow reduces the number and average size of typical PCR-induced gaps in coverage, minimizing library bias and improving coverage uniformity across the genome. Using the streamlined TruSeq Nano DNA protocol, libraries can be prepared in less than 1 day.

Table 2: HiSeq X System Performance Parameters[a]

Parameter	Specification
Output per Run	Dual flow cell: 1.6-1.8 Tb
Single Reads Passing Filter	Dual flow cell: 5.3-6 billion
Supported Read Length	2 × 150 bp
Run Time	< 3 days
Quality	≥ 75% of bases above Q30 at 2 × 150 bp
Supported Library Preparation	TruSeq DNA PCR-Free Library Prep Kit TruSeq Nano DNA Library Prep Kit

a. Specifications based on Illumina PhiX control library at supported cluster densities (1255–1412 K clusters/mm^2) on 1 HiSeq X System. Supported library preparation kit includes TruSeq Nano DNA Kit and TruSeq PCR-Free DNA Kit with 350 bp or 450 bp target insert size and HiSeq X Reagent Kit v2.5. The HiSeq X System was designed, optimized, and licensed for WGS. Other applications are not permitted.

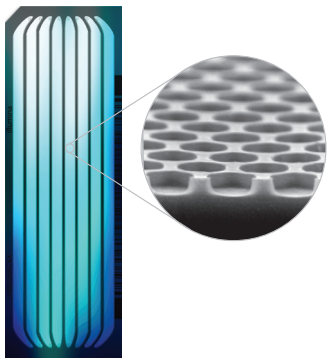

Figure 2: Advanced Patterned Flow Cell Design Enables Maximum Throughput—Patterned flow cells contain billions of nanowells at fixed locations providing even cluster spacing and uniform feature size to deliver extremely high cluster density.

High Operational Efficiency

To drive operational efficiency for HiSeq X laboratories, Illumina, together with select third-party vendors, has developed Illumina SeqLab. Illumina SeqLab is a combination of products and services that includes high-throughput liquid-handling robotics fully integrated with a laboratory information management system (LIMS), WGS analysis software, and personalized consulting. Each component is optimized specifically for the HiSeq X Five and HiSeq X Ten Systems to maximize quality, throughput, and cost efficiency, while minimizing turnaround time.

Fully Integrated LIMS

Illumina offers a fully automated workflow for the HiSeq X series that incorporates the BaseSpace® Clarity LIMS X Edition, the Hamilton Microlab STAR liquid-handling robotics, and defined auxiliary equipment to provide complete positive sample tracking. It is preconfigured to support both the TruSeq DNA PCR-Free and TruSeq Nano DNA workflows using Illumina Automated Workflow Manager for Hamilton. The intuitive user interface allows quick system adoption for immediate process tracking and scalability.

For Research Use Only. Not for use in diagnostic procedures.

AATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTA
AACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAC
ACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGT
CGTACCATTAAGAGCTACCGTGCAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACA
AATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTA
TTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGACGAA
TATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAAAAGAATGATAACAGTAAC

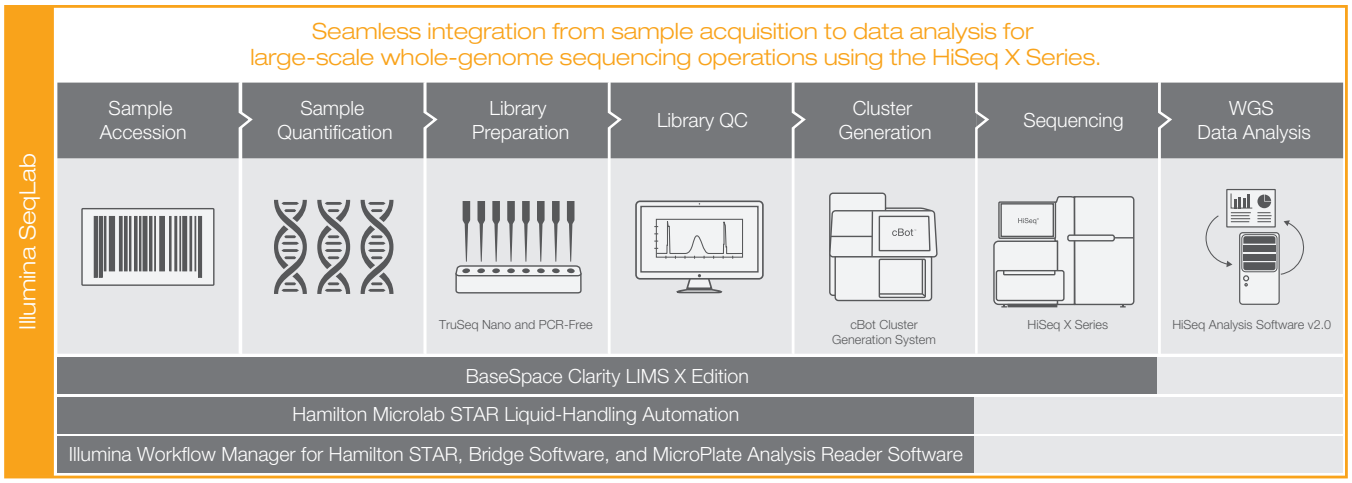

Figure 3: Illumina SeqLab Workflow—Seamless integration from sample accessioning to data analysis using Illumina methods and software: Illumina Automated Workflow Manager for the Hamilton Microlab STAR liquid-handling automation workstations, Illumina Automated Bridge Software for BaseSpace Clarity LIMS X Edition, and Illumina MicroPlate Analysis Reader Software for DNA quantification integration with a defined reference architecture for auxiliary equipment. Positive sample tracking throughout the workflow provides confidence in WGS results while streamlined processes maximize efficiencies.

Fast, Accurate WGS Analysis

Illumina redefines WGS analysis with the HiSeq® Analysis Software v2.0. Offering a fast, accurate solution to high-throughput WGS, HiSeq Analysis Software v2.0 processes data up to 6× faster than existing analysis methods. It uses the proven Isaac™ workflow to provide a full spectrum of variant types, including single nucleotide variants (SNVs), indels, structural variants (SVs), and copy number variants (CNVs) from BCL and FASTQ files. The pipeline can be run through command-line on commodity hardware, reducing the need for significant IT infrastructure investment. By analyzing data faster than the rate of HiSeq X sequence acquisition, HiSeq Analysis Software v2.0 eliminates costly informatics bottlenecks while maintaining exceptional data quality.

Illumina SeqLab Consulting Service

The Illumina SeqLab Consulting Service includes a suite of custom high-throughput implementation solutions for the HiSeq X Series. Personalized consulting engagement delivers accurate and expedient solutions aligned to the unique business objectives and laboratory environment of each customer in a collaborative manner. This enables each facility to realize the full potential of their HiSeq X Systems and achieve operational excellence. The Illumina SeqLab Consulting Service includes a full spectrum of guidelines for running a successful production sequencing operation, including capacity planning, fleet management, risk mitigation, performance and QC trending, troubleshooting, bioinformatics, data management, and IT infrastructure. At the end of the consultation, Illumina provides personalized recommendations and customized solutions to implement production-scale sequencing operations expeditiously and at a low total cost of ownership.

Summary

The HiSeq X Ten and HiSeq X Five Systems continue to break down sequencing barriers, reshaping the economics of whole-genome sequencing, and laying the foundation for visionary scientists, institutions, and nations working to perform groundbreaking research that will forever change our understanding of the human genome.

Just as true population-scale genome sequencing projects are beginning to take shape around the world, the HiSeq X Series delivers truly affordable human and nonhuman genomes—on a massive scale. By providing the capacity to sequence thousands to tens of thousands of genomes, the HiSeq X Series will bring genome sequencing to an inflection point. These high-performing systems will pave the way to a comprehensive catalog of human and nonhuman variation, forge population-based references, drive far-reaching discoveries, and accelerate a deeper understanding of biology and genetic disease.

We've taken sequencing to the next level. Now it's time to make your vision for human health and genome science a reality.

Learn More

To learn more about the HiSeq X Series, visit www.illumina.com/hiseqxseries.

To learn more about Illumina SeqLab, visit www.illumina.com/illuminaseqlab.

References

1. Bentley DR, Balasubramanian S, Swerdlow HP et al. Accurate whole human genome sequencing using reversible terminator chemistry. *Nature.* 2008;456:53-59.
2. Ley TJ, Mardis ER, Ding L, et al. DNA sequencing of a cytogenetically normal acute myeloid leukemia genome. *Nature.* 2008;456(7218):66-72.
3. Saunders CJ, Miller NA, Soden SE, et al. Rapid whole-genome sequencing for genetic disease diagnosis in neonatal intensive care units. *Sci Transl Med.* 2008;4(154):154ra135.

For Research Use Only. Not for use in diagnostic procedures.

AAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAA
AATCAACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACC
AACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTA
TTAACGTACCATTAAGAGCTACCGTGCAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGAT
AAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAA
AAGATTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGA
AACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAAAAGAATGATAACAG

HiSeq X System Specifications

Parameter	Specification[a]
Instrument Configuration	Computer and touch screen display Installation setup and accessories Data collection and analysis software
Instrument Control Computer	Base Unit: 2× Intel Xeon E5-2697V2 64 BIT 2.7 GHz CPU 30 MB Cache Memory: 128 GB RAM Hard Drive: 8 × 1.0 TB SATA 7200 RPM 3.5" Constellation ES.3 (2 RAID 0 drives, 6 RAID 5 drives) Solid-State Drive: 5 × 400 GB (5 RAID 0 drives) Operating System: Microsoft Windows 7 Professional Note: Computer specifications will be regularly upgraded. Contact your local account manager for current configuration.
Operating Environment	Temperature: 22°C ± 3°C Humidity: Noncondensing 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	W × D × H: 118.6 cm × 76.0 cm × 94.0 cm (46.7 in × 30.0 in × 37.0 in) Weight: 225.9 kg (498 lbs) Crated Weight: 316.6 kg (698 lbs)
Power Requirements	100–240V AC 50/60Hz, 20A, 1500 W Illumina provides a region-specific uninterruptible power supply for all HiSeq instruments
Product Safety	CE-marked and ETL-listed instrument

a. Specifications refer to an individual HiSeq X System.

Ordering Information

Product	Catalog No.
HiSeq X Ten Products	
HiSeq X Ten System[a]	SY-412-1001
HiSeq X Ten Reagent Kit v2.5	FC-501-2501
HiSeq X Ten Reagent Kit v2.5 - 10 pack	FC-501-2521
HiSeq X Five Products	
HiSeq X Five System[b]	SY-412-1011
HiSeq X Five Reagent Kit v2.5	FC-502-2501
HiSeq X Five Reagent Kit v2.5 - 10 pack	FC-502-2521

a. Catalog No. refers to an individual system. Minimum order for the HiSeq X Ten is 10 systems.
b. Catalog No. refers to an individual system. Minimum order for the HiSeq X Five is 5 systems.

Illumina • 1.800.809.4566 toll-free (U.S.) • +1.858.202.4566 tel • techsupport@illumina.com • www.illumina.com

For Research Use Only. Not for use in diagnostic procedures.

© 2016 Illumina, Inc. All rights reserved.
Illumina, BaseSpace, HiSeq, HiSeq X, Isaac, TruSeq, and the pumpkin orange color are trademarks of Illumina, Inc. and/or its affiliate(s) in the U.S. and/or other countries. All other names, logos, and trademarks are the property of their respective owners
Pub. No. 770-2014-056 Current as of 22 March 2016

illumina®

AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
TCAACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTT
CGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACC
AACGTACCATTAAGAGCTACCGTGCAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAA
AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
GATTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGACG
CGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAAAAGAATGATAACAGTA