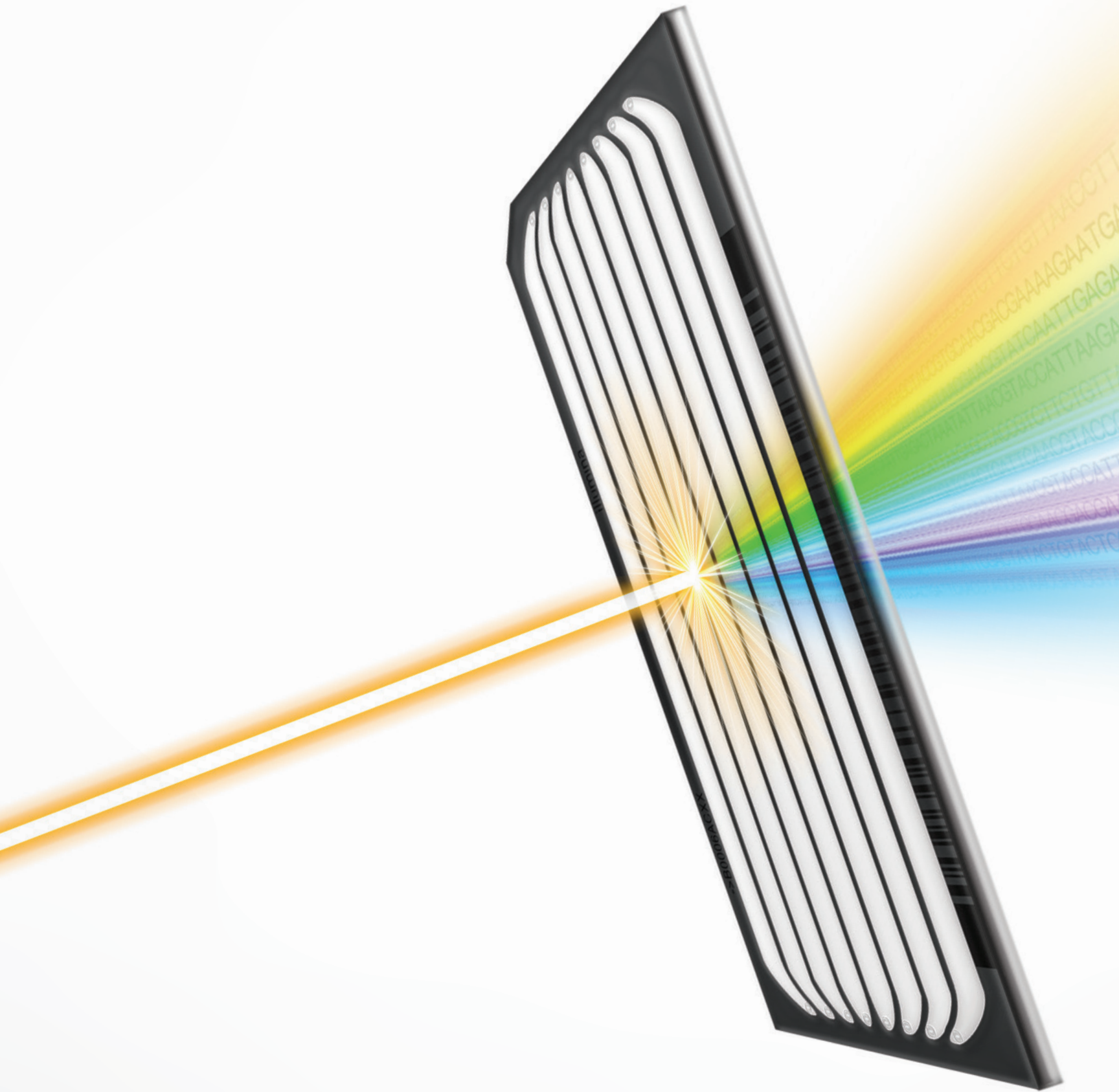


Sequencing power for every scale.

Systems for every application, for every lab.







Proven sequencing technology.

Accelerate your research. Achieve your next breakthrough.

What started as novel Illumina chemistry, sequencing by synthesis (SBS) technology, has fueled a sequencing revolution.

Every day, researchers are using Illumina next-generation sequencing (NGS) systems to unlock the power of the genome. Studying cancer, genetic disease, microbiology, and agriculture. Enhancing research in emerging fields such as reproductive health and forensic science. Making breakthrough discoveries that increase our understanding of genotypic and phenotypic variation.

A complete portfolio.

Systems for every application, for every lab.



MiniSeq™ System

Leveraging industry-leading sequencing in our simplest, smallest, most affordable system, the MiniSeq System supports a broad range of targeted DNA and RNA applications for examining single genes or entire pathways. An intuitive user interface, load-and-go operation, and onboard data analysis make it easy to learn and easy to use.

- Cost efficient to run and affordable to acquire
- Ideal for targeted sequencing

MiSeq® System

Combining proven data quality, ease of use, and longer read lengths, the MiSeq System is well-suited for a broad range of applications, including targeted DNA and RNA, and small genome sequencing.

- Most adopted benchtop sequencer in the world
- Ideal for longer read applications
- Cost-effective and scalable alternative to capillary electrophoresis

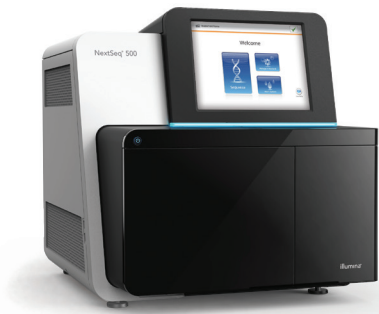


MiSeqDx™ System

Featuring all the capabilities of the MiSeq System, the MiSeqDx System is specifically designed for clinical laboratories performing screening and diagnostic testing.

- The first FDA-cleared in vitro diagnostic system
- An expanding menu of IVD assays, including cystic fibrosis
- Integrated software enabling sample tracking, user traceability, and results interpretation





NextSeq® 500 System*

Delivering the power of high-throughput sequencing with the simplicity of a desktop sequencer, the NextSeq 500 System transforms exome, transcriptome, and whole-genome sequencing (WGS) into everyday research tools. This versatile and flexible platform lets you easily switch from one application to another. Streamlined NGS workflows enable you to perform low- and high-throughput studies to support many project sizes.

- Configurable output and fast run time to support a wide range of applications and sample sizes
- Ideal for exome and transcriptome sequencing
- Only desktop system capable of sequencing a human whole genome in a single run

* The NextSeq 550 System has identical sequencing specifications to the NextSeq 500 System and includes array scanning functionality for cytogenomic and karyomapping applications.

The HiSeq® Series

HiSeq 2500 System

Offering a high-powered, cost-effective sequencing solution, the HiSeq 2500 System enables you to perform large-scale high-throughput exome, transcriptome, and WGS projects. The system can process 1 or 2 flow cells in parallel and has flexible run modes. These features let you adjust data output to support your studies.

- Proven powerhouse configurable for a wide range of applications and sample sizes
- Rapid and high-throughput modes for increased flexibility



HiSeq 3000 and HiSeq 4000 Systems†

Building on the proven HiSeq 2500 System and leveraging innovative patterned flow cell technology, the HiSeq 3000 and HiSeq 4000 Systems provide unparalleled speed and performance. Perform large-scale, high-throughput exome, transcriptome, and WGS projects quickly and economically.

- Ideal for high-throughput exome and transcriptome projects
- The standard for multi-application production-scale sequencing

† Available in single (HiSeq 3000 System) and dual (HiSeq 4000 System) flow cell configurations.





* Depreciation schedules and labor may differ due to differences in institutional accounting and staffing.
For Research Use Only. Not for use in diagnostic procedures.



Empowering population and production-scale human whole-genome sequencing.

The HiSeq X™ Series. Maximum throughput.
Lowest cost per genome.

HiSeq X Ten System

The HiSeq X Ten System is the first and only sequencing platform to break the \$1,000 barrier for a human genome at 30x coverage. Composed of 10 or more individual instruments, the HiSeq X Ten System is ideal for population-scale projects focused on the discovery of genotypic variation. It can rapidly sequence tens of thousands of genomes at high coverage, delivering a comprehensive catalog of human variation within and outside of coding regions. With its ultra-high throughput and unprecedented low price per genome, the HiSeq X Ten System makes population-scale human WGS a reality.

- Sequences tens of thousands of human whole genomes per year
- Achieves the \$1,000 human genome milestone, including instrument depreciation, sample preparation, and labor*

HiSeq X Five System

The HiSeq X Five System, a set of 5 or more individual HiSeq X instruments, delivers fast, affordable, production-scale human WGS. With a lower initial capital investment than the HiSeq X Ten System, the HiSeq X Five System provides an accessible entry point to human WGS with an upgradable path to population-scale sequencing and the \$1,000 genome. This empowers researchers to complete large-scale human WGS projects rapidly, in their own labs.

- Sequences more than 9,000 human whole genomes per year
- Offers an affordable price per human whole genome

Accessible sequencing solutions.

Power tailored for every researcher, application, and scale of study.



Product	MiniSeq	MiSeq	NextSeq 500*	
Description	Simplicity and accessibility for examining single genes or entire pathways	Speed and simplicity for targeted and small-genome sequencing	Speed and simplicity for everyday genomics	
Key methods	Targeted DNA and targeted RNA sequencing	Small genome, amplicon, targeted gene panel sequencing	Everyday genome, exome, transcriptome sequencing, and more	
Run mode	—	—	Mid-output	High-output
Flow cells processed per run	1	1	1	1
Output range	0.6–7.5 Gb	0.3–15 Gb	20–39 Gb	30–120 Gb
Run time	4–24 hours	5–55 hours	15–26 hours	12–30 hours
Reads per flow cell†	25 million	25 million [§]	130 million	400 million
Maximum read length	2 x 150 bp	2 x 300 bp	2 x 150 bp	2 x 150 bp

* The NextSeq 550 System has identical sequencing specifications to the NextSeq 500 System and includes array scanning functionality for cytogenomic and karyomapping applications.

† Specifications shown for an individual HiSeq X System. The HiSeq X System is available only as part of the HiSeq X Five or HiSeq X Ten System.



HiSeq 2500

HiSeq 3000

HiSeq 4000

HiSeq X Five[†]

HiSeq X Ten[†]

Power and efficiency for large-scale genomics

Maximum throughput and lowest cost for production-scale genomics

Maximum throughput and lowest cost for population- and production-scale human WGS

Production-scale genome, exome, transcriptome sequencing, and more

Population-scale human WGS

Rapid run

High-output

—

—

—

—

1 or 2

1 or 2

1

1 or 2

1 or 2

1 or 2

10–300 Gb

50–1000 Gb

125–750 Gb

125–1500 Gb

900–1800 Gb

900–1800 Gb

7–60 hours

< 1–6 days

< 1–3.5 days

< 1–3.5 days

< 3 days

< 3 days

300 million

2 billion

2.5 billion

2.5 billion

3 billion

3 billion

2 × 250 bp

2 × 125 bp

2 × 150 bp

2 × 150 bp

2 × 150 bp

2 × 150 bp

[†] Clusters passing filter.

[§] For MiSeq Reagent Kit v3 only.

^{||} For MiniSeq High Output Kit only.

Industry-leading data quality.

Trusted technology. Highest confidence.

Your studies deserve the best data quality. That's what our systems are proven to deliver.

It's no wonder more than 90% of the world's sequencing data is generated using SBS technology from Illumina.

- Obtain the greatest accuracy with the highest percentage of sequenced bases above Q30
- Achieve the highest yield of error-free reads
- Improve efficiency with the fewest false positives, false negatives, and miscalls

The performance you need.

Every Illumina sequencing system leverages our proprietary cluster generation and SBS chemistry, the most widely adopted sequencing technology in the world. Using a single base extension and competitive addition of nucleotides, SBS chemistry results in highly accurate sequencing that virtually eliminates homopolymer-related errors. You'll get industry-leading data quality with the highest percentage of sequenced bases above Q30, the fewest false positive and false negative calls, and the utmost confidence in your results.

All Illumina sequencing systems perform fully automated paired-end sequencing, improving alignment and genome assembly, and enabling accurate detection of structural variants, gene fusions, and transcript isoforms.

A stylized world map in a dark orange color, centered on the Atlantic Ocean, serving as a background for the text.

> 90%

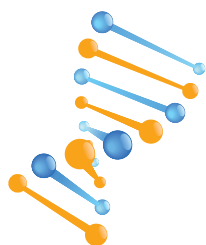
of the world's sequencing data is
generated using Illumina SBS technology.*

Comprehensive library prep solutions optimized for Illumina systems.

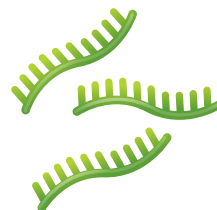
A depth of applications.

Developed to seamlessly integrate with our NGS workflows, our extensive high-quality library prep solutions support the broadest diversity of applications and sample types.

Select from a broad range of applications:*



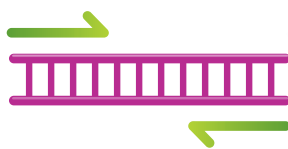
Whole genome



Transcriptome



Exome



Amplicon



Targeted panels



NeoPrep™ Library Prep System

Featuring the precision of digital microfluidics and unparalleled ease of use, the NeoPrep System radically simplifies library prep. Now you can dramatically reduce hands-on time and achieve reproducible, high-quality libraries, even with limited starting material.

- Accepts 10x lower input for some assays
- Takes just 30 minutes of hands-on time per run
- Delivers walkaway library prep, quantification, and normalization
- Works with all Illumina sequencing systems



Library prep

In addition to manual options, Illumina offers the NeoPrep System for reproducible sequencing-ready libraries with just 30 minutes of hands-on time per run.



Sequencing

With power for every scale, Illumina offers a complete portfolio NGS solutions that are accessible for every study and every lab.



Informatics

Intuitive informatics tools provide critical insights. Essential data can be transferred, stored, analyzed, and shared securely in BaseSpace® Onsite or in the BaseSpace Cloud.



Optimize your work with simply smart workflow solutions.

One seamless process. One complete resource.

From library prep to sequencing and informatics, Illumina offers seamless NGS workflow solutions that optimize your process from start to finish and accelerate your progress. As the innovators of next-generation technology, we're here to deliver the experience and expertise to help propel your success.

Industry-leading solutions.

A community of support.

From library prep, arrays, and sequencing to informatics, Illumina genomic solutions empower researchers and clinical researchers across the globe to find the answers they seek.

When you join the Illumina community, you become part of a dynamic scientific movement that includes thousands of researchers and industry thought leaders. Throughout the year, we host user group meetings, symposia, consortia, online forums, and other initiatives—all designed to bring the best minds together to share ideas and advance science.

In addition to on-site training, ongoing support, and phone consults, we offer webinars and courses at various Illumina locations. We're here with all the resources you need to accelerate progress.

Find the right Illumina system for your needs.

www.illumina.com/sequencer

A global genomics leader, Illumina provides complete next-generation sequencing workflow solutions to the basic and translational research communities. Illumina technology is responsible for generating more than 90% of the world's sequencing data.* Through collaborative innovation, Illumina is fueling groundbreaking advancements in the fields of oncology, reproductive health, genetic disease, microbiology, agriculture, and forensic science.

*Data calculations on file. Illumina, Inc., 2015.

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