NextSeq® Series of Sequencing Systems

Fast, flexible, high-throughput desktop sequencers enable transcriptome and targeted resequencing applications with the accuracy of Illumina SBS technology.

Highlights

- **Highly Flexible to Fit Research Demands**
  Supports a broad range of sequencing applications and offers tunable read length and multiple output configurations
- **Fast Turnaround Time**
  Generate data faster for time-critical studies and complete projects in record time
- **Industry-Leading Illumina Chemistry**
  Highly accurate SBS chemistry delivers high-quality results with no homopolymer issues
- **Push-Button Operation and Easy Data Analysis**
  Walk away sample-to-results solution with streamlined informatics performed on premises or in the cloud
- **End-to-End Illumina Scientific Support**
  Illumina scientists and engineers are there every step of the way, providing installation, training, applications, and data analysis support

Introduction

A transformative addition to the industry-leading Illumina next-generation sequencing (NGS) system portfolio, the NextSeq Series of systems delivers the power of high-throughput sequencing with the simplicity of a desktop sequencer (Figure 1). Its fast, integrated, sample-to-results workflow enables rapid sequencing of exomes, targeted panels, and transcriptomes in a single run, with the flexibility to switch to lower-throughput sequencing as needed (Figure 2). The systems fit seamlessly into research laboratories, with no need for specialized equipment. Illumina scientists are available at every point along the way with support and guidance, enabling researchers to focus on making the next breakthrough discovery.

Enabling New Discoveries

The NextSeq Series enables researchers to keep pace with technology, putting them in control of their sequencing projects. These robust, scalable systems turn a broad range of high-throughput applications into affordable everyday research tools. The flexible NextSeq Series enables researchers to switch quickly from one application to another and configure output based on sample volume and coverage needs. Now, even the smallest laboratory can perform any combination of sequencing applications to advance their studies, supporting faster publication of landmark research.

Figure 1: NextSeq System—By leveraging the latest advances in SBS chemistry and the industry's simplest workflow, the NextSeq Series of systems delivers high-quality results for exome, transcriptome, and targeted resequencing applications.

Fast and Easy Workflow

The intuitive user interface and load-and-go operation enable researchers to perform more sequencing applications at the highest depth and resolution. It takes less than 10 minutes to load and set up a NextSeq System. While other platforms require several pieces of specialized equipment, the NextSeq Series integrates cluster generation and sequencing into a single instrument and offers a seamless transition for onsite or cloud-based data analysis.

After preparation using a simple, streamlined Illumina library prep kit, libraries are loaded into a NextSeq System where sequencing is automated and fast. Data are generated in as little as 12 hours for a 75-cycle sequencing run and less than 30 hours for paired 150-cycle reads. By employing the Illumina industry-leading sequencing by synthesis (SBS) chemistry and file format conventions, the NextSeq Series offers customers access to the broadest ecosystem of established protocols, workflows, data sets, and data analysis tools.

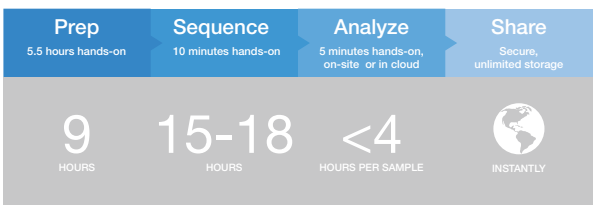

Figure 2: NextSeq Series Sequencing Workflow—The NextSeq Series offers a simple, integrated workflow from sample preparation to data analysis. Workflow times will vary by experiment and assay type. Details shown are for an mRNA expression profiling experiment assuming 2 × 75 bp on instrument, analysis results include differential expression and identification of alternative transcripts.

Table 1: Unprecedented Flexibility for Multiple Applications

Application	High-Output Flow Cell Configuration		Mid-Output Flow Cell Configuration	
	No. of Samples	Time	No. of Samples	Time
Gene Expression Profiling > 10 M Reads 1 × 75 bp	40	11 hours	13	11 hours
mRNA-Seq > 40 M Reads 2 × 75 bp	10	18 hours	3	15 hours
Enrichment Panel 12 Mb Region > 20× coverage at > 95% targets	36	29 hours	12	26 hours
Whole-Exome Sequencing > 90% at > 10× coverage	9	18 hours	3	15 hours
Small Whole-Genome Sequencing 130 Mb Genome > 30× coverage 2 × 150 bp	30	29 hours	10	26 hours

Industry-Leading SBS Chemistry Delivers Highest Accuracy

At the core of the NextSeq Series is industry-leading Illumina SBS chemistry—the most widely adopted NGS technology. This proprietary reversible terminator–based method enables the massively parallel sequencing of millions of DNA fragments, detecting single bases as they are incorporated into growing DNA strands. The method virtually eliminates errors and missed calls associated with strings of repeated nucleotides (homopolymers).

Furthermore, the latest evolution in sequencing chemistry—SBS v2 sequencing reagents—deliver improved signal intensities and the lowest number of false positives, false negatives, and error rates yet. With SBS v2 chemistry, the NextSeq Series provides exceptional accuracy for human genome, targeted panel, exome, or transcriptome data at any coverage level. SBS chemistry on the MiSeq® Series and HiSeq® Series Systems also provides consistency and reliability across all Illumina platforms.

Versatile and Flexible to Support the Widest Range of Applications

The NextSeq Series offers the right sequencer for any project size and sequencing throughput, providing users with optimal operational efficiency. It is the only desktop sequencing system capable of sequencing a high-coverage (30×) whole human genome in one run. The NextSeq Series also delivers a one-day turnaround for numerous popular sequencing applications. With these instruments, researchers can sequence a broad range of samples per run:

- 1–16 exomes
- 1–20 transcriptomes
- 6–96 targeted panels
- 12–40 gene expression profiling samples

The NextSeq Series is easily configured providing researchers with scalability to handle low to high-throughput project sizes for maximum operational efficiency. Based on sample volume and coverage needs, researchers can choose between 2 flow cell configurations (High Output and Mid Output), easily shifting from low- to higher-throughput processing with each sequencing run (Table 1). The NextSeq Series provides integrated support for paired-end sequencing, offering user-defined read lengths up to 2 × 150 bp. The system is supported by the full suite of Illumina library preparation and target enrichment solutions, offering library compatibility across the Illumina sequencing portfolio. This allows researchers to scale up studies easily to the higher throughput HiSeq Series Systems or perform follow-up studies on the MiSeq Series Systems (Figure 3).

HiSeq Series
Power and efficiency for large-scale genomics.

NextSeq Series
Speed and simplicity for personal-scale genomics.

MiSeq Series
Speed and simplicity for targeted and small genome sequencing.

Figure 3: Illumina NGS Portfolio Makes Sequencing Accessible to All Researchers—Illumina NGS systems offer solutions for every application, sample type, and sequencing scale. Each delivers high data quality and accuracy with flexible throughput and simple, streamlined workflows. Data can be seamlessly compared, exchanged, and analyzed in BaseSpace.

Streamlined Bioinformatics

The NextSeq Series supports several data analysis options. Integrated instrument computers perform base calling and quality scoring. Sequencing run data can be run through a wide range of open-source or commercial pipelines developed for Illumina data, or instantly transferred, analyzed, and stored securely in BaseSpace® (Cloud or Onsite), the Illumina genomics computing environment. BaseSpace downstream data analysis includes alignment and variant detection, annotation, visualization, and interpretation.

BaseSpace also includes Illumina data analysis apps for exome, transcriptome, whole-genome, and somatic variant calling. Thanks to industry-standard data formats, third-party developers have created

Table 2: NextSeq Series Performance Parameters

NextSeq Series Sequencing Performance[a]					
Flow Cell Configuration	**Read Length (bp)**	**Output (Gb)**	**Run Time**	**Data Quality**	**Required Input**
High-Output Flow Cell Up to 400 M single reads Up to 800 M paired-end reads	2 × 150	100–120	29 hours	> 75% > Q30	100 ng–1 µg with TruSeq® Library Prep Kits
	2 × 75	50–60	18 hours	> 80% > Q30	
	1 × 75	25–30	11 hours	> 80% > Q30	
Mid-Output Flow Cell Up to 130 M single reads Up to 260 M paired-end reads	2 × 150	32–39	26 hours	> 75% > Q30	
	2 × 75	16–19	15 hours	> 80% > Q30	

NextSeq 550 System Array Scanning Parameters		
BeadChip	**Scan Time Per BeadChip**	**Scan Time Per Sample**
Infinium® CytoSNP-850K BeadChip	40 minutes	5 minutes
HumanCytoSNP-12 BeadChip	40 minutes	3.3 minutes
Infinium HumanKaryomap-12 BeadChip	40 minutes	3.3 minutes

a. Total times include cluster generation, sequencing, and base calling on a NextSeq System. Install specifications are based on Illumina PhiX control library at supported cluster densities (between 129 and 165 k/mm^2 clusters passing filter). Actual performance parameters may vary based on sample type, sample quality, and clusters passing filter. The percentage of bases > Q30 is averaged over the entire run.

a rich ecosystem of commercial and open-source tools for more extensive downstream data analysis.

BlueFuse® Multi software provides a single framework for analyzing data from array-based molecular cytogenetics studies or combined array and NGS data from *in vitro* fertilization (IVF) applications. The software is designed to manage, search, and display the wealth of data generated by whole-genome analysis experiments using sophisticated processing algorithms and an intuitive visualization format.

NextSeq 550 System Enables Array Scanning

The NextSeq 550 System combines microarray scanning with the proven and robust NextSeq 500 sequencing system (Table 2).* By leveraging microarray scanning on the NextSeq 550 System, researchers have instant access to a powerful, complementary technology for further exploration or confirmation of copy number variants detected through sequencing. With the NextSeq 550 System, the menu of cutting-edge research applications is maximized while the instrument costs are simultaneously minimized. The NextSeq 550 System supports flexible options by enabling a broad range of applications in reproductive, genetic health, and oncology research.

Summary

The NextSeq 500 and NextSeq 550 Systems are transformative sequencers that enable NGS to become an everyday tool in laboratories worldwide. Incorporating the latest advancements in SBS chemistry, the flexible NextSeq Series features push-button operation and streamlined sample-to-results workflow that allow researchers to perform the most popular high-throughput applications in less than a day. Its multiple flow cell and reagent configurations enable low-throughput sequencing as needed, providing researchers with the operational efficiency to handle a range of project sizes.

Table 3: NextSeq Series Specifications

Instrument Configuration
RFID tracking for consumables
Instrument Control Computer (Internal)[a]
Base Unit: Dual Intel Xeon ES-2448L 1.8 GHz CPU
Memory: 96 GB RAM
Hard Drive: 750 GB
Operating System: Windows 7 embedded standard
Operating Environment
Temperature: 19°C to 25°C (22°C ± 3°C)
Humidity: Noncondensing 20%–80% relative humidity
Altitude: Less than 2,000 m (6,500 ft)
Air Quality: Pollution degree rating of II
Ventilation: Up to 2,048 BTU/hr @ 600 W
For Indoor Use Only
Light Emitting Diode (LED)
520 nm, 650 nm; Laser diode: 780 nm, Class IIIb
Dimensions
W×D×H: 53.3 cm × 63.5 cm × 58.4 cm (21.0 in × 25.0 in × 23.0 in)
Weight: 83 kg (183 lbs)
Crated Weight: 151.5 kg (334 lbs)
Power Requirements
100–120 VAC 15 A
220–240 VAC 10 A
Radio Frequency Identifier (RFID)
Frequency: 13.56 MHz
Power: Supply current 120 mA, RF output power 200 mW
Product Safety and Compliance
NRTL certified IEC 61010-1
CE marked
FCC/IC approved

a. Computer specifications are subject to change.

* Microarray scanning is only supported on the NextSeq 550 System. Microarray scanning includes support for the CytoSNP-850K, HumanCytoSNP-12, and HumanKaryomap-12 DNA BeadChips.

Ordering Information

System Name	Catalog No.
NextSeq 500 System	SY-415-1001
NextSeq 550 System	SY-415-1002
Output Kit Name	**Catalog No.**
NextSeq 500 Mid-Output Kit (150 cycles)	FC-102-1001
NextSeq 500 Mid-Output Kit (300 cycles)	FC-404-1003
NextSeq 500 High-Output Kit (75 cycles)	FC-404-1005
NextSeq 500 High-Output Kit (150 cycles)	FC-404-1002
NextSeq 500 High-Output Kit (300 cycles)	FC-404-1004
NextSeq 500/550 Mid-Output v2 Kit (150 cycles)	FC-404-2001
NextSeq 500/550 High-Output v2 Kit (150 cycles)	FC-404-2002
NextSeq 500/550 Mid-Output v2 Kit (300 cycles)	FC-404-2003
NextSeq 500/550 High-Output v2 Kit (300 cycles)	FC-404-2004
NextSeq 500/550 High-Output v2 Kit (75 cycles)	FC-404-2005

Learn More

Go to www.illumina.com/nextseq to learn more about the next revolution in sequencing.

Maximize Performance and Productivity with Illumina Services, Training, and Consulting

Whether immediate help is needed during an instrument run, or in-depth consultations are required for sophisticated workflows, Illumina can help. Illumina service and support teams provide a full suite of expedient, customized solutions from initial trainings, to instrument support, and ongoing NGS consultations. Our support offerings include:

Product Care Services

- Tiered Instrument Service Plans + Add-On Services
- Instrument Compliance Services
- Instrument On-Demand Services

Illumina University Training

- Instructor-Led Training at Your Chosen Facility
- Instructor-Led Training at an Illumina Training Center
- Online Courses
- Webinars

Illumina Consulting

- Proof-of-Concept Services for instrument and library preparation testing
- Concierge Services for design assistance and product optimization

For more on Illumina support offerings, visit: www.illumina.com/services/instrument-services-training.html

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