

Table 1: Unprecedented Flexibility for Multiple Applications

Table with 5 columns: Application, High-Output Flow Cell Configuration (No. of Samples, Time), and Mid-Output Flow Cell Configuration (No. of Samples, Time). Rows include Gene Expression Profiling, mRNA-Seq, Enrichment Panel, Whole-Exome Sequencing, and Small Whole-Genome Sequencing.

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...

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.

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 (30x) whole human genome in one 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



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.

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 x 150 bp. The system is supported by the full suite of Illumina library preparation and target enrichment solutions...

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...

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	2 × 150	100–120	29 hours	> 75% > Q30	100 ng–1 µg with TruSeq® Library Prep Kits
Up to 400 M single reads	2 × 75	50–60	18 hours	> 80% > Q30	
Up to 800 M paired-end reads	1 × 75	25–30	11 hours	> 80% > Q30	
Mid-Output Flow Cell	2 × 150	32–39	26 hours	> 75% > Q30	
Up to 130 M single reads	2 × 75	16–19	15 hours	> 80% > Q30	
Up to 260 M paired-end reads					

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/mm² 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.

* 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.

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
WxDxH: 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.

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



