illumina®

NextSeq™ 1000 and NextSeq 2000 Sequencing Systems

Explore current and emerging applications with higher efficiency and fewer restraints

- **Scale for the future while driving efficiencies today**

  Innovative, scalable platform empowers deeper investigation, larger studies, and higher resolution on a benchtop system

- **Achieve capacity for breakthroughs, support to sustain them**

  Cost-efficient, high-throughput system delivers accurate results for emerging applications of increasing complexity

- **Maximize time and resources with an intuitive experience**

  Easy-to-use system and onboard informatics streamline workflow and analysis, making NGS accessible to novice and expert users

Gain greater capacity for deeper exploration and discovery through significantly reduced sequencing costs, simplified workflows, and more flexibility to support new and emerging applications at virtually any scale.

Innovations in next-generation sequencing (NGS) are helping the genomics community ask, and answer, increasingly complex scientific questions. Across the spectrum of oncology, microbiome research, single-cell studies, and other emerging applications, researchers need sequencing power to help fuel larger studies of more samples at greater sequencing depth and at a lower cost.

To support this expansion in research, Illumina is committed to enabling the exploration of the genome, transcriptome, and epigenome by providing users with innovative advances in technology and systems. Over the last 20 years, Illumina has led the charge to improve sequencing capabilities across the entire workflow, making it easier to use while driving down costs. This tradition continues with the NextSeq 1000 and NextSeq 2000 Sequencing Systems (Figure 1, Table 1). These game-changing platforms offer breakthrough system design, chemistry innovations, compatibility with an expansive list of library preparation options, and onboard integrated informatics for rapid secondary analysis.

The result: Illumina NextSeq 1000 and NextSeq 2000 Sequencing Systems are scalable platforms that will support the research of today and tomorrow.

Figure 1: The NextSeq 2000 Sequencing System—The NextSeq 2000 system offers innovative design features, advanced chemistry, simplified bioinformatics, and an intuitive workflow that enable the widest range of applications and flexibility of scale on a benchtop sequencing system.

Table 1: Performance parameters for the NextSeq 1000 and 2000 Sequencing Systems

Read length	NextSeq 1000/2000 P1 Reagents	NextSeq 1000/2000 P2 Reagents	NextSeq 2000 P3 Reagents
Output per flow cell[a]			
1 × 50 bp (P3 only)	–	–	60 Gb
2 × 50 bp	–	40 Gb	120 Gb
2 × 100 bp	–	80 Gb	240 Gb
2 × 150 bp	30 Gb	120 Gb	360 Gb
Reads CPF	100M	400M	1.2B
Quality scores[b]			
1 × 50 bp		≥ 90% of bases higher than Q30	
2 × 50 bp		≥ 90% of bases higher than Q30	
2 × 100 bp		≥ 85% of bases higher than Q30	
2 × 150 bp		≥ 85% of bases higher than Q30	
Run time			
1 × 50 bp	–	–	~11 hours
2 × 50 bp	–	~13 hours	~19 hours
2 × 100 bp	–	~21 hours	~33 hours
2 × 150 bp	~19 hours	~29 hours	~48 hours

a. Output specifications based on a single flow cell using Illumina PhiX control library at supported cluster densities; CPF, clusters passing filter
b. Quality scores are based on an Illumina PhiX control library; performance may vary based on library type and quality, insert size, loading concentration, and other experimental factors

Discover more with our groundbreaking benchtop systems

The NextSeq 1000 and NextSeq 2000 Sequencing Systems leverage the latest advances in optics, instrument design, and reagent chemistry to miniaturize the volume of the sequencing reaction while increasing output and reducing the cost per run. Now, users can obtain the throughput, data quality, and cost needed to expand the size and scope of their studies, all on a benchtop sequencing system.

Increased output powered by our most intuitive experience yet

The NextSeq 1000 and NextSeq 2000 Sequencing Systems use patterned flow cells similar to those that power the NovaSeq™ 6000 System. The result is a highly flexible, robust, and scalable benchtop system that offers the highest cluster density flow cell of any on-market NGS system to date, driving down the cost per gigabase (Gb) of the sequencing run.

To take full advantage of these higher density flow cells, the NextSeq 1000 and NextSeq 2000 Sequencing Systems feature a novel super resolution optics system that yields highly accurate imaging data with greater resolution and higher sensitivity than traditional benchtop systems. This miniaturization provides scalability for a variety of output quantities while maintaining the same high standards of data quality enjoyed by NextSeq 550 System users.

High-quality data and lower run costs with enhanced reagent chemistry

Building on decades of expertise, the NextSeq 1000 and NextSeq 2000 systems feature the next iteration of industry-leading sequencing by synthesis (SBS) chemistry, optimized to increase cluster brightness, reduce channel cross talk, and improve signal-to-noise ratio. The combination of this advancement with formulation improvements that reduce the actual reaction size enables NextSeq 1000/2000 reagent users to realize high-quality data and an overall reduction in reagent volume and waste, minimizing physical storage requirements. Additionally, the improved robustness and stability enables ambient shipment of the flow cell.

Pioneer breakthrough studies with access to broader capabilities

With fast, accurate results, extensibility from 30 Gb up to 360 Gb, and flexible informatics options, the NextSeq 1000 and NextSeq 2000 Sequencing Systems are ideal for wide-ranging applications (Table 2) across oncology, genetic disease, reproductive health, agrigenomics, and more. Add in unwavering expert support and labs are set for today's workload and future emerging applications.

Table 2: Some of the broader applications available on the NextSeq 1000 and NextSeq 2000 Sequencing Systems

Application	NextSeq 1000/2000 P1 Reagents		NextSeq 1000/2000 P2 Reagents		NextSeq 2000 P3 Reagents	
	No. samples	Time	No. samples	Time	No. samples	Time
Small whole-genome sequencing (300 cycles) 130 Mb genome; > 30× coverage	7	~19 hours	30	~29 hours	90	~48 hours
Whole-exome sequencing (200 cycles) 50× mean targeted coverage; 90% targeted coverage at 20×	4 (300 cycles)	~19 hours	16	~21 hours	48	~33 hours
Single-cell RNA-Seq (100 cycles)[a] 4K cells, 10K-50K reads/cell	–	–	2-10	~13 hours	6-30	~19 hours
miRNA-Seq or small RNA analysis (50 cycles) 11M reads/sample	–	–	–	–	108	~11 hours

a. Recommended sequencing depth will largely depend on sample type and experimental objective and will need to be optimized for each study

A powerful, simplified workflow driven by an integrated system and advanced informatics

At Illumina, customer experience is at the center of every innovation, making it as easy as possible to prepare samples, sequence, and analyze data. The NextSeq 1000 and NextSeq 2000 Sequencing Systems offer a simplified workflow, combining load-and-go ease and advanced informatics (Figures 2 and 3) benefiting both new and advanced users.

Easy-to-use cartridge-based platform

The NextSeq 1000 and NextSeq 2000 Sequencing Systems take advantage of an integrated cartridge that includes reagents, fluidics, and the waste holder, simplifying library loading and instrument use. Simply thaw the reagent cartridge, insert the flow cell into the cartridge, load the library into the cartridge, and insert the assembled cartridge into the instrument. Denaturation and dilution steps occur onboard automatically.

In addition to ease of use, the fully integrated cartridge design improves efficiency throughout the sequencing run. By miniaturizing many of the sequencing reactions, the unique design:

- Lowers sequencing costs
- Improves recyclability
- Minimizes waste volume

Because the reagents never leave the cartridge, the dry instrument design does not require washing, enabling streamlined instrument maintenance and optimizing instrument efficiency.

Flexible options for run setup

Runs can be set up locally or in the cloud. For local setup, users can create their own sample sheet or take advantage of a convenient, preset Illumina template. Cloud-based setup uses the Run Planner app in BaseSpace™ Sequence Hub. Once the run setup information is ready, it is imported into the NextSeq 1000 and NextSeq 2000 systems. Users then select and start the run of interest. Optimized instrument software provides a cleaner interface with easy-to-read screens, easier-to-understand run metrics, and improved visualization of instrument and run status compared to earlier benchtop systems. The NextSeq 1000 and NextSeq 2000 systems output industry-standard file formats used by various laboratory information management systems (LIMS) for secure, automated sample tracking and information management.

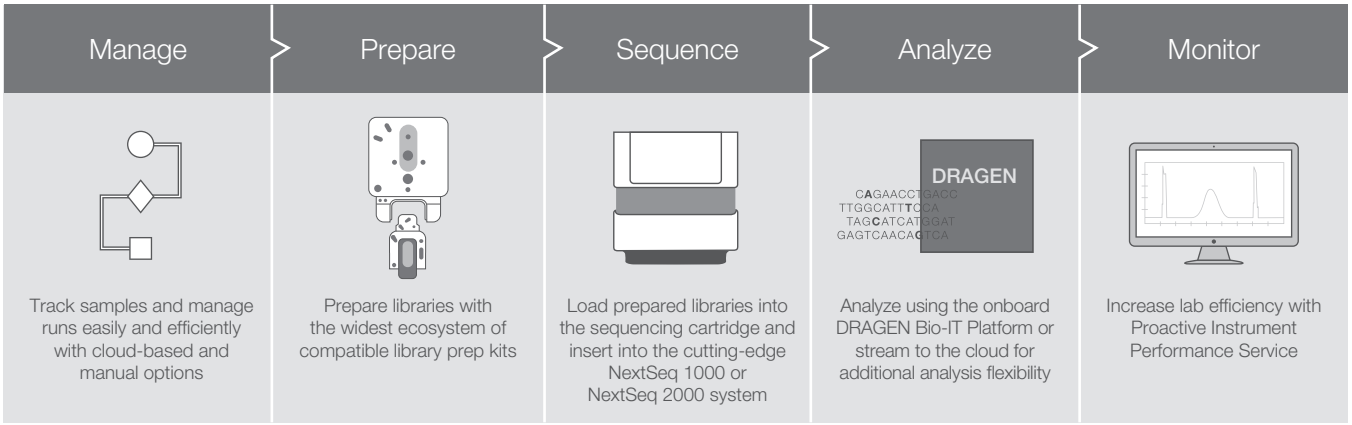

Figure 2: Intuitive library-to-analysis workflow—The NextSeq 1000 and NextSeq 2000 Sequencing Systems provide a comprehensive workflow that includes user-friendly run setup, the widest ecosystem of compatible library prep kits, load-and-go operation, and integrated, onboard secondary analysis.

Simplified analysis, flexible options

The NextSeq 1000 and NextSeq 2000 systems offer access to onboard, local, and cloud-based analysis software, giving users the flexibility to analyze data in a manner that meets their needs.

Fast analysis with the onboard DRAGEN™ Bio-IT Platform

The onboard DRAGEN (Dynamic Read Analysis for GENomics) Bio-IT Platform offers an ultrarapid, accurate solution for secondary analysis. The DRAGEN platform uses optimized, hardware-accelerated algorithms for a wide variety of genomic analysis solutions, including base call (BCL) file conversion, compression, mapping, alignment, sorting, duplicate marking, and variant calling. New pipelines will be made available for a variety of new and emerging applications. The onboard solution provides access to select DRAGEN informatics pipelines (Table 3), enabling users to generate results in as little as two hours. DRAGEN informatics use best-in-class pipeline algorithms to help novice and expert users overcome bottlenecks in data analysis and reduce reliance on external informatics experts. Users spend less time and effort running production-level pipelines and can focus more on results.

An ecosystem of apps in BaseSpace Sequence Hub

Users who prefer to use a cloud-based analysis solution can do so with BaseSpace Sequence Hub, a genomics cloud-computing platform that brings simplified data management and analytical sequencing tools directly to researchers in a user-friendly format. In the cloud, users can access a wide selection of bioinformatics tools, and share data globally. Data generated using the NextSeq 1000 and NextSeq 2000 systems is compatible with industry-standard formats for convenient import into the solution of choice.

Table 3: Push-button DRAGEN informatics pipelines integrated into the NextSeq 1000 and NextSeq 2000 systems

Pipeline[a]	Applications	Key functionality
DRAGEN Enrichment	• Whole-exome sequencing • Targeted resequencing	• Alignment • Small variant calling • Germline and somatic (tumor only) modes • Structural variant (SV) calling • Custom manifest files
DRAGEN RNA	• Whole-transcriptome gene expression • Gene fusion detection	• Alignment • Fusion detection • Gene expression • Differential expression
DRAGEN Single-Cell RNA	• Single-cell whole-transcriptome sequencing	• Cell barcodes and error correction • Alignment • Gene expression • Cell filtering • Basic reporting and visualization
DRAGEN ORA[b] Compression	• Compression of FASTQ files	• Lossless compression • Up to 5× reduction in file size
DRAGEN Germline	• Whole-genome sequencing	• Alignment • Small variant calling • SV/CNV[c] calling • Repeat expansion[c] • Regions of homozygosity[c] • CYP2D6 genotyping[c]
DRAGEN Amplicon[d]	• DNA amplicon panels • Targeted resequencing	• Alignment • Small variant calling • Germline and somatic (tumor only) modes

a. Additional DRAGEN informatics pipelines are available in the cloud; visit illumina.com/DRAGEN for a complete list
b. ORA, original read archive
c. Feature available for human genomes only; CNV, copy number variant
d. Supported for DNA samples only; available beginning with DRAGEN v3.8

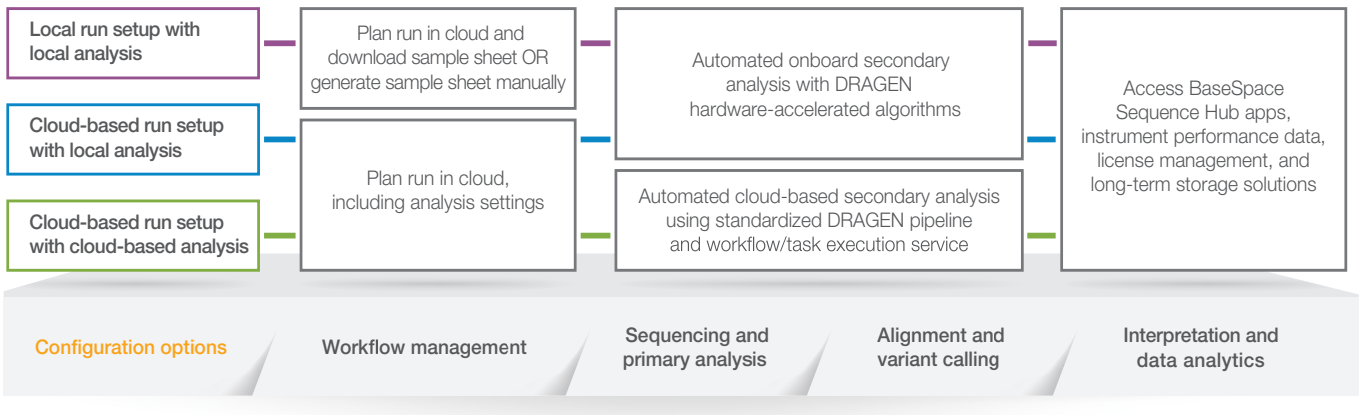

Figure 3: Flexible informatics suite—The NextSeq 1000 and NextSeq 2000 systems feature both local and cloud-based options for run setup, run management, and data analysis, enabling users to run their sequencing their way.

Modular construction for simpler, faster support

The NextSeq 1000 and NextSeq 2000 systems are built in a modular fashion, simplifying service and support. Onboard sensors monitor system performance and alert users to possible issues. Troubleshooting and repairs are easier for the service engineer to perform, ultimately saving time and reducing frustration.

World-class service for more sample control and reduced downtime

Illumina Proactive is a secure and remote instrument performance support service designed to detect risk failure preemptively, troubleshoot runs more efficiently, and prevent in-run failures. The service helps minimize unplanned downtime and avoid unnecessary sample loss by anticipating repairs and alerting Illumina field personnel to schedule maintenance visits.

Capacity for breakthroughs, support to sustain them

To help you maximize investment, support peak performance, and minimize interruptions, Illumina provides a world-class support team comprised of experienced scientists who are experts in library prep, sequencing, and analysis. This dedicated team includes highly qualified field service engineers (FSE), technical applications scientists (TAS), field application scientists (FAS), system support engineers, bioinformaticians, and IT network experts, all deeply familiar with next-generation sequencing and the applications that Illumina customers perform around the globe. Technical support is available via phone 5 days a week or access online support 24/7, worldwide and in multiple languages. Either way, support teams are available when you need them.

Each system purchase includes a one-year service warranty. Comprehensive maintenance, repair, and qualification solutions are also available. In addition, Illumina offers on-site training, ongoing support, phone consults, webinars, and courses at various Illumina locations globally. We're here with all the resources you need to accelerate progress.

Join the world's largest genomics ecosystem

With > 17,000 active systems, Illumina is setting the standard for NGS solutions. Joining this community provides access to a large ecosystem of applications, protocols, and informatics that have been built in collaboration with thousands of researchers and industry thought leaders across the globe.

Scale for the future while driving efficiencies today

Illumina has a proven track record of producing genomics solutions that empower researchers to perform studies at the throughput, scale, and price meeting their research objectives. With two systems and three flow cell configurations to choose from, users can select the data output requirements suitable to their needs. The NextSeq 2000 system provides higher throughput options to meet the needs of new and emerging applications while achieving better run economics for current applications. The NextSeq 1000 system has lower throughput relative to the NextSeq 2000 system and is available at a lower system price. To ensure flexible future scalability, customers who purchase a NextSeq 1000 system can easily upgrade to the NextSeq 2000 system.

Summary

The NextSeq 1000 and NextSeq 2000 Sequencing Systems revolutionize what can be accomplished with a benchtop sequencing system. With improved technology, advanced chemistry, simplified workflows, and onboard secondary analysis, researchers will have unprecedented flexibility to seek, and discover, more.

Learn more

NextSeq 1000 and NextSeq 2000 Sequencing Systems, illumina.com/NextSeq2000

Ordering information

Product	Catalog no.
NextSeq 2000 Sequencing System	20038897
NextSeq 1000 Sequencing System	20038898
NextSeq 1000 to NextSeq 2000 upgrade	20047256
NextSeq 1000/2000 P1 Reagents (300 cycles)	20050264
NextSeq 1000/2000 P2 Reagents (100 cycles)	20046811
NextSeq 1000/2000 P2 Reagents (200 cycles)	20046812
NextSeq 1000/2000 P2 Reagents (300 cycles)	20046813
NextSeq 2000 P3 Reagents (50 cycles)	20046810
NextSeq 2000 P3 Reagents (100 cycles)	20040559
NextSeq 2000 P3 Reagents (200 cycles)	20040560
NextSeq 1000/2000 Read and Index Primers	20046115
NextSeq 1000/2000 Index Primer Kit	20046116
NextSeq 1000/2000 Read Primer Kit	20046117

NextSeq 1000 and NextSeq 2000 system specifications

Specifications
Instrument configuration Self-contained, dry instrument with integrated DRAGEN Bio-IT field-programmable gate array (FPGA) secondary analysis
Instrument control computer Base Unit: 2U Microserver located inside the instrument Memory: 288 GB Hard Drive: 3.8 TB SSD Operating System: Linux CentOS 7.6
Operating environment Temperature: 15°C-30°C Humidity: 20%-80% relative humidity, non-condensing Altitude: 0 meters-2000 meters For Indoor Use Only
Laser Wavelengths: 449 nm, 523 nm, 820nm Safety: Class 1 Laser Product
Dimensions W × D × H: 60 cm × 65 cm × 60 cm Weight: 141 kg **Crated Dimensions** Crated W × D × H: 92 cm × 120 cm × 118 cm Crated Weight: 232 kg
Power requirements Instrument Input Voltage: 100 VAC to 240 VAC Instrument Input Frequency: 50/60 Hz
Bandwidth for network connection 200 Mb/s/instrument for internal network uploads 200 Mb/s/instrument for BaseSpace Sequence Hub uploads 5 Mb/s/instrument for Instrument Operational Data uploads
Product safety and compliance NRTL certified IEC 61010-1 CE marked FCC/IC approved

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