MiSeq® System

Focused power. Speed and simplicity for targeted and small-genome sequencing.

MiSeq System Highlights

- **Exceptional data quality**
  Highest quality data demonstrated through peer-reviewed, scientific comparison
- **Simple and intuitive instrument workflow**
  Highly automated system features a simple, easy-to-use instrument interface
- **Fastest turnaround time**
  Most rapid sequencing and variant detection for time-critical studies
- **Optimized for key applications**
  Adjustable read length and flow cell options provide ultimate flexibility across a broad range of applications

Introduction

The MiSeq system offers the first end-to-end sequencing solution, integrating cluster generation, amplification, sequencing, and data analysis into a single instrument. Its small footprint—approximately two square feet—fits easily into virtually any laboratory environment (Figure 1). The MiSeq system employs Illumina sequencing by synthesis technology (SBS), the most widely used, proven next-generation sequencing chemistry with over 4,800 publications to date, making it the ideal platform for any lab seeking to perform rapid and cost-effective genetic analysis.

Exceptional Data Quality

Illumina's sequencing by synthesis chemistry is the most widely adopted next-generation sequencing technology. Exceptional data quality is acheived by a proprietary, reversible terminator-based method that detects single bases as they are incorporated into massively parallel DNA strands. Fluorescent terminator dyes are imaged as each dNTP is added and then cleaved to allow incorporation of the next base. With all four reversible, terminator-bound dNTPs present during each cycle, natural competition minimizes incorporation bias. Base calls are made directly from signal intensity measurements during each cycle, greatly reducing raw error rates compared to other technologies.[1–5] The end result is highly accurate base-by-base sequencing that virtually eliminates sequence context-specific errors, even within repetitive sequence regions or homopolymers. Illumina sequencing—powered by TruSeq technology—delivers the highest yield of error-free data for the most sensitive or complex sequencing samples (Figure 3).

Simple and Intuitive Instrument Workflow

The MiSeq system offers straightforward, easy-to-follow instrument control software. Perform simple instrument operations with an intuitive touch screen interface, use plug-and-play reagent cartridges with RFID tracking, consult on-screen video tutorials, and enjoy step-by-step guides throughout each sequencing workflow.

All MiSeq systems include access to BaseSpace®—Illumina's genomic analysis cloud platform. BaseSpace provides real-time data uploading, simple data analysis tools, internet-based run monitoring, and a secure, scalable storage solution. A suite of data analysis tools, as well as a growing list of third-party BaseSpace Apps, empowers researchers to perform their own informatics. BaseSpace also enables fast and easy data sharing with colleagues or customers (learn more at www.illumina.com/basespace).

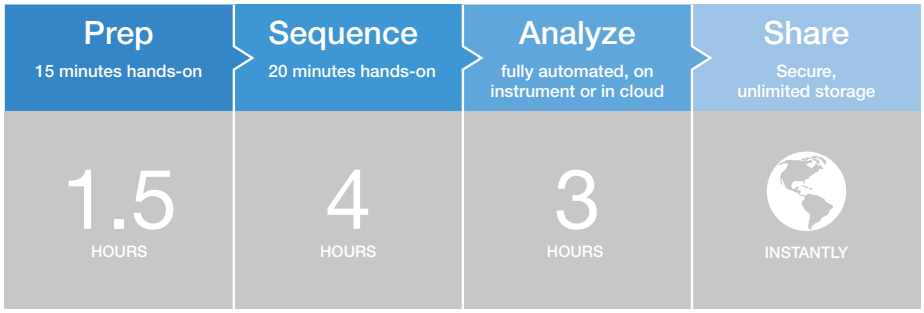
Fastest Turnaround Time

For results in hours rather than days, the combination of rapid sample preparation and the MiSeq system delivers the simplest and fastest turnaround time of any next-generation desktop sequencing system (Figure 2). Prepare your sequencing library in just 90 minutes with Nextera® sample prep reagents, then move to automated clonal amplification, sequencing, and quality-scored basecalling in as little as four hours on the MiSeq instrument. Variant calling and sequence alignment can be completed directly on the integrated instrument computer or in the BaseSpace cloud within three hours.

Figure 1: MiSeq System

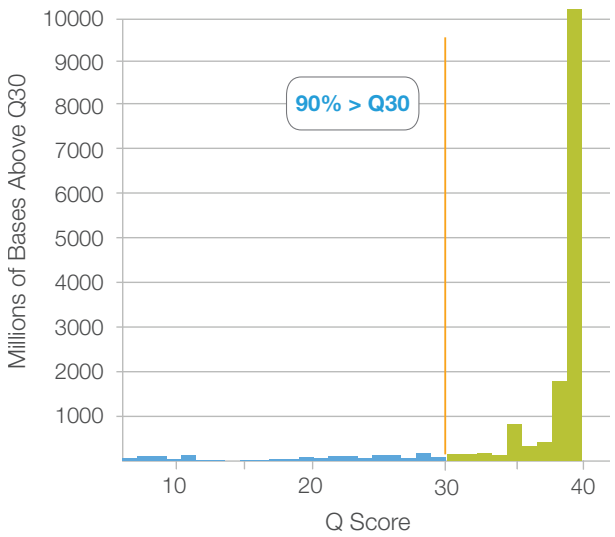
Illumina's compact MiSeq system is well suited for rapid, cost-effective next-generation sequencing.

Figure 2: MiSeq Workflow



The MiSeq system's revolutionary workflow enables very fast turnaround time among next-generation desktop sequencing systems. Samples were prepared with the Nextera XT sample prep kit. Four-hour sequence time includes cluster generation, sequencing, and quality-scored basecalling with dual surface scanning for a 1 × 36 base pair run on a MiSeq system with MCS 2.4.

Figure 3: MiSeq Quality Score Distribution



Quality scores for a PhiX control library, 2 × 300 base pair run on a MiSeq System with MCS 2.4. This example shows 90% of bases sequenced above Q30.

Optimized for Key Applications

Explore an ever-increasing range of sequencing applications. With its faster turnaround time and simplified workflows, the MiSeq offers a cost-effective alternative to capillary electrophoresis (CE) for applications such as clone checking, amplicon sequencing, and targeted transcript sequencing. Optimized analysis workflows are also available for small genome resequencing, *de novo* sequencing, small RNA sequencing, library QC, 16S metagenomics studies, as well as highly multiplexed applications such as TruSeq Custom Amplicon and TruSeq Custom Enrichment. Adjustable read lengths, flow cell options, and choice of single or paired-end reads allow unprecedented flexibility for matching data output to a broad range of experimental needs.

MiSeq System Specifications

Instrument Configuration
RFID tracking for consumables
MiSeq Control Software
MiSeq Reporter Software

Instrument Control Computer (Internal)*
Base Unit: Intel Core i7-2710QE 2.10 GHz CPU
Memory: 16 GB RAM
Hard Drive: 750 GB
Operating System: Windows 7 embedded standard
*Computer specifications are subject to change.

Operating Environment
Temperature: 22°C ± 3°C
Humidity: Non-condensing 20%–80%
Altitude: Less than 2,000 m (6,500 ft)
Air Quality: Pollution degree rating of II
Ventilation: Maximum of 1,364 BTU/h
For Indoor Use Only

Light Emitting Diode (LED)
530 nm, 660 nm

Dimensions
W×D×H: 68.6 cm × 56.5 cm × 52.3 cm (27.0 in × 22.2 in × 20.6 in)
Weight: 54.5 kg (120 lbs)
Crated Weight: 90.9 kg (200 lbs)

Power Requirements
100–240V AC @ 50/60Hz, 10A, 400W

Radio Frequency Identifier (RFID)
Frequency: 13.56 MHz
Power: 100 mW

Product Safety and Compliance
NRTL certified IEC 61010-1
CE marked
FCC/IC approved

MiSeq System Performance Parameters

MiSeq Reagent Kit v2

Read Length	Total Time*	Output
1 × 36 bp	~4 hours	540–610 Mb
2 × 25 bp	~5.5 hours	750–850 Mb
2 × 150 bp	~24 hours	4.5–5.1 Gb
2 × 250 bp	~39 hours	7.5–8.5 Gb

Reads Passing Filter†

Single Reads	12–15 M
Paired-End Reads	24–30 M

Quality Scores††

> 90% bases higher than Q30 at 1 × 36 bp
> 90% bases higher than Q30 at 2 × 25 bp
> 80% bases higher than Q30 at 2 × 150 bp
> 75% bases higher than Q30 at 2 × 250 bp

MiSeq Reagent Kit v3

Read Length	Total Time*	Output
2 × 75 bp	~21 hours	3.3–3.8 Gb
2 × 300 bp	~56 hours	13.2–15 Gb

Reads Passing Filter†

Single Reads	22–25 M
Paired-End Reads	44–50 M

Quality Scores††

> 85% bases higher than Q30 at 2 × 75 bp
> 70% bases higher than Q30 at 2 × 300 bp

* Total times include cluster generation, sequencing, and basecalling on a MiSeq system enabled with dual surface scanning.

† Install specifications based on Illumina PhiX control library at supported cluster densities between 467-583 k/mm2 clusters passing filter for v2 chemistry and 727-827 k/mm2 clusters passing filter for v3 chemistry. Actual performance parameters may vary based on sample type, sample quality, and clusters passing filter.

†† The percentage of bases > Q30 is averaged across the entire run.

bp = base pairs, Mb = megabases, Gb = gigabases, M = millions

Learn More

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

Ordering Information

Instrument Name	Catalog No.
MiSeq System	SY-410-1003

References

1. Junemann S, Sedlazeck FJ, Prior K, Albersmeier A, Uwe J, et al. (2013) Updating benchtop sequencing performance comparison. Nat Biotechnol 31:294–296.
2. Ross MG, Russ C, Costello M, Hollinger A, Lennon NJ, et al. (2013) Characterizing and measuring bias in sequence data. Gen Biol 14:R51.
3. Loman NJ, Misra RV, Dallman TJ, Constantinidou C, Gharbia SE, et al. (2012) Performance comparison of benchtop high-throughput sequencing platforms. Nat Biotechnol 30:434-439.
4. Quail MA, Smith M, Coupland P, Otto TD, Harris SR, et al. (2012) A tale of three next generation sequencing platforms: comparison of Ion Torrent, Pacific Biosciences and Illumina MiSeq sequencers. BMC Genomics 13:341.
5. Liu L, Li Y, Li S, Hu N, He Y, et al. (2012) Comparison of Next-Generation sequencing systems. J Biomed Biotechnol 2012:251364.

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

FOR RESEARCH USE ONLY

Pub. No. 770-2011-001 Current as of 27 May 2014

illumina®

AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
TCAACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTT
CGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACC
AACGTACCATTAAGAGCTACCGTGCAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAA
AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
GATTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGAGC
CGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAAAAGAATGATAACAGTA