illumina®

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 2 square feet—fits easily into virtually any laboratory environment (Figure 1). The MiSeq System leverages Illumina sequencing by synthesis technology (SBS), the most widely used, next-generation sequencing chemistry. With over 4,800 publications to date, the MiSeq System is the ideal platform for rapid and cost-effective genetic analysis.

Exceptional Data Quality

Illumina SBS chemistry is the most widely adopted next-generation sequencing technology. Exceptional data quality is achieved by SBS chemistry: 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 4 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 result is highly accurate base-by-base sequencing that virtually eliminates sequence context-specific errors, even within repetitive sequence regions or homopolymers. Illumina sequencing 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®— the Illumina 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, and 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. To learn more, visit www.illumina.com/basespace.

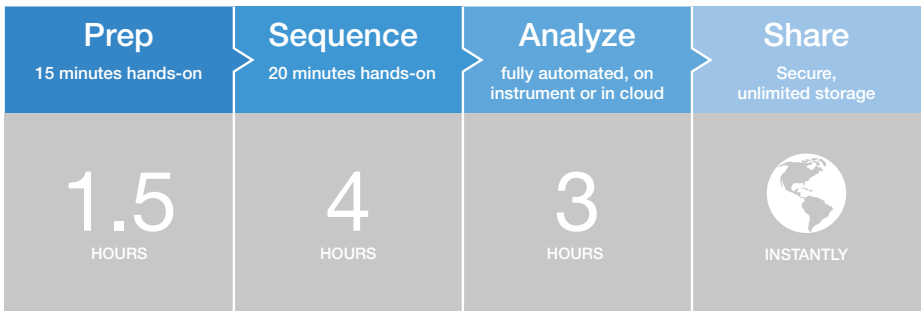
Fastest Turnaround Time

For results in hours rather than days, the combination of rapid library 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® library prep reagents, then move to automated clonal amplification, sequencing, and quality-scored base calling in as little as 4 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 3 hours.

Figure 1: MiSeq System

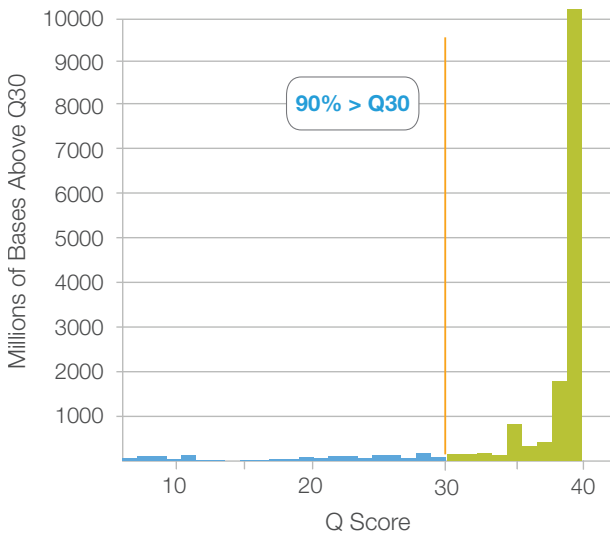
The compact MiSeq System is well suited for rapid, cost-effective next-generation sequencing.

Figure 2: MiSeq Workflow



The revolutionary workflow of the MiSeq System enables fast turnaround time among next-generation desktop sequencing systems. Samples were prepared with the Nextera XT library prep kit. Four-hour sequence time includes cluster generation, sequencing, and quality-scored base calling 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 faster turnaround time and simplified workflows, the MiSeq System 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: Noncondensing 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, 400 W

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 base calling on a MiSeq system enabled with dual surface scanning.

† Install specifications based on Illumina PhiX control library at supported cluster densities between 865–965 k/mm^2 clusters passing filter for v2 chemistry and 1200–1400 k/mm^2 clusters passing filter for v3 chemistry. Actual performance parameters can 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, John U, Kalinowski J, et al. Updating benchtop sequencing performance comparison. *Nat Biotechnol*. 2013;31:294-296.
2. Ross MG, Russ C, Costello M, Hollinger A, Lennon NJ, Hegarty R, et al. Characterizing and measuring bias in sequence data. *Gen Biol*. 2013;14:R51.
3. Loman NJ, Misra RV, Dallman TJ, Constantinidou C, Gharbia SE, Wain J, et al. Performance comparison of benchtop high-throughput sequencing platforms. *Nat Biotechnol*. 2012;30:434-439.
4. Quail MA, Smith M, Coupland P, Otto TD, Harris SR, Connor TR, et al. A tale of three next generation sequencing platforms: comparison of Ion Torrent, Pacific Biosciences and Illumina MiSeq sequencers. *BMC Genomics*. 2012;13:341.
5. Liu L, Li Y, Li S, Hu N, He Y, Pong R, et al. Comparison of Next-Generation sequencing systems. *J Biomed Biotechnol*. 2012;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. Not for use in diagnostic procedures.

© 2015 Illumina, Inc. All rights reserved. Illumina, BaseSpace, MiSeq, Nextera, TruSeq, and the pumpkin orange color are trademarks or registered trademarks of Illumina, Inc and/or its affiliates in the U.S. and/or other countries.
Pub. No. 770-2011-001 Current as of 23 April 2015

illumina®

AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
TCAACGTACCGTAACGAACGTATCATTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTT
CGACGAAAAGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACC
AACGTACCATTAAGAGCTACCGTGCAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGACGAAAAGAATGATAA
AGAATGATAACAGTAACACACTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAAC
GATTACTTGATCCACTGATTCAACGTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGCTTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAGCAACGACG
CGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGTCTGTTAACCTTAAGATTACTTGATCCACTGATTCAACGTACCGTAACGAACGTATCAATTGAGACTAAATATTAACGTACCATTAAGAGCTACCGTGCAACGAAAAGAATGATAACAGTA