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MiSeq™ System

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

Highlights

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

Figure 1: MiSeq System—The compact MiSeq System is well suited for rapid, cost-effective next-generation sequencing.

Introduction

The MiSeq System offers the first DNA-to-data sequencing platform, 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 leverages Illumina sequencing by synthesis (SBS) technology, the most widely used, next-generation sequencing chemistry worldwide.[1] With the power of next-generation sequencing (NGS) delivered in a compact footprint, the MiSeq System is the ideal platform for rapid and cost-effective genetic analysis.

Simple, intuitive instrument workflow

The MiSeq System offers straightforward, easy-to-follow instrument control software. Perform 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 guidance throughout each sequencing workflow. All MiSeq Systems include onboard data analysis and access to BaseSpace™ Sequence Hub— the Illumina genomic analysis 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 analysis apps empowers researchers to perform their own informatics. BaseSpace also enables fast and easy data sharing with colleagues or customers.

Fast turnaround time

For results in hours rather than days, the combination of rapid library preparation and the MiSeq System delivers a simple, accelerated turnaround time (Figure 2). Prepare your sequencing library in just 90 minutes with Nextera™ XT library prep reagents, then move to automated clonal amplification, sequencing, and quality-scored base calling in as little as 5.5 hours on the MiSeq
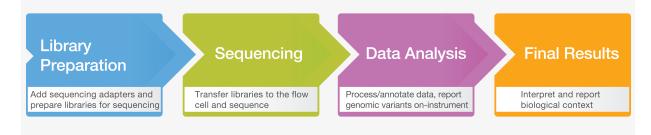
Library Preparation	Sequencing	Data Analysis	Final Results
Add sequencing adapters and prepare libraries for sequencing	Transfer libraries to the flow cell and sequence	Process/annotate data, report genomic variants on-instrument	Interpret and report biological context

Figure 2: MiSeq Workflow—The streamlined workflow of the MiSeq System enables rapid turnaround time for next-generation benchtop sequencing. Libraries can be prepared with any Nextera library preparation kit. Five and a half hour sequence time includes cluster generation, sequencing, and quality-scored base calling with dual surface scanning for a 2 × 25 base pair run on a MiSeq System with MiSeq Control Software.

Table 1: MiSeq System performance parameters

Read length	Total time[a]	Output	Quality scores[b]	Single reads[c]	Paired-end reads[c]
MiSeq Reagent Kit v2					
2 × 25 bp	~5.5 hours	750-850 Mb	>90% bases higher than Q30	12-15 M	24–30 M
2 × 150 bp	~24 hours	4.5-5.1 Gb	>80% bases higher than Q30		
2 × 250 bp	~39 hours	7.5-8.5 Gb	>75% bases higher than Q30		
MiSeq Reagent Kit v3					
2 × 75 bp	~21 hours	3.3-3.8 Gb	>85% bases higher than Q30	22-25 M	44-50 M
2 × 300 bp	~56 hours	13.2-15 Gb	>70% bases higher than Q30		
MiSeq Reagent Kit v2 Micro					
2 × 150 bp	~19 hours	1.2 Gb		4 M	8 M
MiSeq Reagent Kit v2 Nano					
2 × 150 bp	~17 hours	300 Mb		1 M	2 M
2 × 250 bp	~28 hours	500 Mb			

a. Total times include cluster generation, sequencing, and base calling on a MiSeq System enabled with dual surface scanning.
b. The percentage of bases > Q30 is averaged across the entire run.
c. Install specifications based on Illumina PhiX control library at supported cluster densities between 467-583 k/mm^2 clusters passing filter for v2 chemistry and 727-827 k/mm^2 clusters passing filter for v3 chemistry. Actual performance parameters may vary based on library type, library quality, and clusters passing filter.

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

instrument. Sequence alignment can be completed directly on the onboard instrument computer with MiSeq Local Run Manager software or through BaseSpace Sequence Hub within three hours.

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 enables the massively parallel sequencing of billions of DNA fragments, detecting single bases as they are incorporated into growing 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. The result is highly accurate base-by-base sequencing that virtually eliminates sequence context-specific errors, even within repetitive sequence regions or homopolymers (Figure 3).[2]

Extensive suite of 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 sequencing by capillary electrophoresis and qPCR for applications such as targeted resequencing, clone checking, amplicon sequencing, and RNA expression. Local Run Manager Software and BaseSpace Sequence Hub offer optimized analysis workflows for small

genome sequencing, 16S metagenomics, RNA sequencing, targeted resequencing, and preimplantation genetic screening (PGS), as well as highly multiplexed applications such as AmpliSeq™ for Illumina. 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.
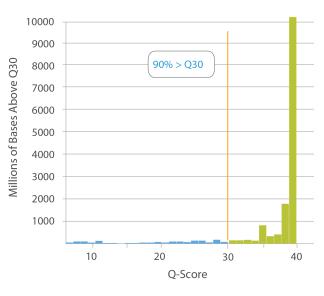

Figure 3: MiSeq quality score distribution—Quality scores for a PhiX control library, 2 × 300 base pair run on a MiSeq System with MiSeq Control Software v2.4. This example shows 90% of bases sequenced above Q30.

Table 2: MiSeq System specifications

Parameter	Specifications
Instrument Configuration	RFID tracking for consumables MiSeq Control Software Local Run Manager Software
Instrument Control Computer (Internal)[a]	Base Unit: Intel Core i7-2710QE 2.10 GHz CPU Memory: 16 GB RAM Hard Drive: 750 GB Operating System: Windows 7 embedded standard
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: 57.2 kg (126 lbs) Crated Weight: 93.6 kg (206 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

a. Computer specifications are subject to change.

Ordering Information

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

Learn More

To learn more about the MiSeq System, visit
www.illumina.com/systems/sequencing-platforms/miseq.html.

References

1. Data calculations on file. Illumina, Inc., 2015..
2. Bentley DR, Balasubramanian S, Swerdlow HP, et al. Accurate Whole Human Genome Sequencing using Reversible Terminator Chemistry. *Nature*. 2008;456(7218):53-59.

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