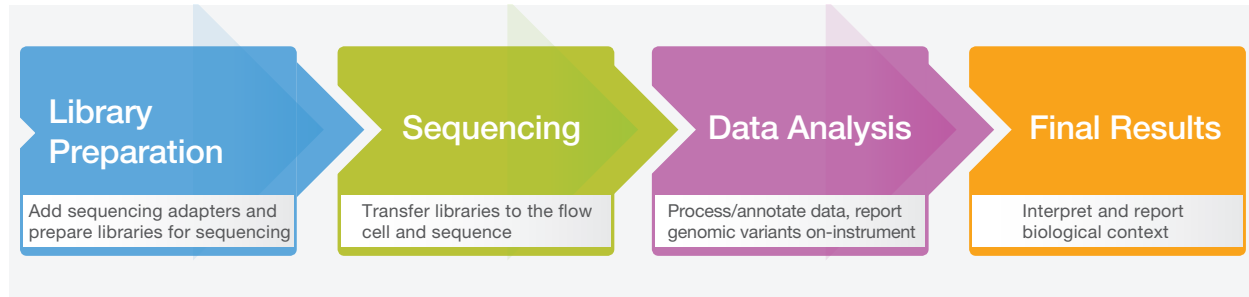
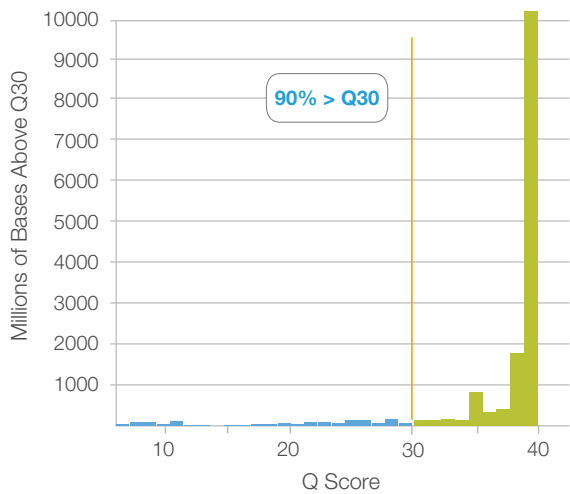


Figure 2: MiSeq Workflow



The revolutionary workflow of the MiSeq System enables rapid turnaround time for next-generation desktop sequencing. 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 x 36 base pair run on a MiSeq system with MiSeq Control Software v2.4.

Figure 3: MiSeq Quality Score Distribution



Quality scores for a PhiX control library, 2 x 300 base pair run on a MiSeq System with MiSeq Control Software v2.4. This example shows 90% of bases sequenced above Q30.

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 capillary electrophoresis (CE) for applications such as targeted resequencing, clone checking, and amplicon sequencing. Optimized analysis workflows are also available for small genome sequencing, 16S metagenomics, RNA sequencing, HLA sequencing, forensics, preimplantation genetic screening (PGS), and preimplantation genetic diagnosis (PGD), 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

WxDxH: 68.6 cm x 56.5 cm x 52.3 cm (27.0 in x 22.2 in x 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

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/mm² clusters passing filter for v2 chemistry and 1200–1400 k/mm² 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

Ordering Information

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

Learn More

To learn more about the next revolution in desktop sequencing, visit:
www.illumina.com/miseq

References

- 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.
- 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.
- 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.
- 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.
- 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.

Maximize Performance and Productivity with Illumina Services, Training, and Consulting

Whether immediate help is needed during an instrument run, or in-depth consultations are required for sophisticated workflows, Illumina can help. Illumina service and support teams provide a full suite of expedient, customized solutions from initial trainings, to instrument support, and ongoing NGS consultation. Our support offerings include:

Product Care Services

- Tiered Instrument Service Plans + Add-On Services
- Instrument Compliance Services
- Instrument On-Demand Services

Illumina University Training

- Instructor-Led Training at Your Chosen Facility
- Instructor-Led Training at an Illumina Training Center
- Online Courses and Webinars

Illumina Consulting

- Proof-of-Concept Services for instrument and library preparation testing
- Concierge Services for design assistance and product optimization

For more on Illumina support offerings, visit: www.illumina.com/services/instrument-services-training.html



