

HiSeq System Performance Parameters

High-Output Run Mode				Rapid-Run Mode			
Read Length	Dual Flow Cell	Single Flow Cell	Dual Flow Cell Run Time	Read Length	Dual Flow Cell	Single Flow Cell	Dual Flow Cell Run Time
1 x 36	128–144 Gb	64–72 Gb	29 hours	1 x 36	18–22 Gb	9–11 Gb	7 hours
2 x 50	360–400 Gb	180–200 Gb	2.5 days	2 x 50	50–60 Gb	25–30 Gb	16 hours
2 x 100	720–800 Gb	360–400 Gb	5 days	2 x 100	100–120 Gb	50–60 Gb	27 hours
2 x 125*	900 Gb–1 Tb	450–500 Gb	6 days	2 x 150	150–180 Gb	75–90 Gb	40 hours
				2 x 250*	250–300 Gb	125–150 Gb	60 hours
Reads Passing Filter†	Up to 4 billion	Up to 2 billion		Reads Passing Filter†	Up to 600 million	Up to 300 million	
Quality	≥ 85% of bases above Q30 at 2 x 50 bp ≥ 80% of bases above Q30 at 2 x 100 bp ≥ 80% of bases above Q30 at 2 x 125 bp			Quality	≥ 85% of bases above Q30 at 2 x 50 bp ≥ 80% of bases above Q30 at 2 x 100 bp ≥ 75% of bases above Q30 at 2 x 150 bp		

Install specifications based on Illumina PhiX control library at supported cluster densities (between 870–930 k clusters/mm² passing filter using HiSeq v4 or 700–820 K clusters/mm² passing filter using HiSeq Rapid v2 kits). Run times for rapid-run mode correspond to on-board cluster generation (1.5 hours) and sequencing; for high-output mode, run times correspond to sequencing only. Performance may vary based on sample quality, cluster density, and other experimental factors. *Maximum supported read length is 2 x 125 bp for high-output mode and 2 x 250 bp for rapid-run mode. †Single-end reads.

Simple Intuitive Instrument Control Software

The HiSeq 2500 features HiSeq Control Software (HCS): an easy-to-use, touchscreen-operated instrument control interface. With optimized step-by-step workflows, HCS guides you through experimental set-up, loading flow cells and reagents, flow-checks and post-run washes. Quality statistics from one or multiple runs can be monitored in real-time either on the instrument, from the lab, or from the comfort of your own home via BaseSpace on any browser.

Learn More

For more information about the HiSeq 2500 System, visit www.illumina.com/hiseq

To learn more about BaseSpace, visit www.illumina.com/software/basespace.ilmn

To see how Illumina fuels powerful science, visit www.illumina.com/science/publications.ilmn

References

- Nakazato T, Ohta T, Bono H. (2013) Experimental design-based functional mining and characterization of high-throughput sequencing data in the sequence read archive. *PLoS One* 22;8(10): e77910.
- Ross MG, Russ C, Costello M, Hollinger A, Lennon NJ, et al. (2013) Characterizing and measuring bias in sequence data. *Gen Biol* 14: R51.
- Liu L, Li Y, Li S, Hu N, He Y, et al. (2012) Comparison of next-generation sequencing systems. *J Biomed Biotechnol* 2012: 251364.

HiSeq 2500 System Specifications

Instrument Configuration

Computer and touch screen display
 Installation setup and accessories
 Data collection and analysis software

Instrument Control Computer

Base Unit: Intel® Xeon® CPU E5-2620 @ 2.00 GHz (2 processors)
 Memory: 64 GB RAM
 Hard Drive: 8 x 1.0 TB 3.5" Enterprise SATA (2 OS - RAID1 drives, 6 data RAID 5 drives)
 Operating System: Microsoft Windows 7

Note: Computer specifications will be regularly modified. Contact your local account manager for current configuration.

Operating Environment

Temperature: 22°C ± 3°C
 Humidity: Non-condensing 20%–80%
 Altitude: Less than 2000 m (6500 ft)
 Air Quality: Pollution degree rating of II
 Ventilation: Maximum of 4000 BTU/h
 For Indoor Use Only

Laser

532 nm, 660 nm, 650 nm (barcode reader)

Dimensions

WxDxH: 118.6 cm x 76.0 cm x 94.0 cm (46.7 in x 30.0 in x 37.0 in)
 Weight: 221.4 kg (488 lbs)
 Crated Weight: 312 kg (688 lbs)

Power Requirements

100–240V AC 50/60Hz, 20A, 1500 W
 Illumina provides a region-specific uninterruptible power supply for all HiSeq instruments

Product Safety

CE-marked and ETL-listed instrument

