

Part 1 of 4	Illumina info@illumina.com San Diego, CA 858-202-4500 www.illumina.com	Illumina info@illumina.com San Diego, CA 858-202-4500 www.illumina.com	Illumina info@illumina.com San Diego, CA 858-202-4500 www.illumina.com
For additional information about next-generation sequencing instruments, see www.greenarrowdx.com			
Name of instrument	iSeq 100 System	MiniSeq System	MiSeq System
Name of model/Model has been upgraded	—/no	—/no	—/no
Country where designed/Manufactured/FDA cleared or approved	U.S./Singapore/not required	U.S./Singapore/not required	U.S./U.S./not required
First year sold in U.S./Outside U.S./First year installed	2018/2018/2018	2016/2016/2016	2011/2011/2011
Dimensions in inches (H × W × D)/Footprint of all instrumentation and computing hardware	16.8 × 12 × 13/1.1 sq. ft.	20.4 × 18 × 18.9/2.4 sq. ft.	20.6 × 27 × 22.2/4.2 sq. ft.
Equipment supplied with system/Automation for library preparation	single unit inclusive of amplification, paired-end sequencing/yes	single unit inclusive of amplification, paired-end sequencing/yes	single unit inclusive of amplification, paired-end sequencing/yes
Necessary equipment not included with system (additional cost)	—	—	—
Bioinformatics tools provided/For use by biologist or bioinformatician	Local Run Manager, BaseSpace/biologist	Local Run Manager, BaseSpace/biologist	Local Run Manager, MiSeq Reporter, BaseSpace/biologist
Supplied with UPS/Entire workflow can occur in same lab	no/yes	no/yes	no/yes
Clean room requirements/Electrical connection	—/100–240 VAC at 50–60 Hz	—/100–240 VAC at 50–60 Hz	—/100–240 VAC at 50–60 Hz
List price/Total list price for equipment (not typically found in lab) needed to perform simplest and fastest workflow from amplification through variant calling	\$19,900/—	\$49,000/—	\$99,000/—
Purchase options	purchase	purchase, reagent rental, lease	purchase, reagent rental, lease (financing available)
Warranties offered	first year included with purchase, extended warranty available	first year included with purchase, extended warranty available	first year included with purchase, extended warranty available
Training included/Total time for standard install and basic training	no/customer installable, <1 day training	yes/<1 day installation, <1 day training	yes/<1 day installation, <1 day training
Training location/Follow-up training available	on site, off site/yes (extra charge)	on site/yes (extra charge)	on site/yes (extra charge)
Instrument core performance:			
Maximum No. of libraries amplified in single amplification event	384 samples (>384 samples with custom barcodes)	384 samples (>384 samples with custom barcodes)	384 samples (>384 samples with custom barcodes)
Read length/Percent bases >Q30	up to 2 × 150 bp/80%	up to 2 × 150 bp/80%	up to 2 × 300 bp/70% (for 2 × 300 bp)
Paired-end capability/Tag lengths/Spans	yes/up to 2 × 150 bp/up to 350 bp	yes/up to 2 × 150 bp/up to 350 bp	yes/up to 2 × 300 bp/up to 550 bp
Fragment/Tag lengths/Spans	yes/up to 2 × 150 bp/up to 350 bp	yes/up to 2 × 150 bp/up to 350 bp	yes/up to 2 × 300 bp/up to 550 bp
Mate pair/Tag lengths/Spans	yes/up to 2 × 150 bp/2–12 kb	yes/up to 2 × 150 bp/2–12 kb	yes/up to 2 × 150 bp/2–12 kb
Single end/Tag lengths/Spans	yes/up to 1 × 300 bp/up to 300 bp	yes/up to 1 × 300 bp/up to 300 bp	yes/up to 1 × 300 bp/up to 300 bp
RNA sequencing/Tag lengths/Spans	yes/up to 2 × 150 bp/up to 350 bp	yes/up to 2 × 150 bp/up to 350 bp	yes/up to 2 × 300 bp/up to 550 bp
ChIP sequencing/Tag lengths/Spans	yes/up to 2 × 150 bp/up to 350 bp	yes/up to 2 × 150 bp/up to 350 bp	yes/up to 2 × 300 bp/up to 550 bp
Bisulfite sequencing/Tag lengths/Spans	yes/up to 2 × 150 bp/up to 350 bp	yes/up to 2 × 150 bp/up to 350 bp	yes/up to 2 × 300 bp/up to 550 bp
Output per run	up to 1.2 Gb	up to 7.5 Gb	up to 15 Gb
Total time from library construction to variant calling to achieve output per run/Technical bench time/Bioinformatics time	9–19 hours (depends on read length; sequencing only)/<30 min. (sequencing only)/varies	7–24 hours (depends on read length; sequencing only)/<30 min. (sequencing only)/varies	4–56 hours (depends on read length; sequencing only)/<30 min. (sequencing only)/varies
Sample preparation:			
Total time for generating standard gDNA library	<3.5 hours (Illumina DNA Prep)	<3.5 hours (Illumina DNA Prep)	<3.5 hours (Illumina DNA Prep)
• Paired end	<3.5 hours (Illumina DNA Prep)	<3.5 hours (Illumina DNA Prep)	<3.5 hours (Illumina DNA Prep)
• Fragment	<7 hours (AmpliSeq for Illumina); <6.5 hours (Illumina DNA Prep with Enrichment)	<7 hours (AmpliSeq for Illumina); <6.5 hours (Illumina DNA Prep with Enrichment)	<7 hours (AmpliSeq for Illumina); <6.5 hours (Illumina DNA Prep with Enrichment)
• Mate pair	—	—	—
• Single end	<1 day (TruSeq Small RNA)	<1 day (TruSeq Small RNA)	<1 day (TruSeq Small RNA)
• RNA sequencing	<9 hours	<9 hours	<9 hours
• ChIP sequencing	<1.5 days (TruSeq ChIP)	<1.5 days (TruSeq ChIP)	<1.5 days (TruSeq ChIP)
• Bisulfite sequencing	—	—	—
Hands-on time each:			
• Paired end	<1.5 hours (Illumina DNA Prep)	<1.5 hours (Illumina DNA Prep)	<1.5 hours (Illumina DNA Prep)
• Fragment	<1.5 hours (AmpliSeq for Illumina); <2 hours (Illumina DNA Prep with Enrichment)	<1.5 hours (AmpliSeq for Illumina); <2 hours (Illumina DNA Prep with Enrichment)	<1.5 hours (AmpliSeq for Illumina); <2 hours (Illumina DNA Prep with Enrichment)
• Mate pair	—	—	—
• Single end	<4 hours (TruSeq Small RNA)	<4 hours (TruSeq Small RNA)	<4 hours (TruSeq Small RNA)
• RNA sequencing	<4.5 hours	<4.5 hours	<4.5 hours
• ChIP sequencing	—	—	—
• Bisulfite sequencing	—	—	—
Equipment required for library construction	standard lab equipment	standard lab equipment	standard lab equipment
Reagents and controls:			
Cost per run	\$495 (pricing based on iSeq 8-pack reagent kit)	\$615–\$1,725	\$325–\$1,705
Cost per sample*	—	—	—
Reagent tracking method on instrument	RFID	RFID	RFID
• Information tracked	serial number, expiration date, lot and part numbers, number of cycles	serial number, expiration date, lot and part numbers, number of cycles	serial number, expiration date, lot and part numbers, number of cycles
Reagent shipping conditions**/Storage conditions**	dry ice, ambient/cartridge: -15°– -25°C; flow cell: 2°–8°C	box 1: dry ice; box 2: gel pack/box 1: -15°– -25°C; box 2: 2°–8°C	box 1: dry ice; box 2: gel pack/box 1: -15°– -25°C; box 2: 2°–8°C
Shelf life of amplification and sequencing reagents	guaranteed 3 months (minimum)	guaranteed 3 months (minimum)	guaranteed 3 months (minimum)
Controls introduced during creation of library/Sequencing control avail.	yes/yes	yes/yes	yes/yes
Capable of complete walkaway automation for amplification, sequencing, and variant calling/Remote system monitoring	yes/yes	yes/yes	yes/yes
Instrument control software and devices to start run/for data analysis	iSeq Control/Local Run Manager, BaseSpace	MiniSeq Control/Local Run Manager, BaseSpace	MiSeq Control/Local Run Manager, MiSeq Reporter, BaseSpace
Total time required for setup of amplification, sequencing, and variant calling steps	5 minutes	10 minutes	10 minutes
Maximum No. of libraries sequenced in a single run	384 samples (>384 samples with custom barcodes)	384 samples (>384 samples with custom barcodes)	384 samples (>384 samples with custom barcodes)
Types of maintenance plans available	Advanced Exchange	parts only, bronze, silver, gold, dedicated on site	parts only, bronze, silver, gold, dedicated on site
No. of field application scientists and engineers based in U.S.	—	—	—
Maintenance required: weekly/monthly/prerun	none/none/none (post-run wash not necessary; fluidics discarded with cartridge)	none (manual wash if instrument idle for 7 days)/none/none (automatic wash completed after every run)	none (manual wash if instrument idle for 7 days)/maintenance wash/none (post-run wash required after every run)
System offers secondary data analysis software developed by instrument vendor	yes	yes	yes
Variant report can be generated on instrument	no	yes	yes
Data analysis software available	yes, BaseSpace	yes, BaseSpace	yes, BaseSpace
Ability of software to detect mutations	substitutions, indels, copy number changes	substitutions, indels, copy number changes	substitutions, indels, copy number changes
Total No. of peer-reviewed publications for this platform	—	—	>5,300 publications
Published applications in pathology-related research	—	—	—
Fastest published turnaround time from sample to analyzed result	—	—	1.5 days (Koser, et al.)
Lowest published variant sensitivity level	—	—	<5% (Harismendy, et al.)
Distinguishing features of sequencer (supplied by company)	lowest capital cost to obtain high accuracy results with Sequencing by Synthesis; low instrument footprint, clustering and sequencing all in one, analysis onboard or in the cloud; 19-hour run time for overnight results	affordable to acquire and cost-efficient to run, even with low numbers of samples; push-button operation and simple data analysis; based on industry's most-adopted sequencing technology	quality scores with >70% of bases higher than Q30 at 2 × 300 bp and >85% bases higher than Q30 at 2 × 75 bp; benchtop sequencer (per Loman, et al.) based on industry's most-adopted sequencing technology; simple, streamlined workflow with as little as 30 minutes hands-on time from sample to answer
<i>*inclusive of sample prep for multiple configurations, using 1 Mb and 30x average coverage per sample</i>			
<i>**for amplification and sequencing</i>			
<i>Note: a dash in lieu of an answer means company did not answer question or question is not applicable</i>			

Part 2 of 4	illumina info@illumina.com San Diego, CA 858-202-4500 www.illumina.com	illumina info@illumina.com San Diego, CA 858-202-4500 www.illumina.com	illumina info@illumina.com San Diego, CA 858-202-4500 www.illumina.com
For additional information about next-generation sequencing instruments, see www.greenarrowdx.com Name of instrument Name of model/Model has been upgraded Country where designed/Manufactured/FDA cleared or approved First year sold in U.S./Outside U.S./First year installed	MiSeqDx System —/no U.S./U.S./yes 2013/2013/2013	NextSeq 550 System —/no U.S./Singapore/not required NextSeq 500: 2014/2014/2014; NextSeq 550: 2015/2015/2015	NextSeq 550Dx System —/no U.S./Singapore/yes 2017/2017/2017
Dimensions in inches (H x W x D)/Footprint of all instrumentation and computing hardware Equipment supplied with system/Automation for library preparation Necessary equipment not included with system (additional cost) Bioinformatics tools provided/For use by biologist or bioinformatician Supplied with UPS/Entire workflow can occur in same lab Clean room requirements/Electrical connection	20.6 x 27 x 22.2/4.2 sq. ft. single unit inclusive of amplification, paired-end sequencing/yes — Local Run Manager, MiSeq Reporter, BaseSpace/biologist yes (extra charge)/yes —/100–240 VAC at 50–60 Hz	23 x 21 x 25/3.6 sq. ft. single unit inclusive of amplification, paired-end sequencing/yes — Local Run Manager, BaseSpace/biologist no/yes —/100–240 VAC at 50–60 Hz	23 x 21 x 25/3.6 sq. ft. single unit inclusive of amplification, paired-end sequencing/yes — Local Run Manager, BaseSpace/biologist no/yes —/100–120 VAC at 50–60 Hz
List price/Total list price for equipment (not typically found in lab) needed to perform simplest and fastest workflow from amplification through variant calling Purchase options Warranties offered	\$125,000/— purchase, reagent rental, lease (financing available) first year included with purchase, extended warranty available	\$275,000/— purchase, reagent rental, lease first year included with purchase, extended warranty available	\$347,000/— purchase first year included with purchase, extended warranty available
Training included/Total time for standard install and basic training Training location/Follow-up training available	yes/<1 day installation, <1 day training on site/yes (extra charge)	yes/1 day installation, 2 days training on site/yes (extra charge)	yes/1 day installation, 2 days training on site/yes (extra charge)
Instrument core performance: Maximum No. of libraries amplified in single amplification event Read length/Percent bases >Q30 Paired-end capability/Tag lengths/Spans Fragment/Tag lengths/Spans Mate pair/Tag lengths/Spans Single end/Tag lengths/Spans RNA sequencing/Tag lengths/Spans ChIP sequencing/Tag lengths/Spans Bisulfite sequencing/Tag lengths/Spans Output per run	384 samples (>384 samples with custom barcodes) up to 2 x 300 bp/80% (for 2 x 150 bp) yes/up to 2 x 300 bp/up to 550 bp yes/up to 2 x 300 bp/up to 550 bp yes/up to 2 x 150 bp/2–12 kb yes/up to 1 x 300 bp/up to 300 bp yes/up to 2 x 300 bp/up to 550 bp yes/up to 2 x 300 bp/up to 550 bp yes/up to 2 x 300 bp/up to 550 bp up to 15 Gb	384 samples (>384 samples with custom barcodes) up to 2 x 150 bp/75% yes/up to 2 x 150 bp/up to 350 bp yes/up to 2 x 150 bp/up to 350 bp yes/up to 2 x 150 bp/2–12 kb yes/up to 1 x 300 bp/up to 300 bp yes/up to 2 x 150 bp/up to 350 bp yes/up to 2 x 150 bp/up to 350 bp yes/up to 2 x 150 bp/up to 350 bp up to 120 Gb	384 samples (>384 samples with custom barcodes) up to 2 x 150 bp/75% yes/up to 2 x 150 bp/up to 350 bp yes/up to 2 x 150 bp/up to 350 bp yes/up to 2 x 150 bp/2–12 kb yes/up to 1 x 300 bp/up to 300 bp yes/up to 2 x 150 bp/up to 350 bp yes/up to 2 x 150 bp/up to 350 bp yes/up to 2 x 150 bp/up to 350 bp up to 120 Gb
Total time from library construction to variant calling to achieve output per run/Technical bench time/Bioinformatics time	4–56 hours (depends on read length; sequencing only)/<30 min. (sequencing only)/varies	11–29 hours (depends on read length; sequencing only)/<30 min. (sequencing only)/varies	11–29 hours (depends on read length; sequencing only)/<30 min. (sequencing only)/varies
Sample preparation: Total time for generating standard gDNA library • Paired end • Fragment • Mate pair • Single end • RNA sequencing • ChIP sequencing • Bisulfite sequencing Hands-on time each: • Paired end • Fragment • Mate pair • Single end • RNA sequencing • ChIP sequencing • Bisulfite sequencing Equipment required for library construction	<3.5 hours (Illumina DNA Prep) <3.5 hours (Illumina DNA Prep) <7 hours (AmpliSeq for Illumina); <6.5 hours (Illumina DNA Prep with Enrichment) — <1 day (TruSeq Small RNA) <9 hours <1.5 days (TruSeq ChIP) — <1.5 hours (Illumina DNA Prep) <1.5 hours (AmpliSeq for Illumina); <2 hours (Illumina DNA Prep with Enrichment) — <4 hours (TruSeq Small RNA) <4.5 hours — — standard lab equipment	<3.5 hours (Illumina DNA Prep) <3.5 hours (Illumina DNA Prep) <7 hours (AmpliSeq for Illumina); <6.5 hours (Illumina DNA Prep with Enrichment) — <1 day (TruSeq Small RNA) <9 hours <1.5 days (TruSeq ChIP) — <1.5 hours (Illumina DNA Prep) <1.5 hours (AmpliSeq for Illumina); <2 hours (Illumina DNA Prep with Enrichment) — <4 hours (TruSeq Small RNA) <4.5 hours — — standard lab equipment	<3.5 hours (Illumina DNA Prep) <3.5 hours (Illumina DNA Prep) <7 hours (AmpliSeq for Illumina); <6.5 hours (Illumina DNA Prep with Enrichment) — <1 day (TruSeq Small RNA) <9 hours <1.5 days (TruSeq ChIP) — <1.5 hours (Illumina DNA Prep) <1.5 hours (AmpliSeq for Illumina); <2 hours (Illumina DNA Prep with Enrichment) — <4 hours (TruSeq Small RNA) <4.5 hours — — standard lab equipment
Reagents and controls: Cost per run Cost per sample* Reagent tracking method on instrument • Information tracked Reagent shipping conditions**/Storage conditions** Shelf life of amplification and sequencing reagents Controls introduced during creation of library/Sequencing control avail.	\$2,205 — RFID serial number, expiration date, lot and part numbers, number of cycles box 1: dry ice; box 2: gel pack/box 1: -15°–-25°C; box 2: 2°–8°C guaranteed 3 months (minimum) yes/yes	\$1,205–\$5,065 — RFID serial number, expiration date, lot and part numbers, number of cycles dry ice, gel pack, ambient/reagent cartridge, HT1: -15°–-25°C; flow cell: 2°–8°C; buffer cartridge: 15°–30°C guaranteed 3 months (minimum) yes/yes	\$2,195–\$6,335 — RFID serial number, expiration date, lot and part numbers, number of cycles dry ice, gel pack, ambient/reagent cartridge, HT1: -15°–-25°C; flow cell: 2°–8°C; buffer cartridge: 15°–30°C guaranteed 6 months (minimum) yes/yes
Capable of complete walkaway automation for amplification, sequencing, and variant calling/Remote system monitoring Instrument control software and devices to start run/for data analysis Total time required for setup of amplification, sequencing, and variant calling steps Maximum No. of libraries sequenced in a single run Types of maintenance plans available	yes/yes MiSeq Control/Local Run Manager, MiSeq Reporter, BaseSpace 10 minutes 384 samples (>384 samples with custom barcodes) parts only, bronze, silver, gold, Dx, dedicated on site	yes/yes NextSeq Control/Local Run Manager, BaseSpace 10 minutes 384 samples (>384 samples with custom barcodes) parts only, bronze, silver, gold, dedicated on site	yes/yes NextSeq 550Dx Control, NextSeq 550Dx Operating/Local Run Manager, BaseSpace 10 minutes 384 samples (>384 samples with custom barcodes) parts only, bronze, silver, gold, dedicated on site
No. of field application scientists and engineers based in U.S. Maintenance required: weekly/monthly/prerun System offers secondary data analysis software developed by instrument vendor Variant report can be generated on instrument Data analysis software available Ability of software to detect mutations Total No. of peer-reviewed publications for this platform Published applications in pathology-related research Fastest published turnaround time from sample to analyzed result Lowest published variant sensitivity level	— none (manual wash if instrument idle for 7 days)/maintenance wash/none (post-run wash required after every run) yes yes yes, BaseSpace substitutions, indels, copy number changes >5,300 publications (MiSeq technology) — 1.5 days (Koser, et al.) <5% (Harismendy, et al.)	— none (manual wash if instrument idle for 2 weeks)/none/none (automatic wash completed after every run) yes yes yes, BaseSpace substitutions, indels, copy number changes >350 publications — — >5% (Siravegna, et al.)	— none (manual wash if instrument idle for 2 weeks)/none/none (automatic wash completed after every run) yes yes yes, BaseSpace substitutions, indels, copy number changes >350 publications (NextSeq technology) — — —
Distinguishing features of sequencer (supplied by company) *inclusive of sample prep for multiple configurations, using 1 Mb and 30x average coverage per sample **for amplification and sequencing Note: a dash in lieu of an answer means company did not answer question or question is not applicable	FDA-cleared NGS platform; available menu of FDA-cleared content including Extended RAS Panel, MiSeqDx Cystic Fibrosis 139-Variant Assay, MiSeqDx Cystic Fibrosis Clinical Sequencing Assay, MiSeqDx Universal Kit; leverages proven MiSeq technology, providing high-quality data and simple workflow on a single instrument	fast and simple workflow, powerful desktop sequencer capable of panels, exomes, RNA sequencing, and WGS; high-quality data with >75% bases higher than Q30 at 2 x 150 bp; ability to scan microarrays including the Infinium MethylationEPIC BeadChip and other select BeadChips	FDA-regulated NGS platform allows clinical diagnostics in Dx mode and clinical research applications in research mode; FDA-regulated content includes NextSeq 550Dx High-Output Reagent Kit v2, TruSeq Custom Amplicon Kit Dx, and FFPE QC Kit; flexible output for sample multiplexing and different research applications, from targeted panels to whole genome

Part 3 of 4	Illumina info@illumina.com San Diego, CA 858-202-4500 www.illumina.com	Illumina info@illumina.com San Diego, CA 858-202-4500 www.illumina.com	Illumina info@illumina.com San Diego, CA 858-202-4500 www.illumina.com
For additional information about next-generation sequencing instruments, see www.greenarrowdx.com			
Name of instrument	NextSeq 1000 System	NextSeq 2000 System	NovaSeq 6000 System
Name of model/Model has been upgraded	—/no	—/no	—/no
Country where designed/Manufactured/FDA cleared or approved	U.S./Singapore/not required	U.S./Singapore/not required	U.S./U.S./not required
First year sold in U.S./Outside U.S./First year installed	2020/2020/2020	2020/2020/2020	2017/2017/2017
Dimensions in inches (H × W × D)/Footprint of all instrumentation and computing hardware	23.6 × 23.6 × 25.6/3.9 sq. ft.	23.6 × 23.6 × 25.6/3.9 sq. ft.	65.2 × 31.5 × 37.2/8.2 sq. ft.
Equipment supplied with system/Automation for library preparation	single unit inclusive of amplification, paired-end sequencing/yes	single unit inclusive of amplification, paired-end sequencing/yes	single unit inclusive of amplification, paired-end sequencing/yes
Necessary equipment not included with system (additional cost)	—	—	—
Bioinformatics tools provided/For use by biologist or bioinformatician	onboard DRAGEN BIO-IT platform includes hardware and various analysis software pipelines	onboard DRAGEN BIO-IT platform includes hardware and various analysis software pipelines	BaseSpace/biologist; DRAGEN/bioinformatician
Supplied with UPS/Entire workflow can occur in same lab	yes/yes	yes/yes	yes/yes
Clean room requirements/Electrical connection	—/100–240 VAC at 50–60 Hz	—/100–240 VAC at 50–60 Hz	—/200–240 VAC at 50–60 Hz
List price/Total list price for equipment (not typically found in lab) needed to perform simplest and fastest workflow from amplification through variant calling	\$210,000/—	\$335,000/—	\$985,000/—
Purchase options	purchase, lease	purchase, lease	purchase, lease
Warranties offered	first year included with purchase, extended warranty available	first year included with purchase, extended warranty available	first year included with purchase, extended warranty available
Training included/Total time for standard install and basic training	yes/~8 hours installation, 1–2 days training	yes/~8 hours installation, 1–2 days training	yes/2 days installation, 2 days training
Training location/Follow-up training available	on site/yes (extra charge)	on site/yes (extra charge)	on site/yes (extra charge)
Instrument core performance:			
Maximum No. of libraries amplified in single amplification event	384	384	384 samples (>384 samples with custom barcodes)
Read length/Percent bases >Q30	up to 2 × 150 bp/75%	up to 2 × 150 bp/75%	up to 2 × 250 bp/75% (for 2 × 250 bp)
Paired-end capability/Tag lengths/Spans	yes/up to 2 × 150 bp/—	yes/up to 2 × 150 bp/—	yes/up to 2 × 250 bp/up to 550 bp
Fragment/Tag lengths/Spans	yes/up to 2 × 150 bp/—	yes/up to 2 × 150 bp/—	yes/up to 2 × 250 bp/up to 550 bp
Mate pair/Tag lengths/Spans	yes/up to 2 × 150 bp/—	yes/up to 2 × 150 bp/—	yes/up to 2 × 150 bp/2–12 kb
Single end/Tag lengths/Spans	yes/up to 2 × 150 bp/—	yes/up to 2 × 150 bp/—	yes/up to 1 × 300 bp/up to 350 bp
RNA sequencing/Tag lengths/Spans	yes/up to 2 × 150 bp/—	yes/up to 2 × 150 bp/—	yes/up to 2 × 250 bp/up to 550 bp
ChIP sequencing/Tag lengths/Spans	yes/up to 2 × 150 bp/—	yes/up to 2 × 150 bp/—	yes/up to 2 × 250 bp/up to 550 bp
Bisulfite sequencing/Tag lengths/Spans	yes/up to 2 × 150 bp/—	yes/up to 2 × 150 bp/—	yes/up to 2 × 250 bp/up to 550 bp
Output per run	up to 120 Gb	up to 330 Gb	up to 3,000 Gb
Total time from library construction to variant calling to achieve output per run/Technical bench time/Bioinformatics time	13–29 hours (depends on read length; sequencing only)/<30 min. (sequencing only)/<2 hours onboard analysis time	13–48 hours (depends on read length; sequencing only)/<30 min. (sequencing only)/<2 hours onboard analysis time	13–44 hours (depends on read length; sequencing only)/<30 min. (sequencing only)/varies
Sample preparation:			
Total time for generating standard gDNA library	<3.5 hours (Illumina DNA Prep)	<3.5 hours (Illumina DNA Prep)	<3.5 hours (Illumina DNA Prep)
• Paired end	<3.5 hours (Illumina DNA Prep)	<3.5 hours (Illumina DNA Prep)	<3.5 hours (Illumina DNA Prep)
• Fragment	<7 hours (AmpliSeq for Illumina); <6.5 hours (Illumina DNA Prep with Enrichment)	<7 hours (AmpliSeq for Illumina); <6.5 hours (Illumina DNA Prep with Enrichment)	<7 hours (AmpliSeq for Illumina); <6.5 hours (Illumina DNA Prep with Enrichment)
• Mate pair	—	—	—
• Single end	<1 day (TruSeq Small RNA)	<1 day (TruSeq Small RNA)	<1 day (TruSeq Small RNA)
• RNA sequencing	<9 hours	<9 hours	<9 hours
• ChIP sequencing	<1.5 days (TruSeq ChIP)	<1.5 days (TruSeq ChIP)	<1.5 days (TruSeq ChIP)
• Bisulfite sequencing	—	—	—
Hands-on time each:			
• Paired end	<1.5 hours (Illumina DNA Prep)	<1.5 hours (Illumina DNA Prep)	<1.5 hours (Illumina DNA Prep)
• Fragment	<1.5 hours (AmpliSeq for Illumina); <2 hours (Illumina DNA Prep with Enrichment)	<1.5 hours (AmpliSeq for Illumina); <2 hours (Illumina DNA Prep with Enrichment)	<1.5 hours (AmpliSeq for Illumina); <2 hours (Illumina DNA Prep with Enrichment)
• Mate pair	—	—	—
• Single end	<4 hours (TruSeq Small RNA)	<4 hours (TruSeq Small RNA)	<4 hours (TruSeq Small RNA)
• RNA sequencing	<4.5 hours	<4.5 hours	<4.5 hours
• ChIP sequencing	—	—	—
• Bisulfite sequencing	—	—	—
Equipment required for library construction	standard lab equipment	standard lab equipment	standard lab equipment
Reagents and controls:			
Cost per run	\$1,420–\$3,540	\$1,420–\$6,000	\$2,100–\$14,400
Cost per sample*	—	—	—
Reagent tracking method on instrument	RFID	RFID	RFID
• Information tracked	serial number, expiration date, lot and part numbers, number of cycles	serial number, expiration date, lot and part numbers, number of cycles	serial number, expiration date, lot and part numbers, number of cycles
Reagent shipping conditions**/Storage conditions**	dry ice, gel pack, ambient/-15°–-25°C; 2°–8°C; 15°–30°C	dry ice, gel pack, ambient/-15°–-25°C; 2°–8°C; 15°–30°C	dry ice, gel pack, ambient/cluster, SBS cartridges: -15°–-25°C; flow cell: 2°–8°C; buffer cartridge: 15°–30°C
Shelf life of amplification and sequencing reagents	guaranteed 3 months (minimum)	guaranteed 3 months (minimum)	guaranteed 3 months (minimum)
Controls introduced during creation of library/Sequencing control avail.	yes/yes	yes/yes	yes/yes
Capable of complete walkaway automation for amplification, sequencing, and variant calling/Remote system monitoring	yes/yes	yes/yes	yes/yes
Instrument control software and devices to start run/for data analysis	NextSeq Control/Local Run Manager, BaseSpace, DRAGEN	NextSeq Control/Local Run Manager, BaseSpace, DRAGEN	NovaSeq Control/BaseSpace, DRAGEN
Total time required for setup of amplification, sequencing, and variant calling steps	varies, minimum ~15 hours	varies, minimum ~15 hours	5–30 minutes
Maximum No. of libraries sequenced in a single run	384	384	384 samples (>384 samples with custom barcodes)
Types of maintenance plans available	parts only, bronze, silver, gold, dedicated on site	parts only, bronze, silver, gold, dedicated on site	parts only, bronze, silver, gold, dedicated on site
No. of field application scientists and engineers based in U.S.	—	—	—
Maintenance required: weekly/monthly/prerun	none/none/none (automatic wash completed after every run)	none/none/none (automatic wash completed after every run)	none (manual wash if instrument idle for 2 weeks)/none/none (automatic wash completed after every run)
System offers secondary data analysis software developed by instrument vendor	yes	yes	yes
Variant report can be generated on instrument	yes	yes	no
Data analysis software available	yes, BaseSpace, DRAGEN	yes, BaseSpace, DRAGEN	yes, BaseSpace, DRAGEN
Ability of software to detect mutations	substitutions, indels, copy number changes	substitutions, indels, copy number changes	substitutions, indels, copy number changes
Total No. of peer-reviewed publications for this platform	—	—	>2,900 publications
Published applications in pathology-related research	—	—	—
Fastest published turnaround time from sample to analyzed result	—	—	—
Lowest published variant sensitivity level	—	—	—
Distinguishing features of sequencer (supplied by company)	onboard DRAGEN BIO-IT informatics hardware/software for secondary analysis and FASTQ generation in <2 hours; dry instrument; fluid handling components contained within consumable cartridge reduces run-to-run contamination; up to 34% cost savings over NextSeq 500/550 run costs	onboard DRAGEN BIO-IT informatics hardware/software for secondary analysis and FASTQ generation in <2 hours; dry instrument; fluid handling components contained within consumable cartridge reduces run-to-run contamination; up to 50% cost savings over NextSeq 500/550 run costs	match data output, time to results, and price per sample to study needs; configure sequencing method, flow cell type, and read length to support a broad range of applications; increase lab efficiency with a simplified workflow and reduced hands-on time
<i>*inclusive of sample prep for multiple configurations, using 1 Mb and 30x average coverage per sample</i>			
<i>**for amplification and sequencing</i>			
<i>Note: a dash in lieu of an answer means company did not answer question or question is not applicable</i>			

Part 4 of 4	Thermo Fisher Scientific customerservice@thermofisher.com Carlsbad, CA 800-955-6288 www.thermofisher.com/genestudio	Thermo Fisher Scientific customerservice@thermofisher.com Carlsbad, CA 800-955-6288 www.thermofisher.com/pgmdx	Thermo Fisher Scientific customerservice@thermofisher.com Carlsbad, CA 800-955-6288 www.thermofisher.com/genexus
For additional information about next-generation sequencing instruments, see www.greenarrowdx.com			
Name of instrument	Ion GeneStudio S5 System	Ion PGM Dx System	Ion Torrent Genexus Integrated Sequencer A45727/no
Name of model/Model has been upgraded	—/no	—/no	—/no
Country where designed/Manufactured/FDA cleared or approved	U.S./U.S./—	U.S./Singapore/yes	U.S./Singapore/underway
First year sold in U.S./Outside U.S./First year installed	2018/2018/2018	2014/2014/2014	2019/2019/2019
Dimensions in inches (H x W x D)/Footprint of all instrumentation and computing hardware	21.3 x 31.7 x 20/—	21 x 24 x 20/8 sq. ft.	open: 81.1 x 58.5 x 43.5; closed: 66.1 x 41.9 x 32.1/open: 17.67 sq. ft.; closed: 9.36 sq. ft.
Equipment supplied with system/Automation for library preparation	Ion GeneStudio S5 sequencer/yes	Ion PGM Dx sequencer, Chip Minifuge, wireless scanner; Ion OneTouch Dx instrument, ES Dx instrument; Ion Torrent server with Ion PGM Dx Torrent Suite software/no	single unit inclusive of automated library preparation and amplification/yes
Necessary equipment not included with system (additional cost)	Ion Chef System for automated library and template prep, general laboratory supplies	Veriti Dx Thermal Cycler or equivalent	—
Bioinformatics tools provided/For use by biologist or bioinformatician	Torrent Suite, Ion Reporter, OncoPrint Reporter, Torrent Circuit/biologist	Torrent Suite Dx/both	sample management, assay management, run planning, results review, report generation/both
Supplied with UPS/Entire workflow can occur in same lab	no/yes	no/yes	no/yes
Clean room requirements/Electrical connection	none/100–240 VAC, 50–60 Hz, 6.5–14.5 A	none/60 Hz, 9 VA	—/100–240 VAC
List price/Total list price for equipment (not typically found in lab) needed to perform simplest and fastest workflow from amplification through variant calling	—	—/\$120,000	—
Purchase options	purchase, trade-in, lease (financing available)	purchase or lease (financing available)	purchase, trade-in, lease, reagent rental
Warranties offered	first year included with purchase, extended warranty available	first year included with purchase, extended warranty available	first year included with purchase, extended warranty available
Training included/Total time for standard install and basic training	yes/1 day	yes/~5 days	yes/6 days
Training location/Follow-up training available	on and off site/yes (extra charge)	on site/yes (extra charge)	on site/yes (extra charge)
Instrument core performance:			
Maximum No. of libraries amplified in single amplification event	384 (with custom barcodes)	16	96
Read length/Percent bases >Q30	up to 600 bp/—	up to 200 bp/—	up to 400 bp/—
Paired-end capability/Tag lengths/Spans	—	—	—
Fragment/Tag lengths/Spans	yes/—/up to 600 bp	yes/up to 200 bp/—	—
Mate pair/Tag lengths/Spans	yes/—/—	—	—
Single end/Tag lengths/Spans	yes/—/up to 400 bp	yes/up to 200 bp/—	—
RNA sequencing/Tag lengths/Spans	yes/—/up to 400 bp	—	—
ChIP sequencing/Tag lengths/Spans	—	—	—
Bisulfite sequencing/Tag lengths/Spans	yes/—/up to 400 bp	—	—
Output per run	20–25 Gb (Ion 550); 10–15 Gb (Ion 540); 3–4 Gb (Ion 530); 0.6–1 Gb (Ion 520); 0.3–0.5 Gb (Ion 510 chip)	up to 1 Gb; 200 bp workflow on Ion 318 Dx chip	—
Total time from library construction to variant calling to achieve output per run/Technical bench time/Bioinformatics time	<24 hours/<45 minutes/<1 hour	<2 days/<4.5 hours/<6 hours	14 hours/1 hour/5 minutes
Sample preparation:			
Total time for generating standard gDNA library	varies	<5 hours	—
• Paired end	—	—	—
• Fragment	4–6 hours	<5 hours	—
• Mate pair	2.5 days	—	—
• Single end	5–7 hours	<5 hours	—
• RNA sequencing	<6 hours	—	—
• ChIP sequencing	—	—	—
• Bisulfite sequencing	—	—	—
Hands-on time each:	varies	—	—
• Paired end	—	—	—
• Fragment	1 hour	<2 hours	—
• Mate pair	6 hours	—	—
• Single end	15 minutes	<2 hours	—
• RNA sequencing	1 hour (with Ion AmpliSeq Transcriptome)	—	—
• ChIP sequencing	—	—	—
• Bisulfite sequencing	15 minutes	—	—
Equipment required for library construction	Ion Chef System for Ion AmpliSeq libraries	Veriti Dx Thermal Cycler or equivalent	—
Reagents and controls:			
Cost per run	—	~\$2,250 on Ion 318 Dx chip for 16 samples	—
Cost per sample*	—	~\$140	—
Reagent tracking method on instrument	RFID	barcode reader	barcode reader
• Information tracked	expiration date, lot number, part number	expiration date, lot number, part number (with external barcode reader)	—
Reagent shipping conditions**/Storage conditions**	-20°C, 4°C, ambient/-20°C, 4°C, ambient	-20°C, 4°C, ambient/-20°C, 4°C, ambient	room temperature or on wet or dry ice/-30°–30°C
Shelf life of amplification and sequencing reagents	varies	1 year	14 days
Controls introduced during creation of library/Sequencing control avail.	yes/yes	yes/yes	yes/yes
Capable of complete walkaway automation for amplification, sequencing, and variant calling/Remote system monitoring	yes/yes	yes/yes	yes/yes
Instrument control software and devices to start run/for data analysis	Torrent Suite/Torrent Suite, Ion Reporter, OncoPrint Reporter	Torrent Suite Dx/Torrent Suite Dx	Genexus Software/Genexus Software
Total time required for setup of amplification, sequencing, and variant calling steps	<30 minutes	<4.5 hours	—
Maximum No. of libraries sequenced in a single run	384	up to 16	32, on instrument library prep; 96, off instrument library prep
Types of maintenance plans available	AB Assurance, AB Complete, AB Maintenance Plus, AB Maintenance Service	AB Assurance, AB Complete, AB Maintenance Plus, AB Maintenance Service	AB Complete, AB Assurance, AB Maintenance Plus, IQOQ
No. of field application scientists and engineers based in U.S.	—	—	116 field application scientists, 177 engineers
Maintenance required: weekly/monthly/prerun	none (post-run cleans automated)/none/initialization part of run setup	yes/—/run utilization	none (maintenance tasks are automatic)/none (maintenance tasks are automatic)/none
System offers secondary data analysis software developed by instrument vendor	yes	no	yes
Variant report can be generated on instrument	yes	no	yes
Data analysis software available	yes, Ion Reporter, OncoPrint Reporter	no	yes, Genexus Software
Ability of software to detect mutations	substitutions, indels, copy number changes	substitutions, indels	substitutions, indels, copy number changes
Total No. of peer-reviewed publications for this platform	>250	>845 based on RUO platform	>5
Published applications in pathology-related research	—	>195 based on RUO platform	0
Fastest published turnaround time from sample to analyzed result	<15 hours based on RUO platform	<15 hours based on RUO platform	14 hours
Lowest published variant sensitivity level	.01 fresh frozen; .02 FFPE based on RUO platform	.01 fresh frozen; .02 FFPE based on RUO platform	—
Distinguishing features of sequencer (supplied by company)	a single sequencer supports 2–130 million reads per run, enabling different throughput and application needs; fast turnaround DNA-to-data workflow (<24 hours) with minimal hands-on time (<45 minutes); start with as little as 1 ng FFPE DNA with Ion AmpliSeq technology	delivers highly reproducible, accurate genetic variant analysis with 10 ng of input DNA derived from whole blood coupled with highly multiplexed amplicon generation using Ion AmpliSeq technology (RUO); produces accurate long reads with >99% raw-read accuracy; speed and simplicity of Ion Torrent platform; affordable, flexible sequencer meets a range of applications, budgets, project sizes; rapid TAT from sample to variant analysis in <2 days; integrated secure software enables role-based workflows, supports tracking of samples to reagents management and variant analysis throughout each run; provides traceability and auditable run analysis, a necessary part of 21 CFR Part 11 compliance	automated workflow with 2 user touch points, 5 minutes hands-on time, sample to report in 14 hours; start with as little as 1 ng FFPE DNA input with automated Ion AmpliSeq library preparation; scalable reagent architecture allows for cost-efficient sequencing of small and large batches on one system
<i>*inclusive of sample prep for multiple configurations, using 1 Mb and 30x average coverage per sample</i>			
<i>**for amplification and sequencing</i>			
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