

NEXT-GENERATION SEQUENCING INSTRUMENTS

Part 1 of 5	Illumina info@illumina.com 5200 Illumina Way, San Diego, CA 92122 858-202-4500 www.illumina.com	Illumina info@illumina.com 5200 Illumina Way, San Diego, CA 92122 858-202-4500 www.illumina.com
See captodayonline.com/productguides for an interactive version of guide		
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	MiniSeq —/no U.S./Singapore/not required 2016/2016/2016	MiSeq —/no U.S./U.S./not required 2011/2011/2011
Dimensions in inches (H × W × D)/Footprint of all instrumentation and computing hardware Equipment supplied with system/Automation for library preparation Necessary equipment not included with system and additional cost Bioinformatics tools provided/For use by biologist or bioinformatician	20.4 × 18 × 18.9/2.4 square feet system is a single unit inclusive of amplification, paired-end sequencing, and analysis/yes — Local Run Manager/biologist; BaseSpace/biologist	20.6 × 27 × 22.2/~4.2 square feet system is a single unit inclusive of amplification, paired-end sequencing, and analysis/yes — MiSeq Reporter/biologist; BaseSpace/biologist
Supplied with UPS/Entire workflow can occur in same lab Clean room requirements/Electrical connection	no/yes —/100–240 VAC at 50–60 Hz	no/yes —/100–240 VAC at 50–60 Hz, 400 W
List price/Total list price for equipment needed to perform simplest and fastest workflow from amplification through variant calling (not typically found in lab) Purchase options Warranties offered Training included/Total time for standard install and basic training Training location/Follow-up training available	\$49,500/\$49,500 purchase, reagent rental, or lease first year included with instrument purchase, extended options available yes/<1 day on site/yes, extra charge	\$99,000/— purchase, reagent rental, or lease (financing available) first year included with instrument purchase, extended options available yes/<1 day on site/yes, extra charge
Instrument core performance:		
Maximum No. of libraries amplified in single amplification event	384 for some applications	384 for some applications
Read length/Percent bases >Q30	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 350 bp/2 × 150 bp	yes/up to 2 × 300 bp/200–550 bp
Fragment/Tag lengths/Spans	yes/up to 350 bp/2 × 150 bp	yes/up to 2 × 300 bp/200–550 bp
Mate-pair/Tag lengths/Spans	yes/up to 350 bp/2 × 150 bp	yes/up to 2 × 150 bp/3–15 kb
Single-end/Tag lengths/Spans	yes/up to 350 bp/2 × 150 bp	yes/1 × 600 bp/550 bp
RNA sequencing/Tag lengths/Spans	yes/up to 350 bp/2 × 150 bp	yes/up to 2 × 300 bp/100–300 bp
ChIP sequencing/Tag lengths/Spans	yes/up to 350 bp/2 × 150 bp	yes/up to 2 × 300 bp/100–300 bp
Bisulfite sequencing/Tag lengths/Spans	yes/up to 350 bp/2 × 150 bp	yes/2 × 300 bp/100–300 bp
Output per run	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	4–24 hours depending on read length/2 hours/2 hours	4–55 hours depending on read length/2 hours/2 hours
Sample preparation:		
Total time for generating standard gDNA library	<2 hours	<2 hours
• Paired-end	<2 hours	<2 hours
• Fragment	<2 hours	<2 hours
• Mate-pair	<2 days	<2 days
• Single-end	<2 hours	<2 hours
• RNA sequencing	<9 hours	<9 hours
• ChIP sequencing	<9 hours	<9 hours
• Bisulfite sequencing	5 hours	5 hours
Hands-on time each:		
• Paired-end	15 minutes	15 minutes
• Fragment	<3 hours	<3 hours
• Mate-pair	<2 hours	<2 hours
• Single-end	15 minutes	15 minutes
• RNA sequencing	<5.5 hours	<5.5 hours
• ChIP sequencing	<5.5 hours	<5.5 hours
• Bisulfite sequencing	3 hours	3 hours
Equipment required for library construction	standard lab equipment	standard lab equipment
Reagents and controls:		
Cost per run	\$550–\$1,545	\$290–\$1,530
Cost per sample*	—	—
Reagent tracking method on instrument	RFID	RFID
Information contained in tracking method	serial number, expiration date, lot and part numbers, number of cycles, PE-SR	serial number, expiration date, lot and part numbers, number of cycles, PE-SR
Reagent shipping conditions/Storage conditions	box 1: dry ice; box 2: gel pack/box 1: -15°–-20°C; box 2: 2°–8°C	box 1: dry ice; box 2: gel pack/box 1: -15°–-20°C; box 2: 2°–8°C
Shelf life of amplification and sequencing reagents	guaranteed 3 months	guaranteed 3 months
Controls introduced during creation of library/Sequencing control avail.	yes/yes	yes/yes
Capable of complete walkaway automation for amplification, sequencing, and variant calling/Remote system monitoring	yes/yes	yes/yes
Instrument control software and devices to start run/for data analysis	Local Run Manager/Local Run Manager	10 minutes/2 hours
Total time required for setup of amplification, sequencing, and variant calling steps	10 minutes	10 minutes
Maximum No. of libraries sequenced in a single run	384	up to 96 (384 for targeted RNA)
Types of maintenance plans available	parts only, basic, comprehensive, advantage, dedicated on site	parts only, basic, comprehensive, advantage, dedicated on site
No. of field apps scientists and engineers based in U.S.	—	—
Weekly maintenance required/Monthly/Pre-run	wash/wash/wash	water wash/water wash/water wash
System offers secondary analysis software developed by instrument vendor	yes	yes
Variant report generated directly on instrument	yes	yes
Third-party analysis software available	yes, BaseSpace apps store	yes, BaseSpace apps store
Ability of software to detect mutations	substitutions, indels, copy number changes	substitutions, indels, copy number changes
Total No. of peer-reviewed publications for this platform	8 publications total	>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 percent (Harismendy, et al.)
Distinguishing features of sequencer (supplied by company)	smallest benchtop sequencer available; based on industry's most-adopted sequencing technology; single instrument goes from prepared library through paired-end sequencing and analysis with no ancillary equipment	quality scores with >70% of bases higher than Q30 at 2 × 300 bp and >85% bases higher than Q30 at 2 × 75 bp and benchtop sequencer (per Loman, et al.) based on industry's most-adopted sequencing technology (>5,300 publications); single instrument takes samples from library prep through secondary analysis with no ancillary equipment needed; 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>Note: a dash in lieu of an answer means company did not answer question or question is not applicable</i>		

NEXT-GENERATION SEQUENCING INSTRUMENTS

Part 2 of 5	Illumina info@illumina.com 5200 Illumina Way, San Diego, CA 92122 858-202-4500 www.illumina.com	Illumina info@illumina.com 5200 Illumina Way, San Diego, CA 92122 858-202-4500 www.illumina.com
See captodayonline.com/productguides for an interactive version of guide		
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 —/no U.S./U.S./yes 2013/2013/2013	NextSeq 550 Sequencing System —/no U.S./Singapore/— NextSeq 500: 2014/2014/2014; NextSeq 550: 2015/2015/2015
Dimensions in inches (H × W × D)/Footprint of all instrumentation and computing hardware	20.6 × 27 × 22.2/~4.2 square feet	25 × 23 × 21/4 square feet
Equipment supplied with system/Automation for library preparation	system is a single unit inclusive of amplification, paired-end sequencing, and analysis/yes	system is inclusive for flowcell clustering and sequencing; library preparation and data analysis are done off board/yes
Necessary equipment not included with system and additional cost	—	BaseSpace (no charge), custom informatics pipeline (variable), general laboratory supplies
Bioinformatics tools provided/For use by biologist or bioinformatician	Local Run Manager/biologist; MiSeq Reporter/biologist; BaseSpace/biologist	BaseSpace/biologist
Supplied with UPS/Entire workflow can occur in same lab Clean room requirements/Electrical connection	yes, for extra charge/yes —/100–240 VAC at 50–60 Hz, 400 W	no/yes —/100–120 VAC 15 A or 220–240 VAC 10 A
List price/Total list price for equipment needed to perform simplest and fastest workflow from amplification through variant calling (not typically found in lab)	\$125,000/\$125,000	\$275,000/—
Purchase options Warranties offered Training included/Total time for standard install and basic training Training location/Follow-up training available	purchase, reagent rental, or lease (financing available) first year included with instrument purchase, extended options available yes/<1 day on site/yes, extra charge	purchase, reagent rental, lease first year included, extended options available yes/1 day install, 2 days training on site/yes, extra charge
Instrument core performance:		
Maximum No. of libraries amplified in single amplification event	384 for some applications	384 for some applications
Read length/Percent bases >Q30	up to 2 × 300 bp/70 (for 2 × 300 bp)	up to 150 bp/75
Paired-end capability/Tag lengths/Spans	yes/up to 2 × 300 bp/200–550 bp	yes/up to 550 bp/up to 2 × 150 bp
Fragment/Tag lengths/Spans	yes/up to 2 × 300 bp/200–550 bp	yes/up to 550 bp/up to 2 × 150 bp
Mate-pair/Tag lengths/Spans	yes/up to 2 × 150 bp/3–15 kb	yes/2–12 kb/up to 2 × 150 bp
Single-end/Tag lengths/Spans	yes/1 × 600 bp/550 bp	yes/up to 550 bp/up to 1 × 150 bp
RNA sequencing/Tag lengths/Spans	yes/up to 2 × 300 bp/100–300 bp	yes/up to 550 bp/up to 2 × 150 bp
ChIP sequencing/Tag lengths/Spans	yes/up to 2 × 300 bp/100–300 bp	yes/up to 550 bp/up to 2 × 150 bp
Bisulfite sequencing/Tag lengths/Spans	yes/up to 2 × 300 bp/100–300 bp	yes/up to 550 bp/up to 2 × 150 bp
Output per run	up to 15 Gb	20–120 Gb
Total time from library construction to variant calling to achieve output per run/Technical bench time/Bioinformatics time	4–55 hours depending on read length/2 hours/2 hours	22–45 hours depending on application/90 minutes–12 hours/ 30 minutes–12 hours
Sample preparation:		
Total time for generating standard gDNA library	<2 hours	<2 hours
• Paired-end	<2 hours	<2 hours
• Fragment	<2 hours	<2 hours
• Mate-pair	<2 days	<2 days
• Single-end	<2 hours	<2 hours
• RNA sequencing	<9 hours	<9 hours
• ChIP sequencing	<9 hours	<9 hours
• Bisulfite sequencing	5 hours	5 hours
Hands-on time each:		
• Paired-end	15 minutes	15 minutes
• Fragment	<3 hours	<3 hours
• Mate-pair	<2 hours	<2 hours
• Single-end	15 minutes	15 minutes
• RNA sequencing	<5.5 hours	<5.5 hours
• ChIP sequencing	<5.5 hours	<5.5 hours
• Bisulfite sequencing	3 hours	3 hours
Equipment required for library construction	standard lab equipment	standard lab equipment
Reagents and controls:		
Cost per run	\$545–\$3,600	\$1,060–\$4,450
Cost per sample*	—	—
Reagent tracking method on instrument Information contained in tracking method Reagent shipping conditions/Storage conditions Shelf life of amplification and sequencing reagents Controls introduced during creation of library/Sequencing control avail.	RFID serial number, expiration date, lot and part numbers, number of cycles, PE-SR box 1: dry ice; box 2: gel pack/box 1: -15°–-20°C; box 2: 2°–8°C guaranteed 3 months yes/yes	RFID serial number, expiration date, lot and part numbers, number of cycles dry ice, gel pack, or ambient/-20°C, 4°C, 25°C guaranteed 3 months 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	yes/yes 10 minutes/2 hours 10 minutes up to 384	yes/yes 10 minutes/5 minutes (performed off board in BaseSpace) 10 minutes 384
Types of maintenance plans available No. of field apps scientists and engineers based in U.S. Weekly maintenance required/Monthly/Pre-run	parts only, basic, comprehensive, advantage, Dx, dedicated on site — water wash/water wash/water wash	parts only, basic, comprehensive, advantage, dedicated on site — none/manual wash if instrument is idle for 2 weeks/none, automatic wash is completed after every run
System offers secondary analysis software developed by instrument vendor Variant report generated directly on instrument Third-party analysis software available Ability of software to detect mutations	yes yes yes, BaseSpace apps store substitutions, indels, copy number changes	yes no yes substitutions, indels, copy number changes
Total No. of peer-reviewed publications for this platform	>5,300 publications (MiSeq technology)	>340 publications using NextSeq Sequencing Systems; >11,000 publications using core Illumina sequencing chemistry
Published applications in pathology-related research Fastest published turnaround time from sample to analyzed result Lowest published variant sensitivity level	— 1.5 days (Koser, et al.) <5 percent (Harismendy, et al.)	— — >5 percent (Siravegna, et al.)
Distinguishing features of sequencer (supplied by company)	FDA-cleared NGS platform; available menu of FDA-cleared content including Extended RAS Panel, the MiSeqDx Cystic Fibrosis 139-Variant Assay, MiSeqDx Cystic Fibrosis Clinical Sequencing Assay, and the MiSeqDx Universal Kit v1.0; 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 whole-genome sequencing; mid- and high-output kits allow for flexibility in sample multiplexing based on coverage needs and applications; leverages the industry's most-adopted sequencing technology; generates high-quality data with >75% bases higher than Q30 at 2 × 150 bp
<i>*inclusive of sample prep, for multiple configurations, using 1 Mb and 30x average coverage per sample</i>		
<i>Note: a dash in lieu of an answer means company did not answer question or question is not applicable</i>		

NEXT-GENERATION SEQUENCING INSTRUMENTS

Part 3 of 5	Illumina info@illumina.com 5200 Illumina Way, San Diego, CA 92122 858-202-4500 www.illumina.com	Thermo Fisher Scientific Mauricio Minotta mauricio.minotta@thermofisher.com 5791 Van Allen Way, Carlsbad, CA 92008 760-929-2456 www.lifetechnologies.com
See captodayonline.com/productguides for an interactive version of guide		
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	NextSeq 550Dx Instrument —/no U.S./Singapore/yes 2017/2017/2017	Ion S5 and Ion S5 XL Systems —/no U.S./U.S./not required 2015/2015/2015
Dimensions in inches (H x W x D)/Footprint of all instrumentation and computing hardware	23 x 21 x 27/4 square feet	20 x 21.4 x 31.8/7.2 square feet
Equipment supplied with system/Automation for library preparation	system is inclusive for flowcell clustering, sequencing, and data analysis; library preparation is done off board/yes	Ion S5 Sequencer/yes
Necessary equipment not included with system and additional cost	general laboratory supplies (variable)	general laboratory supplies
Bioinformatics tools provided/For use by biologist or bioinformatician	Local Run Manager/biologist	Ion Reporter, Torrent Suite software, Torrent Circuit/biologist
Supplied with UPS/Entire workflow can occur in same lab Clean room requirements/Electrical connection	yes (extra charge)/yes —/100–120 VAC 15 A or 220–240 VAC 10 A	no/yes none/100–240 V, 14.5 A, 5060 Hz, 1350 W
List price/Total list price for equipment needed to perform simplest and fastest workflow from amplification through variant calling (not typically found in lab)	\$347,000/\$347,000	Ion S5: \$65,000; Ion S5 XL: \$150,000/\$120,000–\$170,000
Purchase options Warranties offered Training included/Total time for standard install and basic training Training location/Follow-up training available	purchase, reagent rental, or lease first year included, extended options available yes/1 day install, 2 days training on site/yes, extra charge	purchase or lease (financing available) 1 year included, extended warranty available yes/1 day on and off site/yes, extra charge
Instrument core performance:		
Maximum No. of libraries amplified in single amplification event	384 for some applications	384, with custom barcodes
Read length/Percent bases >Q30	up to 150 bp/75	up to 400 bp/—
Paired-end capability/Tag lengths/Spans	yes/up to 550 bp/up to 2 x 150 bp	—
Fragment/Tag lengths/Spans	yes/up to 550 bp/up to 2 x 150 bp	yes/—/up to 400 bp
Mate-pair/Tag lengths/Spans	yes/2–12 kb/up to 2 x 150 bp	yes/—/—
Single-end/Tag lengths/Spans	yes/up to 550 bp/up to 2 x 150 bp	yes/—/up to 400 bp
RNA sequencing/Tag lengths/Spans	yes/up to 550 bp/up to 2 x 150 bp	yes/—/up to 400 bp
ChIP sequencing/Tag lengths/Spans	yes/up to 550 bp/up to 2 x 150 bp	—
Bisulfite sequencing/Tag lengths/Spans	yes/up to 550 bp/up to 2 x 150 bp	—
Output per run	up to 120 Gb	0.6–2 Gb (Ion 520 chip), 3–8 Gb (Ion 530 chip), 10–15 Gb (Ion 540 chip)
Total time from library construction to variant calling to achieve output per run/Technical bench time/Bioinformatics time	22–45 hours depending on application/90 minutes–12 hours/ 30 minutes–12 hours	<24 hours/<45 minutes/<1 hour
Sample preparation:		
Total time for generating standard gDNA library	<2 hours	varies
• Paired-end	<2 hours	—
• Fragment	<2 hours	4–6 hours
• Mate-pair	<2 days	2.5 days
• Single-end	<2 hours	5–7 hours
• RNA sequencing	<9 hours	<6 hours
• ChIP sequencing	<9 hours	customer demonstrated
• Bisulfite sequencing	5 hours	customer demonstrated
Hands-on time each:		
• Paired-end	15 minutes	—
• Fragment	<3 hours	1 hour
• Mate-pair	<2 hours	6 hours
• Single-end	15 minutes	15 minutes
• RNA sequencing	<5.5 hours	1 hour with Ion AmpliSeq Transcriptome
• ChIP sequencing	<5.5 hours	—
• Bisulfite sequencing	3 hours	—
Equipment required for library construction	standard lab equipment	Ion Chef System for Ion AmpliSeq libraries, standard laboratory equipment
Reagents and controls:		
Cost per run	\$1,060–\$5,562	\$928 (Ion 520 chip), \$1,088 (Ion 530 chip), \$1,250 (Ion 540 chip)
Cost per sample*	—	varies
Reagent tracking method on instrument Information contained in tracking method Reagent shipping conditions/Storage conditions Shelf life of amplification and sequencing reagents Controls introduced during creation of library/Sequencing control avail.	RFID serial number, expiration date, lot and part numbers, number of cycles dry ice, gel pack, or ambient/-20°C, 4°C, 25°C guaranteed 3 months yes/yes	RFID expiration date, lot number, part number -20°C, 4°C, and ambient/-20°C, 4°C, and ambient varies 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	yes/yes 10 minutes/5 minutes 35 minutes up to 384	yes/yes Torrent Suite software/Torrent Suite software, Ion Reporter software <30 minutes 384
Types of maintenance plans available No. of field apps scientists and engineers based in U.S. Weekly maintenance required/Monthly/Pre-run	parts only, basic, comprehensive, advantage plan — none/manual wash if instrument is idle for 2 weeks/none, automatic wash is completed after every run	AB Assurance, AB Complete, AB Maintenance Plus, AB Maintenance Service — none required, post-run cleans are automated/none required/initialization is part of run setup
System offers secondary analysis software developed by instrument vendor Variant report generated directly on instrument Third-party analysis software available Ability of software to detect mutations	yes yes yes substitutions, indels, copy number changes	yes yes yes substitutions, indels, copy number changes
Total No. of peer-reviewed publications for this platform	>11,000 publications using Illumina sequencing chemistry	>1,600 for Ion sequencing
Published applications in pathology-related research Fastest published turnaround time from sample to analyzed result Lowest published variant sensitivity level	— — —	>300 <15 hours based on RUO platform .01 fresh frozen; .02 FFPE based on RUO platform
Distinguishing features of sequencer (supplied by company)	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	setting up a sequencing run requires less than 15 minutes of hands-on time on the Ion S5 Systems; start with as little as 1 ng FFPE DNA with Ion AmpliSeq technology; sequencing run time is as few as 2.5 hours for a 1 x 200 bp sequencing run
<i>*inclusive of sample prep, for multiple configurations, using 1 Mb and 30x average coverage per sample</i>		
<i>Note: a dash in lieu of an answer means company did not answer question or question is not applicable</i>		

NEXT-GENERATION SEQUENCING INSTRUMENTS

Part 4 of 5	Thermo Fisher Scientific customerservice@lifetech.com 5791 Van Allen Way, Carlsbad, CA 92008 800-955-6288 www.lifetechnologies.com	Thermo Fisher Scientific customerservice@lifetech.com 5791 Van Allen Way, Carlsbad, CA 92008 800-955-6288 www.lifetechnologies.com
See captodayonline.com/productguides for an interactive version of guide		
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	Ion PGM Dx System —/no U.S./Singapore/listed 2014/2014/2014	Ion Personal Genome Machine (PGM) System (RUO) 508-U001/yes U.S./U.S., Singapore/no 2010/2010/2010
Dimensions in inches (H x W x D)/Footprint of all instrumentation and computing hardware Equipment supplied with system/Automation for library preparation	21 x 24 x 20/8 square feet Ion PGM Dx Sequencer, Chip Minifuge, and Wireless Scanner; Ion OneTouch Dx Instrument and ES Dx Instrument; Ion Torrent Server with Ion PGM Dx Torrent Suite software/no	21 x 20 x 24/5 square feet Dell Precision T7500 Server/yes
Necessary equipment not included with system and 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	Veriti Dx Thermal Cycler (or equivalent) Ion PGM Dx Torrent Suite software/— no/yes no/60 Hz, 9 VA	general laboratory supplies Ion Reporter, Torrent Suite software, Torrent Circuit/biologist no/yes no/standard voltage 100–240 VAC, 50–60 Hz, 9 VA
List price/Total list price for equipment needed to perform simplest and fastest workflow from amplification through variant calling (not typically found in lab) Purchase options Warranties offered Training included/Total time for standard install and basic training Training location/Follow-up training available	—/\$115,000 purchase or lease (financing available) 1 year included, extended warranty available yes/~5 days on site/yes, extra charge	\$37,500/\$50,000 purchase or lease (financing available) 1 year included, extended warranty available yes/<2 days on and off site/yes, extra charge
Instrument core performance:		
Maximum No. of libraries amplified in single amplification event	16	384 samples, by employing custom barcoding
Read length/Percent bases >Q30	up to 200 bp/—	200 bp, 400 bp/Manfred
Paired-end capability/Tag lengths/Spans	—	—
Fragment/Tag lengths/Spans	yes/up to 200 bp/—	yes/200 bp, 400 bp/100–400 bp
Mate-pair/Tag lengths/Spans	—	yes/200 bp, 400 bp/100–400 bp
Single-end/Tag lengths/Spans	yes/up to 200 bp/—	yes/200 bp, 400 bp/100–400 bp
RNA sequencing/Tag lengths/Spans	—	yes/200 bp, 400 bp/100–400 bp
ChIP sequencing/Tag lengths/Spans	—	yes/200 bp, 400 bp/100–400 bp
Bisulfite sequencing/Tag lengths/Spans	—	no/customer demonstrated/100–400 bp
Output per run	up to 1Gb; 200 bp workflow on Ion 318 Dx chip	100 Mb (Ion 314 chip, 400 bp kit); 1Gb (Ion 316 chip, 400 bp kit); 2 Gb (Ion 318 chip, 400 bp kit)
Total time from library construction to variant calling to achieve output per run/Technical bench time/Bioinformatics time	<2 days/<4.5 hours/<6 hours	<1 day/<2 hours/20 minutes
Sample preparation:		
Total time for generating standard gDNA library	<5 hours	<2 hours
• Paired-end	—	—
• Fragment	<5 hours	<2 hours
• Mate-pair	—	2.5 days
• Single-end	<5 hours	<2 hours
• RNA sequencing	—	<6 hours
• ChIP sequencing	—	customer demonstrated
• Bisulfite sequencing	—	customer demonstrated
Hands-on time each:		
• Paired-end	—	—
• Fragment	<2 hours	~10 minutes (Ion AmpliSeq 2.0)
• Mate-pair	—	~6 hours
• Single-end	<2 hours	~10 minutes (Ion AmpliSeq 2.0)
• RNA sequencing	—	~40 minutes (whole transcriptome library, small RNA library); ~55 minutes for small RNA library with enrichment
• ChIP sequencing	—	customer demonstrated
• Bisulfite sequencing	—	—
Equipment required for library construction	Veriti Dx Thermal Cycler (or equivalent)	standard laboratory equipment
Reagents and controls:		
Cost per run	~\$2,250 on Ion 318 Dx chip for 16 samples	\$349 (Ion 314 chip), \$549 (Ion 316 chip), \$749 (Ion 318 chip)
Cost per sample*	~\$140	30x coverage, 200 bp: \$88.06 (Ion 318 chip), \$213.75 (Ion 316 chip), \$750.83 (Ion 314 chip)
Reagent tracking method on instrument	barcode reader	barcode reader
Information contained in tracking method	external barcode reader for sample and reagent tracking and expiration date, lot, and part numbers	external barcode reader for sample and reagent tracking information
Reagent shipping conditions/Storage conditions	-20°C, 4°C, and ambient/-20°C, 4°C, and ambient	-20°C, 4°C, and ambient/-20°C, 4°C, and ambient
Shelf life of amplification and sequencing reagents	1 year	9 months
Controls introduced during creation of library/Sequencing control avail.	yes/yes	yes/yes
Capable of complete walkaway automation for amplification, sequencing, and variant calling/Remote system monitoring	yes/yes	yes/yes
Instrument control software and devices to start run/for data analysis	~10 minutes/automated	10 minutes/20 minutes–4.5 hours (100 Mb–2 Gb)
Total time required for setup of amplification, sequencing, and variant calling steps	<4.5 hours	<30 minutes
Maximum No. of libraries sequenced in a single run	up to 16	384
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
No. of field apps scientists and engineers based in U.S.	—	—
Weekly maintenance required/Monthly/Pre-run	yes/—/run initialization	weekly cleaning/—/instrument initialization
System offers secondary analysis software developed by instrument vendor	no	yes
Variant report generated directly on instrument	no	yes
Third-party analysis software available	no	yes (AB Assurance, AB Complete, AB Maintenance Plus, AB Maintenance Service)
Ability of software to detect mutations	substitutions, indels	substitutions, indels, copy number changes, fusion transcript**
Total No. of peer-reviewed publications for this platform	>845 based on RUO platform	>845 based on RUO platform
Published applications in pathology-related research	>195 based on RUO platform	>195 based on RUO platform
Fastest published turnaround time from sample to analyzed result	<15 hours based on RUO platform	<15 hours based on RUO platform
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)	delivers highly reproducible and 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 more than 99% raw-read accuracy; provides the speed and simplicity of the Ion Torrent platform; affordable and flexible sequencer that meets a range of applications, budgets, and project sizes; provides rapid turnaround time from sample to variant analysis in <2 days; integrated secure software enables role-based workflows and 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	affordable, accurate, and flexible sequencer meets a range of research applications, budgets, project sizes, and input DNA amounts (as low as 10 ng of FFPE-derived sample) by employing scalable semiconductor technology (no laser or camera) with the Ion 3 series chips, coupled with highly multiplexed amplicon generation using Ion AmpliSeq technology; delivers fast run times, enabling a single-day workflow from sample to annotated variants for gene-panel sequencing featuring Ion AmpliSeq; produces accurate long reads with more than 99% raw-read accuracy; majority of bases at ≥Q30
*inclusive of sample prep, for multiple configurations, using 1 Mb and 30x average coverage per sample		
Note: a dash in lieu of an answer means company did not answer question or question is not applicable		**Ion Reporter

NEXT-GENERATION SEQUENCING INSTRUMENTS

Part 5 of 5	Thermo Fisher Scientific customerservice@lifetech.com 5791 Van Allen Way, Carlsbad, CA 92008 800-955-6288 www.lifetechnologies.com	Thermo Fisher Scientific customerservice@lifetech.com 5791 Van Allen Way, Carlsbad, CA 92008 800-955-6288 www.lifetechnologies.com
See captodayonline.com/productguides for an interactive version of guide		
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	Ion Proton System —/no U.S./U.S./no 2012/2012/2012	5500 Series Genetic Analyzers 5500, 5500xl, 5500xl Wildfire/— U.S., Japan/Japan/no 2011/2011/2011
Dimensions in inches (H × W × D)/Footprint of all instrumentation and computing hardware Equipment supplied with system/Automation for library preparation Necessary equipment not included with system and additional cost	34.5 × 29 × 38/14 square feet Torrent Suite Server, Ion OneTouch2, ES Station/yes general laboratory supplies	45.1 × 47.5 × 29.5/100 square feet 5500xl workstation, instruction control software, installation kit, training/yes Covaris S220 System: \$44,500; UPS: \$6,500; AB Library Builder system: \$35,000; LifeScope workstation or cluster (or cloud) \$22,500 or \$48,000, respectively; Thermocycler: \$5,000; SOLiD EZ Bead system (enricher, amplifier, emulsifier): \$60,000 (replaced by on-FlowChip template preparation on 5500xl Wildfire) BAM file generation, SAM file generation, LifeScope Genomics Analysis Solution/biologist yes, for extra charge/yes none/200–400 VAC
Bioinformatics tools provided/For use by biologist or bioinformatician Supplied with UPS/Entire workflow can occur in same lab Clean room requirements/Electrical connection	Torrent Suite software, Ion Reporter/biologist no/yes no/standard voltage	BAM file generation, SAM file generation, LifeScope Genomics Analysis Solution/biologist yes, for extra charge/yes none/200–400 VAC
List price/Total list price for equipment needed to perform simplest and fastest workflow from amplification through variant calling (not typically found in lab) Purchase options Warranties offered Training included/Total time for standard install and basic training Training location/Follow-up training available	\$225,000/— purchase or lease (financing available) 1 year included, extended warranty available yes/<2 days on and off site/yes, extra charge	\$595,000 (xl), \$349,000 (5500), \$250,000 (upgrade from SOLiD4)/\$350,000 — 1 year warranty yes/5 days on and off site/yes, extra charge
Instrument core performance:		
Maximum No. of libraries amplified in single amplification event	96	1,152
Read length/Percent bases >Q30	200 bp/>70	75 bp forward, 35 bp reverse/>85
Paired-end capability/Tag lengths/Spans	—	yes/75 bp × 35 bp/150–300 bp
Fragment/Tag lengths/Spans	yes/up to 200 bp/—	yes/75 bp/150–300 bp
Mate-pair/Tag lengths/Spans	yes/2 × 100 bp/up to 10 kb	yes/60 bp × 60 bp/0.5–10 kb supported; >10 kb enabled
Single-end/Tag lengths/Spans	yes/up to 200 bp/—	75 bp/<3 kb/—
RNA sequencing/Tag lengths/Spans	yes/up to 200 bp/—	yes/75 bp × 35 bp/150–200 bp
ChIP sequencing/Tag lengths/Spans	yes/up to 200 bp/—	yes/35–75 bp/150–300 bp
Bisulfite sequencing/Tag lengths/Spans	no/—/—	yes/75 bp/150–300 bp
Output per run	>10 Gb	240 Gb
Total time from library construction to variant calling to achieve output per run/Technical bench time/Bioinformatics time	<1 day/<4 hours/—	5–26 days (template prep: 2 hours on FlowChip, sequencing 2–21 days; data analysis: 2 days)/1–2 days/0.5–2 days
Sample preparation:		
Total time for generating standard gDNA library	<2 hours	—
• Paired-end	—	3 hours
• Fragment	<2 hours	3 hours
• Mate-pair	2.5 days	2–3 days
• Single-end	<2 hours	3 hours
• RNA sequencing	<6 hours	2 days or 3 hours post-RNA extraction
• ChIP sequencing	customer demonstrated	3 hours post ChIP
• Bisulfite sequencing	—	3 hours
Hands-on time each:		
• Paired-end	—	30 minutes
• Fragment	~15 minutes	30 minutes
• Mate-pair	~8 hours	8 hours
• Single-end	~15 minutes	30 minutes
• RNA sequencing	<1 hour	2 hours
• ChIP sequencing	customer demonstrated	30 minutes post ChIP
• Bisulfite sequencing	—	45 minutes
Equipment required for library construction	standard laboratory equipment	standard lab equip., magnetic bead separator, Covaris system, AB library building
Reagents and controls:		
Cost per run	varies based on application	\$2,000 5500xl Wildfire
Cost per sample*	varies based on application	1Mb, 200x to 2,000x coverage per sample, in one-lane run of multiplexed samples (includes library prep): \$116 (12 samples), \$108 (24 samples), \$104 (48 samples), \$102 (96 samples)
Reagent tracking method on instrument	yes	real-time reagent monitoring
Information contained in tracking method	—	current reagent volume predicted time to replenish reagents
Reagent shipping conditions/Storage conditions	ambient, 8°–20°C/ambient, 20°C	-20°C, 4°C, and ambient/-20°C, 4°C, and ambient
Shelf life of amplification and sequencing reagents	≥6 months	1 year
Controls introduced during creation of library/Sequencing control avail.	yes/yes	yes/no
Capable of complete walkaway automation for amplification, sequencing, and variant calling/Remote system monitoring	yes/yes	yes/yes
Instrument control software and devices to start run/for data analysis	10 minutes/7 hours	ICS on system workstation/LifeScope or cloud
Total time required for setup of amplification, sequencing, and variant calling steps	<1 hour	5–26 days
Maximum No. of libraries sequenced in a single run	384	1,152
Types of maintenance plans available	AB Assurance, AB Complete, AB Maintenance Plus, AB Maintenance Service	AB Assurance (fixed-price planned maintenance)
No. of field apps scientists and engineers based in U.S.	—	24 field applications scientists, 31 engineers
Weekly maintenance required/Monthly/Pre-run	chlorite cleaning/none/automated cleaning of instrument after run	—
System offers secondary analysis software developed by instrument vendor	yes	yes
Variant report generated directly on instrument	yes	no
Third-party analysis software available	yes, Partek, DNASTar, NextGene, Ingenuity, more	yes, Partek, SoftGenetics, GenoLogics, CLC Bio
Ability of software to detect mutations	substitutions, indels, copy number changes	substitutions, indels, copy number changes
Total No. of peer-reviewed publications for this platform	>845 based on RUO platform	225
Published applications in pathology-related research	>195 based on RUO platform	60 related publications
Fastest published turnaround time from sample to analyzed result	<15 hours based on RUO platform	3 months
Lowest published variant sensitivity level	25 percent	<1 percent
Distinguishing features of sequencer (supplied by company)	fast exome capture workflow leverages the power and simplicity of AmpliSeq target enrichment technology; competitive pricing matched with capacity means economical exomes; custom and fixed panels enable targeted resequencing technology; low input requirements (as little as 10 ng DNA or 500 pg total RNA) are compatible with FFPE samples; users can design custom panels tailored to their own research interests using a simple Web application, order consortium-developed targeted gene panels, or purchase ready-to-use gene panels	two-base encoding and exact call chemistry delivers 99.99% accuracy, which enables detection of low-frequency variants; pay-per-lane sequencing; application-per-lane sequencing
*inclusive of sample prep, for multiple configurations, using 1 Mb and 30x average coverage per sample		
Note: a dash in lieu of an answer means company did not answer question or question is not applicable		