Next-generation sequencing instruments

Part 1 of 3 *See* captodayonline.com/productguides *for an interactive version of guide*	**Illumina** **Laura Trotter** ltrotter@illumina.com **5200 Research Place, San Diego, CA 92121** **858-202-4500** www.illumina.com	**Ion Torrent, part of Life Technologies** customerservice@lifetech.com **7000 Shoreline Court, Suite 201, South San Francisco, CA 94080** **800-955-6288** www.lifetechnologies.com
Name of instrument	MiSeq	Ion Personal Genome Machine (PGM)
Name of model/Model has been upgraded	—/yes	508-U001/no
Country where designed/Manufactured/FDA-cleared or approved	U.S./U.S./underway	U.S./Singapore/pre-IDE submission
First year sold in U.S./Outside U.S./First year installed	2011/2011/2011	2010/2010/2010
Dimensions in inches (H × W × D)/Footprint of all instrumentation and computing hardware	20.6 × 27 × 22.2/~4.2 square feet	21 × 24 × 20/5 square feet
Equipment supplied with system/Automation for library preparation	system is a single unit inclusive of amplification, sequencing, paired-end, and analysis hardware/yes	Dell Precision T7500 Server/yes
Necessary equipment not included with system and additional cost	—	compressed nitrogen cylinder (for pressurizing the Ion PGM Sequencer): ~$70, Ion OneTouch System (automated template preparation): ~$14,500, Elga Purelab Flex 3 water purification system (fresh 18MΩ water) ~$5,000
Bioinformatics tools provided/For use by biologist or bioinformatician	MiSeq Reporter/biologist	Ion Reporter (biologist), Torrent Suite software (biologist), Torrent Circuit (biologist)
Supplied with UPS/Entire workflow can occur in same lab	no/yes	no/yes
Clean room requirements/Electrical connection	none/100–240 VAC at 50–60 Hz, 400 W	clean room always recommended for pre-amp steps/100–240 VAC, 50–60 Hz, 9 VA
List price/Total list price for equipment needed to perform simplest and fastest workflow from amplif through variant calling (not typically found in lab)	$125,000/—	$49,500/$49,500 (Ion PGM Sequencer), $16,500 (Torrent Server), $14,500 (Ion OneTouch System), $5,700 (Elga Purelab water purification system, plus nitrogen gas)
Purchase options	purchase, reagent rental, lease, financing	purchase, reagent rental, or lease (financing available)
Warranties offered	first year included with instrument purchase, extended options available	1-year included, extended warranty available
Training included/Total time for standard install and basic training	yes/~1.5 days	yes/install: 1 day; training: 2 days
Training location/Follow-up training available	on site/yes (extra charge)	on site and off site/yes, extra charge
Instrument core performance:		
Maximum No. of libraries amplified in single amplification event	up to 96 (dependent on Illumina sample preparation method used)	384 samples, by employing custom bar-coding
Read length/Percent bases >Q30	up to 2 × 150 bp/70	200+ bp, 300+ bp* (Q3 of 2012), 400+ bp (Q4 of 2012)*/75*
Paired-end capability/Tag lengths/Spans	yes/up to 2 × 250 bp/200–500 bp	yes/2 × 100 bp/~100–400*
Fragment/Tag lengths/Spans	yes/up to 2 × 250 bp/200–500 bp	yes/200 bp, 300 bp (Q3 of 2012)*, 400 bp (Q4 of 2012)*/~100–400*
Mate-pair/Tag lengths/Spans	yes/2 × 150 bp Q4 2012*/3–15 kb	yes/60 bp/~2–10 kb
Single-end/Tag lengths/Spans	yes/1 × 500 bp/500 bp	yes/200 bp, 300 bp (Q3 of 2012)*, 400 bp (Q4 of 2012)*/~100–400*
RNA sequencing/Tag lengths/Spans	yes/2 × 50 bp–2 × 100 bp/80–300 bp	yes/200 bp, 300 bp (Q3 of 2012)*, 400 bp (Q4 of 2012)*/~100–400*
ChIP sequencing/Tag lengths/Spans	yes/1 × 50 bp/100–300 bp	yes/200 bp, 300 bp (Q3 of 2012)*, 400 bp (Q4 of 2012)*/~100–400*
Bisulfite sequencing/Tag lengths/Spans	yes/2 × 50 bp–2 × 100 bp/100–300 bp	yes, customer demonstrated/~100–400*
Output per run	540–610 Mb for 1 × 36 bp, 7.5–8.5 Gb for 2 × 250 bp	20 Mb (Ion 314 chip, 200 bp kit); 200 Mb (Ion 316 chip, 200 bp kit); ≤1 Gb (Ion 318 chip, 200 bp kit)
Total time from library construction to variant calling to achieve output per run/Technical bench time/Bioinformatics time	~4 hours for 1 × 36 bp, ~39 hours for 2 × 250 bp using Nextera Library Prep/2 hours/2 hours	7–14 hours (35 to 300 bp*)/2 hours (library, template, PGM, Ion Chip preparation)/≤30 minutes
Sample preparation:		
Total time for generating standard gDNA library	<2 hours with Nextera, ~9 hours with TruSeq	<2 hours
• Paired-end	<2 hours with Nextera, ~9 hours with TruSeq	~3 hours
• Fragment	<2 hours with Nextera, ~9 hours with TruSeq	<2 hours
• Mate-pair	<2 days Q4 2012*	~18 hours
• Single-end	<2 hours with Nextera, ~9 hours with TruSeq	<2 hours
• RNA sequencing	<2 hours with Nextera, <= 2hours with TruSeq	~6 hours
• ChIP sequencing	<2 hours with Nextera, <= 2hours with TruSeq	customer demonstrated
• Bisulfite sequencing	~9 hours	customer demonstrated
Hands-on time each:		
• Paired-end	~15 minutes with Nextera, ~2.5 hours with TruSeq	~15 minutes (IonXpress Fragment), ~10 minutes (Ion AmpliSeq 2.0)
• Fragment	~15 minutes with Nextera, ~2.5 hours with TruSeq	~15 minutes (IonXpress Fragment), ~10 minutes (Ion AmpliSeq 2.0)
• Mate-pair	~4.5 hours	~6 hours
• Single-end	~15 minutes with Nextera, ~2.5 hours with TruSeq	~15 minutes (IonXpress Fragment), ~10 minutes (Ion AmpliSeq 2.0)
• RNA sequencing	2.5 hours	~40 minutes (whole transciptome library, small RNA library); ~55 minutes for small RNA library with enrichment
• ChIP sequencing	2.5 hours	customer demonstrated
• Bisulfite sequencing	~3 hours	customer demonstrated
Equipment required for library construction	standard lab equipment	if automation required, recommend AB Library Builder system
Reagents and controls:		
Cost per run	$695–$965	$349 (Ion 314 chip), $549 (Ion 316 chip), $749 (Ion 318 chip)
Cost per sample*	$63 (11 samples per 50-cycle kit) $35 (27 samples per 300-cycle kit)	30x coverage, 200 bp: $88.06 (Ion 318 chip), $213.75 (Ion 316 chip), $750.83 (Ion 314 chip)
Reagent tracking method on instrument	RFID	bar-code reader
Information contained in tracking method	serial No., expiration date, lot and part numbers, number of cycles, PE	external bar-code reader for sample and reagent tracking information
Reagent shipping conditions/Storage conditions	box 1: dry ice; box 2: gel pack/box 1: -15°– -25°C; box 2: 2°–8°C	-20°C, 4°C, and ambient/-20°C, 4°C, and ambient
Shelf life of amplification and sequencing reagents	at least 3 months of shelf life on shipped reagents	≤12 months
Controls introduced during creation of library/Sequencing control avail.	yes/yes	yes/yes
Capable of complete walkaway automation for amp, seq, var calling	yes	yes
Remote system monitoring	yes	yes
Instrument control software and devices to start run/for data analysis	10 minutes/2 hours	touchscreen user interface/Torrent Suite
Total time required for setup of amplification, sequencing, and variant calling steps	10 minutes	30 minutes
Maximum No. of libraries sequenced in a single run	up to 96	384
Types of maintenance plans available	parts only, standard, silver, and gold	AB Assurance, AB Complete, AB Maintenance Plus, AB Maintenance Service
No. of field apps scientists and engineers based in U.S.	—	field applications scientists: 40; engineers: 90
Weekly maintenance required/Monthly/Pre-run	weekly: post-run wash; monthly: post-run wash; pre-run: post-run wash	weekly: chlorite cleaning; monthly: none; pre-run: daily wash solution cleaning
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 or Avadis NGS	yes (DNAStar SoftGenetics, Partek, Avadis NGS, CLC Bio, Bio Team)
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	>3,200	22
Published applications in pathology-related research	—	8
Fastest published turnaround time from sample to analyzed result	1.5 days (Koser, et al.)	62 hours
Lowest published variant sensitivity level	somatic variations detected at 1.1 percent on MiSeq based on internal analysis; ~5 percent for published (Harismendy, et al.)	0.25–5.5 percent (Yang, et al.)
Distinguishing features of sequencer (supplied by company)	quality scores with >80 percent of bases higher than Q30 at 2 × 150 bp and >70 percent bases higher than Q30 at 2 × 250 bp and benchtop sequencer (per Loman, et al.) based on industry's most adopted sequencing technology (>3,200 publications); propietary Nextera and Nextera XT sample-preparation kits provide fast, easy, and low-input sample preparation; ability to multiplex samples: highly multiplexed amplicon sequencing-up to 1,536 targets per reaction, 96 samples per run with TruSeq custom Amplicon Assay; short hands-on time	flexibility to meet a range of applications, budgets, project sizes, and input DNA amounts (as low as 10 ng of FFPE-derived sample), by employing scalable semiconductor technology with the Ion 3 series chips, coupled with highly multiplexed amplicon generation using Ion AmpliSeq technology; delivers fast sequencing run times, while maintaining high accuracy, i.e., 30 minutes for 35 bp, 2 hours for 200+ bp, with concomitant Q30 (>99.9 percent) accuracy; high-throughput, low-cost capital acquisition; no optics, lasers, or cameras enables low maintanance and run costs **expected performance; product not officially released, information subject to change without notice*

**inclusive of sample preparation, 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

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Next-generation sequencing instruments

Part 2 of 3 *See* captodayonline.com/productguides *for an interactive version of guide*	**Ion Torrent, part of Life Technologies** customerservice@lifetech.com **7000 Shoreline Court, Suite 201, South San Francisco, CA 94080** **800-955-6288** www.lifetechnologies.com	**Life Technologies** customerservice@lifetech.com **5791 Van Allen Way, Carlsbad, CA 92008** **800-955-6288** www.lifetechnologies.com
Name of instrument	Ion Proton System	5500 Series Genetic Analyzers
Name of model/Model has been upgraded	IONPROTON/no	5500, 5500xl, 5500xl Wildfire/—
Country where designed/Manufactured/FDA-cleared or approved	U.S./U.S./no	U.S., Japan/Japan/no
First year sold in U.S./Outside U.S./First year installed	2012/2012/2012	2011/2011/2011
Dimensions in inches (H × W × D)/Footprint of all instrumentation and computing hardware	18.7 × 21.3 × 30.5/5 square feet	45.1 × 47.5 × 29.5/100 square feet
Equipment supplied with system/Automation for library preparation	Porton Torrent Server/yes	5500xl workstation, instrument control software, installation kit, training/yes
Necessary equipment not included with system and additional cost	compressed nitrogen cylinder (for pressurizing the Ion Proton Sequencer): ~$70, Ion OneTouch 2 System (automated template preparation): ~$18,985, Elga Purelab Flex 3 water purification system (fresh 18MΩ water) ~$5,000	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: $5000
Bioinformatics tools provided/For use by biologist or bioinformatician	Ion Reporter (biologist), Torrent Suite software (biologist), Torrent Circuit (biologist)	LifeScope Genomics Analysis Solution
Supplied with UPS/Entire workflow can occur in same lab	no/yes	yes, for extra charge/yes
Clean room requirements/Electrical connection	clean room always recommended for pre-amp steps/100–240 VAC, 50–60 Hz, 14 VA	none/200–400 VAC
List price/Total list price for equipment needed to perform simplest and fastest workflow from amplif through variant calling (not typically found in lab)	$224,000/224,000, (Ion Proton Sequencer and Proton Torrent Server); $18,985 (Ion OneTouch 2 System for automated template prep); ~$5,070, (source of fresh 18MΩ water, plus nitrogen gas)	$595,000 (XL), $349,000 (5500), $250,000 (upgrade from SOLiD4)/$350,000
Purchase options	purchase, reagent rental, or lease (financing available)	—
Warranties offered	1-year included, extended warranty available	1-year warranty
Training included/Total time for standard install and basic training	yes/install: 2 days; training: 3 days	yes/5 days
Training location/Follow-up training available	on site and off site/yes, for extra charge	on site and off site/yes, for extra charge
Instrument core performance:		
Maximum No. of libraries amplified in single amplification event	384 samples, by employing custom bar-coding	1,152
Read length/Percent bases >Q30	up to 200 bp/75* Note: This metric is reported as the percentage of bases that for a given read length is measured to have an accuracy of Q30 or better	75 bp forward, 35 bp reverse/>85
Paired-end capability/Tag lengths/Spans	no	yes/75 bp × 35 bp/150–300 bp
Fragment/Tag lengths/Spans	yes/up to 200 bp*/up to 245 bp*	yes/75 bp/150–300 bp
Mate-pair/Tag lengths/Spans	no	yes/60 bp × 60 bp/0.5–10 kb supported; >10 kb enabled
Single-end/Tag lengths/Spans	yes/up to 200 bp*/up to 245 bp*	75 bp/<3 kb
RNA sequencing/Tag lengths/Spans	yes/up to 200 bp*/up to 245 bp*	yes/75 bp × 35 bp/150–200 bp
ChIP sequencing/Tag lengths/Spans	yes/up to 200 bp*/up to 245 bp*	yes/35–75 bp/150–300 bp
Bisulfite sequencing/Tag lengths/Spans	yes/up to 200 bp*/up to 245 bp*	yes/75 bp/150–300 bp
Output per run	≤10 Gb on Ion Proton I Chip, ≤20x human-scale genome on Ion Proton II chip	240 gb
Total time from library construction to variant calling to achieve output per run/Technical bench time/Bioinformatics time	24 hours/3 hours (library, template, Proton and Ion chip)/≤90 minutes	5–26 days (template preparation: 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	—	2–3 days
• Single-end	<2 hours	3 hours
• RNA sequencing	~6 hours	2 days or 3 hours post-RNA extraction
• ChIP sequencing	customer demonstrated on semiconductor sequencing	3 hours post chip
• Bisulfite sequencing	customer demonstrated on semiconductor sequencing	3 hours
Hands-on time each:		
• Paired-end	—	30 minutes
• Fragment	~15 minutes (IonXpress Fragment), ~10 minutes (Ion AmpliSeq 2.0)	30 minutes
• Mate-pair	—	8 hours
• Single-end	~15 minutes (IonXpress Fragment), ~10 minutes (Ion AmpliSeq 2.0)	30 minutes
• RNA sequencing	~40 minutes (whole transcriptome, small RNA), ~55 minutes (small RNA with enrichment)	2 hours
• ChIP sequencing	customer demonstrated on semiconductor sequencing	30 minutes post chip
• Bisulfite sequencing	customer demonstrated on semiconductor sequencing	45 minutes
Equipment required for library construction	if automation required, recommend AB Library Builder system	standard lab equipment, Covaris system, AB Library Builder system
Reagents and controls:		
Cost per run	$1,000 for template, sequencing, and Ion Proton chip (excludes sample preparation)	$2000 5500xl Wildfire
Cost per sample*	$133 (12 samples, ~800x coverage of 1 Mb); $92 (24 samples, ~400x coverage); $71 (48 samples, ~200x coverage); $60 (96 samples, ~100x coverage)	1Mb, 200x to 2000x coverage per sample, in one-lane run of multiplexed samples (includes library preparation): $116 (12 samples), $108 (24 samples), $104 (48 samples), $102 (96 samples)
Reagent tracking method on instrument	bar-code reader	real-time reagent monitoring
Information contained in tracking method	external bar-code reader for sample and reagent tracking	current reagent volume predicted time to replenish reagents
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	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	touchscreen user interface/Torrent Suite	ICS on system workstation/LifeScope or cloud
Total time required for setup of amplification, sequencing, and variant calling steps	30 minutes	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 application scientists and engineers based in U.S.	field applications scientists: 40; engineers: 90	field applications scientists: 24; engineers: 31
Weekly maintenance required/Monthly/Pre-run	chlorite cleaning/none/daily wash solution cleaning	—
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, DNAStar, SoftGenetics, Partek, Avadis NGS, CLC Bio, Bio Team	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	22 using semiconductor sequencing	225
Published applications in pathology-related research	8 using semiconductor sequencing	60 clinically related publications
Fastest published turnaround time from sample to analyzed result	62 hours using semiconductor sequencing	3 months
Lowest published variant sensitivity level	0.25–5.5 percent (Yang, et al.)	<1 percent
Distinguishing features of sequencer (supplied by company)	flexibility to meet a range of applications, budgets, project sizes, and input DNA amounts, by employing scalable semiconductor technology delivering human-scale genome sequencing and mulitplexed exome and transcriptome sequencing; delivers fast sequencing run times, while maintaining high accuracy; high-throughput, low-cost capital acquisition; no optics, lasers, or cameras enables low maintanance and run costs	two-base encoding and exact call chemistry delivers 99.99 percent accuracy, which enables detection of low frequency variants; pay-per-lane sequencing; application-per-lane sequencing

*inclusive of sample preparation, for multiple configurations, using 1 Mb and 30x average coverage per sample

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Next-generation sequencing instruments

Part 3 of 3 *See* captodayonline.com/productguides *for an interactive version of guide*	**Roche Diagnostics Corp.** **Clotilde Teiling** clotilde.teiling@roche.com **9115 Hague Road** **Indianapolis, IN 46256** **317-521-2000** www.my454.com	**Roche Diagnostics Corp.** **Clotilde Teiling** clotilde.teiling@roche.com **9115 Hague Road** **Indianapolis, IN 46256** **317-521-2000** www.my454.com
Name of instrument	GS Junior**	GS FLX+**
Name of model/Model has been upgraded	GS Junior/no	GS FLX+/yes
Country where designed/Manufactured/FDA-cleared or approved	U.S./U.S./—	U.S./U.S./—
First year sold in U.S./Outside U.S./First year installed	2010/2010/2010	2005/2006/2005
Dimensions in inches (H × W × D)/Footprint of all instrumentation and computing hardware	16 × 16 × 24/30 square feet	51 × 30 × 36/50 square feet
Equipment supplied with system/Automation for library prep	sequencing instrument, emulsion creation device, attendant computer, control and analysis software/yes	sequencing instrument, attendant computer, control and analysis software/yes
Necessary equipment not included with system and additional cost	microplate centrifuge, thermal cycler/—	data analysis workstation, Qiagen TissueLyser II, bead counter, microplate centrifuge, thermal cycler, hood/—
Bioinformatics tools provided/For use by biologist or bioinformatician	GS Amplicon Variant Analyzer, GS De Novo Assembler, GS Reference Mapper (all are GUI-based)/biologist	GS Amplicon Variant Analyzer, GS De Novo Assembler, GS Reference Mapper (all are GUI-based)/biologist
Supplied with UPS/Entire workflow can occur in same lab	no/yes	yes/yes
Clean room requirements/Electrical connection	none/110–240 V, 50 or 60 Hz	none/120 V or 230 V, 50 or 60 Hz
List price/Total list price for equipment needed to perform simplest and fastest workflow from amplif through variant calling (not typically found in lab)	$108,000/—	$425,000/—
Purchase options	purchase, lease, or rent	purchase, lease, or rent
Warranties offered	1-year manufacturing, extended service contracts	1-year manufacturing, extended service contracts
Training included/Total time for standard install and basic training	yes/3 days	yes/5 days
Training location/Follow-up training available	on site and off site/yes (no additional charge)	on site and off site/yes (no additional charge)
Instrument core performance:		
Maximum No. of libraries amplified in single amplification event	100+	192+
Read length/Percent bases >Q30	up to 600 bp (400 bp average mode)/86	up to 1,000 bp (700 bp average mode)/88
Paired-end capability/Tag lengths/Spans	yes/180 average/3 kb, 8 kb, 20 kb, 40 kb	yes/180 average/3 kb, 8 kb, 20 kb, 40 kb
Fragment/Tag lengths/Spans	yes/full read length/—	yes/full read length/—
Mate-pair/Tag lengths/Spans	yes/180 average/3 kb, 8 kb, 20 kb, 40 kb	yes/180 average/3 kb, 8 kb, 20 kb, 40 kb
Single-end/Tag lengths/Spans	yes/full read length/—	yes/full read length/—
RNA sequencing/Tag lengths/Spans	yes/full read length/—	yes/full read length/—
ChIP sequencing/Tag lengths/Spans	yes/full read length/—	yes/full read length/—
Bisulfite sequencing/Tag lengths/Spans	yes/full read length/—	yes/full read length/—
Output per run	~40 Mb (70–100k reads)	~700 Mb (1,000,000+ reads)
Total time from library construction to variant calling to achieve output per run/Technical bench time/Bioinformatics time	24 hours/6.5 hours/3 hours (full titanium run)	36 hours/6.5 hours/3 hours (full titanium run)
Sample preparation:		
Total time for generating standard gDNA library	3 hours	3 hours
• Paired-end	36 hours	36 hours
• Fragment	1.5 hours	1.5 hours
• Mate-pair	36 hours	36 hours
• Single-end	3 hours	3 hours
• RNA sequencing	36 hours	36 hours
• ChIP sequencing	1.5 hours	1.5 hours
• Bisulfite sequencing	1.5 hours	1.5 hours
Hands-on time each:	2 hours	2 hours
• Paired-end	8 hours	8 hours
• Fragment	.75 hours	.75 hours
• Mate-pair	8 hours	8 hours
• Single-end	2 hours	2 hours
• RNA sequencing	8 hours	8 hours
• ChIP sequencing	.75 hours	.75 hours
• Bisulfite sequencing	.75 hours	.75 hours
Equipment required for library construction	supplied with kit	supplied with kit
Reagents and controls:		
Cost per run	$930 (approximate)	$4,490 (approximate)
Cost per sample	depends on experimental design	depends on experimental design
Reagent tracking method on instrument	bar-coded reagents	bar-coded reagents
Information contained in tracking method	part and lot numbers, expiration date	part and lot numbers, expiration date
Reagent shipping conditions/Storage conditions	ambient and dry ice/ambient, 4°C, -20°C	ambient and dry ice/ambient, 4°C, -20°C
Shelf life of amplification and sequencing reagents	12–18 months	12–18 months
Controls introduced during creation of library/Sequencing control avail.	no/yes	no/yes
Capable of complete walkaway automation for amp, seq, var calling	no	no
Remote system monitoring	yes	yes
Instrument control software and devices to start run/for data analysis	GUI-based, on instrument computer/GUI-based, on instrument computer and available off instrument	GUI-based, on instrument/GUI-based, off instrument
Total time required for setup of amplification, sequencing, and variant calling steps	3.5 hours	6 hours
Maximum No. of libraries sequenced in a single run	100+	192+
Types of maintenance plans available	full service	full coverage
No. of field apps scientists and engineers based in U.S.	259	259
Weekly maintenance required/Monthly/Pre-run	monthly: maintenance wash; pre-run: fully integrated wash with run protocol	monthly: maintenance wash; pre-run: fully integrated wash with run protocol
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 (multi-vendor capability)	yes (multi-vendor capability)
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	1,500+	1,500+
Published applications in pathology-related research	300+	300+
Fastest published turnaround time from sample to analyzed result	24 hours	24 hours
Lowest published variant sensitivity level	0.01 percent	0.01 percent
Distinguishing features of sequencer (supplied by company)	up to 600 base pair reads in NGS benchtop; long reads suited to a variety of applications, including mutation detection, infectious disease, and cancer research; integrated bioinformatics software allows analysis of amplicon variants in minutes	up to 1,000 base pair reads (comparable to Sanger); long reads allow accurate linkage of variants and transcript assemblies; GS FLX system technology available in benchtop format with the GS Junior system

**inclusive of sample preparation, 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

***For life science research only. Not for use in diagnostic procedures.*

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