Next-generation sequencing instruments

Part 1 of 2 *See accompanying article on page 1*	**Illumina** **Laura Trotter** ltrotter@illumina.com **9885 Towne Centre Drive, San Diego, CA 92121** **800-809-4566** www.illumina.com	**Ion Torrent, part of Life Technologies** **Graham Scott** graham.scott@lifetech.com **7000 Shoreline Court, Suite 201, South San Francisco, CA 94080** **650-243-6550** www.lifetechnologies.com
Name of instrument	MiSeq	Ion Personal Genome Machine (PGM)
Name of model/Model has been upgraded	—/no	508-U001/no
Country where designed/Manufactured/FDA-cleared or approved	U.S./U.S./submit in 2012	U.S./U.S./submit in 2012
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 sq. ft.	21 × 24 × 20/~7.2 sq. ft. (sequencer: 2 × 1.7 sq. ft.; server: .7 × 1.8 sq. ft.)
Equipment supplied with system/Automation for library prep	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 argon cylinder for pressurizing PGM ($500); source of fresh 18MΩ water (~$2,000)
Bioinformatics tools provided/For use by biologist or bioinformatician	MiSeq Reporter/biologist	bioinformatic tools provided for basecalling, alignment and somatic or germline mutation identification
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 (sequencer); $16,500 (Torrent Server)/~$2,500 (18MΩ water and argon 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 amplif event	up to 96 (dependent on Illumina sample prep method used)	384 samples by employing custom bar-coding
Read length/Percent bases >Q30	up to 2 × 150 bp/75%	200+ bp (Q4, 2011); 400+ bp* (2012)/80%
Paired-end capability/tag lengths/spans	yes/up to 2 × 150 bp/200–500 bp	yes/2 × 100 bp; 2 × 200 bp*/~100–300
Fragment/tag lengths/spans	yes/up to 2 × 150 bp/200–500 bp	yes/200+ bp in Q4/400+ bp* (2012)
Mate-pair/tag lengths/spans	yes/2 × 35 bp/2–5 kb	yes/60 bp/up to 10 kb
Single-end/tag lengths/spans	yes/up to 2 × 150 bp/200–500 bp	yes/200+ bp in Q4/400+ bp* (2012)
RNA sequencing/tag lengths/spans	yes/up to 2 × 100 bp/200–500 bp	yes/100 bp, 200+ bp in Q4, 2011*/—
ChIP sequencing/tag lengths/spans	yes/1 × 35 bp/200–500 bp	no/expected in 2012, customer demonstrated
Bisulfite sequencing/tag lengths/spans	no/expected in 2012	no/expected in 2012, customer demonstrated
Output per run	175–245 Mb with 1 × 35 bp, 1.5–2 Gb with 2 × 150 bp	10 Mb (Ion 314 chip kit); 100 Mb (Ion 316 chip kit); 1 Gb (Ion 318 chip kit)**
Total time from library construction to variant calling to achieve output per run/Technical bench time/Bioinformatics time	8 hours for 1 × 35 bp, 31 hours for 2 × 150 bp using Nextera Library Prep/2 hours/2 hours	<8 hours (35 bp run)/30 minutes (library and template prep)/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	~3 days	~18 hours
• Single-end	<2 hours with Nextera, ~9 hours with TruSeq	<2 hours
• RNA sequencing	~9 hours with TruSeq	~6 hours
• ChIP sequencing	~9 hours with TruSeq	expected in 2012, customer demonstrated
• Bisulfite sequencing	~9 hours	expected in 2012
Hands-on time each:		
• Paired-end	~15 minutes with Nextera, ~2.5 hours with TruSeq	~15 minutes
• Fragment	~15 minutes with Nextera, ~2.5 hours with TruSeq	~15 minutes
• Mate-pair	~4.5 hours	~6 hours
• Single-end	~15 minutes with Nextera, ~2.5 hours with TruSeq	~15 minutes
• RNA sequencing	~3 hours	~2 hours
• ChIP sequencing	~3 hours	expected in 2012, customer demonstrated
• Bisulfite sequencing	~3 hours	expected in 2012
Equipment required for library construction	standard lab equipment	if automation required, recommend AB Library Builder system
Reagents and controls:		
Cost per run	$695–$965	$281: 314 chip with spec. of 10 Mb (3 samples @ 30x coverage)
Cost per sample*	$63 (11 samples per 50 cycle kit) $35 (27 samples per 300 cycle kit)	$45: 316 chip with spec of 100 Mb (48 samples @ 30x coverage) $45: 318 chip (96 samples @ 30x coverage)
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/-20°C–4°C
Shelf life of amplification and sequencing reagents	at least 3 months of shelf life on shipped reagents	six 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/5 minutes	touch screen user interface/Torrent Suite
Total time required for setup of amplification, sequencing, and variant calling steps	30 minutes	30 minutes
Maximum No. of libraries sequenced in a single run	up to 96 (dependent on Illumina sample prep method used)	384
Types of maintenance plans available	parts only, standard, silver, and gold	PGM sequencer and server: rapid exchange, AB Complete and Dx, IQ/OQ, IPV
No. of field apps scientists and engineers based in U.S.	—	75 engineers, 22 applications specialists
Weekly maintenance required/monthly/pre-run	weekly: post-run wash; monthly: post-run wash; pre-run: post-run wash	weekly: chlorite cleaning; 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	no	yes (Dnastar Seqman Ngen, Partek Genomics Suite, Avadis NGS, NextGENe)
Ability of software to detect mutations	substitutions, indels	substitutions, indels, copy number changes
Total No. of peer-reviewed publications for this platform	>1,900 original research publications using Illumina SBS chemistry (same chemistry in MiSeq)	4 (*Nature, New England Journal of Medicine, PLoS One*)
Published applications in pathology-related research	—	2
Fastest published turnaround time from sample to analyzed result	—	62 hours (Mellmann, et al.)
Lowest published variant sensitivity level	somatic variations detected at 1.1% on MiSeq based on internal analysis	somatic variations detected at 5% on internal analysis, no published somatic var studies
Distinguishing features of sequencer (supplied by company)	rapid, scalable, cost-effective variant ID; prepare and enrich 384 amplicons per sample and 96 samples per plate simultaneously using standard lab equipment; range of DNA sequencing apps in 90 minutes enables users to go from DNA to analyzed data in a single workday; BaseSpace eliminates need for expensive IT infrastructure to support platforms, making it simple to put a personal sequencer into labs of any size and experience	100x increase in throughput within nine months of launch demonstrates rapidly scalable semiconductor technology with 314 and 316 Ion chips (318 chip** available Q4, 2011); >99% per base accuracy measured at 100 bp and improving; read lengths reached 200 bp in Oct. 2011 and expected to reach 400 bp in 2012**; consensus accuracy of Q50 (99.999%) demonstrated; uniform genome coverage with minimal bias; using simple, natural chemistry (no optics or lasers, eliminates many sources of error) sequencing runs in as little as 30 minutes at 35 bp, 2 hours for 200+ bp

*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

*expected performance; **product not officially released, info. subject to change without notice

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Next-generation sequencing instruments

Part 2 of 2	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 sq. ft.	51 × 30 × 36/50 sq. ft.
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 amplif 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 hour	.75 hour
• Mate-pair	8 hours	8 hours
• Single-end	2 hours	2 hours
• RNA sequencing	8 hours	8 hours
• ChIP sequencing	.75 hour	.75 hour
• Bisulfite sequencing	.75 hour	.75 hour
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%	0.01%
Distinguishing features of sequencer (supplied by company)	up to 600 base pair reads in NGS benchtop; long reads suited to wide 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
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.*	***For life science research only. Not for use in diagnostic procedures.*

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