Genome Analyzer$_{II}$ System

Based on revolutionary massively parallel sequencing technology, Illumina provides a high-speed, whole-genome analysis system that offers an unmatched combination of read lengths, paired-end insert size ranges, and high genomic coverage to enable the broadest spectrum of applications.

A REVOLUTION IN GENOMICS

The Illumina Genome Analyzer, a groundbreaking platform for genetic analysis and functional genomics, is transforming the way experiments are developed and executed. The massively parallel sequencing technology leverages clonal cluster formation and proprietary reversible terminator chemistry to dramatically improve the speed and reduce the cost of large-scale sequencing applications.

BROADEST APPLICATIONS FLEXIBILITY

The Genome Analyzer supports a range of applications including whole-genome and candidate region resequencing. Transcriptome analysis, small RNA discovery, methylation profiling, and protein-nucleic acid interaction analysis at the genome-wide scale are also now made affordable by a single system.

GENOME ANALYZER SYSTEM HIGHLIGHTS

- **Broadest Applications Flexibility:** Study the genome, epigenome, and transcriptome
- **Simplest Workflow:** Reduce hands-on time with application-specific kits and walk-away automation
- **Short- and Long-Insert Paired-End Reads:** Use insert sizes from 200 bp to 5 kb
- **Unmatched Combination of Read Length and Number of Reads:** Achieve 75 bp reads and up to 200 million reads per paired-end run
- **Unrivaled Output:** Generate the highest throughput per day and highest output of perfect reads per run

SIMPLE, FAST, AND AUTOMATED

The Genome Analyzer System offers the simplest and fastest workflow for a broad range of high-throughput sequencing applications. Sample libraries can be prepared in just a few hours with ready-to-use kits. The Cluster Station is a standalone system for automated generation of clonal clusters on Illumina Genome Analyzer flow cells. In less than five hours, up to twelve multiplexed samples can be isothermally amplified in each flow cell channel.

Illumina Sequencing technology provides an easy-to-use workflow that does not require emulsion PCR. This allows for a self-contained system that minimizes handling errors and contamination concerns, eliminating the need for robotics or clean rooms. The fast and simple workflow maximizes the capacity of the Genome Analyzer, while the walk-away automation reduces overall project time and cost. The system is designed to fit in any lab, from individual researcher labs to core labs and genome centers.

SCALABLE ULTRA-HIGH OUTPUT

The Genome Analyzer currently generates billions of bases of high-quality filtered data per paired-end run on a single flow cell. The scalable nature of the technology delivers unmatched data densities and output, supporting more complex projects at lower costs. The performance of the Genome Analyzer is continuously improving. As a result, specifications listed in this document may have already been surpassed. Please contact Illumina for the latest system specifications.

HIGHEST YIELD OF QUALITY DATA

The quality of raw data generated by a sequencing system is the most fundamentally important factor in the success of an experiment. The high accuracy of Genome Analyzer data, with quality metrics available for each base sequenced, mean that a given experiment can be accomplished with fewer runs and with higher confidence.

SINGLE OR PAIRED-END SUPPORT

The Genome Analyzer System supports sequencing of both single-read and paired-end libraries. This system is the only platform that offers a short-insert paired-end capability for high-resolution sequencing as well as long-insert paired-end reads for efficient assembly, *de novo* sequencing, and large-scale structural variation detection. Illumina's simple library construction protocol minimizes the time from sample isolation to obtaining usable results. Single-read or short-insert paired-end sample preparation of genomic DNA takes six hours with only three hours of hands-on time. The combination of short inserts and 2 × 50 bp or longer reads increases the ability to align and sample the genome, and expand the utility for other applications.

NOVEL SEQUENCING CHEMISTRY

The Genome Analyzer uses sequencing by synthesis (SBS) to support massively parallel sequencing. Based on novel reversible fluorescently labeled terminators, this technology allows detection of single-base incorporation events into growing DNA strands. Since all four reversible-terminator dNTPs are present during each sequencing cycle, natural competition minimizes incorporation bias. Homopolymers pose no problem because each cycle interrogates only one base at a time per template. The reversible terminator chemistry ensures strict base-by-base sequencing.

AUTOMATED WORKFLOW

1. SAMPLE PREPARATION

~6 hours (~3 hours hands-on)

- Sample collection, genomic DNA sheared
- DNA end-repair
- Adapter ligation

2. CLUSTER GENERATION

~5 hours

- Flow cell and reagents placed into Cluster Station
- Samples applied to flow cell
- Complete walk-away automation

3. SEQUENCING BY SYNTHESIS

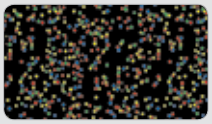
~1 day (25 bp), ~5.5 days (2 × 50 bp)

- Flow cell and reagents placed on Genome Analyzer
- Complete walk-away automation

4. PAIRED END MODULE

- Add-on module for automated reagent delivery
- Second read prepared and sequenced while flow cell remains on Genome Analyzer

5. DATA ANALYSIS



~1–2 days

- Real-time image analysis
- Data transfer to automated analysis pipeline
- Automated base calling
- Paired-end alignment
- Polymorphism detection

LOW INPUT REQUIREMENTS

The Genome Analyzer System requires sample inputs as low as 100 ng, enabling a host of applications where sample is limited (e.g., immunoprecipitates, laser-dissected materials, and small model systems).

DATA ANALYSIS SUPPORT

Illumina provides analysis software and hardware that contribute to an end-to-end sequencing system to rapidly move from raw data acquisition to publishable, biologically meaningful results.

The IPAR (Integrated Primary Analysis and Reporting) system facilitates real-time image analysis of the primary data output. After image analysis, the Pipeline software automates base calling and read alignment to a reference sequence. Illumina's GenomeStudio™ data analysis software supports intuitive graphical secondary analysis of sequence data for DNA and RNA applications.

PRODUCTS AND CATALOG NUMBERS FOR GENOME ANALYZER$_{IIx}$ APPLICATIONS

APPLICATION	LIBRARY PREPARATION	CLUSTER GENERATION	SEQUENCING
DNA Sequencing			
Genomic DNA Paired-End Library Sequencing (200 bp–500 bp inserts)	Paired-End Genomic DNA Sample Prep Kit	Paired-End Cluster Generation Kit	Standard Sequencing Kit (36 cycle)
Catalog Number	*PE-102-1001*	*PE-203-2001*	*FC-104-3002*
Mate Pair Library Sequencing (2 kb–5 kb inserts)	Mate Pair Library Prep Kit	Paired-End Cluster Generation Kit	Standard Sequencing Kit (36 cycle)
Catalog Number	*PE-112-1002*	*PE-203-2001*	*FC-104-3002*
Genomic DNA Single-Read Sequencing	Genomic DNA Sample Prep Kit	Single-Read Cluster Generation Kit	Standard Sequencing Kit (36 cycle)
Catalog Number	*FC-102-1001*	*GD-203-2001*	*FC-104-3002*
Transcriptome Analysis			
mRNA-Seq (full-length cDNA sequencing)	mRNA-Seq Sample Prep Kit	mRNA-Seq Cluster Generation Kit	Standard Sequencing Kit (36 cycle)
Catalog Number	*RS-100-0801*	*SR-203-1001*	*FC-104-3002*
mRNA Tag Profiling (16 or 17 bp mRNA tags)	Tag Profiling Sample Prep Kit	Tag Profiling Cluster Generation Kit	Standard Sequencing Kit (18 cycle)
Catalog Number	*FC-102-1007* (DpnII) *FC-102-1005* (NlaIII)	*TP-203-1001* (DpnII) *TP-203-1003* (NlaIII)	*FC-104-3001*
Small RNA Discovery and Analysis	Small RNA Sample Prep Kit	Small RNA Cluster Generation Kit	Standard Sequencing Kit (36 cycle)
Catalog Number	*FC-102-1009*	*SR-203-1001*	*FC-104-3002*
Gene Regulation and Control Analysis			
Protein-Nucleic Acid Interaction Analysis	ChIP-Seq Sample Prep Kit	Single-Read Cluster Generation Kit	Standard Sequencing Kit (36 cycle)
Catalog Number	*IP-102-1001*	*GD-203-2001*	*FC-104-3002*
Sample Multiplexing			
Multiplex up to 12 samples per flow cell channel	Multiplexing Sample Prep Oligonucleotide Kit	Single-Read or Paired-End Cluster Generation Kit	Standard Sequencing Kits (18 or 36 cycle)
Catalog Number	*PE-400-1001*		

PERFORMANCE PARAMETERS*

READ LENGTH†	RUN TIME (DAYS)	# OF READS (PER FLOW CELL)	HIGH-QUALITY OUTPUT (GB)‡	HIGH-QUALITY OUTPUT (GB PER DAY)‡	BASE CALLS WITH Q ≥ 30	PER BASE READ ACCURACY	% PERFECT READS
1 × 35 bp	~ 2	80–100 million	2-3	~ 1–1.5	70–85%	> 99%	≥ 90%
2 × 35 bp	~ 4	80–100 million	4-6	~ 1–1.5	70–85%	> 99%	≥ 90%
2 × 50 bp	~ 5.5	80–100 million	8–10	~1.5–1.8	70–85%	> 98.5%	≥ 80%
2 × 75 bp	~ 8	80–100 million	12–15	~1.5–1.9	> 70%	> 98%	≥ 70%

SAMPLES

Throughput: eight channels per flowcell, up to 12 samples per channel
Input requirement: 0.1–1.0 µg (single- and paired-end reads), 10 µg (Mate Pair reads)
Genomic DNA sample prep: 3 hours hands-on, 6 hours total for single or paired-end libraries
Flow cell: Genome Analyzer$_{IIx}$ uses 1.4 mm channel flow cell

SERVICE AND SUPPORT

Illumina will ensure that your Genome Analyzer system is properly installed and qualified, and will provide ongoing maintenance and service. This industry-leading support is available in North America, Europe, and Asia.

* Sequencing output generated at cluster densities between 100,000 and 125,000 per tile that pass filters, SBS v3 kits and Sequencing Control Software (SCS) 2.3. Analysis performed with IPAR 1.3 and Pipeline software v1.3.

† 2 × 50 bp reads supported, 2 × 75 bp reads enabled.

‡ Data generated from clusters that pass Pipeline software v1.3 quality filters.

SPECIFICATIONS FOR THE GENOME ANALYZER$_{II}$ SYSTEM

ILLUMINA GENOME ANALYZER	ILLUMINA CLUSTER STATION	ILLUMINA PAIRED-END MODULE
CATALOG NUMBER		
SY-301-1201	SY-301-2001	SE-301-1002
INSTRUMENT CONFIGURATION		
CE Marked and ETL Listed instrument	CE Marked and ETL Listed instrument	CE Marked and ETL Listed instrument
Computer and flat panel display	Computer and flat panel display	Installation setup and accessories
Installation setup and accessories	Installation setup and accessories	
Data collection and analysis software		
INSTRUMENT CONTROL COMPUTER		
Base Unit: 3.6 GHz Dual Processor	Base Unit: 2.8 GHz Processor	
Memory: 4 GB RAM	Memory: 512 MB RAM	
Hard Drive: 4 × 300 GB SCSI	Hard Drive: 80 GB	
Operating System: Windows XP	Operating System: Windows XP	
Monitor: 19" LCD flat panel	Monitor: 17" LCD flat panel	
Note: The computer specifications may be regularly upgraded. Contact your local sales representative for current configuration.		
INTEGRATED PRIMARY ANALYSIS AND REPORTING (IPAR) SYSTEM		
Base Unit: HP DL380, X5460 3.16 GHz Processor		
Memory: 3.1TB in total; (25) 146 GB 2.5" SAS drives with SmartArray P800 RAID Controller		
Operating System: Windows XP		
Rack: 12U with UPS unit		
OPERATING ENVIRONMENT		
Temperature: 22°C ± 3°C	Temperature: 22°C ± 3°C	Temperature: 22°C ± 3°C
Humidity: Non-Condensing 20%–80%	Humidity: Non-Condensing 20%–80%	Humidity: Non-Condensing 20%–80%
Altitude: Less than 2,000 m (6,500 ft)	Altitude: Less than 2,000 m (6,500 ft)	Altitude: Less than 2,000 m (6,500 ft)
Air Quality: Pollution Degree Rating of II	Air Quality: Pollution Degree Rating of II	Air Quality: Pollution Degree Rating of II
Ventilation: Maximum of 3400 Btu/h (1000W)		
For Indoor Use Only	For Indoor Use Only	For Indoor Use Only
LASER		
3 laser system: 660, 635, and 532 nm		
DIMENSIONS		
W×D×H: 102 cm × 67 cm × 92 cm	W×D×H: 58 cm × 62 cm × 38 cm	W×D×H: 24 cm × 61 cm × 44 cm
Weight: 187 kg	Weight: 27 kg	Weight: 13 kg
Crated Weight: 232 kg	Crated Weight: 41 kg	Crated Weight: 34 kg
POWER REQUIREMENTS		
100–240V AC 50/60 Hz, 20A, 900 Watts	100–240V AC 50/60 Hz, 15A, 750 Watts	100–240V AC 50/60 Hz, 3A Max, 250 Watts
Illumina recommends an uninterruptible power supply (UPS) with an output capacity of at least 3 kVA.		
INSTRUMENT BENCH		
Illumina recommends a movable table with locking casters capable of supporting the weight of the instrument and computers.		

ADDITIONAL INFORMATION

Visit our website or contact us to learn more about Illumina Sequencing products and services. Contact Customer Solutions for the most up-to-date throughput specifications.

Illumina, Inc.
Customer Solutions
9885 Towne Centre Drive
San Diego, CA 92121-1975
1.800.809.4566 (toll free)
1.858.202.4566 (outside the U.S.)
techsupport@illumina.com
www.illumina.com

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