Genome Analyzer$_{IIx}$ System

The most proven, widely adopted next-generation sequencing platform

Highlights

- **Broadest Applications Flexibility**
  Study the genome, epigenome, and transcriptome
- **Broadest Spectrum of Genomic Variation**
  Characterize genomic variants with short- and long-insert paired-end reads with insert sizes from 200 bp to 5 kb
- **Unmatched Combination of Read Length and Number of Reads**
  Achieve 2 × 150 bp reads and > 640 million reads per flow cell
- **High Data Quality Generation**
  Yield greater than 85% of bases higher than Q30 at 2 x 50 bp

A Revolution in Genomics

Illumina's Genome Analyzer$_{IIx}$ is a proven platform for genetic analysis and functional genomics, and has transformed the way experiments are developed and executed (Figure 1). 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.

Broadest Applications Flexibility

The Genome Analyzer$_{IIx}$ supports a wide range of applications, including whole-genome and candidate region resequencing, transcriptome analysis, small RNA discovery, methylation profiling, and genome-wide protein-nucleic acid interaction analysis.

Simple, Fast, and Automated

The Genome Analyzer$_{IIx}$ system offers the simplest and- fastest workflow for a broad range of high-throughput sequencing applications. Sample libraries are prepared in just a few hours with ready-to-use kits. Clonal clusters are automatically generated on Illumina Genome Analyzer$_{IIx}$ flow cells using the cBot cluster generation system. In less than four hours, up to 12 multiplexed samples can be isothermally amplified in each channel of the eight-channel flow cell.

Illumina sequencing technology provides an easy-to-use protocol 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 system is designed to fit in any lab, from individual research labs to core labs and genome centers. The streamlined workflow of the Genome Analyzer$_{IIx}$ system generates meaningful data quickly and efficiently, while reducing project time lines and costs (Figure 2).

TruSeq™ Technology

The TruSeq family of reagents represents the latest advancement of Illumina's sequencing by synthesis (SBS) chemistry. From sample prep through DNA sequencing, TruSeq technology enables Illumina sequencing to deliver the most accurate data across a broad range of applications.

SBS chemistry enables massively parallel sequencing of millions of fragments using a proprietary reversible terminator-based method that detects single bases as they are incorporated into growing DNA strands. A fluorescently-labeled terminator is imaged as each dNTP is added and then cleaved to allow incorporation of the next base. Since all four reversible terminator-bound dNTPs are present during each sequencing cycle, natural competition minimizes incorporation bias. Base calls are made directly from signal intensity measurements during each cycle, which greatly reduces raw error rates compared to other technologies. The end result is highly accurate base-by-base sequencing that eliminates sequence-context specific errors, enabling robust base calling across the genome, including repetitive sequence regions and within homopolymers.

Illumina sequencing delivers the most accurate human genome at any level of coverage. The highest yield of error free reads and most base calls above Q30 provide researchers the highest confidence in their data integrity to draw sound biological conclusions.

Figure 1: Genome Analyzer System

The Genome Analyzer$_{IIx}$ gives you the power to go from DNA or RNA to data in under a week with less than four hours of hands-on time, with superior raw-read accuracy and the industry's simplest automated workflow.

Single- or Paired-End Read Support

The Genome Analyzer$_{IIx}$ system supports sequencing of both single-read and paired-end libraries. It is the only platform available that offers a short-insert paired-end capability for high-resolution sequencing as well as long-insert paired-end reads for efficient sequence assembly, *de novo* sequencing, and large-scale structural variation detection. The TruSeq library construction protocol minimizes the time from sample isolation to usable results. Single-read or short-insert paired-end sample preparation of genomic DNA takes as few as two hours (5 minutes of hands-on time) using Nextera Library Prep Kits. The combination of short inserts and 2 × 150 bp or longer reads increases the ability to align and sample the genome, expanding the Genome Analyzer's utility for other applications.

Low Input Requirements

The Genome Analyzer$_{IIx}$ 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).

Genome Analyzer$_{IIx}$ Performance Parameters

Read Length	Run Time (Days)	Output (Gb)
1 × 35 bp	~2	10 – 12
2 × 50 bp	~5	25 – 30
2 × 75 bp	~7	37.5 – 45
2 × 100 bp	~9.5	54 – 60
2 × 150 bp	~14	85 – 95

*Sequencing output generated using TruSeq SBS V5 kit with PhiX library and cluster densities between 508,000-630,000 clusters/mm^2 that pass filtering on a GA$_{IIx}$

Throughput

Up to 6.5 Gb per day for a 2 x 100 bp run

Reads

Up to 320 million clusters passing filter and up to 640 million paired-end reads

Performance

The Genome Analyzer$_{IIx}$ generates a significant yield of bases greater than Q30

- Greater than 85% bases higher than Q30 at 2 x 50 bp
- Greater than 80% bases higher than Q30 at 2 x 100 bp

Service and Support

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

Figure 2. Simple, Automated Workflow

1. Library Preparation

~2 hours [15 min. hands-on (Nextera)]
~6 hours [~3 hours hands-on (TruSeq)]

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

2. Cluster Generation

~4 hours (<10 min. hands-on)

- Flow cell and pre-filled reagents placed into cBot with no reagent preparation time
- Walk-away automation with remote monitoring

3. Sequencing by Synthesis

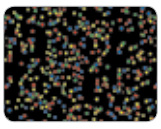
~14 days for 2 ×150 bp (< 10 min hands-on)

- Flow cell and pre-filled reagents placed on Genome Analyzer$_{IIx}$
- Complete walk-away automation, including support for longer reads

4. Paired-End module

- Add-on module for automated reagent delivery
- Second read prepared and sequenced while flow cell remains on Genome Analyzer$_{IIx}$

5. Data Analysis



- Real-time image analysis and base calling
- Automated data transfer to analysis pipeline
- Gapped paired-end alignment
- Variant detection

Data Analysis Support

The analysis software and hardware included with the Genome Analyzer$_{IIx}$ contribute to an end-to-end sequencing approach that enables researchers to rapidly move from raw data acquisition to publishable, biologically meaningful results. Illumina's Sequencing Control Software (SCS) offers real-time analysis processing that automatically produces image intensities and quality-scored base calls directly on the instrument computer. These reads can be aligned to a reference sequence and analyzed using the Pipeline analysis software. In combination with the Consensus Assessment of Sequence and Variation (CASAVA) software, GenomeStudio® data analysis software provides intuitive, graphical analysis and interaction with DNA and RNA data.

Additional Information

For more information about the Genome Analyzer$_{IIx}$ go to http://www.illumina.com/systems/genome_analyzer_iix.ilmn

Specifications for the Genome Analyzer$_{IIx}$ System

Illumina Genome Analyzer$_{IIx}$	Illumina cBot	Illumina Paired-End Module
Catalog No.		
SY-301-1301	SY-301-2002	SE-301-1002
Instrument Configuration		
CE Marked and ETL Listed instrument Installation, setup, and accessories Computer and flat panel display Data collection and analysis software	CE Marked and ETL Listed instrument Installation, setup, and accessories	CE Marked and ETL Listed instrument Installation setup and accessories
Instrument Control Computer		
Base Unit: Intel Xeon x5560 2.8 GHz, Quad Core Memory: 4 GB RAM Hard Drive: 4 × 300 GB SCSI Operating System: Windows XP Monitor: 19" LCD flat panel	Embedded Mini-ITX Board with Celeron M Processor Memory: 1 GB RAM Hard Drive: 80 GB Operating System: Windows Embedded Monitor: Integrated 8" touch screen	
Note: The computer specifications may be regularly upgraded. Contact your local Account Manager for current configuration.		
Operating Environment		
Temperature: 22°C ± 3°C Humidity: Non-Condensing 20%–80% Altitude: Less than 2,000 m (6,500 ft) Air Quality: Pollution Degree Rating of II Ventilation: Maximum of 3400 BTU/h (1000W) For Indoor Use Only	Temperature: 22°C ± 3°C Humidity: Non-Condensing 20%–80% Altitude: Less than 2,000 m (6,500 ft) Air Quality: Pollution Degree Rating of II For Indoor Use Only	Temperature: 22°C ± 3°C Humidity: Non-Condensing 20%–80% Altitude: Less than 2,000 m (6,500 ft) Air Quality: Pollution Degree Rating of II For Indoor Use Only
Laser		
Three laser system: 660, 635, and 532 nm	Class 2 laser: 630–650 nm	
Dimensions		
W×D×H: 102 cm × 67 cm × 92 cm Weight: 187 kg Crated Weight: 232 kg	W×D×H: 38 cm × 62 cm × 40 cm Weight: 34 kg Crated Weight: 36 kg	W×D×H: 24 cm × 61 cm × 44 cm Weight: 13 kg Crated Weight: 34 kg
Power Requirements		
100–240V AC 50/60 Hz, 20A, 900 Watts	100–240V AC 50/60 Hz, 4A, 400 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.		

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