

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/mm² that pass filtering on a GA_{IIx}.

Throughput

Up to 6.5 Gb per day for a 2 × 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

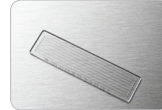
- Greater than 85% bases higher than Q30 at 2 × 50 bp
- Greater than 80% bases higher than Q30 at 2 × 100 bp

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)

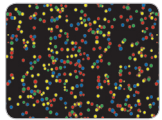
- Flow cell and pre-filled reagents placed on Genome Analyzer_{IIx}
- Complete walk-away automation, including support for longer reads

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

