

Single and Paired-End Reads, Short and Long Inserts

The Genome Analyzer_{IIe} supports single read and paired-end library sequencing. The combination of both short and long insert paired end sequencing, coupled with 2x150 base read lengths, greatly expands the available range of applications. The Genome Analyzer_{IIe} requires the standard Illumina Paired-End Module for automated reagent delivery and second read sequencing (Figure 2).

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).

Proven Sequencing Chemistry

The Genome Analyzer_{IIe} uses sequencing by synthesis 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.

Genome Analyzer_{IIe} Performance Parameters

Read Length	Run Time (Days)	Output (Gb)
1 x 35 bp	~2	4 – 4.5
2 x 50 bp	~5	6.5 – 8
2 x 75 bp	~7.5	16 – 18
2 x 100 bp	~9.5	21 – 24
2 x 150 bp	~14	34 – 38

*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_{IIe}

Throughput

Up to 2.7 Gb per day

Reads

Up to 128 million clusters passing filter and up to 256 million paired-end reads

Performance

The Genome Analyzer_{IIe} generates a significant yield of bases greater than Q30

- Greater than 90% bases higher than Q30 at 2 x 50 bp
- Greater than 85% bases higher than Q30 at 2 x 100 bp

Service and Support

Illumina will ensure that your Genome Analyzer_{IIe} 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. Sample Preparation



~6 hours (~3 hours hands-on)

- 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 x 150 bp (< 10 min. hands-on)

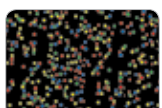
- Flow cell and pre-filled reagents placed on Genome Analyzer_{IIe}
- Complete walk-away automation, including support for longer reads

4. Paired-End module



- Add-on module for automated reagent delivery
- Second read prepared and sequenced while flow cell remains on Genome Analyzer_{IIe}

5. Data Analysis



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

