

# Introducing HiSeq™ 2000

Redefining the trajectory  
of sequencing.



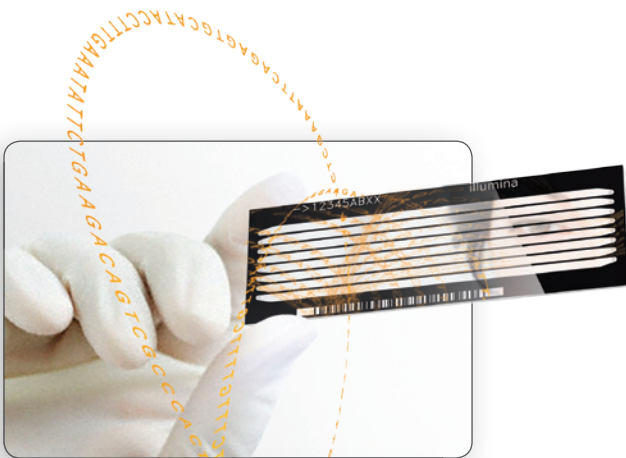
# Redefining the trajectory of sequencing.

HiSeq 2000 combines Illumina's proven sequencing by synthesis (SBS) chemistry with innovative engineering to set new standards in output, user experience, and cost-effectiveness.

Sequence on a scale never before possible.

- Sequence a normal and a cancer human genome at 30x coverage
- Perform gene expression profiling on 200 samples
- Sequence a genome on one flow cell and its epigenome and transcriptome on the other flow cell
- Analyze two human methylomes
- Sequence >16 whole transcriptomes

Each in a single run.



## Unprecedented output.

- Highest sequencing output: up to 200 Gb of data per run
- Highest number of reads: one billion single- and two billion paired-end reads
- Fastest data generation rate: ~25 Gb per day

## Breakthrough user experience.

- Streamlined single-operator workflow: Simple flow cell loading; pre-configured, plug-and-play reagents; touch screen-enabled user interface
- Enhanced experimental flexibility: Single or dual flow cell mode operation; simultaneous processing of different applications
- Simple and efficient data analysis solution: Rapid alignment and variant discovery; intuitive, graphical analysis software

## Unmatched cost-effectiveness.

- 30x coverage of human genome for less than \$10,000 (USD)<sup>1</sup>
- 200 gene expression profiles per run for less than \$200/sample<sup>2</sup>

<sup>1</sup> Reagent costs at list price for shipments to North America

<sup>2</sup> Includes sample/library prep



# HiSeq 2000

Accelerate your research. Perform large-scale studies on complex genomes and transcriptomes more rapidly and economically. Make human genome sequencing routine. Set a new trajectory for your lab.

Sequence more at [www.illumina.com/HiSeq2000](http://www.illumina.com/HiSeq2000)



**WORLDWIDE HEADQUARTERS**

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