





Aleatoriedade, amostragem e reprodutibilidade

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Throughput NGS





				
	iSeq 100 System	MiniSeq System	MiSeq Series	NextSeq Series
Popular Applications & Methods	Key Application	Key Application	Key Application	Key Application
Large Whole-Genome Sequencing (human, plant, animal)				
Small Whole-Genome Sequencing (microbe, virus)				
Exome Sequencing				
Targeted Gene Sequencing (amplicon, gene panel)				
Whole-Transcriptome Sequencing				
Gene Expression Profiling with mRNA-Seq				
Targeted Gene Expression Profiling				
Long-Range Amplicon Sequencing*				
miRNA & Small RNA Analysis				
DNA-Protein Interaction Analysis				
Methylation Sequencing				
16S Metagenomic Sequencing				

How to Choose a Benchtop Sequencer

This Benchtop Sequencing Buyer's Guide has tips to help you make a smooth transition to next-generation sequencing and select the best benchtop sequencing system to achieve your research objectives.

[Read Benchtop Buyer's Guide](#)

Run Time	9–17.5 hours	4–24 hours	4–55 hours	12–30 hours
Maximum Output	1.2 Gb	7.5 Gb	15 Gb	120 Gb
Maximum Reads Per Run	4 million	25 million	25 million †	400 million
Maximum Read Length	2 × 150 bp	2 × 150 bp	2 × 300 bp	2 × 150 bp

				
	NextSeq Series	HiSeq Series	HiSeq X Series†	NovaSeq 6000 System
Popular Applications & Methods	Key Application	Key Application	Key Application	Key Application
Large Whole-Genome Sequencing (human, plant, animal)				
Small Whole-Genome Sequencing (microbe, virus)				
Exome Sequencing				
Targeted Gene Sequencing (amplicon, gene panel)				
Whole-Transcriptome Sequencing				
Gene Expression Profiling with mRNA-Seq				
miRNA & Small RNA Analysis				
DNA-Protein Interaction Analysis				
Methylation Sequencing				
Shotgun Metagenomics				

Optimized NGS Sample Tracking and Workflows

See how BaseSpace Clarity LIMS (Laboratory Information Management System) enabled this large genomics lab to standardize lab procedures and cope with increasing sample volumes from diverse clients.

[Read Case Study](#)

Run Time	12–30 hours	< 1–3.5 days (HiSeq 3000/HiSeq 4000) 7 hours–6 days (HiSeq 2500)	< 3 days	16–36 hours (Dual S2 flow cells) 44 hours (Dual S2 flow cells)
Maximum Output	120 Gb	1500 Gb	1800 Gb	6000 Gb
Maximum Reads Per Run	400 million	5 billion	6 billion	20 billion
Maximum Read Length	2 × 150 bp	2 × 150 bp	2 × 150 bp	2 × 150 bp