

Available equipment and applications for Massive Parallel Sequencing (MPS / NGS)

	MiSeq	HiSeq 1500	NovaSeq 6000
MAIN CHARACTERISTICS*			
Output (Gigabase)	0,3-15	9-500	134-3000
Output (Single reads)	1×10^6 - 50×10^6	300×10^6 - 2000×10^6	1300×10^6 - 10000×10^6
Read length (base)	25-300	36-250	50-150
Run time (h)	4-56	7-144	13-44
Cost/base	High	Medium	Low
No. of simultaneous runs	1	1	2
APPLICATIONS			
Large Whole-Genome Sequencing (human, plant, animal)	-	~	++
Shallow genome sequencing	-	++	++
Small Whole-Genome Sequencing (microbe, virus)	++	+	+
Exome Sequencing	-	++	++
Targeted Sequencing (amplicon based)	++	+	+
Targeted Sequencing (capture based)	+	++	++
Whole-Transcriptome Sequencing	-	++	++
Gene Expression Profiling with mRNA-Seq	-	+	+
Targeted Gene Expression Profiling	~	+	+
Long-Range Amplicon Sequencing	+	+	+
Mitochondrial resequencing	+	+	+
miRNA & Small RNA Analysis	~	+	+
DNA-Protein Interaction Analysis	~	+	+
Methylation Sequencing	-	+	++
Shotgun Metagenomics	-	+	+
16S Metagenomic Sequencing	+	+	+

* Indicative range per run. Values presented for lowest and highest possible outputs.

- Not a compatible application

+ Compatible application

++ Key application

~ Compatible application but not advised