Accessible sequencing solutions

Make a smooth transition to next-generation sequencing

Product	iSeq™ 100	MiniSeq™		MiSeq™Dx*†	MiSeq†			NextSeq™ 550Dx*§
Key methods	Targeted gene sequencing, direct amplicon sequencing, small-genome sequencing	Targeted gene sequencing, targeted gene expression profiling, small-genome sequencing		Targeted DNA sequencing (Dx Mode) All associated MiSeq methods (Research Mode‡)	Targeted gene sequencing, metagenomic sequencing, small-genome sequencing			Targeted DNA sequencing (Dx Mode) All associated NextSeq methods (Research Mode‡)
Flow cell	–	Mid-output	High-output	–	—	Micro	Nano	High-output (Dx Mode)
Flow cells processed per run	1	1	1	1	1	1	1	1
Output range	1.2 Gb	2.1–2.4 Gb	1.9–7.5 Gb	> 5 Gb	3.8–15 Gb	600 Mb–1.2 Gb	300Mb–500 Mb	> 90 Gb
Run time	8–19 hours	4–17 hours	4–24 hours	< 28 hours	21–56 hours	10–19 hours	17–28 hours	< 35 hours
Clusters passing filter per flow cell	4 million	8 million	25 million	15 million	25 million	4 million	1 million	400 million
Maximum read length	2 × 150 bp	2 × 150 bp	2 × 150 bp	2 × 300 bp	2 × 300 bp	2 × 150 bp	2 × 250 bp	2 × 150 bp

*For In Vitro Diagnostic Use

†For MiSeq Reagent Kit v3 only

‡Refer to MiSeq System and NextSeq 550 System for Research Mode specifications

§The NextSeq 550 System has identical sequencing specification to the NextSeq 500 System and includes array scanning functionality for cytogenomic and karyomapping applications.

Large-scale sequencing solutions

Power tailored for population and production studies

Product	NextSeq 550*		HiSeq™ 4000	HiSeq X Ten†	NovaSeq™ 6000			
Key methods	Gene expression profiling, coding and non-coding RNA, exome, targeted gene sequencing, whole-genome sequencing		Exome, whole-transcriptome, whole-genome sequencing	Whole-genome sequencing	Exome, whole-transcriptome sequencing, liquid biopsy development, methylation, single-cell applications, whole-genome sequencing			
Flow cell	Mid-output	High-output	–	–	SP	S1	S2	S4
Flow cells processed per run	1	1	1 or 2	1 or 2	1 or 2	1 or 2	1 or 2	1 or 2
Output range	20–39 Gb	30–120 Gb	125–1500 Gb	900–1800 Gb	80–800 Gb	167–1000 Gb	417–2500 Gb	2000–6000 Gb
Run time	15–26 hours	11–29 hours	< 1–3.5 days	< 3 days	13–38 hours	13–25 hours	16–36 hours	36–44 hours
Clusters passing filter per flow cell	130 million	400 million	2.5 billion	3 billion	800 million	1.6 billion	4.1 billion	10 billion
Maximum read length	2 × 150 bp	2 × 150 bp	2 × 150 bp	2 × 150 bp	2 × 250 bp	2 × 150 bp	2 × 150 bp	2 × 150 bp

*The NextSeq 550 System has identical sequencing specification to the NextSeq 500 System and includes array scanning functionality for cytogenomic and karyomapping applications.

†Specifications shown are for an individual HiSeq X instrument. The HiSeq X System is available only as part of the HiSeq X Five or HiSeq X Ten System.