

**Supplementary Table 3. Strategy, technology and performance of NGS platforms.**

Platform	Instrument	Output per Run	Maximum Read Length	Read per Run	Run Time	Error Bias	Sequencing Technology	Library amplification	Advantages	Limitations
ABI/SOLiD <sup>a</sup>	SOLiD 5500 W	160–260 Gb	75 bp	3 B	5–8 d	mismatch	Sequencing by ligation	EmPCR	High throughput	Cumbersome emPCR; long run time
	SOLiD 5500 xl W	160–320 Gb	75 bp	6 B	4–8 d	mismatch				
Illumina <sup>a</sup>	NovaSeq 6000 System	65–3000 Gb	2 × 150 bp	1.3–20 B	13–44 h	mismatch	Reversible terminator sequencing by synthesis	Bridge amplification	Very high throughput	Run and read length; high investment for the instrument
	HiSeq X Series	1.6–1.8 Tb	2 × 150 bp	5.3–6 B	< 3 d	mismatch				
	HiSeq 4000 System	105–1500 Gb	2 × 150 bp	2.1 M–5 B	<1–3.5 d	mismatch				
	NextSeq Series	25–120 Gb	2 × 150 bp	130–400 M	12–30 h	mismatch				
	MiSeq Series	540 Mb–15 Gb	2 × 300 bp	1–25 M	4–55 h	mismatch				
	MiniSeq System	1.65–7.5 Gb	2 × 150 bp	7–25M	4–24 h	mismatch				
iSeq 100 System	144–1.2 Gb	2 × 150 bp	4 M	9–17.5 h	mismatch					
Ion Torrent <sup>a</sup>	Ion PGM	100 Mb–2 Gb	400 bp	0.6–5.5 M	2–7 h	indel	Sequencing by synthesis	EmPCR	Read length; short run time	Increased errors rate by multiple PCR steps
	Ion Proton	10–32 Gb	200 bp	82–330 M	2–4 h	indel				
	Ion GeneStudio S5	0.5–50 Gb	600 bp	2–130 M	3–24 h	indel				
Pacific Biosystems <sup>b</sup>	PacBio RSII	500 Mb–1 Gb	13500 bp	560–660 M	0.5–4 h	indel	Single-molecule, real-time DNA sequencing by synthesis	No PCR	Long reads; short run time	Reads per run low; high error rates
	Sequel	5–10 Gb	10000 bp	350 M	8 h	N/A				
Oxford Nanopore <sup>b</sup>	MinION	1–5 Gb	100 kb	100 M	1–2 d	indel mismatch	Nanopore exonuclease sequencing	No PCR	Long reads; low cost	High error rates
BGI Group <sup>b</sup>	BGI500SEQ	20 Gb	100		24 h	N/A	Probe-Anchor Synthesis (cPAS) and DNA Nanoballs (DNB)	Rolling circle replication	High throughput; low error rate	Read length

Abbreviations: M=million; B=billion; h=hours; d=days

(a) Second generation sequencing

(b) Third generation sequencing