PARAMETER	BASIC SPECS OF SEQUENCING PLATFORMS[1]			
	NovaSeq6000	**MiSeq**	**iSeq**	**PacBio SEQUEL IIe**
Chemistry	SBS reverse terminators Two-color	SBS reverse terminators Four-color	SBS reverse terminators Two-color	Direct SBS, Single molecule seq, cleavable fluor (gammaP)
Seq Configurations	Four types of flow cells (S4, S2, S1, SP) SE or PE 35-250 cycles	Single loading port per flow cell run	One flow cell	8 independent SMRT cells per run
Most common error	Substitutions, G-C bias	Substitutions, G-C bias	Substitutions, G-C bias	Insertions GC deletions
% Error rate[3]	<0.1	<0.1	<0.1	CLR (12-15), CCS/HiFi <0.1)
Seq Read length	35-250 bp PE 250 only on SP	35-300 bp	35-150 bp	Large-insert genomic: 10-30 kb Amplicon, IsoSeq: 30-50 kb
SE Reads/full run	S4: 10 Billion S2: 4 Billion S1: 1.6 Billion SP: 800 Million	10-13 M (v2) 20-25 M (v3)	4 M	3-5 M
Max output/ PE run (in Gb)	S4: 3000 Gb S2: 1250 Gb S1: 500 Gb SP: 250 Gb PE150, 400 Gb PE250	V3: 4-15 Gb V2: 0.75-7.5 Gb Micro: 1.2 Gb Nano: 0.5 Gb	1.2 Gb	Library- and movie-dependent • Large-insert genomic: 60-120 Gb • Amplicon, IsoSeq: 80-200 Gb
Run time	1-2 days	1-3 days	10-20 hr	10h- 30h/ SMRT cell
[4]Cost/Gb in USD	S4: ~5-8 (format dependent) S2: ~8-20 S1: ~12-26 SP: ~12-35	V3: 127-325 V2: 200-1500 Micro: 542 Nano: 1100-1650	550	Library- and movie- dependent 12-30
Most common app	• Ultra-high throughput • Whole genome seq • Variant Analysis, genotyping • Transcriptome (RNAseq) • ChIP seq, SeqCap (ExomeSeq) • Methylation Anal (WGBS, RRBS) • ATAC-Seq • Single-cell Seq	• Amplicon (e.g., 16S metagenomics) • Targeted RNAseq • Variant Analysis	• Library QC for balancing pools • Small amplicon pools	• *De novo* sequencing • Isoform analysis (IsoSeq) • Amplicon Seq • SNP validation • Direct methyl-seq • Microbial seq • Variant analysis