**S1 Table. Development of sequencing technologies over time** [1–6]**.**

| Time frame | <2005 | 2005 | 2008 | 2010 | 2011 | 2011 | 2011 | 2011 | 2012 | 2012 | 2013 | 2013 | 2013 | 2015 | Future |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Sequencing technology** | Sanger (ABIXXX) [2] | 454 GS20 [3] | 454 GS FLX Titanium [3] | Illumina Hiseq 1000 [4] | 454 GS FLX+ [3] | Illumina Miseq [4] | Ion Torrent PGM [2] | PacBio RS [5] | Ion Torrent PGM [2] | Illumina Hiseq 2000/2500 [4] | Illumina Miseq v3 [4] | TruSeq Synthetic Long-Reads (Moleculo) [4] | PacBio RS II [5] | Illumina Hiseq 3000/ 4000 [4] | Oxford nanopore MiniON [6] |
| **Read length [bp]** | 800-1200 | 100 | ~400 | 100 | ~700 | 150 | 50-100 | 5000-9000 | 400 | 100-150 | 300 | ~10,000 | 15,000 | 150 | >10,000 |
| **Technique** | PCR | Emulsion PCR amplification | Emulsion PCR amplification | Cluster amplification | Emulsion PCR amplification | Cluster amplification | Emulsion PCR amplification | Single molecule real-time sequencing (SMRT) | Emulsion PCR amplification | Cluster amplification | Cluster amplification | Labelled sublibraries, cluster amplification & local pre-assembly | Single molecule real-time sequencing (SMRT) | Normalized cluster amplification | Single molecule nanopore threading |
| **Output per run** | 96 Kb | 20 Mb | ~400 Mb | 300 Gb | ~700 Mb | 2Gb | 100-200 Mb | 100 Mb per SMRT cell | >1Gb | 600-1000 Gb | 15 Gb | >600 Mb long read data per library & lane (+) | 1 Gb per SMRT cell | 750-1500 Gb | NA |
| **Costs per Mb** | $2400 | $166 | $12 | $0.04 | $9 | $0.50 | $0.70 | $2 | $1 | $0.04 | $0.08 | <$1.4 (+) | $0.60 | NA | NA |
| **Time per run** | 12h | 24h | 24h | 9 days | 24h | 20-36 h | 3h | 2h | 4 h | 4-11 days | 20-36 h | ~2-6 days (+) | 4 h | 4 days | NA |
| **Problems/ pitfalls** | Cloning bias for shotgun libraries | Homopolymer stretches | Homopolymer stretches | GGCxG motifs | Homopolymer stretches | GGCxG motifs | Homopolymer stretches | High random error rates | Homopoly-mer stretches | GGCxG motifs | GGCxG motifs | Local pre-assembly breaks at repeats | Quite high random error rate | GGCxG motifs | High random error rates |

(+) Depends on sequencing machine and size of target genome

**References:**


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