**Supplementary Information.**

**Table S1.** Comparison of the most commonly used sequencing platforms for SARS-CoV-2 sequencing.

| Platform | Cost and maintenance | Advantages | Limitations | Genome SARS-CoV-2 cost and coverage | Sequencing yield and samples per run | Pipeline |
|---|---|---|---|---|---|---|
| Illumina | Moderate sequencing cost, high start-up cost. Frequent maintenance [240]. | High capacity to sequence large volumes of samples. High accuracy in SNV. Well-established methods of analysis [240]. Clinical application use [241] | High cost of maintenance. 300pb maximum read size [240]. | 32.5 USD per genome on Illumina NextSeq 550. Coverage 300-600x, ≥ 99%, [242,243] Sample viral load up to 30 Ct value | 1.2-6000Gb[243] 12-3072 samples per run. | Base calling and demultiplexing with Bcl2Fastq [244]. Removal adaptors and trimming with Cutadapt [245] and Trimmomatic [246]. Alignment with Bowtie2 [247]. Variant calling with Samtools mpileup and BCFtools [248]. |

| | | | | | | |
|---|---|---|---|---|---|---|
| Oxford Nanopore | Low cost of sequencing, low start-up cost. Without maintenance [240]. | Very portable sequencer. It is obtaining data in real-time. Long reads 13-20 kb. RNA-direct sequencing [240]. | They are constantly changing analysis methods.<br><br>Moderate accuracy in SNV [249].<br><br>Homopolymers complicated to sequence. | 29 USD per genome on MinION[249].<br><br>Coverage 800-1000x, ≥ 99%,<br><br>Sample viral load up to 31 Ct value [249] | 1.8-245Gb[250]<br><br>12-2,304 samples per run. | Base calling and demultiplexing with Guppy [251].<br><br>Alignment with Minimap2 [252].<br><br>Variant calling with Nanopolish [253] or Medaka [254]. |
| Ion Torrent | Moderate start-up and sequencing cost. Frequent maintenance [240]. | Library generation automatic. High accuracy in SNV. Fast sequencing. | Homopolymers complicated to sequence. | 122 USD per genome on GeneStudio S5<br><br>Coverage 3,000x, ≥ 99%, [255]<br><br>Sample viral load up to 38 Ct value[256] | 0.5-50Gb[257]<br><br>2-80 samples per run. | Similar pipeline to Illumina can be used. |
| Pacific Biosciences | Moderately high cost of sequencing and start-up. Frequent maintenance [240]. | Long reads 10-16 kb. Sequencing genomic regions such as high/low G + C, tandem repeat, and interspersed repeat regions. RNA-direct | High raw error rate up to 8%, Low accuracy in SNV [258]. | | 18-680Gb [259] Up to 900 samples per run [260]. | Demultiplexing with lima, USEARCH to reoriented 5′-3′ direction, Cutadapt for trimming. Variant calling with Minimap2 [252]. |

sequencing [240].