# NANOPORE

As a potent fourth generation sequencing technology, Nanopore, provides a platform for comprehensive and rapid sequencing of Nucleic Acids for various applicationsSequencing of amplified genome fragments as well as native long read genome with specificity and accuracy is possible along with real time data analysis. This application of Nanopore providing real time data analysis allows the user to examine the data while it is being generated. . With enough data produced, one can stop the sequencing at any point of time and also re-sequence , if the need arises.

Nanopore provides a platform to sequence amplified products using ARTIC primers pool specific for covid-19, which eliminates the problem of a maximum occupancy of false reads on different platforms of NGS, when RNA is isolated from the patient and might have more than 90% of human RNA contamination. Due to the enrichment of the target panel, minimal input or even poor-quality DNA can be efficiently sequenced with the promising Oxford Nanopore technology.

The Oxford Nanopore Technology, offers user friendly and less time-consuming library prep protocol (from RNA to full SARS-CoV-2 consensus sequence in ~7hours) with multiplexed samples. This technique can be used to analyze variants and mutations thus, identifying the various strains of the Virus.

# MiSeq & NextSeq

MiSeq and NextSeq are Illumina sequencing platforms that perform on the reversible-terminator sequencing-by-synthesis principle to provide high throughput end-to-end sequencing results.

Small genomes like Covid-19 can be efficiently sequenced with the help of Nextera XT lib preparation kit (Illumina) within 90 minutes,where cDNA libraries can be prepared using Nextera XT library preparation kit without any enrichment protocol and can further be sequenced on the MiSeq and NextSeq illumina platforms efficiently. This can also be beneficial for validating the results of the nanopore sequencing.

In terms of efficiency, initially, when the results were compared, Multiplex sequencing on the MiSeq platform with 301 paired end reads generated data with 75% of the success rate. Then after, with the hike in the sample numbers, in order to generate more data for efficient analysis, NextSeq was performed with 151 paired end reads. In addition to the validation of the Nanopore results of the Covid-19 sequencing, Miseq and NextSeq sequencing also provide a privilege of scrutinizing human trancriptomics and host body responses which speaks lot about their potential applications at large.