Related work

Nanopore sequencing offers an alternative to established short-read platforms for viral WGS with several advantages. ONT devices: are relatively inexpensive, highly portable and require minimal associated laboratory infrastructure; enable rapid generation of sequencing data and even real-time data analysis; require comparatively simple procedures for library preparation and; offer flexibility in sample throughput, accommodating single , multiple or tens/hundreds of specimens per flow-cell16,18.

Due to the relatively low mutation rate observed in SARS-CoV-226, accurate sequence determination is vital to correctly define the phylogenetic structure of disease outbreaks. With ONT sequencing known to exhibit higher read-level sequencing error rates than short-read technologies23,24,25, reasonable concerns exist about suitability of the technology for SARS-CoV-2 genomics.

The present study resolves these concerns, demonstrating accurate consensus-level SARS-CoV-2 sequence determination with ONT data. Although SNVs alone are sufficient for routine phylogenetic analysis, small indels and large structural variants can profoundly impact gene function and are, therefore, of interest to studies of virus evolution and pathogenicity15.

While short-read sequencing platforms remain the gold-standard for high-throughput viral sequencing, the advantages to portability, cost and turnaround-time afforded by nanopore sequencing imply that this emerging technology can serve an important complementary role in local, national and international COVID-19 response strategies.