We prepared RNA extractions for Oxford Nanopore (ONT) MinION sequencing of SARS-CoV-2 viral genomes. We made modifications to the ARCTIC Network Protocol ([v2](https://www.protocols.io/view/ncov-2019-sequencing-protocol-v2-bdp7i5rn)) (Tyson *et al.*, 2020), to optimize sequencing for environmental samples. Our complete protocol is available online (protocols.io, forthcoming). In brief: we conducted random hexamer primed reverse transcription and amplified cDNA using v3 primers, which tile the entire viral genome (save for non-coding regions at the genome ends) with overlapping 400bp fragments. We concentrated PCR products using the Zymo Select-a-Size DNA Clean & Concentrator Kit (Zymo Research, Irvine CA), ligated barcodes using the Oxford Nanopore Native Barcoding kit, and ligated sequencing adaptors. Samples were run on ONT R9.4 flow cells. We followed the [ARTIC Network bioinformatics SOP](https://artic.network/ncov-2019/ncov2019-bioinformatics-sop.html), which in brief involved high accuracy basecalling and demultiplexing using ONT Guppy, mapping reads to the Wuhan-Hu-1 (accession MN908947) reference, polishing with Nanopolish, and consensus generation.

Tyson JR, James P, Stoddart D, Sparks N, Wickenhagen A, Hall G, *et al.* (2020). Improvements to the ARTIC multiplex PCR method for SARS-CoV-2 genome sequencing using nanopore. *bioRxiv*. e-pub ahead of print, doi: 10.1101/2020.09.04.283077.