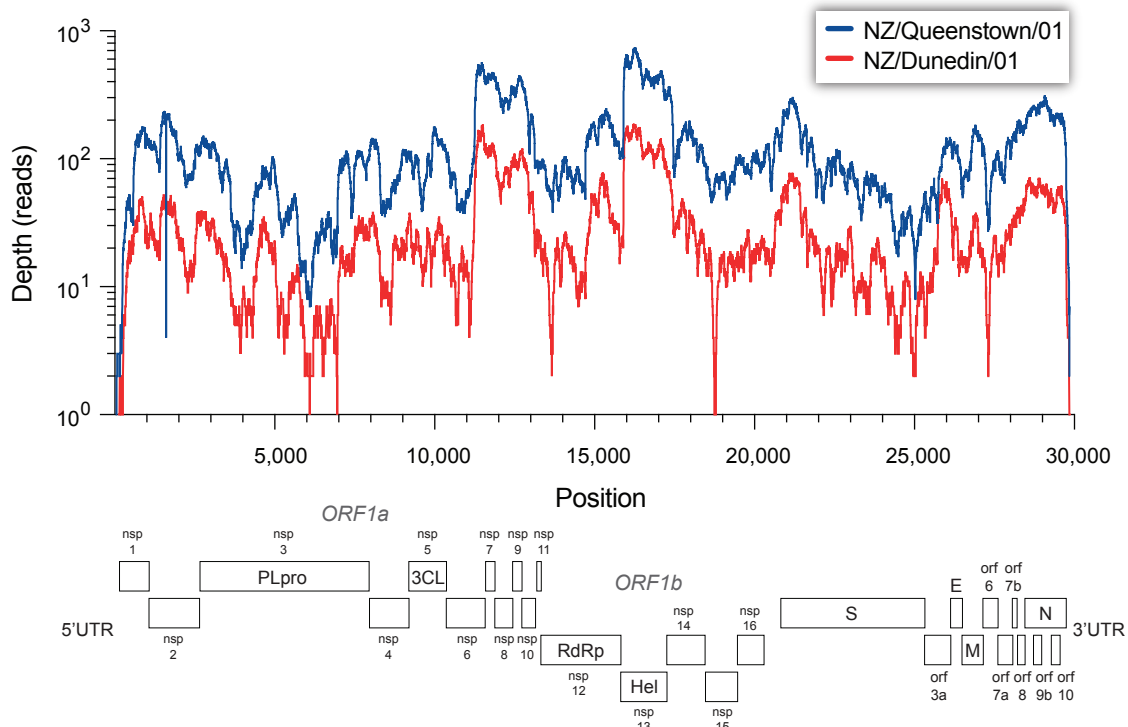
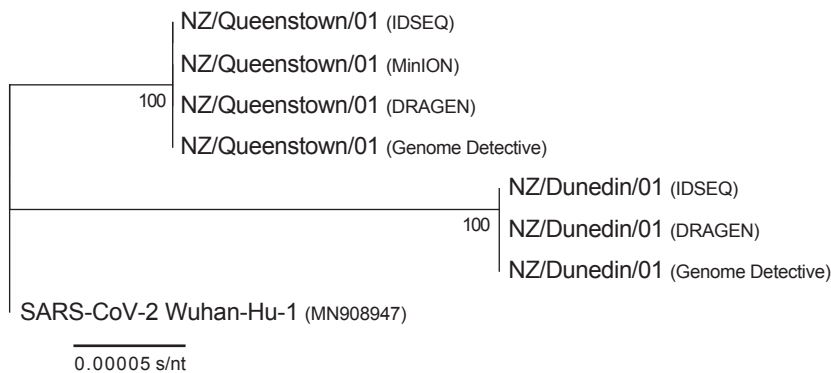


A. Coverage



B. Phylogenetic analysis



Supplementary Figure S1. (A) Coverage, i.e., number of reads per nucleotide position, obtained by deep sequencing of the first two COVID-19 cases identified in South Island, New Zealand. Near whole genome SARS-CoV-2 sequences were obtained as described in Materials and Methods. The position relative to the Wuhan-Hu-1 (NC_045512) SARS-CoV-2 reference strain is indicated. (B) Maximum Likelihood phylogenetic tree constructed using whole genome SARS-CoV-2 sequences generated (mapped and aligned) using four different software tools: GISAID, DRAGEN Bio-IT Platform (Illumina), Genome Detective Virus Tool, and IDSEQ (see Materials & Methods for details). Bootstrap resampling (1,000 data sets) of the multiple alignments testing the statistical robustness of the trees (%) is indicated. s/nt, substitutions per nucleotide.