S1 FIG: Sequencing of SARS-CoV-2 from 6/9 healthcare workers with active infection (numbers on y-axis correspond to those in Supplementary Table 3). A multiple sequence alignment of all consensus reads and the MN908947.3 reference was generated, then used to build a phylogenetic tree using augur (https://github.com/nextstrain/augur). Variants were called using scripts developed as part of the nCoV-tools package (https://github.com/jts/ncov-tools). Sites with single base substitutions are shown, with N indicating no coverage at the site. For genome completeness, a cut-off of 75% was used to sequence samples. Three of the nine samples did not meet this cut-off. Genome completeness ranged between 83.7-97.1%. Results demonstrate 3 variants. The D614G mutation, which occurs at nucleotide position 23403 of the reference strain, is indicated with an arrow.