RESEARCH ARTICLE

# Figures and figure supplements

Screening of healthcare workers for SARS-CoV-2 highlights the role of asymptomatic carriage in COVID-19 transmission

**Lucy Rivett *et al***

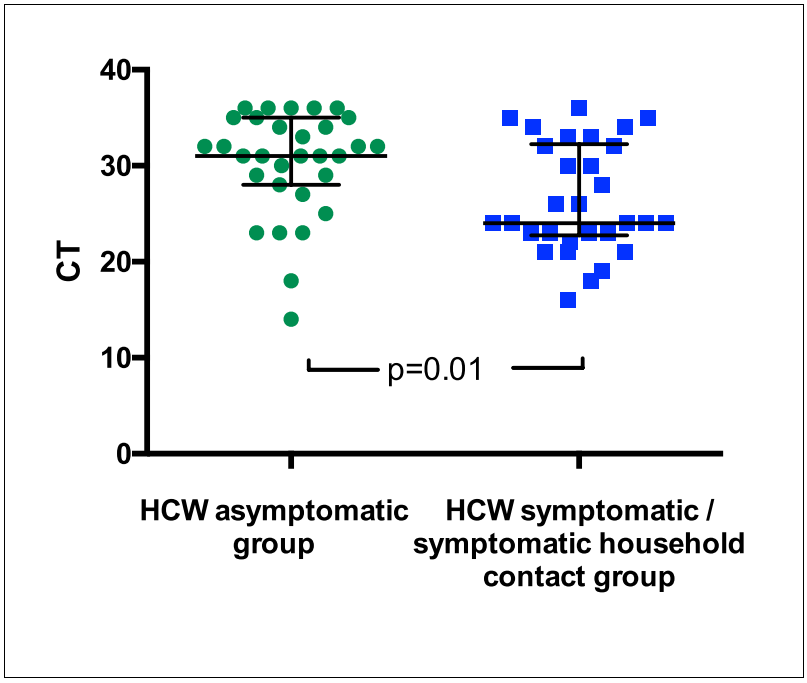


**Figure 1.** SARS-CoV-2 RNA CT (cycle threshold) values for those individuals who tested positive shown according to HCW group. *HCW asymptomatic screening group* (green circles); *HCW symptomatic* or *symptomatic household contact screening groups* (blue squares). A Mann Whitney test was used to compare the two groups. Bars: median + / - interquartile range. Note that lower CT values correspond to earlier detection of the viral RNA in the RT-PCR process and therefore identify swabs with higher numbers of copies of the viral genome.

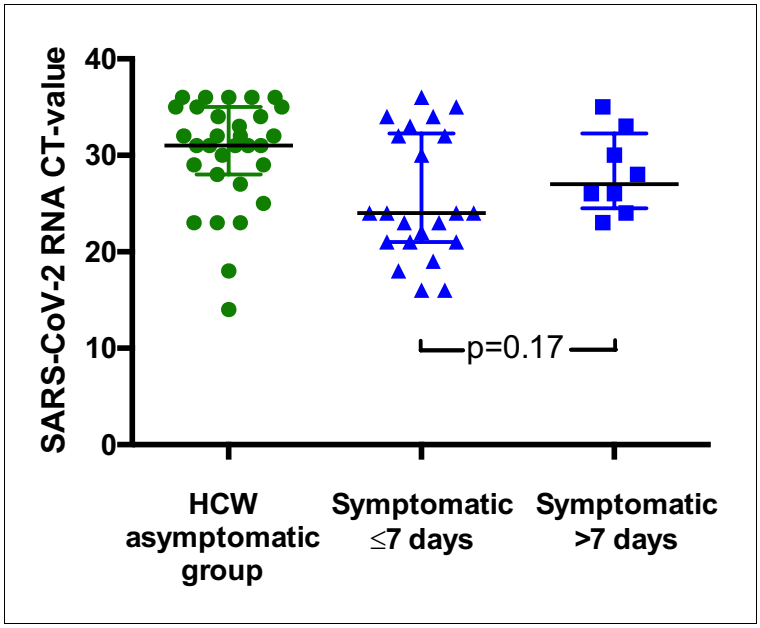


**Figure 1—figure supplement 1.** SARS-CoV-2 RNA CT values for HCWs testing positive according to presence and duration of symptoms. Results from the HCW symptomatic and HCW symptomatic contact groups are considered together in this figure. Individual CT values are shown, along with median and interquartile range for each group. (A). (B).

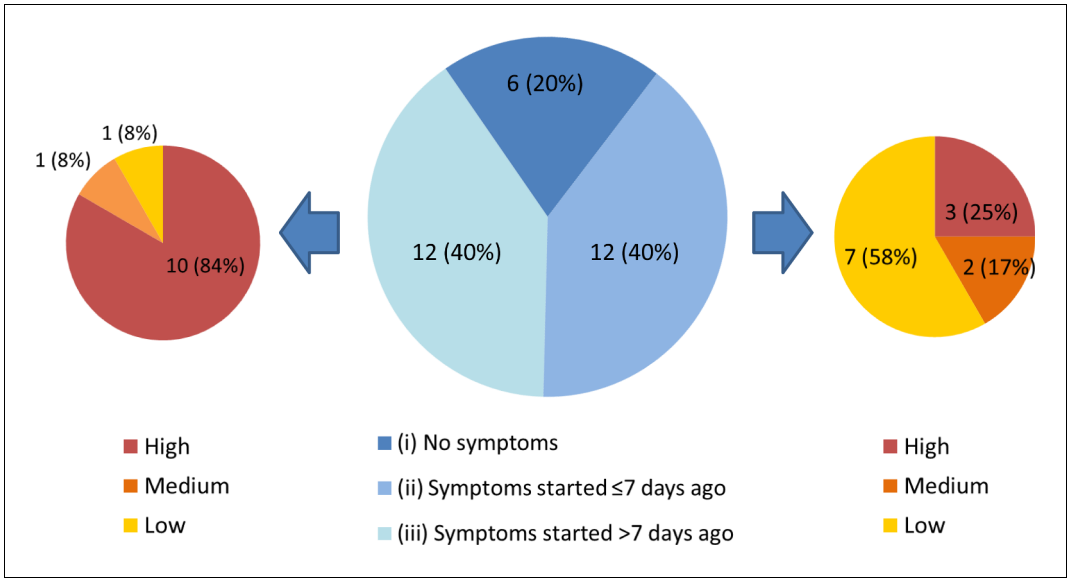


**Figure 2.** Three subgroups of staff testing SARS-CoV-2 positive from the *HCW asymptomatic screening group*. (central pie chart, described in detail in the main text). n = number of individuals (% percentage of total). The peripheral pie charts show number and percentage of individuals in groups (ii – right pie chart) and (iii – left pie chart) with low, medium and high COVID-19 probability symptoms upon retrospective analysis.

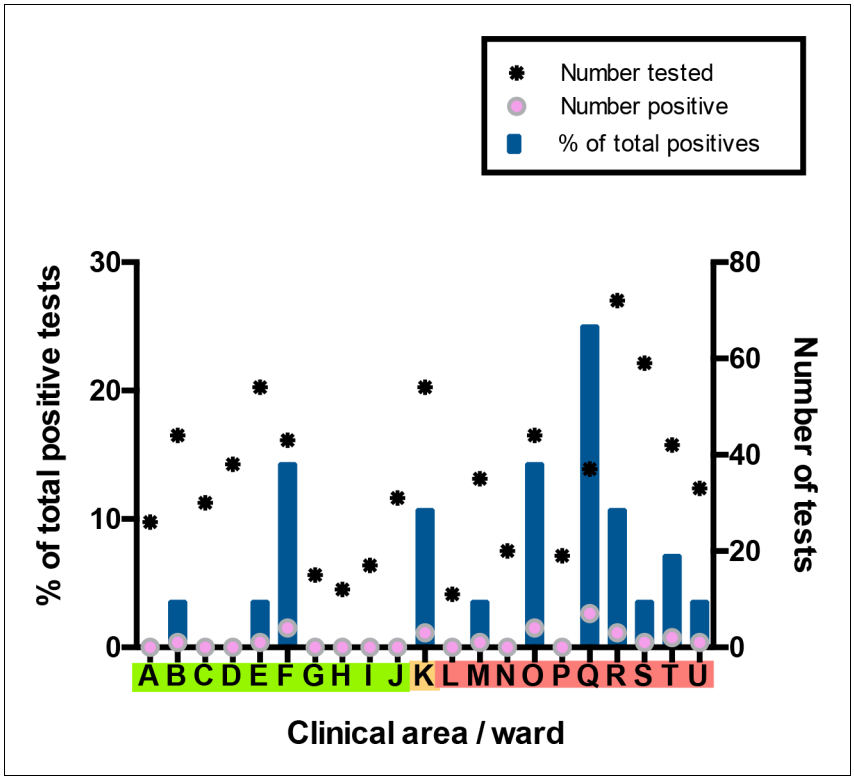


**Figure 3.** Distribution of SARS-CoV-2 positive cases across 21 clinical areas, detected by ward-based asymptomatic screening. (underlying data shown in 'Source Data'). Wards are coloured ('green', 'amber', 'red') according to risk of anticipated exposure to COVID-19 (***Table 4***). HCWs working across >1 ward were counted for each area. The left-hand y-axis shows the percentage of positive results from a given ward compared to the total positive results from the *HCW asymptomatic screening group* (blue bars). The right-hand y-axis shows the total number of SARS-CoV-2 tests (stars) and the number positive (pink circles). Additional asymptomatic screening tests were subsequently performed in an intensified manner on ward F and ward Q after identification of clusters of positive cases on these wards (***Figure 4***). Asymptomatic screening tests were also performed for a number of individuals from other clinical areas on an opportunistic basis; none of these individuals tested positive. Results of these additional tests are included in summary totals in ***Table 1***, but not in this figure.

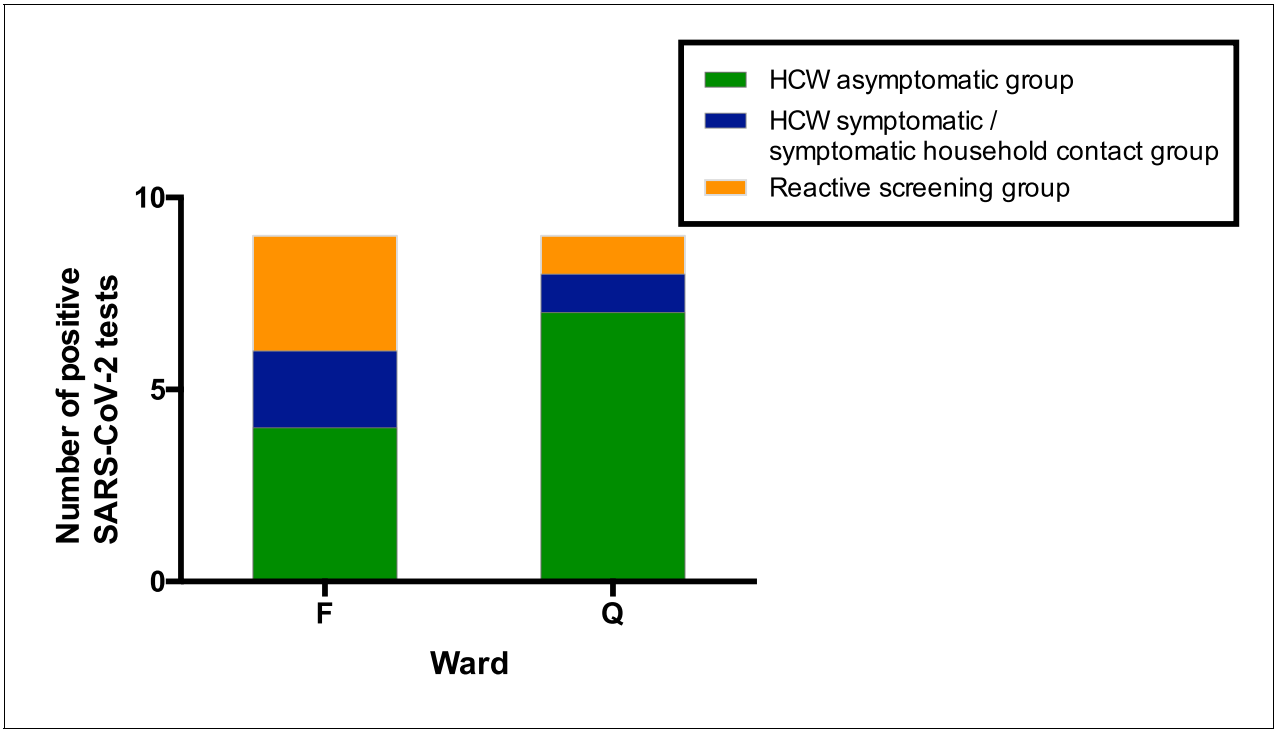


**Figure 4.** All SARS-CoV-2 positive HCW identified in Wards F and Q, stratified by their mechanism of identification. Individuals testing positive for SARS-CoV-2 in the '*HCW asymptomatic screening group*' were identified by the asymptomatic screening programme. Individuals testing positive in the '*HCW symptomatic/symptomatic household contact groups*' were identified by self-presentation after developing symptoms. Individuals testing positive in the '*Reactive screening group*' were identified by an intensified screening programme after initial positive clusters had been recognised.

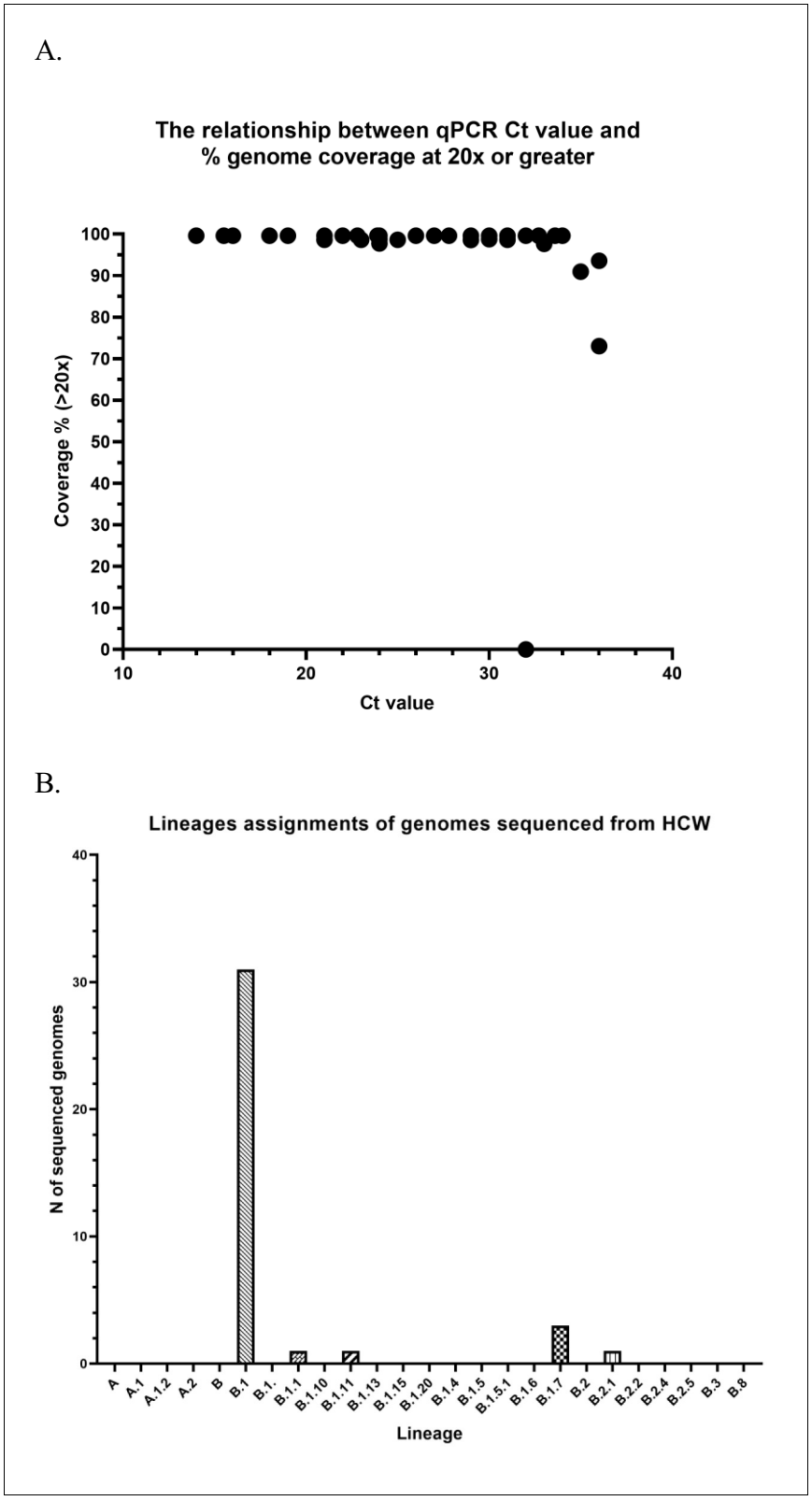


**Figure 4—figure supplement 1.** Further details of sequencing data. (**A**) Comparisons of sequencing success rate vs Ct of HCW samples. Samples with CT less than 33 typically yielded genomes > 90% coverage at a minimum depth of 20x. (**B**) Lineage assignment of SARS CoV-2 genomes from HCW positive samples. Lineage assignments were generated using the PANGOLIN utility using a comparison against all currently circulating reference lineages.

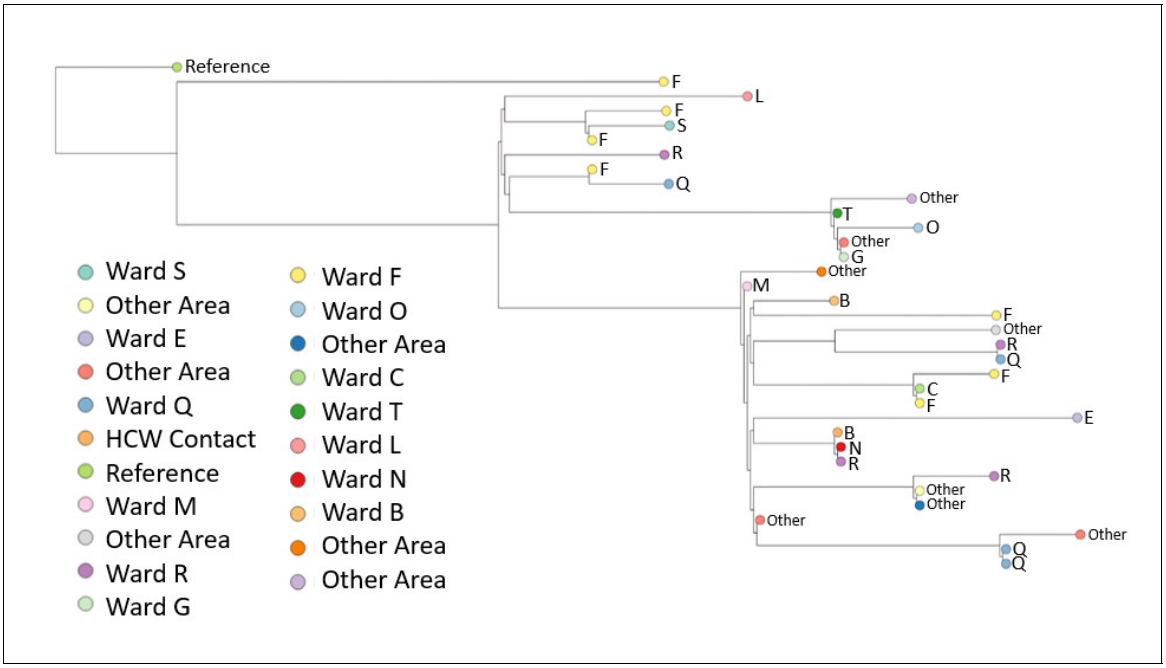


**Figure 4—figure supplement 2.** Phylogenetic tree of 34 healthcare worker (HCW) SARS-CoV-2 genomes. Branch tips are coloured by HCW base ward. 34/35 sequenced genomes passed the filter of <2990 (~10%) N. A SARS-CoV-2 genome collected in Wuhan in December 2019 was selected to root the tree, visualised initially on Nextstrain (https://nextstrain.org/) and the fasta file was downloaded from GISAID (ID: EPI ISL 402123) (https://www.gisaid.org/). Multiple sequence alignment of consensus fasta files was performed using MAFFT with default settings (Katoh K. MAFFT version 7. https://mafft.cbrc.jp/alignment/software/). The alignment was manually inspected using AliView (University U. AliView. https://ormbunkar.se/aliview/). A maximum likelihood tree was produced using IQ-TREE software (http://www.iqtree.org/) with ModelFinder Plus option (-m MFP), which chooses the nucleotide substitution model that minimises Bayesian information criterion (BIC) score. The model 'chosen' was TPM2u+F (details: http://www.iqtree.org/doc/Substitution-Models). The tree was manually inspected in FigTree (http://tree.bio.ed.ac.uk/software/figtree/), rooted on the 2019 Wuhan sample, ordered by descending node and exported as a Newick file. The tree was visualised in the online software Microreact (https://microreact.org/showcase) in a private account, exported as a png image, which is shown here. Due to low genetic diversity in the virus (very recent introduction) genomic similarity alone cannot be used to infer transmission chains, as viruses can be identical by chance. Achieving higher resolution on transmission chains requires integrating clinical and detailed epidemiological data with genomic data from HCW and patients to uncover plausible transmission pathways.