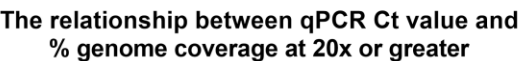
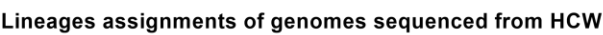


A.



B.



**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.