Figure Legends

Figure 1) Schematic of the CRICK COVID-19 Consortium test and reporting pipelines A) For the CRICK COVID-19 Consortium test, specimen barcodes are scanned at sample reception, prior to viral inactivation in a Class I or II safety cabinet, processing through RNA extraction using an in-house protocol and RT-PCR testing using a commercial kit (BGI). **B)** CRICK COVID-19 Consortium reporting pipeline. Test results are reported through a custom-made remote web application, allowing remote clinical scientists and pathologists working outside of the institute to authorise reports, in line with the established SOP.

Figure 2) CRICK-COVID-19 Consortium RT-PCR test validity and specificity. A) Dot plot demonstrating the COVID-19 Ct values obtained from 2 repeats of processing 37 samples through the CCC test (red and orange dots) alongside Ct values derived from the reference laboratory using the N gene assay (gray dots). The clinical call from the reference laboratory is indicated above the boxes; POSITIVE, NEGATIVE, BORDERLINE POSITIVE or NON COVID VIRUS. All repeats were independently re-extracted from the original inactivated virus solution. Ct values of 'undetermined' are plotted as ">40" for illustrative purposes. This set of 37 includes 27 current clinical samples taken for diagnosis of COVID-19 and a further 10 samples classified as Non-COVID virus from patients known to be infected with other viruses such as Flu A, Flu B, RSV, rhinovirus, metapneumovirus, parainfluenza virus. **B)** Dot plot demonstrating the COVID-19 Ct values obtained from a repeat (1 test performed at the research institute using the BGI kit, 1 performed at the reference laboratory using the N gene assay) of processing an independent batch of 29 samples through the RT-PCR assay. All repeats were independently re-extracted from the original inactivated virus solution. Ct values of 'undetermined' are plotted as ">40" for illustrative purposes. CCC 'failed' swabs, with negative internal control signal, are marked with the '*' symbol. **C)** Table to summarise the concordance of the CCC test with the reference laboratory results for the 56 COVID-19 testing

specimens from A and B. **C)** ROC curve illustrating CCC test specificity and sensitivity. The positive predictive value is 100% and the negative predictive value is 90.9%.

Figure 3) CRICK COVID-19 Consortium test sensitivity and reproducibility A) SARS-CoV-2 titration curve. Ten-fold serial dilutions of patient samples were carried out by the reference laboratory. Following RNA extraction, RT-PCR was performed to determine the linearity of the detection process using the BGI kit. **B)** Dot plot showing assay precision. Five aliquots of one COVID-19 positive sample were processed through independent repeats of RNA extraction and RT-PCR using the BGI kit to determine the precision of the CCC test. Data are shown for COVID-19 target (left) and internal control target (right). CV = coefficient of variation.

Supplementary Figure 1) Example amplification plots from the CRICK COVID-19 Consortium test. Illustrations of results that were called **A)** Positive by the reference laboratory, negative by the CCC; **B)** Borderline positive by the reference laboratory, negative by the CCC; **C)** Positive by both the reference laboratory and the CCC; **D)** Negative by the reference laboratory, failed by the CCC.

Supplementary Figure 2) CRICK COVID-19 Consortium test specificity A) CRICK COVID-19 assay specificity using RNA extracted from cell lines. RNA extracted from human cell lines (95 wells) were analysed alongside 1 well of positive control RNA. Only the positive control well displayed a COVID-19 amplification signal (red). The average internal control Ct for human cell line RNA (blue) is 25.55±0.15. **B)** CRICK COVID-19 Consortium assay specificity in “non-sample” wells during “live” runs. For specificity assessment, COVID-19 Ct values from ‘non-sample’ wells (elution buffer + PCR master mix only) were determined during live runs. 24/25 wells showed no detectable Ct value (n=3).

Supplementary Figure 3) CCC test specificity determined using water or guanidine buffer and RNA elution buffer. Amplification plots derived from a plate of 48 no template

controls (water), plus one positive control well. Late-rising curves above the manually set threshold occur at Ct>39.0 in one well for COVID-19 **(A)** and 2 wells at Ct>36.0 for internal control **(B)**. There is no overlap between the well giving late non-specific COVID-19 signal and the 2 wells showing late internal control signal. Amplification plots derived from a plate of 48 no template controls (guanidine + RNA elution buffer), plus one positive control well. Late-rising curves above the manually set threshold occur at Ct>37.0 in 2 wells for COVID-19 **(C)** and 8 wells out of 48 at Ct>35.0 for internal control **(D)**. There is no overlap between the 2 wells giving late non-specific COVID-19 signals and the 8 wells showing late internal control signals. Cts of late rising curves reduce by 1-2 cycles from water control to guanidine + RNA elution buffer.

Supplementary Figure 4) CCC test BGI kit batch reproducibility assessment. A) Amplification plots from a 96 well plate with four columns of 10 fold serial dilutions and 2 columns of negative control run in parallel with 2 different batches of RT-PCR kit from BGI. **B)** Amplification plots illustrated for one column from each kit, which is a 2-fold dilution of positive control down the column. **C)** Amplification plots of 2 columns of negative control loaded wells demonstrating similar numbers of late stage amplification. **D)** Titration curve calculated from data in A for the two batches (blue, batch A, orange batch B).