

# Stability of SARS-CoV-2 RNA in Nonsupplemented Saliva

## Appendix

### Methods

#### RNA extraction and SARS-CoV-2 detection

Saliva samples were self-collected by COVID-19 inpatients and healthcare workers at the Yale-New Haven Hospital (Yale Human Research Protection Program Institutional Review Boards FWA00002571, Protocol ID. 2000027690) (2), into plain wide-mouth containers without the addition of stabilizing buffers. RNA was extracted from saliva samples (1) and tested by RT-qPCR for SARS-CoV-2 RNA (N1) and human *RNase P* (RP) (3) on day of collection ( $\leq 12$  hours post sample collection) and at various time points after the storage of the remaining, unsupplemented samples at temperatures of  $-80^{\circ}\text{C}$ ,  $-20^{\circ}\text{C}$ ,  $+4^{\circ}\text{C}$ , room temperature (measured at an average of  $\sim 19^{\circ}\text{C}$ ), or  $30^{\circ}\text{C}$ .

#### Cell culture

Vero-E6 cells (ATCC) were cultured in Dulbecco's Modified Eagle Medium (Gibco) supplemented with 10% heat-inactivated fetal bovine serum (VWR), 1% Penicillin/Streptomycin (Gibco), 100  $\mu\text{g}/\text{mL}$  gentamicin (Gibco), and 0.5  $\mu\text{g}/\text{mL}$  amphotericin B (Gibco). All cells were incubated at  $37^{\circ}\text{C}$  and 5%  $\text{CO}_2$ . All cell culture experiments were performed in a biosafety level 3 laboratory at Yale University and approved by the Yale University Biosafety Committee.

#### Saliva inoculation and virus culture in Vero-E6 cells

Saliva samples were diluted 1:1 in 1X Dulbecco's PBS (Gibco). Diluted saliva samples were incubated for one hour at  $37^{\circ}\text{C}$  with  $2.5 \times 10^5$  Vero-E6 cells in a 24-well plate (Corning). Unbound virus was aspirated and the media were replaced. Infected Vero-E6 cells were frozen at  $-80^{\circ}\text{C}$  at 1 and 72 hours post-inoculation. Thawed samples were used for plaque assays and RNA extraction. Prior to RNA extraction (1) and RT-qPCR detection of SARS-CoV-2 RNA (3) the Vero-E6 cells from 1 and 72 hours post-inoculation were thawed at room temperature and further

lysed by diluting 1:3 in MagMax Binding Solution (ThermoFisher). RNA was extracted from the two timepoints and tested in RT-qPCR for SARS-CoV-2 N1. We interpreted a Ct reduction  $>2$  as a difference which could potentially be explained by viral replication during the two timepoints.

### **Plaque assay**

Vero-E6 cells were seeded at  $4 \times 10^5$  cells/well in 12-well plates (Corning). The following day, media were removed and replaced with 100  $\mu$ l of 10-fold serial dilutions of thawed 1 hour or 72 hour post-inoculation saliva samples. Plates were incubated at 37°C for 1 hour with gentle rocking every 15 mins. Unbound inocula was aspirated from each well and overlay media (DMEM, 2% FBS, 0.6% Avicel RC-581 (DuPont)) were added to each well. At 48 hours post-infection, plates were fixed with 5-10% formaldehyde for 30 min then stained with crystal violet solution (0.5% crystal violet in 20% ethanol) for 30 mins. Crystal violet solution was then aspirated and plates were washed in tap water to visualize plaques.

### **Statistical analyses**

We fit a linear regression to the experimental stability data to model the change in Ct values of positive samples following stability conditions using the equation below. Let  $dct$  be the change in Ct value from fresh testing following each storage condition and let  $condition$  be the categorical storage condition (e.g. freeze/thaw, room temperature, 30°C, etc).

$$dct \sim condition$$

Robust confidence intervals were simulated from this model using the `mvrnorm`, in the R package “MASS”, and quantile functions. This regression was also used to model the effect of prolonged storage in stability conditions on RP.

For extended timepoint analyses of N1 we used a linear mixed effects model to predict the change in Ct values of positive samples under each stability condition for greater durations of time using the equation below. Let  $timepoint$  be the number of days under stability conditions and let  $sample$  be the patient number.

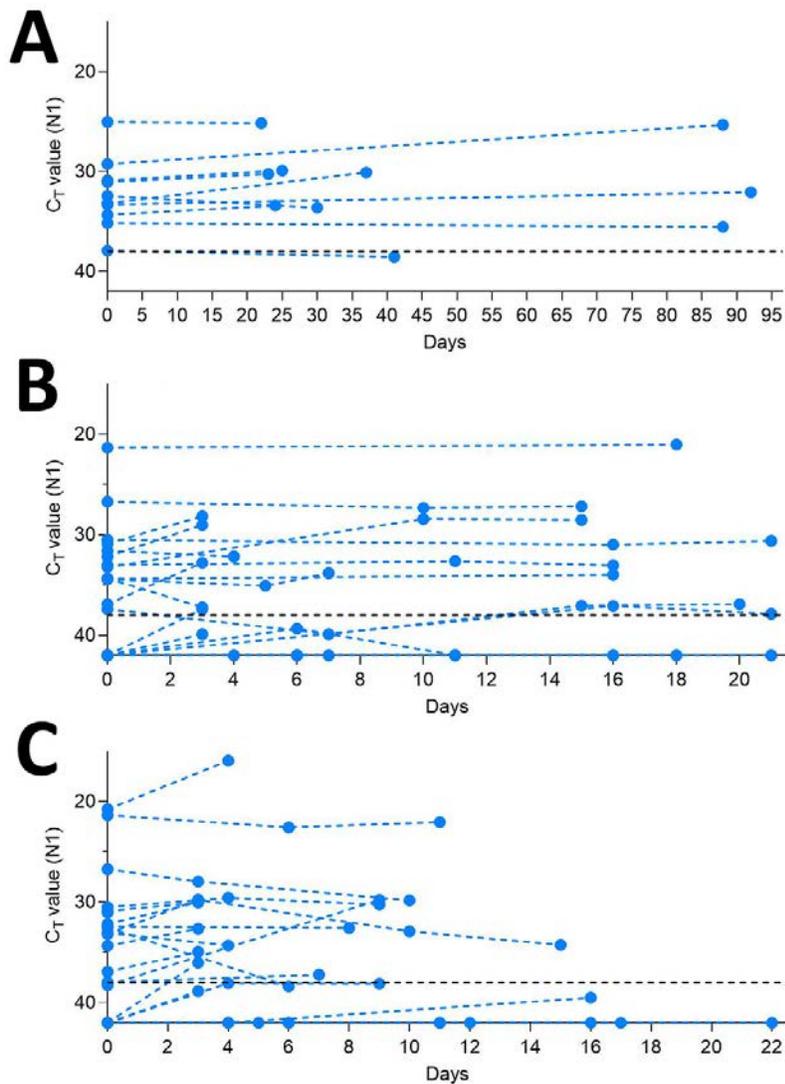
$$dct \sim timepoint + (1|sample)$$

Confidence intervals were computed for this model using `confint.merMod`, in the R package “lme4”.

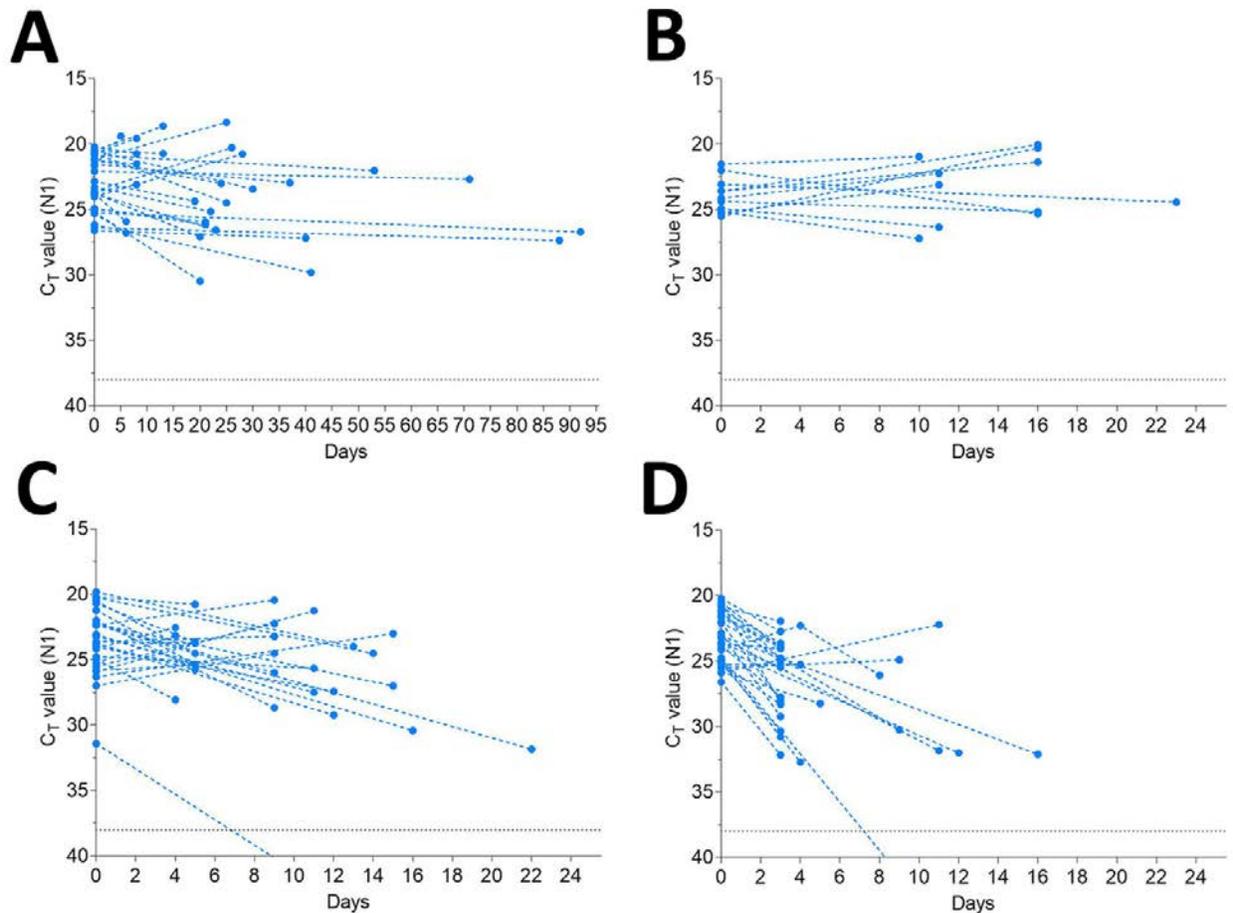
Further statistical analyses were conducted in GraphPad Prism 8.0.0 as described in the text and figure legends.

## References

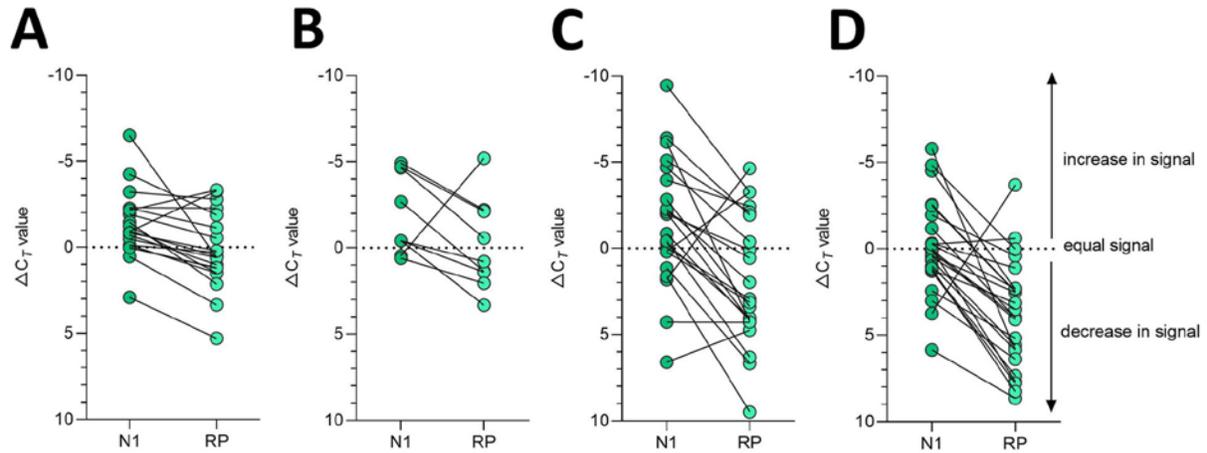
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<http://dx.doi.org/10.17504/protocols.io.bg3pjymn>
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3. Vogels CBF, Brito AF, Wyllie AL, Fauver JR, Ott IM, Kalinich CC, et al. Analytical sensitivity and efficiency comparisons of SARS-CoV-2 RT-qPCR primer-probe sets. *Nat Microbiol*. 2020;5:1299–305. [PubMed https://doi.org/10.1038/s41564-020-0761-6](https://doi.org/10.1038/s41564-020-0761-6)



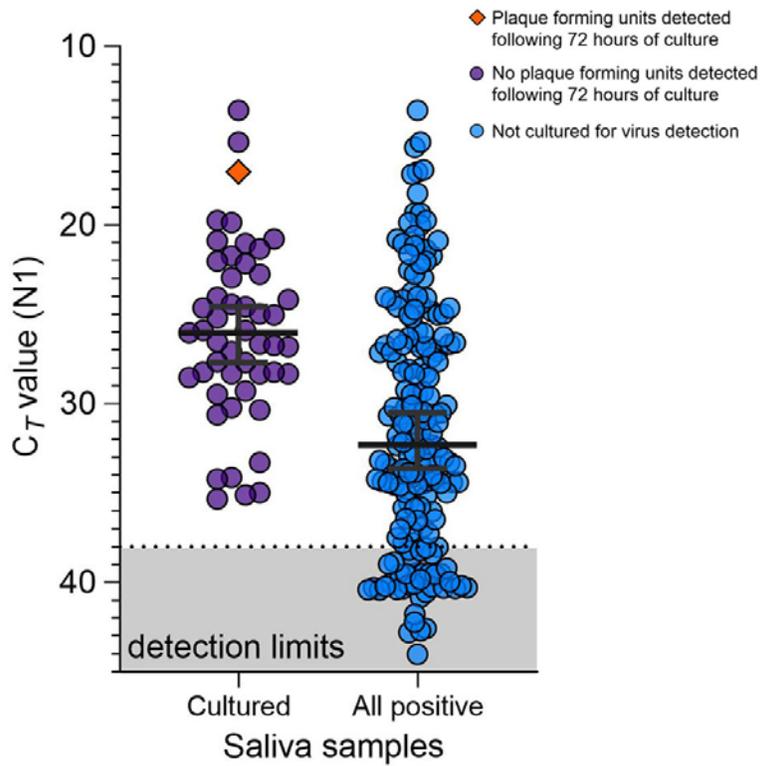
**Appendix Figure 1.** Stability of SARS-CoV-2 RNA (N1) detection in saliva. SARS-CoV-2 RNA detection in saliva on day of sample collection (0) or after prolonged storage at  $-80^{\circ}\text{C}$ ,  $4^{\circ}\text{C}$  or  $30^{\circ}\text{C}$ . Ct values from the same original sample are connected by a dotted line. The  $-80^{\circ}\text{C}$  and  $4^{\circ}\text{C}$  conditions were found to have a weakly beneficial effect on signal detection by the mixed effects model, while the  $30^{\circ}\text{C}$  condition resulted in a slight increase in Ct. The  $-80^{\circ}\text{C}$  storage alone did not cross zero suggesting a mildly stronger effect than the other conditions (95% CI:  $-0.038$ ,  $-0.010$ ). The black dashed line represents Ct 38 which we applied as the cut-off to determine sample positivity. Samples that remained not detected (ND) after 45 cycles are depicted as Ct 42.



**Appendix Figure 2.** Detection of human *RNase P* (RP) declines over time when stored in saliva in warmer conditions. Detection of human RP in saliva on day of collection (0) or after prolonged storage at  $-80^{\circ}\text{C}$ ,  $4^{\circ}\text{C}$ , room temperature ( $\sim 19^{\circ}\text{C}$ ) or  $30^{\circ}\text{C}$ . Ct values from the same original sample are connected by a dotted line. Prolonged storage at  $-80^{\circ}\text{C}$  and  $4^{\circ}\text{C}$  had minimal effect on RP detection with Ct changes of 0.832 (95% CI: -0.402, 2.038) and -0.315 (95% CI: -2.336, 1.687), respectively. However, storage at room temperature (Ct +1.837, 95% CI: 0.468, 3.188) and  $30^{\circ}\text{C}$  (Ct +3.526, 95% CI: 1.750, 5.349) was detrimental to RP, exhibiting a more substantial decrease in signal at these warmer conditions. The black dashed line represents Ct 38 which we applied as the cut-off to determine sample positivity. Samples that remained not detected (ND) after 45 cycles are below the y-axis limit.



**Appendix Figure 3.** Detection of SARS-CoV-2 RNA (N1) in saliva remained more stable over time than human *RNase P* (RP). Delta Ct was calculated as the difference in Ct value from the day of saliva collection and after storage at  $-80^{\circ}\text{C}$ ,  $4^{\circ}\text{C}$ , room temperature ( $\sim 19^{\circ}\text{C}$ ) or  $30^{\circ}\text{C}$ . Delta Ct values from the same sample are joined by a solid line. While the change in detection of SARS-CoV-2 N1 and RP was similar in saliva samples stored at  $4^{\circ}\text{C}$  (Wilcoxon signed rank test,  $p = 0.129$ ), a greater difference was observed between the change in N1 and RP for samples stored at  $-80^{\circ}\text{C}$  ( $p = 0.001$ ), room temperature ( $p = 0.001$ ) and  $30^{\circ}\text{C}$  ( $p < 0.0001$ ).



**Appendix Figure 4.** Saliva samples of relatively high viral load were cultured to evaluate the infectiousness of SARS-CoV-2 in saliva. Saliva samples cultured on Vero-E6 to test for infectious virus were of higher SARS-CoV-2 RNA (N1) load as compared to the overall saliva samples collected by Yale IMPACT (2) which tested positive for SARS-CoV-2 (Mann-Whitney,  $p = <0.0001$ ). The orange diamond depicts the only sample that produced plaque forming units following 72 hours of culture (PFU; titer increase of  $3.79e4$  PFU/mL)