

Smartphone Screen Testing, a novel pre-diagnostic method to identify SARS-CoV-2 infectious individuals

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Abstract

The COVID-19 pandemic will likely take years to control globally, and constant epidemic surveillance will be required to limit the spread of SARS-CoV-2, especially considering the emergence of new variants that could hamper the effect of vaccination efforts. We developed a simple and robust - *Phone Screen Testing (PoST)* - method to detect positive SARS-CoV-2 individuals by RT-PCR testing of smartphone screen swab samples. We show that 81.3-100% of individuals with high-viral load SARS-CoV-2 nasopharyngeal positive samples also test positive for *PoST*, suggesting this method is effective in identifying COVID-19 contagious individuals. Furthermore, we successfully identified polymorphisms associated with SARS-CoV-2 Alpha, Beta and Gamma variants, in SARS-CoV-2 positive *PoST* samples. Overall, we report that *PoST* is a new non-invasive, cost-effective, and easy to implement smartphone-based smart alternative for SARS-CoV-2 testing, which could help to contain COVID-19 outbreaks and identification of variants of concern in the years to come.

Introduction

The coronavirus disease 2019 (COVID-19) pandemic, caused by the SARS-CoV-2 virus, has had a massive impact on human lives, health and quality of life, challenging countries healthcare systems and their economies worldwide. Several countries are now facing a second or third wave of COVID-19 cases. Moreover, the development of this pandemic is still difficult to predict considering the emergence of SARS-CoV-2 mutations located in the receptor-binding domain of the surface Spike protein, which creates a new hazard as evolved viral strains may be more infectious or evade the immune response and hinder vaccination efforts (CDC, 2021a; Collier et al., 2021; Greaney et al., 2021a; Volz et al., 2021; Wang et al., 2021; Wibmer et al., 2021). Particularly the more infectious Alpha (B.1.1.7, Frampton et al., 2021; Rambaut et al., n.d.),

together with the Beta (B.1.351, Tegally et al., 2020) and Gamma (P.1, Faria et al., n.d.), which share the antigenic drift E484K, and the signature mutations K417N and N501Y in the region of the spike protein that is recognised by neutralising antibodies (Collier et al., 2021; Greaney et al., 2021b; Wang et al., 2021; Wibmer et al., 2021).

Early in the pandemic, the RNA sequence of the SARS-CoV-2 virus was made available (Wu et al., 2020), enabling the testing of infected patients by Reverse Transcription (RT)-PCR (Arnaout et al., 2020; Corman et al., 2020). Regular and broad testing of SARS-CoV-2 seems essential to contain the propagation of SARS-CoV-2, as many infected individuals express no symptoms, inadvertently spreading the infection (Ferretti et al., 2020; Kronbichler et al., 2020; Petersen and Phillips, 2020; Pollock and Lancaster, 2020; Sayampanathan et al., 2021). Therefore, successful epidemiological surveillance strategies required to monitor the spread of SARS-CoV-2 and the outbreak of new strains should include large-scale screening methods that enable periodic and continuous testing of the general population.

However, testing capacity has been limited, hampering attempts to control the spread of SARS-CoV-2. One obstacle is that reliable nasopharyngeal sampling and RT-PCR testing is highly invasive and requires both specialised staff and appropriate conditions for the manipulation and transport of the samples to comply with clinical standards and protocols expected by regulatory bodies (CDC, 2021b; UK-Government, 2021). Lateral flow device antigen tests are cheaper, accurate when detecting individuals with high viral load, and an epidemiologically effective option to identify SARS-CoV-2 contagious people (Dinnes et al., 2021; Pavelka et al., 2021; Wagenhäuser et al., 2021). Yet, correct testing also requires nasopharyngeal sampling. Therefore, regular large-scale testing is difficult because accurate tests are either too invasive, expensive or logistically complicated to implement, which make them unviable for the task.

To provide a simple alternative to identify SARS-CoV-2 infected individuals, we designed and validated a method by which SARS-CoV-2 RNA can be RT-PCR detected from samples taken from

a person's smartphone screen. This Phone Screen Testing (*PoST*) method shows high sensitivity (81-100%) compared to nasopharyngeal RT-PCR SARS-CoV-2 test results from individuals with a high viral load, making the smartphone screen a good proxy of the health status of contagious individuals. Furthermore, the SARS-CoV-2 variants present in *PoST* samples with low RT-PCR Ct value were successfully identified. Overall, our results provide a new, non-invasive, cost-effective and efficient method to identify COVID-19 contagious infected cases and limit the transmission of the disease.

Results

Phone Screen Testing (*PoST*) pilot to identify COVID-19 positive cases.

SARS-CoV-2 RNA can be detected from many different kinds of surfaces, places and devices, including phones (Marshall et al., 2020; Santarpia et al., 2020; Ye et al., 2020; Zhou et al., 2020). Furthermore, active SARS-CoV-2 virus is more likely to be recovered from some surfaces when expelled from individuals with seemingly high viral load (Bullard et al., 2020; Jefferson et al., 2020; Sonnleitner et al., 2021). Smartphones are personal objects that are constantly exposed to peoples' mouths, their screens becoming a likely contaminated surface. Therefore, we hypothesised that COVID-19 contagious individuals will regularly deposit aerosols, droplets of saliva, or upper respiratory tract secretions containing shed SARS-CoV-2 virions, over the screen of their phone, which could then be sampled and detected by RT-PCR.

To facilitate test-trace and isolating strategies of COVID-19 infected individuals, we assessed the RT-PCR detection of SARS-CoV-2 RNA from smartphone screen swab samples *via Phone Screen Testing - PoST*. The presence of SARS-CoV-2 RNA in phone screens was then correlated with clinical COVID-19 nasopharyngeal RT-PCR positive diagnosis of the phones' owner. The cohort sample in this pilot study consisted of both symptomatic and asymptomatic or pre-symptomatic individuals who required SARS-CoV-2 testing due to a suspected SARS-CoV-2

infection, close contact to SARS-CoV-2 positive individuals, or return to work and travel authorisation requests in Santiago, Chile, between September and October 2020 (3.81%±1.0 average positivity rate in Santiago, Figure 1- figure supplement 1C-E).

Polyester swabs embedded in saline solution were used by a member of our team to sweep the bottom half of smartphone screens of individuals (Figure 1A). Out of 540 individuals, 51 tested positive for SARS-CoV-2 by nasopharyngeal RT-PCR detection (9.4% positivity rate, Figure 1B (whole bar), Figure 1-figure supplement 1A, Source file 1). Remarkably, all samples with low Ct value, under 20, also tested positive for *PoST* (n=15, Figure 1B (blue segment of bars), Figure 1C, Source file 1). Our results suggest that the ability for *PoST* to correctly identify positive nasopharyngeal individuals, sensitivity, is 100% in individuals with high viral load, Ct value under 20. As shown in Figure 1C (red line, Source file 1), the accumulated sensitivity of *PoST* in nasopharyngeal samples with medium Ct values below 30 is 89.7% (n=29, medium and low viral load). Therefore, our results suggest that testing samples from smartphone screens is effective in identifying COVID-19 positive patients with low and medium Ct RT-PCR result values, which are thought to be actively contagious and expelling virus particles (Bullard et al., 2020; Jefferson et al., 2020; Sonnleitner et al., 2021). The study was performed in double-blind conditions such that the *PoST* and the nasopharyngeal RT-PCR tests were carried out in different laboratories by independent teams which were not aware of each other's result outcome.

Of all the *PoST* and nasopharyngeal positive samples in this cohort, 76% (n=22/29) corresponded to individuals with no specific COVID-19 symptoms (Figure supplement 1E, Source file 1). Therefore, testing smartphone screens is effective in identifying COVID-19 infected individuals regardless of their symptoms at the time of testing.

The overall ability of *PoST* to correctly identify a negative nasopharyngeal test, specificity, in this pilot was 98.8% (Figure supplement 1A, Source file 1). Of this cohort, 6 samples were identified as *PoST*-positive/nasopharyngeal-negative, which could be interpreted as *PoST* false

positives (Figure supplement 1, Source file 1). However, in two cases that were contacted after testing, the individuals had three clear COVID-19 symptoms (Source file 1), suggesting that rather than a *PoST* false positive, these cases could be a nasopharyngeal false-negative result.

To further evaluate the apparent bimodal distribution observed in the Ct values from this cohort of positive COVID-19 clinical samples, we analysed the RT-PCR Ct dataset results of SARS-CoV-2 positive cases from the Davila Clinic (Santiago, Chile) adding up to over seven thousand samples (Figure supplement 2 A-H, Source File 3). When this data set was grouped in month intervals, we did observe a specific distribution of Ct values consistent with the pilot data at the months this cohort was tested (Figure 1B, Figure supplement 2G-H).

The results of our pilot study were encouraging and suggested that the *PoST* method could be a good alternative to more invasive tests with similar sensitivity, like lateral flow antigen test screening (Dinnes et al., 2021; Jääskeläinen et al., 2021; Wagenhäuser et al., 2021). Therefore, validation with higher sample number was required to generate more conclusive evidence.

Validation of Phone Screen Testing in a high positivity rate cohort.

To further validate the *PoST* method, we increased the sample size by testing a new set of 764 individuals at the same clinic and similar cohort kind as before, between the 5th and the 16th of April 2021. At this time, Santiago presented a high positivity rate ($12.4\% \pm 2.2$, (Chilean Department of Health, 2021) as a consequence of the second COVID-19 wave in the country, which enabled identifying 182 positive SARS-CoV-2 individuals (24% positivity rate in this cohort at the clinic), by nasopharyngeal swabbing (Figure 1D, Figure supplement 1B). The distribution of RT-PCR results in this study is unimodal and tends towards lower Ct values compared to the distribution observed in the pilot study (Figure 1B, C).

Similar to what was observed in the pilot cohort, the sensitivity of *PoST* ranges between 81.3% and 100% in nasopharyngeal samples with low Ct value, under 20 (high viral load, Figure 1D, E); and the sensitivity decays at higher Ct values (Figure 1E, red line). In this cohort, 35% of

PoST and nasopharyngeal positive samples corresponded to COVID-19 asymptomatic or pre-symptomatic individuals at the time of testing (n=43/122, Source file 2). This validation study was also performed in the same double-blind conditions as the pilot study described above.

The overall specificity of *PoST* during this validation was 97.6% (Figure supplement 1B); 14 negative SARS-CoV-2 nasopharyngeal samples were identified positively by *PoST* (Figure supplement 1B, Source file 2). Of these cases, we could contact 4 individuals, of which three had clear COVID-19 symptoms, one of which tested positive when the nasopharyngeal sample was repeated (Source file 2). This suggests that some of the discrepancies may be due to nasopharyngeal false-negative test results.

Early in the pandemic, the notion that SARS-CoV-2 could spread via surfaces made regular disinfection of surfaces a common practice (Goldman, 2020). We therefore evaluated whether cleaning smartphone screens before *PoST* sampling could affect the test results. Of all the SARS-CoV-2 *PoST* and nasopharyngeal positive samples where the screen had been cleaned within 24 hrs (n=23), 22% (5/23) were taken from phones that had been sanitised the same day (<6 hrs), and 48% (8/23) less than 2 hrs before the *PoST* sample was taken (Source file 3). This suggests that sanitising or cleaning the smartphone before the *PoST* sampling may not affect the detection of SARS-CoV-2 traces on the phone screen.

This validation study confirms that the *PoST* method shows a high sensitivity when identifying SARS-CoV-2 infected individuals with a low RT-PCR Ct value, regardless of their symptoms, providing a new valuable tool to tackle the COVID-19 pandemic.

SARS-CoV-2 variant identification in *PoST* samples

The current challenge in COVID-19 diagnostics is to find ways to distinguish the specific SARS-CoV-2 variant present in the tested samples to aid in containing outbreaks of variants with higher virulence or infectivity. To aid this task, we performed a screen to address whether SARS-CoV-2 variants can be identified from *PoST* samples. Fluorescent probe-based multiplexed or

single RT-PCR reactions in 69 *PoST* samples from the 2021 cohort was used to identify the following variations in the Spike (S) SARS-CoV-2 gene: del69/70, K417N/T, E484K, N501Y, P681H. From this analysis, 36 samples fulfilled the criteria of amplifying SARS-CoV-2 control genes S and N. Out of this group, 7 samples tested positive for at least one SNP associated with new SARS-CoV-2 variants. Two samples had all three variations described to be present in Beta (B.1.351-South African) or Gamma (P.1-Brasilian) variants (K417T, E484K, N501Y). Another three samples showed variations E484K and N501, which are only found together in Gamma and Beta variants. Even though these samples did not test positive for K417T, it is still likely that the virus in these samples corresponds to either Beta or Gamma, as the combination of variations that tested positive have only been found together in these two SARS-CoV-2 variants. One sample only tested positive for SNP K417T, which is only found in Gamma and Beta SARS-CoV-2 variants. Lastly, we identified one sample with variation del69/70 and P681H which are only found together in the Alpha (B.1.1.7- UK) SARS-CoV-2 variant. The remaining 28 samples showed no variation, and hence are likely to contain original Wuhan SARS-CoV-2.

Our results imply that the capacity to identify SARS-CoV-2 RNA by the primer/probe set we used for *PoST* is not affected by the mutations described for the variant of concern we identified. The capacity of identifying SARS-CoV-2 variants from *PoST* samples, differentiates this assay from lateral flow device antigen testing which can only identify the presence of the virus and not discriminate specific variants.

Discussion

A recent study suggests that socioeconomic status and delay in testing for SARS-CoV-2 was a significant factor in the high mortality rate observed during 2020 in Santiago, Chile (Mena et al., 2021). Therefore, finding new methods to enhance epidemiological surveillance strategies are necessary to limit the struggle generated by the COVID-19 pandemic.

Our study suggests that the *PoST* method could be an effective non-invasive way to rapidly identify COVID-19 positive contagious individuals who actively spread the virus, regardless of their symptoms. This method does not require specialised operators or conditions for sampling. Furthermore, because *PoST* is an environmental test, the protocols and reagents required to manipulate and process the samples for RT-PCR have been optimised to make *PoST* substantially more cost-effective, circumventing the need for clinical grade reagents and standards. All which makes *PoST* a good alternative for large-scale population testing.

Interpretation of the *PoST* method results

PoST positive tests correlate with nasopharyngeal samples with low RT-PCR Ct values, which suggests that individuals with low Ct clinical RT-PCR results are probably passing through the peak of a COVID-19 infection and are contagious, shedding SARS-CoV-2 viral particles which can be detected on their smartphone screens. The Ct value of RT-PCR results from nasopharyngeal samples may present a level of variability that is intrinsic to the nature of the technique, the sampling process, and because the results are not standardised to an internal reference (Dahdouh et al., 2021). However, considering these inherent limitations, correlations have been found between nasopharyngeal samples with low RT-PCR Ct value results and the level of infectivity assessed by the capacity to propagate the SARS-CoV-2 virus *in vitro* from such samples (Bullard et al., 2020; Jefferson et al., 2020; Sonnleitner et al., 2021). Our results add support to the possibility that patients with low Ct RT-PCR results from nasopharyngeal samples present a high viral load and are actively shedding SARS-Cov-2, which can be detected on the screen of smartphones.

Of all the *PoST* positive samples, most of which had low nasopharyngeal RT-PCR Ct results, 76% of the pilot and 35% in the validation study were asymptomatic or pre-symptomatic at the moment of testing (Figure supplement 1E, Source file 1, 2). Suggesting that *PoST* is effective in identifying COVID-19 positive individuals regardless of their symptoms.

SARS-CoV-2 variant identification is required to further enhance epidemiological surveillance to contain the spreading of variants of concern that are more pathogenic or infective, to contain and isolate their dissemination. We successfully identified one *PoST* sample that presented all three polymorphisms present in Beta (B.1.351) and Gamma (P.1) variants. The rest of the tests did not unequivocally show which SARS-CoV-2 variant was present in the sample but was enough to conclude the nature of the variant present in the sample. Even though optimisation will be required to enhance SARS-CoV-2 variant identification in *PoST* samples, our results are encouraging, and could make *PoST* a viable option to screen for variants of concern. In this scenario, and although the output of results would take longer, PCR and sequencing will likely enhance the performance of variant detection in *PoST* samples.

Regarding nasopharyngeal RT-PCR results with a high Ct value (i.e., lower-viral load), these are probably in transition, and either starting or ending a COVID-19 infection. Therefore, they are less likely to shed SARS-CoV-2 virions that can be detected by *PoST*. This transition is the reason why periodic regular testing is required to identify those infected individuals once they enter a contagious phase.

To a lesser extent and against the overall trend we observe for *PoST* detection, *PoST* positive results were identified in this high Ct value nasopharyngeal RT-PCR results group. Given the unstable nature of the SARS-CoV-2 virus on surfaces (Goldman, 2020), and the pervasive activity of RNases which are ubiquitously present in the environment (Probst et al., 2006), it is unlikely that these positive *PoST* results are due to the detection of long-lasting virus or RNA on the phone screen surface. Hence, we could exclude the possibility that these *PoST* positive results are the consequence of detecting RNA from when individuals were passing through a moment of higher COVID-19 infection. Therefore, one could speculate that these results are the consequence of suboptimal nasopharyngeal sampling, which would explain the low amount of virus in the sample and hence, a high Ct value. Alternatively, it is plausible that these samples

belong to individuals with a low viral load that are still actively contagious, which is against the observed trend (Bullard et al., 2020; Jefferson T et al., 2020; Sonnleitner et al., 2021), but cannot be excluded as a possibility. It will be interesting to perform a follow-up study on these individuals as they could be part of a group with a higher capacity to shed SARS-CoV-2 along their infectious cycle, potentially explaining the COVID-19 superspreading capacity observed in some people (Lewis, 2021).

The distribution profile of the nasopharyngeal RT-PCR Ct test results in our study was different in the pilot and validation cohorts. The pilot Ct results presented an apparent bimodal distribution with low and high Ct value populations (Figure 1B). On the other hand, in the validation study, the distribution was unimodal and most samples tended towards low RT-PCR Ct results (Figure 1D). We speculate that this stark difference could be due to an inherent characteristic of these cohorts related to the positivity rates in the population of Santiago at the time of sampling. In fact, the distribution profile of the pilot nasopharyngeal Ct values is similar to that corresponding to samples taken when the pilot sampling was performed (Figure supplement 2G-H). At the time the pilot study was performed, Santiago, Chile, presented a low average positivity rate ($3.8\% \pm 1.0$, Chilean Department of Health, 2021), and was recovering from the first COVID-19 wave. Likewise, the distribution profile of the validation cohort nasopharyngeal Ct results was similar to when Santiago was passing through the middle of first the COVID-19 wave, at a high average positivity rate (9.5-26.4%, Figure supplement 2B-D). This observation suggests that the RT-PCR Ct value results distribution could show specific profile signatures that express the epidemiological status of the population. Confirming this observation will further require a deeper analysis of this kind of dataset.

Advantages and limitations of the *PoST* method

a. Cost effective

One of the main advantages of *PoST* is its low cost compared to clinical nasopharyngeal tests. Excluding staff and premises, the net cost of a nasopharyngeal test in Chile ranges between \$20-25 USD which includes: sample tube, transport media, swab, RNA extraction kit and RT-PCR kit. Because *PoST* does not use clinical-grade consumables and reagents, its net cost for the same items ranges between \$2-3USD when it is the result of a single sample tested RT-PCR reaction. This net cost can go below \$1USD when *PoST* samples are pooled and groups of 5 and a single RT-PCR reaction is performed, which we have shown to produce reliable results for *PoST* samples (data not shown).

Besides *PoST* not using clinical-grade consumables and reagents, one key optimisation is that *PoST* does not require an RNA extraction step, which reduces the cost by approximately \$7USD. Furthermore, instead of purchasing an RT-PCR kit specifically designed for SARS-CoV-2 detection, we assembled a combination of off-the-shelf probe/primers to detect the SARS-CoV-2 gene 'N' together with a generic RT-PCR kit. All together this optimisation enables a 10-fold price reduction of the net cost of *PoST* compared to a regular nasopharyngeal RT-PCT test.

b. High sensitivity and specificity

The *PoST* method has a similar sensitivity and specificity, compared to antigen lateral flow devices, which are extensively used for routine testing (Dinnes et al., 2021; Jääskeläinen et al., 2021; Wagenhäuser et al., 2021). Clinical grade diagnostic RT-PCR kits include the detection of three SARS-CoV-2 genes, plus a human positive control, either multiplexed or individually detected. The specificity reached by *PoST* in this study was achieved only when detecting the 'N' SARS-CoV-2 gene. This could explain why *PoST* can miss identifying some positive nasopharyngeal RT-PCR samples in the low Ct range. A study adding the detection of two or three SARS-CoV-2 genes in the *PoST* protocol to assess if a higher sensitivity is achieved would enable us to calculate whether this trade-off is enough to justify increasing the net cost of the *PoST* assay. Especially considering that the sensitivity described in this study is already high

enough to detect positive COVID-19 individuals to affect limiting the transmission of the SARS-CoV-2 virus (Kennedy-Shaffer et al., 2021; Larremore et al., 2021; Mina et al., 2020).

c. Sampling speed, result turnaround of *PoST*.

One other advantage of the *PoST* method is that the sampling process takes around a minute at most, and does not require a particular setup besides having a sterile swab and sample tube. To maximise the speed and minimise errors in the *PoST* processing of samples, we developed a barcode-based smartphone application (unpublished), which enables the efficient tracking of the samples through the testing pipeline, ending with the delivery of results to the tested individuals' smartphone via SMS. Moreover, pooling samples can reduce the number of RT-PCR reactions required to process, further decreasing the time to deliver results, when the positivity rate is below 5% to justify pooling. With all this in place, a minimal non-automatised laboratory set up with one 96 well plate real-time PCR machine has the potential to deliver 940 test results per day, when processed by two technicians, and working on two rounds of 470 samples.

Altogether, this enables an efficient turnaround of results such that after the samples arrive at the lab, the results of 940 can be delivered in approximately 5.5 hours, if no positive SARS-CoV-2 samples are found, and 6.5 hours if positive individual samples are to be identified from pools. These times consider two technicians processing the samples to feed one 96 well plate real-time PCR machine. Therefore, under these conditions, results for 940 tests could be provided within the same day of sampling, which is ideal to isolate contagious cases, and effectively curb the spreading of COVID-19.

d. *PoST* as an alternative self-testing method

Due to its high sensitivity, specificity, and rapid result turnaround time, lateral flow device antigen testing has become widely used to screen for COVID-19 cases operated by trained staff (Pavelka et al., 2021), and self-administered (Riley et al., 2021). Because this method uses highly invasive nasopharyngeal swabbing, trained operators are the preferred option to deliver

accurate and reliable results from these tests. From this point of view, the *PoST* method offers a valuable alternative for accurate self-tests results as it is much easier and more reliable to effectively swab the screen of a smartphone than performing a self-administered nasopharyngeal test. This, together with the fact that SARS-CoV-2 variants can be identified in *PoST* samples, gives this method further advantages compared to lateral flow antigen testing.

e. Penetration of smartphone use in the population

One aspect that is important to mention is that although it is estimated that there are around 3.8 billion smartphones in the world and their penetration is very high among the young and adult population, their global distribution is not equitable (Turner, 2021). While penetration is almost total among adults in developed countries, in countries such as India or Bangladesh it does not exceed 33% of the population (Berenguer et al., 2016). On the other hand, among senior citizens, who are precisely a vulnerable population, even in developed countries some do not use a telephone or have older devices.

Overall, this study was aimed to validate *PoST* as method to identify infected COVID-19 cases by using the smartphone as a proxy from which traces of the SARS-CoV-2 virus of the owner can be detected. We propose that this highly-sensitive, non-invasive and cost-effective method could well be used for mass testing and help to contain the spreading of other airborne contagious diseases and outbreaks when tackling future epidemics. This could be particularly useful as an early warning system for rapid detection of respiratory pathogens in public health efforts to contain local outbreaks to prevent further escalating to other areas.

Materials and Methods

Smartphone screen swab sampling, sample processing and RT-PCR.

323 Informed consent and consent to publish was obtained from all the individuals that participated
324 in this study before performing the sampling process. Dacron swabs were briefly dipped in
325 Weise medium (Merck, 1.09468.0100) and then used to swab the bottom half of mobile phone
326 screens by a member of our team as shown in Figure 1A. Swabs were then introduced in sterile
327 conical tubes containing Weise medium and briefly hand spun. Samples were processed for RT-
328 PCR within 8 hours.

329 Aliquots of swab samples were incubated at 70°C for 10min as previously described (Miranda et
330 al., 2020). Samples were left to cool at room temperature and 3.3µl aliquots were used for RT-
331 PCR using Promega GoTaq Probe 1-Step RT-qPCR system (A6121) according to the manufacturer
332 instructions and supplemented with SARS-CoV-2 N2 probes and primers (IDT#10006606) on an
333 Illumina Eco Real-Time PCR System. We considered a test as positive if the PCR amplification
334 obtained followed the expected standard sigmoidal kinetics of amplification.

335 **Clinical sampling and RT-PCR.**

336 For each patient, nasopharyngeal swabs were collected using standard technique, as
337 recommended by the manufacturer (Allplex™ 2019-nCoV Assay insert) and transported to the
338 laboratory in viral transport medium (prepared according to the standard operating procedure
339 of the CDC, USA). For all samples, RNA extraction was performed using STARmag kit (Seegene,
340 Korea), and following the manufacturer's instructions. For the analysis of the pilot cohort
341 samples, target gene amplification of SARS-Cov-2 was performed using the Allplex™ 2019-nCoV
342 Assay kit (Seegene, Korea), according to the manufacturer's procedure. The RT-qPCR preparation
343 was carried out in the Starlet equipment (Hamilton, USA, distributed by Seegene) and the qPCR
344 amplification in a CFX-96 thermal cycler (Biorad, USA). The Allplex™ 2019-nCoV Assay kit
345 detects 3 viral genes (N, RdRP and E). We considered a test as positive if PCR amplification was
346 obtained with N gene and RdRP. If only the E gene was amplified, the test was considered

presumably positive, thus requiring repetition by another extraction instrument (MagNAPure Compact System, Roche).

Identification of SARS-CoV-2 variants

The detection of different SARS-CoV-2 single nucleotide and deletion variants was performed using the Applied Biosystems™ TaqMan™ SARS-CoV-2 Mutation Panel kit (ThermoFisher) according to the conditions recommended by the manufacturer, on the AriaMx Real-time PCR system (Agilent Technologies) thermal cycler for fluorescence detection on VIC (reference sequence) and FAM channels (mutation sequence); and the AccuPower® SARS-CoV-2 Variants ID Real-Time RT-PCR kit (Bioneer) according to manufacturer conditions, on the Exicycler 96 V4 Real Time thermal cycler (Bioneer) to detect fluorescence on the TET, TexasRed, FAM, TAMRA and Cyanine5 channels.

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368 Bibliography

- 369 Arnaout R, Lee RA, Lee GR, Callahan C, Yen CF, Smith KP, Arora R, Kirby JE. 2020. SARS-CoV2
 370 Testing: The Limit of Detection Matters. *bioRxiv Prepr Serv Biol*. doi:10.1101/2020.06.02.131144
- 371 Berenguer A, Goncalves J, Hosio S, Ferreira D, Anagnostopoulos T, Kostakos V. 2016. Are
 372 Smartphones Ubiquitous? *IEEE Consum Electron Mag* **6**:104–110.
- 373 Bullard J, Dust K, Funk D, Strong JE, Alexander D, Garnett L, Boodman C, Bello A, Hedley A,
 374 Schiffman Z, Doan K, Bastien N, Li Y, Van Caesele PG, Poliquin G. 2020. Predicting Infectious
 375 Severe Acute Respiratory Syndrome Coronavirus 2 From Diagnostic Samples. *Clin Infect Dis*
 376 **71**:2663–2666. doi:10.1093/cid/ciaa638
- 377 CDC. 2021a. SARS-CoV-2 Variant Classifications and Definitions. *Centers Dis Control Prev*.
 378 [https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-](https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html)
 379 [info.html](https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/variant-info.html)
- 380 CDC. 2021b. Interim Guidelines for Collecting and Handling of Clinical Specimens for COVID-19
 381 Testing. *Centers Dis Control Prev*. [https://www.cdc.gov/coronavirus/2019-ncov/lab/guidelines-](https://www.cdc.gov/coronavirus/2019-ncov/lab/guidelines-clinical-specimens.html)
 382 [clinical-specimens.html](https://www.cdc.gov/coronavirus/2019-ncov/lab/guidelines-clinical-specimens.html)
- 383 Collier DA, De Marco A, Ferreira IATM, Meng B, Datir R, Walls AC, Kemp S SA, Bassi J, Pinto D,
 384 Fregni CS, Bianchi S, Tortorici MA, Bowen J, Culap K, Jaconi S, Cameroni E, Snell G, Pizzuto MS,
 385 Pellanda AF, Garzoni C, Riva A, Elmer A, Kingston N, Graves B, McCoy LE, Smith KGC, Bradley JR,
 386 Temperton N, Lourdes Ceron-Gutierrez L, Barcenas-Morales G, Harvey W, Virgin HW,
 387 Lanzavecchia A, Piccoli L, Doffinger R, Wills M, Veessler D, Corti D, Gupta RK. 2021. Sensitivity of
 388 SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies. *Nature*. doi:10.1038/s41586-021-
 389 03412-7
- 390 Corman VM, Landt O, Kaiser M, Molenkamp R, Meijer A, Chu DK, Bleicker T, Brünink S, Schneider
 391 J, Luisa Schmidt M, GJC Mulders D, Haagmans BL, van der Veer B, van den Brink S, Wijsman L,
 392 Goderski G, Romette J-L, Ellis J, Zambon M, Peiris M, Goossens H, Reusken C, Koopmans MP,

393 Drosten C, Victor CM, Olfert L, Marco K, Richard M, Adam M, Daniel CK, Tobias B, Sebastian B,
 394 Julia S, Marie Luisa S, Daphne GJC M, Bart HL, der Veer Bas V, den Brink Sharon V, Lisa W, Gabriel
 395 G, Jean-Louis R, Joanna E, Maria Z, Malik P, Herman G, Chantal R. 2020. Detection of 2019 -nCoV
 396 by RT-PCR. *Euro Surveill* **25**:1–8.

397 Dahdouh E, Lázaro-Perona F, Romero-Gómez MP, Mingorance J, García-Rodríguez J. 2021. Ct
 398 values from SARS-CoV-2 diagnostic PCR assays should not be used as direct estimates of viral
 399 load. *J Infect* **82**:414–451. doi:<https://doi.org/10.1016/j.jinf.2020.10.017>

400 Dinnes J, Jj D, Berhane S, Taylor M, Adriano A, Davenport C, Dittrich S, Emperador D, Takwoingi
 401 Y, Cunningham J, Beese S, Domen J, Dretzke J, Im H, Hoo L, Mmg L, Mdf M, Spijker R, A VDB,
 402 Domen J, Dretzke J, Im H, Mj P, Hoo L, Mmg L, Mdf M, Spijker R. 2021. Rapid, point-of-care
 403 antigen and molecular-based test for diagnosis of SARS-CoV-2 infection (Review).
 404 doi:10.1002/14651858.CD013705.pub2.www.cochranelibrary.com

405 Faria NR, Morales I, Candido D, Moyses LA, Andrade PS, Coletti TM, Silva CAM, Sales FC, Manuli
 406 ER, Aguiar RS, Gaburo N, Camilo C da C, Fraiji NA, Esashika MA, Carvalho M do P, Rambaut A,
 407 Loman N, Pybus OG, Sabino EC. n.d. Genomic characterisation of an emergent SARS-CoV-2
 408 lineage in Manaus: preliminary findings. *Preprints*. [https://virological.org/t/genomic-](https://virological.org/t/genomic-characterisation-of-an-emergent-sars-cov-2-lineage-in-manaus-preliminary-findings/586)
 409 [characterisation-of-an-emergent-sars-cov-2-lineage-in-manaus-preliminary-findings/586](https://virological.org/t/genomic-characterisation-of-an-emergent-sars-cov-2-lineage-in-manaus-preliminary-findings/586)

410 Ferretti L, Wymant C, Kendall M, Zhao L, Nurtay A, Abeler-Dörner L, Parker M, Bonsall D, Fraser
 411 C. 2020. Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact
 412 tracing. *Science (80-)* **368**:0–8. doi:10.1126/science.abb6936

413 Frampton D, Rampling T, Cross A, Bailey H, Heaney J, Byott M, Scott R, Sconza R, Price J,
 414 Margaritis M, Bergstrom M, Spyer MJ, Miralhes PB, Grant P, Kirk S, Valerio C, Mangera Z,
 415 Prabhakar T, Moreno-Cuesta J, Arulkumaran N, Singer M, Shin GY, Sanchez E, Paraskevopoulou
 416 SM, Pillay D, McKendry RA, Mirfenderesky M, Houlihan CF, Nastouli E. 2021. Genomic
 417 characteristics and clinical effect of the emergent SARS-CoV-2 B.1.1.7 lineage in London, UK: a

418 whole-genome sequencing and hospital-based cohort study. *Lancet Infect Dis*.
419 doi:10.1016/S1473-3099(21)00170-5

420 Goldman E. 2020. Exaggerated risk of transmission of COVID-19 by fomites. *Lancet Infect Dis*
421 **20**:892–893. doi:10.1016/S1473-3099(20)30561-2

422 Greaney AJ, Loes AN, Crawford KHD, Starr TN, Malone KD, Chu HY, Bloom JD. 2021a.
423 Comprehensive mapping of mutations in the SARS-CoV-2 receptor-binding domain that affect
424 recognition by polyclonal human plasma antibodies. *Cell Host Microbe* **29**:463-476.e6.
425 doi:10.1016/j.chom.2021.02.003

426 Greaney AJ, Loes AN, Crawford KHD, Starr TN, Malone KD, Chu HY, Bloom JD. 2021b.
427 Comprehensive mapping of mutations to the SARS-CoV-2 receptor-binding domain that affect
428 recognition by polyclonal human serum antibodies. *bioRxiv* 2020.12.31.425021.
429 doi:10.1101/2020.12.31.425021

430 Jääskeläinen AE, Ahava MJ, Jokela P, Szirovicza L, Pohjala S, Vapalahti O, Lappalainen M,
431 Hepojoki J, Kurkela S. 2021. Evaluation of three rapid lateral flow antigen detection tests for the
432 diagnosis of SARS-CoV-2 infection. *J Clin Virol* **137**:104785.
433 doi:https://doi.org/10.1016/j.jcv.2021.104785

434 Jefferson T, Spencer EA, Brassey J, Heneghan C. 2020. Viral cultures for COVID-19 infectious
435 potential assessment – a systematic review. *Clin Infect Dis*. doi:10.1093/cid/ciaa1764

436 Kennedy-Shaffer L, Baym M, Hanage WP. 2021. Perfect as the enemy of good: tracing
437 transmissions with low-sensitivity tests to mitigate SARS-CoV-2 outbreaks. *The Lancet Microbe*.
438 doi:10.1016/S2666-5247(21)00004-5

439 Kronbichler A, Kresse D, Yoon S, Lee KH, Effenberger M, Shin J Il. 2020. Asymptomatic patients as
440 a source of COVID-19 infections: A systematic review and meta-analysis. *Int J Infect Dis* **98**:180–
441 186. doi:https://doi.org/10.1016/j.ijid.2020.06.052

442 Larremore DB, Wilder B, Lester E, Shehata S, Burke JM, Hay JA, Tambe M, Mina MJ, Parker R.

443 2021. Test sensitivity is secondary to frequency and turnaround time for COVID-19 screening. *Sci*
 444 *Adv* **7**:eabd5393. doi:10.1126/sciadv.abd5393
 445 Lewis D. 2021. Superspreading drives the COVID pandemic - and could help to tame it. *Nature*
 446 **590**:544–546. doi:10.1038/d41586-021-00460-x
 447 Marshall DL, Bois F, Jensen SKS, Linde SA, Higby R, Rémy-McCort Y, Murray S, Dieckelman B,
 448 Sudradjat F, Martin GG. 2020. Sentinel Coronavirus environmental monitoring can contribute to
 449 detecting asymptomatic SARS-CoV-2 virus spreaders and can verify effectiveness of workplace
 450 COVID-19 controls. *Microb Risk Anal* **16**:100137. doi:10.1016/j.mran.2020.100137
 451 Mena GE, Martinez PP, Mahmud AS, Marquet PA, Buckee CO, Santillana M. 2021. Socioeconomic
 452 status determines COVID-19 incidence and related mortality in Santiago, Chile. *Science* (80-)
 453 eabg5298. doi:10.1126/science.abg5298
 454 Mina MJ, Parker R, Larremore DB. 2020. Rethinking Covid-19 Test Sensitivity — A Strategy for
 455 Containment. *N Engl J Med* **383**:e120. doi:10.1056/NEJMp2025631
 456 Chilean Department of Health. 2021. Base de Datos COVID-19.
 457 <https://www.minciencia.gob.cl/covid19/>
 458 Miranda JP, Osorio J, Videla M, Angel G, Camponovo R, Henríquez-Henríquez M. 2020. Analytical
 459 and Clinical Validation for RT-qPCR Detection of SARS-CoV-2 Without RNA Extraction. *Front Med*
 460 **7**:1–9. doi:10.3389/fmed.2020.567572
 461 Pavelka M, Van-Zandvoort K, Abbott S, Sherratt K, Majdan M, Analýz IZ, Jarčuška P, Krajčí M,
 462 Flasche S, Funk S. 2021. The impact of population-wide rapid antigen testing on SARS-CoV-2
 463 prevalence in Slovakia. *Science* (80-) eabf9648. doi:10.1126/science.abf9648
 464 Petersen I, Phillips A. 2020. Three quarters of people with SARS-CoV-2 infection are
 465 asymptomatic: Analysis of english household survey data. *Clin Epidemiol* **12**:1039–1043.
 466 doi:10.2147/CLEP.S276825
 467 Pollock AM, Lancaster J. 2020. Asymptomatic transmission of covid-19. *BMJ* **371**.

doi:10.1136/bmj.m4851

Probst J, Brechtel S, Scheel B, Hoerr I, Jung G, Rammensee H-G, Pascolo S. 2006. Characterization of the ribonuclease activity on the skin surface. *Genet Vaccines Ther* **4**:4. doi:10.1186/1479-0556-4-4

Rambaut A, Loman N, Pybus O, Barclay W, Barrett J, Carabelli A, Connor T, Peacock T, Robertson DL, Volz E. n.d. Preliminary genomic characterisation of an emergent SARS-CoV-2 lineage in the UK defined by a novel set of spike mutations. *Preprints*. <https://virological.org/t/preliminary-genomic-characterisation-of-an-emergent-sars-cov-2-lineage-in-the-uk-defined-by-a-novel-set-of-spike-mutations/563>

Riley S, Ainslie KEC, Eales O, Walters CE, Wang H, Atchison C, Fronterre C, Diggle PJ, Ashby D, Donnelly CA, Cooke G, Barclay W, Ward H, Darzi A, Elliott P. 2021. Resurgence of SARS-CoV-2: detection by community viral surveillance. *Science (80-)* eabf0874. doi:10.1126/science.abf0874

Santarpia JL, Rivera DN, Herrera VL, Morwitzer MJ, Creager HM, Santarpia GW, Crown KK, Brett-Major DM, Schnaubelt ER, Broadhurst MJ, Lawler J V, Reid SP, Lowe JJ. 2020. Aerosol and surface contamination of SARS-CoV-2 observed in quarantine and isolation care. *Sci Rep* **10**:12732. doi:10.1038/s41598-020-69286-3

Sayampanathan AA, Heng CS, Pin PH, Pang J, Leong TY, Lee VJ. 2021. Infectivity of asymptomatic versus symptomatic COVID-19. *Lancet* **397**:93–94. doi:10.1016/S0140-6736(20)32651-9

Sonnleitner ST, Dorigi J, Jansen B, Schönegger C, Gietl S, Koblmüller S, Sturmhuber C, Posch W, Walder G. 2021. An in vitro model for assessment of SARS-CoV-2 infectivity by defining the correlation between virus isolation and quantitative PCR value: isolation success of SARS-CoV-2 from oropharyngeal swabs correlates negatively with Cq value. *Virology* **18**:71. doi:10.1186/s12985-021-01542-y

Tegally H, Wilkinson E, Giovanetti M, Iranzadeh A, Fonseca V, Giandhari J, Doolabh D, Pillay S, San EJ, Msomi N, Mlisana K, von Gottberg A, Walaza S, Allam M, Ismail A, Mohale T, Glass AJ,

493 Engelbrecht S, Van Zyl G, Preiser W, Petruccione F, Sigal A, Hardie D, Marais G, Hsiao M, Korsman
 494 S, Davies M-A, Tyers L, Mudau I, York D, Maslo C, Goedhals D, Abrahams S, Laguda-Akingba O,
 495 Alisoltani-Dehkordi A, Godzik A, Wibmer CK, Sewell BT, Lourenço J, Alcantara LCJ, Pond SLK,
 496 Weaver S, Martin D, Lessells RJ, Bhiman JN, Williamson C, de Oliveira T. 2020. Emergence and
 497 rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2)
 498 lineage with multiple spike mutations in South Africa. *medRxiv* 2020.12.21.20248640.
 499 doi:10.1101/2020.12.21.20248640
 500 Turner A. 2021. HOW MANY SMARTPHONES ARE IN THE WORLD?
 501 <https://www.bankmycell.com/blog/how-many-phones-are-in-the-world>
 502 UK-Government U. 2021. Guidance COVID-19: safe handling and processing for samples in
 503 laboratories. [https://www.gov.uk/government/publications/wuhan-novel-coronavirus-guidance-](https://www.gov.uk/government/publications/wuhan-novel-coronavirus-guidance-for-clinical-diagnostic-laboratories/wuhan-novel-coronavirus-handling-and-processing-of-laboratory-specimens)
 504 [for-clinical-diagnostic-laboratories/wuhan-novel-coronavirus-handling-and-processing-of-](https://www.gov.uk/government/publications/wuhan-novel-coronavirus-handling-and-processing-of-laboratory-specimens)
 505 [laboratory-specimens](https://www.gov.uk/government/publications/wuhan-novel-coronavirus-handling-and-processing-of-laboratory-specimens)
 506 Volz E, Mishra S, Chand M, Barrett JC, Johnson R, Geidelberg L, Hinsley WR, Laydon DJ, Dabrera
 507 G, O'Toole Á, Amato R, Ragonnet-Cronin M, Harrison I, Jackson B, Ariani C V, Boyd O, Loman NJ,
 508 McCrone JT, Gonçalves S, Jorgensen D, Myers R, Hill V, Jackson DK, Gaythorpe K, Groves N,
 509 Sillitoe J, Kwiatkowski DP, Flaxman S, Ratmann O, Bhatt S, Hopkins S, Gandy A, Rambaut A,
 510 Ferguson NM. 2021. Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: Insights from linking
 511 epidemiological and genetic data. *medRxiv* 2020.12.30.20249034.
 512 doi:10.1101/2020.12.30.20249034
 513 Wagenhäuser I, Knies K, Rauschenberger V, Eisenmann M, McDonogh M, Petri N, Andres O,
 514 Flemming S, Gawlik M, Papsdorf M, Taurines R, Böhm H, Forster J, Weismann D, Weißbrich B,
 515 Dölken L, Liese J, Kurzai O, Vogel U, Krone M. 2021. Clinical performance evaluation of SARS-
 516 CoV-2 rapid antigen testing in point of care usage in comparison to RT-qPCR. *medRxiv*
 517 2021.03.27.21253966. doi:10.1101/2021.03.27.21253966

518 Wang Z, Schmidt F, Weisblum Y, Muecksch F, Barnes CO, Finkin S, Schaefer-Babajew D, Cipolla
 519 M, Gaebler C, Lieberman JA, Oliveira TY, Yang Z, Abernathy ME, Huey-Tubman KE, Hurley A,
 520 Turroja M, West KA, Gordon K, Millard KG, Ramos V, Da Silva J, Xu J, Colbert RA, Patel R, Dizon J,
 521 Unson-O'Brien C, Shimeliovich I, Gazumyan A, Caskey M, Bjorkman PJ, Casellas R, Hatzioannou
 522 T, Bieniasz PD, Nussenzweig MC. 2021. mRNA vaccine-elicited antibodies to SARS-CoV-2 and
 523 circulating variants. *Nature* **592**:616–622. doi:10.1038/s41586-021-03324-6
 524 Wibmer CK, Ayres F, Hermanus T, Madzivhandila M, Kgagudi P, Oosthuysen B, Lambson BE, de
 525 Oliveira T, Vermeulen M, van der Berg K, Rossouw T, Boswell M, Ueckermann V, Meiring S, von
 526 Gottberg A, Cohen C, Morris L, Bhiman JN, Moore PL. 2021. SARS-CoV-2 501Y.V2 escapes
 527 neutralization by South African COVID-19 donor plasma. *Nat Med* **27**:622–625.
 528 doi:10.1038/s41591-021-01285-x
 529 Wu F, Zhao S, Yu B, Chen YM, Wang W, Song ZG, Hu Y, Tao ZW, Tian JH, Pei YY, Yuan ML, Zhang
 530 YL, Dai FH, Liu Y, Wang QM, Zheng JJ, Xu L, Holmes EC, Zhang YZ. 2020. A new coronavirus
 531 associated with human respiratory disease in China. *Nature* **579**:265–269. doi:10.1038/s41586-
 532 020-2008-3
 533 Ye G, Lin H, Chen S, Wang S, Zeng Z, Wang W, Zhang S, Rebmman T, Li Y, Pan Z, Yang Z, Wang Y,
 534 Wang F, Qian Z, Wang X. 2020. Environmental contamination of SARS-CoV-2 in healthcare
 535 premises. *J Infect* **81**:e1–e5. doi:10.1016/j.jinf.2020.04.034
 536 Zhou J, Otter JA, Price JR, Cimpeanu C, Garcia DM, Kinross J, Boshier PR, Mason S, Bolt F, Holmes
 537 AH, Barclay WS. 2020. Investigating SARS-CoV-2 surface and air contamination in an acute
 538 healthcare setting during the peak of the COVID-19 pandemic in London. *Clin Infect Dis*.
 539 doi:10.1093/cid/ciaa905

Figure 1. Phone Screen Testing and RT-PCR can identify individuals with high SARS-CoV-2 viral load. (A) Schematic of smartphone sampling. Swabbing follows the dashed line indicated trajectory. (B, D) Histograms showing the distribution of individuals on ranges of clinical RT-PCR Ct value results for the pilot cohort (B, full dataset in Source File 1) and validation cohort (D, full dataset in Source file 2). For example, bar Ct value 11 corresponds to samples with Ct between [11-13[interval. Whole bar, all individuals with positive nasopharyngeal RT-PCR result. Blue bar section, those individuals also *PoST* positive. (C, E) Bars represent the accumulated number of individuals with positive RT-PCR clinical results under the Ct value number associated with the bar for, (C) pilot cohort, and (E) validation cohort. Red line in both plots depicts the sensitivity observed relative to clinical nasopharyngeal RT-PCR testing at the corresponding accumulated Ct value results. Left axis, percentage of sensitivity; right axis, number of accumulated individuals under the corresponding Ct value.

Figure supplement 1 - Pilot and Validation study cohort data analysis.

(A, B) Two-by-two tables for sensitivity and specificity of *PoST* method compared to nasopharyngeal RT-PCR results in the (A) pilot cohort (Source file 1) and (B) validation cohort (Source file 2). (C-F) Bar plots representing the number of individuals in the pilot (left bar) and validation (right bar) studies showing age distribution (C), sex distribution (D), symptomatic and asymptomatic patients (E), and COVID-19 symptoms score (F). Each COVID-19 symptom (anosmia, coughing and fever) was assigned a value of 1. Score 1=1 symptom, score 2=2 symptoms.

Figure supplement 2. SARS-CoV2-19 RT-PCR Cycle threshold (Ct) values in Chilean individuals.

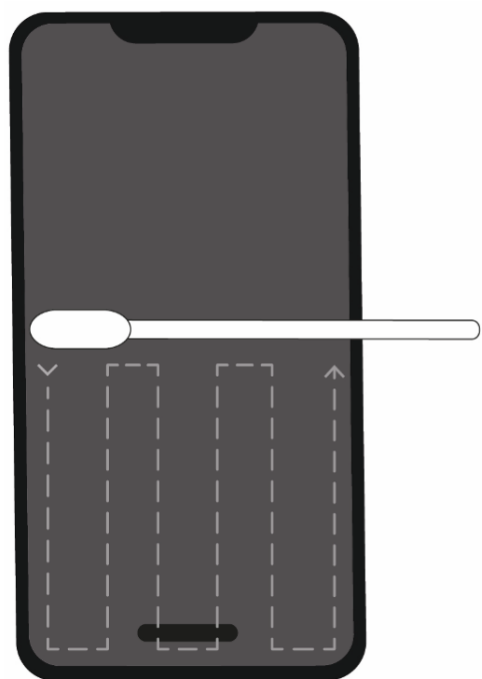
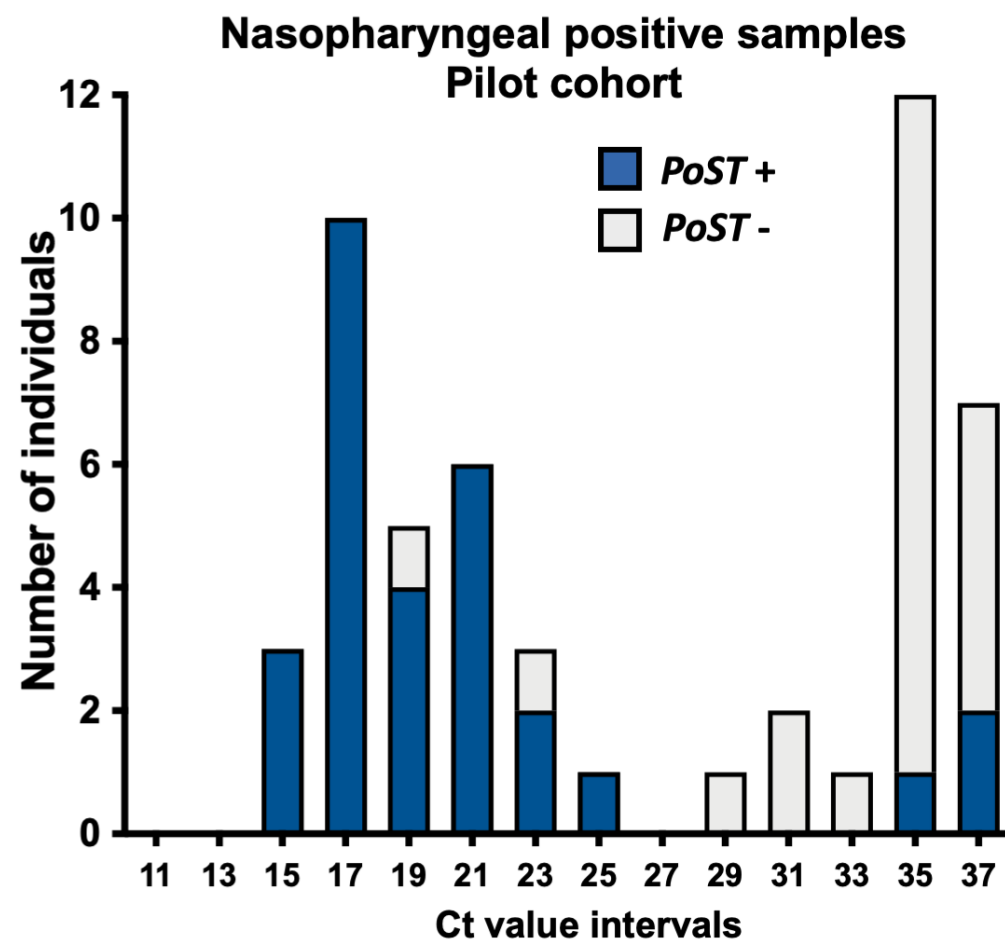
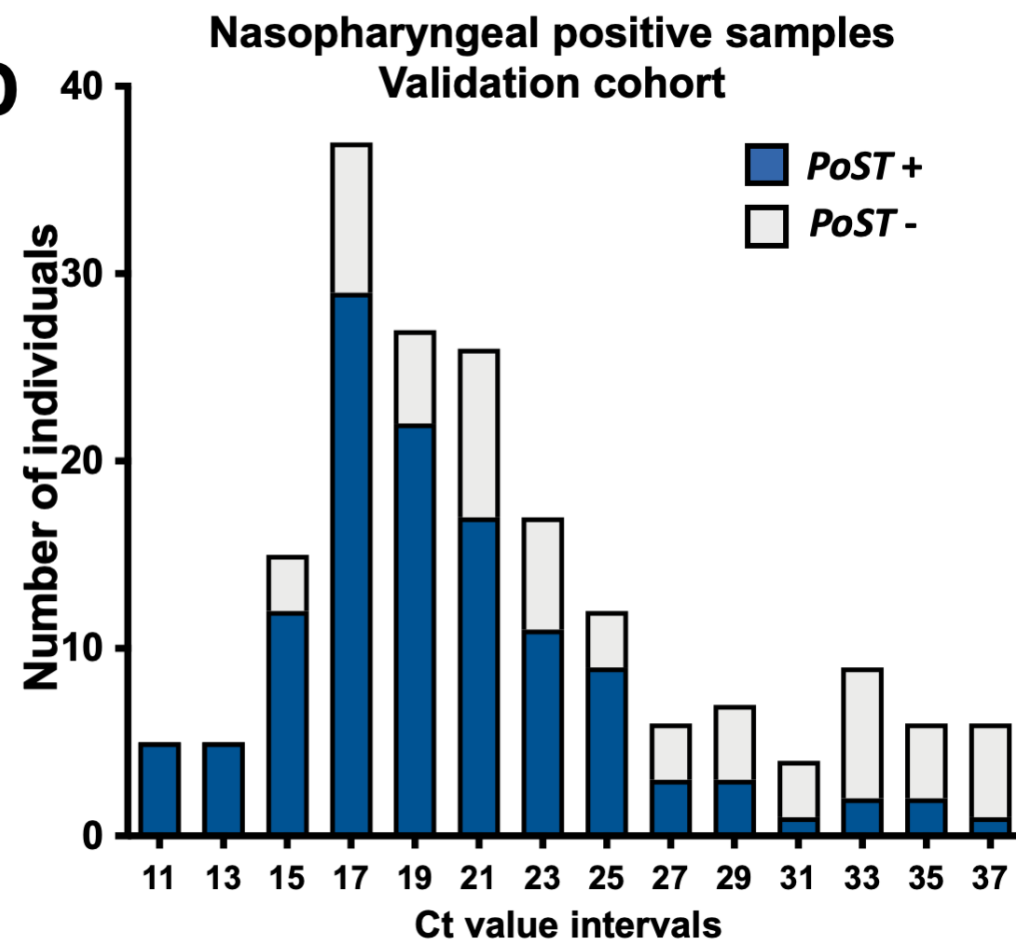
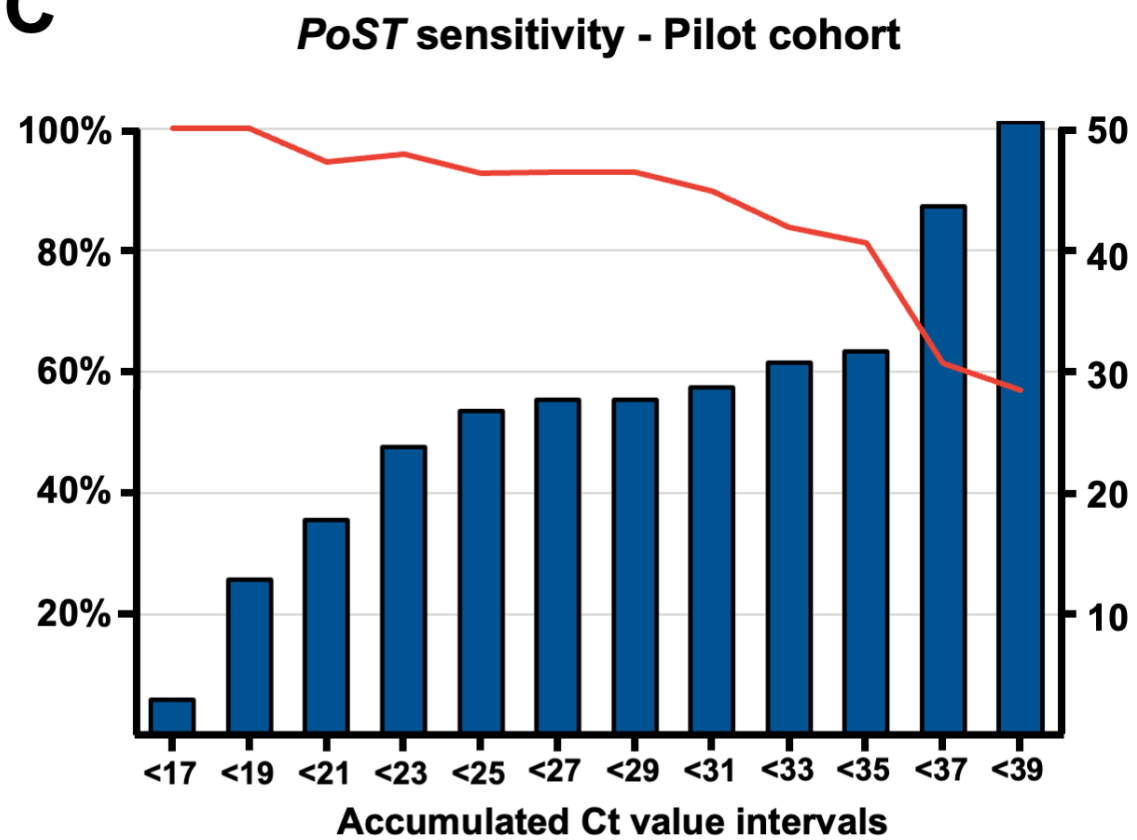
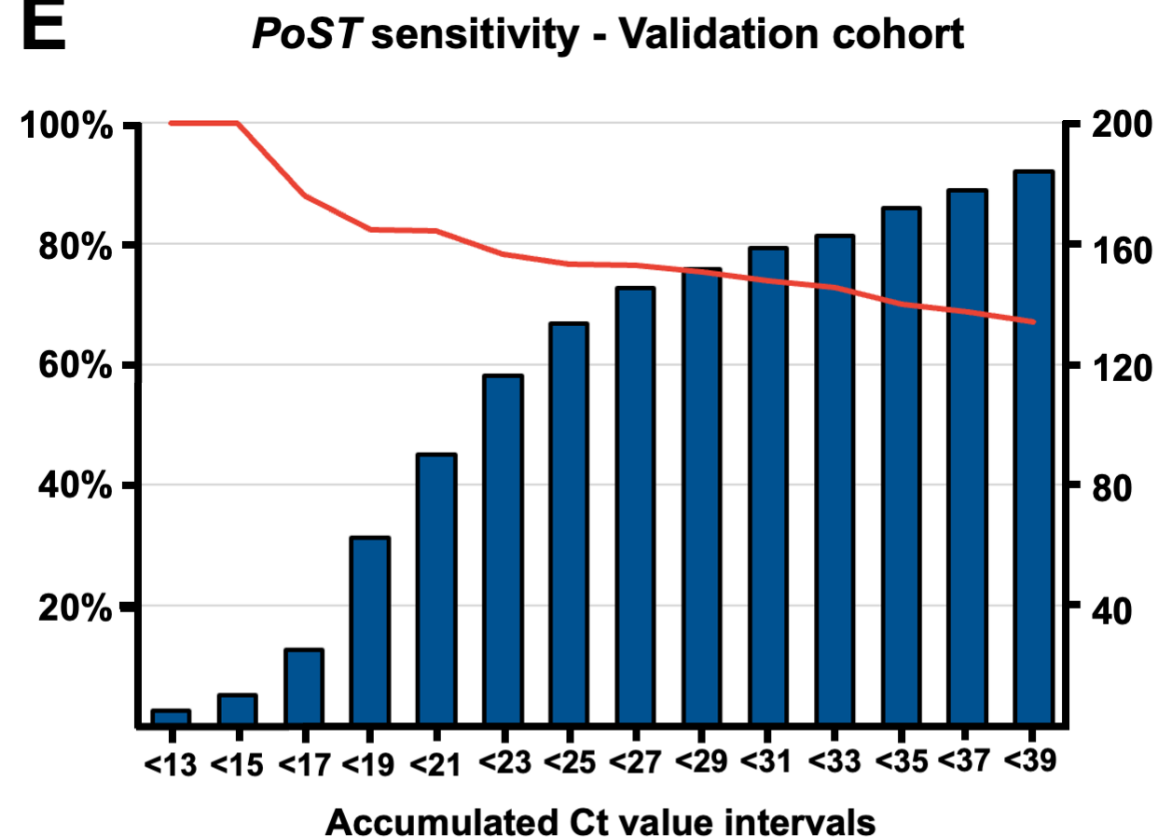
(A-H) Histograms representing the Ct value distribution of the patients from Dávila Clinic (Santiago, Chile) between March and October 2020 (n=7569, Source file 3).

565

566 **Source File 1.** Table 1 including all data generated by the 2020 cohort study.

567 **Source File 2.** Table 2 including all data generated by the 2020 cohort study.

568 **Source File 3.** Table 1 including all data generated by the 2020 cohort study.

A**B****D****C****E**

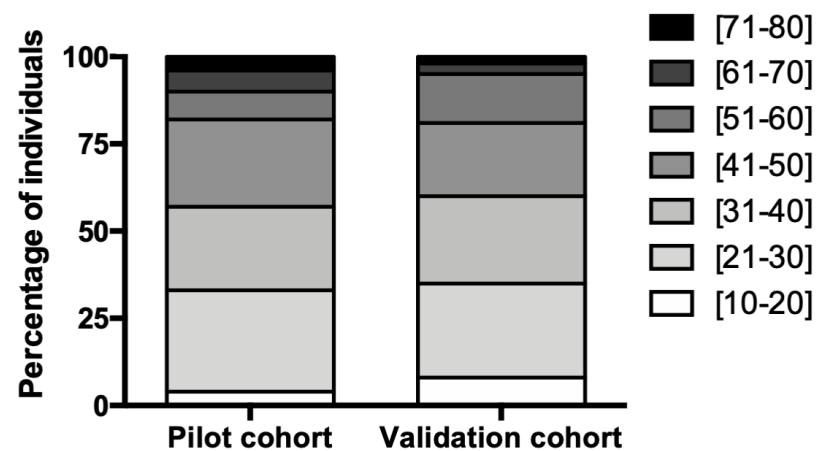
— % PoST Sensitivity ■ # Nasopharyngeal Samples

A**Pilot cohort**

		NF - PCR		
		+	-	
<i>PoST</i>	+	29	6	35
	-	22	483	505
		51	489	540

B**Validation cohort**

		NF - PCR		
		+	-	
<i>PoST</i>	+	122	14	136
	-	60	568	628
		182	582	764

C**Age distribution****D****Gender distribution****E****COVID-19 Symptom distribution**