

1 **Title: Accessioning and automation compatible anterior nares swab** 2 **design**

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15

16 **ABSTRACT**

17 The COVID-19 pandemic has resulted in an unparalleled need for viral testing capacity across the
18 world and is a critical requirement for successful re-opening of economies. The logistical barriers to near-
19 universal testing are considerable. We have designed an injection molded polypropylene anterior nares
20 swab, the RHINOstick, with a screw cap integrated into the swab handle that is compatible with fully
21 automated sample accessioning and processing. The ability to collect and release both human and viral
22 material is comparable to that of several commonly used swabs on the market. SARS-CoV-2 is stable on
23 dry RHINOstick swabs for at least 3 days, even at 42°C, and elution can be achieved with small volumes.
24 The swab and barcoded tube set can be produced, sterilized, and packaged at < 2 USD per unit and can

25 easily be adopted by large research institutes to increase throughput and dramatically reduce the cost of a
26 standard SARS-CoV-2 detection pipeline.

27

28 **INTRODUCTION**

29 As of September 8th 2020, at least 27 million cases of COVID-19 and 890,000 deaths have been
30 reported world-wide (1). To determine if a patient has COVID-19, in most cases, a nasopharyngeal (NP)
31 swab is collected by a trained professional. The swab is then deposited in 1-3 mL of transport media
32 followed by RNA purification and RT-qPCR. NP swabs are around 15 cm in length with a collection
33 head coated with short synthetic filaments, flock, or spun fibers (2); collection is often an uncomfortable
34 process. The high demand for testing during this pandemic has outstripped the supply of NP swabs (and
35 many other critical reagents for testing) resulting in a testing bottleneck (3). These supply limitations
36 together with a drive towards patient self-collection has spurred the development of alternatives to the
37 standard NP swab. A promising alternative is anterior nares (AN) swabs, commonly referred to as nasal
38 swabs. AN swabs offer a testing sensitivity similar to NP swabs (4, 5) but are easier to use and more
39 comfortable for the patient.

40 The choice of swab and collection device can have a major impact on the testing speed in clinical
41 labs. Upon receiving samples, a typical procedure in a testing facility is to first accession the delivered
42 patient samples by scanning the barcoded label to upload relevant patient data into the system, then swabs
43 are manually removed from each collection tube and disposed of. The sample transport media is then
44 processed to purify RNA, which is used as input for RT-qPCR. The initial steps in this procedure are hard
45 to automate, slow, and expose staff to infection. Standard 1D barcoding systems and the manual removal
46 of swabs is time consuming and thus costly. There are machines that can perform the entire procedure
47 from accessioning to results, one tube at a time, e.g. a cobas® 8800, but this process is slow, 1056 tubes
48 per 8-hour shift (6), and the machines are expensive.

49 In an effort to meet the dramatic increase in demand for nasal swabs, several groups have
50 designed and 3D printed new swabs (2, 7). The performance of these swabs is comparable to that of

51 standard swabs; however, they aim to reproduce the existing status quo, rather than to address some of the
52 limitations caused by the standard swab design. An ideal swab would be one that is comfortable for
53 patients to self-administer without sacrificing performance, while also allowing for automated specimen
54 accessioning and processing. Additionally, the swab would be made from non-absorbent material,
55 allowing samples to be diluted into smaller volumes of transport media than those used in the current
56 procedure, rendering the sample more concentrated and allowing for more sensitive detection of viral
57 RNA. Here we present the RHINOstick, a swab that 1) performs as well as existing AN swabs; 2) is
58 compatible with direct input to RT-qPCR for extraction free SARS-CoV-2 detection; and 3) is compatible
59 with a collection system (swab and tube) that enables automated sample accessioning and processing.

60

61 **MATERIALS AND METHODS**

62 **Swab design.** The swabs were designed in SolidWorks (Dassault Systèmes) and manufactured
63 using single-shot rapid injection molding (Protolabs) from medical grade FHR P5M4R polypropylene
64 (Flint Hills), a material compatible with autoclaving (121°C, 20 min), ethylene oxide, gamma radiation,
65 and e-beam sterilization. The stacked rings of the swab head enable collection of nasal matrix without the
66 need for an absorbent coating, using a design previously developed at the Wyss Institute. The cap cavity
67 is compatible with automated decapping robot systems using a square profile adapter head, while the 2
68 mm pitch external threading mates with the interior threading of sample collection tubes from several
69 major manufacturers (e.g. Matrix, Micronics, and LVL). As the new swab we developed in this study is
70 useful for the collection of nasal samples for diagnostic tests we call it the RHINOstick swab.

71 **Absorption of liquid by swab.** The swabs used in this study were weighed on an analytical
72 balance before and after a 15 second incubation in 1 mL of nuclease free water. Six replicates were
73 measured and results are reported in Table 1.

74 **Anterior nares self-swabbing to compare swab performance.** We compared several swab
75 types for performance in anterior nares (AN) specimen collection: the RHINOstick prototype, Proctor &
76 Gamble (P&G) blue prototype, a Wyss Institute flocked prototype, Puritan hydraflock, Puritan foam,

77 Puritan polyester, US Cotton, and Microbrush®. Per CDC guidelines, volunteers were instructed to insert
78 the swab 0.5 inch into a nostril, rotate three times along the membrane of the nose firmly and leave in
79 place for 10 to 15 seconds, remove, and then repeat this procedure on the other nostril with the same swab
80 to collect nasal matrix (8). The volunteer was then instructed to place the used swab in a dry 1.5 mL
81 microcentrifuge tube and break the handle if necessary so the tube could close for transport. Prior to RT-
82 qPCR reactions all swabs were suspended in 200 μ L of nuclease free 1x PBS. All experiments in this
83 study were approved by the Institutional Review Board of the Harvard Faculty of Medicine, IRB20-0581,
84 and informed written consent was obtained from volunteers.

85 **RT-qPCR.** RT-qPCR reactions were prepared to reach a final volume of 10 μ L using 8 μ L of
86 master mix and 2 μ L of sample. The Luna Universal One Step RT-qPCR kit (NEB) was used for all RT-
87 qPCR reactions. The master mix protocol was adjusted to include 0.25 U/ μ L of RNaseIn Plus (Promega)
88 for every 10 μ L reaction. RT-qPCR reactions were run on the QuantStudio 6 Real Time PCR system
89 (Thermo Fisher Scientific) following the manufacturer recommended Luna RT-qPCR protocol. For all
90 reactions, melt curves were used to determine if products were specific or non-specific. All non-specific
91 T_{ms} , >0.5 °C from the expected melting temperature, are presented as having a Ct of 40. All experiments
92 included at least one negative control which was either 1x PBS or water. The sequences of all primers
93 used are listed in Table S1.

94 **Recovery of human mRNA from AN swabs.** SARS-CoV-2 negative volunteers performed AN
95 swabbing as directed with each type of swab tested (Fig. 2, Table 1) to collect nasal matrix. There were
96 three biological replicates for each AN swab measurement, taken on at least two different days. For every
97 condition in which a swab was tested, an unused swab, without nasal matrix, was processed in parallel as
98 a negative control. To recover the sample from the swabs, all swabs were suspended in 200 μ L of 1x
99 PBS, vortexed for 10 sec, spun down in a microcentrifuge, and input directly to the RT-qPCR for
100 GAPDH mRNA detection (Fig. 2C).

101 **Contrived samples using packaged synthetic SARS-CoV-2 spiked onto unused swabs.**
102 AccuPlex SARS-CoV-2 verification panel v2 (Seracare), a packaged synthetic virus, containing the N

103 gene, E gene, ORF1a, S gene, and RdRp was used to simulate the expected viral recovery from AN swabs
104 near the limit of detection (Fig. 2D, S2C). 10 μ L of 100 copies/ μ L packaged synthetic virus was directly
105 applied to the collection head of each swab. Swabs were left in a fume hood for about 20 min until the
106 swabs appeared dry to the eye indicating absorption of the packaged synthetic virus into the collection
107 material. At least three biological replicates were used for every swab tested and replicate data was
108 collected on at least two different days. Swabs were then inserted into a 1.5 mL microcentrifuge tube
109 containing 200 μ L of 1x PBS, vortexed for 10 sec, spun down in a microcentrifuge, and 2 μ L was input
110 directly to RT-qPCR for N gene detection. The positive control was 10 μ L of 100 copies/ μ L packaged
111 synthetic virus directly input to 190 μ L of PBS.

112 **Clinical samples.** NP swabs from SARS-CoV-2 patient samples were purchased from
113 BocaBiolistics, FL. The NP swabs are remnant samples obtained through BocaBiolistics and partner labs
114 that were de-identified by BiocaBiolistics with their IRB reviewed and approved SOP for de-linking
115 specimens. These NP swabs arrived in 1-3 mL of viral, multitrans, or universal transport media (VTM,
116 MTM, or UTM). 40 μ L of each sample was aliquoted and frozen at -80°C to limit freeze-thawing of
117 samples.

118 **Contrived samples from a clinical source spiked onto swabs with nasal matrix.** Nasal matrix
119 was collected from volunteers as described above using RHINOstick and Puritan foam swabs. 5 μ L of
120 clinical sample, with either a higher (~ 1600 copies/ μ L), or lower titer (~ 140 copies/ μ L), were applied to
121 the collection head of used swabs, and swabs were air dried in the BSL2+ biosafety cabinet for 20 min.
122 Each swab was then placed in a 1.5 mL microcentrifuge tube containing 200 μ L of 1x PBS, manually
123 spun for 10 sec in the media, and 2 μ L was directly input to the RT-qPCR for both N gene (Fig. 2E) and
124 GAPDH mRNA detection (Fig. S2C). To assess maximum possible viral recovery from the swab, the
125 positive control was 5 μ L of either the higher or lower titer clinical sample in 195 μ L of 1x PBS.
126 Negative controls are unused RHINOstick and Puritan foam swabs suspended in 200 μ L of 1x PBS.
127 Three biological replicates were performed for each titer and type of swab tested.

128 **Assessment of stability of SARS-CoV-2 on swabs with nasal matrix over time.** To assess the
129 stability of the SARS-CoV-2 virus on swabs with nasal matrix over time, two volunteers self-swabbed
130 three independent times with both the RHINOstick and Puritan foam swabs for a total of six swabs at
131 each time point. The handles of the Puritan foam swabs were broken in order to safely close the collection
132 vial, a 1.5 mL microcentrifuge tube. Several clinical samples were mixed together to generate a pooled
133 clinical sample with a viral titer of ~10,200 copies/ μ L. The pooled clinical sample was then aliquoted into
134 50 μ L volumes and refrozen at -80°C. At each time point (72, 48, 24, 2, and 0 hrs) an aliquot was thawed
135 and 3 μ L of pooled clinical sample was applied to each swab. One RHINOstick and one Puritan foam
136 swab with nasal matrix from each volunteer was incubated dry at room temperature (25°C) or 42°C in a
137 1.5 mL microcentrifuge tube to assess stability at room temperature or elevated temperatures that may
138 occur during transport. A matched RHINOstick or Puritan foam swab with nasal matrix from each
139 volunteer was immediately put into a 1.5 mL microcentrifuge tube containing 0.4 mL of 1x PBS to assess
140 the relative stability of a wet swab vs dry swab. An additional 3 μ L of the pooled clinical sample was
141 applied to an unused RHINOstick and unused Puritan foam swab at each time point and kept dry over the
142 time course at 25°C, to assess the effect of nasal matrix on viral recovery. At the end of the time course,
143 dry swabs were suspended in 0.4 mL of 1x PBS. The samples from both wet and dry tubes were mixed by
144 vortexing for 10 sec, then spun down in a microcentrifuge. 2 μ L of each sample was directly input to RT-
145 qPCR for GAPDH and N gene detection. The positive control was 3 μ L of the pooled clinical sample in
146 197 μ L of 1x PBS at time 0.

147

148 **RESULTS**

149 **Swab design for automated accessioning and analysis.** NP swabs are long, making it
150 challenging to use these swabs with automation-compatible tubes. AN swabs in contrast do not need to be
151 as long as NP swabs and can be designed with a shorter handle, opening up the possibility of making AN
152 swabs that can be directly paired with automation-compatible tubes for an effective collection system. As
153 part of the design, RHINOstick swabs have a cap that can be directly screwed onto a 96-well format

154 automation-compatible tube, such as a 1.0 mL Matrix tube (Thermo Fisher Scientific) (Fig. 1A). The
155 swabs were made by single shot injection molding with medical grade polypropylene (Fig. S1 and
156 Methods). Injection molding of swabs allows for high volume production at low prices. While the swabs
157 can fit onto many tubes, we believe the optimal design is in collection tubes pre-labeled (by the
158 manufacturer) with a serialized Type 128 1D barcode plus human readable code on the side with a
159 matching 2D data matrix barcode on the bottom. (Fig. 1). This design allows for the collection tube and
160 swab to be accessioned and used by the patient in an unobserved manner without having to pre-register
161 each barcode manually, reducing costs and labor. In addition, the matching 2D barcode on the bottom
162 allows a whole rack of tubes to be accessioned in seconds by a barcode reader.

163 **Swab performance.** We compared the RHINOstick to several other swabs on the market or
164 under development (Fig. 2A, Table 1). First, we tested for absorption of water. Water absorption is
165 sometimes used as a proxy for the amount of material that a swab will collect (9, 10), although it does not
166 necessarily correlate with effective collection of cells and viral particles. The RHINOstick, as well as the
167 Proctor and Gamble (P&G) blue swab absorbed very little water compared to the majority of available
168 swabs on the market or prototypes. This lack of absorption is likely because polypropylene is more
169 hydrophobic than the other collection materials, such as cotton and spun polyester.

170 To test swab performance more directly, we measured the performance of 8 different AN swabs
171 using several approaches (Fig. 2). We tested collection and recovery of 1) human mRNA in nasal matrix
172 from swabs, 2) mRNA from viral particles added to swabs, and 3) mRNA from viral particles added to
173 swabs coated in nasal matrix (Fig. 2B). Human mRNA was used as a process control to assess successful
174 collection and recovery of cells from swabs. The process control also assesses the efficiency of the
175 reverse transcription (RT) reaction as the primers span two exons to ensure the assay quantifies mRNA
176 not DNA (11). A single volunteer swabbed with 8 different brands of AN swabs in triplicate (Fig. 2B,
177 scheme I) and the eluent was used as direct input for RT-qPCR for GAPDH mRNA to quantify the
178 amount of human mRNA recovered (Fig. 2C). All 8 swabs performed similarly in this assay and no

179 GAPDH was detected on any of the unused swabs (Fig. 2C). For all evaluations of AN swabs in this work
180 we performed direct RT-qPCR on the swab eluant without RNA purification.

181 Recovery of viral particles was first assessed on a contrived sample by applying packaged
182 synthetic SARS-CoV-2 viral particles (Seracare reference) to an unused swab for each of the 8 AN swabs
183 tested (Fig. 2B, scheme II). The packaged synthetic virus was dried onto the swab and eluted into PBS by
184 vortexing. In a similar experiment, we found that elution into PBS by gentle swirling of the swabs
185 releases the virus at equivalent or superior levels to vortexing in the same amount of time (Fig. S2A and
186 B). The level of viral particles released by each swab was quantified by RT-qPCR for the SARS-CoV-2 N
187 gene (Fig. 2D). The RHINOstick performed as well as the other swabs tested, and released an equivalent
188 number of viral particles to the positive control (Fig. 2D). The lower detection of viral RNA for other
189 swabs such as the Puritan foam is likely due to the fact that these swabs absorb significant volumes of
190 liquid (Table 1) making it hard to elute the contents off the swab efficiently, especially given that the
191 maximal recovery of AccuPlex possible is 10 molecules per reaction. Going forward, due to swab
192 availability, and its common use we performed all comparisons to the RHINOstick with only the Puritan
193 foam swabs.

194 To test recovery of SARS-CoV-2 RNA from contrived clinical samples in the presence of nasal
195 matrix, volunteers self-swabbed using either the RHINOstick or Puritan foam swab, then transport media
196 from SARS-CoV-2 clinical samples was applied to the used swabs (Fig.2B, scheme III). After drying, the
197 viral material was recovered by spinning the swabs in PBS. This experiment was performed with both a
198 lower and a higher titer clinical sample (Methods), and the presence of both SARS-CoV-2 N gene and
199 GAPDH mRNA was detected by RT-qPCR using the PBS/swab solution as direct input to RT-qPCR
200 (Fig. 2E, Fig. S2C). Additionally, the equivalent performance of the RHINOstick to the positive control
201 demonstrates the robustness of RT-qPCR to nasal matrix. The clinical sample titers were determined
202 using an N gene standard curve (Fig. S2D, Supplementary Methods). RHINOstick swabs were not
203 statistically distinguishable from the positive control at either titer, but the Puritan foam swabs showed

204 lower recovery ($P < 0.001$ by an independent t-test). Replicate Ct values shows the high reproducibility of
205 the qPCR data (Fig. S2E and F).

206 **Virus stability on swabs.** A key issue with swabs is the stability of viral particles on the swabs
207 during transport from the collection site to the test lab. To test the stability of SARS-CoV-2 on swabs
208 over time we added SARS-CoV-2 from clinical samples to swabs containing nasal matrix (Fig. 3A). The
209 contrived samples were left wet or dry at 25°C as well as dry at 42°C, to simulate storage in a hot car or
210 truck, for up to 72 hours before elution into PBS. The presence of both SARS-CoV-2 N gene RNA and
211 GAPDH mRNA was detected by using the swab eluent as direct input into RT-qPCR (Fig. 3 and S3).
212 SARS-CoV-2 viral particles on the RHINOstick swabs were stable under all conditions tested both in the
213 presence and absence of nasal matrix (Fig. 3B and S3A) whereas the Puritan foam swabs showed much
214 greater variation in N gene detection when in the presence of nasal matrix, particularly when the sample
215 was left out for 72 hours (Fig. 3D and S3A). Overall, GAPDH detection was more consistent for both the
216 RHINOstick and Puritan foam swabs (Fig. 3C and D, S3B-D) across all conditions in the time course, but
217 was slightly more variable for the Puritan foam swabs stored wet at room temperature for 72 hours (Fig
218 3E). The variability in the N gene as well as GAPDH data collected from Puritan foam swabs during the
219 time course is also observed when comparing the Ct's between two technical replicates in the RT-qPCR
220 data (Fig. S3E and F).

221

222 **DISCUSSION**

223 Our improved AN swab is comfortable to use, allows patients to perform swabs for themselves,
224 and enables rapid accessioning and processing. The RHINOstick performs comparably to currently
225 available swabs, releasing similar amounts of human and viral material into solution after use (Fig. 2). We
226 found that RHINOstick and Puritan foam swabs detected similar levels of GAPDH mRNA (Fig. 3), while
227 SARS-CoV-2 was detected more consistently from the RHINOstick swab with lower titer contrived
228 samples (Fig. 2D and E) or after long periods of storage (Fig. 3). All RT-qPCR reactions performed in

229 this study used direct input of swab eluant to the reaction mix without any RNA extraction and we were
230 able to detect as low as 10 molecules per assay (Fig. 2D).

231 SARS-CoV-2 viral particles on the RHINOstick swab proved to be very stable with no
232 statistically significant loss of Ct under all the conditions tested (Fig. 3). One of the key design elements
233 of the RHINOstick swab is the ability for a patient to self-collect their AN swab for sample processing.
234 To best use this feature, it is preferred to use dry swabs in which the swab is put into the collection tube
235 after self-collection in the absence of any buffer. This swab may then be mailed in or collected at a central
236 location without the need for concern over sample leakage in transport. The stability of SARS-CoV-2 on
237 the RHINOstick swab for up to 72 hours before processing (Fig. 3B and C) demonstrates the feasibility of
238 the dry swab method which is consistent with other studies (12). An additional advantage of the new
239 swab design is the ability to elute the sample in a low volume of liquid (200 μ L), potentially increasing
240 the sensitivity of the direct RT-qPCR method by 5-15 fold compared to standard methods. Most
241 commercial swabs cannot be used with this low elution volume, due to the high volume of liquid
242 absorbed by the swab (Table 1).

243 We envision the RHINOstick swabs being used in the following workflow: the patient will scan
244 the side of the barcode on the side of the tube using a cellphone app, phone-accessed website, or scanner
245 and an ID card at the collection site to link the patient and sample together. After swabbing with the
246 RHINOstick swab, the patient would screw the swab into the barcoded tube. The sample would then be
247 packaged for Category B compliant transport. In an unsupervised self-collection setting, the tube could be
248 rescanned at the sample deposition site to help track sample custody. The tubes would be deposited in a
249 lockbox at the site, which would periodically be sent to the testing center. All swabs would be stored and
250 transported dry avoiding the risk of liquid leakage. In the testing facility, the samples would be received
251 and loaded into 96-well racks by hand (Fig. 1B). Each rack of tubes would then be put onto a robot that
252 scans the 2D matrix codes on the bottom of the tubes thereby linking the sample ID to each plate and
253 plate location in seconds. After accessioning, the samples can pass to a de-capping robot which removes
254 the caps and the samples can then be eluted, inactivated, and processed for viral quantitation.

255 Here we demonstrate that the RHINOstick, a newly designed injection molded polypropylene
256 swab with a screw cap integrated into the swab handle, performs equal to several commonly used AN
257 swabs on the market at capturing and releasing SARS-CoV-2 viral particles from AN swabs. This
258 innovative AN swab design has the potential to expedite SARS-CoV-2 diagnostic testing while
259 significantly reducing costs. We anticipate that these swabs will be generally useful for pathogen panel
260 testing at large research institutes.

261

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270 paper. All authors reviewed the manuscript.

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303

304 **FIGURE LEGENDS**

305 **FIG 1** 96-well format automation and accession compatible AN swab design. (A) Custom injection
306 molded AN swab that can be produced at large scale and is compatible with 96-well format automation. A
307 sample tube compatible with the RHINOstick swab is shown with barcodes on the side and bottom. The
308 RHINOstick swab is 4.9 cm long with a collection head length of 1.6 cm. 1 cm scale bar shown for
309 reference. (B) 96-well rack of swabs and tubes with 2D matrix codes printed on the bottom of the tubes,
310 allows for rapid accessioning.

311

312 **FIG 2** Comparison of swab performance. (A) AN swabs tested in this study, from left to right:
313 RHINOstick, Proctor & Gamble (P&G) blue, Wyss Institute flocked prototype, Puritan hydroflock,
314 Puritan foam, Puritan polyester, US Cotton, and Microbrush®. 1 cm scale bar shown for reference. (B)
315 Schematic of swab experiments performed in C-D. **I**; SARS-CoV-2 negative volunteer self-collected
316 nasal matrix on a swab. **II**; unused swab, without nasal matrix, was either treated with packaged synthetic
317 SARS-CoV-2 virus or left untreated (clean, unused swab). **III**; SARS-CoV-2 negative volunteer self-
318 collected nasal matrix on a swab which was then treated with packaged synthetic SARS-CoV-2 or SARS-
319 CoV-2 clinical sample (Methods). All samples were eluted in PBS and used as direct input to RT-qPCR
320 assays. Images created with BioRender.com. (C) RT-qPCR quantitation of human GAPDH mRNA from
321 used swabs containing nasal matrix (pink bars) or matched unused swabs (grey bars). (D) RT-qPCR
322 quantitation of the SARS-CoV-2 N gene from packaged synthetic virus applied to clean, unused swabs.
323 The grey bar is the negative control, PBS input into RT-qPCR. The pink line is a guideline for complete
324 recovery based on the positive control. (E) RT-qPCR quantitation of SARS-CoV-2 N gene from swabs in

325 the presence of nasal matrix spiked with a lower (~140 copies/ μ L, pink bars) or higher (~1600 copies/ μ L,
326 green bars) titer clinical sample. The grey bar is the negative control, PBS, and the positive controls are
327 the lower or higher titer clinical samples directly input to RT-qPCR. RT-qPCR data in C-E all show
328 technical replicates of at least 3 biological experiments.

329

330 **FIG 3** Stability of SARS-CoV-2 on swabs in the presence of nasal matrix. (A) Schematic of the
331 experimental workflow in B-E. SARS-CoV-2 clinical sample was applied to unused swabs or self-
332 collected AN swabs, with nasal matrix, (Methods) and left dry or wet at 25°C, for up to 72 hours. All
333 samples were quantified by direct input of eluent into RT-qPCR. Images created with BioRender.com.
334 (B,C) The stability of SARS-CoV-2 on RHINOstick swabs with nasal matrix left dry or wet at 25°C or
335 dry at 42°C was analyzed over the course of 72 hours by RT-qPCR for the SARS-CoV-2 N gene (B) or
336 GAPDH (C). (D,E) The stability of SARS-CoV-2 on Puritan foam swabs with nasal matrix left dry or
337 wet at 25°C or dry at 42°C was analyzed over the course of 72 hours by RT-qPCR for the SARS-CoV-2
338 N gene (D) or GAPDH (E). Data points in B-E are technical replicates of 2 biological replicates. The
339 positive control in B-E is the SARS-CoV-2 clinical sample directly added to PBS at time 0. The negative
340 control is an unused RHINOstick (B, C) or Puritan foam (D, E) swab in PBS.

341

342 **FIGURES and TABLES**

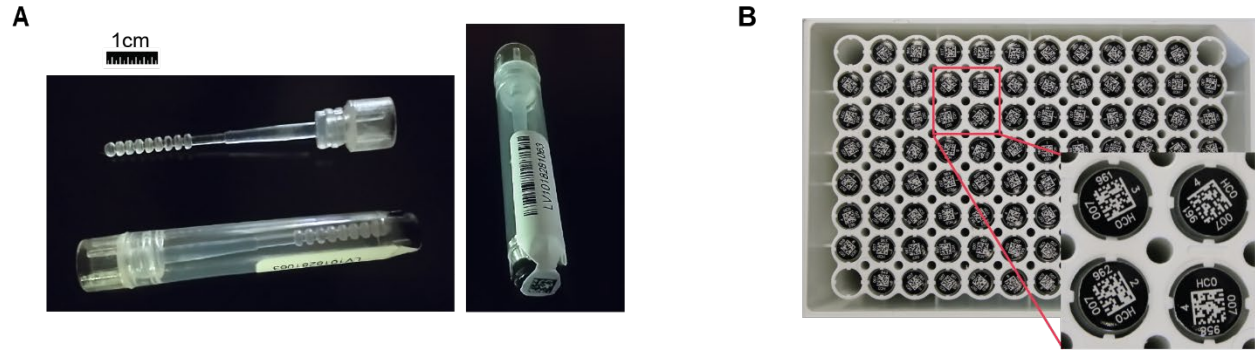
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344 **Table 1:**

Swab	Collection Material	Average volume absorbed (μL)	Standard deviation (μL)	Purchasable as of 09/17/20
RHINOstick	Polypropylene	14.4	2.2	N
P&G blue	Polypropylene	0.7	1.0	N
Wyss flock	Polypropylene and polyester flock	65.8	3.9	N
Puritan hydraflock	Polyester flock	154.1	8.9	Y
Puritan foam	Polyurethane foam	41.3	14.4	Y
Puritan polyester	Polyester	155.9	9.6	Y
US Cotton	Cotton	168.8	25.4	Y
Microbrush	Nylon Flock	64.9	10.1	Y

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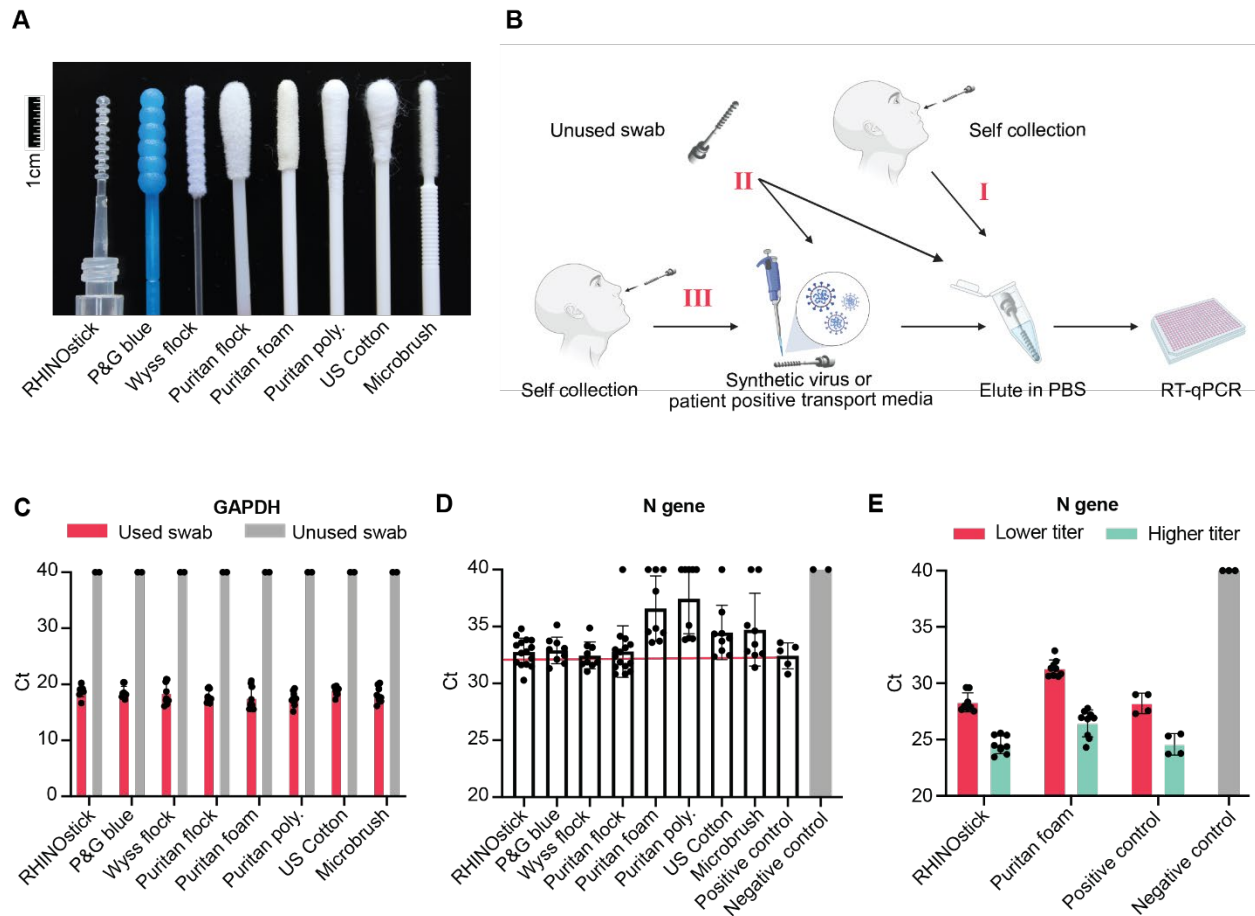
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348 **FIG 1** 96-well format automation and accession compatible AN swab design. (A) Custom injection
349 molded AN swab that can be produced at large scale and is compatible with 96-well format automation. A
350 sample tube compatible with the RHINOstick swab is shown with barcodes on the side and bottom. The
351 RHINOstick swab is 4.9 cm long with a collection head length of 1.6 cm. 1 cm scale bar shown for
352 reference. (B) 96-well rack of swabs and tubes with 2D matrix codes printed on the bottom of the tubes,
353 allows for rapid accessioning.

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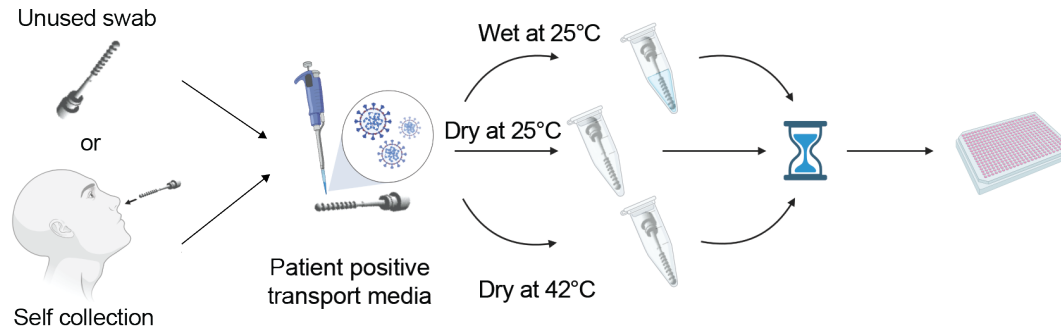


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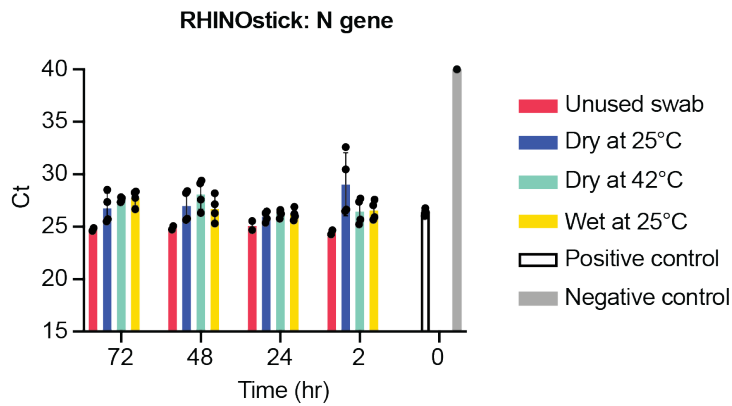
356 **FIG 2** Comparison of swab performance. (A) AN swabs tested in this study, from left to right:
 357 RHINOstick, Proctor & Gamble (P&G) blue, Wyss Institute flocked prototype, Puritan hydraflock,
 358 Puritan foam, Puritan polyester, US Cotton, and Microbrush®. 1 cm scale bar shown for reference. (B)
 359 Schematic of swab experiments performed in C-D. **I**; SARS-CoV-2 negative volunteer self-collected
 360 nasal matrix on a swab. **II**; unused swab, without nasal matrix, was either treated with packaged synthetic
 361 SARS-CoV-2 virus or left untreated (clean, unused swab). **III**; SARS-CoV-2 negative volunteer self-
 362 collected nasal matrix on a swab which was then treated with packaged synthetic SARS-CoV-2 or SARS-
 363 CoV-2 clinical sample (Methods). All samples were eluted in PBS and used as direct input to RT-qPCR
 364 assays. Images created with BioRender.com. (C) RT-qPCR quantitation of human GAPDH mRNA from
 365 used swabs containing nasal matrix (pink bars) or matched unused swabs (grey bars). (D) RT-qPCR
 366 quantitation of the SARS-CoV-2 N gene from packaged synthetic virus applied to clean, unused swabs.
 367 The grey bar is the negative control, PBS input into RT-qPCR. The pink line is a guideline for complete

368 recovery based on the positive control. (E) RT-qPCR quantitation of SARS-CoV-2 N gene from swabs in
369 the presence of nasal matrix spiked with a lower (~140 copies/ μ L, pink bars) or higher (~1600 copies/ μ L,
370 green bars) titer clinical sample. The grey bar is the negative control, PBS, and the positive controls are
371 the lower or higher titer clinical samples directly input to RT-qPCR. RT-qPCR data in C-E all show
372 technical replicates of at least 3 biological experiments.
373

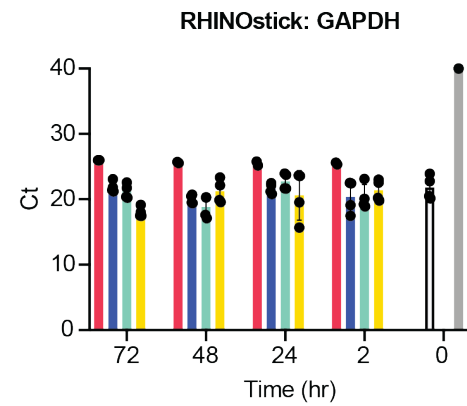
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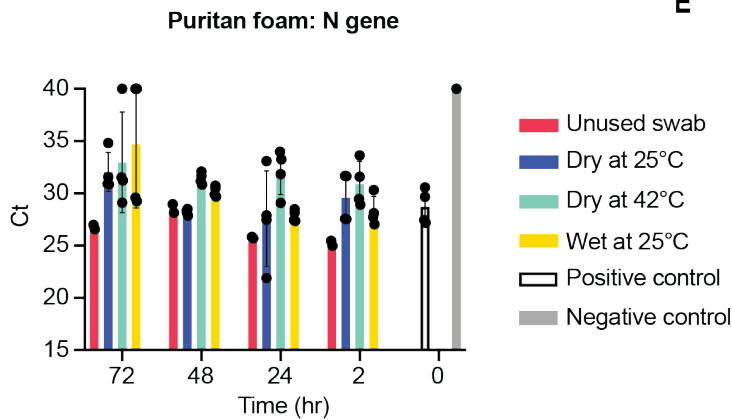
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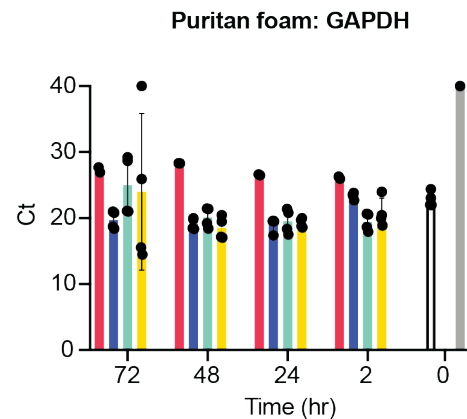
C



D



E



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375 **FIG 3** Stability of SARS-CoV-2 on swabs in the presence of nasal matrix. (A) Schematic of the
376 experimental workflow in B-E. SARS-CoV-2 clinical sample was applied to unused swabs or self-
377 collected AN swabs, with nasal matrix, (Methods) and left dry or wet at 25°C, for up to 72 hours. All

378 samples were quantified by direct input of eluent into RT-qPCR. Images created with BioRender.com.
379 (B,C) The stability of SARS-CoV-2 on RHINOstick swabs with nasal matrix left dry or wet at 25°C or
380 dry at 42°C was analyzed over the course of 72 hours by RT-qPCR for the SARS-CoV-2 N gene (B) or
381 GAPDH (C). (D,E) The stability of SARS-CoV-2 on Puritan foam swabs with nasal matrix left dry or
382 wet at 25°C or dry at 42°C was analyzed over the course of 72 hours by RT-qPCR for the SARS-CoV-2
383 N gene (D) or GAPDH (E). Data points in B-E are technical replicates of 2 biological replicates. The
384 positive control in B-E is the SARS-CoV-2 clinical sample directly added to PBS at time 0. The negative
385 control is an unused RHINOstick (B, C) or Puritan foam (D, E) swab in PBS.
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