

1 **Clinical evaluation of the cobas SARS-CoV-2 test and a diagnostic platform**
2 **switch during 48 hours in the midst of the COVID-19 pandemic**

3 **Running title:** Evaluation of the cobas SARS-CoV-2 test

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19 **Abstract**

20 Laboratories are currently witnessing extraordinary demand globally for sampling devices,
21 reagents, consumables, and diagnostic instruments needed for timely diagnosis of SARS-CoV-2
22 infection. To meet diagnostic needs as the pandemic grows, the US Food and Drug
23 Administration (FDA) recently granted several commercial SARS-CoV-2 tests Emergency Use
24 Authorization (EUA), but manufacturer-independent evaluation data are scarce. We performed
25 the first manufacturer-independent evaluation of the fully automated sample-to-result two-
26 target test cobas 6800 SARS-CoV-2 (cobas) (Roche Molecular Systems, Branchburg, NJ), which
27 received US FDA EUA on March 12, 2020. The comparator was a standardized 3-hour SARS-CoV-
28 2 protocol, consisting of RNA extraction using an automated portable instrument, followed by a
29 two-target RT-PCR, which our laboratory has routinely used since January 2020 (Corman VM et
30 al. EuroSurveill 25(3):2000045). Cobas and the comparator showed overall agreement of 98.1%
31 and a kappa value of 0.95 on an in-house validation panel consisting of 217 well-characterized
32 retrospective samples. Immediate prospective head-to-head comparative evaluation followed
33 on 502 samples, and the diagnostic approaches showed overall percent agreement of 99.6%
34 and a kappa value of 0.98. A good correlation ($r^2 = 0.96$) between cycle threshold values for
35 SARS-CoV-2 specific targets obtained by cobas and the comparator was observed. Our results
36 showed that cobas is a reliable assay for qualitative detection of SARS-CoV-2 in nasopharyngeal
37 swab samples collected in the UTM-RT system. Under the extraordinary circumstances that
38 laboratories are facing worldwide, a safe diagnostic platform switch is feasible in only 48 hours
39 and in the midst of the COVID-19 pandemic if carefully planned and executed.

40

41 **Keywords:** SARS-CoV-2, COVID-19, cobas, cobas 6800

42 **INTRODUCTION**

43 Coronavirus disease 2019 (COVID-19), a severe acute respiratory syndrome first linked to a
44 seafood market in Wuhan (Hubei, China) in December 2019 (1, 2), has become a major public
45 health concern all over the world. The pandemic is rapidly evolving, and as of April 08, 2020
46 there have been 1,447,466 laboratory-confirmed cases of COVID-19 with 83,471 deaths. The
47 causative agent of COVID-19 is a severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2;
48 previously known as 2019-nCoV) (2, 3), which is genetically related to but distinct from two
49 other coronaviruses responsible for largescale outbreaks in the past: severe acute respiratory
50 syndrome coronavirus (SARS-CoV; about 79% sequence identity) and Middle East respiratory
51 syndrome coronavirus (MERS-CoV; about 50%) (2, 3).

52 As evidenced in previous coronavirus epidemics caused by SARS-CoV and MERS-CoV (4, 5),
53 highly reliable laboratory diagnostics for COVID-19 are essential for case identification, patient
54 management, and contact tracing. Due to the current limitations of other laboratory
55 approaches (viral culture, antigen testing, and serology), reverse transcription real-time PCR
56 (RT-PCR) remains the most suitable laboratory diagnostic test for COVID-19 (6-8). The rapid
57 availability of the complete genome of SARS-CoV-2 early in the pandemic (9, 10) facilitated the
58 development of standardized laboratory PCR protocols for COVID-19 in January 2020 (7, 8, 10-
59 12), followed by the launch of a range of commercial SARS-CoV-2 PCR-based assays in the last 3
60 months. Despite the fact that the US Food and Drug Administration (FDA) granted several
61 commercial SARS-CoV-2 amplification assays Emergency Use Authorization (EUA), as of March
62 29, 2020 no manufacturer-independent evaluation data for any commercial SARS-CoV-2 assay
63 with US FDA EUA is available in peer-reviewed literature.

64 Here we present the results of the first manufacturer-independent evaluation of the fully
65 automated sample-to-result two-target test cobas 6800 SARS-CoV-2 (cobas) (Roche Molecular
66 Systems, Branchburg, NJ, USA), which received US FDA EUA on March 12, 2020. The
67 performance of cobas was first evaluated on a well-characterized in-house validation panel
68 consisting of 217 samples. The comparator was a standardized 3-hour SARS-CoV-2 detection
69 protocol, consisting of RNA extraction using an automated portable instrument, followed by RT-
70 PCR targeting the envelope (E) and the RNA-dependent RNA polymerase (RdRp) coronavirus
71 genes (11). The comparator protocol, which has been in routine use in our laboratory since
72 January 2020, was originally developed by Christian Drosten's team (Charité Hospital, Berlin,
73 Germany) (11) and is recommended by the World Health Organization (WHO) (13, 14). The
74 protocol is currently considered the gold standard for SARS-CoV-2 detection in Europe (6, 15).
75 The initial evaluation on the validation panel was followed by immediate prospective head-to-
76 head comparison on 502 routinely collected clinical samples against the same comparator. The
77 entire cobas evaluation procedure followed by a successful diagnostic platform switch lasted
78 only 48 hours and was performed in the midst of the COVID-19 pandemic.

79

80 MATERIALS AND METHODS

81 **In-house validation panel and comparator protocol.** The well-characterized in-house
82 validation panel consisted of 217 undiluted 600 μ l aliquots of nasopharyngeal (N=211) or
83 combined nasopharyngeal/oropharyngeal swabs (N=6) collected in a Universal Transport
84 Medium System (UTM-RT) (Copan, Brescia, Italy). The panel was designed to test sensitivity on
85 a number of SARS-CoV-2 positive samples, with a wide range of viral loads and specificity using

86 SARS-CoV-2 negative samples, as well as samples positive for other respiratory viruses related
87 and not related to SARS-CoV-2. The clinical samples used in the validation panel were collected
88 from 217 individuals referred for COVID-19 testing from March 7, 2020 to March 23, 2020.

89 All samples in the validation panel were routinely tested for the presence of SARS-CoV-2
90 immediately upon arrival in the laboratory using a standardized 3-hour protocol implemented
91 in our laboratory in early January 2020. Briefly, swabs were vortexed for 1 minute at maximum
92 speed followed by automatic nucleic acid extraction from 200 μ l of UTM-RT carried out on a
93 MagNa Pure Compact instrument (Roche Applied Science, Mannheim, Germany) using a
94 MagNA Pure Compact Nucleic Acid Isolation Kit I (Roche), following the manufacturer's
95 instructions. Equine arteritis virus, a positive-sense single-stranded RNA virus, was added to all
96 clinical specimens prior to RNA extraction and served as an internal extraction and amplification
97 control (16). For detection of SARS-CoV-2, two-target RT-PCRs (SARS-CoV-2 specific and pan-
98 Sarbecovirus) were performed using previously described commercially available primers and
99 FAM-labeled hydrolysis probes (11). LightMix Modular SARS and Wuhan CoV E-gene kit (Tib-
100 Molbol, Berlin Germany) amplifying a 76 bp long fragment from a conserved region in the E
101 gene (pan-Sarbecovirus target) and LightMix Modular Wuhan CoV RdRP-gene kit (Tib-Molbol)
102 amplifying a 100 bp long fragment from a conserved region of the RNA-dependent RNA
103 polymerase (RdRP) gene (a SARS-CoV-2 specific target) was used in combination with TaqMan
104 Fast Virus 1-Step MasterMix (Thermo Fisher Scientific, Grand Island, NY, USA). RT-PCR was
105 performed on the StepOnePlus Real-Time PCR System (Applied Biosystems, Thermo Fisher
106 Scientific) following recommended cycling conditions: reverse transcription at 50 °C for 5 min
107 and 95 °C for 20 sec, followed by 45 cycles of PCR at 95 °C for 3 sec and 60 °C for 30 sec

108 (Corman). Cycle threshold (Ct) values for the LightMix two-target RT-PCR (LightMix) were
109 always set to 0.1 normalized reporter dye intensity (ΔR_n). Ct values above 37.0 were
110 considered negative. The tested sample was considered SARS-CoV-2 positive if LightMix showed
111 positive results for either both the E (pan-Sarbecovirus target) and RdRP genes (SARS-CoV-2
112 specific target) or the RdRP gene only. In the case of positivity for the E gene only, the result
113 was reported as SARS-CoV-2 presumptive positive and a follow-up sample was requested. The
114 SARS-CoV-2 positive control panel needed for initial assay implementation was obtained from
115 European Virus Archive Global (EVAg; www.european-virus-archive.com).

116 All samples included in the validation panel that tested negative using LightMix were
117 additionally tested for the presence of other common respiratory viruses using the
118 commercially available Respiratory Viruses 16-well assay (AusDiagnostics, Mascot, Australia), as
119 previously described (17, 18). The assay utilizes a multiplex-tandem PCR (MT-PCR) for
120 enrichment of targets followed by amplification of targeted DNA and/or RNA. The viruses
121 targeted are influenza virus A (H1, H3, H5, and H7), influenza virus B (Yamagata and Victoria
122 lineages), respiratory syncytial virus (types A and B), rhinovirus (types A, B, and C), enterovirus
123 (types A, B, C, and D), human bocavirus 1, human parainfluenza virus (types 1–4), human
124 parechovirus (types 1–8), human adenovirus (groups B, C, and E, and some from groups A and
125 D), human coronavirus (229E, HKU-1, NL63, and OC43), and human metapneumovirus (types A
126 and B). The assay uses a human reference gene for sample adequacy and amplification control.
127 All samples positive for coronaviruses using the AusDiagnostics assay were further typed using
128 four specific in-house coronavirus type-specific one-step RT-PCRs. Briefly, 5 μ l of total nucleic
129 acid was added to 15 μ l of reaction mixture using TaqMan Fast Virus 1-Step Master Mix

130 (Thermo Fisher Scientific, Grand Island, NY) and four Custom TaqMan Gene Expression assays
131 (Thermo Fisher Scientific) specific for each of the four human coronaviruses (229E, HKU-1,
132 NL63, and OC43). Cycling conditions were as follows: 5 minutes at 50 °C, 20 seconds at 95 °C,
133 and 40 cycles of 3 seconds at 95 °C and 30 seconds at 60 °C. Cycling conditions were universal
134 for all four specific RT-PCRs.

135 The final composition of the in-house validation panel consisting of 217 clinical samples was
136 64 SARS-CoV-2 positives, 17 coronavirus (hCoV) positives (nine NL63 positives, five 229E
137 positives, two HKU-1 positives, and one OC43 positive), 14 human rhinovirus (hRV) positives,
138 nine respiratory syncytial virus (RSV) positives, eight human metapneumovirus (hMPV)
139 positives, eight influenza virus B positives, six influenza virus A (Flu A) positives and one human
140 parechovirus positive. Four samples each contained multiple respiratory viruses: RSV and hCoV;
141 RSV and hRV; hRV and hCoV-229E; and Flu A and hMPV. Eighty-six samples were negative for all
142 respiratory viruses tested. All samples included in the validation panel were undiluted original
143 600 µl aliquots of UTM-RT. Aliquots were kept frozen after initial testing at -30 °C and thawed 1
144 hour before cobas testing. The median sample storage time at -30 °C was 3 days (range 1-17
145 days). Cobas testing of the in-house validation panel was performed in three runs on the
146 afternoon of March 24, 2020.

147 **Head-to-head prospective comparison.** Prospective cobas evaluation on 502 routinely
148 collected clinical samples against the same comparator (LightMix) was performed in six runs on
149 March 25, 2020 and March 26, 2020. The nasopharyngeal (N=489) or combined
150 nasopharyngeal/oropharyngeal swab (N=13) samples used in prospective head-to-head
151 evaluation were collected in UTM-RT from 502 individuals referred for COVID-19 testing on

152 March 25, 2020 and March 26, 2020. The median transport time of samples from the collection
153 site to the laboratory was 1 hour and 32 minutes. Upon arrival in the laboratory, swabs were
154 vortexed for 1 minute at maximum speed and two UTM-RT aliquots were prepared: 600 μ l for
155 cobas testing and 200 μ l for LightMix testing.

156 **Cobas 6800 SARS-CoV-2 testing.** Cobas is intended for fully automated sample-to-result
157 qualitative detection of SARS-CoV-2 in nasopharyngeal and oropharyngeal swab samples
158 collected in UTM-RT or Becton Dickinson Universal Viral Transport System (UVT) from patients
159 with signs and symptoms suggestive of COVID-19. The test could be performed on either the
160 cobas 6800 or cobas 8800 instrument (Roche Molecular Diagnostics, Pleasanton, CA, USA). The
161 cobas 6800 instrument consists of the sample supply module, the transfer module, the
162 processing module, and the analytic module. For detection of SARS-CoV-2, a two-target RT-PCR
163 is used: one targeting ORF1, a non-structural region that is unique to SARS-CoV-2 (target 1), and
164 the second targeting a conserved region in the structural protein envelope E gene for pan-
165 Sarbecovirus detection (target 2). The pan-Sarbecovirus primers and probe should also detect
166 the SARS-CoV-2 virus. The test utilizes RNA internal control for sample preparation and PCR
167 amplification process control. Uracil-N-glycosylase is included in the PCR mix to destroy
168 potential contaminating amplicons from previous PCR runs. Automated data management is
169 performed by the manufacturer's software, which assigns test results for all tests. The results
170 can be reviewed directly on the system screen, printed as a report, or transferred to a
171 laboratory information system. According to the manufacturer's instructions, a tested sample
172 was considered SARS-CoV-2 positive if cobas showed positive results either for both ORF1

173 (target 1) and E (target 2) genes or for the ORF1 gene only. In the case of positivity for the E
174 gene only (target 2), the result should be reported as SARS-CoV-2 presumptive positive.

175 In our study, 600 μ l of UTM-RT aliquots equilibrated to room temperature were transferred
176 into barcoded secondary tubes, loaded on the cobas 6800 System, and tested following the
177 manufacturer's instructions. Testing was performed in batches of 94 samples plus one negative
178 and positive control each.

179 **Data analysis.** Contingency tables were constructed to assess overall agreement with 95%
180 confidence intervals (CIs), and the McNemar test was applied to assess differences between
181 matched proportions. The level of agreement between tests was assessed using Kappa
182 statistics, and simple linear regression analysis was used for Ct comparative analysis. All
183 statistical analyses were performed using Excel (Microsoft, Redmond, WA, USA) and R software
184 version 3.2.5 (Free Software Foundation, Boston, MA, USA).

185

186 RESULTS

187 **In-house validation panel.** The results of comparative evaluation of the cobas and LightMix
188 on the in-house validation panel consisting of 217 well-characterized samples are summarized
189 in Table 1. Two samples were excluded from analysis due to invalid cobas results. The
190 diagnostic approaches showed overall percent agreement of 98.1% (211/215; 95% CI: 95.0-
191 99.4%), positive percent agreement of 95.2% (60/63; 95% CI: 85.8-98.8%), negative percent
192 agreement of 99.3% (151/152; 95% CI: 95.8-100.0%) and a high kappa value of 0.95 on 215
193 samples with valid results for both assays. Four discordant results were obtained. Three
194 samples were positive with LightMix and negative by cobas. All three samples with LightMix-

195 positive/cobas-negative results had very low SARS-CoV-2 viral loads with LightMix Ct values for
196 E and RdRP genes of 33.1 and 35.7 (Sample 1), 36.5 and 36.9 (Sample 2), and 36.9 and 36.0
197 (Sample 3), respectively. Before cobas testing, these three samples with LightMix-
198 positive/cobas-negative results were frozen at -30°C for 12, 5, and 1 day, respectively. Sample
199 3 was a follow-up/control nasopharyngeal swab of a patient that tested SARS-CoV-2 positive 14
200 days earlier. As shown in Table 1, one sample (Sample 4) tested cobas-positive/LightMix-
201 negative with cobas Ct values for ORF1 (target 1) and E (target 2) genes of 33.3 and 35.9.

202 **Head-to-head prospective comparison.** The results of head-to-head comparative evaluation
203 of the cobas and LightMix on 502 samples prospectively collected from the same number of
204 individuals are summarized in Table 2. One sample was excluded from analysis due to an invalid
205 cobas result. The diagnostic approaches showed overall percent agreement of 99.6% (499/501;
206 95% CI: 98.4-99.9%), positive percent agreement of 100.0% (63/63; 95% CI: 92.8-100.0%),
207 negative percent agreement of 99.5% (436/438; 95% CI: 98.2-99.9%) and a high kappa value of
208 0.98 on 501 samples with valid results of both assays. Two discordant results were obtained.
209 One sample (Sample 5) with a cobas-positive/LightMix-negative result had a very low SARS-
210 CoV-2 viral load with cobas Ct values for ORF1 (target 1) and E (target 2) genes of 33.8 and 36.5.
211 According to the cobas manufacturer's instructions, Sample 5 is considered SARS-CoV-2
212 positive. Sample 5 was a follow-up/control nasopharyngeal swab of a patient that tested SARS-
213 CoV-2 positive using LightMix 15 days earlier. One sample (Sample 6) with a cobas presumptive
214 positive/LightMix-negative result had a very low SARS-CoV-2 viral load with cobas Ct values for
215 the E gene (target 2) of 38.1, whereas amplification for the ORF1 gene (target 1) showed a
216 negative result. According to the cobas manufacturer's instructions, Sample 6 was considered

217 SARS-CoV-2 presumptive positive. Sample 6 was also a follow-up/control nasopharyngeal swab
218 obtained from a patient that tested SARS-CoV-2 positive using LightMix 19 days earlier.

219 As shown in Figure 1, a remarkably good correlation ($r^2 = 0.96$) between Ct values for SARS-
220 CoV-2 specific targets obtained by LightMix (RdRP gene) and cobas (ORF1; target 1) was
221 observed on 63 samples positive for SARS-CoV-2 by both diagnostic approaches in a prospective
222 head-to-head evaluation part of our study.

223 **Additional data supporting the informed decision for a diagnostic approach switch.** After
224 extensive evaluation, our laboratory implemented LightMix-based SARS-CoV-2 testing on
225 January 17, 2020. Routine SARS-CoV-2 testing started on January 27, 2020, and the first positive
226 sample was detected on March 4, 2020 after testing 353 routine samples. As of April 08, 2020, a
227 total of 30,669 SARS-CoV-2 tests have been performed in Slovenia (1,533 tests per million
228 inhabitants), 1,103 laboratory confirmed cases of COVID-19 have been detected, and 40 deaths
229 reported. During a 1-month period before implementation of cobas in routine SARS-CoV-2
230 testing on March 26, 2020 the workforce needed for SARS-CoV-2 testing using the LightMix
231 approach at our institution gradually increased from a single technician to a total of 14 highly
232 skilled technicians working in two six-member laboratory teams covering 7 am to 11 pm shifts
233 plus two technicians for an 8-hour night shift. At the time of the diagnostic approach switch,
234 using the LightMix approach the COVID-19 diagnostic team was able to process 600 to 700
235 samples per day with an average bench time of 9.6 minutes per sample. The approximate
236 bench time per sample for cobas testing of 600 to 700 samples per day is around one-tenth of
237 the time needed previously. From March 27, 2020 until April 07, 2020 a total of 2,296 samples
238 has been routinely tested using cobas in 28 runs with a total of 3 samples showing invalid result

239 (1 in 765). All invalid cobas results noticed in our laboratory were caused by either
240 clots/mucus/physical contamination detected by the instrument during sample aspiration or
241 insufficient sample volume identified in sample tubes/processing plates.

242

243 **DISCUSSION**

244 In addition to the unprecedented health and economic impact of the COVID-19 pandemic,
245 we are witnessing extraordinary demand on the global scale for personal protective equipment
246 and medical devices such as ventilators as well as sampling devices, reagents, consumables, and
247 diagnostic instruments needed for timely diagnosis of SARS-CoV-2 infection. To meet diagnostic
248 needs and as the pandemic grows, the US FDA recently dramatically expanded enforcement
249 discretion to speed up COVID-19 test access, resulting in granting EUA to 30 different SARS-
250 CoV-2 commercial assays and 5 laboratory developed tests as of April 08, 2020
251 ([https://www.fda.gov/medical-devices/emergency-situations-medical-devices/emergency-use-
253 independent evaluation data for any commercial SARS-CoV-2 assay with the US FDA EUA is
254 available in peer-reviewed literature. EUA-granted assays range from those with rapid
255 turnaround time allowing point-of-care testing to those performed on high-throughput
256 diagnostic platforms allowing for large numbers of patients to be tested in a reasonable
257 timeframe.](https://www.fda.gov/medical-devices/emergency-situations-medical-devices/emergency-use-
252 authorizations#covid19ivd)

258 Cobas 6800 is a fully automated instrument allowing sample-to-result qualitative and
259 quantitative detection of several microorganisms. A range of cobas 6800 assays have been
260 approved by the US FDA in recent years (<https://www.fda.gov/medical-devices/vitro->

261 diagnostics/nucleic-acid-based-tests). Due to the high demand for SARS-CoV-2 testing, problems in
262 further scaling up testing using the LightMix approach, the limited and delayed supply of
263 reagents needed for the LightMix approach, and the availability of cobas 6800 in our laboratory,
264 we decided to evaluate the cobas 6800 SARS-CoV-2 test as soon as it become commercially
265 available. Due to production problems with the cobas 6800/8800 Buffer Negative Control Kit
266 the first reagents arrived in the laboratory with 7-days delay on March 24, 2020. In the
267 meantime, a well-characterized in-house validation panel was prepared and immediately tested
268 with cobas in three runs on the afternoon of March 24, 2020. Cobas showed excellent overall
269 agreement with the comparator LightMix on the in-house validation panel with four discordant
270 results (Table 1). All three samples with LightMix-positive/cobas-negative results had very low
271 SARS-CoV-2 viral loads and were most probably cobas-negative due to degradation of SARS-
272 CoV-2 RNA during storage/freezing/thawing. Due to the encouraging results obtained on the in-
273 house validation panel, we started immediate prospective head-to-head evaluation of cobas on
274 502 routinely collected clinical samples against the same comparator. As in the first part of the
275 study, both diagnostic approaches showed excellent overall agreement and a high kappa value
276 also on prospectively collected samples, with only two discordant results (Table 2). Both cobas-
277 positive/LightMix-negative samples had a very low SARS-CoV-2 viral load, suggesting slightly
278 higher analytical sensitivity of cobas over the LightMix approach. Based on favorable results
279 obtained in both the retrospective and prospective parts of our study, we decided to start
280 routine SARS-CoV-2 testing with cobas on March 26, 2020. The entire cobas evaluation
281 procedure followed by a successful diagnostic platform switch lasted only 48 hours.

282 Apart from the commercially available cobas 6800 SARS-CoV-2 test that was evaluated in this
283 study, the cobas 6800 instrument can also be used for SARS-CoV-2 detection following a
284 recently published laboratory-developed protocol and the open channel (utility channel) of the
285 cobas 6800 instrument (19). In the study, authors demonstrated good analytical performance
286 of an adapted SARS-CoV-2 assay on swab samples with the limit of detection comparable to the
287 LightMix approach used in our evaluation (19). A similar laboratory-developed open-access
288 protocol was also recently published for another US FDA-approved high-throughput
289 instrument: Panther Fusion (Hologic, Marlborough, MA) (20).

290 In conclusion, the results of the first manufacturer-independent evaluation of cobas
291 performed on a well-characterized in-house validation panel consisting of 217 samples followed
292 by immediate prospective head-to-head comparison on 502 routine samples against the
293 current diagnostic standard showed that cobas is a reliable assay for qualitative detection of
294 SARS-CoV-2 in nasopharyngeal and combined nasopharyngeal/oropharyngeal swab samples
295 collected in the UTM-RT system. Our study showed that, under the extraordinary circumstances
296 that laboratories are currently facing worldwide, a safe diagnostic platform switch is feasible in
297 only 48 hours and in the midst of the COVID-19 pandemic, if carefully planned and executed.

298

299 **Conflicts of interest**

300 All the authors declare no competing interest. The manufacturer of the cobas 6800 SARS-CoV-2
301 had no role in the study design, data collection and analysis, interpretation of the results,
302 writing of the manuscript, and decision to submit the work for publication.

303

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311 Ljubljana, Slovenia.

312 REFERENCES

- 313 1. Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, Zhang L, Fan G, Xu J, Gu X, Cheng Z, Yu T, Xia J, Wei
314 Y, Wu W, Xie X, Yin W, Li H, Liu M, Xiao Y, Gao H, Guo L, Xie J, Wang G, Jiang R, Gao Z, Jin Q,
315 Wang J, Cao B. 2020. Clinical features of patients infected with 2019 novel coronavirus in
316 Wuhan, China. *Lancet* 395:497–506. [https://10.1016/S0140-6736\(20\)30183-5](https://10.1016/S0140-6736(20)30183-5).
- 317 2. Zhu N, Zhang D, Wang W, Li X, Yang B, Song J, Zhao X, Huang B, Shi W, Lu R, Niu P, Zhan F, Ma
318 X, Wang D, Xu W, Wu G, Gao GF, Tan W; China Novel Coronavirus Investigating and Research
319 Team. 2020. A novel coronavirus from patients with pneumonia in China, 2019. *N Engl J Med*
320 382:727–33. <https://10.1056/NEJMoa2001017>.
- 321 3. Lu R, Zhao X, Li J, Niu P, Yang B, Wu H, Wang W, Song H, Huang B, Zhu N, Bi Y, Ma X, Zhan F,
322 Wang L, Hu T, Zhou H, Hu Z, Zhou W, Zhao L, Chen J, Meng Y, Wang J, Lin Y, Yuan J, Xie Z, Ma J,
323 Liu WJ, Wang D, Xu W, Holmes EC, Gao GF, Wu G, Chen W, Shi W, Tan W. 2020. Genomic
324 characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and
325 receptor binding. *Lancet* 395:565–74. [https://10.1016/S0140-6736\(20\)30251-8](https://10.1016/S0140-6736(20)30251-8).
- 326 4. Berger A, Drosten C, Doerr HW, Stürmer M, Preiser W. 2004. Severe acute respiratory
327 syndrome (SARS)—paradigm of an emerging viral infection. *J Clin Virol* 29:13–22.
328 <https://10.1016/j.jcv.2003.09.011>.
- 329 5. Memish ZA, Perlman S, Van Kerkhove MD, Zumla A. 2020. Middle East respiratory syndrome.
330 *Lancet* 395:1063–77. [https://doi.org/10.1016/S0140-6736\(19\)33221-0](https://doi.org/10.1016/S0140-6736(19)33221-0)
- 331 6. Loeffelholz MJ, Tang YW. 2020. Laboratory diagnosis of emerging human coronavirus
332 infections—The state of the art. *Emerg Microbes Infect* 20:1–26.
333 <https://10.1080/22221751.2020.1745095>.

- 334 7. Chan JF, Yip CC, To KK, Tang TH, Wong SC, Leung KH, Fung AY, Ng AC, Zou Z, Tsoi HW, Choi
335 GK, Tam AR, Cheng VC, Chan KH, Tsang OT, Yuen KY. 2020. Improved molecular diagnosis of
336 COVID-19 by the novel, highly sensitive and specific COVID-19-RdRp/HeI real-time reverse
337 transcription-polymerase chain reaction assay validated in vitro and with clinical specimens. *J*
338 *Clin Microbiol* 00310–20. <https://10.1128/JCM.00310-20>.
- 339 8. Pang J, Wang MX, Ang IYH, Tan SHX, Lewis RF, Chen JI, Gutierrez RA, Gwee SXW, Chua PEY,
340 Yang Q, Ng XY, Yap RK, Tan HY, Teo YY, Tan CC, Cook AR, Yap JC, Hsu LY. 2020. Potential rapid
341 diagnostics, vaccine and therapeutics for 2019 novel coronavirus (2019-nCoV): A systematic
342 review. *J Clin Med* 9:623. doi: <https://doi.org/10.3390/jcm9030623>.
- 343 9. Zhou P, Yang XL, Wang XG, Hu B, Zhang L, Zhang W, Si HR, Zhu Y, Li B, Huang CL, Chen HD,
344 Chen J, Luo Y, Guo H, Jiang RD, Liu MQ, Chen Y, Shen XR, Wang X, Zheng XS, Zhao K, Chen QJ,
345 Deng F, Liu LL, Yan B, Zhan FX, Wang YY, Xiao GF, Shi ZL. 2020. A pneumonia outbreak
346 associated with a new coronavirus of probable bat origin. *Nature* 579:270–3.
347 <https://10.1038/s41586-020-2012-7>.
- 348 10. Wu F, Zhao S, Yu B, Chen YM, Wang W, Song ZG, Hu Y, Tao ZW, Tian JH, Pei YY, Yuan ML,
349 Zhang YL, Dai FH, Liu Y, Wang QM, Zheng JJ, Xu L, Holmes EC, Zhang YZ. 2020. A new
350 coronavirus associated with human respiratory disease in China. *Nature* 579:265–9.
351 <https://10.1038/s41586-020-2008-3>.
- 352 11. Corman VM, Landt O, Kaiser M, Molenkamp R, Meijer A, Chu DK, Bleicker T, Brünink S,
353 Schneider J, Schmidt ML, Mulders DG, Haagmans BL, van der Veer B, van den Brink S, Wijsman
354 L, Goderski G, Romette JL, Ellis J, Zambon M, Peiris M, Goossens H, Reusken C, Koopmans MP,

- 355 Drosten C. 2020. Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR. Euro
356 Surveill 25(3):2000045. <https://10.2807/1560-7917.ES.2020.25.3.2000045>.
- 357 12. Holshue ML, DeBolt C, Lindquist S, Lofy KH, Wiesman J, Bruce H, Spitters C, Ericson K,
358 Wilkerson S, Tural A, Diaz G, Cohn A, Fox L, Patel A, Gerber SI, Kim L, Tong S, Lu X, Lindstrom S,
359 Pallansch MA, Weldon WC, Biggs HM, Uyeki TM, Pillai SK; Washington State 2019-nCoV Case
360 Investigation Team. 2020. First case of 2019 novel coronavirus in the United States. N Engl J
361 Med 382:929–36. <https://10.1056/NEJMoa2001191>.
- 362 13. World Health Organization. Laboratory testing for 2019 novel coronavirus (2019-nCoV) in
363 suspected human cases: interim guidance, 19 March 2020. [https://www.who.int/publications-](https://www.who.int/publications-detail/laboratory-testing-for-2019-novel-coronavirus-in-suspected-human-cases-20200117)
364 [detail/laboratory-testing-for-2019-novel-coronavirus-in-suspected-human-cases-20200117](https://www.who.int/publications-detail/laboratory-testing-for-2019-novel-coronavirus-in-suspected-human-cases-20200117).
- 365 14. World Health Organization. Laboratory testing strategy recommendations for COVID-19:
366 interim guidance, 22 March 2020. <https://apps.who.int/iris/handle/10665/331509>.
- 367 15. Haveri A, Smura T, Kuivanen S, Österlund P, Hepojoki J, Ikonen N, Pitkäpaasi M, Blomqvist S,
368 Rönkkö E, Kantele A, Strandin T, Kallio-Kokko H, Mannonen L, Lappalainen M, Broas M, Jiang M,
369 Siira L, Salminen M, Puumalainen T, Sane J, Melin M, Vapalahti O, Savolainen-Kopra C. 2020.
370 Serological and molecular findings during SARS-CoV-2 infection: the first case study in Finland,
371 January to February 2020. Euro Surveill 25(11):2000266. [https://10.2807/1560-](https://10.2807/1560-7917.ES.2020.25.11.2000266)
372 [7917.ES.2020.25.11.2000266](https://10.2807/1560-7917.ES.2020.25.11.2000266).
- 373 16. Hue KD, Tuan TV, Thi HT, Bich CT, Anh HH, Wills BA, Simmons CP. 2011. Validation of an
374 internally controlled one-step real-time multiplex RT-PCR assay for the detection and
375 quantitation of dengue virus RNA in plasma. J Virol Methods 177:168–73.
376 <https://doi:10.1016/j.jviromet.2011.08.002>.

- 377 17. Anderson TP, Werno AM, Barratt K, Mahagamasekera P, Murdoch DR, Jennings LC. 2013.
378 Comparison of four multiplex PCR assays for the detection of viral pathogens in respiratory
379 specimens. *J Virol Methods* 191:118–21. <https://10.1016/j.jviromet.2013.04.005>.
- 380 18. Szewczuk E, Thapa K, Anninos T, McPhee K, Higgins G, Dwyer DE, Stanley KK, Iredell JR. 2010.
381 Rapid semi-automated quantitative multiplex tandem PCR (MT-PCR) assays for the differential
382 diagnosis of influenza-like illness. *BMC Infect Dis* 10:113. <https://10.1186/1471-2334-10-113>.
- 383 19. Pfefferle S, Reucher S, Nörz D, Lütgehetmann M. 2020. Evaluation of a quantitative RT-PCR
384 assay for the detection of the emerging coronavirus SARS-CoV-2 using a high throughput
385 system. *Euro Surveill* 25(9):2000152. <https://10.2807/1560-7917.ES.2020.25.9.2000152>.
- 386 20. Cordes AK, Heim A. 2020. Rapid random access detection of the novel SARS-coronavirus-2
387 (SARS-CoV-2, previously 2019-nCoV) using an open access protocol for the Panther Fusion. *J*
388 *Clin Virol* 125:104305. <https://10.1016/j.jcv.2020.104305>.
- 389

390 **TABLE 1** Results of comparative evaluation of the cobas 6800 SARS-CoV-2 (cobas) and
 391 standardized SARS-CoV-2 detection protocol consisting of RNA extraction using the MagNA
 392 Pure Compact instrument followed by RT-PCR targeting the E and RdRp coronavirus genes
 393 (LightMix) on an in-house validation panel consisting of 217 samples. Two samples were
 394 excluded from analysis due to an invalid cobas result. Interpretation of discordant results is
 395 given in the manuscript body.

396

LightMix	Cobas 6800			Overall agreement (95% CI)	Kappa value (95% CI)	McNemar's test
	Positive	Negative	Total			
Positive	60	3	63	98.1% (95.0–99.4%)	0.95 (0.91–1.00)	$p = 0.617$
Negative	1	151	152			
Total	61	154	215			

397

398 **TABLE 2.** Results of prospective head-to-head comparative evaluation of the cobas 6800 SARS-
 399 CoV-2 (cobas) and standardized SARS-CoV-2 detection protocol consisting of RNA extraction
 400 using the MagNA Pure Compact instrument followed by RT-PCR targeting the E and RdRp
 401 coronavirus genes (LightMix) on 502 samples. One sample was excluded from analysis due to an
 402 invalid cobas result. Interpretation of discordant results is given in the manuscript body.

403

LightMix	Cobas 6800			Overall agreement (95% CI)	Kappa value (95% CI)	McNemar's test
	Positive	Negative	Total			
Positive	63	0	63	99.6%	0.98	$p = 0.480$
Negative	2	436	438	(98.4–99.9%)	(0.96–1.00)	
Total	65	436	501			

404

405 **FIG 1** Correlation between cycle threshold (Ct) values obtained by LightMix Modular Wuhan
406 CoV (RdRP gene – SARS-CoV-2 specific target) and cobas 6800 SARS-CoV-2 (target 1 – ORF1 –
407 SARS-CoV-2 specific target) in the prospective head-to-head evaluation performed on 502
408 samples. Ct values for the LightMix assay were always set to 0.1 normalized reporter dye
409 intensity (delta Rn). Linear regression of the Ct values was performed using samples positive for
410 SARS-CoV-2 by both diagnostic approaches ($n = 63$). The r^2 correlation value is indicated.

