

1 **Transmission potential of vaccinated and unvaccinated persons infected with the SARS-CoV-2 Delta**  
2 **variant in a federal prison, July—August 2021**

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33 **Disclaimer.** The findings and conclusions in this report are those of the author(s) and do not necessarily  
34 represent the official position of Centers for Disease Control and Prevention (CDC).

35

36 **Abstract**

37 *Background*

38 The extent to which vaccinated persons who become infected with SARS-CoV-2 contribute to  
39 transmission is unclear. During a SARS-CoV-2 Delta variant outbreak among incarcerated persons with  
40 high vaccination rates in a federal prison, we assessed markers of viral shedding in vaccinated and  
41 unvaccinated persons.

42 *Methods*

43 Consenting incarcerated persons with confirmed SARS-CoV-2 infection provided mid-turbinate  
44 nasal specimens daily for 10 consecutive days and reported symptom data via questionnaire. Real-time  
45 reverse transcription-polymerase chain reaction (RT-PCR), viral whole genome sequencing, and viral  
46 culture was performed on these nasal specimens. Duration of RT-PCR positivity and viral culture  
47 positivity was assessed using survival analysis.

48 *Results*

49 A total of 978 specimens were provided by 95 participants, of whom 78 (82%) were fully  
50 vaccinated and 17 (18%) were not fully vaccinated. No significant differences were detected in duration  
51 of RT-PCR positivity among fully vaccinated participants (median: 13 days) versus those not fully  
52 vaccinated (median: 13 days;  $p=0.50$ ), or in duration of culture positivity (medians: 5 days and 5 days;  
53  $p=0.29$ ). Among fully vaccinated participants, overall duration of culture positivity was shorter among  
54 Moderna vaccine recipients versus Pfizer ( $p=0.048$ ) or Janssen ( $p=0.003$ ) vaccine recipients.

55 *Conclusions*

56 As this field continues to develop, clinicians and public health practitioners should consider vaccinated  
57 persons who become infected with SARS-CoV-2 to be no less infectious than unvaccinated persons.  
58 These findings are critically important, especially in congregate settings where viral transmission can  
59 lead to large outbreaks.

## 60 **Introduction**

61 COVID-19 vaccines are highly effective in preventing severe illness and death from SARS-CoV-2  
62 (the virus that causes COVID-19). However, because COVID-19 vaccines are not 100% effective in  
63 preventing infection, some infections among vaccinated persons are expected to occur. As global  
64 vaccination coverage increases, the role of vaccinated persons in transmission will be a critical  
65 determinant of the pandemic's future trajectory.<sup>1</sup> The extent to which vaccinated persons who become  
66 infected contribute to transmission of SARS-CoV-2, including the B.1.617.2 (Delta) variant, is not yet well  
67 understood. Some preprint manuscripts have reported comparable indicators of transmission potential  
68 regardless of vaccination status,<sup>2</sup> while others have reported reduced viability of virus isolated from  
69 vaccinated persons.<sup>3</sup>

70 The Delta variant has been associated with a peak in COVID-19 cases in the United States  
71 beginning in July 2021 that included large outbreaks among vaccinated and unvaccinated persons in  
72 crowded settings.<sup>4-6</sup> These findings are of particular concern for congregate living environments such as  
73 correctional and detention facilities and long-term care facilities because of the potential for rapid  
74 transmission of SARS-CoV-2 and the high prevalence of underlying health conditions associated with  
75 severe COVID-19.<sup>7-9</sup>

76 In a recent outbreak involving the Delta variant in a federal prison in Texas, the cumulative  
77 incidence of infection in two affected housing units was 74%; it was 93% and 70% among unvaccinated  
78 and vaccinated incarcerated persons, respectively.<sup>6</sup> Using serial mid-turbinate nasal specimens collected  
79 from a subset of incarcerated persons infected during this outbreak, this report assesses reverse  
80 transcription-polymerase chain reaction (RT-PCR) and viral culture characteristics as surrogate markers  
81 of transmission potential among persons fully vaccinated and those not fully vaccinated over time. This  
82 report is one of the first longitudinal investigations of viral shedding from vaccinated persons infected

83 with the Delta variant and contributes to the evidence base guiding infection prevention and control  
84 procedures across a variety of settings.

85

## 86 **Methods**

### 87 *Investigational Setting*

88 On July 12, 2021, an outbreak of SARS-CoV-2 among vaccinated and unvaccinated persons was  
89 detected in a federal prison in Texas. Staff from the Centers for Disease Control and Prevention (CDC)  
90 and Federal Bureau of Prisons (BOP) deployed to the prison to investigate the outbreak as previously  
91 reported.<sup>6</sup> As part of this outbreak investigation, a subset of incarcerated persons provided serial mid  
92 turbinate nasal specimens which were analyzed to evaluate the potential role of infected vaccinated and  
93 unvaccinated persons in transmission of SARS-CoV-2. This activity was reviewed and approved by the  
94 BOP Research Review Board and CDC and conducted consistent with applicable federal law and CDC  
95 policy.\*

96

### 97 *Participant Enrollment and Serial Specimen Collection*

98 Incarcerated persons living in four housing units where COVID-19 cases had been identified  
99 were invited to participate in serial swabbing. Persons were eligible to enroll if they had tested positive  
100 for SARS-CoV-2 between July 12 (the start of the outbreak) and August 4, 2021. CDC and BOP staff held  
101 information sessions to explain the purpose of the project and to answer questions, including privacy  
102 protections and how results of the study would be made available to participants. All persons choosing  
103 to participate signed informed consent forms, which were provided in English and Spanish.

104 Specimen collection occurred during July 18—August 9, 2021. CDC and BOP staff collected one  
105 nasal mid-turbinate specimen daily for 10 consecutive days from participants who had tested positive,

106 beginning on July 19 or, for cases identified after July 19, beginning on the date of participants' first  
107 positive test. All incarcerated persons residing in housing units where cases were identified were placed  
108 under quarantine precautions. To assist in case-finding, consenting persons who were quarantined were  
109 tested every other day beginning on July 19 or on their first full day of quarantine; those who tested  
110 positive during quarantine were invited to participate in the 10 consecutive days of specimen collection.  
111 All participants were asked to provide a specimen on August 6 to provide data additional data on viral  
112 shedding, which corresponds to a late timepoint in infection for most participants (Figure 1).

113 On the tenth day of specimen collection, participants were asked to complete a paper-based  
114 questionnaire to report COVID-19-like symptoms during the course of their illness, including date of  
115 symptom onset and symptom duration. Information on demographic characteristics, COVID-19  
116 vaccination history, previous positive SARS-CoV-2 diagnostic tests, and underlying medical conditions  
117 was extracted from BOP electronic medical records for all participants.

118

### 119 *Laboratory Methods*

120 Specimens were collected using nylon flocked minitip swabs, transferred into  
121 universal viral transport media (VTM) (Becton Dickinson, Franklin Lakes, NJ) immediately stored at 2-8°C  
122 and frozen at -20°C or colder within 72 hours, and sent to CDC for RT-PCR testing using the CDC  
123 Influenza SARS-CoV-2 Multiplex Assay. Remnant aliquots were stored at -70°C or below for viral culture.  
124 Due to capacity limitations, viral culture was performed on a subset of collected specimens. Specimens  
125 were included for viral culture if they had been collected 0, 3, 5, 7, or 9 days since onset and had an  
126 accompanying positive RT-PCR test with cycle threshold (Ct) value less than 35. For verification that this  
127 selected Ct cutoff did not exclude specimens containing culturable virus, viral culture was also  
128 performed on 25 of 102 specimens with Ct>35. (25/25 of these specimens were culture negative.) For  
129 more granular detail across the time-course of infection, viral culture was also performed on a subset of

130 specimens collected on other days (see Supplemental Figures 1-2 for details on specimens included for  
131 viral culture).

132 Specimens selected for culture were used to perform limiting-diluting inoculation of Vero CCL-  
133 81 cells expressing TMPRSS2, and cultures showing evidence of cytopathic effect were tested by RT-PCR  
134 for the presence of SARS-CoV-2 RNA. Viral recovery was as previously described.<sup>10</sup> Whole genome  
135 sequencing (WGS) was performed for one RT-PCR-positive specimen per participant with Ct less than 30  
136 (per sequencing laboratory standard protocols).

137

### 138 *Statistical Methods*

139 Onset (used as time 0 in longitudinal analyses below) was defined to be either a) date of first  
140 onset of self-reported symptom(s) meeting the case definition of COVID-19,<sup>11</sup> or b) date of first positive  
141 diagnostic SARS-CoV-2 test, whichever occurred first. In two instances where a participant without  
142 symptoms had an initial positive test followed by at least 3 negative tests before subsequent positive  
143 tests, the date of second positive test was used.

144 Participants were considered fully vaccinated if  $\geq 14$  days had elapsed since they had completed  
145 all recommended doses of a COVID-19 primary vaccine series before the start of the outbreak. (No  
146 participant had completed a primary vaccine series  $< 14$  days before the outbreak.) Participants were  
147 considered not fully vaccinated if they had not received any doses of a vaccine or if they had not  
148 completed all doses of a vaccine series. Demographic characteristics of participants stratified by  
149 vaccination status were assessed using Fisher's exact tests.

150 Three surrogate markers for assessing transmission potential were analyzed as primary  
151 outcomes: RT-PCR positivity (an indicator of current/recent infection), RT-PCR Ct value (a semi-  
152 quantitative indicator of relative level of viral nucleic acid), and viral culture positivity (an indicator of  
153 viable/infectious virus). Dichotomous laboratory results (RT-PCR positivity and viral culture positivity)

154 were analyzed longitudinally with time 0 defined as the date of onset and the primary endpoints defined  
155 by a participant's last positive test. Specimens for which viral culture was not performed were presumed  
156 to be culture negative if an accompanying RT-PCR test was negative or was positive with Ct>35. To  
157 account for variation in the interval between onset and enrollment, and intermittent participation in  
158 specimen collection by some participants (which can result in interval and right censoring), survival  
159 analyses were performed using Turnbull estimation using the "interval" package implementation in R.<sup>12</sup>  
160 Hypothesis testing of survival functions was performed using the generalized Wilcoxon-Mann-Whitney  
161 method for interval-censored data.

162 As a post-hoc evaluation of potential interactions between vaccination status and known prior  
163 SARS-CoV-2 infections, a stratified analysis was conducted using Fisher's exact test to compare RT-PCR  
164 and viral culture results across these two variables among specimens collected on days with complete  
165 viral culture coverage (0, 3, 5, 7, and 9 days since onset).

166 Non-dichotomous laboratory results (RT-PCR Ct values) were characterized by days since onset  
167 using medians and interquartile ranges (IQRs). Because Ct values are semi-parametric, distributions  
168 were compared non-parametrically using the Mann-Whitney U test with ties (for dichotomous variables)  
169 or the Kruskal-Wallis test (for categorical variables with more than 2 levels); negative RT-PCR results  
170 were assigned higher ranks than any Ct value from positive RT-PCR results. To account for multiple  
171 hypothesis testing across days,  $\alpha$  thresholds were adjusted using Bonferroni correction. All hypothesis  
172 tests performed are detailed in Supplementary Tables 1 and 2. All statistical analyses were performed in  
173 R version 4.0.2 (R Core Team, Vienna, Austria).

174

## 175 **Results**

### 176 *Population Characteristics*

177           Among 189 persons with SARS-CoV-2 infection eligible to enroll, a total of 96 persons consented  
178 to participate in serial specimen collection; one participant had a single positive diagnostic test (Ct=36.2)  
179 followed by seven negative diagnostic tests and reported no symptoms and was excluded as a non-case.  
180 Of the 95 included participants, 78 (82%) were documented as being fully vaccinated against SARS-CoV-  
181 2, 15 (16%) were unvaccinated and 2 (2%) were partially vaccinated and categorized as not fully  
182 vaccinated in further analyses (Table 1). Among fully vaccinated participants, a majority (57/78, 73%)  
183 received the Pfizer vaccine; smaller proportions received the Moderna vaccine (14/78, 18%) or Janssen  
184 vaccine (7/78, 9%). A majority (47/78, 60%) of fully vaccinated participants completed their vaccination  
185 series more than 120 days prior to the start of the outbreak (IQR: 81-140 days prior to start). Recipients  
186 of Pfizer vaccines completed their series earlier (IQR: 131-131 days) than recipients of Moderna (IQR:  
187 81-82 days prior to start) or Janssen (IQR: 46-70 days prior to start) vaccines ( $p<0.001$ ). A small number  
188 of participants (2/78 fully vaccinated, 3%, and 2/17 not fully vaccinated, 12%,  $p=0.10$ ) had a documented  
189 prior SARS-CoV-2 infection. Based on symptom self-report at the end of sampling, 76% of participants  
190 reported at least one symptom in the COVID-19 case definition [CSTE 2021]. The most commonly  
191 reported symptoms were runny or stuffy nose (58%), loss of smell or taste (54%), and cough (45%). Of  
192 95 specimens from 95 participants for which sequencing was attempted, 64 were successfully  
193 sequenced and passed quality metrics; all 64 (100%) belonged to the B.1.617.2 (Delta) lineage and AY.3  
194 sublineage.

195

#### 196 *RT-PCR Positivity*

197           From the 95 included participants, 978 specimens were collected for RT-PCR testing (825/978,  
198 84% from fully vaccinated participants). Specimens were collected ranging from 13 days prior to onset  
199 (among participants tested during quarantine prior to diagnosis) to 32 days following onset. See Figure 1  
200 for a diagrammatic representation of RT-PCR specimen collection from participants, and see



201 Supplemental Figure 1 for details of specimen collection by day since onset (stratified by vaccination  
202 status). A median of 6 days elapsed between onset and enrollment among fully vaccinated participants,  
203 compared with a median of 7 days among participants who were not fully vaccinated ( $p=0.33$ ). Overall,  
204 499 of the 978 (51%) specimens tested positive by RT-PCR.

205 No significant differences in time to last RT-PCR positive test were found. Median duration of  
206 RT-PCR positivity was 13 days among fully vaccinated participants versus 13 days among participants  
207 who were not fully vaccinated ( $p=0.50$ ; Figure 2); and 10 days among participants with known history of  
208 prior SARS-CoV-2 infection (regardless of vaccination) versus 13 days among participants without any  
209 known prior infection ( $p=0.12$ ). Among fully vaccinated participants, median duration of positivity was  
210 10 days among Moderna vaccine recipients versus 13 days among Pfizer recipients and 13 days among  
211 Janssen recipients ( $p=0.39$ ); and 13 days among participants fully vaccinated more than 120 days prior  
212 to the outbreak versus 11 days among participants vaccinated 120 days or less prior to the outbreak  
213 ( $p=0.32$ ).

214

#### 215 *Ct Values*

216 Ct values from specimens testing positive by RT-PCR increased with the number of days since  
217 onset (Figure 3). Among specimens from fully vaccinated participants, Ct values increased from a  
218 median of 26.4 (IQR: 23.5-28.4) on the day of onset to a median of 32.9 on day 10 (IQR: 30.5-34.6), while  
219 Ct values from specimens from participants who were not fully vaccinated increased from a median of  
220 28.5 (IQR:24.8-31.8) on the day of onset to a median of 34.5 on day 10 (IQR: 29.4-35.2). Across the time-  
221 course of infection, no statistically significant difference was observed among Ct values by vaccination  
222 status on any day after Bonferroni correction (all  $p>0.0026$ , the Bonferroni-corrected  $\alpha$  threshold).  
223 Additionally, no significant differences were observed among Ct values when stratified by vaccine  
224 product, time since vaccination, or known prior SARS-CoV-2 infection. While not statistically significant,

225 lower Ct values were observed early in the time-course of infection among Janssen vaccine recipients  
226 (day 3 median: 17.9; IQR: 17.6-19.4) than among Moderna (day 3 median: 27.4; IQR: 23.7-28.1) or Pfizer  
227 recipients (day 3 median: 24.8; IQR: 23.1-26.8;  $p=0.016$  while Bonferroni  $\alpha=0.0026$ ).

228

#### 229 *Viral Culture Positivity*

230 Of the 978 specimens collected, viral culture was performed on 286 (29%); an additional 556  
231 (57%) were included as presumptive negative viral culture results due to an accompanying negative RT-  
232 PCR test ( $n=479$ ) or a positive RT-PCR test with a Ct value greater than 35 ( $n=77$ ). Viral culture capture  
233 by day since onset stratified by vaccination status is detailed in Supplementary Figure 2. Among the 842  
234 specimens with a viral culture result, 75 (9%) had a positive viral culture. Virus was recovered from  
235 57/690 (8%) of specimens from fully vaccinated participants, compared with 18/152 (12%) of specimens  
236 from participants who were not fully vaccinated ( $p=0.16$ ).

237 No statistically significant difference was detected in the duration of viral culture positivity  
238 (Figure 4) between participants who were fully vaccinated (median: 5 days) compared with those who  
239 were not fully vaccinated (median: 5 days;  $p=0.29$ ). (Viral culture results are illustrated as a function of  
240 days since onset and grouped by RT-PCR result in Supplementary Figure 4). Cumulative hazard functions  
241 indicate overall shorter culture positivity for fully vaccinated participants who received the Moderna  
242 vaccine than those who received Pfizer ( $p=0.048$ ) or Janssen vaccines ( $p=0.003$ ), but there was no  
243 significant difference between recipients of Pfizer and Janssen vaccines ( $p=0.12$ ). No statistically  
244 significant differences in duration of culture positivity were detected when stratified according to time  
245 since vaccination ( $p=0.79$ ) or known prior infection ( $p=0.99$ ).

246

#### 247 *Factorial Stratification: Vaccination Status and History of Prior Infection*

248 Figure 5 illustrates a post-hoc stratification of RT-PCR and viral culture results by vaccination  
249 status and prior SARS-CoV-2 infection. No statistically significant difference in RT-PCR or viral culture  
250 positivity was detected on any day; however, bivariate stratification resulted in small population sizes in  
251 some groups (n=2 participants each for those fully vaccinated with a known prior infection and those  
252 not fully vaccinated with a known prior infection), which limits the ability to draw conclusions about  
253 these groups.

254

## 255 Discussion

256 During a high-transmission outbreak of the SARS-CoV-2 Delta variant in a prison setting, we  
257 failed to find different durations of RT-PCR positivity, Ct values, or durations of viral culture positivity in  
258 fully vaccinated persons compared with persons who were not fully vaccinated. However, vaccinated  
259 persons who received the Moderna vaccine had a shorter duration of culture positivity compared with  
260 Pfizer or Janssen vaccine recipients. (However, Moderna vaccine recipients also were more recently  
261 vaccinated than Pfizer vaccine recipients.) Collectively, our findings suggest that, as evidence continues  
262 to emerge in this developing field, vaccinated persons who become infected should be regarded as not  
263 significantly less infectious than unvaccinated persons for the purposes of public health action.

264 As viral infections in vaccinated persons can result from either a failure to mount a protective  
265 immune response following initial vaccination or a gradual waning of immunological protection  
266 following initially robust protection, the infectiousness of vaccinated persons may be variable. It is  
267 plausible that some participants in this investigation who became infected despite vaccination had weak  
268 or waning vaccine-induced protection and were therefore similar to unvaccinated persons in the  
269 markers of transmission potential that we evaluated.

270           This report adds to a limited body of scientific literature evaluating the transmission potential of  
271 SARS-CoV-2 infections in vaccinated persons. Reports of infections in vaccinated persons have found  
272 mixed results using markers of transmission potential, and no longitudinal studies of viral culture  
273 characteristics in vaccinated persons with Delta infections have been published. A multi-site serial  
274 testing investigation involving Alpha (B.1.1.7) and Gamma (P.1) infections found that duration of culture  
275 positivity was shorter among vaccinated persons compared with unvaccinated persons.<sup>13, 14</sup> One report  
276 using surveillance data found lower Ct values among unvaccinated persons, but this difference was only  
277 observed for two of three RT-PCR probes and only during one of three months.<sup>15</sup> One cross-sectional  
278 report found no difference in Ct value by vaccination status.<sup>2</sup> However, extrapolating from cross-  
279 sectional and surveillance data may be challenging without data to account for timing of specimen  
280 collection in the course of infection. Nevertheless, this finding is corroborated by analysis of a clinical  
281 convenience sample which found vaccination did not impact Ct values and reduced viral recovery of  
282 Alpha variant but did not reduce recovery of Delta variant virus;<sup>16</sup> similar findings were mirrored by two  
283 retrospective health-system cohorts.<sup>17, 18</sup> A report of health system workers found that viral culture  
284 positivity was reduced in vaccinated persons despite similar Ct values as those in unvaccinated persons.<sup>3</sup>  
285 A separate report found that early in the clinical course of infection, Ct values were comparable  
286 between vaccinated and unvaccinated persons, but among individuals who presented to care later in  
287 their course of illness, Ct values were higher in vaccinated persons.<sup>19</sup> A study of household transmission  
288 of Delta infections found similar peak viral loads regardless of vaccination status, but noted faster  
289 declines in vaccinated persons.<sup>20</sup> Cumulatively, available data have not clearly or consistently identified  
290 markers of reduced transmission potential in vaccinated persons with SARS-CoV-2 infection. This report,  
291 which to our awareness represents the first longitudinal investigation of viral culture characteristics of  
292 vaccinated persons with Delta variant infections, further demonstrates the potential of vaccinated  
293 persons to contribute to SARS-CoV-2 transmission.

294           While our investigation did not find evidence of reduced transmission potential from vaccinated  
295 persons with infection, vaccination is known to reduce the risk of infection,<sup>6, 21</sup> which prevents  
296 secondary transmission. In addition, vaccination remains a strongly protective factor against morbidity  
297 and mortality due to SARS-CoV-2.<sup>22</sup> Protection against infection, morbidity, and mortality underscores  
298 the importance of maximizing vaccination coverage, particularly in settings where challenges to physical  
299 distancing can result in rapid, widespread transmission when infections do occur.

300           The evidence that vaccinated persons can transmit SARS-CoV-2 to others suggests that there is  
301 continued risk of widespread outbreaks when the virus is introduced into congregate settings, even  
302 when vaccination coverage is high. In particular, because of the potential for rapid transmission and high  
303 prevalence of underlying health conditions in incarcerated populations,<sup>7, 8</sup> persons living or working in  
304 correctional facilities should quarantine after exposure to SARS-CoV-2, regardless of vaccination status.  
305 Post-exposure quarantine is especially important where the risk of transmission is high (e.g., in dorm-  
306 style housing, and where staff and/or incarcerated persons frequently interact across housing units) or  
307 where the population is at high risk of severe outcomes from COVID-19. Facilities can continue to  
308 minimize the need for quarantine by enforcing consistent indoor masking to the extent possible,  
309 continuing recommended disinfection, cleaning, and ventilation, and maintaining routine test-based  
310 screening programs that can identify cases early and facilitate timely action (including isolation) to limit  
311 exposure to others. Facilities that implement routine test-based screening should continue to include  
312 vaccinated persons in their frame.

313           This report is subject to several limitations. Due to the small proportion of participants who  
314 were not fully vaccinated (19%), statistical comparisons on the basis of vaccination status were  
315 underpowered, and negative findings reported here warrant cautious interpretation. To increase the  
316 sample size of this group, two partially vaccinated participants were included, potentially diluting the  
317 characteristics of unvaccinated participants. However, our conclusions did not change when analyses

318 were performed excluding these two participants. Similarly, only four participants had known prior  
319 infection, of which a higher proportion occurred in those not fully vaccinated; therefore, these  
320 participants may appear to have slightly greater immunological protection than those without prior  
321 infection. On average, unvaccinated participants enrolled earlier in the outbreak and later in their  
322 course of infection than vaccinated participants; we utilized Turnbull estimation in survival analyses to  
323 account for the possibility of interval censoring in this population. All symptom data was self-reported  
324 and collected at the end of the specimen collection period, which may have impacted the accuracy of  
325 participants' recall related to the date of symptom onset. Ct values are semi-quantitative indicators of  
326 viral RNA levels and cannot be interpreted as quantitative markers of viral load or infectiousness. To  
327 avoid drawing quantitative conclusions around Ct values, we conservatively utilized non-parametric  
328 rank-based statistics (Mann-Whitney and Kruskal-Wallis) with Bonferroni correction to describe Ct  
329 values in this investigation. Information on prior SARS-CoV-2 infection was obtained from medical  
330 records; persons with earlier infections that were undiagnosed or diagnosed prior to incarceration and  
331 not documented in the BOP medical system may not have been correctly characterized. Finally, we did  
332 not attempt viral culture for 561 specimens with Ct>35 and classified them as presumptively negative.  
333 This decision was based on negative viral culture results from 25/25 specimens with Ct>35 for which  
334 viral culture was performed during this investigation, as well as previously published findings  
335 demonstrating an inability to recover viable virus from specimens that were RT-PCR negative.<sup>23</sup>

336 In this investigation, we found no statistically significant difference in transmission potential  
337 between vaccinated persons and persons who were not fully vaccinated. Therefore, our findings  
338 indicate that prevention and mitigation measures should be applied without regard to vaccination status  
339 for persons in high-risk settings or those with significant exposures. In congregate settings, and  
340 correctional and detention facilities in particular, post-exposure testing and quarantine remain essential  
341 tools to limit transmission when cases are identified, in addition to other recommended prevention

342 measures.<sup>24</sup> Our data add to a growing body of evidence characterizing transmission potential from  
343 vaccinated persons. Future studies of transmission potential from vaccinated persons with infection,  
344 incorporating similar laboratory-based markers as well as evidence of transmission from secondary  
345 attack rates and network analysis, may help to further describe the contributions of vaccinated persons  
346 in chains of transmission as the pandemic evolves and new variants emerge.

347 **Conflict of Interest Statement**

348 The authors have no conflicts of interest to report. All authors have completed the ICMJE Conflict of  
349 Interest declaration.

350

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354

355 **Footnotes**

356 \* 45 C.F.R. part 46, 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et  
357 seq.

358



359 **Table 1. Characteristics of enrolled participants who tested positive for SARS-CoV-2, Federal prison,**  
 360 **Texas, July 12—August 9, 2021**

	All participants		Fully vaccinated		Not fully vaccinated*		p-value†
	n	%	n	%	n	%	
<b>Total</b>	95	100%	78	81%	17	19%	
<b>Sex</b>							
Male	95	100%	78	100%	17	100%	
<b>Age</b>							0.4
18-29	5	5%	3	4%	2	12%	
30-39	22	23%	19	24%	3	18%	
40-49	28	29%	22	28%	6	35%	
50-59	25	26%	20	26%	5	29%	
≥ 60	15	16%	14	18%	1	6%	
<b>Race/Ethnicity</b>							<b>0.008</b>
American Indian/Alaska Native	2	2%	2	3%	0	0%	
Asian	1	1%	1	1%	0	0%	
Black	16	17%	8	10%	8	47%	
Hispanic	12	13%	10	13%	2	12%	
White	64	67%	57	73%	7	41%	
<b>Country of birth</b>							0.6
Non US-born	4	4%	3	4%	1	6%	
US-born	91	96%	75	96%	16	94%	
<b>Vaccination status</b>							
Fully vaccinated	78	82%	78	100%	0	0%	
Not fully vaccinated*	17	18%	0	0%	17	100%	
<i>Partially vaccinated</i>	2	2%	0	0%	2	12%	
<i>Unvaccinated</i>	15	16%	0	0%	15	88%	
<b>Vaccine product received</b>							
Janssen	7	7%	7	9%	0	0%	
Moderna	14	15%	14	17%	0	0%	
Pfizer	57	60%	57	74%	0	0%	
<b>Time from full vaccination to outbreak (if fully vaccinated)</b>							
≤120 days	31	33%	31	33%	0	0%	
>120 days	47	49%	47	61%	0	0%	
<b>Medical comorbidities</b>							
Overweight‡	31	33%	24	31%	7	41%	0.3
Obesity‡	47	49%	42	54%	5	29%	
Severe obesity ‡	7	7%	6	8%	1	6%	
History of smoking	46	48%	42	54%	4	24%	<b>0.03</b>
Hypertension	43	45%	38	49%	5	29%	0.1

Diabetes	15	16%	14	18%	1	6%	0.3
Moderate/severe asthma	10	11%	8	10%	2	12%	1.0
Chronic obstructive pulmonary disease	6	6%	6	8%	0	0%	0.6
Cancer	1	1%	1	1%	0	0%	1.0
Chronic kidney disease	2	2%	2	3%	0	0%	1.0
Immunocompromised state	2	2%	2	3%	0	0%	1.0
HIV	0	0%	0	0%	0	0%	
Serious cardiac conditions	0	0%	0	0%	0	0%	
Liver disease	0	0%	0	0%	0	0%	
<b>Documented prior SARS-CoV-2 infection</b>							0.1
No	91	96%	76	97%	15	88%	
Yes	4	4%	2	3%	2	12%	
<b>COVID-19 disease outcomes</b>							
Hospitalization	2	2%	1	1%	1	6%	
Death	0	0%	0	0%	0	0%	
<b>Reported Symptoms</b>							
Reported any symptoms in CSTE case definition§	66	70%	54	70%	12	71%	0.7
Reported any symptoms	72	76%	59	76%	13	76%	0.4
Runny/Stuffy Nose	55	58%	48	62%	7	41%	0.4
Loss of Smell or Taste	51	54%	43	55%	8	44%	1.0
Cough	43	45%	35	45%	8	47%	0.8
Headache	40	42%	33	42%	7	41%	1.0
Muscle Aches	40	42%	30	38%	10	59%	0.08
Subjective Fever	34	36%	27	35%	7	41%	0.6
Measured Fever	10	11%	6	8%	4	24%	0.06
Chills	29	31%	21	27%	8	47%	0.06
Sore Throat	24	25%	21	27%	3	18%	0.7
Shortness of Breath	20	21%	14	18%	6	35%	0.08
Abdominal Pain, Nausea, Vomiting	17	18%	12	15%	5	28%	0.2
Diarrhea	16	17%	11	14%	5	28%	0.1
Other	6	6%	6	8%	0	0%	1.0
None Reported ¶	23	24%	19	24%	4	24%	1.0

361 \*Not fully vaccinated participants include 15 who have not received any dose of a SARS-CoV-2 vaccine and 2 who  
 362 receive only the first dose of a two-dose SARS-CoV-2 vaccine series.

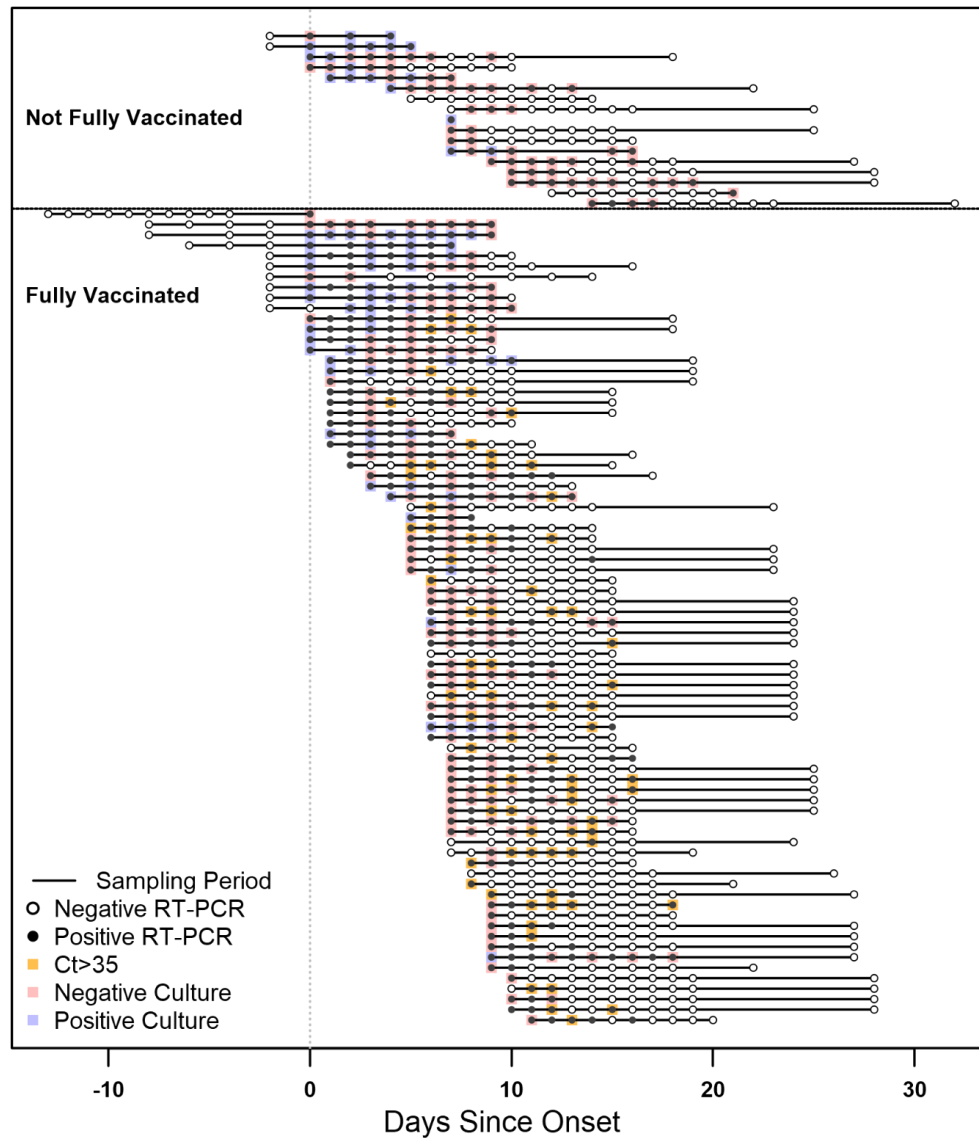
363 †P-values correspond to results of Fisher's exact tests.

364 ‡Overweight was defined as a body mass index (BMI) >25 kg/m<sup>2</sup> but <30 kg/m<sup>2</sup>; obesity was defined as BMI ≥30  
 365 kg/m<sup>2</sup> but <40 kg/m<sup>2</sup>; severe obesity was defined as BMI ≥40 kg/m<sup>2</sup>.

366 §The COVID-19 case definition of the Council of State and Territorial Epidemiologists (CSTE) includes fever, chills,  
 367 muscle aches, headache, sore throat, nausea/vomiting, diarrhea, fatigue, stuffy/runny nose, cough, shortness of  
 368 breath, or loss of taste or smell. [CSTE 2021]

369 ¶ 8 participants (5 fully vaccinated and 3 not fully vaccinated) declined to report symptoms in addition to 15 (14  
 370 and 1, respectively) who reported that they had no symptoms

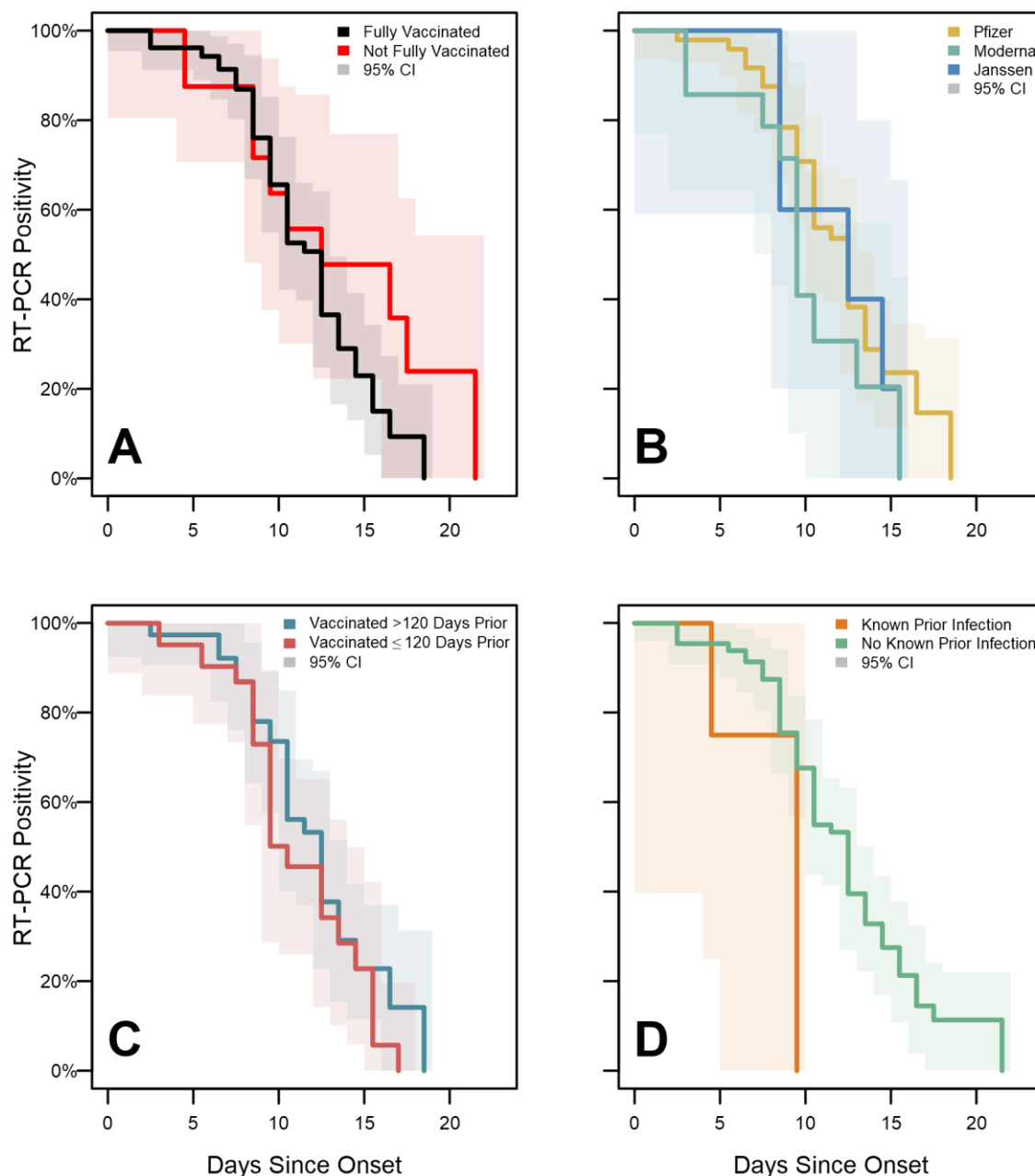
371 **Figure 1. Timelines and results of nasal mid-turbinate specimens collected from enrolled participants,**  
372 **Federal prison, Texas, July 12—August 9, 2021**



373

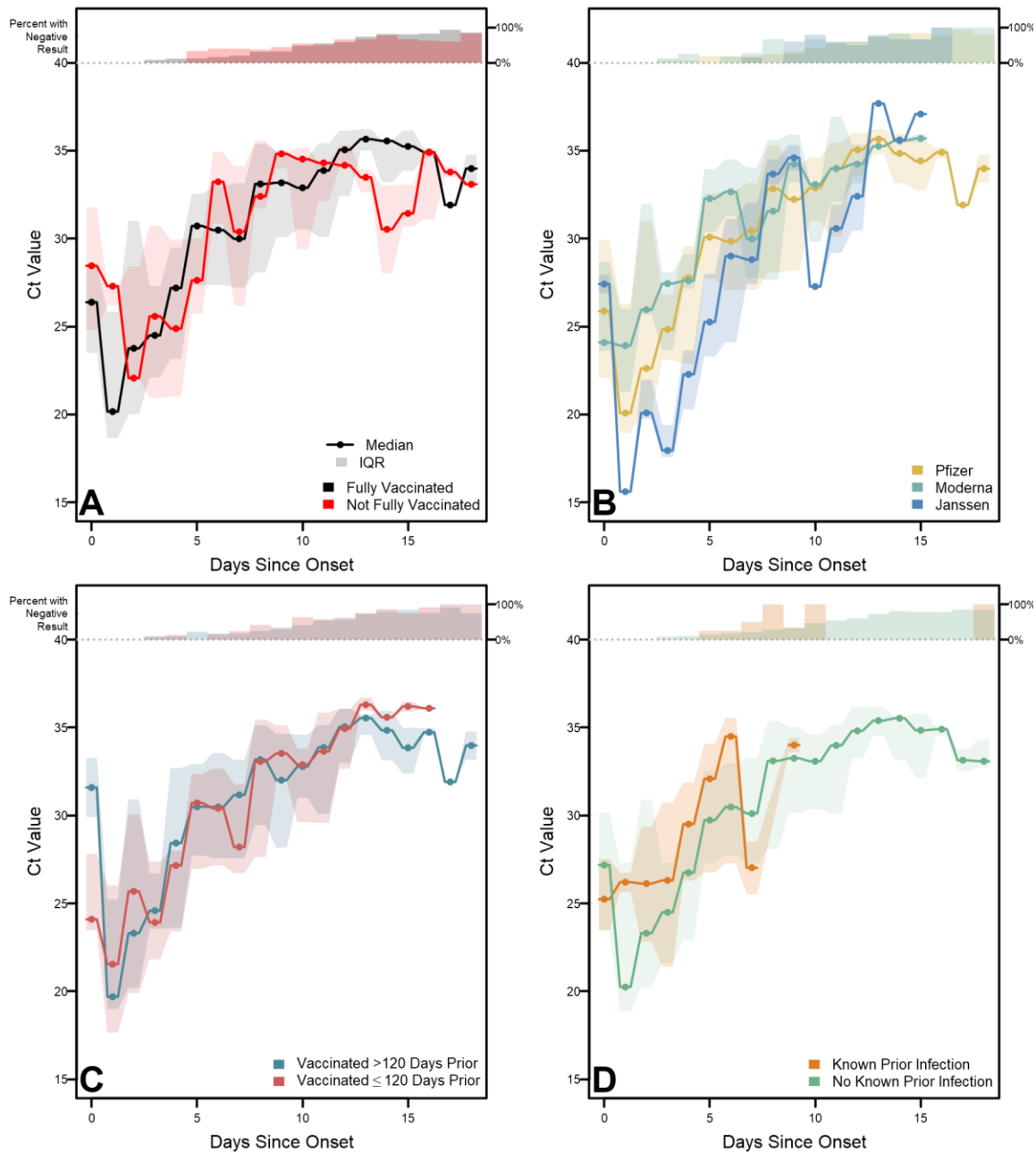
374 The timelines of specimen collection and laboratory results for 95 included participants are represented  
375 diagrammatically, indexed by the day of onset. Onset was determined to be either a) date of first onset of self-  
376 reported symptom(s) meeting the case definition of COVID-19 or b) date of first positive diagnostic SARS-CoV-2  
377 test, whichever occurred first. Each participant is represented by a horizontal line corresponding to the  
378 investigation sampling period during their time-course of illness. Participants who were not fully vaccinated  
379 (including 2 participants who received only the first dose of a two-dose COVID-19 vaccine series) are depicted at  
380 the top of the figure, while fully vaccinated participants are depicted at the bottom. RT-PCR results are  
381 represented by solid circles (positive results) or open circles (negative results). For specimens with positive RT-PCR  
382 results for which viral culture was performed, culture results are indicated by overlaid blue boxes (positive culture  
383 results) or red boxes (negative culture results). Specimens with positive RT-PCR results with a cycle threshold (Ct)  
384 value greater than 35 for which viral culture was not performed are indicated by overlaid orange boxes (indicated  
385 a presumptive negative viral culture result). Some participants provided specimens during case-finding testing  
386 while in quarantine and may have RT-PCR negative specimens collected prior to onset.

387 **Figure 2. SARS-CoV-2 RT-PCR test positivity survival curves for enrolled participants, Federal prison,**  
388 **Texas, July 12—August 9, 2021**



389  
390 Panels illustrate the results of Turnbull estimation survival functions with a primary endpoint of last positive  
391 reverse transcription-polymerase chain reaction (RT-PCR) test result. Solid lines indicate nonparametric maximum  
392 likelihood estimates and shaded regions correspond to 95% confidence intervals estimated through modified  
393 bootstrap. Survival functions are plotted by Turnbull interval midpoints. Onset was determined to be either a) date  
394 of first onset of self-reported symptom(s) meeting the case definition of COVID-19 or b) date of first positive  
395 diagnostic SARS-CoV-2 test, whichever occurred first. Panel A depicts RT-PCR positivity by vaccination status (not  
396 fully vaccinated participants include 2 participants who received only the first dose of a two-dose COVID-19  
397 vaccine series). Panel B depicts positivity by vaccine product among fully vaccinated participants. Panel C depicts  
398 positivity according to the time from completion of a COVID-19 vaccine/series to onset. Panel D depicts positivity  
399 according to history of known prior SARS-CoV-2 infection.

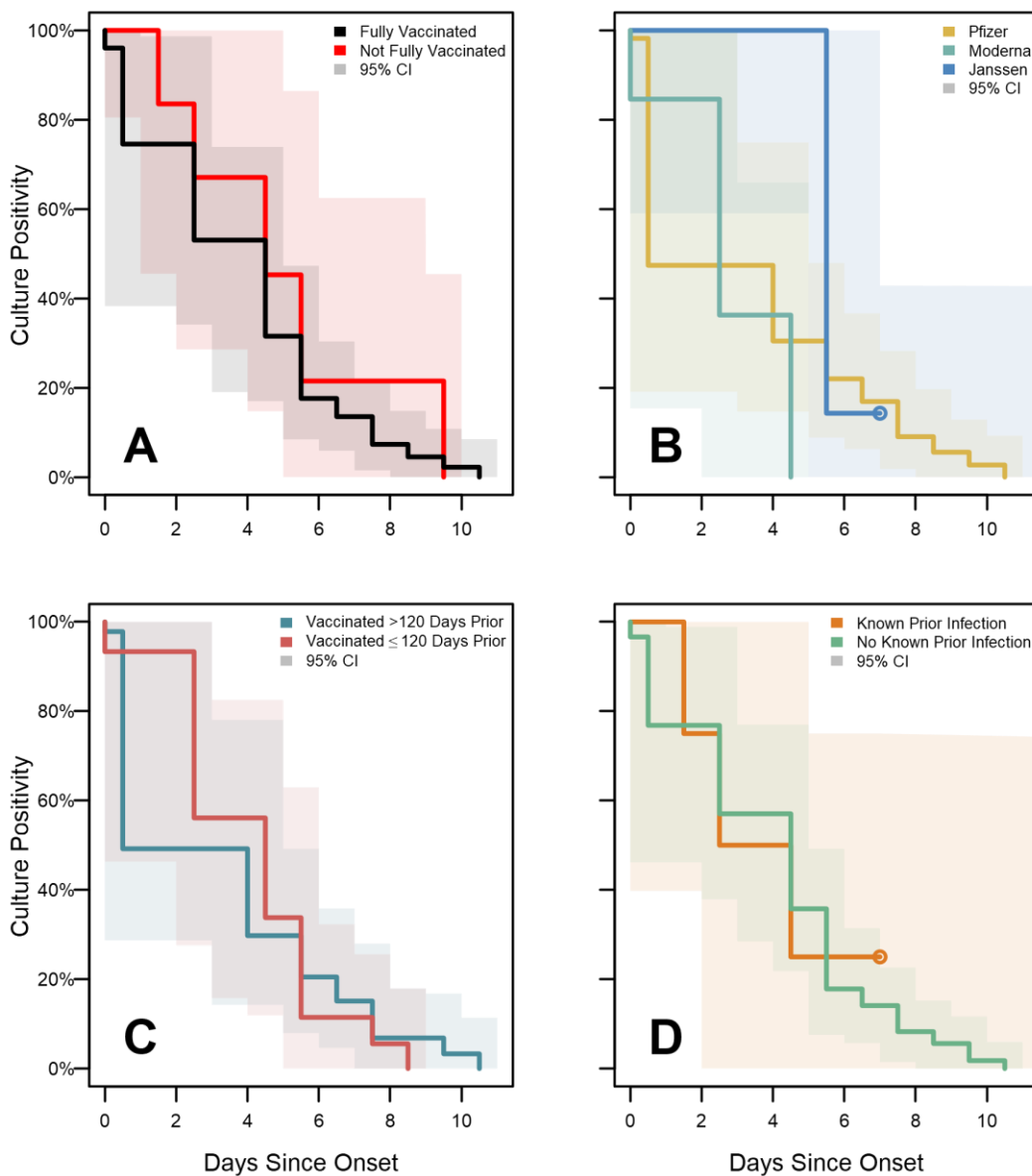
400 **Figure 3. RT-PCR Cycle Threshold distributions for enrolled participants with confirmed SARS-CoV-2**  
401 **infection, Federal prison, Texas, July 12—August 9, 2021**



402

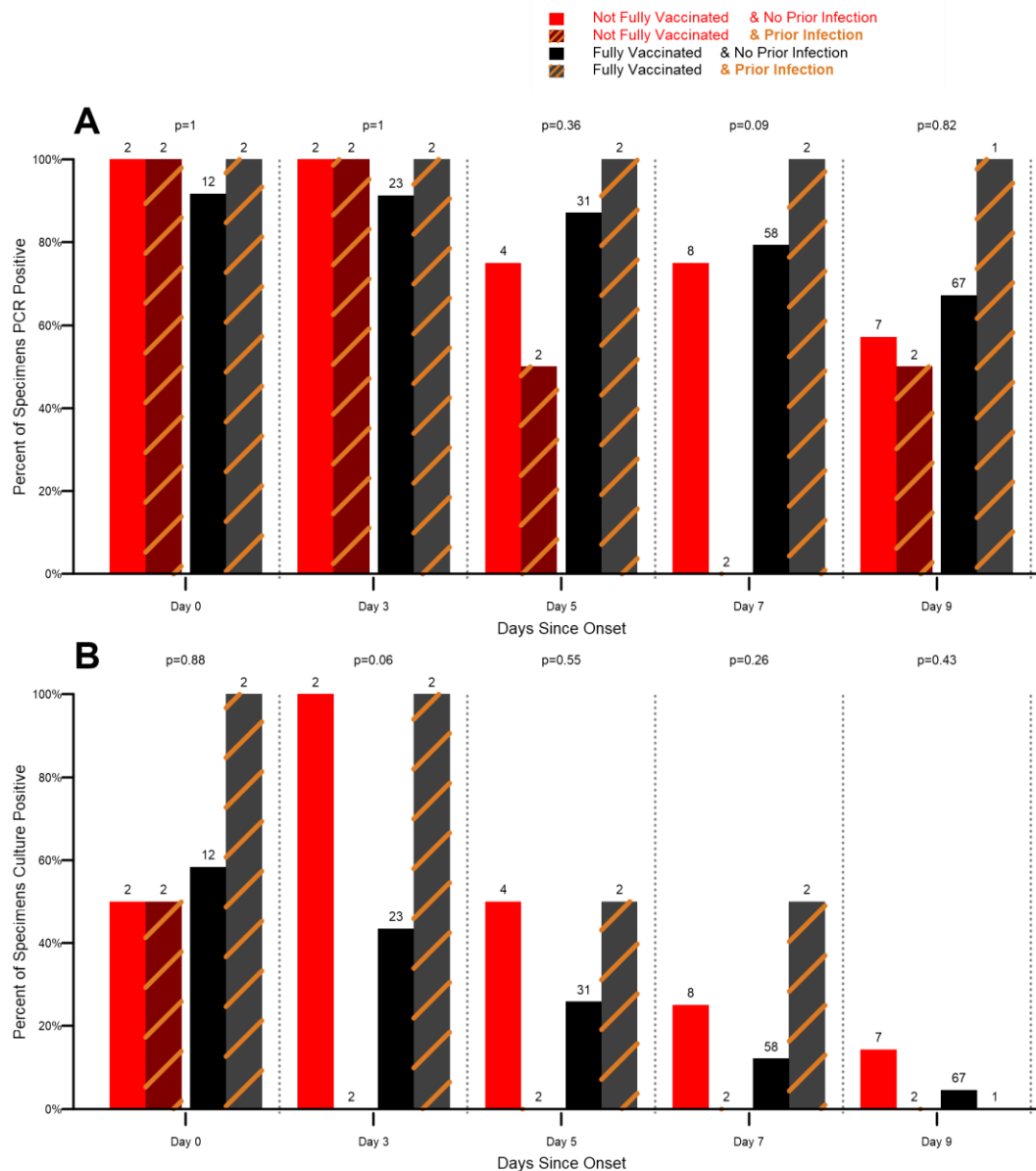
403 Panels illustrate daily medians and interquartile ranges (IQRs) for reverse transcription-polymerase chain reaction  
404 (RT-PCR) cycle threshold (Ct) values among specimens with positive RT-PCR results. Solid lines indicate median Ct  
405 values and shaded regions indicate IQRs. Percentages at the top of each panel indicate the proportion of  
406 specimens with negative RT-PCR results each day Onset was determined to be either a) date of first onset of self-  
407 reported symptom(s) meeting the case definition of COVID-19 or b) date of first positive diagnostic SARS-CoV-2  
408 test, whichever occurred first. Panel A depicts RT-PCR positivity by vaccination status (not fully vaccinated  
409 participants include 2 participants who received only the first dose of a two-dose COVID-19 vaccine series). Panel B  
410 depicts positivity by vaccine product among fully vaccinated participants. Panel C depicts positivity according to  
411 the time from completion of a COVID-19 vaccine/series to onset. Panel D depicts positivity according to history of  
412 known prior SARS-CoV-2 infection.

413 **Figure 4. SARS-CoV-2 viral culture test positivity survival curves for enrolled participants, Federal**  
414 **prison, Texas, July 12—August 9, 2021**



415  
416 Panels illustrate the results of Turnbull estimation survival functions with a primary endpoint of last positive viral  
417 culture test result. Specimens were included as presumptive negative results if no culture was performed but were  
418 accompanied by negative RT-PCR results or positive RT-PCR results with Ct>35. Solid lines indicate nonparametric  
419 maximum likelihood estimates and shaded regions correspond to 95% confidence intervals estimated through  
420 modified bootstrap. Survival functions are plotted by Turnbull interval midpoints. When Turnbull intervals are  
421 bounded by positive infinity (resulting from right-censoring in subgroups), survival functions are truncated by open  
422 points at the rightmost non-infinite intervals. Onset was determined to be either a) date of first onset of self-  
423 reported symptom(s) meeting the case definition of COVID-19 or b) date of first positive diagnostic SARS-CoV-2  
424 test, whichever occurred first. Panel A depicts RT-PCR positivity by vaccination status (not fully vaccinated  
425 participants include 2 participants who received only the first dose of a two-dose COVID-19 vaccine series). Panel B  
426 depicts positivity by vaccine product among fully vaccinated participants. Panel C depicts positivity according to  
427 the time from completion of a COVID-19 vaccine/series to onset. Panel D depicts positivity according to history of  
428 known prior SARS-CoV-2 infection.

429 **Figure 5. SARS-CoV-2 RT-PCR test positivity (A) and viral culture test positivity (B) stratified by**  
 430 **vaccination status and prior infection status for enrolled participants, Federal prison, Texas, July 12–**  
 431 **August 9, 2021**



432

433 Panels illustrate the proportions of specimens for which RT-PCR test results (panel A) or viral culture test results  
 434 (panel B) were positive, stratified by both vaccination status and history of prior SARS-CoV-2 infection. Solid bars  
 435 indicate results for participants with no known prior infections, and striped bars indicate results for participants  
 436 with documented prior infections. Specimens were included as presumptive negative results if no culture was  
 437 performed but were accompanied by negative RT-PCR results or positive RT-PCR results with Ct>35. Onset was  
 438 determined to be either a) date of first onset of self-reported symptom(s) meeting the case definition of COVID-19  
 439 or b) date of first positive diagnostic SARS-CoV-2 test, whichever occurred first. Results are depicted only for days  
 440 0, 3, 5, 7, and 9 since onset, representing days for which 100% of eligible specimens had viral culture performed.  
 441 Bar labels indicate the number of specimens collected from participants in each group for each day. P-values are  
 442 reported at the top of each daily grouping and correspond to Fisher's exact test of proportions across the four  
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