

1 Transmission of SARS-CoV-2
2 Omicron VOC subvariants BA.1 and BA.2:
3 Evidence from Danish Households

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NOTE: This preprint reports new research that has not been certified by peer review and should not be used to guide clinical practice.

6 1 Abstract

7 The Omicron SARS-CoV-2 variant of concern (VOC lineage B.1.1.529), which became
8 dominant in many countries during early 2022, includes several subvariants with strikingly
9 different genetic characteristics. Several countries, including Denmark, have observed the
10 two Omicron subvariants: BA.1 and BA.2. In Denmark the latter has rapidly replaced
11 the former as the dominant subvariant.

12 Based on nationwide Danish data, we estimate the transmission dynamics of BA.1 and
13 BA.2 following the spread of Omicron VOC within Danish households in late December
14 2021 and early January 2022.

15 Among 8,541 primary household cases, of which 2,122 were BA.2, we identified a total
16 of 5,702 secondary infections among 17,945 potential secondary cases during a 1-7 day
17 follow-up period. The secondary attack rate (SAR) was estimated as 29% and 39% in
18 households infected with Omicron BA.1 and BA.2, respectively.

19 We found BA.2 to be associated with an increased susceptibility of infection for unvacci-
20 nated individuals (Odds Ratio (OR) 2.19; 95%-CI 1.58-3.04), fully vaccinated individuals
21 (OR 2.45; 95%-CI 1.77-3.40) and booster-vaccinated individuals (OR 2.99; 95%-CI 2.11-
22 4.24), compared to BA.1. We also found an increased transmissibility from unvaccinated
23 primary cases in BA.2 households when compared to BA.1 households, with an OR of
24 2.62 (95%-CI 1.96-3.52). The pattern of increased transmissibility in BA.2 households
25 was not observed for fully vaccinated and booster-vaccinated primary cases, where the
26 OR of transmission was below 1 for BA.2 compared to BA.1.

27 We conclude that Omicron BA.2 is inherently substantially more transmissible than BA.1,
28 and that it also possesses immune-evasive properties that further reduce the protective
29 effect of vaccination against infection, but do not increase its transmissibility from vacci-
30 nated individuals with breakthrough infections.

31 2 Introduction

32 The current pandemic with SARS-CoV-2 is characterized by continuous emergence of
33 new variants taking over from previous variants as a result of natural selection (Darwin,
34 1859). Most recently, the Omicron variant of concern (VOC), Pango lineage B.1.1.529,
35 has become the most prevalent in most countries in Europe as well as the rest of the world
36 (Ritchie & Roser, 2020). Of the previously identified Omicron subvariants (Mullen et al.,
37 2022; SSI, 2022), three subvariants have been detected in Denmark, namely BA.1.1, BA.1
38 and BA.2, where the latter two by far have been the most abundant. BA.1 and BA.2
39 differ by approximately 40 mutations (Majumdar & Sarkar, 2021) in addition to a key
40 deletion at position 69-70 in the spike region of BA.1 compared to BA.2 (Public Health
41 England, 2022; Chowdhury et al., 2022).

42 By 1 January 2022, BA.2 accounted for 5% of all subvariants found in England, with an
43 ongoing increase in this proportion (Public Health England, 2022). BA.1 was first detected
44 in Denmark on 25 November 2021, and BA.2 was first detected on 5 December 2021. Since
45 then, the prevalence of BA.2 has been increasing faster than that of BA.1. In week 52 of
46 2021, BA.2 accounted for around 20% of all Danish SARS-CoV-2 cases; in week 2 in 2022
47 this had increased to around 45%, indicating that BA.2 carries an advantage over BA.1
48 within the highly vaccinated population of Denmark. The RT-PCR test used in Denmark
49 does not target the S-gene deletion to detect Omicron cases, but instead targets the spike
50 position L452 Wt (Spiess et al., 2021). Thus in the current set-up, Danish RT-PCR data
51 cannot distinguish between BA.1 and BA.2. However, whole genome sequencing (WGS) is
52 conducted routinely in Denmark (www.covid19genomics.dk), providing the opportunity
53 to identify and differentiate between BA.1 and BA.2.

54 We have previously used a model of household transmission to quantify the transmissibility
55 of VOCs, and applied this model to show that the Omicron VOC had an advantage over
56 the Delta VOC due to immune evasiveness (Lyngse et al., 2021b).

57 The increasing numbers of BA.2 cases justify the questions we address in this study;

58 1) Is there a difference in the household transmission patterns between Omicron VOC

59 subvariant BA.1 and BA.2; and 2) if there is a difference, is it due to a difference in
60 susceptibility, transmissibility, or both, and could this indicate a difference in immune
61 evasiveness between the subvariants?

62 **3 Methods**

63 **3.1 Study design and participants**

64 In this study, we used Danish register data comprising all individuals in Denmark. We
65 linked all individuals to households by their personal identification number. We only in-
66 cluded households with 2-6 members to exclude care facilities etc. We linked this with
67 information on all antigen and RT-PCR tests for SARS-CoV-2 from the Danish Microbi-
68 ology Database (MiBa; Schönning et al. (2021)), and records in the Danish Vaccination
69 Register (Krause et al., 2012). We used data on primary cases from 20 December 2021 to
70 11 January 2022, and allowed a 7-day follow-up period for potential secondary cases, i.e.
71 until 18 January 2022.

72 A primary case was defined as the first individual in a household testing positive with
73 an RT-PCR test within the study period and being identified with the Omicron VOC
74 BA.1 or BA.2 by WGS. We followed all tests of other household members in the follow-
75 up period. A positive secondary case was defined by either a positive RT-PCR test or
76 a positive antigen test (Jakobsen et al., 2021). Households were categorized as BA.1 or
77 BA.2 households depending on the WGS result of the sample from the primary case.

78 In the study period, a total of approximately 25,000 mid- and high-quality SARS-CoV-2
79 genomes were produced (appendix Table 4) at the time of analysis. Briefly, sequencing
80 of positive SARS-CoV-2 samples was performed using short read Illumina technology
81 (Illumina) with the Illumina COVIDSeq Test kit (Illumina). The library preparation
82 was performed as described by the manufacturer with spike-in of amplicon 64, 70 and 74
83 from the ARTIC v3 amplicon sequencing panel (<https://artic.network>). Samples were
84 sequenced on either the NextSeq or NovaSeq platforms (Illumina). Consensus sequences

85 were called using an in-house implementation of IVAR (version 1.3.1) with a custom
86 BCFtools (Li, 2011) command for consensus calling. The resulting consensus sequences
87 were considered for variant calling when containing <3,000 ambiguous sites including
88 N's. Variants were called using Pangolin (version 3.1.17) with PangoLEARN assignment
89 algorithm (version 2022-01-05) on the consensus sequences (O'Toole et al., 2021).

90 The vaccination status of all individuals was classified into three groups following Lyngse
91 et al. (2021b): i) unvaccinated (including partially vaccinated individuals); ii) fully vac-
92 cinated (defined by the vaccine used, Comirnaty (Pfizer/BioNTech): 7 days after second
93 dose; Vaxzevria (AstraZeneca): 15 days after second dose; Spikevax (Moderna): 14 days
94 after second dose; Janssen (Johnson & Johnson): 14 days after vaccination, and 14 days
95 after the second dose for cross vaccinated individuals) or 14 days after previous infection;
96 or iii) booster-vaccinated, defined by 7 days after the booster vaccination, (Pfizer, 2021;
97 Bomze et al., 2021). By 22 December 2021, of all vaccinated individuals in Denmark, 85%
98 were vaccinated with Comirnaty, 14% with Spikevax, 1% with Janssen, and approximately
99 0% with AstraZeneca (SSI, 2021).

100 **3.2 Statistical analyses**

101 The secondary attack rate (SAR) was defined as the proportion of potential secondary
102 cases within the same household that tested positive between 1-7 days following the pos-
103 itive test of the primary case in that household. We estimated the adjusted odds ratios
104 (OR) for infection in a multivariable logistic regression model. The outcome variable in
105 this model was the binary test result of each potential secondary case. We used the sub-
106 variant as an explanatory variable as well as fixed effects for other potentially confounding
107 variables; age and sex of the primary case, age and sex of the potential secondary case,
108 household size (2-6 members), and primary case sample date to control for time related
109 effects. To test if the subvariants behaved differently depending on the immune status of
110 the primary cases (i.e. different transmissibility) and the potential secondary cases (i.e.
111 different susceptibility), we included interactions between household subvariant and vac-
112 cination status of the primary cases and the potential secondary cases, respectively.

113 To investigate the robustness of the results, we conducted a number of additional sensitiv-
114 ity analyses, which can be found in the appendix. Here, we also describe the distribution of
115 BA.1 and BA.2 cases over the study period and the characteristics of samples selected for
116 WGS. We also provide statistics for a 14-day follow-up period. Additionally, we provide
117 measures of model fit and estimates under a number of alternative specifications of the
118 logistic regression model to assess the robustness of the findings, as well as a more detailed
119 investigation of the pairwise OR between vaccination groups for each subvariant.

120 **3.3 Ethical statement**

121 This study was conducted using data from national registers only. According to Dan-
122 ish law, ethics approval is not needed for this type of research. All data management
123 and analyses were carried out on the Danish Health Data Authority's restricted research
124 servers with project number FSEID-00004942. The study only contains aggregated results
125 and no personal data. The study is, therefore, not covered by the European General Data
126 Protection Regulation (GDPR).

127 **3.4 Data availability**

128 The data used in this study are available under restricted access due to Danish data
129 protection legislation. The data are available for research upon reasonable request to The
130 Danish Health Data Authority and Statens Serum Institut and within the framework
131 of the Danish data protection legislation and any required permission from Authorities.
132 We performed no data collection or sequencing specifically for this study. Consensus
133 genome data from the Danish cases are routinely shared publicly at GISAID (www.gisaid.org).
134 [org](http://www.gisaid.org)).

135 **4 Results**

136 We identified 2,122 households with BA.2 comprising a total of 4,587 potential secondary
137 cases, of which 1,792 tested positive within 7 days, resulting in a SAR of 39%. Similarly,

138 we identified 6,419 households with BA.1 comprising a total of 13,358 potential secondary
139 cases, of which 3,910 tested positive, resulting in a SAR of 29%. The distributions of age,
140 sex, household size and vaccination status in primary and potential secondary cases were
141 broadly comparable between BA.1 and BA.2 households (Table 1).

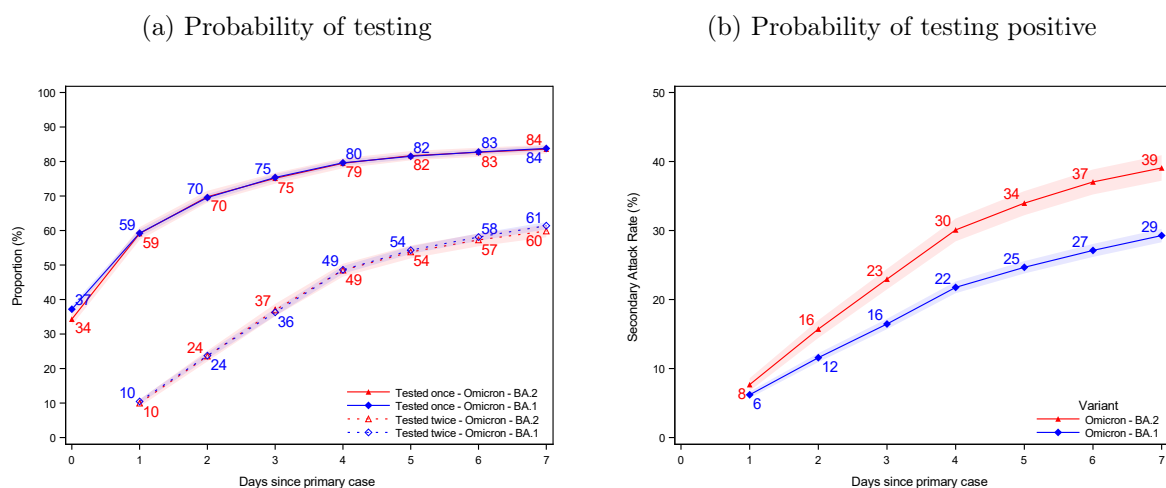
Table 1: Summary statistics

	Omicron - BA.2				Omicron - BA.1			
	Primary Cases	Potential Secondary Cases	Positive Secondary Cases	SAR (%)	Primary Cases	Potential Secondary Cases	Positive Secondary Cases	SAR (%)
Total, N	2,122	4,587	1,792	39	6,419	13,358	3,910	29
Sex, %								
Male	49	50	49	38	49	50	48	28
Female	51	50	51	40	51	50	52	31
Age, %								
0-10	8	17	19	42	5	17	19	33
10-20	25	18	16	34	23	19	17	26
20-30	23	14	13	38	27	15	16	31
30-40	15	12	18	56	15	11	15	42
40-50	11	18	17	38	12	18	17	27
50-60	11	14	12	32	11	14	10	22
60-70	4	4	3	35	5	4	4	25
70+	3	2	2	30	3	2	2	26
Household size, %								
2	37	17	19	44	40	19	22	33
3	24	23	21	37	25	24	22	27
4	26	36	38	41	23	34	35	31
5	10	18	16	34	9	18	17	28
6	2	6	5	35	2	5	4	23
Immunity, %								
Unvaccinated	21	26	29	43	16	26	30	34
Fully vaccinated / previous infection	52	42	44	41	59	44	47	31
Booster vaccinated	26	32	27	34	25	30	23	22

Notes: The secondary attack rate (SAR) is expressed as a percentage (%). Total numbers (N) is presented in the first row. Summary statistics based on primary cases are shown separately from summary statistics of potential secondary cases, positive secondary cases and SAR. The raw numbers (N) for each category is presented in appendix Table 5. The summary statistics stratified by the primary case level are presented in appendix Tables 6 and 7.

142 Within 7 days of the identification of the primary cases, 84% of the potential secondary
143 cases had been tested once, regardless of subvariant, and 60-61% had been tested twice
144 (Figure 1, panel a). In households infected with the Omicron BA.2 (red), the SAR was
145 8% on day 1 and 39% on day 7. Similarly, in households infected with BA.1 (blue), the
146 SAR was 6% and 29%, respectively.

Figure 1: Probability of being tested and testing positive



Notes: Panel (a) shows the probability of potential secondary cases being tested after a primary case has been identified within the household. Panel (b) shows the probability of potential secondary cases that test positive subsequently to a primary case being identified within the household. Note that the latter is not conditional on being tested, i.e. the denominator contains test-negative individuals and untested individuals. The x-axes show the days since the primary case tested positive, and the y-axes show the proportion of individuals either being tested (a) or testing positive (b) with either antigen or RT-PCR tests, stratified for the subvariant of the primary case. The SAR for each day according to the subvariant primary case can be read directly from panel (b). For example, the SAR on day 7 is 39% for BA.2 (red) and 29% for BA.1 (blue), whereas the SAR on day 4 is 30% and 22%, respectively. The shaded areas show the 95% confidence bands clustered on the household level. Appendix Figure 3 presents the two panels with a 14 day follow-up period. Appendix Figure 4 presents the 14 day SAR for Omicron BA.1, BA.2, and Delta VOC, as well as those without a known variant.

147 We observed a general gradient in both Omicron BA.1 and BA.2 households such that
 148 the susceptibility of potential secondary cases was highest among the unvaccinated and
 149 lowest among the booster vaccinated, but the effect of vaccination appeared to be lower
 150 for Omicron BA.2 than for BA.1 (see Table 2, and the interactions in Figure 6). We
 151 observed lower transmissibility in both BA.1 and BA.2 households when the primary case
 152 was booster vaccinated rather than fully vaccinated.

Table 2: Effect of Vaccination

	Susceptibility		Transmissibility	
	Omicron BA.2 households	Omicron BA.1 households	Omicron BA.2 households	Omicron BA.1 households
Unvaccinated	1.10 (0.92-1.32)	1.23 (1.09-1.40)	1.21 (0.97-1.50)	0.93 (0.80-1.08)
Fully vaccinated	ref (.)	ref (.)	ref (.)	ref (.)
Booster vaccinated	0.80 (0.67-0.94)	0.65 (0.58-0.73)	0.79 (0.64-0.98)	0.77 (0.70-0.88)
Number of observations	17,945	17,945	17,945	17,945
Number of households	8,541	8,541	8,541	8,541

Notes: This table shows odds ratio estimates for susceptibility and transmissibility by vaccination status. Column 1 shows the susceptibility based on the vaccination status of the potential secondary case, conditional on being in a household infected with BA.2. Column 2 shows the susceptibility based on the vaccination status of the potential secondary case, conditional on being in a household infected with BA.1. Column 3 shows the transmissibility based on the vaccination status of the primary case, conditional on being in a household infected with BA.2. Column 4 shows the transmissibility based on the vaccination status of the primary case, conditional on being in a household infected with BA.1. Note that all estimates are from the same model, but with a different reference category across column 1-4. The estimates are adjusted for age and sex of the primary case, age and sex of the potential secondary case, size of the household, and primary case sample date. The estimates are furthermore adjusted for vaccination status of the potential secondary case and primary case interacted with the household subvariant. 95% confidence intervals are shown in parentheses. Standard errors are clustered on the household level. The odds ratio estimates for the full model are presented in the appendix Table 12, column I.

153 Relative to Omicron BA.1 households, we found an increased susceptibility for both un-
154 vaccinated (OR 2.19; 95%-CI 1.58-3.04), fully vaccinated (OR 2.45; 95%-CI 1,77-3,40)
155 and booster-vaccinated individuals (OR 2.99; 95%-CI 2.11-4.24) in BA.2 households (Ta-
156 ble 3). We also observed increased transmissibility in BA.2 households from unvaccinated
157 primary cases when compared to BA.1 households with an OR of 2.62 (95%-CI 1.96-3.52).
158 The pattern of increased transmissibility in BA.2 households was not observed for fully
159 vaccinated and booster-vaccinated primary cases, where the estimates were below 1 for
160 BA.2 compared to BA.1 (Table 3).

Table 3: Relative effect of Omicron VOC BA.2 vs. BA.1

	Susceptibility			Transmissibility		
	Unvaccinated	Fully vaccinated	Booster vaccinated	Unvaccinated	Fully vaccinated	Booster vaccinated
Omicron BA.2 households	2.19 (1.58-3.04)	2.45 (1.77-3.40)	2.99 (2.11-4.24)	2.62 (1.96-3.52)	0.60 (0.42-0.85)	0.62 (0.42-0.91)
Omicron BA.1 households	ref (.)	ref (.)	ref (.)	ref (.)	ref (.)	ref (.)
Number of observations	17,945	17,945	17,945	17,945	17,945	17,945
Number of households	8,541	8,541	8,541	8,541	8,541	8,541

Notes: This table shows odds ratio estimates for the effect of living in a household infected with BA.2 relative to BA.1. Column 1 and 4 shows the relative transmission of BA.2, conditional on being unvaccinated. Column 2 and 5 shows the relative transmission of BA.2, conditional on being fully vaccinated. Column 3 and 6 shows the relative transmission of BA.2, conditional on being booster vaccinated. Note, all estimates are from the same model, but with a different reference category across column 1-6. The estimates are adjusted for age and sex of the primary case, age and sex of the potential secondary case, size of the household, and primary case sample date. The estimates are furthermore adjusted for vaccination status of the potential secondary case and primary case interacted with the household subvariant. 95% confidence intervals are shown in parentheses. Standard errors are clustered on the household level. The odds ratio estimates for the full model are presented in Appendix Table 12, column I.

161 In the appendix, where we allowed for a 14-day follow-up, we found a 14-day SAR of 42%
162 for BA.2 and 36% for BA.1 (appendix Figure 3).

163 The distribution of sample Ct values for unvaccinated primary cases showed that the viral
164 load was overall higher for BA.2 cases than for BA.1 cases. This was not the case for fully
165 vaccinated and booster-vaccinated individuals, where the distribution appeared to be the
166 same (appendix Figure 5 and appendix Table 8).

167 5 Discussion

168 The present study shows that infection with the Omicron BA.2 subvariant generally lead
169 to a higher SAR compared to BA.1 across all groups of sex, age, household sizes and
170 immunity groups (Table 1). Furthermore, we found that booster-vaccinated individuals
171 had a reduced susceptibility and transmissibility for both BA.1 and BA.2 compared to
172 fully vaccinated individuals (Table 2). Efficient transmission to vaccinated individuals
173 corroborates previous findings that the Omicron VOC possess immune evasive properties
174 (Zhang et al., 2021; Lyngse et al., 2021b; Ferguson et al., 2021; Planas et al., 2021). How-
175 ever, both booster-vaccinated individuals and fully-vaccinated individuals had reduced
176 susceptibility and transmissibility compared to unvaccinated individuals for both subvari-

177 ants, suggesting that the effectiveness of vaccines remains significant (appendix Figure
178 6).

179 Both unvaccinated, fully vaccinated and booster-vaccinated individuals had a higher sus-
180 ceptibility for BA.2 compared to BA.1, indicating an inherent increased transmissibility of
181 BA.2 (Table 3). However, the relative increase in susceptibility was significantly greater in
182 vaccinated individuals compared to unvaccinated individuals (appendix Figure 6), which
183 points towards immune evasive properties of the BA.2 conferring an even greater advan-
184 tage for BA.2 in a highly vaccinated population such as Denmark. Because previous
185 studies of the Omicron VOC has focused on the BA.1 (Pearson et al., 2021; Planas et al.,
186 2021), new studies are needed to further investigate these properties for BA.2.

187 Unvaccinated individuals had a higher transmissibility with BA.2 compared to BA.1.
188 Contrary to this, fully vaccinated and booster-vaccinated individuals had a reduced trans-
189 missibility, due to a significant negative interaction between subvariant and booster/fully
190 vaccinated individuals compared to unvaccinated individuals (appendix Figure 6). This
191 indicates that after a breakthrough infection, vaccination protects against further trans-
192 mission, and more so for BA.2 than BA.1. This mechanism is only possible to identify in
193 studies that take into account the exposure of individuals.

194 A potential mechanism for the higher transmissibility of unvaccinated individuals infected
195 with BA.2 compared to BA.1 could be a higher viral load (appendix 7.3). No such
196 difference was found for fully or booster-vaccinated individuals, which could be a result of
197 a lower viral load in vaccinated individuals with a breakthrough infection (Puhach et al.,
198 2022; Levine-Tiefenbrun et al., 2021; Lyngse et al., 2022).

199 The higher susceptibility and transmissibility among unvaccinated will likely result in
200 even more extensive transmission of BA.2 in unvaccinated children in school settings and
201 day care.

202 This study has a number of strengths. Firstly, Denmark is, to the best of our knowledge,
203 the only country in the world that have been able to identify a large amount of both
204 BA.1 and BA.2 cases in December 2021 and January 2022. Secondly, any bias introduced

205 in the identification of the subvariants will presumably affect both BA.1 and BA.2 in
206 a similar way. Third, this study draws on exhaustive population registers with a high
207 quality of information covering the whole population. Fourth, potential secondary cases
208 were frequently being tested: 84% one time, and 60-61% two times.

209 Some limitations apply to this study. The study period runs over Christmas 2021 and New
210 Year's Eve 2021/22, which are public holidays in Denmark. Despite government advice to
211 limit social activity, it is likely that there has been considerable social mixing with family
212 and friends outside the households during this period. Social mixing over the holidays
213 in conjunction with the high incidence levels in Denmark during this period likely means
214 that some secondary cases in this study are actually misclassified co-primary cases, i.e.
215 infections picked up outside the household and testing positive after each other. However,
216 this potential bias would be applicable to both subvariants. Moreover, our estimates were
217 robust when only including primary cases from 5-11 January 2022 (appendix Table 12,
218 model II) and when only including secondary cases found on day 2-7 or 3-7 (appendix
219 Table 13, model VII and VIII).

220 The present household study showed a transmission advantage of Omicron BA.2 over
221 BA.1. Although vaccinations, in particular booster vaccinations, did protect against
222 infection, the 2.45 (fully vaccinated) and 2.99 (booster vaccinated) fold higher odds of
223 infection in BA.2 households indicate that BA.2 as a phenotype represents a further step
224 in immune evasion in the Omicron lineage. However, it is likely that this change came
225 with an evolutionary cost for BA.2. To our surprise, we found a decreased transmissibility
226 of BA.2 relative to BA.1 among fully vaccinated and booster vaccinated, with estimates
227 of 0.60 and 0.62, respectively. Based on such a considerable loss in transmissibility among
228 vaccinated individuals, it is not straightforward to predict the future trajectory of BA.2
229 relative to BA.1 or other potentially emerging variants.

230 Evolution of SARS-CoV-2 variants, including the Omicron VOC, is constantly evolving,
231 especially during the current record high transmission in many countries. For public
232 health, it is reassuring that BA.2, like BA.1, seems to be associated with favorable out-

233 comes relative to the Delta variant, and that vaccines protect in particular against hospital
234 admissions and severe illness (Wolter et al., 2022; Bager et al., 2022). Even with the emer-
235 gence of BA.2, vaccines have an effect against infection, transmission and severe disease,
236 although reduced compared to the ancestral variants. The combination of high incidence
237 of a relative innocuous subvariant has raised optimism (Sundhedsministeriet, 2022). It is,
238 however, important to follow the future evolution of the BA.2 subvariant closely, as well
239 as future emergent subvariants. Thus, it is critical to maintain rapid high-quality WGS
240 with random sampling as part of surveillance to continuously support the risk assessment
241 of new variants, their impact on public health and to inform public health policy makers,
242 when navigating during a pandemic.

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355 **Contributions**

356 FPL performed all data analyses. MD calculated the contrasts between vaccination
357 groups. FPL, CTK and LHM wrote the first draft. All other authors contributed to
358 the discussion, revised the first draft and approved the submitted version.

359 **Competing interests**

360 The authors declare no competing interests.

361 **Supplementary Appendix**

362 **6 Background**

363 This section provides some background characteristics for all of Denmark, i.e. not re-
364 stricted to the study sample used for the analysis of household transmission.

365 **6.1 Number of tests**

366 Table 4 shows the number of antigen (AG) tests and RT-PCR tests in Denmark from 1
367 December 2021 to 19 January 2022. The table also provides information on the number
368 of successfully sequenced positive RT-PCR tests by SARS-CoV-2 variant, including their
369 relative proportion. On 20 December 2021, Omicron BA.2 comprised 5% of all infections,
370 and Omicron BA.1 comprised 64%, while Delta comprised 30%. By 11 January 2022, the
371 proportions were 47%, 53%, and 0%, respectively.

Table 4: Number of tests in Denmark, 1 December 2021–19 January 2022

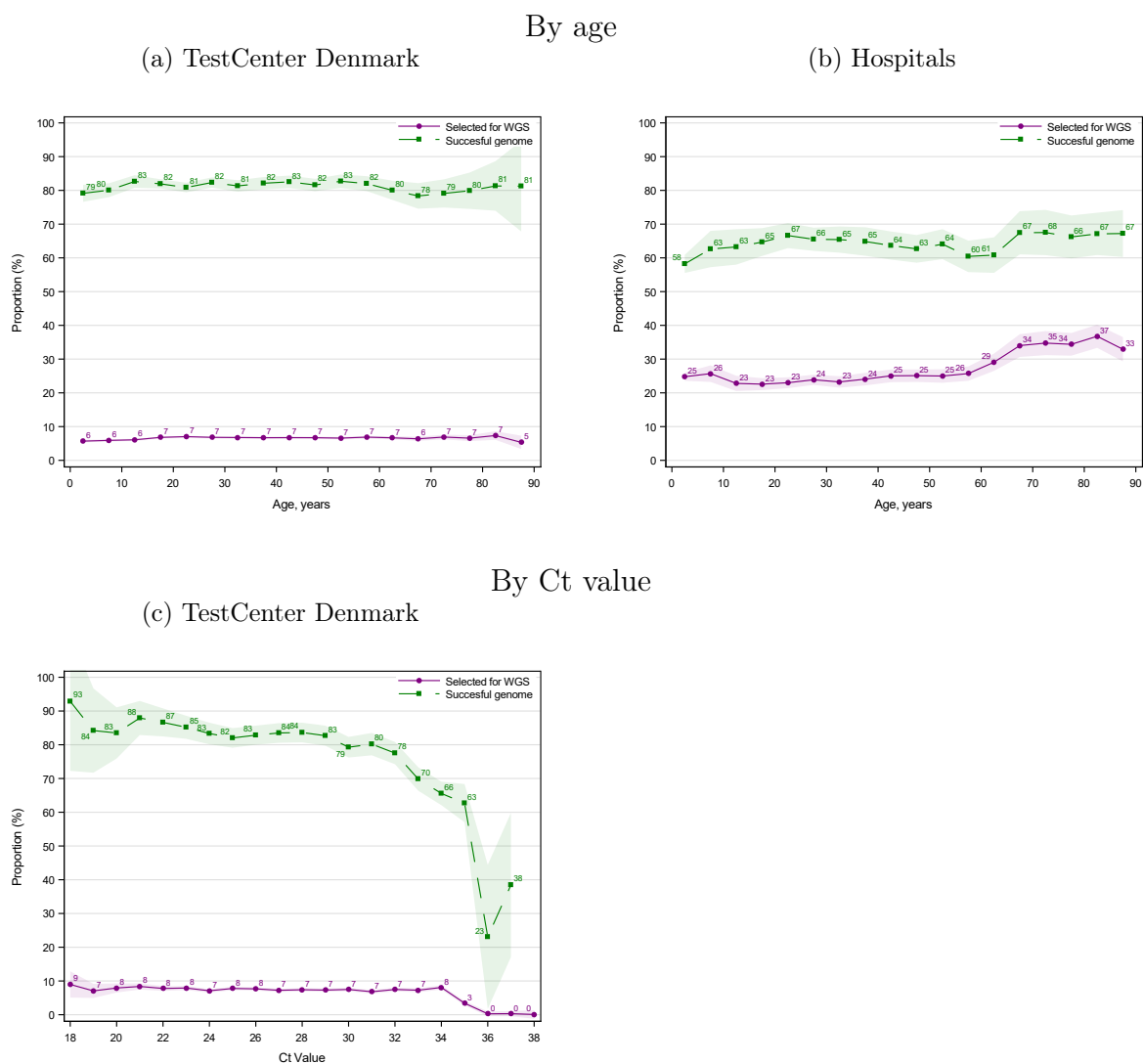
Sample date	AG tests		RT-PCR tests		Variant					
	Tests N	Positives N	Tests N	Positives N	Omicron N	BA.2 %	Omicron N	BA.1 %	Delta N	%
01-12-2021	177,466	1,946	188,052	4,874	0	0	56	2	2,298	98
02-12-2021	217,978	1,908	216,548	4,960	0	0	43	2	2,630	98
03-12-2021	237,466	1,891	189,592	5,599	0	0	34	1	2,342	99
04-12-2021	143,557	1,566	142,053	5,524	0	0	58	2	2,910	98
05-12-2021	144,767	2,133	149,098	5,401	<5	0	102	3	3,330	97
06-12-2021	228,350	2,882	211,711	7,546	0	0	211	5	4,206	95
07-12-2021	233,073	2,778	211,038	7,814	0	0	203	10	1,825	90
08-12-2021	239,456	2,885	207,141	7,088	0	0	199	11	1,533	89
09-12-2021	268,385	2,807	245,057	7,092	0	0	193	15	1,074	85
10-12-2021	274,849	2,596	213,063	7,427	<5	0	202	12	1,462	88
11-12-2021	178,176	2,166	155,858	7,159	0	0	197	17	983	83
12-12-2021	178,068	3,087	167,670	7,669	<5	0	238	20	937	80
13-12-2021	261,259	4,380	232,666	11,221	13	1	391	29	961	70
14-12-2021	254,258	4,529	225,263	12,157	16	2	405	44	499	54
15-12-2021	225,026	4,744	219,477	11,940	13	1	544	48	587	51
16-12-2021	255,302	4,676	258,490	11,316	19	2	498	46	563	52
17-12-2021	273,106	4,550	236,644	11,831	20	4	272	53	222	43
18-12-2021	221,579	4,305	176,424	11,350	32	4	519	57	360	40
19-12-2021	220,878	5,263	182,974	11,637	49	4	680	59	426	37
20-12-2021	248,231	6,379	271,191	15,093	70	6	752	64	355	30
21-12-2021	251,443	6,408	258,469	14,778	62	7	561	67	216	26
22-12-2021	275,255	6,172	272,965	13,584	52	8	476	71	139	21
23-12-2021	277,452	5,037	246,286	14,573	65	9	513	70	156	21
24-12-2021	155,248	4,466	72,578	8,253	24	8	200	67	74	25
25-12-2021	128,703	4,787	73,516	9,163	45	12	264	72	56	15
26-12-2021	168,399	6,072	82,131	12,212	114	16	502	70	105	15
27-12-2021	207,265	7,393	186,664	24,968	342	17	1,399	71	231	12
28-12-2021	213,340	7,253	195,094	24,145	232	17	1,019	72	155	11
29-12-2021	238,567	6,813	216,571	19,207	79	19	300	72	38	9
30-12-2021	314,614	6,387	229,325	21,573	144	17	632	74	82	10
31-12-2021	181,564	4,507	72,615	10,978	86	22	281	70	32	8
01-01-2022	70,576	3,248	75,054	9,821	117	26	318	70	21	5
02-01-2022	224,366	8,394	156,448	22,461	1,073	22	3,447	72	250	5
03-01-2022	239,585	9,284	224,060	28,810	552	25	1,528	70	108	5
04-01-2022	260,020	8,579	207,726	27,044	88	25	248	71	15	4
05-01-2022	225,865	6,023	186,594	20,330	383	26	1,034	70	53	4
06-01-2022	247,962	5,205	212,979	17,996	255	32	525	65	26	3
07-01-2022	240,998	4,777	185,196	16,690	774	35	1,414	63	46	2
08-01-2022	145,731	3,999	136,728	15,682	266	37	437	61	15	2
09-01-2022	204,489	5,890	151,107	18,550	199	41	277	57	14	3
10-01-2022	242,588	6,932	211,919	26,243	449	44	556	55	12	1
11-01-2022	238,640	6,548	197,537	25,646	201	47	225	53	<5	0
12-01-2022	232,320	6,408	190,105	25,504	-	-	-	-	-	-
13-01-2022	255,218	7,167	225,495	26,775	-	-	-	-	-	-
14-01-2022	254,373	7,647	207,485	28,934	-	-	-	-	-	-
15-01-2022	158,305	6,738	158,450	28,218	-	-	-	-	-	-
16-01-2022	229,717	10,724	175,178	31,223	-	-	-	-	-	-
17-01-2022	275,634	11,886	251,447	45,876	-	-	-	-	-	-
18-01-2022	267,751	11,955	239,012	44,841	-	-	-	-	-	-
19-01-2022	250,051	10,857	226,241	42,031	-	-	-	-	-	-

Notes: This tables shows the number of antigen (AG) tests and RT-PCR tests in Denmark from 1 December 2021 to 19 January 2022. The table also provides information on the number of successfully sequenced positive RT-PCR tests by SARS-CoV-2 variant, including their relative proportion. On any given day, fewer than 5 of the successfully sequenced samples were classified as another variant than Omicron BA.2, Omicron BA.1, or Delta.

372 **6.2 Sample selection to WGS**

373 In Denmark, individuals can be tested in the community track (TestCenter Denmark) or
374 in the healthcare track (Hospitals), which includes hospitalized patients, nursing home
375 residents, and healthcare personnel (see Schønning et al. (2021) for elaboration). Only
376 a proportion of all positive RT-PCR tests were sampled for whole genome sequencing
377 (WGS). Both TestCenter Denmark and Hospitals sample positive RT-PCR tests ran-
378 domly for WGS. However, all hospitalized patients were tested for SARS-CoV-2 and all
379 positive tests were subject to WGS for treatment purposes. Figure 2 shows the sampling
380 probability for WGS for within the study period by TestCenter Denmark and Hospitals.
381 Panel a and b shows the sampling probability by age. For positive RT-PCR tests at
382 TestCenter Denmark, there was no selection bias on age, whereas in hospitals, there was
383 an increased sampling probability by age for young children and elderly. Panel c shows
384 the sampling probability for WGS by sample Ct value for TestCenter Denmark (we only
385 obtained Ct values from TestCenter Denmark). There was no sampling bias for Ct values
386 < 35 . The probability of obtaining a successfully sequenced genome was correlated with
387 the sample Ct value.

Figure 2: WGS sampling probability of positive RT-PCR tests



Notes: This figure shows the sampling probability of positive RT-PCR tests for WGS by testing place (TestCenter Denmark and Hospitals). Only Ct values from TestCenter Denmark were available. The shaded areas show the 95% confidence bands clustered on the household level.

388 7 Descriptive analyses

389 7.1 Summary statistics

390 In this section, we present additional summary statistics.

Table 5: Summary Statistics

	Omicron - BA.2				Omicron - BA.1			
	Primary Cases	Potential Secondary Cases	Positive Secondary Cases	SAR (%)	Primary Cases	Potential Secondary Cases	Positive Secondary Cases	SAR (%)
Total, N	2,122	4,587	1,792	39	6,419	13,358	3,910	29
Sex, N								
Male	1,032	2,312	871	38	3,174	6,724	1,882	28
Female	1,090	2,275	921	40	3,245	6,634	2,028	31
Age, N								
0-10	180	799	336	42	302	2,280	747	33
10-20	523	845	289	34	1,468	2,556	673	26
20-30	484	633	240	38	1,714	2,056	633	31
30-40	328	573	321	56	958	1,408	595	42
40-50	241	804	303	38	784	2,393	650	27
50-60	225	660	213	32	692	1,838	400	22
60-70	79	175	61	35	324	572	145	25
70+	62	98	29	30	177	255	67	26
Household size, N								
2	790	790	345	44	2,577	2,577	853	33
3	517	1,034	378	37	1,605	3,210	862	27
4	550	1,650	683	41	1,504	4,512	1,379	31
5	212	848	292	34	606	2,424	667	28
6	53	265	94	35	127	635	149	23
Immunity, N								
Unvaccinated	449	1,210	518	43	1,016	3,421	1,171	34
Fully vaccinated / previous infection	1,114	1,917	783	41	3,781	5,921	1,856	31
Booster vaccinated	559	1,460	491	34	1,622	4,016	883	22

Notes: The secondary attack rate (SAR) is expressed as a percentage (%). Summary statistics based on primary cases are shown separately from summary statistics on potential secondary cases, positive secondary cases and SAR. The summary statistics stratified by the primary case level are presented in appendix Tables 6 and 7.

Table 6: Summary Statistics, stratified by primary case level

	Omicron - BA.2				Omicron - BA.1			
	Primary Cases	Potential Secondary Cases	Positive Secondary Cases	SAR (%)	Primary Cases	Potential Secondary Cases	Positive Secondary Cases	SAR (%)
Total, N	2,122	4,587	1,792	39	6,419	13,358	3,910	29
Sex of primary case, %								
Male	49	49	49	38	49	50	49	29
Female	51	51	51	40	51	50	51	30
Age of primary case, %								
0-10	8	11	18	65	5	6	9	43
10-20	25	30	21	28	23	28	18	19
20-30	23	19	16	32	27	22	18	24
30-40	15	17	19	44	15	17	22	38
40-50	11	12	14	45	12	14	17	36
50-60	11	7	8	42	11	8	9	33
60-70	4	2	2	41	5	3	4	38
70+	3	1	2	42	3	1	2	37
Household size of primary case, %								
2	37	17	19	44	40	19	22	33
3	24	23	21	37	25	24	22	27
4	26	36	38	41	23	34	35	31
5	10	18	16	34	9	18	17	28
6	2	6	5	35	2	5	4	23
Immunity of primary case, %								
Unvaccinated	21	24	30	50	16	18	21	34
Fully vaccinated / previous infection	52	55	49	35	59	61	59	28
Booster vaccinated	26	22	21	38	25	21	20	28

Notes: The secondary attack rate (SAR) is expressed as a percentage (%). Potential and positive secondary cases are grouped based on the primary case characteristics. See Table 1 and appendix Table 5 for potential and positive secondary cases grouped by their own characteristics.

Table 7: Summary Statistics, stratified by primary case level

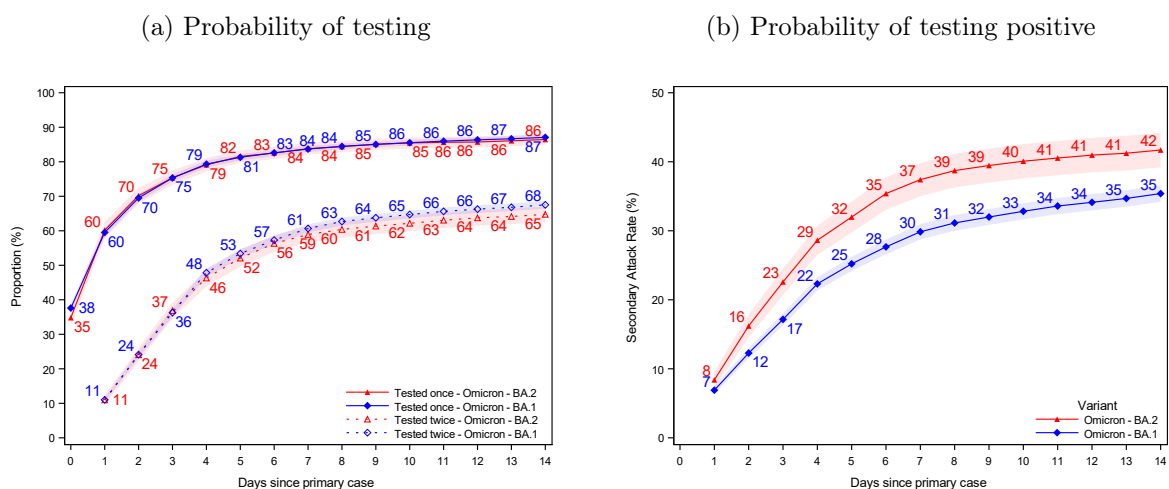
	Omicron - BA.2				Omicron - BA.1			
	Primary Cases	Potential Secondary Cases	Positive Secondary Cases	SAR (%)	Primary Cases	Potential Secondary Cases	Positive Secondary Cases	SAR (%)
Total, N	2,122	4,587	1,792	39	6,419	13,358	3,910	29
Sex of primary case, N								
Male	1,032	2,270	873	38	3,174	6,643	1,928	29
Female	1,090	2,317	919	40	3,245	6,715	1,982	30
Age of primary case, N								
0-10	180	495	324	65	302	828	353	43
10-20	523	1,360	375	28	1,468	3,782	720	19
20-30	484	873	278	32	1,714	2,903	707	24
30-40	328	783	348	44	958	2,242	860	38
40-50	241	572	256	45	784	1,886	681	36
50-60	225	342	144	42	692	1,134	369	33
60-70	79	95	39	41	324	391	149	38
70+	62	67	28	42	177	192	71	37
Household size of primary case, N								
2	790	790	345	44	2,577	2,577	853	33
3	517	1,034	378	37	1,605	3,210	862	27
4	550	1,650	683	41	1,504	4,512	1,379	31
5	212	848	292	34	606	2,424	667	28
6	53	265	94	35	127	635	149	23
Immunity of primary case, N								
Unvaccinated	449	1,083	543	50	1,016	2,417	816	34
Fully vaccinated / previous infection	1,114	2,507	875	35	3,781	8,152	2,315	28
Booster vaccinated	559	997	374	38	1,622	2,789	779	28

Notes: The secondary attack rate (SAR) is expressed as a percentage (%). Potential and positive secondary cases are grouped based on the primary case characteristics. See Table 1 and appendix Table 5 for potential and positive secondary cases grouped by their own characteristics.

391 7.2 Testing dynamics, 14-day follow-up

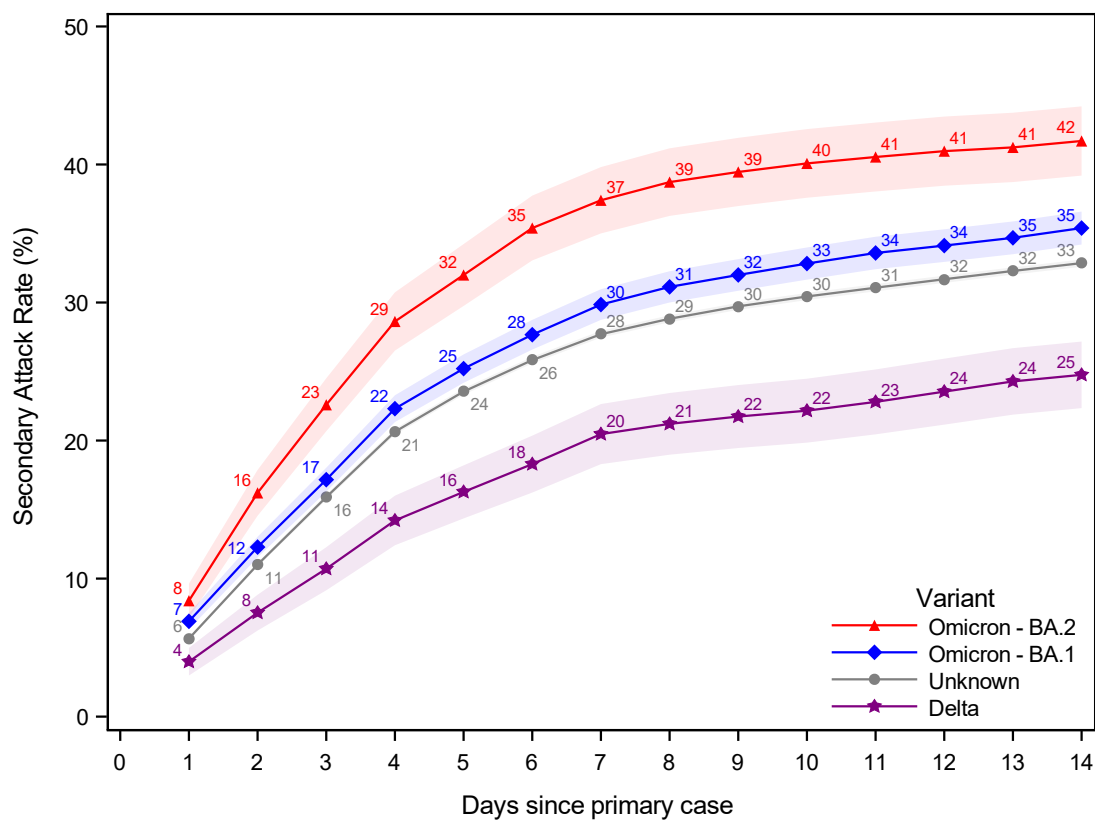
392 In this section, we present evidence of the testing dynamics over a 14-day follow-up period.
 393 Figure 3 presents the probability of being tested and testing positive over a 14-day follow-
 394 up period instead of a 7-day follow-up period, as used in Figure 1. Figure 4 presents the
 395 SAR for households infected with the Omicron BA.1, BA.2, and Delta VOC, as well as
 396 those without an identified variant.

Figure 3: Probability of being tested and testing positive, 14-day follow-up



Notes: Panel (a) shows the probability of potential secondary cases being tested after a primary case has been identified within the household. Panel (b) shows the probability of potential secondary cases that test positive subsequently to a primary case being identified within the household. Note that the latter is not conditional on being tested, i.e. the denominator contains test negative individuals and untested individuals. The x-axes shows the days since the primary case tested positive, and the y-axes shows the proportion of individuals either being tested (a) or testing positive (b) with either antigen or RT-PCR tests, based on the subvariant of the primary case. The SAR for each day relative to the primary case can be read directly from panel (b). For example, the SAR on day 7 is 37% for BA.2 (red) and 30% for BA.1 (blue), whereas the SAR on day 14 is 42% and 35%, respectively. The shaded areas show the 95% confidence bands clustered on the household level. To allow for a 14-day follow-up, only primary cases with samples from 20 December 2021 to 5 January 2022 were included in this figure. Appendix Figure 4 also presents the 14-day SAR for the Delta VOC and those without a known variant.

Figure 4: Probability of testing positive, 14-day follow-up

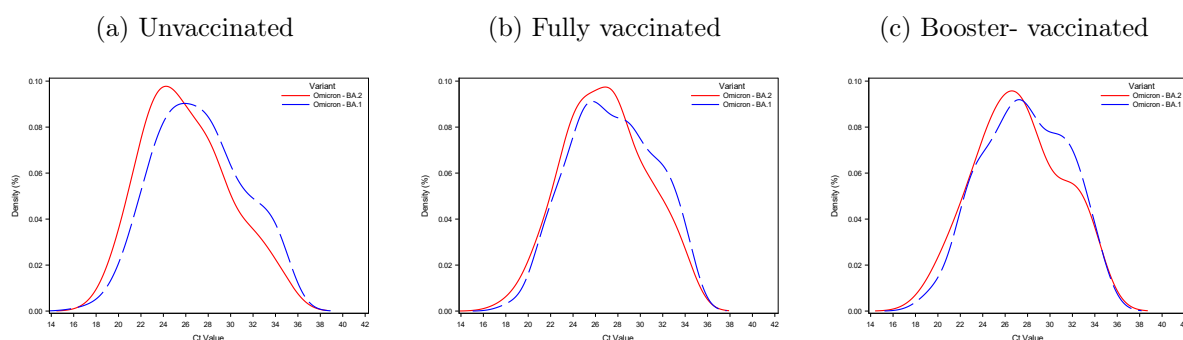


Notes: This figure shows the probability of potential secondary cases that test positive subsequently to a primary case being identified within the household in a 14-day follow-up period. Note that the latter is not conditional on being tested, i.e. the denominator contains test negative individuals and untested individuals. The x-axis shows the days since the primary case tested positive, and the y-axis shows the proportion of individuals testing positive with either antigen or RT-PCR tests, based on the subvariant of the primary case. The SAR for each day relative to the primary case can be read directly from the figure. For example, the SAR on day 14 is 42% for Omicron BA.2, 35% for BA.1, 33% for those without a known variant, and 25% for Delta. The shaded areas show the 95% confidence bands clustered on the household level. To allow for a 14-day follow-up, only primary cases with samples from 20 December 2021 to 5 January 2022 were included in this figure.

397 7.3 Viral load of primary cases

398 This section provides descriptive statistics on the viral load of the primary case samples.
 399 Figure 5 shows the density plots of sample Ct values for primary cases infected with
 400 Omicron BA.1 and BA.2 stratified by their vaccination status. The distributional values
 401 are presented in Table 8. In particular, unvaccinated primary cases infected with BA.2
 402 have a higher sample viral load (lower Ct value), with the median primary case having a
 403 1.6 point lower sample Ct value, corresponding to 0.4 of a standard deviation.

Figure 5: Ct values of primary cases



Notes: This figure shows the density plots for primary cases infected with Omicron BA.1 and BA.2 stratified by their vaccination status.

Table 8: Ct values of primary cases

Vaccination status	Subvariant	Q1	Median	Q3	Mean	STD	N
Booster vaccinated	Omicron - BA.1	25.01	27.65	30.80	27.72	3.71	1,622
	Omicron - BA.2	24.48	27.09	30.06	27.20	3.82	559
	Difference / STD	-0.14	-0.14	-0.19	-0.13		
Fully vaccinated	Omicron - BA.1	24.65	27.33	30.48	27.50	3.76	3,781
	Omicron - BA.2	24.10	26.97	29.47	26.88	3.68	1,114
	Difference / STD	-0.15	-0.09	-0.26	-0.16		
Not vaccinated	Omicron - BA.1	24.14	27.02	29.97	27.20	3.91	1,016
	Omicron - BA.2	23.20	25.42	28.55	26.07	3.80	449
	Difference / STD	-0.24	-0.41	-0.36	-0.29		

Notes: This table provides distributional values for the Ct values of primary case samples. "Difference / STD" denotes the difference of primary cases with BA.2 and BA.1 relative to the standard deviation of BA.1 primary cases, within vaccination group.

404 8 Alternative presentation of main results

405 8.1 Contrasts

406 In this section, we present some of our main estimates in an alternative way, showing the
407 estimates for comparison of different vaccination groups.

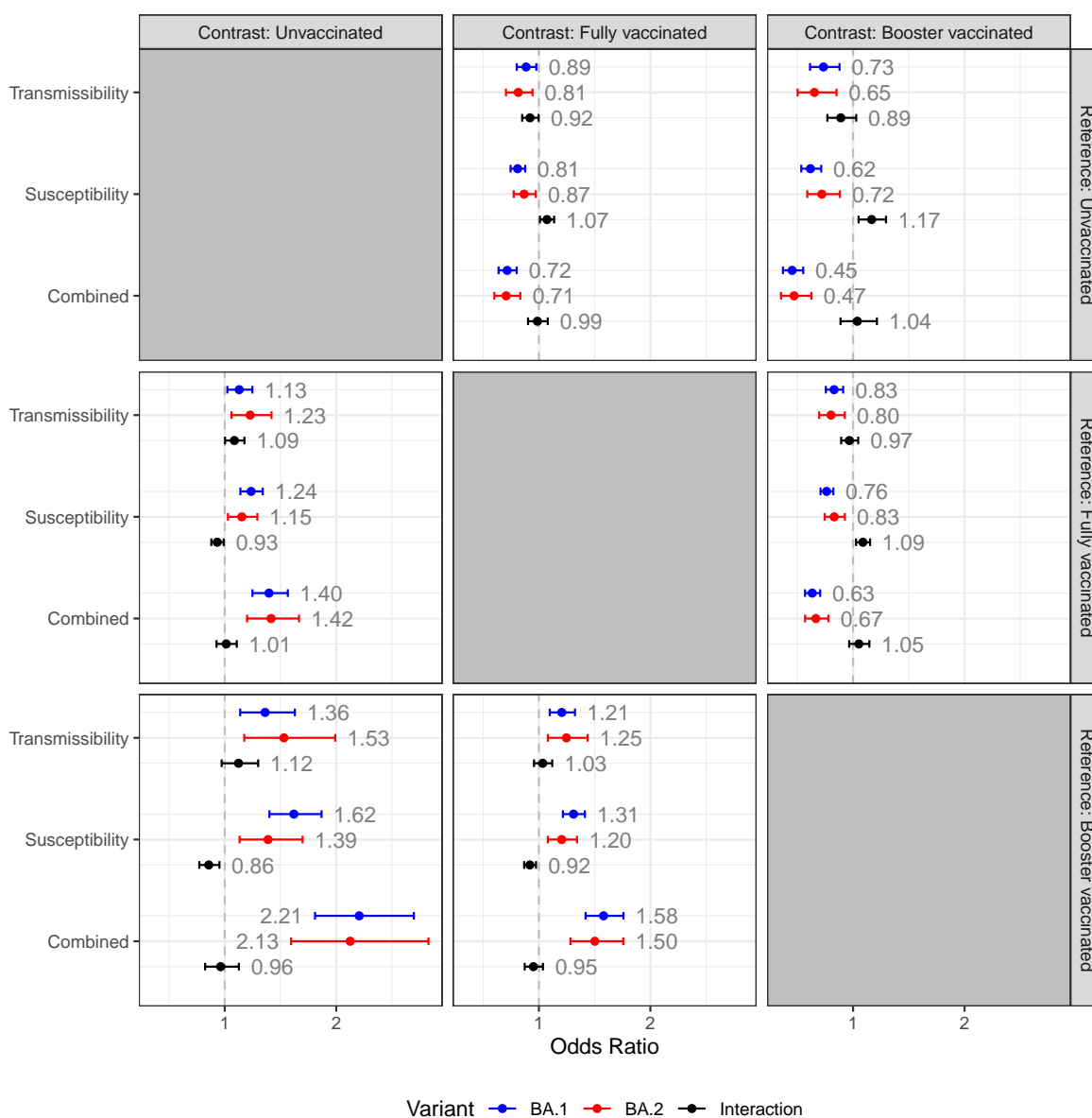
408 Figure 6 shows a full comparison of our main estimates across vaccination groups with
409 different reference groups. We can see the relative effect of vaccination dependent on their
410 vaccination status by choosing the *Contrast* (column) and compare their *Transmissibility*
411 to the vaccination status of a similar primary case by choosing the *Reference* (row). For
412 example, unvaccinated primary cases (Contrast=unvaccinated) compared to fully vacci-
413 nated primary cases (Reference=fully vaccinated) have an increased transmissibility of
414 OR=1.13 when infected with BA.1 (blue) and OR=1.23 when infected with BA.2 (red).
415 The interaction term of BA.2 on transmissibility has an OR=1.09 (black). This inter-
416 action term can be interpreted as the additional OR associated with BA.2 (relative to
417 BA.1) within the comparison. Similarly, we can see the relative transmissibility for unvac-
418 cinated primary cases (Contrast=unvaccinated) compared to booster-vaccinated primary
419 cases (Reference=booster). Primary cases with BA.1 have an OR=1.36 for transmissibil-
420 ity and primary cases with BA.2 have an OR=1.53 for transmissibility. The interaction
421 term is OR=1.12. The estimates for *Susceptibility* is read in a similar way, but for po-
422 tential secondary cases. Lastly, the *Combined* effect of vaccination shows the effect of
423 both the primary case and potential secondary case having the same vaccination status.
424 Thus, for households infected with BA.1, the OR=1.40 if both the primary case and
425 potential secondary case are unvaccinated (Contrast=Unvaccinated) compared to when
426 both are fully vaccinated (Reference=Fully vaccinated). Note, the model estimates for
427 reference=Fully vaccinated are found in Table 10.

428 Table 9 shows the OR for infection with BA.2 compared to BA.1 for each combination of
429 vaccination status of both the primary case and potential secondary case. The relative
430 transmission of BA.2 compared to BA.1 is higher across all combinations of vaccination

431 groups. The relative transmission of BA.2 compared to BA.1 is generally higher for un-
432 vaccinated primary cases across all vaccination groups of potential secondary cases.

433 Table 10 shows the model estimates (similar to Table 12, model I) with interaction terms
434 instead of a full specification of contrasts.

Figure 6: Effect of vaccination, contrast plot



Notes: This figure shows a full comparison of our main estimates across vaccination groups with different reference groups. We can see the relative effect of vaccination dependent on their vaccination status by choosing the *Contrast* (column) and compare their *Transmissibility* to the vaccination status of a similar primary case by choosing the *Reference* (row). For example, unvaccinated primary cases (Contrast=unvaccinated) compared to fully vaccinated primary cases (Reference=fully vaccinated) have an increased transmissibility of OR=1.13 when infected with BA.1 (blue) and OR=1.23 when infected with BA.2 (red). The interaction term of BA.2 on transmissibility has an OR=1.09 (black). This interaction term can be interpreted as the additional OR associated with BA.2 (relative to BA.1) within the comparison. Note that the top/right subplots are simply the inverse of the lower/left subplots. 95%-confidence intervals. Standard errors are clustered on the household level.

Table 9: OR estimates of BA.2 compared to BA.1 by vaccination status

	Primary Case		
	Unvaccinated	Fully vaccinated	Booster-vaccinated
Potential secondary case			
Unvaccinated	1.31 (1.17-1.46)	1.21 (1.11-1.31)	1.17 (1.03-1.32)
Fully vaccinated	1.41 (1.27-1.55)	1.29 (1.23-1.36)	1.25 (1.13-1.38)
Booster-vaccinated	1.53 (1.35-1.73)	1.41 (1.31-1.52)	1.36 (1.23-1.51)

Notes: This table shows the OR for BA.2 compared to BA.1 for each combination of vaccination status of both the primary case and potential secondary case. 95% confidence intervals in parentheses. Standard errors clustered on the household level.

435 Method for estimating the contrast

436 To estimate the contrast, we used the estimates and variance-covariance matrix from the
 437 fitted model (Table 10) to generate 10,000 correlated Monte Carlo estimates of the model
 438 parameters. These estimates were then used to calculate log odds ratios representing the
 439 total effect of BA.2 compared to BA.1 for all possible pairwise contrasts within vaccination
 440 groups. This was done for transmissibility and susceptibility, as well as a combined
 441 effect calculated as the sum of these. In addition, the interaction between subvariant
 442 and vaccination group was also calculated for each pairwise contrast within vaccination
 443 groups. Results were summarised as mean and 95%-confidence intervals of the estimates,
 444 before exponentiation for interpretation as odds ratios (Figure 6). These analyses were
 445 performed in R version 4.1.2 (R Core Team, 2021).

Table 10: Model estimates

	Estimate	(95%-CI)
Intercept	-0.58	(-0.68;-0.48)
Omicron BA.2	0.26	(0.21;0.31)
Potential secondary case, vaccination status		
Booster-vaccinated	-0.27	(-0.35;-0.19)
Fully vaccinated	ref	(.)
Not-vaccinated	0.21	(0.13;0.29)
Primary case, vaccination status		
Booster-vaccinated	-0.19	(-0.28;-0.09)
Fully vaccinated	ref	(.)
Not-vaccinated	0.12	(0.02;0.22)
Potential secondary case, vaccination status		
Omicron BA.2 X Booster-vaccinated	0.08	(0.03;0.14)
Omicron BA.2 X Fully vaccinated	ref	(.)
Omicron BA.2 X Not-vaccinated	-0.07	(-0.13;-0.01)
Primary case, vaccination status		
Omicron BA.2 X Booster-vaccinated	-0.03	(-0.11;0.04)
Omicron BA.2 X Fully vaccinated	ref	(.)
Omicron BA.2 X Not-vaccinated	0.08	(0.01;0.16)
Primary case age		
0-10	0.30	(0.12;0.49)
10-20	-0.76	(-0.88;-0.64)
20-30	ref	(.)
30-40	-0.06	(-0.18;0.06)
40-50	0.09	(-0.03;0.21)
50-60	0.03	(-0.10;0.17)
60-70	0.38	(0.17;0.59)
70+	0.71	(0.38;1.04)
Potential secondary case age		
0-10	-0.11	(-0.23;0.02)
10-20	-0.12	(-0.22;-0.02)
20-30	ref	(.)
30-40	0.48	(0.37;0.58)
40-50	0.26	(0.16;0.36)
50-60	0.00	(-0.11;0.11)
60-70	-0.18	(-0.35;-0.01)
70+	-0.56	(-0.84;-0.27)
Household size		
2	0.27	(0.18;0.36)
3	-0.02	(-0.11;0.06)
4	0.07	(-0.01;0.15)
5	-0.08	(-0.19;0.03)
6	ref	(.)
Primary case sex		
Male	ref	(.)
Female	0.14	(0.07;0.20)
Potential secondary case sex		
Male	ref	(.)
Female	0.06	(-0.02;0.15)
Primary case sample date		
20DEC2021	-0.15	(-0.34;0.05)
21DEC2021	0.02	(-0.21;0.24)
22DEC2021	0.15	(-0.08;0.39)
23DEC2021	0.09	(-0.17;0.34)
24DEC2021	0.20	(-0.20;0.59)
25DEC2021	0.46	(0.12;0.80)
26DEC2021	0.20	(-0.08;0.47)
27DEC2021	0.06	(-0.10;0.23)
28DEC2021	-0.01	(-0.19;0.18)
29DEC2021	0.14	(-0.16;0.44)
30DEC2021	-0.04	(-0.26;0.18)
31DEC2021	ref	(.)
01JAN2022	-0.03	(-0.32;0.25)
02JAN2022	-0.05	(-0.16;0.05)
03JAN2022	-0.09	(-0.23;0.05)
04JAN2022	-0.16	(-0.48;0.15)
05JAN2022	-0.36	(-0.54;-0.19)
06JAN2022	-0.21	(-0.43;0.00)
07JAN2022	-0.15	(-0.29;-0.01)
08JAN2022	-0.09	(-0.32;0.14)
09JAN2022	0.00	(-0.24;0.24)
10JAN2022	-0.04	(-0.21;0.14)
11JAN2022	0.02	(-0.26;0.31)
Number of observations	17,945	
Number of households	8,541	

Notes: This table provides model estimates of our main specification (model 1) with an interaction effect. 95% confidence intervals are shown in parentheses. Standard errors are clustered on the household level.

446 9 Robustness

447 9.1 Model selection

Table 11: Model selection

Model	I	II	III	IV
AIC	21,245	21,249	21,260	21,263
Omicron BA.2 household	YES	YES	YES	YES
Potential secondary case vaccination status	YES	YES	YES	YES
Primary case vaccination status	YES	YES	YES	YES
Potential secondary case vaccination status X Omicron BA.2 household	YES	YES	NO	NO
Primary case vaccination status X Omicron BA.2 household	YES	NO	YES	NO
Primary case age	YES	YES	YES	YES
Potential secondary case age	YES	YES	YES	YES
Household size	YES	YES	YES	YES
Primary case sex	YES	YES	YES	YES
Potential secondary case sex	YES	YES	YES	YES
Number of observations	17,945	17,945	17,945	17,945
Number of households	8,541	8,541	8,541	8,541

Notes: This table provides estimates of the goodness of fit for the model. Model I includes an interaction with Omicron BA.2 both for susceptibility and transmissibility, and is the one used in the study. Model II includes an interaction with Omicron BA.2 only for susceptibility. Model III includes an interaction with Omicron BA.2 only for transmissibility. Model IV includes neither an interaction with Omicron BA.2 only for susceptibility nor transmissibility. AIC = Akaike information criterion.

448 9.2 Intra-household correlation of variants

449 An obvious concern in transmission studies is the linkage of primary cases to their potential
450 secondary cases and positive secondary cases. In previous studies we have used the same
451 method as in the current study (Lyngse et al., 2021a,b). In those studies, we investigated
452 the household transmission between different SARS-CoV-2 variants and found an intra-
453 household correlation of variants (i.e. the probability that a positive secondary case was
454 infected with the same variant as the primary case) of 96-99%. In the present study, we
455 are limited by only having a low number of positive secondary cases with a successfully
456 sequenced genome. This is due to both the laboratory time needed from a positive test
457 result to having a successfully sequenced genome from the sample and a relatively low
458 sampling probability for WGS. Of all the 5,702 positive secondary samples in the current
459 study, only 23 of them had a successfully sequenced genome at the time of analysis. All
460 of these 23 samples were the exact same subvariant as the primary case, implying an
461 intra-household correlation of subvariants of 100%.

462 **9.3 Robustness of main results**

463 This section provides additional analyses to investigate the robustness of our main results.
464 Model I in Tables 12 and 13 provides the odds ratio (OR) estimates of our main model
465 specification. In model II, we only include households with primary cases identified in the
466 period 5-11 January 2022, in order to exclude the atypical transmission patterns between
467 Christmas 2021 and New Year's Eve 2021/22. In model III, we only include households,
468 where the primary cases have been identified by TestCenter Denmark to account for
469 the potential sampling bias from the healthcare track (Section 6.2). In model IV, we
470 only include households with two persons to account for the natural weighting bias from
471 different sizes of households. In model V, we exclude households, where the primary case
472 was below 10 years of age. In model VI, we exclude households that have previously
473 been infected (defined by having a positive RT-PCR test), to exclude possible hybrid
474 immunity (i.e. immunity from both vaccination and previous infection). In model VII,
475 we only include positive secondary cases that tested positive on day 2-7 (in model I, this
476 window is 1-7), as these could potentially be misclassified co-primary cases. Similarly, in
477 model VIII, we only include positive secondary cases that tested positive on day 3-7. In
478 model IX, we additionally adjust for the primary case sample Ct value, as differences in
479 the viral load could potentially affect the results.

480 To investigate the sensitivity of our results presented in Table 3, we estimated our model
481 by stratifying the sample (Table 14).

Table 12: Robustness I

Model	I		II		III		IV		V	
	OR	Main (95%-CI)	5-11 January OR	January (95%-CI)	Only OR	Test Center DK (95%-CI)	2-person OR	households (95%-CI)	Primary OR	cases >10years (95%-CI)
Potential secondary case, vaccination status										
<i>Omicron BA.1 households</i>										
Booster-vaccinated	0.65	(0.58-0.73)	0.57	(0.46-0.70)	0.61	(0.54-0.70)	0.89	(0.71-1.12)	0.65	(0.58-0.73)
Fully vaccinated	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
Not-vaccinated	1.23	(1.09-1.40)	1.27	(1.01-1.60)	1.24	(1.08-1.43)	0.97	(0.71-1.33)	1.20	(1.05-1.36)
<i>Omicron BA.2 households</i>										
Not-vaccinated	1.95	(1.37-2.78)	1.95	(1.19-3.20)	1.72	(1.16-2.55)	2.29	(1.00-5.23)	1.29	(0.84-2.00)
Fully vaccinated	2.45	(1.77-3.40)	2.46	(1.57-3.85)	2.04	(1.42-2.94)	2.36	(1.08-5.15)	1.70	(1.12-2.56)
Not-vaccinated	2.70	(1.95-3.74)	2.57	(1.63-4.03)	2.59	(1.81-3.72)	2.05	(1.01-4.17)	1.84	(1.23-2.75)
Primary case, vaccination status										
<i>Omicron BA.1 households</i>										
Booster-vaccinated	0.77	(0.67-0.88)	0.85	(0.65-1.12)	0.74	(0.63-0.86)	0.72	(0.57-0.90)	0.76	(0.66-0.87)
Fully vaccinated	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
Not-vaccinated	0.93	(0.80-1.08)	1.11	(0.85-1.44)	0.94	(0.80-1.11)	1.00	(0.74-1.36)	0.96	(0.82-1.12)
<i>Omicron BA.2 households</i>										
Booster-vaccinated	0.47	(0.32-0.71)	0.55	(0.31-0.97)	0.51	(0.33-0.81)	0.52	(0.22-1.22)	0.69	(0.43-1.11)
Fully vaccinated	0.60	(0.42-0.85)	0.70	(0.42-1.14)	0.69	(0.47-1.01)	0.67	(0.30-1.48)	0.89	(0.58-1.36)
Not-vaccinated	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
Primary case age										
0-10	2.69	(2.18-3.33)	2.29	(1.67-3.15)	2.43	(1.91-3.09)	2.27	(1.20-4.29)	-	-
10-20	0.93	(0.81-1.07)	0.83	(0.65-1.07)	0.92	(0.79-1.07)	0.72	(0.52-1.01)	0.91	(0.79-1.06)
20-30	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
30-40	1.88	(1.63-2.16)	1.59	(1.23-2.04)	1.90	(1.63-2.23)	1.19	(0.90-1.57)	1.85	(1.60-2.13)
40-50	2.19	(1.87-2.55)	1.40	(1.03-1.89)	2.15	(1.81-2.57)	1.67	(1.19-2.34)	2.15	(1.84-2.51)
50-60	2.06	(1.74-2.44)	1.46	(1.07-2.01)	2.06	(1.70-2.50)	2.04	(1.51-2.75)	2.04	(1.72-2.42)
60-70	2.90	(2.24-3.77)	2.55	(1.36-4.76)	2.99	(2.19-4.09)	2.16	(1.49-3.13)	2.83	(2.18-3.67)
70+	4.06	(2.73-6.03)	5.47	(2.30-13.05)	5.15	(3.16-8.39)	3.44	(2.09-5.68)	3.95	(2.66-5.87)
Potential secondary case age										
0-10	0.72	(0.61-0.84)	0.84	(0.64-1.10)	0.71	(0.60-0.85)	0.85	(0.54-1.34)	0.77	(0.65-0.90)
10-20	0.71	(0.62-0.81)	0.82	(0.64-1.04)	0.75	(0.64-0.87)	0.56	(0.38-0.82)	0.73	(0.64-0.84)
20-30	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
30-40	1.28	(1.11-1.48)	1.52	(1.19-1.94)	1.32	(1.12-1.55)	0.88	(0.65-1.19)	1.33	(1.15-1.55)
40-50	1.04	(0.90-1.19)	1.19	(0.93-1.51)	1.05	(0.90-1.23)	0.83	(0.61-1.15)	1.07	(0.92-1.24)
50-60	0.80	(0.69-0.92)	1.05	(0.80-1.37)	0.81	(0.69-0.96)	0.72	(0.53-0.97)	0.83	(0.72-0.97)
60-70	0.67	(0.53-0.83)	0.75	(0.49-1.15)	0.66	(0.51-0.85)	0.69	(0.48-0.99)	0.70	(0.56-0.88)
70+	0.46	(0.33-0.65)	0.37	(0.18-0.76)	0.53	(0.35-0.78)	0.44	(0.27-0.72)	0.48	(0.34-0.68)
Household size										
2	1.22	(1.08-1.37)	1.13	(0.92-1.40)	1.21	(1.07-1.38)	-	-	1.22	(1.09-1.38)
3	0.91	(0.82-1.01)	0.94	(0.78-1.13)	0.91	(0.81-1.03)	-	-	0.89	(0.80-1.00)
4	ref	(.)	ref	(.)	ref	(.)	-	-	ref	(.)
5	0.86	(0.75-0.99)	0.95	(0.76-1.19)	0.87	(0.75-1.01)	-	-	0.88	(0.76-1.02)
6	0.74	(0.58-0.93)	0.65	(0.43-0.98)	0.75	(0.57-0.98)	-	-	0.74	(0.57-0.95)
Primary case sex										
Male	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
Female	1.15	(1.08-1.22)	1.13	(1.01-1.25)	1.16	(1.08-1.24)	1.18	(1.00-1.39)	1.15	(1.08-1.23)
Potential secondary case sex										
Male	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
Female	1.07	(0.98-1.16)	1.08	(0.94-1.26)	1.07	(0.98-1.18)	1.02	(0.86-1.20)	1.07	(0.98-1.16)
Primary case sample date										
20DEC2021	0.81	(0.56-1.17)	-	-	0.89	(0.57-1.38)	0.86	(0.46-1.61)	0.79	(0.54-1.16)
21DEC2021	0.95	(0.65-1.41)	-	-	1.01	(0.63-1.62)	1.05	(0.54-2.04)	0.90	(0.60-1.35)
22DEC2021	1.10	(0.74-1.62)	-	-	1.21	(0.72-2.06)	0.91	(0.46-1.79)	1.09	(0.73-1.63)
23DEC2021	1.02	(0.68-1.54)	-	-	0.90	(0.55-1.46)	0.50	(0.25-1.01)	1.05	(0.69-1.60)
24DEC2021	1.14	(0.68-1.91)	-	-	0.98	(0.51-1.89)	0.59	(0.25-1.40)	0.97	(0.57-1.64)
25DEC2021	1.49	(0.93-2.39)	-	-	1.77	(0.91-3.43)	0.73	(0.31-1.73)	1.33	(0.81-2.19)
26DEC2021	1.14	(0.75-1.74)	-	-	0.87	(0.53-1.43)	0.79	(0.40-1.56)	1.10	(0.71-1.70)
27DEC2021	1.00	(0.70-1.43)	-	-	0.87	(0.58-1.31)	0.68	(0.38-1.23)	0.97	(0.68-1.40)
28DEC2021	0.93	(0.65-1.34)	-	-	0.86	(0.57-1.30)	0.65	(0.35-1.20)	0.91	(0.62-1.33)
29DEC2021	1.08	(0.69-1.67)	-	-	1.13	(0.68-1.87)	0.76	(0.36-1.59)	1.04	(0.66-1.64)
30DEC2021	0.90	(0.61-1.32)	-	-	0.77	(0.49-1.19)	0.80	(0.42-1.54)	0.86	(0.58-1.29)
31DEC2021	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
01JAN2022	0.91	(0.59-1.39)	-	-	0.80	(0.48-1.33)	0.97	(0.47-2.00)	0.84	(0.54-1.31)
02JAN2022	0.89	(0.64-1.24)	-	-	0.80	(0.55-1.16)	0.61	(0.35-1.07)	0.87	(0.62-1.22)
03JAN2022	0.86	(0.61-1.21)	-	-	0.76	(0.52-1.13)	0.70	(0.39-1.27)	0.84	(0.59-1.20)
04JAN2022	0.80	(0.51-1.25)	-	-	0.86	(0.50-1.49)	0.41	(0.18-0.94)	0.77	(0.48-1.22)
05JAN2022	0.65	(0.45-0.94)	0.68	(0.48-0.96)	0.59	(0.39-0.88)	0.40	(0.22-0.76)	0.64	(0.44-0.93)
06JAN2022	0.76	(0.52-1.11)	0.80	(0.56-1.15)	0.71	(0.46-1.08)	0.47	(0.24-0.90)	0.75	(0.50-1.12)
07JAN2022	0.81	(0.57-1.14)	0.85	(0.62-1.17)	0.74	(0.51-1.09)	0.63	(0.35-1.14)	0.76	(0.53-1.08)
08JAN2022	0.86	(0.58-1.27)	0.93	(0.64-1.34)	0.81	(0.52-1.26)	0.34	(0.16-0.73)	0.74	(0.48-1.13)
09JAN2022	0.94	(0.63-1.40)	0.99	(0.68-1.44)	0.81	(0.51-1.29)	0.86	(0.42-1.76)	0.91	(0.60-1.39)
10JAN2022	0.91	(0.63-1.30)	0.93	(0.66-1.30)	0.83	(0.55-1.24)	0.58	(0.30-1.11)	0.89	(0.61-1.31)
11JAN2022	0.96	(0.62-1.48)	ref	(.)	0.92	(0.58-1.45)	0.48	(0.21-1.11)	1.01	(0.64-1.60)
Number of observations	17,945		6,275		14,523		3,367		16,622	
Number of households	8,541		2,818		6,860		3,367		8,059	

Notes: This table provides model estimates for the main specification (model I) as well as different robustness specifications. 95% confidence intervals are shown in parentheses. Standard errors are clustered on the household level.

Table 13: Robustness II

Model	I		VI		VII		VIII		IX	
	OR	Main (95%-CI)	Excl. OR	prev. HH infect. (95%-CI)	Cases day 2-7 OR	(95%-CI)	Cases day 3-7 OR	(95%-CI)	Control for Ct OR	(95%-CI)
Potential secondary case, vaccination status										
<i>Omicron BA.1 households</i>										
Booster-vaccinated	0.65	(0.58-0.73)	0.59	(0.52-0.66)	0.67	(0.60-0.76)	0.72	(0.62-0.82)	0.57	(0.47-0.68)
Fully vaccinated	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
Not-vaccinated	1.23	(1.09-1.40)	1.07	(0.92-1.24)	1.24	(1.08-1.41)	1.17	(1.01-1.36)	1.14	(0.93-1.39)
<i>Omicron BA.2 households</i>										
Not-vaccinated	1.95	(1.37-2.78)	1.83	(1.24-2.71)	1.94	(1.34-2.82)	1.75	(1.17-2.60)	2.24	(1.31-3.83)
Fully vaccinated	2.45	(1.77-3.40)	2.56	(1.77-3.68)	2.30	(1.63-3.25)	2.02	(1.40-2.90)	2.29	(1.40-3.76)
Not-vaccinated	2.70	(1.95-3.74)	2.36	(1.65-3.36)	2.55	(1.81-3.59)	2.05	(1.42-2.97)	2.75	(1.65-4.60)
Primary case, vaccination status										
<i>Omicron BA.1 households</i>										
Booster-vaccinated	0.77	(0.67-0.88)	0.76	(0.65-0.88)	0.74	(0.64-0.85)	0.75	(0.64-0.88)	0.71	(0.56-0.89)
Fully vaccinated	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
Not-vaccinated	0.93	(0.80-1.08)	0.95	(0.80-1.12)	0.93	(0.80-1.10)	0.93	(0.78-1.11)	0.94	(0.75-1.18)
<i>Omicron BA.2 households</i>										
Booster-vaccinated	0.47	(0.32-0.71)	0.45	(0.29-0.70)	0.52	(0.34-0.79)	0.63	(0.40-0.98)	0.33	(0.18-0.61)
Fully vaccinated	0.60	(0.42-0.85)	0.60	(0.41-0.88)	0.64	(0.45-0.92)	0.72	(0.49-1.05)	0.57	(0.34-0.97)
Not-vaccinated	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
Primary case age										
0-10	2.69	(2.18-3.33)	2.66	(2.10-3.36)	2.74	(2.19-3.42)	2.96	(2.33-3.76)	2.23	(1.60-3.10)
10-20	0.93	(0.81-1.07)	0.87	(0.74-1.02)	0.98	(0.84-1.14)	1.02	(0.86-1.21)	0.85	(0.68-1.06)
20-30	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
30-40	1.88	(1.63-2.16)	1.84	(1.58-2.16)	1.88	(1.62-2.18)	1.94	(1.65-2.28)	1.66	(1.32-2.07)
40-50	2.19	(1.87-2.55)	2.15	(1.81-2.56)	2.01	(1.70-2.37)	1.98	(1.65-2.38)	1.86	(1.46-2.37)
50-60	2.06	(1.74-2.44)	2.08	(1.73-2.51)	1.98	(1.65-2.37)	2.02	(1.66-2.46)	1.80	(1.39-2.34)
60-70	2.90	(2.24-3.77)	2.86	(2.17-3.77)	2.61	(1.97-3.44)	2.51	(1.85-3.39)	2.72	(1.79-4.14)
70+	4.06	(2.73-6.03)	3.72	(2.46-5.64)	4.21	(2.78-6.38)	4.03	(2.62-6.21)	6.18	(2.87-13.32)
Potential secondary case age										
0-10	0.72	(0.61-0.84)	0.69	(0.58-0.83)	0.79	(0.67-0.93)	0.90	(0.75-1.08)	0.84	(0.65-1.08)
10-20	0.71	(0.62-0.81)	0.63	(0.54-0.74)	0.77	(0.67-0.89)	0.79	(0.67-0.93)	0.89	(0.72-1.10)
20-30	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
30-40	1.28	(1.11-1.48)	1.20	(1.03-1.40)	1.31	(1.12-1.52)	1.31	(1.11-1.54)	1.34	(1.07-1.67)
40-50	1.04	(0.90-1.19)	1.00	(0.85-1.17)	1.07	(0.92-1.25)	1.11	(0.94-1.31)	1.13	(0.90-1.40)
50-60	0.80	(0.69-0.92)	0.74	(0.63-0.87)	0.82	(0.70-0.97)	0.84	(0.70-1.00)	0.93	(0.74-1.17)
60-70	0.67	(0.53-0.83)	0.59	(0.47-0.75)	0.67	(0.53-0.85)	0.73	(0.56-0.94)	0.71	(0.49-1.02)
70+	0.46	(0.33-0.65)	0.44	(0.30-0.63)	0.49	(0.34-0.70)	0.52	(0.36-0.77)	0.53	(0.29-1.00)
Household size										
2	1.22	(1.08-1.37)	1.15	(1.02-1.31)	1.23	(1.09-1.40)	1.19	(1.04-1.36)	1.27	(1.06-1.52)
3	0.91	(0.82-1.01)	0.90	(0.80-1.01)	0.90	(0.80-1.02)	0.88	(0.77-0.99)	0.94	(0.80-1.11)
4	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
5	0.86	(0.75-0.99)	0.89	(0.76-1.04)	0.88	(0.76-1.01)	0.90	(0.77-1.04)	0.83	(0.67-1.02)
6	0.74	(0.58-0.93)	0.76	(0.57-1.01)	0.75	(0.59-0.97)	0.79	(0.61-1.03)	0.80	(0.56-1.15)
Primary case sex										
Male	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
Female	1.15	(1.08-1.22)	1.16	(1.08-1.24)	1.14	(1.06-1.22)	1.12	(1.03-1.20)	1.14	(1.03-1.26)
Potential secondary case sex										
Male	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
Female	1.07	(0.98-1.16)	1.09	(0.99-1.19)	1.06	(0.97-1.16)	1.06	(0.96-1.16)	1.08	(0.95-1.23)
Primary case sample date										
20DEC2021	0.81	(0.56-1.17)	0.80	(0.54-1.18)	0.78	(0.54-1.14)	0.95	(0.63-1.45)	0.92	(0.53-1.57)
21DEC2021	0.95	(0.65-1.41)	0.95	(0.63-1.42)	0.86	(0.58-1.28)	1.06	(0.68-1.65)	1.20	(0.68-2.15)
22DEC2021	1.10	(0.74-1.62)	0.97	(0.64-1.47)	1.05	(0.71-1.58)	1.33	(0.85-2.09)	1.32	(0.64-2.72)
23DEC2021	1.02	(0.68-1.54)	1.02	(0.66-1.57)	0.98	(0.65-1.47)	1.23	(0.78-1.94)	0.81	(0.43-1.55)
24DEC2021	1.14	(0.68-1.91)	1.21	(0.70-2.09)	1.15	(0.68-1.94)	1.29	(0.73-2.26)	1.00	(0.49-2.05)
25DEC2021	1.49	(0.93-2.39)	1.53	(0.91-2.57)	1.37	(0.84-2.22)	1.51	(0.88-2.59)	1.16	(0.51-2.63)
26DEC2021	1.14	(0.75-1.74)	1.17	(0.75-1.84)	0.85	(0.55-1.30)	0.94	(0.58-1.53)	1.07	(0.61-1.88)
27DEC2021	1.00	(0.70-1.43)	1.00	(0.69-1.46)	0.77	(0.53-1.11)	0.88	(0.58-1.33)	0.96	(0.59-1.56)
28DEC2021	0.93	(0.65-1.34)	0.93	(0.63-1.37)	0.82	(0.56-1.20)	0.85	(0.55-1.31)	1.00	(0.61-1.64)
29DEC2021	1.08	(0.69-1.67)	1.05	(0.66-1.68)	0.79	(0.49-1.26)	0.98	(0.58-1.66)	1.34	(0.74-2.40)
30DEC2021	0.90	(0.61-1.32)	0.82	(0.54-1.23)	0.85	(0.57-1.27)	1.08	(0.69-1.69)	0.97	(0.56-1.69)
31DEC2021	ref	(.)	ref	(.)	ref	(.)	ref	(.)	ref	(.)
01JAN2022	0.91	(0.59-1.39)	1.03	(0.65-1.61)	0.75	(0.48-1.16)	0.83	(0.51-1.36)	0.94	(0.50-1.76)
02JAN2022	0.89	(0.64-1.24)	0.86	(0.61-1.22)	0.72	(0.52-1.01)	0.80	(0.55-1.17)	0.89	(0.57-1.39)
03JAN2022	0.86	(0.61-1.21)	0.86	(0.60-1.24)	0.68	(0.48-0.97)	0.85	(0.57-1.27)	0.79	(0.51-1.21)
04JAN2022	0.80	(0.51-1.25)	0.85	(0.53-1.36)	0.73	(0.45-1.18)	0.78	(0.45-1.36)	0.77	(0.40-1.46)
05JAN2022	0.65	(0.45-0.94)	0.66	(0.45-0.96)	0.62	(0.43-0.90)	0.74	(0.49-1.13)	0.70	(0.42-1.16)
06JAN2022	0.76	(0.52-1.11)	0.77	(0.51-1.17)	0.68	(0.45-1.00)	0.81	(0.52-1.26)	0.80	(0.49-1.32)
07JAN2022	0.81	(0.57-1.14)	0.80	(0.56-1.15)	0.81	(0.57-1.14)	0.96	(0.65-1.41)	0.87	(0.56-1.36)
08JAN2022	0.86	(0.58-1.27)	0.88	(0.58-1.33)	0.84	(0.56-1.24)	1.00	(0.64-1.55)	0.86	(0.53-1.40)
09JAN2022	0.94	(0.63-1.40)	0.96	(0.63-1.45)	0.84	(0.56-1.27)	0.95	(0.60-1.49)	1.00	(0.55-1.84)
10JAN2022	0.91	(0.63-1.30)	0.87	(0.59-1.27)	0.78	(0.54-1.13)	0.88	(0.58-1.34)	0.79	(0.47-1.30)
11JAN2022	0.96	(0.62-1.48)	1.01	(0.64-1.61)	0.81	(0.52-1.27)	0.95	(0.58-1.57)	1.04	(0.63-1.73)
Ct value										
16-18	-	-	-	-	-	-	-	-	1.76	(0.73-4.23)
18-20	-	-	-	-	-	-	-	-	1.57	(0.97-2.53)
20-22	-	-	-	-	-	-	-	-	1.31	(1.00-1.71)
22-24	-	-	-	-	-	-	-	-	1.51	(1.20-1.90)
24-26	-	-	-	-	-	-	-	-	1.15	(0.92-1.42)
26-28	-	-	-	-	-	-	-	-	1.04	(0.83-1.30)
28-30	-	-	-	-	-	-	-	-	ref	(.)
30-32	-	-	-	-	-	-	-	-	0.90	(0.70-1.15)
32-34	-	-	-	-	-	-	-	-	0.74	(0.57-0.98)
34-36	-	-	-	-	-	-	-	-	1.05	(0.60-1.81)
Number of observations	17,945		14,497		16,765		15,678		7,349	
Number of households	8,541		7,119		8,206		7,861		3,505	

Notes: This table provides model estimates for the main specification (model I) as well as different robustness specifications. 95% confidence intervals are shown in parentheses. Standard errors are clustered on the household level.

Table 14: Relative effect of Omicron BA.2 vs. BA.1, by stratification

	Susceptibility			Transmissibility		
	Unvaccinated	Fully vaccinated	Booster vaccinated	Unvaccinated	Fully vaccinated	Booster vaccinated
Omicron BA.2 households	2.74 (1.76-4.27)	1.99 (1.26-3.16)	3.54 (1.86-6.76)	3.92 (2.49-6.16)	1.59 (1.10-2.29)	1.11 (0.58-2.14)
Omicron BA.1 households	ref (.)	ref (.)	ref (.)	ref (.)	ref (.)	ref (.)
Number of observations	4,631	7,838	5,476	3,500	10,659	3,786
Number of households	3,030	5,391	4,084	1,465	4,895	2,181

Notes: This table provides model estimates similar to Table 3, but with stratification of the sample. For the susceptibility estimates, we stratify by the vaccination status of the potential secondary case. For the transmissibility estimates, we stratify by the vaccination status of the primary case. 95% confidence intervals are shown in parentheses. Standard errors are clustered on the household level.