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# 1 Digital measurement of SARS-CoV-2 transmission risk from 7 2 million contacts

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20 Summary

How likely is it to become infected by SARS-CoV-2 after being exposed? Virtually everyone has wondered about this question during the COVID-19 pandemic. Contact tracing apps<sup>1,2</sup> recorded measurements of proximity<sup>3</sup> and duration between nearby smartphones. Contacts - individuals exposed to confirmed cases - were notified according to public health policies such as the 2-metre 15-minute guideline<sup>4,5</sup>, despite limited evidence supporting this threshold. Here we analysed 7 million contacts notified by the NHS COVID-19 app<sup>6,7</sup> in England and Wales to infer how app measurements translated to actual transmissions. Empirical metrics and statistical modelling showed a strong relation between app-computed risk scores and actual transmission probability. Longer exposures at greater distances had similar risk to shorter exposures at closer distances. The probability of transmission confirmed by a reported positive test increased initially linearly with duration of exposure (1.1% per hour) and continued increasing over several days. While most exposures were short (median 0.7 hours, IQR 0.4-1.6), transmissions typically resulted from exposures lasting one hour to several days (median 6 hours, IQR 1.4-28). Households accounted for about 6% of contacts but 40% of transmissions. With sufficient preparation, privacy-preserving yet precise

37 analyses of risk that would inform public health measures, based on digital contact  
38 tracing, could be performed within weeks of a new pathogen emerging.

39 **Introduction**

40  
41 Non-pharmaceutical measures such as social distancing, testing, contact tracing and  
42 quarantine are effective approaches to control the spread of epidemics, but they also  
43 entail significant social and economic costs<sup>8,9</sup>. It would be desirable to adjust these  
44 measures throughout an epidemic as epidemiological understanding increases or as the  
45 pathogen evolves. Optimising such interventions requires methods to quantify  
46 transmission risk factors.

47  
48 Despite the large amount of SARS-CoV-2 data collected globally, quantitative risk  
49 assessments at the level of individual exposures have been limited to a few large-scale  
50 manual contact tracing studies<sup>10,11</sup>. Another approach is provided by contact tracing  
51 apps on smartphones, which were implemented for COVID-19 in many countries. These  
52 apps digitised the process of contact tracing based on recording close-proximity events  
53 between smartphones<sup>1</sup>, performing quantitative risk assessment by measuring  
54 proximity<sup>3,12,13</sup> and duration of exposure to cases, although their real-life accuracy has  
55 been questioned<sup>14–17</sup>. Contact tracing apps are useful for public health if they are able to  
56 estimate the risk of pathogen transmission and should be evaluated to improve their  
57 functionality and ensure public trust<sup>2,18</sup>.

58  
59 For contact tracing and more generally for distancing guidelines, public health  
60 authorities worldwide often used a binary classification of risk, e.g. whether or not  
61 individuals spent 15 minutes or more at a distance of 2 metres or less from a case<sup>4,5</sup>.  
62 Contact tracing apps were calibrated to approximately match these heuristic rules. In  
63 the UK, which experienced a large-scale epidemic and implemented a substantial test-  
64 and-trace infrastructure, this advice led to more than 20 million notifications and  
65 quarantine requests from manual<sup>19</sup> and digital<sup>20</sup> contact tracing, with a peak of over 1.5  
66 million per week in July 2021. The socioeconomic costs could have been significantly  
67 mitigated by improved, fine-tuned guidelines for contact tracing and quarantine. Doing  
68 this would require two ingredients: (i) data and methods for quantitative assessment of  
69 how the probability of transmission varies with different factors, (ii) tools to measure  
70 those risk factors for contacts, to estimate their individual level of risk and respond  
71 appropriately.

72  
73 Digital contact tracing in England and Wales was implemented through the NHS  
74 COVID-19 App<sup>6</sup> which was active on 13 to 18 million smartphones each day during  
75 2021<sup>7</sup>. The app recorded measurements of the proximity and duration of exposure to an

76 index case using the privacy-preserving Exposure Notification framework<sup>21</sup> with custom  
77 analysis of Bluetooth signal attenuation between smartphones to estimate proximity<sup>22</sup>.  
78 By relating this data to whether the exposed individual subsequently reported a positive  
79 test through the app, we provide the first analysis of how the probability of SARS-CoV-2  
80 transmission varied with app-recorded measurements. We analysed 7 million exposure  
81 notifications from April 2021 to February 2022 comprising 23 million hours of cumulative  
82 exposure and 240,000 positive tests reported after notification. We demonstrate that the  
83 NHS COVID-19 app accurately translated proximity and duration of exposure into a  
84 meaningful epidemiological risk score and we quantify how these factors affected the  
85 actual probability of transmission.

## 86 Results

87 We use the term *case* to mean an individual whose infection was confirmed by testing,  
88 *index case* to mean a case who triggered a contact tracing process, and *contact* to  
89 mean an individual identified as having had some level of exposure to an index case  
90 (including, in general, individuals whose level of exposure is evaluated as being below  
91 some risk threshold).

92  
93 The NHS COVID-19 app assessed the transmission risk for a contact by partitioning the  
94 full exposure event into a set of non-overlapping ‘exposure windows’, each lasting at  
95 most 30 minutes. For each window, the app calculated a risk score<sup>23,24</sup>:

96 *Risk score = proximity score × duration within the 30-minute window × infectiousness*  
97 *score*

98 The proximity score was constant below 1 metre, and decreased as the inverse square  
99 of the distance if greater than 1 metre. A scaling of risk in proportion to duration follows  
100 from microbial risk assessment expectations. Infectiousness was scored as either  
101 ‘standard’, ‘high’ (2.5x), or zero depending on the timing of exposure relative to the  
102 index case symptom onset date (or positive test date when no symptom onset was  
103 recorded)<sup>23,25</sup>. For ease of interpretation, we normalised the risk score such that it  
104 equals 1 for an exposure at 2 metres’ distance from an index case with standard  
105 infectiousness for 15 minutes (i.e. the typical threshold for manual contact tracing),  
106 implying a maximum possible score of 20.

107  
108 Contacts were notified of a risky exposure if they had at least one exposure window with  
109 a risk score exceeding the threshold for notification, which was 1.11 with our  
110 normalisation (Extended Data Figure 1 shows the threshold in distance-duration space).  
111 When a contact was notified, their app sent anonymous exposure data to the central  
112 server. This data was sent in separate unlinked data ‘packets’, one for each exposure  
113 window that had a risk score over the notification threshold (about half of the contacts  
114 had more than one exposure window, see Extended Data Table 1). These packets

115 formed the basis for our analysis: we analysed only contacts who were notified and had  
116 at least one exposure above the risk threshold. We grouped windows likely to have  
117 come from the same contact as a recording of the whole exposure history between that  
118 contact and the associated index case (excluding windows below the notification  
119 threshold). If a given individual was notified multiple times during our study, each  
120 notification was treated as though it were of a separate contact due to the absence of  
121 unique identifiers.

122

123 The data also indicated whether the contact reported a positive SARS-CoV-2 test  
124 through the app during an interval beginning with their notification and ending 14 days  
125 after the exposure. The fraction of contacts doing so defines the *probability of reported*  
126 *infection*. This is a proxy for the true probability of being infected, though it is  
127 significantly underestimated: an unknown but likely appreciable fraction of infected app  
128 users either did not seek a test, or did not report their positive result through the app, or  
129 reported it outside of the aforementioned interval. As a reference, the number of  
130 infections in adults in the same period in the UK was 2-3 times greater than the number  
131 of cases<sup>26</sup>.

132

133 The linkage between exposure measurements and reported test positivity enables apps  
134 to be used for precision epidemiological estimation while preserving privacy. We  
135 analysed how contacts' exposure data, recorded in separate 30-minute windows, can  
136 predict their probability of reporting a positive test following their exposure. The peak  
137 risk experienced by an individual can be summarised by the maximum risk score  
138 measured by the app among all of their 30-minute exposure windows. This summary  
139 metric is what the app actually used: contacts were notified only when it was above the  
140 threshold. We found an increasing probability of reported infection as the maximum risk  
141 score increased (Figure 1a). This pattern holds irrespective of season or epidemic wave  
142 (Figure 1b). This simple analysis demonstrates that the approach used by the app to  
143 calculate risk correlates with the actual risk of transmission.

144

145 We defined two more summary metrics of risk measurements for each contact: the total  
146 duration of the exposure and the cumulative risk score, both aggregated over all  
147 exposure windows from the contact. Both of these metrics are more discriminatory than  
148 the maximum risk score. The probability of reported infection continues increasing as  
149 the duration and cumulative risk increase, even after several days of cumulative  
150 exposure (Figure 1).

151

152 These results suggest that the instantaneous level of risk and the duration of exposure  
153 both affect the risk of transmission. We also expect a background level of risk from  
154 exposures not recorded or not reported by the app; we estimated this level by

155 statistically modelling it as proportional to the local risk of infection among app users at  
156 that time (see Methods). We therefore stratified contacts by two summary metrics of  
157 their app-recorded measurements simultaneously: the duration of their exposure and  
158 their mean risk score per unit time. For each stratum of contacts we calculated the  
159 fraction reporting a positive test through the app during the observation window, as  
160 previously, now also subtracting the estimated background risk; we refer to the resulting  
161 quantity as the *probability of reported transmission*. (This differs from the *probability of*  
162 *reported infection* in that the background has been subtracted, and thus we attribute  
163 transmission to the exposures measured by the app. Both of these probabilities are  
164 lower than the corresponding true probabilities due to incomplete reporting.) As  
165 expected, we found that the level of risk measured by the app and the duration of the  
166 exposure both contribute to the probability of reported transmission (Figure 2). Duration  
167 is the more important predictor. For short exposures the probability of reported  
168 transmission grows linearly with duration at a rate of 1.1% per hour, increasing  
169 sublinearly only after a few hours (Extended Data Figure 2).

170  
171 These results suggest that overall risk is determined by contributions from each  
172 separate exposure window, with greater contributions from riskier windows, in addition  
173 to the background risk. To disentangle these effects we used a statistical model for  
174 combined contributions to overall risk, estimating the separate contributions from each  
175 window and from the background. We refer to these separate contributions from each  
176 exposure window as the *probability of reported transmission per exposure window*. We  
177 found that the probability of reported transmission per exposure window was  
178 proportional to the app's risk score for that window with remarkable accuracy,  
179 increasing by 0.3% per unit, providing validation that the app's risk calculation is  
180 epidemiologically meaningful. Figure 3 shows this relationship for exposures lasting  
181 between 1 and 3 hours. The relationship is robust with respect to individual  
182 heterogeneities or underreporting of positive tests among contacts (Extended Data  
183 Figure 3).

184  
185 Heterogeneities in the context of an exposure are expected to have a large effect on  
186 transmission risk. While the context is not recorded by the app, date and geographical  
187 area may be correlated with context and other causal factors. As an example, the  
188 probability of transmission from low-risk exposures is higher over the weekend than on  
189 weekdays (Extended Data Figure 4), while the probability of transmission appears to be  
190 lower in London and other conurbations than in rural and urban areas (towns and  
191 cities), particularly at the lower end of the risk spectrum (Extended Data Figure 4).

192  
193 The impact of transmission control measures that target risk factors is determined by  
194 the distribution of these factors in the population, as well as how predictive they are of

195 risk. Figures 4a-c show the population distributions over contacts of the maximum and  
196 cumulative risk score and the total duration of the exposure. We show the distributions  
197 separately for (i) all contacts, and (ii) transmissions, i.e. only those contacts who  
198 reported a positive test result through the app in the observation window, for whom we  
199 attributed the infection to the recorded exposure. All distributions are strongly left-  
200 skewed, with low risk scores and short durations most common among contacts, in  
201 agreement with previous observations in specific contexts such as university  
202 campuses<sup>27</sup>. Larger risk scores and longer durations are seen disproportionately more  
203 for transmissions than for all contacts, in keeping with our earlier results and  
204 mechanistic understanding of pathogen transmission risk. Across all contacts, most  
205 exposures are brief (median duration 40 minutes), yet most detected exposures that  
206 result in transmission last several hours (median duration 6 hours; 82% last more than 1  
207 hour) (Figure 4e), suggesting that contact tracing for SARS-CoV-2 would retain >80% of  
208 its effectiveness if applied with a threshold of one hour. Cumulative risk and duration  
209 show a bimodal distribution for transmissions; duration has a wide distribution (IQR 1.4-  
210 28 hours) with a peak at around 1-2 hours of exposure and another peak at around 1-2  
211 full days of cumulative exposure, the latter most likely corresponding to household  
212 contacts.

213  
214 To clarify the contribution of different exposure patterns and contexts to SARS-CoV-2  
215 spread, we classified contacts into four categories intended to approximately reflect  
216 different contexts: contacts exposed for at least 8 hours in a day (household contacts),  
217 non-household contacts with recurring exposures on multiple days, contacts exposed  
218 during a single day (between 30 minutes and 8 hours), and fleeting contacts (less than  
219 30 minutes). Household and recurring contacts accounted for 6% and 14% of all app-  
220 recorded contacts but were responsible for 41% and 24% of transmissions respectively  
221 (Figure 4d). The long duration of household exposures—33 hours on average—and  
222 their closer proximity explain their disproportionate role in transmissions (Extended Data  
223 Table 2).

224  
225 How effective are these app-measured predictors for binary risk classification for  
226 contacts? Panels e-f of Figure 4 show the sensitivity-specificity tradeoff among contacts  
227 from using different thresholds on duration. Extended Data Figure 5 shows the tradeoff  
228 for several predictors, including machine-learning classifiers using binned counts of risk  
229 scores and extra information such as background risk, date and region. There was a  
230 small improvement in classification by using duration or cumulative risk instead of  
231 maximum risk, and the only significant further gain came from the inclusion of  
232 background risk. In fact, duration and background risk alone were enough for a near-  
233 optimal prediction with an area under the receiver operating characteristic curve of 0.73.  
234

235 These quantitative risk measurements enable optimisation of a variety of management  
236 strategies based on simple and effective predictors such as duration of exposure to a  
237 case. As an example, we previously proposed milder ‘amber’ notifications as an  
238 alternative to quarantine for intermediate-risk contacts during the pandemic<sup>1,28</sup> and  
239 these were implemented in some settings<sup>29</sup>. If amber notifications would be optimally  
240 assigned for intermediate durations of exposure, pursuing an optimised strategy of PCR  
241 testing following an amber notification could reduce the socioeconomic costs of an  
242 illustrative intervention by 30-50% for a similar epidemiological impact (Extended Data  
243 Figure 6), or increased its effectiveness by 30-50% for similar costs (Extended Data  
244 Figure 7).

## 245 Discussion

246  
247 We performed the first large-scale study of how SARS-CoV-2 transmission probability  
248 varies with app-recorded risk measurements of the proximity and duration of exposures,  
249 analysing data from 7 million contacts notified by the NHS COVID-19 app in England  
250 and Wales. We found that the probability of infection strongly correlated with duration of  
251 exposure, as well as with the maximum and cumulative risk scores measured by the  
252 app. As a measure of proximity, the app’s risk score for individual exposure windows  
253 captured the relative probability of transmission with remarkable accuracy. Furthermore,  
254 the app-measured cumulative risk score was the best single predictor of probability of  
255 transmission among those tested, in agreement with expectations from microbial risk  
256 modelling (see Supplementary Methods Section 1.5). This provides highly encouraging  
257 validation for the risk modelling underlying the NHS COVID-19 App<sup>23,30</sup> and for future  
258 development of similar tools.

259  
260 Our results have immediate implications for contact tracing. We found that the  
261 cumulative duration of exposure to infected individuals is a key predictor of transmission  
262 in the COVID-19 pandemic, and needs to be accounted for in preparation for future  
263 epidemics of respiratory pathogens. Since duration of exposure to known cases can  
264 usually be recalled without the support of digital tools, it could be immediately  
265 incorporated into manual contact tracing interviews. Contacts should be notified and  
266 managed based on duration of exposure as well as other risk factors; knowledge  
267 transfer should prove relatively easy, e.g. through automated tools to support manual  
268 contact tracing staff with their interview-based risk assessment. Beyond identification of  
269 predictors of infection, our quantitative risk measurements also enable optimisation of  
270 different public health outcomes and epidemic management strategies such as amber  
271 notifications and post-exposure prophylaxis.

272

273 A result of particular importance beyond contact tracing is our empirical demonstration  
274 of the continuing increase in probability of transmission with the duration of exposure to  
275 an infected individual. Spending a long time at greater distance from an infected person  
276 carries similar risk to shorter times at smaller distances. ‘Physical distancing’ strategies  
277 to reduce risk should therefore consider the relevance of time as well as space. The  
278 continued increase in risk that we observed over multiple days shows that individuals  
279 can still benefit by beginning precautionary measures even after having already spent  
280 days exposed to an index case, for example in the same household.

281

282 The effectiveness of epidemic control measures depends on the population distribution  
283 of risk. Exposures are highly skewed towards short and low-risk encounters; on the  
284 other hand, transmissions are caused by exposures in a wide range of risk, with  
285 duration varying from an hour to several days. Our results can pave the way towards  
286 more targeted and graded interventions that account for the different frequency and risk  
287 of different exposures.

288

289 The main limitation of our analysis is the absence of data on the context of an exposure:  
290 setting, immunity, level of ventilation etc. The observed risks we report are averages  
291 over these unknown factors. Some of these factors might affect the risk score recorded  
292 by the app and the true risk in different ways: for example being indoors is linked to  
293 poorer ventilation, which increases true risk but not risk score. Manual tracing can  
294 obtain contextual data through interviews; in practice this data is sometimes used to  
295 assess risk, but it should be collected more systematically to build a more informed  
296 classification of risk. Recording direct or indirect information on the context of  
297 exposures, either through the app (e.g. by implementing indoor/outdoor detection) or  
298 linking it from external sources, could significantly improve risk assessment.

299

300 Another limitation of our study is the inclusion of exposures only when their risk score  
301 crossed the app’s notification threshold, excluding transmissions resulting from a large  
302 number of very low-risk exposures. These transmissions are likely to play a role in the  
303 spreading of SARS-CoV-2 in specific settings, but are unlikely to be a major driver of  
304 the epidemic. Also, testing was not compulsory for contacts, therefore infections were  
305 likely under-reported and absolute transmission rates must be interpreted with caution.  
306 Biases in testing or reporting, such as increased propensity to get tested after learning  
307 that a close contact tested positive, could also have affected our results.

308

309 In summary, if deployed at scale, contact tracing apps for infectious diseases have  
310 potential not only as interventions to reduce transmission<sup>6,7</sup> but also as tools to develop  
311 quantitative epidemiological understanding. Doing this and translating it into improved  
312 interventions takes time. We should strive to accelerate and improve this process as a

313 key step toward preparedness for future epidemics. Tools and methods for quantitative  
314 risk measurement and assessment should be further developed and integrated into the  
315 public health toolbox for the benefits they can bring now and in readiness for rapid  
316 deployment at the start of the next pandemic.

317

318 Recent decades have seen increasing focus on ‘personalised’ or ‘precision medicine’:   
319 using an individual’s biomarkers to inform their treatment and disease prevention.  
320 Epidemiological interventions that are concerned with population health, based on  
321 exposures and risks, have a long way to go to catch up. But the benefit of doing so is  
322 clear: dynamically tailoring responses according to individual risks measured at scale  
323 could turn blunt instruments into sharp ones. Digital contact tracing and the analysis  
324 presented here are a step forward on the path to precision epidemiology.

325

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399            Exposure Notification Framework to Inform Quarantine Recommendations. *Risk Anal.* **42**,  
400            162–176 (2022).

401

402 **Figure legends**

403

404 **Figure 1: App risk score and duration of exposure correlate with probability of**  
405 **infection.** (a) The probability of reported infection, i.e. the probability of a contact  
406 reporting a positive test through the app shortly after receiving an exposure notification,  
407 as a function of three summary metrics of their exposure measurements ('predictors'): (i)  
408 the maximum risk score from any exposure window (each lasting 30 minutes), (ii) the  
409 cumulative risk score, summed over all exposure windows, (iii) the total duration of the  
410 exposure, summed over all exposure windows. The grey point illustrates our estimate  
411 for the probability of reported infection after 15 minutes at 2 metres' distance from an  
412 individual with standard infectiousness. Black points in the top panels indicate the bins  
413 used for the risk predictor. (b) Probability of reported infection disaggregated by month  
414 of notification. Central values correspond to maximum likelihood estimates, shading and

415 (small) whiskers indicate the 95% confidence intervals ( $n=7,047,541$  contacts).  
416 Tabulated values can be found in Supplementary Tables S6,S7.  
417  
418  
419 **Figure 2: The probability of transmission is affected by both duration and**  
420 **proximity as captured by the risk score.** Log-log plot of the probability of reported  
421 transmission, i.e. the probability that the contact reported a positive test that we  
422 attributed to the transmission event traced, as a function of the binned duration of  
423 exposure and the mean risk score per hour (i.e. cumulative risk score divided by  
424 duration). The solid lines connect the maximum likelihood estimates for each bin and  
425 the shading around these shows the 95% confidence intervals. Tabulated values can be  
426 found in Supplementary Table S8.

427  
428  
429 **Figure 3: The transmission probability per exposure window increases almost**  
430 **linearly with risk score.** The probability of reported transmission per exposure window,  
431 i.e. the estimated probability of transmission in an individual 30-minute exposure  
432 window followed by reporting of a positive test, as a function of the app-measured risk  
433 score for that window. Points show the maximum-likelihood estimate ( $n=2,507,879$   
434 contacts); error bars on the points indicate the 95% confidence intervals. We fit a  
435 weighted robust linear regression without intercept to the points, with shading around  
436 the line indicating the 95% confidence intervals in its gradient, highlighting that the  
437 probability of reported transmission is proportional to the app-measured risk score.  
438 Tabulated values can be found in Supplementary Table S9.

439  
440  
441 **Figure 4: Short, intermediate and long exposures all contribute to SARS-CoV-2**  
442 **transmissions in the population.** Distributions over contacts of summary metrics for  
443 their app-recorded exposure measurements, shown separately for all contacts in the  
444 dataset (all of whom were notified, shown in blue) and for ‘transmissions’, i.e. only those  
445 contacts who reported a positive test result through the app in the observation window,  
446 for whom we attributed the transmission to the recorded exposure rather than the  
447 background risk (shown in red). Panel a: the distribution of the maximum risk score.  
448 Panel b: the distribution of the duration of exposure. Panel c: the distribution of the  
449 cumulative risk score over all exposure windows. Panel d: categories of contacts  
450 reflecting the context of their exposure. The first bar shows the fraction of contacts in  
451 each category; the other bars show the fraction of the overall cumulative duration of  
452 exposure, cumulative risk score and number of transmissions that are associated with  
453 each category. Panel e: the fraction of all actually traced transmissions that would still

454 be traced if only contacts with exposures longer than a given duration would be traced.  
455 This relative effectiveness of contact tracing at different thresholds corresponds also to  
456 the reduction in  $R_t$  in a counterfactual scenario with a higher notification threshold  
457 relative to the reduction in  $R_t$  in the factual scenario. Panel f: the fraction of contacts  
458 being infected during the recorded exposure and reporting a positive test, i.e. the ratio  
459 of transmissions to contacts, among all contacts with exposures longer than a given  
460 duration. Shading at the top of the bars in panels e-f shows the 95% confidence  
461 intervals from uncertainty on background risk. Tabulated values can be found in  
462 Supplementary Table S10.

463

464

## 465 Methods

466

467 For all Methods subsections, greater detail is provided in Supplementary Methods.

468

### 469 Data

470

471 All data for this study comes from contacts notified by the NHS COVID-19 contact  
472 tracing app between April 2021 and February 2022 inclusive. The data generating  
473 process for app data was non-trivial: the primary aim was successfully implementing a  
474 privacy-preserving and data-minimising contact tracing process, not generating data for  
475 epidemiological study. We analysed data recorded by the app with three different  
476 timings/frequencies: first, daily ‘analytics’ data; second, exposure data sent when a contact  
477 is notified of risky exposure; and third, exposure data sent when a contact  
478 reports a positive test. Nowhere in the data is there a unique identifier for each app  
479 user, and so connecting these three data sources required some application of logic,  
480 some assumption, and some subsetting of the data. We next explain each of these  
481 three data sources in turn.

482

483 First, we have described the daily analytics data previously<sup>6,7</sup>. Each correctly functioning  
484 installation of the app sent one ‘analytics packet’ of data daily (at midnight, regardless  
485 whether the user was notified that day). Each packet indicated whether or not the app  
486 user was notified of risky exposure on that day, and included four fields of ‘individual  
487 characteristics’ which we assumed were usually constant for an individual over the time  
488 scale of one round of contact tracing and testing (i.e. are effectively constant for the  
489 individual): their device model (e.g. ‘iPhone X’), their operating system version on this  
490 device, the postcode district (an area with mean population size of about 20,000  
491 individuals) in which they reported residing, and their lower-tier local authority (LTLA, if  
492 ambiguous from the postcode district).

493

494 Second, when a contact was notified of a risky exposure to an anonymous case, their  
495 app sent one ‘event packet’ of data to the central server for each exposure window  
496 (lasting a maximum of 30 minutes) that had a risk score over the threshold for  
497 notification. These were sent separately from the daily analytics packets, and only at the  
498 time of notification. Data about proximity to any individual not reporting a positive test  
499 are never sent to the central server. Event packets included information on exposure  
500 proximity, duration and date, and the same four fields of individual characteristics as in  
501 the daily analytics packets. Events packets contained no information about the index  
502 case to whom the contact was exposed (such information is irretrievable by the app by  
503 design) except for whether their infectiousness at the time of exposure was encoded as  
504 ‘high’ or ‘standard’. If a single continuous exposure event lasted more than 30 minutes,  
505 it was automatically split into multiple exposure windows that were considered  
506 separately; multiple exposures occurring at different times (i.e. a discontinuous meeting  
507 between the individuals) also resulted in separate exposure windows. Risk calculations  
508 were performed separately on each exposure window. As explained in Results, the  
509 overall risk score used by the app for each window was calculated by multiplying scores  
510 from proximity, duration and index infectiousness, and we normalised these overall  
511 scores by the value for a 15-minute exposure to an index case of standard  
512 infectiousness at a proximity of 2m. With this normalisation the threshold for notification  
513 used by the app was a risk score of 1.11 throughout the period analysed; this value was  
514 chosen as part of the intervention deployment, not as part of analysis here.

515

516 Third, if an individual reported a positive test in the app during the ‘observation  
517 interval’—starting with their notification and ending 14 days after the exposure—the  
518 same event packets that were sent when the individual was notified were sent once  
519 more to the central server, identical except for a flag indicating that this is the report-  
520 positive stage not the notification stage.

521

522 Jointly analysing the second and third data sources—the event packets sent at  
523 notification and again at positive test—we could assign to each exposure window the  
524 binary outcome of ‘positive test reported or not’. This follows because we could see  
525 which event packets were sent a second time with all data fields identical except for the  
526 flag indicating either notification or report-positive stage, and which event packets were  
527 not. An assignment of a reported-positive-test outcome to a given exposure window  
528 does not imply that that exposure window was causal for the individual becoming  
529 infected: the transmission event could have been caused by background risk or by any  
530 other exposure window for the same contact if they had multiple exposure windows.

531

532 When more than one risky exposure window was recorded between a contact and the  
533 index case, these were analysed separately for the risk calculation and sent as separate  
534 event packets to the central server. The absence of a unique individual identifier means  
535 that in general one cannot know whether  $N$  event packets sent on the same day (as  
536 determined by the date received centrally) with matching individual characteristics for  
537 the contact (device model, operating system version, postcode district and LTLA) were  
538 sent by (i) 1 contact with  $N$  risky exposure windows, or (ii)  $N$  contacts, who were notified  
539 on the same day and had matching individual characteristics, with 1 risky exposure  
540 window each, or (iii) anything in between. We therefore restricted the dataset of event  
541 packets to an unambiguous subset constructed as follows. From the daily analytics data  
542 we identified the subset of notifications (of risky exposure) when exactly one contact  
543 with a given combination of individual characteristics was notified on a given day; for  
544 each such notification, we assumed that all event packets with identical characteristics  
545 originated from the same contact, i.e. scenario (i) above. When more than one contact  
546 with given characteristics was notified on a given day, all event packets that day with  
547 those characteristics were excluded from analysis for simplicity. This procedure for  
548 grouping multiple event packets as being from the same contact is specifically for a  
549 single notification event of a given contact: if the same individual is notified multiple  
550 times during our study, each notification event (which will be at least a quarantine period  
551 apart from other notifications, by design) is treated as being from a separate individual,  
552 with a set of event packets associated to each event.

553  
554 Extended Data Table 1 summarises sample sizes for the final dataset analysed in this  
555 paper. Supplementary Table S1 summarises sample sizes and aspects of the events  
556 packet data at three of the stages described above: before and after the grouping stage,  
557 and also for only those contacts who reported a positive test. The grouping stage—  
558 subsetting to instances when only a single contact with given characteristics was  
559 notified on a given day, for which the matching event packets can be grouped as from  
560 one contact—retains 60% of the events packets.

561  
562 **Empirical estimation of individuals' probability of testing positive from summary  
563 statistics**

564  
565 In general, each contact in our dataset had multiple exposure windows, each of which  
566 had a duration (anything up to 30 minutes) and a risk score. We summarised this data  
567 for each contact into metrics including the maximum risk score from any of the windows,  
568 the cumulative risk score over all windows, and the cumulative duration over all  
569 windows. We binned (grouped) contacts by the value of their summary metrics, and  
570 within each bin calculated the fraction of contacts reporting a positive test in the  
571 observation interval. Confidence intervals on this fraction were calculated through the

associated binomial distribution (defined with the number of ‘trials’ equal to the group size and the number of ‘successes’ equal to the number of contacts reporting a positive test). We extrapolated our estimates to risk score 1 (i.e. 2 metres away from an index case with standard infectiousness for 15 minutes, indicated with a grey circle in Figure 1 as a point of comparison) via a quadratic fit. In Figures 2 and 4, the background risk estimate from the maximum-likelihood approach outlined below was subtracted from the result. In all figures, the x coordinate for each bin corresponds to the mean of all scores within the bin.

580

## 581 Statistical modelling of the per-exposure-window probability of transmission

582

583 In reality, a given individual that reported a positive test was either infected by the  
584 background, or was infected in their first recorded window, or in their second recorded  
585 window etc. but which of these was actually the case is unknown. Hence we modelled  
586 the process in terms of risk parameters, shared between individuals, which are to be  
587 estimated. We developed a statistical model for the separate contributions to each  
588 individual's overall risk from each of their exposure windows and from background risk.  
589 Specifically, we modelled the probability of individual  $i$  *not* reporting a positive test  
590 during the observation interval as

591  $(1 - B_i) \times (1 - P_t(i\text{'s first window})) \times (1 - P_t(i\text{'s second window})) \times \dots \times (1 - P_t(i\text{'s last})$   
 592  $\text{window}))$

where  $B_i$  is the probability of background transmission (followed by reporting a positive test), and  $P_t(i's\ nth\ window)$  is the probability of transmission during the  $i$ 's  $n$ th window (followed by reporting a positive test). The justification for this form is that if an individual does not report a positive test, this implies that they were not infected by the background (with subsequent reporting) and were not infected during their first window (with subsequent reporting) and not during their second window etc. The probabilities for each of these events not happening should thus be multiplied together to give the overall probability for none of them happening. We modelled  $B_i$  as  $1 - (1 - b_i)^\beta$ , defining  $b_i$  as the sum, over the 14 days following  $i$ 's notification, of the weekly-smoothed mean daily fraction of geographically matched not-recently-notified app users that reported a positive test (and  $\beta$  is the associated regression coefficient for this term). For small values of  $b_i$  the background risk is simply rescaled by a factor  $\beta$ , i.e.  $B_i \approx \beta b_i$ ; for larger values of  $b_i$  the functional form accounts for saturation of risk. We modelled  $P_t(i's\ nth\ window)$  as depending only on the risk score recorded by the app for  $i$ 's  $n$ th window. We binned risk scores into 8 bins, defining a single independent  $P_t$  parameter for each bin, such that the expression above could be rewritten

$$609 \quad (1 - B_i) \times \prod_{j=1}^8 (1 - P_{t,i}(\text{bin } j))^{\text{(number of windows from } i \text{ with risk score in bin } j)}$$

610 The probability that an individual  $i$  would report a positive test during the observation  
611 interval is one minus the expression above (the expression for them *not* reporting a

positive test in the interval). The likelihood is given by the product of all individuals' probabilities for their reported outcome for testing positive. We maximised the likelihood to estimate the parameters  $\beta$  and the per-window transmission probability for each of the 8 bins of risk score, plotted in Figure 3, and profiled the likelihood to obtain the confidence intervals. Figure 3 shows that the per-window transmission risk estimated for each of the 8 bins is proportional to the app-recorded risk score of that bin. We used a binning approach to allow the data to reveal this proportionality—instead of taking it to be true as a modelling assumption—because this proportionality serves as validation for the app's risk score capturing real risk.

As a robustness check, we developed likelihoods based on frailty models with several sources of heterogeneity among case-contact pairs in the model (see Supplementary Methods Section 1.6.2).

## Predictors and machine-learning classifiers

As basic input predictors for machine learning we used the maximum, mean and cumulative risk score, the duration, and the number of exposures in each bin of risk score. Additional predictors include date, region, rural/urban score, background rate of infections, day of the week with more exposure windows and peak daily duration. Classifiers used include logistic regression, gradient boosting machines<sup>31</sup> and extreme gradient boosting XGBoost<sup>32</sup> with 10, 100 and 400 rounds. Optimal strategies for amber notifications were obtained using a general approach for targeted interventions<sup>33</sup> presented in Supplementary Discussion.

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655 (DHSC).

656 **Author contributions**

657 L.F., C.W., J.P., A.L., M.C., M.B., C.F. conceptualised this work. L.F., C.W., J.P., A.F.,  
658 M.K., D.T., C.F. did the analyses. All authors contributed to the writing and reviewing of  
659 this manuscript.

660 **Competing interests**

661 L.F., C.W., and C.F. were named researchers on a grant from DHSC to Oxford University. M.K.  
662 has a data sharing agreement with UKHSA. D.T. was an employee of Zühlke which provided  
663 consultancy to UKHSA. M.C., M.B., A.L., J.P.G. and A.D.F. were employees or affiliated to  
664 UKHSA.

665

666 **Additional information**

667 Supplementary Information is available for this paper. Correspondence and requests for  
668 materials should be addressed to Luca Ferretti <[luca.ferretti@bdi.ox.ac.uk](mailto:luca.ferretti@bdi.ox.ac.uk)> and Christophe  
669 Fraser <[christophe.fraser@bdi.ox.ac.uk](mailto:christophe.fraser@bdi.ox.ac.uk)>.

670 **Data availability statement**

671 Data access is managed by UKHSA, who will make available on request the data needed to  
672 replicate the key results, either via the UK Data Service or through direct request for data  
673 access to UKHSA (details on the process can be found at  
674 <https://www.gov.uk/government/publications/accessing-ukhsa-protected-data>). Access is  
675 controlled for privacy reasons.

676 **Code availability statement**

677 Code to replicate the analysis will be made available as part of the data sharing process by  
678 UKHSA at [https://github.com/ukhsa-collaboration/risk\\_scoring\\_nhs\\_covid19\\_app](https://github.com/ukhsa-collaboration/risk_scoring_nhs_covid19_app).

679

680 **Extended Tables**

681

682 *Extended Data Table 1: Summary statistics for the NHS COVID-19 app exposure dataset.*  
683 We report statistics only for exposure windows that were successfully grouped and assigned to  
684 a single contact. These windows represent about 60% of the whole dataset. See Supplementary  
685 Table S1 for further details on the raw exposure window data before the grouping stage.

686

687

688 *Extended Data Table 2: Summary statistics for different types of contacts in our dataset.*

689 Household contacts (defined as contacts whose exposures cover more than 15 windows in a  
690 single day), recurring contacts (defined as non-household contacts whose multiple exposure  
691 windows occur on two different days or more), one-day contacts (defined as non-household  
692 contacts whose multiple exposure windows occur all in a single day) and fleeting contacts  
693 (defined as contacts with a single exposure window).

694

695 **Extended Figures**

696

697 *Extended Data Figure 1: The app has more nuanced distance-duration rules than*  
698 **manual contact tracing.** Coloured regions show regions of the distance-duration space  
699 where contacts are notified digitally (depending on the infectiousness of the index case)  
700 or manually. These boundaries apply in theory, though in practice distances are  
701 imperfectly estimated from Bluetooth signal attenuation.

702

703

704 *Extended Data Figure 2: The probability of transmission depends linearly on*  
705 **duration and cumulative risk for short exposures, then sublinearly.** Log-log plots of  
706 the probability of reported infection (the fraction of notified contacts who report a  
707 positive test shortly after notification) and transmission (subtracting the maximum-  
708 likelihood correction for background risk) as a function of cumulative risk score and  
709 duration of exposure. Points correspond to maximum likelihood estimates. The brown  
710 bands show the 95% confidence interval for linear regressions on the points shown, i.e.  
711 a power-law relation between risk predictors and the probability of reporting a positive

712 test. The maximum-likelihood estimates for the exponents are  $P_t \sim r_{cum}^{0.46 \pm 0.01}$ ,  $P_t \sim$   
713  $d^{0.47 \pm 0.01}$  (infection) and  $P_t \sim r_{cum}^{0.69 \pm 0.04}$ ,  $P_t \sim d^{0.76 \pm 0.04}$  (transmission). For the regressions  
714 of the probability of transmission, when restricting to low values of the risk predictor  
715 (cumulative risk <20, duration <3 hours), the relationships were approximately linear:  $P_t \sim r_{cum}^{0.95 \pm 0.07}$ ,  
716  $P_t \sim d^{0.99 \pm 0.09}$  (orange bands), as expected from theoretical arguments. The  
717  $\pm$  values shown in the exponents are standard deviations.

718

719

720 **Extended Data Figure 3: The monotonic relationship between the risk score per**  
721 **window and the probability of transmission in that window is robust with respect**  
722 **to the inclusion of individual heterogeneities in the model.** Maximum-likelihood  
723 estimates of the probability of reported transmission per exposure window, i.e. the  
724 estimated probability of transmission in an individual exposure window followed by  
725 reporting of a positive test, as a function of the binned app-measured risk score for that  
726 window. The grey line and shading show the maximum-likelihood monotonic risk (and  
727 the corresponding 95% CI) shown in Figure 3. Lines of different colours show  
728 maximum-likelihood estimates from models that do not assume monotonicity; these  
729 models include positive-test ascertainment and/or different functional forms for  
730 heterogeneities in risk (see Supplementary Methods Section 1.6.2).

731

732

733 **Extended Data Figure 4: The transmission probability per exposure window**  
734 **decreases for contacts located in conurbations and increases for low-risk**  
735 **exposures during the weekend.** The probability of reported transmission per exposure  
736 window, i.e. the estimated probability of transmission in an individual 30-minute  
737 exposure window followed by reporting of a positive test, is shown as a function of the  
738 app-measured risk score for that window, as in Figure 3 but with stratifications of  
739 contacts. Panel a: Stratification by weekday or weekend. Panel b: Stratification by rural  
740 area, urban area (town or city) and conurbation (urban agglomeration). Lines connect  
741 the maximum-likelihood estimates for each bin; shaded areas indicate 95% confidence  
742 intervals.

743

744

745 **Extended Data Figure 5: Duration and cumulative risk are the best predictors of**  
746 **infection, only marginally improved by machine learning.** Sensitivity/specificity  
747 (receiver operating characteristic) curve for different methods and thresholds to classify  
748 individuals exposed to an index case as at risk or not. Our dataset contained only  
749 individuals who were actually notified; we varied the classification thresholds to  
750 interpolate between continuing to notify all of these individuals (top right) and notifying  
751 none of these individuals (bottom left). Different colours show different classification  
752 methods. For each method we varied thresholds to explore their balance between

753 sensitivity (notifying individuals who would report a subsequent positive test) and  
754 specificity (not notifying individuals who would not). ML abbreviates machine learning,  
755 AUC the area under the curve.

756

757

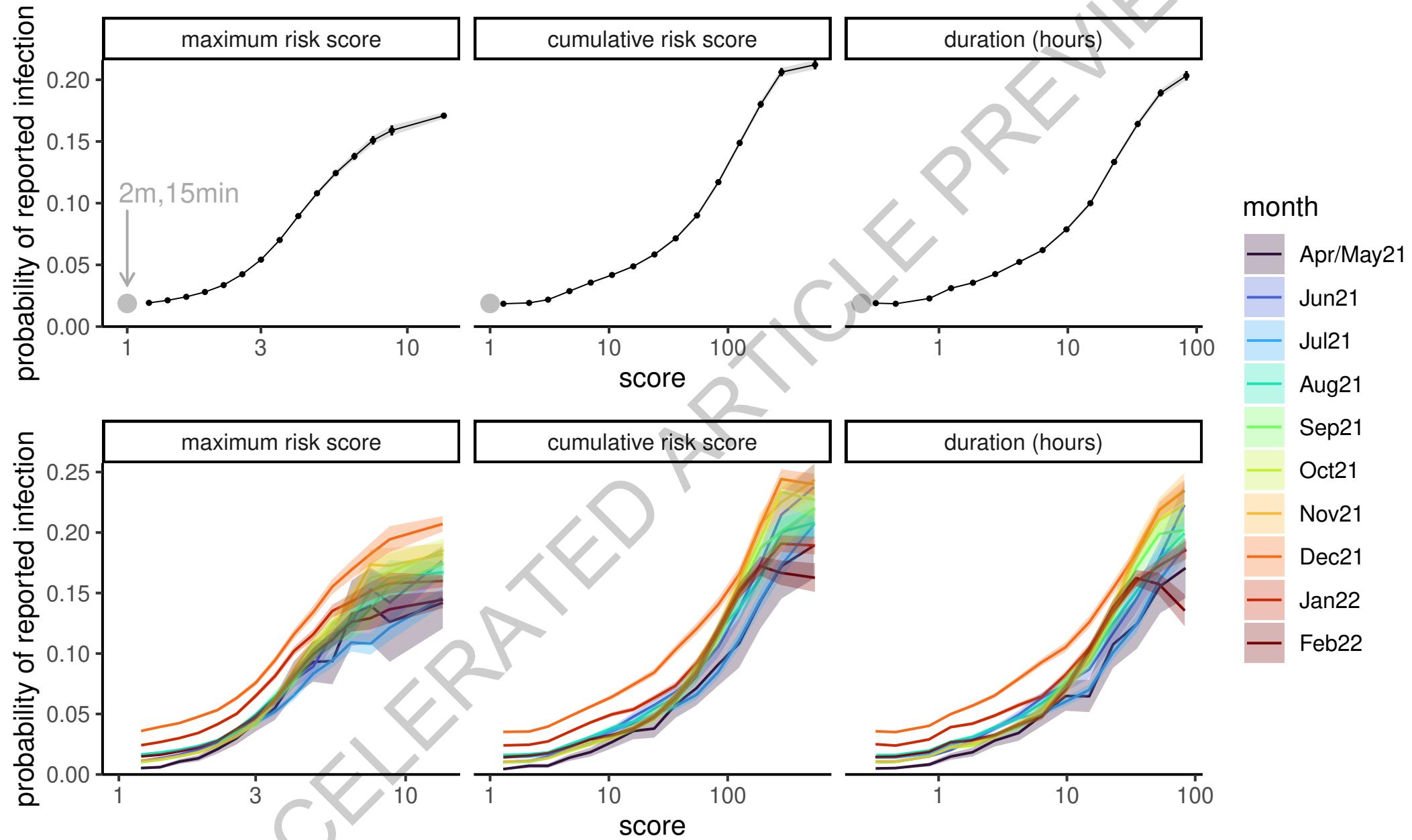
758 **Extended Data Figure 6: Illustration of optimal strategies to reduce social costs of**  
759 **contact tracing via amber/red alert notifications.** In this illustrative scenario we  
760 considered combinations of three measures: red notification leading to quarantine after  
761 notification, amber notification leading to PCR test after notification (followed by self-  
762 isolation if positive), and no notification. We assume that the risk of infection would be  
763 assessed based on duration of exposure. We consider optimal strategies leading to  
764 minimisation of total costs for patient and public health for a given epidemiological  
765 effectiveness; see Supplementary Discussion for details and assumptions on relative  
766 costs and effectiveness. Panel a: each horizontal line represents an optimal strategy  
767 (quarantining high-risk contacts, testing intermediate-risk contacts, not tracing low-risk  
768 contacts) that has the same effectiveness as a baseline quarantine-only strategy for  
769 contacts above a threshold duration of exposure (y axis). Panel b: the decrease in cost  
770 of the optimal strategy relative to the baseline strategy (quarantine for all traced  
771 contacts).

772

773

774 **Extended Data Figure 7: Illustration of optimal strategies to increase effectiveness**  
775 **of contact tracing via amber/red alert notifications.** Same as Extended Data Figure  
776 6, but considering optimal strategies that keep the total costs fixed while maximising  
777 epidemiological effectiveness. Panel a: each horizontal line represents an optimal  
778 strategy that has the same cost as a baseline quarantine-only strategy for contacts  
779 above a threshold duration of exposure (y axis). Panel b: the increase in effectiveness  
780 of the optimal strategy relative to the baseline strategy.

781



probability of reported transmission

0.100

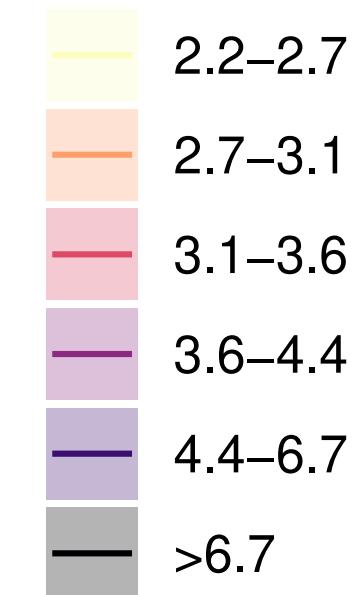
0.030

0.010

0.003

duration (hours)

risk score  
per hour



probability of reported transmission  
per exposure window

0.020

0.015

0.010

0.005

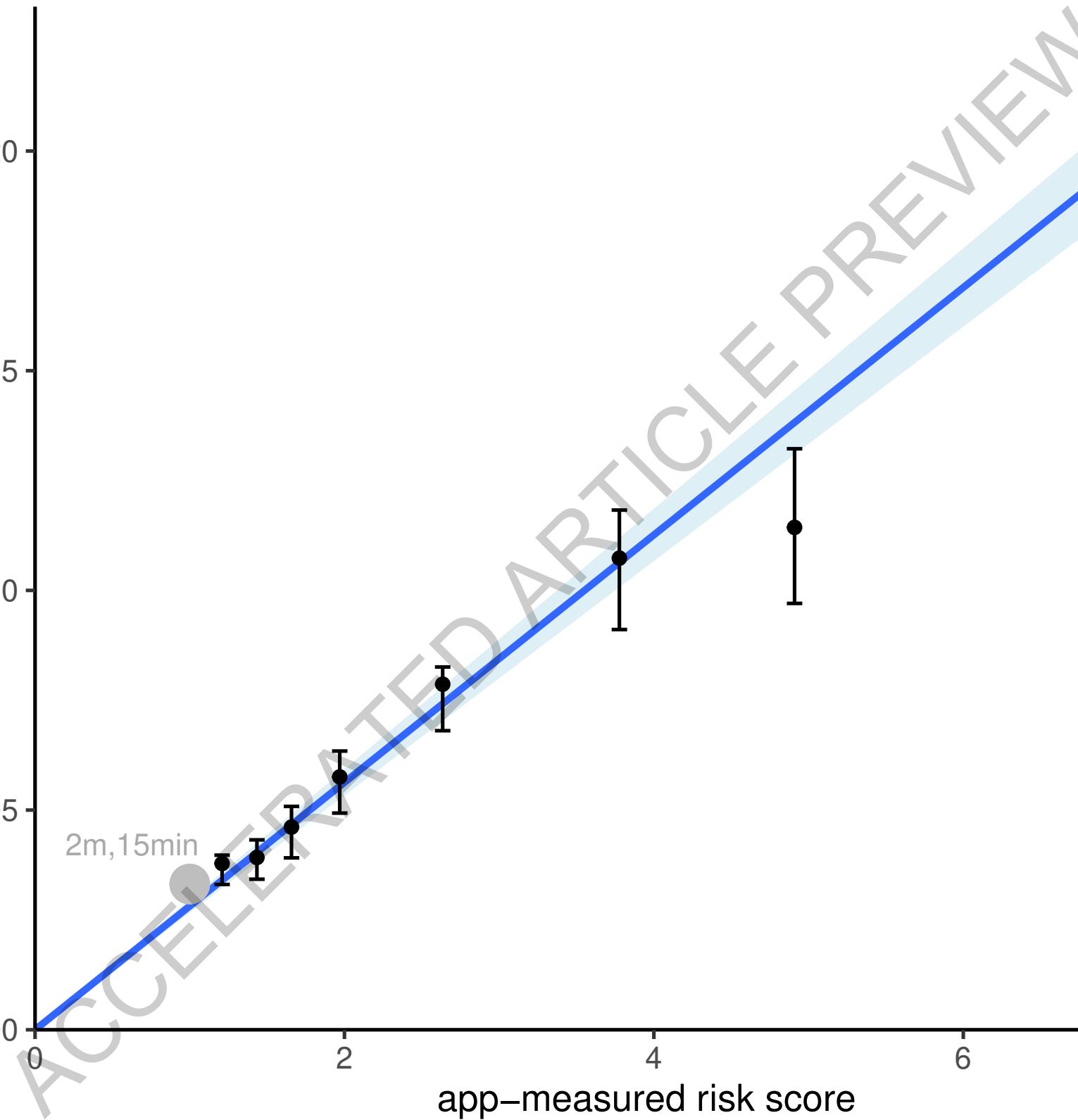
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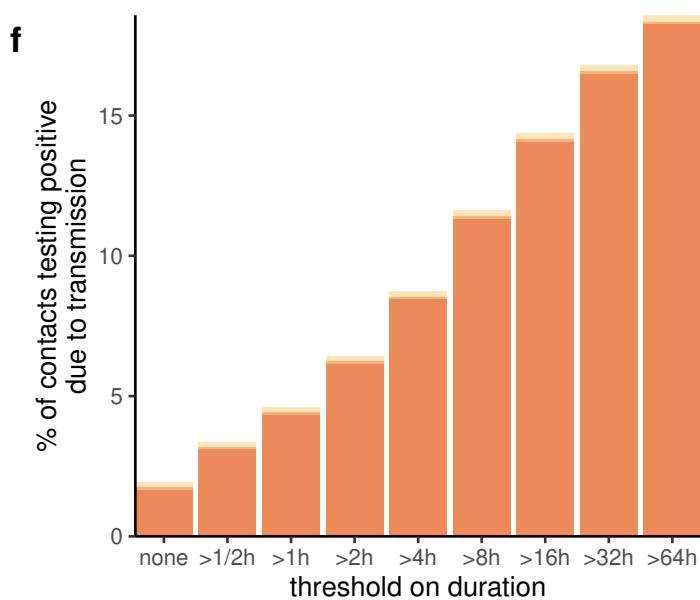
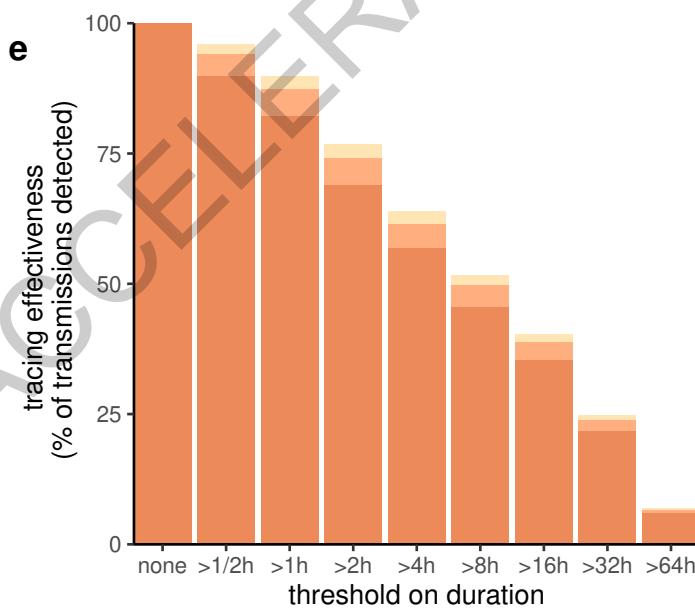
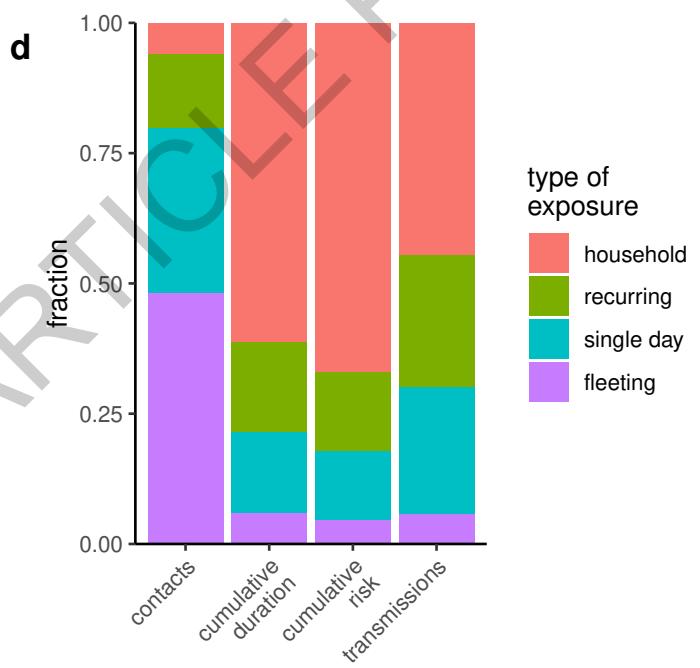
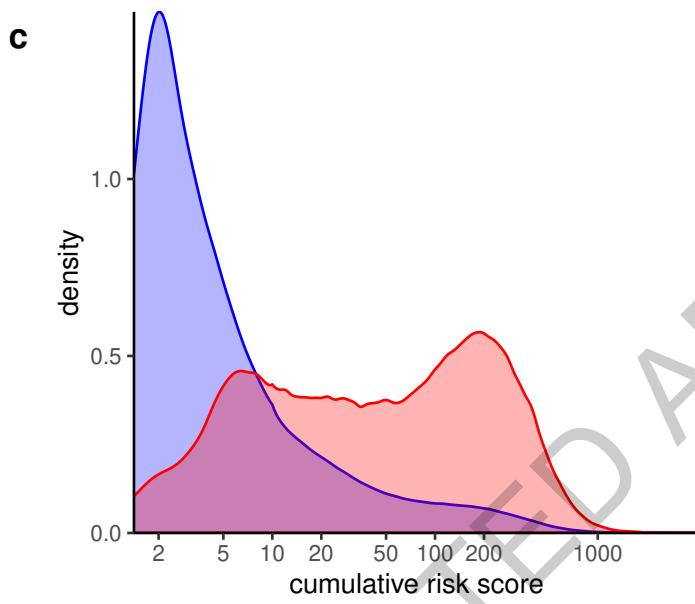
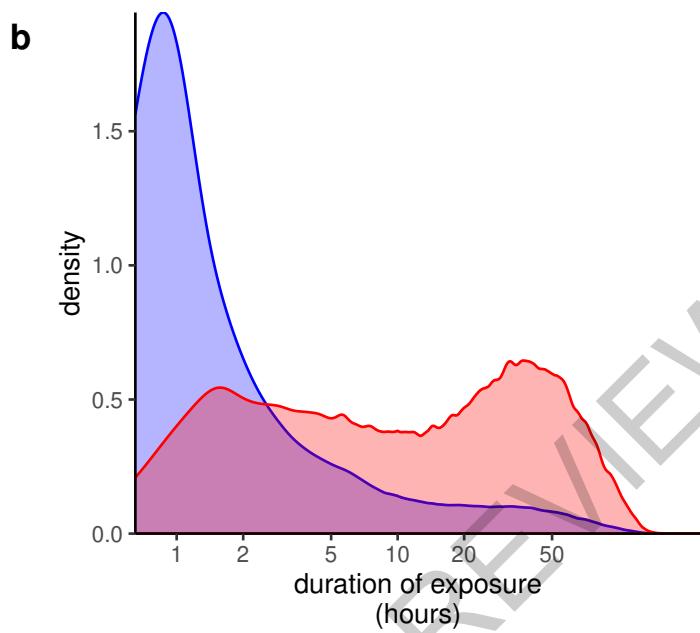
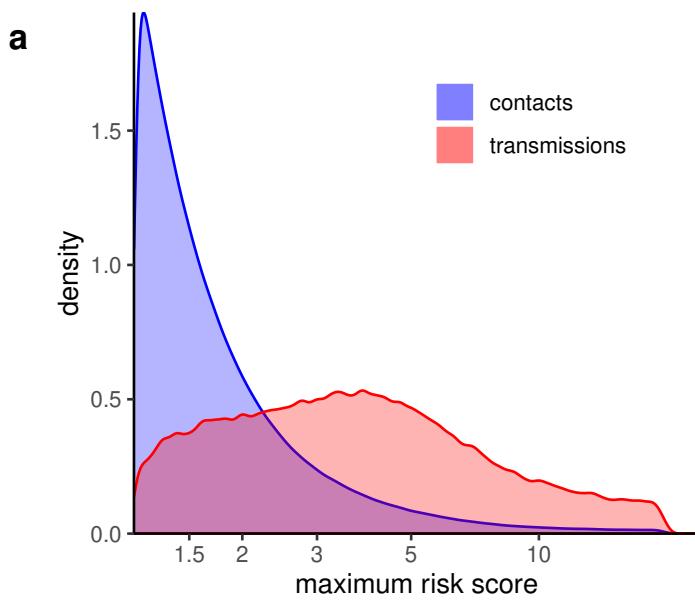
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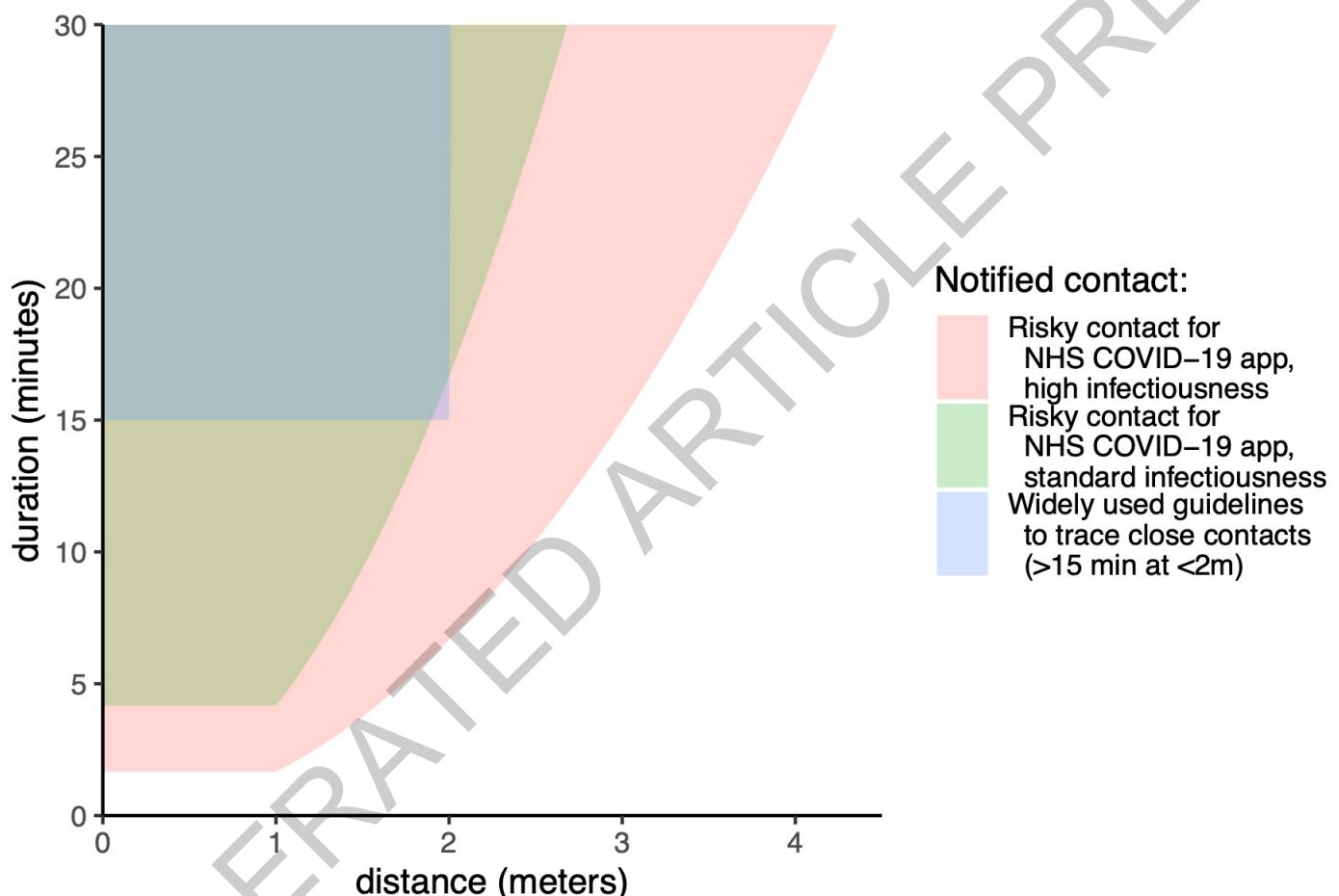
2 4 6

app-measured risk score

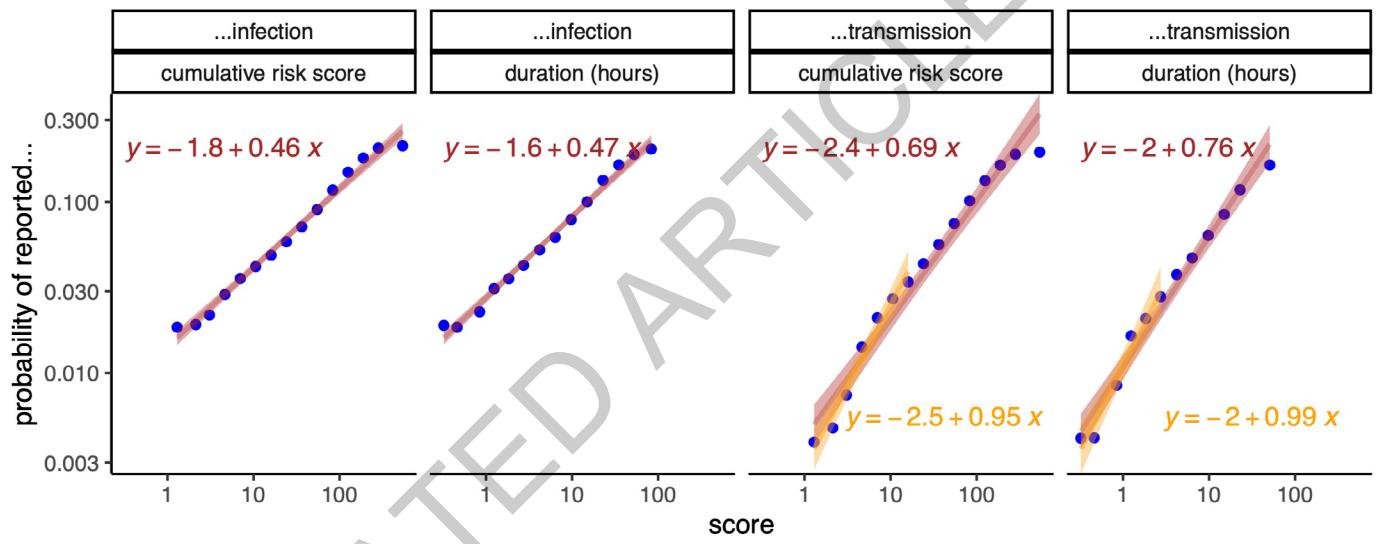
2m, 15min



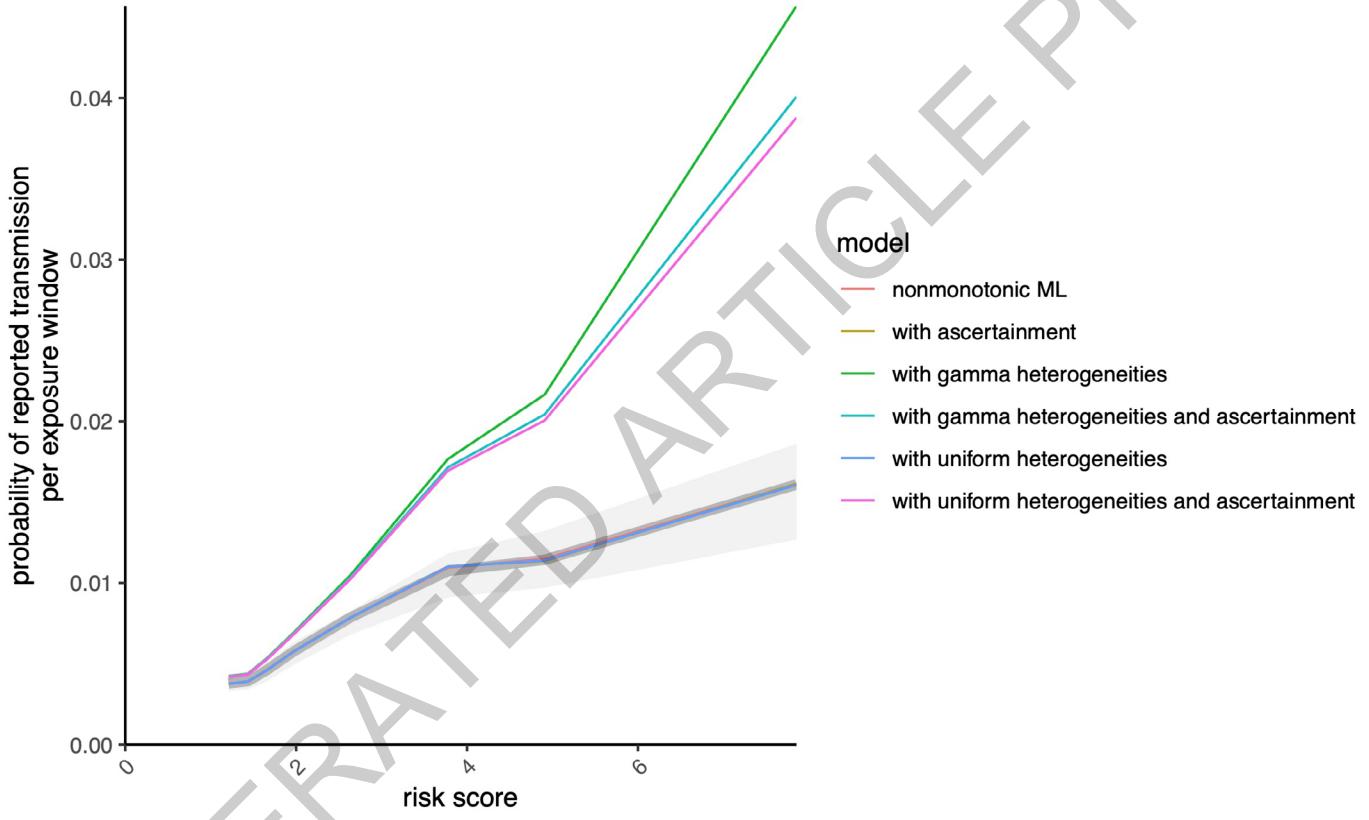




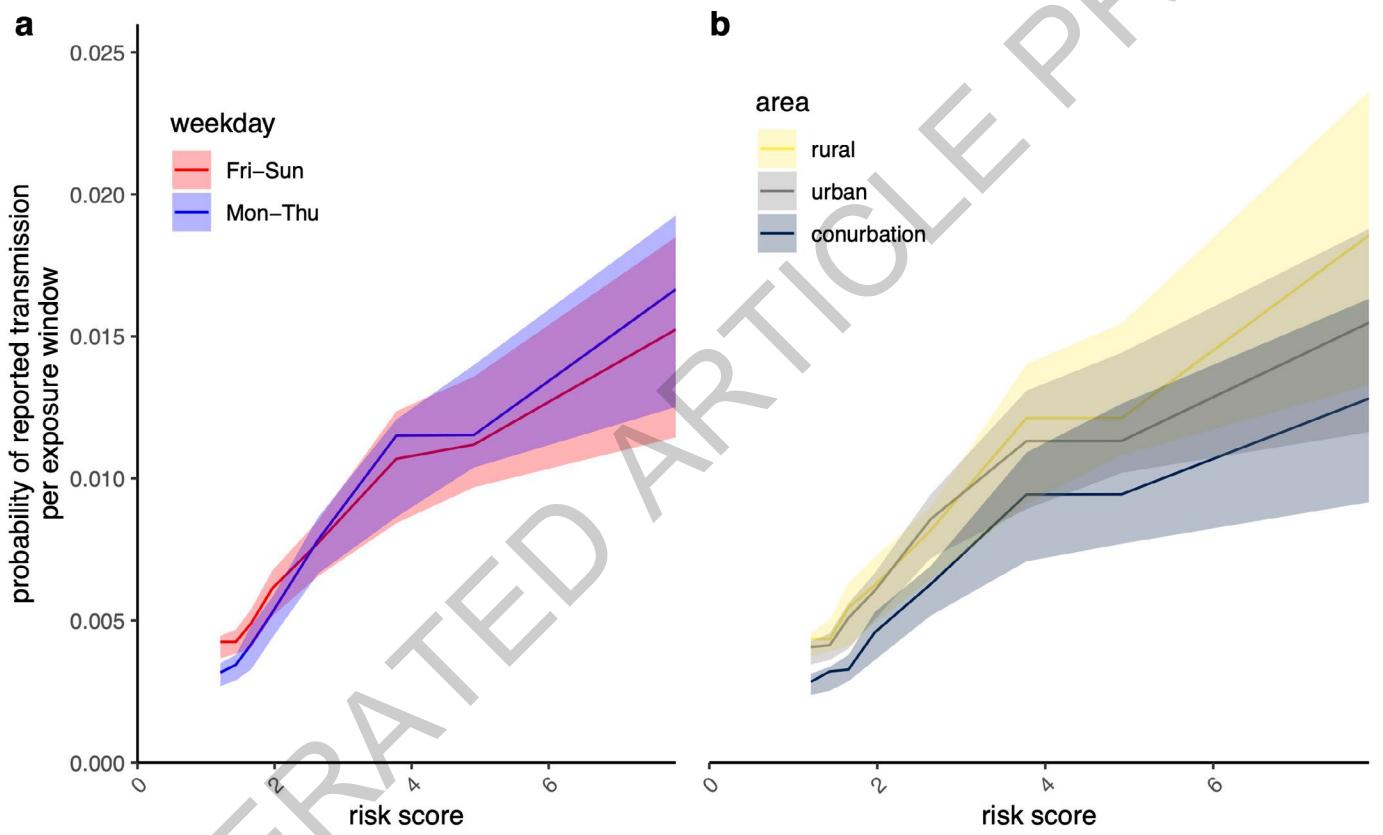
Extended Data Fig. 1



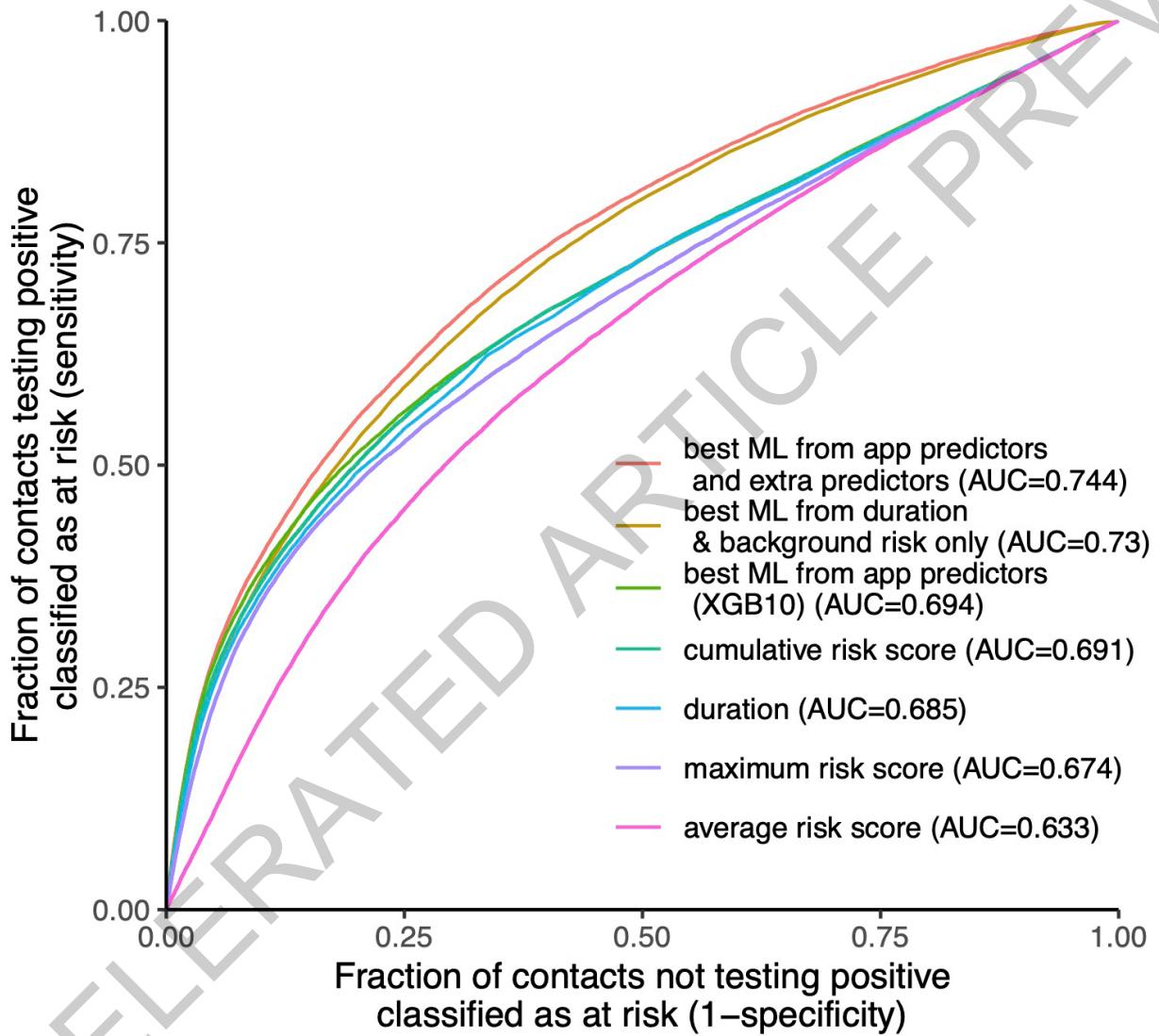
Extended Data Fig. 2



Extended Data Fig. 3

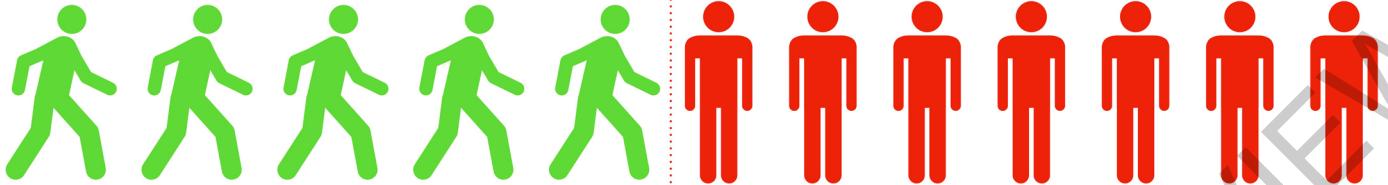


Extended Data Fig. 4



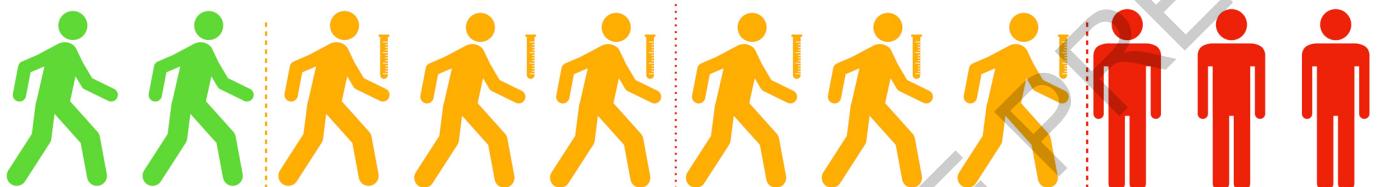
Extended Data Fig. 5

## Quarantine for risky contacts



**Alternative:**

## quarantine for high-risk contacts, testing for low-risk contacts

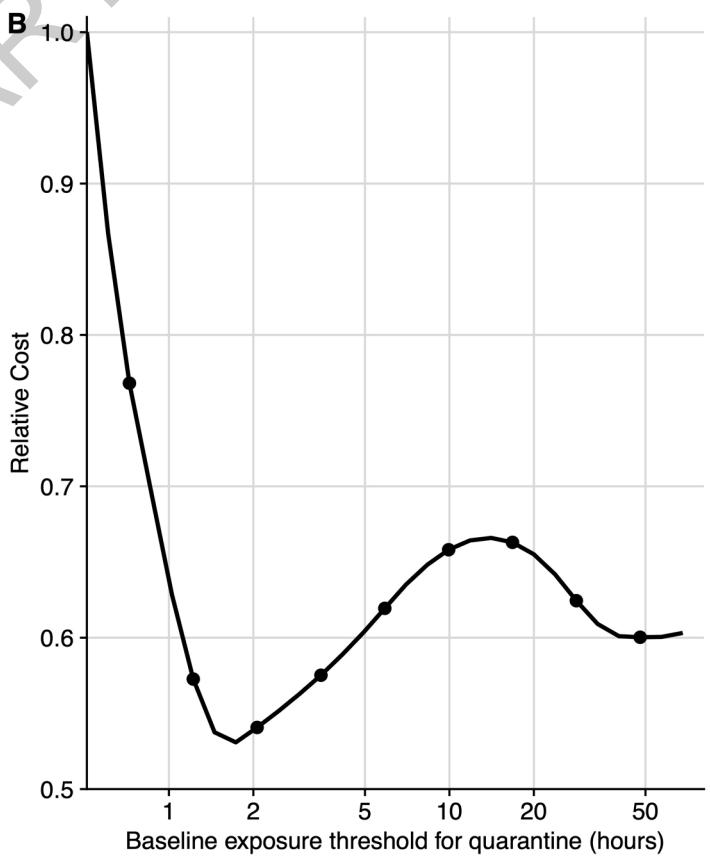
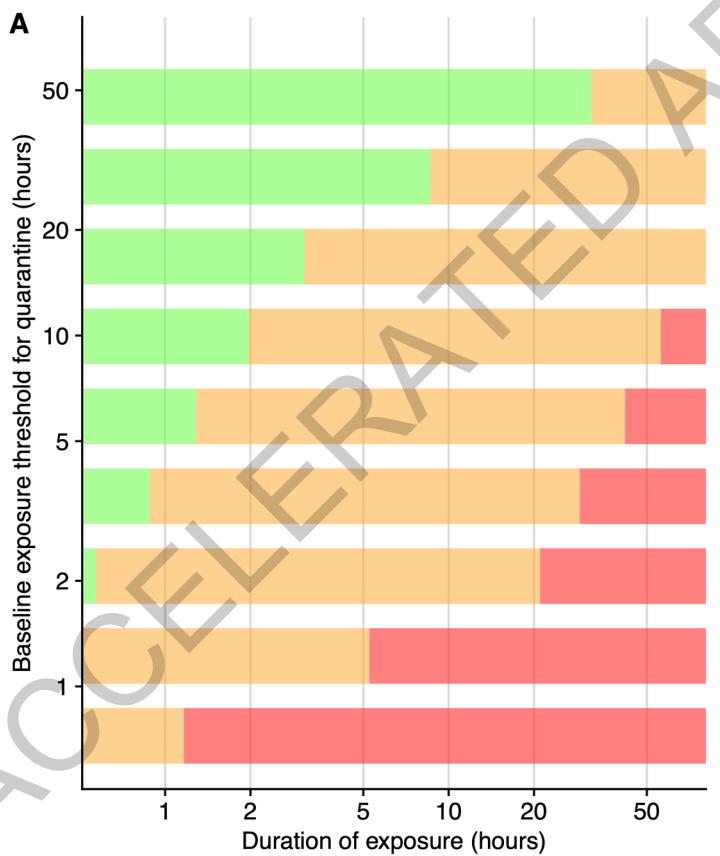


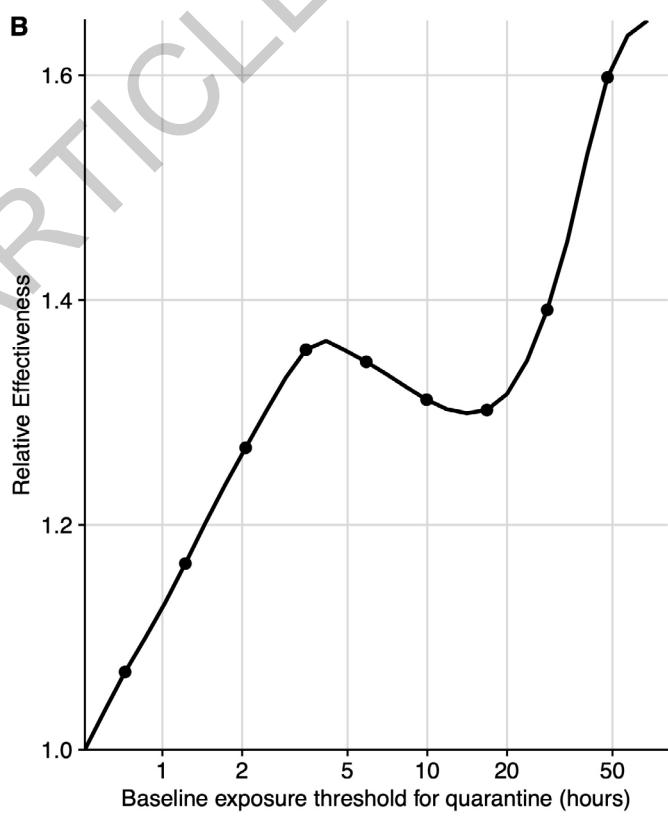
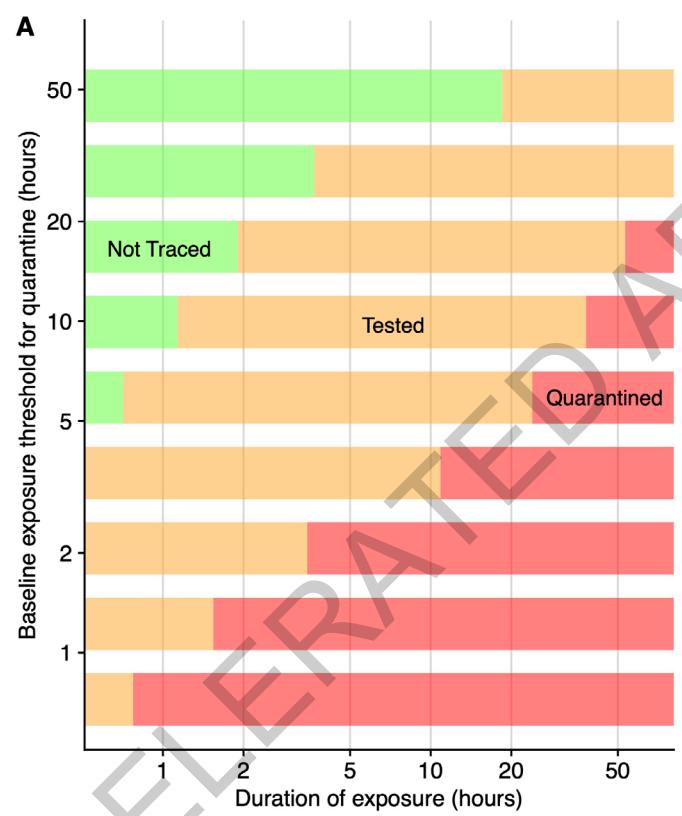
threshold for tracing & testing

Quarantine-only  
threshold for tracing

threshold for quarantine

**Duration of exposure**





Extended Data Fig. 7

	<b>Grouped events packets</b>	<b>Grouped event packets for individuals reporting a positive test</b>
<b>Number of packets</b>	52,979,100	6,137,896
<b>Cumulative duration (hours)</b>	22,877,575	2,670,167
<b>Mean duration per window (minutes)</b>	26	26
<b>Number of contacts</b>	7,047,541	239,683
<b>Mean duration per contact</b>	3 hours and 15 minutes	11 hours and 8 minutes
<b>Mean number of packets per contact</b>	7.52	25.61

Extended Data Table 1

Type of contact	mean duration (hours)	mean risk score	% testing positive	mean risk score per hour	% of all contacts	% of duration from all exposures	% of cumulative risk score from all exposures	% of all transmissions
<i>household</i>	32.9	173.9	13	5.3	6	61	67	41
<i>recurring</i>	3.9	16.6	3.3	4.2	14	17	15	24
<i>single day</i>	1.6	6.6	1.5	4.2	32	15	13	25
<i> fleeting</i>	0.4	1.5	0.4	3.7	48	6	4.5	10

Extended Data Table 2

## Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

### Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement
- A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided  
*Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g.  $F$ ,  $t$ ,  $r$ ) with confidence intervals, effect sizes, degrees of freedom and  $P$  value noted  
*Give  $P$  values as exact values whenever suitable.*
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's  $d$ , Pearson's  $r$ ), indicating how they were calculated

*Our web collection on [statistics for biologists](#) contains articles on many of the points above.*

### Software and code

Policy information about [availability of computer code](#)

Data collection	Data collection was performed using RAthena (v2.6.1) queries of the database of private app data.
Data analysis	Analysis was performed in R, version 4.0.4, with use of packages data.table (v1.14.2), tidyverse (v1.3.2), gbm (v2.1.8.1), xgboost (v1.6). Code to replicate the analysis will be made available as part of the data sharing process by UKHSA at <a href="https://github.com/ukhsa-collaboration/risk_scoring_nhs_covid19_app">https://github.com/ukhsa-collaboration/risk_scoring_nhs_covid19_app</a> .

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All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
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Data access is managed by UKHSA, who will make available on request the data needed to replicate the key results, either via the UK Data Service or through direct

request for data access to UKHSA (details on the process can be found at <https://www.gov.uk/government/publications/accessing-ukhsa-protected-data>). Access is controlled for privacy reasons.

## Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

N/A

Reporting on race, ethnicity, or other socially relevant groupings

N/A

Population characteristics

N/A

Recruitment

N/A

Ethics oversight

Research Ethics Committee approval was not required because our analysis was performed on routinely collected, anonymised data that cannot be traced back to individuals, from a database built with the primary purpose of supporting public health.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

## Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences

Behavioural & social sciences

Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://nature.com/documents/nr-reporting-summary-flat.pdf)

## Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size

We used all available data

Data exclusions

No data were excluded from the analyses

Replication

This is a one-off observational study, with no replication possible.

Randomization

Not relevant - no use of experimental groups

Blinding

Not relevant - no use of experimental groups

## Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

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| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology and archaeology |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms   |
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### Methods

- |                                     |   |
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| <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |