

Using contact data to model the impact of contact tracing and physical distancing to control the SARS-CoV-2 outbreak in Kenya - Supplementary Appendix

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S1. Shorter delay to isolation from symptom onset

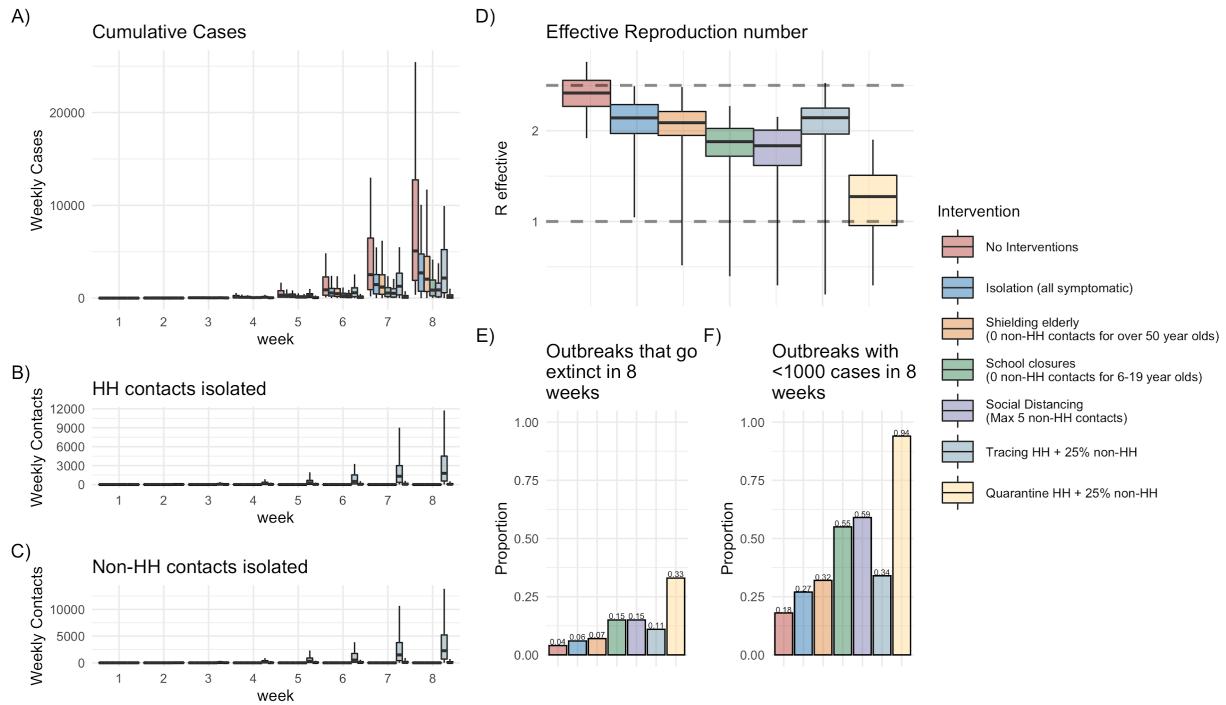


Figure 5.

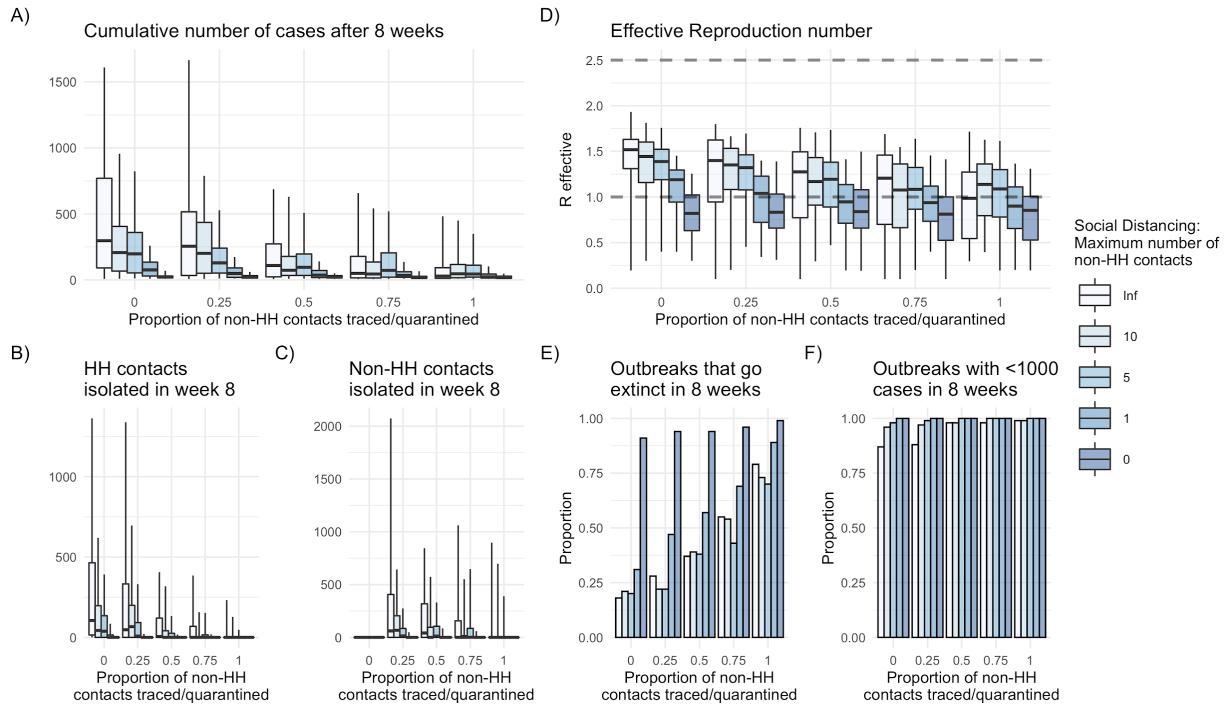


Figure 6.

S2. Higher overdispersion of R₀

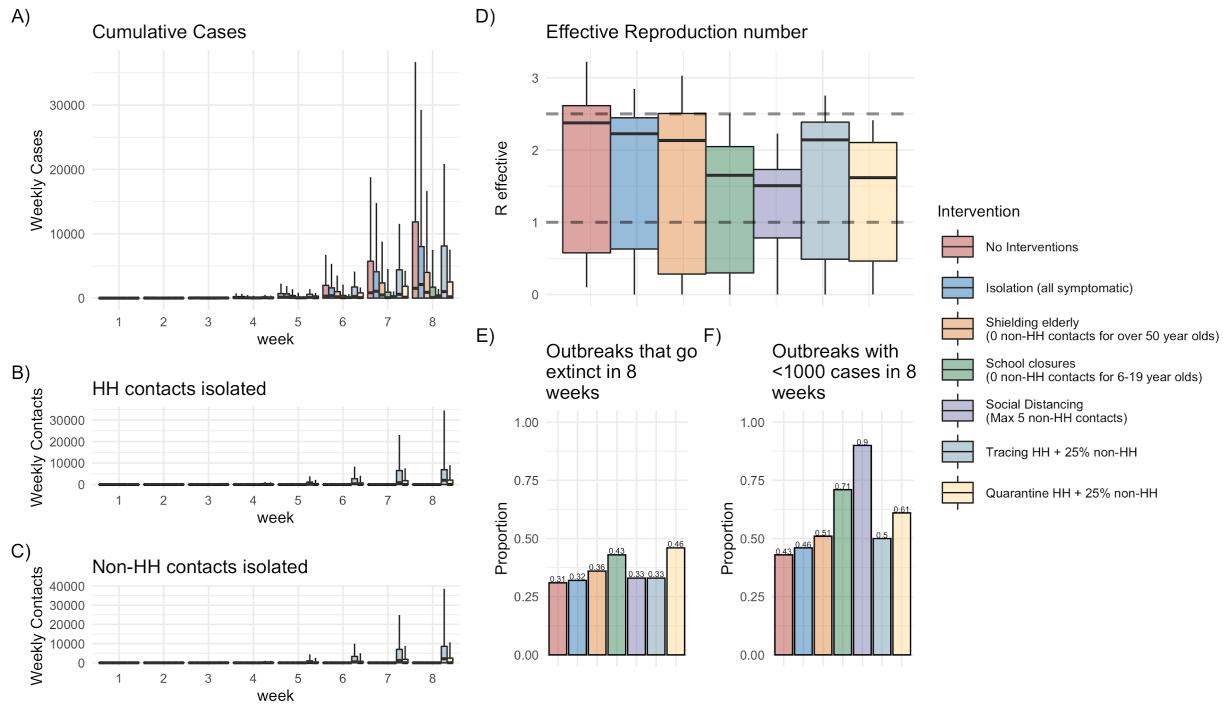


Figure 7.

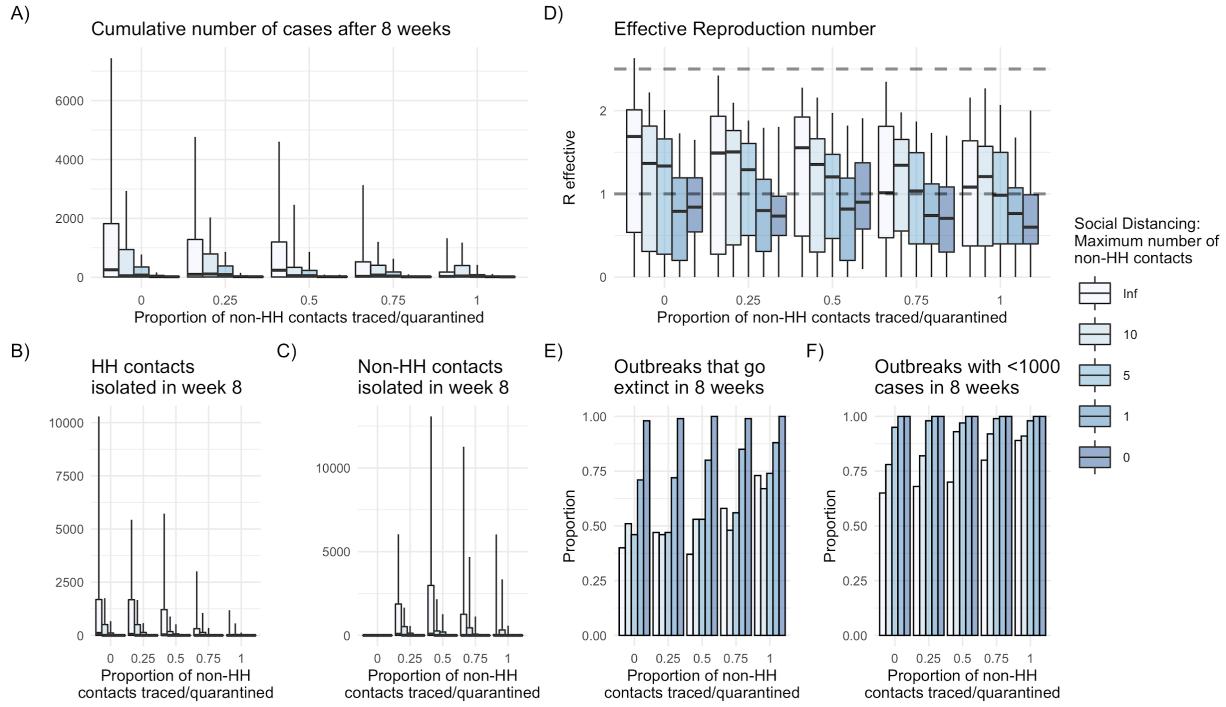


Figure 8.

S3. Higher overdispersion of R₀ and a shorter delay to isolation

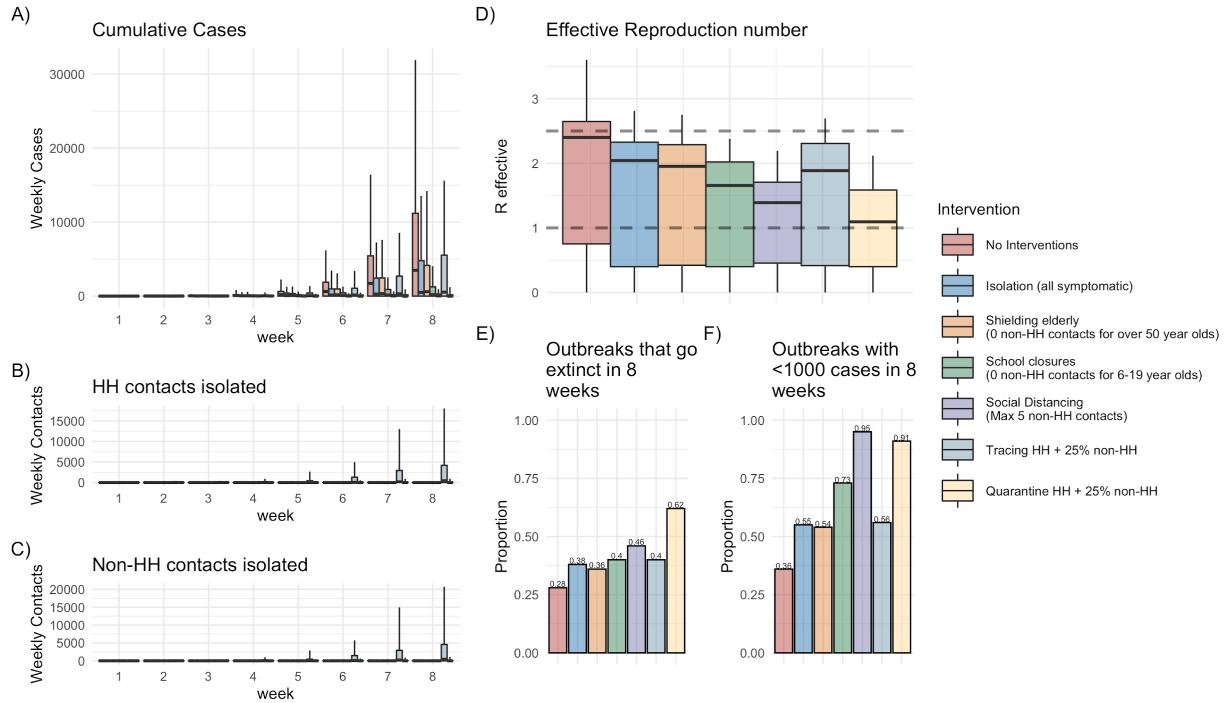


Figure 9.

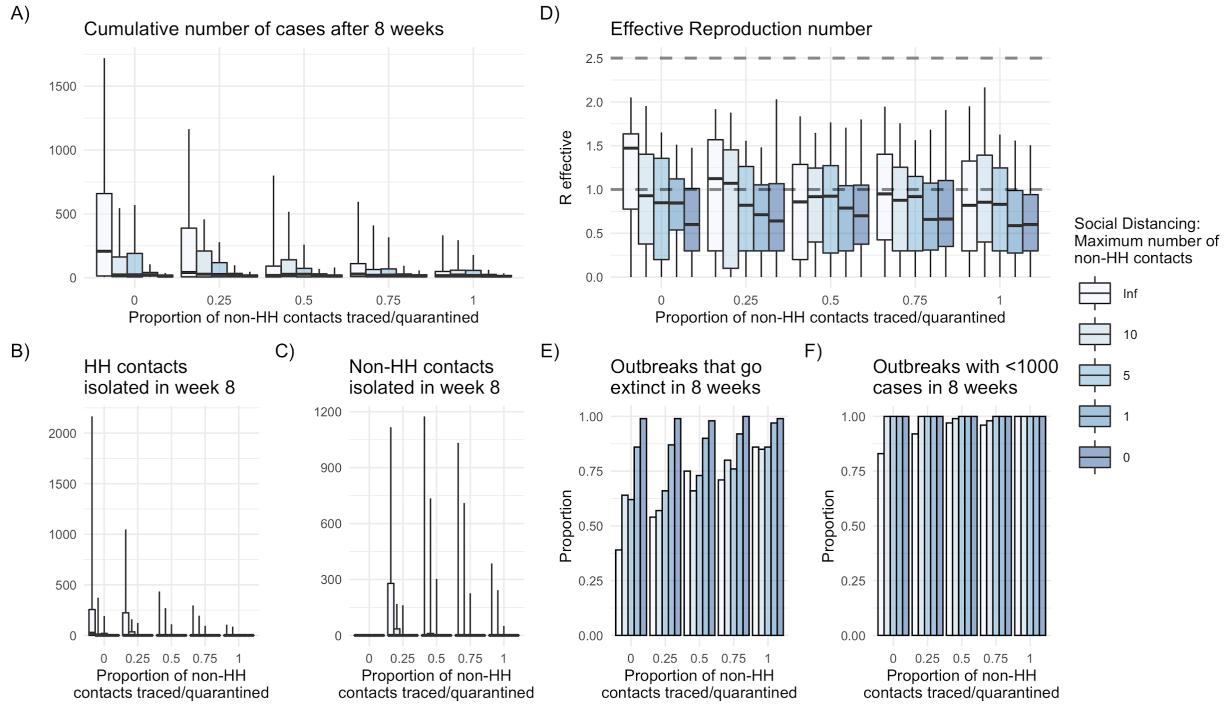


Figure 10.

S4. Pre-symptomatic transmission

Less pre-symptomatic transmission (15%)

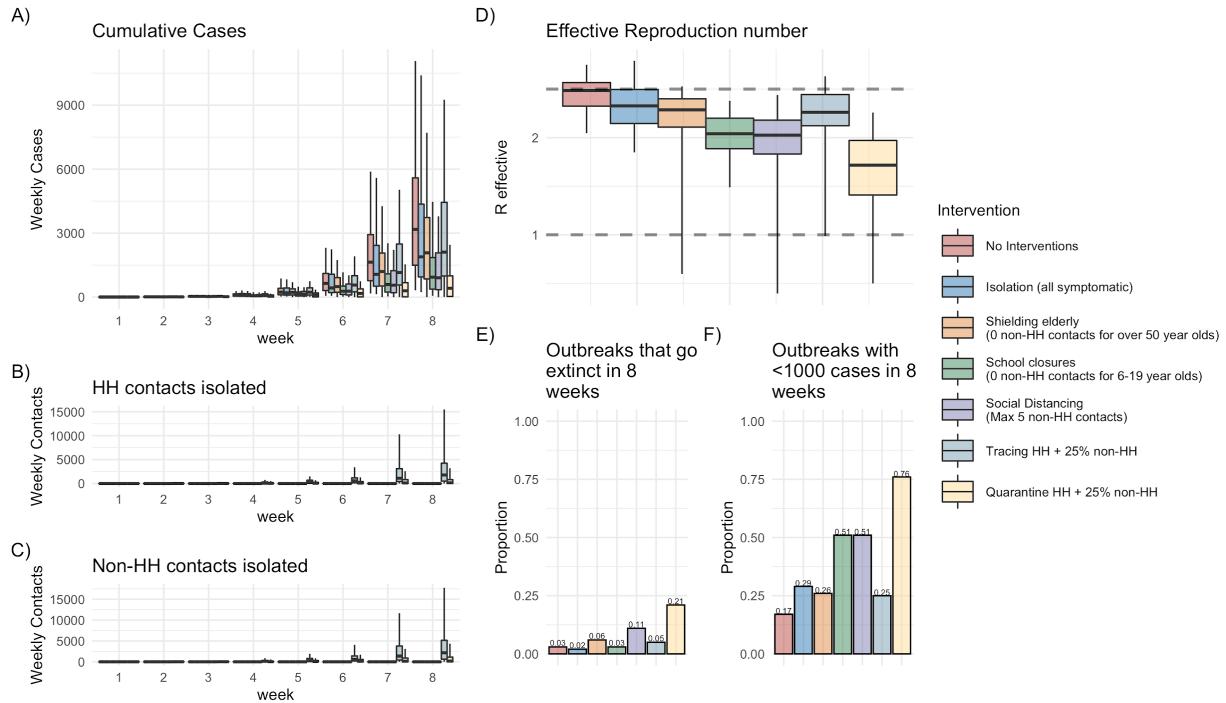


Figure 11.

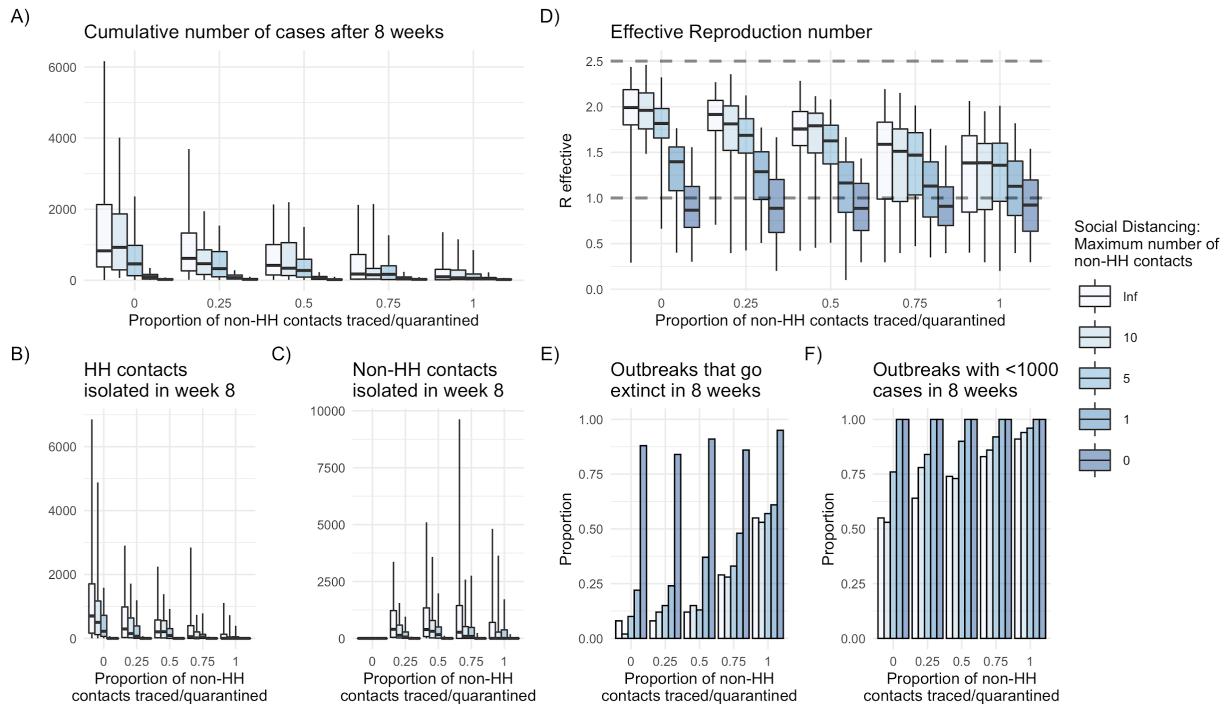


Figure 12.

More pre-symptomatic transmission (45%)

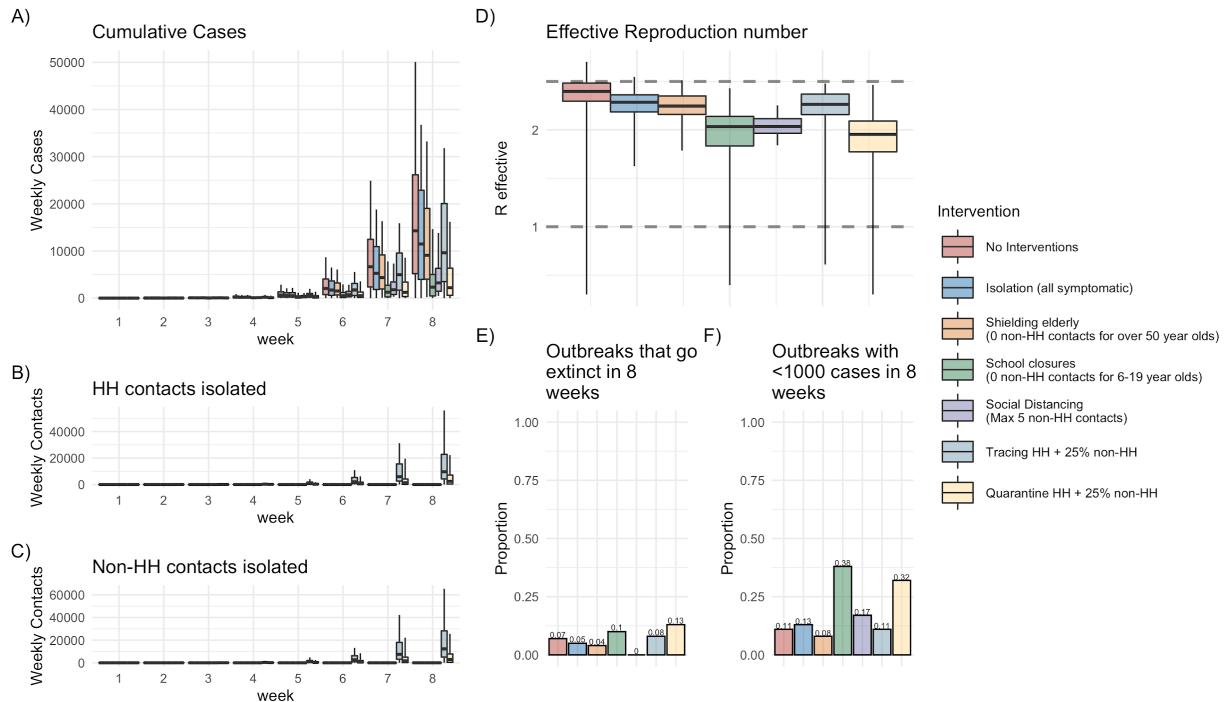


Figure 13.

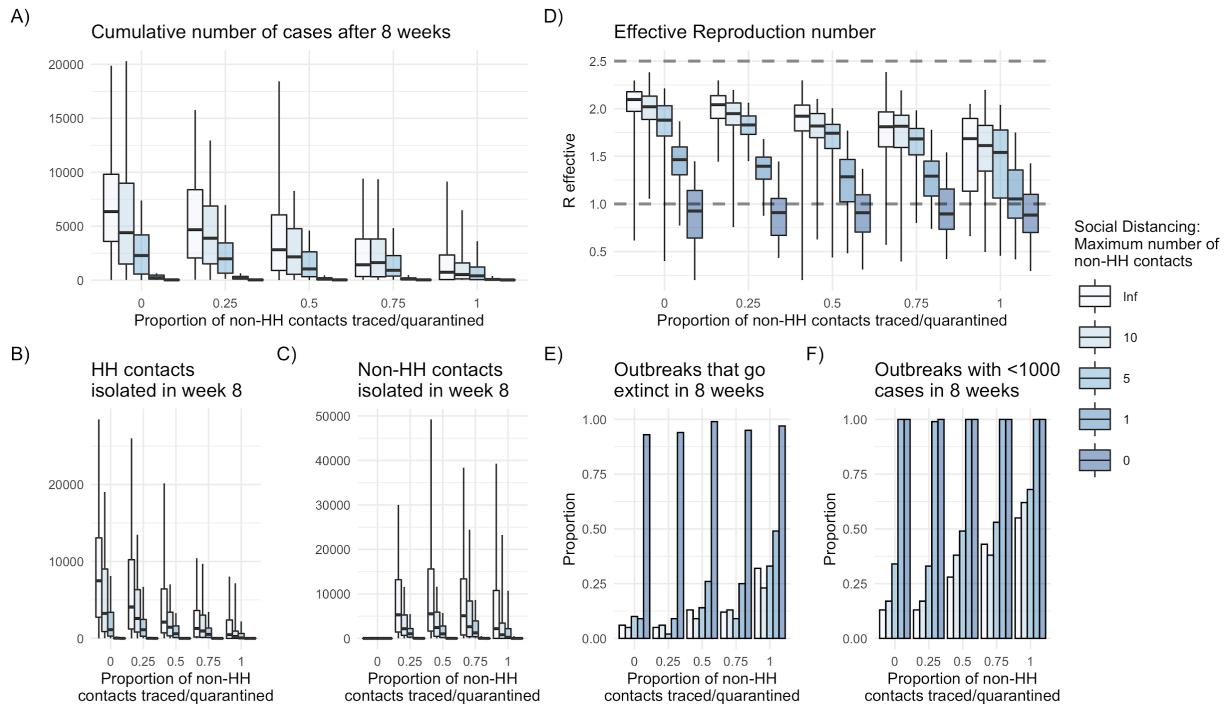


Figure 14.

S5. Lower R₀=2

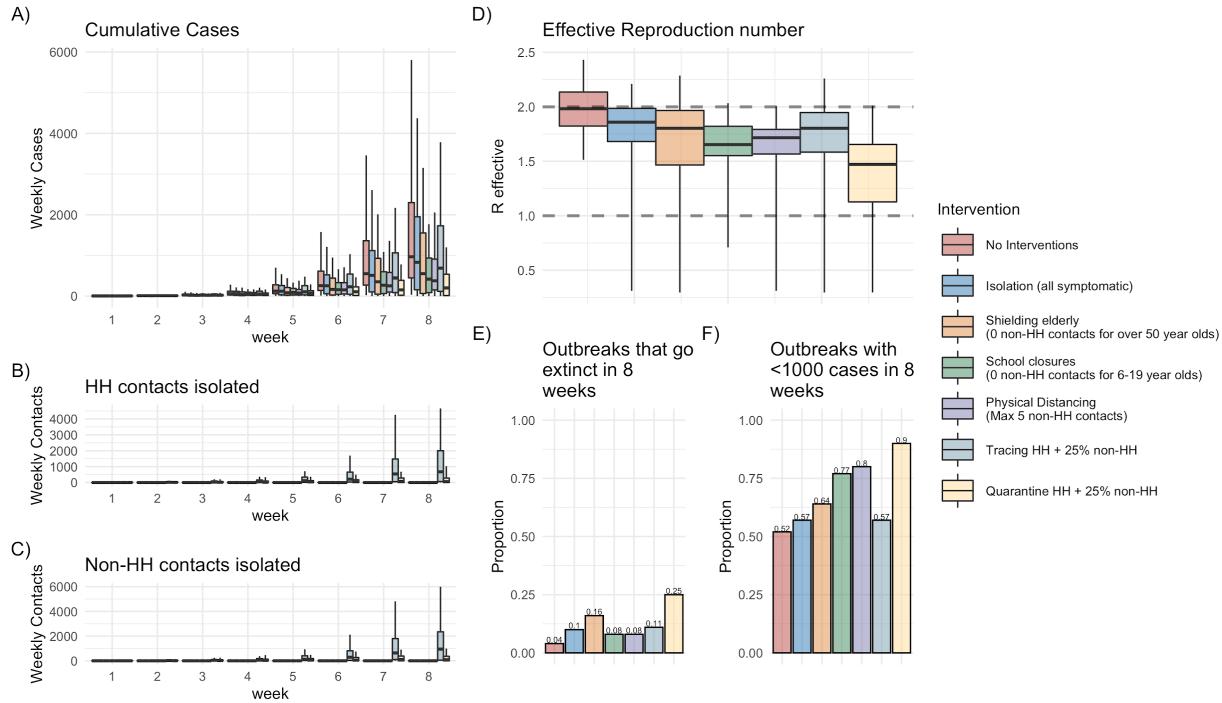


Figure 15.

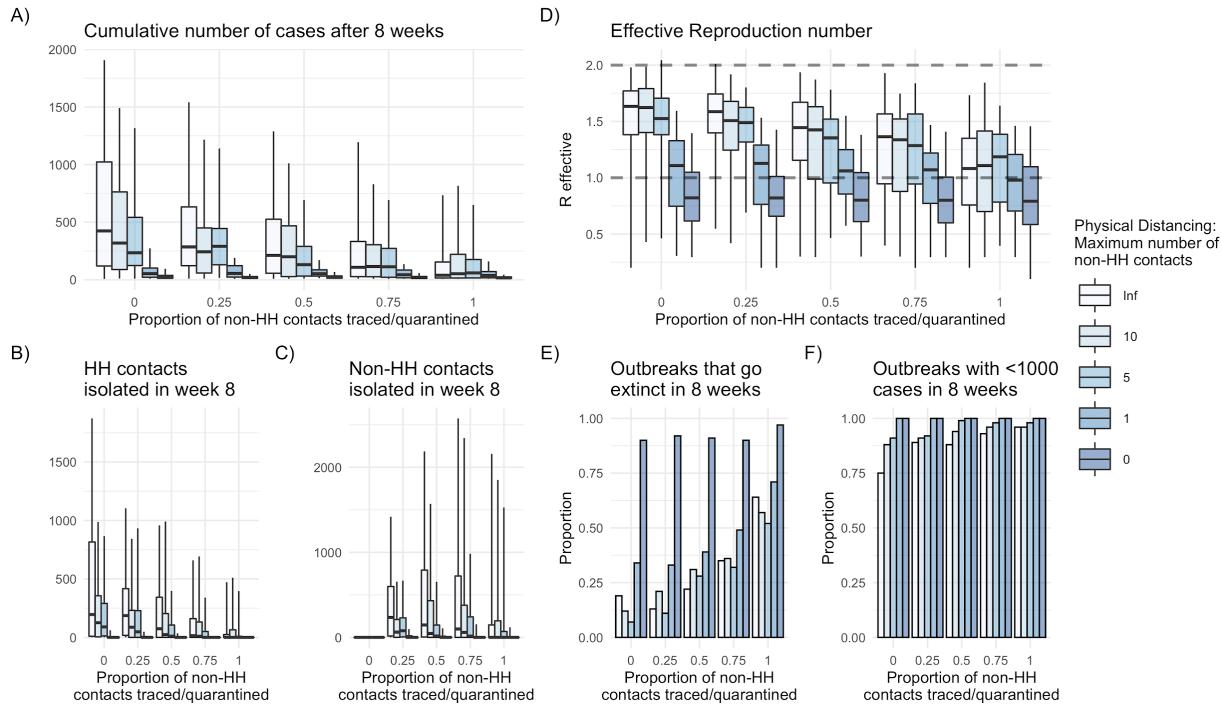


Figure 16.

S6. Reduced infectiousness of asymptomatics (50%)

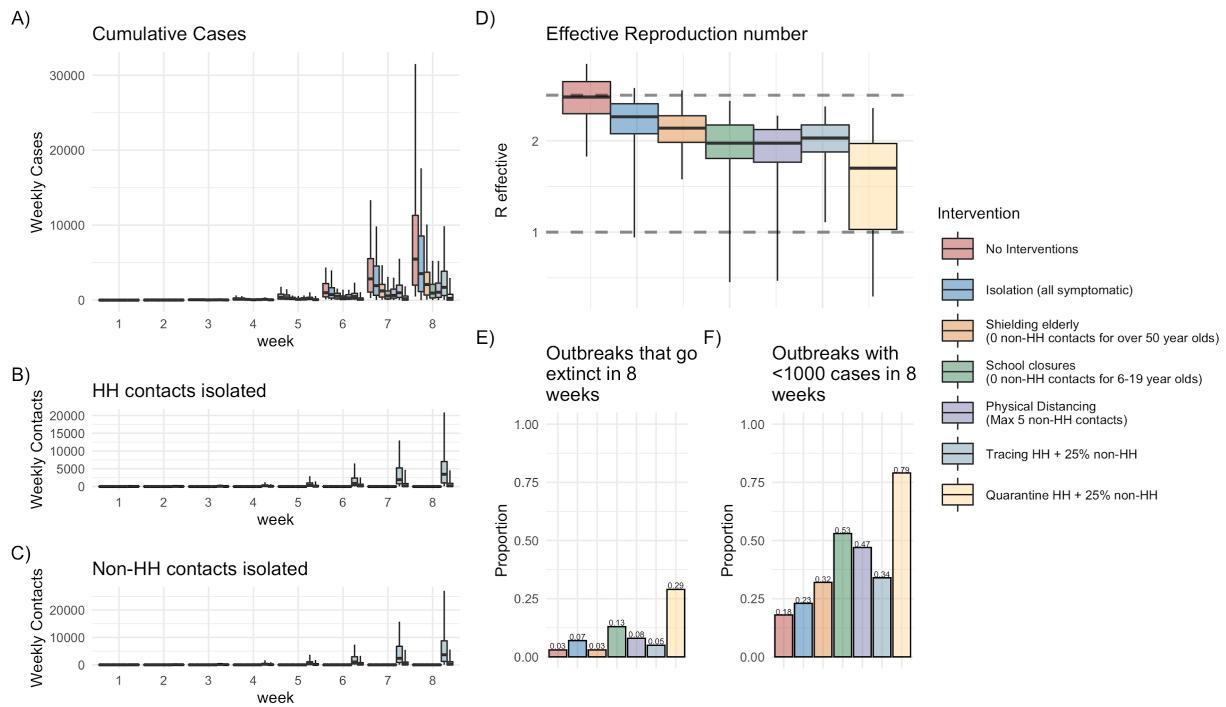


Figure 17.

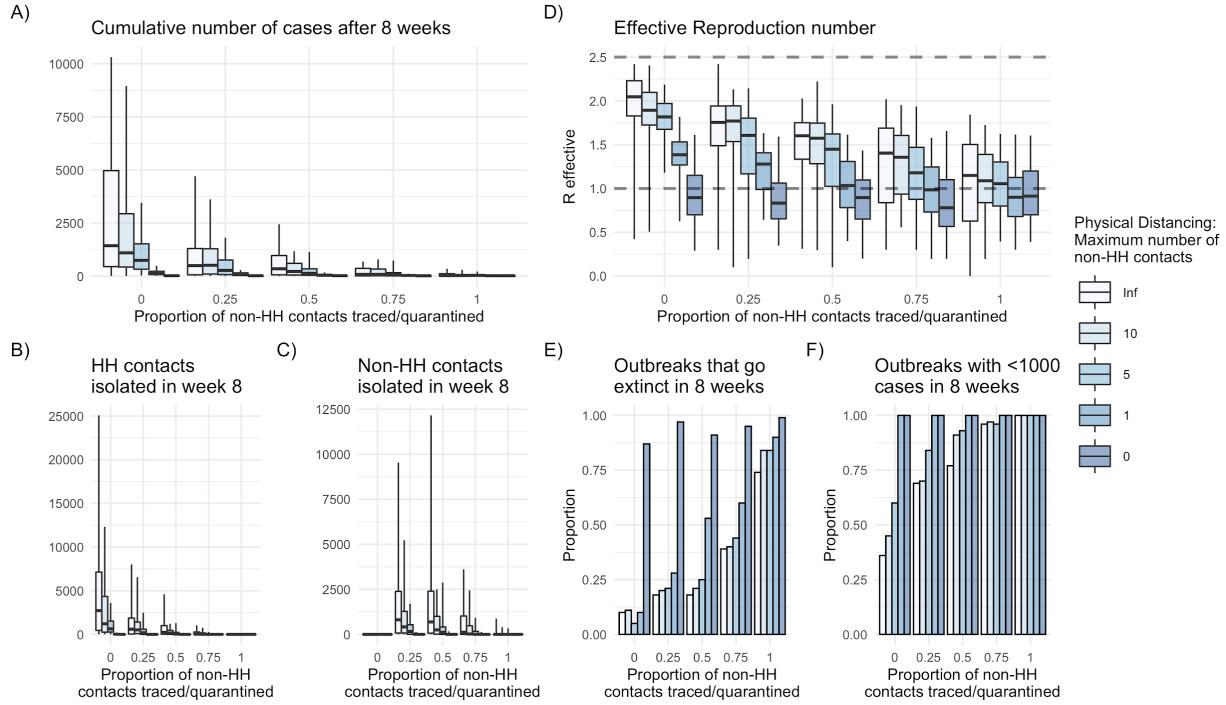


Figure 18.

S7. Proportion of cases by age

All infections

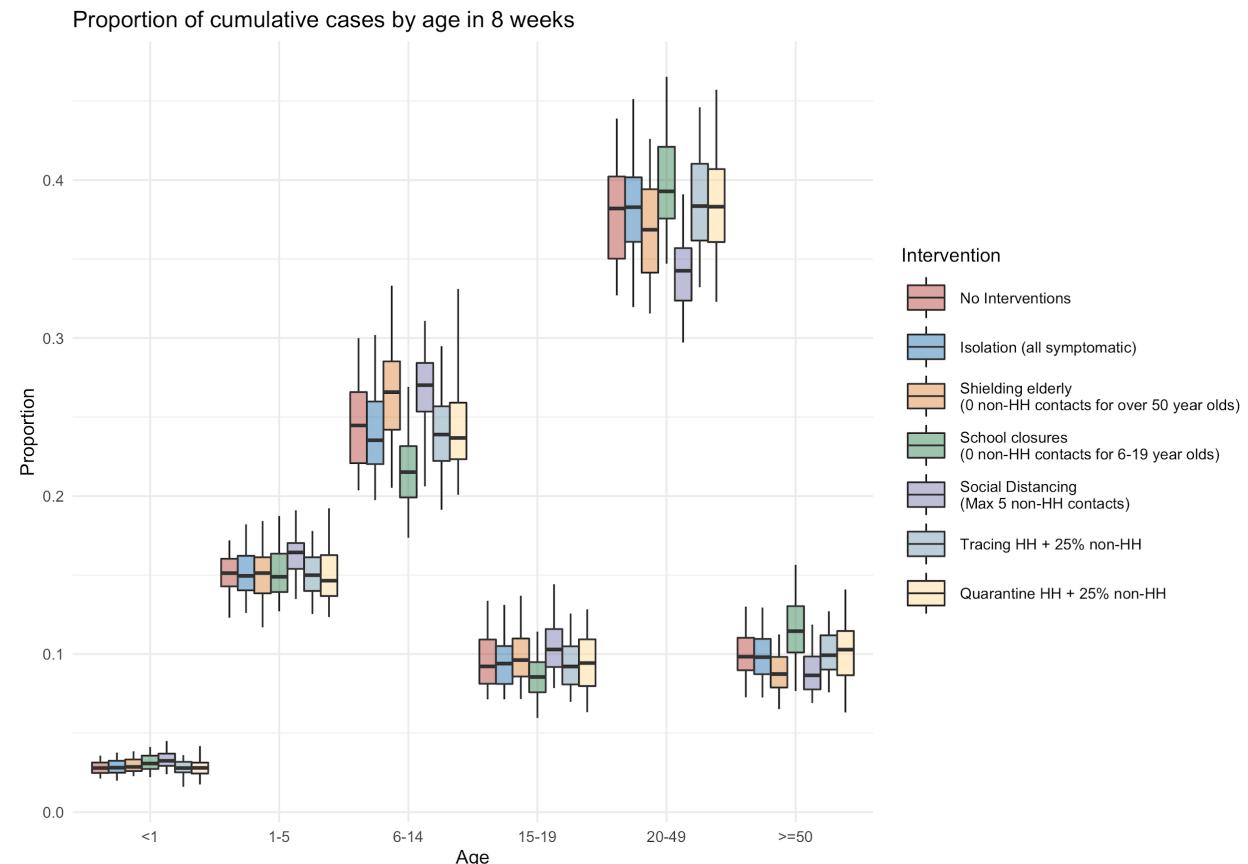


Figure 19.

Symptomatic infections

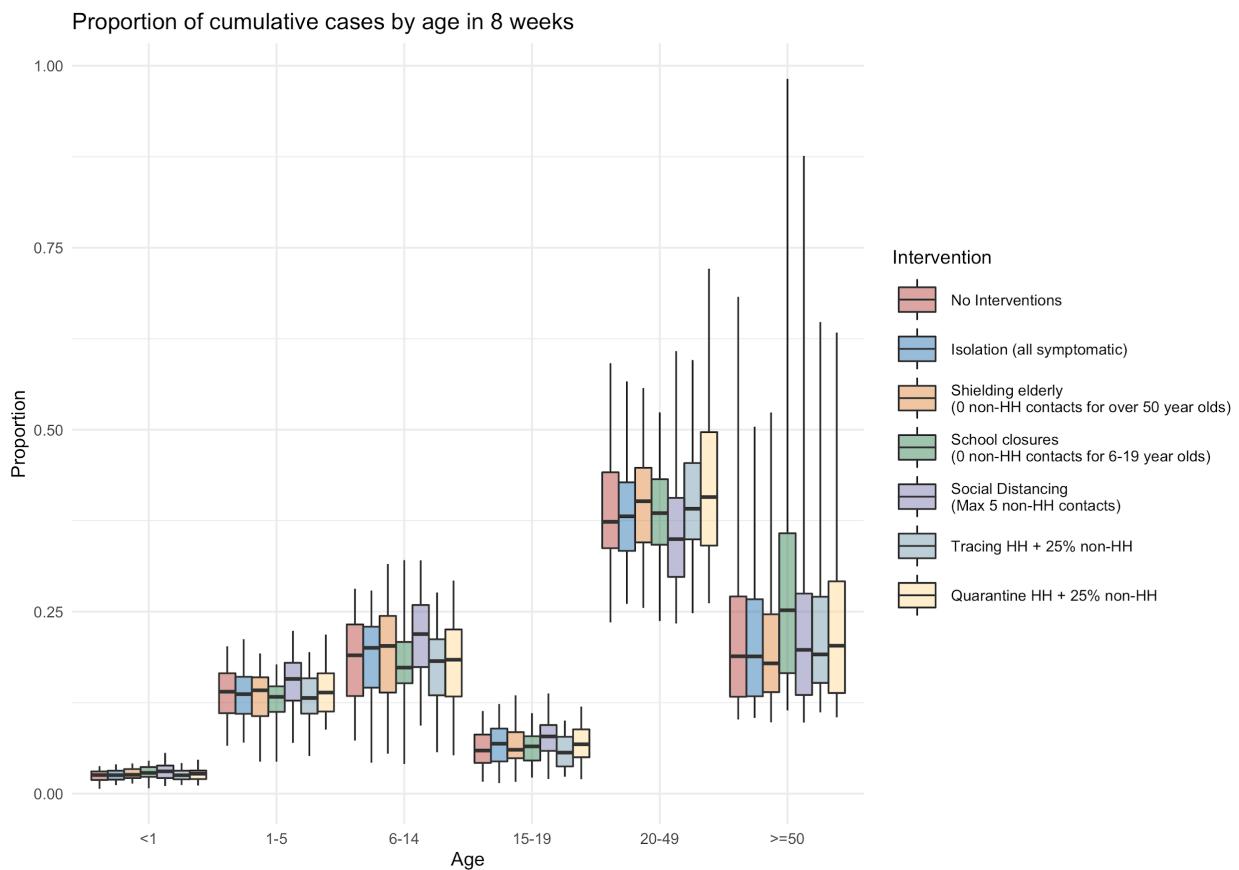


Figure 20.

S8. Repeated and unique contacts in a given time period

We have information on the frequency of a contact and the survey definitions of these, so we can assign a probability p of meeting that contact on a given day:

- Daily: $p=1$
- Often: 1-2 times per week $p=(1.5/7)$
- Regular: 1-2 times per month $p=(1.5/30)$
- Rarely: <1 times per month $p=(0.5/30)$
- Never: $p=0$

We assume that, given a participant, the contacts for a single day are representative of any other day. So if we have a single contact of a certain frequency on day one, this contact is repeated for the remaining $t-1$ days. Then, based on the frequencies above, this contact has probability p of being repeated. So for each day, $1-p$ gives the probability that a contact is a new contact. If a new contact occurs, the probability of a further new contact on the following days is $(1-p)^2$, and so on. Random numbers between 0 and 1 are drawn each day to determine whether new contacts have occurred. Weights are added to these contacts according to the expected frequency of contact during that period. Thus for $t=7$ days, “Daily” contacts will have a weight of 7, while the “Never” contacts have a weight of 1. In addition, we multiply these by relative susceptibility estimates by age from a previous modelling study to from our final weights [17]. Infections are later matched according to these weights during the infection step, thus incorporating relative susceptibility by age as well as the frequency of contacts.

The final output is a full contact data set with participant and contact ids. This defines the susceptible population during the outbreak and for each id (contact and participant), we keep track of who becomes infected.

S9. Matching infections to contacts

Here we extend the LSHTM model to include realistic contact data stratified by age and household. Given an infector with a number of potential infecteds (based on a sample from R_0), infections are matched to the infector's contacts. In our contact data, individuals are either study participants or study contacts. We consider two scenarios:

1. The infector is a study participant: We know all their contacts already.
2. The infector is a study contact: We don't know the full set of contacts here and have to sample from the rest of the contact data. Again we have two scenarios: (a) The individual was infected through the household (HH), thus we know their HH contacts, as these are linked to their infector. The non-household (non-HH) contacts are sampled from the non-HH contacts of a participant of the same age group. Note that this may introduce some biases as there may be a relationship between the number of HH and non-HH contacts by age; (b) The individual was infected outside the HH. In this case we sample a random participant of the same age and use their HH and non-HH contacts.

We then assign which of the contacts become infected based on their weight (see [section on repeated and unique contacts](#)). There are three scenarios that reduce the pool of susceptible contacts:

1. The amount of contacts available to an infector. There will be random draws of R_0 that are larger than the total contacts available. In this case we assume the occurrence of a super-spreading event (SSE), where the available contacts are not captured by the contact data, e.g. larger group gatherings. We extend the number of contacts available to match R_0 by sampling further non-HH contacts from participants of the same age.
2. A contact has already been infected. If the study population is large most of these pre-existing infections will be HH contacts formed through HH clusters.
3. Duplicate infections. The model is run in generations, where each generation represents all the infections that occur from the infecteds of the previous generation. During the infection step, multiple infectors may infect the same individual. Again if the study population is large most of these duplicated infections will be within the same HH.

S9. Detailed table of intervention scenarios

Scenario	Details
No intervention	No isolation of cases and infected individuals infect according to their contacts. Note that this is an unlikely scenario, as symptomatic individuals are likely to change their contact behaviour upon onset of symptoms, especially if severe. It provides a theoretical benchmark to which to compare the other scenarios.
Isolation of all symptomatic cases	Using previous age-specific estimates of the proportion of infecteds that develop symptoms [?], all symptomatic cases are isolated after a delay following symptom onset. This may be equivalent to ensuring that anyone with symptoms self-isolates as well as isolating any infected individuals that present to hospital.
Shielding elderly	The oldest age group limit their contacts to HH contacts only. For the contact data used the oldest age group available were the over 50 year olds, which represents a larger age group than would realistically be included in shielding efforts. Thus this is likely to provide an overestimate of the impact of shielding. SSEs do not occur in the oldest age group.

School closures	We limit the contacts of 6-19 year olds to HH contacts only. Data on school contacts were not available, so this is likely to provide an overestimate of the impact of school closures. SSEs do not occur in 6-19 year olds.
Physical distancing	Contacts of all individuals are limited to 5 unique non-HH contacts per week. HH contacts remain the same. SSEs do not occur across all age groups.
Tracing HH + 25% non-HH	All symptomatic HH contacts and 25% of symptomatic non-HH contacts of an isolated individual are traced and isolated immediately upon symptom onset. All non-traced symptomatic individuals are isolated after a delay following symptom onset (as in 2.).
Quarantine HH + 25% non-HH	All infected household contacts and 25% of infected non-household contacts of an isolated individual are traced and isolated immediately (not following symptom onset). All non-traced symptomatic individuals are isolated after a delay following symptom onset (as in 2.).

Table 3.

S10. Synthetic contact data

To explore the accumulation of contacts across multiple days, we built a shiny app (https://moritzwagner.shinyapps.io/Counting_Contacts/). This allows you to sample from the original contact data by a given urban-rural divide, set a time period of accumulating contacts and produces boxplots of the expected number of contacts overall, by household and non-household, and by frequency of contact. Figure 2 shows an example output of the app for a 30% urban population accumulating contacts across 7 days, we estimate that there are around 38 distinct contacts made with 6 and 32 within and outside of the household, respectively. A mean of 40 contacts is in line with what has been reported for tracing efforts in other settings [14].

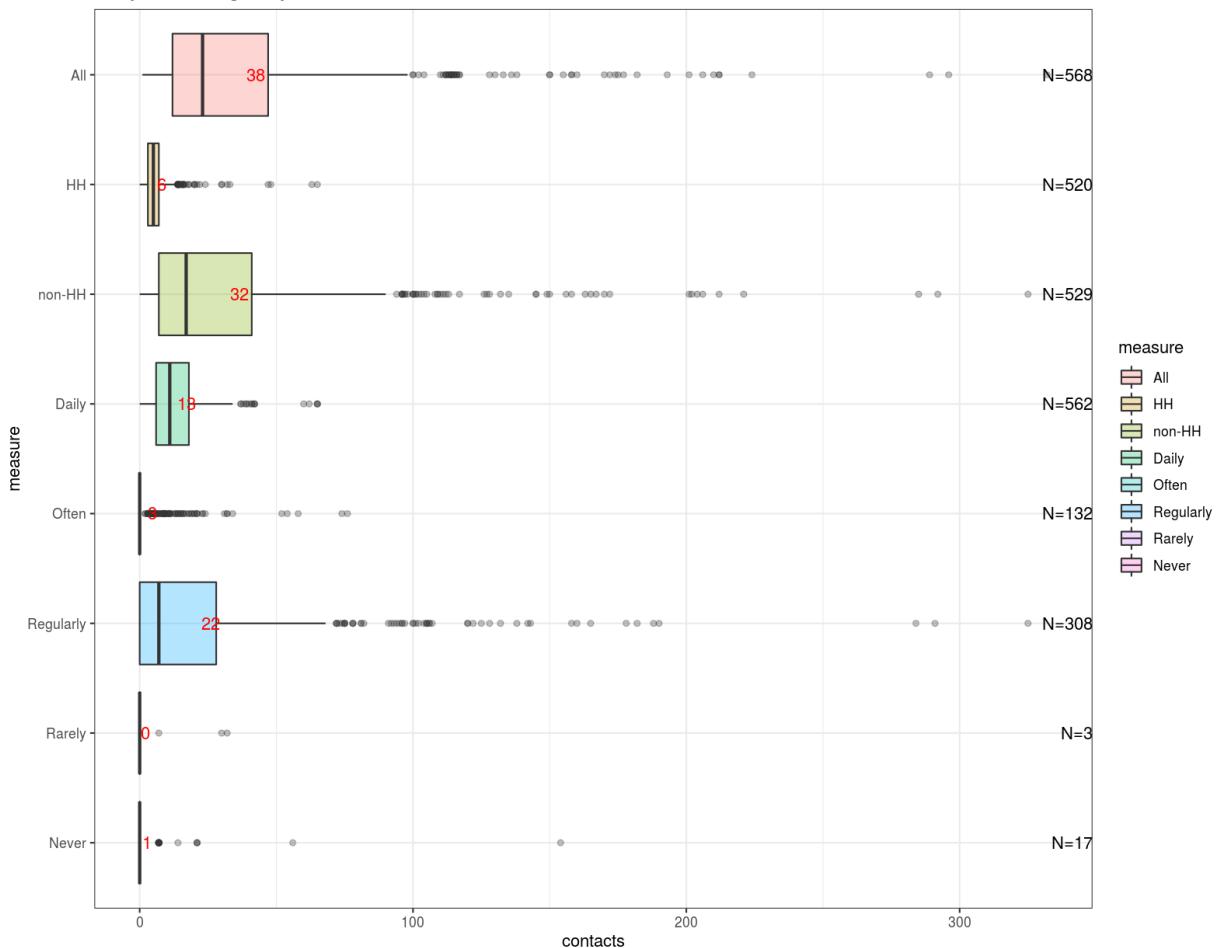


Figure 2.

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