TECHNICAL APPENDIX

A.1. Model Details

A.1.1 Response policies

Response policies consist of vaccination, contact tracing, lockdown, and quarantine strategies.

Vaccination

The effect of Pfizer and AstraZeneca vaccines are included in the model. Vaccinated agents aged 60+ are assumed to be vaccinated with AstraZeneca. All other agents are assumed to be vaccinated with Pfizer. Vaccines are assumed to decrease both susceptibility to infection and the probability of developing symptoms, given infection. These reductions depend on vaccine type, the number of doses received, the time since vaccination, and the assumed model of vaccine protection (detailed below).

Vaccine protection. In the main report, we consider a leaky model of vaccine protection. In the leaky model, the effect of vaccination is determined for each contact – there is a per-exposure probability (which depends on age, and the time since receiving their last dose) that vaccinated individuals in the model are protected against infection or the development of symptoms.

Agents reach the maximum dose/vaccine-type vaccine efficacy 3 weeks after their first dose, and 2 weeks after their second dose

In the supplementary results (Section A.3), we also consider an all-or-nothing model of vaccine protection. In this model, the effect of vaccination is to fully protect a proportion (which depends on vaccine efficacy after receiving i doses, $V_{E,i}$) of vaccinated individuals from ever becoming infected, while the complementary proportion will receive zero protection against infection or the development of symptoms. In this model, once an individual receives their first dose of a vaccine, there is a probability, p_1, each timestep for the following *k* timesteps (which equates to three weeks) that they will develop full protection, where,

$$p_1 = 1 - \left(1 - V_{E,1}\right)^{\frac{1}{k}}.$$

This probability per time step p_1 equates to having a probability $V_{E,1}$ that a vaccinated agent will end up being fully protected 3 weeks after receiving their first dose. For individuals who did not develop full protection after their first dose, there is a probability, p_2, each timestep following their second dose (up to *l* timesteps, which equates to two weeks) that they will develop full protection, where,

$$p_2 = 1 - \left(1 - \hat{V}_{E,2}\right)^{\frac{1}{l}} \text{ and } \hat{V}_{E,2} = \left(\frac{V_{E,2} - V_{E,1}}{1 - V_{E,1}}\right).$$

This probability per time step p_2 equates to having a probability $V_{E,2}$ that a vaccinated agent will end up being fully protected 2 weeks after receiving their second dose.

Test, Trace, Isolate, Quarantine (TTIQ) and lockdown.

TTIQ. When an infected individual becomes symptomatic, they get tested without delay and self-isolate. It is assumed that all symptomatic individuals will get tested. There is a delay, d_1, in receiving their test result. If they receive a negative test result, they leave self-isolation. If they receive a positive test result, contact tracing is implemented, and after a delay d_2, they enter isolation for 10 days (Figure A1a).

Contacts of a case are quarantined (there is a delay d_3 between case identification and contacts entering quarantine). Quarantined contacts are immediately tested. There is a delay, d_1, in receiving their test result. If they receive a positive test result, contact tracing is implemented, and after a delay d_2, they enter isolation for 10 days. Quarantined contacts with a negative test result remain in quarantine for 14 days. A clearance test is conducted on day 12 of quarantine. If they have a negative test result, they leave quarantine on day 14. Otherwise, contact tracing is implemented, and after a delay d_2, they enter isolation for 10 days (Figure A1b).

Cases in isolation undergo a clearance test on day 8 of isolation. If they have a negative test result, they leave isolation on day 10, otherwise their isolation period restarts (Figure A1a).

Lockdown. Upon identification of the first case in the community, the whole community goes into lockdown (there is a delay d_4 between case identification and lockdown implementation). Upon entering lockdown, all community members get tested. There is a delay d_5 until the test results are available. Individuals that test positive enter isolation for 10 days and contact tracing is initiated. Individuals that test negative remain in quarantine for 14 days. A clearance test is conducted on day 12. If they have a negative test result, they leave lockdown on day 14. Otherwise, contact tracing is implemented, and after a delay d_2, they enter isolation for 10 days. (Figure A1c).

Contact tracing. When a case is identified, contact tracing is initiated. Contacts are defined to be all household and community contacts of the case, from either

- 3 days before symptom onset (for symptomatic cases)
- 3 days before the day of testing (for asymptomatic cases)

to the day they entered isolation. Contact tracing is assumed to be 100% effective (all contacts are found). Effectiveness can be reduced if it is considered more feasible.

Effect of TTIQ and Lockdown on contact rates and between-household mobility. Self-isolation, isolation, quarantine and lockdown impact the rate at which agents make household and community contacts in the model, and the rate at which they move between households in the community. In the results presented in the main report, all scenarios assume the following effects of TTIQ and lockdown:

Policy	Self-isolated or isolated. Relative reduction in rate of:			Quarantined. Relative reduction in rate of:			Individuals in lockdown. Relative reduction in rate of:		
	Household contact	Comm. contact	Household mobility	Household contact	Comm. contact	Household mobility	Household contact	Comm. contact	Household mobility
CTP1	1	1	1	1	1	1	0	0.9	1
CTP2	1	1	1	0	1	1	0	0.9	1

Delays. In the results presented in the main report, all scenarios have the following delays:

Delay	Values
From onset of symptoms to receiving results of test for a case (includes delay to receiving test, and receiving result) (d_1)	1 day
From time of case identification to case isolation (d_2)	1 day
From time of case identification to quarantining contacts of a case (d_3)	1 day
From time of quarantining contacts to receiving results of test for contact (d_1)	1 day
From time of case identification to enacting lockdown (d_4)	1 day
From time of enacting lockdown to receiving results of testing whole community (includes delay to receiving test, and receiving result) (d_5)	2 days

A.1.2. Severity data for General and Aboriginal and Torres Strait Islander populations, and comparison to general population severity shifted downwards 10 years and 20 years, for ages 20+

Table A1. Percentage of cases hospitalised only (not ICU, not died) in the General and Aboriginal and Torres Strait Islander populations, and comparison to percentages in the general population that have been shifted downwards 10 years and 20 years for ages 20+. General Population data: COVID-19 cases by age group and severity, selected jurisdictions, 1 January 2021 – 12 September 2021. Aboriginal and Torres Strait Islander Population data: as of the 13th of September 2021

Age group	Percentage hospitalised only (total cases)		10-year age shift (for 20+)	20-year age shift (for 20+)
	General Population	Aboriginal and Torres Strait Islander		
0-11	5 (8302)	3 (475)	5	5
12-17	5 (4685)	7 (255)	5	5
18-29	10 (13086)	12 (502)	14	17
30-39	14 (9051)	17 (298)	17	20
40–49	17 (6349)	20 (250)	20	25
50–59	20 (4639)	18 (130)	25	36
60–69	25 (2530)	39 (54)	36	47
70–79	36 (1123)	40 (10)	47	48
80–89	47 (553)	67 (3)	48	48
90+	48 (146)	100 (1)	48	48

Table A2. Percentage of cases ICU only (not hospital only, not died) in the General and Aboriginal and Torres Strait Islander populations, and comparison to percentages in the general population that have been shifted downwards 10 years and 20 years for ages 20+. General Population data: COVID-19 cases by age group and severity, selected jurisdictions, 1 January 2021 – 12 September 2021. Aboriginal and Torres Strait Islander Population data: as of the 13th of September 2021

Age group	Percentage ICU only (total cases)		10-year age shift (for 20+)	20-year age shift (for 20+)
	General Population	Aboriginal and Torres Strait Islander		
0-11	<1 (8302)	<1 (475)	<1	<1
12-17	<1 (4685)	1 (255)	<1	<1
18-29	1 (13086)	<1 (502)	1	3
30-39	1 (9051)	<1 (298)	3	5
40–49	3 (6349)	2 (250)	5	7
50–59	5 (4639)	5 (130)	7	7
60–69	7 (2530)	9 (54)	7	7*
70–79	7 (1123)	40 (10)	7*	7*
80–89	4 (553)	<1 (3)	7*	7*
90+	0 (146)	<1 (1)	7*	7*

** At any point where the probability of a severe outcome decreased by age in the general population, the severity in the Aboriginal and Torres Strait Islander population was assumed to remain constant.*

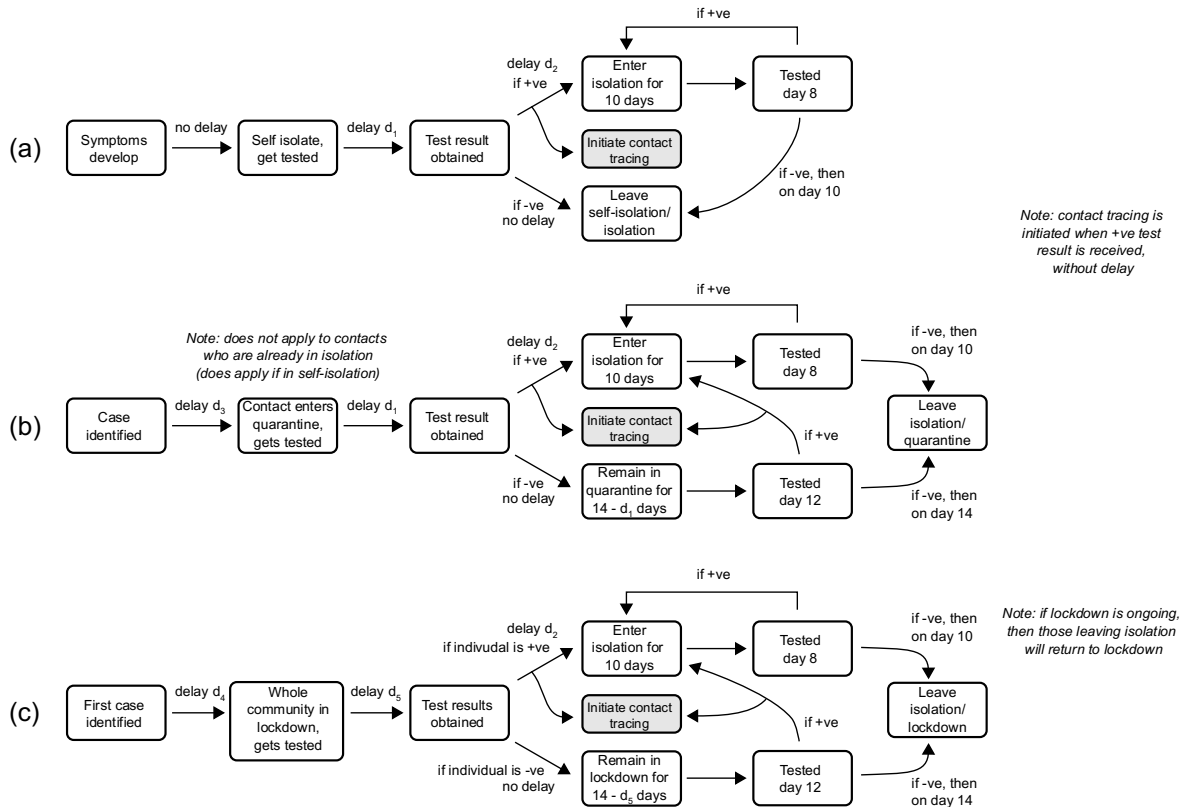

Figure A1. Schematic diagram of the isolation, contact tracing and quarantine in the disease model: (a) represents scenario where case is identified after symptoms develop, (b) represents scenario where case is identified by contact tracing, (c) represents lockdown scenario.

A.2. Model calibration

We applied The Bayesian Optimization for Likelihood-Free Inference (BOLFI) framework to calibrate the model. We used the set of summary statistics (that describe key epidemiological quantities for which we have some prior knowledge) shown in Table A6. These include the basic reproduction number, the mean generation interval, the secondary household attack rate, and the probability of the time of symptom onset being n days earlier than the time of first transmission (TOST), where n is set as -5, -1, 0, 1, 5.

The set of free parameters (estimated by the calibration process) include:

- The mean and standard deviation of the natural logarithm of the distribution describing the duration of symptomatic infection (assuming a lognormal distribution),
- the base probability of transmission per contact,

The values of these free parameters that we use in the model are those which were found to minimise the discrepancy between the model generated summary statistics, and the values of the observed summary statistics. The values of these free parameters that are used in the model are shown in Table A4.

Table A3: Parameters describing community and dwelling characteristics ('AG'= Age Group)

<table>
<tr><th>Parameter/s</th><th>Value</th><th>Source</th></tr>
<tr><td>Community and household size</td><td>
<table>
<tr><th>Scenarios</th><th>Pre-emptive</th><th colspan="3">Reactive</th></tr>
<tr><td>Community size</td><td>1000</td><td>220</td><td>580</td><td>1018</td></tr>
<tr><td>Number of houses</td><td>130</td><td>36</td><td>121</td><td>291</td></tr>
<tr><td>Mean core household size</td><td>7.7</td><td>6.1</td><td>4.8</td><td>3.5</td></tr>
</table>
</td><td>Defined in consultation with the Aboriginal and Torres Strait Islander Advisory Group on COVID-19</td></tr>
<tr><td>Age distribution</td><td>Pre-emptive: Reflective of Aboriginal and Torres Strait Islander Australians in the Northern Territory, Australia.
Reactive: Defined in consultation with the Aboriginal and Torres Strait Islander Advisory Group on COVID-19</td><td>[2]</td></tr>
<tr><td>Within-community mobility</td><td>Individuals stay at main household (core) 66% of the time, second household (regular) 23% of the time, third household (on/off) 9% of the time, and spend their remaining time (i.e. 2%) at a randomly allocated household</td><td>[3,4]</td></tr>
<tr><td>Daily number of contacts with each current household member</td><td>1</td><td>Assumption</td></tr>
<tr><td>Daily number of community contacts (row is age of contact, column is age of agent)
Work package 2 estimate for remote communities (see demographic analysis)</td><td>
<table>
<tr><th>AG</th><th>0,5</th><th>5,10</th><th>10,15</th><th>15,20</th><th>20,25</th><th>25,30</th><th>30,35</th><th>35,40</th><th>40,45</th><th>45,50</th><th>50,55</th><th>55,60</th><th>60,65</th><th>65,70</th><th>70,75</th><th>75,80</th><th>80+</th></tr>
<tr><td>0,5</td><td>2.71</td><td>1.03</td><td>0.23</td><td>0.18</td><td>0.33</td><td>0.49</td><td>0.51</td><td>0.45</td><td>0.39</td><td>0.40</td><td>0.40</td><td>0.29</td><td>0.17</td><td>0.11</td><td>0.11</td><td>0.15</td><td>0.11</td></tr>
<tr><td>5,10</td><td>1.11</td><td>7.54</td><td>1.47</td><td>0.32</td><td>0.37</td><td>0.57</td><td>0.71</td><td>0.73</td><td>0.68</td><td>0.70</td><td>0.73</td><td>0.51</td><td>0.29</td><td>0.19</td><td>0.15</td><td>0.15</td><td>0.13</td></tr>
<tr><td>10,15</td><td>0.36</td><td>1.60</td><td>11.34</td><td>1.84</td><td>0.59</td><td>0.62</td><td>0.77</td><td>0.89</td><td>0.92</td><td>0.89</td><td>0.87</td><td>0.61</td><td>0.35</td><td>0.26</td><td>0.19</td><td>0.13</td><td>0.09</td></tr>
<tr><td>15,20</td><td>0.28</td><td>0.40</td><td>2.02</td><td>10.50</td><td>1.89</td><td>0.82</td><td>0.81</td><td>0.91</td><td>0.98</td><td>0.99</td><td>0.89</td><td>0.63</td><td>0.38</td><td>0.29</td><td>0.25</td><td>0.14</td><td>0.07</td></tr>
<tr><td>20,25</td><td>0.39</td><td>0.34</td><td>0.55</td><td>2.19</td><td>4.94</td><td>1.73</td><td>1.08</td><td>1.04</td><td>1.03</td><td>1.03</td><td>1.00</td><td>0.76</td><td>0.46</td><td>0.33</td><td>0.31</td><td>0.20</td><td>0.07</td></tr>
<tr><td>25,30</td><td>0.62</td><td>0.48</td><td>0.40</td><td>0.72</td><td>2.22</td><td>3.29</td><td>1.76</td><td>1.46</td><td>1.28</td><td>1.16</td><td>1.17</td><td>1.04</td><td>0.65</td><td>0.40</td><td>0.36</td><td>0.28</td><td>0.09</td></tr>
<tr><td>30,35</td><td>0.72</td><td>0.71</td><td>0.51</td><td>0.52</td><td>1.05</td><td>2.04</td><td>2.27</td><td>1.82</td><td>1.56</td><td>1.24</td><td>1.13</td><td>1.09</td><td>0.79</td><td>0.47</td><td>0.37</td><td>0.32</td><td>0.11</td></tr>
<tr><td>35,40</td><td>0.54</td><td>0.70</td><td>0.61</td><td>0.51</td><td>0.70</td><td>1.15</td><td>1.50</td><td>1.69</td><td>1.59</td><td>1.24</td><td>0.98</td><td>0.89</td><td>0.73</td><td>0.48</td><td>0.36</td><td>0.29</td><td>0.11</td></tr>
<tr><td>40,45</td><td>0.34</td><td>0.48</td><td>0.53</td><td>0.52</td><td>0.57</td><td>0.79</td><td>0.93</td><td>1.16</td><td>1.36</td><td>1.22</td><td>0.91</td><td>0.72</td><td>0.57</td><td>0.42</td><td>0.34</td><td>0.27</td><td>0.10</td></tr>
<tr><td>45,50</td><td>0.23</td><td>0.29</td><td>0.35</td><td>0.42</td><td>0.50</td><td>0.64</td><td>0.69</td><td>0.78</td><td>0.96</td><td>1.10</td><td>0.95</td><td>0.70</td><td>0.50</td><td>0.36</td><td>0.30</td><td>0.26</td><td>0.10</td></tr>
<tr><td>50,55</td><td>0.18</td><td>0.19</td><td>0.21</td><td>0.26</td><td>0.37</td><td>0.49</td><td>0.52</td><td>0.53</td><td>0.59</td><td>0.71</td><td>0.84</td><td>0.71</td><td>0.49</td><td>0.32</td><td>0.26</td><td>0.24</td><td>0.11</td></tr>
<tr><td>55,60</td><td>0.15</td><td>0.13</td><td>0.11</td><td>0.12</td><td>0.20</td><td>0.31</td><td>0.35</td><td>0.35</td><td>0.33</td><td>0.36</td><td>0.47</td><td>0.57</td><td>0.46</td><td>0.31</td><td>0.22</td><td>0.19</td><td>0.10</td></tr>
<tr><td>60,65</td><td>0.10</td><td>0.08</td><td>0.06</td><td>0.05</td><td>0.08</td><td>0.14</td><td>0.19</td><td>0.20</td><td>0.17</td><td>0.16</td><td>0.19</td><td>0.28</td><td>0.33</td><td>0.28</td><td>0.19</td><td>0.13</td><td>0.07</td></tr>
<tr><td>65,70</td><td>0.05</td><td>0.04</td><td>0.03</td><td>0.03</td><td>0.03</td><td>0.05</td><td>0.07</td><td>0.10</td><td>0.09</td><td>0.07</td><td>0.07</td><td>0.10</td><td>0.15</td><td>0.19</td><td>0.17</td><td>0.10</td><td>0.04</td></tr>
<tr><td>70,75</td><td>0.02</td><td>0.02</td><td>0.02</td><td>0.01</td><td>0.02</td><td>0.02</td><td>0.03</td><td>0.04</td><td>0.05</td><td>0.04</td><td>0.04</td><td>0.04</td><td>0.06</td><td>0.08</td><td>0.12</td><td>0.09</td><td>0.03</td></tr>
<tr><td>75,80</td><td>0.01</td><td>0.01</td><td>0.01</td><td>0.01</td><td>0.01</td><td>0.01</td><td>0.01</td><td>0.02</td><td>0.02</td><td>0.03</td><td>0.02</td><td>0.02</td><td>0.02</td><td>0.03</td><td>0.05</td><td>0.07</td><td>0.03</td></tr>
<tr><td>80+</td><td>0.00</td><td>0.00</td><td>0.00</td><td>0.01</td><td>0.01</td><td>0.01</td><td>0.01</td><td>0.01</td><td>0.02</td><td>0.02</td><td>0.02</td><td>0.02</td><td>0.02</td><td>0.02</td><td>0.03</td><td>0.04</td><td>0.04</td></tr>
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Table A4: Parameters related to transmission and progression of infection ('AG' = Age Group).

Parameter	Distribution / value	Source
Basic reproduction number	10.7, 5	Highest value: Work package 2 estimate for remote communities (see demographic analysis)
Latent period	Lognormal(mu=1.3, sigma=0.4) which results in mean 4 days, Pr(Latent period < x) = 0.95 of 7.23 days	[6]
Incubation period	Lognormal(mu=1.51, sigma=0.46) which results in mean 5 days, Pr(Incubation period < x) = 0.95 of 9.6 days	[7]
Duration of symptomatic infection	Lognormal(mu=1.40, sigma=0.10) which results in mean 4 days, Pr(Symptomatic period < x) = 0.95 of 4.7 days	Calibrated
Probability of developing symptoms	**AG** **[0,10)** **[10,20)** **[20,30)** **[30,40)** **[40,50)** **[50,60)** **[60,70)** **70+** 0.29 0.21 0.27 0.33 0.4 0.49 0.63 0.69	[8]
Relative susceptibility in community	**AG** **[0,5)** **[5,10)** **[10,15)** **[15,20)** **[20,25)** **[25,30)** **[30,35)** **[35,40)** 0.081 0.098 0.115 0.139 0.197 0.232 0.245 0.243 **AG** **[40,45)** **[45,50)** **[50,55)** **[55,60)** **[60,65)** **[65,70)** **[70,75)** **[75,80)** 0.234 0.230 0.234 0.241 0.248 0.243 0.223 0.210 **AG** **80+** 0.205	Work package 2 estimate for remote communities (see demographic analysis)
Relative susceptibility in household	**AG** **[0,5)** **[5,10)** **[10,15)** **[15,20)** **[20,25)** **[25,30)** **[30,35)** **[35,40)** 0.216 0.264 0.313 0.385 0.571 0.704 0.755 0.747 **AG** **[40,45)** **[45,50)** **[50,55)** **[55,60)** **[60,65)** **[65,70)** **[70,75)** **[75,80)** 0.711 0.696 0.708 0.737 0.770 0.746 0.668 0.620 **AG** **80+** 0.602	Work package 2 estimate for remote communities (see demographic analysis)

Table A5: Parameters related to vaccination and testing

Parameter	Distribution	Source
Test sensitivity	Bernoulli with Pr(positive at t |C, T_{Inc}) = 0, t <= - T_{Inc} , [1 + exp(-(1.5 + 2.2 s))]^(-1) , - T_{Inc} <= t <= - C , [1 + exp(-(1.5 - 0.22 s))]^(-1) , t > - C where s = t + C, C ~ Uniform[0, min(T_{Inc} , 3.5)].	[9]
Vaccine efficacies	Vaccine and dose | Reduction in susceptibility | Reduction in symptomatic infection | Reduction in onwards transmission AstraZeneca Dose 1 | 0.18 | 0.33 | 0.02 AstraZeneca Dose 2 | 0.6 | 0.61 | 0.36 Pfizer BNT Dose 1 | 0.3 | 0.33 | 0.13 Pfizer BNT Dose 2 | 0.79 | 0.83 | 0.65	Doherty modelling consortium, based on literature and expert consultation

Table A6: Summary statistics used in the model calibration process

Summary statistic	Observed values	Source
Basic reproduction number	10.7, 5	Highest value: Work package 2 estimate for remote communities (see demographic analysis)
Generation Interval	4.65 days	Consistent with transmission potential calculation by the Doherty modelling consortium
Secondary household attack rate	0.311	[9]
Pr(TOST < -5)	0.034	[10]
Pr(TOST < -1)	0.325	[10]
Pr(TOST < 0)	0.515	[10]
Pr(TOST < 1)	0.7	[10]
Pr(TOST < 5)	0.9682	[10]

A.3. Supplementary results

A.3.1. Pre-emptive vaccination, leaky vs all-or-nothing vaccine protection

Given uncertainty in the mechanism of vaccine protection, we consider the sensitivity of our transmission model when assuming leaky vaccine protection, versus all-or-nothing vaccine protection. In the scenarios presented in Figure A.2, there is a slight difference in the size of the outbreak peak, with slightly higher peaks observed in the leaky scenarios (top row), compared to the corresponding all-or-nothing scenarios (bottom row). There is little difference in the timing of outbreak peaks and duration of outbreaks.

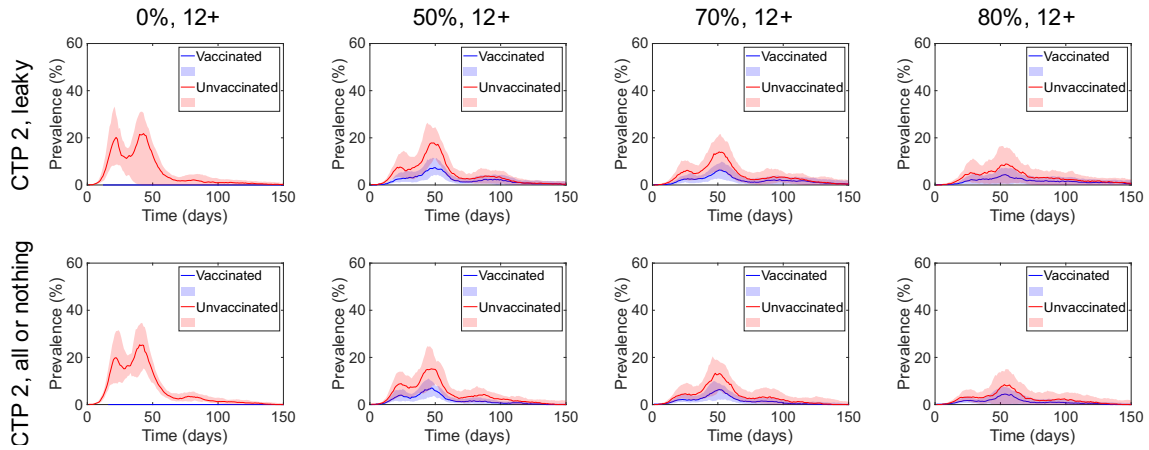

Figure A.2. ***Leaky vs all-or-nothing vaccine protection.*** *Prevalence of infection within the vaccinated (blue) and non-vaccinated (red) subpopulations over time (top row) for response policy CTP2, R0=10.7, leaky vaccine protection; (bottom row) for response policy CTP2, R0=10.7, all-or-nothing vaccine protection, and for each achieved uniform vaccination coverage level (column 1: 0%; column 2: 50%, 12+; column 3: 70%, 12+; column 4: 80%, 12+). Results presented assume 90% level of compliance with lockdown. Solid lines: median prevalence, shaded regions: interquartile range of 100 simulations.*

A.3.2. Pre-emptive vaccination, R_0 = 5 scenarios

Given uncertainty in the basic reproduction number, R_0, for remote communities, the Aboriginal and Torres Strait Islander Advisory Group on COVID-19 was interested in understanding the likely impact of contain and trace response policies with pre-emptive vaccination under the assumption of R_0=5. In the results presented in Figures A3 and Tables A7-A9, it is clear that with a lower starting transmission potential of R_0=5, the impact of contain and trace response policies and pre-emptive vaccination on reducing outbreak size and clinical burdens is far greater, compared to the R_0=10.7 scenarios.

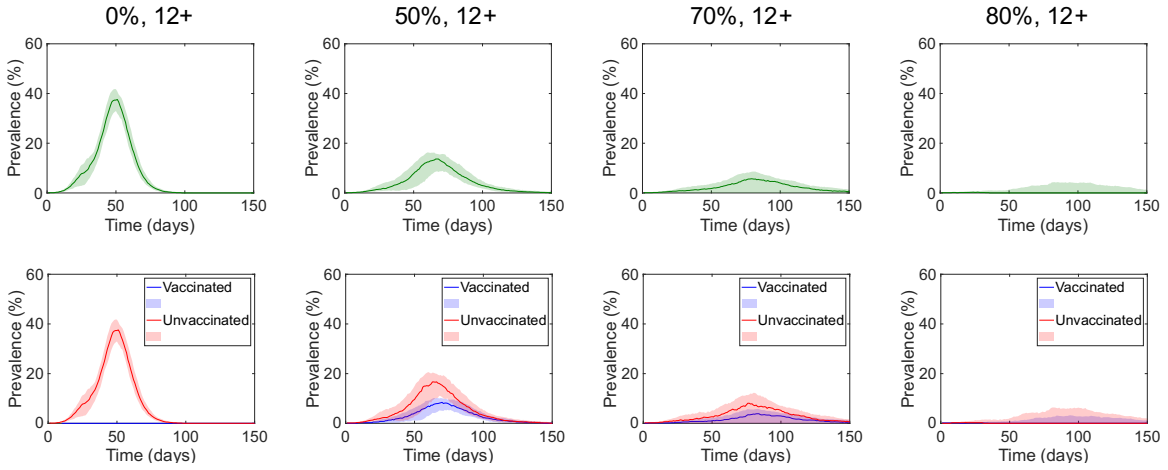

Figure A3. ***Basic reproduction number, R_0=5****. Prevalence of infection (top row) in the whole community; (bottom row) within the vaccinated (blue) and non-vaccinated (red) subpopulations, over time. Here, we assume response policy CTP1 for each achieved uniform vaccination coverage level (column 1: 0%; column 2: 50%, 12+; column 3: 70%, 12+; column 4: 80%, 12+;). Results presented assume 90% level of compliance with lockdown. Solid lines: median prevalence, shaded regions: interquartile range of 100 simulation.*

*Table A7. **Basic reproduction number, R_0=5**. Total cumulative infections for a community of 1000 people, stratified by age and vaccination status. Median and interquartile range of cumulative infections are shown by age group and vaccination status. Results presented assume 90% level of compliance with lockdown and response policy **CTP1**.*

Achieved vaccination coverage scenario	Vaccination status of infected	Age groups				
		<12	12-<15	15-<40	40-<60	60+
No coverage (12+, 0%)	Vaccinated	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 0)	0 (0, 0)
	Not vaccinated	171 (162, 178)	48 (44, 52)	414 (403, 423)	212 (203, 221)	64 (58, 68)
Uniform coverage 1 (12+, 50%)	Vaccinated	0 (0, 0)	3 (2, 5)	80 (72, 86)	43 (38, 49)	18 (14, 21)
	Not vaccinated	126 (113, 136)	27 (22, 31)	178 (167, 187)	93 (88, 100)	29 (24, 32)
Uniform coverage 2 (12+, 70%)	Vaccinated	0 (0, 0)	3 (0, 5)	82 (1, 94)	48 (0, 56)	18 (0, 22)
	Not vaccinated	97 (1, 114)	17 (0, 22)	94 (1, 100)	49 (0, 56)	14 (0, 17)
Uniform coverage 3 (12+, 80%)	Vaccinated	0 (0, 0)	0 (0, 4)	2 (0, 91)	1 (0, 48)	1 (0, 21)
	Not vaccinated	1 (0, 102)	1 (0, 16)	2 (0, 61)	1 (0, 33)	1 (0, 10)

*Table A8. **Basic reproduction number, R_0=5**. Average cumulative number of symptomatic infections, ward admissions and ICU admissions over the course of outbreaks for achieved two dose vaccine threshold targets of 50, 70, and 80% for ages 12+. Results presented assume 90% level of compliance with lockdown, response policy CTP1, and using the 10-year age shift in severity estimates.*

Average cumulative number	Achieved vaccination coverage scenario		
	50%, 12+	70%, 12+	80%, 12+
Symptomatic infections	138	68	34
Ward admissions	30	14	6
ICU admissions	12	6	2

*Table A9. Average cumulative number of symptomatic infections, ward admissions and ICU admissions over the course of outbreaks for achieved two dose vaccine threshold targets of 50, 70, and 80% for ages 12+, stratified by age and vaccination status. Results presented assume 90% level of compliance with lockdown, response policy CTP1, a basic reproduction number **R_0 = 5**, and using the 10-year age shift in severity estimates.*

Average cumulative number	Achieved coverage scenario	<15 yrs		15-39 yrs		40-59 yrs		60+ yrs	
		Vacc'd	Unvac	Vacc'd	Unvac	Vacc'd	Unvac	Vacc'd	Unvac
Symptomatic infections	50%	0	37	3	43	3	34	3	14
	70%	0	22	3	18	2	15	2	6
	80%	0	13	2	8	1	6	2	3
Ward admissions	50%	0	1	0	3	0	11	2	13
	70%	0	0	0	1	0	5	2	6
	80%	0	0	0	1	0	2	1	2
ICU admissions	50%	0	0	0	1	0	5	1	6
	70%	0	0	0	0	0	2	1	3
	80%	0	0	0	0	0	1	0	1

A.3.3. Pre-emptive vaccination, 20-year age shift in severity

Given uncertainty in the severity of disease in Australian Aboriginal and Torres Strait Islander people, relative to the general population (due to limited data), we also calculated clinical burden in pre-emptive vaccination response scenarios assuming a 20-year age shift in severity estimates (clinical burdens shown in the main report assume a 10-year age shift in severity relative to the general population, which is consistent with the limited data we have to date). In all scenarios, the clinical burden (excluding symptomatic infections) is increased compared to the 10-year age shift scenarios.

*Table A10. **20-year age shift in severity and $R_0 = 10.7$**. Average cumulative number of symptomatic infections, ward admissions and ICU admissions over the course of outbreaks for achieved two dose vaccine threshold targets of 50, 70, and 80% for ages 12+. Results presented assume 90% level of compliance with lockdown, response policy CTP1, a basic reproduction number $R_0 = 10.7$, and using the 20-year age shift in severity estimates.*

Average cumulative number	Achieved vaccination coverage scenario		
	50%, 12+	70%, 12+	80%, 12+
Symptomatic infections	203	147	112
Ward admissions	66	41	29
ICU admissions	27	17	11

*Table A11. **20-year age shift in severity and $R_0 = 5$.** Average cumulative number of symptomatic infections, ward admissions and ICU admissions over the course of outbreaks for achieved two dose vaccine threshold targets of 50, 70, and 80% for ages 12+. Results presented assume 90% level of compliance with lockdown, response policy CTP1, a basic reproduction number **$R_0 = 5$**, and using the **20 year age shift** in severity estimates.*

Average cumulative number	Achieved vaccination coverage scenario		
	50%, 12+	70%, 12+	80%, 12+
Symptomatic infections	138	68	34
Ward admissions	47	22	10
ICU admissions	20	9	4

A.3.4. Reactive vaccination, $R_0 = 5$ scenarios

Given uncertainty in the basic reproduction number, R_0, for remote communities, the Aboriginal and Torres Strait Islander Advisory Group on COVID-19 was interested in understanding the likely impact of contain and trace response policies with reactive vaccination under the assumption of $R_0=5$. In the results presented in Figure A4-A6 and Tables A12-A17, it is clear that with a lower starting transmission potential of $R_0=5$, the impact of contain and trace response policies and reactive vaccination on reducing outbreak size and clinical burdens is far greater, compared to the $R_0=10.7$ scenarios.

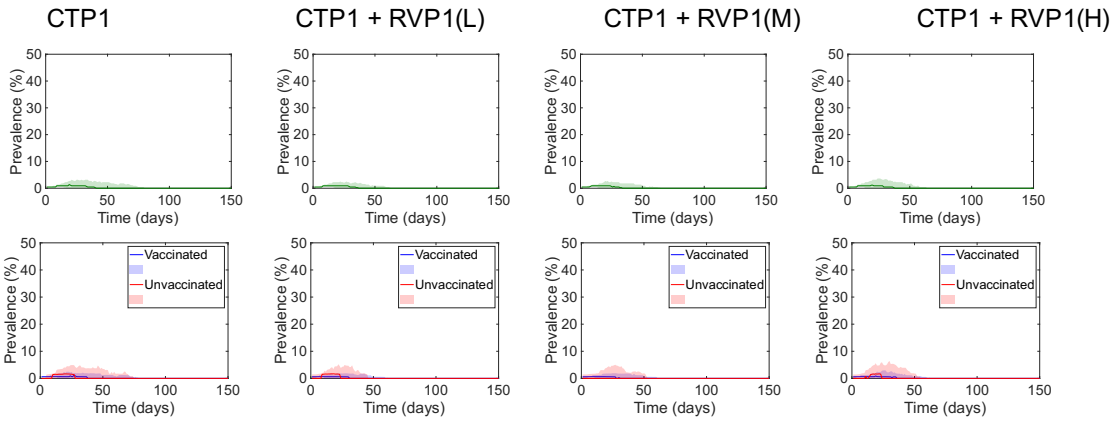

Figure A4. ***Basic reproduction number, R_0=5, exemplar community 1*** *(N = 220, high coverage). Prevalence of infection (top row) in the whole community; (bottom row) within the vaccinated (blue) and non-vaccinated (red) subpopulations, over time, for response policies (column 1) CTP1; (column 2) CTP1+RVP1 (low rate); (column 3) CTP1+RVP1 (medium rate); (column 4) CTP1+RVP1 (high rate). Results presented assume 90% level of compliance with lockdown. Solid lines: median prevalence, shaded regions: interquartile range of 100 simulations.*

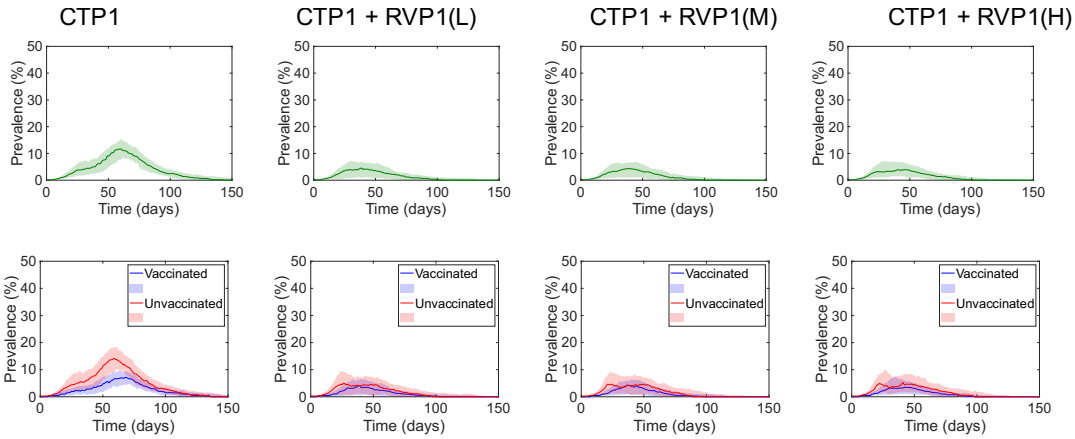

Figure A5. ***Basic reproduction number, R_0=5, exemplar community 2*** *(N = 580, medium coverage). Prevalence of infection (top row) in the whole community; (bottom row) within the vaccinated (blue) and non-vaccinated (red) subpopulations, over time, for response policies (column 1) CTP1; (column 2) CTP1+RVP1 (low rate); (column 3) CTP1+RVP1 (medium rate); (column 4) CTP1+RVP1 (high rate). Results presented assume 90% level of compliance with lockdown. Solid lines: median prevalence, shaded regions: interquartile range of 100 simulations.*

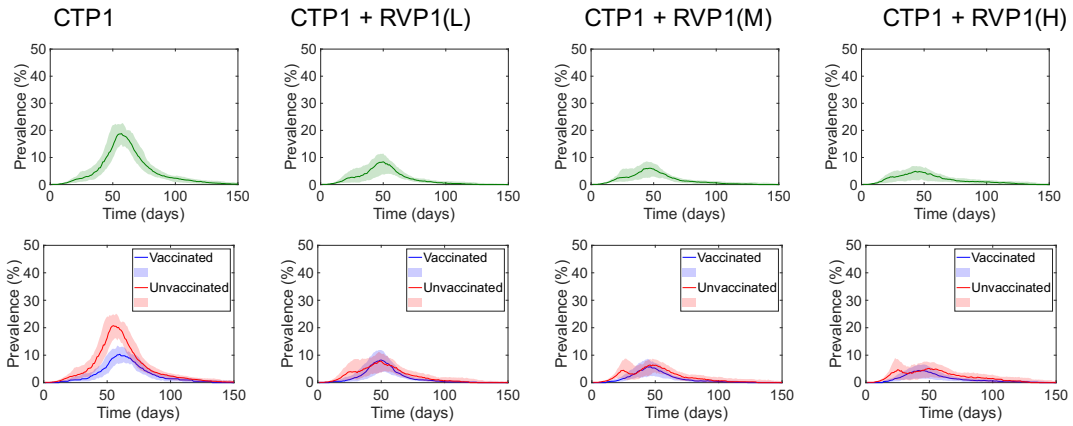

Figure A6. ***Basic reproduction number, R_0=5, exemplar community 3*** *(N = 1018, low coverage). Prevalence of infection (top row) in the whole community; (bottom row) within the vaccinated (blue) and non-vaccinated (red) subpopulations, over time, for response policies (column 1) CTP1; (column 2) CTP1+RVP1 (low rate); (column 3) CTP1+RVP1 (medium rate);. (column 4) CTP1+RVP1 (high rate). Results presented assume 90% level of compliance with lockdown. Solid lines: median prevalence, shaded regions: interquartile range of 100 simulations*

Table A12. ***Basic reproduction number, R_0=5, exemplar community 1*** *(N = 220, high coverage). Total cumulative infections stratified by age and vaccination status. Median and interquartile range of cumulative infections are shown by age group, vaccination status. Results presented assume 90% level of compliance with lockdown, response policy* ***CTP1*** *and reactive vaccination policy* ***RVP1*** *for low, medium and high vaccination rates, R_0=5.*

Reactive vaccination rate	Vaccination status of infected	Age groups				
		<12	12-<15	15-<40	40-<60	60+
0	Vaccinated	0 (0, 0)	0 (0, 0)	3 (0, 10)	1 (0, 6)	1 (0, 4)
	Not vaccinated	2 (0, 9)	0 (0, 2)	1 (0, 4)	0 (0, 1)	0 (0, 0)
Low (30/day)	Vaccinated	0 (0, 0)	0 (0, 0)	3 (0, 8)	1 (0, 4)	1 (0, 2)
	Not vaccinated	1 (0, 5)	0 (0, 1)	0 (0, 2)	0 (0, 0)	0 (0, 0)
Medium (60/day)	Vaccinated	0 (0, 0)	0 (0, 1)	2 (0, 8)	1 (0, 4)	0 (0, 2)
	Not vaccinated	1 (0, 5)	0 (0, 1)	0 (0, 1)	0 (0, 0)	0 (0, 0)
High (100/day)	Vaccinated	0 (0, 0)	0 (0, 1)	2 (0, 8)	1 (0, 4)	1 (0, 2)
	Not vaccinated	2 (0, 7)	0 (0, 2)	0 (0, 2)	0 (0, 0)	0 (0, 0)

Table A13. ***Basic reproduction number, R_0=5, exemplar community 2*** *(580 people, medium coverage). Total cumulative infections stratified by age and vaccination status. Median and interquartile range of cumulative infections are shown by age group, vaccination status. Results presented assume 90% level of compliance with lockdown, response policy* ***CTP1*** *and reactive vaccination policy* ***RVP1*** *for low, medium and high vaccination rates, R_0=5.*

Reactive vaccination rate	Vaccination status of infected	Age groups				
		<12	12-<15	15-<40	40-<60	60+
0	Vaccinated	0 (0, 0)	1 (0, 1)	34 (28, 39)	25 (21, 30)	15 (12, 18)
	Not vaccinated	77 (67, 85)	19 (15, 22)	121 (112, 126)	36 (33, 40)	10 (8, 12)
Low (30/day)	Vaccinated	0 (0, 0)	2 (0, 4)	43 (15, 54)	21 (7, 28)	9 (3, 13)
	Not vaccinated	40 (11, 54)	5 (2, 10)	13 (5, 23)	3 (1, 6)	1 (0, 2)
Medium (60/day)	Vaccinated	0 (0, 0)	2 (1, 3)	39 (20, 56)	19 (10, 26)	9 (3, 12)
	Not vaccinated	39 (17, 54)	6 (2, 8)	12 (6, 24)	4 (1, 7)	1 (0, 1)
High (100/day)	Vaccinated	0 (0, 0)	2 (0, 5)	42 (22, 56)	19 (7, 26)	9 (4, 13)
	Not vaccinated	40 (16, 54)	5 (2, 7)	12 (6, 23)	3 (2, 6)	1 (0, 2)

Table A14. ***Basic reproduction number, R_0=5, exemplar community 3*** *(1018 people, low coverage). Total cumulative infections stratified by age and vaccination status. Median and interquartile range of cumulative infections are shown by age group, vaccination status. Results presented assume 90% level of compliance with lockdown, response policy* ***CTP1*** *and reactive vaccination policy* ***RVP1*** *for low, medium and high vaccination rates, R_0=5.*

Reactive vaccination rate	Vaccination status of infected	Age groups				
		<12	12-<15	15-<40	40-<60	60+
0	Vaccinated	0 (0, 0)	1 (0, 1)	18 (14, 20)	35 (31, 40)	29 (25, 33)
	Not vaccinated	129 (116, 142)	40 (32, 45)	314 (302, 327)	101 (92, 107)	29 (25, 32)
Low (30/day)	Vaccinated	0 (0, 0)	8 (3, 10)	98 (70, 115)	44 (33, 53)	23 (15, 30)
	Not vaccinated	77 (61, 87)	13 (10, 17)	38 (22, 62)	9 (5, 16)	2 (1, 3)
Medium (60/day)	Vaccinated	0 (0, 0)	6 (3, 8)	79 (63, 97)	37 (24, 46)	18 (12, 26)
	Not vaccinated	66 (51, 88)	12 (7, 14)	28 (17, 48)	8 (4, 12)	1 (0, 3)
High (100/day)	Vaccinated	0 (0, 0)	5 (3, 7)	77 (49, 98)	37 (23, 48)	18 (11, 23)
	Not vaccinated	69 (46, 87)	11 (6, 15)	31 (14, 42)	9 (3, 12)	1 (0, 3)

Table A15. ***Basic reproduction number, R_0=5, exemplar community 1*** *(N = 220, high coverage). Average cumulative number of symptomatic infections, ward admissions and ICU admissions over the course of outbreaks with CTP1 and RVP1 (medium rate) switched on or off. Results presented assume 90% level of compliance with lockdown, R0=5, a 2-day delay to initiation of the reactive vaccination program and using the 10-year age shift in severity estimates.*

Average cumulative number	CTP1	CTP1 and RVP1(M)
Symptomatic infections	4	2
Ward admissions	1	0
ICU admissions	0	0

Table A16. ***Basic reproduction number, R_0=5, exemplar community 2*** *(580 people, medium coverage). Average cumulative number of symptomatic infections, ward admissions and ICU admissions over the course of outbreaks with CTP1 and RVP1 (medium rate) switched on or off. Results presented assume 90% level of compliance with lockdown, R0=5, a 2-day delay to initiation of the reactive vaccination program and using the 10-year age shift in severity estimates.*

Average cumulative number	CTP1	CTP1 and RVP1(M)
Symptomatic infections	79	28
Ward admissions	15	4
ICU admissions	6	2

Table A17. ***Basic reproduction number, R_0=5, exemplar community 3*** *(1018 people, low coverage). Average cumulative number of symptomatic infections, ward admissions and ICU admissions over the course of outbreaks with CTP1 and RVP1 (medium rate) switched on or off. Results presented assume 90% level of compliance with lockdown, R0=5, a 2-day delay to initiation of the reactive vaccination program and using the 10-year age shift in severity estimates.*

Average cumulative number	CTP1	CTP1 and RVP1(M)
Symptomatic infections	178	53
Ward admissions	36	8
ICU admissions	14	3

A.3.5. Reactive vaccination, 20-year age shift in severity

Given uncertainty in the severity of disease in Australian Aboriginal and Torres Strait Islander people, relative to the general population (due to limited data), we also calculated clinical burden in reactive vaccination response scenarios assuming a 20-year age shift in severity estimates (clinical burdens shown in the main report assume a 10-year age shift in severity relative to the general population, which is consistent with the limited data we have to date). In all scenarios, the clinical burden (excluding symptomatic infections) is increased compared to the 10-year age shift scenarios.

*Table A18. **20-year age shift in severity and R_0 = 10.7, exemplar community 3** (1018 people, low coverage). Average cumulative number of symptomatic infections, ward admissions and ICU admissions over the course of outbreaks with CTP1 and RVP1 (medium rate) switched on or off. Results presented assume 90% level of compliance with lockdown, R0=10.7, a 2-day delay to initiation of the reactive vaccination program and using the 10-year age shift in severity estimates.*

Average cumulative number	CTP1	CTP1 and RVP1(M)
Symptomatic infections	248	166
Ward admissions	74	40
ICU admissions	31	15

*Table A19. **20-year age shift in severity and R_0=5, exemplar community 3** (1018 people, low coverage). Average cumulative number of symptomatic infections, ward admissions and ICU admissions over the course of outbreaks with CTP1 and RVP1 (medium rate) switched on or off. Results presented assume 90% level of compliance with lockdown, R0=5, a 2-day delay to initiation of the reactive vaccination program and using the 10-year age shift in severity estimates.*

Average cumulative number	CTP1	CTP1 and RVP1(M)
Symptomatic infections	178	53
Ward admissions	55	12
ICU admissions	23	5

References

[1] Bailie, R.S. and K.J. Wayte, *Housing and health in Indigenous communities: key issues for housing and health improvement in remote Aboriginal and Torres Strait Islander communities.* Aust J Rural Health, 2006. **14**(5): p. 178-83.

[2] Australian Bureau of Statistics. Life tables for Aboriginal and Torres Strait Islander Australians, 2015–2017, 'Table 1.6: life tables for Aboriginal and Torres Strait Islander Australians, Northern Territory—2015–2017', data cube: excel spreadsheet, cat. no. 3302.0.55.003. Canberra: Australian Bureau of Statistics.

[3] Musharbash, Y., Yuendumu Everyday: Contemporary life in remote Aboriginal Australia. 2008: Aboriginal Studies Press;.

[4] Chisholm RH, Crammond B, Wu Y, Bowen AC, Campbell PT, Tong SY, et al. A model of population dynamics with complex household structure and mobility: implications for transmission and control of communicable diseases. PeerJ. 2020;8:e10203

[5] Kiti MC, Kinyanjui TM, Koech DC, Munywoki PK, Medley GF, Nokes DJ. Quantifying age-related rates of social contact using diaries in a rural coastal population of Kenya. PLoS One. 2014;9:e104786

[6] Min Kang, Hualei Xin, Jun Yuan, Sheikh Taslim Ali, Zimian Liang, Jiayi Zhang, Ting Hu, Eric H. Y. Lau, Yingtao Zhang, Meng Zhang, Benjamin J. Cowling, Yan Li, Peng Wu. Transmission dynamics and epidemiological characteristics of Delta variant infections in China. medRxiv 2021.08.12.21261991;

[7] Davies, N.G., Klepac, P., Liu, Y. et al. Age-dependent effects in the transmission and control of COVID-19 epidemics. Nat Med 26, 1205–1211 (2020)

[8] Hellewell, J., Russell, T.W., The SAFER Investigators and Field Study Team. et al. Estimating the effectiveness of routine asymptomatic PCR testing at different frequencies for the detection of SARS-CoV-2 infections. BMC Med 19, 106 (2021).

[9] Madewell ZJ, Yang Y, Longini IM, Halloran ME, Dean NE. Factors Associated With Household Transmission of SARS-CoV-2: An Updated Systematic Review and Meta-analysis. JAMA Netw Open. 2021;4(8):e2122240.

[10] Luca Ferretti, Alice Ledda, Chris Wymant, Lele Zhao, Virginia Ledda, Lucie Abeler-Dörner, Michelle Kendall, Anel Nurtay, Hao-Yuan Cheng, Ta-Chou Ng, Hsien-Ho Lin, Rob Hinch, Joanna Masel, A. Marm Kilpatrick, Christophe Fraser. The timing of COVID-19 transmission. medRxiv 2020.09.04.20188516