THE
ROYAL
SOCIETY

30 November 2020

Appendix

SARS-CoV-2: Where Do People Acquire Infection and ‘Who Infects Whom’?

This is the appendix of the rapid review of the science of infection and COVID-19 from the Royal Society provided to assist SAGE in relation to COVID-19.

Appendix 1

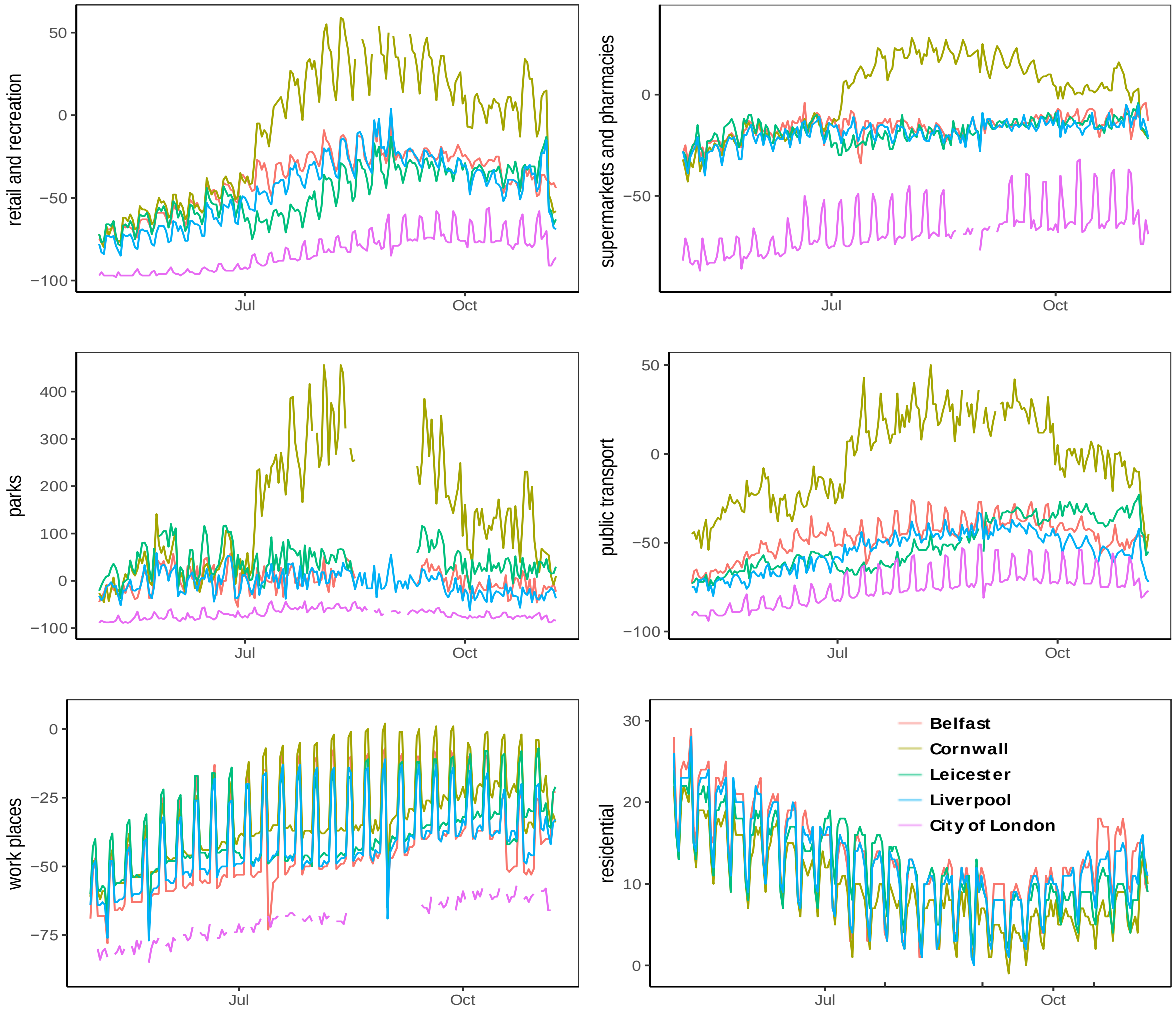


Figure A1: Mobility trends for selected, contrasting areas of the UK, 1st May to 8th November 2020. Figures show how visits and length of stay at different places change compared to a baseline (zero value), which is the median value, for the corresponding day of the week, during the five-week period 3rd January to 6th February 2020. The category “Retail and recreation” includes places such as restaurants, cafés, shopping centres, theme parks, museums, libraries and cinemas; “parks” includes beaches and public gardens. Missing data may be due to data not meeting quality and privacy thresholds for that day. Figure drawn by authors using Google Mobility data, accessed 12th November 2020.[1]

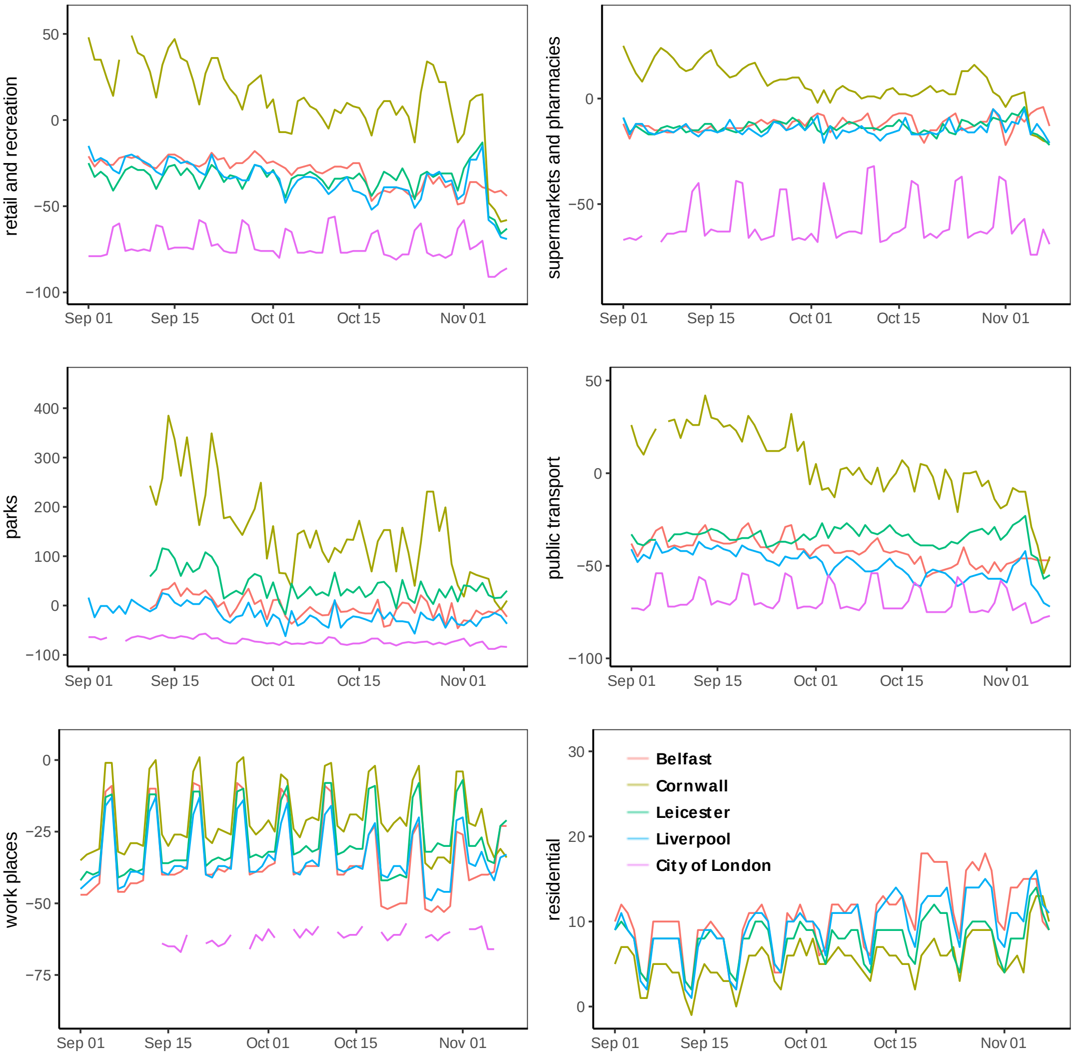


Figure A2: Mobility trends for selected, contrasting areas of the UK, 1st September to 8th November 2020. Figures show how visits and length of stay at different places change compared to a baseline (zero value), which is the median value, for the corresponding day of the week, during the five-week period 3rd January to 6th February 2020. The "Retail and recreation" category includes places such as restaurants, cafés, shopping centres, theme parks, museums, libraries and cinemas; "parks" includes beaches and public gardens. Missing data may be due to data not meeting quality and privacy thresholds for that day. Figure drawn by authors using data from Google Mobility data, accessed 12th November 2020.[1]

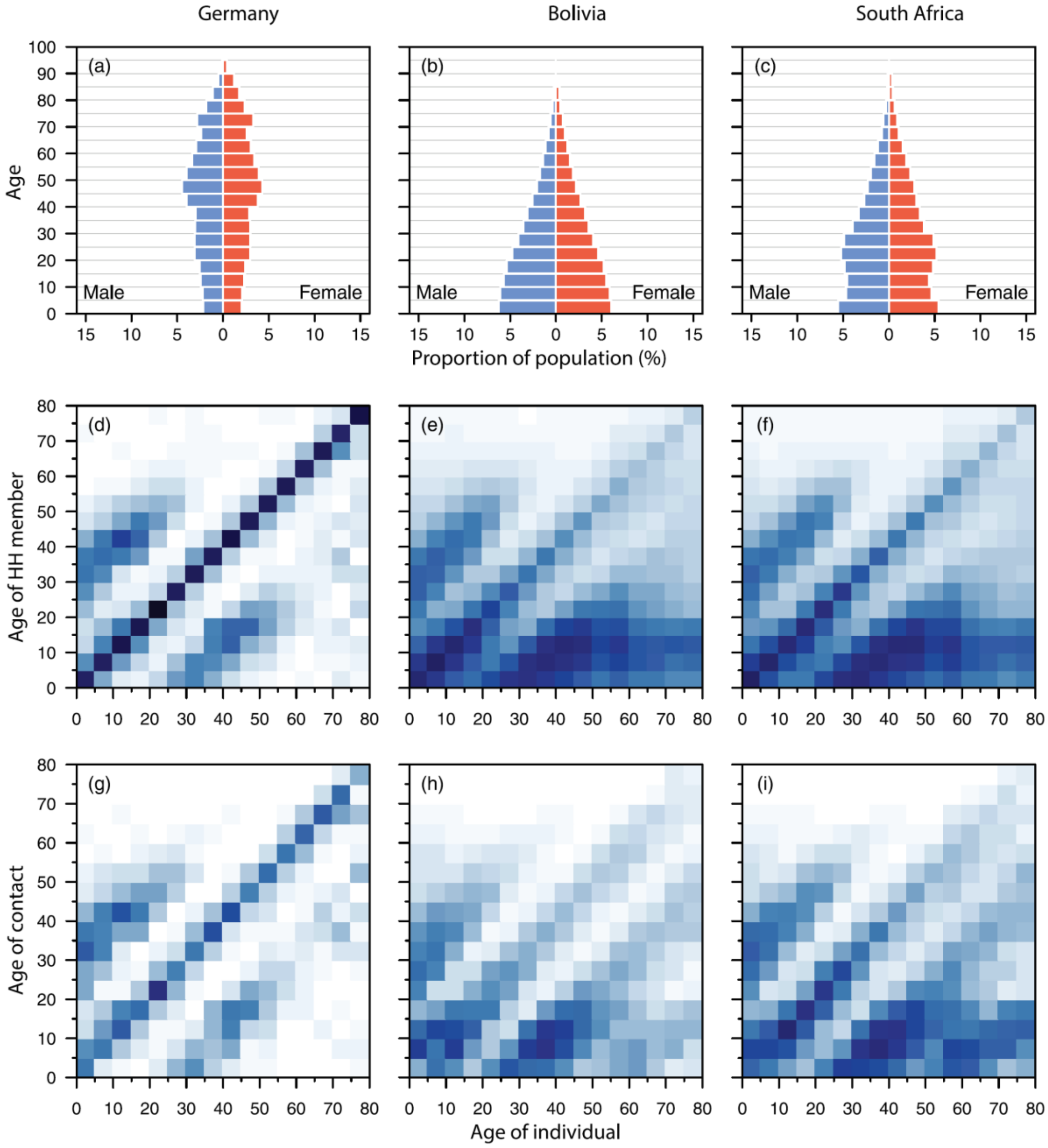


Figure A3: Population and household age distribution, and age specific contacts at home. The top row shows age pyramids for three countries. The next row shows household structure by age and the bottom row shows reported contacts by age in households. The dark shading shows high frequency contacts and low to zero shading intensity shows limited or no reported contacts. The tight relationships in Germany which would be most closely associated with the UK in some social groups shows strong parent-child contacts. In Bolivia and South Africa, the matrices show broader contact between children, parents and grandparents due to multiple generations living in the same household. Figure taken from Prem et al 2016[20].

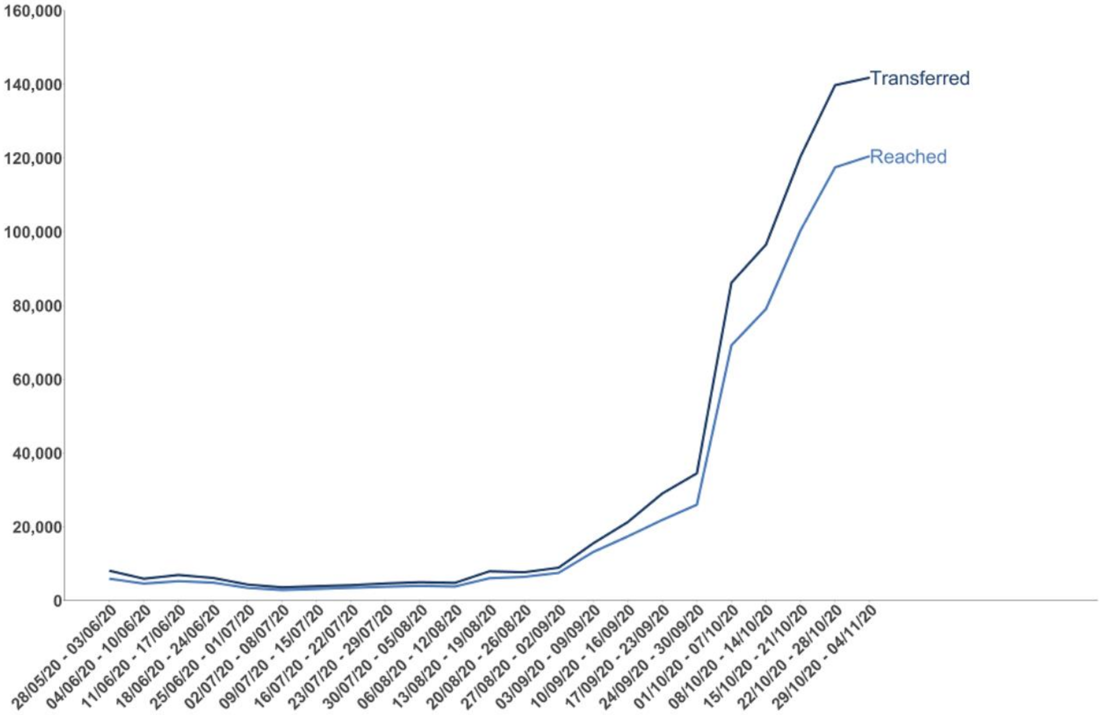
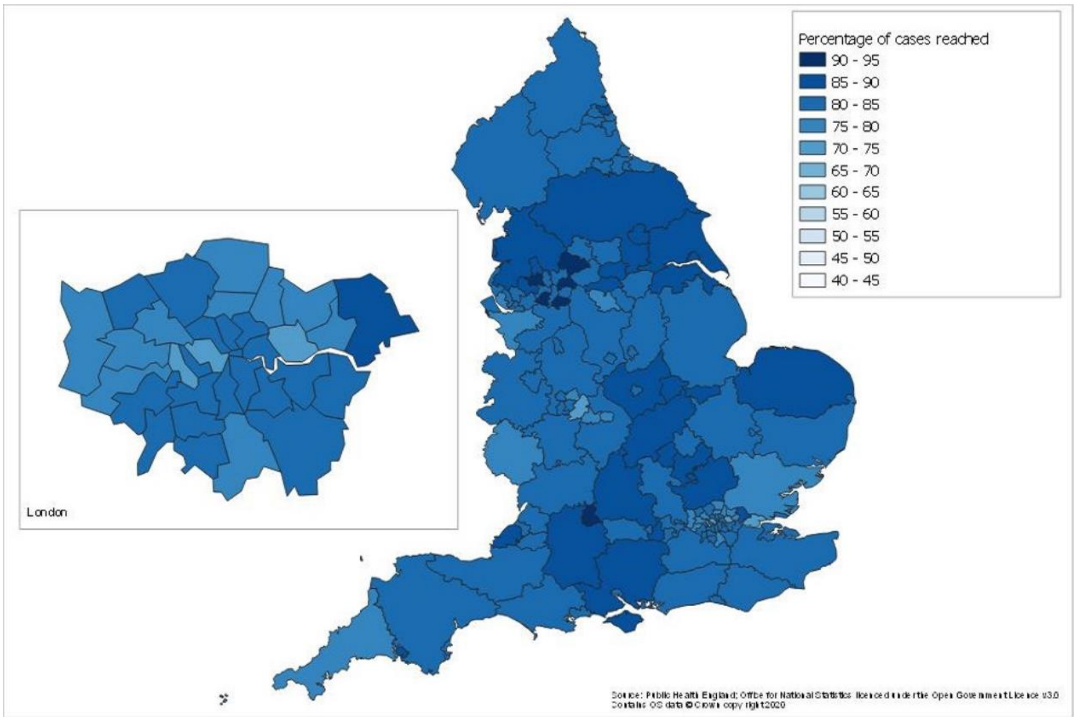


Figure A4: Number of people transferred to the contact tracing system and number of people transferred who were reached and asked to provide details of recent close contacts (includes cases managed and not managed by local HPTs), England. Figure taken from GOV.UK COVID -19 dashboard[47].



Source: Public Health England; Office for National Statistics licenced under the Open Government Licence v3.0
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Figure A5: Percentage of cases reached and asked to provide details of recent close contacts by upper tier local authority since Test and Trace began in England. Figure taken GOV.UK COVID -19 dashboard[47].

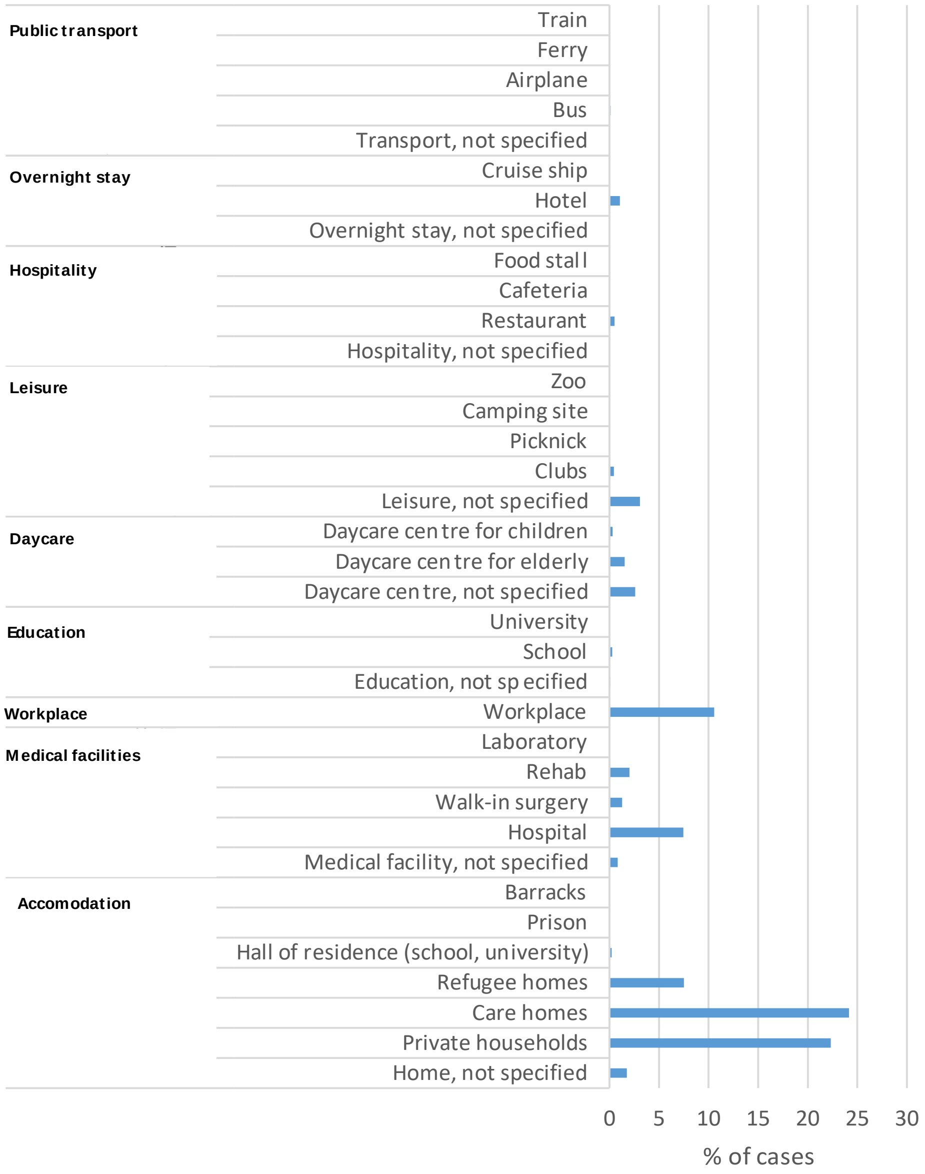


Figure A6: Percentage of COVID-19 cases assigned to an outbreak, by infection setting: contact tracing data from Germany up to 11th August 2020. Figure taken from Robert Koch Institute.[2]

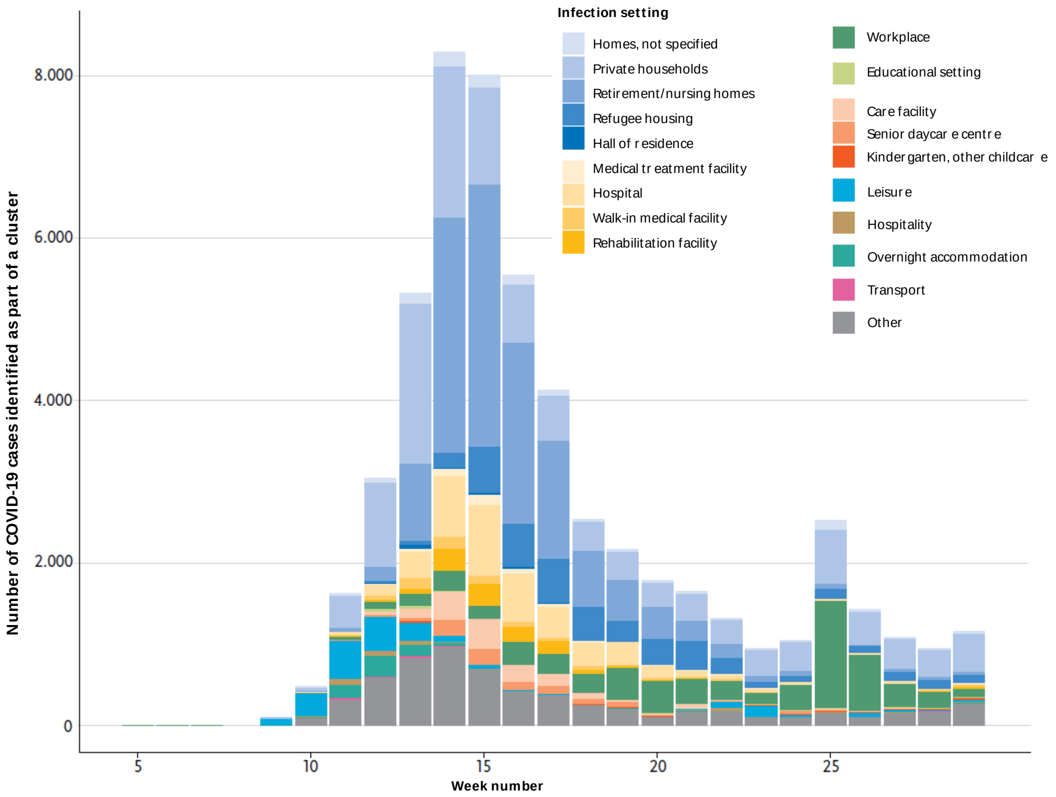
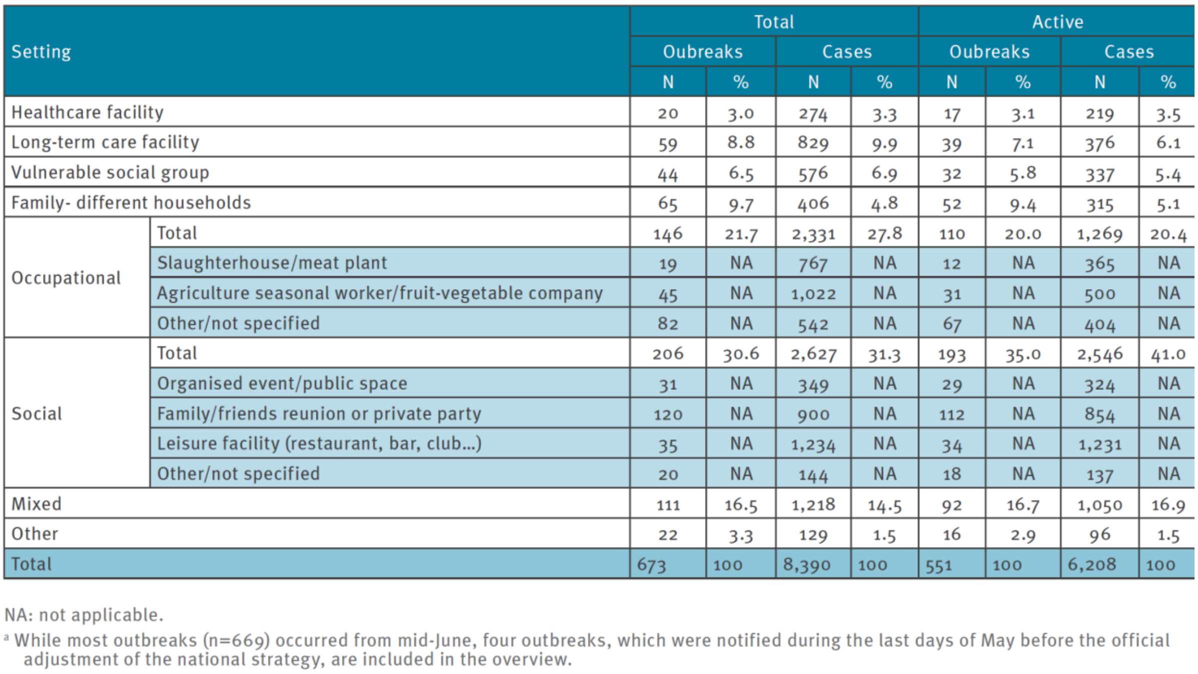


Figure A7: Laboratory-confirmed COVID-19 cases assigned to an outbreak, by infection setting and reporting week (up to 11th August 2020). Graph adapted from Robert Koch Institute report, 17th September 2020.[11]



Setting		Total				Active			
		Oubreaks		Cases		Oubreaks		Cases	
		N	%	N	%	N	%	N	%
Healthcare facility		20	3.0	274	3.3	17	3.1	219	3.5
Long-term care facility		59	8.8	829	9.9	39	7.1	376	6.1
Vulnerable social group		44	6.5	576	6.9	32	5.8	337	5.4
Family- different households		65	9.7	406	4.8	52	9.4	315	5.1
Occupational	Total	146	21.7	2,331	27.8	110	20.0	1,269	20.4
	Slaughterhouse/meat plant	19	NA	767	NA	12	NA	365	NA
	Agriculture seasonal worker/fruit-vegetable company	45	NA	1,022	NA	31	NA	500	NA
	Other/not specified	82	NA	542	NA	67	NA	404	NA
Social	Total	206	30.6	2,627	31.3	193	35.0	2,546	41.0
	Organised event/public space	31	NA	349	NA	29	NA	324	NA
	Family/friends reunion or private party	120	NA	900	NA	112	NA	854	NA
	Leisure facility (restaurant, bar, club...)	35	NA	1,234	NA	34	NA	1,231	NA
	Other/not specified	20	NA	144	NA	18	NA	137	NA
Mixed		111	16.5	1,218	14.5	92	16.7	1,050	16.9
Other		22	3.3	129	1.5	16	2.9	96	1.5
Total		673	100	8,390	100	551	100	6,208	100

NA: not applicable.

[a] While most outbreaks (n=669) occurred from mid-June, four outbreaks, which were notified during the last days of May before the official adjustment of the national strategy, are included in the overview.

Table A1 Examination of outbreaks and settings of outbreaks of COVID-19 infection in Spain in the first wave of the epidemic in that country.[53]

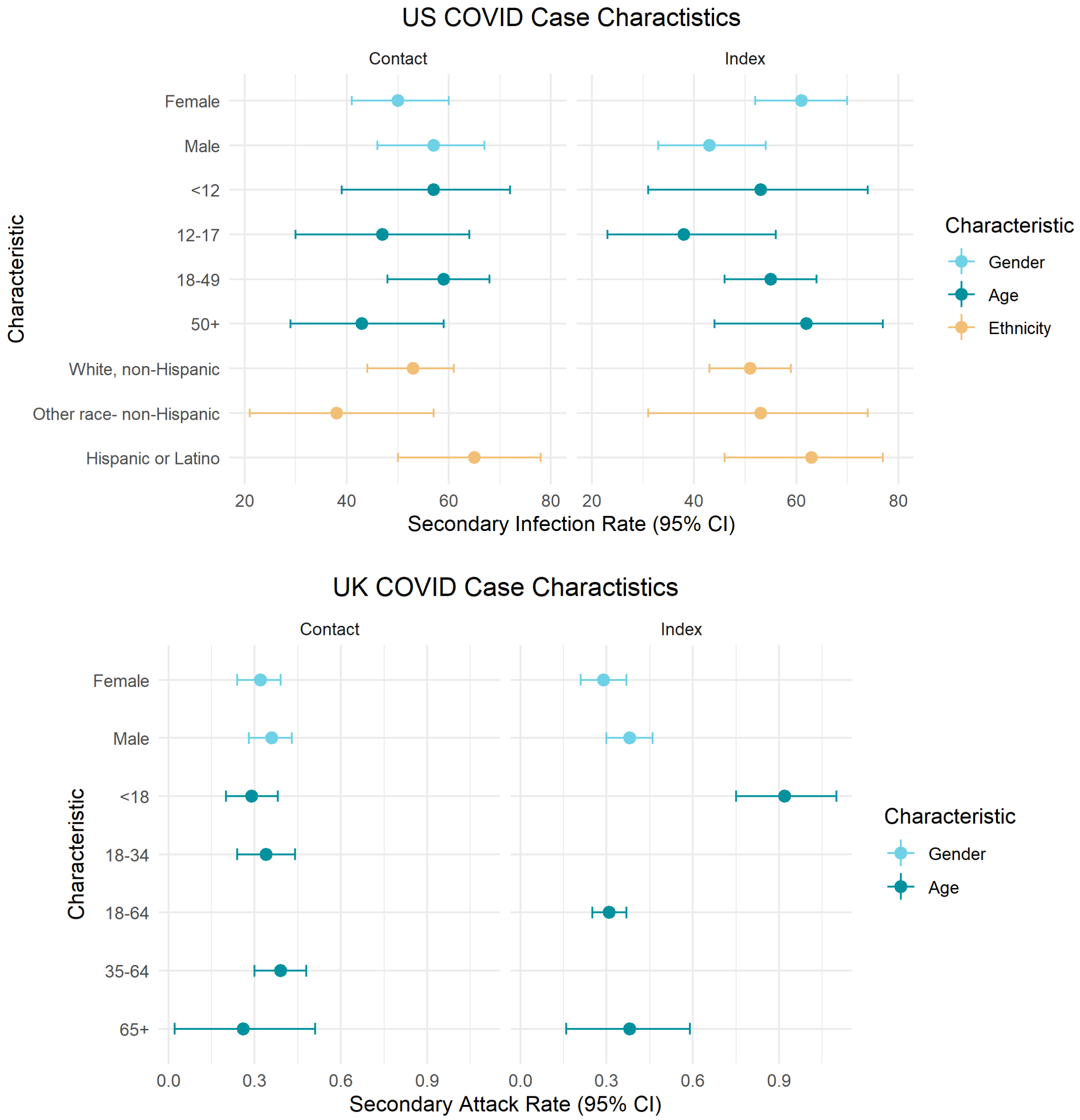


Figure A8: Forest plot comparing UK[71] and US[70] data measuring index and contact case characteristics; namely age, gender and ethnicity (US only). Overall, the data show mirrored rates between index and contacts. Note: UK data measures unadjusted secondary attack rate, whilst US data measures secondary infection rate.

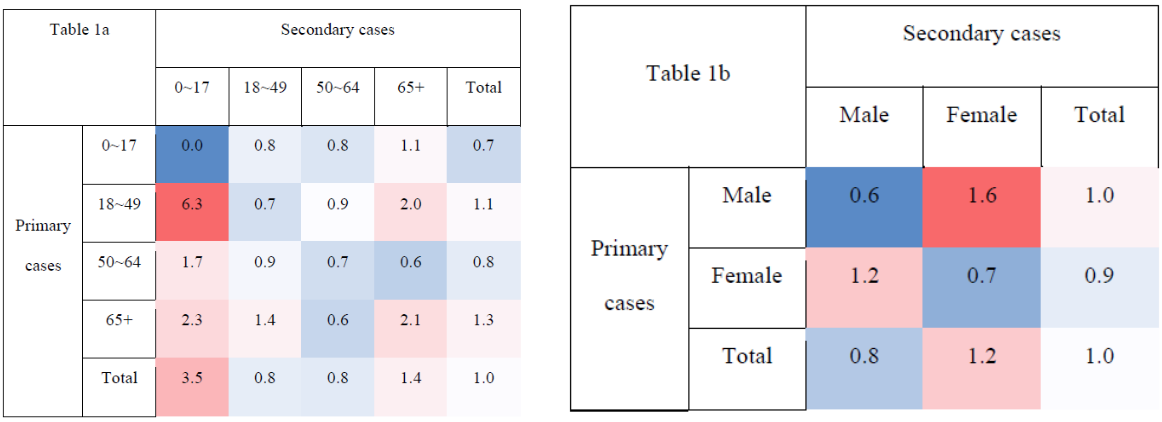


Table 1a		Secondary cases				
		0~17	18~49	50~64	65+	Total
Primary cases	0~17	0.0	0.8	0.8	1.1	0.7
	18~49	6.3	0.7	0.9	2.0	1.1
	50~64	1.7	0.9	0.7	0.6	0.8
	65+	2.3	1.4	0.6	2.1	1.3
	Total	3.5	0.8	0.8	1.4	1.0

Table 1b		Secondary cases		
		Male	Female	Total
Primary cases	Male	0.6	1.6	1.0
	Female	1.2	0.7	0.9
	Total	0.8	1.2	1.0

Table A2: Hazard of infection stratified by age or gender. The risk of being infected outside of households is higher for age groups between 18 and 64 years, whereas the hazard of being infected within households is higher for age groups of young (<18) and elderly (>65) people. (1a) Age-stratified hazard of infection for the household relative to non-household transmission. (1b) Gender-specific hazard of infection for the household relative to non-household transmission. Red or blue shades indicate an increased or decreased hazard of infection within households relative to outside of households, respectively. Figure taken Xu et al et al.[89]

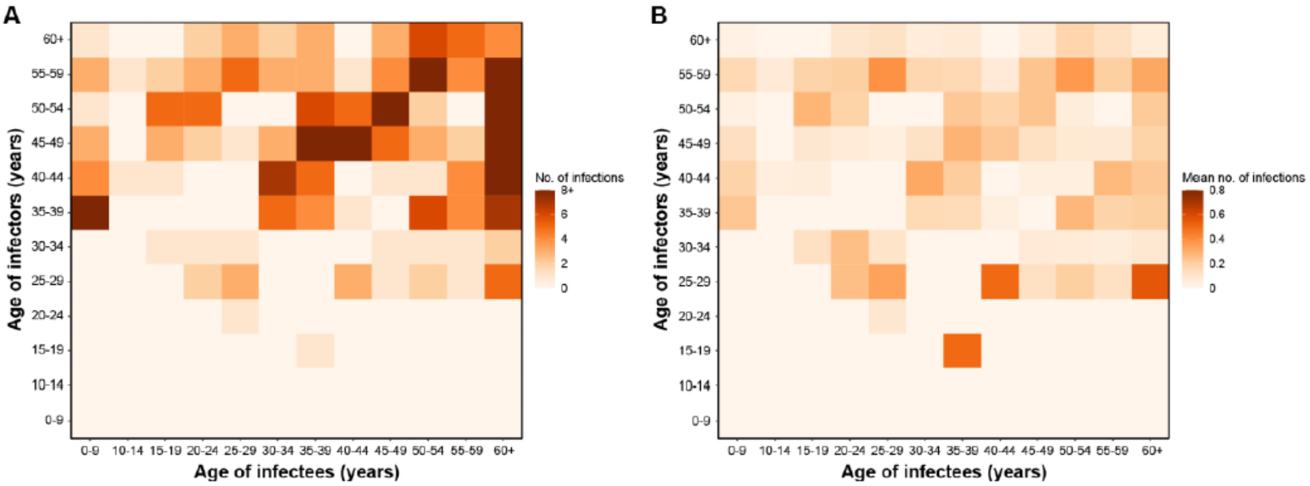


Figure A9: Number of infections by age of infector and infectee. Each cell in the matrices refers to the total number of infections (A) and the mean number of infections (B) caused by an infector of a given age. Figure taken from Hu et al.[54]

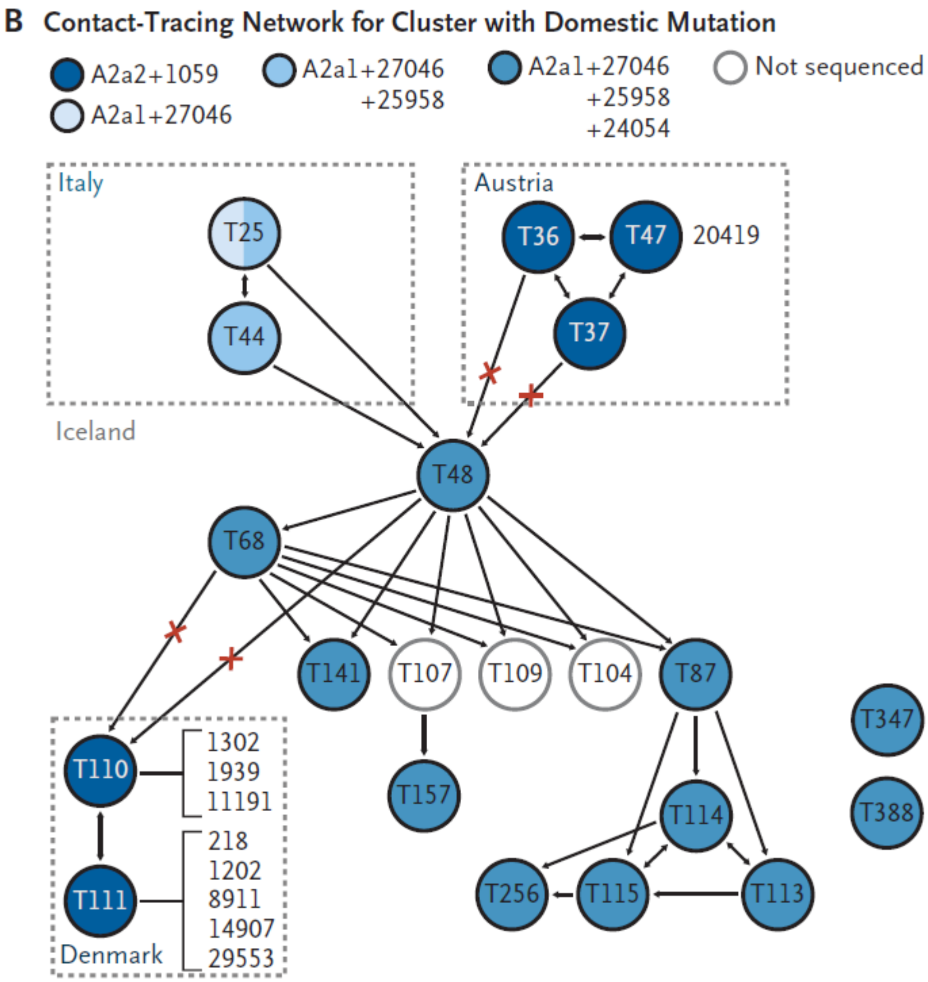


Figure A10: Contact tracing network overlaid by Whole-Genome Sequencing (WGS) information that enabled the identification of the source of origin of the transmission cluster and led to the identification of two previously unlinked cases to the same transmission cluster. Figure taken from Gudbjartsson et al, 2020[14].

Appendix 2

The NHS TTI system was launched in late May 2020. The results from a recent week (22nd October to the 28th of October 2020) give an idea of the volume of testing undertaken weekly during the first phase of the second wave in the UK. There are 4 pillars or tiers of testing. For pillar 1, this starts with a person having a coronavirus test in hospital. For pillar 2, this starts with a person booking or ordering a coronavirus test. Pillar 2 tests can either be conducted at a regional test site, local test site or mobile test unit; or a satellite or home test can be conducted. Pillar 3 tests are serological tests made available as part of research studies that show whether people have antibodies against SARS-CoV-2 following infection.[90] For pillar 4, this starts with a person having a coronavirus test as part of a prevalence study (those who are tested as part of anonymous studies do not get passed on to contact tracing). After tests have been taken, they are sent to a laboratory for processing. Once processed, a person will be emailed or texted their result.

In the week of 22nd-28th October in England, 137,180 people tested positive for coronavirus (SARS-CoV-2) at least once in England. Positive cases had been rising steeply since the end of August, and in the last week in October there had been an increase of 8% compared to the previous week. 9.3% of people tested had a positive result and this rate has been increasing since the end of August. A total of 1,482,528 people were tested at least once for COVID-19, similar to the previous week. A total of 10,218,475 people have been tested at least once since TTI began. Turnaround times for pillar 2 (swab testing for the wide population) for all in-person testing routes have improved compared to the previous week but continue to be longer than they were at the end of June. In the most recent week, 61.8% of in person test results were received the next day after the test was taken. Turnaround times for satellite/home tests have also improved since the previous week, with 52.4% of results received within 48 hours.

The median distance to in-person testing sites (pillar 2) for booked tests has decreased over the past month. Between 22 October and 28 October, the median distance was 2.7 miles, similar to the previous week but continuing the downwards trend seen over the past 6 weeks. Of those tested, 139,781 people were transferred to the contact tracing system between 22 October and 28 October, a 16% increase compared to the previous week. The number of people transferred has been increasing steeply over the past 8 weeks with over 15 times as many people being transferred in the most recent week compared to the end of August. Of those transferred to the contact tracing system between 22 October and 28 October, 82.7% were reached and asked to provide information about their contacts. This has remained similar over the past month. In this week, 27,203 people were identified as coming into close contact with someone who had tested positive between 22 October and 28 October. This is an increase of 14% compared with the previous week, continuing the sharp upward trend since the end of August. For those where communication details were available, 77.8% were reached and asked to self-isolate. Taking into account all the contacts identified, only 59.9% were reached. This is clearly insufficient to have a very marked impact on transmission unless all contact had not or did not transmit on and fully adhered to isolation rules.

Testing capacity in the UK across all pillars between 22 October and 28 October was at 3,596,069 tests, an increase of 11% compared to the previous week. Testing capacity for all swab testing was at 2,748,369 tests, a 64% increase since the start of September. 1,206,106 tests were sent out across the UK within pillars 2 and 4 in the latest week. The number of tests sent out had decreased since the end of September. After a notable increase between 15 October and 21 October, it has decreased slightly in the latest week. 2,227,054 tests were processed in the UK, across all pillars, in the latest week, a 6% increase compared with the previous week. Since the beginning of September there has been a 57% increase in tests processed. 2,178,983 swab tests were processed in the latest week, which is 4 times higher than in mid-June. A summary Flow chart of how people move through the TTI system is shown in **Figure A11**, based on the government website.[46]

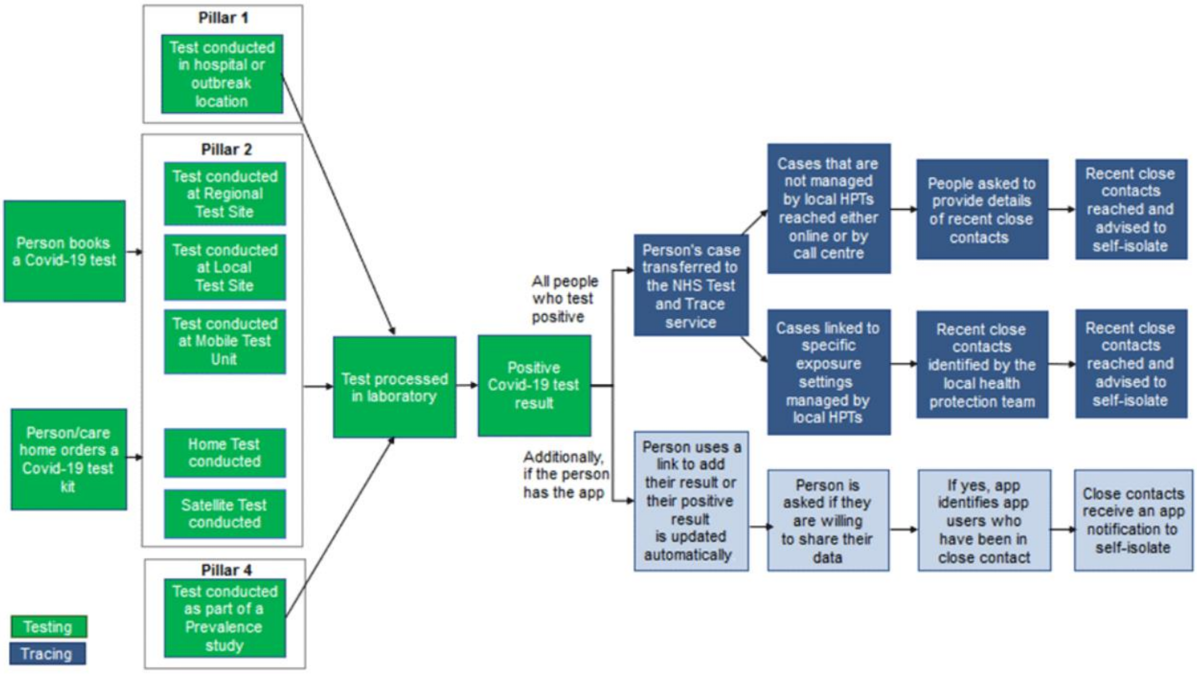


Figure A11: Flow chart of how people move through the Test and Trace system in the UK (note this includes only Pillars 1, 2 & 4).

Appendix 3

Table A3: Summary of published and pre-print studies evaluating COVID-19 contact tracing interventions in Western Europe and North America, plus selected Asian countries known to have effective contact tracing programmes

First author	Setting	Population	Evaluation or intervention period (2020)	COVID-19 prevalence	Methods	Key findings
PREPRINT[a]						
Salathé[91]	Switzerland	National coverage (population 8.7 million[92])	23rd Jul – 10th Sept	16-55/100,000[b]	SwissCovid app: each phone generates a daily Temporary Exposure Key (TEK), from which fast rotating proximity identifiers (RPI) are derived and exchanged with neighbouring phones via Bluetooth Low Energy (BLE) beacons. Positive RT-PCR test gives user a Covidcode, assumes contagious period started 2 days before symptoms. Notifies via TEK those in proximity to infected.	12,456 confirmed cases, issued 2,447 Covidcodes of which 1645 (67%) were used by users. Embedded cohort of "Zurich SARS-CoV-2 Cohort" longitudinal study 7th Aug – 11th Sep. App downloaded 2.36 million times, daily active 1.62 million
Fateh-Moghadam[52]	Independent Province of Trento, Italy	2,812 laboratory-diagnosed community cases of COVID-19 had 6,690 community contacts	March and April (province mainly in lockdown)	12-14/100,000 per day[93]	Contact tracing website developed for the province. Information on contacts was collected by telephone interviews following a standard questionnaire. Contacts were followed via telephone, emails, or the app.	6,690 contacts included in analysis originating from 2,812 cases. 890 developed symptoms, 13.3% attack rate. Overall, 606 outbreaks were identified, 74% of which consisted of only two cases, 16.3% three cases, 7% four cases and 3% having ≥5 connected cases. Greatest risk of transmission (contacts developing symptoms or having a positive test) increased with age of contact. There was no major difference by gender. Workplace exposure was associated with higher risk of becoming a case than cohabiting with a case or having a non-cohabiting family member/friend who was a case. Secondary attack rate by characteristic of contact:

First author	Setting	Population	Evaluation or intervention period (2020)	COVID-19 prevalence	Methods	Key findings
						Age of contact, years (n=6687) 0-14: 8.4% (86/1024) 25-29: 9.2% (126/1372) 30-49: 14.9% (245/1646) 50-64: 15.4% (264/1712) 65-74: 16.9% (79/467) ≥75: 18.9% (88/466) **Gender of contact (n= 6406)** Women: 13.5% (426/3156) Men: 13.1% (427/3250) **Nature of contact with case (n= 6255)** Cohabitant: 14.1% (500/3546) Non-cohabiting family/friend: 12.9% (206/1596) Work colleague: 15.8% (79/499) Other: 9.0% (55/614) Contagiousness (% of contacts who became cases) by characteristic of case: **Age of index, years (n=1,489)** 0-14: 22.4% (11/49) 25-29: 13.1% (62/475) 30-49: 10.6% (250/2361) 50-64: 13.6% (303/2222) 65-74: 15.2% (85/559) ≥75: 17.1% (155/909) **Gender of index (n= 1,442)** Women: 12.1% (414/427) Men: 14.0% (416/2973)
Kendall[94]	Isle of Wight, UK	Population size 141,500	6th May – 26th May	6.7-2.7/100,000[95]	Pilot of the UK's Test, Trace and Isolate (TTI) programme: combined approach of 1) individually questioning index cases on past close proximity contact events; and 2) using version 1 of the NHS contact tracing app to pass anonymised notifications between	App downloaded 54,000 times (38% of population). During evaluation, manual contact tracing led to 163 notifications to isolate. 1,524 reported symptoms in the app leading to 1,188 exposure notifications. Reproductive number Rt decreased after the TTI intervention on the Isle of Wight more sharply than the national trend.

First author	Setting	Population	Evaluation or intervention period (2020)	COVID-19 prevalence	Methods	Key findings
					new index cases and their past contacts.	
Smith[40]	UK	68.0 million[92]	2nd March – 5th August 2020	3.2/100,000 daily cases[e]	Time series of cross-sectional online surveys (21 survey waves) evaluating the UK's Test, Trace and Isolate programme.	42,127 responses from 31,787 people living in the UK. Self-reported adherence to test, trace and isolate behaviours was low (self-isolation 18%, 95%CI 16-20%; requesting an antigen test 12%, 95%CI 10-14%; intention to share details of close contacts 76%, 95%CI 75-77%; quarantining 11%, 95%CI 8-14%) and largely stable over time. Self-reported adherence to test, trace and isolate behaviours is low; intention to carry out these behaviours is much higher. Identification of COVID-19 symptoms is also low.
PUBLISHED[a]						
Burke[96]	Tennessee and Wisconsin, US	Intensive contact tracing of the first 10 patients with travel-related COVID-19 in the US	As of 26th February 2020	Near zero (first 10 patients in US)	Active symptom monitoring of identified contacts for 14 days.	445 persons (range 1–201 persons per case) who had close contact with one of the 10 patients on or after the date of the patient's symptom onset were identified. 19/445 (4%) contacts were members of a patient's household, and five of these continued to have household exposure to the patient during their isolation period. 104/445 (23%) were community members who spent at least 10 minutes within 6 feet of a patient; 100/445 (22%) were community members who were exposed to a patient in a healthcare setting; 222/445 (50%) were health care personnel. Two household contacts of patients tested positive for SARS-CoV-2 (secondary attack rate 0.45% (95%CI 0.12%–1.6%) among all close contacts, and a symptomatic secondary attack rate of 10.5% (95% CI 2.9%–31.4%) among household members. No other close contacts who were tested for SARS-CoV-2 had a positive test, including the five household members who were continuously exposed during the period of isolation of their household member with confirmed COVID-19.
Baraniuk[51]	Northern Ireland, UK	1.9 million[97]	Pilot programme went live 27th April; article published 18th June	0.5-4.6/100,000[d] daily cases	Pilot programme. Cases are called within 24h and asked about close contacts, who are then also called. Close contacts are identified as e.g., people who have been living in the same home as a case	92% of all positive covid-19 cases and their contacts were traced within 24h. High responsiveness attributed to information put on local media about how the contact tracing programme would work, to raise awareness.

First author	Setting	Population	Evaluation or intervention period (2020)	COVID-19 prevalence	Methods	Key findings
					or have spent >15min with a case at a distance <2m. Those deemed to be at risk are advised to self-isolate.	
Iacobucci[98]	England	56.2 million[97]	1st – 7th October	19.5[10.4-34.5]/100,000 daily cases[e]		62.6% of close contacts of people who tested positive for covid-19 Cases handled by local public health protection teams: 97.7% Cases handled either online or by call centres: 57.6% 32.6% of people receiving their result within 24 hours, compared with 27.4% the previous week
Valent[99]	6000-inhabitant town, Remanzacco, Italy	6000[99]	29th Feb – 16th Mar	142.9[19.7-266.1]/100,000 daily cases in Friuli Venezia Giulia[100]		143 persons were traced and followed. Test results were available in mean 5h. All quarantined persons were periodically monitored by telephone to assess clinical conditions. "This experience shows that prompt contact tracing of confirmed cases and extensive collection of nasal swabs from close, even asymptomatic, contacts of cases, with consequent isolation or quarantine, can be effective in extinguishing the COVID-19 epidemic. In our setting, synergic work with the Infectious Disease Clinic, Prevention Department, and Virology and Microbiology Laboratories made these resource-consuming activities possible and effective."
Lash[101]	Two counties, North Carolina, US	1,110,356 143,667	1st June – 12th July	Mean 24 cases/100,000/day		Median interval from specimen collection from the index patient to notification of identified contacts was 6 days in both counties. Health department staff members investigated 5,514 (77%) persons with COVID-19 in Mecklenburg County and 584 (99%) in Randolph Counties. No contacts were reported for 48% of cases in Mecklenburg and for 35% in Randolph. Among contacts provided, 25% in Mecklenburg and 48% in Randolph could not be reached by telephone and were classified as nonresponsive after at least one attempt on 3 consecutive days of failed attempts.
Koetter[102]	Single academic		24th Mar – 28th May	207 – 666 daily cases (peak in		Completed contact tracing for 536 confirmed cases, which resulted in the identification of 953 contacts

First author	Setting	Population	Evaluation or intervention period (2020)	COVID-19 prevalence	Methods	Key findings
	institution, US			April 30, 2,033 cases)[103]		
Robert Koch Institute[2]	Germany	National coverage (population 83.8 million[92])	All data to 11th Aug[c]	Maximum 86/100,000 (9th Apr); 13/100,000 on 11th August[b]		Of 202,225 cases in total, only 55,141 could be linked to an outbreak and a probable infection setting.
Lee[104]	South Korea	51.3 million[92]	29th Feb – 15th Mar	0.7[0.1-1.8]/100,000 daily cases[105]	Descriptive review analysing factors contributing to the country's success in containing viral transmission. Findings were based on the actual field experience of the Korean government's COVID-19 response team.	South Korea has slowed the spread of COVID-19 and flattened the curve of new infections without taking extreme measures that restrict the movement of people and core businesses. Authors attribute this success to agile and comprehensive testing to identify positive cases and robust contact tracing of their contacts to prevent further spread; plus rigorous treating those infected at the earliest stage possible. Contacts of cases are traced by tracking down their credit card transactions, CCTV recordings, and GPS data on their mobile phones when necessary. Anonymised information is disclosed to the public so that those who were in the vicinity of confirmed patients will go through the testing themselves. Those identified through epidemiological investigations are instructed to self-quarantine and monitored one-on-one by staff of the Ministry of the Interior and Safety and local governments.
Park[74]	South Korea	51.3 million[92]	20th Jan – 27th Mar 2020	0.3[0-1.8]/100,000 daily cases[105]	Findings from the national COVID-19 contact tracing programme.	5,706 COVID-19 index patients reported 59,073 contacts. Of 10,592 household contacts, 11.8% had COVID-19. Of 48,481 non-household contacts, 1.9% had COVID-19. Use of personal protective measures and social distancing reduces the likelihood of transmission.
Tran[106]	Hai Phong city, Vietnam	2.1 million[106]	Up to 18th May 2020	0.002[0-0.03]/100,000 daily cases[105] (2.4[0-26] average daily cases)[105]	Case history of how Hai Phong city implemented the initial COVID-19 response	Vietnam had only 320 cases, no deaths, and no verified community transmission, up to 18th May 2020. Hai Phong was the first city in Vietnam to implement preventive activities (on 1st March) such as active screening, contact tracing, and quarantining people from pandemic areas. By 18th May 2020, Hai Phong had not detected any confirmed COVID-19 cases. Of 417 suspected exposure cases, all were quarantined at a health facility.
Pham[107]	Vietnam	97.6 million[92]	Cases during first 100 days after first confirmed case	0.002[0-0.03]/100,000	Clinical and demographic data on the first 270 SARS-CoV-2 infected cases	Vietnam has controlled SARS-CoV-2 spread through early introduction of mass communication, meticulous contact-tracing with strict quarantine, and international travel restrictions. Cases and their contacts were quarantined for

First author	Setting	Population	Evaluation or intervention period (2020)	COVID-19 prevalence	Methods	Key findings
			reported in Vietnam on 23rd Jan	2.3[0-26] average daily cases[105]	and the timing and nature of Government control measures, including numbers of tests and quarantined individuals, were analysed.	14 days in Government facilities to prevent onward transmission. A mobile phone app for contact tracing and symptom reporting was launched on February 8th. One hundred days after the first case, 60% of the first 270 cases were imported, 43% were asymptomatic and 27% of transmissions occurred before symptoms. No community transmission had been detected since April 15th. Through identification of 33 infector-infectee pairs, serial intervals were calculated and used to estimate the proportion of pre-symptomatic transmission events and time-varying reproduction numbers. Up to May 1st, around 70,000 individuals have been quarantined in Government facilities and a further 140,000 at home or in hotels. 266,122 PCR tests have been performed, with a ratio of around 1 positive person: 1000 tests conducted.
Vo[108]	Vietnam	97.6 million[92]	569 confirmed cases, divided into pre-lockdown (23/01 - 22/04) and post lockdown (23/04 - 31/07)		Pre- and post-lockdown evaluation of case epidemiology.	Patients were older in the post-lockdown group, patients remained hospitalised for treatment for longer. Patient pre-lockdown mean age 35.89 (0-88), post-lockdown mean age 40.93 (0-90). 21-30 year group recorded most cases pre-lockdown (96) and post-lockdown (84), followed by 31-40 year group 44 pre-lockdown, 42 post-lockdown. All deaths occurred in the post-lockdown group. 100% of pre-lockdown patients were discharged, whereas 64% of post-lockdown patients were still under treatment at the end of the study.
Phucharoen[109]	Phuket, Thailand	417,000	Up to 29th April 2020	0.03[0-0.4]/100,000 daily cases[105] (Used Thailand population as denominator, as Phuket level data not available) 25.7[0-263] average daily cases	Analysis of high-risk contacts in Phuket recorded by Phuket Provincial Public Health Office contact tracing programme. Thailand's quarantine policy mandated individual isolation in state provided facilities for all high-risk contacts.	<10% of all confirmed cases in Phuket were foreign imported cases. Infections through local transmissions sharply increased after the initial imported transmissions decreased. 15.6% of 1108 high-risk contacts had COVID-19, accounting for 80% of 214 confirmed cases in Phuket up to 29th April 2020. 10.7% of all high-risk contacts were confirmed to be infected before quarantine, and 4.6% after the policy was enforced. Living in the same household as a confirmed case increased infection risk 25% compared to contacts not sharing a household. Contacts' infection probability was negatively linked with their age. There was a higher risk of infection from certain cases than others (super spreaders).

First author	Setting	Population	Evaluation or intervention period (2020)	COVID-19 prevalence	Methods	Key findings
				"Cases in Thailand have remained at approximately 3300"		
Doug-ngern[110]	Thailand	69.4 million			Retrospective case-control study, 211 asymptomatic cases (testing positive later) and 839 controls.	Assessment of mask wearing, social distancing and handwashing. Adjusted odd ratio: men = 0.0.76 (0.41–1.41), <1 m without physical contact = 1.09 (0.58–2.07), >1m = 0.15 (0.04–0.63), duration of contact >15–60 min = 0.67 (0.29–1.55), <15 min = 0.24 (0.07–0.90), handwashing often = 0.33 (0.13–0.87), wearing mask sometimes = 0.87 (0.41–1.84), always wearing a mask = 0.23 (0.09–0.60).
Yong[111]	Singapore	5.9 million[92]	Up to 6th April 2020	0.2[0-2.4]/100,000 daily cases[105] 13.4[0-138] average daily cases "As of 6th April 2020, Singapore had recorded 1375 cases of COVID-19, of which 554 were imported and 821 locally transmitted"	Epidemiological investigation plus serological assays, establishing links between three COVID-19 clusters. In Singapore, active case-finding and contact tracing have been undertaken for all cases.	Three clusters of 28 locally-transmitted cases were from two churches and a family gathering. Links were primarily made by PCR confirmation of cases, but a case linking the two church clusters was eventually diagnosed with past infection by serological testing. Authors concluded that development and application of a serological assay helped to establish connections between COVID-19 clusters in Singapore. Serological testing can have a crucial role in identifying convalescent cases or people with milder disease who might have been missed by other surveillance methods. "Linking disease transmission to an imported source and contact tracing for each identified case has facilitated a high capture of cases in Singapore. This successful linking of a large proportion of cases to imported sources provides encouraging evidence that the intense containment measures undertaken in Singapore have been effective."
Yap[112]	Singapore	5.9 million[92]	No evaluation period reported; paper received by journal 21st March 2020	0.08[0-0.8]/100,000 daily cases[105] 4.7[0.47] average daily cases (from first case to 21st March)	Description of the COVID-19 Symptom Monitoring and Contact Tracking Record (CoV-SCR) web-app (http://bit.ly/covscrapp)	Authors describe the COVID-19 Singapore web-app as a bottom-up, proactive approach to supplement the current management strategies for COVID-19. It enables individuals to keep a personal record of their close contacts and monitor their symptoms on a daily basis, so that they can provide relevant and accurate details when they see the doctor and during the contact tracing process. Individuals can record their temperature and rate their symptoms on a 5-point severity scale, as well as record details of their travel and contact history for the last 14 days. The recorded information

First author	Setting	Population	Evaluation or intervention period (2020)	COVID-19 prevalence	Methods	Key findings
						is sent to their email address for potential symptom monitoring and contact tracing purposes.
Liu[113]	Taiwan	23.8 million[92]	28th Jan to 12th Apr 2020	0.02[0-0.1]/100,000 daily cases[105] 5[0-31] average daily cases	Analysis of demographic characteristics and transmission dynamics of community-acquired COVID-19 cases. Data collected from open-access data and press releases on COVID-19 in Taiwan	All 55 community-acquired confirmed COVID-19 cases were included. 16.4% of community-acquired cases were asymptomatic. 58.2% were identified via contact tracing. The median incubation period was 6 days (range 1 to 13 days) and the median serial interval was 4 days (range -3 to 24 days). Twenty-six cases (47.3%) were transmitted from pre-symptomatic cases, eleven cases (20%) from symptomatic cases, and two cases (3.6%) from an asymptomatic case. The contagious period of symptomatic cases was from 7 days before to 15 days after the onset of symptoms.
Jian[56]	Taiwan	23.8 million[92]	Up to 26th Aug 2020	0.009[0-0.1]/100,000 daily cases[105] (21/01-26/08 date range) 2.2[0-31] average daily cases	Description and reporting of contact tracing in Taiwan: traditional contact tracing measures supplemented with symptom tracking and contact management system. A centralised contact tracing system was developed to support data linkage, cross-jurisdictional coordination, and follow-up of contacts' health status.	Among the 8051 close contacts of the 487 confirmed cases (16.5 close contacts/case, 95%CI 13.9-19.1), the median elapsed time from last exposure to quarantine was three days (IQR 1–5). Implementing self-reporting using automatic text-messages and the web-app increased self-reporting of health status updates from 22.5% to 61.5%. Among the 487 cases, 42 were secondary cases, among whom 37 (88%) were detected via contact tracing. Authors stated that the high proportion of secondary cases detected via contact tracing (88%) might reduce the R0 to under one and minimise the impact of local transmission in the community.
Cheng[114]	Taiwan	23.8 million[92]	15th Jan to 18th March	0.009[0-0.1]/100,000 daily cases[105]	Prospective case-ascertained study of 100 laboratory-confirmed patients, 2761 close contacts	Of the 100 patients, median age 44 (11-88), 56 were women. 2,761 close contacts, 22 of which were index-secondary paired cases. Secondary clinical attack rate 0.7% (95% CI, 0.4-1.0%). Attack rate higher in 1818 contacts whose contact with index case started within 5 days of symptom onset. 299 contacts with pre-symptomatic had an attack rate of 0.7% (95%CI, 0.2-2.4%). Household attack rate 4.6% (95%CI, 2.3-9.3%). Non-household attack rate 5.3% (95%CI, 2.1-12.8%). Older age groups had higher attack rates, 40-59 year 1.1 (95%CI, 0.6-2.1%), 60+ 0.9% (95%CI, 0.3-2.6%).

IQR – interquartile range; PCR – polymerase chain reaction-based SARS-CoV-2 test; TTI – United Kingdom's Test, Trace and Isolate programme.

[a] Publication status as of 28th October 2020.

[b] Estimated number of COVID-19 cases per 100,000 inhabitants over the evaluation or intervention period (European Centre for Disease Prevention and Control data[115]).

[c] Includes all information reported up to 11th August 2020, but only data up to the 29th calendar week were used for analysis (to account for reporting delays).

[d] Derived using an estimate of between 4 and 78 cases per day for period 27th April to 18th June[38] and an estimate of 1.885 million population for Northern Ireland.

[e] Raw case data downloaded from https://coronavirus.data.gov.uk/details/cases.

Table A4: Summary of routine data published from contact tracing interventions and apps from Western Europe and internationally.

Country	App/programme name	Users	Time period	Comments
Western Europe				
England, UK	1) NHS COVID-19 Test and Trace[39] 2) COVID Symptom tracker (ZOE)[40]	1) 10 million (17% of England/Wales population) downloads of by 24/09/2020 2) 4.4 million users of COVID Symptom tracker (ZOE)	1) Launched 24th September 2) Launched in March	
Scotland, UK	Test and Protect[41,42]	600,000 users as of 11/09 (11% of population)	28th May – 25th Oct	Contact tracing primarily focused on SMS messages: contacts with a mobile number receive a SMS message with advice to self-isolate. Once the SMS message has been delivered, the contact is marked as complete. 39,115 individuals were recorded in the contact tracing software, from whom 150,446 contacts were traced (112,632 unique contacts). 40,495 confirmed cases during this period: (of whom 35,331 completed contact tracing). 18,248 (13.6%) of close contacts subsequently had a positive COVID-19 result.
Germany	Corona-Warn-App	21.1 million downloads till 29th Oct 2020 (25.2% of population)	Launched 16 June 2020	More than 2.4 million test results have been sent via the app; of these 45,262 were positive, and of these 60% were shared with contacts via the app (as of 28th Oct 2020)[43,44]
Italy	Immuni	9,513,635 million downloads by 02/11/2020	Launched 15 June 2020	Online dashboard shows notifications and positive cases per region.
Iceland	Rakning	38% of 364,000 by May	Launched early April	
France	StopCovid	2.6 million downloads (4% of population) since June. Re-launch total 4 million downloads.	Launched 2 June 2020	“Tous Anti-Covid” or “all against Covid” launched on 22/10/2020
Spain	Radar Covid	4 million downloads (9% of population) by Sept		
Norway	Smittestop			Suspended use – replacement currently in development
Switzerland	SwissCorona	2 million downloads (24% of population) by 23/07/2020	Launched 25 June 2020	
Austria	Stopp Corona	600,000 downloads		
International				

Country	App/programme name	Users	Time period	Comments
New Zealand	NZ Covid Tracer	2,228,300 users as of 17/09/2020	Launched 20 March 2020	Compulsory QR codes placed in businesses for users to scan from 17/08/2020, from 03/09/2020 compulsory for public transport providers, including buses, trains, ferries, ride-share vehicles and train operators, to provide the QR codes for passengers to use. The app has recorded a total of 62,533,146 poster scans, and users have created 2,984,321 manual diary entries in NZ COVID Tracer.
Australia	COVIDSafe	6.1 million downloads (24% of population) by June	Launched 26 April 2020	
India	Aarogya Setu	140.6 million downloads (13.8% of population) by August	Launched 2 April 2020	
Singapore	TraceTogether	2.4 million users (43% of population) by 4 September 2020	Launched 20 March 2020	Mobile app (and token for those without mobile phone) uses bluetooth. Also SafeAlert for arrivals into Singapore

Table A5: Published studies that used Whole-Genome Sequencing (WGS) of SARS-CoV-2 specimens to analyse origin and spread of the virus. The list is not exhaustive but contains the key references.

Study	Genomes sequenced	Purpose of analysis and findings	Additional benefits for contact tracing
Meredith 2020[60]	747 high-quality genomes from samples collected between 13 March and 12 April 2020 from patients in East Anglia, UK 299 genomes from samples from 299 patients in a hospital in Cambridge, UK	Investigate healthcare associated SARS-CoV-2 infections and inform infection control measures 35 clusters of infections involving 159 patients 58% of patients had strong epidemiological links as confirmed by patient records, clinical details and ward movements 20% had intermediate links and 22% had no evidence of connected transmission Clusters with strong links included suspected HAIs and care-home outbreaks involving healthcare workers based in hospital and community settings	Genome sequencing facilitated the identification of distinct infection clusters In combination with patient and hospital records likely transmission settings inside hospital wards and importation of infection from hospital to care home settings could be identified
du Plessis 2020[80]	50,887 genomes including 26,181 genomes from the UK form samples collected up to 26 June 2020	Quantify the size, spatio-temporal origins and persistence of genetically-distinct UK transmission lineages In total 1179 UK transmission lineages were identified By 1 June >73% of lineages had gone extinct This suggests that SARS-CoV-2 was introduced hundreds of times independently into the UK Lineages that were introduced into the country early (mainly from Italy, Spain and France) grew larger (before NPIs were introduced) and lasted longer than lineages that were introduced later	Genome sequencing and analysis identified the number of independent introductions of SARS-CoV-2 into the UK which would not have been possible without WGS because of the high number of asymptomatic infections WGS also identified the most common source countries from where introduction took place
Lythgoe 2020[86]	Targeted RNA sequencing of 413 clinical samples from two UK locations (Basingstoke and Oxford) collected between 8 March and 14 April	Characterise the within-host diversity of SARS-CoV-2 to provide increased resolution for the identification of transmission clusters Within-host diversity of SARS-CoV-2 is probably generated by super-infection and co-transmission of lineages which lead to regionally distinct clusters of co-transmitted lineages	None demonstrated in practice yet, could potentially be used to reconstruct complex transmission networks

Study	Genomes sequenced	Purpose of analysis and findings	Additional benefits for contact tracing
Ladhani 2020[63]	SARS-CoV-2 genomes isolated from 105 RT-PCR positive residents and 53 RT-PCR positive staff in 6 care homes in London in April 2020	Identify routes of introduction and transmission of SARS-CoV-2 among care home residents and staff WGS identified multiple routes of introduction into individual care homes (up to 9) Half of care home residents and staff were asymptomatic and potential sources of unnoticed onward transmission	WGS could identify multiple independent transmission events into individual care homes
Ladhani 2020[116]	SARS-CoV-2 genomes isolated from 53 RT-PCR positive staff in 6 care homes in London in April 2020	Identify routes of introduction and transmission of SARS-CoV-2 among care home residents and staff WGS identified SARS-CoV-2 identified SARS-CoV-2 clusters involving staff only, including staff with minimal resident contact	WGS could distinguish transmission clusters that involved residents and those involving only staff
Murphy 2020[117]	5 genomes from samples collected from travellers on the same flight	Confirm if 59 SARS-CoV-2 infections on a flight originate from the same source The genomes of the samples were near-identical which points to a single source of infection on the flight	WGS confirmed that a single infected traveller is likely to be the source if onward transmission to 59 SARS-CoV-2 cases
Lucey 2020[118]	50 SARS-CoV-2 genomes collected from patients with hospital-acquired COVID-19 in a tertiary referral centre in Ireland in March/April 2020	Analyse transmission routes of SARS-CoV-2 in a hospital Phylogenetic analysis identified 6 independent clusters of infection in the hospital and that different patients without an obvious epidemiological link had acquired the infection during a previous hospital stay WGS also revealed that asymptomatic staff working on multiple wards was responsible for carrying the virus between wards	WGS revealed transmission chains that would not have been obvious from epidemiological data and patient records alone
Zhang 2020[84]	192 genomes isolated from RT-PCR positive patients from the Los Angeles metropolitan area from 22 March to 15 April 2020	Determine transmission routes of SARS-CoV-2 to southern California and investigate local community spread in the Los Angeles metropolitan area The analysis found community transmission of 13 patients within a 3.81 km^2 radius and a cluster of 10 patients involving residents of different care homes, healthcare staff and 1 relative of a care home resident 15% of isolates resembled Asian SARS-CoV-2 lineages 80% of isolates resembled SARS-CoV-2 lineages from Europe	WGS identified distinct transmission networks and the geographic origin of the circulating SARS-CoV-2 lineages
Deng 2020[119]	36 genomes isolated from patients from 9 counties in northern California and the Grand Princess cruise ship from late January to mid-March 2020	Identify introduction events and transmission pathways of SARS-CoV-2 in northern California	WGS identified multiple introduction events and the likely geographic origin of the source of a SARS-CoV-2 outbreak on a cruise ship

Study	Genomes sequenced	Purpose of analysis and findings	Additional benefits for contact tracing
		WGS revealed the cryptic introduction of at least 7 distinct SARS-CoV-2 lineages into California The outbreak on the Grand Princess cruise ship was likely caused by a lineage from Washington	
Long 2020[120]	5,058 genomes from two COVID-19 outbreaks in metropolitan Houston, Texas (early March till mid-May, and mid-May till early July 2020)	Understand SARS-CoV-2 molecular population genomic evolution and the relationship between virus genotypes and patient features SARS-CoV-2 was introduced into Houston multiple times independently SARS-CoV-2 from the second wave was characterised by an amino acid replacement in the spike protein which is associated with higher transmission and infectivity but with higher virulence	The WGS data were not used to identify transmission pathways
Lemieux 2020[121]	772 genomes from patients in Boston, Massachusetts, collected between 29 January and 18 April, including nearly all confirmed cases of the first week of the epidemic and hundreds of cases from major outbreaks at a conference, a nursing facility and among homeless shelter guests and staff	Investigate the introduction, spread, and epidemiology of COVID-19 in the Boston area SARS-CoV-2 was introduced into the Boston area more than 80 times independently, and with sources from four continents, SARS-CoV-2 genomes from the Boston area were most similar to genomes from other areas in North America, notably New York, and Europe Analysis of the genomes isolated from patients belonging to the same cluster showed that two different lineages were involved in this cluster WGS showed that all cases associated with the conference formed a monophyletic cluster, indicating a single superspreading event, derived from a lineage that was widely spread in Europe in January/February 2020; the lineage was onward transmitted into the community via conference attendees WGS identified at least 7 independent introductions of SARS-CoV-2 into the Boston homeless population, two of the clusters were descended from the lineage introduced into Boston at the conference demonstrating that homeless people were affected by community transmission WGS identified three independent introductions of SARS-CoV-2, one of which resulted in a cluster of 75 infections,	WGS enabled investigators to trace the geographic origins of SARA-CoV-2 lineages and resolve transmission networks in different settings (conference, homeless shelter, nursing home, hospital)

Study	Genomes sequenced	Purpose of analysis and findings	Additional benefits for contact tracing
		into a skilled nursing facility; the low genetic diversity in the large cluster may be the consequence of high-dose transmission so that each patient contained at least some virus particles carrying the consensus sequence WGS showed that several cases of COVID-19 at a hospital were not linked and likely not the result of nosocomial transmission	
Thielen 2020[122]	114 genomes collected in March 2020 by the John Hopkins Health System	Understand the initial spread of SARS-CoV-2 in the US Capital Region Sequenced genomes belonged to all major SARS-CoV-2 clades suggesting multiple independent introduction events Clade did not correlate with patient outcomes	WGS revealed multiple independent introduction events of SARS-CoV-2 into the US Capital Region
Taylor 2020[123]	SARS-CoV-2 specimens from residents and staff at two skilled nursing facilities were sequenced Facility A: 18 specimens from residents and 7 from staff, collected between 14 April and 11 June 2020 Facility B: 75 specimens from residents and five from staff, collected between 29 April and 12 June 2020	Inform infection risk at two skilled nursing facilities Facility A: specimens from 17 residents and 5 staff were genetically similar suggesting transmission within the facility Facility B: all specimens were genetically similar suggesting transmission within the facility	WGS revealed spread of SARS-CoV-2 lineages within skilled nursing facilities
Candido 2020[124]	427 SARS-CoV-2 genomes from all regions of Brazil collected between 5 March and 30 April 2020 For each state the time between the first detected case and sequencing of the first sample was on average only 4.5 days	Evaluate impact of non-pharmaceutical interventions on spread of SARS-CoV-2 in Brazil and determine geographic sources of imported cases Genomic analysis identified >100 independent introductions of SARS-CoV-2 into Brazil, 76% of SARS-CoV-2 strains fell into three clades that were introduced from Europe between 22 February and 11 March 2020, during the early epidemic SARS-CoV-2 spread mainly locally but later the virus was exported from urban centres and travelled large distances despite an overall decrease in air travel	WGS was used to infer independent introduction events and to reconstruct the spatiotemporal spread of different viral lineages across Brazil
Rockett 2020[83]	209 genomes from isolate collected in New South Wales from 21 January to 28 March 2020	Evaluate the added value of near real-time WGS of SARS-CoV-2 in a subpopulation in Australia for containment and epidemic management	WGS revealed multiple independent introduction events of SARS-CoV-2 into New South Wales and helped to identify a proportion of transmission chains that could not be identified using epidemiological data alone.

Study	Genomes sequenced	Purpose of analysis and findings	Additional benefits for contact tracing
		WGS indicates multiple independent introductions of SARS-CoV-2 over time, all clusters remained active during the study period indicating continued onward transmission Due to the low genetic diversity of SARS-CoV-2, both genomic and epidemiological data were needed to define SARS-CoV-2 clusters. Genomic evidence was used to cluster 38.7% (81 out of 209) of cases for which the available epidemiological data could not identify direct links. WGS was used to confirm transmission in institutional outbreaks.	
Speake 2020[125]	25 genomes isolated from infected passengers on a domestic flight in Australia travelling on 19 March 2020	Investigate potential transmission of SARS-CoV-2 during a domestic flight within Australia WGS confirmed that SARS-CoV-2 must have spread from passengers who had previously travelled on the Ruby Princess cruise ship, at least 9 of them were infective at the time of travel on the plane	WGS was used to confirm the epidemiological link between flight-associated SARS-CoV-2 transmission and an outbreak on a cruise ship
Gudbjartsson 2020[14]	643 genomes from specimens collected in Iceland between 29 January and 4 April 2020	Investigate how SARS-CoV-2 entered and spread in the Icelandic population At least 42 separate introductions of SARS-CoV-2 into Iceland occurred The geographic origin of recoredededSARS-CoV-2 lineages changed over time, but this was partly due to changing targeted testing strategies (e.g. including or excluding travellers from high-risk areas) WGS data confirmed epidemiological links established by contact tracing and was used to reconstruct complex transmission networks <u>Example:</u> In a particular contact tracing network, WGS was used to determine that the SARS-CoV-2 strain had been imported from northern Italy and had mutated in Iceland – one person had both wild-type and mutant virus and subsequently infected individuals only had mutant virus; search for persons carrying the mutant strain who were not associated with the cluster identified two individuals who must have been infected by someone in the cluster through an unknown link	WGS has been used to identify sources of introduction of SARS-CoV-2 into Iceland and to reconstruct complex transmission networks

Study	Genomes sequenced	Purpose of analysis and findings	Additional benefits for contact tracing
Oude Munnink 2020[82]	189 genomes isolated from patients in the Netherlands between 27 February and 15 March 2020	Use WGS to inform public health decision making WGS revealed multiple introduction events of SARS-CoV-2 into the Netherlands, mainly from Italy, Austria, Germany and France, followed by local amplification first in the south of the Netherlands and later also in other regions	WGS was used to identify introduction events and to distinguish between imported cases and local community transmission
Oude Munnink 2020[126]	SARS-CoV-2 genomes from infected mink and 18 from infected humans from 16 mink farms in the Netherlands collected between 23 April and 21 June 2020 1775 genomes from the Dutch National SARS-CoV-2 database	Investigate SARS-CoV-2 outbreaks on 16 mink farms in the Netherlands SARS-CoV-2 was introduced into the mink populations by humans, spread widely in the mink populations and was eventually transmitted back to humans Human-mink and mink-human transmission events occurred independently on at least 5 different occasions, but genetic similarity indicates farm-to-farm transmission in 5 distinct clusters; however, the links between farms could not be identified and geographic distance could not explain clustering Although several mink farm workers were from Poland WGS did not show any links between the SARS-CoV-2 lineages on Dutch mink farms and lineages circulating in Poland	WGS was used to show SARS-CoV-2 transmission between humans and animals and to reconstruct complex transmission networks involving humans and mink on 16 mink farms in the Netherlands
Voeten 2020[15]	83 SARS-CoV-2 genomes isolated from 7 care home residents who attended a church service, 35 who did not attend, 20 healthcare workers, 21 inhabitants of the island where the care home is located	Investigate sources and chains of transmission in a nursing home in the Netherlands following and on-site church service WGS identified at least 17 different introduction events of SARS-CoV-2 into the care home The 7 care home residents who attended the church service were all infected with different viral lineages, making a single source of infection unlikely. 4 church service attendees were infected with a viral lineage that belonged to a large regional cluster which likely reflects widespread circulation rather than a single transmission cluster inside the care home. Other clusters identified within the care home are likely transmission clusters	WGS showed that the church service which was attended by care home residents was unlikely a superspreading event and that multiple independent introductions of SARS-CoV-2 into the care home had happened.
Böhmer 2020[127]	16 genomes from isolates from patients belonging to one transmission cluster in Germany in January/February 2020	WGS was used to confirm epidemiological links and to clarify transmission events where contact histories were ambiguous	WGS was used to reconstruct the direction of transmission events which would not have been possible in all cases looking at contact tracing data alone

Study	Genomes sequenced	Purpose of analysis and findings	Additional benefits for contact tracing
		SNPs were used to reconstruct the transmission chain and who infected whom at a medium-size business in Germany	
Walker 2020[85]	55 genomes, 10 from a superspreading event in a small municipality (Heinsberg) in western Germany in mid-February 2020, and 45 from an outbreak in a nearby city (Düsseldorf) in early March 2020	Investigate two outbreaks in nearby locations in western Germany The 10 genomes from Heinsberg displayed a clonal origin in accordance with a single superspreading event during carnival, the origin of the viral lineage responsible for the outbreak remains unclear The 45 genomes from Düsseldorf fall into at least 5 distinct clusters indicating multiple independent introduction events There was no evidence of widespread community transmission of the Heinsberg lineage outside of Heinsberg	WGS was used to confirm a superspreading event and to show that two outbreaks in nearby locations did not involve the same SARS-CoV-2 lineage
Lai 2020[128]	59 SARS-CoV-2 genomes obtained in Northern and Central Italy till end of April 2020	Characterisation of SARS-CoV-2 genome sequences from Northern and Central Italy All isolates except one belonged to lineage B.1, the most widespread lineage in Europe; only one isolate belonged to lineage B The time to most recent common ancestor obtained from phylogenetic analysis suggests a start of the epidemic in late January/early February 2020 and rapid expansion of the viral population during February/March 2020 with an estimated reproduction number R=2.3	WGS was used to determine the lineages of SARS-CoV-2 isolates and to estimate transmission in the past
Gong 2020[129]	26 SARS-CoV-2 genomes isolated from patients in Taiwan between 25 January and 20 March 2020	Investigate the diversity and evolution of SARS-CoV-2 strains in Taiwan In the first wave most identified strains in Taiwan originated from China In the second wave strains originated from different countries	WGS showed that SARS-CoV-2 strains isolated in Taiwan are from different lineages and that no single lineage was dominantly circulating in Taiwan
Puenpa 2020[130]	40 genomes isolated from patients in Thailand from January to May 2020	Assess the genomic variation patterns of SARS-CoV-2 over time in Thailand The 40 genomes belonged to 5 major lineages and different genotypes were introduced at different times Locally transmitted strains belonged to the T lineage and imported strains belonged to the L, GH, GR and O lineages	WGS was used to distinguish between imported cases and local transmission
Batty 2020[131]	27 genomes isolated from patients at Ramathibodi Hospital, Bangkok, Thailand collected between 13-28 March 2020	Genomic surveillance of SARS-CoV-2 in Thailand At least 6 independent introductions of SARS-CoV-2 into Thailand with lineages originating from the US and Europe	WGS was used to identify the likely geographic origins of SARS-CoV-2 lineages circulating in Thailand

Study	Genomes sequenced	Purpose of analysis and findings	Additional benefits for contact tracing
		One lineage closely related to Chinese lineages expanded in Thailand but its origins could not be exactly identified from the sampled viral sequences	
Kumar 2020[132]	104 high-quality SARS-CoV-2 genomes isolated from laboratory-confirmed cases of COVID-19 from targeted testing and available samples at NCDC in India which represent different geographic locations or states and travel history from different countries from the early phase of the SARS-CoV-2 epidemic in India	Understand the genetic diversity, evolution, and epidemiology of SARS-CoV-2 across India to support contact tracing, effective diagnostic development, and drug and vaccine development WGS revealed multiple introductions of SARS-CoV-2 genomes, including the A2a cluster from Europe and the USA, A3 cluster from Middle East and A4 cluster (haplotype redefined) from Southeast Asia (Indonesia, Thailand and Malaysia) and Central Asia (Kyrgyzstan) The most prevalent lineage was a novel A4 lineage similar to strains found elsewhere in South-East Asia but with multiple mutations specific to India	WGS identified the likely origins of the multiple introductions of SARS-CoV-2 into India during the early phase of the epidemic in India
To 2020[133]	2 SARS-CoV-2 genomes isolated from the same patient in Hong Kong 142 days apart, prior to the second infection the patient had travelled from Spain via the UK	Confirm re-infection with SARS-CoV-2 WGS showed that the same patient had been infected with two different strains of SARS-CoV-2 on two different occasions	WGS confirmed re-infection with a different SARS-CoV-2 strain as opposed to persistent infection with the same strain
Xavier 2020[134]	40 SARS-CoV-2 genomes from 15 different municipalities in Minas Gerais, Brazil, collected between 24-26 March 2020	Understand the introduction and spread of SARS-CoV-2 in Minas Gerais, Brazil 17 of the 40 patients sampled had a recent travel history inside or outside of Brazil The majority of genomes belonged to the B.1 lineage that at the point of sampling had spread across many different countries in accordance with the travel histories of investigated cases	WGS was used to confirm the origin of independent introductions of SARS-CoV-2 into Minas Gerais, Brazil
Chau 2020[135]	11 SARS-CoV-2 genomes obtained from individuals infected at a superspreading event in a bar in Ho Chi Minh City, Vietnam, on 14 March 2020	WGS was used to investigate transmission of SARS-CoV-2 at a superspreading event The genomes in the infection cluster resulting from the superspreading event were identical or near-identical but different from the genomes of other SARS-CoV-2 strains recorded in Ho Chi Minh City at the time The identity of the index patient could not be confirmed	WGS revealed that all cases in the infection cluster must have been derived from a single source of infection that differed from other strains circulating in Ho Chi Minh City at the time
Choi 2020[136]	4 genomes from 4 patients who travelled on the same flight from Boston,	Confirm transmission among travellers on the same airplane	WGS was used to confirm a transmission cluster and revealed that the index patient was likely infected in Boston

Study	Genomes sequenced	Purpose of analysis and findings	Additional benefits for contact tracing
	Massachusetts to Hong Kong on 9/10 March 2020	The viral genomes isolated from the 4 patients were 100% identical confirming a recent transmission event on the flight The genome sequence was similar to those of other SARS-CoV-2 strains circulating in North America at the time of the flight	
Tayoun 2020[137]	49 genomes from the earliest confirmed COVID-19 cases in the UAE collected between 29 January and 18 March 2020	Analyse the introduction and beginning of community transmission of SARS-CoV-2 in the UAE WGS showed that most introductions of SARS-CoV-2 into the UAE were from Europe and the Middle East/Iran WGS revealed an international transmission chain of residents of different countries (Germany, Mexico, UAE) all of whom had recently travelled to Italy	WGS revealed multiple independent introductions of SARS-CoV-2 into the UAE and in one example a recent unknown transmission event in which otherwise unconnected individuals were involved
Sekizuka 2020[138]	435 genome sequences collected in Japan up to 6 April 2020	Evaluate origin and spread of SARS-CoV-2 in Japan WGS indicated at least 4-5 independent introductions of SRAS-CoV-2 but epidemiological analysis suggests a higher number of independent events From January – March 2020 most genomes isolated in Japan originated from China, from March onwards most the proportion of isolates from Europe increased	WGS identified two distinct series of introduction of SARS-CoV-2 into Japan, first from China and later from Europe
Sekizuka 2020[139]	148 SARS-CoV-2 genomes isolated from RT-PCR positive passengers and crew on the Diamond Princess cruise ship collected in February 2020	Analyse the outbreak of SARS-CoV-2 on the Diamond Princess cruise ship WGS indicates that the outbreak was due to a single introduction of SARS-CoV-2 on the cruise ship before the beginning of the quarantine Haplotype analyses suggests that transmission first occurred at mass gatherings prior to the beginning of quarantine but onward transmission continued among individuals sharing the same cabin after the beginning of quarantine	WGS revealed a single introduction of SARS-CoV-2 on a cruise ship and different transmission routes on board
Takenouchi 2020[87]	33 genomes from cases (15 patients, 18 staff) in a hospital outbreak of SARS-CoV-2 in Tokyo, Japan, collected between 24 March and 15 May 2020	Investigate seemingly separate clusters of SARS-CoV-2 infections in a hospital WGS confirmed two distinct clusters of infection, cluster 1 contained 5 cases, and cluster two the remaining cases including cases that could previously not be linked to a cluster via source of infection	WGS confirmed two independent outbreaks of SARS-CoV-2 in a hospital and could like previously unattributed cases to one of the outbreaks

Study	Genomes sequenced	Purpose of analysis and findings	Additional benefits for contact tracing
Forster 2020[140]	160 SARS-CoV-2 genomes deposited in the GISAID database by researchers in countries around the world from December 2019 to early March 2020	Understand the evolution of this virus within humans, and to assist in tracing infection pathways and designing preventive strategies WGS revealed three different clades, one prevalent in Eastern Asia and the other two spread mainly in European and North American countries WGS identified the geographic origins of introductions of SARS-CoV-2 into various countries and in at least one example a transmission chain across four different countries (China, Germany, Italy, Mexico)	WGS was used to analyse the geographic spread of different SARS-CoV-2 lineages

Table A6: Summary of transmission rates by index and contact characteristics.

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
Studies from Western Europe and North America						
Thompson[3] India, USA, China, Germany, Brunei, The Netherlands, Taiwan, Singapore, Israel, South Korea, Spain	Systematic review	No significant difference in SARs in index cases aged under 20 and those over 20 (p = 0.12)		No significant difference in SARs in contacts aged under 20 and those over 20 (p = 0.43)		Overall pooled household SAR: 0.21 (95%CI 0.17-0.25) **By duration of exposure** ≤5 days exposure: 0.15 (95%CI 0.06-0.23) >5 days exposure: 0.28 (95%CI 0.18-0.38) **Exposure locations** **Workplace:** 0.02 (95%CI 0.00-0.04) **Healthcare:** Patient contacts: 0.02 (95%CI 0.01-0.03) Healthcare staff contacts: 0.05 (95%CI 0.00-0.10) All healthcare contacts: 0.04 (95%CI 0.01-0.07) **Social contact environments:** Casual contacts: 0.01 (95%CI 0.00-0.02) Family and friends: 0.06 (95%CI 0.04-0.08) Travel: 0.05 (95%CI 0.00-0.10)
Lopez Bernal[71] United Kingdom	Prospective study of 233 households with two or more people, totalling 472 contacts. Household secondary attack rate,	**Adjusted SARs:** <18: 0.92 (95%CI 0.75-1.1) 18-64: 0.31(95%CI 0.25-0.37) 65<: 0.38 (95%CI 0.16-0.59) **OR, secondary infection** <18: 61 (95%CI 2.2-1133)	**Adjusted SARs:** Female: 0.29 (95%CI 0.21-0.37) Male: 0.38 (95%CI 0.3-0.46) **OR, secondary infection** Female: 0.6 (95%CI 0.3-1.2)	**Adjusted SARs:** <18: 0.29 (95%CI 0.2-0.38) 18-34: 0.34 (95%CI 0.24-0.44) 35-64: 0.39 (95%CI 0.3-0.48) ≥65: 0.26 (95%CI 0.021-0.51)	**Adjusted SARs:** Female: 0.32(95%CI 0.24-0.39) Male: 0.36 (95%CI 0.28-0.43) **OR, secondary infection** Female: 0.8 (95%CI 0.44-1.5)	**Index Case Hospital Admission (SAR)** Without Admission: 0.4 (95%CI 0.33-0.48) With Admission: 0.25 (95%CI 0.17-0.33) Hospital Admission (OR) Without Admission: Reference

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
	serial intervals, individual and household reproduction number estimated	18-64: Reference 65<: 1.4 (95%Ci 0.41-5.1)	Male: Reference	**OR, secondary infection** <18: 0.73(95%CI 0.34-1.6) 18-34: Reference 35-64: 1.3 (95%CI 0.66-2.6) ≥65 0.62 (95%CI 0.12-3.3)	Male: Reference	With Admission: 0.4 (95%CI 0.2-0.8) **Cough or Sneezing (SAR)** Neither: 0.29 (95%CI 0.15-0.43) Either: 0.34 (95%CI 0.28-0.41) **Household Size (SAR)** 2: 0.48 (95%CI 0.35-0.6) 3: 0.4 (95%CI 0.29- 0.52) 4: 0.33 (95%CI 0.23-0.44) 5< 0.22 (95%CI 0.12-0.32) **Household Size (OR)** 2: Reference 3: 0.67 (95%CI 0.27-1.6) 4: 0.46 (95%CI 0.18-1.1) 5<: 0.22 (0.078-0.64
Fateh-Moghadam[52] Italy	Contact tracing	**Age of index, years (n=1,489)** 0-14: 22.4% (11/49) 25-29: 13.1% (62/475) 30-49: 10.6% (250/2361) 50-64: 13.6% (303/2222) 65-74: 15.2% (85/559) ≥75: 17.1% (155/909)	**Gender of index (n= 1,442)** Female: 12.1% (414/427) Male: 14.0% (416/2973)	**Age of contact, years (n=6687)** 0-14: 8.4% (86/1024) 25-29: 9.2% (126/1372) 30-49: 14.9% (245/1646) 50-64: 15.4% (264/1712) 65-74: 16.9% (79/467) ≥75: 18.9% (88/466)	**Gender of contact (n= 6406)** Women: 13.5% (426/3156) Men: 13.1% (427/3250)	**Nature of contact with case (n= 6255)** Cohabitant: 14.1% (500/3546) Non-cohabiting family/friend: 12.9% (206/1596) Work colleague: 15.8% (79/499) Other: 9.0% (55/614) Contagiousness (% of contacts who became cases) by characteristic of case:
Grijalva[70] United States	Prospective household study[a]	<12: 53% (31-74, 9/17)[b] 12-17: 38% (23-56, 11/29) 18-49: 55% (46-64, 64/116) ≥50: 62% (44-77, 18/29)	Female: 61% (52-70, 66/108)[b] Male: 43% (33-54, 36/83)	<12: 57% (39-72, 18/32)[b] 12-17: 47% (30-64, 14/30) 18-49: 59% (48-68, 54/92) ≥50: 43% (29-59, 16/37)	Female: 50% (41-60, 52/103)[b] Male: 57% (46-67, 50/88)	**Ethnicity of index** White, non-Hispanic: 51% (43-59, 71/139) Other race, non-Hispanic: 53% (31-74, 9/17) Hispanic/Latino: 63% (46-77, 22/35) **Ethnicity of contact**

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
						White, non-Hispanic: 53% (44-61, 67/127) Other race, non-Hispanic: 38% (21-57, 9/24) Hispanic/Latino: 65% (50-78, 26/40) **Household size** 2: 68% (53-81, 26/38) 3: 61% (46-74, 25/41) 4: 45% (31-60, 18/40) ≥5: 46% (35-57, 33/72)
Lewis[141] United States	Prospective household study[a]			**Child of index:** <10: 18% (3/17) 10-17: 58% (15/26) ≥18: 35% (6/17) **Not a child of index:** <10: 0% (0/12) 10-17: 8% (1/13) ≥18: 26% (27/103)		Child of index (<18): 42% (18/43) Child of index (≥18): 35% (6/17) Spouse: 33% (11/33) Sibling: 20% (6/30) Parent: 17% (4/24) Extended family: 5% (1/20) Non-family household contact: 29% (6/21) **Household secondary attack rate:** 0%: 47 households 1-20%: 3 households 21-40%: 11 households 41-60%: 6 households 61-80%: 4 households 81-99%: 0 households 100%: 7 households
Adamik[142] Poland	Analysis of 16,115 surveillance records	0-39: 66.2% (4232/6400) 40-59: 80.8% (4918/6084) 60-79: 76.1% (2206/2900) >80: 75.1% (532/708) Unknown: 0% (0/23)	Female: 73.1% (6084/8322) Male: 74.5% (5804/7793)	0-39: 33.9% (2168/6400) 40-59: 19.2% (1166/6084) 60-79: 23.9% (694/2900) >80: 24.9% (176/708) Unknown: 100% (23/23)	Female: 26.9% (2238/8322) Male: 25.5% (1989/7793)	**Hospitalisation (Index)** Hospitalised: 82.4% (3602/4373) Hospitalised > 10 days: 82.5% (1978/2399) Hospitalised > 14 days: 83.1% (1505/1811) **Outcome (Index)** Recovered: 72.3% (4246/5872) Deceased: 93.2% (455/488)

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
						Hospitalisation (Secondary) Hospitalised: 17.6% (771/4373) Hospitalised > 10 days: 17.5% (421/2399) Hospitalised > 14 days: 16.9% (306/1811) **Outcome (Secondary)** Recovered: 27.7% (1626/5872) Deceased: 6.8% (33/488)
Maltezou[143] Greece	Transmission dynamic study of 23 clusters of families with children. Data collected between 26-Feb and 03-May.			OR, risk of acquisition: 0-17: 1.69 (95%CI 0.7-4.2) ≥18: Reference		
Buonsenso[144] Italy	Study of families with children, from 30 index cases.			OR, risk of acquisition: 0-17: 0.77 (95%CI 0.27-2.17) ≥18: Reference		
Bi[145] Switzerland	Household serosurvey of 4,524 household members >5 from 2,267 households. Apr to Jun					**Overall Seropositive:** 5-9: 5% (8/167), OR: 0.5(0.2-1.0) 10-19: 7% (31/459), OR: 0.7(0.5-1.1) 20-49: 9% (119/1302) OR: Reference 50-64: 7% (96/1443), OR: 0.7(0.5-0.9) >65: 4% (44/1163), OR: 0.4(0.3-0.6) Female: 6% (137/2432), OR: Reference

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
						Male: 8% (161/2102), OR: 1.4(1.1-1.8) Reduced Contact Yes: 6% (254/3914), OR: 0.8(0.5-1.15) No: 8% (17/224), OR: Reference
Kuwelker[146] Norway	Prospective case-ascertained study of 112 households and 291 participants. 28-Feb to 4-Apr.	<20: 33.3% (2/6) 20-59: 43.3% (68/157) >60: 68.8% (11/16)	Female: 48.2% (40/83) Male: 42.7% (41/96)	0-10: 47.8% (11/23) 11-20: 26.5% (9/34) 21-30: 41.7% (15/36) 31-40: 61.1% (11/18) 41-50: 37.5% (9/24) 51-60: 51.7% (15/29) >60: 73.3% (11/15)	Female: 73.7% (73/99) Male: 71.3% (57/80)	Overall household attack rate: 45% **Household Size** 2: 56.8% (25/44) 3: 44.4% (16/36) >4 40.4% (40/99)
Burke[147] USA	Contact tracing of travellers.					All contacts: 0.45% (95%CI 0.12-1.6) **n=445** Household contacts: 10.5% (95%CI 2.9-31.4)
Rosenberg[148] USA	Surveillance data from New York.			0-4: 20.0% (5/25) 5-17: 28.2% (37/131) 18-29: 41.7% (10/24) 30-49: 43.7% (31/71) 50-64: 53.4% (31/58) ≥65: 55.2% (16/29)		
Yousaf[149] USA	Prospective study of 198 households, and their 47 contacts. Data collected from 22-Mar to 22-Apr.			0-17: 20.3% (95%CI 11.6-31.7) 18-64: 25.4% (95%CI 17.9-34.3) ≥65: 37.5% (95%CI 8.5-75.5)	Female: 29.3% (95%CI 20.6-39.3) Male: 18.8% (95%CI 11.5-28.0)	
Fontanet[59] France	Retrospective closed cohort study: sero-epidemiological investigation of			≤14: 2.7% (1/37)[b] 15-17: 40.0% (82/205)[b] 18-44: 22.0% (39/177)[b]	Female: 28.3% (116/410)[b] Male: 21.9% (55/251)[b]	Pupil: 38.3% (92/240)[b] Teacher: 43.4% (23/53)[b] School staff: 59.3% (16/27)[b] Parent of a pupil: 11.4% (24/211)[b]

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
	high-school pupils, their parents and siblings, teachers and non-teaching staff after Oise outbreak			45-64: 20.5% (49/239)[b] ≥65: 0.0% (0/2)[b]		Sibling of a pupil: 10.2% (13/127)[b] Other: 100.0% (3/3)[b]
van der Hoek[150] Netherlands	Prospective observational study in families with children, focusing on 54 households with 227 participants.			0-17: 24.3% (95%CI 16.5-33.5) 18-60: 27.8% (95%CI 14.2-45.2) >45: 41.9% (95%CI 24.6-60.9)		
Paul[151] Canada	Cohort study of all confirmed cases in Ontario, 18,159 cases from households with no secondary transmission and 3,067 index cases from households with secondary transmission.	**No household transmission** <10: 0.9% (164/18,159) 10-19: 3.0% (536/18,159) 20-29: 18.7% (3,387/18,159) 30-39: 17.5% (3,169/18,159) 40-49: 17.9% (3,256/18,159) 50-59: 20.4% (3,711/18,159) 60-69: 12.5% (2,271/18,159) 70-79: 5.4% (972/18,159) >80: 3.8% (692/18,159) **Household transmission** <10: 0.8% (26/3,067) 10-19: 4.1% (127/3,067) 20-29: 17.1% (523/3,067) 30-39: 15.7% (481/3,067) 40-49: 18.6% (571/3,067) 50-59: 23.7% (726/3,067)	**No household transmission** Female: 54.5% (9,898/18,159) Male: 45.2% (8,214/18,159) **Household transmission** Female: 47.7% (1,464/3,067) Male: 52.0% (1,595/3,067)			**Any household transmission (OR)** <10: 0.87 (0.57 - 1.34) 10-19: 1.20 (0.97 - 1.49) 20-29: 0.78 (0.69 - 0.89) 30-39: 0.80 (0.71 - 0.91) 40-49: 0.90 (0.80 - 1.02) 50-59: Reference 60-69: 0.93 (0.81 - 1.06) 70-79: 0.78 (0.64 - 0.95) >80: 0.58 (0.45 - 0.76) Female: Reference Male: 1.28 (1.18 - 1.38) **Household transmission >60 years** <10: 0.18 (0.02 - 1.27) 10-19: 0.65 (0.37 - 1.17) 20-29: 0.60 (0.45 - 0.80) 30-39: 0.72 (0.55 - 0.94) 40-49: 0.66 (0.50 - 0.86) 50-59: Reference 60-69: 2.15 (1.72 - 2.69)

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
		60-69: 13.2% (404/3,067) 70-79: 4.5% (138/3,067) >80: 2.3% (70/3,067)				70-79: 2.67 (2.04 - 3.49) >80: 2.07 (1.49 - 2.88) Female: Reference Male: 1.19 (1.02 - 1.38) **Household transmission to severe cases (ICU/death)** <10: Insufficient data 10-19: 0.83 (0.25 - 2.74) 20-29: 0.54 (0.30 - 1.00) 30-39: 0.50 (0.27 - 0.93) 40-49: 0.92 (0.56 - 1.51) 50-59: Reference 60-69: 0.90 (0.52 - 1.56) 70-79: 1.66 (0.90 - 3.05) >80: 1.97 (1.04 - 3.76) Female: Reference Male: 0.94 (0.68 - 1.32)
Studies from elsewhere						
Park[74] South Korea	Analysis of 5,706 confirmed cases and their 59,073 contacts reported between 20-Jan and 27-Mar.	Among household contacts: 0-9: 5.3% (1.3-13.7, n=57) 10-19: 18.6% (14.0-24.0, n=231) 20-29: 7.0% (6.2-7.9, n=3417) 30-39: 11.6% (9.9-13.5, n=1229) 40-49: 11.8% (10.3-13.4, n=1749) 50-59: 14.7% (13.2-16.3, n=2045) 60-69: 17.0% (14.8-19.4, n=1039) 70-79: 18.0% (14.8-21.7, n=477) ≥80: 14.4% (11.0-18.4, n=348)				Among non-household contacts (by age of index): 0-9: 1.1% (0.2-3.6, n=180) 10-19: 0.9% (0.1-2.9, n=226) 20-29: 1.1% (0.9-1.3, n=12,393) 30-39: 0.9% (0.7-1.2, n=407) 40-49: 2.0% (1.7-2.3, n=7960) 50-59: 1.8% (1.5-2.1, n=9308) 60-69: 2.9% (2.5-3.3, n=7451) 70-79: 4.8% (3.9-5.8, n=1912) ≥80: 4.6% (3.6-5.7, n=1644)

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
Park[152] South Korea	Contact tracing study from call centre, testing and tracking 1,143 people.	0-19: 16.0% (95%CI 11.9-20.7) 20-59: 10.5% (95%CI 9.9-11.2) ≥60: 16.8% (95%CI 15.1-18.6)				
Hu[54] China	Contact tracing assessment	0-14: 1.0% (2/193) 15-64: 3.0% (188/6833) ≥65: 2.0% (19/1133) OR, risk of transmission: 0-14: 0.25 (95%CI 0.04-1.75) 15-64: Reference ≥65: 0.64 (95%CI 0.26-1.59)	OR, risk of transmission: Female: Reference Male: 1.76 (95%CI 0.97-3.21)	0-14: 2.4% (22/936) 15-64: 2.0% (154/6411) ≥65: 4.1% (33/812) OR, risk of acquisition: 0-14: 0.58 (95%CI 0.34-0.98) 15-64: Reference ≥65: 1.65 (95%CI 1.03-2.65)	OR, risk of acquisition: Female: Reference Male: 1.02 (95%CI 0.74-1.40)	OR, risk of transmission: Household: Reference Relative: 0.11 (95%CI 0.07-0.17) Social: 0.06 (95%CI 0.03-0.11) Other: 0.07 (95%CI 0.04-0.13)
Xin[73] China	Prospect cohort study of 106 household contacts from all confirmed cases in Qingdao Municipal. Data collected from 20-Jan to 27-Mar.	Adults: 12.5% (95%CI 5.9-22.4) Older adults (≥55): 29.4% (95%CI 15.1-47.5)		0-54: 20.5% (95%CI 12.4-30.8) ≥55: 8.7% (95%CI 1.1-28.0)	Female: 21.6% (95%CI 11.3-35.3) Male: 14.5% (95%CI 6.5-26.7)	Spouse: 25.0% Non-spouse: 16.7%
Dattner[153] Israel	Study of 637 households, testing all members.			0-19: 25.4% (95%CI 23.3-27.5) 20-59: 43.9% (95%CI 40.4-47.4) ≥60: 45.7% (95%CI 38.0-53.6)		
Bi[154] China	Data from surveillance programme, identifying 391 cases and 1,286 close contacts.			0-9: 7.4% (95%CI 4.2-12.8), OR 2.33(0.38-14.05) 10-19: 7.1% (3.3–14.6), OR 3.5(0.53-23.24)	Female: 10.4% (58/558), OR: Reference Male: 5.3% (26/486), OR: 0.43 (0.21-0.86)	Household: 11.2% (95%CI 9.1-13.8) Travel: 5.7% (3.6-8.8), OR 9.13(1.85-45.08) Meal:[g] 8.6% (6.8–10.9), OR 23.01(2.51-11.2)

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
	Between 14-Jan and 12-Feb.			20-29: 6.1%(3.0-12.1), OR 4.91(0.74-32.64) 30-39: 6.0% (3.7–9.5), OR (1.84(0.34-9.80) 40-49: 4.9% (2.4–9.8), OR 3.46(0.55-21.92) 50-59: 9.1% (5.0–15.9), OR Reference 60-69: 15.4% (10.2–22.6), OR 5.68(1.01-32.09 >70: 9.7% (4.8–18.7), OR 4.26(0.64-28.44)		
Jing[155] China	Retrospective cohort study of 215 cases and their 2,098 contacts, traced between 07-Jan and 18-Feb.			0-19: 6.4% (95%CI 2.8-12.2) 20-59: 18.5% (95%CI 14.4-23.2) ≥60: 28.0% (95%CI 19.1-38.2)	Female: 18.9% (95%CI 14.5-24.0) Male: 15.5% (95%CI 11.3-20.5)	Household size: <6 people: 20·4% (16·5–24·7) >6 people: 9·1% (5·1–14·8)
Li[156] China	Household cohort study of 105 index cases and their 392 contacts. Data collected from 1-Jan to 20-Feb.			0-17: 4.0% (95%CI 1.1-9.9) 18-60: 22.4% (95%CI 17.2-28.2) >60: 12.7% (95%CI 5.3-24.5)	Female: 17.1% (95%CI 11.9-23.4) Male: 15.6% (95%CI 11.0-21.3)	Spouse: 27.8% Other: 17.3%
Yung[157] Singapore	Household study of 213 children in 137 households. Data collected from 5-Mar to 30-Apr.			0-16: 6.1% (95%CI 3.3-10.2)	Female: 5.0% (95%CI 1.6-11.2)[a] Male: 7.1% (95%CI 3.1-13.6)[a]	

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
Wu[158] China	Study of 35 cases and their 148 household contacts, between Jan and Feb.			0-18: 16.1% (95%CI 5.5-33.7) 19-60: 37.0% (95%CI 24.2-52.0) >60: 41.9% (95%CI 23.5-62.9)	Female: 36.3% (95%CI 24.6-49.7) Male: 30.2% (95%CI 18.5-45.1)	Spouse: 52.2% (95%CI 32.5-71.2) First degree relative: 37.3% (95%CI 22.3-55.2) Other: 23.0% (95%CI 12.5-38.3)
Liu[159] China	Retrospective cohort study, investigating 11,580 contacts of confirmed COVID cases. Data collected from 10-Jan to 15-Mar.					Spouse: 23.3% Non-spouse family: 10.6%
Chaw[160] Brunei	Surveillance survey data from a superspeading event from a Tablighi Jama' event. Of the 75 attending, 19 tested positive, infecting 52 close contacts.					Spouse: 41.9% (95%CI 24.1-60.7) Children: 14.1% (95%CI 7.8-23.8)
Kim[161] South Korea	Retrospective observational household study	0-18: 0.5% (95%CI 0.0-2.6)				
Wang[162] China	Retrospective case series, enrolling 85 hospital patients and their 155 household contacts. Admission date			Children: 11% (2/18) Adults: 33% (45/137)		

First author, country	**Study type**	**Attack rate by age of index**	**Attack rate by gender of index**	**Attack rate by age of contact**	**Attack rate by gender of contact**	**Other attack rates reported**
	of admission 13-Feb to 14-Feb.					
Sun[163] China	Family cluster study of 389 cases from and initial 149 index family cases.			Children: 11% (15/134) Adults: 40% (225/563)		
Pung[164] Singapore	Prospective household study, first 400 cases in Singapore			10: 4.3% (95%CI 2.1-8.6) 20: 5.3% (95%CI 2.9-9.6) 30: 6.5% (95%CI 3.8-10.8) 40: 7.9% (95%CI 4.9-12.6) 50: 9.6% (95%CI 5.9-15.2) 60: 11.7% (95%CI 7.0-18.8) 70: 14.0% (95%CI 7.9-23.7) 80: 16.8% (95%CI 8.8-29.8)		
Cheng[114] Taiwan	Contact tracing assessment			0-19: 0.0% (95%CI 0.0-1.4) 20-39: 0.5% (95%CI 0.2-1.1) 40-59: 1.1% (95%CI 0.6-2.1) ≥60: 0.9% (95%CI 0.3-2.6)		Overall: 0.7% (95%CI 0.4-1.0) **n=2761** Household contact: 4.6% (95%CI 2.3-9.3) Non-household family contact: 5.3% (2.1-12.8) Healthcare contact: 0.9% (95%CI 0.4-1.9) Other contact: 0.1% (95%CI 0.0-0.3)
Korea Centers for Disease Control and Prevention[165] South Korea	Contact tracing, first 30 cases in South Korea					Overall: 0.55% (95%CI 0.31-0.96) **n=2370** Household: 7.56% (95%CI 3.7-14.26)
Xu[89] China	Retrospective study of 643					Hazard of infection for household relative to non-household transmission[d]

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
	transmission clusters					By age of contacts: 0-17: 3.5 18-49: 0.8 50-64: 0.8 ≥65: 1.4 By gender of contacts: Female: 1.2 Male: 0.8
Yu[166] China	Contact tracing assessment			NS[e]	NS[e]	**n=1587** Family member: 10.2% (143/1396) Colleague/classmate/travel companion: 1.8% (3/170) Doctor-patient contact: 40.0% (2/5) Other: 12.5% (2/16)
Zhang[167] China	Contact survey data			OR, risk of acquisition: 0-14: 0.34 (95%CI 0.24-0.49) 15-64: Reference ≥65: 1.47 (95%CI 1.12-1.92)		
Luo[168] China	Prospective cohort			0-17: 3.9% (14/357) 18-44: 2.8% (50/1784) 45-59: 3.6% (29/818) ≥60: 7.5% (34/451) OR, risk of acquisition: 0-17: 0.78 (95%CI 0.41-1.50) 18-44: Reference 45-59: 1.16 (95%CI 0.70-1.92) ≥60: 2.34 (95%CI 1.39-3.97)		Household: 10.3% (105/1015) Healthcare settings: 1.0% (7/679) Public transport: 0.1% (1/818) Entertainment/workplace: 1.3% (11/875) Multiple settings: 13.0% (3/23) OR, risk of transmission: Household: Reference Healthcare settings: 0.09 (95%CI 0.04-0.20) Public transport: 0.01 (95%CI 0.00-0.08)

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
Laxminarayan[169] India	Comparison of contract tracing data from two Indian states, Tamil Nadu and Andhra Predesh.			Tamil Nadu: 0-4: 95 5-17: 656 18-29: 4408 30-39: 5044 40-49: 3600 50-64: 3081 65-74: 1320 75-84: 162 ≥85: 103 Andhra Pradesh: 0.4: 5529 5-17: 36,337 18-29: 158, 029 30-39: 152, 120 40-49: 117, 512 50-64: 116,587 65-74: 34486 75-84: 945 ≥85:1100	Tamil Nadu: Female: 5021 Male: 13457 Andhra Pradesh: Female: 193,286 Male: 362,445	Close social or direct contacts: 10.7% (95%CI 10.5-10.9) Low-risk contacts:[f] 4.7% (95%CI 4.6-4.8)
Fisher[68] United States	Study of 154 cases and 160 controls, determining community transmission dynamics.	18-29: 44 (28.6%) 30-44: 46 (29.9%) 45-59: 46 (29.9%) >60: 18 (11.7%)	Female: 79 (51.3%) Male: 75 (48.7%)			Ethnicity White, non-Hispanic: 92 (59.7%) Hispanic/Latino: 29 (18.8%) Black, non-Hispanic: 27 (17.5%) Other, non-Hispanic: 6 (3.9%) Education Less than high school: 16 (10.5%) High school degree/some college: 60 (39.2%) College degree or more: 75 (48.7%) Community Exposure Shopping: 131 (85.6%)

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
						Home <10 persons: 79 (51.3%) Home > 10 persons: 21 (13.6%) Restaurant: 63 (40.9%) Office: 37 (24.0%) Salon: 24 (15.6%) Gym: 12(7.8%) Public transportation: 8 (5.2%) Bar/coffee shop: 13 (8.5%) Religious gathering: 12 (7.8%) Mask Wearing Never: 6 (3.9%) Rarely: 6 (3.9%) Sometimes: 11 (7.2%) Often: 22 (14.4%) Always: 108 (70.6%)
Wei[170] China	Household study of 23 households, with 139 individuals, including 60 confirmed cases. 01-Jan to 14-Feb.	Mean age: 33.9 (range 2-67)	Female: 58.3% (35/60)	0-17: 28.6% (6/21) 18-49: 42.9% (9/21) >50: 28.6% (6/21)	Female: 66.7% (14/21) Male: 33.3% (7/21)	Secondary Infection Risk Household with children: 26.6% (21/79) **Secondary Cases** Extended family: 33.3% (7/21) Immediate family: 66.7% (14/21) Gathering without living together: 0% Living together for visiting period: 28.6% (6/21) Living together: 71.4% (15/21) Wearing mask at home: 10.3% (3/29) No mask wearing at home: 31.0% (9/29)

First author, country	Study type	Attack rate by age of index	Attack rate by gender of index	Attack rate by age of contact	Attack rate by gender of contact	Other attack rates reported
Angulo-Bazan[171] Peru	Retrospective, secondary database review of 326 people from 52 households and their contacts. 23-Apr to 02-May.					Overall: 53.0%

OR – odds ratio; SAR – secondary attack rate.

[a] 0-16 year olds.

[b] Proportion of study participants with anti-SARS-CoV-2 antibodies.

[c] Mean risk of infection adjusted by age, gender and household size. Values assuming 10 days' exposure shown; values for 5, 15 and 20 days' exposure reported in the publication[164]).

[d] Attack rates not stated. Authors present matrices for hazard of infection for household relative to non-household transmission, stratified by age and gender of both index cases and their contacts (see **Appendix 3 Table A3**). Of 9120 confirmed cases, 34 primary cases were identified as super spreaders, and 5 household super-spreading events were observed.

[e] Authors reported that female close contacts with older age and frequent contacts had higher rates of infection, but secondary attack rates were not presented.

[f] "Low -risk" contacts defined as contacts who were in the proximity of index cases but did not meet these criteria for high-risk exposure.

[g] Sharing a meal with a case.

Table A7: Methods of Epidemiological Investigation used in South Korea, as reported by Lee et al[172] based on information from the Korea Centers for Disease Control and Prevention.[173]

Methods	Description
1. Interview	An epidemiology investigation is done mainly by conducting an interview in person. However, if this is not possible, an interview may be conducted with family, travel companions, or acquaintances.
2. Medical history records	Additional information may be obtained through patient care and interviews with nursing personnel and access to all medical records.
3. Closed-circuit television	If necessary, images and detailed data of the patient's circulation and movement path may be requested.
4. Credit card & Transportation	If necessary, the route of transportation, etc., credit card, debit card, or prepaid card usage statements may be requested.
5. Immigration	If necessary, immigration records may be requested and checked.
6. Hospital records	If necessary, health insurance inquiries may be made to check if there is a history of visiting or using medical institutions.

Appendix 4

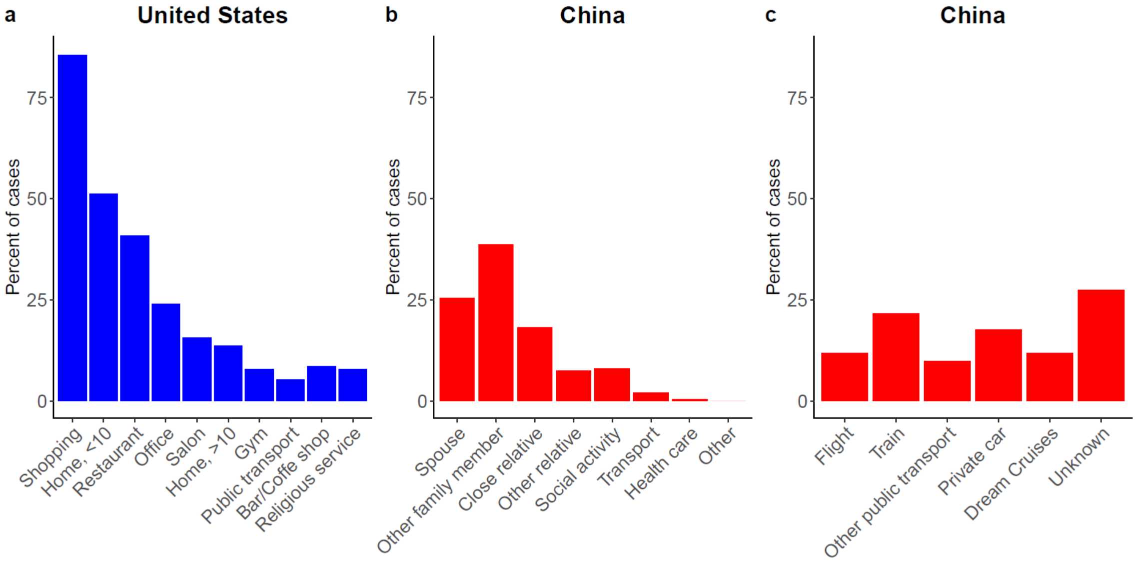


Figure A12: Reported exposure settings and relationships in the US and China. a) Settings that were reported by patients testing positive for SARS-CoV-2 as possible places of exposure before onset of symptoms in the United States. Patients were interviewed at 11 outpatient healthcare facilities.[68] b) Relationships of close contacts of individuals testing positive for SARS-CoV-2 in a cohort study conducted in Guangdong, China.[159] c) Transport settings where individuals testing positive for SARS-CoV-2 had contacts with other infected individuals in a cohort study conducted in Guangdong, China.[159]

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