

 Open access • Posted Content • DOI:10.1101/2020.03.02.20029868

## Household transmissions of SARS-CoV-2 in the time of unprecedented travel lockdown in China. — [Source link](#)

[Xiaoke Xu](#), [Xiao Fan Liu](#), [Lin Wang](#), [Lin Wang](#) ...+5 more authors

**Institutions:** [Minzu University of China](#), [City University of Hong Kong](#), [University of Cambridge](#), [Pasteur Institute](#) ...+3 more institutions

**Published on:** 30 Mar 2020 - [medRxiv](#) (Cold Spring Harbor Laboratory Press)

**Topics:** [Secondary infection](#)

Related papers:

- [Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia.](#)
- [Epidemiology and transmission of COVID-19 in 391 cases and 1286 of their close contacts in Shenzhen, China: a retrospective cohort study.](#)
- [Reconstruction of Transmission Pairs for Novel Coronavirus Disease 2019 \(COVID-19\) in Mainland China: Estimation of Superspreading Events, Serial Interval, and Hazard of Infection.](#)
- [HOSTED-England's Household Transmission Evaluation Dataset: preliminary findings from a novel passive surveillance system of COVID-19.](#)
- [Characteristics of and Important Lessons From the Coronavirus Disease 2019 \(COVID-19\) Outbreak in China: Summary of a Report of 72 314 Cases From the Chinese Center for Disease Control and Prevention](#)

Share this paper:    

View more about this paper here: <https://typeset.io/papers/household-transmissions-of-sars-cov-2-in-the-time-of-521385alg2>

1 **Title:** Household transmissions of SARS-CoV-2 in the time of unprecedented travel  
2 lockdown in China

3

4 **Authors:** Xiao-Ke Xu, PhD <sup>1,+</sup>, Xiao-Fan Liu, PhD <sup>2,+</sup>, Lin Wang, PhD <sup>3,4,+</sup>, Sheikh Taslim Ali, PhD <sup>5,+</sup>,  
5 Zhanwei Du, PhD <sup>6,+</sup>, Paolo Bosetti, PhD <sup>3</sup>, Benjamin J. Cowling, PhD <sup>5</sup>, Ye Wu, PhD <sup>7,8</sup>

6 **Affiliations:**

7 1. College of Information and Communication Engineering, Dalian Minzu University, Dalian 116600,  
8 China

9 2. Web Mining Lab, Department of Media and Communication, City University of Hong Kong, Hong  
10 Kong Special Administrative Region, China

11 3. Department of Global Health, Institut Pasteur, UMR2000, CNRS, Paris 75015, France

12 4. Department of Genetics, University of Cambridge, Cambridge CB2 3EH, UK

13 5. WHO Collaborating Centre for Infectious Disease Epidemiology and Control, School of Public  
14 Health, Li Ka Shing Faculty of Medicine, The University of Hong Kong, Hong Kong Special  
15 Administrative Region, China

16 6. Department of Integrative Biology, University of Texas at Austin, Austin, Texas 78705, USA

17 7. Computational Communication Research Center, Beijing Normal University, Zhuhai, 519087, China

18 8. School of Journalism and Communication, Beijing Normal University, Beijing, 100875, China

19

20 Corresponding email: [wuye@bnu.edu.cn](mailto:wuye@bnu.edu.cn) and [lin.wang@pasteur.fr](mailto:lin.wang@pasteur.fr)

21 <sup>+</sup> These authors are joint first authors with equal contribution.

22

23

24

25

26 Abstract (words limit: 335 / 350)

27 Main Text (words limit: 1,214 / 1200)

28

29

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

## 31 **Key Points**

32 **Question:** What epidemiological characteristics and risk factors are associated with household and  
33 non-household transmissions of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in  
34 China outside of Hubei Province?

35 **Findings:** In this epidemiological study analyzing 1,407 SARS-CoV-2 infection events reported  
36 between 20 January 2020 and 19 February 2020, 643 transmission clusters were reconstructed to  
37 demonstrate the non-negligible frequency of super-spreading events, short duration of serial intervals,  
38 and a higher risk of being infected outside of household for male people of age between 18 and 64  
39 years.

40 **Meaning:** These findings provide epidemiological features and risk estimates for both household and  
41 non-household transmissions of SARS-CoV-2 in China outside of Hubei Province.

42

## 43 **Abstract**

44 **Importance** Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerged in the city of  
45 Wuhan, China, in December 2019 and then spread globally. Limited information is available for  
46 characterizing epidemiological features and transmission patterns in the regions outside of Hubei  
47 Province. Detailed data on transmission at the individual level could be an asset to understand the  
48 transmission mechanisms and respective patterns in different settings.

49 **Objective** To reconstruct infection events and transmission clusters of SARS-CoV-2 for estimating  
50 epidemiological characteristics at household and non-household settings, including super-spreading  
51 events, serial intervals, age- and gender-stratified risks of infection in China outside of Hubei Province.

52 **Design, Setting, and Participants** 9,120 confirmed cases reported online by 264 Chinese urban Health  
53 Commissions in 27 provinces from January 20 to February 19, 2020. A line-list database is established  
54 with detailed information on demographic, social and epidemiological characteristics. The infection  
55 events are categorized into the household and non-household settings.

56 **Exposures** Confirmed cases of SARS-CoV-2 infections.

57 **Main Outcomes and Measures** Information about demographic characteristics, social relationships,  
58 travel history, timelines of potential exposure, symptom onset, confirmation, and hospitalization were  
59 extracted from online public reports. 1,407 infection events formed 643 transmission clusters were  
60 reconstructed.

61 **Results** In total 34 primary cases were identified as super spreaders, and 5 household super-spreading  
62 events were observed. The mean serial interval is estimated to be 4.95 days (standard deviation: 5.24  
63 days) and 5.19 days (standard deviation: 5.28 days) for households and non-household transmissions,  
64 respectively. The risk of being infected outside of households is higher for age groups between 18 and  
65 64 years, whereas the hazard of being infected within households is higher for age groups of young  
66 (<18) and elderly (>65) people.

67 **Conclusions and Relevance** The identification of super-spreading events, short serial intervals, and a  
68 higher risk of being infected outside of households for male people of age between 18 and 64 indicate a  
69 significant barrier to the case identification and management, which calls for intensive non-  
70 pharmaceutical interventions (e.g. cancellation of public gathering, limited access of public services) as  
71 the potential mitigation strategies.

72

73

74

75

76

77

78

79

80

81

82

83

84

85

## 86 **Introduction**

87 In December 2019, a novel coronavirus (severe acute respiratory syndrome coronavirus 2, SARS-CoV-  
88 2) emerged in Wuhan city of Hubei Province in China. World Health Organization (WHO) announced  
89 a public health emergency of international significance on 30 January 2020 <sup>1</sup> and classified the threat as  
90 a global pandemic on 11 March 2020 <sup>2</sup>. More than 118,326 confirmed cases and 4,292 deaths have  
91 been reported as of 11 March 2020. The majority of cases in China (67,773) were from Hubei  
92 Province<sup>3</sup>.

93 On 23 January 2020, China raised the national emergency response to the highest level, triggered an  
94 unprecedented travel ban starting from the lockdown of Wuhan on 23 January, and 14 cities nearby  
95 Wuhan on 24 January, and more than 30 provinces thereafter (Figure 1a). Although this countrywide  
96 travel lockdown was aimed to interrupt case exportations from the epicenter, we have estimated 130  
97 (95% CrI: 190, 369) high-risk cities that have introduced SARS-CoV-2 cases prior to Wuhan's  
98 lockdown <sup>4</sup>. Recent studies<sup>5,6</sup> report similar estimates for the rapid geographic expansion of SARS-  
99 CoV-2. These coincide with the frequent reporting of infection events in China outside of Hubei  
100 Province during the three weeks following Wuhan's lockdown (Figure 1c).

101 Since the last week of January 2020, more than 260 Chinese cities have implemented intensive non-  
102 pharmaceutical controls (Figure 1b), which brought the epidemic under control <sup>7,8,9</sup>. However, as of 19  
103 February 2020, this epidemic still has caused >10,000 cases in China outside of Hubei Province. To  
104 enhance public health preparedness and public awareness, Chinese health authorities have publicly  
105 reported detailed records of confirmed cases since 20 January 2020. This provides a unique resource  
106 and an opportunity for understanding the transmission patterns, routes, and risk factors of the COVID-  
107 19 epidemic.

## 108 **Methods**

### 109 **Data Collection**

110 In China, 27 provincial and 264 urban health commissions have publicly posted 9,120 confirmed case  
111 reports online since 20 January 2020, which comprises 72.7% of all cases confirmed in China outside  
112 of Hubei Province by 19 February (Table S9). We compiled a line-list database from these reports with  
113 extracted demographic characteristics, social relationships, travel history, timelines of potential  
114 exposure, symptom onset, confirmation and hospitalization. We obtained the daily population

115 movement data in China between 1 January and 13 February 2020 from Baidu Qianxi Web Portal  
116 (<https://qianxi.baidu.com/>). We estimated the daily number of passengers leaving each province by  
117 using the migration scale index for moving out of that province each day. More details on our real-time  
118 mobility and line-list case data are provided in Supplemental Material and will be available at our  
119 GitHub.

## 120 **Statistical Analysis**

121 We identified 1,407 infection events with known social relationships. For each infection event, we term  
122 the infector the *primary* case and the infectee the *secondary* case. We also consider connected chains of  
123 confirmed cases; we term the original case the *index* and the entire chain of cases, including the index,  
124 the *transmission cluster* (Figure 2a).

125 We stratify infection events by household versus non-household transmissions, where household  
126 includes any infection event among members within the same family (e.g., between parents and  
127 children), and non-household include all others (e.g. colleagues, classmates). The numbers of  
128 household (662) and non-household (745) infection events are almost even.

129 For each infection event with known symptom onset timelines, we compute the serial interval, i.e., the  
130 number of days between the reported symptom onset date for the primary case and that for the  
131 secondary case. We estimate the distribution of serial intervals by fitting a normal distribution to 679  
132 infection events with known serial intervals (Supplemental Material).

133 The age-stratified hazard of infection for household relative to non-household contacts is estimated by  
134 the ratio between the probability that a secondary case of age group  $b$  was infected by a primary case of  
135 age group  $a$  within the same household and the probability that a secondary case of age group  $b$  was  
136 infected by a primary case of age group  $a$  outside of households. Gender-specific hazard of infection is  
137 measured similarly (Supplemental Material).

## 138 **Results**

139 We reconstructed 643 transmission clusters from 1,407 infection events (Figure 2a). The sizes of 587  
140 transmission clusters are smaller than 5, whereas the size of the largest cluster exceeds 20. We  
141 observed 34 primary cases acting as super spreaders. Stratification by household shows that 356, 92,  
142 and 34 primary cases infected only 1 member, 2 members, and at least 3 familial members within  
143 households, respectively; 276, 78, and 75 primary cases infected 1, 2, and at least 3 secondary cases  
144 outside households, respectively (Figure 2b). Only 5 household super-spreading events were observed.

145 The mean serial interval is estimated to be 4.95 days (standard deviation: 5.24 days) within households,  
146 and 5.19 days (standard deviation: 5.28 days) for non-household transmissions. Notably, 26 of 339  
147 household- and 29 of 340 non-household infection events reported negative-valued serial intervals,  
148 implying pre-symptomatic transmission.

149 The hazard of being infected within households is higher for age groups of young (<18) and elderly  
150 (>65) people, whereas the hazard of being infected outside of households is higher for age groups  
151 between 18 and 64 years (Table 1a). Primary cases of elderly (>65) people are more prone to cause  
152 household infections. Hazard of infection between different genders is higher for households than non-  
153 household transmission (Table 1b).

## 154 **Discussion**

155 We reconstructed 1,407 infection events formed 643 transmission clusters from 9,120 COVID-19 cases  
156 confirmed in China outside of Hubei Province as of 19 February 2020. The entire database will be  
157 available at our GitHub.

158 Although super-spreading events have been reported by media reports and a recent study <sup>11</sup> which  
159 focuses on special settings (e.g., restaurant, chalet) before February 2020, systematic analyses with a  
160 sufficiently large sample size is lacking. Here, we identified 34 primary cases classified as super-  
161 spreader. Majority of the super-spreading events involve more non-household transmissions than  
162 household transmissions. This indicates the importance of non-pharmaceutical interventions (e.g.  
163 cancellation of public gatherings, limited access of public services) as the potential mitigation  
164 strategies (see Table S2).

165 Household study helps identify risk factors for certain demographic groups <sup>12</sup>. The age-stratified and  
166 gender-specific hazard of infection suggests a higher risk of infection within households for age groups  
167 of young (<18) and elderly (>65) and female people. The higher risk of being infected outside of  
168 households for male people of age between 18 and 64 years indicates their role in driving household  
169 secondary infections in the households included in our data, perhaps because these were travelers from  
170 Wuhan of working age.

171 We identified 55 infection events (~4%) with the secondary case reporting symptom onset prior to the  
172 primary case, which is consistent with our preliminary analysis <sup>4</sup> and recent clinical reports <sup>13,14</sup>.

173 Negative-valued serial intervals indicate the potential occurrence of pre-symptomatic transmissions.

174 We estimate that the mean serial interval is ~5 days for both household and non-household infections,

175 which is considerably shorter than the mean serial interval estimated for SARS (e.g., 8.4 days<sup>15</sup>) and  
176 MERS (e.g. 7.6 days<sup>16</sup>). These evidences impose a significant barrier to case identification and  
177 management.

178 Our findings have several limitations. First, the size of each household and the primary cases without  
179 secondary infections are unknown from original disclosures. This may give biased estimates if we  
180 estimate the household reproduction number and secondary attack rate from raw data. Field surveys  
181 will be helpful to adjust biases. Second, the information on nosocomial infections is unknown from  
182 original disclosures, so that the observation of super-spreading events may be less common from our  
183 dataset.

184

185

186

187

188

189

190

191

192

193

194

195

196

197

198

199

200

201

202

203



204

205

## 206 **References**

- 207 1. Statement on the second meeting of the International Health Regulations (2005) Emergency  
208 Committee regarding the outbreak of novel coronavirus (2019-nCoV). [https://www.who.int/news-](https://www.who.int/news-room/detail/30-01-2020-statement-on-the-second-meeting-of-the-international-health-regulations-(2005)-emergency-committee-regarding-the-outbreak-of-novel-coronavirus-(2019-ncov))  
209 [room/detail/30-01-2020-statement-on-the-second-meeting-of-the-international-health-regulations-](https://www.who.int/news-room/detail/30-01-2020-statement-on-the-second-meeting-of-the-international-health-regulations-(2005)-emergency-committee-regarding-the-outbreak-of-novel-coronavirus-(2019-ncov))  
210 [-\(2005\)-emergency-committee-regarding-the-outbreak-of-novel-coronavirus-\(2019-ncov\).](https://www.who.int/news-room/detail/30-01-2020-statement-on-the-second-meeting-of-the-international-health-regulations-(2005)-emergency-committee-regarding-the-outbreak-of-novel-coronavirus-(2019-ncov))  
211 Accessed March 16, 2020.
- 212 2. WHO Director-General's opening remarks at the media briefing on COVID-19 - 11 March 2020.  
213 [https://www.who.int/dg/speeches/detail/who-director-general-s-opening-remarks-at-the-media-](https://www.who.int/dg/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19---11-march-2020)  
214 [briefing-on-covid-19---11-march-2020.](https://www.who.int/dg/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19---11-march-2020) Accessed March 16, 2020.
- 215 3. Novel Coronavirus (2019-nCoV) situation reports.  
216 [https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports.](https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports) Accessed  
217 March 16, 2020.
- 218 4. Du Z, Wang L, Cauchemez S, et al. Risk for Transportation of 2019 Novel Coronavirus Disease  
219 from Wuhan to Other Cities in China. *Emerg Infect Dis.* 2020;26(5). doi:10.3201/eid2605.200146
- 220 5. Wu JT, Leung K, Leung GM. Nowcasting and forecasting the potential domestic and international  
221 spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. *Lancet.*  
222 2020;395(10225):689-697. doi:10.1016/S0140-6736(20)30260-9
- 223 6. Chinazzi M, Davis JT, Ajelli M, et al. The effect of travel restrictions on the spread of the 2019  
224 novel coronavirus (COVID-19) outbreak. *Science.* March 2020. doi:10.1126/science.aba9757
- 225 7. Kraemer MUG, Yang C-H, Gutierrez B, et al. The effect of human mobility and control measures  
226 on the COVID-19 epidemic in China. *medRxiv.* 2020.  
227 [https://www.medrxiv.org/content/10.1101/2020.03.02.20026708v1.abstract.](https://www.medrxiv.org/content/10.1101/2020.03.02.20026708v1.abstract)
- 228 8. Tian H, Liu Y, Li Y, et al. The impact of transmission control measures during the first 50 days of  
229 the COVID-19 epidemic in China. *medRxiv.* 2020.  
230 [https://www.medrxiv.org/content/10.1101/2020.01.30.20019844v4.](https://www.medrxiv.org/content/10.1101/2020.01.30.20019844v4)
- 231 9. Lai S, Ruktanonchai NW, Zhou L, Prosper O, Luo W. Effect of non-pharmaceutical interventions  
232 for containing the COVID-19 outbreak: an observational and modelling study. *medRxiv.* 2020.  
233 [https://www.medrxiv.org/content/10.1101/2020.03.03.20029843v2.full.pdf+html.](https://www.medrxiv.org/content/10.1101/2020.03.03.20029843v2.full.pdf+html)
- 234 10. Liu Y, Eggo RM, Kucharski AJ. Secondary attack rate and superspreading events for SARS-CoV-  
235 2. *Lancet.* 2020;395(10227):e47. doi:10.1016/S0140-6736(20)30462-1
- 236 11. Cowling BJ, Leung GM. Epidemiological research priorities for public health control of the  
237 ongoing global novel coronavirus (2019-nCoV) outbreak. *Euro Surveill.* 2020;25(6).  
238 doi:10.2807/1560-7917.ES.2020.25.6.2000110
- 239 12. Bai Y, Yao L, Wei T, et al. Presumed Asymptomatic Carrier Transmission of COVID-19. *JAMA.*  
240 February 2020. doi:10.1001/jama.2020.2565
- 241 13. Pan X, Chen D, Xia Y, et al. Asymptomatic cases in a family cluster with SARS-CoV-2 infection.  
242 *Lancet Infect Dis.* February 2020. doi:10.1016/S1473-3099(20)30114-6
- 243 14. Lipsitch M. Transmission Dynamics and Control of Severe Acute Respiratory Syndrome. *Science.*  
244 2003;300(5627):1966-1970. doi:10.1126/science.1086616
- 245 15. Hospital Outbreak of Middle East Respiratory Syndrome Coronavirus. *New England Journal of*  
246 *Medicine.* 2013;369(9):886-886. doi:10.1056/nejmx130042

247

248

249

250 **Acknowledgements**

251 We thank Simon Cauchemez, Lauren Ancel Meyers, Henrik Salje, Juliette Paireau, Dongsheng Luo,  
252 and Lanfang Hu for helpful discussions.

253

254 **Funding/Support**

255 We acknowledge the financial support from the National Institutes of Health (grant no. R01AI114703-  
256 01, U01 GM087719), the Open Fund of Key Laboratory of Urban Land Resources Monitoring and  
257 Simulation, Ministry of Land and Resources (grant no. KF-2019-04-034), the Investissement d’Avenir  
258 program, the Laboratoire d’Excellence Integrative Biology of Emerging Infectious Diseases program  
259 (grant no. ANR-10-LABX-62-IBEID), European Union V.E.O project, European Research Council  
260 (grant no. 804744), National Natural Science Foundation of China (grant no. 61773091, 11875005,  
261 61976025, 11975025), Major Project of The National Social Science Fund of China (grant no.  
262 19ZDA324), and a Commissioned Grant from the Health and Medical Research Fund, Food and Health  
263 Bureau, Government of the Hong Kong Special Administrative Region,

264

265 **Conflict of Interest Disclosures:**

266 BJC reports honoraria from Sanofi Pasteur and Roche. The authors report no other potential conflicts  
267 of interest.

268

269

270

271

272

## 273 **Figure Legends and Tables**

274

275 **Figure 1: Changing patterns of population movements, non-pharmaceutical control measures,**  
276 **and epidemic curve of infection events in China outside of Hubei Province.** (a) Relative change in  
277 the outbound travel volume (i.e., daily number of passengers) moving out of each province in China  
278 from 1 January to 13 February 2020. The baseline daily outbound travel volume of a given province is  
279 estimated by the mean daily number of passengers moving out of that province between 3 January  
280 2020 and 9 January 2020 (i.e., the last week prior to the start of the Spring Festival travel season). The  
281 relative change in outbound travel volume of province  $i$  on a given date  $T_i$  is measured by the ratio  
282 between the estimated number of passengers moving out of province  $i$  on date  $T_i$  and the baseline daily  
283 outbound travel volume of province  $i$ . Each row denotes a province, with Hubei Province highlighted  
284 in red. Columns from left to right are ordered by calendar days. For the color bar, the dark red and blue  
285 indicate a significant decrease and increase in the outbound travel volume, respectively. The Spring  
286 Festival travel season officially started on 10 January 2020. The Lunar New Year holiday started on 25  
287 January 2020 and was extended to 8 February 2020. The lockdown of Wuhan started on 23 January  
288 2020. The end date of Spring Festival travel season is not clear because of the countrywide travel  
289 lockdown. (b) The timing of epidemiological events and implementation of non-pharmaceutical control  
290 measures in 263 cities in China. The size of circles is proportional to the number of cities. The vertical  
291 grey dashed line indicates the timing of Wuhan's lockdown. (c) The date of symptom onset for  
292 secondary cases caused by household (light pink) and non-household (light blue) primary infections.  
293  
294

295

296 **Figure 2: COVID-19 transmission clusters.** (a) 643 transmission clusters, stratified by the size of  
297 cluster  $n$ . Red, green and blue nodes denote primary cases, household secondary cases and non-  
298 household secondary cases, respectively. (b) Distribution of the number of secondary infections caused  
299 by each of the 809 primary cases. (c) Distribution of serial intervals, which is fitted to 679 infection  
300 events with known symptom onset timelines. For household transmissions, fitting with a normal  
301 distribution suggests a mean serial interval of 4.95 days (standard deviation: 5.24 days); for non-  
302 household transmissions, fitting with a normal distribution suggests a mean serial interval of 5.19 days  
303 (standard deviation: 5.28 days). Alternative distributions fitted for the serial interval can be found in  
304 Table S5.

305

306

307 **Table 1: Hazard of infection stratified by age or gender.** (a) Age-stratified hazard of infection for  
 308 the household relative to non-household transmission. (b) Gender-specific hazard of infection for the  
 309 household relative to non-household transmission. Red or blue shades indicate an increased or  
 310 decreased hazard of infection within households relative to outside of households, respectively.  
 311

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

312

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

313

314

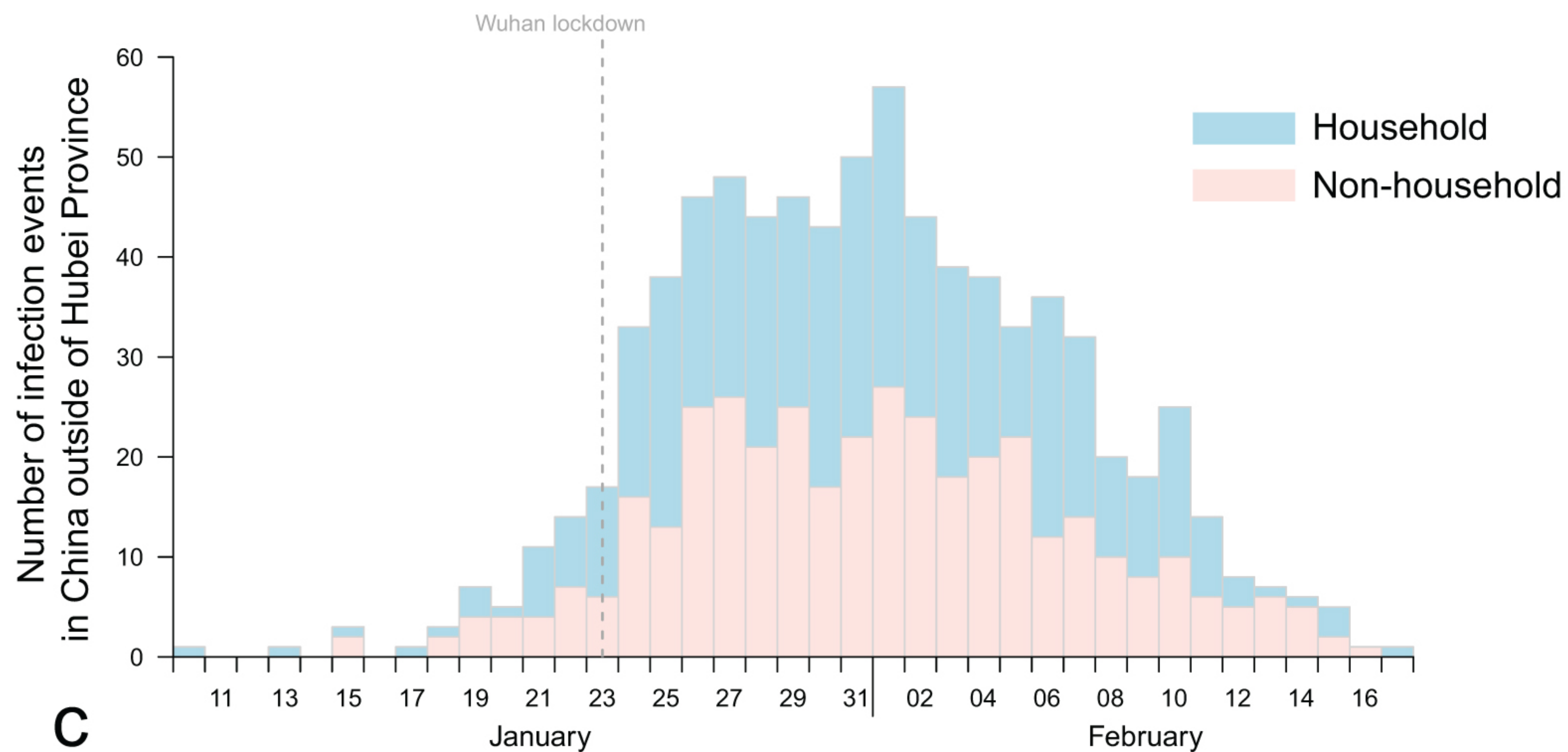
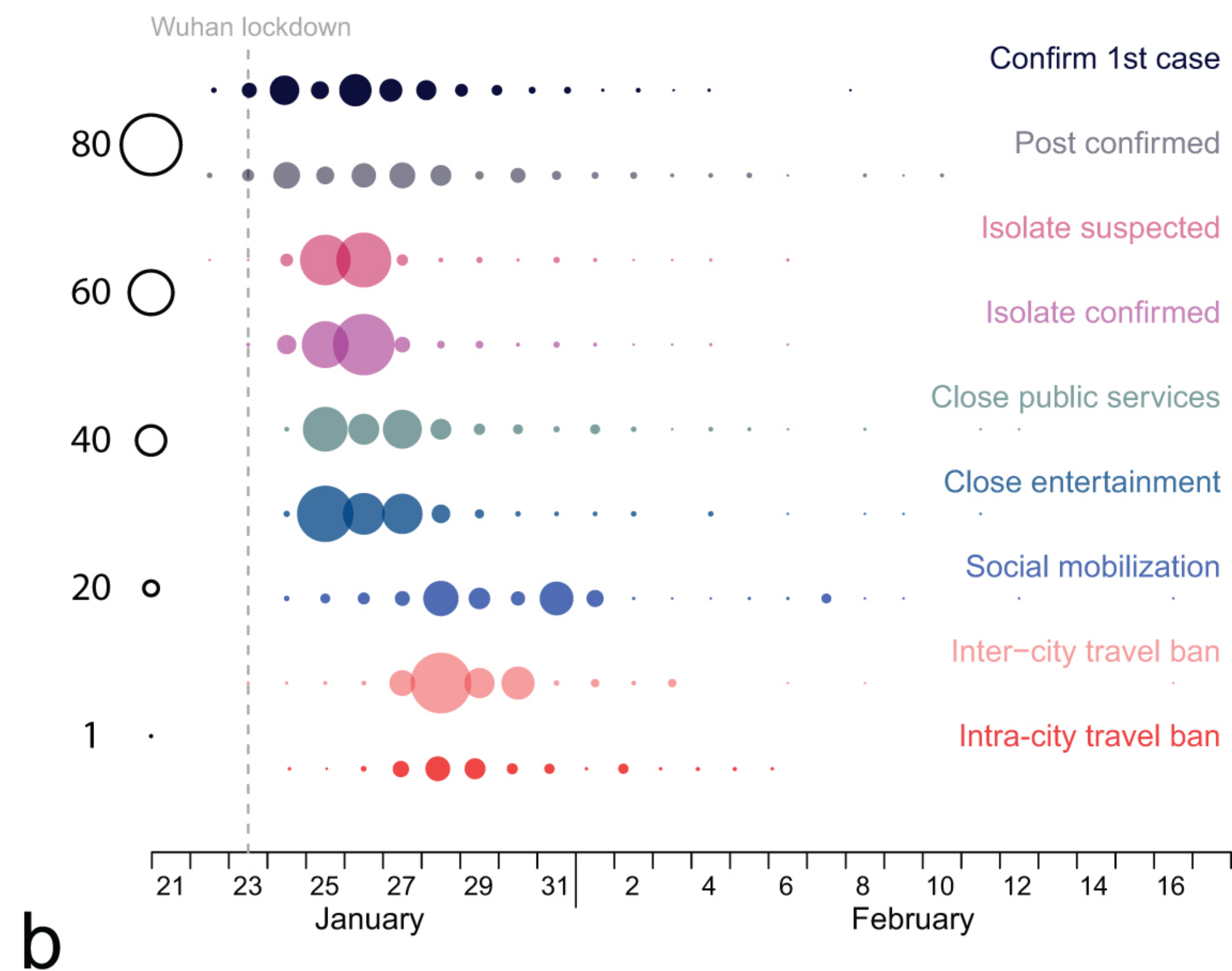
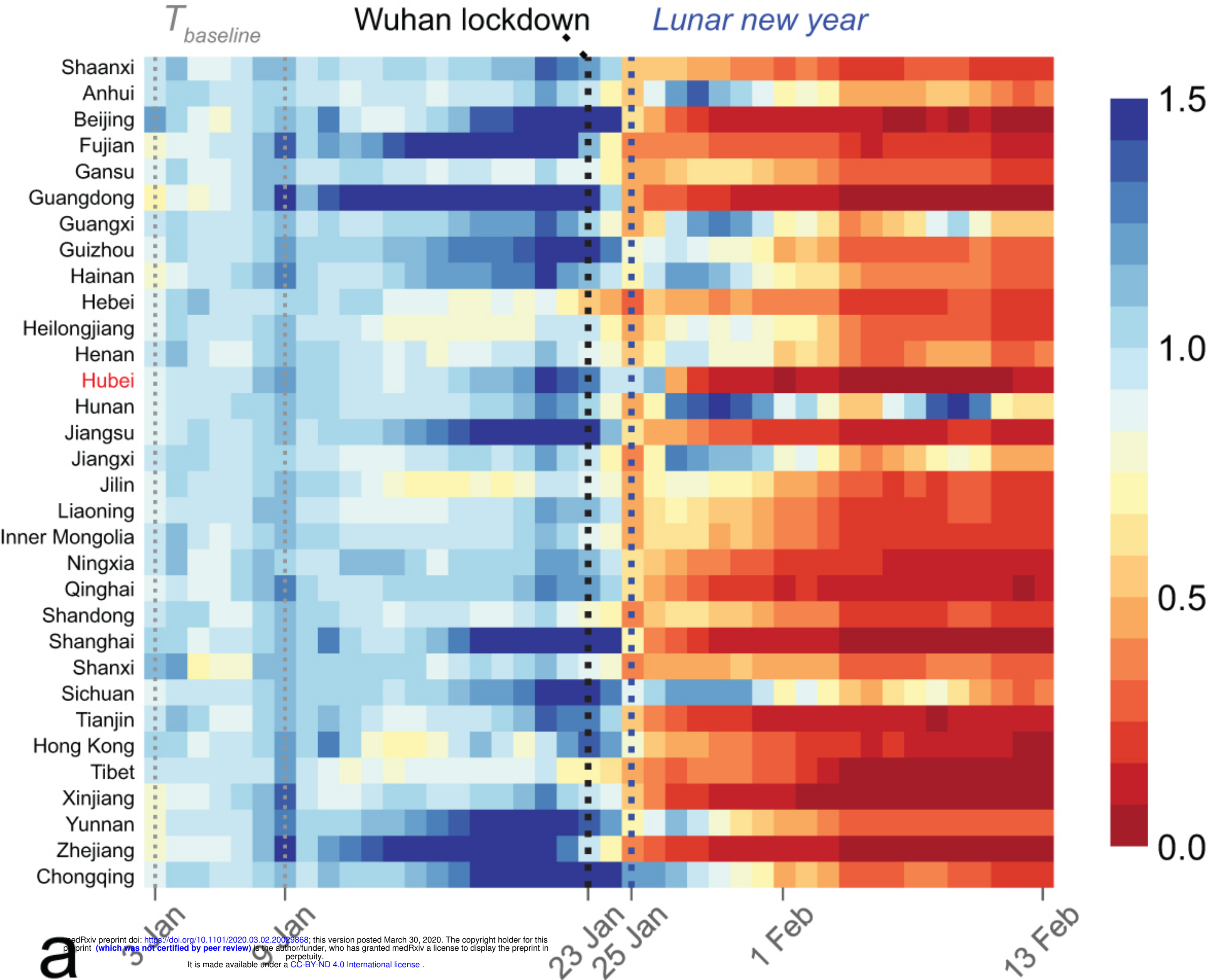
315

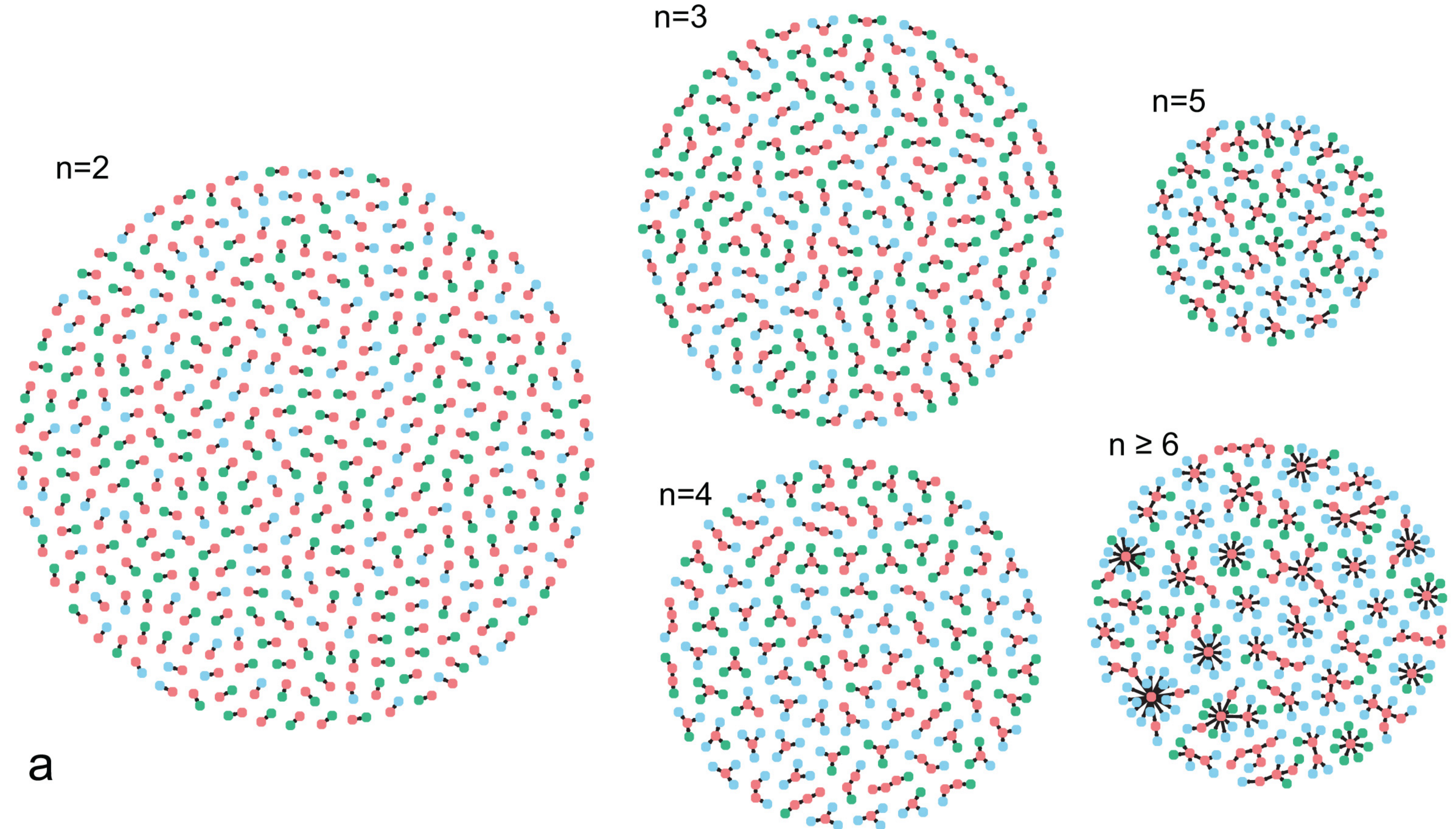
316

317

318

319





medRxiv preprint doi: <https://doi.org/10.1101/2020.03.02.20029868>; this version posted March 30, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted medRxiv a license to display the preprint in perpetuity. It is made available under a [CC-BY-ND 4.0 International license](#).

