

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

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26 Abstract (words limit: 335 / 350)

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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.

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.

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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 ¹ and classified the threat as
90 a global pandemic on 11 March 2020 ². 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 Province³.

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 ⁴. Recent studies^{5,6} 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 ^{7,8,9}. 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 ¹¹ 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 ¹². 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 ⁴ and recent clinical reports ^{13,14}.

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 days¹⁵) and
176 MERS (e.g. 7.6 days¹⁶). 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.

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265 **Conflict of Interest Disclosures:**

266 BJC reports honoraria from Sanofi Pasteur and Roche. The authors report no other potential conflicts
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273 **Figure Legends and Tables**

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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.
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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.

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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.
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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

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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

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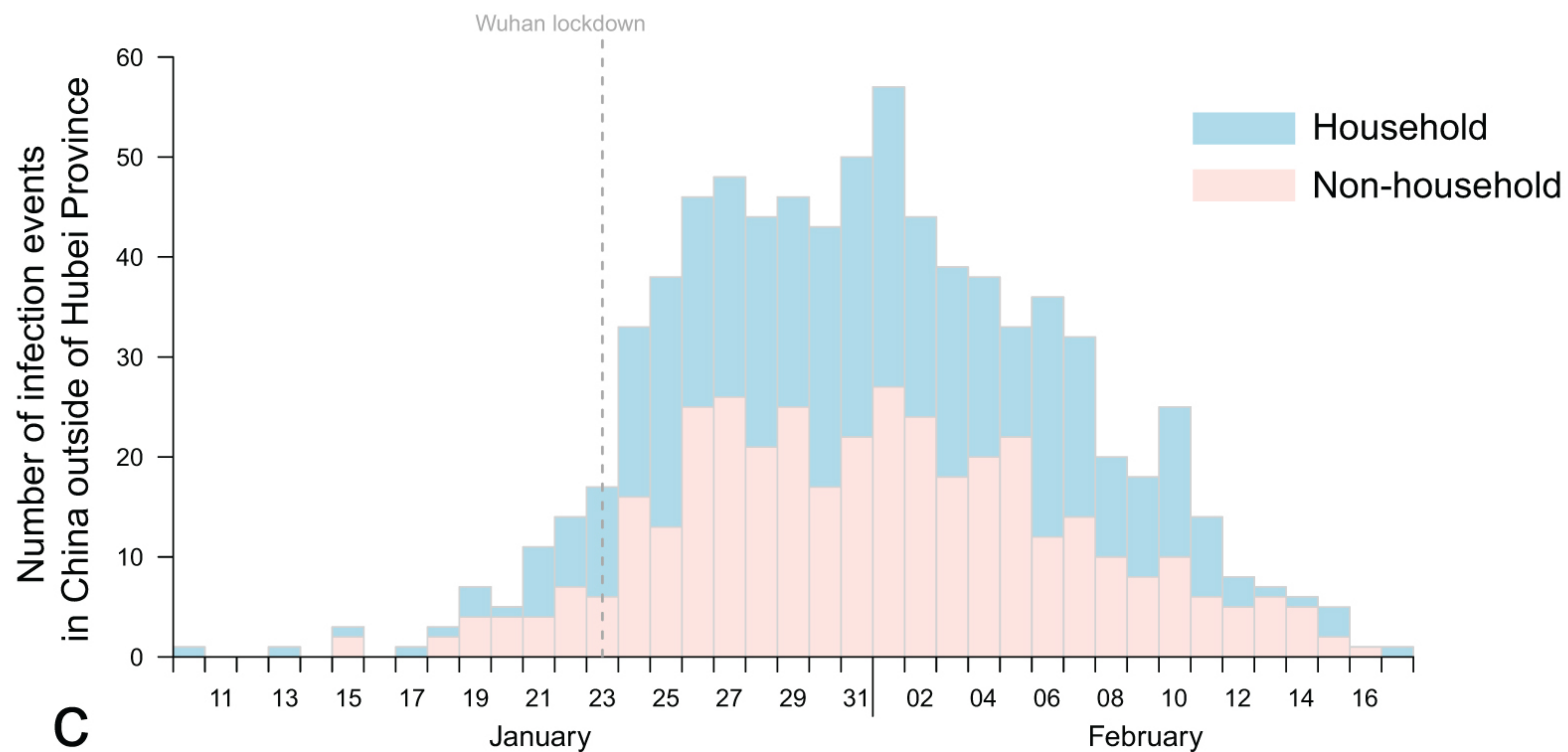
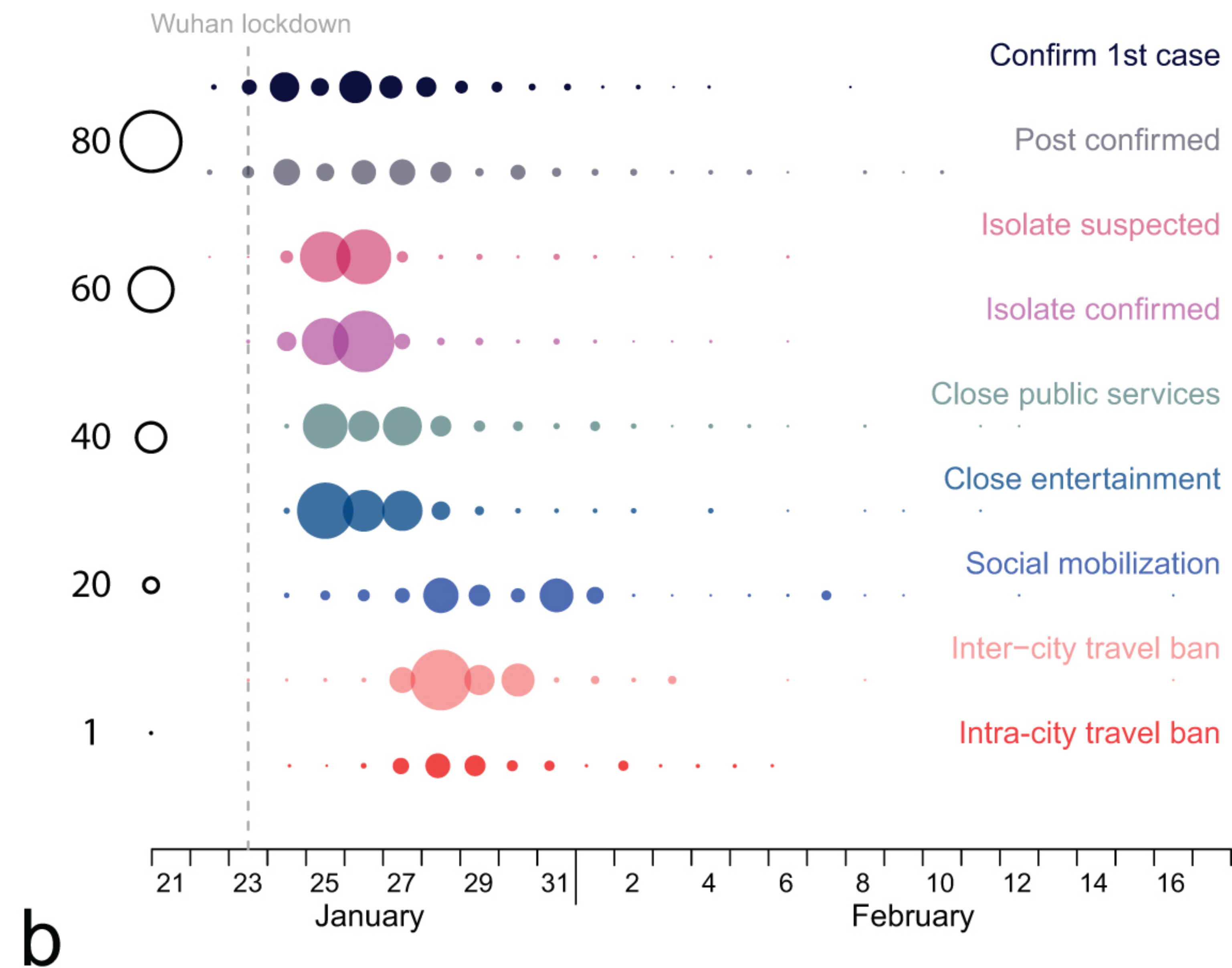
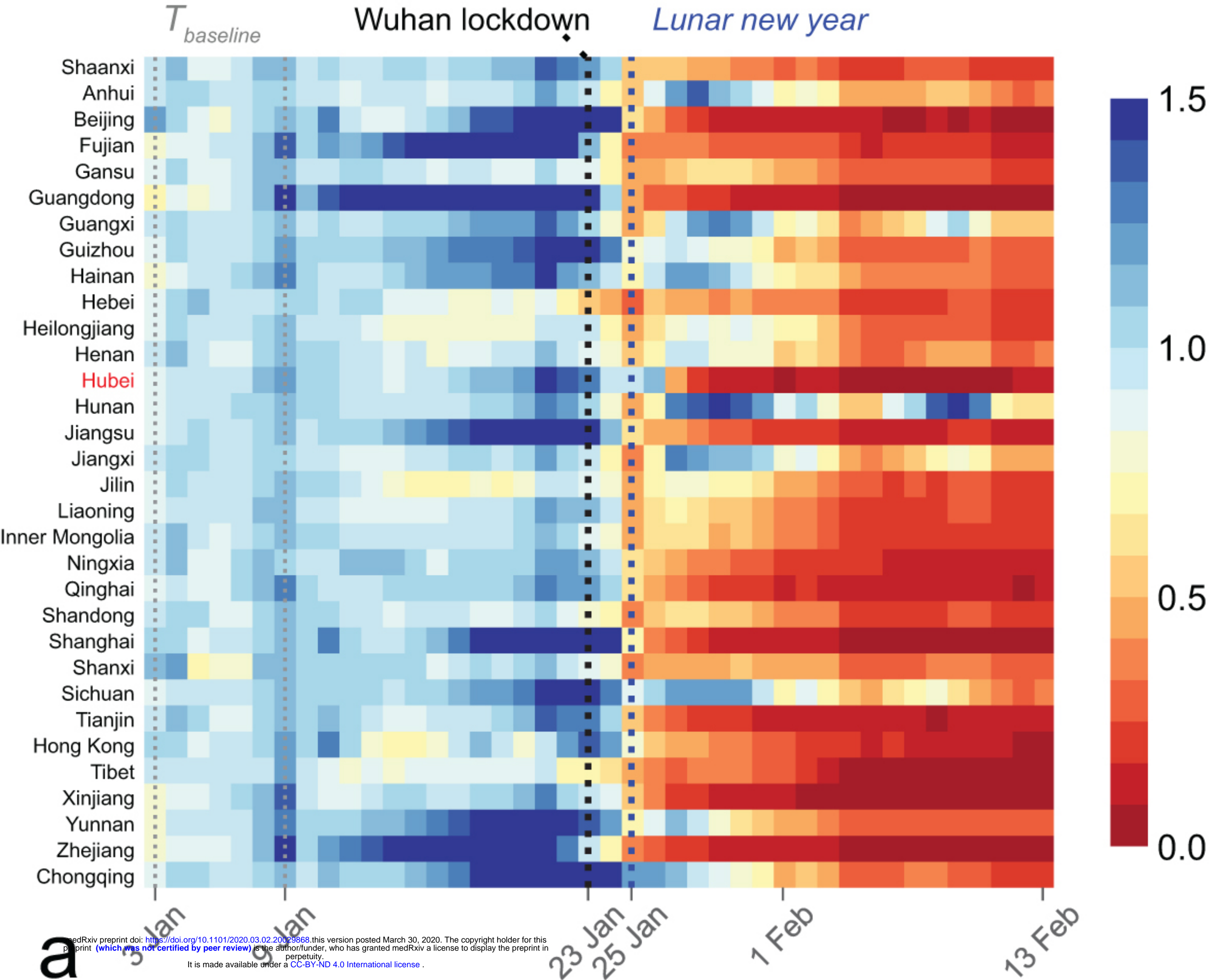
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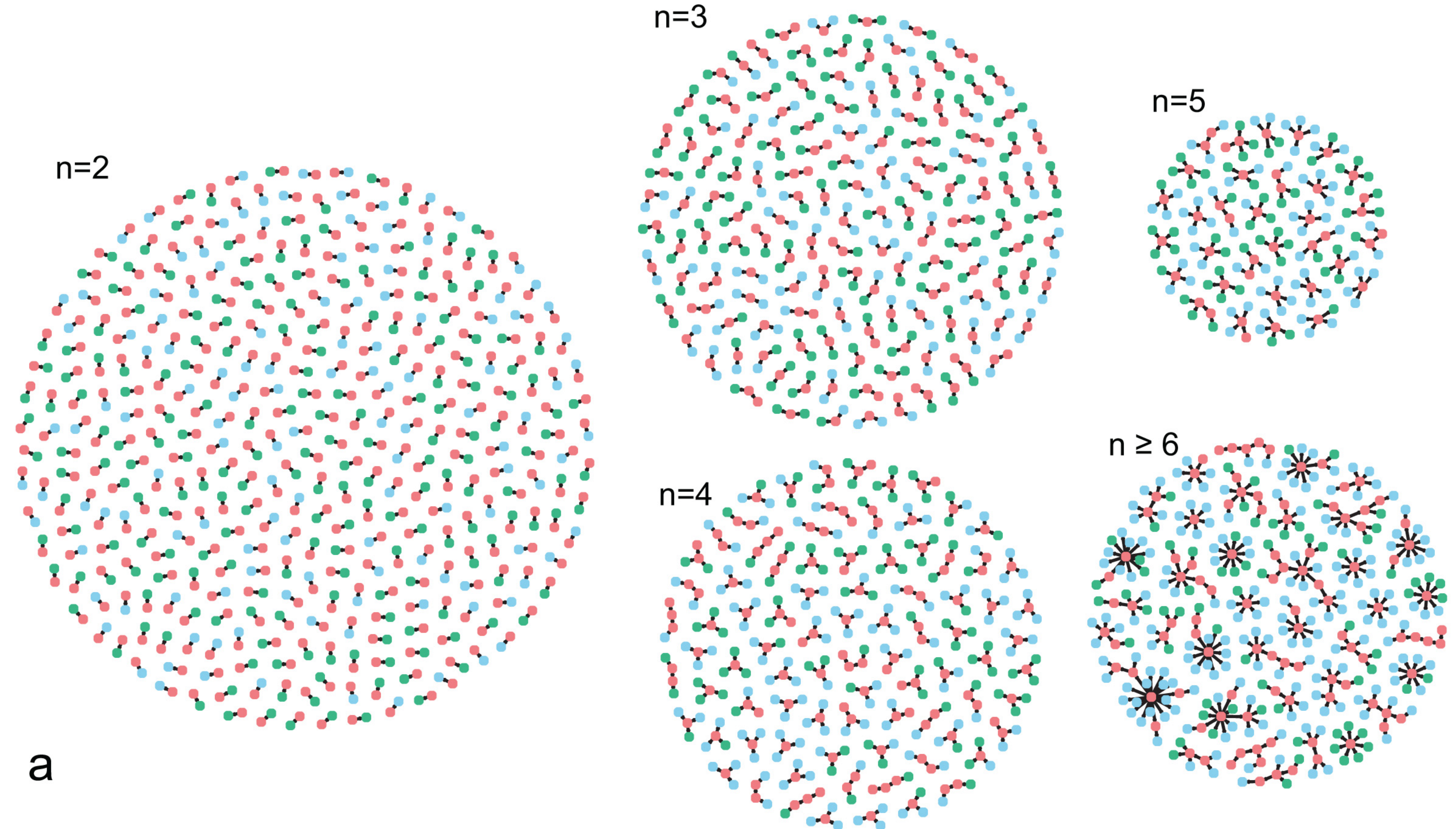
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