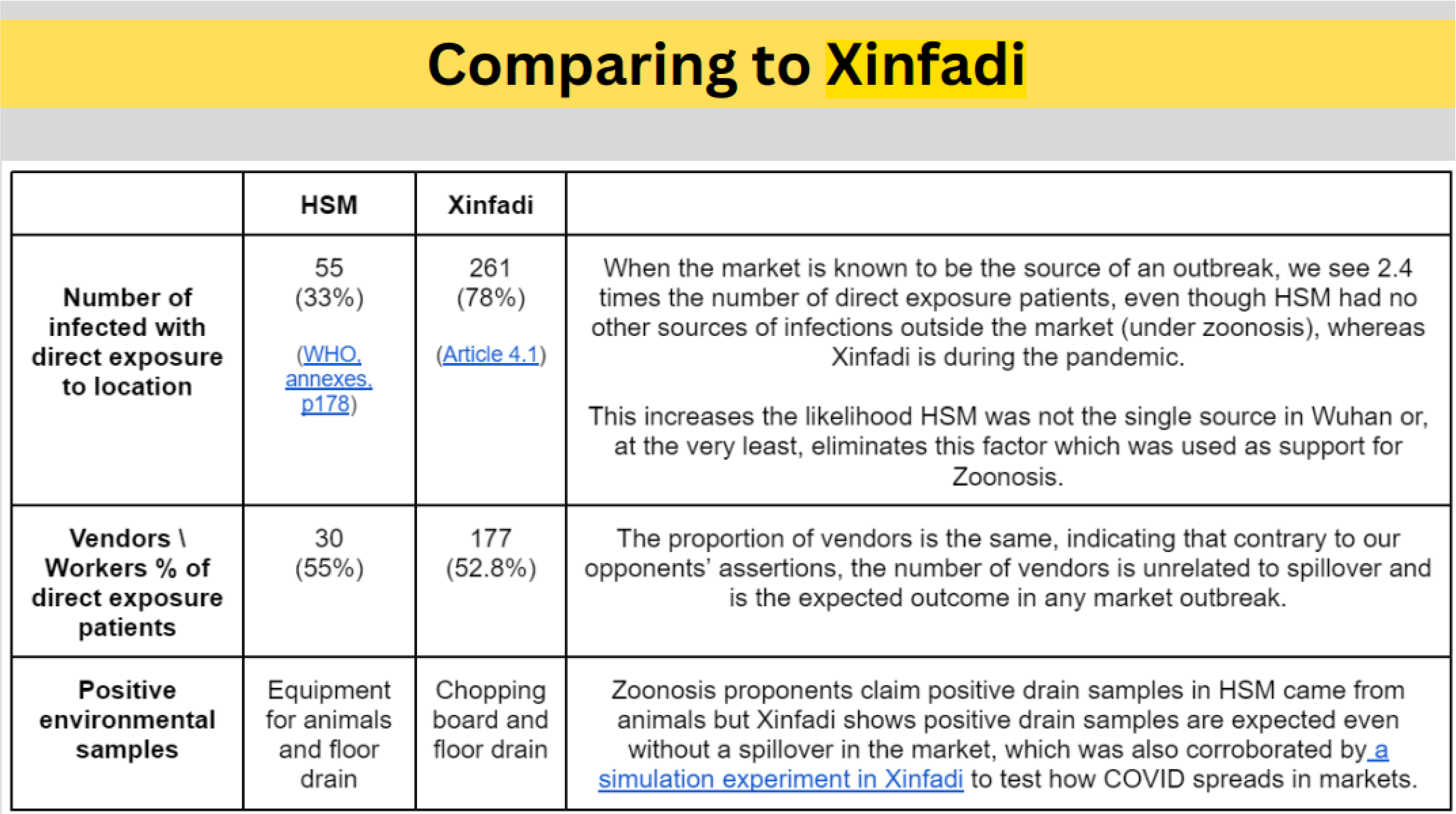
Day 1 slides shown at debate

Xinfadi market

Rootclaim offers this summary:



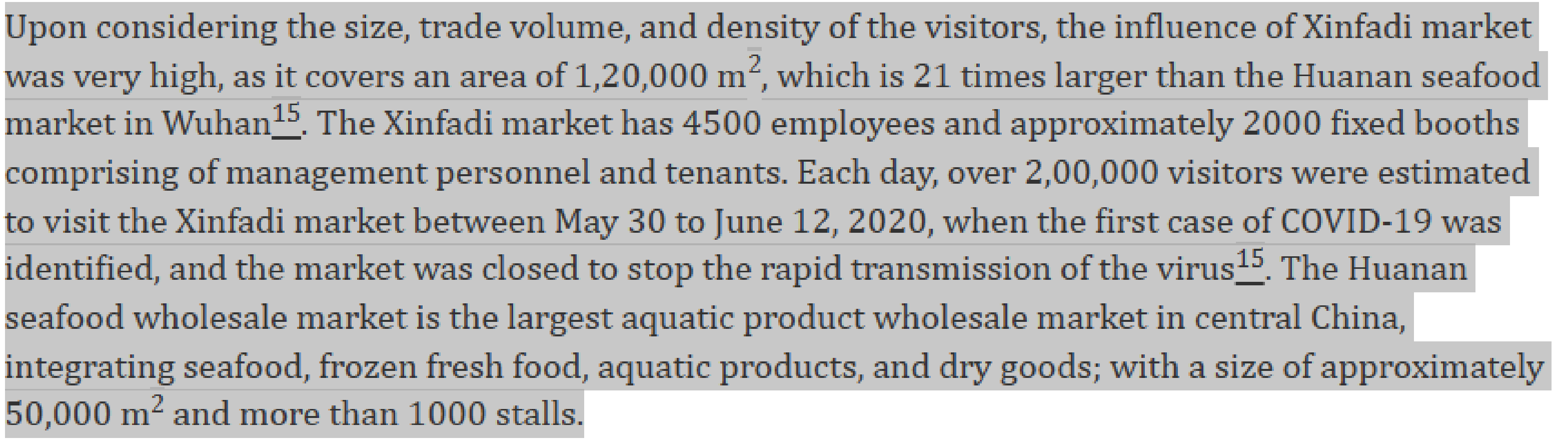
Comparing to Xinfadi

	HSM	Xinfadi	
Number of infected with direct exposure to location	55 (33%) (WHO, annexes, p178)	261 (78%) (Article 4.1)	When the market is known to be the source of an outbreak, we see 2.4 times the number of direct exposure patients, even though HSM had no other sources of infections outside the market (under zoonosis), whereas Xinfadi is during the pandemic. This increases the likelihood HSM was not the single source in Wuhan or, at the very least, eliminates this factor which was used as support for Zoonosis.
Vendors \ Workers % of direct exposure patients	30 (55%)	177 (52.8%)	The proportion of vendors is the same, indicating that contrary to our opponents' assertions, the number of vendors is unrelated to spillover and is the expected outcome in any market outbreak.
Positive environmental samples	Equipment for animals and floor drain	Chopping board and floor drain	Zoonosis proponents claim positive drain samples in HSM came from animals but Xinfadi shows positive drain samples are expected even without a spillover in the market, which was also corroborated by a simulation experiment in Xinfadi to test how COVID spreads in markets.

Why are the total case numbers higher?

Xinfadi market is the biggest market in the city of Beijing, and actually the largest wholescale food market in all of Asia.

Xinfadi was 21 times larger than the Huanan market, with far more employees and visitors:



> Upon considering the size, trade volume, and density of the visitors, the influence of Xinfadi market was very high, as it covers an area of 1,20,000 m^2, which is 21 times larger than the Huanan seafood market in Wuhan[15]. The Xinfadi market has 4500 employees and approximately 2000 fixed booths comprising of management personnel and tenants. Each day, over 2,00,000 visitors were estimated to visit the Xinfadi market between May 30 to June 12, 2020, when the first case of COVID-19 was identified, and the market was closed to stop the rapid transmission of the virus[15]. The Huanan seafood wholesale market is the largest aquatic product wholesale market in central China, integrating seafood, frozen fresh food, aquatic products, and dry goods; with a size of approximately 50,000 m^2 and more than 1000 stalls.

Why are the ratios higher?

This is in mid-2020, when PCR tests are readily available, everyone is looking for covid, and China has a zero covid policy. That will boost the absolute case numbers at the market.

But it also means they would detect an outbreak faster.

June 11: cases detected
June 13: market closed
June 16: Beijing shuts schools.
June 17: Beijing cancels flights.

If you contract trace the epidemic better and shut down the city rapidly, it makes sense that the ratios of market linked to non-market linked cases will be higher.

A larger market might also result in more transmission within market than outside of it within an identical timeframe.

Was the Xinfadi outbreak caused by the same thing as the Huanan outbreak?

According to Pang et al. (2020), several original packaged salmon samples in cold storage were tested positive for SARS-CoV-2. They wrote,

"*We examined all salmon in the original sealed package in the cold storage which was located outside XFDM, and six out of 3582 samples were positive for SARS-CoV-2 RNA. Notably, five positive fish were from company X, which supplied the salmon to booth #S14 on May 30. Through genome sequencing we obtained a significant number of SARS-CoV-2 reads from one swab of company X salmon.*"

Booth #S14 employees had the highest infection rates (100%) and is suspected to be the source of the outbreak. They then conclude:

"Given the abovementioned facts, we speculate that the COVID-19 resurgence in Beijing was likely to be initiated by an environment-to-human transmission originated from contaminated imported food via cold-chain logistics. Notably, a recent study found that SARS-CoV-2 showed no decline in infectivity after 21 days at 4°C and −20°C on the surface of chicken, salmon, and pork pieces [9], indicating that the survival period and transmission distance of the virus could be prolonged by cold-chain transportation of contaminated food."

In contrast, no evidence of possible cold-chain importation was found for the source of SARS-CoV-2 in the Huanan market (as far as anyone knows).

Both outbreaks started from animal products introduced to the market, not from outside community transmission.

Density distribution of infected employees shows shop S14 pretty well, but there are other secondary transmission hotspots.

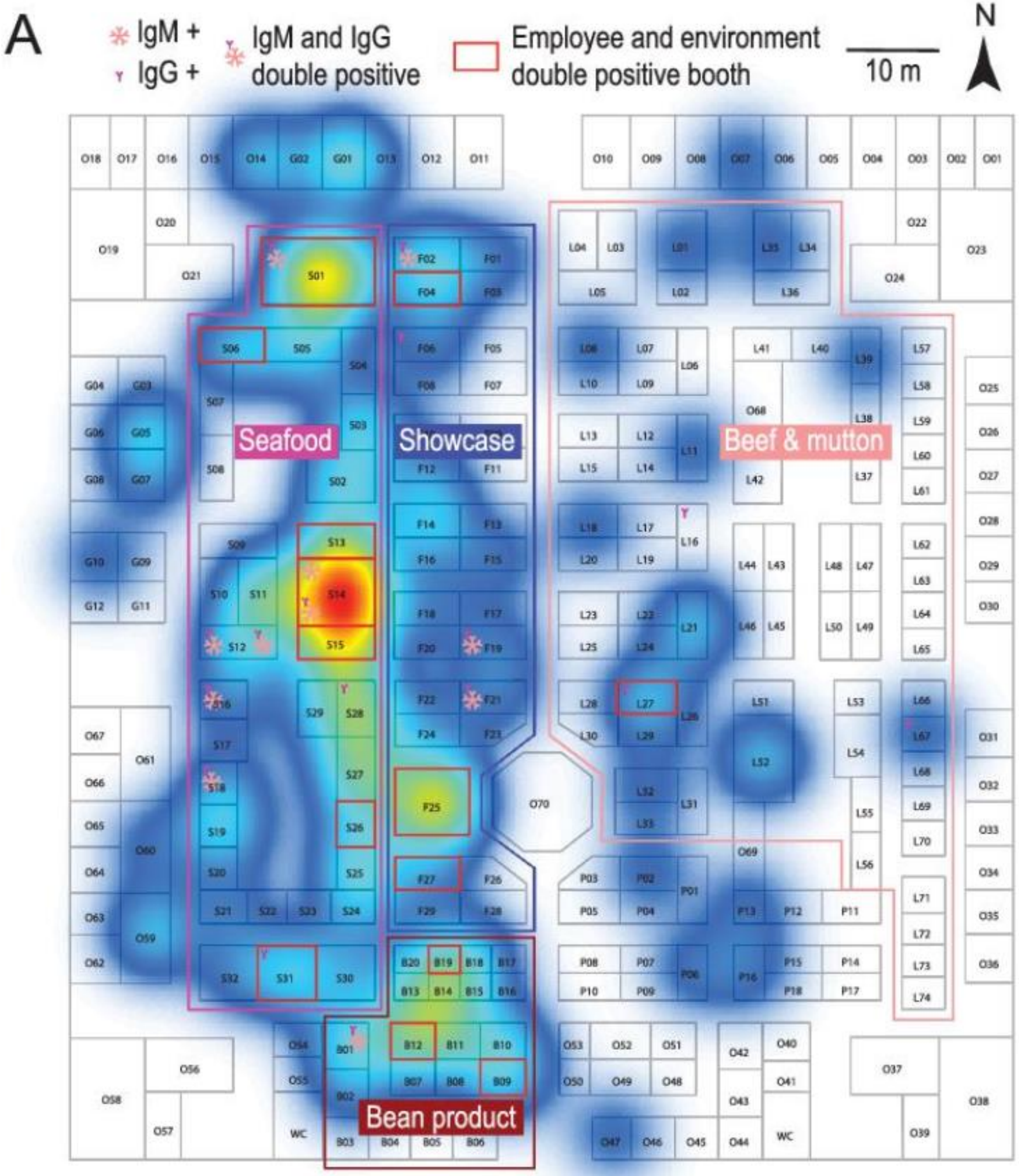


Figure from Pang et al, 2020

And the Xinfadi cases clustered around the market, just like Huanan!

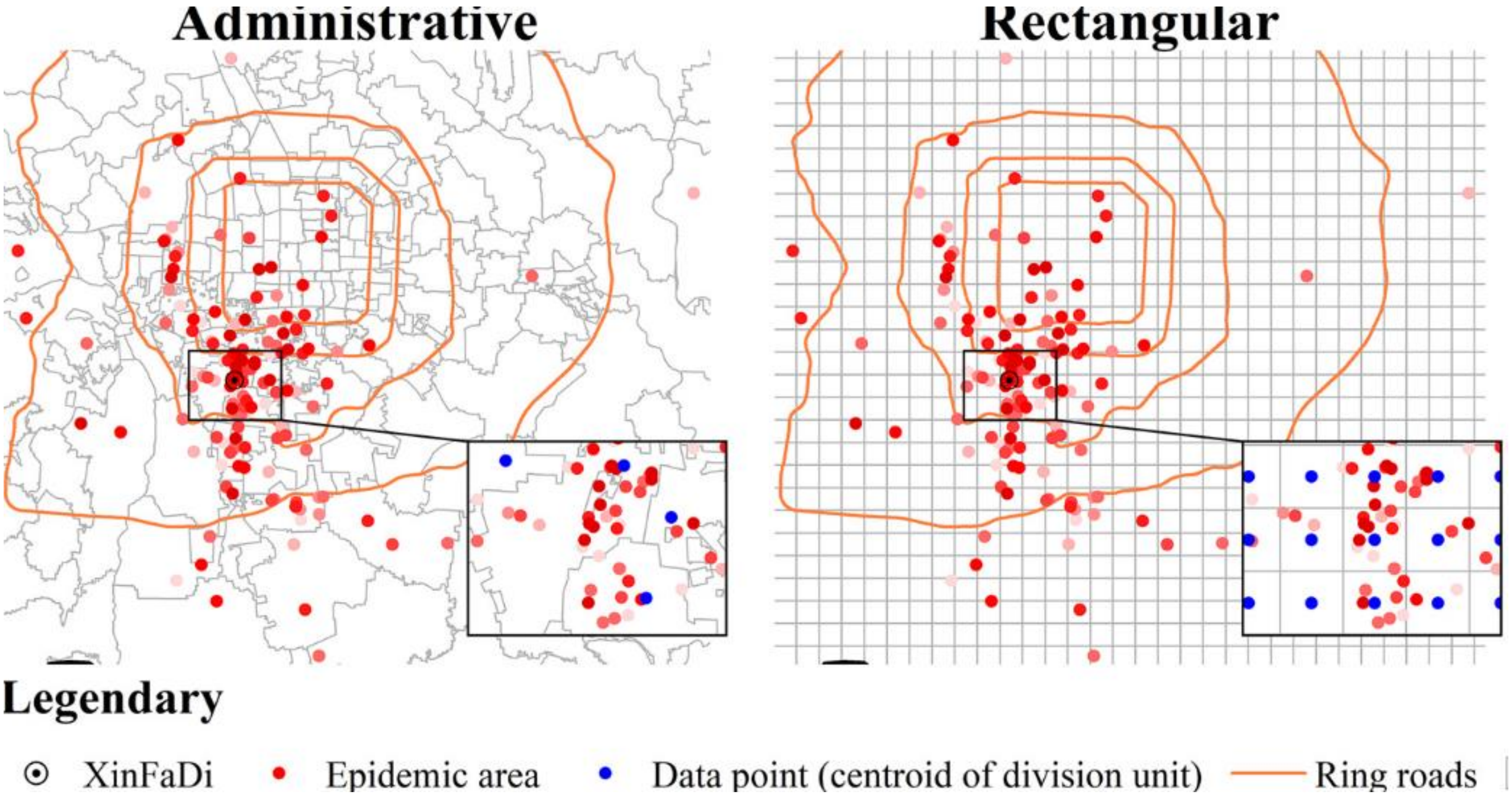
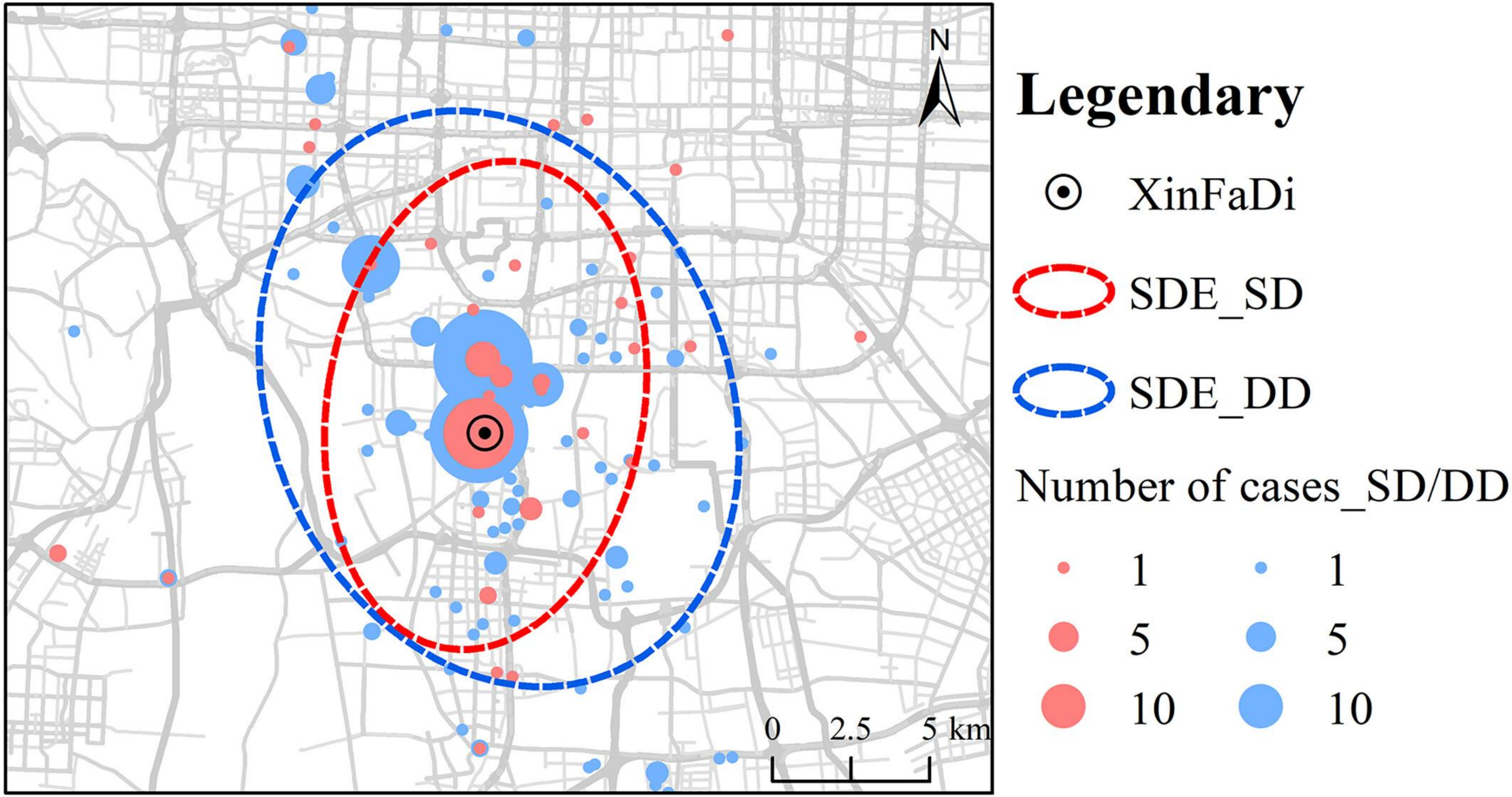


Figure from Zhang et al 2021

The authors didn't use quite the same centering techniques, but made a diagram similar to Worobey's:



Probabilistic arguments can offer the illusion of objectivity

A long series of probabilities multiplied together looks like a factual, scientific process.

Rootclaim says that this eliminates human bias, and allows them to solve problems without investigating.

But the human bias still creeps in – Saar chooses which numbers to multiply together.

In this case, he’s decided to give no weight to the extensive data linking the virus to the Huanan market.

On the other side, he’s made up implausibly high odds for a lab leak, and for lab leaks in general.

It’s easy to come up with any conclusion you want, if you ignore all the evidence you don’t like and exaggerate the evidence you do like.

I’ve also multiplied some probabilities and came up with the opposite conclusion. One of us has to be wrong. How do we resolve this disagreement?

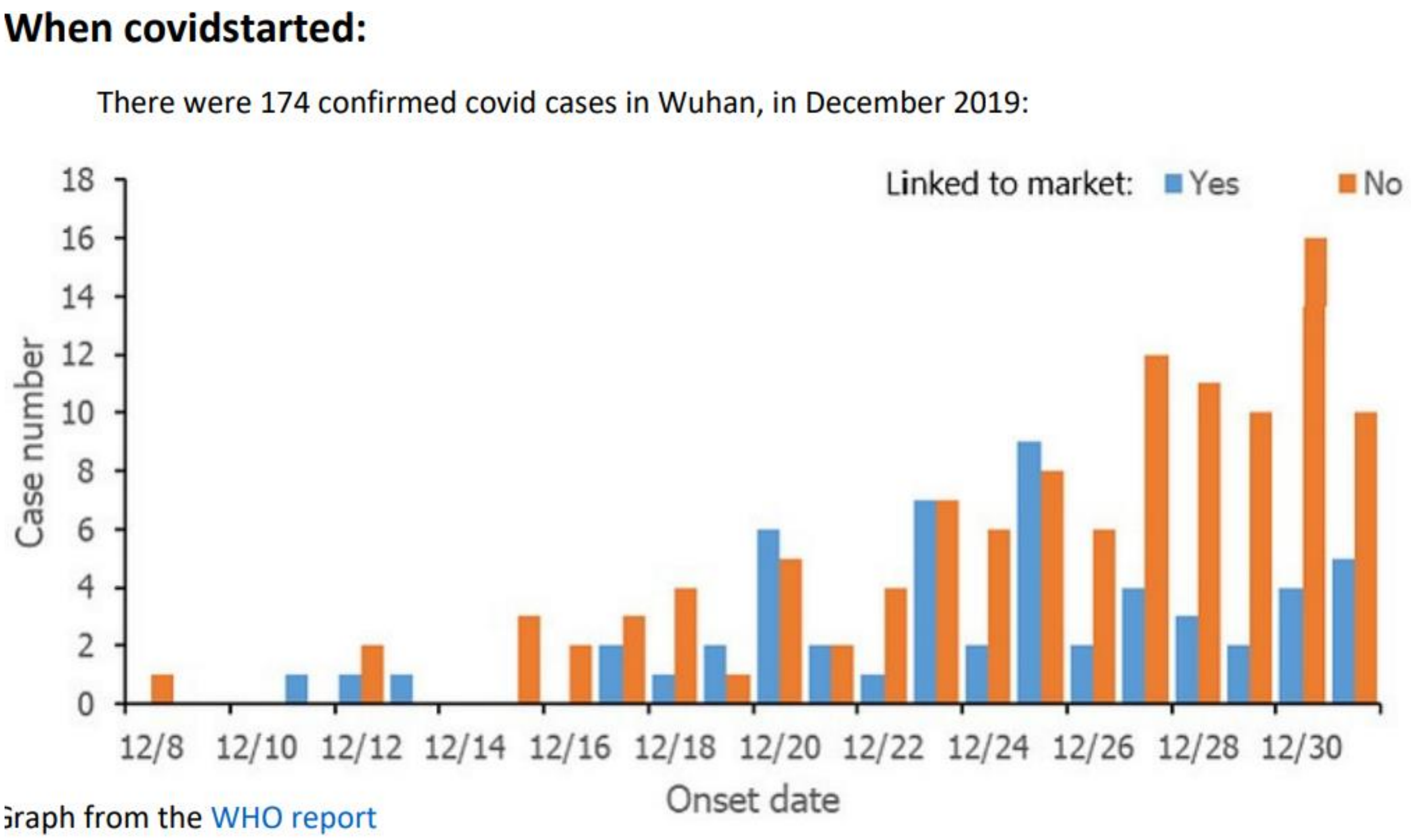
What Rootclaim Doesn’t Do

Fact-Checking

I do agree with this claim. Here are a few key facts Rootclaim has gotten wrong:

“A December 8th case happened before the market outbreak”	**Both sides of this debate agreed that’s false, 2 years ago!**
“The first 2 market cases were visitors that didn’t work there”	**Even members of DRASTIC admit that is false.**
“The early Weibo cases point towards the lab”	**The Weibo data contains at most 3 December cases with unknown locations.**
“Worobey’s data is confounded by population density”	**Not true.**
“The retrospective case search was biased because it happened before January 18th”	**Most of the cases were found after January 18th.** **The market linked cases are unbiased, before December 29th.**
“Excess deaths prove Covid started south of the river”	**Not true, pneumonia deaths are more accurate.**
“There are 90 missing early cases”	**Also not true. We’ll discuss this.**

Rootclaim also wrote that it's "irrelevant when covid started":



When covidstarted:

There were 174 confirmed covid cases in Wuhan, in December 2019:

raph from the WHO report

Irrelevant to us. We don't make any claims based on dates

Probabilities are meaningless if you have the facts wrong

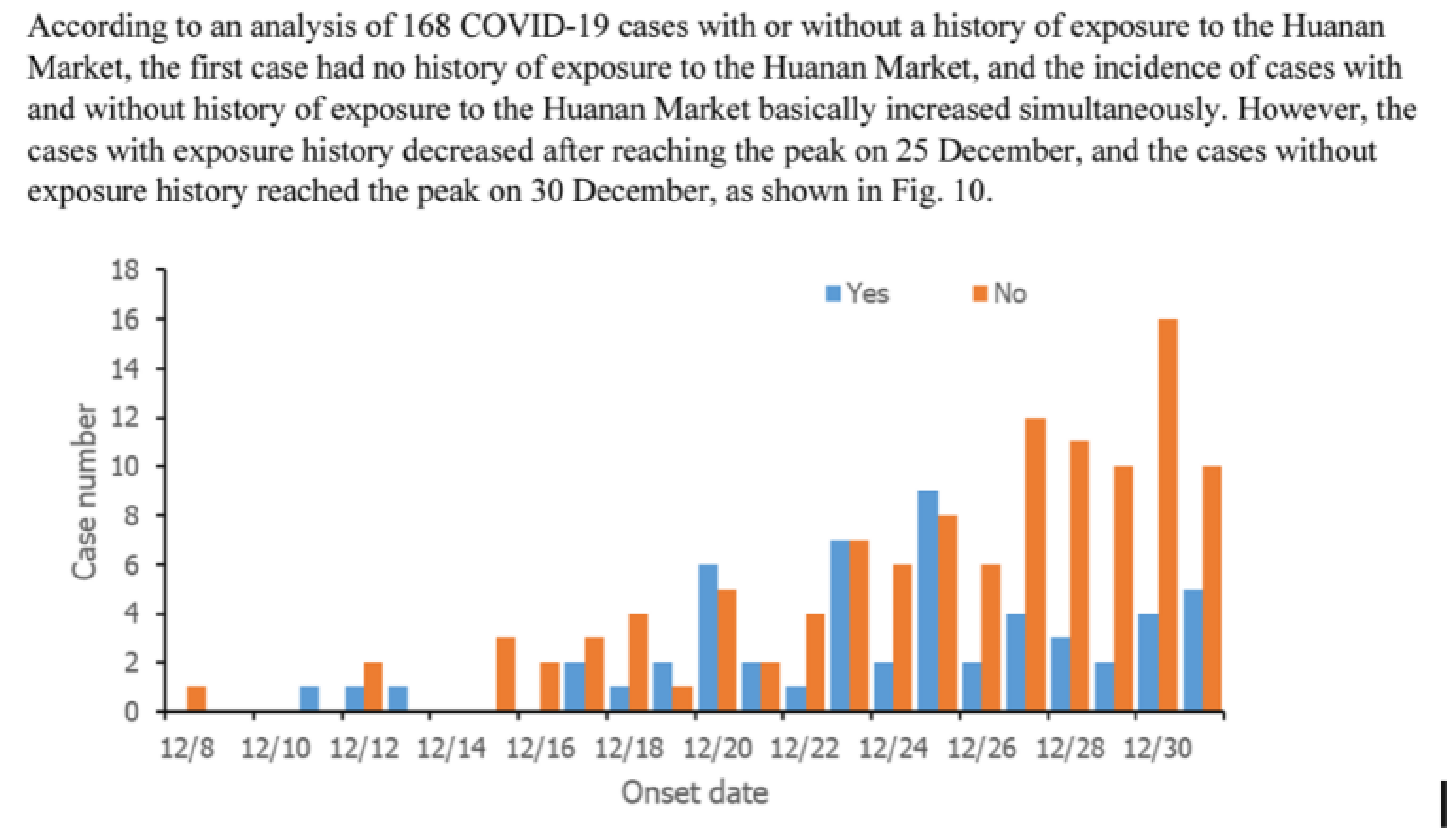
Before we can have a probabilistic discussion, we need to first investigate the evidence.

The focus of this first debate should be on trying to establish some of these facts, and whether the data better links Covid to the Huanan market or to the Wuhan institute of Virology.

I think a good place to start, in investigating a pandemic, is “where” and “when” it started.

Rootclaim cited this disproven December 8th case (actually December 16th).

Early Cases not Connected to Market

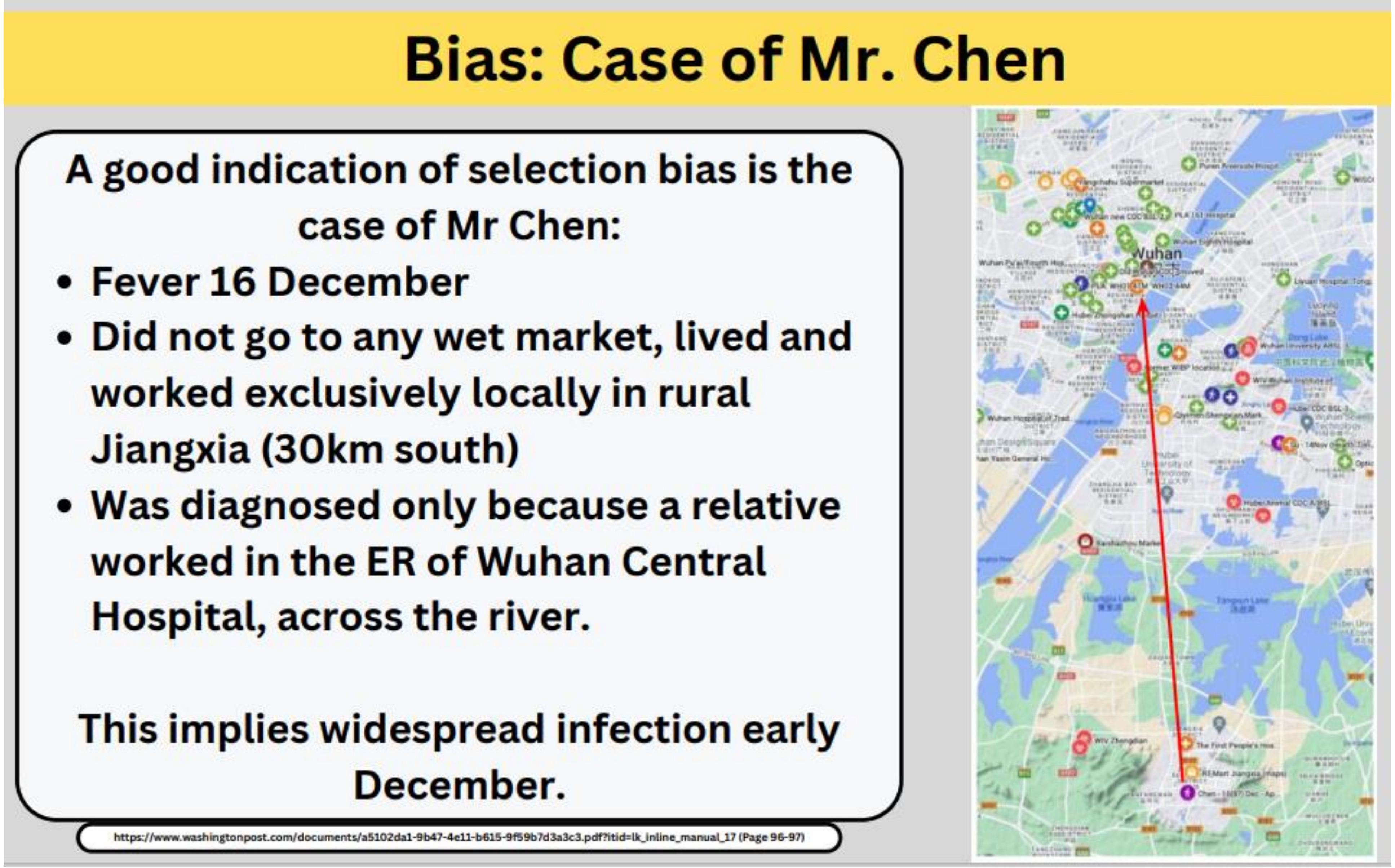


According to an analysis of 168 COVID-19 cases with or without a history of exposure to the Huanan Market, the first case had no history of exposure to the Huanan Market, and the incidence of cases with and without history of exposure to the Huanan Market basically increased simultaneously. However, the cases with exposure history decreased after reaching the peak on 25 December, and the cases without exposure history reached the peak on 30 December, as shown in Fig. 10.

Rates with and without connection to HSM "increased simultaneously". If HSM is GO a likelier distribution would be mostly HSM-related patients at first and only then the rest of Wuhan catching up - but HSM and Wuhan are neck and neck.

https://www.who.int/publications/i/item/who-convened-global-study-of-origins-of-sars-cov-2-china-part

But then 2 slides later, Rootclaim talks about "Mr. Chen" on December 16th – that's the same guy. Rootclaim seems to have not realized they're talking about the same person.



Bias: Case of Mr. Chen

A good indication of selection bias is the case of Mr Chen:

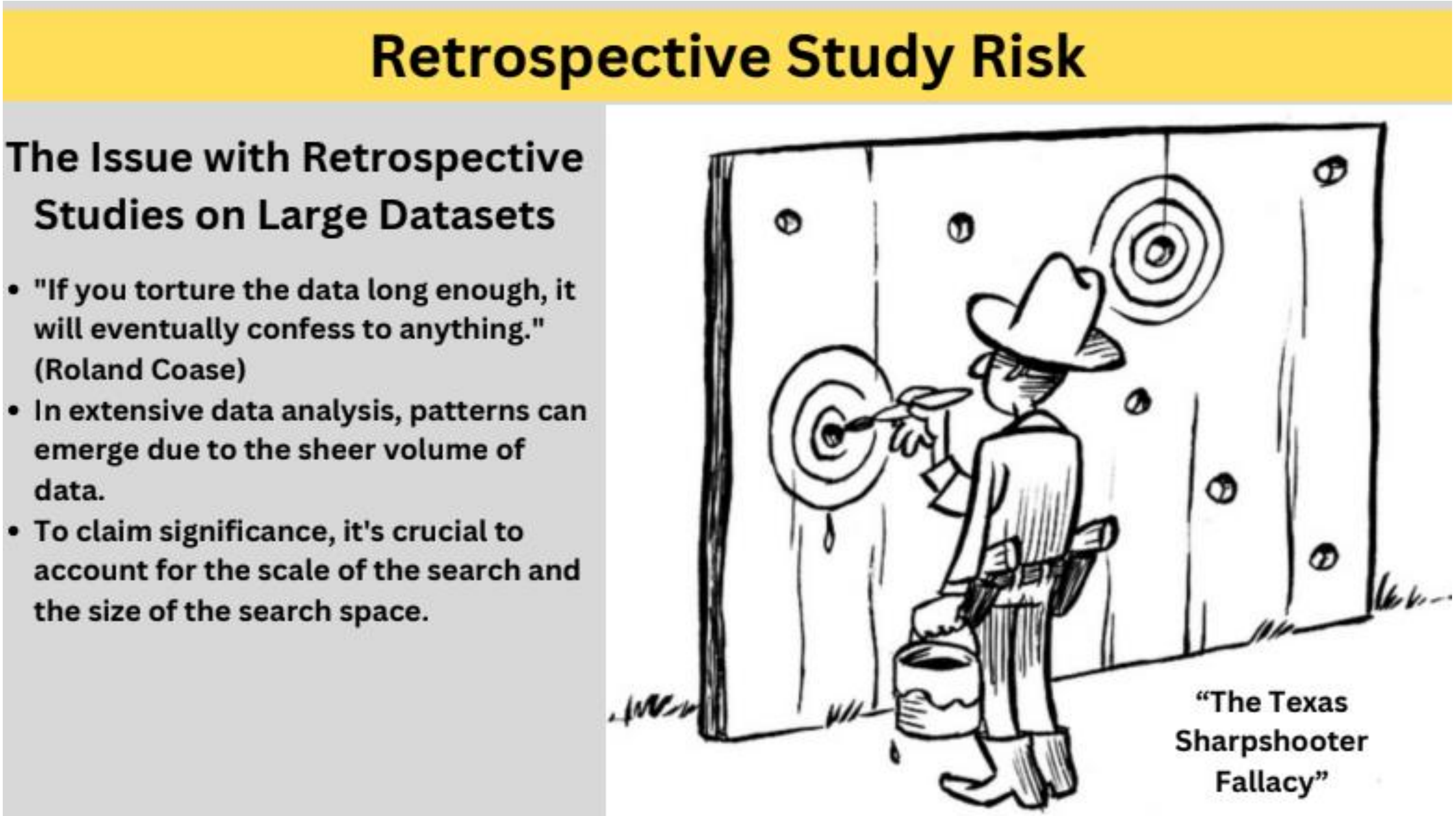
- Fever 16 December
- Did not go to any wet market, lived and worked exclusively locally in rural Jiangxia (30km south)
- Was diagnosed only because a relative worked in the ER of Wuhan Central Hospital, across the river.

This implies widespread infection early December.

https://www.washingtonpost.com/documents/a5102da1-9b47-4e11-b615-9f59b7d3a3c3.pdf?itid=lk_inline_manual_17 (Page 96-97)

Rootclaim dismisses the bulls-eye of cases on the market with the “Texas Sharpshooter fallacy”

I think this fallacy describes many lab leak theories better.
What I see is an actual bullseye on the market, both geographically and genetically.
I see people looking for every reason possible to distract from that: mahjong rooms, bathrooms, speculation about bias in the data, news articles with typos about earlier cases, etc.
That looks like motivated reasoning or intentional obfuscation.



Retrospective Study Risk

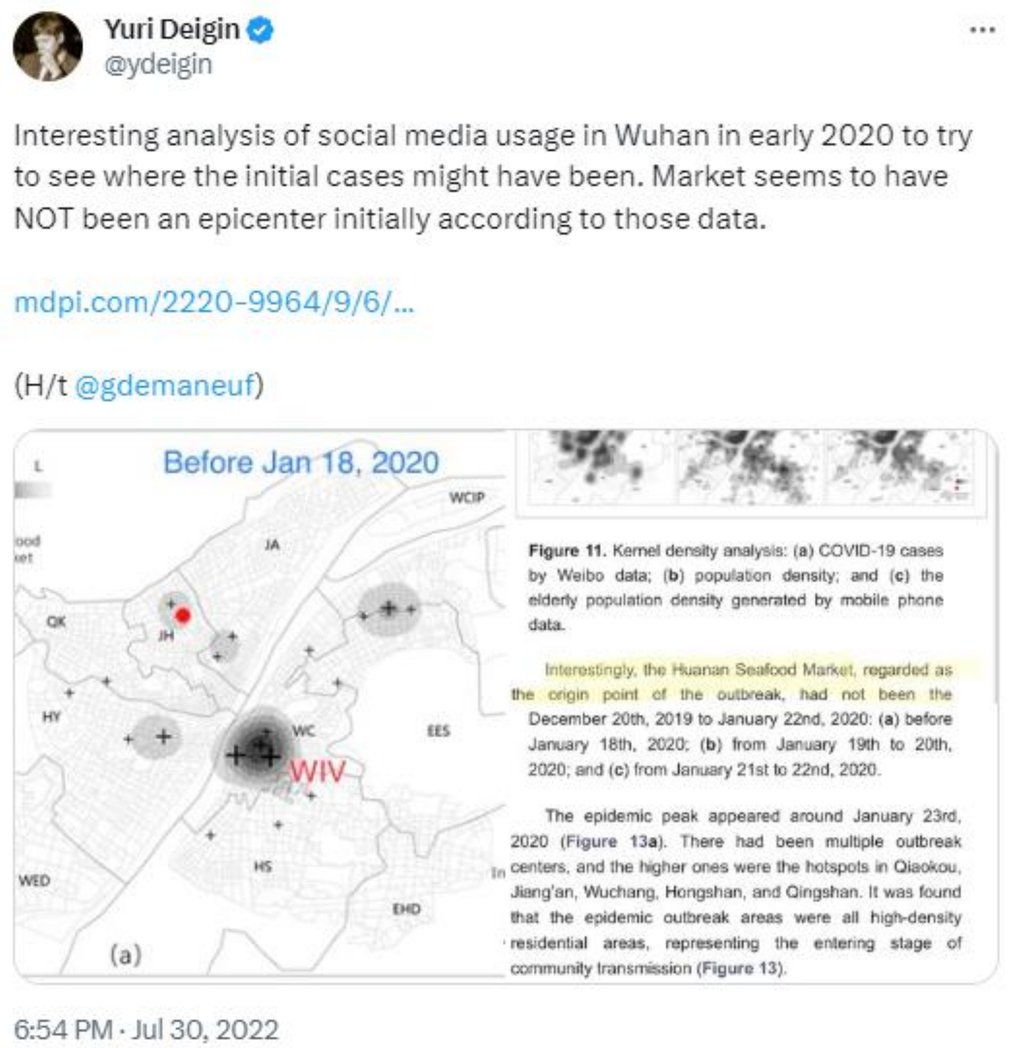
The Issue with Retrospective Studies on Large Datasets

- "If you torture the data long enough, it will eventually confess to anything." (Roland Coase)
- In extensive data analysis, patterns can emerge due to the sheer volume of data.
- To claim significance, it's crucial to account for the scale of the search and the size of the search space.

“The Texas Sharpshooter Fallacy”

People love to use that Weibo data in misleading ways

People cite this heatmap of early Weibo cases to imply that the Wuhan lab was the origin, because one bump shows up on the south side of the river, where they want to see it.
This image also shows up in some of the congressional reports on covid origins.



Yuri Deigin
@ydeigin

Interesting analysis of social media usage in Wuhan in early 2020 to try to see where the initial cases might have been. Market seems to have NOT been an epicenter initially according to those data.

mdpi.com/2220-9964/9/6/...

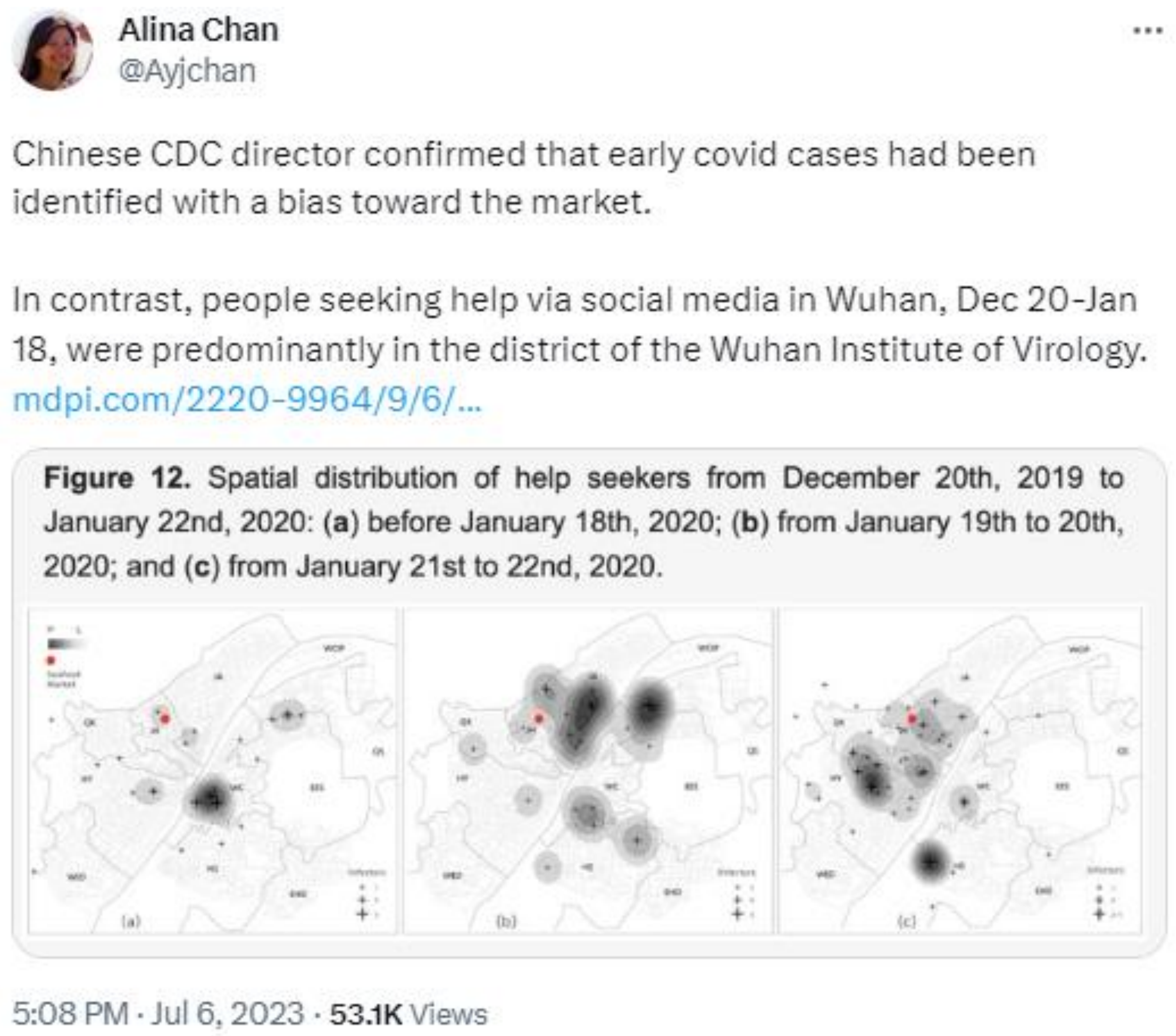
(H/t @gdemaneuf)

Figure 11. Kernel density analysis: (**a**) COVID-19 cases by Weibo data; (**b**) population density; and (**c**) the elderly population density generated by mobile phone data.

Interestingly, the Huanan Seafood Market, regarded as the origin point of the outbreak, had not been the December 20th, 2019 to January 22nd, 2020: (**a**) before January 18th, 2020; (**b**) from January 19th to 20th, 2020; and (**c**) from January 21st to 22nd, 2020.

The epidemic peak appeared around January 23rd, 2020 (Figure 13**a**). There had been multiple outbreak centers, and the higher ones were the hotspots in Qiaokou, Jiang'an, Wuchang, Hongshan, and Qingshan. It was found that the epidemic outbreak areas were all high-density residential areas, representing the entering stage of community transmission (Figure 13).

6:54 PM · Jul 30, 2022



Alina Chan
@Ayjchan

Chinese CDC director confirmed that early covid cases had been identified with a bias toward the market.

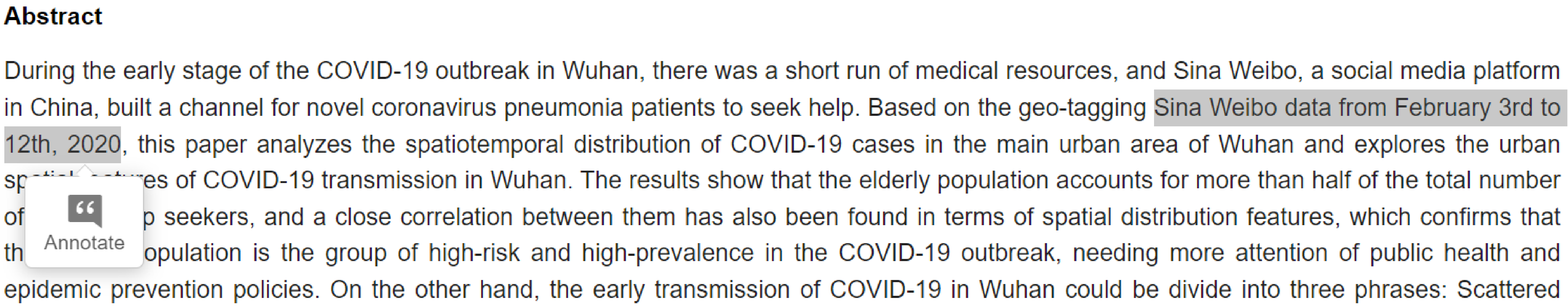
In contrast, people seeking help via social media in Wuhan, Dec 20-Jan 18, were predominantly in the district of the Wuhan Institute of Virology.
mdpi.com/2220-9964/9/6/...

Figure 12. Spatial distribution of help seekers from December 20th, 2019 to January 22nd, 2020: (**a**) before January 18th, 2020; (**b**) from January 19th to 20th, 2020; and (**c**) from January 21st to 22nd, 2020.

5:08 PM · Jul 6, 2023 · **53.1K** Views

Here's what the paper actually says:

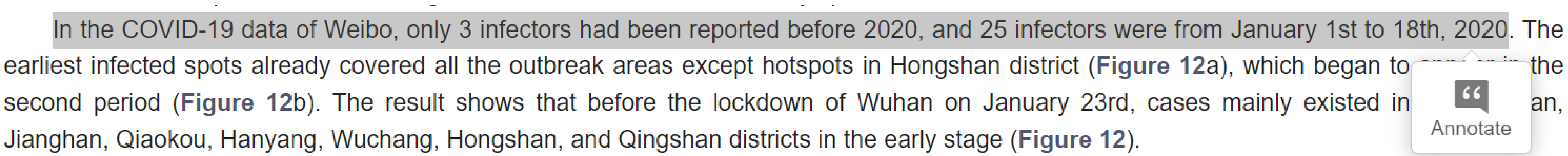
This data is from February:



Abstract

During the early stage of the COVID-19 outbreak in Wuhan, there was a short run of medical resources, and Sina Weibo, a social media platform in China, built a channel for novel coronavirus pneumonia patients to seek help. Based on the geo-tagging Sina Weibo data from February 3rd to 12th, 2020, this paper analyzes the spatiotemporal distribution of COVID-19 cases in the main urban area of Wuhan and explores the urban sp es of COVID-19 transmission in Wuhan. The results show that the elderly population accounts for more than half of the total number of p seekers, and a close correlation between them has also been found in terms of spatial distribution features, which confirms that th opulation is the group of high-risk and high-prevalence in the COVID-19 outbreak, needing more attention of public health and epidemic prevention policies. On the other hand, the early transmission of COVID-19 in Wuhan could be divide into three phrases: Scattered

But people could retrospectively enter their date of infection. Of those, 3 people entered a date in 2019:

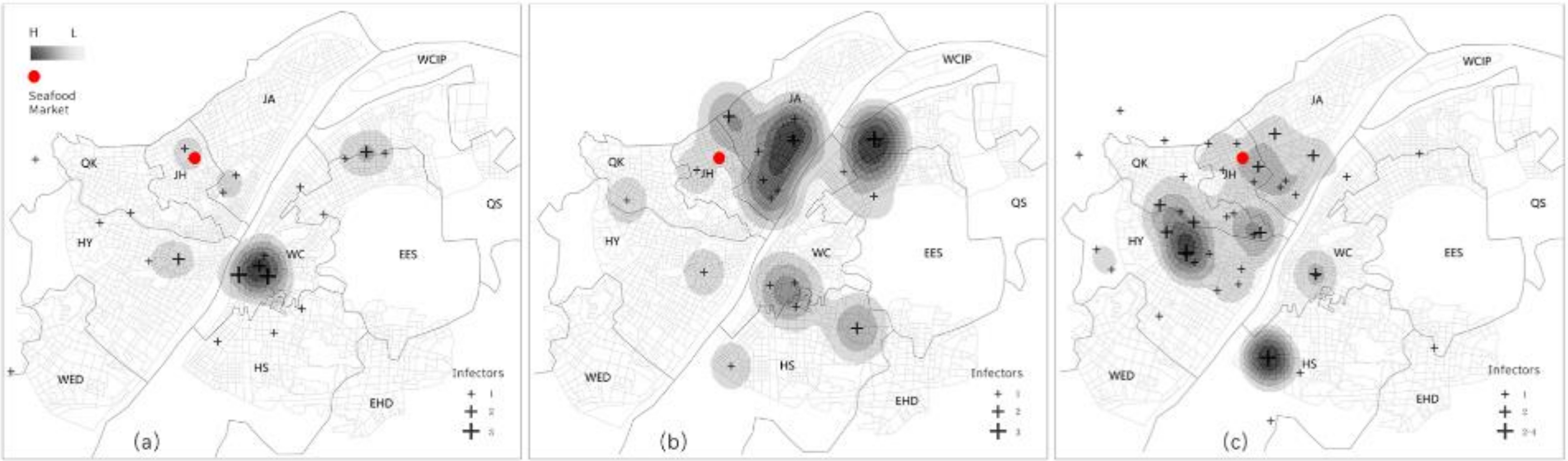


In the COVID-19 data of Weibo, only 3 infectors had been reported before 2020, and 25 infectors were from January 1st to 18th, 2020. The earliest infected spots already covered all the outbreak areas except hotspots in Hongshan district (**Figure 12**a), which began to the second period (**Figure 12**b). The result shows that before the lockdown of Wuhan on January 23rd, cases mainly existed in an, Jianghan, Qiaokou, Hanyang, Wuchang, Hongshan, and Qingshan districts in the early stage (**Figure 12**).

We have no idea which of the 3 points are the 2019 ones, it could be those 3 near the market, for all we know.

This could also just be 3 old people entering the wrong month into the app – symptom onset in December is strange for someone asking for help in February.

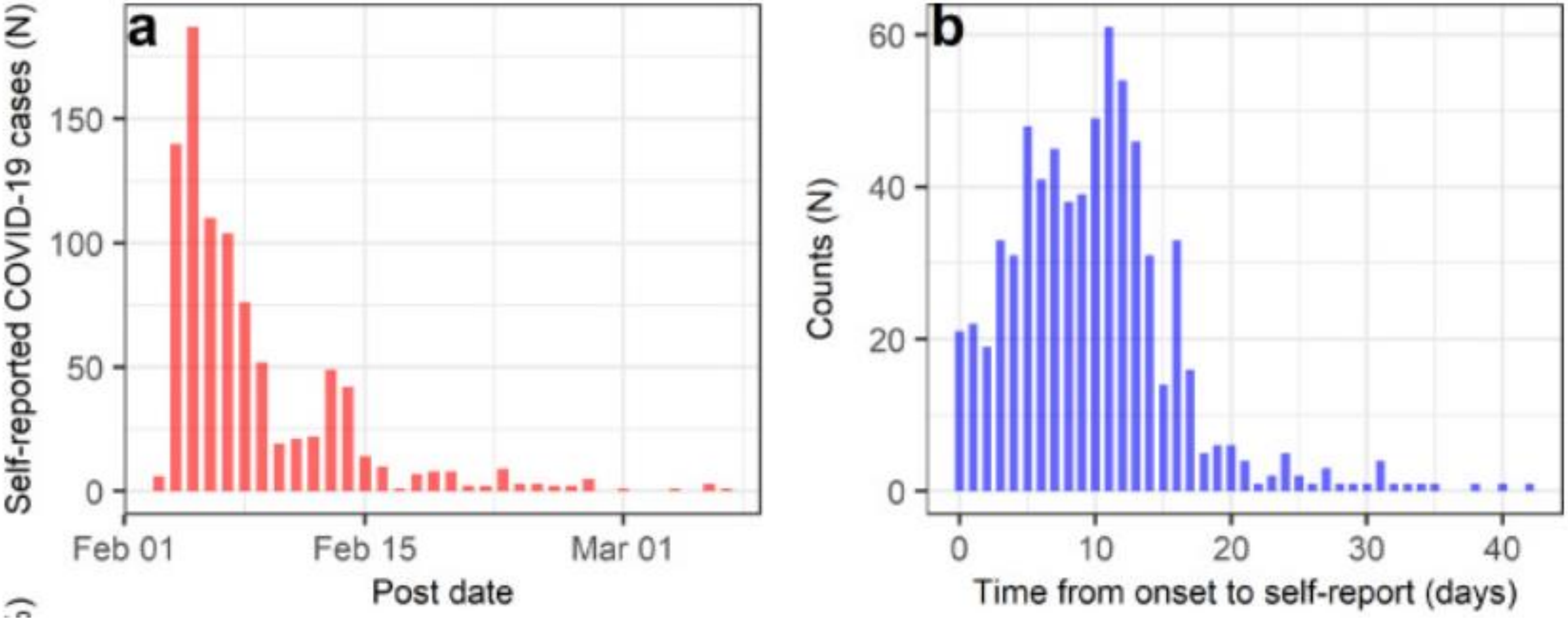
Figure 12. Spatial distribution of help seekers from December 20th, 2019 to January 22nd, 2020: (**a**) before January 18th, 2020; (**b**) from January 19th to 20th, 2020; and (**c**) from January 21st to 22nd, 2020.



It’s also not 100% clear if that paper is using accurate data. I tried to look for a copy of the raw data, and the closest I could find is this [scraped version of the Weibo data]().

But it doesn’t match the paper – the earliest case I could find was January 9th, 2020.
There are no December 2019 cases listed.

A [second paper written on the Weibo data]()lists the dates that people requested help, plus the time between onset and help request. So, you can see 3 possible December 2019 cases if you assume the 40 day “time from onset” cases are also reporting early in February, but it’s not clear if those are December cases.



Does population density, or elderly population density explain the January-February Weibo data?

Yes, it's a pretty good match.

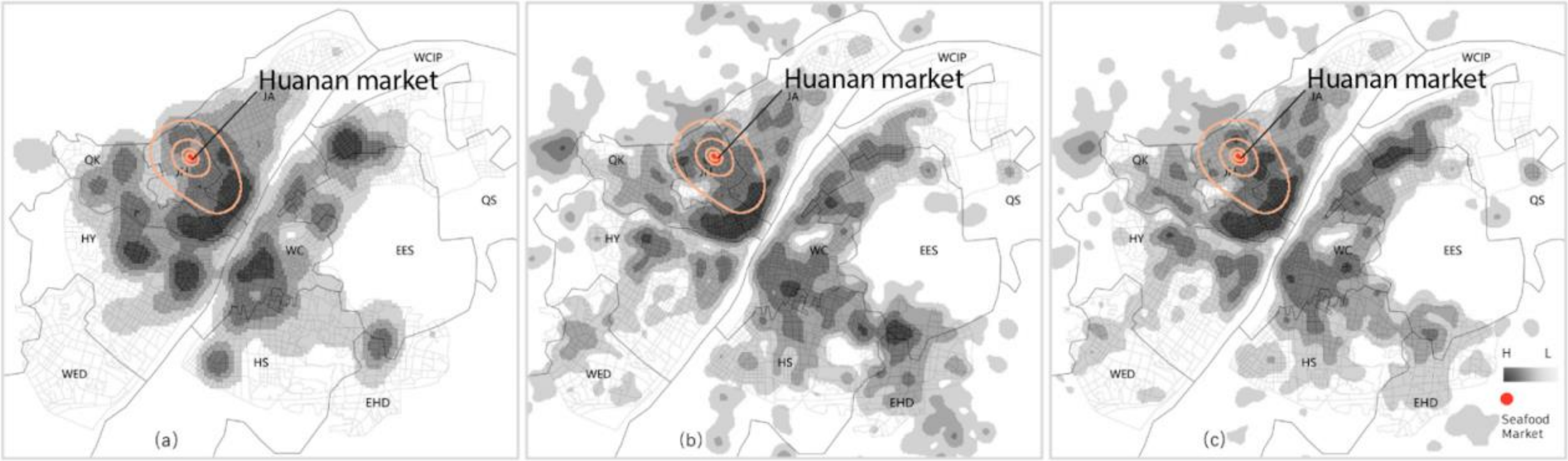


Figure S9, from Worobey et al 2022.

A. Market contours compared to Weibo case density.
B. As compared to Wuhan population density.
C. As compared to elderly population density.

But population density is a poor match for the initial Huanan market case outbreak

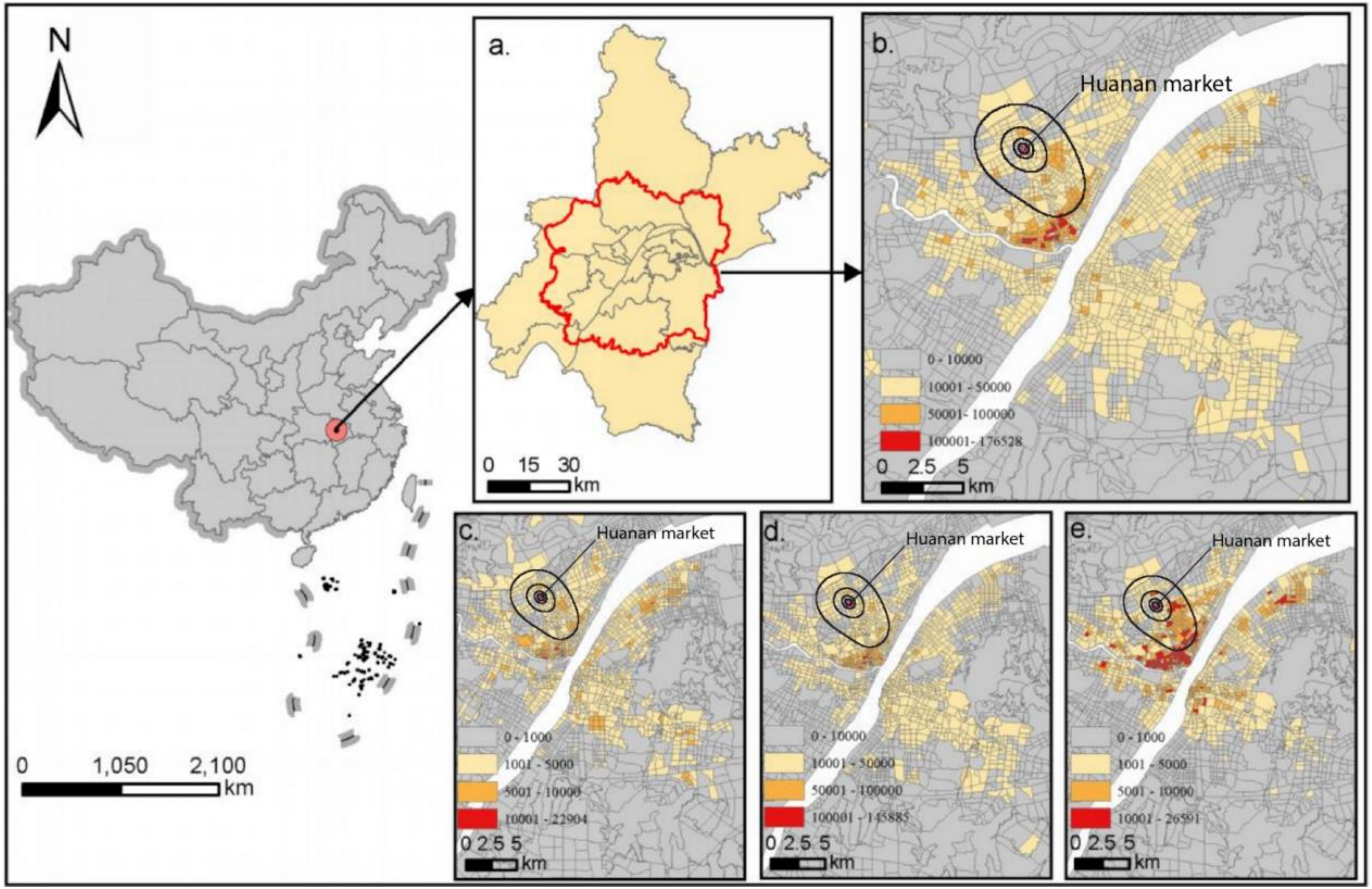
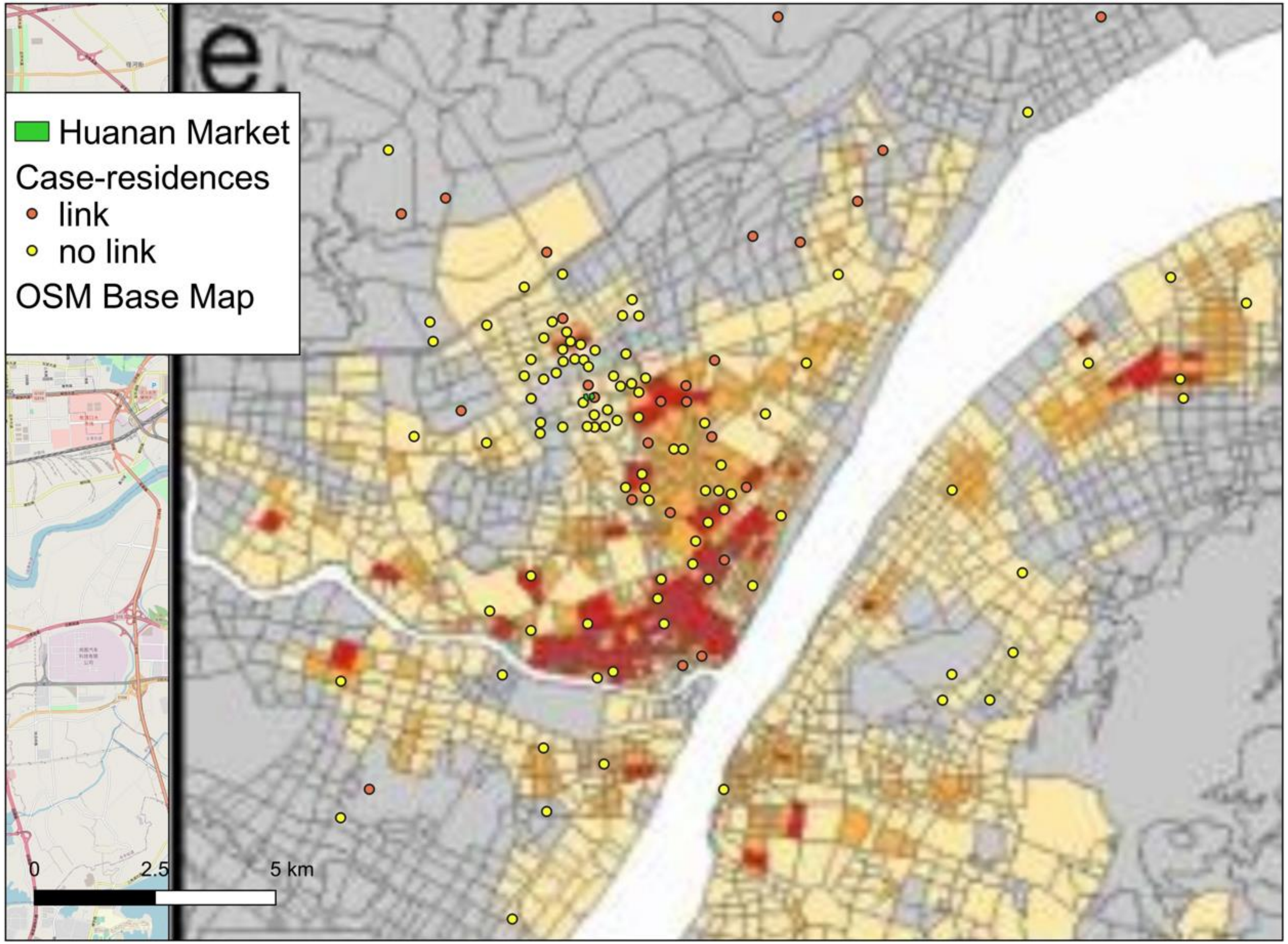


Figure S10 from Worobey et al 2022

B: overall population density, C: child population density, D: adult population density, E: elderly population density

An overlay of raw points on elderly population density makes this clearest:

It looks to me like elderly density can explain some case density south of the market, but not cases centered on the market.



[Image from Dan Walker](), who also made a [thread of similar images]().

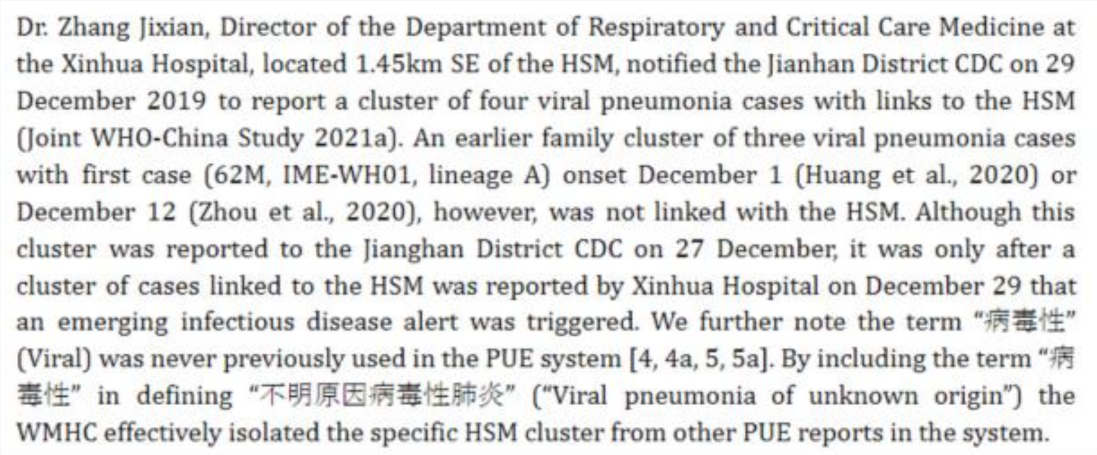
Was the case search biased?

Rootclaim says that the case search was biased:

Bias in Early Cases

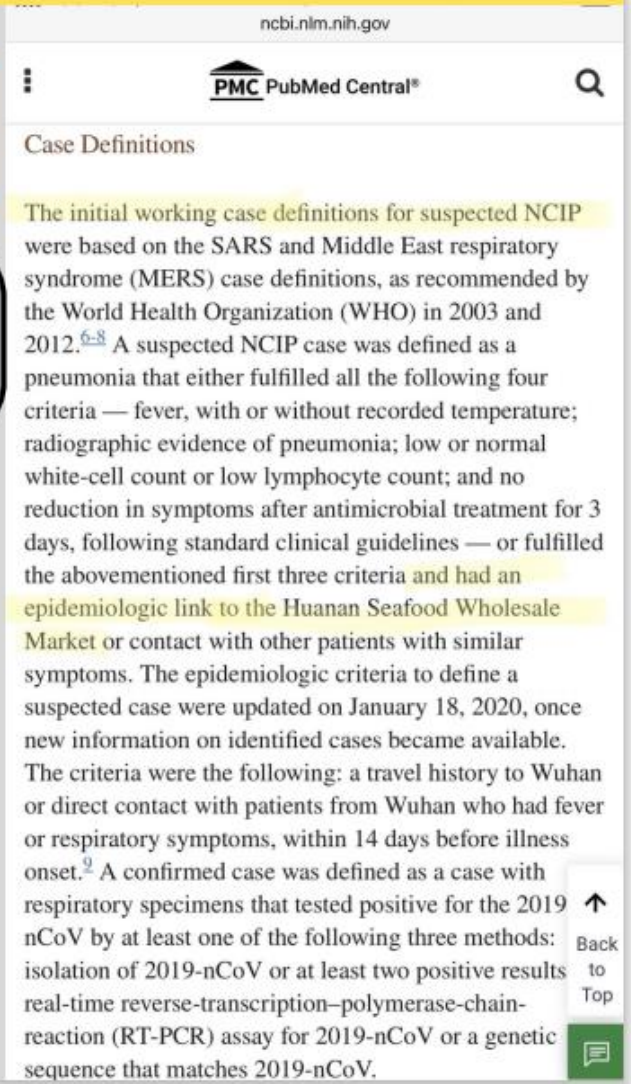
Early in the pandemic, diagnoses were partially given based on whether a patient had a connection to the Huanan Seafood Market.

Until January 18th, 2020 a connection to the market was a requirement for a Covid-19 diagnosis because it was thought to be the source. This led to a selection bias wherein only those connected to the seafood market were diagnosed with covid-19, which further fueled speculation that Huanan was the epicenter and the likely spillover location.



Dr. Zhang Jixian, Director of the Department of Respiratory and Critical Care Medicine at the Xinhua Hospital, located 1.45km SE of the HSM, notified the Jianhan District CDC on 29 December 2019 to report a cluster of four viral pneumonia cases with links to the HSM (Joint WHO-China Study 2021a). An earlier family cluster of three viral pneumonia cases with first case (62M, IME-WH01, lineage A) onset December 1 (Huang et al., 2020) or December 12 (Zhou et al., 2020), however, was not linked with the HSM. Although this cluster was reported to the Jianghan District CDC on 27 December, it was only after a cluster of cases linked to the HSM was reported by Xinhua Hospital on December 29 that an emerging infectious disease alert was triggered. We further note the term "病毒性" (Viral) was never previously used in the PUE system [4, 4a, 5, 5a]. By including the term "病毒性" in defining "不明原因病毒性肺炎" ("Viral pneumonia of unknown origin") the WMHC effectively isolated the specific HSM cluster from other PUE reports in the system.

Due to SARS experience, healthcare workers were more inclined to report new diseases with connection to a market.



Case Definitions

The initial working case definitions for suspected NCIP were based on the SARS and Middle East respiratory syndrome (MERS) case definitions, as recommended by the World Health Organization (WHO) in 2003 and 2012.[6-8] A suspected NCIP case was defined as a pneumonia that either fulfilled all the following four criteria — fever, with or without recorded temperature; radiographic evidence of pneumonia; low or normal white-cell count or low lymphocyte count; and no reduction in symptoms after antimicrobial treatment for 3 days, following standard clinical guidelines — or fulfilled the abovementioned first three criteria and had an epidemiologic link to the Huanan Seafood Wholesale Market or contact with other patients with similar symptoms. The epidemiologic criteria to define a suspected case were updated on January 18, 2020, once new information on identified cases became available. The criteria were the following: a travel history to Wuhan or direct contact with patients from Wuhan who had fever or respiratory symptoms, within 14 days before illness onset.[9] A confirmed case was defined as a case with respiratory specimens that tested positive for the 2019-nCoV by at least one of the following three methods: isolation of 2019-nCoV or at least two positive results real-time reverse-transcription–polymerase-chain-reaction (RT-PCR) assay for 2019-nCoV or a genetic sequence that matches 2019-nCoV.

There can’t be much bias before December 29th, because the market link was not announced or shared between hospitals.

At that point, about 50% of cases were market linked.

From December 29th to January 15th, it’s chaotic, the market link is known, there’s likely some bias towards finding market linked cases.

Between January 15th and January 18th , there’s an official criterion to look for market linked cases (but it’s not the only criterion)

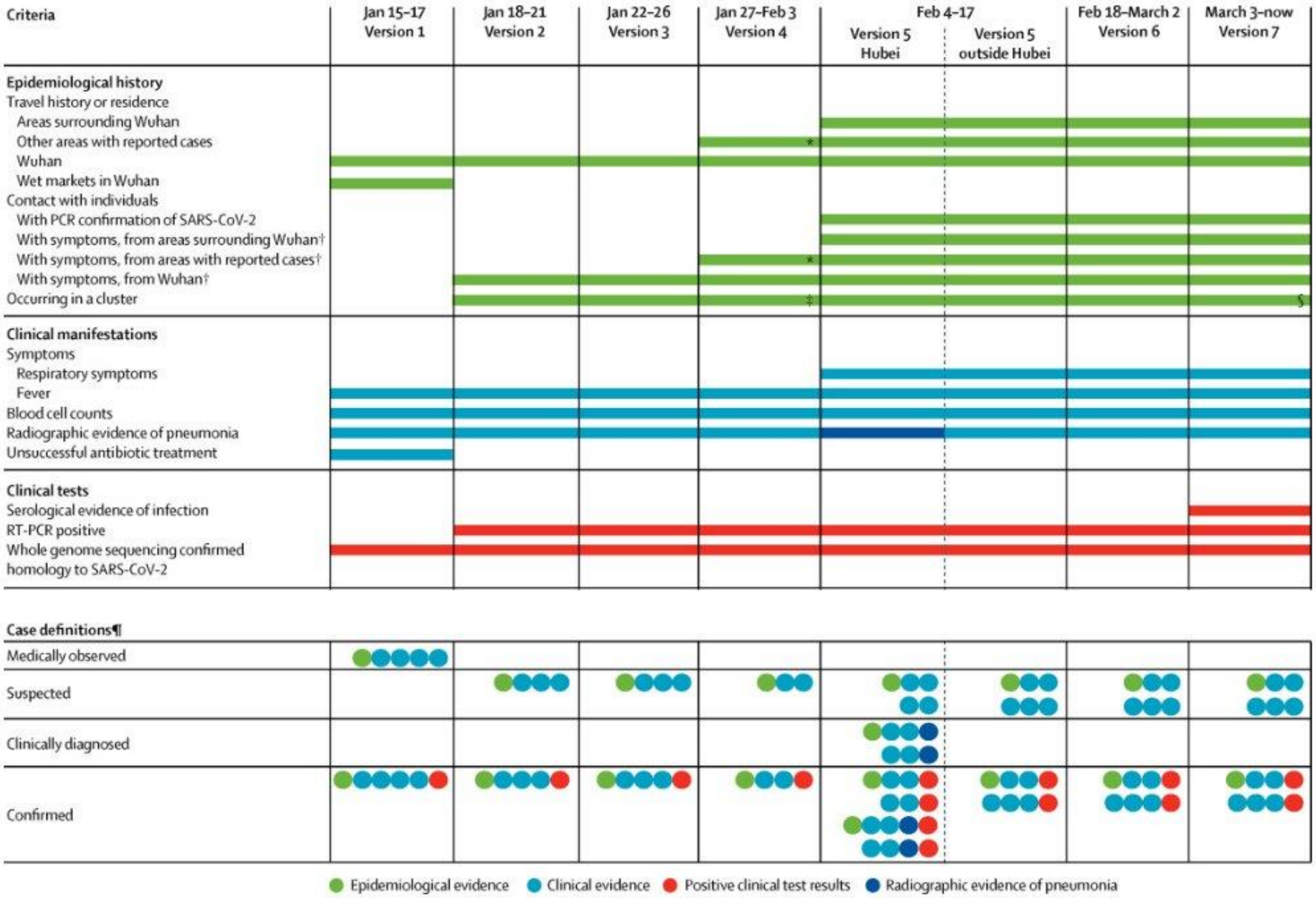
After January 18th, market link was removed from the search criteria. 127 new cases were found in a retrospective search. Many were not market linked, but still happened to live close to the market.
With the WHO report, only 33% are market linked cases.

Cases by time:

Dec 31st (data from 3 hospitals)	16 December cases, 62% linked to market
Jan 2nd data (Huang et al 2020)	40 December cases, 68% linked to market
Jan 22nd data (Li et al 2020)	47 December cases, 55% linked to market
WHO report:	174 December cases, 33% linked to market.

127 of these 174 were added after January 18th, in a retrospective search. That’s after China had recognized human to human transmission and also dropped the link to the market in case searches.

Here’s the changing criteria China used for case searches.



Criteria	Jan 15–17 Version 1	Jan 18–21 Version 2	Jan 22–26 Version 3	Jan 27–Feb 3 Version 4	Feb 4–17 Version 5 Hubei	Feb 4–17 Version 5 outside Hubei	Feb 18–March 2 Version 6	March 3–now Version 7
Epidemiological history								
Travel history or residence								
Areas surrounding Wuhan					🟩	🟩	🟩	🟩
Other areas with reported cases				🟩 *	🟩	🟩	🟩	🟩
Wuhan	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩
Wet markets in Wuhan	🟩							
Contact with individuals								
With PCR confirmation of SARS-CoV-2					🟩	🟩	🟩	🟩
With symptoms, from areas surrounding Wuhan†					🟩	🟩	🟩	🟩
With symptoms, from areas with reported cases†				🟩 *	🟩	🟩	🟩	🟩
With symptoms, from Wuhan†		🟩	🟩	🟩	🟩	🟩	🟩	🟩
Occurring in a cluster		🟩	🟩	🟩 ‡	🟩	🟩	🟩	🟩 §
Clinical manifestations								
Symptoms								
Respiratory symptoms					🟦	🟦	🟦	🟦
Fever	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦
Blood cell counts	🟦	🟦	🟦	🟦	🟦	🟦	🟦	🟦
Radiographic evidence of pneumonia	🟦	🟦	🟦	🟦	🔷	🟦	🟦	🟦
Unsuccessful antibiotic treatment	🟦							
Clinical tests								
Serological evidence of infection								🟥
RT-PCR positive		🟥	🟥	🟥	🟥	🟥	🟥	🟥
Whole genome sequencing confirmed homology to SARS-CoV-2	🟥	🟥	🟥	🟥	🟥	🟥	🟥	🟥
Case definitions¶								
Medically observed	🟢🔵🔵🔵🔵							
Suspected		🟢🔵🔵🔵	🟢🔵🔵🔵	🟢🔵🔵	🟢🔵🔵 🔵🔵	🟢🔵🔵 🔵🔵🔵	🟢🔵🔵 🔵🔵🔵	🟢🔵🔵 🔵🔵🔵
Clinically diagnosed					🟢🔵🔵🔷 🔵🔵🔷			
Confirmed	🟢🔵🔵🔵🔵🔴	🟢🔵🔵🔵🔴	🟢🔵🔵🔵🔴	🟢🔵🔵🔴	🟢🔵🔵🔴 🔵🔵🔴 🟢🔵🔵🔷🔴 🔵🔵🔷🔴	🟢🔵🔵🔴 🔵🔵🔵🔴	🟢🔵🔵🔴 🔵🔵🔵🔴	🟢🔵🔵🔴 🔵🔵🔵🔴

🟢 Epidemiological evidence 🔵 Clinical evidence 🔴 Positive clinical test results 🔷 Radiographic evidence of pneumonia

Figure from Tsang et al, 2020

Worobey also tried simply removing cases, one by one, to see how robust the centering is to any bias.

Using all the cases, you see that clear bulls-eye on the market.

You can remove 1/2 to 2/3 of the nearby cases before you lose an association with the market.

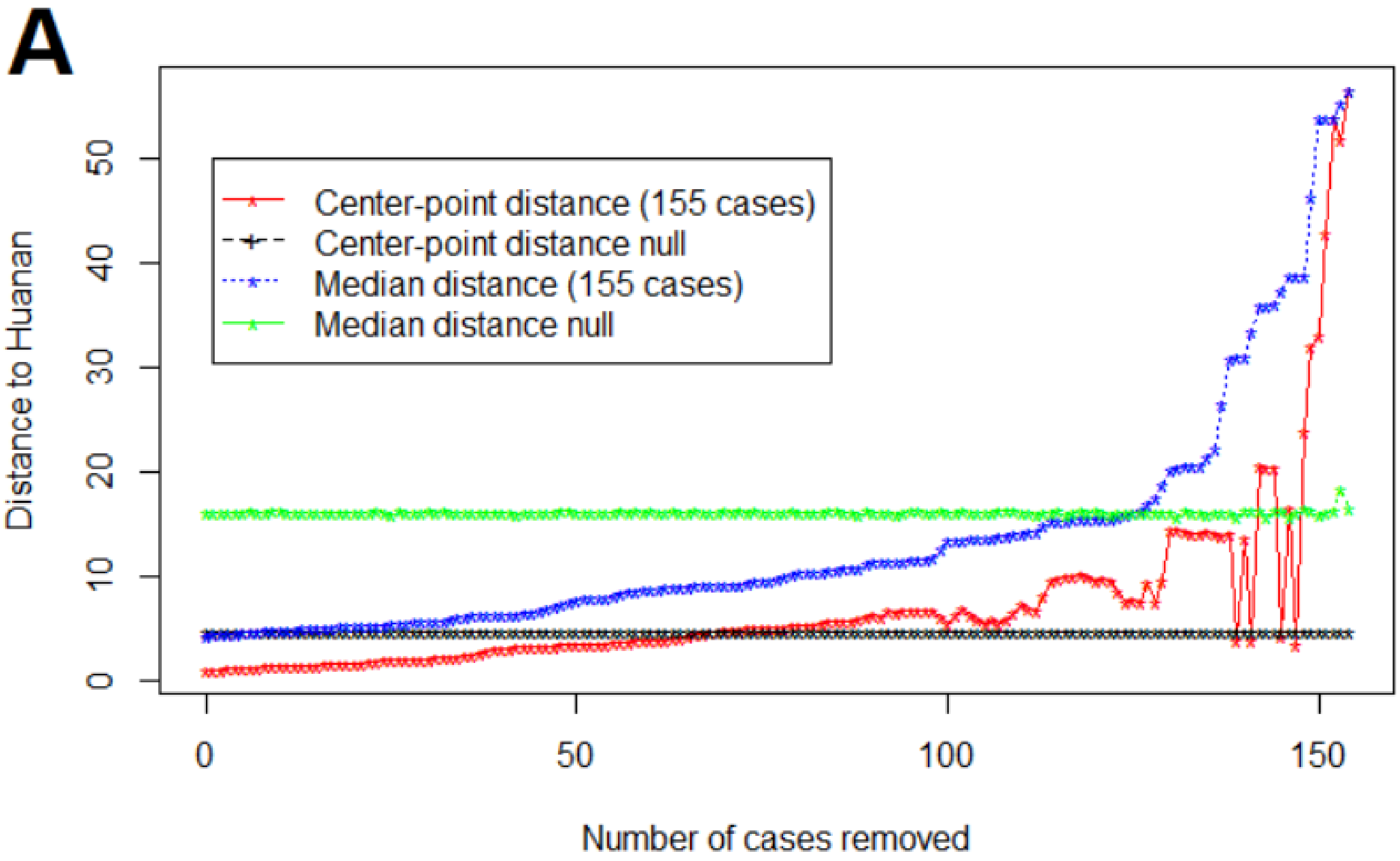
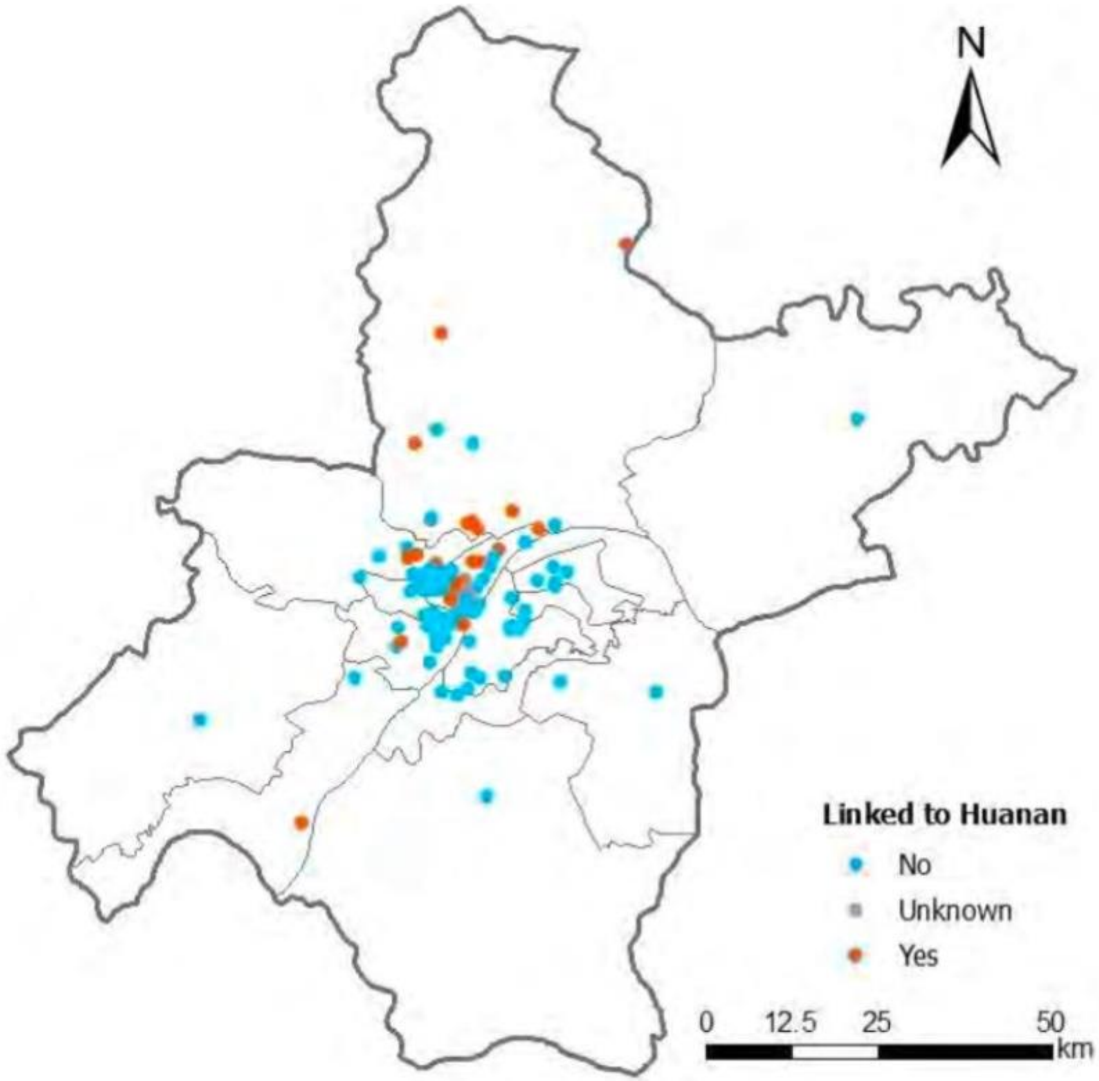


Figure S12 from Worobey et al, 2022: Effect of elimination of cases nearest the market on statistical results.

The search mostly found people with no link to the market and found a few people who lived far away from it.
It's unclear how a biased case search could find those.
The search was done in hospitals, not going door to door.



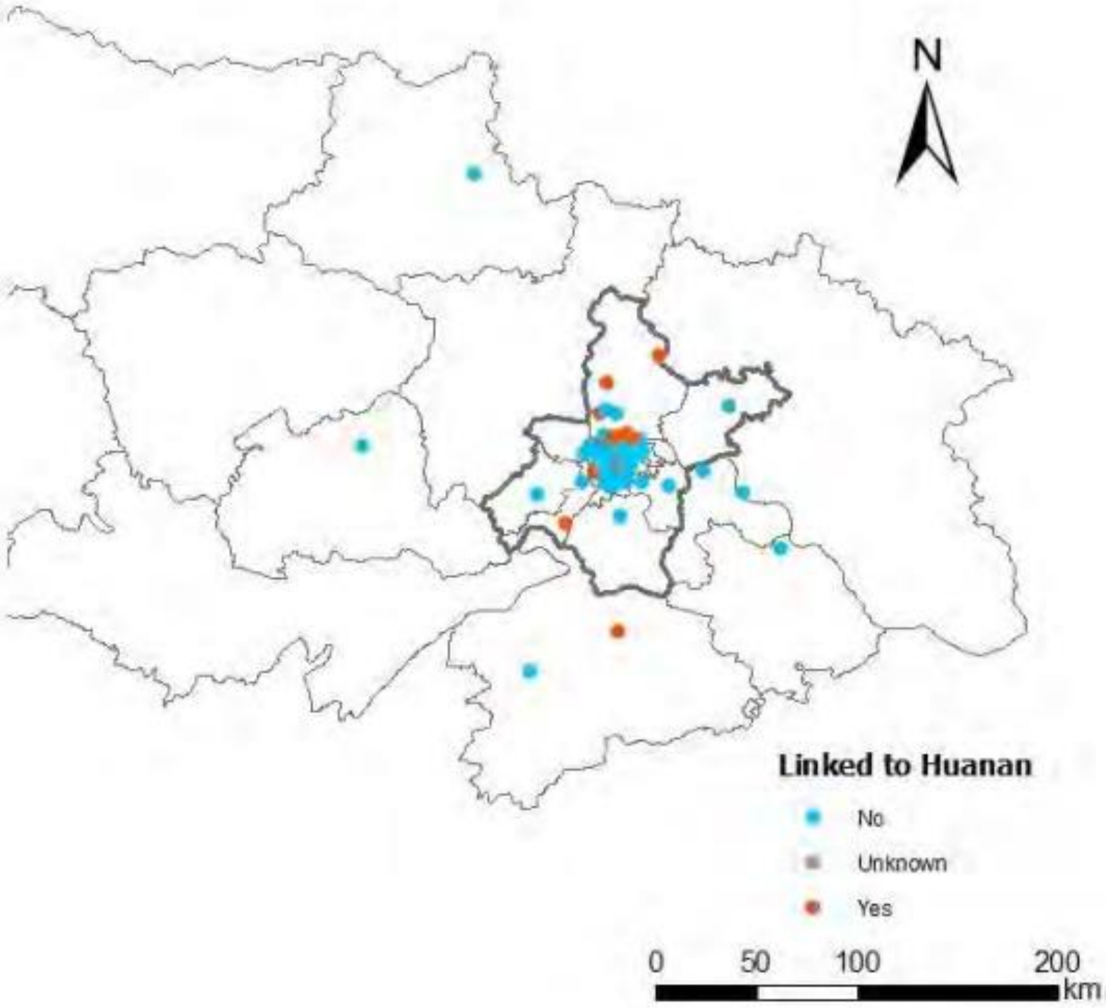


Fig. 3. Spatial distribution of the 174 cases by home address.

Exponential Math

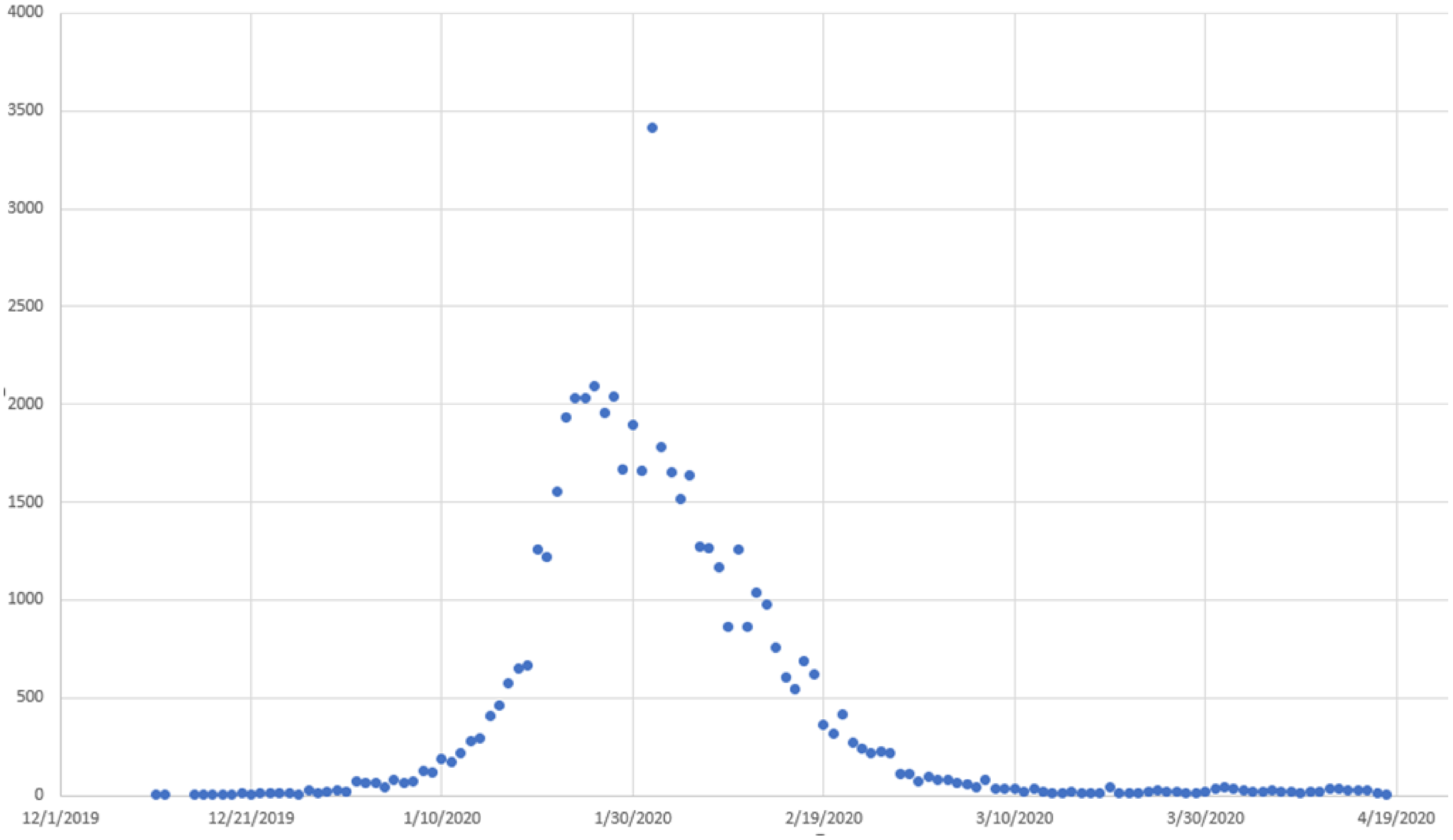
Covid epidemic doubling time is about 3.5 days. That’s 2 doublings per week.

5 known cases on Dec 13th . How many actual cases? Let’s say 50
Assume 5% hospitalization rate, 20% fatality rate for hospitalized cases.

	cases	hospitalizations	deaths
Nov 15:	too early	0	0
Nov 22:	1?	0	0
Nov 29:	3	0	0
Dec 6:	12	< 1	0
Dec 13:	50	2-3	0
Dec 20:	200	8	2
Dec 27:	800	40	8
Jan 3:	3,200	160	32
Jan 10:	12,800	640	128
Jan 17:	51,200	2,560	512
Jan 24:	204,800	10,240	2,048

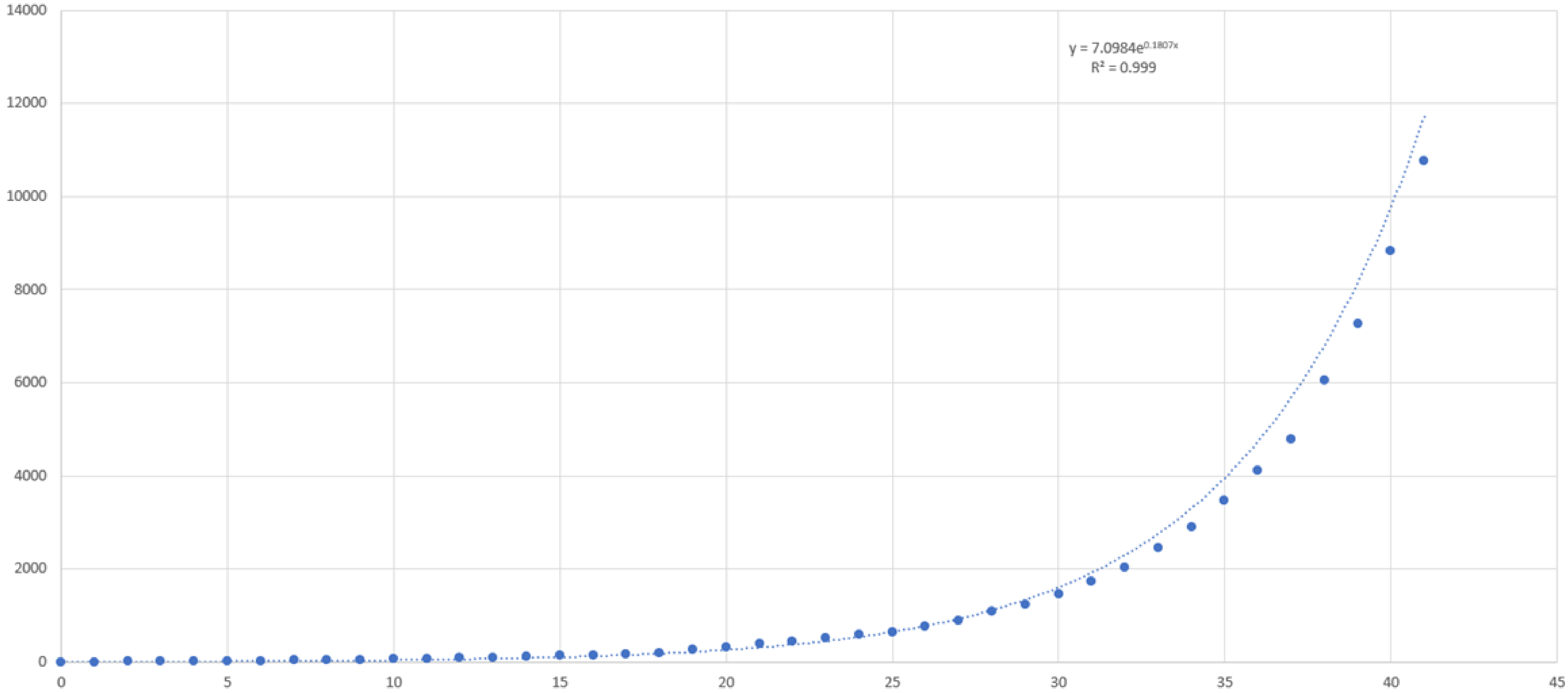
The correct numbers for January 24th are maybe 10,000 hospitalizations and 1,000 to 2,000 (pending) deaths.
That’s not bad, we’re within a factor of 2 of reality. And this gets a similar start date as Pekar’s simulations do.

Covid cases in Wuhan are exponential up until the lockdowns on January 23rd:

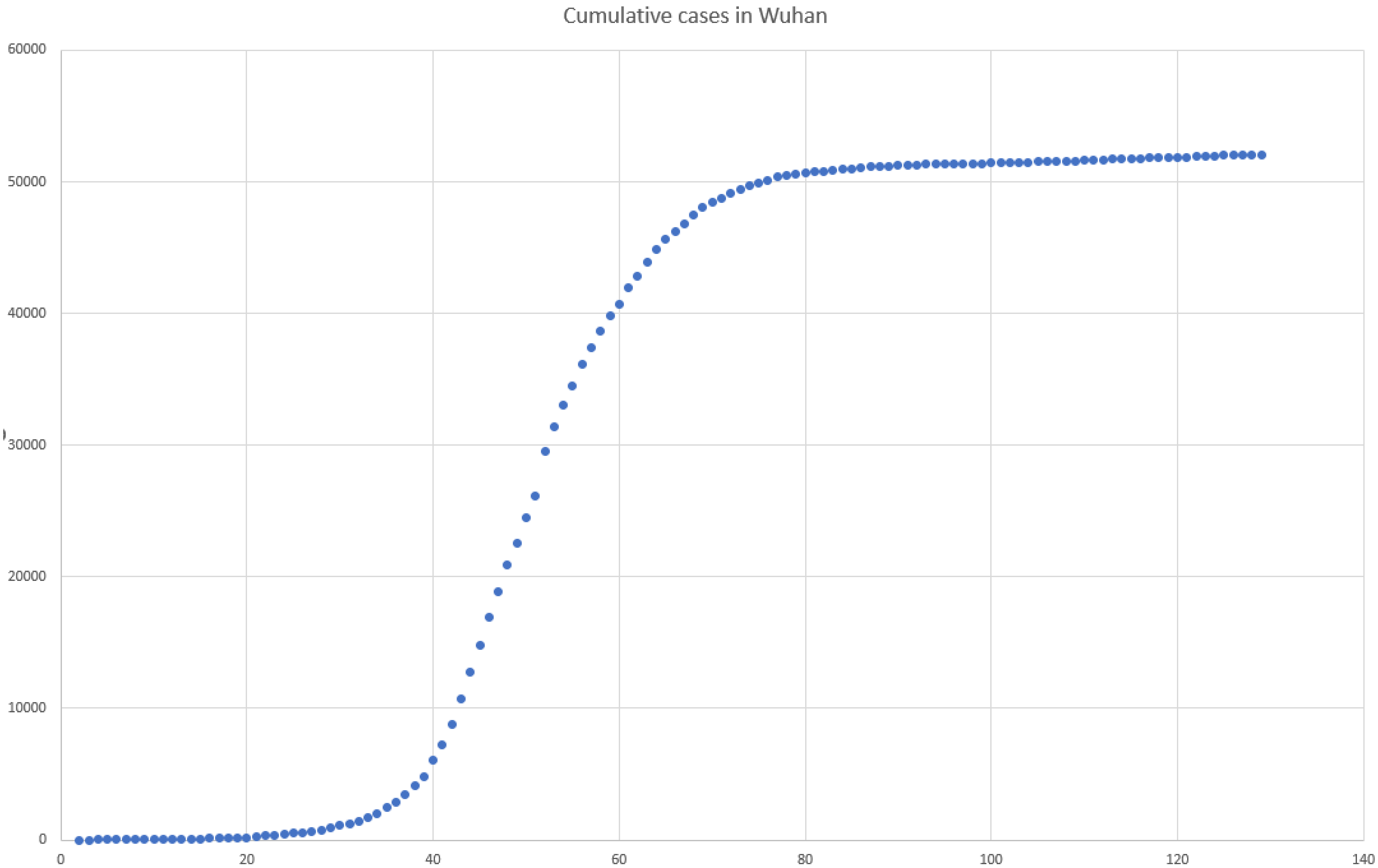


Data source – note this is a graph of daily cases, and my previous slide was “cumulative cases”.
Also, note that “diagnosed cases” isn’t total cases, it’s closer to “number of hospitalizations”.
You can work out the ascertainment rate from case fatality rate if you want to make the model as accurate as possible.

Cumulative cases follow a nice exponential curve up to January 23rd:



Data source


Cumulative cases in Wuhan
60000
50000
40000
30000
20000
10000
0
0
20
40
60
80
100
120
140

Now try 1,000 cases on December 13th:

	cases	hospitalizations	deaths
Dec 13:	1,000	50	10
Dec 20:	4,000	200	40
Dec 27:	16,000	800	160
Jan 3:	64,000	3,200	640
Jan 10:	256,000	12,800	2,560
Jan 17:	1,024,000	51,200	10,240
Jan 24:	4,096,000	204,800	40,960

By the time of the lockdowns, you get 10 times as many deaths in Wuhan as actually happened.

And then you’d have even more during the lockdowns.

The death numbers would have to be fake. So would the seroprevalence numbers in Wuhan.

Now try 10,000 cases on December 13th:

	cases	hospitalizations	deaths
Dec 13:	10,000	500	100
Dec 20:	40,000	2,000	400
Dec 27:	160,000	8,000	1,600
Jan 3:	640,000	32,000	6,400
Jan 10:	2,560,000	128,000	25,600
Jan 17:	10,240,000	512,000	102,400
Jan 24:	40,960,000	2,048,000	409,600

By the time of the lockdowns, 4% of Wuhan ends up dying. And then even more during the lockdowns.
That’s impossibly high, no place in the world has seen a covid death rate that large.

Even if you have 1,000 cases on December 13th, you end up with 10 times too many deaths in Wuhan.

This is a case where human reasoning fails

People don’t intuitively understand exponential math.

They assume that a September origin of covid is equally likely as a November origin.

They assume it’s possible for there to be more early December cases than really happened.

When a covid infection happens, it has to either quickly go extinct or it blows up exponentially.

It’s very hard for it to stay at an in-between rate for much time.

How do we know that doubling rate I used is correct?

It’s confirmed by several sources.

Pekar et al (2022) says 3.47 days.

Liu et al. (2021) says 3.6 days

Simply fitting the cumulative cases data in excel gave me 3.8 days.

Various cities around the world have seen comparable doubling times.

I said 3.5 to keep the math as simple as possible.

The Mahjong Room

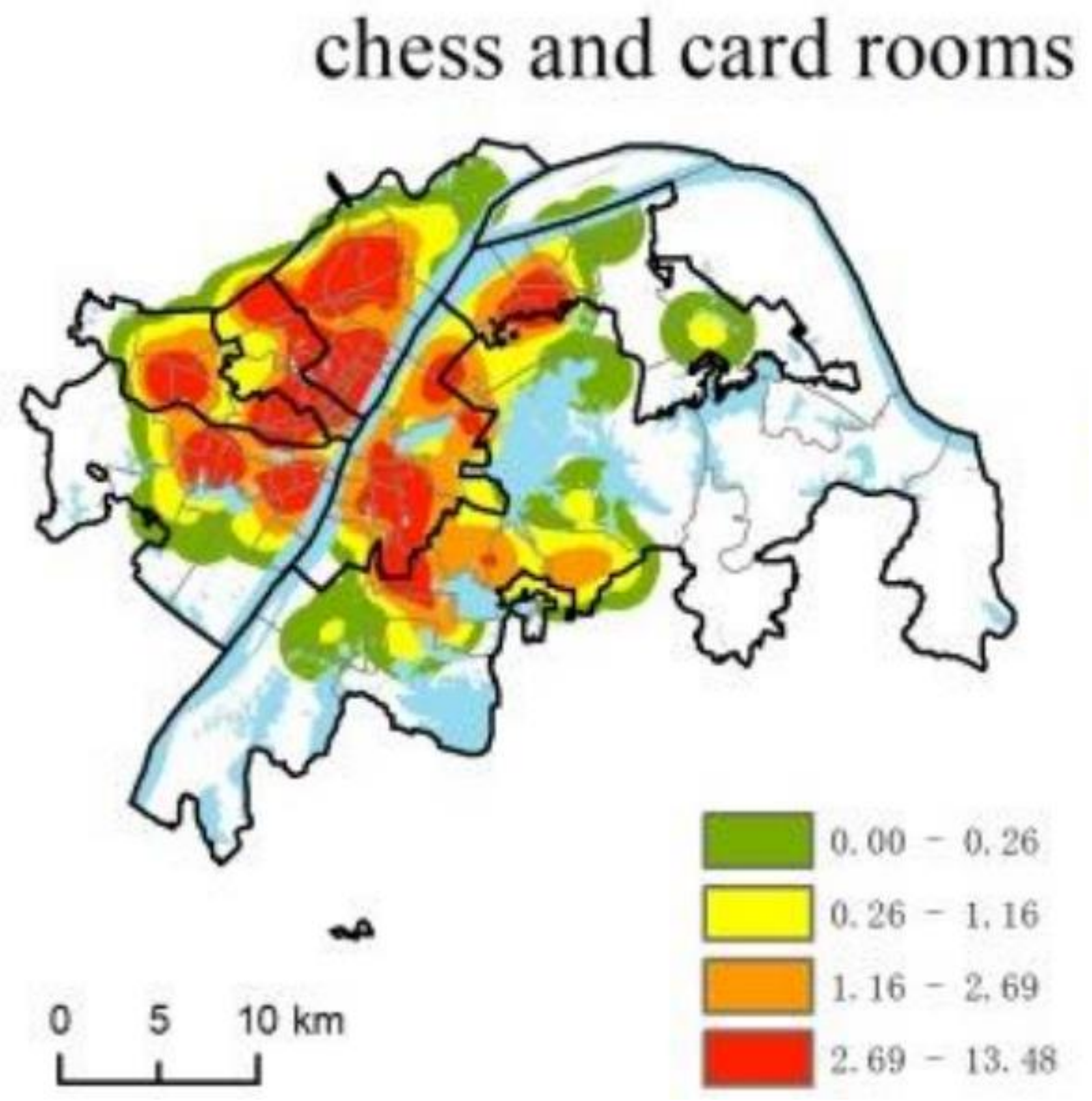
I tried to get an estimate on how many places people play Mahjong, in Wuhan. One study states:

> *“Chess and card rooms: These facilities provide Mahjong, poker and all types of chess activities. They are popular recreational areas for local residents. With the popularity of board games, chess and card rooms have begun to become popular among youth. There are 838 chess and card rooms in the study area.”*

Those places were spread around the city, many were closer to the Wuhan institute of Virology.

Including other “leisure entertainment facilities”, like bars, theatres, cybercafes, karaoke, etc, the study found 2,914 places in the study area.

What are the odds the first super-spreading location just happened to be at the only one of these places that was selling wild animals?



What are the odds that the virus would start in this particular mahjong room?

Naively, 1 in 2,914.

But, you also need to weight that by total number of visitors, many of those places are likely popular and this room is tiny and most outsiders don't know about it.

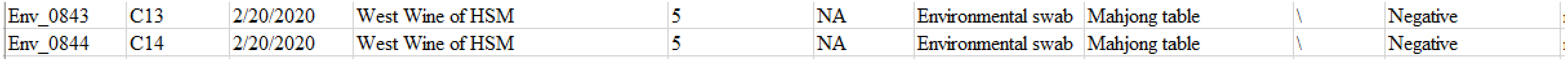
Weighted by traffic, it's probably even lower than the 1 in 10,000 odds I already gave.

I think this may be a video inside the mahjong room

On the other hand, there are only 4 wet markets in town selling wild animals.
The Huanan market has the most shops wildlife shops of any of those markets
(7 out of 17, according to the Xiao Xiao paper)

And wild animals are known to start pandemics.

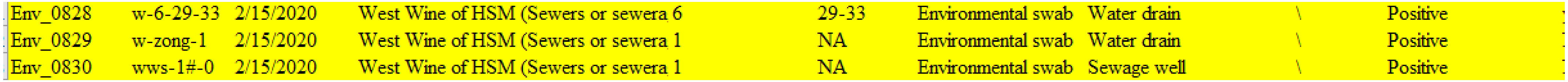
The Chinese teams did test the Mahjong table for covid, and it was negative:



Env_0843	C13	2/20/2020	West Wine of HSM	5	NA	Environmental swab	Mahjong table	\	Negative
Env_0844	C14	2/20/2020	West Wine of HSM	5	NA	Environmental swab	Mahjong table	\	Negative

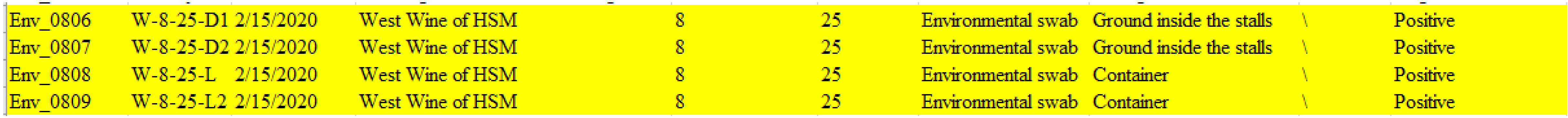
That's on February 20th, 2 months after the market was closed, so the RNA could have degraded.

But on February 15th , the drains were still testing positive for shop 6/29:



Env_0828	w-6-29-33	2/15/2020	West Wine of HSM (Sewers or sewera	6	29-33	Environmental swab	Water drain	\	Positive
Env_0829	w-zong-1	2/15/2020	West Wine of HSM (Sewers or sewera	1	NA	Environmental swab	Water drain	\	Positive
Env_0830	wws-1#-0	2/15/2020	West Wine of HSM (Sewers or sewera	1	NA	Environmental swab	Sewage well	\	Positive

On February 15th, shop 8/25 was also still testing positive:



Env_0806	W-8-25-D1	2/15/2020	West Wine of HSM	8	25	Environmental swab	Ground inside the stalls	\	Positive
Env_0807	W-8-25-D2	2/15/2020	West Wine of HSM	8	25	Environmental swab	Ground inside the stalls	\	Positive
Env_0808	W-8-25-L	2/15/2020	West Wine of HSM	8	25	Environmental swab	Container	\	Positive
Env_0809	W-8-25-L2	2/15/2020	West Wine of HSM	8	25	Environmental swab	Container	\	Positive

Here’s a photo outside of the Mahjong room (it’s that window up there on the left).
What’s more interesting is that sign below the window with one letter cut out:
The sign reads: 鼎盛 _ 味批发商行 = Dingsheng _ wei Wholesale Store
The missing character [is likely 野](). 野味 = yewei = “wild taste”, a term for eating wild animals.

The same character was removed elsewhere in the market:

alamy - 2B7KRNC

Here’s a picture of the Mahjong room from later, during the WHO visit.

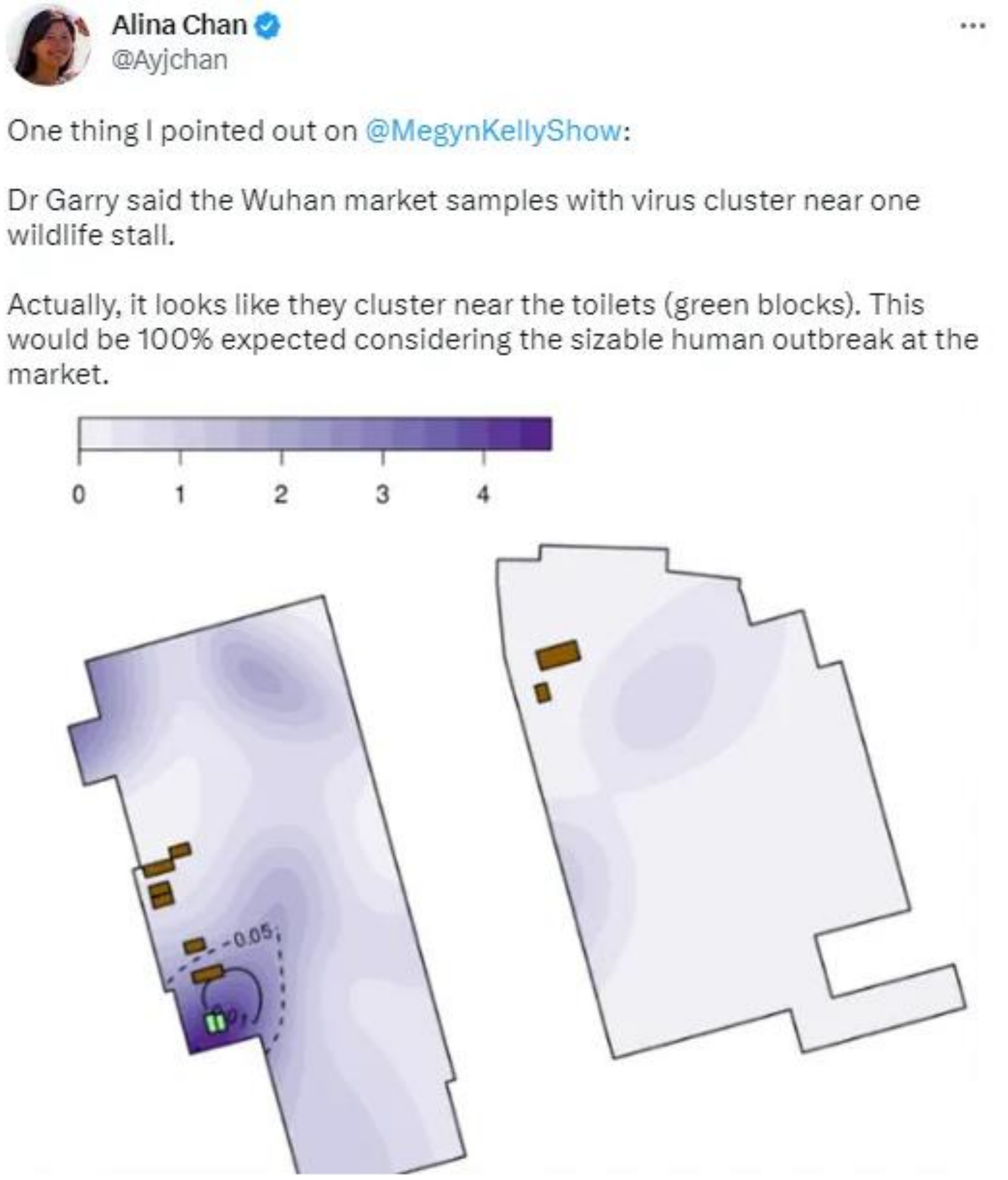
Now the sign has been taken down entirely:

The logic is even more absurd for the “toilets theory”.

There are millions of bathrooms in Wuhan.

But the outbreak started at the one in the market selling the most wildlife?

It happened at a market already flagged as a likely place for a viral outbreak?



Alina Chan
@Ayjchan

One thing I pointed out on @MegynKellyShow:

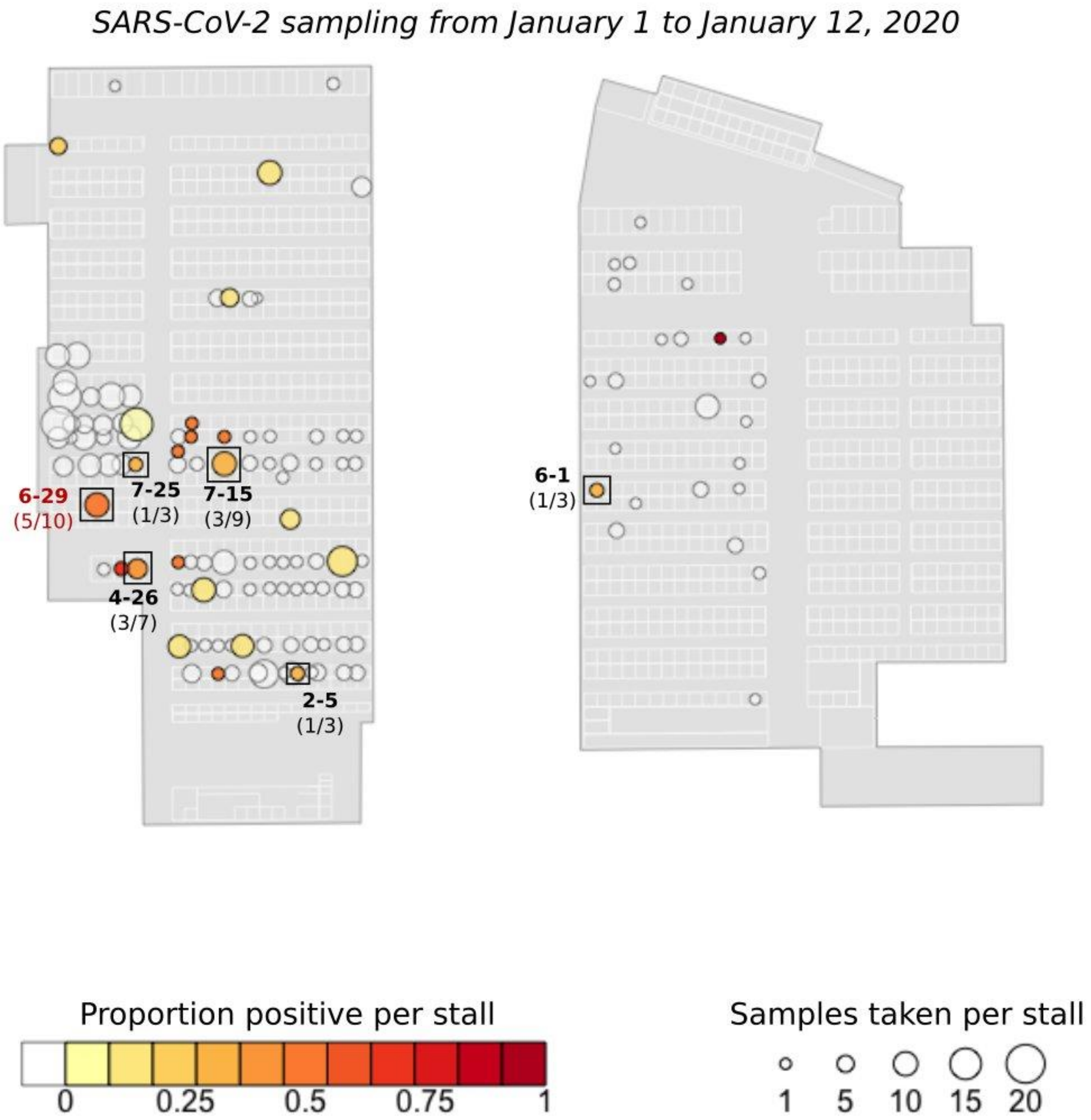
Dr Garry said the Wuhan market samples with virus cluster near one wildlife stall.

Actually, it looks like they cluster near the toilets (green blocks). This would be 100% expected considering the sizable human outbreak at the market.

Both theories fall apart when you look at the sampling maps.

how did the virus spread from the toilets, around a few corners, to the raccoon dog shop, while missing a shops even closer to the bathrooms?

And why did the positive samples have animal DNA, not human DNA, if you think these were contamination from the bathrooms?


SARS-CoV-2 sampling from January 1 to January 12, 2020

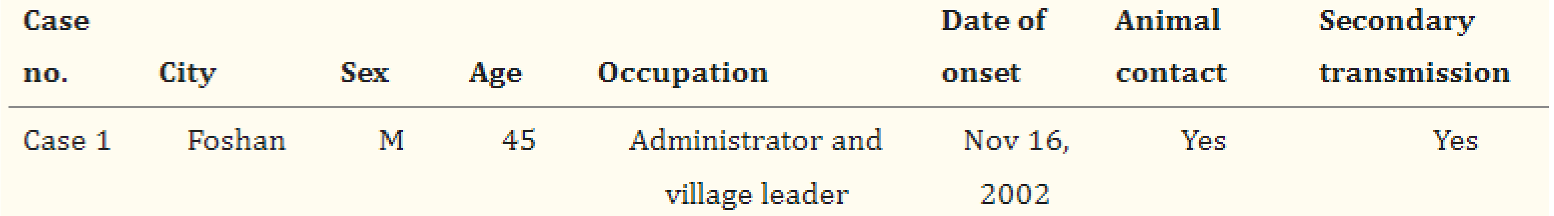
Comparing Covid and SARS

Rootclaim gets many facts wrong for the 2003 SARS pandemic

Rootclaim says that started with a farmer:

Foshan, Guangdong Province, China
(Nov 2002) - Started with a farmer

If you read the research, the man's occupation is unclear:



Case no.	City	Sex	Age	Occupation	Date of onset	Animal contact	Secondary transmission
Case 1	Foshan	M	45	Administrator and village leader	Nov 16, 2002	Yes	Yes

But he definitely wasn't a civet farmer. His "animal contact" was just cooking:

> "Patient 1 had the earliest case, identified by retrospective case searching. He lived with his wife and four children in Foshan city and became ill on November 16, 2002. He had not traveled outside Foshan in the 2 weeks before his illness and had no contact history, but he had prepared food including chicken, domestic cat, and snake"

Many of the index cases for SARS didn’t have animal contact at all:

None of the first 7 index cases are animal traders.

1 is a market vendor, not a trader. (same as covid)
She worked at a market but did not sell animals.

2 are restaurant chefs.

4 aren’t market or restaurant linked at all.

Only 1 of these 7 index cases had known contact with civets.

Rootclaim doesn’t know this, because they don’t do fact checking.

Table 6

Case series of index cases by municipality in SARS epidemic, Guangdong, China, November 2002–April 2003[a]

Case no.	City	Sex	Age	Occupation	Date of onset	Animal contact	Secondary transmission
Case 1	Foshan	M	45	Administrator and village leader	Nov 16, 2002	Yes	Yes
Case 2	Heyuan	M	34	Restaurant chef	Dec 10, 2002	Unknown	Yes
Case 3	Jiangmen	M	26	Factory worker	Dec 21, 2002	No	No
Case 4	Zhongshan	M	30	Restaurant chef	Dec 26, 2002	Yes	Yes
Case 5	Guangzhou	M	49	Office worker	Jan 2, 2003	No	Yes
Case 6	Shenzhen	M	46	Office worker	Jan 15, 2003	No	Yes
Case 7	Zhaoqing	F	39	Market vendor	Jan 17, 2003	Probably	Yes

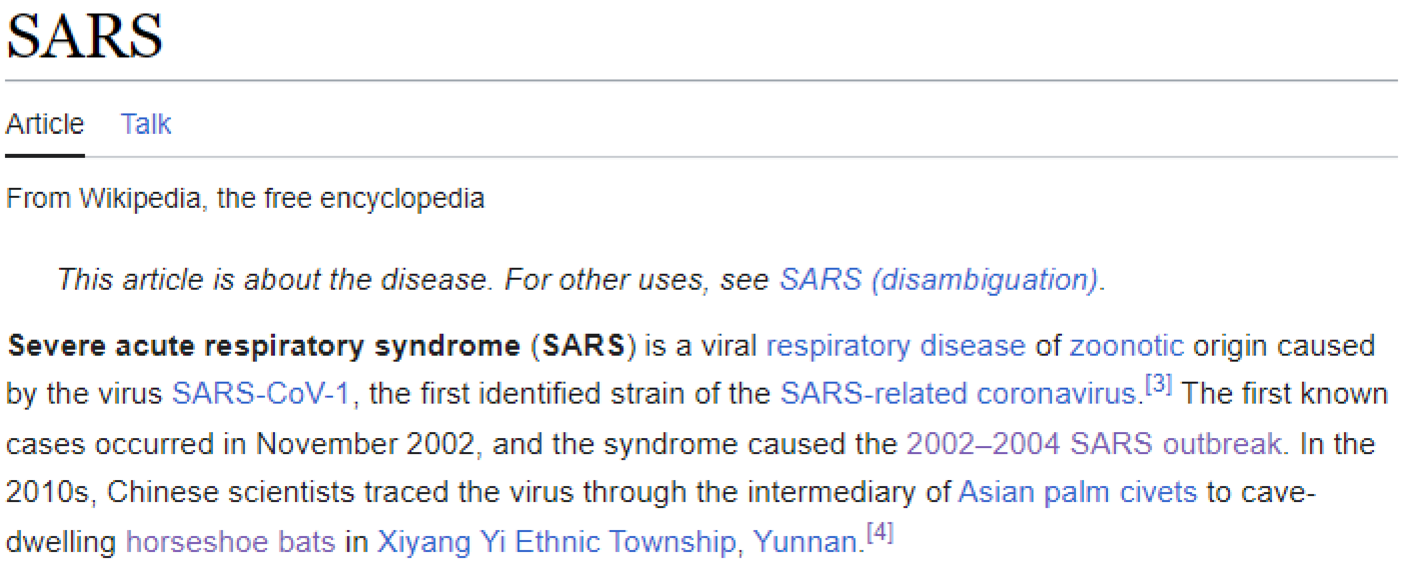
Open in a separate window

[a] SARS, severe acute respiratory syndrome; M, male; F, female.

Where did SARS come from?

Rootclaim says: WIV claimed to find the farm. It's in Yunnan, not Hubei.

The reality is that no SARS infected people or civets were ever found in Yunnan.
Where did Rootclaim get that idea? I have no idea, because Rootclaim didn't provide a source.
I'm guessing maybe they went to Wikipedia:



SARS

Article Talk

From Wikipedia, the free encyclopedia

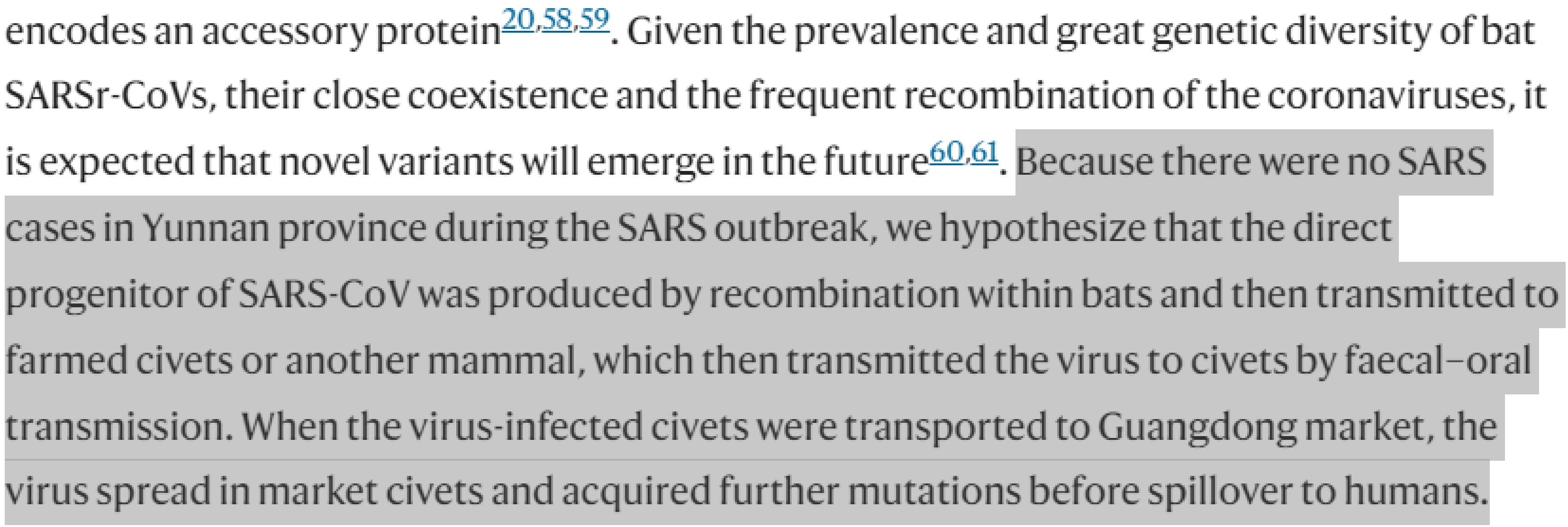
This article is about the disease. For other uses, see SARS (disambiguation).

Severe acute respiratory syndrome (**SARS**) is a viral respiratory disease of zoonotic origin caused by the virus SARS-CoV-1, the first identified strain of the SARS-related coronavirus.[3] The first known cases occurred in November 2002, and the syndrome caused the 2002–2004 SARS outbreak. In the 2010s, Chinese scientists traced the virus through the intermediary of Asian palm civets to cave-dwelling horseshoe bats in Xiyang Yi Ethnic Township, Yunnan.[4]

But if you click through and actually read the linked paper it says:

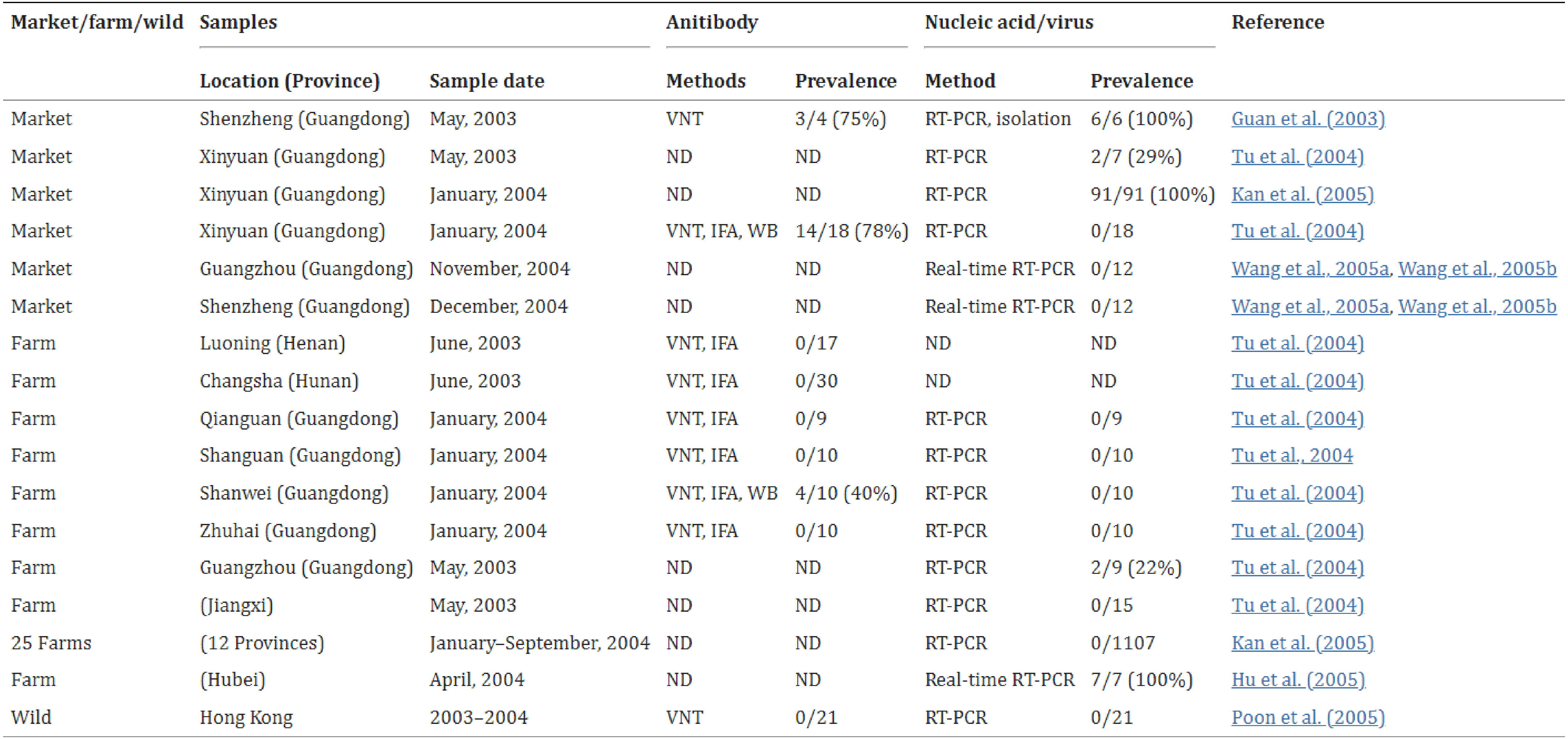
> "We have been conducting longitudinal molecular surveillance of bats for CoVs in Yunnan caves since 2011 and have found that they are inhabited by large numbers of bats including Rhinolophus spp., a major reservoir of SARSr-CoVs. **This region was not involved in the 2002–2003 SARS outbreaks**"

Shi Zhengli has a hypothesis that SARS started in Yunnan:



encodes an accessory protein[20,58,59]. Given the prevalence and great genetic diversity of bat SARSr-CoVs, their close coexistence and the frequent recombination of the coronaviruses, it is expected that novel variants will emerge in the future[60,61]. Because there were no SARS cases in Yunnan province during the SARS outbreak, we hypothesize that the direct progenitor of SARS-CoV was produced by recombination within bats and then transmitted to farmed civets or another mammal, which then transmitted the virus to civets by faecal–oral transmission. When the virus-infected civets were transported to Guangdong market, the virus spread in market civets and acquired further mutations before spillover to humans.

SARS was found in civets in Guangdong, Hubei, and Hunan provinces. One paper lists many of the studies:

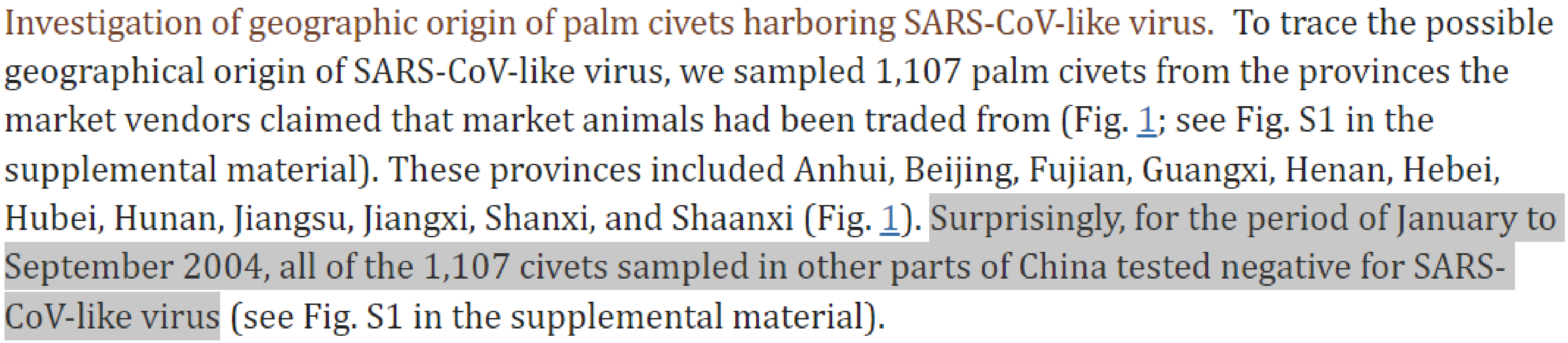


Market/farm/wild	Samples		Anitibody		Nucleic acid/virus		Reference
	Location (Province)	Sample date	Methods	Prevalence	Method	Prevalence	
Market	Shenzheng (Guangdong)	May, 2003	VNT	3/4 (75%)	RT-PCR, isolation	6/6 (100%)	Guan et al. (2003)
Market	Xinyuan (Guangdong)	May, 2003	ND	ND	RT-PCR	2/7 (29%)	Tu et al. (2004)
Market	Xinyuan (Guangdong)	January, 2004	ND	ND	RT-PCR	91/91 (100%)	Kan et al. (2005)
Market	Xinyuan (Guangdong)	January, 2004	VNT, IFA, WB	14/18 (78%)	RT-PCR	0/18	Tu et al. (2004)
Market	Guangzhou (Guangdong)	November, 2004	ND	ND	Real-time RT-PCR	0/12	Wang et al., 2005a, Wang et al., 2005b
Market	Shenzheng (Guangdong)	December, 2004	ND	ND	Real-time RT-PCR	0/12	Wang et al., 2005a, Wang et al., 2005b
Farm	Luoning (Henan)	June, 2003	VNT, IFA	0/17	ND	ND	Tu et al. (2004)
Farm	Changsha (Hunan)	June, 2003	VNT, IFA	0/30	ND	ND	Tu et al. (2004)
Farm	Qianguan (Guangdong)	January, 2004	VNT, IFA	0/9	RT-PCR	0/9	Tu et al. (2004)
Farm	Shanguan (Guangdong)	January, 2004	VNT, IFA	0/10	RT-PCR	0/10	Tu et al., 2004
Farm	Shanwei (Guangdong)	January, 2004	VNT, IFA, WB	4/10 (40%)	RT-PCR	0/10	Tu et al. (2004)
Farm	Zhuhai (Guangdong)	January, 2004	VNT, IFA	0/10	RT-PCR	0/10	Tu et al. (2004)
Farm	Guangzhou (Guangdong)	May, 2003	ND	ND	RT-PCR	2/9 (22%)	Tu et al. (2004)
Farm	(Jiangxi)	May, 2003	ND	ND	RT-PCR	0/15	Tu et al. (2004)
25 Farms	(12 Provinces)	January–September, 2004	ND	ND	RT-PCR	0/1107	Kan et al. (2005)
Farm	(Hubei)	April, 2004	ND	ND	Real-time RT-PCR	7/7 (100%)	Hu et al. (2005)
Wild	Hong Kong	2003–2004	VNT	0/21	RT-PCR	0/21	Poon et al. (2005)

This one study that [looked at 12 different provinces](#) is interesting.

They went to the market vendors in Guangdong and asked them where they got their animals, then went back to the farms and tested 1,107 civets.

None of those farmed civets tested positive!



Investigation of geographic origin of palm civets harboring SARS-CoV-like virus. To trace the possible geographical origin of SARS-CoV-like virus, we sampled 1,107 palm civets from the provinces the market vendors claimed that market animals had been traded from (Fig. 1; see Fig. S1 in the supplemental material). These provinces included Anhui, Beijing, Fujian, Guangxi, Henan, Hebei, Hubei, Hunan, Jiangsu, Jiangxi, Shanxi, and Shaanxi (Fig. 1). Surprisingly, for the period of January to September 2004, all of the 1,107 civets sampled in other parts of China tested negative for SARS-CoV-like virus (see Fig. S1 in the supplemental material).

SARS antibodies were found in wild civets in Hubei province, in one study.

SARS was never found in Yunnan. I'm not sure if it was even searched for in Yunnan.

Scientists did find a bat virus 96% similar to SARS, a decade later.

Perhaps SARS did spill-over in Yunnan and then get shipped to other provinces. Perhaps there was an even closer bat virus in Hubei. We don't know for sure.

It took 5 years of surveillance in one cave to find that bat virus.

By Rootclaim's logic, that study is inadmissible because the WIV did not do 5 years of surveillance in every cave in China.

The reality is that we don't know when and where SARS spilled over from bats, what the first infected animal was, where the first infected civets were, or who the first SARS human case was.

Tracing viruses is very hard. Even after 20 years, we still only have guesses for SARS.

We have already found 2 bat viruses that are > 96% similar to Covid.

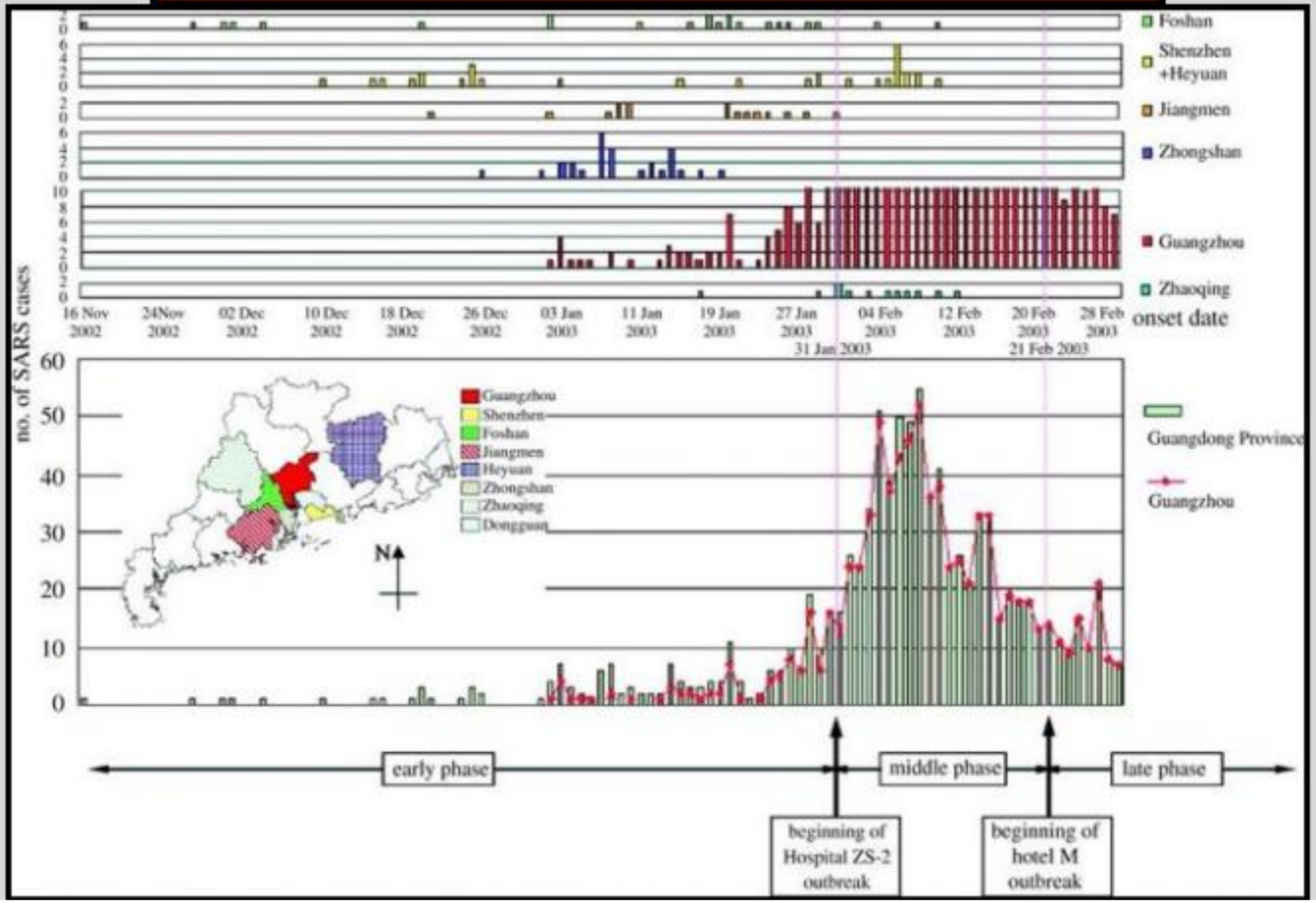
Using the SARS logic, we already found the origin of Covid.

Really, we don't know the origin of either. The big difference is we do know which intermediate animals carried SARS.

Rootclaim asks why SARS1 made it to multiple cities and Covid only spilled over in Hubei

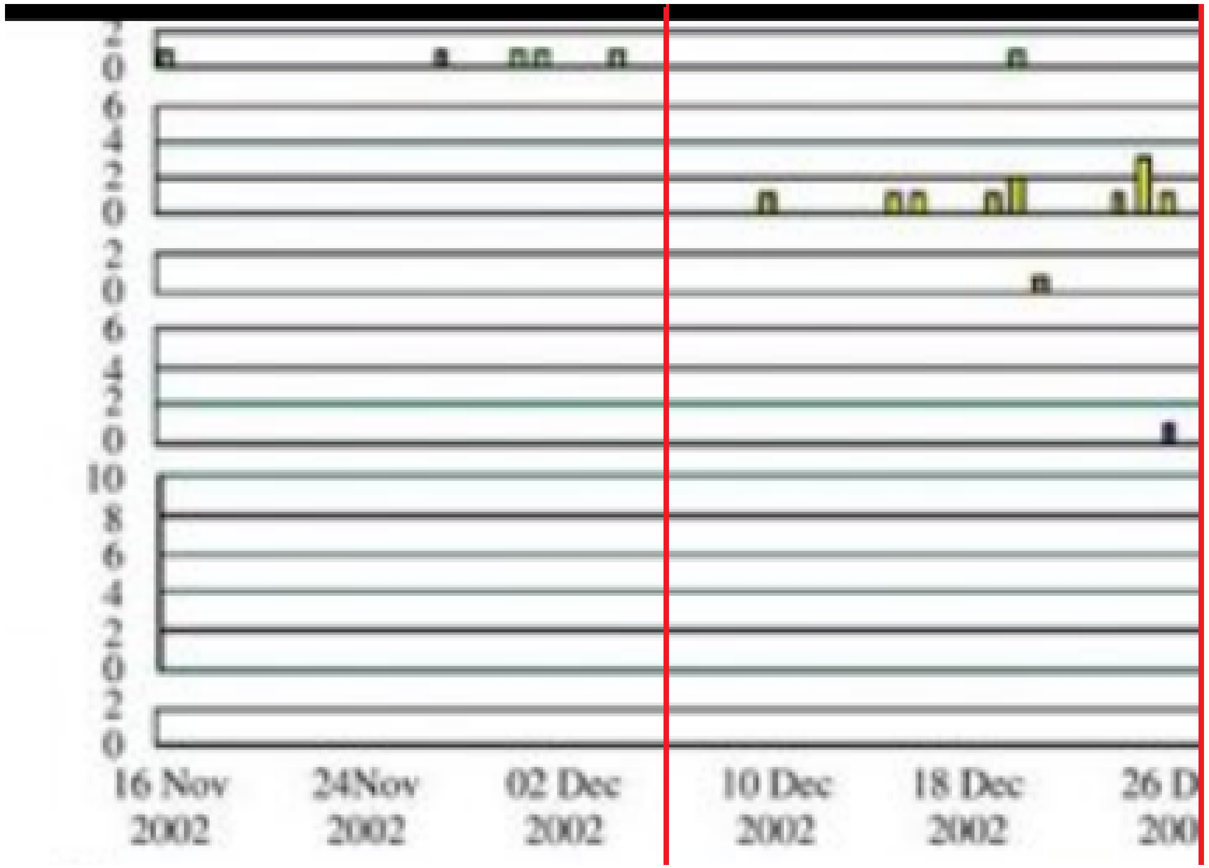
Comparing to SARS1

SARS Infections Over Time



This is what SARS would look like, with the speed of China’s 2020 response:

It wouldn’t even be in another town by the time the market closed, it would barely be in 4 by the Wuhan lockdowns.



Market closed

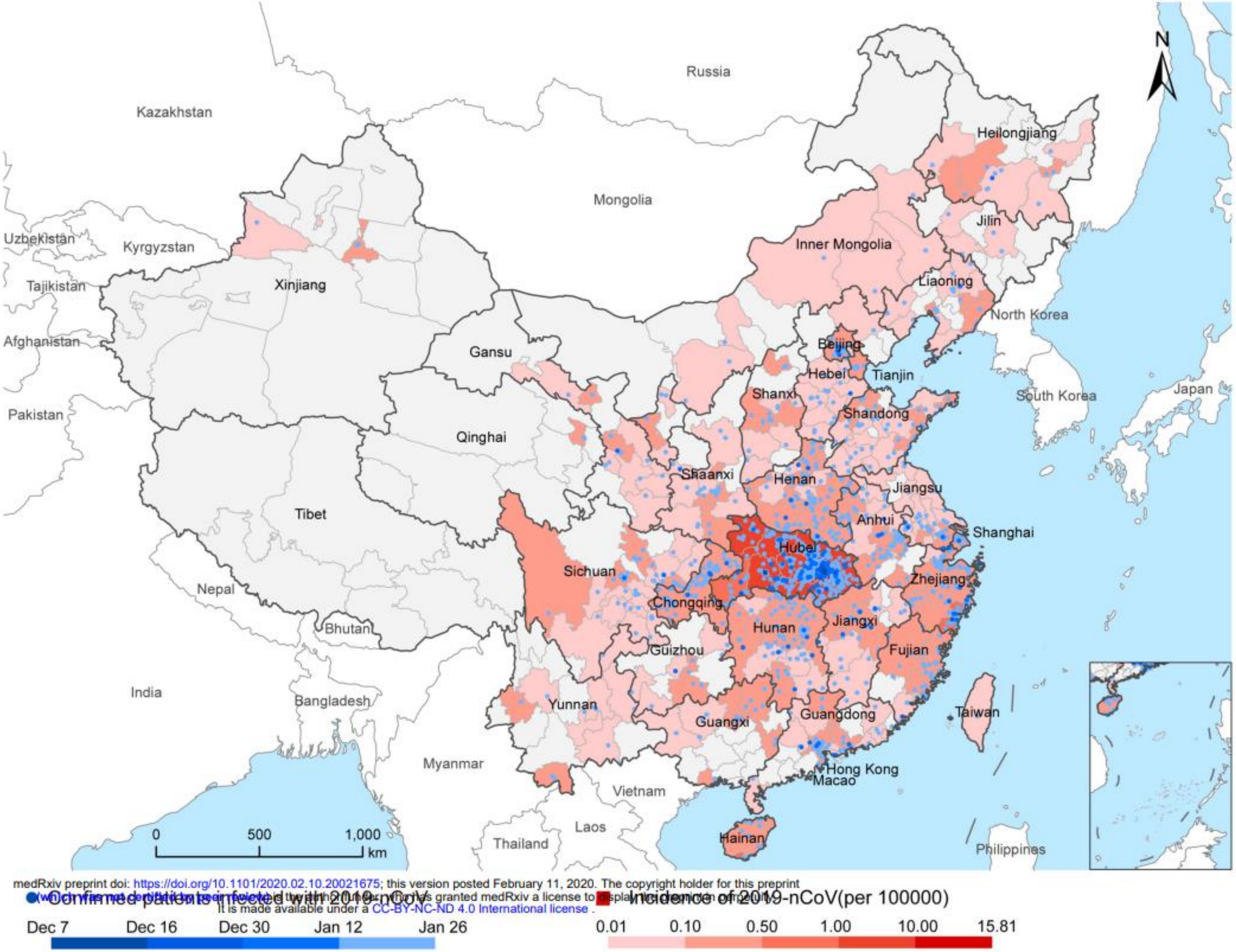
Wuhan lockdown

Here's what actually happened with Covid during that time period.

It's all over China because it's so contagious.

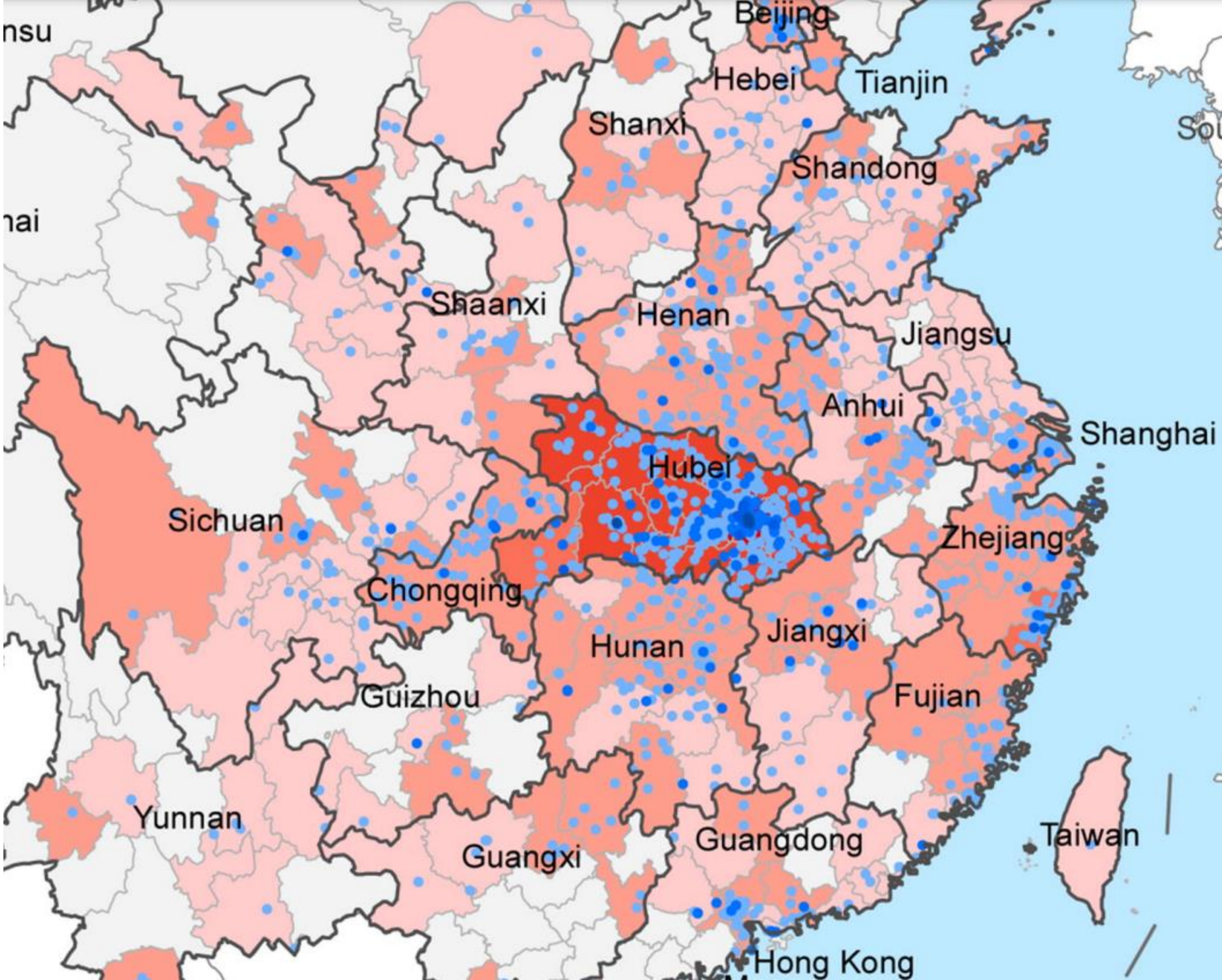
If there was a second, smaller spillover 6 weeks later, would you even notice that?

After this, China locked down and culled millions of animals.

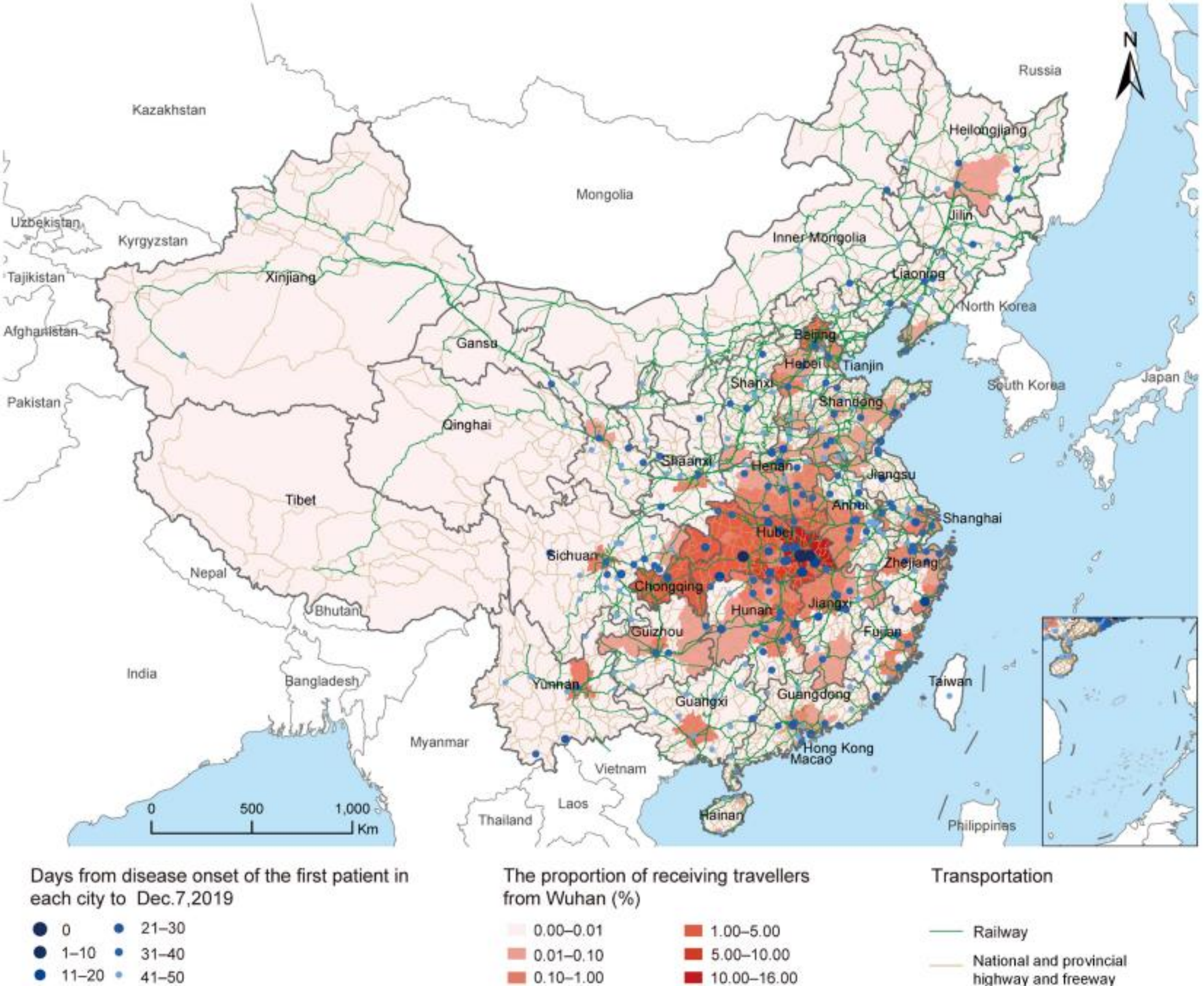


Figures from Yang et al, 2020

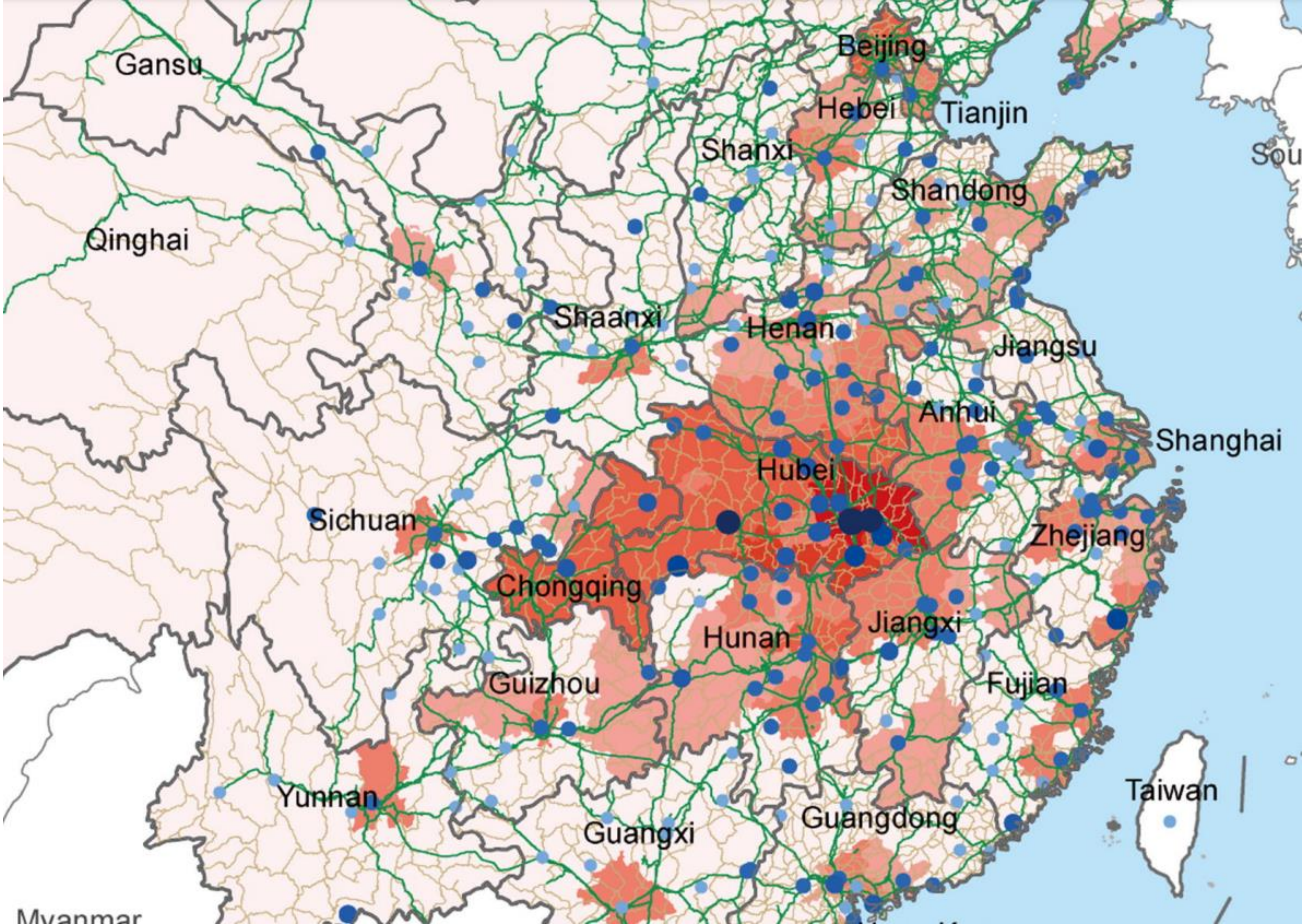
Zoomed in a bit for detail



Mapped along with the railway network.



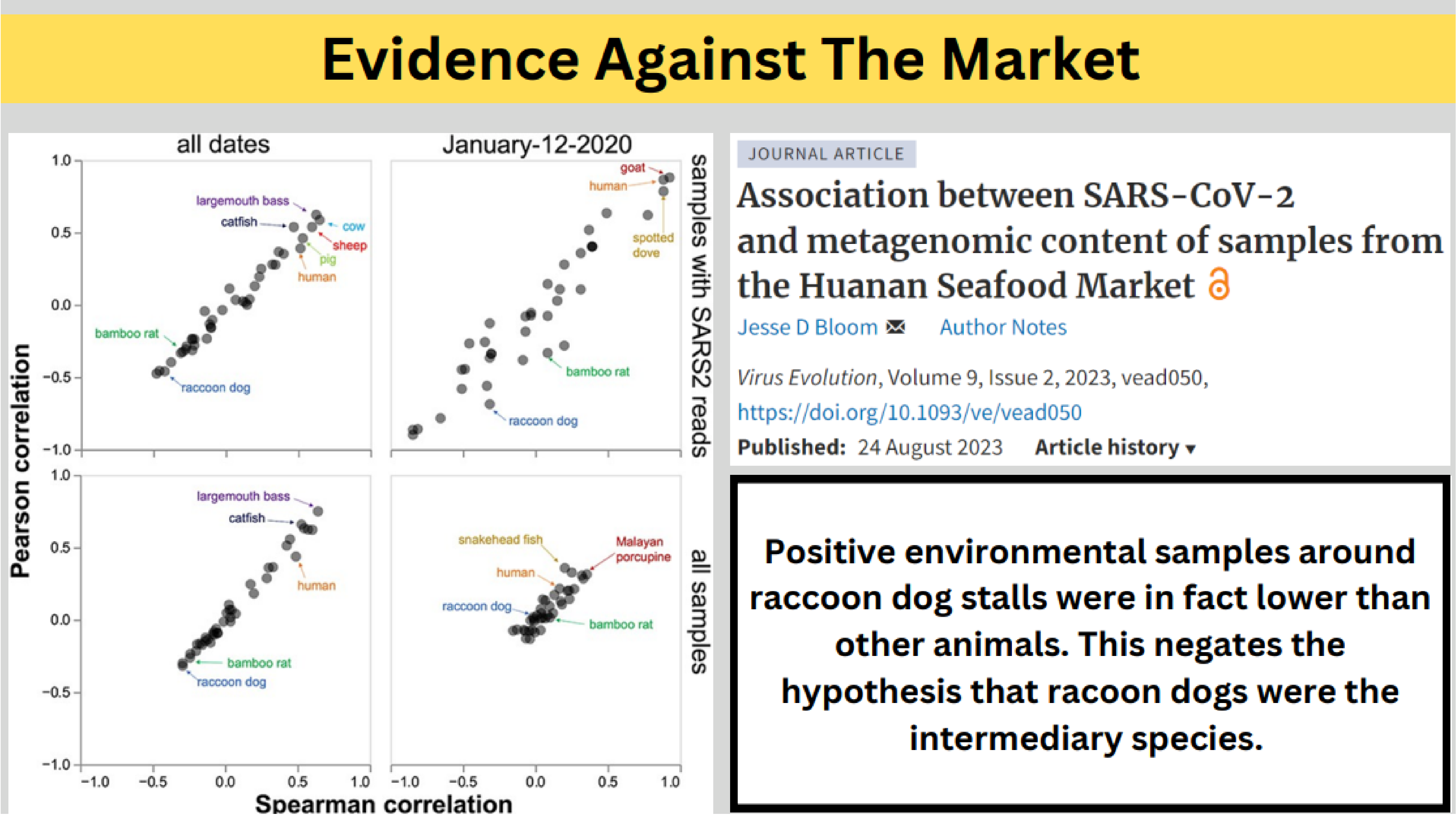
Zoomed In:


Gansu
Beijing
Hebei
Tianjin
Shanxi
Shandong
Qinghai
Shaanxi
Henan
Jiangsu
Anhui
Shanghai
Hubei
Sichuan
Zhejiang
Chongqing
Jiangxi
Hunan
Guizhou
Fujian
Taiwan
Yunnan
Guangdong
Guangxi
Myanmar

Jesse Bloom analysis of market data

There's some fair scientific disagreement about what the positive samples mean

I'm familiar with this paper, I think I'll just debate this live and we can figure out how both sides are interpreting the data.



Evidence Against The Market

JOURNAL ARTICLE

Association between SARS-CoV-2 and metagenomic content of samples from the Huanan Seafood Market

Jesse D Bloom ✉ Author Notes

Virus Evolution, Volume 9, Issue 2, 2023, vead050, https://doi.org/10.1093/ve/vead050

Published: 24 August 2023 **Article history ▾**

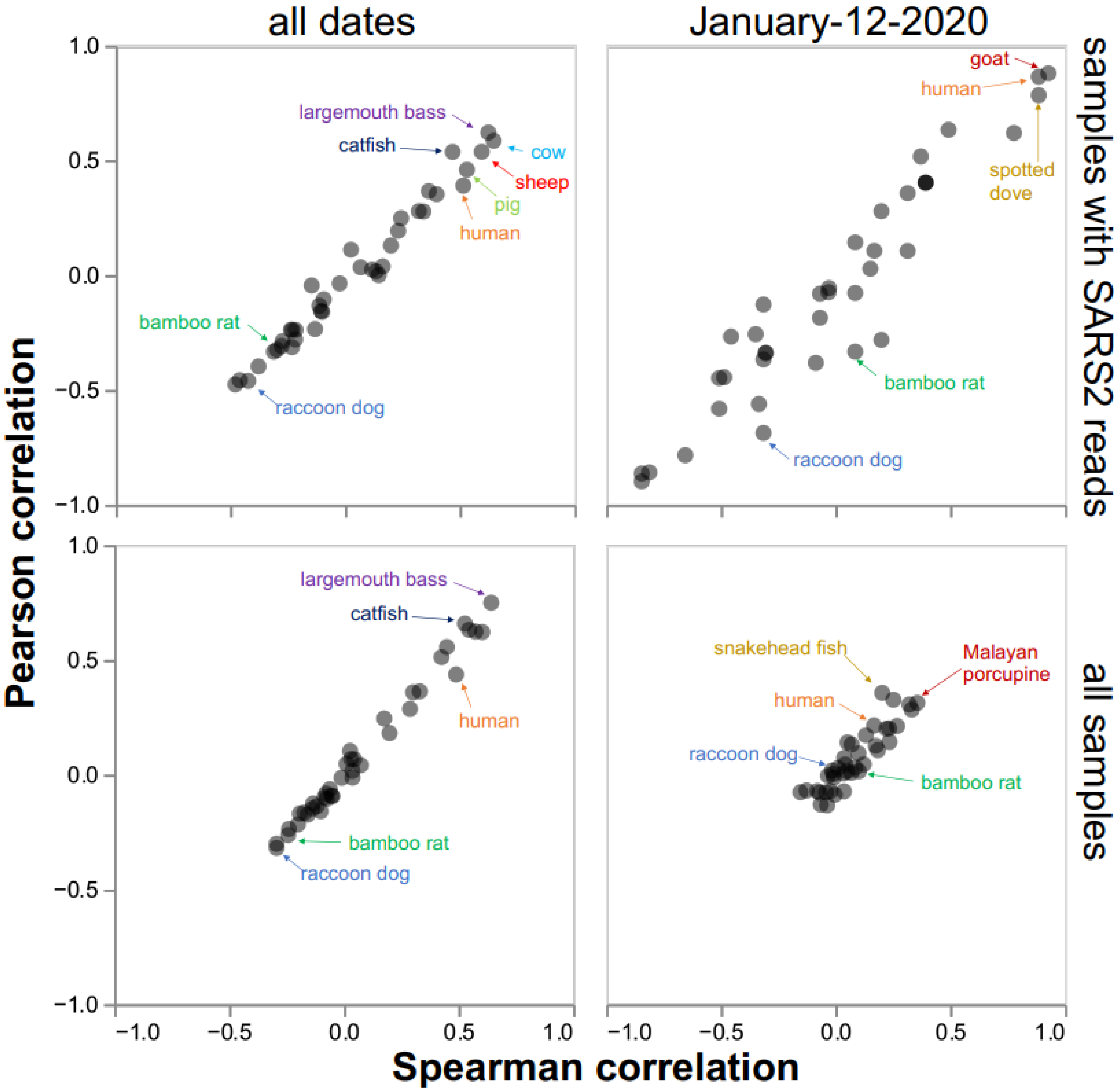
Positive environmental samples around raccoon dog stalls were in fact lower than other animals. This negates the hypothesis that racoon dogs were the intermediary species.

Jesse Bloom analysis

Confirms raccoon dog in Q61 sample (Chinese analysis called this dogs)

Argues no correlation between raccoon dog DNA and covid RNA.

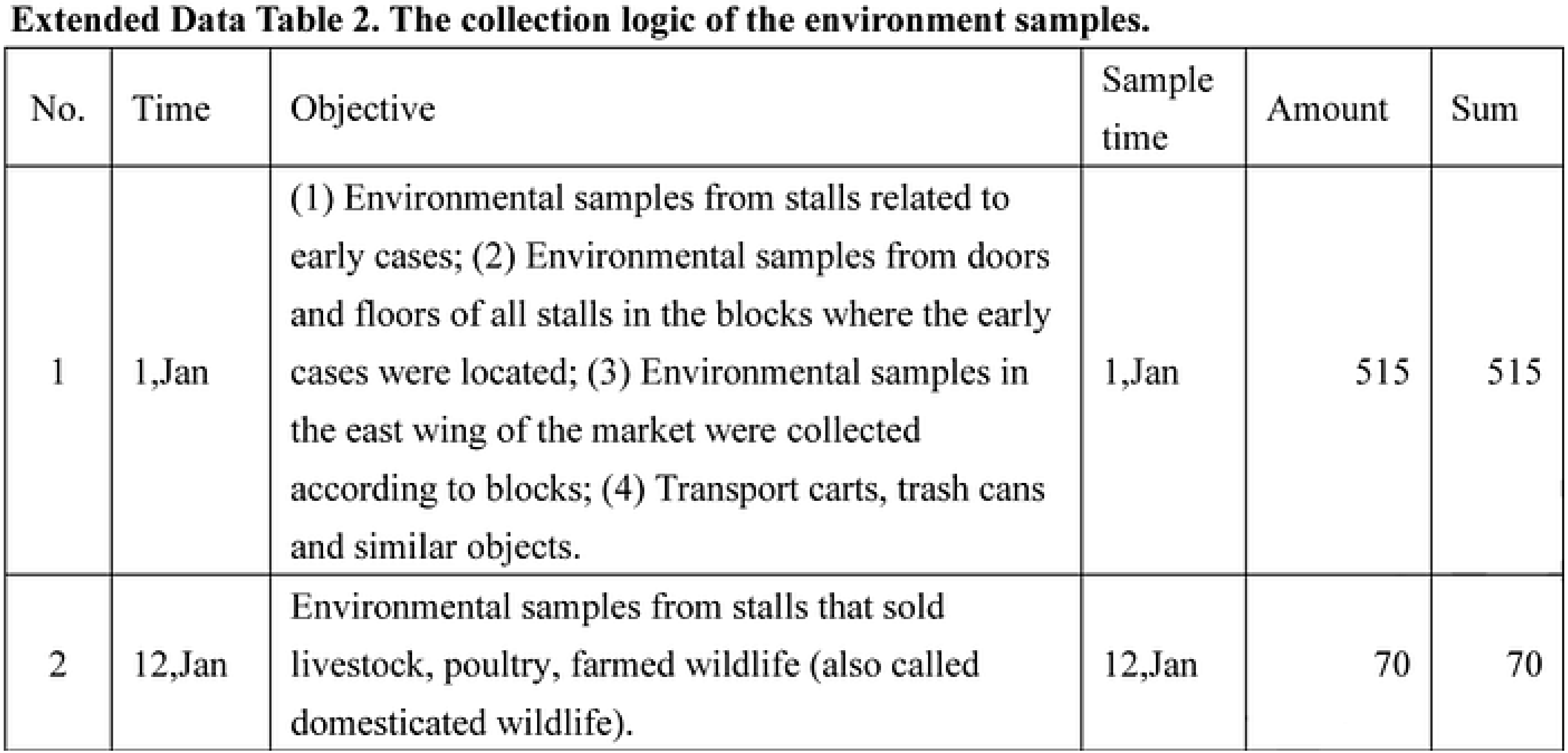
But it really depends on how you run the analysis.



The big problem is that he combined samples from two different dates

January 1st samples were taken where cases were.

January 12th samples were taken from wildlife shops.



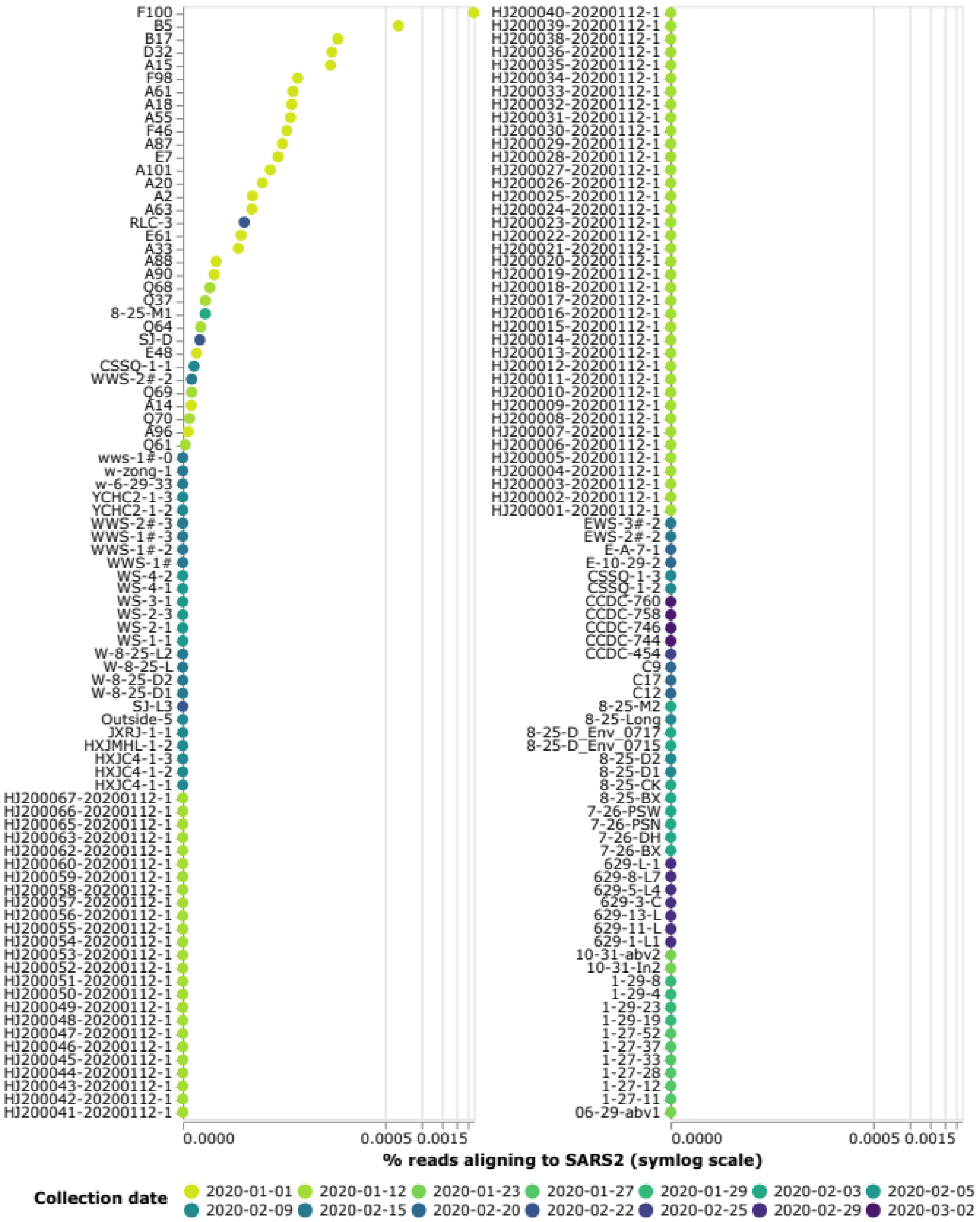
Extended Data Table 2. The collection logic of the environment samples.

No.	Time	Objective	Sample time	Amount	Sum
1	1,Jan	(1) Environmental samples from stalls related to early cases; (2) Environmental samples from doors and floors of all stalls in the blocks where the early cases were located; (3) Environmental samples in the east wing of the market were collected according to blocks; (4) Transport carts, trash cans and similar objects.	1,Jan	515	515
2	12,Jan	Environmental samples from stalls that sold livestock, poultry, farmed wildlife (also called domesticated wildlife).	12,Jan	70	70

Covid RNA degrades over time.

Early samples had more SARS2 reads than later samples.

If you combine the 1/1 and 1/12 samples, your correlation mostly just tells you which date each was taken on.



SARS-CoV-2 read counts drop, over time:

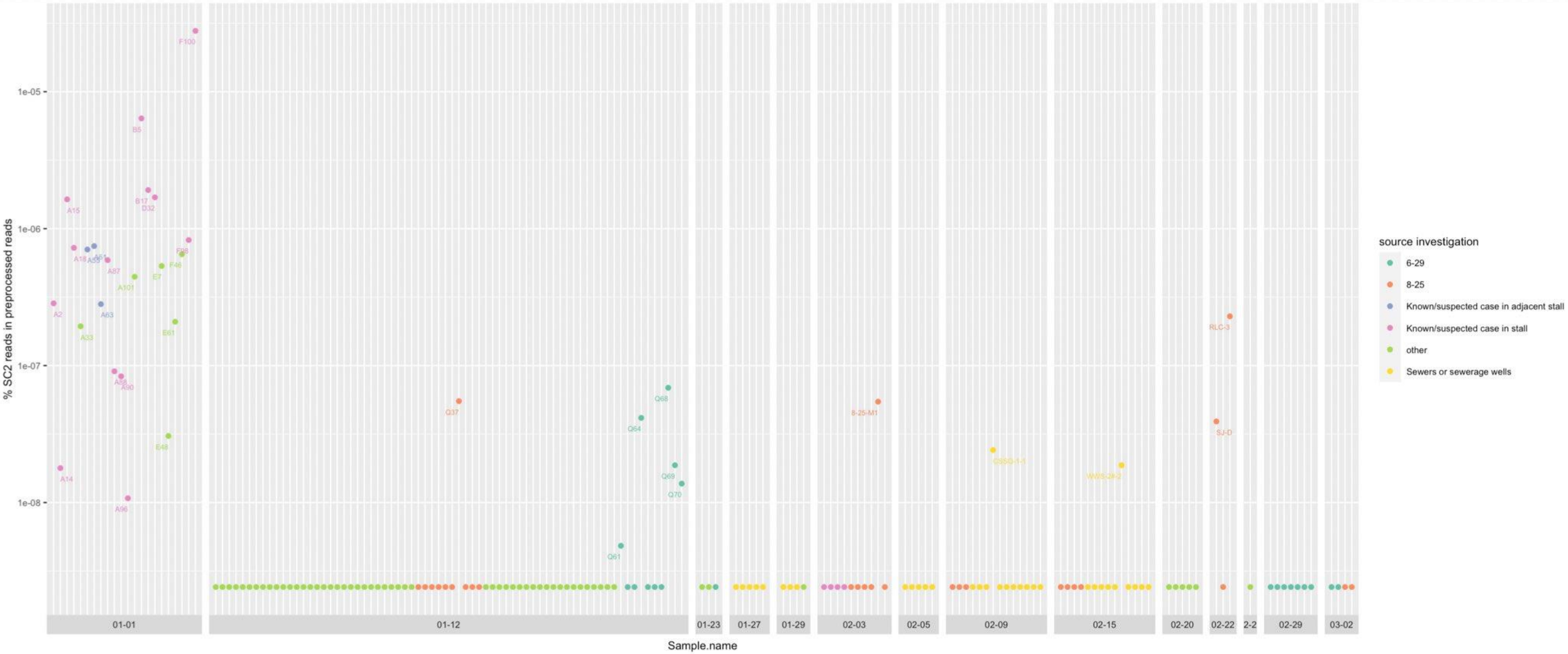
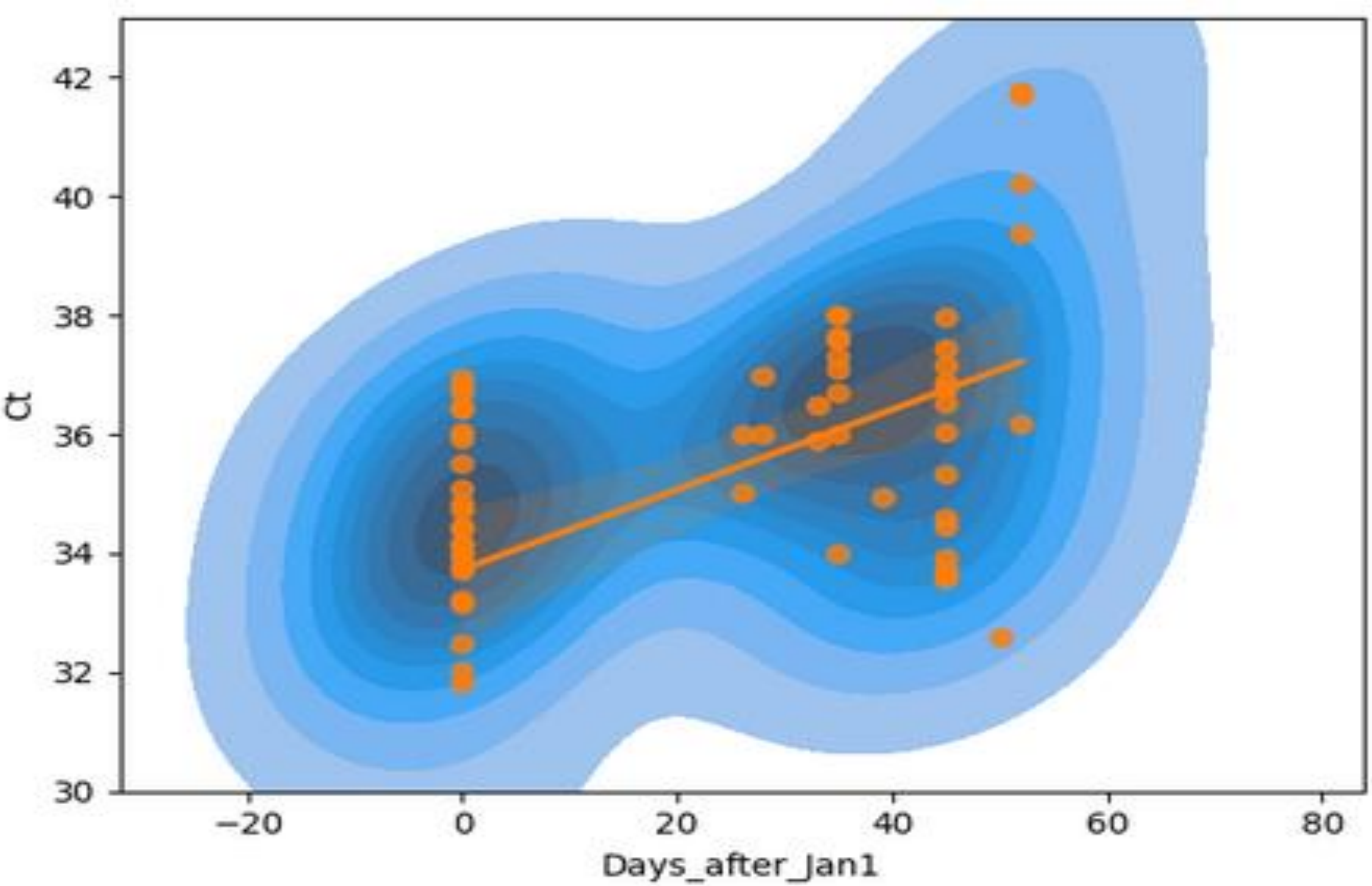


Image from Zhihua Chen

PCR cycle threshold also goes up, over time:



Jesse Bloom correlations are misleading because they combine two days of sampling:

On the human sampling day, human has the highest correlation.
On the wildlife sampling day, wildlife has the highest correlation.
Combine the two and neither stands out.

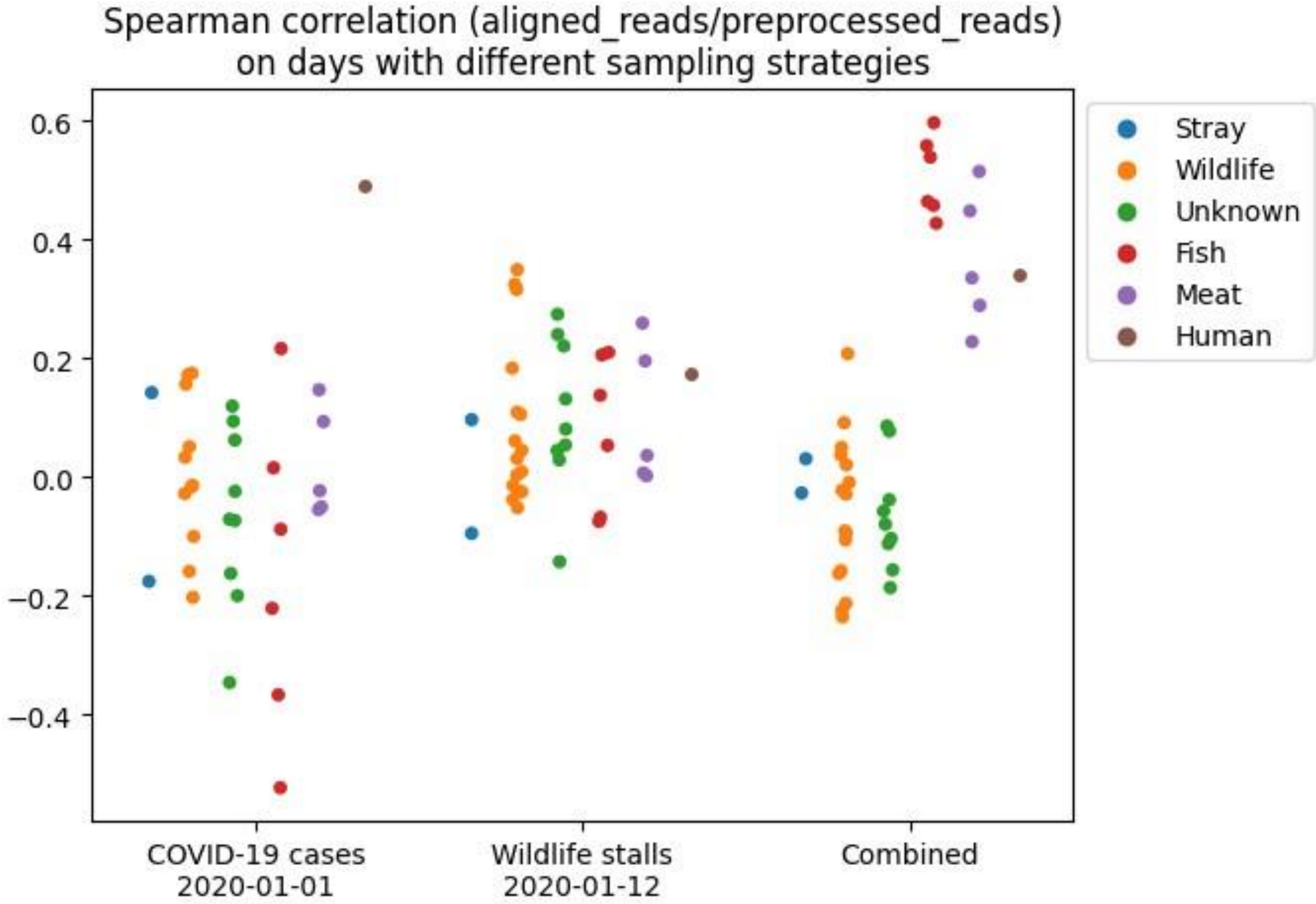


Image from Zach Hensel

Should we even expect to see a correlation?

If infected animals introduced the virus, they would have shed virus **earlier**, but they were sampled **later.**

So the signal from animals will be weaker than from people.

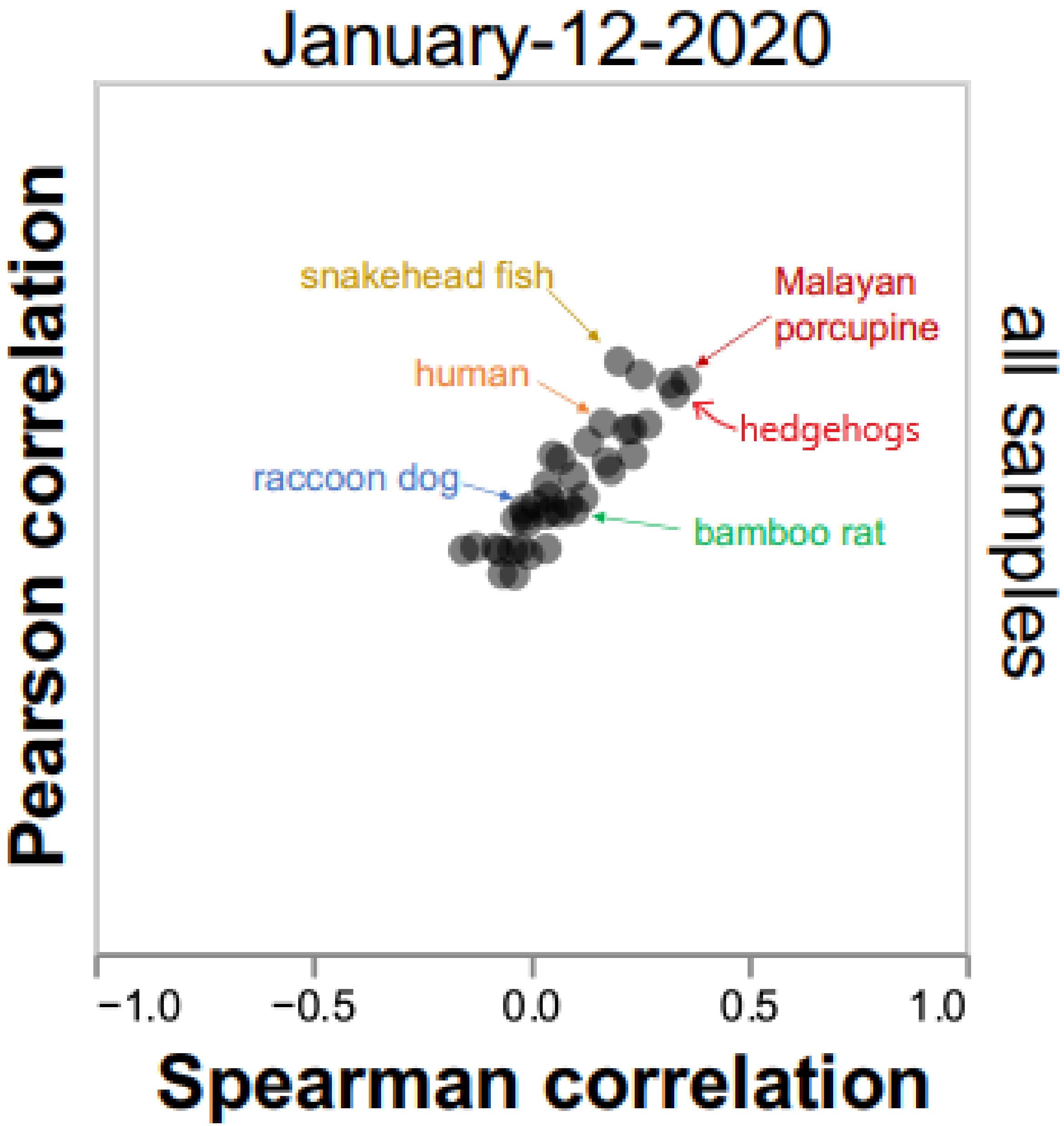
Wildlife stalls are also more diverse, giving a weaker signal than a sample that’s just human DNA.

There’s also a bias in terms of which samples were sequenced:

Positives: all samples (both wildlife and non-wildlife stalls) selected for sequencing.

Negatives: 89 of the 102 selected for sequencing were from wildlife stalls.

If any correlation Bloom came up with is useful, it might be this one, from the wildlife sampling day:



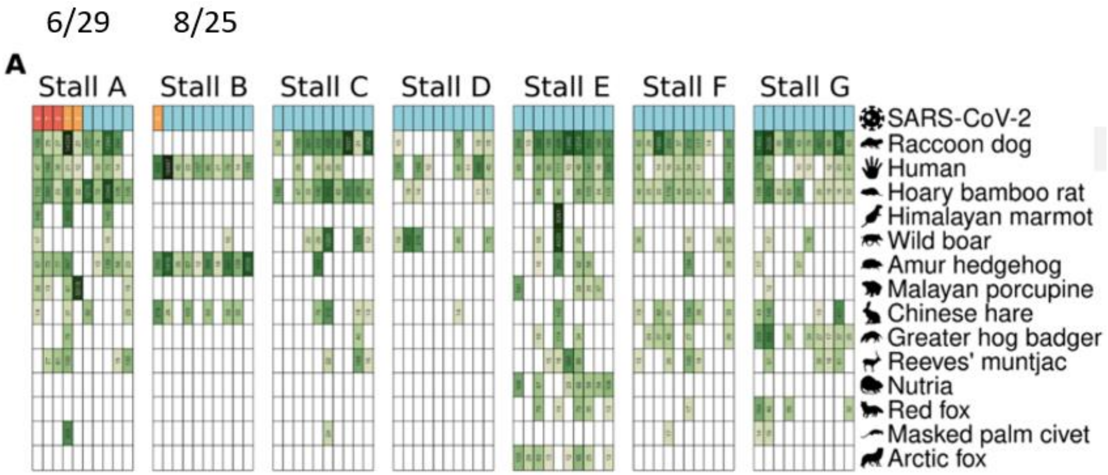
But this doesn't really show us much information beyond what we already know:

2 shops tested positive that day:
five samples in 6/29, and one sample in 8/25.

Both shops sold hedgehogs, so those stand out.

The porcupine sample stands out because porcupines were not sold in many shops besides 6/29.

The one thing Bloom showed is that other shops besides 6/29 also sold raccoon dogs.



Bloom’s table showed that most raccoon dog samples were covid negative, using a 20% DNA cut-off.

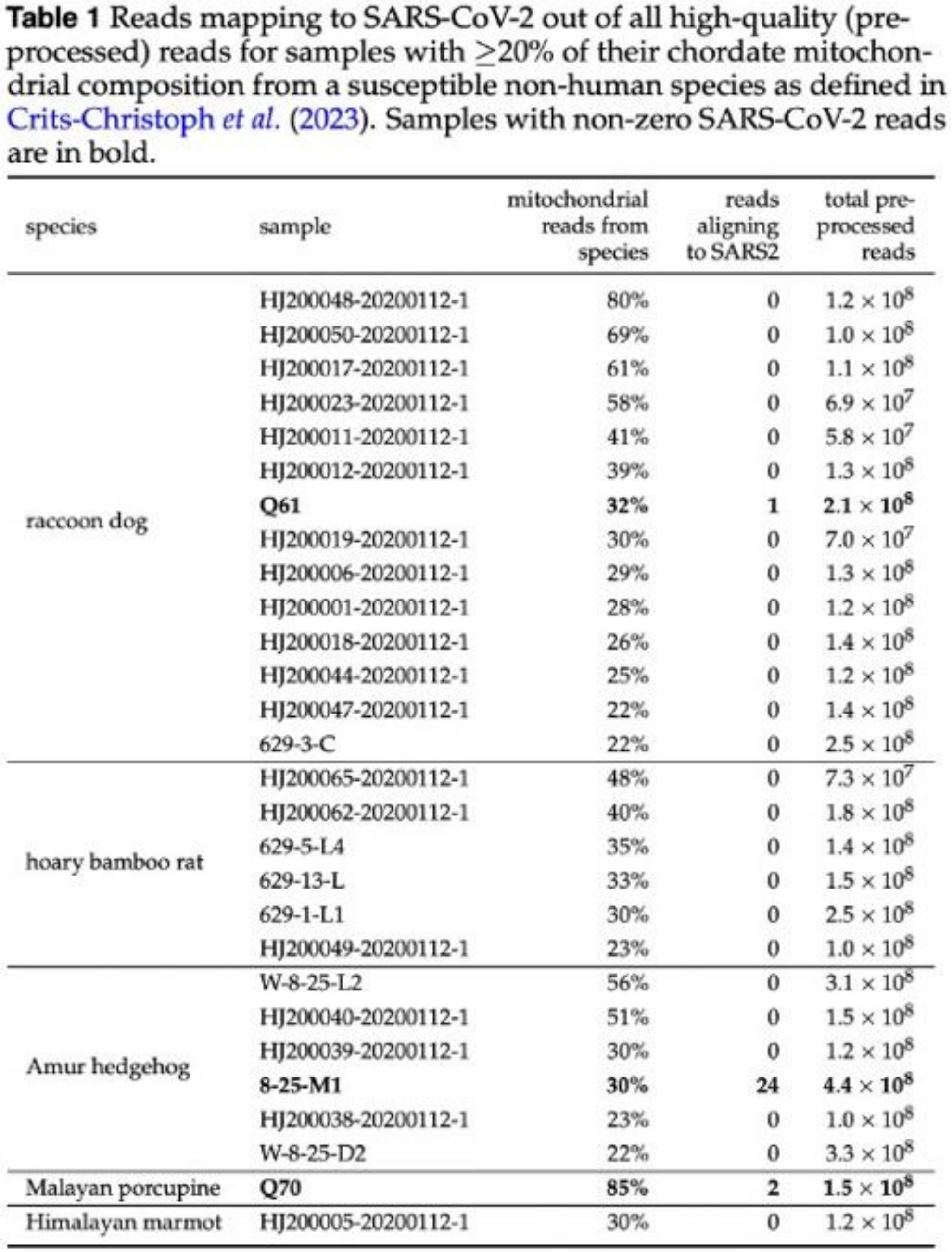
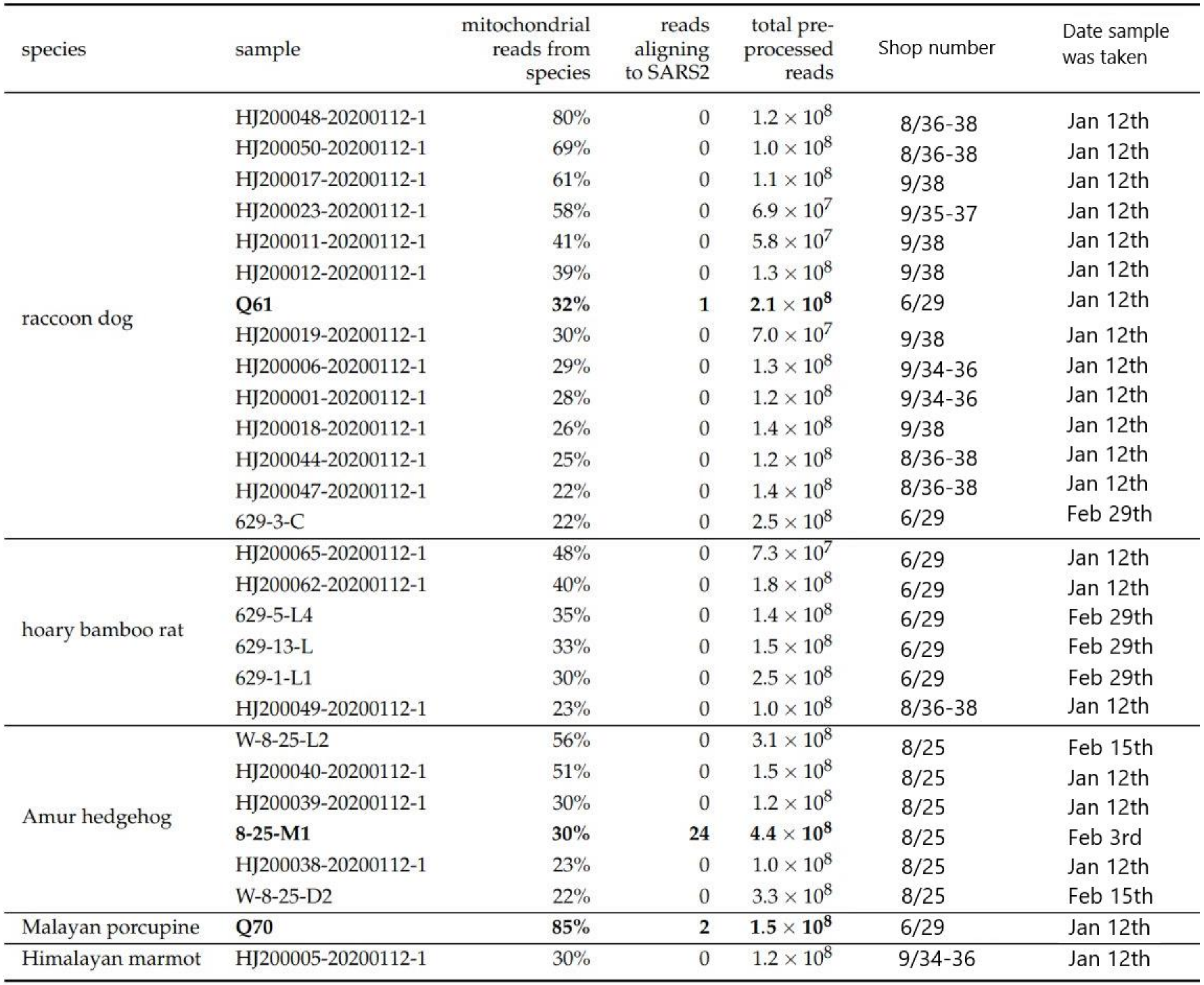


Table 1 Reads mapping to SARS-CoV-2 out of all high-quality (pre-processed) reads for samples with $\geq$20% of their chordate mitochondrial composition from a susceptible non-human species as defined in Crits-Christoph *et al.* (2023). Samples with non-zero SARS-CoV-2 reads are in bold.

species	sample	mitochondrial reads from species	reads aligning to SARS2	total pre-processed reads
raccoon dog	HJ200048-20200112-1	80%	0	1.2×10^8
	HJ200050-20200112-1	69%	0	1.0×10^8
	HJ200017-20200112-1	61%	0	1.1×10^8
	HJ200023-20200112-1	58%	0	6.9×10^7
	HJ200011-20200112-1	41%	0	5.8×10^7
	HJ200012-20200112-1	39%	0	1.3×10^8
	Q61	**32%**	**1**	$\mathbf{2.1 \times 10^8}$
	HJ200019-20200112-1	30%	0	7.0×10^7
	HJ200006-20200112-1	29%	0	1.3×10^8
	HJ200001-20200112-1	28%	0	1.2×10^8
	HJ200018-20200112-1	26%	0	1.4×10^8
	HJ200044-20200112-1	25%	0	1.2×10^8
	HJ200047-20200112-1	22%	0	1.4×10^8
	629-3-C	22%	0	2.5×10^8
hoary bamboo rat	HJ200065-20200112-1	48%	0	7.3×10^7
	HJ200062-20200112-1	40%	0	1.8×10^8
	629-5-L4	35%	0	1.4×10^8
	629-13-L	33%	0	1.5×10^8
	629-1-L1	30%	0	2.5×10^8
	HJ200049-20200112-1	23%	0	1.0×10^8
Amur hedgehog	W-8-25-L2	56%	0	3.1×10^8
	HJ200040-20200112-1	51%	0	1.5×10^8
	HJ200039-20200112-1	30%	0	1.2×10^8
	8-25-M1	**30%**	**24**	$\mathbf{4.4 \times 10^8}$
	HJ200038-20200112-1	23%	0	1.0×10^8
	W-8-25-D2	22%	0	3.3×10^8
Malayan porcupine	**Q70**	**85%**	**2**	$\mathbf{1.5 \times 10^8}$
Himalayan marmot	HJ200005-20200112-1	30%	0	1.2×10^8

But the negative samples were all from other shops, only 2 shops had positive samples on the wildlife sampling day:

Bloom table 1

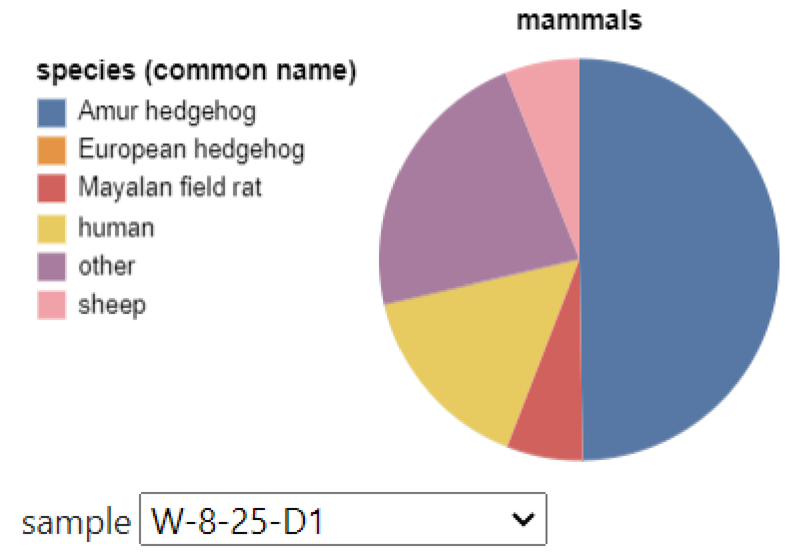


species	sample	mitochondrial reads from species	reads aligning to SARS2	total pre-processed reads	Shop number	Date sample was taken
raccoon dog	HJ200048-20200112-1	80%	0	1.2×10^8	8/36-38	Jan 12th
	HJ200050-20200112-1	69%	0	1.0×10^8	8/36-38	Jan 12th
	HJ200017-20200112-1	61%	0	1.1×10^8	9/38	Jan 12th
	HJ200023-20200112-1	58%	0	6.9×10^7	9/35-37	Jan 12th
	HJ200011-20200112-1	41%	0	5.8×10^7	9/38	Jan 12th
	HJ200012-20200112-1	39%	0	1.3×10^8	9/38	Jan 12th
	Q61	**32%**	**1**	$\mathbf{2.1 \times 10^8}$	6/29	Jan 12th
	HJ200019-20200112-1	30%	0	7.0×10^7	9/38	Jan 12th
	HJ200006-20200112-1	29%	0	1.3×10^8	9/34-36	Jan 12th
	HJ200001-20200112-1	28%	0	1.2×10^8	9/34-36	Jan 12th
	HJ200018-20200112-1	26%	0	1.4×10^8	9/38	Jan 12th
	HJ200044-20200112-1	25%	0	1.2×10^8	8/36-38	Jan 12th
	HJ200047-20200112-1	22%	0	1.4×10^8	8/36-38	Jan 12th
	629-3-C	22%	0	2.5×10^8	6/29	Feb 29th
hoary bamboo rat	HJ200065-20200112-1	48%	0	7.3×10^7	6/29	Jan 12th
	HJ200062-20200112-1	40%	0	1.8×10^8	6/29	Jan 12th
	629-5-L4	35%	0	1.4×10^8	6/29	Feb 29th
	629-13-L	33%	0	1.5×10^8	6/29	Feb 29th
	629-1-L1	30%	0	2.5×10^8	6/29	Feb 29th
	HJ200049-20200112-1	23%	0	1.0×10^8	8/36-38	Jan 12th
Amur hedgehog	W-8-25-L2	56%	0	3.1×10^8	8/25	Feb 15th
	HJ200040-20200112-1	51%	0	1.5×10^8	8/25	Jan 12th
	HJ200039-20200112-1	30%	0	1.2×10^8	8/25	Jan 12th
	8-25-M1	**30%**	**24**	$\mathbf{4.4 \times 10^8}$	8/25	Feb 3rd
	HJ200038-20200112-1	23%	0	1.0×10^8	8/25	Jan 12th
	W-8-25-D2	22%	0	3.3×10^8	8/25	Feb 15th
Malayan porcupine	**Q70**	**85%**	**2**	$\mathbf{1.5 \times 10^8}$	6/29	Jan 12th
Himalayan marmot	HJ200005-20200112-1	30%	0	1.2×10^8	9/34-36	Jan 12th

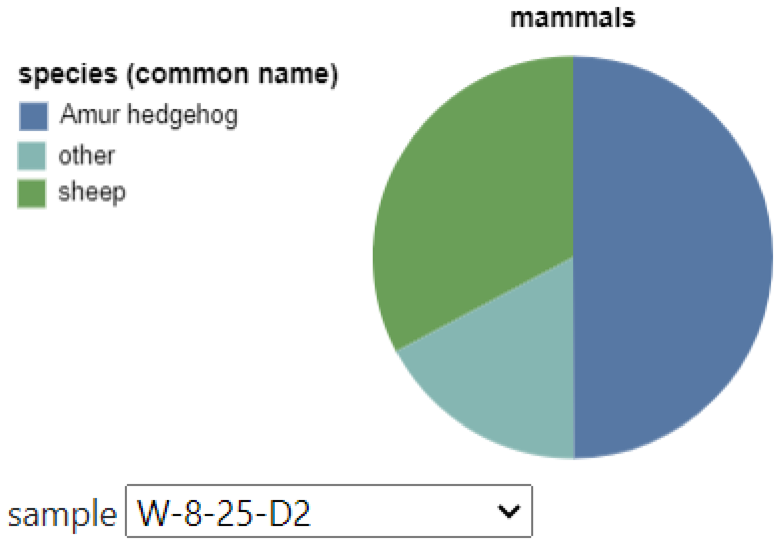
← except for one 6/29 sample taken much later

Also, Bloom left out 4 covid positive samples from 2/15/2020, all with 50%+ hedgehog DNA:

ground samples:

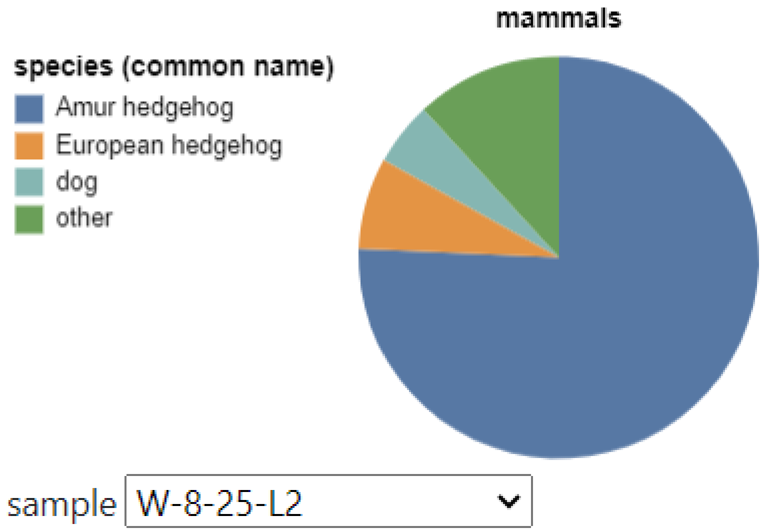


sample W-8-25-D1

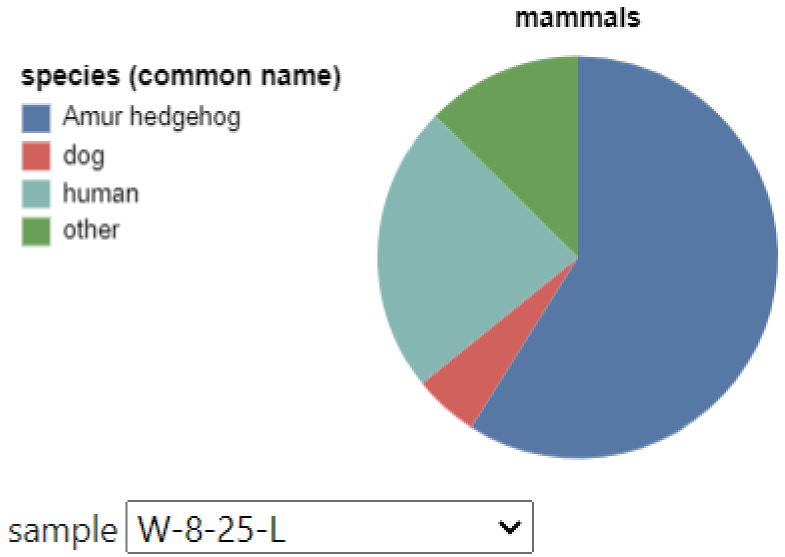


sample W-8-25-D2

Sampled from containers:

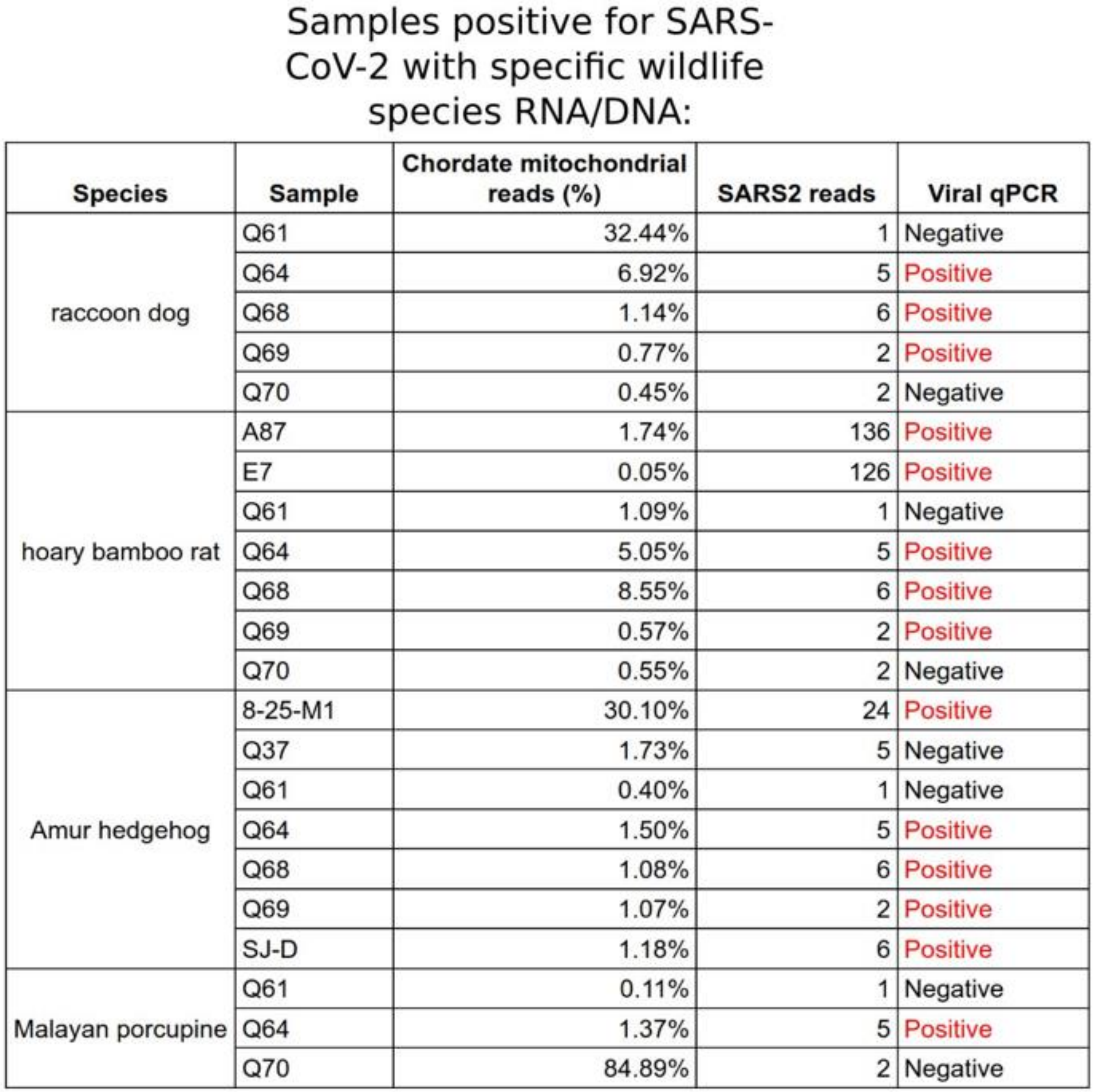


sample W-8-25-L2



sample W-8-25-L

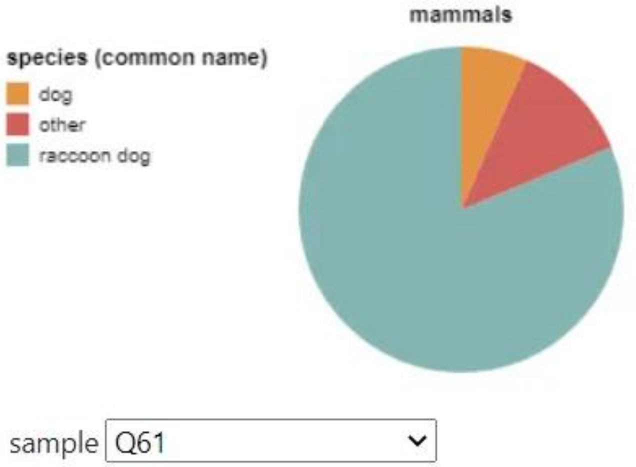
Also, there are many positive samples if you take out the 20% threshold:

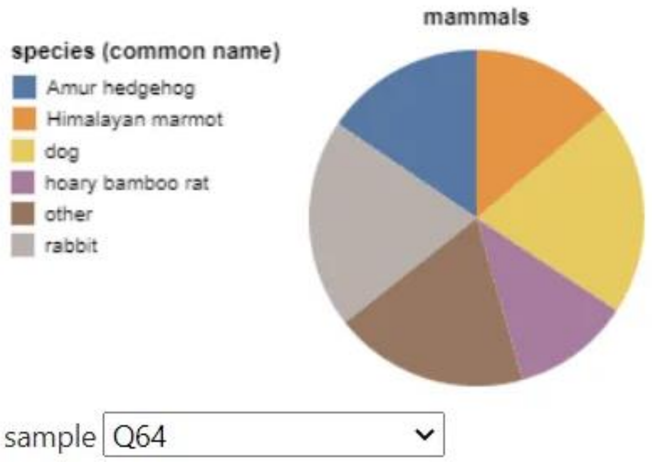


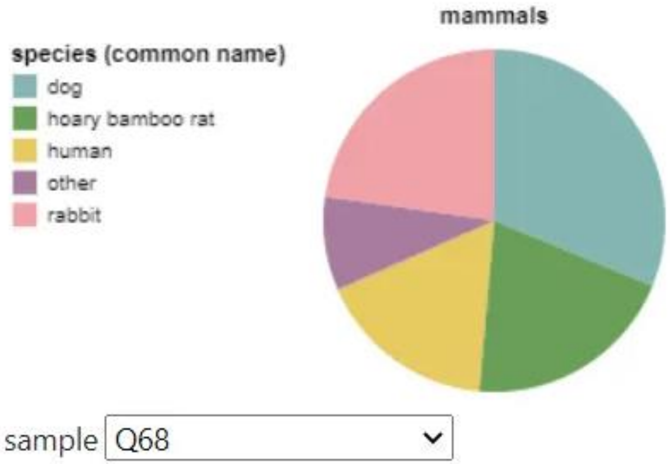
Samples positive for SARS-CoV-2 with specific wildlife species RNA/DNA:

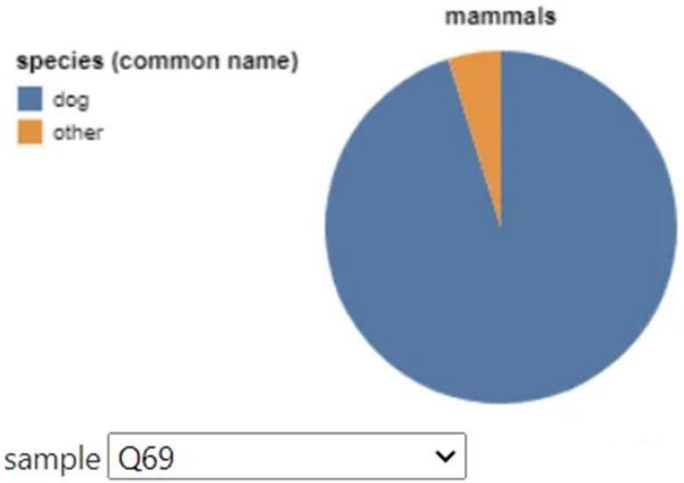
Species	**Sample**	**Chordate mitochondrial reads (%)**	**SARS2 reads**	**Viral qPCR**
raccoon dog	Q61	32.44%	1	Negative
	Q64	6.92%	5	Positive
	Q68	1.14%	6	Positive
	Q69	0.77%	2	Positive
	Q70	0.45%	2	Negative
hoary bamboo rat	A87	1.74%	136	Positive
	E7	0.05%	126	Positive
	Q61	1.09%	1	Negative
	Q64	5.05%	5	Positive
	Q68	8.55%	6	Positive
	Q69	0.57%	2	Positive
	Q70	0.55%	2	Negative
Amur hedgehog	8-25-M1	30.10%	24	Positive
	Q37	1.73%	5	Negative
	Q61	0.40%	1	Negative
	Q64	1.50%	5	Positive
	Q68	1.08%	6	Positive
	Q69	1.07%	2	Positive
	SJ-D	1.18%	6	Positive
Malayan porcupine	Q61	0.11%	1	Negative
	Q64	1.37%	5	Positive
	Q70	84.89%	2	Negative

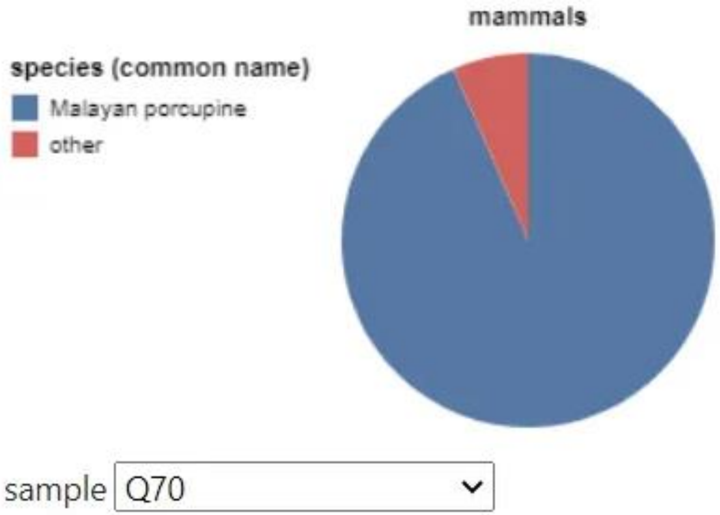
Also, the 6-29 shop sold a lot of different animals, so it's hard to hit 20% on any of them,
Also, Bloom included bird and fish DNA into the count, to make it harder to hit 20%.



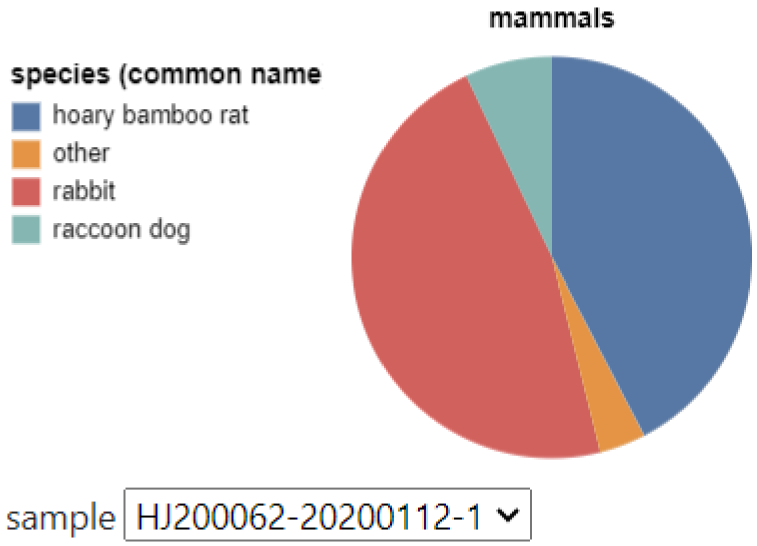




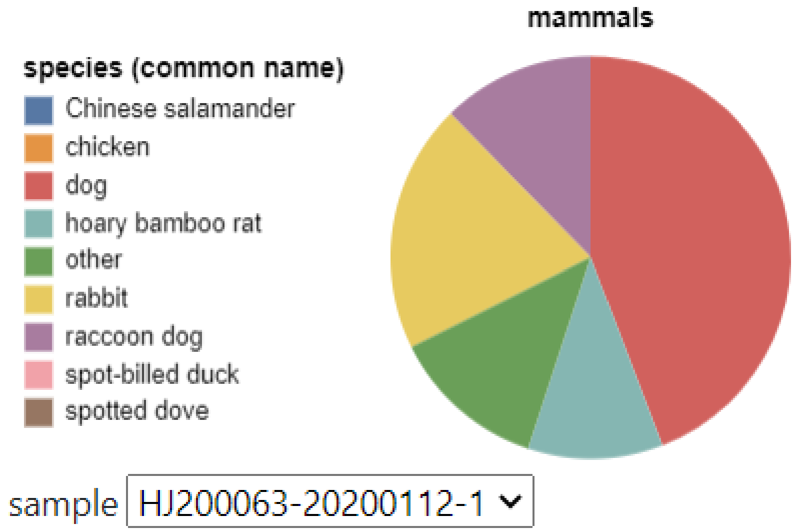




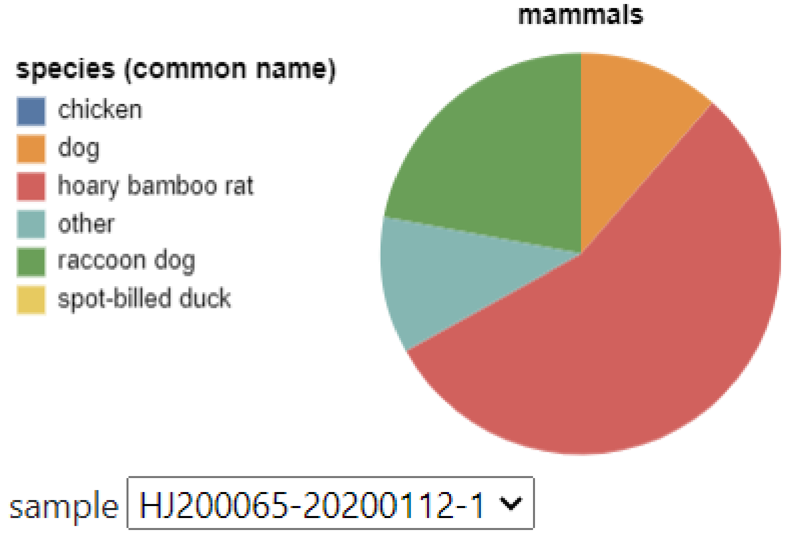
Shop 6-29 also had 5 negative samples, not every wildlife sample is positive:



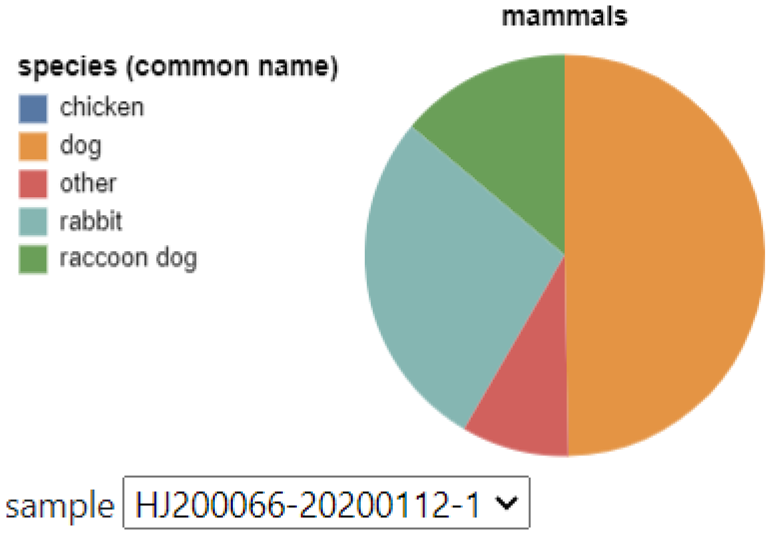
sample HJ200062-20200112-1



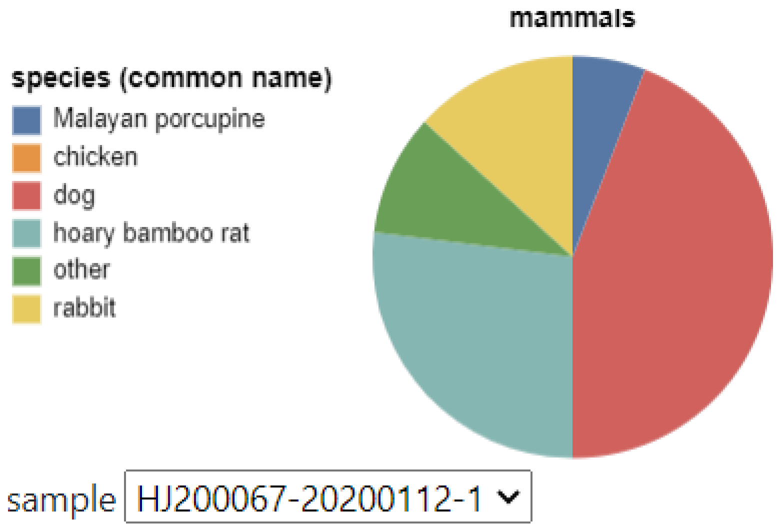
sample HJ200063-20200112-1



sample HJ200065-20200112-1

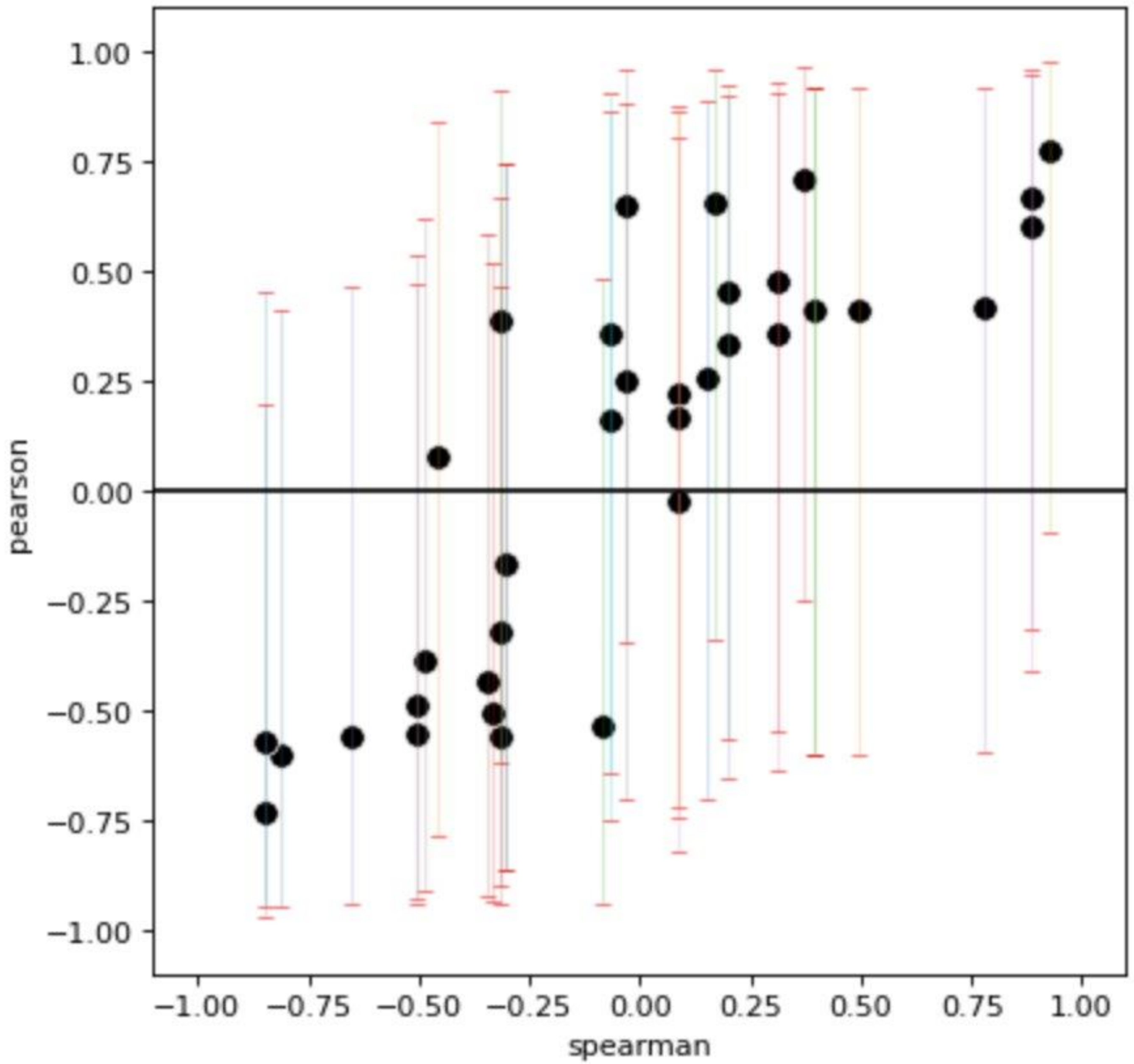


sample HJ200066-20200112-1



sample HJ200067-20200112-1

Also, here's one of Bloom's correlation with 95% error bars:



Bloom also argued that zero equals one, in his paper

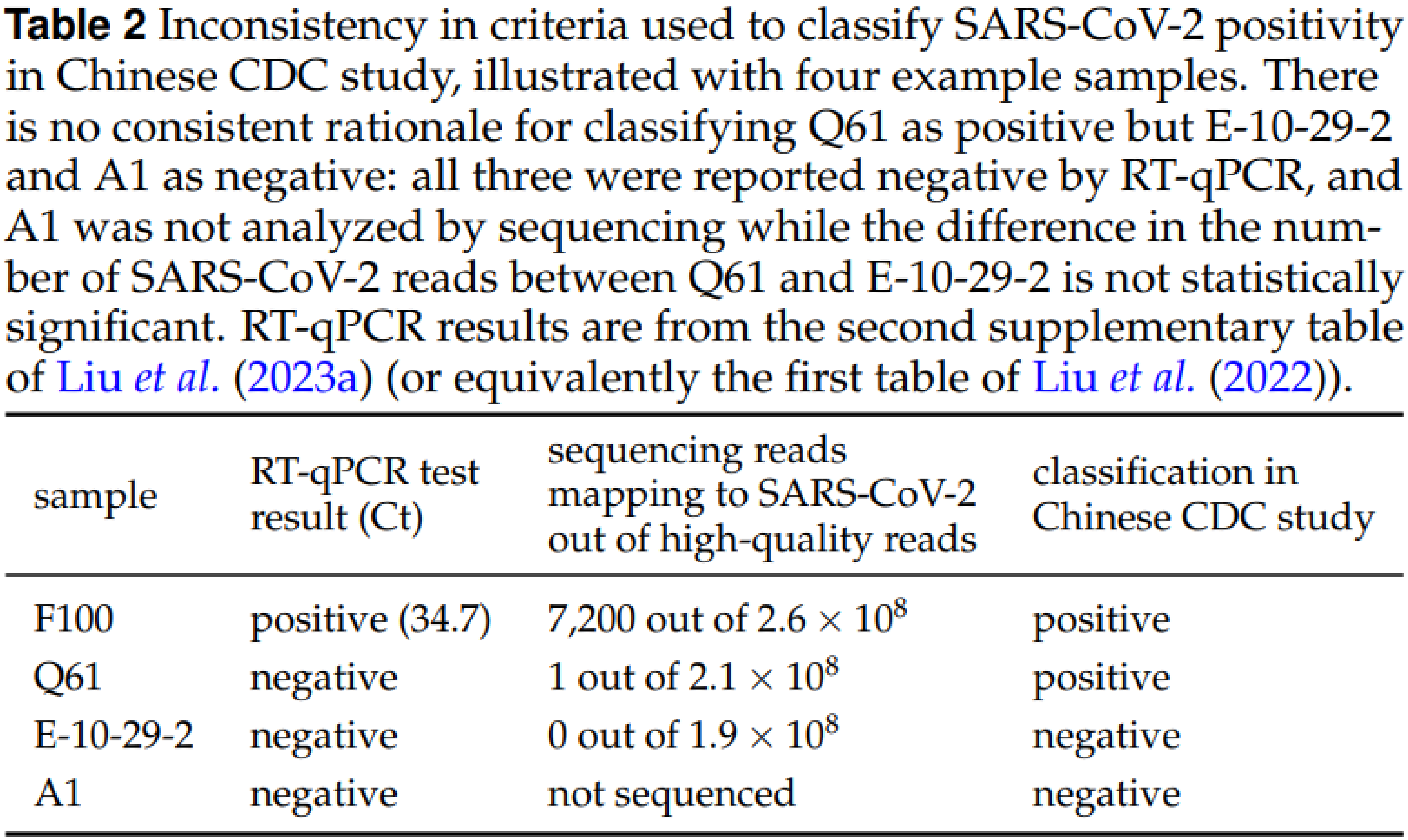


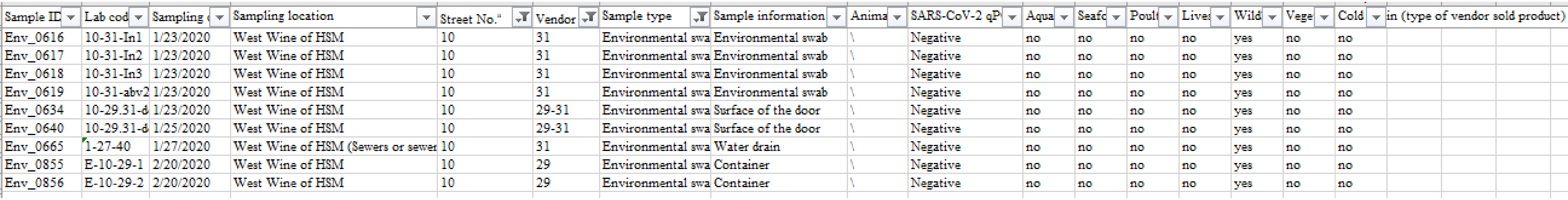
Table 2 Inconsistency in criteria used to classify SARS-CoV-2 positivity in Chinese CDC study, illustrated with four example samples. There is no consistent rationale for classifying Q61 as positive but E-10-29-2 and A1 as negative: all three were reported negative by RT-qPCR, and A1 was not analyzed by sequencing while the difference in the number of SARS-CoV-2 reads between Q61 and E-10-29-2 is not statistically significant. RT-qPCR results are from the second supplementary table of Liu *et al.* (2023a) (or equivalently the first table of Liu *et al.* (2022)).

sample	RT-qPCR test result (Ct)	sequencing reads mapping to SARS-CoV-2 out of high-quality reads	classification in Chinese CDC study
F100	positive (34.7)	7,200 out of 2.6×10^8	positive
Q61	negative	1 out of 2.1×10^8	positive
E-10-29-2	negative	0 out of 1.9×10^8	negative
A1	negative	not sequenced	negative

I have no idea why Bloom even picked that particular sample for his example of 0 reads:

It looks like that’s shop 10/29, or maybe it’s a combined shop 10/29-31

it was tested 9 times in January and February and never tested positive once:



Sample ID	Lab cod	Sampling (	Sampling location	Street No.ª	Vendor	Sample type	Sample information	Anima	SARS-CoV-2 qP	Aqua	Seafc	Poult	Lives	Wild	Vege	Cold	in (type of vendor sold product)
Env_0616	10-31-In1	1/23/2020	West Wine of HSM	10	31	Environmental swa	Environmental swab	\	Negative	no	no	no	no	yes	no	no	
Env_0617	10-31-In2	1/23/2020	West Wine of HSM	10	31	Environmental swa	Environmental swab	\	Negative	no	no	no	no	yes	no	no	
Env_0618	10-31-In3	1/23/2020	West Wine of HSM	10	31	Environmental swa	Environmental swab	\	Negative	no	no	no	no	yes	no	no	
Env_0619	10-31-abv2	1/23/2020	West Wine of HSM	10	31	Environmental swa	Environmental swab	\	Negative	no	no	no	no	yes	no	no	
Env_0634	10-29.31-d	1/23/2020	West Wine of HSM	10	29-31	Environmental swa	Surface of the door	\	Negative	no	no	no	no	yes	no	no	
Env_0640	10-29.31-d	1/25/2020	West Wine of HSM	10	29-31	Environmental swa	Surface of the door	\	Negative	no	no	no	no	yes	no	no	
Env_0665	1-27-40	1/27/2020	West Wine of HSM (Sewers or sewer	10	31	Environmental swa	Water drain	\	Negative	no	no	no	no	yes	no	no	
Env_0855	E-10-29-1	2/20/2020	West Wine of HSM	10	29	Environmental swa	Container	\	Negative	no	no	no	no	yes	no	no	
Env_0856	E-10-29-2	2/20/2020	West Wine of HSM	10	29	Environmental swa	Container	\	Negative	no	no	no	no	yes	no	no	

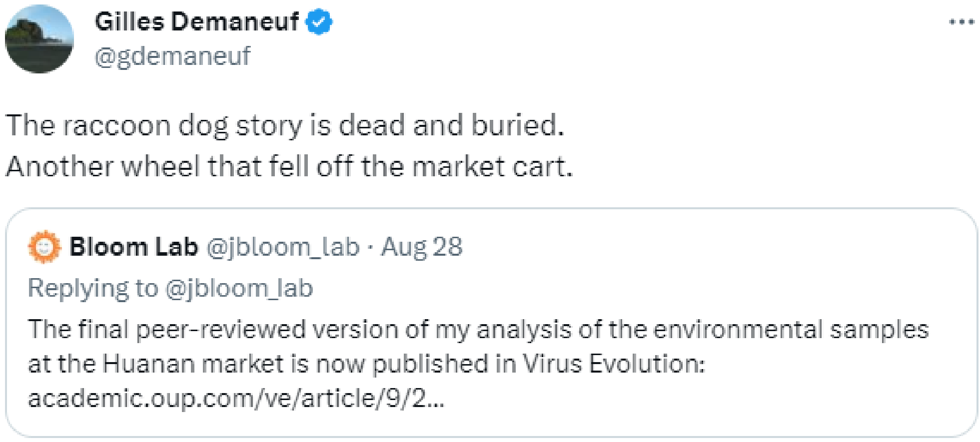
And the specific sample Bloom is pointing out is from February 20th, so… that’s especially not likely to be positive.

The Q61 raccoon dog sample has one read, but it’s also in a shop where 5 of 10 samples tested positive and the drains tested positive (twice). It is reasonable to believe that animals in the shop were shedding virus.

Should we expect every raccoon dog in the market to be infected, if they are infected in one shop?

Maybe not -- people move around, socialize, play mahjong, infect each other. Animals do not.

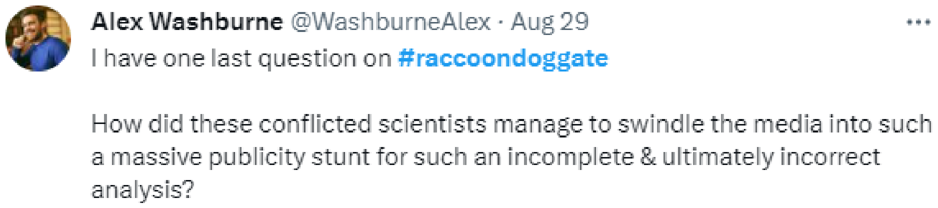
Nevertheless, Lab leak twitter declared the raccoon dog theory dead (and Richard Ebright sure likes to repeat himself)



Gilles Demaneuf
@gdemaneuf

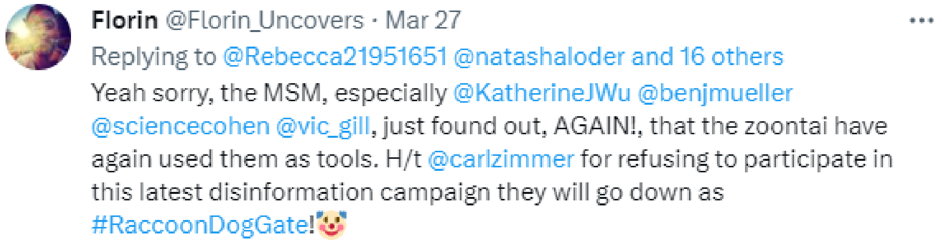
The raccoon dog story is dead and buried.
Another wheel that fell off the market cart.

Bloom Lab @jbloom_lab · Aug 28
Replying to @jbloom_lab
The final peer-reviewed version of my analysis of the environmental samples at the Huanan market is now published in Virus Evolution: academic.oup.com/ve/article/9/2...



Alex Washburne @WashburneAlex · Aug 29
I have one last question on #raccoondoggate

How did these conflicted scientists manage to swindle the media into such a massive publicity stunt for such an incomplete & ultimately incorrect analysis?



Florin @Florin_Uncovers · Mar 27
Replying to @Rebecca21951651 @natashaloder and 16 others
Yeah sorry, the MSM, especially @KatherineJWu @benjmueller @sciencecohen @vic_gill, just found out, AGAIN!, that the zoontai have again used them as tools. H/t @carlzimmer for refusing to participate in this latest disinformation campaign they will go down as #RaccoonDogGate!🤡

Richard H. Ebright @R_H_Ebright · Jun 1
Replying to @KatherineEban and @VanityFair
Only an ignoramus or a fraud would characterize one sequence **read** (of two hundred million sequence reads) in one sample (of 1,380 samples) as "strong," "consequential," or even "significant" evidence for a market origin.
4 · 7 · 70 · 1,968

Richard H. Ebright @R_H_Ebright · Jun 1
Replying to @gdemaneuf and @KatherineEban
Only an ignoramus or a fraud would characterize one sequence **read** (of two hundred million sequence reads) in one sample (of 1,380 samples) as "highly significant," or even "significant," evidence for a market origin.
3 · 7 · 59 · 5,491

Richard H. Ebright @R_H_Ebright · May 30
Replying to @simon_schama and @mattwridley
Only an ignoramus or a fraud would characterize one sequence **read** (of two hundred million sequence reads) in one sample (of 1,380 samples) as "highly significant," or even "significant," evidence for a market origin.
7 · 341

Richard H. Ebright @R_H_Ebright · May 30
Replying to @Muller_Lab and @humblesci
Only an ignoramus or a fraud would characterize one sequence **read** (of two hundred million sequence reads) in one sample (of 1,380 samples) as "consequential" or "strong" evidence for a market origin.
3 · 3 · 31 · 1,654

Richard H. Ebright @R_H_Ebright · May 28
Replying to @Ayjchan @mbalter and 2 others
Only an ignoramus or a fraud would characterize one sequence **read** (of two hundred million sequence reads) in one sample (of 1,380 samples) as "consequential" or "strong" evidence for a market origin.
3 · 2 · 36 · 1,227

Richard H. Ebright @R_H_Ebright · Aug 29
Replying to @zeynep and @mattwridley
Only an **ignoramus** or a fraud would characterize one sequence read (of two hundred million sequence reads) in one sample as evidence for a market origin.
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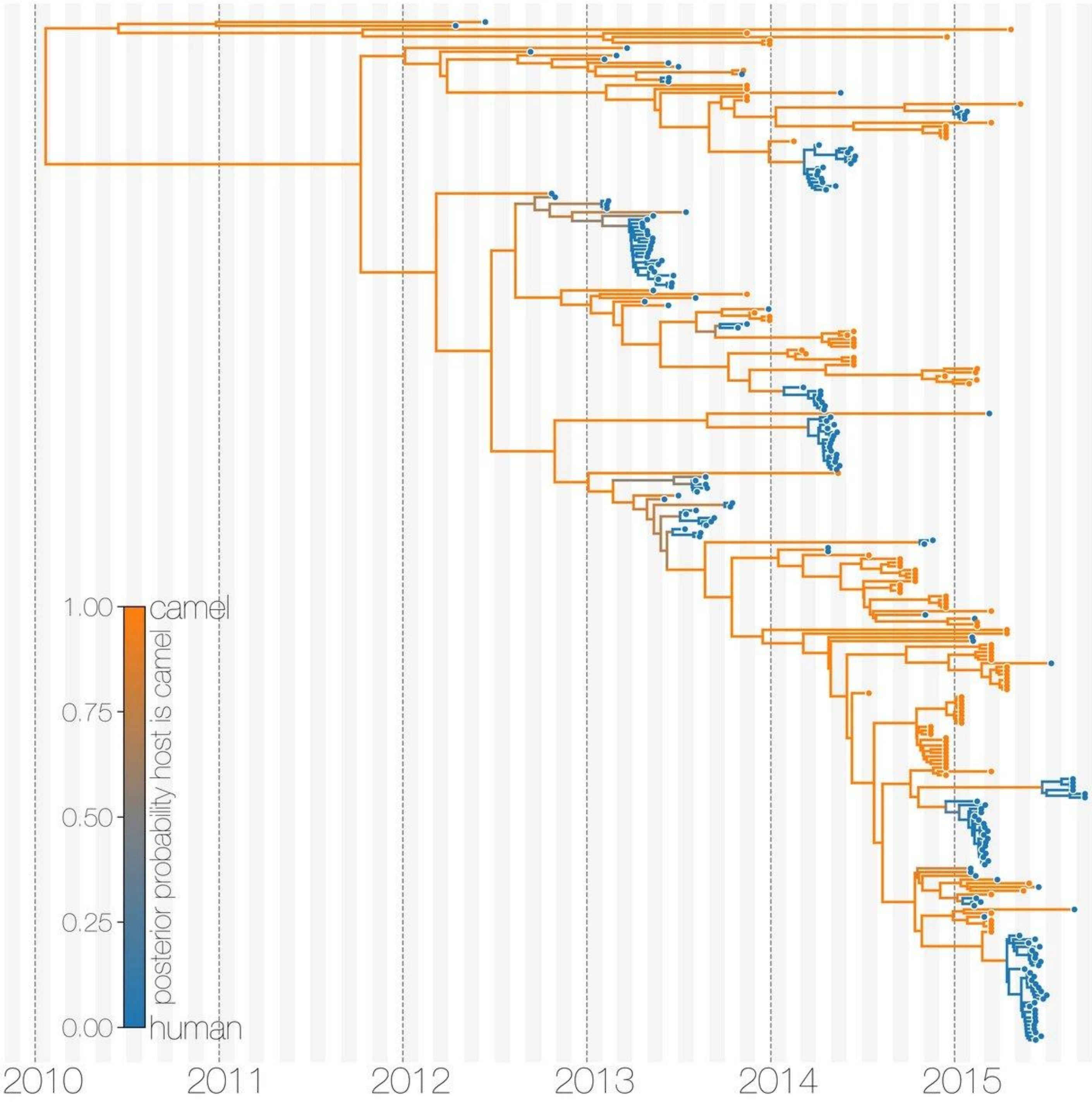
Two spillovers at the market

Multiple spillovers are normal.

SARS had > 10 spillovers.

MERS had multiple spillovers.



When covid infected mink farms, it spilled over back into humans, multiple times.

Covid infected hamsters also reinfected humans, multiple times.

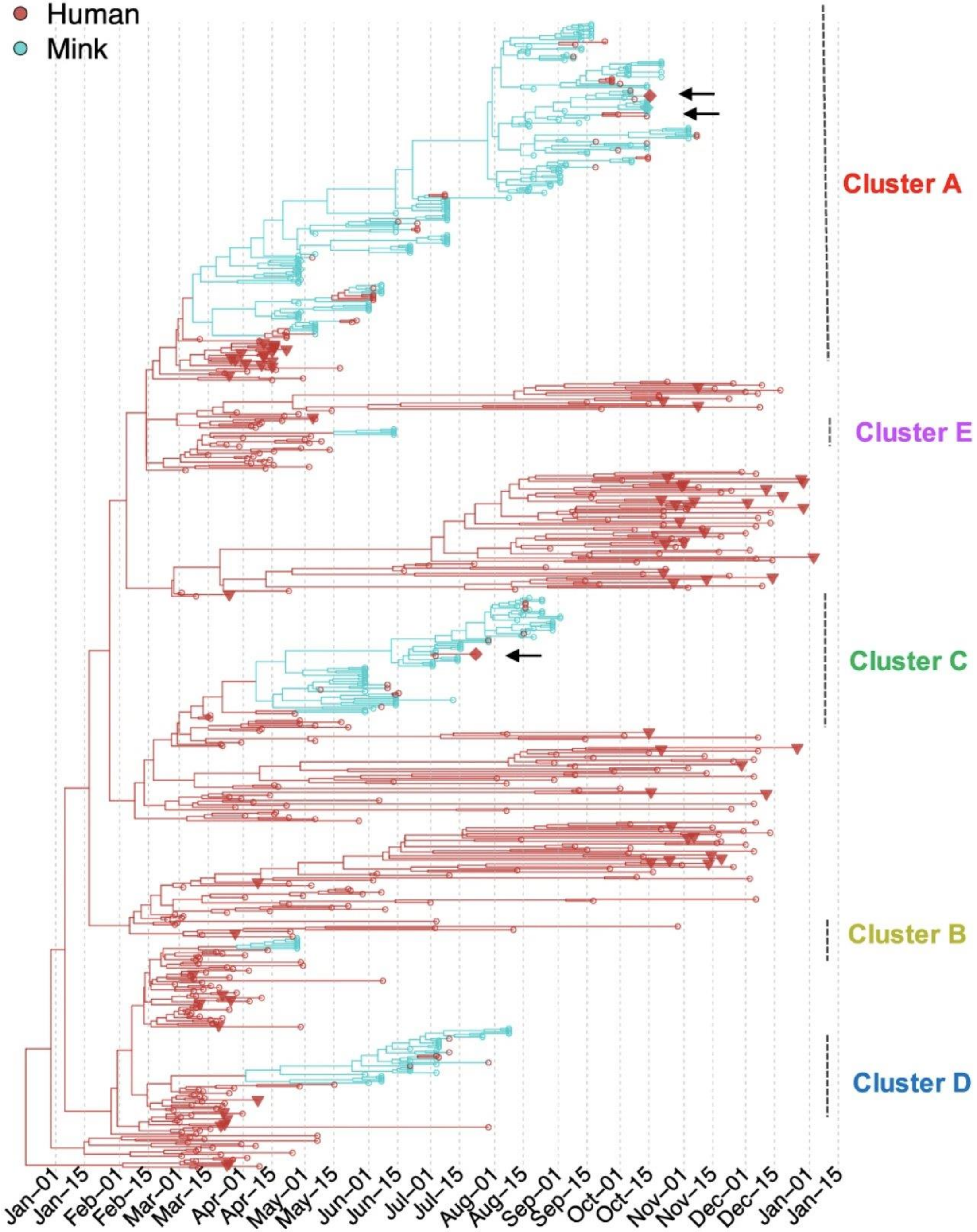
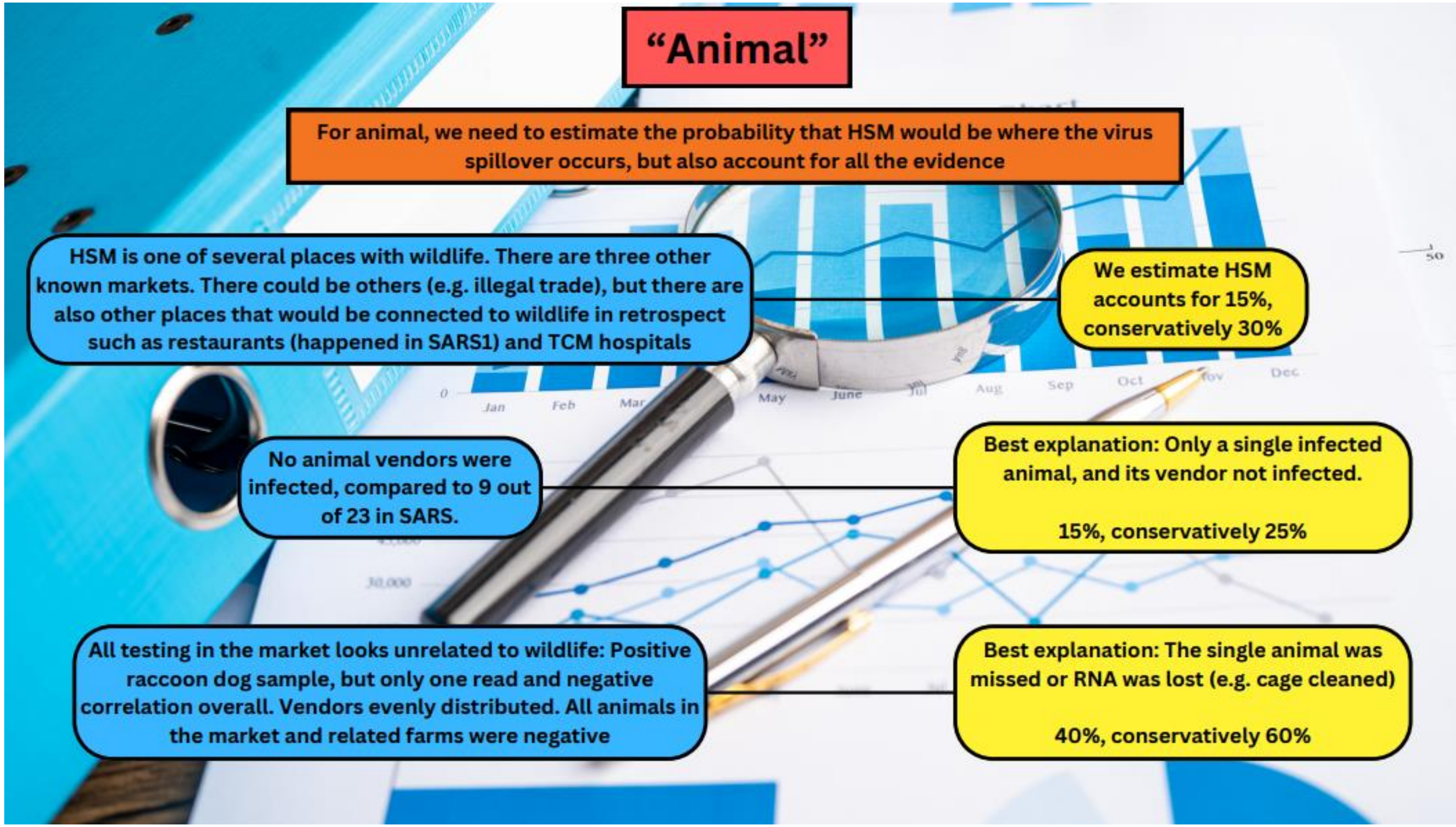


Figure from Lu et al, 2021

Probabilities



“Animal”

For animal, we need to estimate the probability that HSM would be where the virus spillover occurs, but also account for all the evidence

HSM is one of several places with wildlife. There are three other known markets. There could be others (e.g. illegal trade), but there are also other places that would be connected to wildlife in retrospect such as restaurants (happened in SARS1) and TCM hospitals

We estimate HSM accounts for 15%, conservatively 30%

← 7 of 17 shops in xiao xiao study = 41%. Conservatively higher, because we don’t know the species mix in each.

No animal vendors were infected, compared to 9 out of 23 in SARS.

Best explanation: Only a single infected animal, and its vendor not infected.

15%, conservatively 25%

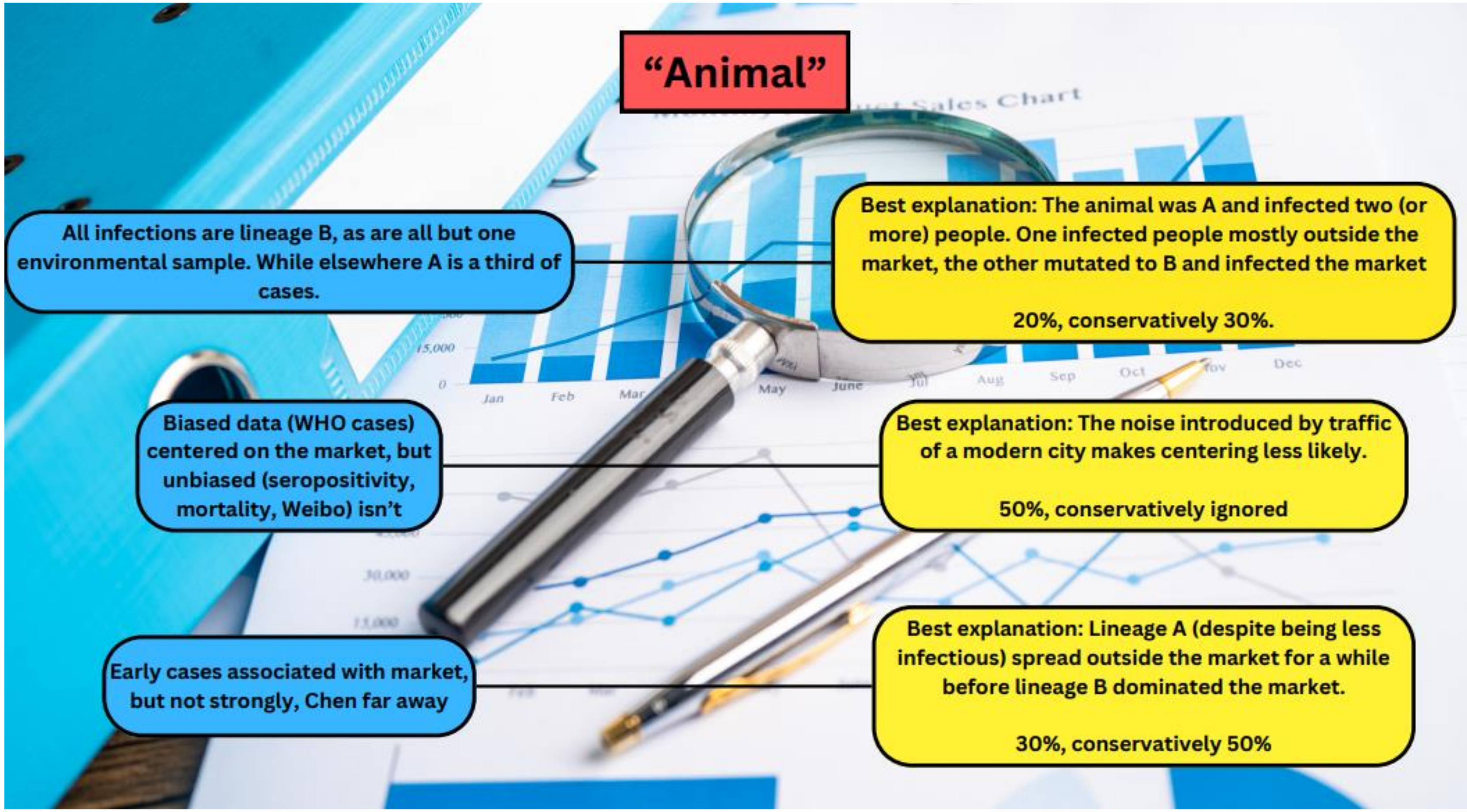
← It’s actually 1 of 7 for earliest SARS cases and SARS2 is harder to contact trace. Conservatively near 100%

All testing in the market looks unrelated to wildlife: Positive raccoon dog sample, but only one read and negative correlation overall. Vendors evenly distributed. All animals in the market and related farms were negative

Best explanation: The single animal was missed or RNA was lost (e.g. cage cleaned)

40%, conservatively 60%

← Conservatively ignored, because zero live animals were tested from shops, and very few relevant dead animals were tested.



"Animal"

All infections are lineage B, as are all but one environmental sample. While elsewhere A is a third of cases.

Best explanation: The animal was A and infected two (or more) people. One infected people mostly outside the market, the other mutated to B and infected the market

20%, conservatively 30%.

Biased data (WHO cases) centered on the market, but unbiased (seropositivity, mortality, Weibo) isn't

Best explanation: The noise introduced by traffic of a modern city makes centering less likely.

50%, conservatively ignored

Early cases associated with market, but not strongly, Chen far away

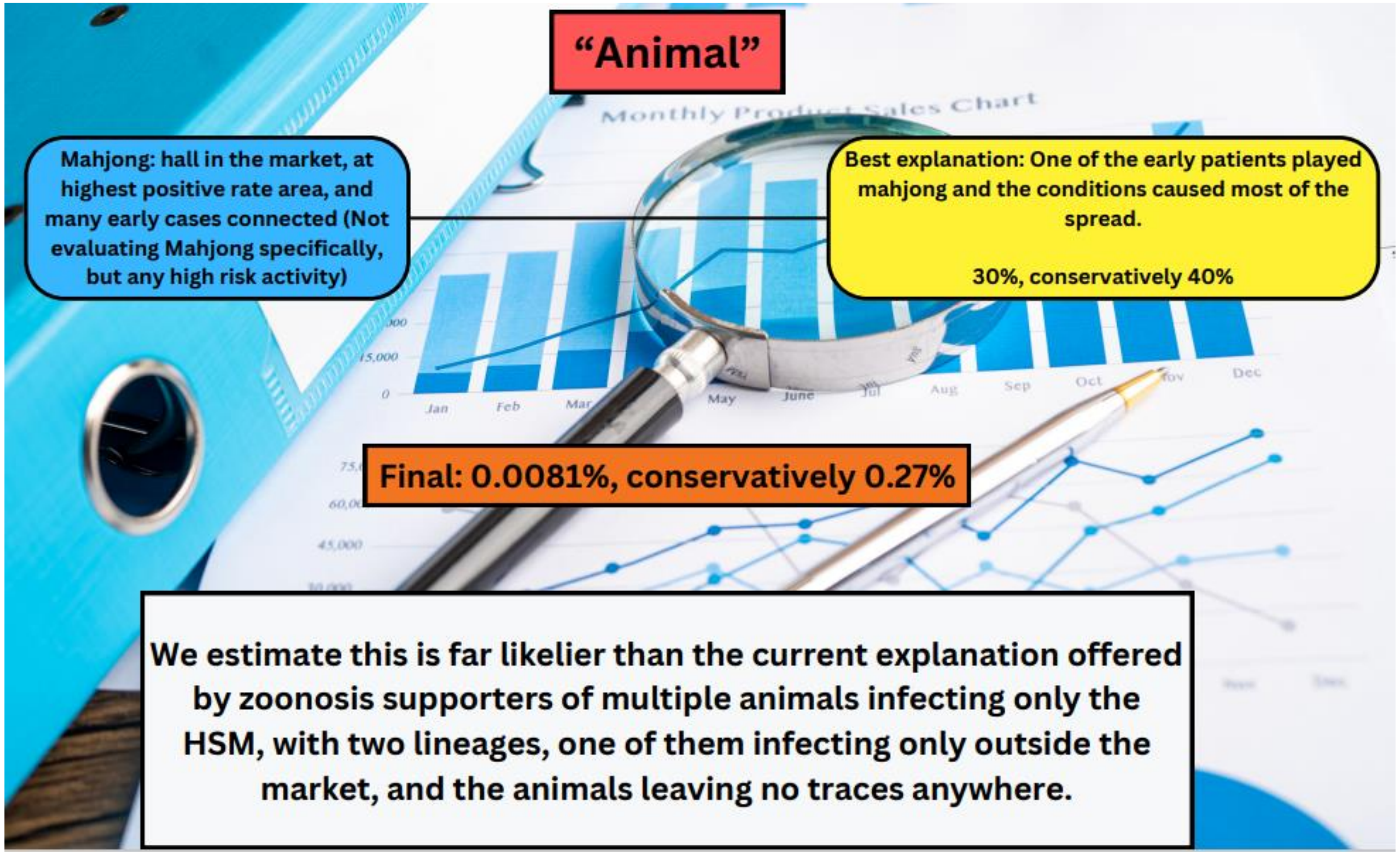
Best explanation: Lineage A (despite being less infectious) spread outside the market for a while before lineage B dominated the market.

30%, conservatively 50%

← Best explanation is two animals caused two spillovers and that explains all the data perfectly. Conservatively ignored.

← Every excuse of bias Rootclaim has given has fallen apart. Conservatively ignored.

← First 5 cases at the market and >50% at multiple hospitals. That's strong association with the market. People can travel across town in less than 5 days. The virus had also been spreading a little before Wei Guixian. There's nothing magical here. Best explanation is that Chen caught it on the subway. Conservatively ignored.



“Animal”

Mahjong: hall in the market, at highest positive rate area, and many early cases connected (Not evaluating Mahjong specifically, but any high risk activity)

Best explanation: One of the early patients played mahjong and the conditions caused most of the spread.

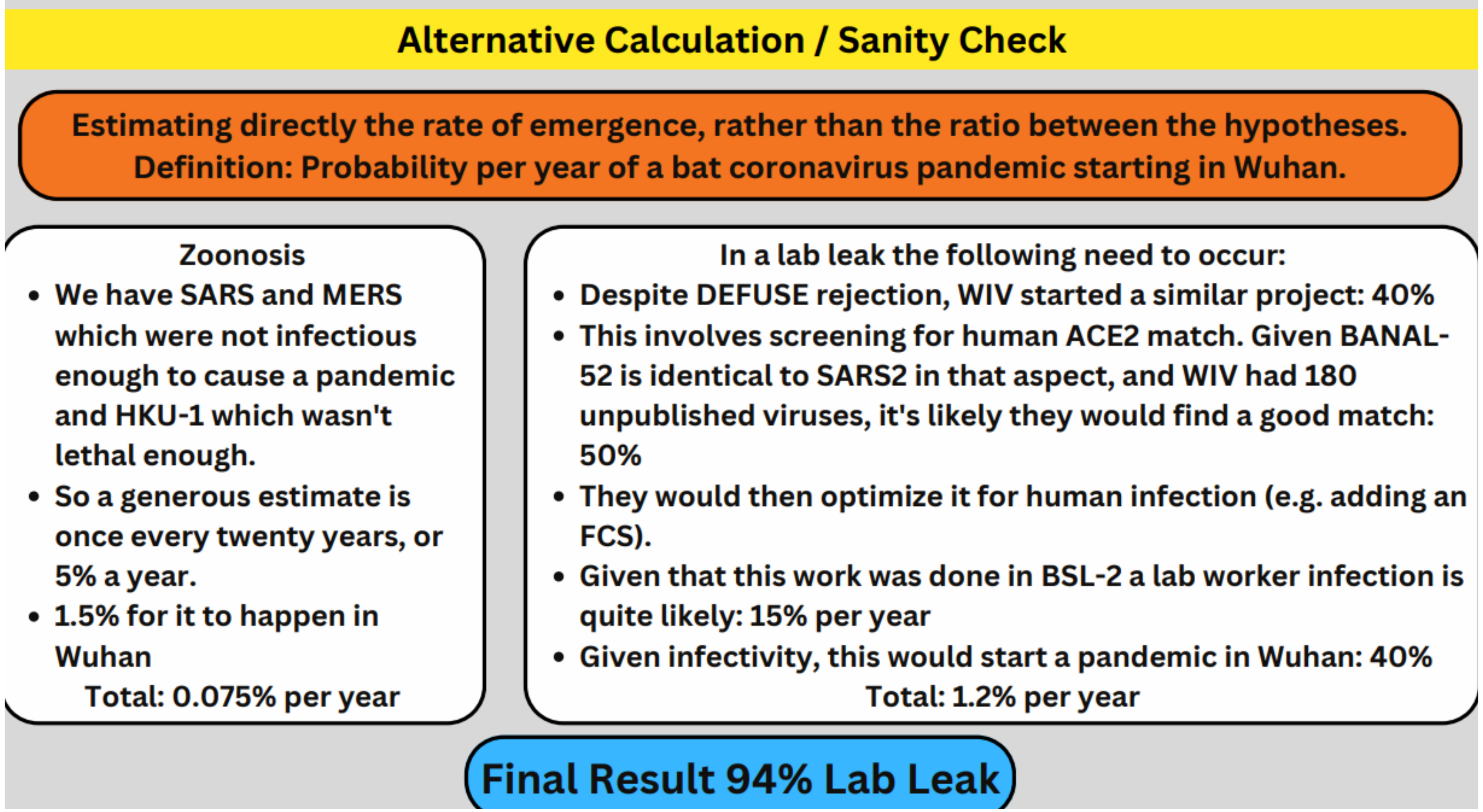
30%, conservatively 40%

Final: 0.0081%, conservatively 0.27%

We estimate this is far likelier than the current explanation offered by zoonosis supporters of multiple animals infecting only the HSM, with two lineages, one of them infecting only outside the market, and the animals leaving no traces anywhere.

← Mahjong board tested negative. Definitely not the highest positivity rate in the market. Covid can spread between people with or without a Mahjong game. For instance, I’ve had covid and I’ve never played Mahjong in my life.

Conservatively ignored.



Alternative Calculation / Sanity Check

Estimating directly the rate of emergence, rather than the ratio between the hypotheses.
Definition: Probability per year of a bat coronavirus pandemic starting in Wuhan.

Zoonosis

- We have SARS and MERS which were not infectious enough to cause a pandemic and HKU-1 which wasn't lethal enough.
- So a generous estimate is once every twenty years, or 5% a year.
- 1.5% for it to happen in Wuhan

Total: 0.075% per year

In a lab leak the following need to occur:

- Despite DEFUSE rejection, WIV started a similar project: 40%
- This involves screening for human ACE2 match. Given BANAL-52 is identical to SARS2 in that aspect, and WIV had 180 unpublished viruses, it's likely they would find a good match: 50%
- They would then optimize it for human infection (e.g. adding an FCS).
- Given that this work was done in BSL-2 a lab worker infection is quite likely: 15% per year
- Given infectivity, this would start a pandemic in Wuhan: 40%

Total: 1.2% per year

Final Result 94% Lab Leak

The calculation on the left isn’t bad, though it misses 2 human coronaviruses since SARS2 and also the odds of Wuhan may be higher than 1.5%.

The calculation on the right is much too high for multiple reasons:
Lab leak rate is too high. (1 in 500 is closer to the average, maybe you can mark that up a bit if you think the WIV is unsafe)
The odds are much lower that they had a secret starting virus.
DEFUSE, as written, couldn’t make SARS2. Even Yuri Deigin agrees with this.
This ignores the odds of: abnormal backbone, abnormal FCS(proline, alanine, out of frame), it’s hard to culture the virus, etc. But we’ll need to have debate #2 to explain why