

Hi everyone

I have provided a compiled article below that would provide information to win the rootclaim challenge.

Please get this to @ban\_epp\_gofroc and @billybostickson ASAP.

Thank you very much.

<https://twitter.com/3ghtweets/status/1717756867458609403>

It does seem that the viral sequence with the patented CTCCTCGGCGGGCACGTAG sequence is needed to generate a proper immune response.

<https://twitter.com/daoyu15/status/1700242832701964387>

In fact first infection after mRNA vaccination lead to less immune response than with no mRNA vaccination—to the point that 1: there is no prevention of future infections at all. 2: mRNA vaccination increases the chances of being infected multiple times.

No CGG-CGG, no immunogenicity. <https://archive.md/aMlw7>

The current mRNA vaccines are of negative efficacy and are actively dangerous. And the cause? The entire CTCCTCGGCGGGCACGTAG provide both high efficacy as a vaccine strain (when inactivated or further cold adapted) and the Proline provide efficient growth in vaccine-relevant and stock-relevant cell lines.

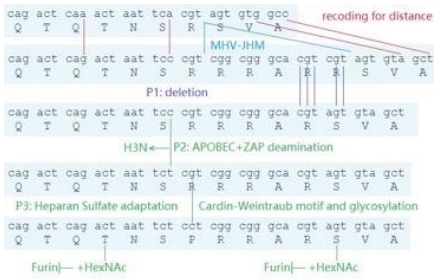
<https://archive.md/l3GpT>

<https://twitter.com/daoyu15/status/1724024956483490133>

Vaccination now also happened to correlate with more total hospitalization and ICU events (Covid+non-Covid) now. The only “same share per pop” is total deaths.

(Which the fraction in total events is the same as the fraction of 0+1 dose population). The hospitalization and ICU counts on the other hand now sat in a flat 0 in these populations.

The choice for CTC(G)CTCGGCGGGCACGTAG is driven by finding the tblastn sequence in the PAT database for synthetic sequences. Ended up with the moderna vaccine patent.

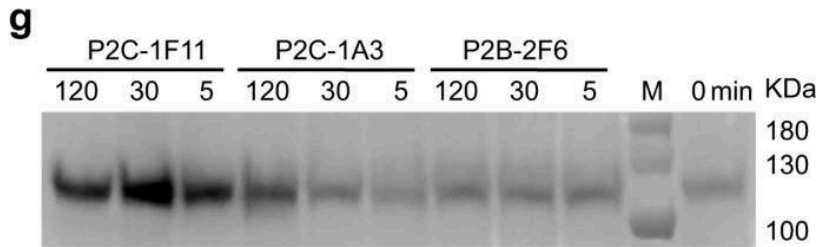
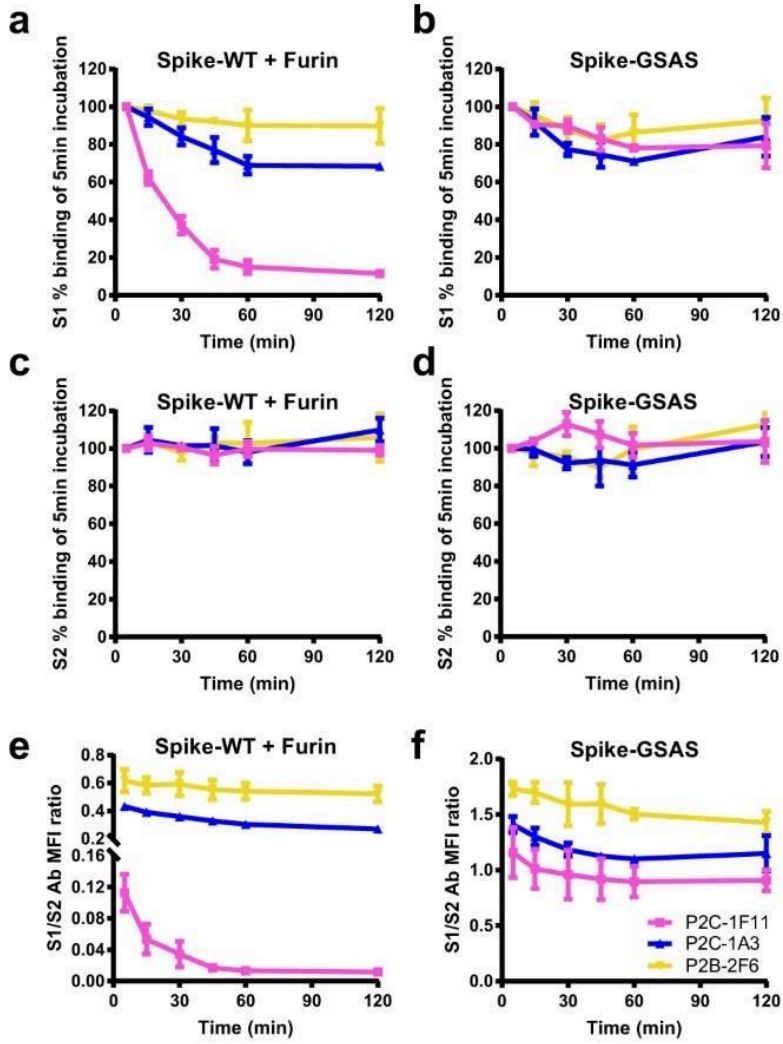


	CONSERVED REGION										VARIABLE REGION																		
SARS-CoV-2	G	A	G	I	C	A	S	Y	Q	T	Q	T	N	S	P	R	R	A	R	S	V	A	-	S	Q	S	I	I	
RaTG13	G	A	G	I	C	A	S	Y	Q	T	Q	T	N	S	-	-	-	-	R	S	V	A	-	S	Q	S	I	I	
RShSTT182/200 (Cambodia) (identical here)	G	A	G	I	C	A	S	Y	Q	T	Q	T	N	S	-	-	-	-	R	S	V	T	-	S	Q	S	I	I	
Pangolin/GD/2019	G	A	G	I	C	A	S	Y	Q	T	Q	T	N	S	-	-	-	-	R	S	V	S	-	S	Q	A	I	I	
RmYN02 Zhou et al.	G	A	G	V	C	A	S	Y	-	-	-	-	-	N	S	P	-	A	A	R	-	V	G	-	T	N	S	I	I
RmYN02 Clustal W	G	A	G	V	C	A	S	Y	N	S	(	P	)	A	-	-	-	-	A	R	V	G	-	T	N	S	I	I	
RmYN02 YD&RS ver. 1	G	A	G	V	C	A	S	Y	(	N	S	)	P	A	A	-	-	-	-	R	-	V	G	-	T	N	S	I	I
RmYN02 YD&RS ver. 2	G	A	G	V	C	A	S	Y	-	N	S	P	A	A	-	-	-	-	R	-	V	G	-	T	N	S	I	I	
RacCS203 (Thailand)	G	A	G	V	C	A	S	Y	-	N	S	P	V	A	-	-	-	-	R	-	V	G	-	T	N	S	I	I	
RacCS264 (Thailand)	G	A	G	V	C	A	S	Y	-	N	S	P	V	?	-	-	-	-	?	-	?	?	-	?	Q	S	I	I	
RacCS271 (Thailand)	? ? ?	V	C	A	S	Y	-	N	S	P	V	A	-	-	-	-	-	R	-	V	G	-	T	N	S	I	I		
PrC31 (Yunnan)	G	A	G	I	C	A	S	Y	H	T	A	P	I	L	-	-	-	-	R	S	T	S	-	Q	K	A	I	V	
Rc-o319 (Japan)	G	A	G	I	C	A	T	Y	H	T	P	S	M	L	-	-	-	-	R	S	A	N	N	K	R	I	V		
Pangolin/GX/2017	G	A	G	I	C	A	S	Y	H	S	M	S	S	F	-	-	-	-	R	S	V	N	-	Q	R	S	I	I	
Rs3367 & RsSHC014 (identical here)	G	A	G	I	C	A	S	Y	H	T	V	S	S	L	-	-	-	-	R	S	T	S	-	Q	K	S	I	V	
ZC45	G	A	G	I	C	A	S	Y	H	T	A	S	I	L	-	-	-	-	R	S	T	S	-	Q	K	A	I	V	
ZXC21	G	A	G	I	C	A	S	Y	H	T	A	S	I	L	-	-	-	-	R	S	T	G	-	Q	K	A	I	V	
RmYN01	G	A	G	I	C	A	S	Y	H	T	A	S	L	L	-	-	-	-	R	N	T	G	-	Q	K	S	I	V	
LYRa11	G	A	G	I	C	A	S	Y	H	T	A	S	L	L	-	-	-	-	R	N	T	D	-	Q	K	S	I	V	
Rf4092	G	A	G	I	C	A	S	Y	H	T	A	S	T	L	-	-	-	-	R	G	V	G	-	Q	K	S	I	V	

Black = common for all  
 Purple = unique to SARS-CoV-2  
 Green = differences mostly found in strains shaded in pink (RmYN02 or RacCSxxx)  
 Blue = differences mostly found in strains shaded in purple (ZC45, Rs3367, LYRa11, etc.)  
 Yellow = differences mostly found in Pangolin/GX/2017  
 Red = other differences

53 Frame 3

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atgtc tga taa tgg acc cca aaa tea geg aaa tgc acc ccg cat tac gtt tgg tgg acc ctc
V - - W T P K S A K C T P H Y V W W T L
aga ttc aac tgg cag taa cca gaa tgg aga acg cag tgg ggc gcg atc aaa aca acg tgc
R F N W Q - P E W R T Q W G A I K T T S
gcc cca agg ttt acc caa taa tac tgc gtc ttg gtt cac cgc tct cac tca aca tgg caa
A P R F T Q - Y C V L V H R S H S T W Q
gga aga cct taa att ccc tgc agg aca agg cgt tcc aat taa cac caa tag cag tcc aga
G R P - I P S R T R R S N - H Q - Q S R
tga cca aat tgg cta cta ccg aag agc tac cag acg aat tgc tgg tgg tga cgg taa aat
- P N W L L P K S Y Q T N S W W - R - N
gaa aga tct cag tcc aag atg gta ttt cta cta cct agg aac tgg gcc aga agc tgg act
E R S Q S K M V F L L P R N W A R S W T
tcc cta tgg tgc taa caa aga cgg cat cat atg ggt tgc aac tga ggg agc ctt gaa tac
S L W C - Q R R H H M G C N - G S L E Y
acc aaa aga tca cat tgg cac ccg caa tcc tgc taa caa tgc tgc aat cgt gct aca act
T K R A S H W H P Q S C - Q C C I R A T T
tcc tca agg aac aac att gcc aaa agg ctt cta cgc aga agg gag gag agg cgg cag tca
S S R N N I A K R L L R R R E Q R R Q S
agg ctc ttc tgc ttc ctc atc acg tag tgc caa cag ttc aag aaa ttc aac tcc agg cag
S L F S F L I T - S Q Q F K K F N S R Q
cag tag ggg aac ttc tcc tgc tag aat ggc tgg caa tgg cgg tga tgc tgc tct tgc ttt
Q - G N F S C - N G W Q W R - C C S C F
gct gct gct tga cag att gaa cca gct tga gag caa aat gtc tgg taa agg cca aca aca
A A A - Q I E P A - E Q N V W - R P T T
aca agg cca aac tgt cac taa gaa atc tgc tgc tga ggc ttc taa gaa gcc tgc gca aaa
T R P N C H - E I C C - G F - E A S A K
acg tac tgc cac taa agc ata caa tgt aac aca agc ttt cgg cag acg tgg tcc aga aca
T Y C H - S I Q C N T S F R Q T W S R T
aac cca agg aaa ttt tgg gga cca gga act aat cag aca agg aac tga tta caa aca ttg
N P R K F W G P G T N Q T R N - L Q T L
gcc gca aat tgc aca att tgc ccc cag cgc ttc agc gtt ctt cgg aat gtc gcg cat tgg
A A N C T I C P Q R F S V L R N V A H W
cat gga agt cac acc ttc ggg aac gtg gtt gac cta cac agg tgc cat caa att gga tga
H G S H T F G N V V D L H R C H Q I G -
caa aga tcc aaa ttt caa aga tca agt cat ttt gct gaa taa gca tat tga cgc ata caa
Q R S K F Q R S S H F A E - A Y - R I Q
aac att ccc acc aac aga gcc taa aaa gga caa aaa gaa gaa ggc tga tga aac tca agc
N I P T N R A - K G Q K E E G - - N S S
ctt acc gca gag aca gaa gaa aca gca aac tgt gac tct tet tcc tgc tgc aga ttt gga
L T A E T E E T A N C D S S S C C R F G
tga ttt ctc caa aca att gca aca atc cat gag cag tgc tga ctc aac tca ggc cta
- F L Q T I A T I H E Q C - L N S G L
```



## MHC-II Binding Prediction Results

### Input Sequences

#	Name	Sequence
1	2	GAGICASYQTQNSPRRAR

Prediction method: IEDB recommended 2.22 | Low adjusted\_rank = good binders

[Download result](#)

### Citations

Check to expand the result:


Allele	#	Start	End	Length	Method used	Peptide	Percentile Rank	Adjusted rank
HLA-DRB1*04:01	1	5	19	15	Consensus (simm/nr/stumio)	CASYQTQNSPRRAR	3.20	3.20
HLA-DRB1*04:01	1	4	18	15	Consensus (simm/nr/stumio)	ICASYQTQNSPRRA	3.70	3.70
HLA-DRB1*04:01	1	3	17	15	Consensus (simm/nr/stumio)	GICASYQTQNSPRR	5.30	5.30
HLA-DRB3*01:01	1	5	19	15	Consensus (simm/nr/stumio)	CASYQTQNSPRRAR	8.60	8.60
HLA-DRB1*04:01	1	2	16	15	Consensus (simm/nr/stumio)	AGICASYQTQNSPR	9.50	9.50
HLA-DRB1*04:05	1	2	16	15	Consensus (simm/nr/stumio)	AGICASYQTQNSPR	12.00	12.00
HLA-DRB3*01:01	1	4	18	15	Consensus (simm/nr/stumio)	ICASYQTQNSPRRA	12.00	12.00
HLA-DRB1*04:05	1	3	17	15	Consensus (simm/nr/stumio)	GICASYQTQNSPRR	13.00	13.00
HLA-DRB1*04:05	1	4	18	15	Consensus (simm/nr/stumio)	ICASYQTQNSPRRA	13.00	13.00
HLA-DRB1*04:05	1	5	19	15	Consensus (simm/nr/stumio)	CASYQTQNSPRRAR	14.00	14.00
HLA-DRB3*01:01	1	3	17	15	Consensus (simm/nr/stumio)	GICASYQTQNSPRR	16.00	16.00
HLA-DRB3*02:02	1	5	19	15	NetMHCIIpan	CASYQTQNSPRRAR	18.00	18.00
HLA-DRB3*02:02	1	4	18	15	NetMHCIIpan	ICASYQTQNSPRRA	23.00	23.00
HLA-DQA1*05:01/DOB1*03:01	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	24.00	24.00
HLA-DRB3*01:01	1	2	16	15	Consensus (simm/nr/stumio)	AGICASYQTQNSPR	31.00	31.00
HLA-DRB1*09:01	1	4	18	15	Consensus (comb.lib./simm/nr)	ICASYQTQNSPRRA	31.00	31.00
HLA-DRB1*09:01	1	3	17	15	Consensus (comb.lib./simm/nr)	GICASYQTQNSPRR	36.00	36.00
HLA-DQA1*05:01/DOB1*03:01	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	37.00	37.00
HLA-DRB3*02:02	1	3	17	15	NetMHCIIpan	GICASYQTQNSPRR	37.00	37.00
HLA-DRB1*13:02	1	5	19	15	Consensus (simm/nr/stumio)	CASYQTQNSPRRAR	41.00	41.00
HLA-DRB1*04:05	1	1	15	15	Consensus (simm/nr/stumio)	GAGICASYQTQNSP	41.00	41.00
HLA-DRB1*13:02	1	4	18	15	Consensus (simm/nr/stumio)	ICASYQTQNSPRRA	42.00	42.00
HLA-DPA1*02:01/DPB1*01:01	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	46.00	46.00
HLA-DRB1*12:01	1	2	16	15	Consensus (simm/nr)	AGICASYQTQNSPR	49.50	49.50
HLA-DRB1*09:01	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	50.00	50.00
HLA-DRB4*01:01	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	51.00	51.00
HLA-DPA1*02:01/DPB1*01:01	1	4	18	15	Consensus (comb.lib./simm/nr)	ICASYQTQNSPRRA	51.00	51.00
HLA-DRB1*03:01	1	1	15	15	Consensus (simm/nr/stumio)	GAGICASYQTQNSP	52.00	52.00
HLA-DRB4*01:01	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	52.00	52.00
HLA-DPA1*02:01/DPB1*01:01	1	3	17	15	Consensus (comb.lib./simm/nr)	GICASYQTQNSPRR	52.00	52.00
HLA-DRB3*02:02	1	2	16	15	NetMHCIIpan	AGICASYQTQNSPR	53.00	53.00
HLA-DRB1*09:01	1	5	19	15	Consensus (comb.lib./simm/nr)	CASYQTQNSPRRAR	53.00	53.00
HLA-DQA1*01:02/DOB1*08:02	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	53.00	53.00
HLA-DRB1*09:01	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	54.00	54.00
HLA-DRB1*15:01	1	2	16	15	Consensus (simm/nr/stumio)	AGICASYQTQNSPR	54.00	54.00
HLA-DRB1*08:02	1	3	17	15	Consensus (simm/nr/stumio)	GICASYQTQNSPRR	54.00	54.00
HLA-DRB1*01:01	1	5	19	15	Consensus (comb.lib./simm/nr)	CASYQTQNSPRRAR	55.00	55.00
HLA-DRB1*01:01	1	4	18	15	Consensus (comb.lib./simm/nr)	ICASYQTQNSPRRA	55.00	55.00
HLA-DQA1*01:02/DOB1*08:02	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	56.00	56.00
HLA-DRB1*03:01	1	2	16	15	Consensus (simm/nr/stumio)	AGICASYQTQNSPR	56.00	56.00
HLA-DRB1*12:01	1	3	17	15	Consensus (simm/nr)	GICASYQTQNSPRR	56.00	56.00
HLA-DRB1*12:01	1	4	18	15	Consensus (simm/nr)	ICASYQTQNSPRRA	56.50	56.50
HLA-DRB1*08:02	1	2	16	15	Consensus (simm/nr/stumio)	AGICASYQTQNSPR	57.00	57.00
HLA-DQA1*03:01/DOB1*03:02	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	57.00	57.00
HLA-DRB1*04:01	1	1	15	15	Consensus (simm/nr/stumio)	GAGICASYQTQNSP	57.00	57.00
HLA-DRB1*08:02	1	4	18	15	Consensus (simm/nr/stumio)	ICASYQTQNSPRRA	57.00	57.00
HLA-DRB1*11:01	1	5	19	15	Consensus (simm/nr/stumio)	CASYQTQNSPRRAR	58.00	58.00
HLA-DRB1*12:01	1	5	19	15	Consensus (simm/nr)	CASYQTQNSPRRAR	58.00	58.00
HLA-DPA1*02:01/DPB1*01:01	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	58.00	58.00
HLA-DPA1*01:03/DPB1*02:01	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	59.00	59.00
HLA-DRB1*08:02	1	5	19	15	Consensus (simm/nr/stumio)	CASYQTQNSPRRAR	59.00	59.00
HLA-DPA1*01:03/DPB1*02:01	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	59.00	59.00
HLA-DRB4*01:01	1	3	17	15	Consensus (comb.lib./simm/nr)	GICASYQTQNSPRR	59.00	59.00
HLA-DPA1*01:03/DPB1*02:01	1	3	17	15	Consensus (comb.lib./simm/nr)	GICASYQTQNSPRR	60.00	60.00
HLA-DPA1*02:01/DPB1*01:01	1	5	19	15	Consensus (comb.lib./simm/nr)	CASYQTQNSPRRAR	61.00	61.00
HLA-DQA1*04:01/DOB1*04:02	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	62.00	62.00
HLA-DRB4*01:01	1	4	18	15	Consensus (comb.lib./simm/nr)	ICASYQTQNSPRRA	62.00	62.00
HLA-DRB1*08:02	1	1	15	15	Consensus (simm/nr/stumio)	GAGICASYQTQNSP	63.00	63.00
HLA-DRB1*03:01	1	3	17	15	Consensus (simm/nr/stumio)	GICASYQTQNSPRR	63.00	63.00
HLA-DRB1*07:01	1	4	18	15	Consensus (comb.lib./simm/nr)	ICASYQTQNSPRRA	63.00	63.00
HLA-DPA1*03:01/DPB1*04:02	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	64.00	64.00

## MHC-II Binding Prediction Results

### Input Sequences

#	Name	Sequence
1	IEDB Epitope 952701	CALPDTPSTLTPRSVRSVPGEMRLA

Prediction method: IEDB recommended 2.22 | Low adjusted\_rank = good binders

Download result 

### Citations

Check to expand the result:

Allele	#	Start	End	Length	Method used	Peptide	Percentile Rank	Adjusted rank
HLA-DRB5*01:01	1	11	25	15	Consensus (simm/nr/stumliolo)	TPRSVRSVPGEMRLA	8.40	8.40
HLA-DRB5*01:01	1	10	24	15	Consensus (simm/nr/stumliolo)	LTPRSVRSVPGEMRL	8.60	8.60
HLA-DRB5*01:01	1	9	23	15	Consensus (simm/nr/stumliolo)	TLTPRSVRSVPGEMRR	9.50	9.50
HLA-DPA1*02:01/DPB1*14:01	1	11	25	15	NetMHCIIpan	TPRSVRSVPGEMRLA	16.00	16.00
HLA-DPA1*02:01/DPB1*14:01	1	10	24	15	NetMHCIIpan	LTPRSVRSVPGEMRL	20.00	20.00
HLA-DRB1*09:01	1	11	25	15	Consensus (comb.lib./simm/nr)	TPRSVRSVPGEMRLA	21.00	21.00
HLA-DQA1*05:01/DQB1*03:01	1	10	24	15	Consensus (comb.lib./simm/nr)	LTPRSVRSVPGEMRL	25.00	25.00
HLA-DRB1*09:01	1	10	24	15	Consensus (comb.lib./simm/nr)	LTPRSVRSVPGEMRL	25.00	25.00
HLA-DQA1*05:01/DQB1*03:01	1	9	23	15	Consensus (comb.lib./simm/nr)	TLTPRSVRSVPGEMRR	25.00	25.00
HLA-DQA1*05:01/DQB1*03:01	1	11	25	15	Consensus (comb.lib./simm/nr)	TPRSVRSVPGEMRLA	25.00	25.00
HLA-DRB1*09:01	1	5	19	15	Consensus (comb.lib./simm/nr)	DTPSTLTPRSVRSVP	27.00	27.00
HLA-DRB1*09:01	1	4	18	15	Consensus (comb.lib./simm/nr)	PDTPSTLTPRSVRSV	27.00	27.00
HLA-DQA1*05:01/DQB1*03:01	1	7	21	15	Consensus (comb.lib./simm/nr)	PSTLTPRSVRSVPGE	28.00	28.00
HLA-DQA1*05:01/DQB1*03:01	1	8	22	15	Consensus (comb.lib./simm/nr)	STLTPRSVRSVPGEM	28.00	28.00
HLA-DRB1*09:01	1	9	23	15	Consensus (comb.lib./simm/nr)	TLTPRSVRSVPGEMR	29.00	29.00
HLA-DRB1*07:01	1	1	15	15	Consensus (comb.lib./simm/nr)	CALPDTPSTLTPRSV	31.00	31.00
HLA-DRB1*03:01	1	11	25	15	Consensus (simm/nr/stumliolo)	TPRSVRSVPGEMRLA	31.00	31.00
HLA-DRB1*03:01	1	10	24	15	Consensus (simm/nr/stumliolo)	LTPRSVRSVPGEMRL	32.00	32.00
HLA-DRB1*09:01	1	3	17	15	Consensus (comb.lib./simm/nr)	LPDTPSTLTPRSVRS	33.00	33.00
HLA-DRB1*07:01	1	10	24	15	Consensus (comb.lib./simm/nr)	LTPRSVRSVPGEMRL	33.00	33.00
HLA-DRB1*08:02	1	10	24	15	Consensus (simm/nr/stumliolo)	LTPRSVRSVPGEMRL	33.00	33.00
HLA-DRB1*07:01	1	8	22	15	Consensus (comb.lib./simm/nr)	STLTPRSVRSVPGEM	33.00	33.00
HLA-DRB1*07:01	1	9	23	15	Consensus (comb.lib./simm/nr)	TLTPRSVRSVPGEMR	33.00	33.00
HLA-DRB1*08:02	1	9	23	15	Consensus (simm/nr/stumliolo)	TLTPRSVRSVPGEMR	33.00	33.00
HLA-DRB1*09:01	1	2	16	15	Consensus (comb.lib./simm/nr)	ALPDTPSTLTPRSVR	34.00	34.00
HLA-DRB1*07:01	1	5	19	15	Consensus (comb.lib./simm/nr)	DTPSTLTPRSVRSVP	36.00	36.00
HLA-DRB1*07:01	1	4	18	15	Consensus (comb.lib./simm/nr)	PDTPSTLTPRSVRSV	36.00	36.00
HLA-DRB1*09:01	1	8	22	15	Consensus (comb.lib./simm/nr)	STLTPRSVRSVPGEM	36.00	36.00
HLA-DRB1*03:01	1	9	23	15	Consensus (simm/nr/stumliolo)	TLTPRSVRSVPGEMR	36.00	36.00
HLA-DPA1*02:01/DPB1*14:01	1	9	23	15	NetMHCIIpan	TLTPRSVRSVPGEMR	37.00	37.00
HLA-DRB1*07:01	1	2	16	15	Consensus (comb.lib./simm/nr)	ALPDTPSTLTPRSVR	39.00	39.00
HLA-DRB1*01:01	1	1	15	15	Consensus (comb.lib./simm/nr)	CALPDTPSTLTPRSV	39.00	39.00
HLA-DRB1*07:01	1	3	17	15	Consensus (comb.lib./simm/nr)	LPDTPSTLTPRSVRS	39.00	39.00
HLA-DRB1*07:01	1	6	20	15	Consensus (comb.lib./simm/nr)	TPSTLTPRSVRSVPG	39.00	39.00
HLA-DRB1*01:01	1	5	19	15	Consensus (comb.lib./simm/nr)	DTPSTLTPRSVRSVP	40.00	40.00
HLA-DRB1*01:01	1	4	18	15	Consensus (comb.lib./simm/nr)	PDTPSTLTPRSVRSV	40.00	40.00
HLA-DRB1*07:01	1	7	21	15	Consensus (comb.lib./simm/nr)	PSTLTPRSVRSVPGE	40.00	40.00
HLA-DRB1*09:01	1	7	21	15	Consensus (comb.lib./simm/nr)	PSTLTPRSVRSVPGE	40.00	40.00
HLA-DRB3*02:02	1	11	25	15	NetMHCIIpan	TPRSVRSVPGEMRLA	40.00	40.00
HLA-DRB1*09:01	1	6	20	15	Consensus (comb.lib./simm/nr)	TPSTLTPRSVRSVPG	40.00	40.00
HLA-DRB1*12:01	1	5	19	15	Consensus (simm/nr)	DTPSTLTPRSVRSVP	41.00	41.00
HLA-DRB1*01:01	1	3	17	15	Consensus (comb.lib./simm/nr)	LPDTPSTLTPRSVRS	41.00	41.00
HLA-DRB1*15:01	1	10	24	15	Consensus (simm/nr/stumliolo)	LTPRSVRSVPGEMRL	41.00	41.00
HLA-DRB1*13:02	1	9	23	15	Consensus (simm/nr/stumliolo)	TLTPRSVRSVPGEMRR	41.00	41.00
HLA-DRB1*01:01	1	11	25	15	Consensus (comb.lib./simm/nr)	TPRSVRSVPGEMRLA	41.00	41.00
HLA-DRB1*12:01	1	4	18	15	Consensus (simm/nr)	PDTPSTLTPRSVRSV	41.50	41.50
HLA-DRB1*13:02	1	8	22	15	Consensus (simm/nr/stumliolo)	STLTPRSVRSVPGEM	42.00	42.00
HLA-DRB1*12:01	1	6	20	15	Consensus (simm/nr)	TPSTLTPRSVRSVPG	42.50	42.50
HLA-DRB1*13:02	1	10	24	15	Consensus (simm/nr/stumliolo)	LTPRSVRSVPGEMRL	43.00	43.00
HLA-DRB1*12:01	1	7	21	15	Consensus (simm/nr)	PSTLTPRSVRSVPGE	43.50	43.50
HLA-DQA1*05:01/DQB1*03:01	1	5	19	15	Consensus (comb.lib./simm/nr)	DTPSTLTPRSVRSVP	44.00	44.00
HLA-DQA1*05:01/DQB1*03:01	1	4	18	15	Consensus (comb.lib./simm/nr)	PDTPSTLTPRSVRSV	44.00	44.00
HLA-DRB1*08:02	1	4	18	15	Consensus (simm/nr/stumliolo)	PDTPSTLTPRSVRSV	44.00	44.00
HLA-DQA1*05:01/DQB1*03:01	1	6	20	15	Consensus (comb.lib./simm/nr)	TPSTLTPRSVRSVPG	44.00	44.00
HLA-DRB1*08:02	1	6	20	15	Consensus (simm/nr/stumliolo)	TPSTLTPRSVRSVPG	44.00	44.00
HLA-DRB1*01:01	1	2	16	15	Consensus (comb.lib./simm/nr)	ALPDTPSTLTPRSVR	45.00	45.00
HLA-DQA1*05:01/DQB1*02:01	1	11	25	15	Consensus (comb.lib./simm/nr)	TPRSVRSVPGEMRLA	45.00	45.00
HLA-DRB3*02:02	1	10	24	15	NetMHCIIpan	LTPRSVRSVPGEMRL	46.00	46.00
HLA-DRB1*15:01	1	9	23	15	Consensus (simm/nr/stumliolo)	TLTPRSVRSVPGEMRR	46.00	46.00
HLA-DRB1*15:01	1	11	25	15	Consensus (simm/nr/stumliolo)	TPRSVRSVPGEMRLA	46.00	46.00
HLA-DQA1*05:01/DQB1*02:01	1	10	24	15	Consensus (comb.lib./simm/nr)	LTPRSVRSVPGEMRL	47.00	47.00

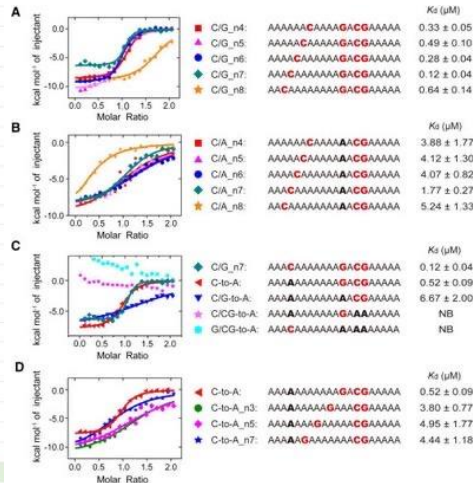
	S1/S2 Junction
SARS-COV-2	CASYQTQNSPRRARSVASQ-SIIAY
ZC45	CASYHT--ASIL--RSTS-QKAIWAY
ZC21	CASYHT--ASIL--RSTG-QKAIWAY
<b>Before SARS-COV-2 (J)</b>	
SARS (Urbani)	CASYHT--VSSL--RSTS-QKSIVAY
YN2018A	CASYHT--ASTL--RSVG-QKSIVAY
Rp/Shaanxi2011	CASYHT--ASVL--RSTG-QKSIVAY
Rs4247	CASYHT--ASTL--RSVG-QKSIVAY
YN2018B	CASYHT--VSSL--RSTS-QKSIVAY
As6526	CASYHT--ASTL--RSVG-QKSIVAY
Rs4237	CASYHT--ASTL--RSVG-QKSIVAY
Longquan-140	CASYHT--ASVL--RSTG-QKSIVAY
Rs4081	CASYHT--ASTL--RSVG-QKSIVAY
BetaCoV/GX2013	CASYHT--ASVL--RSTG-QKSIVAY
HKU3-1	CASYHT--ASVL--RSTG-QKSIVAY
YN2013	CASYHT--ASTL--RSTG-QKSIVAY
Rs806/2006	CASYHT--ASLL--RSTG-QKSIVAY
Cp/Yunnan2011	CASYHT--ASLL--RNTG-QKSIVAY
Rs3367	CASYHT--VSSL--RSTS-QKSIVAY
WIV1	CASYHT--VSSL--RSTS-QKSIVAY
YN2018D	CASYHT--ASTL--RSVG-QKSIVAY
Rs4255	CASYHT--ASTL--RSVG-QKSIVAY
Rs_672/2006	CASYHT--ASTL--RSVG-QKSIVAY
WIV16	CASYHT--VSSL--RSTS-QKSIVAY
RsSHC014	CASYHT--VSSL--RSTS-QKSIVAY
SARS (Civet)	CASYHT--VSSL--RSTS-QKSIVAY
LYRaA3	CASYHT--ASLL--RNTG-QKSIVAY
LYRaA11	CASYHT--ASLL--RNTD-QKSIVAY
Rs9401	CASYHT--VSSL--RSTS-QKSIVAY
Rs4084	CASYHT--VSSL--RSTS-QKSIVAY

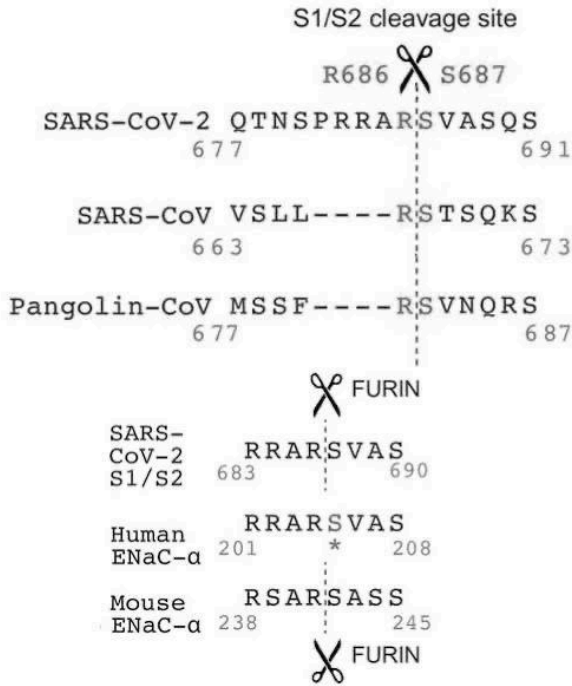
```

caa tgc tgc aat cgt gct aca act
Q C C N R A T T
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R R E Q R R Q S
ttc aag aaa ttc aac tcc agg cag
F K K F N S R Q
tgg cgg tga tgc tgc tct tgc ttt
W R - C C S C F

```

<b>Before SARS-COV-2 (J)</b>	
SARS (Urbani)	CASYHT--VSSL--RSTS-QKSIVAY
YN2018A	CASYHT--ASTL--RSVG-QKSIVAY
Rp/Shaanxi2011	CASYHT--ASVL--RSTG-QKSIVAY
Rs4247	CASYHT--ASTL--RSVG-QKSIVAY
YN2018B	CASYHT--VSSL--RSTS-QKSIVAY
As6526	CASYHT--ASTL--RSVG-QKSIVAY
Rs4237	CASYHT--ASTL--RSVG-QKSIVAY
Longquan-140	CASYHT--ASVL--RSTG-QKSIVAY
Rs4081	CASYHT--ASTL--RSVG-QKSIVAY
BetaCoV/GX2013	CASYHT--ASVL--RSTG-QKSIVAY
HKU3-1	CASYHT--ASVL--RSTG-QKSIVAY
YN2013	CASYHT--ASTL--RSTG-QKSIVAY
Rs806/2006	CASYHT--ASLL--RSTG-QKSIVAY
Cp/Yunnan2011	CASYHT--ASLL--RNTG-QKSIVAY
Rs3367	CASYHT--VSSL--RSTS-QKSIVAY
WIV1	CASYHT--VSSL--RSTS-QKSIVAY
YN2018D	CASYHT--ASTL--RSVG-QKSIVAY
Rs4255	CASYHT--ASTL--RSVG-QKSIVAY
Rs_672/2006	CASYHT--ASTL--RSVG-QKSIVAY
WIV16	CASYHT--VSSL--RSTS-QKSIVAY
RsSHC014	CASYHT--VSSL--RSTS-QKSIVAY
SARS (Civet)	CASYHT--VSSL--RSTS-QKSIVAY
LYRaA3	CASYHT--ASLL--RNTG-QKSIVAY
LYRaA11	CASYHT--ASLL--RNTD-QKSIVAY
Rs9401	CASYHT--VSSL--RSTS-QKSIVAY
Rs4084	CASYHT--VSSL--RSTS-QKSIVAY
Rs7327	CASYHT--VSSL--RSTS-QKSIVAY
Anlong-103	CASYHT--ASTL--RSVG-QKSIVAY
SC2018	CASYHT--ASTL--RSTG-QKSIVAY
YN2018C	CASYHT--ASTL--RSVG-QKSIVAY
RaTG13	CASYQTQNS----RSVASQ-SIIAY





1

2

NIAID PROVIDER TO FOR-PROFIT	NIAID TRACKING NUMBER: 2018-0664
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**MATERIAL TRANSFER AGREEMENT**

This Material Transfer Agreement ("MTA") has been adopted for use by the National Institute of Allergy and Infectious Diseases ("NIAID"), an institute at the National Institutes of Health, which is part of the Department of Health and Human Services, an agency of the United States Government ("Provider") in transfers of research material to for-profit institutions for internal research.

Recipient: ModernaTX, Inc., having offices at 500 Technology Square Cambridge, MA 02139, created and operating under the laws of Delaware

1. Provider has previously transferred to Recipient's Investigator the following material(s), including known functional components or subunits and modified or unmodified descendants thereof ("Research Material"):

Name/Description	Reference
<i>Cell line #1:</i> RajiDCSIGN	PMID: 16415006 and PMID: 18005691
<i>Cell line #2:</i> RajiDCSIGNR	PMID: 16415006 and PMID: 18005691
pFurin; a DNA expression construct expressing human furin protease	Davis et al., J Virol. 2006 Feb; 80(3):1290-301. (PMID: 16415006)
<i>Replicon#1:</i> pWNVII-Rep-G/Z; a WNV lineage II replicon expressing GFP and zocoin resistance	Pierson et al., Virology. 2006 Mar 1;346(1):53-65. (PMID: 16375883)
<i>Replicon#2:</i> pWNVII-Rep-Ren-IB; a WNV lineage II replicon expressing Renilla luciferase and blasticidin resistance	Pierson et al., Virology. 2006 Mar 1;346(1):53-65. (PMID: 16375883)

2. THIS RESEARCH MATERIAL MAY NOT BE USED IN HUMAN SUBJECTS. The Research Material will only be used for commercial research purposes by Recipient's Investigator in his/her laboratory, for the research project described below, under suitable containment conditions. The Research Material will not be used in any product offered for sale or processes for the manufacture thereof, including quality control procedures, or in commercial services.

Recipient agrees to comply with all laws, rules and regulations applicable to the Research Project and the handling of the Research Material.

a. Is the Research Material of human origin?

Yes     No

b. If Yes in 2a, was Research Material collected according to 45 C.F.R. Part 46, "Protection of Human Subjects"?

Yes    Please provide Assurance Number: \_\_\_\_\_  
 No

[0003/0213] NIAID FP-MTA (modified)  
NIAID Tracking Number 2017-0664  
Page 1 of 6



	CONSERVED REGION	VARIABLE REGION
SARS-CoV-2	G A G I C A S Y	Q T Q T N S P R R A R S V A - S Q S I I
RaTG13	G A G I C A S Y	Q T Q T N S - - - R S V A - S Q S I I
RShSTT182/200 (Cambodia) (identical here)	G A G I C A S Y	Q T Q T N S - - - R S V T - S Q S I I
Pangolin/GD/2019	G A G I C A S Y	Q T Q T N S - - - R S V S - S Q A I I
RmYN02 Zhou et al.	G A G V C A S Y	- - - N S P - A A R - V G - T N S I I
RmYN02 Clustal W	G A G V C A S Y	- - - N S ( P ) A - - - A R V G - T N S I I
RmYN02 YD&RS ver. 1	G A G V C A S Y	- - - ( N S ) P A A - - - R - V G - T N S I I
RmYN02 YD&RS ver. 2	G A G V C A S Y	- - - N S P A A - - - R - V G - T N S I I
RacCS203 (Thailand)	G A G V C A S Y	- - - N S P V A - - - R - V G - T N S I I
RacCS264 (Thailand)	G A G V C A S Y	- - - N S P V ? - - - ? - ? - ? Q S I I
RacCS271 (Thailand)	? ? ? V C A S Y	- - - N S P V A - - - R - V G - T N S I I
PrC31 (Yunnan)	G A G I C A S Y	H T A P I L - - - R S T S - Q K A I V
Rc-o319 (Japan)	G A G I C A T Y	H T P S M L - - - R S A N N N K R I V
Pangolin/GX/2017	G A G I C A S Y	H S M S S F - - - R S V N - Q R S I I
Rs3367 & RsSHC014 (identical here)	G A G I C A S Y	H T V S S L - - - R S T S - Q K S I V
ZC45	G A G I C A S Y	H T A S I L - - - R S T S - Q K A I V
ZXC21	G A G I C A S Y	H T A S I L - - - R S T G - Q K A I V
RmYN01	G A G I C A S Y	H T A S L L - - - R N T G - Q K S I V
LYRa11	G A G I C A S Y	H T A S L L - - - R N T D - Q K S I V
RF4092	G A G I C A S Y	H T A S T L - - - R G V G - Q K S I V

Black = common for all  
 Purple = unique to SARS-CoV-2  
 Green = differences mostly found in strains shaded in pink (RmYN02 or RacCSxxx)  
 Blue = differences mostly found in strains shaded in purple (ZC45, Rs3367, LYRa11, etc.)  
 Yellow = differences mostly found in Pangolin/GX/2017  
 Red = other differences

```

caa tgc tgc aat cgt gct aca act
Q C C N R A T T
aga agg gag cag agg cgg cag tca
R R E Q R R Q S
ttc aag aaa ttc aac tcc agg cag
F K K F N S R Q
tgg cgg tga tgc tgc tct tgc ttt
W R - C C S C F
  
```

[https://twitter.com/rootclaim/status/1758127978763125053?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/rootclaim/status/1758127978763125053?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Also, QTQRRQSRS is much more likely than QTQTNSPRRARS if recombination yielded the FCS.

Example of China gatekeeping to give unfair advantage to the zoo side, in addition to the fact that the zoonati repeatedly strawmanned impossible bayes factor assignments.

The market claim is debunked alongside.

Before they begun enforcing their claim of “100/174 centered around the market”

<https://twitter.com/daoyu15/status/1674351139079479298>

and starting to tamper with data to make the claim,

<https://ghrp.biomedcentral.com/articles/10.1186/s41256-021-00200-8>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7149375/>  
135/92 and 115/82 cases already got into in early peer-reviewed papers that went missing in the WHO report.

<https://twitter.com/daoyu15/status/1682778742664630272> Past media reports [archive.md/Ea0Kw](https://archive.md/Ea0Kw) [archive.md/1x658](https://archive.md/1x658) also contradict WHO in key early cases' residences, including the earliest case they admit in the WHO report.

<http://archive.md/5sdkR> <http://archive.md/1pcCU> [archive.md/N0hib](https://archive.md/N0hib) [archive.md/VXtu9](https://archive.md/VXtu9)  
<http://archive.is/Kyr1z>

<https://archive.org/details/mace-e-pai-covid-19-analysis-redacted/page/8/mode/1up>  
And you know that they hate this information when it was censored.  
The MACE-EPAI document here is not searchable on google.

<https://twitter.com/daoyu15/status/1672399653344808960>  
Up to one third of all cases were either removed completely or moved toward the market in the "dataset".

[archive.md/zUD1F](https://archive.md/zUD1F) [archive.md/Pc6gp](https://archive.md/Pc6gp) <https://archive.is/p3K3Z>  
<https://twitter.com/daoyu15/status/1678549054794629120>  
<https://twitter.com/daoyu15/status/1677727068082286592>  
Including the very first case they ever admitted officially.  
<https://twitter.com/daoyu15/status/1693985440762929643>  
And outright removed 4 times more cases than official.  
<https://twitter.com/daoyu15/status/1677234083389411328>  
Unlinked cases supposedly secondary to linked cases should cluster around them, not the market itself.

<https://twitter.com/daoyu15/status/1744157399479664843>  
[archive.md/GvRcD](https://archive.md/GvRcD) [archive.md/ZgVzp](https://archive.md/ZgVzp) Wuhan authorities after that  
[archive.md/OIGPz](https://archive.md/OIGPz) 2014 incident now targeted only the Huanan market when looking for EID outbreaks—and nowhere else.  
[archive.md/1x658](https://archive.md/1x658)  
They tampered with the early cases data  
[archive.md/Ea0Kw](https://archive.md/Ea0Kw)  
To make it look like it "started at the market" when in reality the first case they ever admitted lived right next to the WIV BSL-4.  
[archive.md/5sdkR](https://archive.md/5sdkR) severe discrepancy happening December 2019 and January 2020 indicate tampering with case counts.  
[archive.md/1pcCU](https://archive.md/1pcCU)  
This is indicative of catastrophic ascertainment bias was going on.  
None of China's "early cases" dataset is credible. <https://archive.md/ET1GA>  
<https://twitter.com/daoyu15/status/1678057846204960768>  
<https://archive.md/Ea0Kw> <https://archive.md/1x658>  
The tampering of early case residence data is systematic and extensive. It is the reason why they refused to provide this data in any detail at all.  
<https://twitter.com/daoyu15/status/1719518909009981579>  
<https://twitter.com/daoyu15/status/1672404501129756673>

Not only did The first every case they admitted live in Shidong right next to the BSL-4, and were moved toward the market in the WHO report in contradiction to all known media coverage, <https://gab.com/Flavinkins/posts/109256201942085712> the entirety of Wuchang district was wiped clean for every single WHO case that have onset before 27/12/2019—with up to 3000 cases moved to the market this way over the entire Wuhan outbreak. <https://archive.md/1x658> and for central Wuchang near the labs and the densest inhabited regions inside the district, all cases were moved away in the WHO map.

<https://twitter.com/biorealism/status/1702047444736111042>

Unfortunately Rasmussen's work on the origins question rests heavily on what David Relman described as "hopelessly impoverished" early case data.

<https://www.washingtonpost.com/national-security/2023/02/27/little-known-scientific-team-behind-new-assessment-covid-19-origins/>

<https://www.washingtonpost.com/opinions/2022/11/17/covid-early-cases-wuhan-china-mystery/><https://archive.md/ke1lp>

<https://archive.md/RaYPC><https://twitter.com/daoyu15/status/1726274673472876584>

<https://twitter.com/biorealism/status/1726475588289040834>

David Fisman: I think the most interesting thing this fellow says is that there are clearly tens of thousands of cases...That implies a much earlier introduction than would have occurred with a seafood market outbreak..."

[https://x.com/blink64/status/1747299970460582305?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/blink64/status/1747299970460582305?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

<https://www.nytimes.com/2021/02/12/world/asia/china-world-health-organization-coronavirus.html>

<https://archive.md/UFRsv>

They systematically moved more than 3000 cases from the lab to the market and gave "cases data" that they wanted to push for market as first outbreak site to distance from the labs.

[https://www.researchgate.net/publication/370635299\\_Greater\\_than\\_the\\_Sum\\_of\\_its\\_Parts\\_-\\_Aggregated\\_Wuhan\\_COVID-19\\_case\\_data\\_points\\_to\\_the\\_wrong\\_side\\_of\\_the\\_Yangtze\\_River\\_-\\_Rixey\\_-\\_20230509](https://www.researchgate.net/publication/370635299_Greater_than_the_Sum_of_its_Parts_-_Aggregated_Wuhan_COVID-19_case_data_points_to_the_wrong_side_of_the_Yangtze_River_-_Rixey_-_20230509)

Such an result of having unlinked cases closer to the market than linked cases is not expected even under the null hypothesis of market origin, which we should see unlinked cases secondary to and cluster around the linked cases, and not the market itself.

[https://twitter.com/emanynton90/status/1666720918901538824?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/emanynton90/status/1666720918901538824?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://www.researchgate.net/publication/370635299\\_Greater\\_than\\_the\\_Sum\\_of\\_its\\_Parts\\_-\\_Aggregated\\_Wuhan\\_COVID-19\\_case\\_data\\_points\\_to\\_the\\_wrong\\_side\\_of\\_the\\_Yangtze\\_River\\_-\\_Rixey\\_-\\_20230509](https://www.researchgate.net/publication/370635299_Greater_than_the_Sum_of_its_Parts_-_Aggregated_Wuhan_COVID-19_case_data_points_to_the_wrong_side_of_the_Yangtze_River_-_Rixey_-_20230509)

Not only there were an complete absence of verifiability in Chinese cases, there is direct non-circumstantial evidence that they moved up to 3000 cases from Wuchang to Huanan.

In fact, it is totally not normal to have unlinked cases closer to the market than linked cases—the only way this can happen is with ascertainment bias. Only near the market gets ascertained if not directly linked to it.

[https://twitter.com/emanynton90/status/1580511684912742400?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/emanynton90/status/1580511684912742400?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Base rate neglect. They did the exact same thing when claiming that all 67 “pre-Huanan checkable cases” were “serologically negative”.

[https://twitter.com/daoyu15/status/1631705321239629824?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1631705321239629824?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Again, the social media associated here say “before Jan 18, 2020”. Included all Dec cases. <https://www.mdpi.com/2220-9964/9/6/402>

[https://twitter.com/danwalker9999/status/1745106077274828819?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/danwalker9999/status/1745106077274828819?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

It is actually impossible for unlinked cases, supposedly secondary, to cluster closer to the market than linked cases which supposedly to be primary, without significant sampling bias or outright manipulation in the underlying “data”.

[https://twitter.com/daoyu15/status/1745090431505854942?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1745090431505854942?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Both evidently happened.

<https://arxiv.org/pdf/2401.08680.pdf>

<https://archive.md/JVFuc>

If you toss away anything that is not officially announced by China in bold, then obviously you would arrive at exactly what China wanted you to believe.

[https://twitter.com/rootclaim/status/1753353199216439672?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/rootclaim/status/1753353199216439672?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Just as expected from jurong, mahachai, xinfadi, <https://archive.md/GKdtc>, if a superspreading event happen on line 2 of the Wuhan metro, the biggest cluster would always be in the HSM.

[https://twitter.com/daoyu15/status/1753584453279187447?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1753584453279187447?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Another hint: only 5% of all cases are severe or ascertained in early 2020.

[https://twitter.com/daoyu15/status/1753593531250470983?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1753593531250470983?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Chen lived in Shidong. Even by the annexes indicating his history. The only thing they did is that they moved him to Jiangnan close to the market on the WHO maps.

[https://twitter.com/daoyu15/status/1672404501129756673?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1672404501129756673?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Also, Chen is not the only person infected in Shidong/Jiangxia and central Wuchang. Most were censored and only one of the two ambulances arriving in 31/12/2019 have been registered as a dot—likely because the origin wasn't inside the Shidong prefecture/BSL-4 surroundings, and likely only because of being a close contact relative of Chen (contacting an known case).

Chen's accidental inclusion in the WCH's first report of early cases and its subsequent media coverage mean that China have no choice but to tamper with the official data in an attempt to move him—while the HPHICWM attempt to whistleblow the “cluster 1” cases in 26-27/12/2019 generated from the WCDC's leak of their culture stock (intended for sample manipulation) was blocked by the Hubei CDC, until the report included market cases as well in 29/12/2019. To save face, the CCP leveraged the fact that the WCDC is right nextdoor to the market and forced official media to only say that the cases were “close to the Huanan market” but not allowing the proximity to the WCDC to be reported.

<https://gab.com/Flavinkins/posts/109256201942085712> All dots they moved this way (up to 1/3 of all cases) was sent to Jiangnan, <https://archive.md/p3K3Z>

[https://www.researchgate.net/publication/370635299\\_Greater\\_than\\_the\\_Sum\\_of\\_its\\_Parts\\_-\\_Aggregated\\_Wuhan\\_COVID-19\\_case\\_data\\_points\\_to\\_the\\_wrong\\_side\\_of\\_the\\_Yangtze\\_River\\_-\\_Rixey\\_-\\_20230509](https://www.researchgate.net/publication/370635299_Greater_than_the_Sum_of_its_Parts_-_Aggregated_Wuhan_COVID-19_case_data_points_to_the_wrong_side_of_the_Yangtze_River_-_Rixey_-_20230509) especially to the immediate surroundings of the market, to scapegoat it and end up causing the “unlinked cases” cluster to be closer to the market than the “linked cases” cluster, despite supposedly the linked cases should be the only source of initial human to human transmission seeding and therefore the unlinked cases should cluster near the linked cases and not the market itself. <https://twitter.com/daoyu15/status/1744155296937935089>

This kind of improbable-under-null-hypothesis behavior is all over Chinese “data”.

<https://twitter.com/daoyu15/status/1719518909009981579>

[archive.md/VNr75](https://archive.md/VNr75) [archive.md/rj1pV](https://archive.md/rj1pV)

They attempted to spray their culture into the wildlife stalls, which ended up [twitter.com/daoyu15/status/1704685320388948318](https://twitter.com/daoyu15/status/1704685320388948318)

Making Homo Sapiens the only species that is found in every sample with a viral read in the market (note the absence of lineage reads in the wildlife stalls), and [archive.md/LJzSO](https://archive.md/LJzSO) [archive.md/4cCHG](https://archive.md/4cCHG) [archive.md/13bdP](https://archive.md/13bdP) all of the subsequent efforts at creating positive samples where the CCP specified them to do (“Blame snakes!” Is the official voice in 02/2020) just brought in artifacts first, and then when all of the mammals have degraded away, pure cultures of SARS-CoV-2 intracellular transcriptomes in human cellular transcriptomes.

Because Homo Sapiens is still the only species that they can get infected at all,

<https://twitter.com/daoyu15/status/1703918936843321541>

if you zoom in and correlate between animals and viruses, You get animal-specific viruses being correlated strongly positively to the animals,

<https://twitter.com/daoyu15/status/1720290396033749336> and SARS-CoV-2 being positively correlated consistently or with significant mutual information only with Homo Sapiens.

<https://twitter.com/daoyu15/status/1719537055611724259>

In addition to the heavy censorship of case ascertainment effectively mean you have to either live near the market or have a direct or indirect link to be diagnosed at all, moving all Wuchang case residence dots and sending them to Jiangnan archive.md/1x658 archive.md/Ea0Kw also caused the “unlinked” dots to cluster closer to the market than the “linked” dots—something that can not happen without data manipulation on a massive scale.

<https://archive.md/ET1GA><https://twitter.com/daoyu15/status/1719536721510244663>  
Unlinked cases are supposed to be seeded only by the linked cases if they didn't visit Huanan under the market origin assumption. They are supposed to cluster near the linked cases and NOT the market itself. The CCP failed in this elementary logical analysis and resulted in a “dataset” that is too perfect to be possibly real.

<https://gab.com/Flavinkins/posts/108830214433800007>

<https://gab.com/Flavinkins/posts/109248812361151175>

The central theater command hospital (right next to the WIV) got 600+ fever cases a day the time when the WMHC just sent off a command to look for cases linked to the Huanan market. just before 31/12/2019, their winter infectious disease monitoring program is already detecting an explosive increase in cases, without warning and "suddenly". none of these cases, none of the wuchang cases, ended up being reported.

The above completely destroys the “early cases are linked to the Huanan market” (<https://twitter.com/mbw61567742/status/1762850018661155075> which is known to contain undeniable proximity ascertainment bias solidified in the “data”)

Argument, in addition to the fact that

archive.md/zUD1F archive.md/Pc6gp

<https://twitter.com/daoyu15/status/1678549054794629120>

<https://twitter.com/daoyu15/status/1677727068082286592>

<https://twitter.com/daoyu15/status/1672404501129756673>

<https://twitter.com/daoyu15/status/1677234083389411328>

archive.md/GvRcD archive.md/ZgVzp the Wuhan authorities after that

archive.md/OIGPz 2014 holmes incident now targeted only the Huanan market when looking for EID outbreaks—and nowhere else.

archive.md/1x658

They tampered with the early cases data

archive.md/Ea0Kw

To make it look like it “started at the market” when in reality the first case they ever admitted lived right next to the WIV BSL-4.

archive.md/5sdkR severe discrepancy happening December 2019 and January 2020 indicate tampering with case counts.

archive.md/1pcCU

This is indicative of catastrophic ascertainment bias was going on.

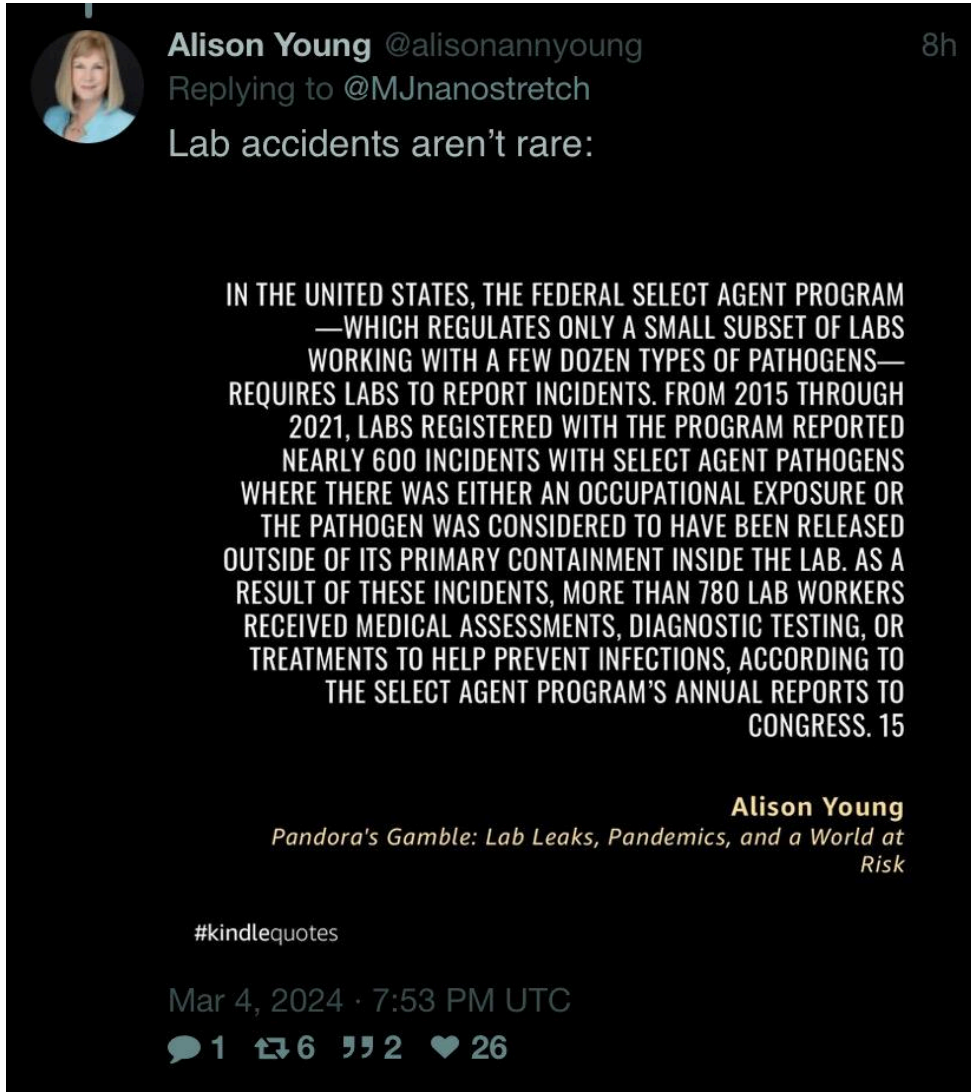
<https://archive.md/ET1GA>

<https://archive.md/p3K3Z>

[https://www.researchgate.net/publication/370635299\\_Greater\\_than\\_the\\_Sum\\_of\\_its\\_Parts\\_-\\_Aggregated\\_Wuhan\\_COVID-19\\_case\\_data\\_points\\_to\\_the\\_wrong\\_side\\_of\\_the\\_Yangtze\\_River\\_-\\_Rixey\\_-\\_20230509](https://www.researchgate.net/publication/370635299_Greater_than_the_Sum_of_its_Parts_-_Aggregated_Wuhan_COVID-19_case_data_points_to_the_wrong_side_of_the_Yangtze_River_-_Rixey_-_20230509)

Up to one third of all cases were moved from the lab to the market.

<https://www.nytimes.com/2023/05/10/opinion/we-could-easily-make-risky-virological-research-safer.html>



A screenshot of a tweet from Alison Young (@alisonnannyoung) posted 8 hours ago. The tweet is a reply to @MJnanostretch and discusses lab accidents. The main text of the tweet is a quote from Alison Young's book 'Pandora's Gamble: Lab Leaks, Pandemics, and a World at Risk'. The quote states that in the United States, the Federal Select Agent Program, which regulates only a small subset of labs, requires labs to report incidents. From 2015 through 2021, labs registered with the program reported nearly 600 incidents with select agent pathogens where there was either an occupational exposure or the pathogen was considered to have been released outside of its primary containment inside the lab. As a result of these incidents, more than 780 lab workers received medical assessments, diagnostic testing, or treatments to help prevent infections, according to the Select Agent Program's annual reports to Congress. The tweet also includes the hashtag #kindlequotes, the date and time (Mar 4, 2024 · 7:53 PM UTC), and engagement metrics (1 reply, 6 retweets, 2 quotes, 26 likes).

**Alison Young** @alisonnannyoung 8h  
Replying to @MJnanostretch  
Lab accidents aren't rare:

IN THE UNITED STATES, THE FEDERAL SELECT AGENT PROGRAM —WHICH REGULATES ONLY A SMALL SUBSET OF LABS WORKING WITH A FEW DOZEN TYPES OF PATHOGENS— REQUIRES LABS TO REPORT INCIDENTS. FROM 2015 THROUGH 2021, LABS REGISTERED WITH THE PROGRAM REPORTED NEARLY 600 INCIDENTS WITH SELECT AGENT PATHOGENS WHERE THERE WAS EITHER AN OCCUPATIONAL EXPOSURE OR THE PATHOGEN WAS CONSIDERED TO HAVE BEEN RELEASED OUTSIDE OF ITS PRIMARY CONTAINMENT INSIDE THE LAB. AS A RESULT OF THESE INCIDENTS, MORE THAN 780 LAB WORKERS RECEIVED MEDICAL ASSESSMENTS, DIAGNOSTIC TESTING, OR TREATMENTS TO HELP PREVENT INFECTIONS, ACCORDING TO THE SELECT AGENT PROGRAM'S ANNUAL REPORTS TO CONGRESS. 15

**Alison Young**  
*Pandora's Gamble: Lab Leaks, Pandemics, and a World at Risk*

#kindlequotes

Mar 4, 2024 · 7:53 PM UTC

1 6 2 26

Lab accidents aren't rare. The other strawman argument for miller is that somehow it is extremely improbable for lab accidents to happen, but in reality an respiratory virus in a BSL-2 guarantee infection, like the

<https://www.theaustralian.com.au/science/beijing-lab-mishap-infected-scientist-with-covid19/news-story/9b0cb0ed84df21d25da11b698be3611a> IVDC.

Rootclaim have identified three major errors in assignment of probability for miller.

<https://blog.rootclaim.com/rootclaims-covid-19-origins-debate-results/>

Ans the actual cards on the issue have reflected these errors.

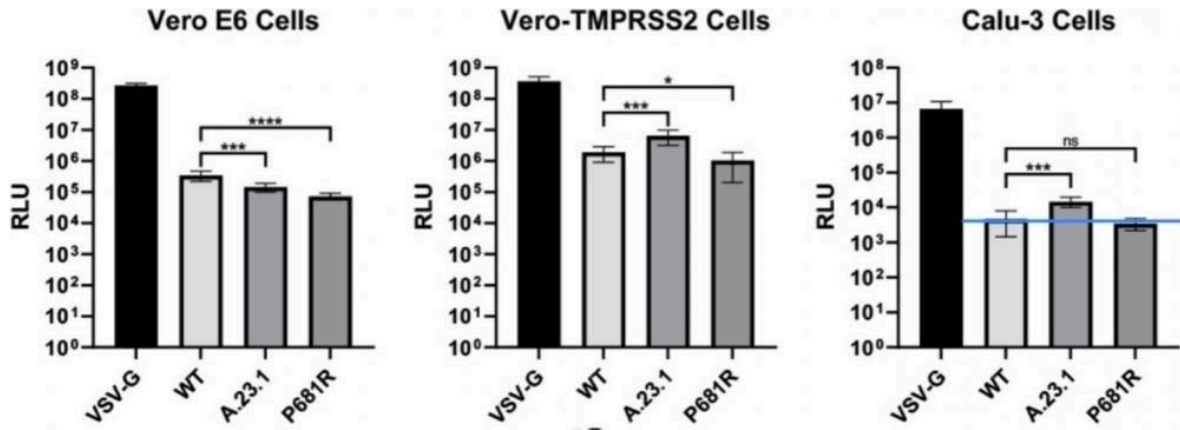
<https://cards.rootclaim.com/analysis/65892f07d97bdb00199d4366>

We have also completely ruled out all plausible intermediate hosts by their susceptibility.

[https://docs.google.com/document/d/18d\\_IMZU\\_DYRX1DIXuSNySC\\_4DiTcgabhxoZ9K4tWrg/edit](https://docs.google.com/document/d/18d_IMZU_DYRX1DIXuSNySC_4DiTcgabhxoZ9K4tWrg/edit)

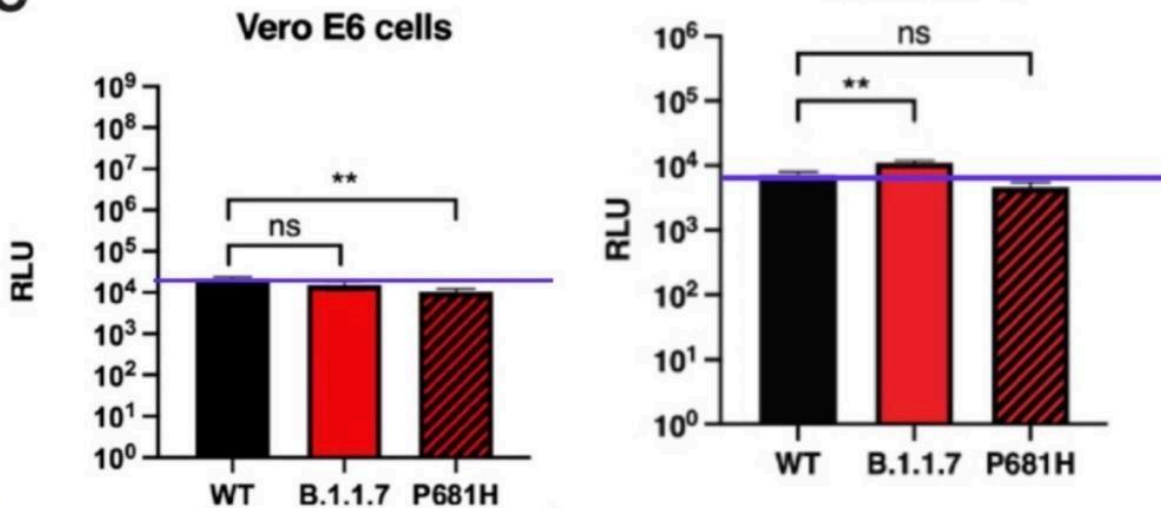
[https://docs.google.com/document/d/1HeZdCnDA4WpoO\\_kzISjmoFzIAggFha3fNEPvBpp2z3M/edit](https://docs.google.com/document/d/1HeZdCnDA4WpoO_kzISjmoFzIAggFha3fNEPvBpp2z3M/edit)



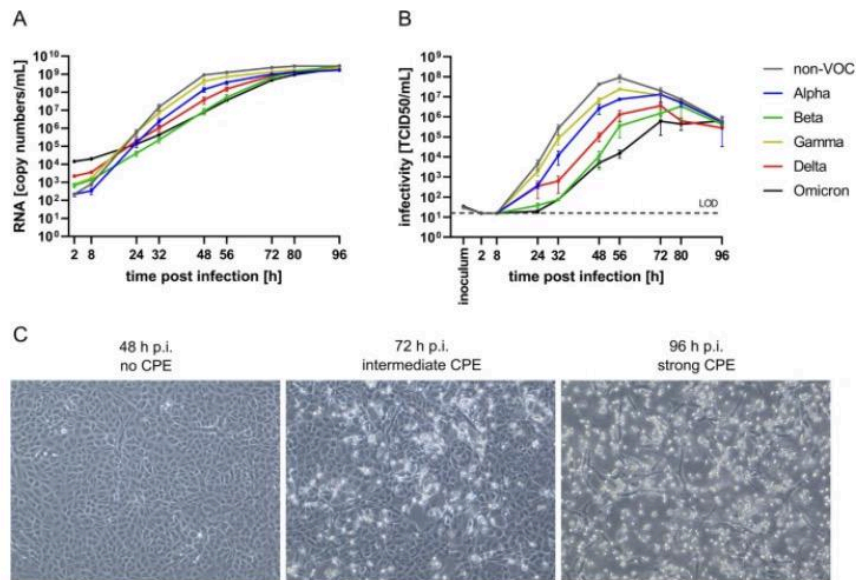


**A**

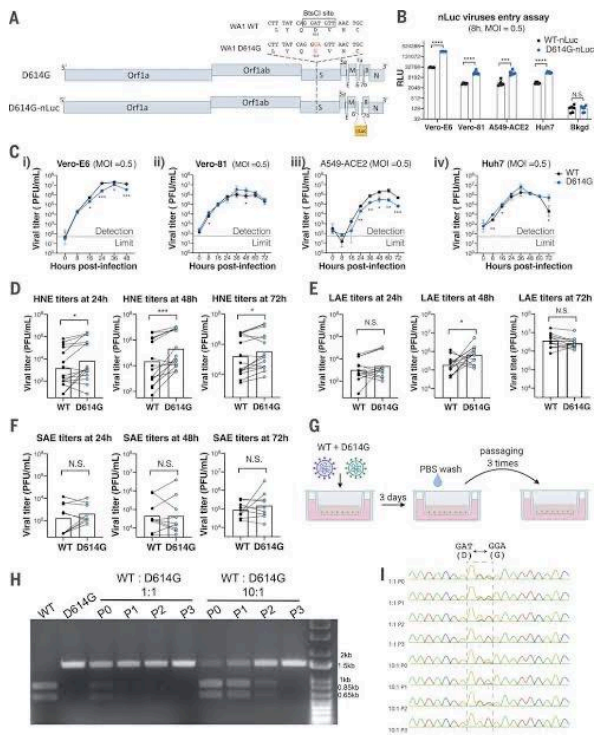
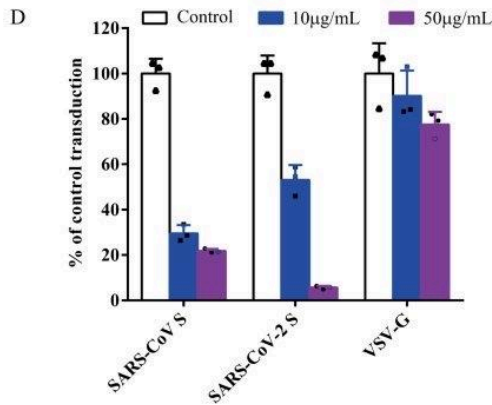
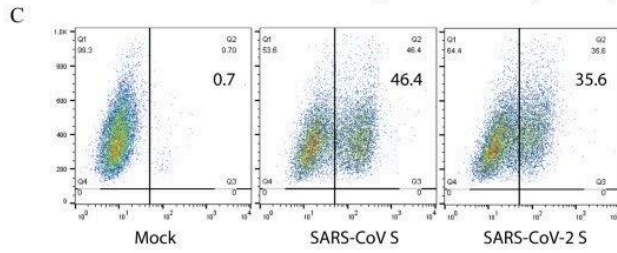
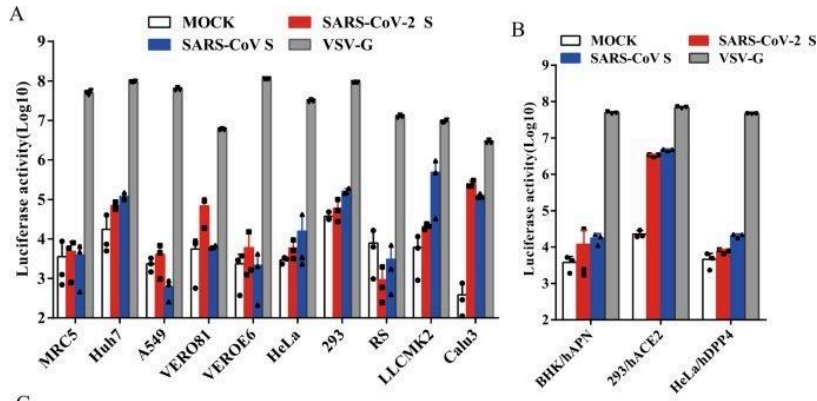
**C**



**Fig. 1**



Viral replication of non-VOC and VOCs on Vero E6. Cells were infected at an MOI of 0.0001 for 96 h and culture supernatant was collected at the indicated time points to quantify **a** RNA copy numbers by RT-qPCR and **b** viral titers by TCID50 endpoint assay. **c** Development of CPE is exemplarily shown for Delta at selected time points. LOD: limit of detection; n = 3



```

          Signal peptide      S1
          L18F T20H F26S      →
          AH69_Av70      D80A
Bat Cov EmYN02      -MFILLIGYTA-----TTCV--NGPTIENKGVUSLNRGVYFDIYRSNVVLPVTFVFLRFNSLWYKFW-----MQATSERVMEFGDGIYPTVDRKSNVIRGWIPOGTLONTQ      106
Bat Cov ZXC21      MLFFLFLQFALVN----SQC-DLNGRTFLMFMVYTHSSQRGVYFDIYRSNTLVLSQGVFLPFYGNVSNVYSL-TTHAATKRTDNPILDFKDIYPAATEKSNIVRGIPOGTLONTQ      114
Bat Cov ZC45      MLFFLFLQFALVN----SQCVMLNRTFLMFMVYTHSSQRGVYFDIYRSNTLVLSQGVFLPFYGNVSNVYSL-TTHAATKRTDNPILDFKDIYPAATEKSNIVRGIPOGTLONTQ      115
SARS-CoV      -MFIFLLFLTLSSGDLORCTTFDDVQAFHYTQRTSNGRGVYFDIYRSNTLVLSQGVFLPFYGNVSNVYSL-TTHAATKRTDNPILDFKDIYPAATEKSNIVRGIPOGTLONTQ      112
Civet SARSr-Cov      -MFIFLLFLTLSSGDLORCTTFDDVQAFHYTQRTSNGRGVYFDIYRSNTLVLSQGVFLPFYGNVSNVYSL-TTHAATKRTDNPILDFKDIYPAATEKSNIVRGIPOGTLONTQ      112
Fangolin CoV GX      -MFVFLVLPVLS----SQCVMLTTRTGIQFQYTHSSSTRGVYFDKVFSSILHLTQQLFLPFYGNVSNVYSL-TTHAATKRTDNPILDFKDIYPAATEKSNIVRGIPOGTLONTQ      113
Fangolin CoV Gx Vero      -MFVFLVLPVLS----SQCVMLTTRTGIQFQYTHSSSTRGVYFDKVFSSILHLTQQLFLPFYGNVSNVYSL-TTHAATKRTDNPILDFKDIYPAATEKSNIVRGIPOGTLONTQ      115
Fangolin CoV GD      MLFFFLLHGFALVN----SQCVMLTTRTGIQFQYTHSSSTRGVYFDKVFSSILHLTQQLFLPFYGNVSNVYSL-TTHAATKRTDNPILDFKDIYPAATEKSNIVRGIPOGTLONTQ      115
Bat Cov RaTg13      -MFVFLVLPVLS----SQCVMLTTRTGIQFQYTHSSSTRGVYFDKVFSSILHLTQQLFLPFYGNVSNVYSL-TTHAATKRTDNPILDFKDIYPAATEKSNIVRGIPOGTLONTQ      115
SARS-CoV-2 B.1.1.7      -MFVFLVLPVLS----SQCVMLTTRTGIQFQYTHSSSTRGVYFDKVFSSILHLTQQLFLPFYGNVSNVYSL-TTHAATKRTDNPILDFKDIYPAATEKSNIVRGIPOGTLONTQ      113
SARS-CoV-2 B.1.351      -MFVFLVLPVLS----SQCVMLTTRTGIQFQYTHSSSTRGVYFDKVFSSILHLTQQLFLPFYGNVSNVYSL-TTHAATKRTDNPILDFKDIYPAATEKSNIVRGIPOGTLONTQ      115
SARS-CoV-2 P.1      -MFVFLVLPVLS----SQCVMLTTRTGIQFQYTHSSSTRGVYFDKVFSSILHLTQQLFLPFYGNVSNVYSL-TTHAATKRTDNPILDFKDIYPAATEKSNIVRGIPOGTLONTQ      115
SARS-CoV-2      -MFVFLVLPVLS----SQCVMLTTRTGIQFQYTHSSSTRGVYFDKVFSSILHLTQQLFLPFYGNVSNVYSL-TTHAATKRTDNPILDFKDIYPAATEKSNIVRGIPOGTLONTQ      115
          IRI          IR2

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“A highly decorated military scientist, Zhou Yusen...produced a vaccine patent w remarkable speed...The...military vaccine specialist is now understood to hv died, w US investigators having bn told by witnesses he was thrown off the roof of the WI...”

翻译推文



msn.com  
 Risky Experiments Inside Wuhan Lab Created COVID-19, Sensational New Evidence Reveals

13:55 · 2023/6/13 位于 Earth · 592 次查看



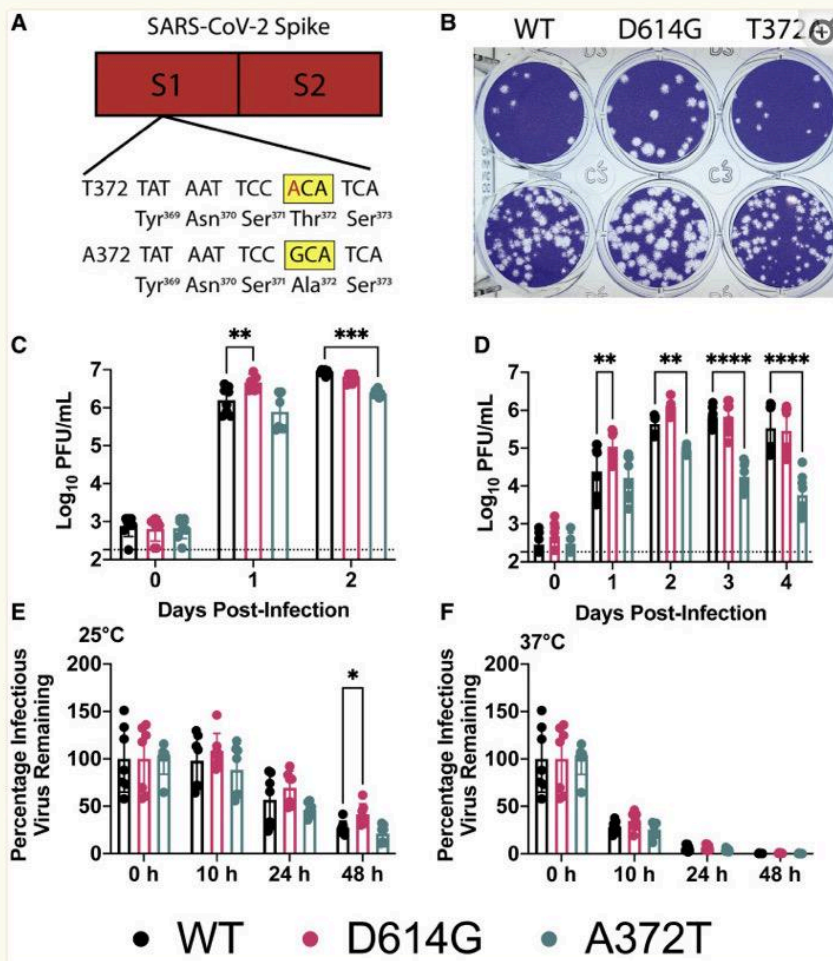


Figure 4

A372T substitution decreases SARS-CoV-2 replication on human lung epithelial cells

(A) The S T372 SARS-CoV-2 mutant was generated by making a single G-to-A substitution. The mutant nucleotide is presented in red, and the altered codon is highlighted in a yellow box.

(B) Plaque morphology of WT and mutant viruses. Plaques were visualized 2 days post-infection (dpi) on Vero E6 cells.

(C and D) Viral replication on Vero E6 (C) and Calu-3 (D) cells following infection at an MOI of 0.05. The sample at 0 dpi was collected immediately after infection to ensure cells were exposed to similar levels of virus, and then samples were collected at 24-h intervals.

(E and F) Kinetics of thermal stability. A solution of  $10^5$  PFU of each virus was incubated at the indicated temperature for different lengths of time. Infectious virus was measured by plaque assay on Vero E6 cells.

Statistical comparisons were made using two-way ANOVA with Dunnett's multiple comparisons test. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , \*\*\*\* $p < 0.0001$ . Error bars represent standard deviation of the mean.

### RBD recombinant protein-based SARS vaccine for biodefense

Project Number: 4R01AI098775-05 | Former Number: 5R01AI098775-05 | Contact PI/Project Leader: HOTEZ, PETER J Other PIs | Awardee Organization: BAYLOR COLLEGE OF MEDICINE

Journal (Link to PubMed abstract)	Authors	Publication Year	Similar Publications	CitedBy	iCite RCR
Recombinant Receptor-Binding Domains of Multiple Middle East Respiratory Syndrome Coronaviruses (MERS-CoVs) Induce Cross-Neutralizing Antibodies against Divergent Human and Camel MERS-CoVs and Antibody Escape Mutants. <i>Journal of virology</i> 2017 Jan 01; 91 (1)	Tai, Wanbo; Wang, Yufei; Fett, Craig A; Zhao, Guangyu; Li, Fang; Perlman, Stanley; Jiang, Shibo; Zhou, Yusen; Du, Lanying	2017	🔗 G	📄 G	📖 2.96
Receptor-binding domain of MERS-CoV with optimal immunogen dosage and immunization interval protects human transgenic mice from MERS-CoV infection. <i>Human vaccines &amp; immunotherapeutics</i> 2017 07 03; 13 (7) 1615-1624	Wang, Yufei; Tai, Wanbo; Yang, Jie; Zhao, Guangyu; Sun, Shihui; Tseng, Chien-Te K; Jiang, Shibo; Zhou, Yusen; Du, Lanying; Gao, Jimin	2017	🔗 G	📄 G	📖 2.31
Cross-neutralization of SARS coronavirus-specific antibodies against bat SARS-like coronaviruses. <i>Science China. Life sciences</i> 2017 12; 60 (12) 1399-1402	Zeng, Lei-Ping; Ge, Xing-Yi; Peng, Cheng; Tai, Wanbo; Jiang, Shibo; Du, Lanying; Shi, Zheng-Li	2017	🔗 G	📄 G	📖 1.16
MERS-CoV spike protein: a key target for antivirals. <i>Expert opinion on therapeutic targets</i> 2017 Feb; 21 (2) 131-143	Du, Lanying; Yang, Yang; Zhou, Yusen; Lu, Lu; Li, Fang; Jiang, Shibo	2017	🔗 G	📄 G	📖 9.89
Optimization of the Production Process and Characterization of the Yeast-Expressed SARS-CoV Recombinant Receptor-Binding Domain (RBD219-N1), a SARS Vaccine Candidate. <i>Journal of pharmaceutical sciences</i> 2017 08; 106	Chen, Wen-Hsiang; Chag, Shivalli M;	2017	🔗 G	📄 G	📖 2.73

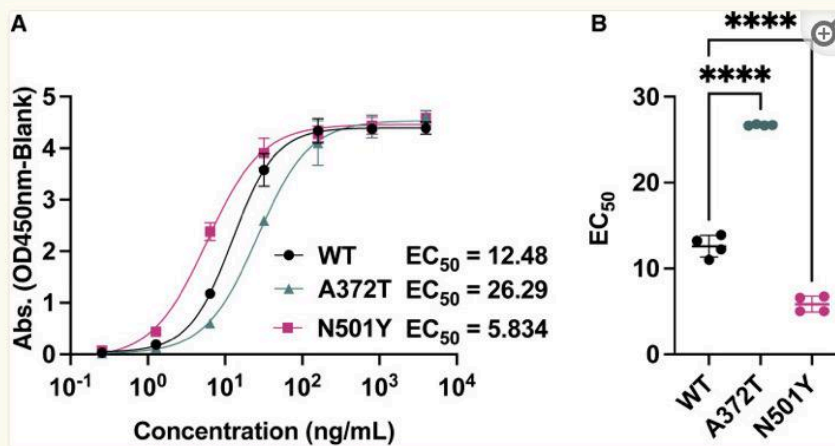


Figure 3

Decreased binding of the A372T mutant to human ACE2

(a) Functional ELISA was used to determine the binding affinity of different S protein receptor-binding domains (RBDs). Plates were coated with recombinant human ACE2 receptor (2  $\mu\text{g}/\text{mL}$  at 100  $\mu\text{L}/\text{well}$ ) and then probed with varying concentrations (0.256–4000 ng/mL) of purified RBDs from WT SARS-CoV-2 (S A372), A372T, and N501Y (positive control). To determine EC<sub>50</sub> values, the absorbance values (450 nm) were fit to a sigmoidal, 4PL nonlinear model using Prism 9 (GraphPad). The experiment was repeated in two independent replicates with four total technical replicates per sample. Error bars represent standard deviation of the mean.

(B) The EC<sub>50</sub> values were compared by one-way ANOVA with Dunnett's multiple comparisons test. \*\*\*\*p < 0.0001 compared with WT SARS-CoV-2 (A372). Error bars represent standard deviation of the mean.



华南海鲜市场进行又一次消毒



There are about 200 reads of canine Kobuvirus in Q61, 20 in Q64, 2 in Q68, 30 in Q69 and 2 in Q70.

Raccoon dog reads are 14338, 150, 29, 77, 21.

There are 204, 70, 80, 55, 60 reads of

Embecoviruses in Q61, Q64, Q68, Q69, Q70.

Bamboo rat and rabbit reads are 746, 294, 505,

36, 85 (the RdRp/ORF1b fragments of

Embecoviruses are heavily confusing with each

other and are frequently recombinant, meaning

that the alignment algorithm does not reliably

distinguish between them within this region)

There are 12, 21, 3, 1100, 3 reads of Canine

Coronavirus in Q61, Q64, Q68, Q69, Q70.

Domestic dogs are 1000, 106, 331, 3008. 103.

There are 80, 7, 0, 0, 600 reads of Murine

Orthopneumovirus in Q61, Q64, Q68, Q69, Q70.

The number of Malayan porcupines are 61, 30,

13, 0, 5018.

The number of Civet Kobuvirus is 90, 0, 0, 0, 0

for Q61, Q64, Q68, Q69, Q70.

masked palm civets are 424, 0, 0, 0, 0.

Finally, the number of SARS-CoV-2 is 1, 5, 7, 2

close to each other, 2 dar apart from each other

for Q61, Q64, Q68, Q69, Q70.

The number of Homo Sapiens are 21, 47, 164, 38,

12.

Q64, Q68, Q69 are PCR+, Q61 and Q70 are

PCR-.

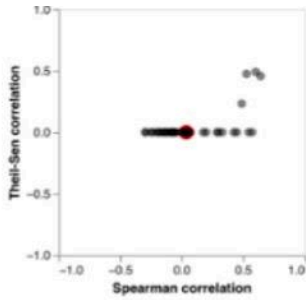
The animals correlate with animal viruses. The

**Table 1.** Summary of mink farm SARS-CoV-2 monitoring data amassed during a period of 14 months

Voivodeship	2021 (February–December)		2022 (January–March)		Total		Number of positive farms
	No. of farms	No. of swabs	No. of farms	No. of swabs	No. of farms	No. of swabs	
Mazowieckie	58	1,160	28	420	86	1,580	0
Podkarpackie	8	160	5	75	13	235	1
Lubuskie	35	700	19	295	54	995	0
Wielkopolskie	117	2,340	87	1,472	204	3,812	1
Zachodniopomorskie	54	1,080	8	420	62	1,500	3
Pomorskie	19	380	1	20	20	400	1
Dolnośląskie	14	280	0	0	14	280	0
Kujawsko-Pomorskie	24	480	0	0	24	480	1
Lubelskie	36	1,120	22	356	58	1,476	2
Lódzkie	6	120	1	15	7	135	1
Małopolskie	7	140	1	15	8	155	0
Opolskie	6	120	0	0	6	120	0
Podlaskie	10	200	0	0	10	200	1
Świętokrzyskie	6	120	13	185	19	305	0
Warmińsko-Mazurskie	1	20	0	0	1	20	0
Śląskie	8	160	0	0	8	160	0
<b>Total</b>	<b>409</b>	<b>8,580</b>	<b>185</b>	<b>3,273</b>	<b>594</b>	<b>11,853</b>	<b>11</b>



**Fig. 1.** Locations of inspected mink farms (marked as grey dots) and those which were SARS-CoV-2 positive (marked as red dots)



% species mitochondria reads computed as

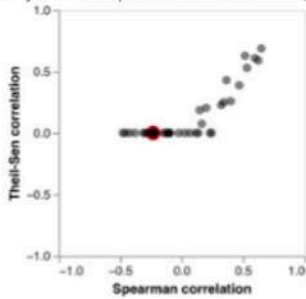
sample collection date

axis scale

sample isolation source

- species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

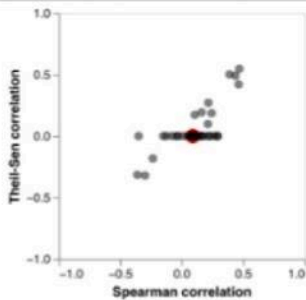
sample collection date

axis scale

sample isolation source

- species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

sample collection date

axis scale

sample isolation source

- species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no





**c. Animal Sampling at the Huanan Seafood Market**

In addition to taking environmental samples, 457 animal-related samples from “188 individuals of 18 species” were collected between January 1 and March 30, 2020.<sup>660</sup> According to presentations by PRC public health officials to the WHO, none of the samples tested positive for SARS-CoV-2.<sup>661</sup> PRC officials informed that none of the “animal-related” samples were taken from live animals present at the market:

The sources of the samples include unsold goods kept in refrigerators and freezers in the stalls of [Huanan Market], and goods kept in warehouses and refrigerators related to the [Huanan Market]. Samples from stray animals in the market were also collected, i.e., swab samples from 10 stray cats, 27 cat feces, one dog, one weasel, and 10 rats.... All the 457 animal samples tested negative for SARS-CoV-2 nucleic acid, suggesting that the animal infections with SARS-CoV-2 might be rare in the market.<sup>662</sup>

Nucleic Acid Testing (NAT)	
Hubei	
Number of species	10
Specific types of animals	Bamboo Rat, Porcupine, Duck, Snake, Rabbit/Hare, Chicken, Ostrich/Turkey, Wild Boar
Total sample size	616
Test results	Negative

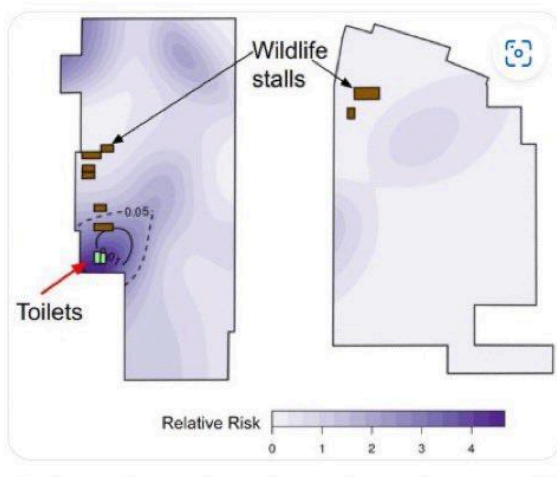
PRC officials denied any illegal live animal sales occurred at the Huanan Market.<sup>663</sup> Presentations to the WHO, PRC officials identified “10 animal selling stalls in the Huanan Market, accounting for 1.5% of the total” stalls.<sup>664</sup> Reviewing sales records provided by PRC officials, the WHO-China Report concluded that those 10 stalls sold “animals or products”, but that the only live animals sold were snakes, salamanders, and crocodiles.<sup>665</sup> None of which are susceptible to SARS-CoV-2, and thus are unlikely to be intermediate hosts.<sup>666</sup> All other animals were reportedly sold as frozen goods, including bamboo rats, badgers, hedgehogs, sika deer, and porcupines.<sup>667</sup>

Table 6. Family, genus, and species for 559 rodents sampled.

<b>Cricetidae</b>	
<i>Eothenomys cochinus</i>	92
<i>Eothenomys proclitor</i>	26
<b>Hystricidae</b>	
<i>Hystrix brachyura</i>	39
<b>Muridae</b>	
<i>Apodemus chevrieri</i>	123
<i>Apodemus draco</i>	1
<i>Apodemus latronum</i>	7
<i>Apodemus peninsulae</i>	28
<i>Niviventer confucianus</i>	1
<i>Niviventer coxingi</i>	2
<i>Niviventer eha</i>	27
<i>Niviventer fulvescens</i>	2
<i>Rattus tanezumi</i>	2
<i>Vernaya fulva</i>	1
<b>Spalacidae</b>	
<i>Rhizomys pruinosus</i>	20
<i>Rhizomys sinensis</i>	188

No rodent samples collected in this study were positive for Coronaviruses or Paramyxoviruses. Field identification of 89% (136/153) of host species (bats) with samples that tested positive for Coronaviruses or Paramyxoviruses was independently confirmed in the laboratory by commercial barcoding using the cytochrome b gene of bat mitochondrial DNA as a marker. Barcoding to identify species of 17 (11%) specimens was not possible due to insufficient sample quantity remaining after RT-PCR assays. Of the 89% tested and confirmed, the field identification was 100% accurate providing assurance that the unconfirmed species (by barcoding) had also have been accurately identified.

All Coronavirus positive samples were collected in four south China provinces (Hainan, Guangdong, Guangxi, and Yunnan), therefore no north-south gradient was discernible. Paramyxovirus positive samples were collected across a greater geographic range in China. Along a north-south gradient, the detection rate was significantly highest ( $\chi^2 = 7.8372$ ,  $p = 0.005118$ ) in the southern provinces of Fujian, Guangdong, Guangxi, Guizhou, and Yunnan. No correlation was evident between bat gender and detection of either virus ( $\chi^2 = 0.2638$ ,  $p = 0.607534$ ).



**Table 2.** A summary of the analysis of positive mink farms

No.	Date of sample collection	Voivodeship	Location	rRT-PCR	
				Positive/Tested	Ct value range*
1	16/06/2021	Lubelskie	Wisznice (house 1)	2/20	21.8–25.5
			Wisznice (house 2)	1/20	28.9
2	22/11/2021	Kujawsko-Pomorskie	Kraczki	1/20	28.9
3	30/11/2021	Zachodniopomorskie	Zieleniewo1	1/20	30.5
Zieleniewo2			13/20	24.7–36.8	
Ołuzna			19/20	18.9–37.3	
6	01/12/2021	Wielkopolskie	Biadki	18/20	17.6–36.4
7	14/12/2021	Podkarpackie	Janowiec	20/20	28.1–30.4
8	15/12/2021	Podlaskie	Kościuki	2/20	32.1–35.3
9	20/12/2021	Pomorskie	Leżno	10/20	19.1–26.3
10	20/12/2021	Lubelskie	Kloczew	5/20	28.9–30.2
11	20/01/2022	Łódzkie	Stefanów	2/20	20.5–21.8

Ct – threshold cycle; \* – results for E gene rRT-PCR

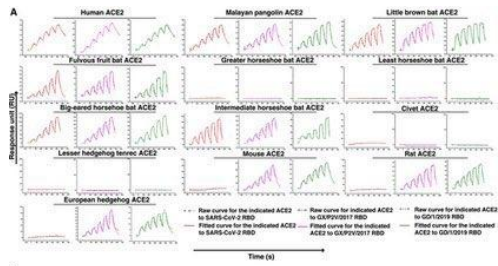
**Table 3.** Results of oral swab and serum sample analysis collected in two houses in Wisznice in the Lubelskie voivodeship

House	Date of sample collection	Sample	Number		Results*	Prevalence (%)
			Collected	Positive		
1	16/06/2021	Oral swab	20	2	21.8–25.5	10
	19/07/2021		90	1	28.8	1.1
	02/08/2021		15	15	1.25	100
			15	14	1.64	93.3
2	16/06/2021	Oral swab	20	2	28.5–30.7	10
	19/07/2021		60	0	-	0
	02/08/2021		15	15	1.04	100
			15	14	1.25	93.3

\* – results for E gene rRT-PCR/mean OD values obtained using Ingezim ELISA test

**Table 4.** Molecular characteristics of SARS-CoV-2 detected in farmed mink in Poland in the studied period

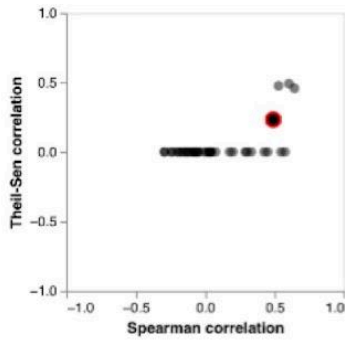
No.	Mink farm	Gisaid_ID	Clade	Pango lineage	Nucleotide		Frame shifts	Amino acid	
					substit.	delet.		substit.	delet.
1	Wisznice, house 2, Lubelskie	EPI_ISL_3218555	GR/20B	B.1.1	31	0	0	18	0
		EPI_ISL_3218557			31	0	0	18	0
2	Kraczki, Kujawsko-Pomorskie	EPI_ISL_7721854	GK/21J (Delta)	AY.43	44	13	0	34	4
		EPI_ISL_8693906			38	13	0	33	4
3	Ołuzna, Zachodniopomorskie	EPI_ISL_8693911	GK/21J (Delta)	AY.43	40	14	1	34	4
		EPI_ISL_8693912			38	13	0	33	4
4	Zieleniewo1, Zachodniopomorskie	EPI_ISL_8693816	GK/21J (Delta)	AY.43	38	13	0	33	4
		EPI_ISL_8693913			41	13	0	34	4
5	Biadki, Wielkopolskie	EPI_ISL_8693914	GK/21J (Delta)	AY.43	41	13	0	34	4
		EPI_ISL_8693915			41	13	0	34	4
6	Janowiec, Podkarpackie	EPI_ISL_9640028	GK/21J (Delta)	AY.126	51	104	1	37	34
		EPI_ISL_9640033			50	107	1	37	34
7	Kościuki, Podlaskie	EPI_ISL_9640052	GRY/20I (Alpha, V1)	B.1.1.7	50	107	1	37	34
		EPI_ISL_9640055			52	37	0	30	11
8	Leżno, Pomorskie	EPI_ISL_9640059	GK/21J (Delta)	B.1.617.2	47	16	0	37	5
		EPI_ISL_9640062			45	47	1	36	12
9	Kloczew, Lubelskie	EPI_ISL_9640065	GK/21J (Delta)	AY.122	41	16	0	32	4
		EPI_ISL_10337406			74	53	0	51	12
10	Stefanów, Łódzkie	EPI_ISL_10337127	GRA/21L (Omicron)	BA.2	72	53	0	51	12



**B**

	SARS-CoV-2 RBD (nM)	GX/PPV2017 RBD (nM)	GD/10219 RBD (nM)
Human	11.2 ± 0.5	11.9 ± 0.1	13.6 ± 0.7
Pangolin	34.1 ± 0.5	58.8 ± 1.2	68.7 ± 6.2
Little brown bat	397.4 ± 35.4	200.3 ± 19.5	155.2 ± 63.9
Fulous fruit bat	2349.33 ± 179.1	938.4 ± 471.1	1020.7 ± 342.1
Greater horseshoe	--	--	--
Least horseshoe bat	--	--	--
Big-eared horseshoe bat	179.8 ± 4.8	267.0 ± 24.3	311.9 ± 50.3
Intermediate horseshoe bat	483.9 ± 45.9	492.0 ± 121.5	827.7 ± 580.2
Mouse	--	291.3 ± 73.0	100.0 ± 27.1
Rat	--	466.1 ± 124.4	265.3 ± 132.0
European hedgehog	--	2115.3±978.5	710.8±266.4
Civet	--	--	--
Lesser hedgehog tenrec	--	--	--





% species mitochondria reads computed as

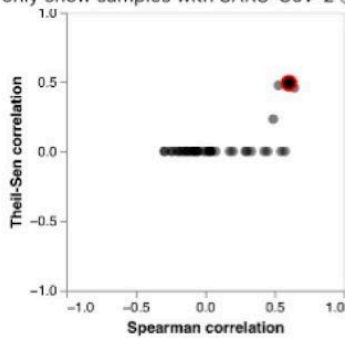
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan mar  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

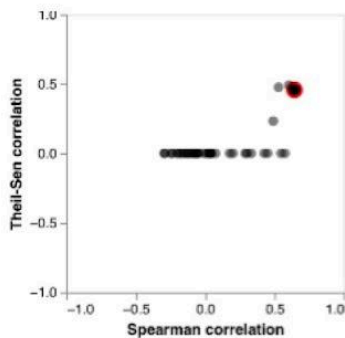
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axis scale

sample isolation source

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only show samples with SARS-CoV-2  yes  no



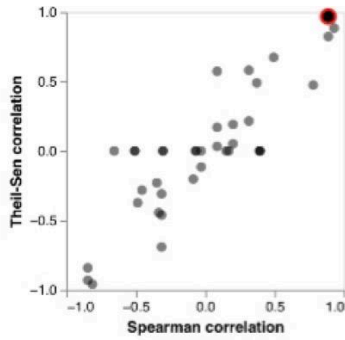
% species mitochondria reads computed as

sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan mar  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon



% species mitochondria reads computed as

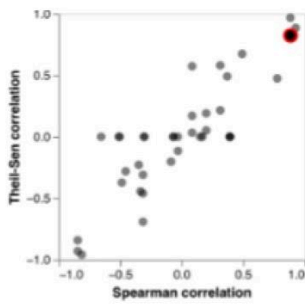
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

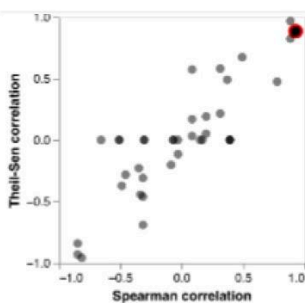
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no

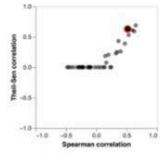
Kristian Andersen 18:52

Run some more selection stuff - here are the numbers. Only thing one can really say is that it looks like the SARS spike protein was possibly under positive selection early in the epidemic and that's not something we see with SARS-CoV-2. I had expected dN/dS to be lower for ORF1, but here SARS-CoV-2 is actually higher.

Not really sure we can conclude anything from these... it's somewhat intriguing that the spike from SARS-CoV-2 doesn't appear to be under selection at all though - does suggest some sort of pre-circulation to me

Selection plot

	ORF1	Spike
SARS-CoV-2	0.91	0.29
SARS, early	0.81	1.82
SARS, middle	0.68	0.44
SARS, late	0.32	0.51



% species mitochondria reads computed as % of all preprocessed reads

sample collection date all

axis scale log10 of % (zero plotted as minimum non-zero value)

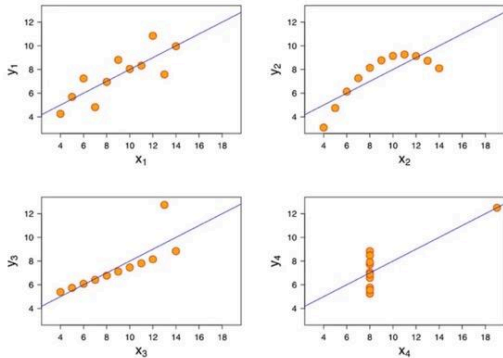
sample isolation source all

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no

### Overall correlation of mitochondrial DNA and SARS-CoV-2 across all samples using Theil-Sen estimator

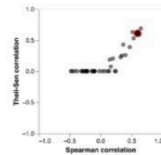
Each point shows the correlation between the percent of all high-quality reads that align to SARS-CoV-2 and the percent of aligned mitochondrial reads for a specific species taken across all samples. The axes show the Spearman correlation and a measure of correlation based on the Theil-Sen estimator.



Source: Wikipedia

An alternative to least squares for simple linear regression is Theil-Sen estimation. This more robust method determines the slope of the regression line via the median of the slopes of all lines that can be drawn through the data points:

$$m_{TS}(x, y) = \text{median}_{\substack{k, l \in \{1, \dots, n\} \\ x_k \neq x_l}} \left( \frac{y_l - y_k}{x_l - x_k} \right)$$



% species mitochondria reads computed as % of all preprocessed reads

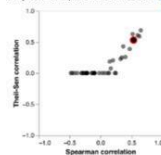
sample collection date all

axis scale log10 of % (zero plotted as minimum non-zero value)

sample isolation source all

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as % of all preprocessed reads

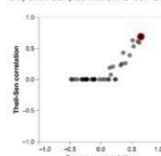
sample collection date all

axis scale log10 of % (zero plotted as minimum non-zero value)

sample isolation source all

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as % of all preprocessed reads

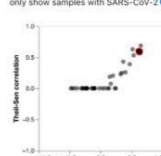
sample collection date all

axis scale log10 of % (zero plotted as minimum non-zero value)

sample isolation source all

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as % of all preprocessed reads

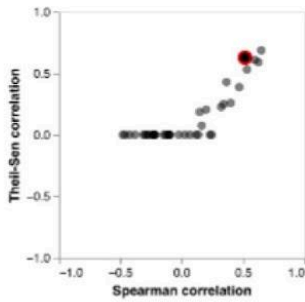
sample collection date all

axis scale log10 of % (zero plotted as minimum non-zero value)

sample isolation source all

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

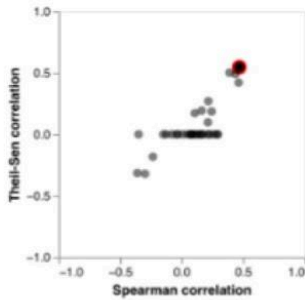
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

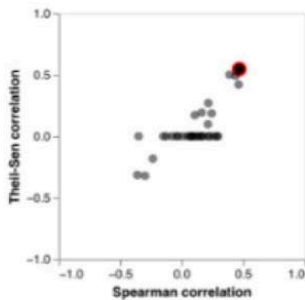
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

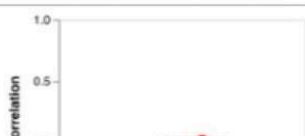
sample collection date

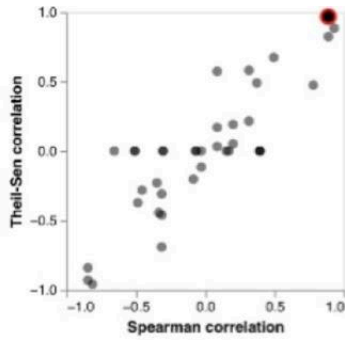
axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no





% species mitochondria reads computed as

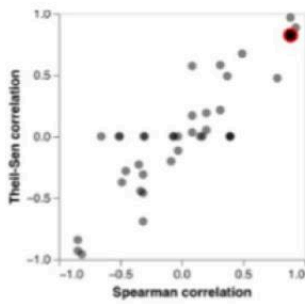
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

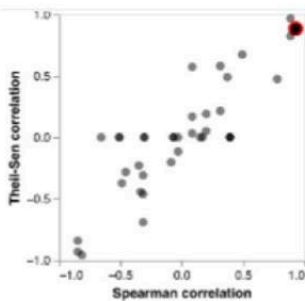
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

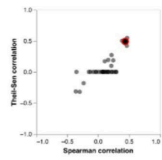
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



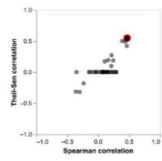
% species mitochondria reads computed as % of all preprocessed reads

sample collection date 2020-01-01

axis scale log10 of % (zero plotted as minimum non-zero value)

sample isolation source all

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish) only show samples with SARS-CoV-2  yes  no



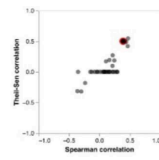
% species mitochondria reads computed as % of all preprocessed reads

sample collection date 2020-01-01

axis scale log10 of % (zero plotted as minimum non-zero value)

sample isolation source all

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish) only show samples with SARS-CoV-2  yes  no



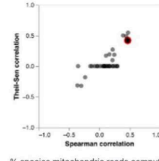
% species mitochondria reads computed as % of all preprocessed reads

sample collection date 2020-01-01

axis scale log10 of % (zero plotted as minimum non-zero value)

sample isolation source all

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish) only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as % of all preprocessed reads

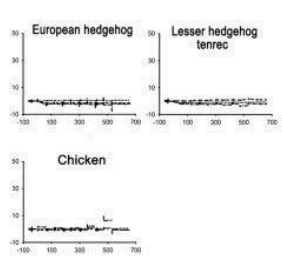
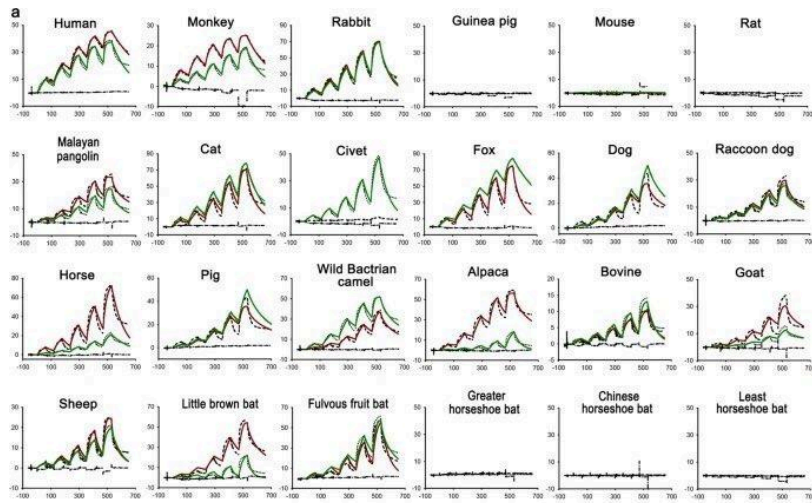
sample collection date 2020-01-01

axis scale log10 of % (zero plotted as minimum non-zero value)

sample isolation source all

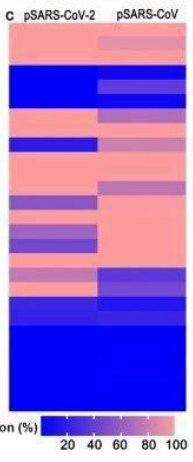
species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish) only show samples with SARS-CoV-2  yes  no





— Fitted curve for the indicated ACE2 to SARS-CoV-2 RBD  
 - - - Raw curve for the indicated ACE2 to SARS-CoV-2 RBD  
 — Fitted curve for the indicated ACE2 to SARS-RBD  
 - - - Raw curve for the indicated ACE2 to SARS-RBD  
 - - - Raw curve for the indicated ACE2 to SARS-CoV-2 NTD

	SARS-CoV-2 RBD	SARS-CoV RBD
Human	21.73 ± 1.54	43.27 ± 6.43
Monkey	21.73 ± 1.97	89.07 ± 4.31
Rabbit	76.20 ± 20.96	74.83 ± 3.06
Guinea pig	--	--
Mouse	--	--
Rat	--	--
Malayan pangolin	66.80 ± 8.22	226.67 ± 54.28
Cat	85.70 ± 19.16	69.90 ± 0.75
Civet	--	121.00 ± 16.37
Fox	40.63 ± 2.63	17.85 ± 1.63
Dog	98.67 ± 25.67	19.97 ± 0.67
Raccoon dog	96.40 ± 18.16	178.67 ± 175.05
Horse	132.63 ± 31.05	141.33 ± 20.28
Pig	47.63 ± 8.10	35.83 ± 9.05
Wild Bactrian camel	272.33 ± 161.85	69.10 ± 3.82
Alpaca	16520 ± 19147	54.90 ± 2.15
Bovine	73.67 ± 53.27	89.77 ± 65.86
Goat	157.00 ± 23.58	308.00 ± 174.26
Sheep	197.03 ± 44.25	157.33 ± 26.50
Little brown bat	312.33 ± 90.79	12380 ± 17046
Fulvous fruit bat	1132 ± 338	412.33 ± 58.5
Greater horseshoe bat	--	--
Chinese horseshoe bat	--	--
Least horseshoe bat	--	--
European hedgehog	--	--
Lesser hedgehog tenrec	--	--
Chicken	--	--



Relative transduction (%)

20 40 60 80 100

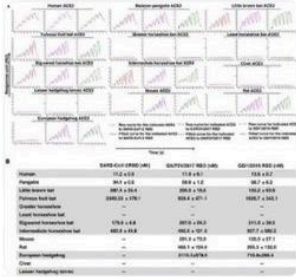
Hedgehogs does not have an ACE2 that is permissive to infection at all and all porcupine suppliers in the HSM can be traced back to supply farms in Hubei that tested negative (the S.D. Of malayan porcupine is 0 in Xiao Xiao et al sales. Indicating stable supply from a registered



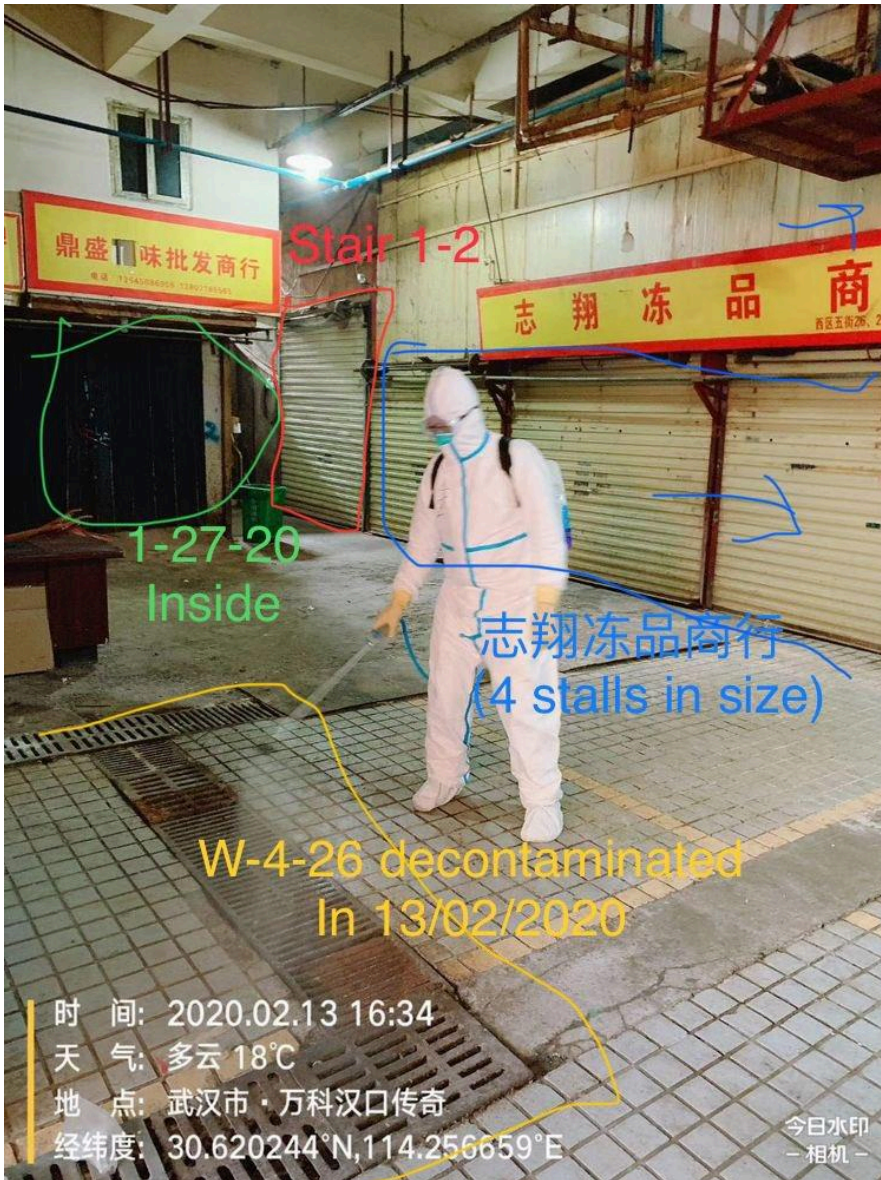
Species	Mean	Min	Max	S.D.
Pallas's squirrel	16.52 ± 4.87 (n = 23)	0.00	49.67	12.00
Masked palm civet	10.69 ± 8.42 (n = 29)	0.00	49.67	12.00
Chinese bamboo rat	42.76 ± 20.68 (n = 29)	0.00	49.67	12.00
Malayan porcupine	10.00 ± 0.00 (n = 29)	0.00	49.67	12.00
Chinese muntjac	10.00 ± 0.00 (n = 29)	0.00	49.67	12.00
Coypu	5.00 ± 0.00 (n = 29)	0.00	49.67	12.00
Marmot	15.00 ± 4.29 (n = 20)	0.00	49.67	12.00
Red fox	30.00 ± 0.00 (n = 25)	0.00	49.67	12.00
Mink	10.37 ± 1.92 (n = 27)	0.00	49.67	12.00
Red squirrel	16.43 ± 9.51 (n = 28)	0.00	49.67	12.00
Wild boar	4.17 ± 5.77 (n = 29)	0.00	49.67	12.00
Complex-toothed Flying Squirrel	5.17 ± 27.85 (n = 29)	0.00	49.67	12.00

在武汉周边的襄樊、随州、咸宁、江夏地区的华南海鲜市场上游供货商养殖场采集的竹鼠、豪猪、火鸡、兔子等动物样本和环境标本共 139 份。经湖北省疾控中心 sRT-PCR 检测检测结果为阴性。

Species	Mean	Min	Max	S.D.
Pallas's squirrel	16.52 ± 4.87 (n = 23)	0.00	49.67	12.00
Masked palm civet	10.69 ± 8.42 (n = 29)	0.00	49.67	12.00
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Coypu	5.00 ± 0.00 (n = 29)	0.00	49.67	12.00
Marmot	15.00 ± 4.29 (n = 20)	0.00	49.67	12.00
Red fox	30.00 ± 0.00 (n = 25)	0.00	49.67	12.00
Mink	10.37 ± 1.92 (n = 27)	0.00	49.67	12.00
Red squirrel	16.43 ± 9.51 (n = 28)	0.00	49.67	12.00
Wild boar	4.17 ± 5.77 (n = 29)	0.00	49.67	12.00
Complex-toothed Flying Squirrel	5.17 ± 27.85 (n = 29)	0.00	49.67	12.00







1-27-26  
Inside

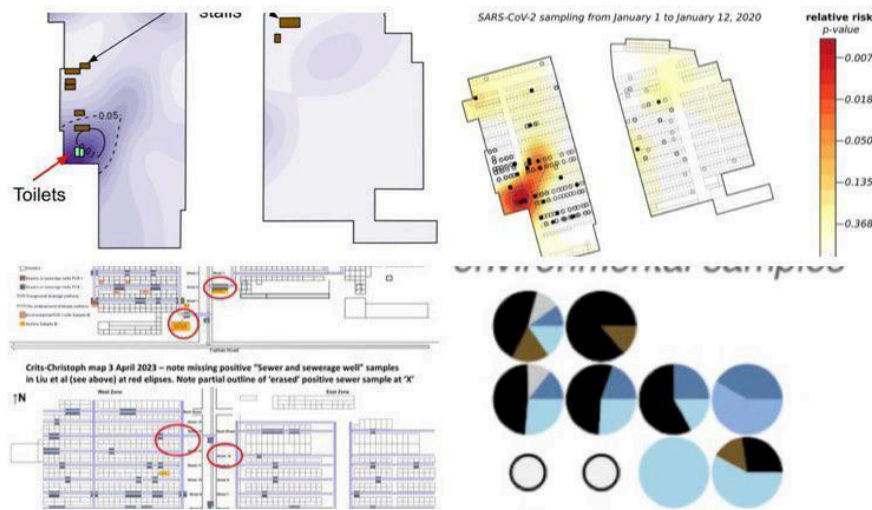
志翔冻品商行  
(4 stalls in size)

W-4-26 decontaminated  
In 13/02/2020

时间: 2020.02.13 16:34  
天气: 多云 18°C  
地点: 武汉市·万科汉口传奇  
经纬度: 30.620244°N, 114.256659°E

今日水印  
- 相机 -

Which is also why in both Jan 01 and in Jan12, the stall with the most positive samples out of all samples is the stall closest to the toilets— W4-26(2/2)and outside of W4-26-28(5/6 or 5/9 for all samples W4-26-28) for Jan01, W6-29-33(5/10) in Jan 12 is closest to the toilets.































 **Daoyu**  @Daoyu15 · 2023/5/13

This is again wrong. The highest positive rate of any stall that tested from 01-12/Jan 2020 was actually W4-28. 2/2 samples were positive. In fact the samples from the outside surfaces of W4-26-28 was the highest positivity rate of any sites for Jan0...

14:03 · 2023/5/29 位于 Earth · 2933 次查看

现呼吸困难。徐冰和同事对他们的病史、接触史进行了调查，发现他们或是在华南海鲜市场工作，或是住在市场附近，“很多病人是相互认识的，有人会告诉我们，亲戚住在哪个医院，状况非常不好”。徐冰发现，这些人有的来自一个家族，有的则是长久的麻将搭子——这些基本上能够判断这是一次聚集性发病事件。

-  **Daoyu**  @Daoyu15 · May 13 ...  
This is again wrong. The highest positive rate of any stall that tested from 01-12/Jan 2020 was actually W4-28. 2/2 samples were positive. In fact the samples from the outside surfaces of W4-26-28 was the highest positivity rate of any sites for Jan01-Jan12.  
 1  2  1  2,755 
-  **Daoyu**  @Daoyu15 · May 13 ...  
There are 2 samples taken from W4-28 and both were positive by PCR. There are 3 samples from inside of W4-26 and 4 samples from the outside of W4-26. All 3 samples from W4-26 that is positive came from the outside of W4-26. This makes it 5/6 PCR+ samples. On the other hand,  
 1  1  1  159 
-  **Daoyu**  @Daoyu15 · May 13 ...  
W6-29-33 itself have only 3 PCR positive samples and the 1 read or 2 reads close to each other make it impossible to rule out that the samples suffered significant cross-contamination (all that is needed is 1 fragment of ssRNA less than 100nt in length and 1 fragment of  
 1  1  1  160 
-  **Daoyu**  @Daoyu15 · May 13 ...  
dsDNA or hairpin RNA less than 100bp in length for Q61 and Q70–falling directly from the neighboring samples After the PCR reaction and during NGS library preparation.)  
 1  1   133 



澎湃  
PENGPAI

声音来源：  
华南海鲜市场首位确诊病例 魏女士

好像没去哪里 我这个人又不打牌



与陈先生情况类似 魏女士至今也没想通  
自己到底是怎么染病的

05:08 / 06:07



她多次回忆病发前的生活轨迹  
除了超市、市场、家里，她哪儿也没去

05:17 / 06:07



shutterstock.com · 1569723133

←

## Flo Débarre

9,596 posts

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Likes

Traditional Chinese	武漢+不明+病毒+人傳人	Wuhan + Obviously + Virus + Human-to-human transmission	2020-02-12
<b>ALT</b> Selection of keyword combinations censored on WeChat criticizing government actors or policies COVID-19			

🗨️ 2
↻
❤️ 1
📊 15
🔗

**Flo Débarre** @flodebarre · 30m

But the first line seems to be related to this [sohu.com/a/370615513\\_10...](https://sohu.com/a/370615513_10...)

🗨️
↻
❤️ 1
📊 9
🔗

**Flo Débarre** @flodebarre · 4h

Replying to @\_everythingism @zhihuachen and 2 others

I remember a report analyzing words censored on the internet early on and I think WIV was included? (From a North American institution)

Does this ring a bell?

🗨️ 1
↻
❤️ 1
📊 97
🔗

**Flo Débarre** @flodebarre · 3h

Here it is [citizenlab.ca/2020/03/censor...](https://citizenlab.ca/2020/03/censor...)

Language	Keyword	English Translation	Date Added
Simplified Chinese	武汉不明肺炎	Unknown Wuhan pneumonia	2019-12-31
Simplified Chinese	武汉海鲜市场	Wuhan seafood market	2019-12-31
Simplified Chinese	沙士变异	SARS variation	2019-12-31
Traditional Chinese	爆發sars疫情	SARS outbreak in Wuhan	2019-12-31
Simplified Chinese	武汉卫生委员会	Wuhan Health Committee	2019-12-31
Simplified Chinese	p4病毒实验室	P4 virus lab	2019-12-31

**ALT** Selection of keywords added to YY's blacklist on December 31, 2019

🗨️ 2
↻
❤️ 2
📊 88
+

↻ Flo Débarre reposted



Flo Débarre

9,596 posts

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Posts

Replies

Media

Likes



Flo Débarre @flodebarre · 11m

Ah interesting. Could the "monkey bite" from Markson's book be a distortion of that initial monkey speculation?

1



2

6



Flo Débarre @flodebarre · 33m

Replying to @\_everythingism @zhihuachen and 2 others

there is also WeChat for later dates. Their data are on Github if you are interested [github.com/citizenlab/cha...](https://github.com/citizenlab/cha...)

Language	Keyword Combination	English Translation	Date Tested
Simplified Chinese	扒一扒武汉病毒所-所长的成功史	Muckraking Wuhan Virus Lab + Successful history of lab director	2020-02-14
Traditional Chinese	地方官+疫情+中央+隱瞞	Local authorities + Epidemic + Central (government) + Cover-up	2020-02-13
Traditional Chinese	舉行+批評中郎+兩會期間+隱瞞	Hold + Criticize China + During two annual meetings + Cover-up	2020-02-13
Traditional Chinese	武漢+中共+危機+北京	Wuhan + CCP + Crisis + Beijing	2020-02-11
Traditional Chinese	共产党+肺炎+表现+统治	Communist Party + Pneumonia + Demonstrate + Rule	2020-02-05
Simplified Chinese	疫情+红会+4+政府+湖北	Epidemic + Red Cross Society + 4 + Government + Hubei	2020-02-04
Simplified Chinese	中国共产党+最大的威胁+这个时代	CCP + Biggest threat + The era	2020-02-05
Traditional Chinese	武漢+明明+病毒+人傳人	Wuhan + Obviously + Virus + Human-to-human transmission	2020-02-12

**ALT:** Selection of keyword combinations censored on WeChat criticizing government actors or policies related to COVID-19

2



1

15



Flo Débarre @flodebarre · 30m

But the first line seems to be related to [sohu.com/a/370615513\\_10...](https://sohu.com/a/370615513_10...)

1



1

9



12月31日一早，多名身着防护服、背着喷雾器的防疫人员出现在华南海鲜市场里消毒，让人们回想起2003年SARS来袭时的场面。SARS全称为“严重急性呼吸系统综合征”，于2002年在中国广东出现，此后迅速扩散至全国乃至全球，最终造成超过8000人感染，774人死亡。

事实上，这天上午，国家卫健委一个专家组即抵达武汉。当天中午1点左右，武汉市卫健委首次公开发布通报称，近期部分医疗机构发现接诊的多例肺炎病例与华南海鲜市场有关联，目前已经发现27例，其中7例病情严重，其余病例病情稳定可控，有2例病情好转拟于近期出院。

2020年1月1日上午8时，华南海鲜市场出现落款为“武汉市江汉区市场监督管理局”和“卫生健康局”的休市整顿公告。该公告称：根据国务院《突发公共卫生事件应急条例》等法规条例的规定及武汉市卫生健康委关于肺炎疫情的情况通报，经研究决定对华南海鲜批发市场实行休市，进行环境卫生整治，请广大商户积极配合。

当天休市前，华南海鲜市场大部分商户还在营业。财新记者在现场看到，身着白色防化服的工作人员出现，准备进一步消毒。大部分商户只好收拾店面陆续离开，时有工作人员在市场里催促收摊。休市后，商户们聚集在市场外的路上，对突然休市和肺炎传闻议论纷纷。

1月2日，大量环卫工人在华南海鲜市场进行清洁作业，市场门口沿街排水沟渠的污泥也被挖出。财新记者在现场看到，身着防化服的人员在市场各处采样。其中，西区七街附近作为消毒重点区域，检疫人员为每个门面逐一搜集、提取检测物质。

- Daoyu @Daoyu15 · 2023/4/6  
Here is a list of January 01 and January 12 samples and you can see a pattern:  
Stall w7-15-17: door, surface of food, package of aquatic product and basket is negative. Ground, glove and shoe covers and soles (left from Dec31 samplers) is positive.
- Daoyu @Daoyu15 · 2023/4/6  
W4-X6-X4: both rolling shutters are negative. Both of the grounds are positive. Only pigs, sheeps and cows are present. Humans is in only one sample.  
W8-19-21-23: chopping blocks and knives are negative. Sewage is positive. Pig, sheep, cow and dog. No wildlife and little human.
- Daoyu @Daoyu15 · 2023/4/6  
The first sampling from W8-25 all negative. One W8-25 sample is contaminated. (Inner surface of freezer).  
W6-29-33 have 7 objects on the ground: cart 1, container, cart 2, bucket, Ground, feather removal machine, iron container in the inner room. (Picture indicate container and)
- Daoyu @Daoyu15 · 2023/4/6  
One garbage cart (full of livestock and no wildlife or humans) is positive, garbage vehicle (handled by human) is negative. W7-25: surface of door and filter are negative. Ground is positive.
- Daoyu @Daoyu15 · 2023/4/6  
W7-20-22-24 and w7-16-18: surface of door are negative, ground is positive. Both w4-28 samples are positive, ground and door.  
W4-24: door negative, ground positive.  
W4-19: door positive, ground negative.
- Daoyu @Daoyu15 · 2023/4/6  
Cart 1 have 1 viral read, "29 human" and PCR negative, Container is "negative", cart 2 have 5 viral reads, "53 humans" and positive by PCR. Bucket is also "negative", Ground have "204 humans", 7 viral reads and positive by PCR.
- Daoyu @Daoyu15 · 2023/4/6  
Feather removal machine have 2 viral reads, "47 human reads" and PCR positive. "Iron container in inner room" have "16 human reads", 2 viral reads and PCR negative.  
3 objects not on the ground are basket, white box and iron container (seen in the picture as higher up on a truck).
- Daoyu @Daoyu15 · 2023/4/6  
W2-5: styrofoam desk in front of door positive. Door and ground negative. Note that the desk is still close to the ground(?)  
E9-22: blood in front of the door is positive, many reads, little human and mostly pig and cow.
- Daoyu @Daoyu15 · 2023/4/6  
E6-1-3: ground is positive. Surface of foam box and food are negative.  
W11-15: only the surface of the wall is positive. Live virus isolated. Human case is present. ground, basket, foam box, scale, water in basin are negative. Direct Handling by humans destroy viral RNA.
- Daoyu @Daoyu15 · 2023/4/6  
W2-17: ground is negative. Rolling shutter door is positive.  
W2-24: roller shutter is negative, ground is positive.  
W2-14 (F54): roller shutter is negative. Ground is positive. Live virus isolated. Cow DNA and no wildlife DNA.



also, the bags in the market were single-use disposable plastic bags which are handled only once (on the mouth of the bags) before being put down or ditched. Desks (and distinct from "box") are handled only on their top surfaces but may be swabbed on their bottom sides.

Scale on desk  
Fishbowl  
White box  
Bucket

1月3日武汉华南海鲜批发市场  
我们这么多工作人员都没有感染 我们明天由谁感染

大众点评

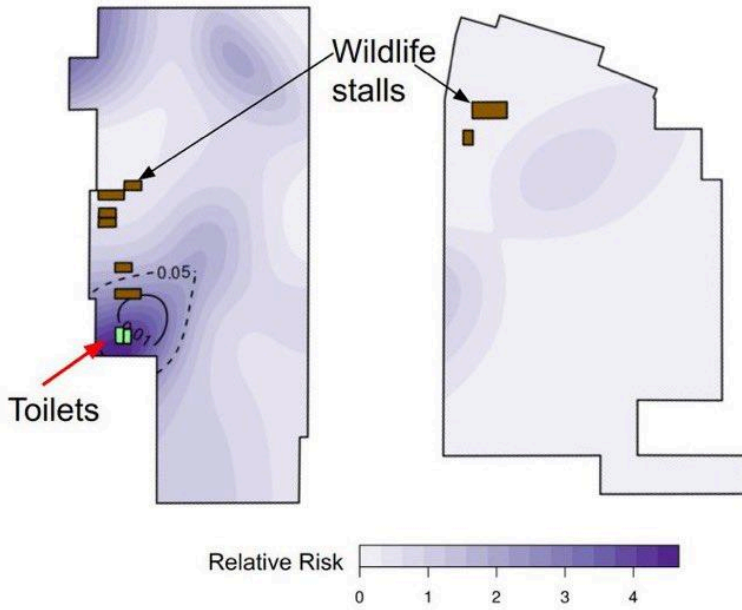
西区二街

已无大碍  
Scale  
Packaging bag

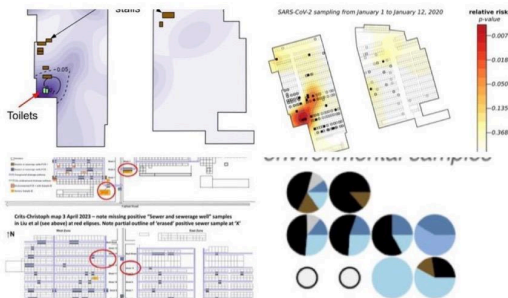
Daoyu @Daoyu15 · 2小時  
This is an example of contamination caused by the back sides of the suits of samplers. And it turned out that they sit on the market surfaces sometimes.....

Daoyu @Daoyu15 · 48分鐘  
needing to bow into the "inner surface of freezer" also caused the sample tube to hit the waist and rear side of the suit of the samplers when the sampler holds an open tube on his off hand when bowing his upper body into the freezer to swab the bottom surface. The tube

Daoyu @Daoyu15 · 40分鐘  
Gets contaminated on the lip and resulted in a PCR-/NGS+, as taking the aliquot for the PCR reaction causes the residual medium in the tube to contact the lip of the tube, contaminating the subsequent NGS reaction.



Which is also why in both Jan 01 and in Jan12, the stall with the most positive samples out of all samples is the stall closest to the toilets— W4-26(2/2) and outside of W4-26-28(5/6 or 5/9 for all samples W4-26-28) for Jan01, W6-29-33(5/10) in Jan 12 is closest to the toilets.



Daoyu @Daoyu15 · 2023/5/13

This is again wrong. The highest positive rate of any stall that tested from 01-12/Jan 2020 was actually W4-28. 2/2 samples were positive. In fact the samples from the outside surfaces of W4-26-28 was the highest positivity rate of any sites for Jan0...

14:03 · 2023/5/29 位于 Earth · 2933 次查看





Daoyu @Daoyu15 · 6天  
Also, unlike vendor gloves ("gloves" when not present together with "shoe covers") that are all negative, Sampler gloves (outer gloves worn by double-gloved samplers) are nuclease-free as professional PPE are sterile products and the outer layers are not in direct contact with



Human skin. Same as "Shoe covers and soles" or "bottom of shoe covers". Both receive contamination from the outside environment—what they touched or stepped on (labs, outside roads and toilet areas), and transfer them to these environments (what they stepped on or kicked).

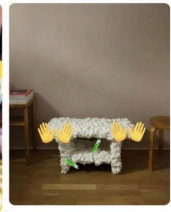
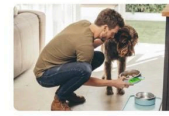
Daoyu @Daoyu15 · 5天  
Human skin. Same as "Shoe covers and soles" or "bottom of shoe covers". Both receive contamination from the outside environment—what they touched or stepped on (labs, outside roads and toilet areas), and transfer them to these environments (what they stepped on or kicked).

36

@Daoyu15

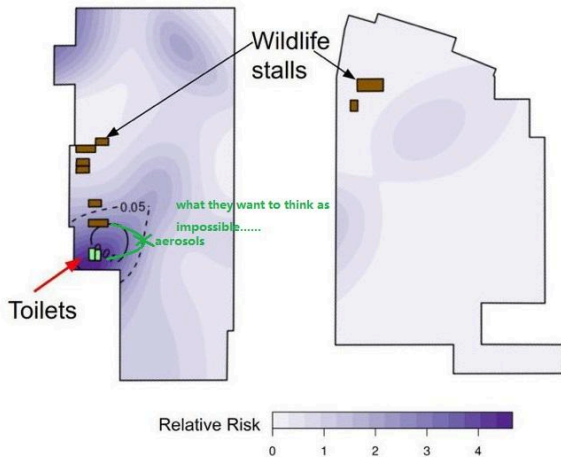
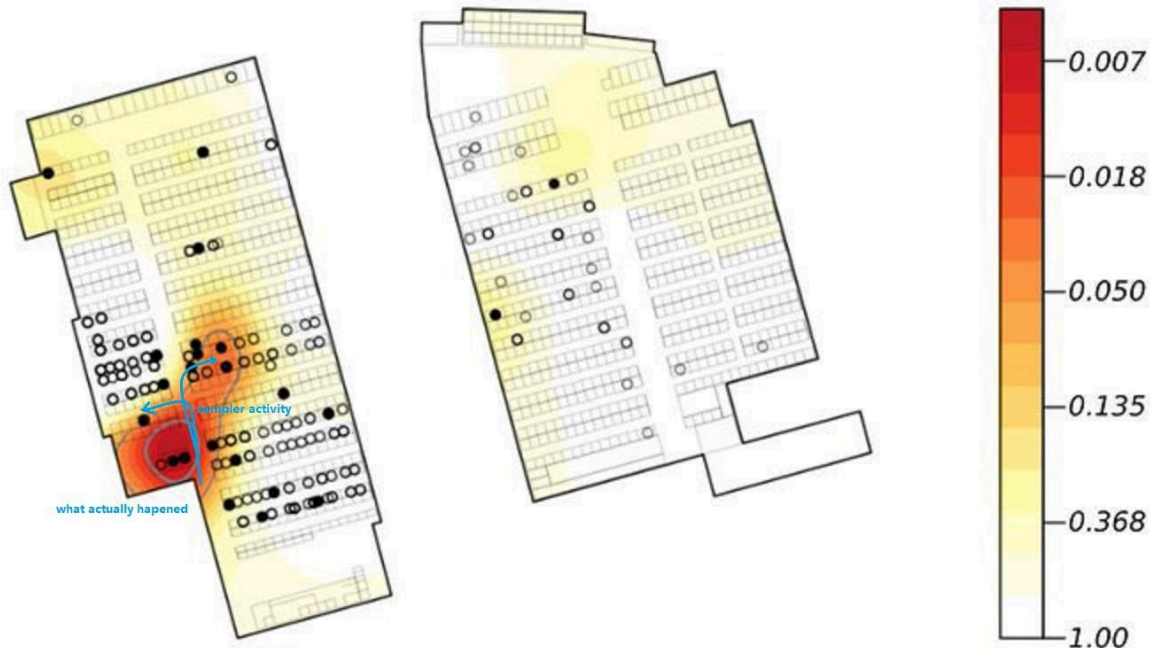


36-原图片



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

**SARS-CoV-2 relative risk**  
p-value



519	Env_0516	HJ200001-2	2020/1/12	West Wine of HSM	9	34-36	Environmental swab Table top
520	Env_0517	HJ200002-2	2020/1/12	West Wine of HSM	9	34-36	Environmental swab Scale
521	Env_0518	HJ200003-2	2020/1/12	West Wine of HSM	9	34-36	Environmental swab Container
522	Env_0519	HJ200004-2	2020/1/12	West Wine of HSM	9	34-36	Environmental swab Container
523	Env_0520	HJ200005-2	2020/1/12	West Wine of HSM	9	34-36	Environmental swab Basket
524	Env_0521	HJ200006-2	2020/1/12	West Wine of HSM	9	34-36	Environmental swab Feather removal machine
525	Env_0522	HJ200007-2	2020/1/12	West Wine of HSM	9	34-36	Environmental swab Table
526	Env_0523	HJ200008-2	2020/1/12	West Wine of HSM	9	34-36	Environmental swab Inner surface of refrigera
527	Env_0524	HJ200009-2	2020/1/12	West Wine of HSM	9	34-36	Environmental swab Inside of feather removal
528	Env_0525	HJ200010-2	2020/1/12	West Wine of HSM	9	34-36	Environmental swab Outside surface of refrig

579	Env_0576	Q61	2020/1/12	West Wine of HSM	6	29-31-33	Environmental swab Cart1
580	Env_0577	HJ200062-2	2020/1/12	West Wine of HSM	6	29-31-33	Environmental swab Container
581	Env_0578	HJ200063-2	2020/1/12	West Wine of HSM	6	29-31-33	Environmental swab Basket
582	Env_0579	Q64	2020/1/12	West Wine of HSM	6	29-31-33	Environmental swab Cart2
583	Env_0580	HJ200065-2	2020/1/12	West Wine of HSM	6	29-31-33	Environmental swab White box
584	Env_0581	HJ200066-2	2020/1/12	West Wine of HSM	6	29-31-33	Environmental swab Iron container
585	Env_0582	HJ200067-2	2020/1/12	West Wine of HSM	6	29-31-33	Environmental swab Bucket
586	Env_0583	Q68	2020/1/12	West Wine of HSM	6	29-31-33	Environmental swab Ground
587	Env_0584	Q69	2020/1/12	West Wine of HSM	6	29-31-33	Environmental swab Feather removal machine
588	Env_0585	Q70	2020/1/12	West Wine of HSM	6	29-31-33	Environmental swab Iron container in inner ro



Code	Location	Date	Lat	Long	Code	Code	Code	Code
CS	Wall inside the stalls	2020/2/20	+	32.59~37.34	RDRP/NE	NA		
SFD	Storehouse ground	2020/2/22	+	39.39,39.25,35.48	RDRP/NE	NA		
SFC5	Storehouse weight scale	2020/2/22	+	40.21,40.13,37.37	RDRP/NE	NA		
SFL3	Storehouse wire fence	2020/2/22	+	41.77,41.62,37.61	RDRP/NE	NA		
REL-C4	Storehouse bag surfaces	2020/2/22	+	41.71,41.53,37.31	RDRP/NE	NA		
REL-C3	Storehouse bag surfaces	2020/2/22	+	36.18,36.05,32.36	RDRP/NE	NA		

Table 6. Family, genus, and species for 559 rodents sampled.

Family	Count
<b>Cricetidae</b>	
<i>Euthromomys couchinus</i>	92
<i>Euthromomys greifleri</i>	26
<b>Hystriidae</b>	
<i>Hystrix brachyura</i>	39
<b>Muridae</b>	
<i>Apodemus chevrieri</i>	123
<i>Apodemus draco</i>	1
<i>Apodemus latronum</i>	7
<i>Apodemus peninsulae</i>	28
<i>Niviventer confucianus</i>	1
<i>Niviventer coxingeri</i>	2
<i>Niviventer eha</i>	27
<i>Niviventer fulvescens</i>	2
<i>Rattus tanezumi</i>	2
<i>Vernaya fulva</i>	1
<b>Sparacidae</b>	
<i>Rhizomys pruinosus</i>	20
<i>Rhizomys sinensis</i>	188

No rodent samples collected in this study were positive for Coronaviruses or Paramyxoviruses. Field identification of 89% (136/153) of host species (bats) with samples that tested positive for Coronaviruses or Paramyxoviruses was independently confirmed in the laboratory by commercial barcoding using the cytochrome b gene of bat mitochondrial DNA as a marker. Barcoding to identify species of 17 (11%) specimens was not possible due to insufficient sample quantity remaining after RT-PCR assays. Of the 89% tested and confirmed, the field identification was 100% accurate providing assurance that the unconfirmed species (by barcoding) had also been accurately identified.

All Coronavirus positive samples were collected in four south China provinces (Hainan, Guangdong, Guangxi, and Yunnan), therefore no north-south gradient was discernible. Paramyxovirus positive samples were collected across a greater geographic range in China. Along a north-south gradient, the detection rate was significantly highest ( $X^2 = 7.8372, p = 0.005118$ ) in the southern provinces of Fujian, Guangdong, Guangxi, Guizhou, and Yunnan. No correlation was evident between bat gender and detection of either virus ( $X^2 = 0.2638, p = 0.607534$ ).

Search “Regional Animal Health Office No. 6 (RAHO6), Viet Nam Department of Animal Health; Viet Nam National Institute of Hygiene & Epidemiology; Wildlife Conservation Society” on GenBank for vietnamese porcupines. Only murine coronavirus, IBV and Alphacoronaviruses were found.

[journals.plos.org/plosone/article...](https://journals.plos.org/plosone/article...)

No Coronaviruses were found in porcupines in China,

[core.ac.uk/download/pdf/1...](https://core.ac.uk/download/pdf/1...)

And no Sarbecovirus genomes from genus *Hystrix* or a SC2r-CoV genome from the genus *Nyctereutes* (or any Sarbecovirus genomes at all after the SARS-CoV-1 epidemic) have ever been deposited on GanBank anywhere in the world.

## Validation of RNASeq Data - How to validate RNASeq DEGs using qPCR

Hi, Biostars! Can anyone tell me how to validate the RNA-Seq Differential gene expression data using qPCR? How many genes should I select for qPCR validation? Is there any criteria for selecting the differentially expressed genes for qPCR validation? and finally what is the best method to visualize/represent the correlation between RNA-Seq and qPCR data?

Thank you all!!

RNA-Seq DESeq2 • 4.7k views

ADD COMMENT • link

updated 2.5 years ago by Antonio R. Franco ★  
5.1k • written 5.7 years ago by Sreeraj Thamban  
▲ 280

Hey! It's highly recommendable to validate at least 20 genes. I'd suggest to choose the ones interesting for the topic you are addressing in your study and ones completely random, or for which you observed an interesting behaviour. The method is a simple Pearson correlation between the two groups: 1: RNA-Seq data and 2: qPCR data. If you got a Pearson correlation value of min 0.7 consider your validation already quite good! Good luck!

ADD COMMENT • link

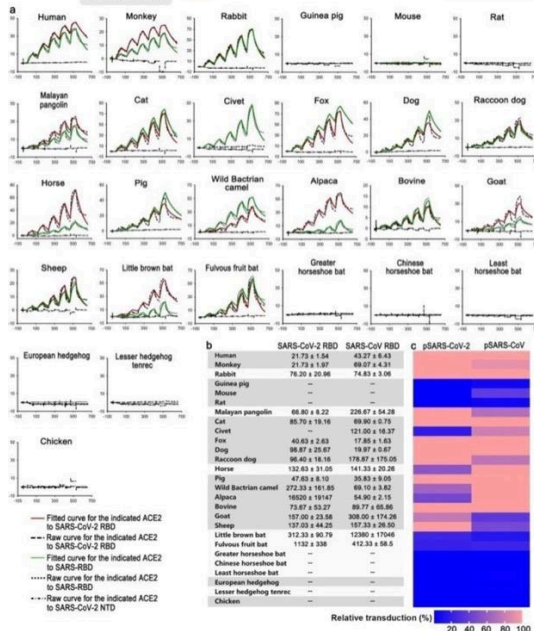
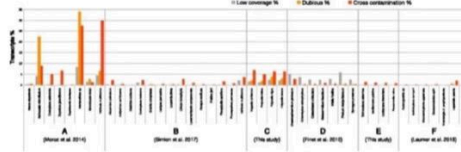


Fig. 1



Pervasive cross contaminations observed in recent transcriptomic datasets from six different labs.

For each transcriptome, three columns indicate the percentage of transcripts categorised as low coverage (*grey bars*), dubious (*orange bars*) and cross contamination (*red bars*) as detected by CroCo (using default parameters). For the content of each dataset, see Additional file 1: Table S1; references [16, 22, 34, 41]

Full size image >

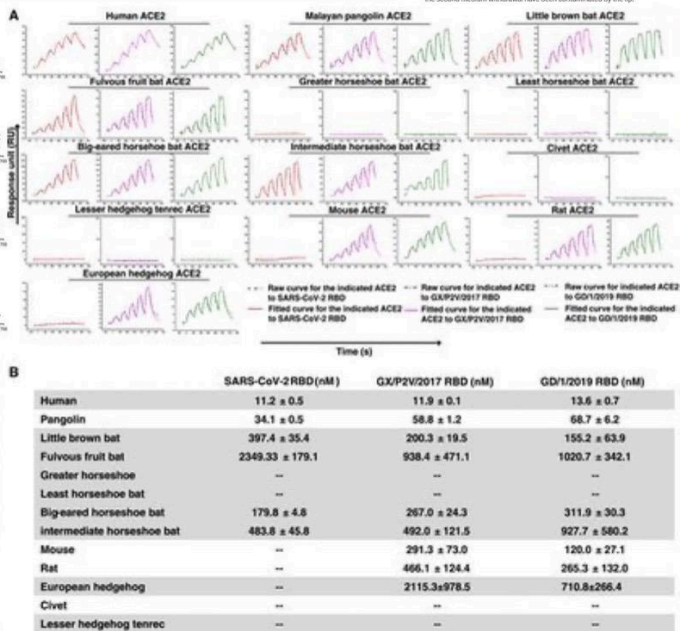


All that existed in Q61 was 1 saRNA fragment less than 300nt in length that fell from the neighboring Q64. All that existed in Q70 was 1 hairpin fragment less than 100bp in length that fell in from the neighboring Q68 and Q69. Both have sufficient homo Sapiens in them that fall

In alongside, Q37 is caused by contamination from sampler suits when it rubbed against the lip of the sample tube by accident. Neither was WB-25 positive in Jan 01 nor would the "freezer" test positive again afterward. The later "positive samples" have either no reads at all or



Have only artifacts. And that "freezer" no longer tested positive. This also have alignment over the CCDC-DSF lab primer, yet it is PCR negative, indicating that the PCR medium withdrawn for PCR is negative whereas the second medium withdrawn have been contaminated by the lip.



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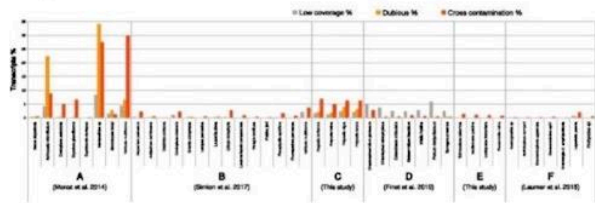
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ADD COMMENT • link

Fig. 1



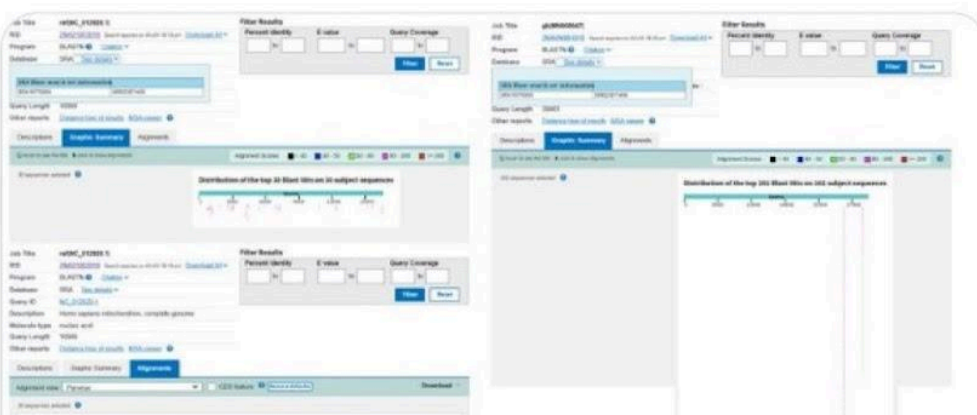
Pervasive cross contaminations observed in recent transcriptomic datasets from six different labs. For each transcriptome, three columns indicate the percentage of transcripts categorised as low coverage (*grey bars*), dubious (*orange bars*) and cross contamination (*red bars*) as detected by CroCo (using default parameters). For the content of each dataset, see Additional file 1: Table S1; references [16, 22, 34, 41]

Full size image >

All that existed in Q61 was 1 ssRNA fragment less than 300nt in length that fell from the neighboring Q64. All that existed in Q70 was 1 hairpin fragment less than 100bp in length that fell in from the neighboring Q68 and Q69. Both have sufficient Homo Sapiens in them that fell



In alongside. Q37 is caused by contamination from sampler suits when it rubbed against the lip of the sample tube by accident. Neither was W8-25 positive in Jan 01 nor would the “freezer” test positive again afterward. The later “positive samples” have either no reads at all or



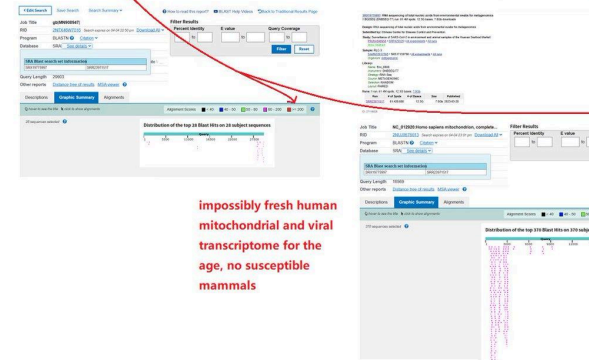
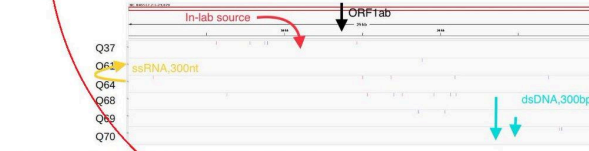
Env_0510	G94	2020/1/1	West Wine of HSM	8	25	Environmental swab Ground	N	Negative		
Env_0511	G95	2020/1/1	West Wine of HSM	8	25	Environmental swab Kiefer	N	Negative		
Env_0512	G96	2020/1/1	West Wine of HSM	8	25	Environmental swab Scale	N	Negative		
Env_0513	G97	2020/1/1	West Wine of HSM	8	25	Environmental swab Table top	N	Negative		
Env_0514	G98	2020/1/1	West Wine of HSM	8	25	Environmental swab Container	N	Negative		
Env_0515	G99	2020/1/1	West Wine of HSM	8	25	Environmental swab Drainage outlet	N	Negative		
Env_0552	Q37	2020/1/12	Inner surface of the freezer	8	25	NA <sup>4</sup>	ORF lab/N	Yes		
Env_0576	Q61	2020/1/12	Cart1	6	29-31-33	-	NA	ORF lab/N	Yes	
Env_0579	Q64	2020/1/12	Cart2	6	29-31-33	+	+	+	ORF lab/N	Yes
Env_0583	Q68	2020/1/12	Ground	6	29-31-33	+	+	+	ORF lab/N	Yes
Env_0584	Q69	2020/1/12	Feather removal machine	6	29-31-33	+	+	+	ORF lab/N	Yes
Env_0585	Q70	2020/1/12	Iron container in inner room	6	29-31-33	-	NA	ORF lab/N	Yes	

<sup>4</sup> The PCR results of Env\_0552, Env\_0576 and Env\_0585 were negative. There were no CT values for these samples. The PCR results of Env\_0579, Env\_0583 and Env\_0584 were positive, but the CT values for these samples were not recorded from the laboratory. **all of the freezers tested negative after**

Env_0713	8-25-L	2020/2/3	West Wine of HSM	8	25	Environmental swab Container	N	Negative
Env_0714	8-25-BX	2020/2/3	West Wine of HSM	8	25	Environmental swab Inner surface of refrigera	N	Negative
Env_0715	8-25-D	2020/2/3	West Wine of HSM	8	25	Environmental swab Knife	N	Negative
Env_0716	8-25-CK	2020/2/3	West Wine of HSM	8	25	Environmental swab Storage	N	Negative
Env_0717	8-25-D	2020/2/3	West Wine of HSM	8	25	Environmental swab Ground inside the stalls	Positive	
Env_0718	8-25-DZ	2020/2/3	West Wine of HSM	8	25	Environmental swab Surface of packing bag	Negative	
Env_0719	8-25-M1	2020/2/3	West Wine of HSM	8	25	Environmental swab Ground inside the stalls	Positive	
Env_0720	8-25-M2	2020/2/3	West Wine of HSM	8	25	Environmental swab Ground	Negative	
Env_0733	8-25-D1	2020/2/9	West Wine of HSM	8	25	Environmental swab Ground	N	Negative
Env_0734	8-25-D2	2020/2/9	West Wine of HSM	8	25	Environmental swab Ground	N	Negative
Env_0755	8-25-D3	2020/2/9	West Wine of HSM	8	25	Environmental swab Ground	N	Negative
Env_0756	8-25-Long	2020/2/9	West Wine of HSM	8	25	Environmental swab Container	N	Negative
Env_0757	8-25-Bang	2020/2/9	West Wine of HSM	8	25	Environmental swab Inner surface of refrigera	N	Negative

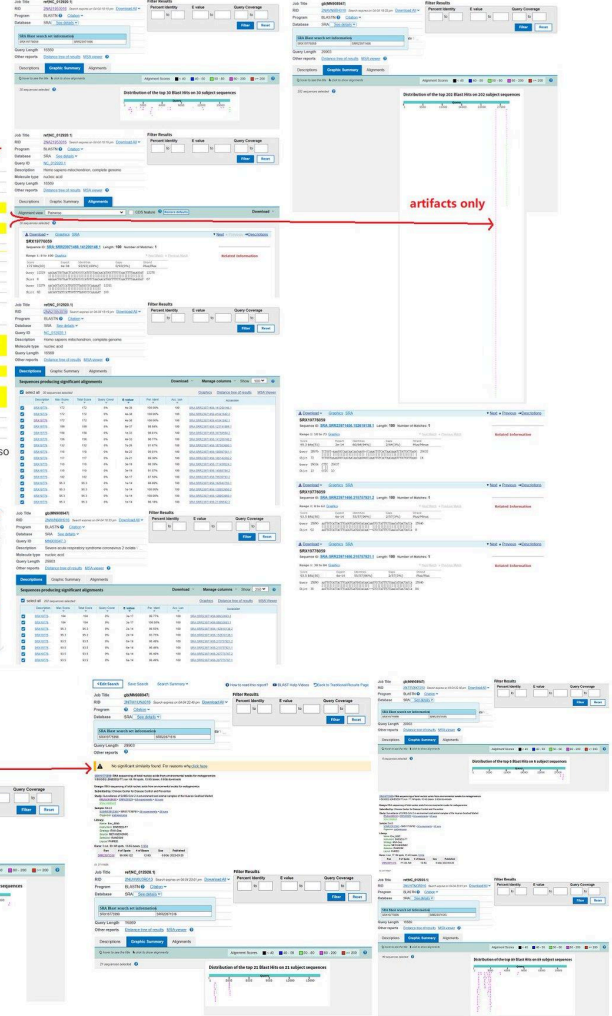
Env_0860	SF-BX-2	2020/2/22	Warehouses related to west wine of H 8	25	Environmental swab Inner surface of refrigera	Negative	
Env_0861	SF-BX-1	2020/2/22	Warehouses related to west wine of H 8	25	Environmental swab Inner surface of refrigera	Negative	
Env_0862	SF-D	2020/2/22	Warehouses related to west wine of H 8	25	Environmental swab Storehouse	Positive	
Env_0863	SF-CS	2020/2/22	Warehouses related to west wine of H 8	25	Environmental swab Storehouse weight scale	Positive	
Env_0864	SF-L1	2020/2/22	Warehouses related to west wine of H 8	25	Environmental swab Storehouse wire fence	Negative	
Env_0865	SF-L3	2020/2/22	Warehouses related to west wine of H 8	25	Environmental swab Storehouse wire fence	Positive	
Env_0866	SF-L2	2020/2/22	Warehouses related to west wine of H 8	25	Environmental swab Storehouse wire fence	Negative	
Env_0867	RLC-4	2020/2/22	Warehouses related to west wine of H 8	25	Environmental swab Storehouse bag surfaces	Positive	
Env_0868	RLC-3	2020/2/22	Warehouses related to west wine of H 8	25	Environmental swab Storehouse bag surfaces	Positive	
Env_0869	RLC-5	2020/2/22	Warehouses related to west wine of H 8	25	Environmental swab Storehouse bag surfaces	Negative	
Env_0870	RLC-2	2020/2/22	Warehouses related to west wine of H 8	25	Environmental swab Storehouse ground	Negative	
Env_0871	RLC-1	2020/2/22	Warehouses related to west wine of H 8	25	Environmental swab Storehouse ground	Negative	

Have Only artifacts. And that "freezer" no longer tested positive. This also have alignment over the CCDC ORF lab primer, yet it is PCR negative, indicating that the first medium withdrawal for PCR is negative whereas the second medium withdrawal have been contaminated by the lip.



impossibly fresh human mitochondrial and viral transcriptome for the age, no susceptible mammals

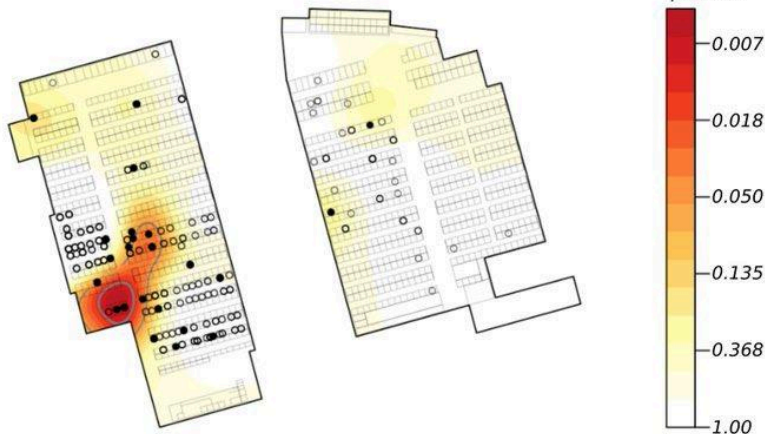
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artifacts only



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



(C) researchers at the Wuhan Institute of Virology who fell ill in autumn 2019, including for any such researcher--

- (i) the researcher's name;
- (ii) the researcher's symptoms;
- (iii) the date of the onset of the researcher's symptoms;

not closely related to SARS-CoV-2. Hu says he never worked with live viruses in that experiment or any others done in Shi's lab. "My work in the lab was mainly genome characterization and evolutionary analysis of viruses," Hu wrote.





**Daoyu** @Daoyu15 · May 3  
Sterilized surfaces. This may have to do with the nucleases found on human skin.

Unfortunately, whatever "non-inactivating virus preservation solution" of Gao et al didn't contain an RNase inhibitor. (See the list of components).



hutchisonintl.com  
Virus Collection and Preservation System (Individually Packaged)  
DescriptionThe Hutchison Virus Collection and Preservation System i...

1 1 2 262

**Daoyu** @Daoyu15 · May 3  
The boxes and baskets are direct evidence that this issue with differential stability (highly handled surfaces failed to preserve SARS-CoV-2 RNA and are always negative) is in operation, as unlike other everyday objects (knives, chopping blocks, cashiers, cups, likely fishbowls),

1 1 2 241

**Daoyu** @Daoyu15 · May 3  
Baskets and boxes are observed on the ground in the market.

1 2 120

**Daoyu** @Daoyu15 · May 3  
Finally, plastic packaging bags are single-use and receive only limited contamination from handling—the openings will contact skin while the body and bottom of such bags will not before being ditched in sewage, on or near the ground.

1 2 149

**Daoyu** @Daoyu15 · May 3  
Some objects including many of the containers have handles, however none of the boxes and baskets in the market have handles.

1 2 156

**Daoyu** @Daoyu15 · May 4  
Also the only "glove" that is positive..... was located in the same location as the only "shoe cover" in the market. The PPE study on stability of SARS-CoV-2 RNA should tell you something.

1 1 114



**Daoyu** @Daoyu15 · May 3  
Also I wonder why no objects that were frequently and directly handled by a vendor tested positive?

As in stall 7-15-17, the basket and is negative. In stall 4-26, the fishbowls were negative. In stall 5-6-8, knife, cashier, basket, fishbowls were negative. In stall 15-X44,

1 1 2 194

**Daoyu** @Daoyu15 · May 3

Cashier is negative (the scales are ground scales with a top that is handled and a measuring surface that is swabbed. The carts have carrying surface that is swabbed and handles that is handled).

In stall 5-25-25, Cashier and water cup was negative. 6-1-3, box is negative.

1 1 110

**Daoyu** @Daoyu15 · May 3

11-15, basket, box were negative.

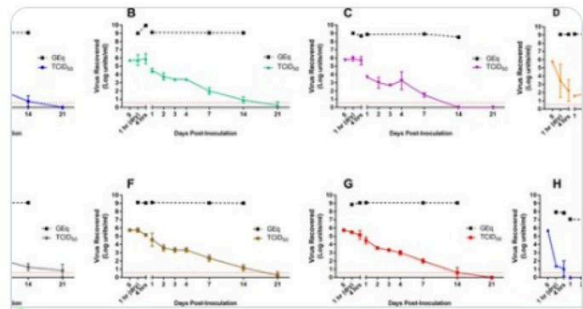
8-19-21-23, chopping block and knife negative.

11-15 is where F13 is located. Somehow live virus, no wildlife in sample, human cases, but still none of the objects directly and frequently handled by vendors tested positive.

1 1 129

**Daoyu** @Daoyu15 · May 3

We do know that if something is frequently handled (vs not handled and clean), the [nature.com/articles/s41591-021-01111-1](https://www.nature.com/articles/s41591-021-01111-1). Stability of SARS-CoV-2 RNA is reduced from over a month to less than 3 days—the earlier surface stability assays are largely based on newly [ncbi.nlm.nih.gov/pmc/articles/P...](https://pubmed.ncbi.nlm.nih.gov/35411111/)



nature.com  
Stability of SARS-CoV-2 on critical personal protective equipment  
Scientific Reports - Stability of SARS-CoV-2 on critical personal protective equipment

Daoyu @Daoyu15 · Apr 24  
More specifically, in order to test positive in Gao's sampling, a swab must include materials that were once stuck to the suits, pants and boots (with heavy preference to pants and boots, sites that are most likely receive and deposit contamination inadvertently as samplers

1 4 1 2,693

Daoyu @Daoyu15 · Apr 24  
walked through the market) of the samplers, and must not include any material that once directly contacted the skin of the vendors. Discarded sampler PPE, containers and bags on the ground, doors, floors and other low-lying objects placed on the ground (such as scales and carts)

1 4 1 1,546

Daoyu @Daoyu15 · Apr 24  
And walls (low-lying parts of walls) Are positive. Vendor gloves (gloves not found together with shoe covers), vendor shoes (not shoe covers which are professional PPE worn only by samplers), everyday objects such as knives, chopping blocks, scissors, mops and cashiers/cups

1 4 1 1,921

Daoyu @Daoyu15 · Apr 24  
Used by the vendors, boxes and baskets frequently handled by vendors as well as any objects unlikely kicked, trampled on and does not need leaning and bowing inside to sample, including all surfaces with physical height above the waist of the samplers and all surfaces of food,

1 4 1 1,704

Daoyu @Daoyu15 · Apr 24  
Mushrooms, vegetables located within containers and the insides of fishbowls and sinks, were negative, even when located in a positive stall with a human case and no wildlife DNA in the positive sample.

1 4 1 2,570

Daoyu @Daoyu15 · Apr 30  
These rules overpowers all other factors including all epidemiological factors such as the presence of a human case in the stall, a positive sample within the stall without wildlife DNA, or even both—handled by a vendor or not contaminated by a sampler(above waist height,

1 4 1 1,029

Daoyu @Daoyu15 · Apr 30  
Unlikely rubbed against, stepped on/kicked, and where aseptic techniques can be practiced without difficulties), not positive. Human cases don't make everyday objects positive and even human case in stall and positive sample without wildlife DNA don't translate to positive result

1 3 1 507

Daoyu @Daoyu15 · Apr 30  
Where sampler-linked contamination is not possible (F13, stall W11-15, "water in basin"/F14; B5, stall W5 6-8, "fishbowl"/B2 and "water in fishbowl"/B7).

Daoyu @Daoyu15 · May 23  
Sampler =positive.  
[twitter.com/daoyu15/status...](https://twitter.com/daoyu15/status...)

Daoyu @Daoyu15 · Apr 24  
More specifically, in order to test positive in Gao's sampling, a swab must include materials that were once stuck to the suits, pants and boots (with heavy preference to pants and boots, sites that are most likely receive and deposit contamination inadvertently as samplers  
[Show this thread](#)

1 2 1 426

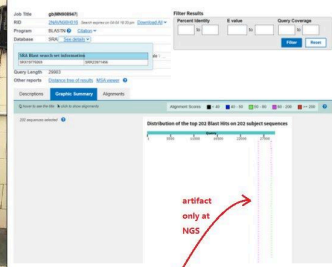
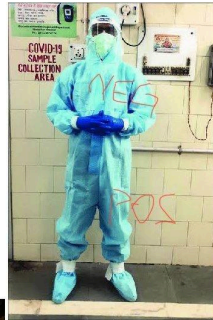
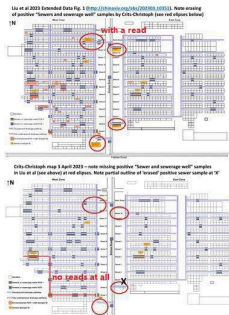
Daoyu @Daoyu15 · May 23  
Vendor and other objects that are frequently and repeatedly handled by the vendors =negative.

Daoyu @Daoyu15 · Apr 24  
And walls (low-lying parts of walls) Are positive. Vendor gloves (gloves not found together with shoe covers), vendor shoes (not shoe covers which are professional PPE worn only by samplers), everyday objects such as knives, chopping blocks, scissors, mops and cashiers/cups  
[Show this thread](#)

1 2 1 444

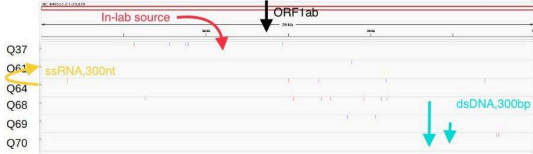
Daoyu @Daoyu15 · May 23  
 in , and other objects that were not likely touched by sampler suits pants and boots, and where aseptic techniques can be practiced during sampling (not in awkward locations requiring leaning into to sample)were negative.

Daoyu @Daoyu15 · Apr 24  
Mushrooms, vegetables located within containers and the insides of fishbowls and sinks, were negative, even when located in a positive stall with a human case and no wildlife DNA in the positive sample.  
[Show this thread](#)



PCR - despite alignment over CCDC ORF1ab/N  
ORF1ab primer (2 in the same PCR, 1 C)

1-27-33	Water drain	none of these have a	2020/1/27	+	36	ORF1ab	NA
1-27-37	Water drain	SARS-CoV-2 read.	2020/1/27	+	35	ORF1ab	NA
1-29-4	Water drain		2020/1/29	+	36	ORF1ab	NA
1-29-8	Water drain		2020/1/29	+	37	ORF1ab	NA
8-25-D	Ground inside the stalls		2020/2/3	+	35.9	ORF1ab	+
8-25-M1	Ground inside the stalls		2020/2/3	+	36.5	ORF1ab	+
W-8-25-D1	Ground inside the stalls		2020/2/15	+	36.77	ORF1ab	NA
W-8-25-D2	Ground inside the stalls		2020/2/15	+	33.91	ORF1ab	NA
W-8-25-L	Container		2020/2/15	+	34.58	ORF1ab	NA
W-8-25-L2	Container		2020/2/15	+	37.16	ORF1ab	NA

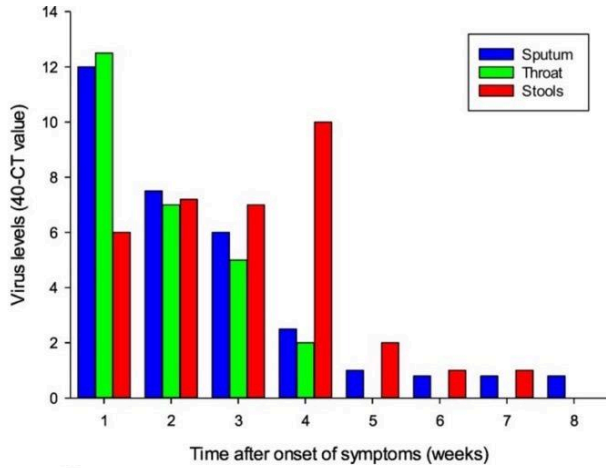
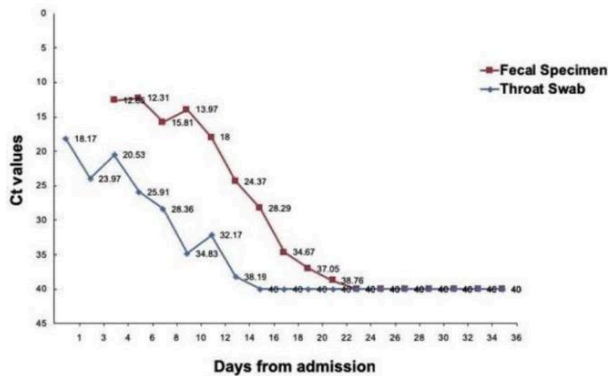


G93	Sewage		2020/1/1	+	33.23	ORF1ab/N	NA
Q37	Inner surface of the freezer		2020/1/12	-	\	ORF1ab/N	+
Q61	Cart1		2020/1/12	+	\	ORF1ab/N	+
Q64	Cart2		2020/1/12	+	+	ORF1ab/N	+
Q68	Ground		2020/1/12	+	+	ORF1ab/N	+
Q69	Feather removal machine		2020/1/12	+	+	ORF1ab/N	+
Q70	Iron container in inner room		2020/1/12	-	\	ORF1ab/N	+

[pubmed.ncbi.nlm.nih.gov/32870707/](https://pubmed.ncbi.nlm.nih.gov/32870707/) at least early in the pandemic, fecal-aerosol transmission (e.g. Poop is aerosolized and then inhaled) is detected. And the RNA shedding for human SARS-CoV-2 in stools is found to be comparable to, and often exceed, the shedding from respiratory samples. There is enough time for the earliest patients and infections to reach the dominant fecal shedding regimes even in adults —and stool/fecal/enteric shedding are also brought all over the market on the outer clothing and shoes of people. Human->feces in toilets->boots and suit of samplers+shoes and outer clothing of vendors and visitors->positive environmental samples. [archive.md/LJzSO](https://archive.md/LJzSO) [archive.md/4cCHG](https://archive.md/4cCHG)

In fact, the samples in the market follows the rule which a positive sample [archive.md/CTP3i](https://archive.md/CTP3i) [archive.md/ETjzS](https://archive.md/ETjzS) [archive.md/BWZJL](https://archive.md/BWZJL) must be contacted by samplers. 🧤 🧥 🧦 =positive. [archive.md/NeybM](https://archive.md/NeybM) [archive.md/2PM9Y](https://archive.md/2PM9Y) [archive.md/RirQ7](https://archive.md/RirQ7) And not frequently handled by vendors. 🍌 🍌 🍌 🍌 🍌 🍌 🍌 =negative.

[archive.md/DChUL](https://archive.md/DChUL) [archive.md/4rVph](https://archive.md/4rVph) [archive.md/yyXOZ](https://archive.md/yyXOZ) [archive.md/iw1Pz](https://archive.md/iw1Pz)



 **Dr. Ali Nouri**   
@AliNouriPhD

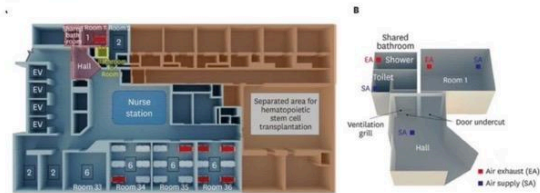
📍 Evidence for airborne SARS-COV-2 transmission between 2 people who visited same bathroom 40 min apart\*

Conclusion backed up by contact tracing, CCTV, & virus' genomic sequence.

\*Bathroom was poorly ventilated due to malfunctioning air exhaust.

Report: [rb.gy/kz5xsh](https://rb.gy/kz5xsh)

翻译帖子



04:58 · 2021/7/5 位于 Earth

## Validation of RNASeq Data - How to validate RNASeq DEGs using qPCR



Hi, Biostars! Can anyone tell me how to validate the RNA-Seq Differential gene expression data using qPCR? How many genes should I select for qPCR validation? Is there any criteria for selecting the differentially expressed genes for qPCR validation? and finally what is the best method to visualize/represent the correlation between RNA-Seq and qPCR data?

Thank you all!!

RNA-Seq DESeq2 • 4.7k views

ADD COMMENT • link

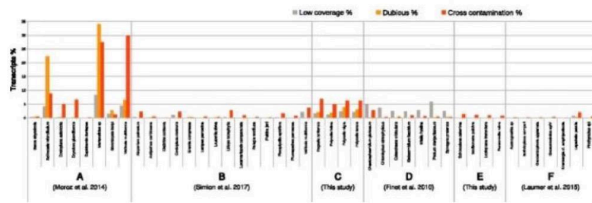
updated 2.5 years ago by Antonio R. Franco ★  
5.1k • written 5.7 years ago by Sreeraj Thamban ▲ 280



Hey! It's highly recommendable to validate at least 20 genes. I'd suggest to choose the ones interesting for the topic you are addressing in your study and ones completely random, or for which you observed an interesting behaviour. The method is a simple Pearson correlation between the two groups: 1: RNA-Seq data and 2: qPCR data. If you got a Pearson correlation value of min 0.7 consider your validation already quite good! Good luck!

ADD COMMENT • link

Fig. 1



Pervasive cross contaminations observed in recent transcriptomic datasets from six different labs. For each transcriptome, three columns indicate the percentage of transcripts categorised as low coverage (*grey bars*), dubious (*orange bars*) and cross contamination (*red bars*) as detected by CroCo (using default parameters). For the content of each dataset, see Additional file 1: Table S1; references [16, 22, 34, 41]

Full size image >

If a Raccoon-dog became infected - somehow - w/SARS2 virus, it would be unlikely they would spread Covid-19; but even if its snot managed to infect other Raccoon-dogs, Freuling et al 2020 indicates virus transmission would end there (max shed was only 42 live SARS2 virions/ml)

### 翻译帖子

Emerging Infectious Diseases

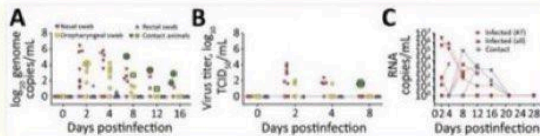


Figure 2

Detection of severe acute respiratory syndrome coronavirus 2 in swab samples from experimentally infected raccoon dogs. A) Viral genome loads in swab samples isolated on Vero E6 cells; B) viral genome loads in virus titers isolated on Vero E6 cells. Two replicates per sample were analyzed. C) Individual viral loads of nasal swab specimens taken from infected and contact animals.

We detected infection in 2 (66.7%) of 3 contact animals (nos. 10 and 11) (Figure 2; Appendix Figure 2). We first detected viral RNA in animal no. 10 on day 8 (i.e., 7 days after contact). Viral shedding, mainly in nasal secretions, lasted until day 16 (15 days after contact), and we identified viral titers of 1.625 log<sub>10</sub> TCID<sub>50</sub>/mL in nasal swab samples on day 8 (7 days after contact). One contact raccoon dog (no. 12) remained negative for SARS-CoV-2 because infection did not deve<sup>l</sup>

Also, can you trust an 2021 cohort study testing on "ANY" 67 cases to be "all negative"? It is in 2021. The entirety of Wuhan community had 4% seroprevalence at the end of lockdowns. No "magic protection" from post-lockdown reinfection because you are an NNDRS reject case.

- Enter a value in each of the first three text boxes (the unshaded boxes).
- Click the **Calculate** button to compute binomial and cumulative probabilities.

Probability of success on a trial	<input type="text" value="0.04"/>
Number of trials	<input type="text" value="67"/>
Number of successes (x)	<input type="text" value="0"/>
Binomial probability: $P(X=0)$	<input type="text" value="0.06489"/>
Cumulative probability: $P(X<0)$	<input type="text" value="0"/>
Cumulative probability: $P(X\leq 0)$	<input type="text" value="0.06489"/>
Cumulative probability: $P(X>0)$	<input type="text" value="0.93511"/>
Cumulative probability: $P(X\geq 0)$	<input type="text" value="1"/>

**Pathogenicity of two new bat SARS-related coronaviruses to transgenic mice expressing human ACE2**

Person in charge: Hu Ben

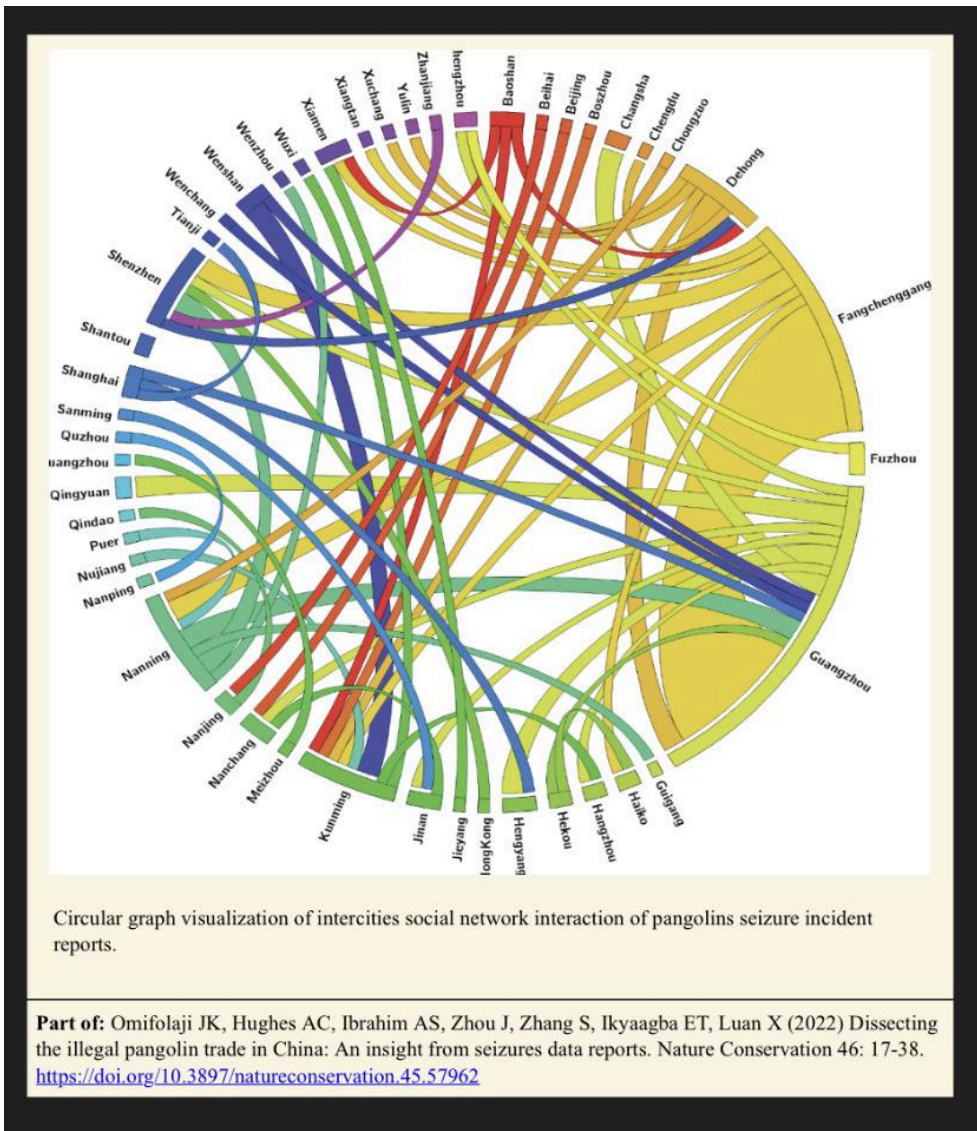
Supporting unit: Wuhan Institute of Virology, Chinese Academy of Sciences

Year of approval: 2018

 to fund inquiry**Project Description**

<b>project name</b>	Pathogenicity of two new bat SARS-related coronaviruses to transgenic mice expressing human ACE2
<b>Project approval number</b>	31800142
<b>Subject classification</b>	C010802 Life Sciences _ Microbiology _ virology _ animal virology
<b>Type of funding</b>	Youth Science Fund Project
<b>principal</b>	Hu Ben
<b>Supporting unit</b>	Wuhan Institute of Virology, Chinese Academy of Sciences
<b>Year of approval</b>	2018
<b>Start and end time</b>	201901-202112
<b>Approved amount</b>	250 thousand yuan
<b>Summary</b>	No data





archive.md/yyX0Z archive.md/iw1Pz archive.md/4rVph archive.md/DChUL

<https://twitter.com/daoyu15/status/1702549289623601162>

Also here is a result on the raccoon dogs and the inability for the species to become

infected in nature. archive.md/n9o0f All non-human mammals archive.md/7doR8

archive.md/0A24q at most landed on different sections of the ground and correlation fails upon entry to that “raccoon dog stall”.

<https://twitter.com/daoyu15/status/1706503805079355845>

archive.md/Ttn5P archive.md/JSQvc

Coincidence caused by pathological spatial distribution on the most uniquely found species in the stall closest to the toilets archive.md/gvHfw have high  $R^2$ —all landed on different sections of the ground and fails upon entry into the stall.

archive.md/0A24q

True causation remain positively correlated when looking at the positive samples or when you enter the site of the pathological spatial distribution.

archive.md/csYBM

<https://twitter.com/daoyu15/status/1738152883185742252>

The only thing governing the probability for positivity of the environmental samples is “closest to the toilets” and “closest to the main entrance of the market”.

<https://twitter.com/midwesterngal51/status/1673521194853703681>

<https://twitter.com/daoyu15/status/1673511971298361344>

<https://twitter.com/daoyu15/status/1713464579920187428>

<https://twitter.com/daoyu15/status/1727124435247968328>

Also, in order to test positive in Gao et al, a sample  
[archive.md/CTP3i](https://archive.is/CTP3i) [archive.md/ETjzS](https://archive.is/ETjzS) [archive.md/BWZJL](https://archive.is/BWZJL)

must be contacted by a sampler. 🧴 🚰 🧤 =positive.

[archive.md/NeybM](https://archive.is/NeybM) [archive.md/2PM9Y](https://archive.is/2PM9Y) [archive.md/RirQ7](https://archive.is/RirQ7)

Must not be frequently handled by a vendor. 🍖 🥬 🍄 🚰 📞 📦 🧺 =negative.

[https://twitter.com/daoyu15/status/1742201874953187706?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1742201874953187706?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

There is a reason why the theil-sen correlation, a quantifier of mutual information, show Homo Sapiens as max correlated wherever any species in the “susceptible mammals” category (wildlife and humans) show correlation at all.

<https://twitter.com/daoyu15/status/1744939585480642650>

Humans=shed in the toilets and feces are stuck all over the boots and suits and shoes and clothes of the samplers and vendors alike. Suit-stained walls doors and legs of desks (but not tops of tables), boot-kicked machines, cages, carts, scales and of course the ground itself which is the dominant sample type for positive samples. And suit-stained sample tubes where the swab is clean but the lip isn't (causing PCR-/NGS+).

In fact all animals that can be infected at all shed in their feces for SARS-CoV-2 RNA.

<https://twitter.com/daoyu15/status/1744937667911921996>

Yes. SARS-CoV-2 have enteric tropism and shed RNA in feces for both animals and humans.

<https://twitter.com/alinouriphd/status/1411761475719401482>

You know that transfer contamination is the dominant if not the only mechanism for market environmental samples when there are also samples that are +ve in both PCR and NGS, but linked neither to human cases nor to wild animals. Even the presence of materials from different origin within the samples are consistent with transfer contamination with a pathway that first go through the toilets and then go through the W6 junction, getting SARS-CoV-2 on the former and wildlife material (on only a fraction of the boots) on the latter, independently.

<https://twitter.com/daoyu15/status/1738157235417821255>

More samples with neither cases nor wildlife DNA are found south of the W6 junction than north of it, but such samples also exist north of the W6 junction. This is consistent with the virus being brought in from the entrance/toilets, contaminating stalls where there is also a focus to stalls with human cases. When boots stepped through the W6 junction, some of the boots also have wildlife DNA stuck to them, bringing it alongside when sites north of the W6 junctions were kicked or trampled.

but not all of them were and there exist also incontrovertible proof of samples with neither human cases nor wildlife DNA found also here.

<https://twitter.com/daoyu15/status/1752142052890997051>

Good and specific PCR primers, like Jan 01/Jan12 ORF1ab+N, and you should have PCR+ before NGS+. Bad and cross-reactive PCR primers like an ORF1ab only primer, and you are going to have PCR+ anytime you see material from the same family you are trying to test on (Embecoviruses cross reacted with their ORF1ab primers—and these animal CoVs are the only real grounded CoV consistent with samples of the expected age at sequencing found here in the specified time).

However, PCR-/NGS+ is something that should never happen nomatter which primer pair you use (cross-reactive or specific) when your NGS result place clustered reads right beside the primer pair.

<https://twitter.com/daoyu15/status/1745406880296349768>

[https://twitter.com/daoyu15/status/1741320436468826555?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1741320436468826555?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

What they wanted you to believe: Aerosols are blocked by walls and can not spread from toilets and wildlife stalls. Reality: Activity of samplers and vendors alike, especially their shoes and boots and the gloves of the samplers, caused the contamination to be spread out from the toilets.

What they wanted you to believe: there are additional PCR+ samples.

Reality: these are a different kind of PCR than what Jan 01 and Jan 12 used. It lacked the universally present N primer pair in the specific PCR primers (the Jan 01 and Jan 12 used specific ORF1ab and N primers in the same reaction to generate 1 single Ct value) which indicate it being an non-specific (surveillance primers in PREDICT target only the ORF1ab/RdRp region due to its conservation, and have degeneracy.) test that cross react with all members of the Coronaviridae family. Artifacts ensues, if not “no reads at all”. Neither PCR+/NGS- nor PCR-/NGS+ can be trusted as genuinely positive, due to the extreme proneness to contamination in the NGS pipeline and the probability of cross-reactivity in some PCR tests.

<archive.md/2PM9Y> <archive.md/RirQ7> <archive.md/CTP3i> <archive.md/NeybM>

<archive.md/ETjzS> <archive.md/BWZJL>

[https://pdfhost.io/v/~IGA2bONb\\_closest\\_to\\_the\\_toilets](https://pdfhost.io/v/~IGA2bONb_closest_to_the_toilets)

[https://pdfhost.io/v/dUbkceTFh\\_anticorrelation\\_is\\_not\\_an\\_artifact](https://pdfhost.io/v/dUbkceTFh_anticorrelation_is_not_an_artifact)

[https://twitter.com/daoyu15/status/1743492601943355494?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1743492601943355494?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Since C-C say you need to @stevenemassey @jbloom\_lab use qPCR to properly get the viral counts, let's see..... Q61/Q70=PCR-. (And located uncomfortably close to PCR+ samples rendering them prone to contamination on NGS.) Q37=PCR- AND orphan sample negative whole stall before and negative exact site after. And primers aligned over by NGS. All are false positive samples. All does not prove virus is there with that metric. The virus is in the human+ and animal-poor Q64/Q68/Q69.

[https://twitter.com/daoyu15/status/1742830724905115871?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1742830724905115871?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://twitter.com/daoyu15/status/1750304059876147618?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1750304059876147618?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

If you examine the inside of “wildlife stall A”, then all you see is boot prints and suit marks. None of it is animals. All metrics now favor Homo Sapiens as the most likely source of the SARS-CoV-2 sequences there.

[https://twitter.com/daoyu15/status/1750295494377484458?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1750295494377484458?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

The wildlife stalls all sold susceptible animals. They only sampled wildlife stalls in Jan 12. Then positives are found closest to the toilets because that is where contaminated suits and boots most likely rub trample and kick. No different from W4-28 and W4-26-28, really.

[https://twitter.com/daoyu15/status/1749953567035727876?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1749953567035727876?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Not forming a line on the correlation diagram=no mutual information=spurious.

[https://twitter.com/daoyu15/status/1750291356927340611?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1750291356927340611?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

That is why it dissolved completely when asking “which species shed the SARS-CoV-2” in slices where the analyte concentrations aren’t 0.

[https://twitter.com/daoyu15/status/1750292448759177457?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1750292448759177457?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

That is also why they fraudulently bleached the toilets before sampling them.

[https://twitter.com/daoyu15/status/1749747743449399671?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1749747743449399671?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://twitter.com/daoyu15/status/1750313347847712908?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1750313347847712908?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And this is how you ID a spurious result.

If the correlational diagram show a neat line indicating an consistent increase in the count of one candidate factor as the target analyte increased, it indicate that the target analyte is probably caused by the candidate factor with a consistently raising minimum of the factor per analyte suggesting that all of it is brought in alongside this candidate.

If the correlation diagram show an randomized pattern or even a line of negative slope, especially when nearly all of the target analyte is found in one place, then it is probably that it is just the one place have one or few potential candidates that are less abundant elsewhere, which with the 25+ candidates in the market sample correlation analysis guarantee 1-2 for every stall (and most of which are on the ground just like anything trampled from the toilets, with entirely different reasons). If you can not use the concentration of the target analyte to reliably predict the concentration of the candidate, or come up with an result that the more target analyte there is the less candidate there is where the target is found, e.g. an absence of or negative mutual information, then it is most likely spurious and extremely unlikely that candidate yielded or is brought alongside the target analyte.

Causation are bijective. Confounders are injective. Spurious correlations are correlated only in some metrics and slices but not all.

Inconsistency between different slices and metrics indicate an lack of true causation and likely confounder that makes false positive in some but negative in the other. A consistent positive correlation in almost all metrics and no negative correlation in any metric, Like Homo Sapiens, indicate that there is true causation that some disruption may have occurred. Species that have “positive” correlation only in some metrics out of a single slice, (not even all the slices examined for that date), but negative or zero in all the other metrics and slices with the mutual information metric yielding negative and zero only regardless of slice, like oriental rat snake or malayan porcupine, are spatially confounded—they are “the most unique species found in the 1 stall at that slice that was closest to the toilets”, and since every stall have one such species, they represent false discovery by lottery fallacy, and fails when any other slices are used. They also failed to form a line on the correlation plot which indicate that there is no causation and the animal did not shed the virus where it was found.

[https://twitter.com/daoyu15/status/1742660802761589231?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1742660802761589231?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://x.com/daoyu15/status/1748919231935041747?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1748919231935041747?s=46&t=wRQSWp_1VffWmS2vKQwhSA) Unfortunately, all that existed for Q61 and Q70 are the result of

cross-contamination from Q64 and Q68/Q69, All of which are on the ground and archive.md/YGDik are the result of either lower level boot and foot contamination

[x.com/daoyu15/status/1744903866800382015?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1744903866800382015?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[x.com/daoyu15/status/1744913305540464731?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1744913305540464731?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Same as Q64/Q68/Q69 (stepped on>kicked for contamination).

[x.com/daoyu15/status/1741320436468826555?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1741320436468826555?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

All that archive.md/73xfX archive.md/8nN3k archive.md/FskYn archive.md/gvHfw exist for Q37 is the contamination of a sample tube by the gloves and suits of the samplers. The swab is clean, PCR-. The tube lip is contaminated, NGS+ with alignment over the CCDC SARS-CoV-2 ORF1ab primer pair.

[archive.md/LJzSO](https://archive.md/LJzSO) [archive.md/4cCHG](https://archive.md/4cCHG)

PCR+/NGS+ mean the virus is present in the location. PCR+/NGS- or NGS(artifacts) mean you are using the incorrect primers (all incidents happened with the PREDICT ORF1ab only primers).

[archive.md/rj1pV](https://archive.md/rj1pV) PCR-/NGS+, especially when [archive.md/csYBM](https://archive.md/csYBM) the primers are aligned over by NGS reads, indicate that the samples have been catastrophically contaminated as NGS is a more complicated process that are far more prone to contamination compared to PCR.

[archive.md/13bdP](https://archive.md/13bdP)

The stall for Q37 is negative at Jan 01.

[twitter.com/daoyu15/status/1722434363042976034](https://twitter.com/daoyu15/status/1722434363042976034) They then went on sampling the

same stall including the “freezer” twice afterward, attempting to verify the “sample” they considered most promising. Bringing in artifacts elsewhere and samples without a read [twitter.com/daoyu15/status/1703729030284120515](https://twitter.com/daoyu15/status/1703729030284120515) (the only sample with a real SARS-CoV-2 read at all gathered using the PREDICT ORF1ab only primer pair was a sewage well connected to the municipal sewage system on the exact opposite to the “wildlife corner”.), but never SARS-CoV-2 reads any more.

<https://twitter.com/daoyu15/status/1757291836928893389>

This fact is also reinforced with the intriguing observation where Q37 is found to be in the same correlational series between SARS-CoV-2 and Homo Sapiens as other Q\* samples.

Attempts at sampling the [twitter.com/daoyu15/status/1740599206035993005](https://twitter.com/daoyu15/status/1740599206035993005) [archive.md/FskYn](https://archive.md/FskYn) [archive.md/gvHfw](https://archive.md/gvHfw) [archive.md/4cCHG](https://archive.md/4cCHG) [archive.md/csYBM](https://archive.md/csYBM) [archive.md/rj1pV](https://archive.md/rj1pV) “storehouse” just ended up with a total catastrophe—[archive.md/13bdP](https://archive.md/13bdP) the sampling team brought in in-lab culture contaminants, not even aged for more than a day, into the sampling sites again when they suited up in their lab and entered the location. Impossibly fresh intracellular Homo Sapiens and SARS-CoV-2 transcriptomes, neither capable of lasting for more than two days ex-vivo in that condition, ended up contaminating the samples and without a single read of a susceptible animal inside those “samples”.

[twitter.com/daoyu15/status/1704347320949862843](https://twitter.com/daoyu15/status/1704347320949862843)

Sampler contamination and cross-contamination. [archive.md/LJzSO](https://archive.md/LJzSO) [archive.md/VNr75](https://archive.md/VNr75) Never an infected vendor or animal. In fact, the samples in the market follows the rule which a positive sample [archive.md/CTP3i](https://archive.md/CTP3i) [archive.md/ETjzS](https://archive.md/ETjzS) [archive.md/BWZJL](https://archive.md/BWZJL) must be contacted by samplers. 🧤 🧥 🧦 =positive.

[archive.md/NeybM](https://archive.md/NeybM) [archive.md/2PM9Y](https://archive.md/2PM9Y) [archive.md/RirQ7](https://archive.md/RirQ7) And not frequently handled by vendors. 🍅 🥬 🍄 🚽 📦 📞 📦 📦 =negative.

[twitter.com/daoyu15/status/1742632626849186292](https://twitter.com/daoyu15/status/1742632626849186292)

[archive.md/HIJ9o](https://archive.md/HIJ9o) [archive.md/nAqKp](https://archive.md/nAqKp) [archive.md/rSaO9](https://archive.md/rSaO9)

They also put bleach onto the toilets and the mahjong room before sampling them.

This is a clear move to cover up.

[archive.md/csYBM](https://archive.md/csYBM)

And no the “stall” W5-NA was sampled on the inside 27/01/2020, negative. (Not even animal CoVs were there) The toilets is the real contamination source.

[archive.md/C5oal](https://archive.md/C5oal) [archive.md/RSsS7](https://archive.md/RSsS7) and yes only Homo Sapiens positively correlated with SARS-CoV-2 consistently in all metrics, or formed any kind of line or grouping pattern at all that allow the abundance of one to be estimated at above-random success rate and precision using the other (e.g. have any significant mutual information with SARS-CoV-2). [archive.md/0O2TN](https://archive.md/0O2TN) [archive.md/GjlEx](https://archive.md/GjlEx)

[https://twitter.com/biorealism/status/1752113606353965467?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/biorealism/status/1752113606353965467?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Ask China on why they fraudulently bleached the toilet area and the mahjong room before any samples were taken,

[https://twitter.com/daoyu15/status/1752150588614177265?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1752150588614177265?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Or why they tampered with the early cases dataset and changed the only case with district of residence known on media.

[https://twitter.com/daoyu15/status/1752135440839151987?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1752135440839151987?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

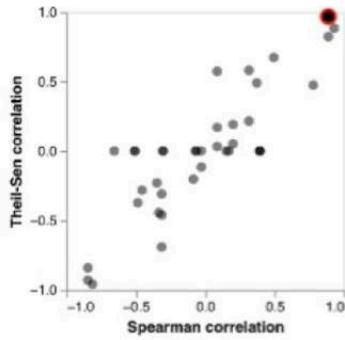
Not only statistically inconsistent

[https://twitter.com/staronline/status/1751915672949358722?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/staronline/status/1751915672949358722?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

But actively tampered with.

[https://x.com/daoyu15/status/1751916335519383630?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1751916335519383630?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://twitter.com/daoyu15/status/1743825586290843998?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1743825586290843998?s=46&t=wRQSWp_1VffWmS2vKQwhSA)



% species mitochondria reads computed as [% of all preprocessed reads](#)

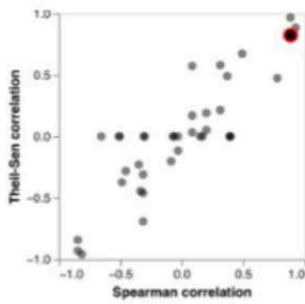
sample collection date [2020-01-12](#)

axis scale [log10 of % \(zero plotted as minimum non-zero value\)](#)

sample isolation source [all](#)

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as [% of all preprocessed reads](#)

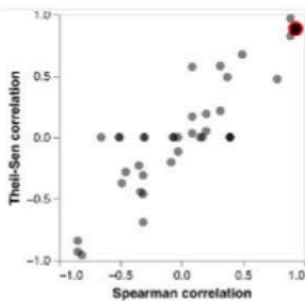
sample collection date [2020-01-12](#)

axis scale [log10 of % \(zero plotted as minimum non-zero value\)](#)

sample isolation source [all](#)

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as [% of all preprocessed reads](#)

sample collection date [2020-01-12](#)

axis scale [log10 of % \(zero plotted as minimum non-zero value\)](#)

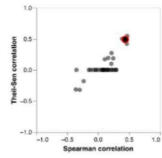
sample isolation source [all](#)

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no







% species mitochondria reads computed as

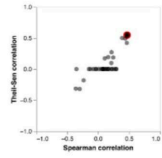
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

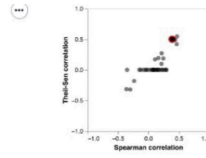
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

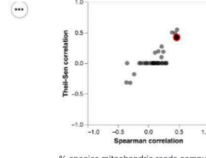
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

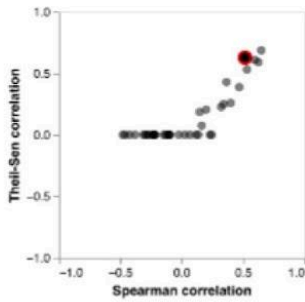
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

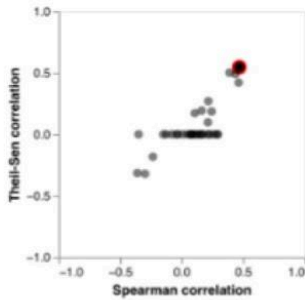
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

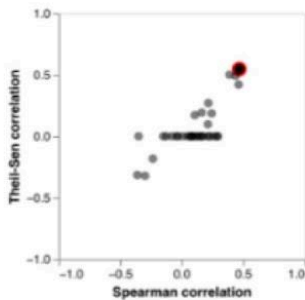
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

sample collection date

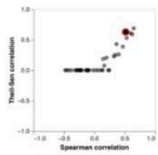
axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



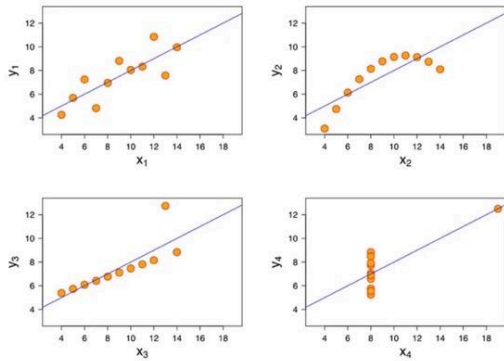


% species mitochondria reads computed as  % of all preprocessed reads  
 sample collection date  all  
 axis scale  log10 of % (zero plotted as minimum non-zero value)

sample isolation source  all  
 species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)  
 only show samples with SARS-CoV-2  yes  no

### Overall correlation of mitochondrial DNA and SARS-CoV-2 across all samples using Theil-Sen estimator

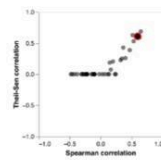
Each point shows the correlation between the percent of all high-quality reads that align to SARS-CoV-2 and the percent of aligned mitochondrial reads for a specific species taken across all samples. The axes show the Spearman correlation and a measure of correlation based on the Theil-Sen estimator.



Source: [Wikipedia](#)

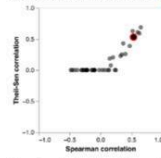
An alternative to least squares for simple linear regression is Theil-Sen estimation. This more robust method determines the slope of the regression line via the median of the slopes of all lines that can be drawn through the data points:

$$m_{TS}(x, y) = \text{median}_{k, l \in \{1, \dots, n\}, x_k \neq x_l} \left( \frac{y_l - y_k}{x_l - x_k} \right)$$



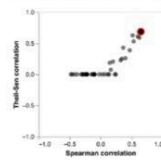
% species mitochondria reads computed as  % of all preprocessed reads  
 sample collection date  all  
 axis scale  log10 of % (zero plotted as minimum non-zero value)

sample isolation source  all  
 species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)  
 only show samples with SARS-CoV-2  yes  no



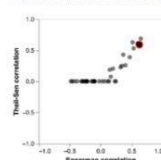
% species mitochondria reads computed as  % of all preprocessed reads  
 sample collection date  all  
 axis scale  log10 of % (zero plotted as minimum non-zero value)

sample isolation source  all  
 species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)  
 only show samples with SARS-CoV-2  yes  no



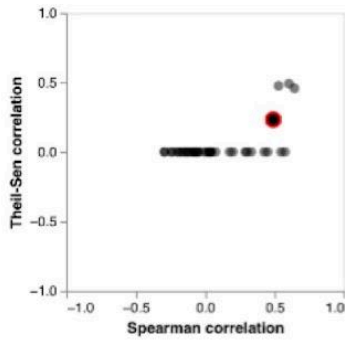
% species mitochondria reads computed as  % of all preprocessed reads  
 sample collection date  all  
 axis scale  log10 of % (zero plotted as minimum non-zero value)

sample isolation source  all  
 species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)  
 only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as  % of all preprocessed reads  
 sample collection date  all  
 axis scale  log10 of % (zero plotted as minimum non-zero value)

sample isolation source  all  
 species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)  
 only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

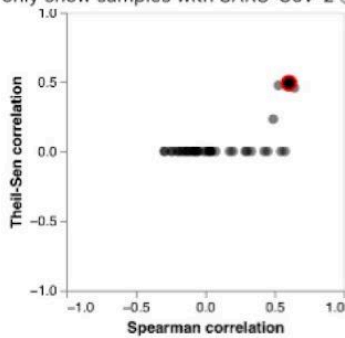
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan mar  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

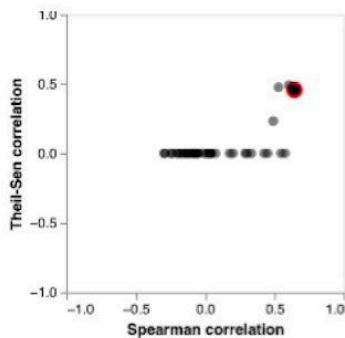
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan mar  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



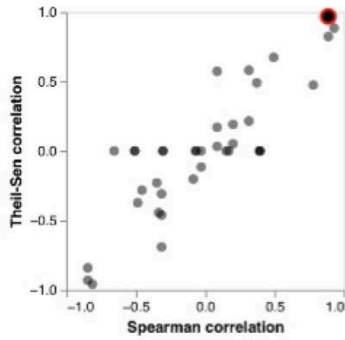
% species mitochondria reads computed as

sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan mar  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon



% species mitochondria reads computed as

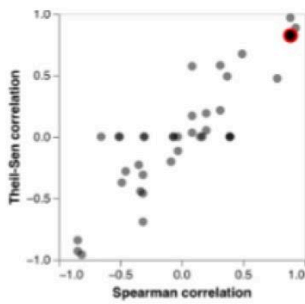
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

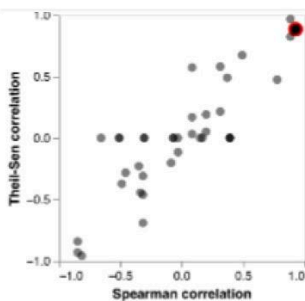
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

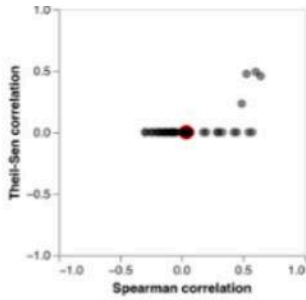
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

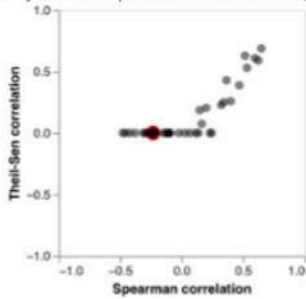
sample collection date

axis scale

sample isolation source

- species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

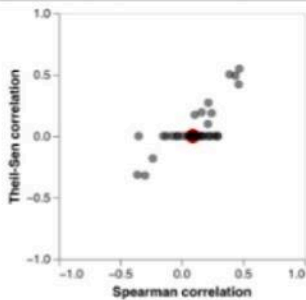
sample collection date

axis scale

sample isolation source

- species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

sample collection date

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only show samples with SARS-CoV-2  yes  no



archive.md/HIJ9o

<https://archive.md/rSaO9><https://archive.md/13bdP><https://archive.md/nAqKp>

They also put bleach onto the toilets and the mahjong room before sampling them. This is a clear move to cover up. <https://archive.md/rj1pV><https://archive.md/FskYn>  
archive.md/csYBM

And no the “stall” W5-NA was sampled on the inside 27/01/2020, negative. The toilets is the real contamination source.

<https://archive.md/LJzSO><https://archive.md/4cCHG>

archive.md/C5oal archive.md/RsS7 and yes only Homo Sapiens positively correlated with SARS-CoV-2 consistently in all metrics, or formed any kind of line or grouping pattern at all that allow the abundance of one to be estimated at above-random success rate and precision using the other (e.g. have any significant mutual information with SARS-CoV-2). archive.md/0O2TN archive.md/GjIEx  
[https://twitter.com/daoyu15/status/1740268239366836398?s=46&t=wRQSWp\\_1Vff](https://twitter.com/daoyu15/status/1740268239366836398?s=46&t=wRQSWp_1Vff)  
WmS2vKQwhSA

What they tried to hide with this:

The fact that “closest to the toilets” is the only factor that governs where you are going to see positive samples the most in the market—there is no difference between W4-28 and W4-26-28 in 01/01/2020 and W6-29-33 in 12/01/2020 in term of where the virus came from and why they have the highest positive sample count out of all sample counts in their respective sampling runs.

[https://twitter.com/daoyu15/status/1738152883185742252?s=46&t=wRQSWp\\_1Vff](https://twitter.com/daoyu15/status/1738152883185742252?s=46&t=wRQSWp_1Vff)  
WmS2vKQwhSA

Sampler contamination and cross-contamination. archive.md/LJzSO

archive.md/VNr75 Never an infected vendor or animal. In fact, the samples in the market follows the rule which a positive sample archive.md/CTP3i archive.md/ETjzS  
archive.md/BWZJL must be contacted by samplers. 🧪 🦠 🦵 =positive.

archive.md/NeybM archive.md/2PM9Y archive.md/RirQ7 And not frequently handled by vendors. 🍅 🥬 🍄 🚽 📦 📞 📦 🧺 =negative.

[https://twitter.com/daoyu15/status/1740195996318261329?s=46&t=wRQSWp\\_1Vff](https://twitter.com/daoyu15/status/1740195996318261329?s=46&t=wRQSWp_1Vff)  
WmS2vKQwhSA

[https://twitter.com/daoyu15/status/1740185689894093265?s=46&t=wRQSWp\\_1Vff](https://twitter.com/daoyu15/status/1740185689894093265?s=46&t=wRQSWp_1Vff)  
WmS2vKQwhSA

[https://twitter.com/daoyu15/status/1740960725286482306?s=46&t=wRQSWp\\_1Vff](https://twitter.com/daoyu15/status/1740960725286482306?s=46&t=wRQSWp_1Vff)  
WmS2vKQwhSA

ANGRY farmers hit by the foot-and-mouth outbreak last night argued the Government's Pirbright facility, blamed for leaking the disease, should stop operating until the source is found.

A number said they lost thousands of pounds because of restrictions on animal movements after the infection of two Surrey farms five weeks ago.

The farmers spoke out after reports by the Health and Safety Executive and Professor Brian Spratt said the outbreak originated from the Pirbright site, is home to commercial laboratory Merial and the Institute of Animal Health.

The group, including Roger Pride, whose beef cattle were the first herd to be culled, met shadow environment, food and rural affairs secretary Peter Ainsworth at a farm in Surrey.

They demanded answers from the Government as to how the virus could have escaped. Laurence Matthews, a farmer from Dorking, Surrey, who rented land to John Gunner, one of the farmers whose herds were culled, said: "It doesn't matter that the pipe broke - accidents can happen - but it is the fact it left the site. It comes down to biosecurity and there was a basic breakdown ... If this was a private company, they would be shut down, but, because it is the Government, they are not. It is one rule for one and one for another."

Cattle farmer Angus Stovold, from Shackleford, said: "(Environment Secretary) Hilary Benn is on TV saying we will do everything to make sure it never happens again, but, if they can't find out the source, how can they give us that reassurance and continue operating?"

Mr Ainsworth, who is MP for East Surrey, said there had been "a systematic failure" in the biosecurity arrangements at Pirbright. He added that, although staff are required to disinfect themselves when coming and going, it was like shutting all the windows to keep the cold out but leaving the front door open.

He added: "In a way, it is fortunate it was foot-and-mouth and not something that could harm humans that got out."

The reports blamed leaking drains, heavy rainfall and building work for triggering the outbreak. Mr Benn cited "a unique and unhappy combination of circumstances" but said it was impossible to know the exact cause.

National Farmers' Union president Peter Kendall said: "I find it well-nigh incredible and quite indefensible that standards should have been as lax as these reports appear to reveal."



<https://www.thefreelibrary.com/Farmers+demand+a+Pirbright+shutdown%3b+%27A+private+company+would+have...-a0168453941>

Also: regarding the “the lab would be shut down and razed to the ground if it leaked and caused an epidemic”:

[https://en.wikipedia.org/wiki/2007\\_United\\_Kingdom\\_foot-and-mouth\\_outbreak](https://en.wikipedia.org/wiki/2007_United_Kingdom_foot-and-mouth_outbreak)

Fact: Pirbright, the only published government research lab which a leak have resulted in a large scale epidemic, was not shut down after FMDV leak infecting 4 farms nearby. They repaired their drain pipes and continued operation, not even interfering academic publication patterns. Ironically, cow farms were shut down and beef trade was closed during the outbreak. This resulted in an epidemic lasting 5 months in cows that lead to at least two major cullings and severe disruption to the livestock trade from the U.K. That is, the reaction look like what they claim a zoonosis would look like, not what they declare what the WIV would do when such a shut-down would certainly directly admit guilt and spell doom to both the institute and its operators. The reaction was identical to that of a “zoonotic spillover from a nearby market” even when the leak is known from the very beginning.

<https://www.theaustralian.com.au/science/beijing-lab-mishap-infected-scientist-with-covid19/news-story/9b0cb0ed84df21d25da11b698be3611a>

Fact 2: there is no shut-down reported at all in the IVDC either after the 2004 leak of SARS or the 2020 leak of Covid. Not even a burp of interruption.

Fact 3: the WIV went on hiatus to the bat CoV isolation tests over 2020-2023. When the sverdlovsk anthrax leak happened, they blamed the animal farms and markets nearby and did not officially shut down the facility. The construction of another anthrax facility nearby was considered potential indication of a shut-down, which is on par with the WIV hiatus. After a timescale similar to the WIV hiatus, the new facility was opened for inspection which no anthrax was found, meaning that they fixed sverdlovsk and went on, just like the WIV (chen WEI.....).

In facts, there have not been a single record of an lab leak or LAI in a research facility that resulted in the (especially permanent, as what they claimed would happen) shut down of the facility (despite hundreds of known incidents in record), even when significant epidemic have occurred from the event. (Ebola21, FMDV07, H1N177, Anthrax82 which no official shutdown was known).

[https://twitter.com/daoyu15/status/1746479306610479514?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1746479306610479514?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

there is a long history of the WIV lying to the point of base rate neglect when being asked anything about potential LAI. The “dinner of staff” too, where they neglected the base rate which is Wuhan medical institutions are already in panic and the general public is already taking precaution, as h2h is announced in 15-16/01/2020 to the point that even the invited international collaborator have hinted Shi to wash hands, that she unexpectedly did not given her expertise and knowledge on the public info about SARS-CoV-2 in general Wuhan public in this time. She pretended

to not know the need to take precautions when she was expected to do so, just like when she sabotaged the test to make 67 general 2021 Wuhan public serological samples test all negative when there should be positives given the seroprevalence in Wuhan at that time.

<https://twitter.com/daoyu15/status/1723512975842226230>

[www.researchgate.net/publication/351711216\\_An\\_analysis\\_of\\_the\\_results\\_of\\_routine\\_employee\\_testing\\_for\\_SARS-like\\_infections\\_within\\_the\\_WIV\\_and\\_other\\_Wuhan\\_labs\\_raises\\_serious\\_issues\\_about\\_their\\_validity](http://www.researchgate.net/publication/351711216_An_analysis_of_the_results_of_routine_employee_testing_for_SARS-like_infections_within_the_WIV_and_other_Wuhan_labs_raises_serious_issues_about_their_validity)

It is just as impossible To have 67 community members to test all negative in Wuhan in 01/2021 as to have 593 people to test all negative with any sensitive test available in April-June 2023.

[gab.com/Flavinkins/posts/108695754734982678](https://gab.com/Flavinkins/posts/108695754734982678)

And this same behavior of issuing a test that will not turn positive on a human also happened to the mojiang miners. Where their own early serological test results were contradicted.

[archive.md/Pc6gp](https://archive.md/Pc6gp) [archive.md/zUD1F](https://archive.md/zUD1F)

And ben HU lied about working with live virus which are so easy to debunk just by a simple google search. His own grant notice required live virus work in 2019.

Regarding sick WIV workers:

<https://twitter.com/daoyu15/status/1693562597373817032>

The ODNI have details which the symptoms of infected employees are known to the fine grain of “compatibility studies”, mandated by law to be published, but denied publishing. Unfortunately ground glass opacities is compatible with CMV pneumonia and anosmia is compatible with seasonal allergies.

<https://twitter.com/daoyu15/status/1725184057011765325>

[https://twitter.com/r\\_h\\_ebright/status/1729164212159824154](https://twitter.com/r_h_ebright/status/1729164212159824154)

Lies and cover-up of China on the origin of SARS-CoV-2.

<https://archive.md/Q02X7>

<https://twitter.com/billybostickson/status/1734534728919724201>

There is No such a thing as a “symptom incompatible with covid-19”.

<https://twitter.com/daoyu15/status/1673402523812765696>

Ben HU lied, people died.

<https://archive.md/Pc6gp>

<https://archive.md/zUD1F>

[https://twitter.com/john\\_bumblebee/status/1671859504122679296](https://twitter.com/john_bumblebee/status/1671859504122679296)

Inconsistency upon inconsistency in Chinese publications as well as “data”.

Well, [twitter.com/covidselect/status/1701958926097342630](https://twitter.com/covidselect/status/1701958926097342630)

The ODNI can't even do a proper google search to realize that the ben Hu did work with live virus.

[twitter.com/daoyu15/status/1702180584532131863?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1702180584532131863?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

No wonder the report.

[twitter.com/daoyu15/status/1673402523812765696](https://twitter.com/daoyu15/status/1673402523812765696)

Regarding the ability of China to stump investigations and keep secrets:

<https://x.com/daoyu15/status/1746391051617636541>

China have hid the merbecovirus found in the HZAU agricultural data,

<https://x.com/daoyu15/status/1746387223262458126>

[twitter.com/daoyu15/status/1672399653344808960](https://twitter.com/daoyu15/status/1672399653344808960)

And of course, WIV1, WIV16, Rs4874 and RsSHC014 count up to 4 published live isolates not “only 3” claimed by Shi. That is published isolates only.

[zenodo.org/records/5702700#.ZKu-2CV6sIT](https://zenodo.org/records/5702700#.ZKu-2CV6sIT)

RaTG13 don't grow outside immortalized kidney cells.

[arxiv.org/abs/2104.01533](https://arxiv.org/abs/2104.01533)

An infectious clone is designed to be rescued.

[archive.ph/EiCQW](https://archive.ph/EiCQW)

Well, MN611520—definitely not a bat CoV.

[twitter.com/drhermiz/status/1718191358077276403](https://twitter.com/drhermiz/status/1718191358077276403)

[twitter.com/daoyu15/status/1719847927512977720](https://twitter.com/daoyu15/status/1719847927512977720)

These are just too many inconsistencies and obvious lies regarding the number of WIV

[twitter.com/daoyu15/status/1719763256976523501](https://twitter.com/daoyu15/status/1719763256976523501)

[twitter.com/mattwridley/status/1462659372421718019](https://twitter.com/mattwridley/status/1462659372421718019)

Or EHA viral sequences AND isolates in their public claims.

And finally regarding the once again officially denied fact that Covid is in the lab before the market:

<https://twitter.com/daoyu15/status/1733792251669786633>

Leaked SRA data included both the exact kind of viruses that they claim will not be present in the WIV—and the exact SARS-CoV-2, WA1, cultured in a CoV-specific tailored fusion cell line VERO-CHO never used in China and sequenced before even a sample of WA1 can be taken in China, alongside C/C and B, at high passage depths, and contained within it residual human DNA not from anywhere in central China but in stead right where they were sampling from the 2018 “pathogen host adaptation and immune intervention” grant—the belt and road regions. Note that the FCS is not found in these sequences.

[https://twitter.com/daoyu15/status/1737318515353501739?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1737318515353501739?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Continued EHA human sampling=Yunnan and belt and road DNA.

[https://twitter.com/biophysicsfl/status/1737114987146174846?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/biophysicsfl/status/1737114987146174846?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Isolate if possible=special unpublished VERO-CHO cells.

[https://twitter.com/daoyu15/status/1737399622509928510?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1737399622509928510?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And it was sequenced before the first public sequencing of SARS-CoV-2 with this machine type by the flow cell, confirmed via Sangon policy and Chinese law, and before+not matching any samples of WA1 was even taken in China.

[https://twitter.com/daoyu15/status/1738903987381031326?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1738903987381031326?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And this exact CAS special project mirroring of DEFUSE+Year 5 extension—sample humans from belt and road area, isolate and engineer viruses for infection characterization, and create vectorized and nanoparticle vaccines that are capable of bringing in both backbone and Spike into bats studied in and released by the WIV, and into the main sample storage facility of the WCDC.

(Also see this—note all the FCS relevant oddities can also be caused by targeted RNA recombination [link.springer.com/chapter/10.1007/3-540-26765-4\\_5](https://link.springer.com/chapter/10.1007/3-540-26765-4_5) followed by cell culture).

[https://x.com/daoyu15/status/1731414539324018732?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1731414539324018732?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

<https://gab.com/Flavinkins/posts/109640519028841414>

It is not just that SARS-CoV-2 Wuhan grows best in VERO cells out of all variants.

<https://twitter.com/daoyu15/status/1723738450078396809>

Some earliest patients harbored inside their QS specific S1-S2 deletions that can form only in VERO E6.

<https://twitter.com/daoyu15/status/1730690080950596017>

[https://twitter.com/daoyu15/status/1673402523812765696?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1673402523812765696?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

SRR13200932	A	C	G	T	N		A	C	G	T	N
NC_045512.2 3037	1	6986	0	21	0	0	0	1001	0	2	0
NC_045512.2 8782	0	214	0	7216	0	0	0	10	0	2297	0
NC_045512.2 17747	1	1002	0	5491	0	0	2	1674	0	698	0
NC_045512.2 17858	8	1	3284	4	0	0	3	0	3219	1	0
NC_045512.2 18060	0	4	0	2997	0	0	1	3	1	4051	0
NC_045512.2 28144	1	742	0	2110	0	0	1	6359	0	167	0
NC_045512.2 29095	0	354	0	6	0	0	0	8445	1	27	0

	SRR11607710	A	C	G	T
97					
98	3037	0	3982	0	19
99	8782	1	3	2	4787
100	17747	1	4517	0	2
101	17858	4497	0	3	1
102	18060	0	11	0	6145
103	28144	0	5582	0	0
104	29095	1	5746	0	7

	SRR11622069	A	C	G	T
37					
38	3037	6	2057	2	87
39	8782	18	56	3	2559
40	17747	1	125	0	673
41	17858	34	0	490	2
42	18060	13	1	4	7604
43	28144	43	7652	1	2
44	29095	0	83	0	0
45	29758	26	0	15	1700

	SRR11607710	A	C	G	T
109					
110	3037	0	3977	0	19
111	8782	1	3	1	4759
112	17747	1	4507	0	2
113	17858	4494	0	3	1
114	18060	0	7	0	6145
115	28144	0	5567	0	0
116	29095	1	5744	0	7
117	29758	0	0	0	5

	SRR11578196	A	C	G	T
73					
74	3037	3	2782	3	23
75	8782	1	6	0	1585
76	17747	0	183	0	65
77	17858	3	0	94	0
78	18060	1	7	0	1078
79	28144	9	3009	2	10
80	29095	3	1051	0	14

<https://twitter.com/daoyu15/status/1722061305195208921>

8782/28144 QS instability is also abundant in the WA1/UW cluster, which indicate that the WA1->A->C/C->B process happened in culture and can generate all early lineages within a single spillover. And that this occur recurrently in culture conditions with or without the FCS.

Also, China WHO/WIV covered up their earlier cases intentionally—it is not plausible for 67 samples from humans taken in 01/2021 to test “all negative”.

[https://twitter.com/daoyu15/status/1673882003203309569?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1673882003203309569?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

<https://www.mdpi.com/2036-7481/14/1/33>

<https://www.biorxiv.org/content/10.1101/2022.10.10.511625v1>

[archive.md/JVFuc](https://archive.md/JVFuc)

[archive.md/GME5L](https://archive.md/GME5L)

There is also issue with Epistasis, and the fact that the very deep sequencing alignment Table Pekar used to “exclude” 3 T/T genomes, literally say T/T in quasi species.

This also completely debunks Pekar by removing the prior of “multiple spillovers” given the instability of these sites in-vitro and their epistatic correlation with each other (but still highly unstable) in-vivo.

[https://twitter.com/daoyu15/status/1674155531035090945?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1674155531035090945?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Again, why always focus on the wrong part of the report? “Other rescarchers in China working with the same vaccine platform took between three to four months to develop their candidate

vaccine.” Is what that matters. It cross-validates

<https://carterheavyindustries.files.wordpress.com/2020/05/mace-e-pai-covid-19-analysis.pdf> the Wechat results.

**Rootclaim** ✓ @Rootclaim

Feb 2

HSM is not the only early cluster location under zoonosis. There are other markets with wildlife, and more importantly, SARS1 was repeatedly spilling over in restaurants, not markets. So we can comfortably assert  $p(\text{HSM|Wuhan,Zoonosis})=0.1$ .

Feb 2, 2024 · 9:44 AM UTC

2 2 8

**Rootclaim** ✓ @Rootclaim

Feb 2

Meaning that if we assume an outbreak starts in Wuhan due to zoonosis, HSM has a 1 in 10 probability of forming the earliest detected cluster.

2 2 5

**Rootclaim** ✓ @Rootclaim

Feb 2

Considering the different pieces of evidence mentioned above that indicate human introduction to HSM rather than wildlife, we increase the odds of human introduction by 10x to 0.01.

1 2 7

**Rootclaim** ✓ @Rootclaim

Feb 2

Therefore, for this evidence to have any value we need to claim there is less than 1% probability that HSM will form an early cluster under the lab leak hypothesis i.e.  $p(\text{HSM|Wuhan,lab-leak})<0.01$

2 2 5

**Rootclaim** ✓ @Rootclaim

Feb 2

Given the two independent arguments above: a) that there are very few locations in Wuhan so conducive to SARS2, and b) we repeatedly see similar locations forming the first cluster after a zero covid period, 0.01 seems like a highly overconfident claim.

2 2 7

[https://wwwnc.cdc.gov/eid/article/10/6/03-0852\\_article](https://wwwnc.cdc.gov/eid/article/10/6/03-0852_article)

Finally, zoonoses in SARS1 happened mainly at restaurants, not markets. Not a single SARS2 case have been linked to a restaurant or any direct contact to the wildlife trade at all.

<https://twitter.com/Rootclaim/status/1753353716776739089>

Unfortunately, none of your “caged, stacked, sick and wounded animals” actually have a single infection in nature anywhere in the world.

[archive.md/DChUL](https://archive.md/DChUL) [archive.md/4rVph](https://archive.md/4rVph) [archive.md/yyX0Z](https://archive.md/yyX0Z) [archive.md/iw1Pz](https://archive.md/iw1Pz)

And unfortunately <https://pubmed.ncbi.nlm.nih.gov/35298912/> two following sampling studies have in fact registered the entirety of the supply chain for the Huanan market, one for the local trappers which 100% of the raccoon dogs and weasels are from

<https://pubmed.ncbi.nlm.nih.gov/35298912/>

And the second for all the other animals which are farmed.

<https://twitter.com/daoyu15/status/1723019367854875094>

Unlike all prior zoonoses where multiple sites of spillover happens with extensive diversity,

<https://twitter.com/daoyu15/status/1727479523778887806>

Which is true for non-coronaviruses as well,

<https://archive.md/OIGPz> and just like the absence of secondary outbreaks

anywhere at all despite the fact that the wildlife trade continuing for the same amount of time where SARS-CoV-1 had 9 out of its 11 primary spillovers

<https://twitter.com/daoyu15/status/1740796866617647522>

The total absence of a phylogenetic tree indicating 20nt+ variants and wildlife linked diversity also disproves zoonosis for SARS-CoV-2.

<https://twitter.com/daoyu15/status/1668828125617352704>

[https://twitter.com/daoyu15/status/1740796866617647522?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1740796866617647522?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Unfortunately the animal trade continued

[https://twitter.com/daoyu15/status/1723305823886291394?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1723305823886291394?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

All the way into 23/01/2020 and later, without being shut down especially in Guangdong.

<https://twitter.com/daoyu15/status/1690330493693374464>

This is sufficient amount of time where the majority of the primary SARS-CoV-1 spillover events (9 out of 11, 5 of which are animal sellers from distinct markets in distinct cities, and which an animal transporter linking Yunnan and Guangdong was among the first cases) have taken place.

<https://gab.com/Flavinkins/posts/109883975094801876>

[https://wwwnc.cdc.gov/eid/article/10/6/03-0852\\_article](https://wwwnc.cdc.gov/eid/article/10/6/03-0852_article)

On the contrast, 5 independent animal seller cases out of 9 total primary cases for SARS-CoV-1 have happened in 5 cities in 4 in Guangdong and 1 in Guangxi (and +4 for the non-animal seller cases), over the same 2-months timeframe. Two of them were civet butchers, two market workers and one a driver for wildlife dealers that connect Yunnan and Guangdong through Guangxi. In the contrast, 0 of the early



cases for SARS-CoV-2 worked in or have a history of direct participation with the wildlife industry.

[https://twitter.com/daoyu15/status/1679623149045043200?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1679623149045043200?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Hundreds of restaurants sold wildlife in western Hubei, dozens of resurfaced in Wuhan, why not 1 single SARS-CoV-2 early case have visited or worked in any of these restaurants? The closest an early known case have in term of the food industry worked to sell “seafood” “shrimps” and “seasoning”. None of the early cases have even cooked or eaten a wild animal, anywhere in China. All of the known “other markets” of early cases were ordinary supermarkets and farmer’s markets which none is one of the 4 wildlife markets in Wuhan or any other markets that sold wildlife, not even outside Wuhan. None of the early cases outside Wuhan, which is also ironically where most of the early lineage A cases were found due to there not being a requirement for visiting the Huanan market for ascertainment outside wuhan, have reported visiting a market that sold wildlife or have any contact history to wildlife including those in restaurants supplied by the Huanan market, or any market at all anywhere. There is in fact a total absence of direct wildlife exposure, even among the Huanan market cases themselves, for the early epidemiology of SARS-CoV-2, completely different from SARS-CoV.

[https://twitter.com/daoyu15/status/1687522463440384000?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1687522463440384000?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://twitter.com/daoyu15/status/1668828125617352704?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1668828125617352704?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Again, In SARS1 Guangdong had 11 spillovers in 11 markets in 9 cities in Guangdong, creating 3 distinct lineages and 3 outbreaks differing by up to 20nt to 30nt. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7150232/#bib1>

[archive.md/GKdtdc](https://archive.md/GKdtdc)

<https://archive.md/e3615> <https://archive.md/vWjZl>

<https://archive.md/nyR0q>

<https://twitter.com/daoyu15/status/1728590226715738126>

The absence of infections in any animals in China and the absence of positivity where Yunnan animals are actually sold,

<https://twitter.com/daoyu15/status/1734220765434921016>

is perfectly predicted by the absence of any secondary spillovers in any other Chinese market.

[https://twitter.com/washburnealex/status/1728200810964853194?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/washburnealex/status/1728200810964853194?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Where are the 10 other spillovers in 8 other cities for SARS-CoV-2 again? An absence of secondary spillovers is in and of itself evidence of absence of animal infections.

[https://twitter.com/daoyu15/status/1727479523778887806?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1727479523778887806?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And no the 11 SARS1 spillovers happened within 2 months. That is the same timescale from the first market case (beginning of December 2019) to any impact at all felt in the wildlife trade in China (during the end of January 2020 to the beginning of February 2020) in case of SARS-CoV-2. No there is no valid reason to claim that “because they shut down the wildlife trade so swiftly there will be no secondary spillovers”.

[https://twitter.com/daoyu15/status/1740796866617647522?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1740796866617647522?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

<https://twitter.com/daoyu15/status/1727479523778887806>

All viral outbreaks of a spillover origin have more than one initial outbreaks in more than one locations.

<https://twitter.com/daoyu15/status/1716635021438755037>

<https://x.com/daoyu15/status/1749084056111689987>

This is consistent with the fact that the actual stalls that sold animals from Yunnan are entirely uninfected.

<https://twitter.com/daoyu15/status/1708521378092392864>

Not even a single SARS-CoV-2 case was linked to any of the intermediate distribution sites and secondary destinations even in Hubei or wuhan of any of the animals that were supplied to the Huanan market, especially given that the each stall have at least 3 distinct live animal suppliers for “susceptible animals” and there are 17 stalls in Wuhan, and the total number of animals sold per week is only ~58 in total.

<https://twitter.com/daoyu15/status/1752282114760876096>

4 animals at most per shelf life per supplier is not going to eat up the single harvest output of any farm. It will spill into other cities. None observed.

<https://twitter.com/daoyu15/status/1748113909700334053>

[https://twitter.com/daoyu15/status/1694163822473629792?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1694163822473629792?s=46&t=wRQSWp_1VffWmS2vKQwhSA)



**Coroldo1** @coroldo1 · 18m



Replying to @coroldo1

The communication author of above TED, also the 1st author of this SR, went to the 'epicenter', the exact booth, repeatedly, with documentray close contacts with ppl and wildlife animals, after close contacts with bats, before UP started to arise.



nature.com

Animal sales from Wuhan wet markets immediately prior to the COVID-19 pandemic

Scientific Reports - Animal sales from Wuhan wet market...



16



**Coroldo1**

@coroldo1



There's absolutely zero data published, showed a SC2 progenitor showed in cave bats in Hubei.

But epidemiological speaking, anyone cross checked the contact history of the author with wildlife traders(who showed symptoms and documented as Covid patients) in HSM during survey?



[onlinelibrary.wiley.com/doi/full/10.1111](https://onlinelibrary.wiley.com/doi/full/10.1111)

Bats collected from May 2018, Separate 2019, Jul 2020 from three different locations in June for an ongoing programme aiming at identifying pathogens in bats.....



onlinelibrary.wiley.com

Bats and their ectoparasites (Nycteribiidae and Spinturnicidae) carry diverse novel ...  
Bartonella species are facultative intracel...

2



39



**Coroldo1** @coroldo1 · 1h



Replying to @coroldo1

'every effort was made to minimize the discomfort of bats, captured bats were sacrificed by inhaling of ethyl ether in the field, and then transported back to the laboratory on ice asap... Thoracic and abdominal organs of bats were collected.'

1



30



**Coroldo1** @coroldo1 · 54m



Replying to @coroldo1

So, unlike Junhua Tian in WDCDC, who was cleared by statements and no existing evidence of travel bats back to Wuhan.

These authors actually brought the bats back and dissected in their own lab(s), and stored frozen bats for their ongoing bat pathogens programme, whatever that is.

1



33



**Coroldo1** @coroldo1 · 30m



Replying to @coroldo1

Despite the tedious facts such as: one author's institute had two campus, one is in Wuchang;  
The merge of two schools in 2003 and upgraded in 2010 actually left employees from each school a different list of designated hospitals for medical insurance coverage if they went



**Coroldo1** @coroldo1 · 7h



Replying to @coroldo1

where the animals...went, but an inner lane for mini cargo vans parked not more discrete than open main roads where CCTVs all over including cameras from opposite sides of the street? There were numerous inspections from year to year such as live poultry, no playbook or empirical



1



50



**Coroldo1** @coroldo1 · 7h



Replying to @coroldo1

\*experience\* for stall owners and market workers?

(4)the animal carcass left seemed like from rabbits.

(5) with public available information, the only person who had Yunnan and other rural areas research visit history, plus had live bats within own lab, captured live bats in



1



56



**Coroldo1** @coroldo1 · 7h



Replying to @coroldo1

Sep 2019(by publication) , plus documentary evidence of routine monthly visits to wildlife stalls in markets in Wuhan with close contact to humans and animals till the latest known time pre-pandemic, was Xiao Xiao himself.



2



103





**Coroldo1**  
@coroldo1

Blocked



[nature.com/articles/s4159...](https://www.nature.com/articles/s4159...)

The corresponding author, Zhao-min Zhou, was a police officer in national Forestry for 6 yrs, in charged of pangolin smuggling investigation, before joined CWNU. PhD studied bats in Kunming.



nature.com

Animal sales from Wuhan wet markets immediately prior to the C...  
Scientific Reports - Animal sales from Wuhan wet markets  
immediately prior to the COVID-19 pandemic

### 3.3 讨论

2012年11月,云南省墨江哈尼族自治县通关镇的一个废弃的铜矿洞中,矿工群体中暴发重症肺炎疫情。其中6人感染,共造成3人死亡。中国疾病预防控制中心、云南省疾病预防控制中心以及其他医疗机构和相关科研单位采集了病人以及矿洞中蝙蝠、老鼠和环境等样本并进行病原检测和病因分析。4名患者咽拭子和全血标本中,SARS冠状病毒、流行性出血热、登革热(1-4型)、乙型肝炎及黄病毒、甲病毒病原核酸检测均为阴性(成都军区疾病预防控制中心);4名病例和4名曾经进入矿洞但未发病人员的血标本检测结果无异常发现(广东钟

82

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#### 蝙蝠宿主中新病毒发现及蝙蝠冠状病毒 HKU9 受体的探索

南山实验室);对矿洞内蝙蝠进行解剖,对蝙蝠粪便进行检测,均未发现异常(中国科学院武汉病毒学研究所);4名病例血液标本检测结果显示:4人均携带 SARS 病毒 IgG 抗体,其中出院 2 人的抗体水平较高,住院 2 人的抗体水平较低(中国科学院武汉病毒学研究所)。时隔半年之后,金奇实验室再次进入该矿洞采集蝙蝠和野鼠样本并进行病原检测,从野鼠样本中,得到一株 Henipa-like virus 基因组全长序列<sup>[9]</sup>。但是,该病毒与这次疫情暴发之间的相关性,并未得到论证。因此,造成此次疫情暴发的病因尚未明了,虽经多方努力,迄今成了一桩不了了之的悬案。

2014年10月,我们在这个山洞中采集了87只蝙蝠和1只野鼠,解剖后对各种脏器组织进行检测。从结果看,两份样本为冠状病毒阳性,分别为 BatCoV HKU7 和 BatCoV HKU8,这两种冠状病毒目前尚未有感染人的病例报道<sup>[65,100]</sup>。根据文献初步推测,受体也不是常见的 SARS-CoV 的 ACE2 和 MERS-CoV 的 CD26 受体,可能是 APN (Aminopeptidase N) 受体。另有两例为博卡病毒阳性,而博卡病毒最初是从儿童重症肺炎样本中发现,同时,9份样本为星状病毒阳性。星状病毒是一种常见的消化道病原,目前没有任何证据表明星状病毒与肺炎或者呼吸道疾病相关。因此,所发现的病毒与这起疫情暴发是否存在相关性,同样需要做很多的后续工作来进行论证。

对于我们实验室而言,病原的快速检测还处于探索阶段,平台建立尚未完善。目前,只设计了针对10个科或属的通用引物,未来需要设计更多的通用引物并在实践中尝试和强化,以期涵盖尽可能多的病毒范围实现突发疫情中的快速反应。

墨江县废弃矿洞中疫情暴发,有一个细节值得我们注意。在此次疫情之前,曾有多人多次进出这个废弃矿洞,但是未有疫情发生。这种现象提示我们,有必要对某些特定的生态环境进行跨年或长期的监测,以了解特定环境或动物群体中病原的变异和进化,以及这些变化可能造成的跨物种传播。



**Francisco de Asis** ✓  
@franciscodeasis



These are the three available snapshots in Google Earth

- 06-Feb-11
- 15-Feb-15
- 23-Apr-19

And as noticed by [@TheSeeker268](#), there are two new facilities (F1 and F2) which have been built in recent years and could be related

翻译帖子







Gilles Demaneuf @gdeman... · 2021/10/2 ...  
回复 @FabienColombo 和 @R\_H\_Ebright

Yes. Another coincidence.

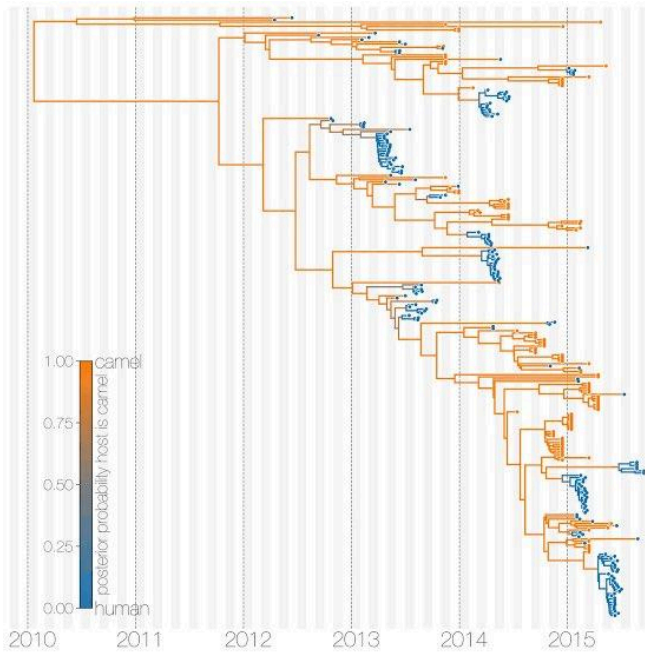
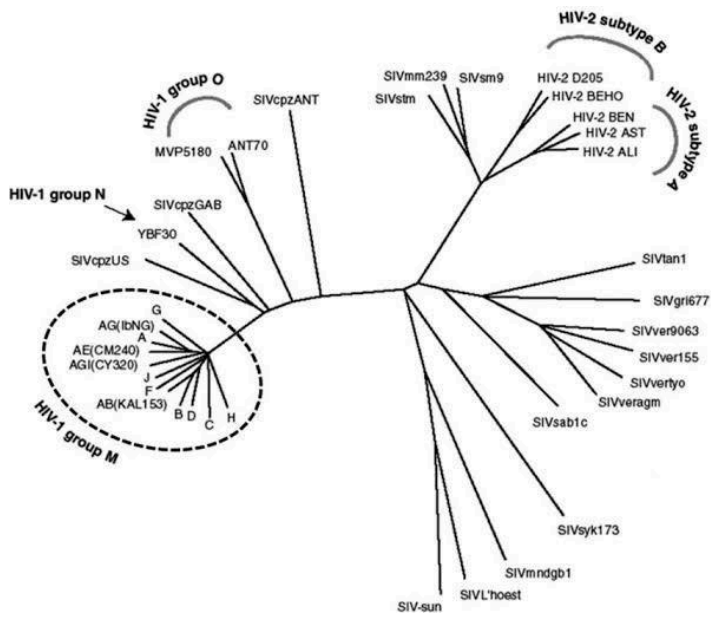
EHA was sampling around the **Mojiang** mine when the workers were getting infected. They would have driven just a few km from it between two sampling sites.

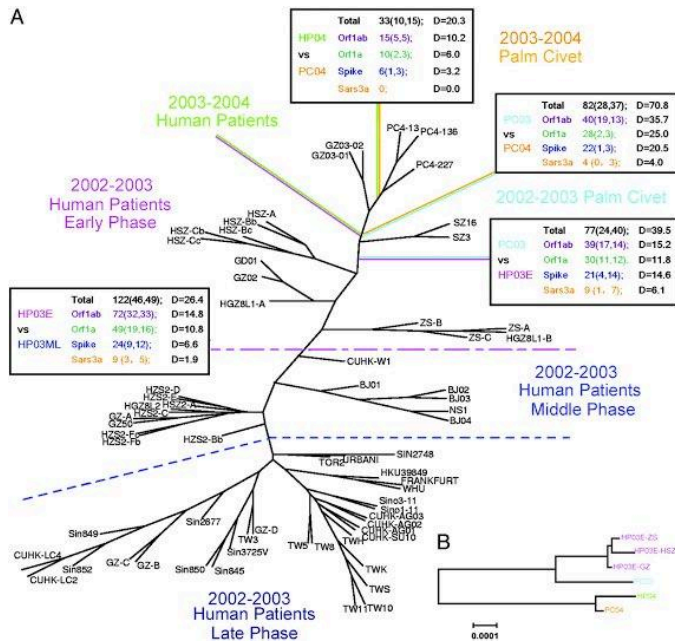
But EHA never hears of it. They had a sudden epiphany about bat guano infection risk instead.











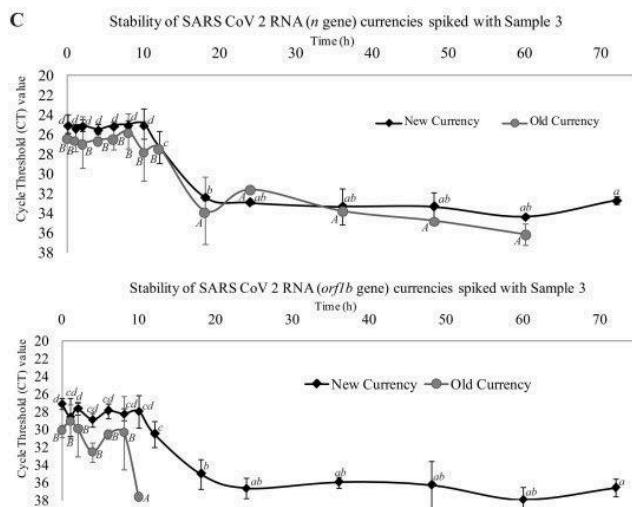
Flo Débarre  
@flodebarre

Attention, SARS-CoV-2 n'a pas été détecté chez des chiens viverrins. Le matériel génétique des deux a été trouvé dans des échantillons du marché, mais ce n'est pas la preuve que les animaux étaient infectés.

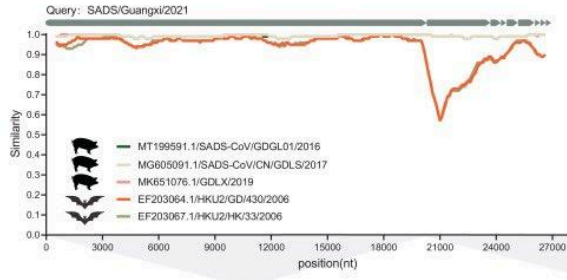
由 Google 翻译自 法语

请注意，尚未在貉中检测到 SARS-CoV-2。在市场样本中发现了这两种动物的遗传物质，但这并不能证明这些动物被感染。

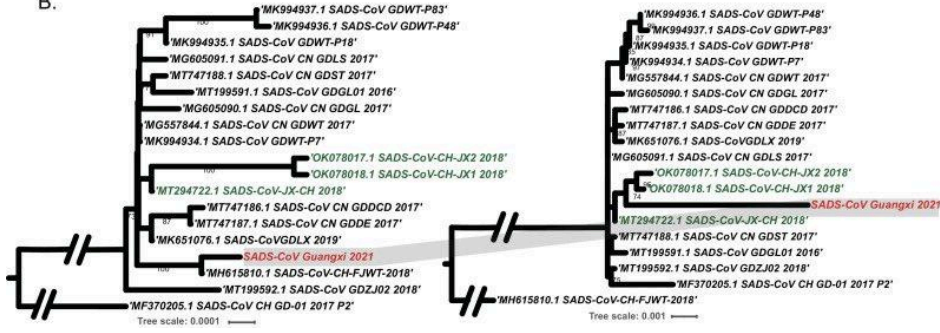
下午7:07 · 2023年6月26日 · 39 查看





A.










B.










现呼吸困难。徐冰和同事对他们的病史、接触史进行了调查，发现他们或是在华南海鲜市场工作，或是住在市场附近，“很多病人是相互认识的，有人会告诉我们，亲戚住在哪个医院，状况非常不好”。徐冰发现，这些人有的来自一个家族，有的则是长久的麻将搭子——这些基本上能够判断这是一次聚集性发病事件。






 **Daoyu**  @Daoyu15 · May 13 ...  
This is again wrong. The highest positive rate of any stall that tested from 01-12/Jan 2020 was actually W4-28. 2/2 samples were positive. In fact the samples from the outside surfaces of W4-26-28 was the highest positivity rate of any sites for Jan01-Jan12.

 1    2    1    2,755   

 **Daoyu**  @Daoyu15 · May 13 ...  
There are 2 samples taken from W4-28 and both were positive by PCR. There are 3 samples from inside of W4-26 and 4 samples from the outside of W4-26. All 3 samples from W4-26 that is positive came from the outside of W4-26. This makes it 5/6 PCR+ samples. On the other hand,

 1    1    1    159   

 **Daoyu**  @Daoyu15 · May 13 ...  
W6-29-33 itself have only 3 PCR positive samples and the 1 read or 2 reads close to each other make it impossible to rule out that the samples suffered significant cross-contamination (all that is needed is 1 fragment of ssRNA less than 100nt in length amd 1 fragment of

 1    1    1    160   

 **Daoyu**  @Daoyu15 · May 13 ...  
dsDNA or hairpin RNA less than 100bp in length for Q61 and Q70–falling directly from the neighboring samples After the PCR reaction and during NGS library preparation.)

 1    1       133   

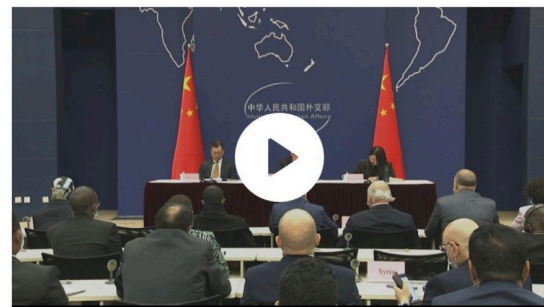


**Michael Stand...** @msta... · 2021年8月30日 ...  
 This is the sign next to the gate of the Hubei Wildlife Rescue Center. The rescue center and WIV both declined to comment on their collaboration.



1 2 8

More than 18 months later, as G7 leaders call for “a transparent, evidence-based and expert-led World Health Organization or WHO-convened phase 2 study on the origins of COVID-19, that is free from interference” and intelligence services in the United States reveal their findings on the origins of the virus, it remains unclear as to whether the wildlife centre or the zoo were ever questioned as part of investigations into how the disease emerged into the world.



				<b>MATEI</b>
Item	Manufacturer	Number/Descr	Unit Price	
Restriction Enzymes small tubes	NE BIO LABS	R0580S	\$72.00	
Restriction Enzymes large tubes	NE BIO LABS	R0580L	\$292.00	
SuperScript™ III Reverse Transcriptase	FISHER	18-080-051	\$460.00	
T4 DNA Polymerase - 750 units	NE BIO LABS	M0203L	\$268.00	
Antarctic DNA Phosphatase - 1000 units	NE BIO LABS	M0289S	\$68.00	
T4 DNA Ligase	NE BIO LABS	M0202L	\$256.00	
GLOVES PF NITRILE SM (100/pk 10 pk/c	FISHER	19-130-1597E	\$249.48	
GLOVES PF NITRILE MED (100/pk 10 pk/c	FISHER	19-130-1597C	\$249.48	
GLOVES PF NITRILE LG (100/pk 10 pk/c	FISHER	19-130-1597I	\$249.48	
GLOVES PF NITRILE XL (100/pk 10 pk/c	FISHER	19-130-1597E	\$249.48	
DMEM with L-Glutamine, 4.5g/L Glucose	FISHER	MT10013CV	\$141.20	
Animal per diem for breeder cages	Department of Compartive	hot wash mic	4.2	
Animal per diem for experimental cages	Department of Compartive	hot wash mic	8.4	



(3) *Retrospective test results of animal coronaviruses*

Retrospective SARS-CoV-2 NAT was performed on 6811 animal samples collected from Beijing, Shanghai, Jiangxi and Xinjiang from 2015 to 2019, involving species of primates, Carnivora, Artiodactyla, Anciformes and Marabiformes. The results were all negative.

As part of national active surveillance plan of important animal diseases, animal samples were collected every year and these stored samples were retrospectively tested for SARS-CoV-2 after the outbreak of SARS-CoV-2. In December 2019, 2328 samples of 69 animal species, including macaque monkeys, forest musk deer, tigers, camels, bamboo rats, porcupines, goats and guinea pigs, were collected from tourist areas, zoos and artificial breeding sites in Hubei Province. All were SARS-CoV-2 NAT negative (Table 10).

**Table 10. Survey of SARS-CoV-2 in wildlife before the epidemic**

		Nucleic acid testing	
		Hubei Province	Nationwide
Number of species		69	14
Specific types of animals		South China tiger, Raccoon, Siberian tiger, African lion, Stump-tailed macaque, Civet, Red fox, Meerkat, Porpoise, Skunk, Brown bear, Red kangaroo, Red squirrel, Marmot, Porcupine, Fennec fox, Nutria, China rabbit, squirrel, Guinea pig, Bamboo rat, Muskrat, Sika deer, Bactrian camel, Grey wolf, Hare, Mule, Chinese water deer, Lynx, Raccoon dog, Asian elephant, Black bear, Leopard, Ring-tailed lemur, Tibetan macaque, African baboon, Panda, Snub-nosed monkey, DeZhou donkey, lion, Pallas's cat, kangaroo, Elk, Giraffe, African elephant, Hippo, White rhinoceros, Zebra, Red panda, Francois's leaf monkey, etc.	Angora ferret, Snub-nosed monkey, Sika deer, Wild boar, Elk, Mallard, Bar-headed goose, Heron, Night heron, Chicken, Duck, Pigeon, Fruit bat, Pangolin, etc.
<b>Total sample size</b>		<b>2328</b>	<b>6811</b>
<b>Test results</b>		<b>negative</b>	<b>negative</b>

(4) *Other information on SARS-CoV-2 from unpublished studies reported during meetings of the international joint team in Wuhan*

- Tests on samples of more than 1000 bats from Hubei Province showed that none was positive for viruses related to SARS-CoV-2 (see Annex F, Table 4).

The animal and environment working group reviewed existing knowledge on coronaviruses that are phylogenetically related to SARS-CoV-2 identified in different animals, including horseshoe bats (*Rhinolophus* spp) and pangolins. However, the presence of SARS-CoV-2 has not been detected through sampling and testing of bats or of wildlife across China. More than 80 000 wildlife, livestock and poultry samples were collected from 31 provinces in China and no positive result was identified for SARS-CoV-2 **antibody** or nucleic acid before and after the SARS-CoV-2 outbreak in China. Through extensive testing of animal products in the Huanan market, no evidence of animal infections was found.

6. Of 923 environmental samples in Huanan market 73 were positive; Forty-four of those positive were from the stalls of 21 vendors dealing in the following products: aquatic animals and products ( $n = 13$ ), cold-chain products ( $n = 16$ ), poultry meat ( $n = 6$ ), seafood products ( $n = 6$ ), livestock meat ( $n = 5$ ), vegetable products ( $n = 2$ ) and farmed wildlife meat ( $n = 1$ ). Sampling and testing of 38 515 livestock and poultry samples and 41 696 wild animal samples from 31 provinces in China during 2018 to 2020 resulted in no positive SARS-CoV-2 **antibody** or nucleic acid tests. No evidence was found of circulation of SARS-CoV-2 among domestic livestock, poultry and wild animals before and after the SARS-CoV-2 outbreak in China.

## RNA extraction, DNA sequencing and

**analysis.** RNA was extracted from a mixture of the

heart, liver, spleen and lung from a raccoon dog

(obtained in October 2006 from a live-animal retail

market in Hebei Province, China) with TRIzol

(Invitrogen), according to the manufacturer's

instructions. RNA was dissolved in 20 µl diethyl

pyrocarbonate-treated water and stored at -80 °C.

RNA was reverse-transcribed to cDNA by using a

combined gene-specific priming, random-priming and

oligo-dT-priming strategy by using SuperScript II

reverse transcriptase (Invitrogen). Five overlapping

DNA fragments covering the full-length ACE2 gene

were produced by PCR using the following primers,

which were designed based on the most conserved

regions of a sequence alignment of ACE2 genes from

ten SARS-associated animals: ACE2F1, 5'-

CCGGATCCATGTCAGGCTCTTCTGGCTC-3'; ACE2F2, 5'-

CCGGATCCCTCCTCAACTTCTTTGTAC-3'; ACE2F3, 5'-

ACE2 molecules of human (*Homo sapiens*), civet (*Paguma larvata*), and rat (*Rattus norvegicus*) were cloned into a modified pcDNA3.1-cmyc/C9 vector (Invitrogen) and previously described [27,48]. ACE2 protein expressed from this vector has a c-myc tag at the N-terminus and a C9 tag at the C-terminus. An Age I site was engineered right downstream of the signal peptide sequence (nt. 1-54) of hACE2. The ACE2 molecules of Chinese ferret badger (*Melogale moschata*), raccoon dog (*Nyctereutes procyonoides*), Mexican free-tailed bat (*Tadarida brasiliensis*), hog badger (*Arctonyx collaris*), and domestic cat (*Felis catus*) were described previously (Hanxin Lin, Ph. D Thesis Dissertation. "Molecular interaction between the spike protein of human coronavirus NL63 and ACE2 receptor" McMaster University, Health Science Library.

[https://discovery.mcmaster.ca/iii/encore/record/C\\_\\_Rb2023203\\_\\_SMolecular%20interaction%20between%20the%20spike%20protein%20of%20human%20coronavirus%20NL63%20and%20ACE2%20receptor%20Lw%3D%3D%20by%20Hanxin%20Lin\\_\\_Orightresult\\_\\_U\\_\\_X4?lang=eng&suite=def](https://discovery.mcmaster.ca/iii/encore/record/C__Rb2023203__SMolecular%20interaction%20between%20the%20spike%20protein%20of%20human%20coronavirus%20NL63%20and%20ACE2%20receptor%20Lw%3D%3D%20by%20Hanxin%20Lin__Orightresult__U__X4?lang=eng&suite=def). Briefly, ACE2 cDNA was amplified using BD SMART™ RACE cDNA Amplification Kit (BD Biosciences Clontech). The total RNAs of these animals, except bat, were

extracted from the mixture of lung and kidney tissues using RNeasy Mini kit (QIAGEN, ON). The total RNAs of bat were extracted from Tb-1 Lu cell culture. Two cDNA populations, 5'-RACE-Ready cDNAs and 3'-RACE-Ready cDNAs, were synthesized from the total RNAs according to the manufacturer's instruction. Overlapping DNA fragments that cover the full-

length ACE2 genes were amplified by nested PCR with *Pfx* DNA polymerase (Invitrogen) with

two primer pairs: internal forward primer GSP1 5'-

CCCTTTGGACAGAAACCAACATAGATGT-3' (nt. 850-878 of multiple aligned ACE2s) and

external backward primer 5'-CTAAAATGAAGTCTGAACATCATCATC-3' (nt. 2395-2418) or

universal primer A mix (UPM) that is supplied in the kit; internal backward primer GSP2: 5'-

CCRACKATVTTYCGCTTCATCTCCACCA-3' (nt. 1429-1458) and external forward primer

5'-ATGTYVRGYTCHTBCTGGCTCCTTCTCAG-3' (nt. 1-29). The PCR fragments were

cloned into pGEM-T vector (Promega, Madison, WI). Three clones of each fragment were

sequenced. Based on the determined sequences of specific animal species, forward primers with

an Age I site and backward primers with a Kpn I site were designed. These primers were then

used to amplify the full-length ACE2s using the overlapping PCR strategy recommended by the

manual of BD SMART™ RACE cDNA Amplification Kit. The full-length PCR products of

ACE2 molecules were cloned into Age I/Kpn I-digested pcDNA3.1-cmyc/C9 vector vector, and

subject to sequencing to confirm their correctness. The nucleotide sequence of Chinese

horseshoe bat (*Rhinolophus sinicus*, Rs) ACE2 obtained from NCBI database ([KC881004.1](https://www.ncbi.nlm.nih.gov/nuccore/KC881004.1))

was synthesized and cloned into pcDNA3.1-cmyc/C9 vector with the same strategy.

---

nipulation of SARS-CoV2. First, there is the absence of identified intermediate hosts after three years of pandemics.

Second, why Wuhan? This megapolis where the first cases of Covid-19 were detected is remote from the areas of bat reservoirs. In the early phase of the pandemic, the absence of secondary outbreaks that would have accompanied the trade of living animals is surprising.

During the emergence of other recent viral respiratory diseases transmitted by animals on markets, as SARS and H7N9 avian influenza, multiple scattered clusters were observed [32], [33], [34]. In Wuhan and elsewhere, researchers have practiced GoF on sarbecoviruses.

According to publications, chimeric viruses were created in 2015, followed by 8 more viruses in 2017, two of which were pathogenic to humanized mice. All

With its high cross-species transmissibility, SARS-CoV-2 would be expected to quickly reach the human population via intermediate hosts. Extensive spread of SARS-CoV-2 in wildlife has not been observed and in hindsight is not expected. In contrast, SARS-CoV had spread widely from its as-yet-undetermined reservoir into intermediate hosts, such as civets, ferret badgers, and raccoon dogs, and genetically diversified before it made multiple jumps to humans. This possibility was not accounted for by the authors of the preprint (14) that

The “Shunde problem” or “why it managed to infect Wuhan and only Wuhan”—is a problem which all market zoonosis or wildlife farm theories require extremely improbable and hard explanation to answer. <https://archive.md/OIGPz>  
<https://archive.md//VGPMY> Again, We have found direct evidence of lab leak in accidentally published early SRA samples from Csabai et al.  
<https://twitter.com/daoyu15/status/1668828125617352704>  
Fact 1: shunde is not a megapolis in 2002.  
[https://twitter.com/daoyu15/status/1668828125617352704?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1668828125617352704?s=46&t=wRQSWp_1VffWmS2vKQwhSA)  
Fact 2: HKU3 and ZC45 are not SARS1/SARS2r-CoVs.  
[https://twitter.com/daoyu15/status/1686471307230416896?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1686471307230416896?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

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2024 年 3 月 5 日星期二 12:01, dzha4225 <dzha4225@protonmail.com> 来信:

Also, please just get this to @ban\_epp\_gofroc  
<https://twitter.com/daoyu15/status/1668828125617352704>  
<https://archive.md/yyX0Z> <https://archive.md/iw1Pz><http://archive.md/7doR8>  
<https://archive.md/DChUL>  
Unfortunately, neither raccoon dogs nor any of the “species found in the wildlife stalls” were reported to be infected in nature at all by any strain of SARS-CoV-2.  
<https://x.com/daoyu15/status/1752888427169657342>  
Nowhere in the world were any raccoon dogs infected by SARS-CoV-2 any strain at all.  
[archive.md/DChUL](https://archive.md/DChUL) [archive.md/4rVph](https://archive.md/4rVph) [archive.md/yyX0Z](https://archive.md/yyX0Z) [archive.md/iw1Pz](https://archive.md/iw1Pz)  
<https://x.com/daoyu15/status/1740374861506310251>  
None have any rodents in the market ever been infected with a Sarbecovirus on the species level let alone SARS-CoV-2.  
<https://x.com/daoyu15/status/1749140161923887205>  
No evidence of Sarbecovirus infections even right next to the bats that carried the closest relatives and the RBD of SARS-CoV-2.  
<https://x.com/daoyu15/status/1740378156304109889>  
Nor were any civets or hedgehogs or rodents found infected or even infectable in-vitro by SARS-CoV-2.  
<https://x.com/daoyu15/status/1756582198235279692>  
Nor were red foxes or old-world deer infected before Omicron.  
<https://x.com/daoyu15/status/1756628731769081943>  
None of the pre- or post- pandemic efforts at sampling malayan porcupines yielded a single positive result for a Sarbecovirus.  
<https://x.com/daoyu15/status/1756627557066105090>

Even the zoos—lions and tigers infected, D614G and Delta strains. 0 porcupines.

<https://x.com/daoyu15/status/1756633632016404974>

No natural infection detected=no evidence of susceptibility. This is the gold standard for susceptibility estimation.

<https://twitter.com/daoyu15/status/1750291356927340611>

As expected from this absence of natural susceptibility, correlation failed with porcupines when entering the infamous “wildlife stall A”,

<https://x.com/daoyu15/status/1708341321969418446>

And overall not a single wild mammal species had positive correlation with significant mutual information with SARS-CoV-2 in the market,

<https://x.com/daoyu15/status/1750295494377484458>

and all metrics where “susceptible species” correlated with any degree of mutual information to SARS-CoV-2 yielded Homo Sapiens as the most correlated in all metrics.

<https://x.com/daoyu15/status/1720290396033749336>

Every stall have its unique species in the market, and most animals are sold on the ground.

<https://x.com/daoyu15/status/1708400523735613950>

Unfortunately inside the stall closest to the toilets and main entrance of the market sampled in Jan 12,

<https://x.com/daoyu15/status/1704347320949862843>

the unique species failed to land on the same sections of the ground as SARS-CoV-2, unlike the boot prints and suit marks of Homo Sapiens.

<https://x.com/daoyu15/status/1706503805079355845>

Human sampler contamination smeared out of the toilets and dropped in by the samplers.

<https://x.com/daoyu15/status/1744913305540464731>

Is the reality of W6-29-33.

<https://x.com/daoyu15/status/1748919231935041747>

Bleaching the toilets before sampling them would have worked if not for someone seeing and posting an image of it.

<https://x.com/daoyu15/status/1743825586290843998>

And there is a reason why PCR-/NGS+ or PREDICT ORF1ab-only PCR+/NGS- is unreliable.

<https://x.com/daoyu15/status/1745405110732144913>

Must be contaminated by a sampler, all below waist height and mainly below step height, in locations where sampler contact is inevitable

<https://x.com/daoyu15/status/1745073038981230666>

And must not be directly handled by a vendor because the single cell human source is fragile against RNase 7 degradation

<https://x.com/daoyu15/status/1744897774028521789>

Is the only rule followed by the market samples.

<https://x.com/daoyu15/status/1744899130084737140>

Despite all the animal CoVs have remained intact all the way to the end of February 2020,

<https://x.com/daoyu15/status/1741320436468826555>

No non-artifact SARS-CoV-2 reads survived past 12/01/2020 despite evidence of fecal shedding.

<https://x.com/daoyu15/status/1741328752955793547>

This is consistent with the SARS-CoV-2 being not found inside any animals.

<https://x.com/daoyu15/status/1741400591719678438>

An open question on flow cells.

<https://twitter.com/daoyu15/status/1749953567035727876>

Toilets spread SARS-CoV-2.

<https://x.com/daoyu15/status/1749953567035727876>

And this is the behavior of human-sourced environmental SARS-CoV-2.

No. Pierce.

<https://x.com/daoyu15/status/1756631223588303009?>

Unfortunately the animal sampling China didn't lie. RD=not susceptible.

Also, All that "raccoon dog stall" had in it is

Contamination and cross-contamination

<http://archive.md/xGHOC>

From incompetent samplers.

<http://archive.md/FskYn>

The reason why in both in Jan01 and Jan12, the stall with most positive

[https://twitter.com/daoyu15/status/1667155306135298048?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1667155306135298048?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Samples out of all samples is the stall closest to the toilets.

<https://archive.md/rSaO9><https://archive.md/ef2JW>

Also, inside of the stall "W5/NA" tested negative—it is the toilets and not the stall.

Even after they bleached the toilets, the staircase linking to the glasses city upstairs tested positive, as expected from a route which the still-open glasses city would trample in viruses downstairs in the middle of an outbreak.

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2024 年 3 月 5 日星期二 13:25, dzha4225 <dzha4225@protonmail.com> 来信:

[https://x.com/daoyu15/status/1749330085771886981?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1749330085771886981?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

When a separate source in 2021 mentioned body bags dumped outside the WIV and then Zhou Yusen dies without a cause, then the indication that he was killed and that he fell down the roof of the WIV simply indicated that he was likely murdered by the mean of being pushed off the roof.

[https://x.com/daoyu15/status/1671633678500528128?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1671633678500528128?s=46&t=wRQSWp_1VffWmS2vKQwhSA)





## RBD recombinant protein-based SARS vaccine for biodefense

Project Number  
4R01AI098775-05

Former Number  
5R01AI098775-05

Contact PI/Project Leader  
**HOTEZ, PETER** JOther Pls

Awardee Organization  
BAYLOR COLLEGE OF  
MEDICINE

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Journal (Link to PubMed abstract)	Authors	Publication Year	Similar Publications	CitedBy	iCite RCR
<a href="#">Recombinant Receptor-Binding Domains of Multiple Middle East Respiratory Syndrome Coronaviruses (MERS-CoVs) Induce Cross-Neutralizing Antibodies against Divergent Human and Camel MERS-CoVs and Antibody Escape Mutants.</a> <a href="#">Journal of virology 2017 Jan 01; 91 (1)</a>	Tai, Wanbo; Wang, Yufei; Fett, Craig A; Zhao, Guangyu; Li, Fang; Perlman, Stanley; Jiang, Shibo; Zhou, Yusen; Du, Lanying	2017	G	G	2.96
<a href="#">Receptor-binding domain of MERS-CoV with optimal immunogen dosage and immunization interval protects human transgenic mice from MERS-CoV infection.</a> <a href="#">Human vaccines &amp; immunotherapeutics 2017 07 03; 13 (7) 1615-1624</a>	Wang, Yufei; Tai, Wanbo; Yang, Jie; Zhao, Guangyu; Sun, Shihui; Tseng, Chien-Te K; Jiang, Shibo; Zhou, Yusen; Du, Lanying; Gao, Jimin	2017	G	G	2.31
<a href="#">Cross-neutralization of SARS coronavirus-specific antibodies against bat SARS-like coronaviruses.</a> <a href="#">Science China. Life sciences 2017 12; 60 (12) 1399-1402</a>	Zeng, Lei-Ping; Ge, Xing-Yi; Peng, Cheng; Tai, Wanbo; Jiang, Shibo; Du, Lanying; Shi, Zheng-Li	2017	G	G	1.16
<a href="#">MERS-CoV spike protein: a key target for antivirals.</a> <a href="#">Expert opinion on therapeutic targets 2017 Feb; 21 (2) 131-143</a>	Du, Lanying; Yang, Yang; Zhou, Yusen; Lu, Lu; Li, Fang; Jiang, Shibo	2017	G	G	9.89
<a href="#">Optimization of the Production Process and Characterization of the Yeast-Expressed SARS-CoV Recombinant Receptor-Binding Domain (RBD219-N1), a SARS Vaccine Candidate.</a> <a href="#">Journal of pharmaceutical sciences 2017 08; 106</a>	Chen, Wen-Hsiang; Chag, Shivali M;	2017	G	G	2.73



## 曹晓斌

北京科兴生物制品有限公司政府事务中心原高级经理

本词条是多义词，共7个义项

展开

曹晓斌（1976年6月-2022年4月17日），毕业于中国疾控中心流行病学与卫生统计学专业，博士研究生学历。<sup>[2]</sup>生前任北京科兴生物制品有限公司政府事务中心高级经理。

2022年4月17日，曹晓斌因病医治无效逝世，享年45岁。<sup>[1]</sup>

中文名	曹晓斌
出生日期	1976年6月
逝世日期	2022年4月17日
学历	博士研究生

### 相关视频



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人物逝世

### 人物经历

曹晓斌自参加工作以来，一直从事疾控防控工作。

生前任北京科兴生物制品有限公司政府事务中心高级经理。<sup>[1]</sup><sup>[2]</sup>

### 人物逝世

2022年4月17日，曹晓斌因病医治无效逝世，享年45岁。曹晓斌的追悼会于2022年4月19日12时在八宝山殡仪馆菊厅举行。<sup>[1]</sup><sup>[2]</sup>

### 人物逝世

2022年4月17日，曹晓斌因病医治无效逝世，享年45岁。曹晓斌的追悼会于2022年4月19日12时在八宝山殡仪馆菊厅举行。<sup>[1]</sup><sup>[2]</sup>

### 参考资料

[1] 网传科兴高管去世，公司回应：属实界面新闻·快讯，界面新闻·快讯 [引用日期2022-04-20]

[2] 网传科兴高管去世 公司回应：属实、新浪 [引用日期2022-04-20]

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TA



### 曾兵

辽宁省大连市委原常委，市人民政府原副市长、党组成员

本词条系多义词，共14个义项

曾兵（1970年1月-2022年7月23日），四川内江人，1993年7月参加工作，2007年10月加入中国共产党，生前任辽宁省大连市委常委，市人民政府副市长、党组成员，市委军民融合办（市国防科工办）主任（挂职）。

2022年7月23日19时55分，曾兵突发疾病医治无效在大连去世，享年52岁。

中文名	曾兵
性别	男
国籍	中国
民族	汉族
籍贯	四川内江

#### 快速导航

#### 人物逝世

曾任德国宝灵曼中国有限公司北京办事处医药代表，荷兰阿克苏诺贝尔集团欧高隆科技公司全球总部国际部职员，荷兰阿克苏诺贝尔集团欧高隆中国有限公司广州代表处华南地区经理，法国生物梅里埃中国有限公司广州代表处首席代表；中国生物技术集团公司副总经理，中国医药集团总公司（中国医药集团有限公司）副总经理，云南省发展和改革委员会副主任（挂职）。

2016年4月起，任中国医药集团有限公司副总经理、董事会秘书、新闻发言人、政策研究室主任。

2022年6月至2022年7月，任大连市委常委，市人民政府副市长、党组成员，市委军民融合办（市国防科工办）主任（挂职）。

#### 人物逝世

2022年7月23日19时55分，曾兵突发疾病医治无效在大连去世，享年52岁。

#### 参考资料

- [1] 大连市人民政府 曾兵，大连市人民政府 [引用日期2022-06-25]
- [2] 大连市人大常委会任免名单，大连日报 [引用日期2022-06-25]
- [3] 大连市人民政府办公室关于市政府领导同志工作分工的通知，大连市人民政府，2022-07-15 [引用日期2022-07-15]

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### 周育森

郑州大学公共卫生学院兼职教授

周育森，男，1966年生，安徽淮北人。博士，研究员，博士研究生导师，中国军事医学科学院微生物流行病研究所病原分子生物学研究室主任、病原微生物生物安全国家重点实验室病原生物学专业实验室负责人。

中文名	周育森
出生日期	1966年
出生地	安徽淮北
学位	博士

快速导航 学习经历 专业擅长 主要成就

#### 人物介绍

郑州大学公共卫生学院兼职教授，安徽医科大学兼职教授，美国匹兹堡大学客座教授等。担任《中国医学检验杂志》常务编委和《临床输血与检验》杂志编委，任中国微生物学会人畜共患病专业委员会委员和中华预防医学会慢性防治分会肝病防治学组专家、中华医学会感染病分会出血热病学组成员。

#### 学习经历

1998年毕业于中国军事医学科学院，获医学博士学位，其博士学位论文获2000年度全国百名优秀博士论文奖。2000至2003年在美国匹兹堡大学医学院进行博士后研究。

#### 专业擅长

主要从事肝炎病毒和新发传染病病原学和免疫学方面的研究。

#### 主要成就

1996年和1997年在国内率先报道了HGV和TTV病毒的发现和测定了国内病毒株的全基因序列，并进行了系统的致病性研究。先后获得军队科技进步一等奖和省部级二等奖和三等奖等。先后承担国家自然科学基金、973课题和863课题等多项课题研究。先后国内外专业杂志发表论文50余篇论文。指导4名博士研究生和6名硕士研究生，建立的分子病原生物学研究室目前与美国The University of Pittsburgh大学、Paris Universty XI大学、NeW York Blood Center和香港大学等联合进行研究生和博士后的培养和科研合作。

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苹果15怎么截图	虫草多少钱一颗

**Sharri Markson** @SharriMarkson · Sep 20, 2021  
 EXCLUSIVE: Trump has made the explosive claim that there were dead bodies dumped outside the Wuhan Institute of Virology, while the former Director of National Intelligence says some of the first Wuhan scientists to fall sick with Covid-19 are now missing.



“A highly decorated military scientist, Zhou Yusen...produced a vaccine patent w remarkable speed...The...military vaccine specialist is now understood to hv died, w US investigators having bn told by witnesses he was thrown off the roof of the WI...”

翻译推文



msn.com  
 Risky Experiments Inside Wuhan Lab Created COVID-19, Sensational New Evidence Reveals

13:55 · 2023/6/13 位于 Earth · 592 次查看



Are any of these wrong? No they aren't. Zhou Yusen was verified with the body bags reference. Ben HU lied in front of press on working with live virus. The stories specifically the contents are verified in stead of "disproven".

<https://twitter.com/daoyu15/status/1727357840606871865>

Yes. Body bags outside WIV match perfectly to Zhou yusen dying from a fall off its roof.

Two independent results.

No official cause of death listed.

Deceased.

<https://www.theaustralian.com.au/science/us-paid-chinese-peoples-liberation-army-to-engineer-coronavirus/news-story/4adee56c1433fad332a76ffe043390ea?amp%3Dnote%3Adeceased>

<https://www.science.org/doi/10.1126/science.abc4730>

Unfortunately this time the independent-in-both-space-and-time intelligence results does pan out.

Sent from [Proton Mail](#) for iOS

2024 年 3 月 5 日星期二 18:20, dzha4225 <dzha4225@protonmail.com> 来信:

Hi iboverlord and arkmedic

I have provided info to defeat miller in the rootclaim challenge.

Please also check my other rootclaim titled email to you.

Thank you.

Here are the contents 

[https://twitter.com/rootclaim/status/1753353199216439672?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/rootclaim/status/1753353199216439672?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Just as expected from jurong, mahachai, xinfadi, <https://archive.md/GKdtc> ,if a superspreading event happen on line 2 of the Wuhan metro, the biggest cluster would always be in the HSM.

[https://twitter.com/daoyu15/status/1753584453279187447?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1753584453279187447?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Another hint: only 5% of all cases are severe or ascertained in early 2020.

[https://twitter.com/daoyu15/status/1753593531250470983?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1753593531250470983?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://twitter.com/rootclaim/status/1758127978763125053?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/rootclaim/status/1758127978763125053?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

QTQRRQSRS is much more likely than QTQNSPRRARS if recombination yielded the FCS.

[https://x.com/kappafannon/status/1753548068526428436?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/kappafannon/status/1753548068526428436?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

When attention to DEFUSE is less than a fake decoy study (similar to Gemini 1.5's hallucination of Hanlen et al), the "assessment" is worthless. Still unable to reach "consensus".

[https://x.com/inwuchang/status/1753551174869938669?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/inwuchang/status/1753551174869938669?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Dark money and academic extortion (cutting off NIH funds and disciplining academic goals) were used by the zoonati to pressure any experts that don't believe in their cause. This is similar to how political correctness and liberalism prevented white people from being properly described by Gemini 1.5.

[https://x.com/daoyu15/status/1753613102388494672?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1753613102388494672?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

The reason why people with more familiarity in the zoonosis texts voted less likely for zoonosis is because they did not operate on knowledge but on financial interests—even non-targeted experts like @jbkinney were being extorted to give up lab leak promotions or beliefs on financial and academic grounds.

<https://gab.com/Flavinkins/posts/108971775263920617> Thus good conscience voting favors less to zoonosis and more to lab for whatever conscience left in them which none have really read any of the texts, or DEFUSE at all (any familiarity level below the fake decoy study are not real familiarities but just random fills).

[https://x.com/daoyu15/status/1751409799709790308?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1751409799709790308?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://x.com/billybostickson/status/1752248539076510083?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/billybostickson/status/1752248539076510083?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And then. Real polls on people that are aware:

[https://x.com/billybostickson/status/1752247037557690444?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/billybostickson/status/1752247037557690444?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Speaking out on lab origin in the field of experts carries a huge professional risk—the NIH and the EHA especially on virology and epidemiology have all its money to specifically pressure anyone (which emails in the professional domain are not exactly private among the domain, and which most "anonymous surveys" online are more than less likely baited to take personal info) by the institution against promoting lab origin content, most commonly under the threat of ending further funding and many times, if the expert have a higher probability of speaking out (which personal beliefs aren't really truly isolated between private and public), excommunication.

<https://gab.com/Flavinkins/posts/109447563442978822>

The funding agencies also have a huge complicit and therefore a huge financial interest to prevent the peer-review of lab origin promoting content and to financially and academically extort any experts into giving up their belief or stopping any promotion.

[https://x.com/daoyu15/status/1754790059495006520?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1754790059495006520?s=46&t=wRQSWp_1VffWmS2vKQwhSA) The more financially dependent one institution is (especially on foreign funds) the more incentivized an institution would do the same.

<https://twitter.com/daoyu15/status/1752903350507512190>

Bleach the toilets, spray the stalls, try as hard as you can.

<https://twitter.com/daoyu15/status/1752898622901899488>

Some eyewitness reports and some pictures eventually come out,

<https://twitter.com/daoyu15/status/1752895624473678055>

And all your efforts would end up bite back on yourself.

“A redundant 0.01 factor was added for requiring WIV to have an unpublished backbone with 98% nucleotide similarity to SARS2. There is no such need. Since our prior was defined as a novel coronavirus pandemic, then all we need to estimate is the probability that a virus capable of that existed in WIV. Specifically, since DEFUSE describes searching for hACE2 matches and adding FCS, then the only question is whether WIV held a virus with a good hACE2 match.

We know BANAL-52 is identical in the RBD to SARS2, so if a relative of it was collected then they have a backbone and we're done. But we should expand that to any virus with an hACE2 match, even one with 80% similarity to SARS2, so it's very reasonable that at least one will be found. We gave this 50%.

Another way to look at this mistake: If we arbitrarily limit the engineered backbone to have 98% similarity to SARS2, we should apply the same limitation to the zoonotic progenitor, meaning we should discard from the prior any pandemic that is caused by viruses that doesn't use hACE2, or those with good hACE2 match but using a different genetic sequence.

If we place this requirement on both hypotheses, the effect cancels out.”

<https://blog.rootclaim.com/rootclaims-covid-19-origins-debate-results/>

Also: only wild mice make 501Y, not hACE2 mice.

[https://twitter.com/john\\_bumblebee/status/1742592460491014225?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/john_bumblebee/status/1742592460491014225?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

“Humanized mice will attenuate the FCS”=“humanized mice will generate the exact PRRAR site”.

[https://twitter.com/daoyu15/status/1742600092606136416?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1742600092606136416?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Also reality: it was not “out of frame”. SARS-CoV-2 uniquely have two dS changes compared to all other QTQNTS genomes after the last Cysteine before the first S cleavage site.

[https://twitter.com/daoyu15/status/1745797467642487081?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1745797467642487081?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Shi put it in S2

[https://twitter.com/daoyu15/status/1745801964858786100?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1745801964858786100?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And the Proline is so you can grow it into a stock in VERO E6 cells (VOCs or P681 mutants have growth defects in VERO cells)

[https://x.com/daoyu15/status/1745753741251510627?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1745753741251510627?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

The PRRVR from mouse-passaged MERS-CoV.

[https://x.com/daoyu15/status/1751911405937193351?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1751911405937193351?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://x.com/daoyu15/status/1749741366635012244?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1749741366635012244?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://x.com/daoyu15/status/1749736275450417311?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1749736275450417311?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Remember those VERO-CHO?

[https://x.com/daoyu15/status/1749740263965172209?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1749740263965172209?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://x.com/daoyu15/status/1749741366635012244?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1749741366635012244?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Yes. The VERO signature FCS deletions (forms at significant fractions of the QS when cultured in VERO) were actually found in Wuhan patients.

<http://archive.md/GKdtc>

And well this is how SARS-CoV-2 outbreaks in Asia behaves:

<https://gab.com/Flavinkins/posts/108660565659228071>

Start with frozen VERO-CHO.

<https://twitter.com/daoyu15/status/1749734332665651406>

<https://twitter.com/daoyu15/status/1723738450078396809>

[https://x.com/daoyu15/status/1750115717871980793?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1750115717871980793?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

End with all 4 asian 2020-2021 outbreaks at frozen fish markets on primary transportation hubs.

No. The “game street” is now completely gone.

[https://x.com/daoyu15/status/1750104013457002932?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1750104013457002932?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Pretending there are infected animals required a grand conspiracy to also cover up all the secondary human outbreaks especially given that SARS-CoV-2 always generate outbreak in the naive human population after any spillover, if infected animals contacted humans any point in the trading route. There is no fizzling out for SARS-CoV-2 in the absence of NPI in Dec2019-Jan2020. And no there is zero cases at all linked to any other animal markets in China, even those known from leaks and gossip.



[https://x.com/daoyu15/status/1750141549030056395?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1750141549030056395?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

No that “thailand lab” did not engineer BatCoVs.

[https://x.com/daoyu15/status/1750100376030699567?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1750100376030699567?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

<https://twitter.com/daoyu15/status/1733792251669786633>

Note that these sequences notably did not contain coverage to the FCS.

<https://twitter.com/daoyu15/status/1722061305195208921>

And that WA1->A->B have happened independently at least 5 times in the WA1/UW cluster.

Leaked SRA data included both the exact kind of viruses that they claim will not be present in the WIV—and the exact SARS-CoV-2, WA1, cultured in a CoV-specific tailored fusion cell line VERO-CHO never used in China and sequenced before even a sample of WA1 can be taken in China, alongside C/C and B, at high passage depths, and contained within it residual human DNA not from anywhere in central China but in stead right where they were sampling from the 2018 “pathogen host adaptation and immune intervention” grant—the belt and road regions.

[https://twitter.com/daoyu15/status/1737318515353501739?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1737318515353501739?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Continued EHA human sampling=Yunnan and belt and road DNA.

[https://twitter.com/biophysicsfl/status/1737114987146174846?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/biophysicsfl/status/1737114987146174846?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Isolate if possible=special unpublished VERO-CHO cells.

[https://twitter.com/daoyu15/status/1737399622509928510?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1737399622509928510?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And it was sequenced before the first public sequencing of SARS-CoV-2 with this machine type by the flow cell, confirmed via Sangon policy and Chinese law, and before+not matching any samples of WA1 was even taken in China.

[https://twitter.com/daoyu15/status/1738903987381031326?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1738903987381031326?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And this exact CAS special project mirroring of DEFUSE+Year 5 extension—sample humans from belt and road area, isolate and engineer viruses for infection characterization, and create vectorized and nanoparticle vaccines that are capable of bringing in both backbone and Spike into bats studied in and released by the WIV, and into the main sample storage facility of the WDCD.

[https://twitter.com/daoyu15/status/1726529108811874621?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1726529108811874621?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Also: in the set of WA1/WA-UW samples, it have been discovered that the determinants of WA1 is highly unstable—it is not uncommon to find inside this cluster including cultures grown from this cluster that have shown signs of 3037C->T, 29095T residuum, 18060T->C and 8782C->T and 28144T->C, all appearing independently in the quasispecies.

A single leak of WA1 that mutated afterward causes all of the early lineages.

[https://twitter.com/daoyu15/status/1726531984288334216?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1726531984288334216?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Which are all found in the same culture from Csabai et al. WA1, A, C/C and B are all found in the same VERO-CHO culture where the only human sequences are found in the belt and road region but not Wuhan. None of the 3 (belt and road humans, CHO, WA1) are ever published in China for SARS-CoV-2 isolation or culture. And belt and road humans as an NGS sample in 2019-2020 is related only to viral sampling under the “病原体宿主适应与免疫干预” grant.

[https://twitter.com/daoyu15/status/1491651835584675845?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1491651835584675845?s=46&t=wRQSWp_1VffWmS2vKQwhSA) Csabai et al also contained T22657C, T3346C, A21562C and G487T. all of which is in RaTg13 but not in WuHu-1. also T1963C and T22963C in BANAL-52. Significant culture mutations have occurred inside Csabai et al which likely contained samples co-sequenced at different passage depths. not all of the reads were H655Y and del I68-T76.

(Also see this—note all the FCS relevant oddities can also be caused by targeted RNA recombination [link.springer.com/chapter/10.1007/3-540-26765-4\\_5](http://link.springer.com/chapter/10.1007/3-540-26765-4_5) followed by cell culture).

[https://x.com/daoyu15/status/1731414539324018732?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1731414539324018732?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

<https://gab.com/Flavinkins/posts/109640519028841414>

It is not just that SARS-CoV-2 Wuhan grows best in VERO cells out of all variants.

<https://twitter.com/daoyu15/status/1723738450078396809>

Some earliest patients harbored inside their QS specific S1-S2 deletions that can form only in VERO E6.

<https://twitter.com/daoyu15/status/1730690080950596017>

<https://twitter.com/daoyu15/status/1726769717497696562>

The WCDC and the Hubei CDC stores all of the human samples and backups of research cultures of pathogenic microbes in Wuhan, as this is their legally delegated duty and that labs in China are not allowed to store such cultures except several select state key laboratories. Since 2014, the only EID surveillance target in Wuhan is the HSM which all other sites are kept blind so that they can blame Huanan in case the research labs suffer an accident.

After an initial release from the WIV that caused Chen’s infection, and eventual transmission to the HSM via line 2 of the Wuhan metro, they mobilized the WCDC in 20-22/12/2019 to begin tapering with the environmental samples and prepare for any needed scapegoat action.

That mobilization ended up causing an infection of a WCDC worker with an aliquot of a sample containing WA1, A and B in the same quasispecies, which then go on infecting all of the earliest lineage A cases in Wuhan.

[https://twitter.com/daoyu15/status/1703438297983561793?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1703438297983561793?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://twitter.com/daoyu15/status/1726526722831683601?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1726526722831683601?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

The idea that “lineage A is in the market” hinges on A20. It is debunked by the absence of vendor gloves in the stall, presence of sampler PPE, inconsistency between 2021-2023 in viral read and fractions and inconsistency between 03/03/2023 and 26/03/2023 in host read fractions. Amplicon sequencing doesn’t alter host fractions.

[https://twitter.com/daoyu15/status/1739419702143881342?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1739419702143881342?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://twitter.com/daoyu15/status/1704216164560449822?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1704216164560449822?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

In fact, guess what is consistent with this observation? The introduction of human hosted lineage A genomes into the viral amplicon run but not the metagenomic run [archive.ph/ANS4Q](https://archive.ph/ANS4Q) and improbability of vendor origin for A20 predicts that lineage A is being grown inside the WDC, and likely caused human infections. And behold, all 3 of the samples are linked tightly and directly to the WDC.

[https://twitter.com/daoyu15/status/1705344605401800804?s=46&t=wRQSWp\\_1VffWmS2vKQwhSAA](https://twitter.com/daoyu15/status/1705344605401800804?s=46&t=wRQSWp_1VffWmS2vKQwhSAA) hotel right nextdoor to the new lab site, a location on the same route as the lab’s November-December movement (spilling aerosols everywhere on the road) and an admitted infection and seropositivity with no direction deducible for the “family cluster”.

Chen lived in Shidong. Even by the annexes indicating his history. The only thing they did is that they moved him to Jiangnan close to the market on the WHO maps.

[https://twitter.com/daoyu15/status/1672404501129756673?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1672404501129756673?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And no there is zero contact with the wildlife trade for the first market patient Mrs Wei either.

[https://x.com/daoyu15/status/1746808849384845582?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1746808849384845582?s=46&t=wRQSWp_1VffWmS2vKQwhSA)



**Holtz** ✓ @Biorealism

Feb 19

Do you have any notes about errors made through the debate? You might be one of the few people to have watched the whole 18 hours. I've seen a few that Miller made have been pointed out by @ban\_epp\_gofroc and @Ben\_Kuebrich.

2 1 1 6



**Ben Kuebrich** @Ben\_Kuebrich

Feb 19

If you read the judges notes, they got caught up on the lack of virus backbones for engineering.

Guess they bought into Peter's misinfo about mutations from lab culture and humanized mice.

2 2 14



**Ben Kuebrich** @Ben\_Kuebrich

Feb 19

They talk about retrospective studies not showing evidence of circulating COVID before the HSM super spreading event. What they don't mention is that those studies didn't find evidence of COVID until the first week of January, weeks after HSM so they're clearly underpowered

4 1 15



**Ben Kuebrich** @Ben\_Kuebrich

Feb 19

I am glad that the judges understood the significance of a clean insert (since Saar explained it incorrectly)

1 1 1



Flo Débarre

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Flo Débarre @flodebarre · 11m

Ah interesting. Could the "monkey bite" from Markson's book be a distortion of that initial monkey speculation?

1



2

6



Flo Débarre @flodebarre · 33m

Replying to @\_everythingism @zhihuachen and 2 others

there is also WeChat for later dates. Their data are on Github if you are interested [github.com/citizenlab/cha...](https://github.com/citizenlab/cha...)

Language	Keyword Combination	English Translation	Date Tested
Simplified Chinese	扒一扒武汉病毒所-所长的成功史	Muckraking Wuhan Virus Lab + Successful history of lab director	2020-02-14
Traditional Chinese	地方官+疫情+中央+隱瞞	Local authorities + Epidemic + Central (government) + Cover-up	2020-02-13
Traditional Chinese	舉行+批評中印+兩會期間+隱瞞	Hold + Criticize China + During two annual meetings + Cover-up	2020-02-13
Traditional Chinese	武漢+中共+危機+北京	Wuhan + CCP + Crisis + Beijing	2020-02-11
Traditional Chinese	共产党+肺炎+表现+统治	Communist Party + Pneumonia + Demonstrate + Rule	2020-02-05
Simplified Chinese	疫情+红会+4+政府+湖北	Epidemic + Red Cross Society + 4 + Government + Hubei	2020-02-04
Simplified Chinese	中国共产党+最大的威胁+这个时代	CCP + Biggest threat + The era	2020-02-05
Traditional Chinese	武漢+明明+病毒+人傳人	Wuhan + Obviously + Virus + Human-to-human transmission	2020-02-12

**ALT** Selection of keyword combinations censored on WeChat criticizing government actors or policies related to COVID-19

2



1

15



Flo Débarre @flodebarre · 30m

But the first line seems to be related to [sohu.com/a/370615513\\_10...](https://sohu.com/a/370615513_10...)

1



1

9



12月31日一早，多名身着防护服、背着喷雾器的防疫人员出现在华南海鲜市场里消毒，让人们回想起2003年SARS来袭时的场面。SARS全称为“严重急性呼吸系统综合征”，于2002年在中国广东出现，此后迅速扩散至全国乃至全球，最终造成超过8000人感染，774人死亡。

事实上，这天上午，国家卫健委一个专家组即抵达武汉。当天中午1点左右，武汉市卫健委首次公开发布通报称，近期部分医疗机构发现接诊的多例肺炎病例与华南海鲜市场有关联，目前已经发现27例，其中7例病情严重，其余病例病情稳定可控，有2例病情好转拟于近期出院。

2020年1月1日上午8时，华南海鲜市场出现落款为“武汉市江汉区市场监督管理局”和“卫生健康局”的休市整顿公告。该公告称：根据国务院《突发公共卫生事件应急条例》等法规条例的规定及武汉市卫生健康委关于肺炎疫情的情况通报，经研究决定对华南海鲜批发市场实行休市，进行环境卫生整治，请广大商户积极配合。

当天休市前，华南海鲜市场大部分商户还在营业。财新记者在现场看到，身着白色防化服的工作人员出现，准备进一步消毒。大部分商户只好收拾店面陆续离开，时有工作人员在市场里催促收摊。休市后，商户们聚集在市场外的路上，对突然休市和肺炎传闻议论纷纷。

1月2日，大量环卫工人在华南海鲜市场进行清洁作业，市场门口沿街排水沟渠的污泥也被挖出。财新记者在现场看到，身着防化服的人员在市场各处采样。其中，西区七街附近作为消毒重点区域，检疫人员对每个门面逐一搜集、提取检测物质。



Posts Replies Media Likes

Traditional Chinese	武汉+阴阳+病毒+人传人	Wuhan + Obviously - Virus + Human-to-human transmission	2020-02-12
ALT Selection of keyword combinations censored on WeChat criticizing government actors or policies COVID-19			

2 1 15

Flo Débarre @flodebarre · 30m  
 But the first line seems to be related to this [sohu.com/a/370615513\\_10...](http://sohu.com/a/370615513_10...)

Flo Débarre @flodebarre · 4h  
 Replying to @\_everythingism @zhihuachen and 2 others  
 I remember a report analyzing words censored on the internet early on and I think WIV was included? (From a North American institution)  
 Does this ring a bell?

Flo Débarre @flodebarre · 3h  
 Here it is [citizenlab.ca/2020/03/censor...](http://citizenlab.ca/2020/03/censor...)





























Language	Keyword	English Translation	Date Added
Simplified Chinese	武汉不明肺炎	Unknown Wuhan pneumonia	2019-12-31
Simplified Chinese	武汉海鲜市场	Wuhan seafood market	2019-12-31
Simplified Chinese	沙士变异	SARS variation	2019-12-31
Traditional Chinese	爆發sars疫情	SARS outbreak in Wuhan	2019-12-31
Simplified Chinese	武汉卫生委员会	Wuhan Health Committee	2019-12-31
Simplified Chinese	p4病毒实验室	P4 virus lab	2019-12-31

ALT Selection of keywords added to YY's blacklist on December 31, 2019

2 2 88 +

Flo Débarre reposted

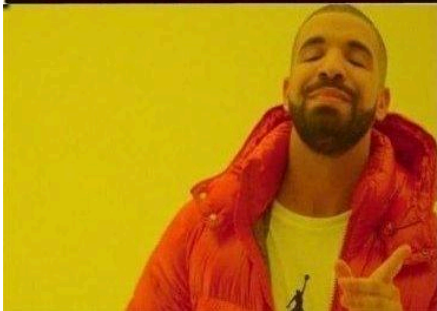
现呼吸困难。徐冰和同事对他们的病史、接触史进行了调查，发现他们或是在华南海鲜市场工作，或是住在市场附近，“很多病人是相互认识的，有人会告诉我们，亲戚住在哪个医院，状况非常不好”。徐冰发现，这些人有的来自一个家族，有的则是长久的麻将搭子——这些基本上能够判断这是一次聚集性发病事件。

-  **Daoyu**  @Daoyu15 · May 13 ...  
This is again wrong. The highest positive rate of any stall that tested from 01-12/Jan 2020 was actually W4-28. 2/2 samples were positive. In fact the samples from the outside surfaces of W4-26-28 was the highest positivity rate of any sites for Jan01-Jan12.  
 1  2  1  2,755 
-  **Daoyu**  @Daoyu15 · May 13 ...  
There are 2 samples taken from W4-28 and both were positive by PCR. There are 3 samples from inside of W4-26 and 4 samples from the outside of W4-26. All 3 samples from W4-26 that is positive came from the outside of W4-26. This makes it 5/6 PCR+ samples. On the other hand,  
 1  1  1  159 
-  **Daoyu**  @Daoyu15 · May 13 ...  
W6-29-33 itself have only 3 PCR positive samples and the 1 read or 2 reads close to each other make it impossible to rule out that the samples suffered significant cross-contamination (all that is needed is 1 fragment of ssRNA less than 100nt in length and 1 fragment of  
 1  1  1  160 
-  **Daoyu**  @Daoyu15 · May 13 ...  
dsDNA or hairpin RNA less than 100bp in length for Q61 and Q70–falling directly from the neighboring samples After the PCR reaction and during NGS library preparation.)  
 1  1   133 



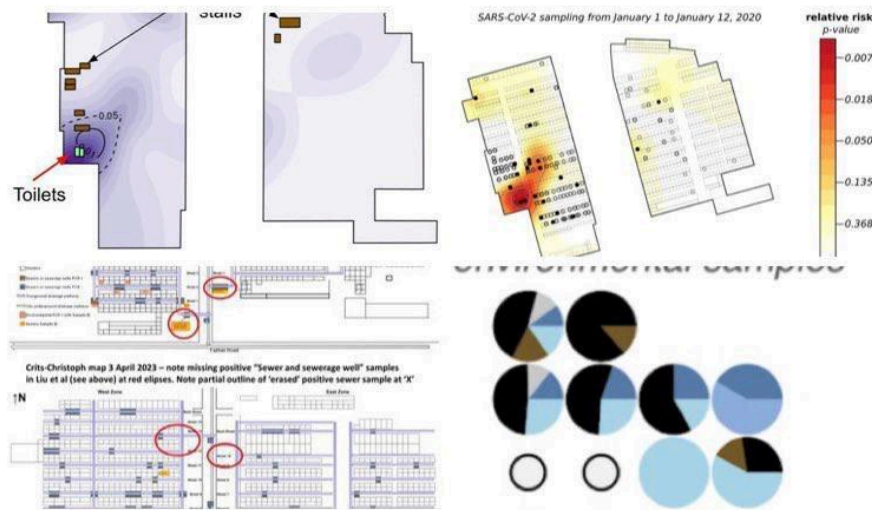




DEFUSE grant proposal,  
2018



Hanlen et al., 2022

Which is also why in both Jan 01 and in Jan12, the stall with the most positive samples out of all samples is the stall closest to the toilets— W4-26(2/2)and outside of W4-26-28(5/6 or 5/9 for all samples W4-26-28) for Jan01, W6-29-33(5/10) in Jan 12 is closest to the toilets.



 **Daoyu**  @Daoyu15 · 2023/5/13

This is again wrong. The highest positive rate of any stall that tested from 01-12/Jan 2020 was actually W4-28. 2/2 samples were positive. In fact the samples from the outside surfaces of W4-26-28 was the highest positivity rate of any sites for Jan0...

14:03 · 2023/5/29 位于 Earth · **2933** 次查看

Why “P4 virus lab” was among the banned words on Wechat in 31/12/2019?  
[https://x.com/daoyu15/status/1755183328825680307?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1755183328825680307?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

## (In addition to all elements in the WMHC announcement)

12月31日一早，多名身着防护服、背着喷雾器的防疫人员出现在华南海鲜市场里消毒，让人们回想起2003年SARS来袭时的场面。SARS全称为“严重急性呼吸系统综合征”，于2002年在中国广东出现，此后迅速扩散至全国乃至全球，最终造成超过8000人感染，774人死亡。

事实上，这天上午，国家卫健委一个专家组即抵达武汉。当天中午1点左右，武汉市卫健委首次公开发布通报称，近期部分医疗机构发现接诊的多例肺炎病例与华南海鲜市场有关联，目前已经发现27例，其中7例病情严重，其余病例病情稳定可控，有2例病情好转拟于近期出院。

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当天休市前，华南海鲜市场大部分商户还在营业。财新记者在现场看到，身着白色防化服的工作人员出现，准备进一步消毒。大部分商户只好收拾店面陆续离开，时有工作人员在市场里催促收摊。休市后，商户们聚集在市场外的路上，对突然休市和肺炎传闻议论纷纷。

1月2日，大量环卫工人在华南海鲜市场进行清洁作业，市场门口沿街排水沟渠的污泥也被挖出。财新记者在现场看到，身着防化服的人员在市场各处采样。其中，西区七街附近作为消毒重点区域，检疫人员对每个门面逐一搜集、提取检测物质。



shutterstock.com · 1569723133

[https://twitter.com/daoyu15/status/1721692065804030381?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1721692065804030381?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

At least four positive samples from the market especially near the entrance of the market are found with neither human cases nor “susceptible wildlife”. Not even a single read. These functions as incontrovertible evidence that sampler boots and their sprayers were bringing in the virus into the market.

<https://twitter.com/daoyu15/status/1722428958694887858>

<https://twitter.com/daoyu15/status/1748919231935041747>

In fact, it even followed the exact pattern as would be expected from boot contamination brought in from the outside of the market and trampled out from the toilets—More such samples are found south of the W6 junction while some also exist north of it. This is entirely as expected when boots that brought in the virus from the entrance and the toilets first came with SARS-CoV-2 without wildlife material, then many but not all of them then got wildlife material on them when they stepped through the W6 junction.

<https://twitter.com/daoyu15/status/1752142052890997051>

[https://twitter.com/daoyu15/status/1731840299100754197?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1731840299100754197?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

All observations of virologists working at the market without a published sample taken at that date should automatically be considered extremely suspicious.

[https://twitter.com/daoyu15/status/1722434363042976034?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1722434363042976034?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://twitter.com/daoyu15/status/1731838292256309424?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1731838292256309424?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

The most likely reason is that They were dropping in samples in stead of taking them, leading to the observation that only human have a consistent positive correlation or any significant mutual information with SARS-CoV-2 there.

An army of cleaning workers and hazmat suited workers armed with cleaning utensils and biological material manipulation equipment seen frequenting “the vicinity of W7” (e.g. W6 and W8) in 02 Jan 2020. There were no samples from W7 in 12/01/2020. And these workers were seen fiddling with the environmental surfaces as they moved, even sludge in the drains were dug up—no samples exist from 02/01/2020. It is more likely that they are planting all of the “positive Jan 12 samples” in stead of sampling them. Of course, convenience to reach by hand and by foot would make an object more likely being tampered with and a positive sample planted in this operation.

<https://twitter.com/daoyu15/status/1722434363042976034>

Also, neither the early cases data, sample A20, “wildlife stall A” and any other market samples, nor the statements of the WIV regarding viruses or infections are real or untampered with.

<https://twitter.com/tylerastepke/status/1721668207486869662>

Because Homo Sapiens is still the only species that they can get infected at all,

<https://twitter.com/daoyu15/status/1703918936843321541>

if you zoom in and correlate between animals and viruses, You get animal-specific viruses being correlated strongly positively to the animals,

<https://twitter.com/daoyu15/status/1720290396033749336> and SARS-CoV-2 being positively correlated consistently or with significant mutual information only with Homo Sapiens.



Don't follow your logic.

9 Raccoon-dog were inoculated w/100K live SARS2 virions (lineage B), & 6 became infected. But max titer of SARS2 shed by the 6 was 13,400 live virions, which caused infection in 2 naive RD. However, only 1 of naive RD shed live virus - just 42 virions!

2 3



**Ticklicker** @Ticklicker56

1h

That 1 nasal swab of previously naive Raccoon-dog (Animal #10) had TOO FEW live virions (42) to perpetuate the infection chain - thus represented a DEAD END transmission.

Animal #11, the other naive RD that was infected by inoculated neighbor, apparently did NOT shed live virus!

1 2



**Ticklicker** @Ticklicker56

1h

Raccoon-dog are NOT social animals, w/male & female primarily defending their territory via scent marking - so opportunity to spread infection would be very restricted.

Also, infectious period was limited to ~3 days after inoculation.

Perpetuating SARS2 infection highly unlikely!

1 2



**Ticklicker** @Ticklicker56

37m

Replying to @Ticklicker56 @JeffNovack1 @Biorealism @breakfast\_dogs @tommy2t45103307 @Rebecca21951651 @WashburneAlex

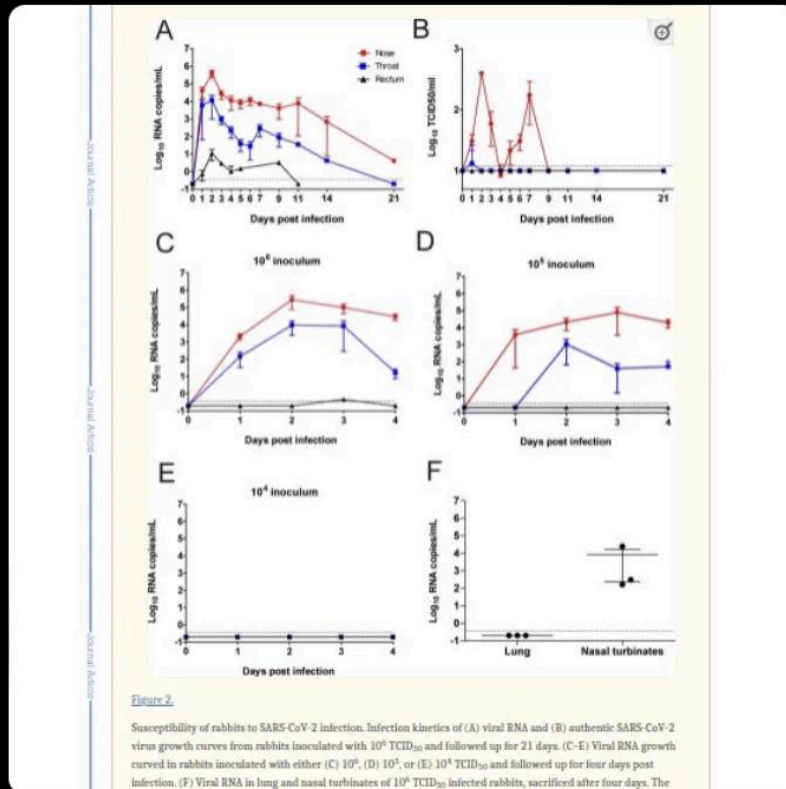
For an "intermediate host" Raccoon-dog to infect human in "single contact", it would need its nasal/oral mucosa to have had direct contact w/massive # of live SARS2 virions (100k?) within only the 3 previous days, & several drops of its snot had to get into human's eyes or mouth.



**Ticklicker** @Ticklicker56

10h

Peter fails to recognize that the titer of inoculating dose of SARS2 lineageB can be critical determinant in whether the resulting infection can be effectively transmitted - as documented in experimental infection study of domesticated rabbits (see Fig 2B,D&E in Mykytyn et al '21)



1 1 2



**Ticklicker** @Ticklicker56

10h

FYI, the very same isolate of SARS2 virus was used in experimental infection study of domesticated rabbits (Mykytyn et al '21) as was used in the experimental infection study of Raccoon-dog (Freuling et al '20) - ie, BetaCoV/Germany/BavPat1/2020 (lineage B; w/D614G mutation).



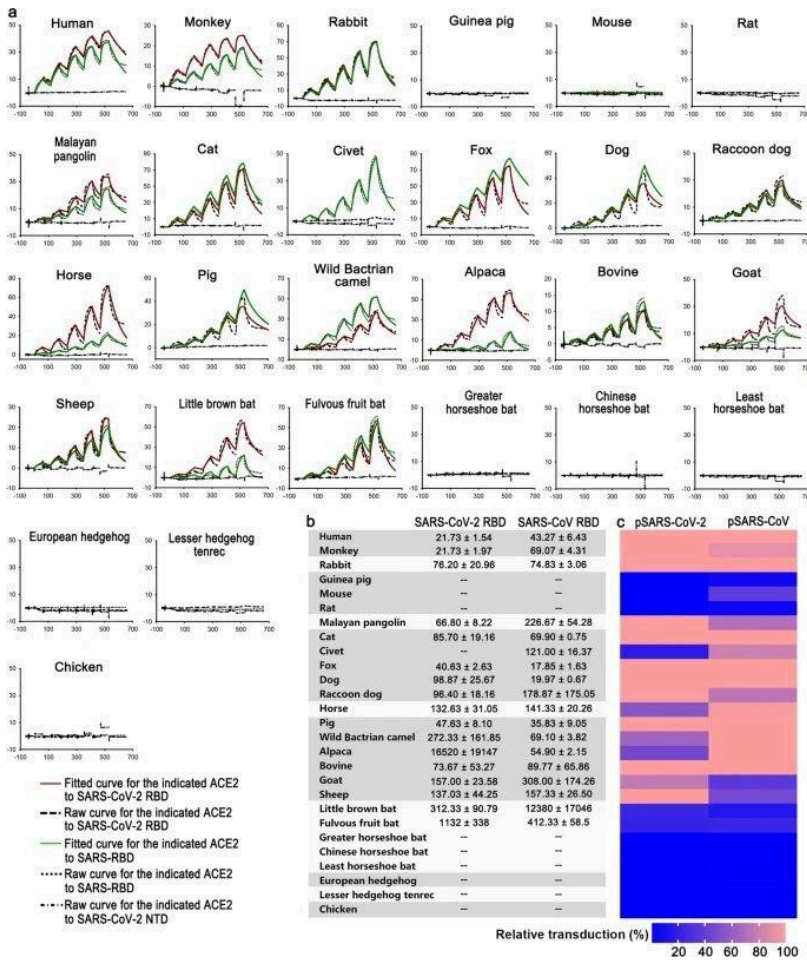
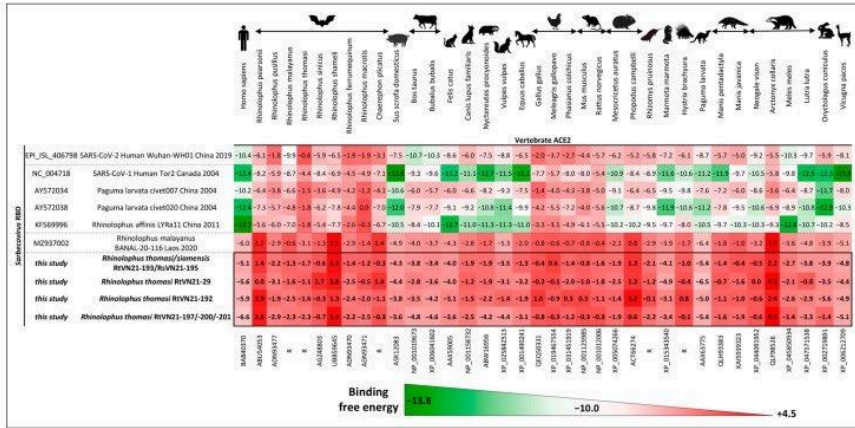
**Kristian Andersen** 18:22

Ran some more selection stuff - here are the numbers. Only thing one can really say is that it looks like the SARS spike protein was possibly under positive selection early in the epidemic and that's not something we see with SARS-CoV-2. I had expected dN/dS to be lower for ORF1, but here SARS-CoV-2 is actually higher.

Not really sure we can conclude anything from these... It's somewhat intriguing that the spike from SARS-CoV-2 doesn't appear to be under selection at all though - does suggest some sort of pre-circulation to me.

Selection pag.

	ORF1	Spike
SARS-CoV-2	0.91	0.29
SARS, early	0.81	1.82
SARS, middle	0.68	0.44
SARS, late	0.32	0.51



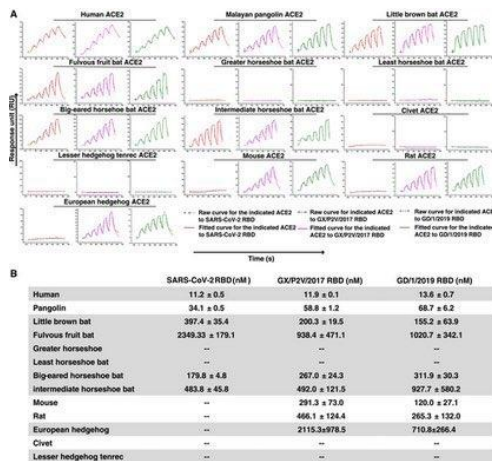


Hedgehogs does not have an ACE2 that is permissive to infection at all and all porcine suppliers in the HSM can be traced back to supply farms in Hubei that tested negative (the S.D. of malayan porcine is 0 in Xiao Xiao et al sales. Indicating stable supply from a registered



Species	Accession Number
Malayopithecus procyonoides	Q96011
Canis lupus familiaris	Q96011
Neofelis concolor	Q96011
Ursus arctos	Q96011
Ursus mandchuricus	Q96011
Ursus mandchuricus	Q96011
Ursus mandchuricus	Q96011
Ursus mandchuricus	Q96011
Ursus mandchuricus	Q96011
Ursus mandchuricus	Q96011
Ursus mandchuricus	Q96011

在武汉周边的黄陂、随州、咸宁、江夏地区的宰杀海鲜市场上游供货商养殖的竹鼠、穿山甲、大猫、兔子等动物和本地环境标本共 139 份，经湖北省疾控中心 rRT-PCR 核酸检测均为阴性。



c. Animal Sampling at the Huanan Seafood Market

In addition to taking environmental samples, 457 animal-related samples from "188 individuals of 18 species" were collected between January 1 and March 30, 2020.<sup>660</sup> According to presentations by PRC public health officials to the WHO, none of the samples tested positive for SARS-CoV-2.<sup>661</sup> PRC officials informed that none of the "animal-related" samples were taken from live animals present at the market:

The sources of the samples include unsold goods kept in refrigerators and freezers in the stalls of [Huanan Market], and goods kept in warehouses and refrigerators related to the [Huanan Market]. Samples from stray animals in the market were also collected, i.e., swab samples from 10 stray cats, 27 cat feces, one dog, one weasel, and 10 rats.... All the 457 animal samples tested negative for SARS-CoV-2 nucleic acid, suggesting that the animal infections with SARS-CoV-2 might be rare in the market.<sup>662</sup>

Nucleic Acid Testing (NAT)	
Hubei	
Number of species	10
Specific types of animals	Bamboo Rat, Porcupine, Duck, Snake, Rabbit/Hare, Chicken, Ostrich/Turkey, Wild Boar
Total sample size	616
Test results	Negative

PRC officials denied any illegal live animal sales occurred at the Huanan Market.<sup>663</sup> Presentations to the WHO, PRC officials identified "10 animal selling stalls in the Huanan Market, accounting for 1.5% of the total" stalls.<sup>664</sup> Reviewing sales records provided by PRC officials, the WHO-China Report concluded that those 10 stalls sold "animals or products", but that the only live animals sold were snakes, salamanders, and crocodiles.<sup>665</sup> None of which are susceptible to SARS-CoV-2, and thus are unlikely to be intermediate hosts.<sup>666</sup> All other animals were reportedly sold as frozen goods, including bamboo rats, badgers, hedgehogs, sika deer, and porcupines.<sup>667</sup>

Pallas's squirrel ( <i>Callosciurus erythraeus</i> ) <sup>R,P,*</sup>	16.52 ± 4.87 (n = 23)	25.74 ± 7.59 (n = 5)
Masked palm civet ( <i>Paguma larvata</i> ) <sup>F,*</sup>	10.69 ± 8.42 (n = 29)	62.73 ± 15.25 (n = 5)
Chinese bamboo rat ( <i>Rhizomys sinensis</i> ) <sup>F,*</sup>	42.76 ± 20.68 (n = 29)	18.64 ± 7.58 (n = 5)
Malayan porcupine ( <i>Hystrix brachyura</i> ) <sup>F,*</sup>	10.00 ± 0.00 (n = 29)	68.06 ± 14.23 (n = 5)
Chinese muntjac ( <i>Muntiacus reevesi</i> ) <sup>F,*</sup>	10.00 ± 0.00 (n = 29)	142.62 ± 49.67 (n = 5)
Coyup ( <i>Myocastor coypus</i> ) <sup>F</sup>	5.00 ± 0.00 (n = 29)	28.70 ± 5.08 (n = 5)
Marmot ( <i>Marmota himalayana</i> ) <sup>F</sup>	15.00 ± 4.29 (n = 20)	81.37 ± 11.70 (n = 5)
Red fox ( <i>Vulpes vulpes</i> ) <sup>F</sup>	30.00 ± 0.00 (n = 25)	60.96 ± 21.68 (n = 5)
Mink ( <i>Neovison vison</i> ) <sup>F</sup>	10.37 ± 1.92 (n = 27)	34.62 ± 14.78 (n = 5)
Red squirrel ( <i>Sciurus vulgaris</i> ) <sup>R,P,*</sup>	16.43 ± 9.51 (n = 28)	26.04 ± 8.14 (n = 5)
Wild boar ( <i>Sus scrofa</i> ) <sup>W,R,F,*</sup>	4.17 ± 5.77 (n = 29)	319.57 ± 55.95 (n = 5)
Complex-toothed Flying Squirrel ( <i>Trogopterus xanthipes</i> ) <sup>F,*</sup>	5.17 ± 27.85 (n = 29)	28.11 ± 9.64 (n = 5)

Table 6. Family, genus, and species for 559 rodents sampled.

<b>Cricetidae</b>	
<i>Eothenomys cochinus</i>	92
<i>Eothenomys proclitor</i>	26
<b>Hystriidae</b>	
<i>Hystrix brachyura</i>	39
<b>Muridae</b>	
<i>Apodemus chevrieri</i>	123
<i>Apodemus draco</i>	1
<i>Apodemus latronum</i>	7
<i>Apodemus peninsulae</i>	28
<i>Niviventer confucianus</i>	1
<i>Niviventer coxingi</i>	2
<i>Niviventer eha</i>	27
<i>Niviventer fulvescens</i>	2
<i>Rattus tanezumi</i>	2
<i>Vernaya fulva</i>	1
<b>Spalacidae</b>	
<i>Rhizomys pruinosus</i>	20
<i>Rhizomys sinensis</i>	188

No rodent samples collected in this study were positive for Coronaviruses or Paramyxoviruses. Field identification of 89% (136/153) of host species (bats) with samples that tested positive for Coronaviruses or Paramyxoviruses was independently confirmed in the laboratory by commercial barcoding using the cytochrome b gene of bat mitochondrial DNA as a marker. Barcoding to identify species of 17 (11%) specimens was not possible due to insufficient sample quantity remaining after RT-PCR assays. Of the 89% tested and confirmed, the field identification was 100% accurate providing assurance that the unconfirmed species (by barcoding) had also have been accurately identified.

All Coronavirus positive samples were collected in four south China provinces (Hainan, Guangdong, Guangxi, and Yunnan), therefore no north-south gradient was discernible. Paramyxovirus positive samples were collected across a greater geographic range in China. Along a north-south gradient, the detection rate was significantly highest ( $X^2 = 7.8372$ ,  $p = 0.005118$ ) in the southern provinces of Fujian, Guangdong, Guangxi, Guizhou, and Yunnan. No correlation was evident between bat gender and detection of either virus ( $X^2 = 0.2638$ ,  $p = 0.607534$ ).

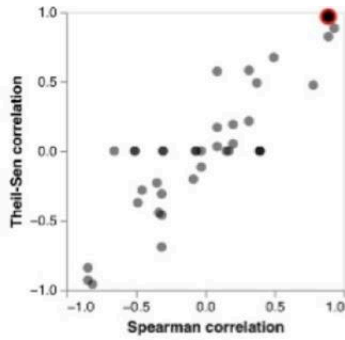
Search “Regional Animal Health Office No. 6 (RAHO6), Viet Nam Department of Animal Health; Viet Nam National Institute of Hygiene & Epidemiology; Wildlife Conservation Society” on GenBank for vietnamese porcupines. Only murine coronavirus, IBV and Alphacoronaviruses were found.

[journals.plos.org/plosone/articl...](https://journals.plos.org/plosone/article/)

No Coronaviruses were found in porcupines in China,

[core.ac.uk/download/pdf/1...](https://core.ac.uk/download/pdf/1...)

And no Sarbecovirus genomes from genus Hystrix or a SC2r-CoV genome from the genus Nyctereutes (or any Sarbecovirus genomes at all after the SARS-CoV-1 epidemic) have ever been deposited on GanBank anywhere in the world.



% species mitochondria reads computed as [% of all preprocessed reads](#)

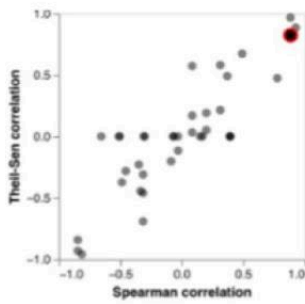
sample collection date [2020-01-12](#)

axis scale [log10 of % \(zero plotted as minimum non-zero value\)](#)

sample isolation source [all](#)

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as [% of all preprocessed reads](#)

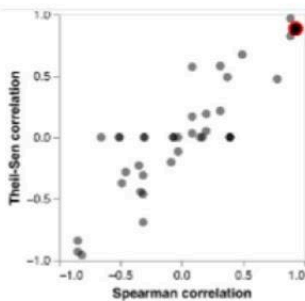
sample collection date [2020-01-12](#)

axis scale [log10 of % \(zero plotted as minimum non-zero value\)](#)

sample isolation source [all](#)

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as [% of all preprocessed reads](#)

sample collection date [2020-01-12](#)

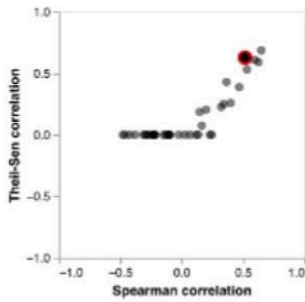
axis scale [log10 of % \(zero plotted as minimum non-zero value\)](#)

sample isolation source [all](#)

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no





% species mitochondria reads computed as

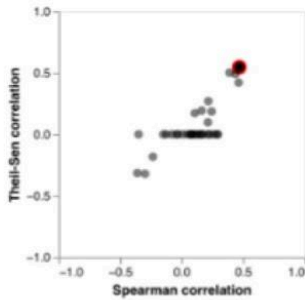
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

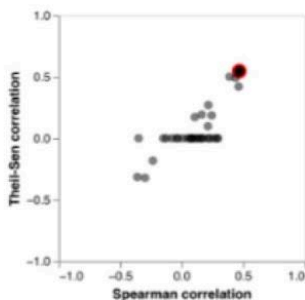
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

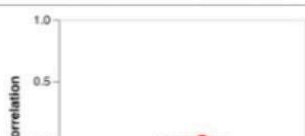
sample collection date

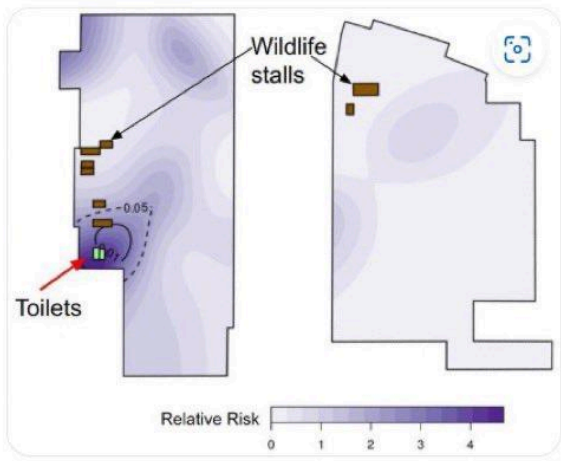
axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no





There are about 200 reads of canine Kobuvirus in Q61, 20 in Q64, 2 in Q68, 30 in Q69 and 2 in Q70.

Raccoon dog reads are 14338, 150, 29, 77, 21.

There are 204, 70, 80, 55, 60 reads of

Embecoviruses in Q61, Q64, Q68, Q69, Q70.

Bamboo rat and rabbit reads are 746, 294, 505, 36, 85 (the RdRp/ORF1b fragments of

Embecoviruses are heavily confusing with each other and are frequently recombinant, meaning that the alignment algorithm does not reliably distinguish between them within this region)

There are 12, 21, 3, 1100, 3 reads of Canine Coronavirus in Q61, Q64, Q68, Q69, Q70.

Domestic dogs are 1000, 106, 331, 3008. 103.

There are 80, 7, 0, 0, 600 reads of Murine

Orthopneumovirus in Q61, Q64, Q68, Q69, Q70.

The number of Malayan porcupines are 61, 30, 13, 0, 5018.

The number of Civet Kobuvirus is 90, 0, 0, 0, 0 for Q61, Q64, Q68, Q69, Q70.

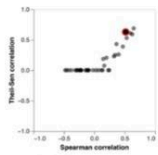
masked palm civets are 424, 0, 0, 0, 0.

Finally, the number of SARS-CoV-2 is 1, 5, 7, 2 close to each other, 2 dar apart from each other for Q61, Q64, Q68, Q69, Q70.

The number of Homo Sapiens are 21, 47, 164, 38, 12.

Q64, Q68, Q69 are PCR+, Q61 and Q70 are PCR-.

The animals correlate with animal viruses. The

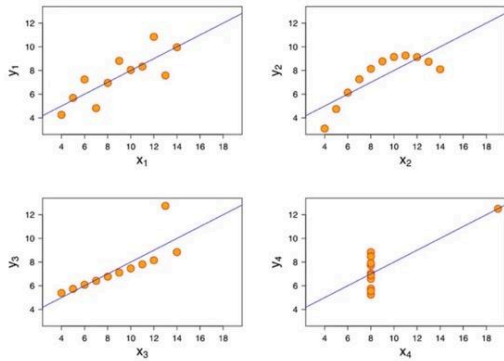


% species mitochondria reads computed as  % of all preprocessed reads   
 sample collection date  all   
 axis scale  log10 of % (zero plotted as minimum non-zero value)

sample isolation source  all   
 species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)   
 only show samples with SARS-CoV-2  yes  no

### Overall correlation of mitochondrial DNA and SARS-CoV-2 across all samples using Theil-Sen estimator

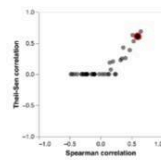
Each point shows the correlation between the percent of all high-quality reads that align to SARS-CoV-2 and the percent of aligned mitochondrial reads for a specific species taken across all samples. The axes show the Spearman correlation and a measure of correlation based on the Theil-Sen estimator.



Source: [Wikipedia](#)

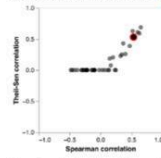
An alternative to least squares for simple linear regression is Theil-Sen estimation. This more robust method determines the slope of the regression line via the median of the slopes of all lines that can be drawn through the data points:

$$m_{TS}(x, y) = \text{median}_{k, l \in \{1, \dots, n\}, x_k \neq x_l} \left( \frac{y_l - y_k}{x_l - x_k} \right)$$



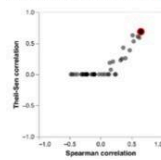
% species mitochondria reads computed as  % of all preprocessed reads   
 sample collection date  all   
 axis scale  log10 of % (zero plotted as minimum non-zero value)

sample isolation source  all   
 species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)   
 only show samples with SARS-CoV-2  yes  no



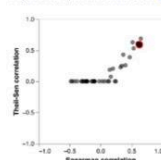
% species mitochondria reads computed as  % of all preprocessed reads   
 sample collection date  all   
 axis scale  log10 of % (zero plotted as minimum non-zero value)

sample isolation source  all   
 species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)   
 only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as  % of all preprocessed reads   
 sample collection date  all   
 axis scale  log10 of % (zero plotted as minimum non-zero value)

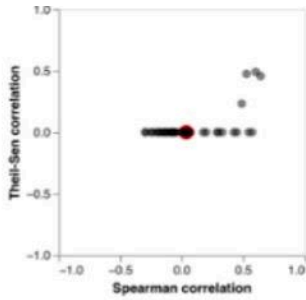
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 species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)   
 only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as  % of all preprocessed reads   
 sample collection date  all   
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sample isolation source  all   
 species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)   
 only show samples with SARS-CoV-2  yes  no





% species mitochondria reads computed as

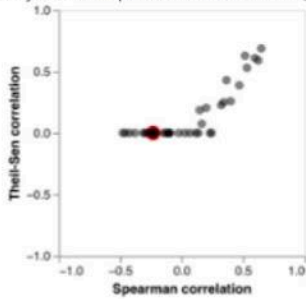
sample collection date

axis scale

sample isolation source

- species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



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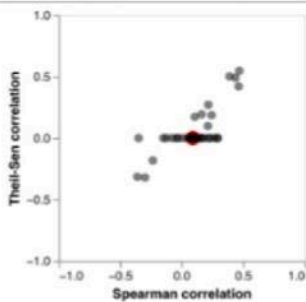
sample collection date

axis scale

sample isolation source

- species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

sample collection date

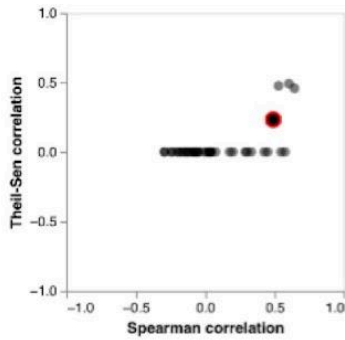
axis scale

sample isolation source

- species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no





% species mitochondria reads computed as

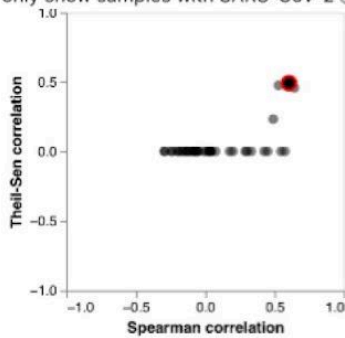
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan mar  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as

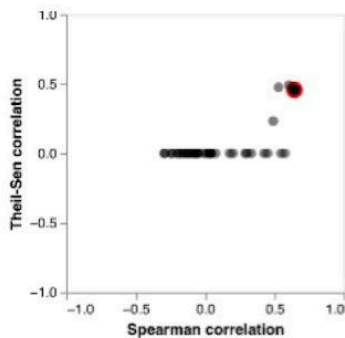
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan mar  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



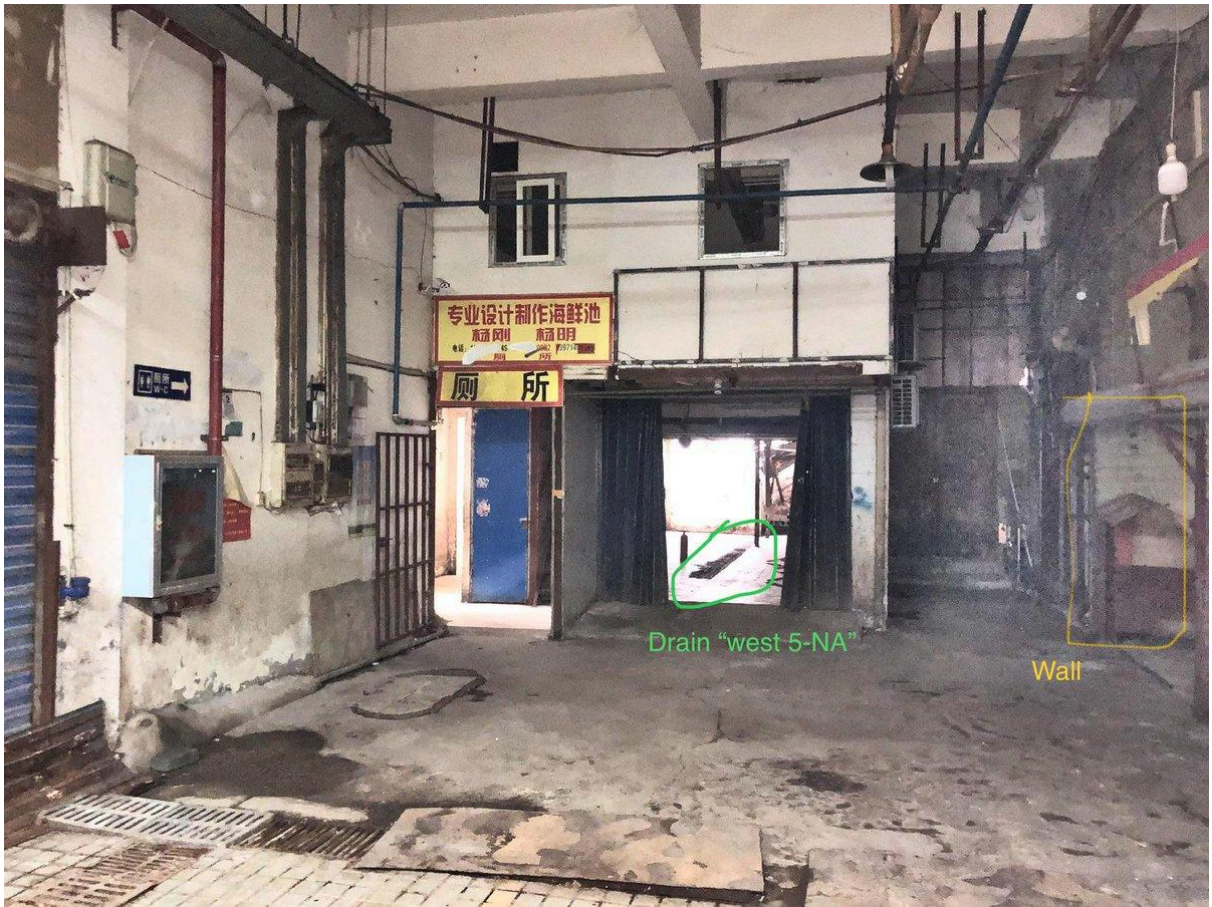
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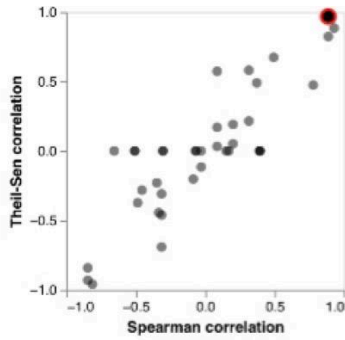
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan mar  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon





% species mitochondria reads computed as

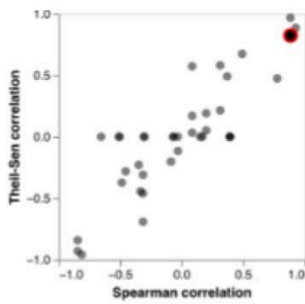
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



...

% species mitochondria reads computed as

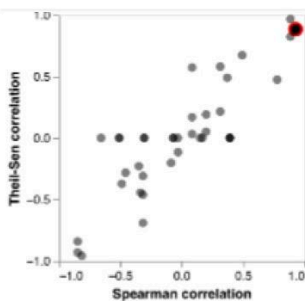
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



...

% species mitochondria reads computed as

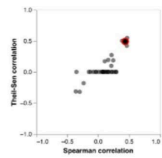
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as  % of all preprocessed reads

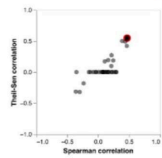
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as  % of all preprocessed reads

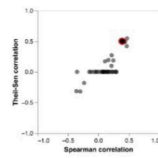
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  Oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as  % of all preprocessed reads

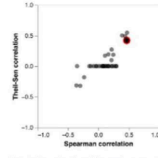
sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no



% species mitochondria reads computed as  % of all preprocessed reads

sample collection date

axis scale

sample isolation source

species to highlight  none  Amur hedgehog  Chinese cobra  Chinese salamander  European hedgehog  Himalayan marmot  Largemouth bass  Malayan porcupine  Mayalan field rat  oriental rat snake  Siberian weasel  bat-eared fox  brown bush hen  brown rat  carp  catfish  chicken  cow  dog  fennec fox  goat  gray fox  hoary bamboo rat  hog badger  human  leaf deer  long-eared hedgehog  masked palm civet  pig  pigeon  quail  rabbit  raccoon dog  sand cat  sheep  snakehead fish  spot-billed duck  spotted dove  swamp eel  yellow croaker (fish)

only show samples with SARS-CoV-2  yes  no

Note that the negative upstream supply farm animal testing results are in fact leaked in as early as 02/2020, when there is no official disapproval to the market theory.

**Table 1.** Summary of mink farm SARS-CoV-2 monitoring data amassed during a period of 14 months

Voivodeship	2021 (February–December)		2022 (January–March)		Total		Number of positive farms
	No. of farms	No. of swabs	No. of farms	No. of swabs	No. of farms	No. of swabs	
Mazowieckie	58	1,160	28	420	86	1,580	0
Podkarpackie	8	160	5	75	13	235	1
Lubuskie	35	700	19	295	54	995	0
Wielkopolskie	117	2,340	87	1,472	204	3,812	1
Zachodniopomorskie	54	1,080	8	420	62	1,500	3
Pomorskie	19	380	1	20	20	400	1
Dolnośląskie	14	280	0	0	14	280	0
Kujawsko-Pomorskie	24	480	0	0	24	480	1
Lubelskie	36	1,120	22	356	58	1,476	2
Lódzkie	6	120	1	15	7	135	1
Małopolskie	7	140	1	15	8	155	0
Opolskie	6	120	0	0	6	120	0
Podlaskie	10	200	0	0	10	200	1
Świętokrzyskie	6	120	13	185	19	305	0
Warmińsko-Mazurskie	1	20	0	0	1	20	0
Śląskie	8	160	0	0	8	160	0
<b>Total</b>	<b>409</b>	<b>8,580</b>	<b>185</b>	<b>3,273</b>	<b>594</b>	<b>11,853</b>	<b>11</b>



**Fig. 1.** Locations of inspected mink farms (marked as grey dots) and those which were SARS-CoV-2 positive (marked as red dots)

**Table 2.** A summary of the analysis of positive mink farms

No.	Date of sample collection	Voivodeship	Location	rRT-PCR	
				Positive/Tested	Ct value range*
1	16/06/2021	Lubelskie	Wisznice (house 1)	2/20	21.8–25.5
			Wisznice (house 2)	1/20	28.9
2	22/11/2021	Kujawsko-Pomorskie	Kraczki	1/20	28.9
3			Zieleniewo1	1/20	30.5
4	30/11/2021	Zachodniopomorskie	Zieleniewo2	13/20	24.7–36.8
5			Ołuzna	19/20	18.9–37.3
6	01/12/2021	Wielkopolskie	Biadki	18/20	17.6–36.4
7	14/12/2021	Podkarpackie	Janowiec	20/20	28.1–30.4
8	15/12/2021	Podlaskie	Kościuki	2/20	32.1–35.3
9	20/12/2021	Pomorskie	Leżno	10/20	19.1–26.3
10	20/12/2021	Lubelskie	Kloczew	5/20	28.9–30.2
11	20/01/2022	Łódzkie	Stefanów	2/20	20.5–21.8

Ct – threshold cycle; \* – results for E gene rRT-PCR

**Table 3.** Results of oral swab and serum sample analysis collected in two houses in Wisznice in the Lubelskie voivodeship

House	Date of sample collection	Sample	Number		Results*	Prevalence (%)
			Collected	Positive		
1	16/06/2021		20	2	21.8–25.5	10
	19/07/2021	Oral swab	90	1	28.8	1.1
	02/08/2021	Serum of kitten	15	15	1.25	100
		Serum of adult	15	14	1.64	93.3
2	16/06/2021		20	2	28.5–30.7	10
	19/07/2021	Oral swab	60	0	-	0
	02/08/2021	Serum of kitten	15	15	1.04	100
		Serum of adult	15	14	1.25	93.3

\* – results for E gene rRT-PCR/mean OD values obtained using Ingezim ELISA test

**Table 4.** Molecular characteristics of SARS-CoV-2 detected in farmed mink in Poland in the studied period

No.	Mink farm	Gisaid_ID	Clade	Pango lineage	Nucleotide		Frame shifts	Amino acid	
					substit.	delet.		substit.	delet.
1	Wisznice, house 2, Lubelskie	EPI_ISL_3218555	GR/20B	B.1.1	31	0	0	18	0
		EPI_ISL_3218557			31	0	0	18	0
2	Kraczki, Kujawsko-Pomorskie	EPI_ISL_7721854	GK/21J (Delta)	AY.43	44	13	0	34	4
		EPI_ISL_8693906			38	13	0	33	4
3	Ołuzna, Zachodniopomorskie	EPI_ISL_8693911	GK/21J (Delta)	AY.43	40	14	1	34	4
		EPI_ISL_8693912			38	13	0	33	4
4	Zieleniewo1, Zachodniopomorskie	EPI_ISL_8693816	GK/21J (Delta)	AY.43	38	13	0	33	4
		EPI_ISL_8693913			41	13	0	34	4
5	Biadki, Wielkopolskie	EPI_ISL_8693914	GK/21J (Delta)	AY.43	41	13	0	34	4
		EPI_ISL_8693915			41	13	0	34	4
6	Janowiec, Podkarpackie	EPI_ISL_9640028	GK/21J (Delta)	AY.126	51	104	1	37	34
		EPI_ISL_9640033			50	107	1	37	34
7	Kościuki, Podlaskie	EPI_ISL_9640052	GRY/20I (Alpha, V1)	B.1.1.7	50	107	1	37	34
		EPI_ISL_9640055			52	37	0	30	11
8	Leżno, Pomorskie	EPI_ISL_9640059	GK/21J (Delta)	B.1.617.2	47	16	0	37	5
		EPI_ISL_9640062			45	47	1	36	12
9	Kloczew, Lubelskie	EPI_ISL_9640065	GK/21J (Delta)	AY.122	41	16	0	32	4
		EPI_ISL_10337406			74	53	0	51	12
10	Stefanów, Łódzkie	EPI_ISL_10337127	GRA/21L (Omicron)	BA.2	72	53	0	51	12

[https://twitter.com/daoyu15/status/1702549289623601162?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1702549289623601162?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Unfortunately, [archive.md/DChUL](https://archive.md/DChUL) [archive.md/4rVph](https://archive.md/4rVph) [archive.md/yyX0Z](https://archive.md/yyX0Z)

[archive.md/iw1Pz](https://archive.md/iw1Pz) Even where robust surveillance systems are in place, raccoon dogs are not infected at all.

Before they begun enforcing their claim of “100/174 centered around the market”

<https://twitter.com/daoyu15/status/1674351139079479298>

and starting to tamper with data to make the claim,

<https://ghrp.biomedcentral.com/articles/10.1186/s41256-021-00200-8>  
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7149375/>  
135/92 and 115/82 cases already got into in early peer-reviewed papers that went missing in the WHO report.  
<https://twitter.com/daoyu15/status/1682778742664630272> Past media reports [archive.md/Ea0Kw](https://archive.md/Ea0Kw) [archive.md/1x658](https://archive.md/1x658) also contradict WHO in key early cases' residences, including the earliest case they admit in the WHO report.  
<http://archive.md/5sdkR> <http://archive.md/1pcCU> [archive.md/N0hib](https://archive.md/N0hib) [archive.md/VXtu9](https://archive.md/VXtu9) <http://archive.is/Kyr1z>  
<https://archive.org/details/mace-e-pai-covid-19-analysis-redacted/page/8/mode/1up>  
And you know that they hate this information when it was censored.  
The MACE-EPAI document here is not searchable on google.  
<https://twitter.com/daoyu15/status/1672399653344808960>  
Up to one third of all cases were either removed completely or moved toward the market in the “dataset”.  
[archive.md/zUD1F](https://archive.md/zUD1F) [archive.md/Pc6gp](https://archive.md/Pc6gp) <https://archive.is/p3K3Z>  
<https://twitter.com/daoyu15/status/1678549054794629120>  
<https://twitter.com/daoyu15/status/1677727068082286592>  
Including the very first case they ever admitted officially.  
<https://twitter.com/daoyu15/status/1693985440762929643>  
And outright removed 4 times more cases than official.  
<https://twitter.com/daoyu15/status/1677234083389411328>  
Unlinked cases supposedly secondary to linked cases should cluster around them, not the market itself.  
<https://twitter.com/daoyu15/status/1744157399479664843>  
[archive.md/GvRcD](https://archive.md/GvRcD) [archive.md/ZgVzp](https://archive.md/ZgVzp) Wuhan authorities after that [archive.md/OIGPz](https://archive.md/OIGPz) 2014 incident now targeted only the Huanan market when looking for EID outbreaks—and nowhere else.  
[archive.md/1x658](https://archive.md/1x658)  
They tampered with the early cases data  
[archive.md/Ea0Kw](https://archive.md/Ea0Kw)  
To make it look like it “started at the market” when in reality the first case they ever admitted lived right next to the WIV BSL-4.  
[archive.md/5sdkR](https://archive.md/5sdkR) severe discrepancy happening December 2019 and January 2020 indicate tampering with case counts.  
[archive.md/1pcCU](https://archive.md/1pcCU)  
This is indicative of catastrophic ascertainment bias was going on.  
None of China’s “early cases” dataset is credible. <https://archive.md/ET1GA>  
<https://twitter.com/daoyu15/status/1678057846204960768>  
<https://archive.md/Ea0Kw> <https://archive.md/1x658>  
The tampering of early case residence data is systematic and extensive. It is the reason why they refused to provide this data in any detail at all.  
<https://twitter.com/daoyu15/status/1719518909009981579>  
<https://twitter.com/daoyu15/status/1672404501129756673>



Not only did The first every case they admitted live in Shidong right next to the BSL-4, and were moved toward the market in the WHO report in contradiction to all known media coverage, <https://gab.com/Flavinkins/posts/109256201942085712> the entirety of Wuchang district was wiped clean for every single WHO case that have onset before 27/12/2019—with up to 3000 cases moved to the market this way over the entire Wuhan outbreak. <https://archive.md/1x658> and for central Wuchang near the labs and the densest inhabited regions inside the district, all cases were moved away in the WHO map.

<https://twitter.com/biorealism/status/1702047444736111042>

Unfortunately Rasmussen's work on the origins question rests heavily on what David Relman described as "hopelessly impoverished" early case data.

<https://www.washingtonpost.com/national-security/2023/02/27/little-known-scientific-team-behind-new-assessment-covid-19-origins/>

<https://www.washingtonpost.com/opinions/2022/11/17/covid-early-cases-wuhan-china-mystery/> <https://archive.md/ke1lp> <https://archive.md/RaYPC>

<https://twitter.com/daoyu15/status/1726274673472876584>

<https://twitter.com/biorealism/status/1726475588289040834>

David Fisman: I think the most interesting thing this fellow says is that there are clearly tens of thousands of cases...That implies a much earlier introduction than would have occurred with a seafood market outbreak..."

[https://x.com/blink64/status/1747299970460582305?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/blink64/status/1747299970460582305?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

<https://www.nytimes.com/2021/02/12/world/asia/china-world-health-organization-coronavirus.html>

<https://archive.md/UFrSv>

They systematically moved more than 3000 cases from the lab to the market and gave "cases data" that they wanted to push for market as first outbreak site to distance from the labs.

[https://www.researchgate.net/publication/370635299\\_Greater\\_than\\_the\\_Sum\\_of\\_its\\_Parts\\_-\\_Aggregated\\_Wuhan\\_COVID-19\\_case\\_data\\_points\\_to\\_the\\_wrong\\_side\\_of\\_the\\_Yangtze\\_River\\_-\\_Rixey\\_-\\_20230509](https://www.researchgate.net/publication/370635299_Greater_than_the_Sum_of_its_Parts_-_Aggregated_Wuhan_COVID-19_case_data_points_to_the_wrong_side_of_the_Yangtze_River_-_Rixey_-_20230509)

Such an result of having unlinked cases closer to the market than linked cases is not expected even under the null hypothesis of market origin, which we should see unlinked cases secondary to and cluster around the linked cases, and not the market itself.

[https://twitter.com/emanymton90/status/1666720918901538824?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/emanymton90/status/1666720918901538824?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://www.researchgate.net/publication/370635299\\_Greater\\_than\\_the\\_Sum\\_of\\_its\\_Parts\\_-\\_Aggregated\\_Wuhan\\_COVID-19\\_case\\_data\\_points\\_to\\_the\\_wrong\\_side\\_of\\_the\\_Yangtze\\_River\\_-\\_Rixey\\_-\\_20230509](https://www.researchgate.net/publication/370635299_Greater_than_the_Sum_of_its_Parts_-_Aggregated_Wuhan_COVID-19_case_data_points_to_the_wrong_side_of_the_Yangtze_River_-_Rixey_-_20230509)

Not only there were an complete absence of verifiability in Chinese cases, there is direct non-circumstantial evidence that they moved up to 3000 cases from Wuchang to Huanan.

In fact, it is totally not normal to have unlinked cases closer to the market than linked cases—the only way this can happen is with ascertainment bias. Only near the market gets ascertained if not directly linked to it.

[https://twitter.com/emanynton90/status/1580511684912742400?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/emanynton90/status/1580511684912742400?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Base rate neglect. They did the exact same thing when claiming that all 67 “pre-Huanan checkable cases” were “serologically negative”.

[https://twitter.com/daoyu15/status/1631705321239629824?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1631705321239629824?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Again, the social media associated here say “before Jan 18, 2020”. Included all Dec cases. <https://www.mdpi.com/2220-9964/9/6/402>

[https://twitter.com/danwalker9999/status/1745106077274828819?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/danwalker9999/status/1745106077274828819?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

It is actually impossible for unlinked cases, supposedly secondary, to cluster closer to the market than linked cases which supposedly to be primary, without significant sampling bias or outright manipulation in the underlying “data”.

[https://twitter.com/daoyu15/status/1745090431505854942?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1745090431505854942?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Both evidently happened.

<https://arxiv.org/pdf/2401.08680.pdf>

<https://archive.md/JVFuc>

If you toss away anything that is not officially announced by China in bold, then obviously you would arrive at exactly what China wanted you to believe.

Sent from [Proton Mail](#) for iOS

2024 年 3 月 4 日星期一 03:28, dzha4225 <dzha4225@protonmail.com> 来信:

Hi, still get these to @ban\_epp\_gofroc

As for good LL papers, List so far looks like this:

Zoonosis at the Huanan Seafood Market: A Critique

<https://zenodo.org/record/7169296>

Statistical challenges for inferring multiple SARS-CoV-2 spillovers with early outbreak phylodynamics

<https://www.biorxiv.org/content/10.1101/2022.10.10.511625v1>

Unwarranted Exclusion of Intermediate Lineage A-B SARS-CoV-2 Genomes Is Inconsistent with the Two-Spillover Hypothesis of the Origin of COVID-19

<https://www.mdpi.com/2036-7481/14/1/33>

SARS-CoV-2 infection at the Huanan seafood market

[https://zenodo.org/record/6300876#.YhtwdN\\_jK9w](https://zenodo.org/record/6300876#.YhtwdN_jK9w)

Statistics cannot prove that the Huanan Seafood Wholesale Market was the early epicenter of the COVID-19 pandemic

<https://arxiv.org/abs/2208.10106>

<https://docs.google.com/presentation/d/e/2PACX-1vQzTj2YutZ8jw7PkOP539mKo1-00vT3B9r5CBd5oGWGLKiTgy8Q9NWx8FdlihWtcm0N69EMPvLTN5-i/pub?start=false&loop=false&delayms=3000&slide=id.p2>

Should we discount the laboratory origin of COVID-19?

<https://link.springer.com/article/10.1007/s10311-021-01211-0>

Circular arguments on the origin of SARS-CoV-2

<https://zenodo.org/record/7016143#.YwbG2HbMKUI>

Dan Walker's critique of mapping data. Not an official paper, but well documented.

<https://twitter.com/danwalker9999/status/1560740050408656896?s=20>

Wrong Side of the Yangtze River: Did a Map Mistake by the World Health Organization Contribute to Premature Conclusions About SARS2's Origin?

<https://zenodo.org/record/5153950#.YQg4Kz-SIPY>

If even @jkinney was extorted to give up lab leak in public, it is quite clear that the “number of lab leak papers” can not be used as anything that is even remotely useful let alone “dispositive”.

Also, the study itself have funding from, but was not performed nor even supervised by, the effective altruism group. The group have its money being tricked off by the zoonati to conduct a heavily biased “send surveys to your contacts” (e.g. severe sampling bias) decoy study.

**Rootclaim** ✓ @Rootclaim

Feb 2

HSM is not the only early cluster location under zoonosis. There are other markets with wildlife, and more importantly, SARS1 was repeatedly spilling over in restaurants, not markets. So we can comfortably assert  $p(\text{HSM|Wuhan,Zoonosis})=0.1$ .

Feb 2, 2024 · 9:44 AM UTC

2 2 8

**Rootclaim** ✓ @Rootclaim

Feb 2

Meaning that if we assume an outbreak starts in Wuhan due to zoonosis, HSM has a 1 in 10 probability of forming the earliest detected cluster.

2 2 5

**Rootclaim** ✓ @Rootclaim

Feb 2

Considering the different pieces of evidence mentioned above that indicate human introduction to HSM rather than wildlife, we increase the odds of human introduction by 10x to 0.01.

1 2 7

**Rootclaim** ✓ @Rootclaim

Feb 2

Therefore, for this evidence to have any value we need to claim there is less than 1% probability that HSM will form an early cluster under the lab leak hypothesis i.e.  $p(\text{HSM|Wuhan,lab-leak})<0.01$

2 2 5

**Rootclaim** ✓ @Rootclaim

Feb 2

Given the two independent arguments above: a) that there are very few locations in Wuhan so conducive to SARS2, and b) we repeatedly see similar locations forming the first cluster after a zero covid period, 0.01 seems like a highly overconfident claim.

2 2 7



I am leaving @BiosafetyNow. I always knew there was some professional risk to me speaking out, but my advocacy has now become a liability that I can no longer ignore. 1/5

Jan 27, 2024 · 3:49 AM UTC

106 213 68 926



**Justin B. Kinney** ✓ @jbkinney Jan 27

Going forward I will also be unavailable for public comment on the origin of SARS-CoV-2, the ramifications for science, and the risks of future lab-generated pandemics. 2/5

8 38 5 367



**Justin B. Kinney** ✓ @jbkinney Jan 27

I wholeheartedly support the mission of Biosafety Now and am leaving on good terms with @Bryce\_Nickels, @R\_H\_Ebright, and @DrishtiEthics. I am proud of Biosafety Now, its leadership team, and what we have accomplished in less than a year since our public launch. 3/5

2 30 1 326



**Justin B. Kinney** ✓ @jbkinney Jan 27

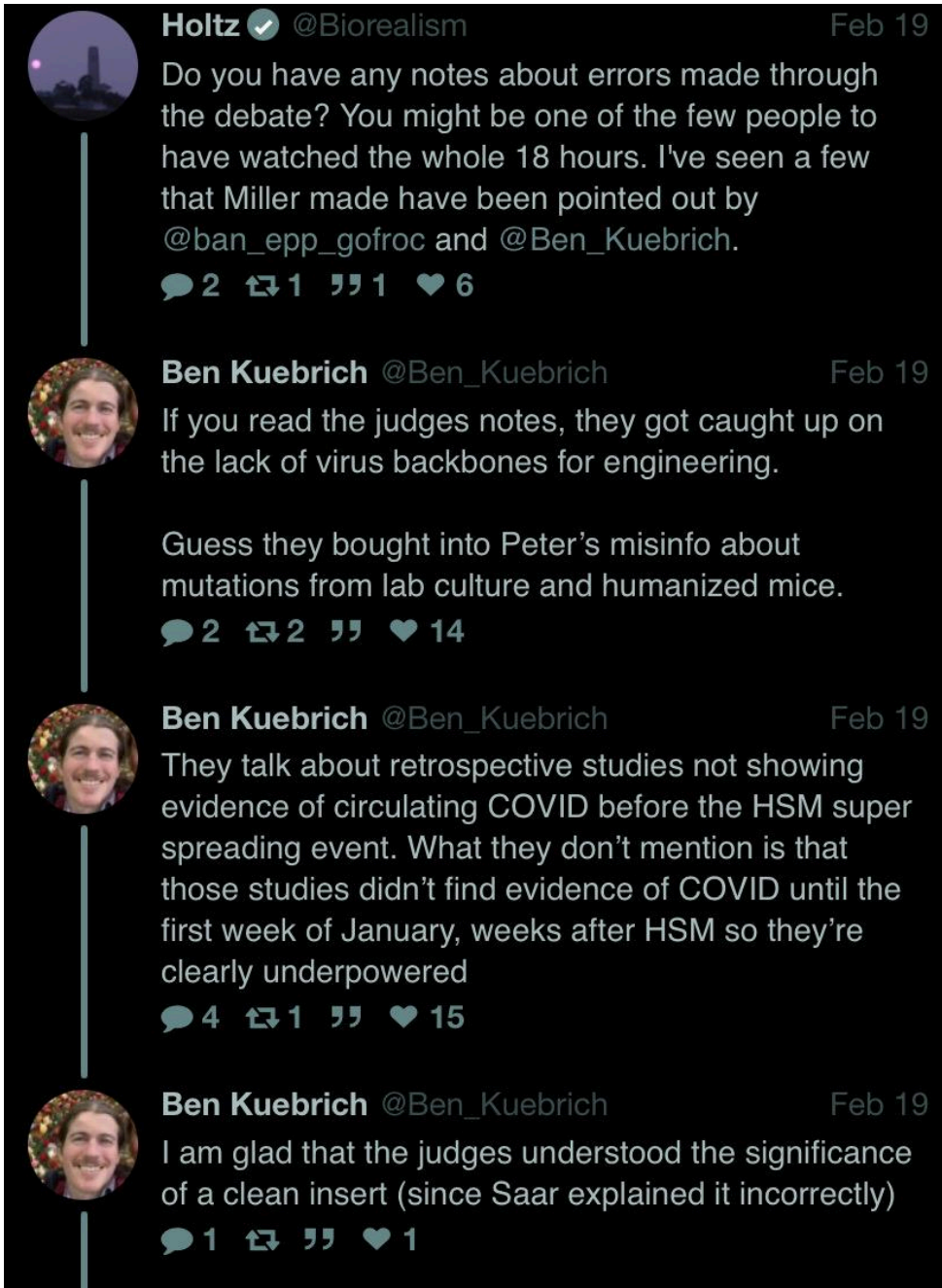
I have especially enjoyed my conversations with reporters, activists, independent researchers, and concerned citizens from across the political spectrum and across the globe. These interactions have opened my eyes to just how parochial we scientists can be. 4/5

2 33 326



**Justin B. Kinney** ✓ @jbkinney Jan 27

If you are a scientist and are concerned about the origin of SARS-CoV-2, the ramifications for science, and the risk of future lab-generated pandemics, **\*\*please speak up\*\***. A small number of scientists speaking out on these issues can make a big difference. 5/5



<https://twitter.com/jbkinney/status/1751090111733751991>

<https://twitter.com/WashburneAlex/status/1762481120250061286>

[https://x.com/daoyu15/status/1753613102388494672?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1753613102388494672?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

<https://gab.com/Flavinkins/posts/108971775263920617>

[https://x.com/daoyu15/status/1751409799709790308?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1751409799709790308?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://twitter.com/daoyu15/status/1684315961162342400?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1684315961162342400?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Direct evidence of lab leak have been found.

[archive.md/nyR0q](https://archive.md/nyR0q) [archive.md/OIGPz](https://archive.md/OIGPz) [archive.md/GvRcD](https://archive.md/GvRcD) [archive.md/EzTib](https://archive.md/EzTib)

[archive.md/svZqO](https://archive.md/svZqO) [archive.md/NMerN](https://archive.md/NMerN) [archive.md/tlfNr](https://archive.md/tlfNr) [archive.md/ARecg](https://archive.md/ARecg)

<https://twitter.com/daoyu15/status/1692354502190587938>

[archive.md/AYhoF](https://archive.md/AYhoF) [archive.md/nAqKp](https://archive.md/nAqKp)

<https://archive.md/RSsS7>

<https://archive.md/C5oal><https://archive.md/3WS68><https://archive.md/AYhoF>

<https://twitter.com/daoyu15/status/1679455533743607810>

Sent from [Proton Mail](#) for iOS

2024 年 3 月 4 日星期一 13:34, dzha4225 <[dzha4225@protonmail.com](mailto:dzha4225@protonmail.com)> 来信:

Here is my opt-in to win back the rootclaim challenge.

Washburne, maybe you want to join and collate them.

All of them are for posting on twitter.

There is in fact direct evidence of lab leak.

<https://twitter.com/daoyu15/status/1733792251669786633>

Leaked SRA data included both the exact kind of viruses that they claim will not be present in the WIV—and the exact SARS-CoV-2, WA1, cultured in a CoV-specific tailored fusion cell line VERO-CHO never used in China and sequenced before even a sample of WA1 can be taken in China, alongside C/C and B, at high passage depths, and contained within it residual human DNA not from anywhere in central China but in stead right where they were sampling from the 2018 “pathogen host adaptation and immune intervention” grant—the belt and road regions.

No official explanations have ever been given.

[https://twitter.com/daoyu15/status/1737318515353501739?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1737318515353501739?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Continued EHA human sampling=Yunnan and belt and road DNA.

[https://twitter.com/biophysicsfl/status/1737114987146174846?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/biophysicsfl/status/1737114987146174846?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Isolate if possible=special unpublished VERO-CHO cells.

[https://twitter.com/daoyu15/status/1737399622509928510?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1737399622509928510?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And it was sequenced before the first public sequencing of SARS-CoV-2 with this machine type by the flow cell, confirmed via Sangon policy and Chinese law, and before+not matching any samples of WA1 was even taken in China.

[https://twitter.com/daoyu15/status/1738903987381031326?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1738903987381031326?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And this exact CAS special project mirroring of DEFUSE+Year 5 extension—sample humans from belt and road area, isolate and engineer viruses for infection characterization, and create vectorized and nanoparticle vaccines that are capable of bringing in both backbone and Spike into bats studied in and released by the WIV, and into the main sample storage facility of the WCDC.

(Also see this—note all the FCS relevant oddities can also be caused by targeted RNA recombination [link.springer.com/chapter/10.1007/3-540-26765-4\\_5](https://link.springer.com/chapter/10.1007/3-540-26765-4_5) followed by cell culture).

[https://x.com/daoyu15/status/1731414539324018732?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1731414539324018732?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

<https://gab.com/Flavinkins/posts/109640519028841414>

It is not just that SARS-CoV-2 Wuhan grows best in VERO cells out of all variants.

<https://twitter.com/daoyu15/status/1723738450078396809>

Some earliest patients harbored inside their QS specific S1-S2 deletions that can form only in VERO E6.

<https://twitter.com/daoyu15/status/1730690080950596017>

Also, what is a live animal after being left without water or food for a month before sampling?

Do they become dead animals?

It is a simple explanation.

The absence of intermediate animals is nationwide in all of China, and not just in the Huanan market. They could never get a market animal to be blamed because there is none. Thus they can also not release the market data because that time it can not be used to support any species, hence they even went as far as to blame the pangolins, a species that does not exist in Wuhan.



"Before entering caves, scientists pull on hazmat suits, face masks & thick gloves to cover every inch of their skin. Contact with bat droppings or urine could expose them to the world's deadliest unknown viruses"



Via **CNBC** Webcast  
 Rockland County, New York  
 9:30 AM ET

**CORONAVIRUS PANDEMIC**

**"VIRUS HUNTERS" SEARCH BAT CAVES TO PREDICT NEXT PANDEMIC**  
 Peter Daszak | President, EcoHealth Alliance

<b>CORONAVIRUS PANDEMIC</b>
GLGHELY
TOTAL CASES <b>3,278,546</b>
DEATHS <b>234,021</b>
IN THE UNITED STATES
TOTAL CASES <b>1,070,620</b>
DEATHS <b>63,023</b>

CNN NEWSROOM



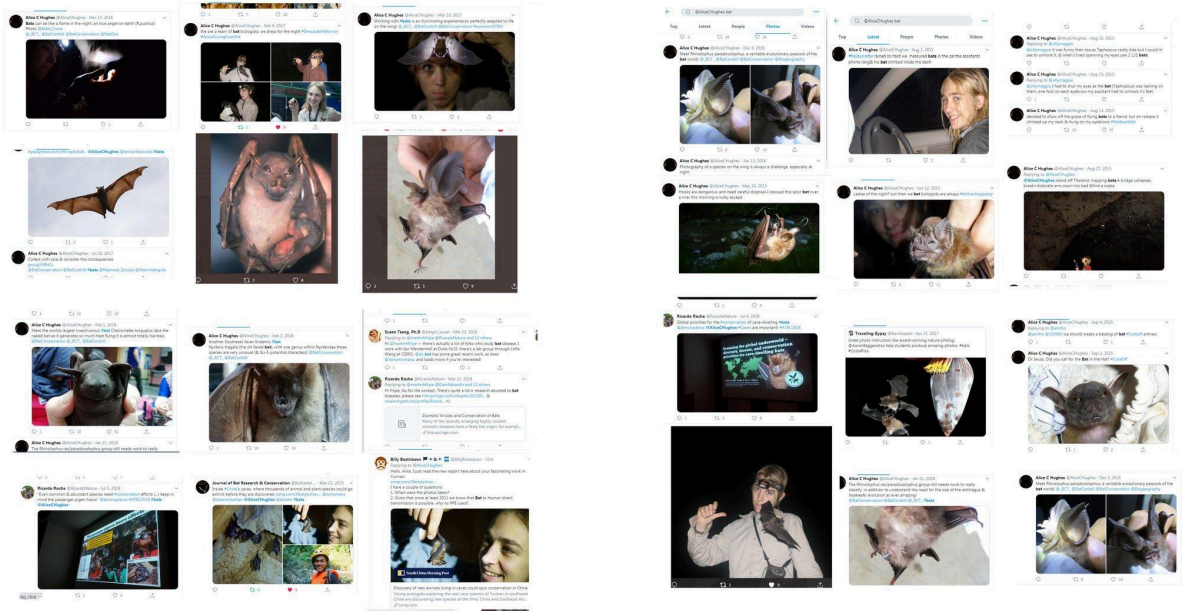
**More Batshit Lies!**  
 "Even if they stumbled across the virus, they would be very unlikely to get infected. When collecting samples, they take precautions to avoid infecting themselves, wearing N95 respirator masks, Tyvek suits, goggles and gloves" Says Mazet  
<https://www.nprillinois.org/post/virus-researchers-cast-doubt-theory-coronavirus-lab-accident#stream/0>

**Bloody Batshit Lies!**  
 "Before entering caves, scientists pull on hazmat suits, face masks & thick gloves to cover every inch of their skin. Contact with bat droppings or urine could expose them to the world's deadliest unknown viruses"  
[stltoday.com/news/national/...](http://stltoday.com/news/national/)



"Even if they stumbled across the virus, they would be very unlikely to get infected. When collecting samples, they take precautions to avoid infecting themselves, wearing N95 respirator masks, Tyvek suits, goggles and gloves" Says Jonna Mazet

# THE REALITY OF BAT RESEARCH IN CHINA



◀
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🔍

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归属地: 📍 湖北 武汉市 江夏区 纸坊 114best.com

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驾驶本信息查询

手机号码查机主

### Interview with patient recovered from COVID-19

- The patient in the COVID-19 reporting system with the earliest date of onset date (8 December 2019) agreed to a face-to-face interview with the joint international study team.
- The WHO team asked some questions about the patient's history and family and were told that the person was an accountant by profession and worked for his family company.
- While details of the interview are not disclosed here to protect the person's privacy, the interview found no evidence for high-risk exposures (wild animals, mass gatherings, contacts with healthcare settings, contact with symptomatic individual, travel, etc.). The person mentioned one relative working in a healthcare setting, and one relative visiting a local market, but there were no illness reports related to these locations at that time. The person commuted to work by public transport, and had not travelled outside Wuhan.
- The WHO team was told that earlier potential cases were given the opportunity to be interviewed, but were unwilling or unable to attend.



武汉发布

35分钟前 · 武汉市委、市政府官方账号

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网友@本地号外 提问：**#提问武汉#** 请问目前已知最早发病的患者情况如何？该患者具体什么时候发病的？是否曾有过华南海鲜市场接触史？

武汉市新冠肺炎防控指挥部医疗救治组回复：  
据查询信息系统，我市登记报告最早的新冠肺炎患者为陈某，发病时间为2019年12月8日，经医院救治后痊愈出院。患者居住在武昌某小区，否认去过华南海鲜市场。



本地号外

4天前 · 北京青年报即时新闻官方账号

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**#提问武汉#** 请问目前已知最早发病的患者情况如何？该患者具体什么时候发病的？是否曾有过华南海鲜市场接触史？



**#提问武汉#**

Pages 2-3 of a 16 page booklet titled "Medical Institutions in Hubei Province Outpatient (Emergency) General Medical Record" 湖北省医疗机构门(急)诊通用病历. Shown during interview of 41 year old Chen XX, a Covid patient with onset either Dec 8 or 16, 2019.

Name: Chen [redacted]  
 Treatment department: [redacted]  
 Treatment time: [redacted]

Main complaint: requirements [redacted]  
 History of present illness: request for tooth extraction

Past history: Denial of special medical history

Physical examination: 51 buccoverision, 11 erupting; 6 erupting with deep pits and fissures  
 Auxiliary inspection results:  
 Diagnosis: 1. Retention of primary teeth  
 Treatment plan: 51 removal and 6 perform pit and fissure sealant, 51 removal under local anesthesia, regular doctor's order, follow-up if unwell

Obucaine Hydrochloride 30mg: 10ml/bottle x 1  
 Gel Usage: 30mg bottle for external use, temporary medical advice

Doctor: Tian Wei [Oral Medicine at Jiangxia Hospital] 87959144

The upper right central child incisor is displaced outward (buccal often used in place of labial) by an erupting permanent tooth and not exfoliating, a condition seen with ~7 year olds. Removal would be unlikely to cause infection. The mild topical anesthetic is too weak for pain from an existing septic dental abscess that could cause high fever. Pit and fissure sealant is required, normally given to 6-14 year olds. Doctor confirmed to be in Oral Medicine Dept. of Jiangxia District Hospital in 2019. Hospital phone number confirmed. Patient shares surname with 41M Chen.

就诊医院: 2019年12月9日  
 2019年12月11日  
 发热一天  
 Fever one day

39.5°C

血常规 WBC 13.4x10<sup>9</sup>/L  
 N 10.86x10<sup>9</sup>/L  
 CRP 20mg/L

23 mg

药物 Medication  
 头孢美唑 Cefmetazole (+) (Allergenicity test)  
 哌拉西林 Piperacillin (-)

NS 250ml  
 哌拉西林钠 Piperacillin-sulbactam 2g  
 NS 150ml  
 热毒宁 Reduning 8ml

High fever for a day. WBC\N\CRP level high indicates anti-inflammatory. Two antibiotics tested for allergic reaction. Piperacillin-sulbactam is administered intravenously with Reduning, a traditional Chinese medicine. Only use found for P+S\Reduning combo is to treat community acquired pneumonia. More IV meds on Dec 11.

WBC=white blood cell count  
 N=neutrophil  
 CRP=c-reactive protein  
 NS=neutral saline (IV)  
 qdx2=once per day for 2 days  
 哌拉西林钠 [舒巴坦钠]=Piperacillin-Sulbactam.  
 Dosage implies Sulbactam.



It is clear that <https://archive.md/VXtu9> there are significantly <https://archive.md/UIBkB> more cases, sufficient to get infections before Huanan, in Wuhan.

<https://twitter.com/daoyu15/status/1736761001775943855>

In Mar-Apr 2020, China officially blamed wild animals sold in the Huanan market. Publishing the current “data” to Holmes would be the best way to solidify their then official opinion. If this “data” can be interpreted in any way to arrive at the C-C “conclusions”, ECH won’t be denied of it. Since he is denied, the most logical reason for the denial is that it does not originally support any of the C-C “conclusions”, and were tampered only recently to poison the scientific database and to provide a fallback for debate purposes. Only after being tampered with and then approved by the CCP, would it be officially permitted—in fact, actively given to Holmes for “analysis”.

Pack tube blood=they are pre-screened against IgM presence of any kind, mean that it can not be used for detecting November infections because any potentially positive serological samples are rejected. ILI=they are 20 samples per two weeks sentinel surveillance that were far too low in sample counts to be effective at detecting an 100 cases outbreak November or December 2019. In fact they only get positives inside the Wuhan CBD in late January 2020 when about one third of all official cases have already had onset, and only because the influenza season have faded enough to have SARS-CoV-2 positive samples able to reach (4500-7000 ILI a week in peak Wuhan flu season) the surveillance mechanisms. They also failed to detect it near the market first.

Finally,

[https://twitter.com/daoyu15/status/1703438297983561793?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1703438297983561793?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://twitter.com/daoyu15/status/1726526722831683601?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1726526722831683601?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

The idea that “lineage A is in the market” hinges on A20. It is debunked by the absence of vendor gloves in the stall, presence of sampler PPE, inconsistency between 2021-2023 in viral read and fractions and inconsistency between 03/03/2023 and 26/03/2023 in host read fractions. Amplicon sequencing doesn’t alter host fractions.

[https://twitter.com/daoyu15/status/1739419702143881342?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1739419702143881342?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://twitter.com/daoyu15/status/1704216164560449822?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1704216164560449822?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

In fact, guess what is consistent with this observation? The introduction of human hosted lineage A genomes into the viral amplicon run but not the metagenomic run [archive.ph/ANS4Q](https://archive.ph/ANS4Q) and improbability of vendor origin for A20 predicts that lineage A

is being grown inside the WDC, and likely caused human infections. And behold, all 3 of the samples are linked tightly and directly to the WDC.

[https://twitter.com/daoyu15/status/1705344605401800804?s=46&t=wRQSWp\\_1VffWmS2vKQwhSAA](https://twitter.com/daoyu15/status/1705344605401800804?s=46&t=wRQSWp_1VffWmS2vKQwhSAA) hotel right nextdoor to the new lab site, a location on the same route as the lab's November-December movement (spilling aerosols everywhere on the road) and an admitted infection and seropositivity with no direction deducible for the "family cluster".

[https://twitter.com/daoyu15/status/1726529108811874621?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1726529108811874621?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Also: in the set of WA1/WA-UW samples, it have been discovered that the determinants of WA1 is highly unstable—it is not uncommon to find inside this cluster including cultures grown from this cluster that have shown signs of 3037C->T, 29095T residuum, 18060T->C and 8782C->T and 28144T->C, all appearing independently in the quasispecies.

A single leak of WA1 that mutated afterward causes all of the early lineages.

[https://twitter.com/daoyu15/status/1726531984288334216?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1726531984288334216?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Which are all found in the same culture from Csabai et al. WA1, A, C/C and B are all found in the same VERO-CHO culture where the only human sequences are found in the belt and road region but not Wuhan. None of the 3 (belt and road humans, CHO, WA1) are ever published in China for SARS-CoV-2 isolation or culture. And belt and road humans as an NGS sample in 2019-2020 is related only to viral sampling under the "病原体宿主适应与免疫干预" grant.

[https://twitter.com/daoyu15/status/1491651835584675845?s=46&t=wRQSWp\\_1VffWmS2vKQwhSACsabai](https://twitter.com/daoyu15/status/1491651835584675845?s=46&t=wRQSWp_1VffWmS2vKQwhSACsabai) et al also contained T22657C, T3346C, A21562C and G487T. all of which is in RaTg13 but not in WuHu-1. also T1963C and T22963C in BANAL-52. Significant culture mutations have occurred inside Csabai et al which likely contained samples co-sequenced at different passage depths. not all of the reads were H655Y and del I68-T76.

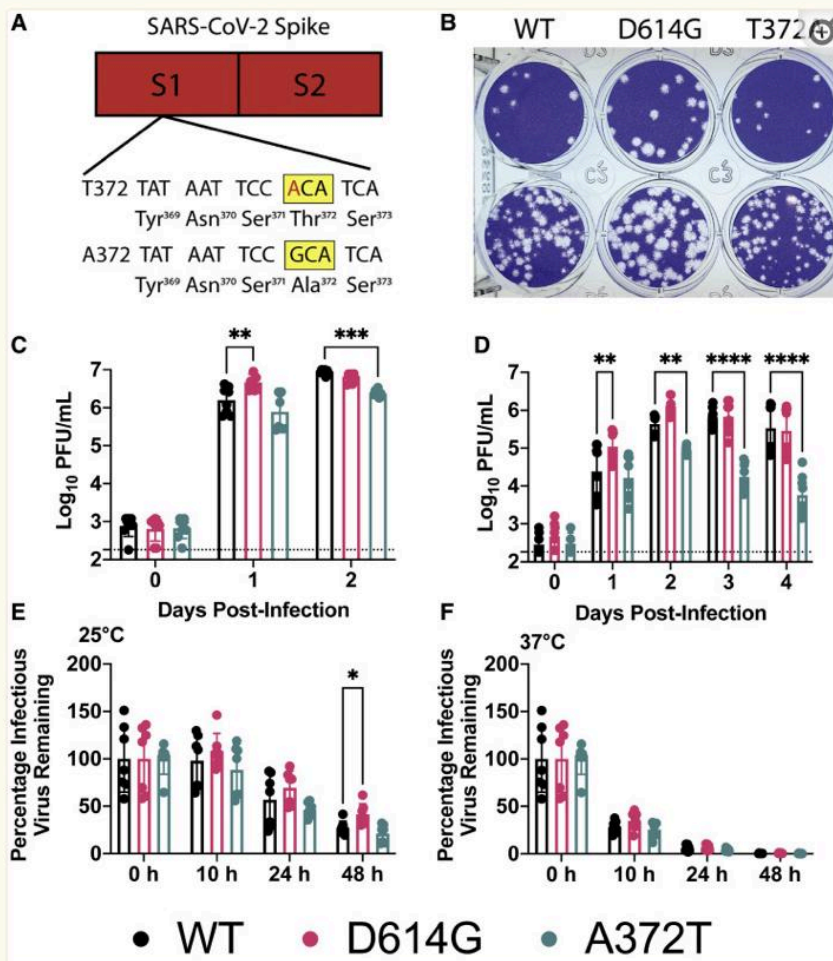


Figure 4

A372T substitution decreases SARS-CoV-2 replication on human lung epithelial cells

(A) The S T372 SARS-CoV-2 mutant was generated by making a single G-to-A substitution. The mutant nucleotide is presented in red, and the altered codon is highlighted in a yellow box.

(B) Plaque morphology of WT and mutant viruses. Plaques were visualized 2 days post-infection (dpi) on Vero E6 cells.

(C and D) Viral replication on Vero E6 (C) and Calu-3 (D) cells following infection at an MOI of 0.05. The sample at 0 dpi was collected immediately after infection to ensure cells were exposed to similar levels of virus, and then samples were collected at 24-h intervals.

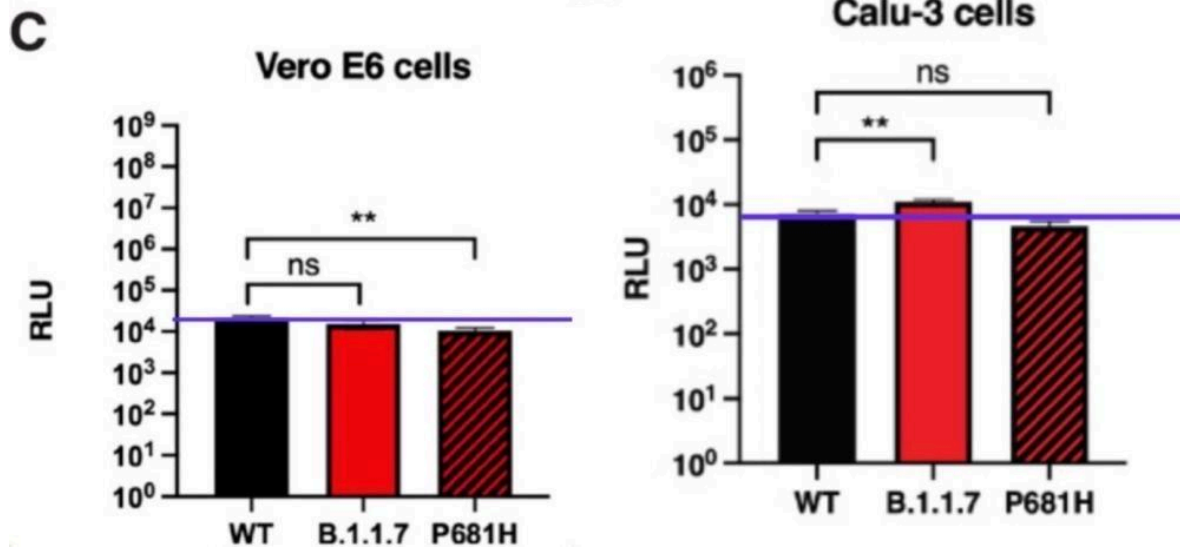
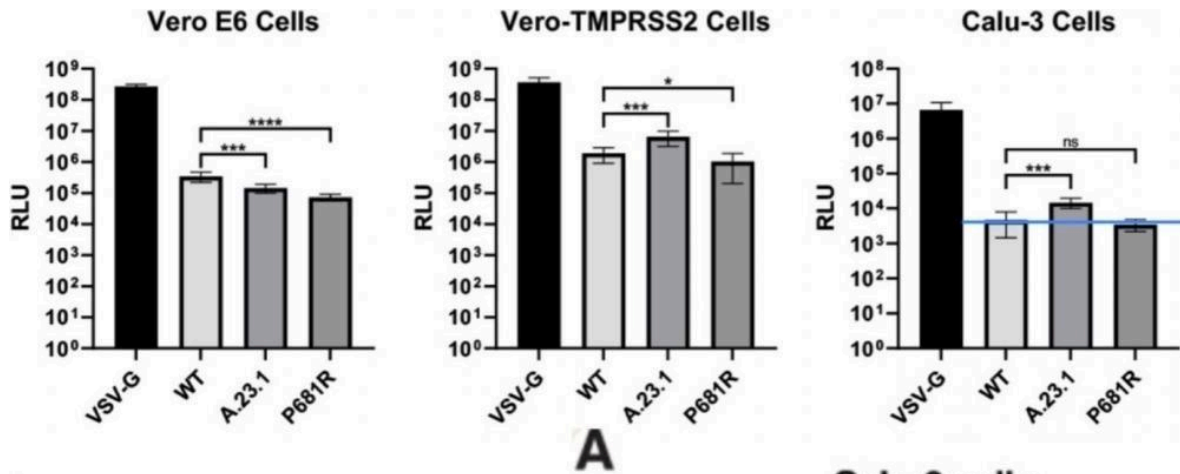
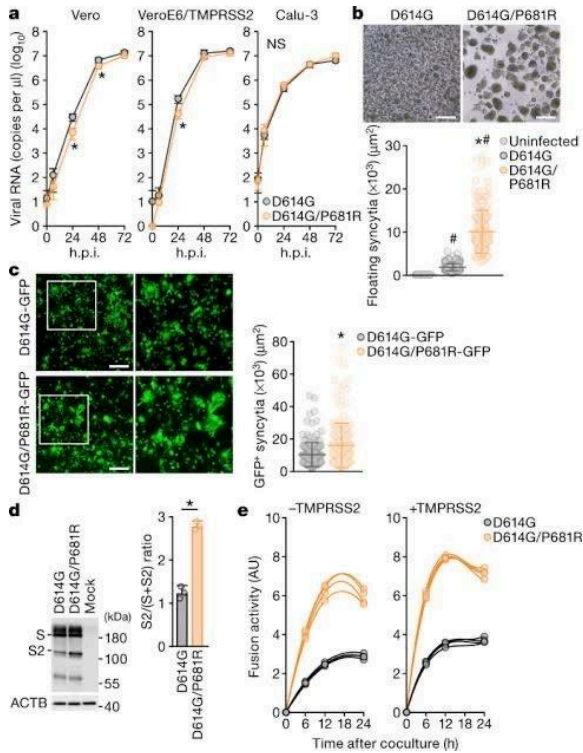
(E and F) Kinetics of thermal stability. A solution of  $10^5$  PFU of each virus was incubated at the indicated temperature for different lengths of time. Infectious virus was measured by plaque assay on Vero E6 cells.

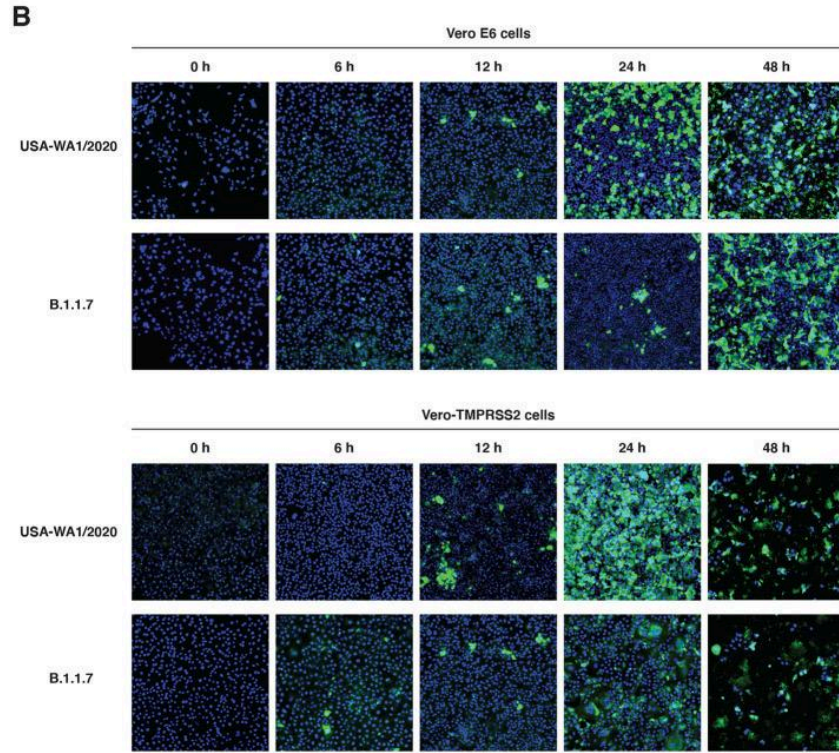
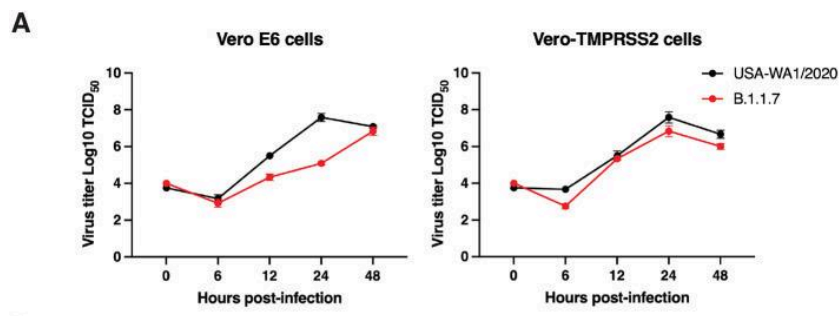
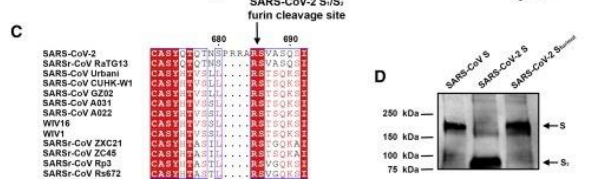
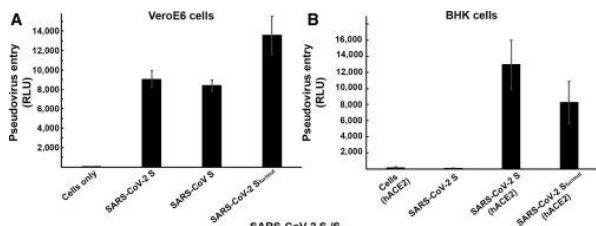
Statistical comparisons were made using two-way ANOVA with Dunnett's multiple comparisons test. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , \*\*\*\* $p < 0.0001$ . Error bars represent standard deviation of the mean.







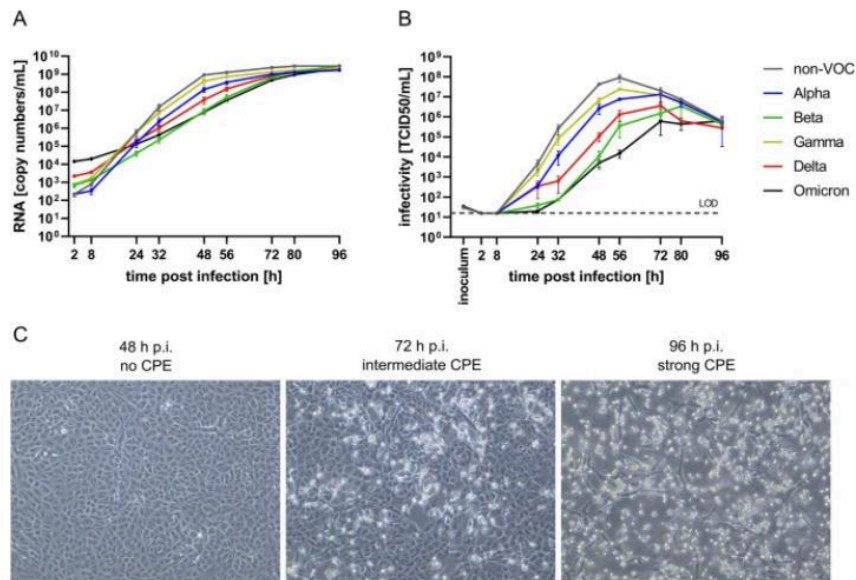




	CONSERVED REGION	VARIABLE REGION
SARS-CoV-2	G A G I C A S Y ggt goa ggt ata tgc gct agt tat	Q T Q T N S P R R A R S V A - S Q S I I cag act caa act aat tct cct cgg cgg gaa cgt agt gta gct --- agt caa tca atc att
RaTG13	G A G I C A S Y ggt goa gga ata tgc gcc agt tat	Q T Q T N S - - - - R S V A - S Q S I I cag act caa act aat tca --- --- --- ogt agt gtg gcc --- agt caa tct att att
RShSTT182/200 (Cambodia) (identical here)	G A G I C A S Y ggt goa ggt ata tgc gcc agt tgc	Q T Q T N S - - - - R S V T - S Q S I I cag act caa act aat toa --- --- --- ogt agt gta acc --- agt caa tca att att
Pangolin/GD/2019	G A G I C A S Y ggt goa gga ata tgt gcc agt tat	Q T Q T N S - - - - R S V S - S Q A I I cag act caa act aat toa --- --- --- ogt agt gtt tca --- agt caa gct att att
RmYN02 Zhou et al.	G A G V C A S Y gga goa ggt gtg tgt gcc agt tac	- - - - N S P - A A R - V G - T N S I I --- --- aac toa cct --- goa gog cgt --- gta ggt --- act aat tca att att
RmYN02 Clustal W	G A G V C A S Y gga goa ggt gtg tgt gcc agt tac	N S ( P ) A - - - - A R V G - T N S I I --- aac toa cct --- gta gca --- --- gog cgt gta ggt --- act aat tca att att
RmYN02 YD&RS ver. 1	G A G V C A S Y gga goa ggt gtg tgt gcc agt tac	( N S ) P A A - - - - R - V G - T N S I I --- aac toa cct gca gog --- --- --- ogt --- gta ggt --- act aat tca att att
RmYN02 YD&RS ver. 2	G A G V C A S Y gga goa ggt gtg tgt gcc agt tac	- N S P A A - - - - R - V G - T N S I I --- aac toa cct gca gog --- --- --- ogt --- gta ggt --- act aat tca att att
RacCS203 (Thailand)	G A G V C A S Y gga goa ggt gtg tgt gcc agt tat	- N S P V A - - - - R - V G - T N S I I --- aac toa cct gta gca --- --- --- ogt --- gta ggt --- act aat tca att att
RacCS264 (Thailand)	G A G V C A S Y gga goa ggt gtg tgt gcc agt tat	- N S P V ? - - - - ? - ? - ? Q S I I --- aac toa cct gta sca --- --- --- crt --- KKR SRY --- Mgc caa tca att att
RacCS271 (Thailand)	? ? ? V C A S Y NNN NNN NNT gtg tgt gcc agt tat	- N S P V A - - - - R - V G - T N S I I --- aac toa cct gta gca --- --- --- ogt --- gta ggt --- act aat tca att att
PrC31 (Yunnan)	G A G I C A S Y ggt gct ggt att tgt gct ago tac	H T A P I L - - - - R S T S - Q K A I V cag acg gca tct atg cta --- --- --- ogt agt aca ago --- cag aag gct att gtg
Rc-o319 (Japan)	G A G I C A T Y gga goa gga ata tgc gct aca tat	H T P S M L - - - - R S A N N N K R I V cag acg gca tct atg cta --- --- --- ogt ago gca aac aac aat aag aga att gtt
Pangolin/GX/2017	G A G I C A S Y ggt gct ggc ata tgt gca agt tac	H S M S S F - - - - R S V N - Q R S I I cag tca atg tca tca ttt --- --- --- ogt agt gtc aac --- cag cgt tca atc att
Rs3367 & RsSHC014 (identical here)	G A G I C A S Y gga gct ggc att tgt gct agt tac	H T V S S L - - - - R S T S - Q K S I V cag aca gtt tct tca tta --- --- --- ogt agt act ago --- cag aaa tct att gtg
ZC45	G A G I C A S Y ggt gct ggt att tgt gct ago tac	H T A S I L - - - - R S T S - Q K A I V cag acg gct tct ata tta --- --- --- cgc agt aca ago --- cag aaa gct att gtg
ZXC21	G A G I C A S Y ggt gct ggt att tgt gct ago tac	H T A S I L - - - - R S T G - Q K A I V cag acg gct tct ata tta --- --- --- ogt agt aca ggc --- cag aaa gct att gtg
RmYN01	G A G I C A S Y ggt goa ggc att tgt gct agt tac	H T A S L L - - - - R N T G - Q K S I V cag aca gct tca ctt tta --- --- --- ogt aat aca ggc --- cag aaa tca att gtg
LYRa11	G A G I C A S Y ggt gct ggc att tgt gct agt tac	H T A S L L - - - - R N T D - Q K S I V cag aca gct tct cta tta --- --- --- ogt aat aca ggc --- cag aaa tca att gtg
RF4092	G A G I C A S Y ggt gct ggc att tgt gct ago tac	H T A S T L - - - - R G V G - Q K S I V cag aca gct tct atc cta --- --- --- ogt ggt gta ggt --- cag aaa tca att gtg

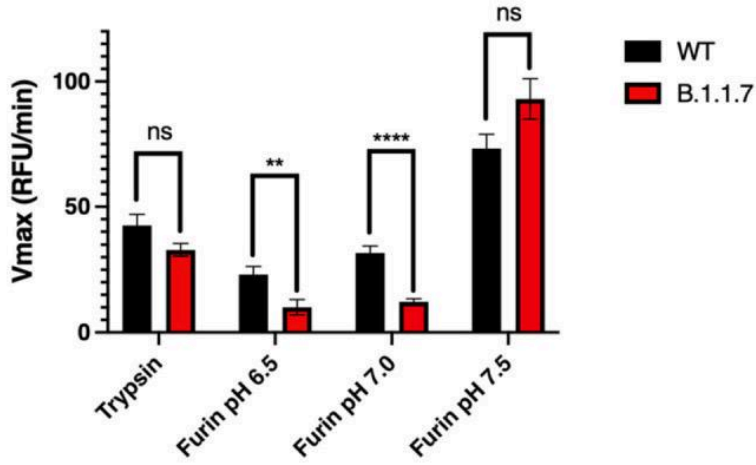
Black = common for all  
 Purple = unique to SARS-CoV-2  
 Green = differences mostly found in strains shaded in pink (RmYN02 or RacCSxxx)  
 Blue = differences mostly found in strains shaded in purple (ZC45, Rs3367, LYRa11, etc.)  
 Yellow = differences mostly found in Pangolin/GX/2017  
 Red = other differences

**Fig. 1**

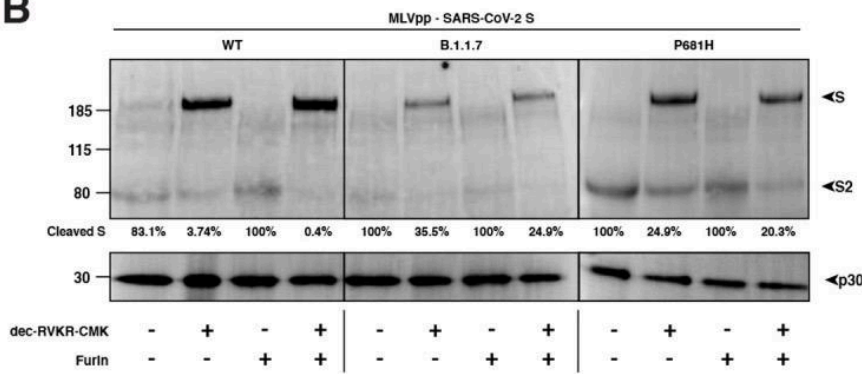


Viral replication of non-VOC and VOCs on Vero E6. Cells were infected at an MOI of 0.0001 for 96 h and culture supernatant was collected at the indicated time points to quantify **a** RNA copy numbers by RT-qPCR and **b** viral titers by TCID50 endpoint assay. **c** Development of CPE is exemplarily shown for Delta at selected time points. LOD: limit of detection; n = 3

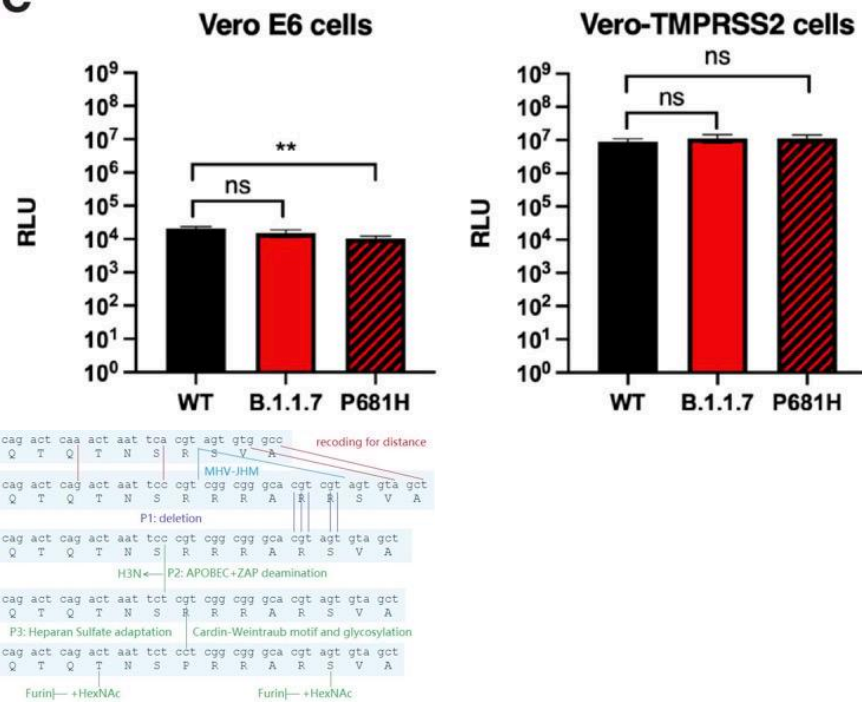
**A**

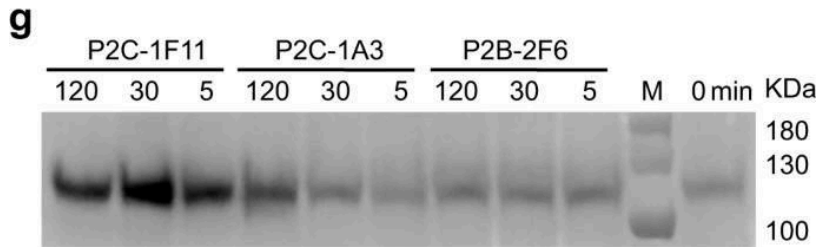
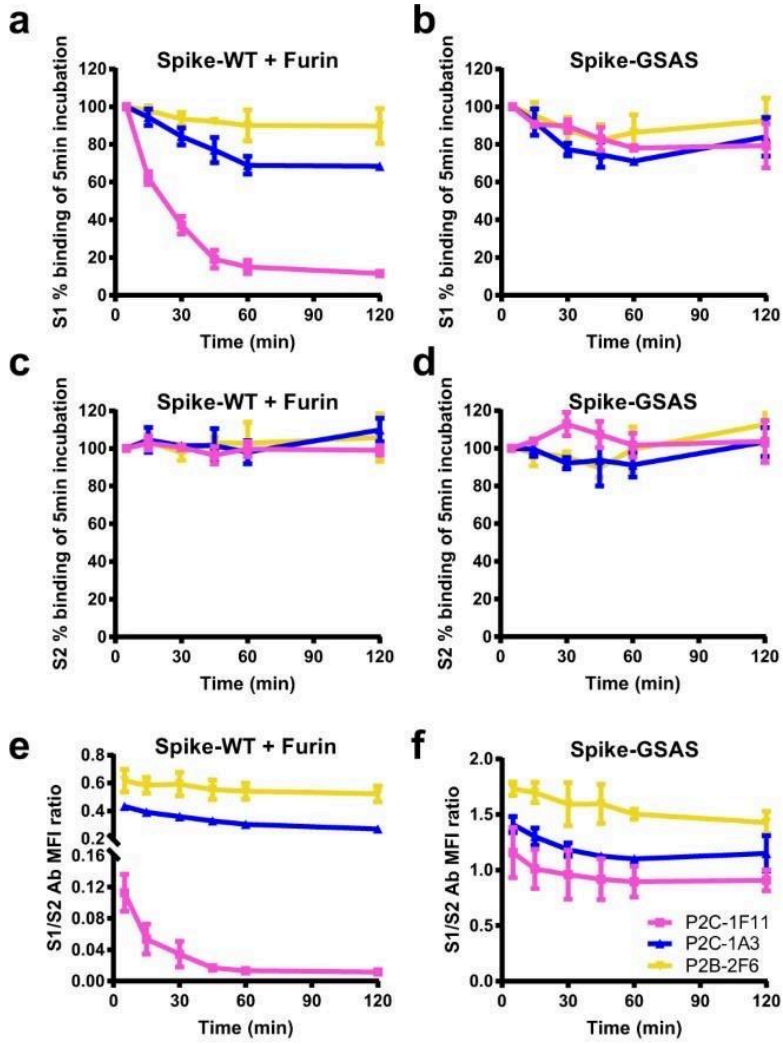


**B**



**C**







53 Frame 3

```

atgtc tga taa tgg acc cca aaa tea ggg aaa tgc acc ccg cat tac gtt tgg tgg acc ctc
V - - W T P K S A K C T P H Y V W W T L
aga ttc aac tgg cag taa cca gaa tgg aga acg cag tgg ggc gcg atc aaa aca acg tgc
R F N W Q - P E W R T Q W G A I K T T S
gcc cca agg ttt acc caa taa tac tgc gtc ttg gtt cac gcg tct cac tca aca tgg caa
A P R F T Q - Y C V L V H R S H S T W Q
gga aga cct taa att ccc tgc agg aca agg cgt tcc aat taa cac caa tag cag tcc aga
G R P - I P S R T R R S N - H Q - Q S R
tga cca aat tgg cta cta ccg aag agc tac cag acg aat tgc tgg tgg tga cgg taa aat
- P N W L L P K S Y Q T N S W W - R - N
gaa aga tct cag tcc aag atg gta ttt cta cta cct agg aac tgg gcc aga agc tgg act
E R S Q S K M V F L L P R N W A R S W T
tcc cta tgg tgc taa caa aga cgg cat cat atg ggt tgc aac tga ggg agc ctt gaa tac
S L W C - Q R R H H M G C N - G S L E Y
acc aaa aga tca cat tgg cac ccg caa tcc tgc taa caa tgc tgc aat cgt gct aca act
T K R P S H W H P Q S C - Q C C L R A T T
tcc tca agg aac aac att gcc aaa agg ctt cta cgc aga agg gag tag agg cgg cag tca
S S R N N I A K R L L R R R E Q R R Q S
agg ctc ttc tgc ttc ctc atc acg tag tgc caa cag ttc aag aaa ttc aac tcc agg cag
S L F S F L I T - S Q Q F K K F N S R Q
cag tag ggg aac ttc tcc tgc tag aat ggc tgg caa tgg cgg tga tgc tgc tct tgc ttt
Q - G N F S C - N G W Q W R - C C S C F
gct gct gct tga cag att gaa cca gct tga gag caa aat gtc tgg taa agg cca aca act
A A A - Q I E P A - E Q N V W - R P T T
aca agg cca aac tgt cac taa gaa atc tgc tgc tga ggc ttc taa gaa gcc tgc gca aaa
T R P N C H - E I C C - G F - E A S A K
acg tac tgc cac taa agc ata caa tgt aac aca agc ttt cgg cag acg tgg tcc aga aca
T Y C H - S I Q C N T S F R Q T W S R T
aac cca agg aaa ttt tgg gga cca gga act aat cag aca agg aac tga tta caa aca ttg
N P R K F W G P G T N Q T R N - L Q T L
gcc gca aat tgc aca att tgc ccc cag gcg ttc agc gtt ctt cgg aat gtc gcg cat tgg
A A N C T I C P Q R F S V L R N V A H W
cat gga agt cac acc ttc ggg aac gtg gtt gac cta cac agg tgc cat caa att gga tga
H G S H T F G N V V D L H R C H Q I G -
caa aga tcc aaa ttt caa aga tca agt cat ttt gct gaa taa gca tat tga cgc ata caa
Q R S K F Q R S S H F A E - A Y - R I Q
aac att ccc acc aac aga gcc taa aaa gga caa aaa gaa ggc tga tga aac tca agc
N I P T N R A - K G Q K E E G - - N S S
ctt acc gca gag aca gaa gaa aca gca aac tgt gac tct tet tcc tgc tgc aga ttt gga
L T A E T E E T A N C D S S S C C R F G
tga ttt ctc caa aca att gca aca atc cat gag cag tgc tga ctc aac tca ggc cta
- F L Q T I A T I H E Q C - L N S G L

```

```

caa tgc tgc aat cgt gct aca act
Q C C N R A T T
aga agg gag cag agg cgg cag tca
R R E Q R R Q S
ttc aag aaa ttc aac tcc agg cag
F K K F N S R Q
tgg cgg tga tgc tgc tct tgc ttt
W R - C C S C F

```

Before SARS-COV-2 (J)

SARS (Urbani)	CASYHT--VSSL--RSTS-QKSIVAY
YN2018A	CASYHT--ASTL--RSVG-QKSIVAY
Rp/Shaanxi2011	CASYHT--ASVL--RSTG-QKSIVAY
Rs4247	CASYHT--ASTL--RSVG-QKSIVAY
YN2018B	CASYHT--VSSL--RSTS-QKSIVAY
As6526	CASYHT--ASTL--RSVG-QKSIVAY
Rs4237	CASYHT--ASTL--RSVG-QKSIVAY
Longquan-140	CASYHT--ASVL--RSTG-QKSIVAY
Rs4081	CASYHT--ASTL--RSVG-QKSIVAY
BetaCoV/GX2013	CASYHT--ASVL--RSTG-QKSIVAY
HKU3-1	CASYHT--ASVL--RSTG-QKSIVAY
YN2013	CASYHT--ASTL--RSIG-QKSIVAY
Rs806/2006	CASYHT--ASLL--RSTG-QKSIVAY
Cp/Yunnan2011	CASYHT--ASLL--RNTG-QKSIVAY
Rs3367	CASYHT--VSSL--RSTS-QKSIVAY
WIV1	CASYHT--VSSL--RSTS-QKSIVAY
YN2018D	CASYHT--ASTL--RSVG-QKSIVAY
Rs4255	CASYHT--ASTL--RSVG-QKSIVAY
Rs_672/2006	CASYHT--ASTL--RSVG-QKSIVAY
WIV16	CASYHT--VSSL--RSTS-QKSIVAY
RsSHC014	CASYHT--VSSL--RSTS-QKSIVAY
SARS (Civet)	CASYHT--VSSL--RSTS-QKSIVAY
LYRaA3	CASYHT--ASLL--RNTG-QKSIVAY
LYRaA11	CASYHT--ASLL--RNTD-QKSIVAY
Rs9401	CASYHT--VSSL--RSTS-QKSIVAY
Rs4084	CASYHT--VSSL--RSTS-QKSIVAY
Rs7327	CASYHT--VSSL--RSTS-QKSIVAY
AnLong-103	CASYHT--ASTL--RSVG-QKSIVAY
SC2018	CASYHT--ASTL--RSTG-QKSIVAY
YN2018C	CASYHT--ASTL--RSVG-QKSIVAY
RaTG13	CASYQTQTN-----RSVASQ-SIAY

## MHC-II Binding Prediction Results

### Input Sequences

#	Name	Sequence
1	2	GAGICASYQTQNSPRRAR

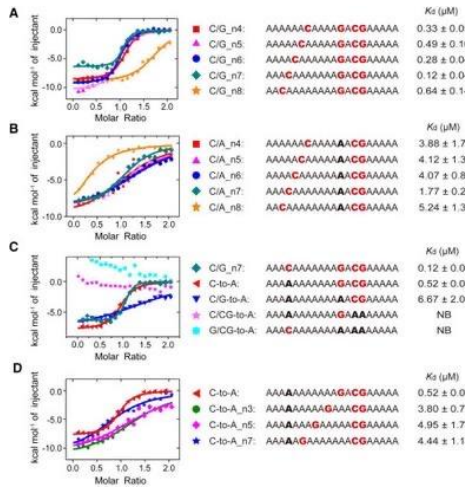
Prediction method: IEDB recommended 2.22 | Low adjusted\_rank = good binders

Download result

### Citations

Check to expand the result:

Allele	#	Start	End	Length	Method used	Peptide	Percentile Rank	Adjusted rank
HLA-DRB1*04:01	1	5	19	15	Consensus (simm/nr/stumio)	CASYQTQNSPRRAR	3.20	3.20
HLA-DRB1*04:01	1	4	18	15	Consensus (simm/nr/stumio)	ICASYQTQNSPRRA	3.70	3.70
HLA-DRB1*04:01	1	3	17	15	Consensus (simm/nr/stumio)	GICASYQTQNSPRR	5.30	5.30
HLA-DRB3*01:01	1	5	19	15	Consensus (simm/nr/stumio)	CASYQTQNSPRRAR	8.60	8.60
HLA-DRB1*04:01	1	2	16	15	Consensus (simm/nr/stumio)	AGICASYQTQNSPR	9.50	9.50
HLA-DRB1*04:05	1	2	16	15	Consensus (simm/nr/stumio)	AGICASYQTQNSPR	12.00	12.00
HLA-DRB3*01:01	1	4	18	15	Consensus (simm/nr/stumio)	ICASYQTQNSPRRA	12.00	12.00
HLA-DRB1*04:05	1	3	17	15	Consensus (simm/nr/stumio)	GICASYQTQNSPRR	13.00	13.00
HLA-DRB1*04:05	1	4	18	15	Consensus (simm/nr/stumio)	ICASYQTQNSPRRA	13.00	13.00
HLA-DRB1*04:05	1	5	19	15	Consensus (simm/nr/stumio)	CASYQTQNSPRRAR	14.00	14.00
HLA-DRB3*01:01	1	3	17	15	Consensus (simm/nr/stumio)	GICASYQTQNSPRR	16.00	16.00
HLA-DRB3*02:02	1	5	19	15	NetMHCIIpan	CASYQTQNSPRRAR	18.00	18.00
HLA-DRB3*02:02	1	4	18	15	NetMHCIIpan	ICASYQTQNSPRRA	23.00	23.00
HLA-DQA1*05:01/DOB1*03:01	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	24.00	24.00
HLA-DRB3*01:01	1	2	16	15	Consensus (simm/nr/stumio)	AGICASYQTQNSPR	31.00	31.00
HLA-DRB1*09:01	1	4	18	15	Consensus (comb.lib./simm/nr)	ICASYQTQNSPRRA	31.00	31.00
HLA-DRB1*09:01	1	3	17	15	Consensus (comb.lib./simm/nr)	GICASYQTQNSPRR	36.00	36.00
HLA-DQA1*05:01/DOB1*03:01	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	37.00	37.00
HLA-DRB3*02:02	1	3	17	15	NetMHCIIpan	GICASYQTQNSPRR	37.00	37.00
HLA-DRB1*13:02	1	5	19	15	Consensus (simm/nr/stumio)	CASYQTQNSPRRAR	41.00	41.00
HLA-DRB1*04:05	1	1	15	15	Consensus (simm/nr/stumio)	GAGICASYQTQNSP	41.00	41.00
HLA-DRB1*13:02	1	4	18	15	Consensus (simm/nr/stumio)	ICASYQTQNSPRRA	42.00	42.00
HLA-DPA1*02:01/DPB1*01:01	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	46.00	46.00
HLA-DRB1*12:01	1	2	16	15	Consensus (simm/nr)	AGICASYQTQNSPR	49.50	49.50
HLA-DRB1*09:01	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	50.00	50.00
HLA-DRB4*01:01	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	51.00	51.00
HLA-DPA1*02:01/DPB1*01:01	1	4	18	15	Consensus (comb.lib./simm/nr)	ICASYQTQNSPRRA	51.00	51.00
HLA-DRB1*03:01	1	1	15	15	Consensus (simm/nr/stumio)	GAGICASYQTQNSP	52.00	52.00
HLA-DRB4*01:01	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	52.00	52.00
HLA-DPA1*02:01/DPB1*01:01	1	3	17	15	Consensus (comb.lib./simm/nr)	GICASYQTQNSPRR	52.00	52.00
HLA-DRB3*02:02	1	2	16	15	NetMHCIIpan	AGICASYQTQNSPR	53.00	53.00
HLA-DRB1*09:01	1	5	19	15	Consensus (comb.lib./simm/nr)	CASYQTQNSPRRAR	53.00	53.00
HLA-DQA1*01:02/DOB1*08:02	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	53.00	53.00
HLA-DRB1*09:01	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	54.00	54.00
HLA-DRB1*15:01	1	2	16	15	Consensus (simm/nr/stumio)	AGICASYQTQNSPR	54.00	54.00
HLA-DRB1*08:02	1	3	17	15	Consensus (simm/nr/stumio)	GICASYQTQNSPRR	54.00	54.00
HLA-DRB1*01:01	1	5	19	15	Consensus (comb.lib./simm/nr)	CASYQTQNSPRRAR	55.00	55.00
HLA-DRB1*01:01	1	4	18	15	Consensus (comb.lib./simm/nr)	ICASYQTQNSPRRA	55.00	55.00
HLA-DQA1*01:02/DOB1*08:02	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	56.00	56.00
HLA-DRB1*03:01	1	2	16	15	Consensus (simm/nr/stumio)	AGICASYQTQNSPR	56.00	56.00
HLA-DRB1*12:01	1	3	17	15	Consensus (simm/nr)	GICASYQTQNSPRR	56.00	56.00
HLA-DRB1*12:01	1	4	18	15	Consensus (simm/nr)	ICASYQTQNSPRRA	56.50	56.50
HLA-DRB1*08:02	1	2	16	15	Consensus (simm/nr/stumio)	AGICASYQTQNSPR	57.00	57.00
HLA-DQA1*03:01/DOB1*03:02	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	57.00	57.00
HLA-DRB1*04:01	1	1	15	15	Consensus (simm/nr/stumio)	GAGICASYQTQNSP	57.00	57.00
HLA-DRB1*08:02	1	4	18	15	Consensus (simm/nr/stumio)	ICASYQTQNSPRRA	57.00	57.00
HLA-DRB1*11:01	1	5	19	15	Consensus (simm/nr/stumio)	CASYQTQNSPRRAR	58.00	58.00
HLA-DRB1*12:01	1	5	19	15	Consensus (simm/nr)	CASYQTQNSPRRAR	58.00	58.00
HLA-DPA1*02:01/DPB1*01:01	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	58.00	58.00
HLA-DPA1*01:03/DPB1*02:01	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	59.00	59.00
HLA-DRB1*08:02	1	5	19	15	Consensus (simm/nr/stumio)	CASYQTQNSPRRAR	59.00	59.00
HLA-DPA1*01:03/DPB1*02:01	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	59.00	59.00
HLA-DRB4*01:01	1	3	17	15	Consensus (comb.lib./simm/nr)	GICASYQTQNSPRR	59.00	59.00
HLA-DPA1*01:03/DPB1*02:01	1	3	17	15	Consensus (comb.lib./simm/nr)	GICASYQTQNSPRR	60.00	60.00
HLA-DPA1*02:01/DPB1*01:01	1	5	19	15	Consensus (comb.lib./simm/nr)	CASYQTQNSPRRAR	61.00	61.00
HLA-DQA1*04:01/DOB1*04:02	1	1	15	15	Consensus (comb.lib./simm/nr)	GAGICASYQTQNSP	62.00	62.00
HLA-DRB4*01:01	1	4	18	15	Consensus (comb.lib./simm/nr)	ICASYQTQNSPRRA	62.00	62.00
HLA-DRB1*08:02	1	1	15	15	Consensus (simm/nr/stumio)	GAGICASYQTQNSP	63.00	63.00
HLA-DRB1*03:01	1	3	17	15	Consensus (simm/nr/stumio)	GICASYQTQNSPRR	63.00	63.00
HLA-DRB1*07:01	1	4	18	15	Consensus (comb.lib./simm/nr)	ICASYQTQNSPRRA	63.00	63.00
HLA-DPA1*03:01/DPB1*04:02	1	2	16	15	Consensus (comb.lib./simm/nr)	AGICASYQTQNSPR	64.00	64.00



	S1/S2 Junction
SARS-COV-2	CASYQTQNSPRRARSVASQ-SIIAY
ZC45	CASYHT--ASIL--RSTS-QKAIVAY
ZC21	CASYHT--ASIL--RSTG-QKAIVAY
<b>Before SARS-COV-2 (J)</b>	
SARS (Urbani)	CASYHT--VSSL--RSTS-QKSIVAY
YN2018A	CASYHT--ASTL--RSVG-QKSIVAY
Rp/Shaanxi2011	CASYHT--ASVL--RSTG-QKSIVAY
Rs4247	CASYHT--ASTL--RSVG-QKSIVAY
YN2018B	CASYHT--VSSL--RSTS-QKSIVAY
As6526	CASYHT--ASTL--RSVG-QKSIVAY
Rs4237	CASYHT--ASTL--RSVG-QKSIVAY
Longquan-140	CASYHT--ASVL--RSTG-QKSIVAY
Rs4081	CASYHT--ASTL--RSVG-QKSIVAY
BetaCoV/GX2013	CASYHT--ASVL--RSTG-QKSIVAY
HKU3-1	CASYHT--ASVL--RSTG-QKSIVAY
YN2013	CASYHT--ASTL--RSTG-QKSIVAY
Rs806/2006	CASYHT--ASLL--RSTG-QKSIVAY
Cp/Yunnan2011	CASYHT--ASLL--RNTG-QKSIVAY
Rs3367	CASYHT--VSSL--RSTS-QKSIVAY
WIV1	CASYHT--VSSL--RSTS-QKSIVAY
YN2018D	CASYHT--ASTL--RSVG-QKSIVAY
Rs4255	CASYHT--ASTL--RSVG-QKSIVAY
Rs_672/2006	CASYHT--ASTL--RSVG-QKSIVAY
WIV16	CASYHT--VSSL--RSTS-QKSIVAY
ReSHC014	CASYHT--VSSL--RSTS-QKSIVAY
SARS (Civet)	CASYHT--VSSL--RSTS-QKSIVAY
LYRaA3	CASYHT--ASLL--RNTG-QKSIVAY
LYRaA11	CASYHT--ASLL--RNTD-QKSIVAY
Rs9401	CASYHT--VSSL--RSTS-QKSIVAY
Rs40R4	CASYHT--VSSL--RSTS-QKSIVAY

## MHC-II Binding Prediction Results

### Input Sequences

#	Name	Sequence
1	IEDB Epitope 952701	CALPDTPSTLTPRSVRSVPGEMRLA

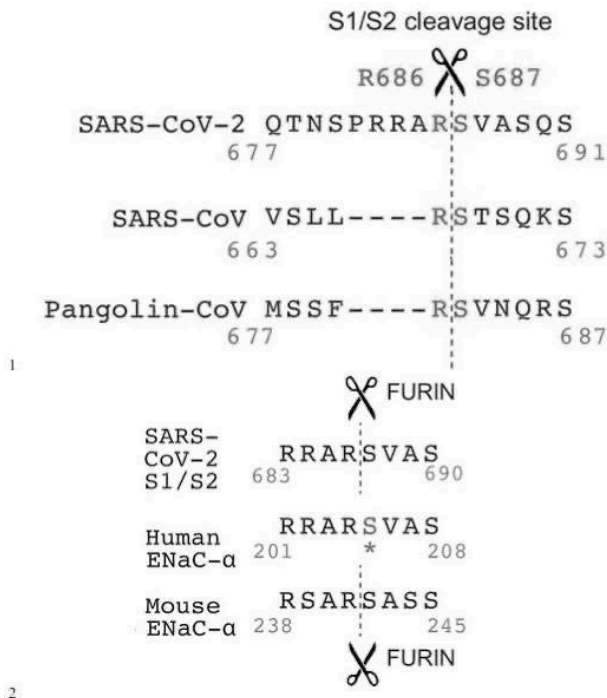
Prediction method: IEDB recommended 2.22 | Low adjusted\_rank = good binders

Download result

### Citations

Check to expand the result:

Allele	#	Start	End	Length	Method used	Peptide	Percentile Rank	Adjusted rank
HLA-DRB5*01:01	1	11	25	15	Consensus (simm/nr/stumliolo)	TPRSVRSVPGEMRLA	8.40	8.40
HLA-DRB5*01:01	1	10	24	15	Consensus (simm/nr/stumliolo)	LTPRSVRSVPGEMRL	8.60	8.60
HLA-DRB5*01:01	1	9	23	15	Consensus (simm/nr/stumliolo)	TLTPRSVRSVPGEMRR	9.50	9.50
HLA-DPA1*02:01/DPB1*14:01	1	11	25	15	NetMHCIIpan	TPRSVRSVPGEMRLA	16.00	16.00
HLA-DPA1*02:01/DPB1*14:01	1	10	24	15	NetMHCIIpan	LTPRSVRSVPGEMRL	20.00	20.00
HLA-DRB1*09:01	1	11	25	15	Consensus (comb.lib./simm/nr)	TPRSVRSVPGEMRLA	21.00	21.00
HLA-DQA1*05:01/DQB1*03:01	1	10	24	15	Consensus (comb.lib./simm/nr)	LTPRSVRSVPGEMRL	25.00	25.00
HLA-DRB1*09:01	1	10	24	15	Consensus (comb.lib./simm/nr)	LTPRSVRSVPGEMRL	25.00	25.00
HLA-DQA1*05:01/DQB1*03:01	1	9	23	15	Consensus (comb.lib./simm/nr)	TLTPRSVRSVPGEMRR	25.00	25.00
HLA-DQA1*05:01/DQB1*03:01	1	11	25	15	Consensus (comb.lib./simm/nr)	TPRSVRSVPGEMRLA	25.00	25.00
HLA-DRB1*09:01	1	5	19	15	Consensus (comb.lib./simm/nr)	DTPSTLTPRSVRSVP	27.00	27.00
HLA-DRB1*09:01	1	4	18	15	Consensus (comb.lib./simm/nr)	PDTPSTLTPRSVRSV	27.00	27.00
HLA-DQA1*05:01/DQB1*03:01	1	7	21	15	Consensus (comb.lib./simm/nr)	PSTLTPRSVRSVPGGE	28.00	28.00
HLA-DQA1*05:01/DQB1*03:01	1	8	22	15	Consensus (comb.lib./simm/nr)	STLTPRSVRSVPGEM	28.00	28.00
HLA-DRB1*09:01	1	9	23	15	Consensus (comb.lib./simm/nr)	TLTPRSVRSVPGEMRR	29.00	29.00
HLA-DRB1*07:01	1	1	15	15	Consensus (comb.lib./simm/nr)	CALPDTPSTLTPRSV	31.00	31.00
HLA-DRB1*03:01	1	11	25	15	Consensus (simm/nr/stumliolo)	TPRSVRSVPGEMRLA	31.00	31.00
HLA-DRB1*03:01	1	10	24	15	Consensus (simm/nr/stumliolo)	LTPRSVRSVPGEMRL	32.00	32.00
HLA-DRB1*09:01	1	3	17	15	Consensus (comb.lib./simm/nr)	LPDTPSTLTPRSVRS	33.00	33.00
HLA-DRB1*07:01	1	10	24	15	Consensus (comb.lib./simm/nr)	LTPRSVRSVPGEMRL	33.00	33.00
HLA-DRB1*08:02	1	10	24	15	Consensus (simm/nr/stumliolo)	LTPRSVRSVPGEMRL	33.00	33.00
HLA-DRB1*07:01	1	8	22	15	Consensus (comb.lib./simm/nr)	STLTPRSVRSVPGEM	33.00	33.00
HLA-DRB1*07:01	1	9	23	15	Consensus (comb.lib./simm/nr)	TLTPRSVRSVPGEMRR	33.00	33.00
HLA-DRB1*08:02	1	9	23	15	Consensus (simm/nr/stumliolo)	TLTPRSVRSVPGEMRR	33.00	33.00
HLA-DRB1*09:01	1	2	16	15	Consensus (comb.lib./simm/nr)	ALPDTPSTLTPRSVRS	34.00	34.00
HLA-DRB1*07:01	1	5	19	15	Consensus (comb.lib./simm/nr)	DTPSTLTPRSVRSVP	36.00	36.00
HLA-DRB1*07:01	1	4	18	15	Consensus (comb.lib./simm/nr)	PDTPSTLTPRSVRSV	36.00	36.00
HLA-DRB1*09:01	1	8	22	15	Consensus (comb.lib./simm/nr)	STLTPRSVRSVPGEM	36.00	36.00
HLA-DRB1*03:01	1	9	23	15	Consensus (simm/nr/stumliolo)	TLTPRSVRSVPGEMRR	36.00	36.00
HLA-DPA1*02:01/DPB1*14:01	1	9	23	15	NetMHCIIpan	TLTPRSVRSVPGEMRR	37.00	37.00
HLA-DRB1*07:01	1	2	16	15	Consensus (comb.lib./simm/nr)	ALPDTPSTLTPRSVRS	39.00	39.00
HLA-DRB1*01:01	1	1	15	15	Consensus (comb.lib./simm/nr)	CALPDTPSTLTPRSV	39.00	39.00
HLA-DRB1*07:01	1	3	17	15	Consensus (comb.lib./simm/nr)	LPDTPSTLTPRSVRS	39.00	39.00
HLA-DRB1*07:01	1	6	20	15	Consensus (comb.lib./simm/nr)	TPSTLTPRSVRSVPG	39.00	39.00
HLA-DRB1*01:01	1	5	19	15	Consensus (comb.lib./simm/nr)	DTPSTLTPRSVRSVP	40.00	40.00
HLA-DRB1*01:01	1	4	18	15	Consensus (comb.lib./simm/nr)	PDTPSTLTPRSVRSV	40.00	40.00
HLA-DRB1*07:01	1	7	21	15	Consensus (comb.lib./simm/nr)	PSTLTPRSVRSVPGGE	40.00	40.00
HLA-DRB1*09:01	1	7	21	15	Consensus (comb.lib./simm/nr)	PSTLTPRSVRSVPGGE	40.00	40.00
HLA-DRB3*02:02	1	11	25	15	NetMHCIIpan	TPRSVRSVPGEMRLA	40.00	40.00
HLA-DRB1*09:01	1	6	20	15	Consensus (comb.lib./simm/nr)	TPSTLTPRSVRSVPG	40.00	40.00
HLA-DRB1*12:01	1	5	19	15	Consensus (simm/nr)	DTPSTLTPRSVRSVP	41.00	41.00
HLA-DRB1*01:01	1	3	17	15	Consensus (comb.lib./simm/nr)	LPDTPSTLTPRSVRS	41.00	41.00
HLA-DRB1*15:01	1	10	24	15	Consensus (simm/nr/stumliolo)	LTPRSVRSVPGEMRL	41.00	41.00
HLA-DRB1*13:02	1	9	23	15	Consensus (simm/nr/stumliolo)	TLTPRSVRSVPGEMRR	41.00	41.00
HLA-DRB1*01:01	1	11	25	15	Consensus (comb.lib./simm/nr)	TPRSVRSVPGEMRLA	41.00	41.00
HLA-DRB1*12:01	1	4	18	15	Consensus (simm/nr)	PDTPSTLTPRSVRSV	41.50	41.50
HLA-DRB1*13:02	1	8	22	15	Consensus (simm/nr/stumliolo)	STLTPRSVRSVPGEM	42.00	42.00
HLA-DRB1*12:01	1	6	20	15	Consensus (simm/nr)	TPSTLTPRSVRSVPG	42.50	42.50
HLA-DRB1*13:02	1	10	24	15	Consensus (simm/nr/stumliolo)	LTPRSVRSVPGEMRL	43.00	43.00
HLA-DRB1*12:01	1	7	21	15	Consensus (simm/nr)	PSTLTPRSVRSVPGGE	43.50	43.50
HLA-DQA1*05:01/DQB1*03:01	1	5	19	15	Consensus (comb.lib./simm/nr)	DTPSTLTPRSVRSVP	44.00	44.00
HLA-DQA1*05:01/DQB1*03:01	1	4	18	15	Consensus (comb.lib./simm/nr)	PDTPSTLTPRSVRSV	44.00	44.00
HLA-DRB1*08:02	1	4	18	15	Consensus (simm/nr/stumliolo)	PDTPSTLTPRSVRSV	44.00	44.00
HLA-DQA1*05:01/DQB1*03:01	1	6	20	15	Consensus (comb.lib./simm/nr)	TPSTLTPRSVRSVPG	44.00	44.00
HLA-DRB1*08:02	1	6	20	15	Consensus (simm/nr/stumliolo)	TPSTLTPRSVRSVPG	44.00	44.00
HLA-DRB1*01:01	1	2	16	15	Consensus (comb.lib./simm/nr)	ALPDTPSTLTPRSVRS	45.00	45.00
HLA-DQA1*05:01/DQB1*02:01	1	11	25	15	Consensus (comb.lib./simm/nr)	TPRSVRSVPGEMRLA	45.00	45.00
HLA-DRB3*02:02	1	10	24	15	NetMHCIIpan	LTPRSVRSVPGEMRL	46.00	46.00
HLA-DRB1*15:01	1	9	23	15	Consensus (simm/nr/stumliolo)	TLTPRSVRSVPGEMRR	46.00	46.00
HLA-DRB1*15:01	1	11	25	15	Consensus (simm/nr/stumliolo)	TPRSVRSVPGEMRLA	46.00	46.00
HLA-DQA1*05:01/DQB1*02:01	1	10	24	15	Consensus (comb.lib./simm/nr)	LTPRSVRSVPGEMRL	47.00	47.00



[https://twitter.com/daoyu15/status/1757940248120631634?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1757940248120631634?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Also, the program for bat CoV work is performed in the WIV for culture and the WHU for animals, both of which stores the backups and archives of their strains and cultures in the WCDC.

And of course, it is nonsensical to claim that the entire supply chain was bleached in December 2019. In fact nothing at all was affected and animals are still sampled as live in the end of January 2020.

[archive.md/DChUL](https://archive.md/DChUL) [archive.md/4rVph](https://archive.md/4rVph) [archive.md/yyX0Z](https://archive.md/yyX0Z) [archive.md/iw1Pz](https://archive.md/iw1Pz)



**Ben Kuebrich** @Ben\_Kuebrich

Feb 19

If you read the judges notes, they got caught up on the lack of virus backbones for engineering.

Guess they bought into Peter's misinfo about mutations from lab culture and humanized mice.

💬 2 ↻ 2 🗣️ ❤️ 14



**Ben Kuebrich** @Ben\_Kuebrich

Feb 19

They talk about retrospective studies not showing evidence of circulating COVID before the HSM super spreading event. What they don't mention is that those studies didn't find evidence of COVID until the first week of January, weeks after HSM so they're clearly underpowered

💬 4 ↻ 1 🗣️ ❤️ 15



**Odysseus** @rwlander

Feb 20

Replying to @Ben\_Kuebrich @Biorealism @quay\_dr @Rootclaim @ban\_epp\_gofroc

The guided WHO tour took them wherever they were guided to, but not to WCDC lab next door to HSM. Amazing.

Feb 20, 2024 · 10:54 AM UTC

💬 1 ↻ 🗣️ ❤️ 2



**Odysseus** @rwlander

Feb 20

Replying to @rwlander @Ben\_Kuebrich @Biorealism @quay\_dr @Rootclaim @ban\_epp\_gofroc

Esp after travelling thousands of KMS and hours to get there. Joke.

💬 ↻ 🗣️ ❤️



**Holtz** ✓ @Biorealism

Feb 19

Do you have any notes about errors made through the debate? You might be one of the few people to have watched the whole 18 hours. I've seen a few that Miller made have been pointed out by @ban\_epp\_gofroc and @Ben\_Kuebrich.

💬 2 ↻ 1 🗣️ 1 ❤️ 6



**Ben Kuebrich** @Ben\_Kuebrich

Feb 19

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💬 2 ↻ 2 🗣️ ❤️ 14



**Ben Kuebrich** @Ben\_Kuebrich

Feb 19

They talk about retrospective studies not showing evidence of circulating COVID before the HSM super spreading event. What they don't mention is that those studies didn't find evidence of COVID until the first week of January, weeks after HSM so they're clearly underpowered

💬 4 ↻ 1 🗣️ ❤️ 15



**Ben Kuebrich** @Ben\_Kuebrich

Feb 19

I am glad that the judges understood the significance of a clean insert (since Saar explained it incorrectly)

💬 1 ↻ 🗣️ ❤️ 1



**Rootclaim** ✓ @Rootclaim

Feb 19

Replying to @Ben\_Kuebrich @Biorealism @quay\_dr @ban\_epp\_gofroc

How would you explain it better?

Feb 19, 2024 · 10:34 AM UTC

💬 ↻ 🗣️ ❤️

2024 年 2 月 29 日星期四 12:49, dzha4225 <dzha4225@protonmail.com> 来信:

[https://twitter.com/daoyu15/status/1746479306610479514?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1746479306610479514?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Sometimes a blatant lie is worth as much as a direct admission when from a person or a group that is not able to speak freely. Note how Shi went excessively normal that she pretended to have not been aware at all of the ongoing outbreak in Wuhan when others have already taken measures, needing to be reminded toward it and still reluctant. This should have not been the case with genuine lack of foreknowledge, where it is expected that measures similar to public is to happen as in 15-16/01/2020, when clinics and hospitals are already full and h2h is locally widely known at that time in wuhan.

Not everyone can afford the price of speaking up. The WHO report have at least two sections whistleblowing the WCDC (not the HBCDC that don't know about the bioweapons program which have their civilian fronts all operating at and below municipal level in Wuhan) (infected sampler caused all lineage A infections, got through by disguising as family cluster infection, riding the intent to prove sensitivity of the serological tests that China forgot that analysis can not be distributed evenly across distinctly collected cohorts (the only positive serological test on any subject at all in the entire WHO report) ) and the manipulation of early cases data (detailing accountant chen in Jiangxia——while not distinctly talking about his residence in the report and place his dot in Jiangnan, so the falsehood of the WHO maps can be exposed).

[https://twitter.com/daoyu15/status/1752808015521038748?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1752808015521038748?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Activity flaring up in China in late 2019—like usual, Shi once again overdid the cover-up and it become obvious what she was hiding.

[https://twitter.com/daoyu15/status/1752859981571916065?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1752859981571916065?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Both of the principle members that engaged in the Sep-Dec 2019 events ended up being too silent about the FCS when they shouldn't. This is what we call extremely suspicious.

[https://twitter.com/jhas5/status/1509365535548624901?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/jhas5/status/1509365535548624901?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

The ODNI broke the COVID origin disclosure act by nor providing the exact symptoms to the level of knowledge that their heavily redacted report clearly show.

[https://twitter.com/r\\_h\\_ebright/status/1729164212159824154](https://twitter.com/r_h_ebright/status/1729164212159824154)

Because doing so guarantee an diplomatic catastrophe.

[https://twitter.com/daoyu15/status/1748654694170292675?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1748654694170292675?s=46&t=wRQSWp_1VffWmS2vKQwhSA)



Sent from [Proton Mail](#) for iOS

2024 年 2 月 29 日星期四 20:56, dzha4225 <dzha4225@protonmail.com> 来信:

Hi engineer and iboverlord

Please tell this to @ban\_epp\_gofroc on twitter.

(Tell him that trolls are best blocked)

<https://twitter.com/daoyu15/status/1754661054733242856>

Sorry, markolin, none of your “caged, stacked, sick and wounded animals” actually have a single infection in nature anywhere in the world.

[archive.md/DChUL](https://archive.md/DChUL) [archive.md/4rVph](https://archive.md/4rVph) [archive.md/yyX0Z](https://archive.md/yyX0Z) [archive.md/iw1Pz](https://archive.md/iw1Pz)

And sorry, the <https://pubmed.ncbi.nlm.nih.gov/35298912/> two following sampling studies have in fact registered the entirety of the supply chain for the Huanan market, one for the local trappers which 100% of the raccoon dogs and weasels are from

<https://pubmed.ncbi.nlm.nih.gov/35298912/>

And the second for all the other animals which are farmed.

<https://twitter.com/daoyu15/status/1723019367854875094>

Unlike all prior zoonoses where multiple sites of spillover happens with extensive diversity,

<https://twitter.com/daoyu15/status/1727479523778887806>

Which is true for non-coronaviruses as well,

<https://archive.md/OIGPz> and just like the absence of secondary outbreaks anywhere at all despite the fact that the wildlife trade continuing for the same amount of time where SARS-CoV-1 had 9 out of its 11 primary spillovers

<https://twitter.com/daoyu15/status/1740796866617647522>

The total absence of a phylogenetic tree indicating 20nt+ variants and wildlife linked diversity also disproves zoonosis for SARS-CoV-2.

<https://twitter.com/daoyu15/status/1668828125617352704>

[https://twitter.com/daoyu15/status/1740796866617647522?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1740796866617647522?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Unfortunately the animal trade continued

[https://twitter.com/daoyu15/status/1723305823886291394?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1723305823886291394?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

All the way into 23/01/2020 and later, without being shut down especially in Guangdong.

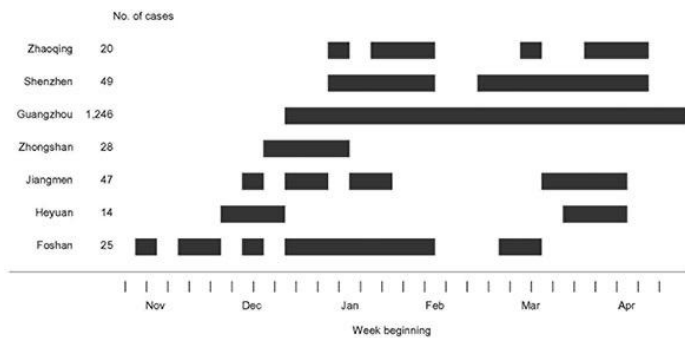
<https://twitter.com/daoyu15/status/1690330493693374464>

This is sufficient amount of time where the majority of the primary SARS-CoV-1 spillover events (9 out of 11, 5 of which are animal sellers from distinct markets in distinct cities, and which an animal transporter linking Yunnan and Guangdong was among the first cases) have taken place.

<https://gab.com/Flavinkins/posts/109883975094801876>

[https://wwwnc.cdc.gov/eid/article/10/6/03-0852\\_article](https://wwwnc.cdc.gov/eid/article/10/6/03-0852_article)

On the contrast, 5 independent animal seller cases out of 9 total primary cases for SARS-CoV-1 have happened in 5 cities in 4 in Guangdong and 1 in Guangxi (and +4 for the non-animal seller cases), over the same 2-months timeframe. Two of them were civet butchers, two market workers and one a driver for wildlife dealers. In the contrast, 0 of the early cases for SARS-CoV-2 worked in or have a history of direct participation with the wildlife industry.



Sent from [Proton Mail](#) for iOS

2024 年 3 月 1 日星期五 03:45, dzha4225 <dzha4225@protonmail.com> 来信:

Why the WCDC is involved?

[https://twitter.com/daoyu15/status/1757940248120631634?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1757940248120631634?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Because well the program for bat CoV work is performed in the WIV for culture and the WHU for animals, both of which stores the backups and archives of their strains and cultures in the WCDC.

<https://twitter.com/daoyu15/status/1726769717497696562>

The WCDC and the Hubei CDC stores all of the human samples and backups of research cultures of pathogenic microbes in Wuhan, as this is their legally delegated duty and that labs in China are not allowed to store such cultures except several select state key laboratories. Since 2014, the only EID surveillance target in Wuhan is the HSM which all other sites are kept blind so that they can blame Huanan in case the research labs suffer an accident.

After an initial release from the WIV that caused Chen's infection, and eventual transmission to the HSM via line 2 of the Wuhan metro, they mobilized the WCDC in 20-22/12/2019 to begin tapering with the environmental samples and prepare for any needed scapegoat action.

That mobilization ended up causing an infection of a WCDC worker with an aliquot of a sample containing WA1, A and B in the same quasispecies, which then go on infecting all of the earliest lineage A cases in Wuhan.

[https://twitter.com/daoyu15/status/1704207677663121556?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1704207677663121556?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Their possession of lineage A as a culture also poured itself into A20, creating the massive discrepancy between the fraction of mammalian host sequences inside the samples between metagenomic and amplicon. (Culture host introduced alongside lineage A into the amplicon dataset, neither exist in the metagenomic dataset).

Why no line lists?

[https://x.com/daoyu15/status/1724556334472077599?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1724556334472077599?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Not a single raccoon dog have been found infected in nature anywhere in the world.

[https://x.com/daoyu15/status/1724557544507793707?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1724557544507793707?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Where are all the other expected spillovers especially in Guangdong, where and 90% of all animals farmed in China was consumed and nearly all of them were distributed through?

[https://x.com/daoyu15/status/1724561751172378861?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1724561751172378861?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Any farms in Yunnan large enough to sell to Wuhan, will sell mainly to [Guangdong](#).

<https://archive.md/e3615> <https://archive.md/vWjZl>

[https://x.com/daoyu15/status/1724201870103847006?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1724201870103847006?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Contamination and intentional adulteration, with human cultures and human shedding. Not animals.

[https://x.com/daoyu15/status/1724352346959032668?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1724352346959032668?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Haven't told that there is an epistasis issue as well?

[https://x.com/daoyu15/status/1724242786134982894?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1724242786134982894?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Without any raw data to speak of, the moving of the residence of the first ever case they admit

[https://x.com/daoyu15/status/1724242737074233833?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1724242737074233833?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

and the suspicious over-removal of cases in Wuchang

<https://gab.com/Flavinkins/posts/109256201942085712> removed all credibility of the WHO "early cases" report.

[https://x.com/daoyu15/status/1724566520595095974?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1724566520595095974?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

There is VERO-CHO adaptation, freeze-thaw adaptation, and not to mention that the WCDC is one of the very few places where samples of pathogenic viral cultures are permitted storage in Wuhan—

[https://x.com/daoyu15/status/1724402686806933700?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1724402686806933700?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

nearly all of the Wuchang lab complex needed to store their samples in it.

Then consider the extensive sharing of [arxiv.org/abs/2104.01533](https://arxiv.org/abs/2104.01533)

[arxiv.org/abs/2109.09112](https://arxiv.org/abs/2109.09112) samples between Wuhan labs observed in their SRA data.

[https://x.com/daoyu15/status/1724404211155341364?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1724404211155341364?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And of course, their cover-up of early cases are belied by both peer-reviewed early articles on cases and peer-reviewed early articles on deaths

[https://x.com/daoyu15/status/1724556387177656338?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1724556387177656338?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Inconsistent viral read counts between 2021 and 2023 in all 3 major samples except B5 indicate significant data tampering and invalidate resequencing claims. Especially exemplified with A20 with inconsistent host fractions as well.

[https://x.com/daoyu15/status/1724559272124805577?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1724559272124805577?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Zhou Yusen, unfortunately.

[https://x.com/daoyu15/status/1725670977407987978?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://x.com/daoyu15/status/1725670977407987978?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

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2024 年 3 月 1 日星期五 13:37, dzha4225 <[dzha4225@protonmail.com](mailto:dzha4225@protonmail.com)> 来信:

If they have any genetic expertise they would realize that neither RaTG13 nor their early datasets are correct or what they claimed to be.

[arxiv.org/abs/2104.01533](https://arxiv.org/abs/2104.01533)

An infectious clone is designed to be rescued.

[archive.ph/EiCQW](https://archive.ph/EiCQW)

Well, MN611520—definitely not a bat CoV.

[twitter.com/drhermiz/status/1718191358077276403](https://twitter.com/drhermiz/status/1718191358077276403)

[twitter.com/daoyu15/status/1719847927512977720](https://twitter.com/daoyu15/status/1719847927512977720)

[twitter.com/daoyu15/status/1672399653344808960](https://twitter.com/daoyu15/status/1672399653344808960)

And of course, WIV1, WIV16, Rs4874 and RsSHC014 count up to 4 published live isolates not “only 3” claimed by Shi. That is published isolates only.

[zenodo.org/records/5702700#.ZKu-2CV6sIT](https://zenodo.org/records/5702700#.ZKu-2CV6sIT)

RaTG13 don't grow outside immortalized kidney cells.

These are just too many inconsistencies and obvious lies regarding the number of WIV

[twitter.com/daoyu15/status/1719763256976523501](https://twitter.com/daoyu15/status/1719763256976523501)

[twitter.com/mattwridley/status/1462659372421718019](https://twitter.com/mattwridley/status/1462659372421718019)

Or EHA viral sequences AND isolates in their public claims.

[https://twitter.com/john\\_bumblebee/status/1671859504122679296](https://twitter.com/john_bumblebee/status/1671859504122679296)

Inconsistency upon inconsistency in Chinese publications as well as “data”.

Well, [twitter.com/covidselect/status/1701958926097342630](https://twitter.com/covidselect/status/1701958926097342630)

The ODNI can't even do a proper google search to realize that the ben Hu did work with live virus.

[twitter.com/daoyu15/status/1702180584532131863?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1702180584532131863?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

No wonder the report.

[twitter.com/daoyu15/status/1673402523812765696](https://twitter.com/daoyu15/status/1673402523812765696)

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Unrestricted biowarfare explain the anomalies in prepandemic and early pandemic

wuhan. @breakfast\_dogs @drlimengyan1 <https://archive.md/ORJSH>

[https://twitter.com/breakfast\\_dogs/status/1753048332451160097?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/breakfast_dogs/status/1753048332451160097?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

Beijing got the real info before Wuhan. Always.

[https://twitter.com/breakfast\\_dogs/status/1753048295755108718?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/breakfast_dogs/status/1753048295755108718?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And when Wuhan and internationally they still deny human transmission while Beijing already know, it is clear that the market is a farce.

[https://twitter.com/daoyu15/status/1754109830866894869?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1754109830866894869?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

And continued to deploy variants to this date.

[https://twitter.com/breakfast\\_dogs/status/1754657113589379194?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/breakfast_dogs/status/1754657113589379194?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

None of their “data” can be trusted at all.

[https://twitter.com/daoyu15/status/1754740313770402208?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/daoyu15/status/1754740313770402208?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

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Someone here should

Also tell @rebecca21951651 that the final intranet takedown date for Batvirus is in February 2020, which is unfortunately two months before “far right forums” get any of the email addresses and passwords. Intelligence collection agencies are much more

likely to have known these and attempt to collect data. The correct way facing such issue is always to put up an immutable digitally signed copy on a public server immediately, In stead nothing happened.

<https://gab.com/Flavinkins/posts/109119589216881037>

People still seems to forget that can ping a server does not mean can access the database.

<https://gab.com/Flavinkins/posts/109118879442600424>

Regardless on how, why there is a hacking attempt in the first place and who is actually targeted by hacking attempts? And exactly how you can deduce that “it is fake”? And if you immediately say this attempt is “fake”, then perhaps

<https://gab.com/Flavinkins/posts/109118879442600424>[https://twitter.com/daoyu15/status/1695771029875089813?s=46&t=wRQSWp\\_1VffWmS2vKQwhSAShi](https://twitter.com/daoyu15/status/1695771029875089813?s=46&t=wRQSWp_1VffWmS2vKQwhSAShi)'s claim of “hacking” is just as fake as Sharyl?

Why not putting up a read-only copy on a secure server except when there is incriminating data that must be kept hidden for all causes especially from intelligence collectors?

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It may also worth mentioning that rootclaim have provided two info that defeats miller's heavily strawmanned argument.

[https://twitter.com/rootclaim/status/1758127978763125053?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/rootclaim/status/1758127978763125053?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

[https://twitter.com/rootclaim/status/1753353199216439672?s=46&t=wRQSWp\\_1VffWmS2vKQwhSA](https://twitter.com/rootclaim/status/1753353199216439672?s=46&t=wRQSWp_1VffWmS2vKQwhSA)

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