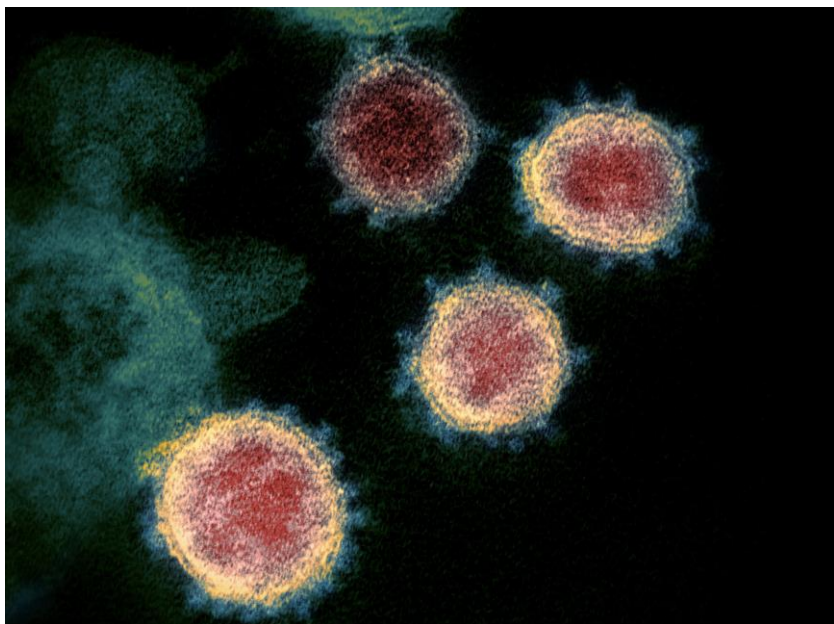




新型冠狀病毒知多少

馬偕兒童醫院 兒童感染科
主治醫師 黃璫寧

DANIEL TSUNG-NING HUANG, M.D., PH.D.



Coronavirus COVID-19 Global Cases by Johns Hopkins CSSE



Total Confirmed

69,186

Confirmed Cases by
Country/Region

68,500 Mainland China

285 Others

72 Singapore

56 Hong Kong

43 Japan

33 Thailand

29 South Korea

22 Malaysia

18 Taiwan

16 Germany

16 Vietnam

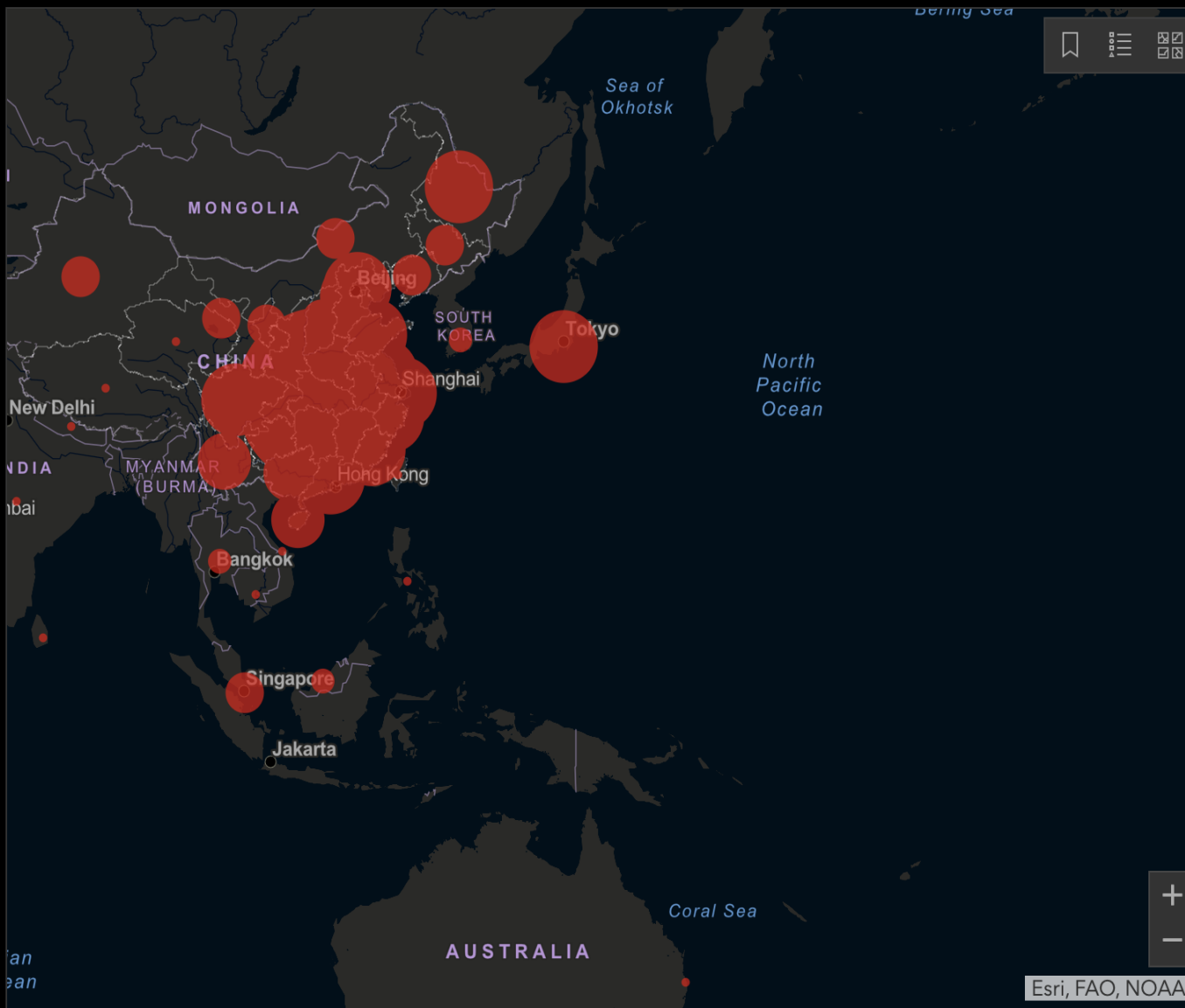
15 Australia

15 US

12 France

Country/Region

Last Updated at (M/D/YYYY)
2/16/2020 11:13:07 上午



Total Deaths

1,669

1,596 deaths

Hubei Mainland China

13 deaths

Henan Mainland China

11 deaths

Heilongjiang Mainland China

6 deaths

Anhui Mainland China

5 deaths

Chongqing Mainland China

4 deaths

Beijing Mainland China

4 deaths

Hainan Mainland China

Total Recovered

9,571

5,623 recovered

Hubei Mainland China

437 recovered

Zhejiang Mainland China

436 recovered

Guangdong Mainland China

430 recovered

Hunan Mainland China

402 recovered

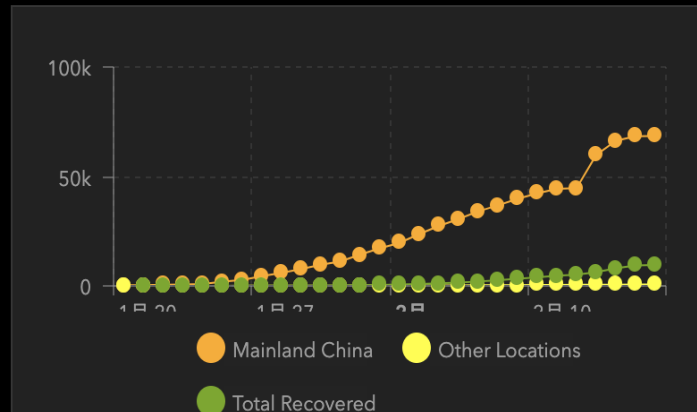
Henan Mainland China

242 recovered

Anhui Mainland China

239 recovered

Jiangxi Mainland China



Actual

Logarithmic

Daily Increase

Mobile Version: [Here](#). Visualization: JHU CSSE. Automation Support: [Esri Living Atlas team](#).

Data sources: [WHO](#), [CDC](#), [ECDC](#), [NHC](#) and [DXY](#). Read more in this [blog](#). [Contact US](#).

Downloadable database: GitHub: [Here](#). Feature layer: [Here](#).

Point level: City level - US, Canada and Australia; Province level - China; Country level - other countries.

COVID-19 CORONAVIRUS OUTBREAK

Last updated: February 16, 2020, 03:10 GMT

[Cases](#) – [Deaths](#) – [Countries](#) – [Death Rate](#) – [Incubation](#) – [Age](#) – [Symptoms](#) – [Opinions](#)

Coronavirus Cases:

69,269

[view by country](#)

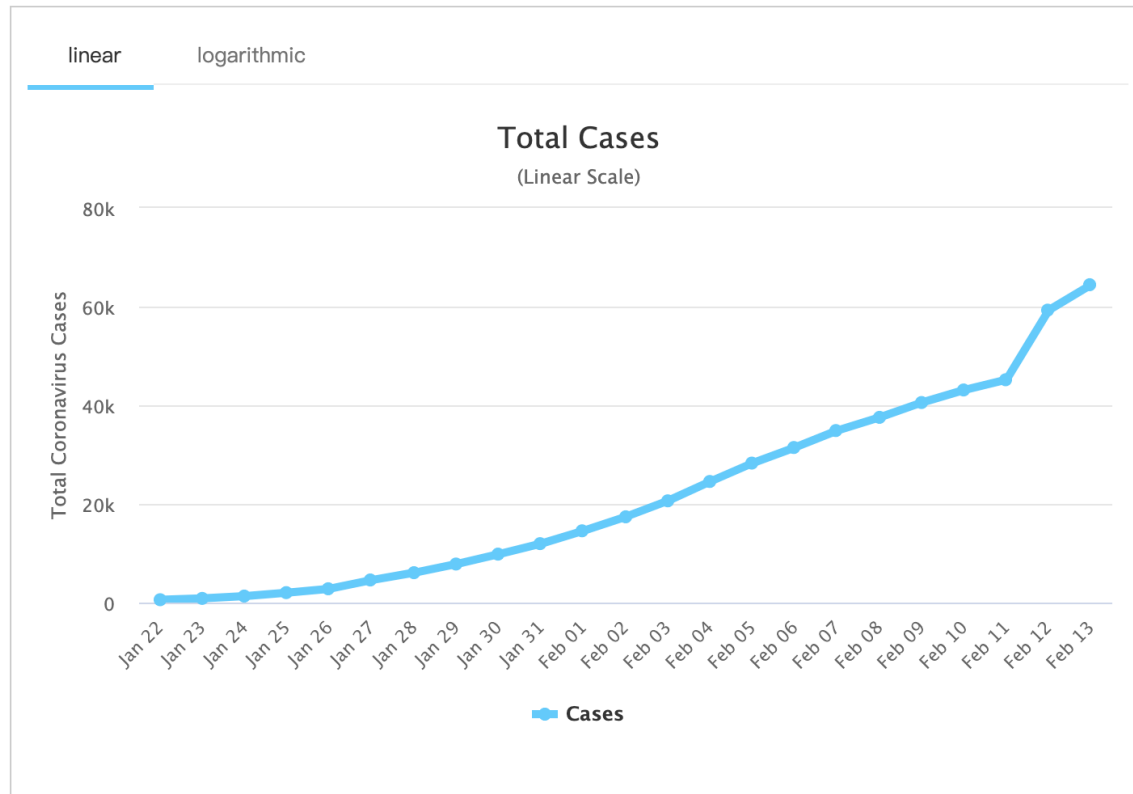
Deaths:

1,669

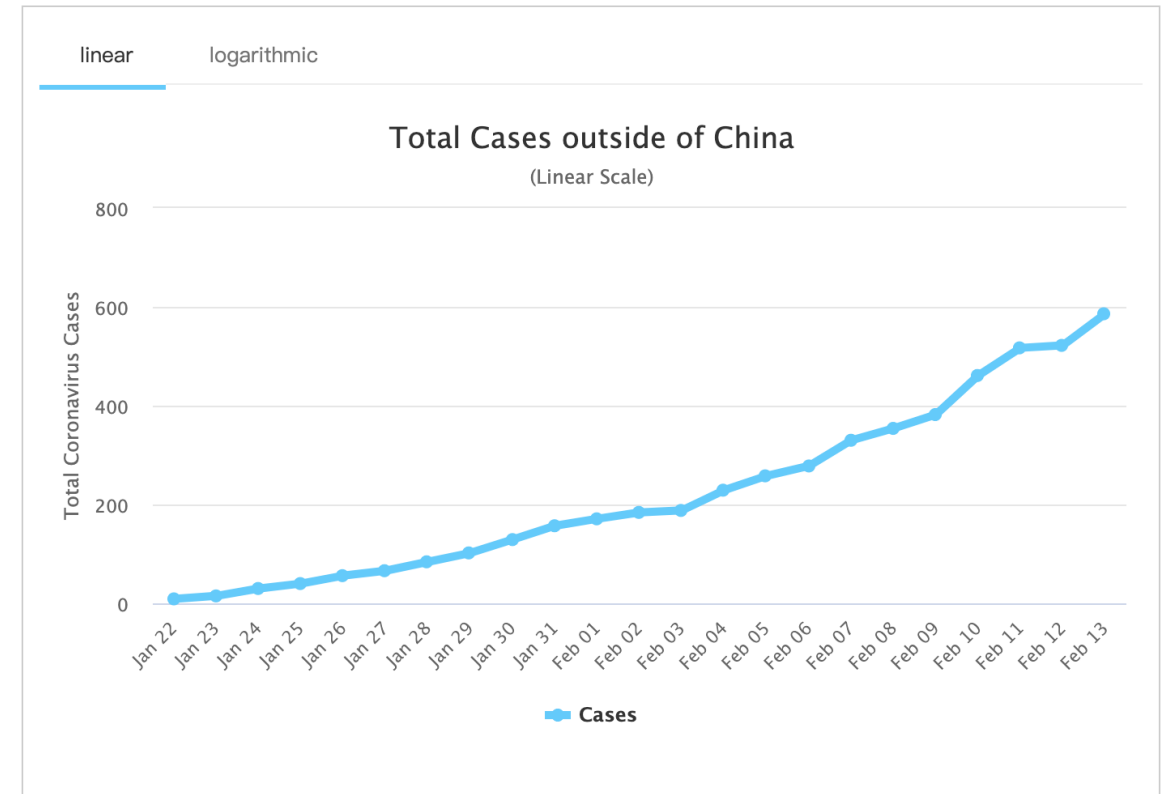
Recovered:

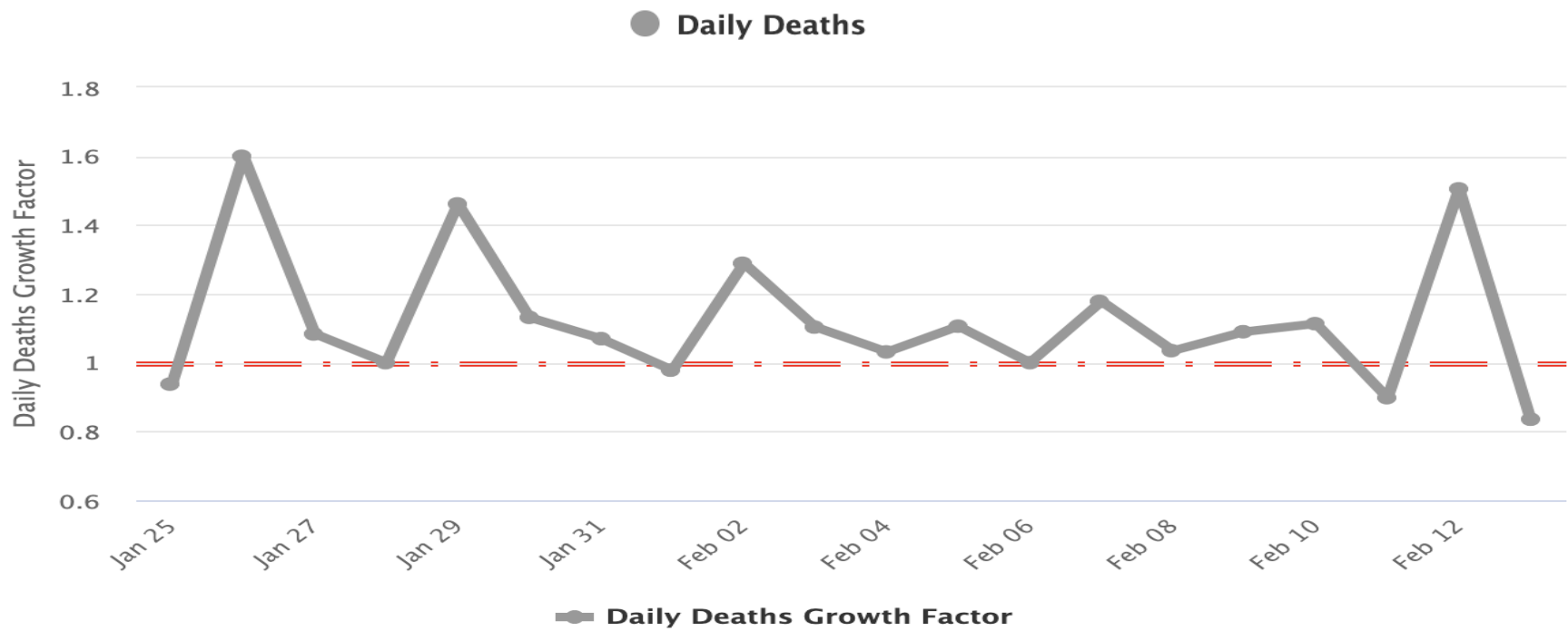
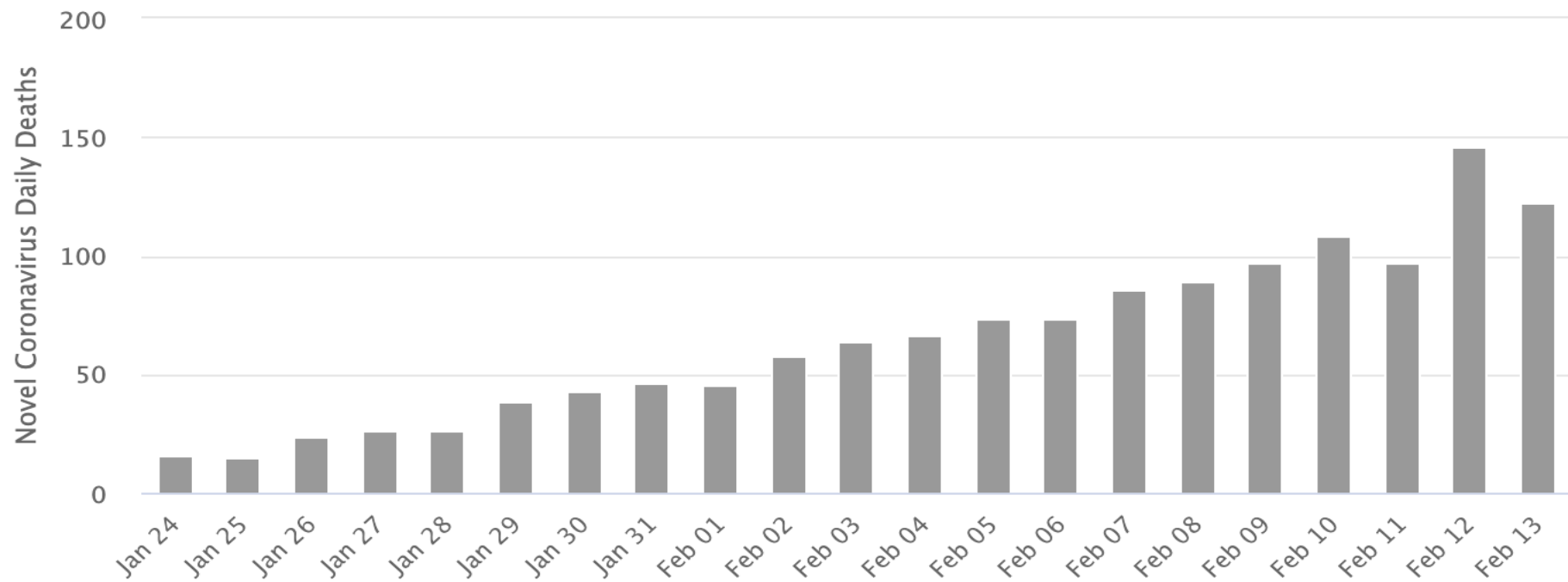
9,586

Total Cases (worldwide)



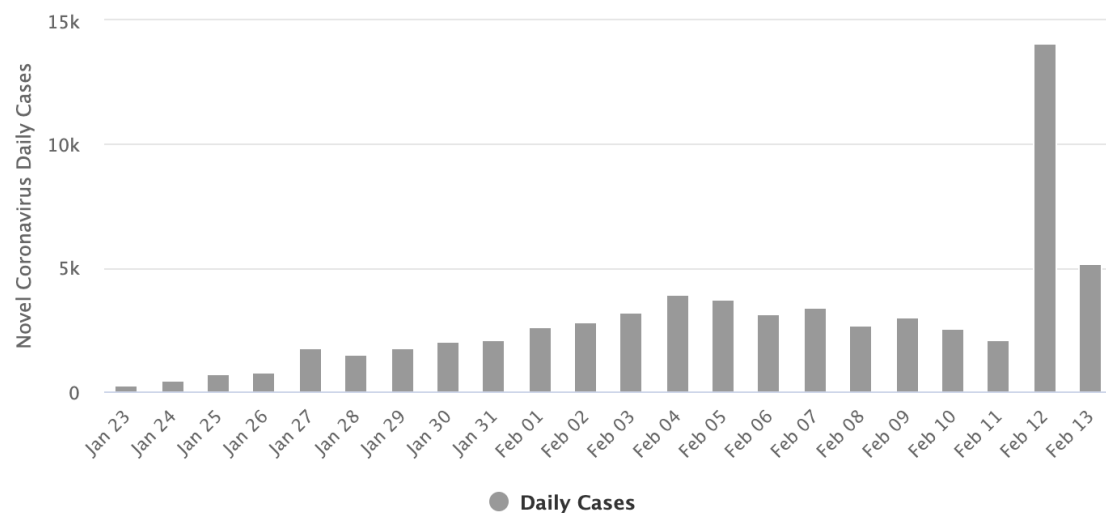
Total Cases excluding mainland China





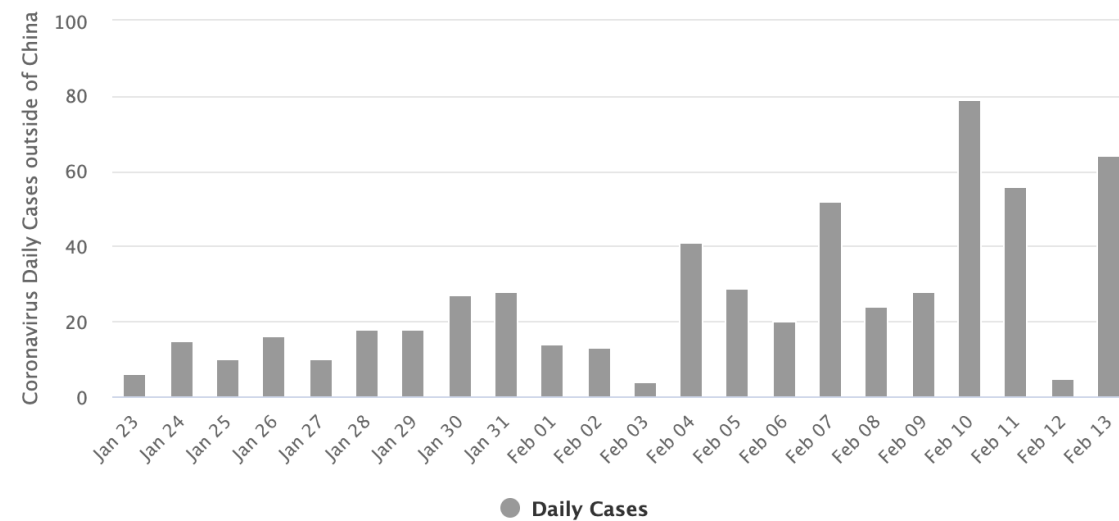
Daily New Cases

Cases per Day
Data as of 0:00 GMT+0



Daily New Cases outside of China

Cases per Day
Data as of 0:00 GMT+0



預測武漢肺炎未來趨勢：之前的統計數字大多已不適用。

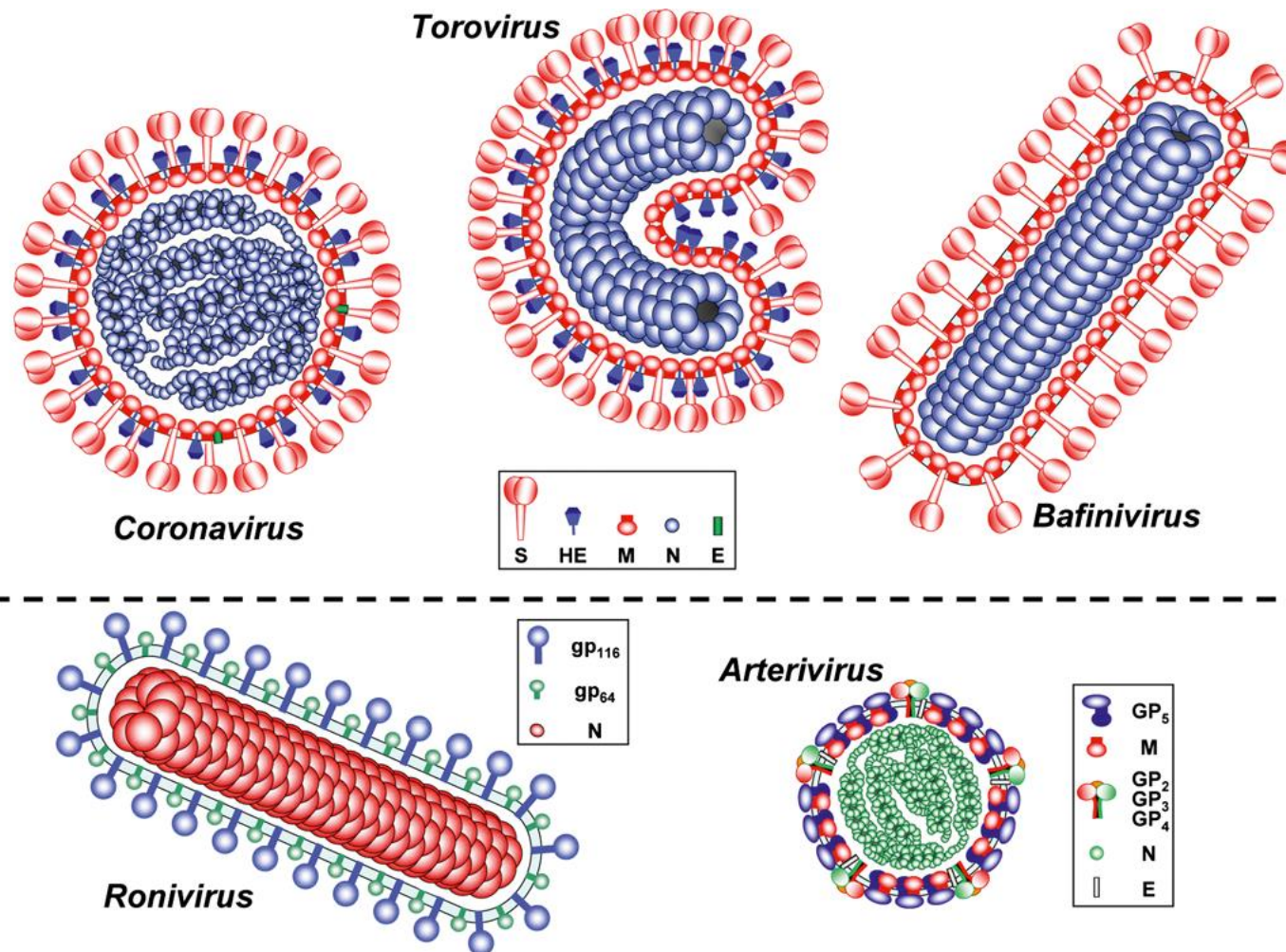
Outline

1. Introduction to coronavirus (CoV)
2. Virology of SARS-CoV-2
3. Genomic epidemiology of SARS-CoV-2
4. Clinical manifestations of COVID19
5. Possible explanations for some crucial questions
6. Future perspectives

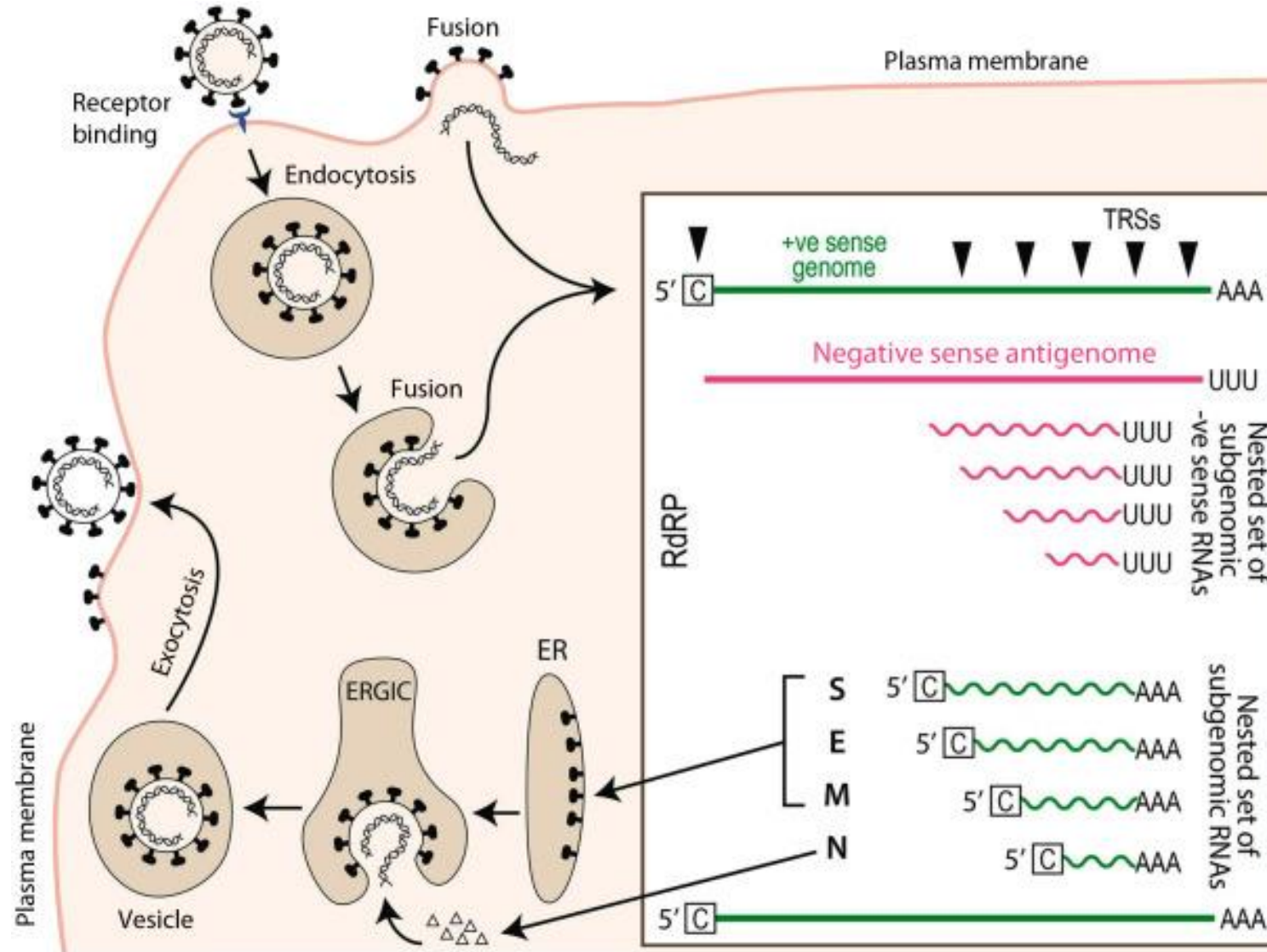
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Nidovirales 網巢病毒目

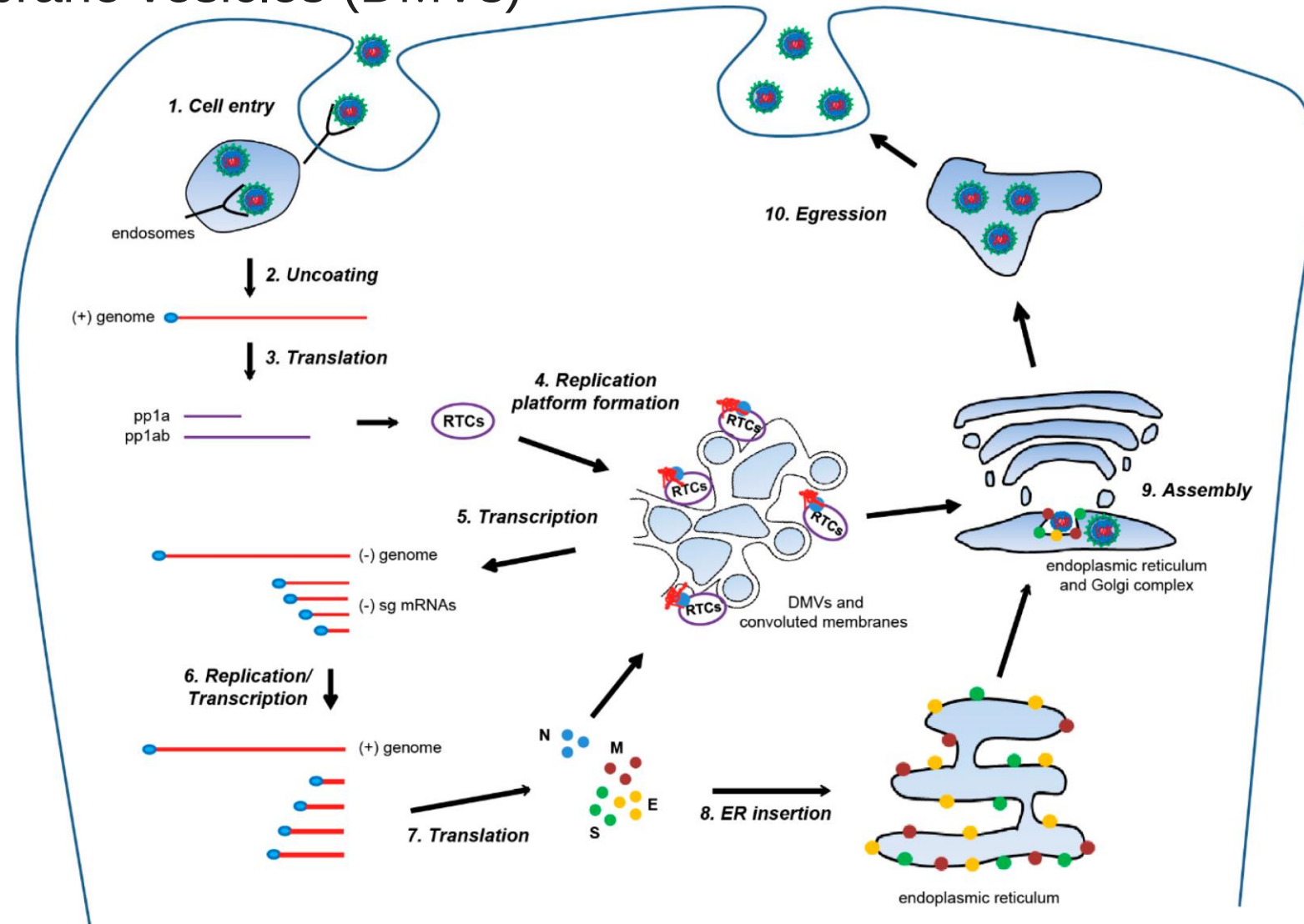


Nidovirales: produce a 3' co-terminal nested set of subgenomic mRNA's during infection.

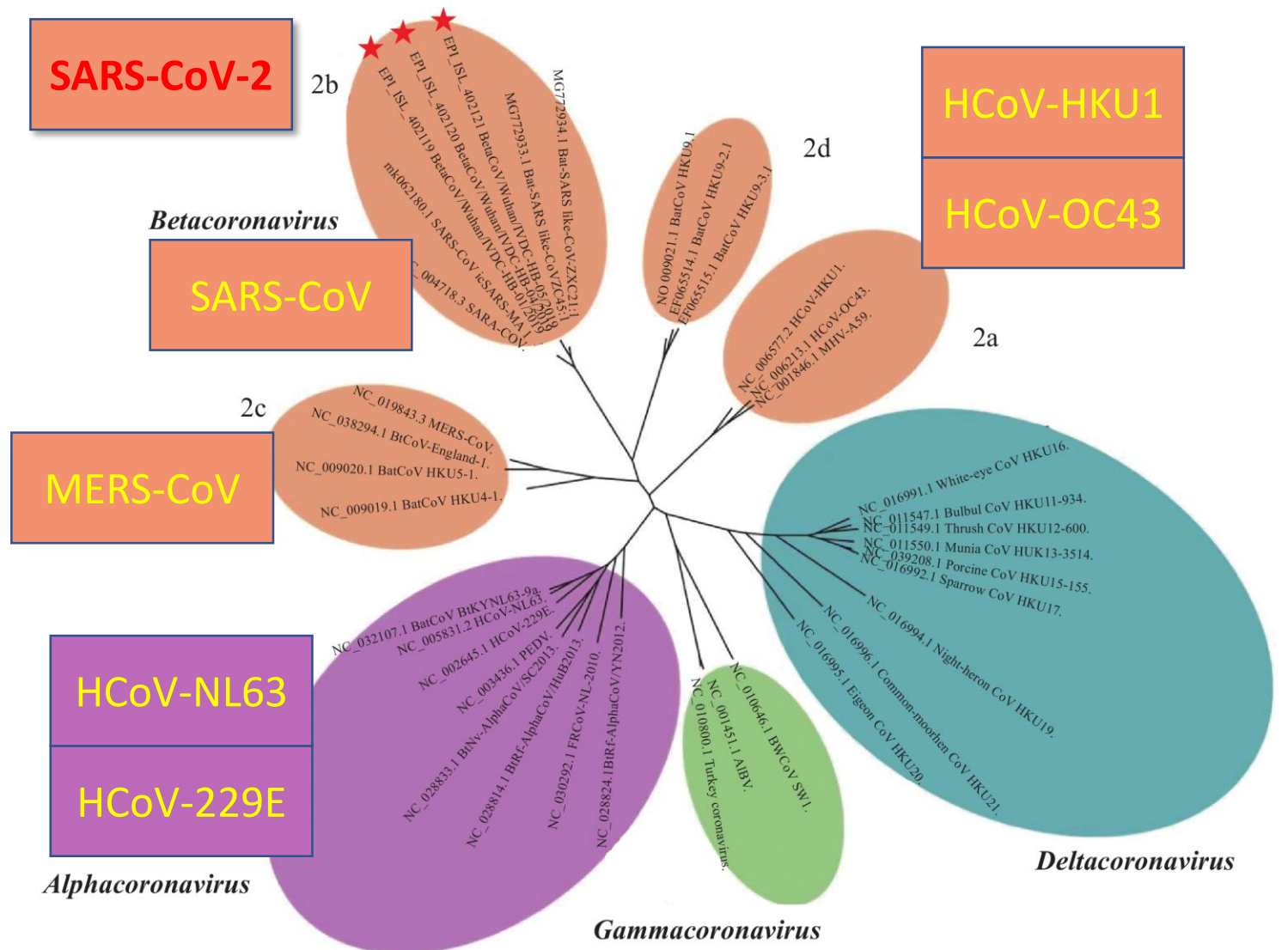
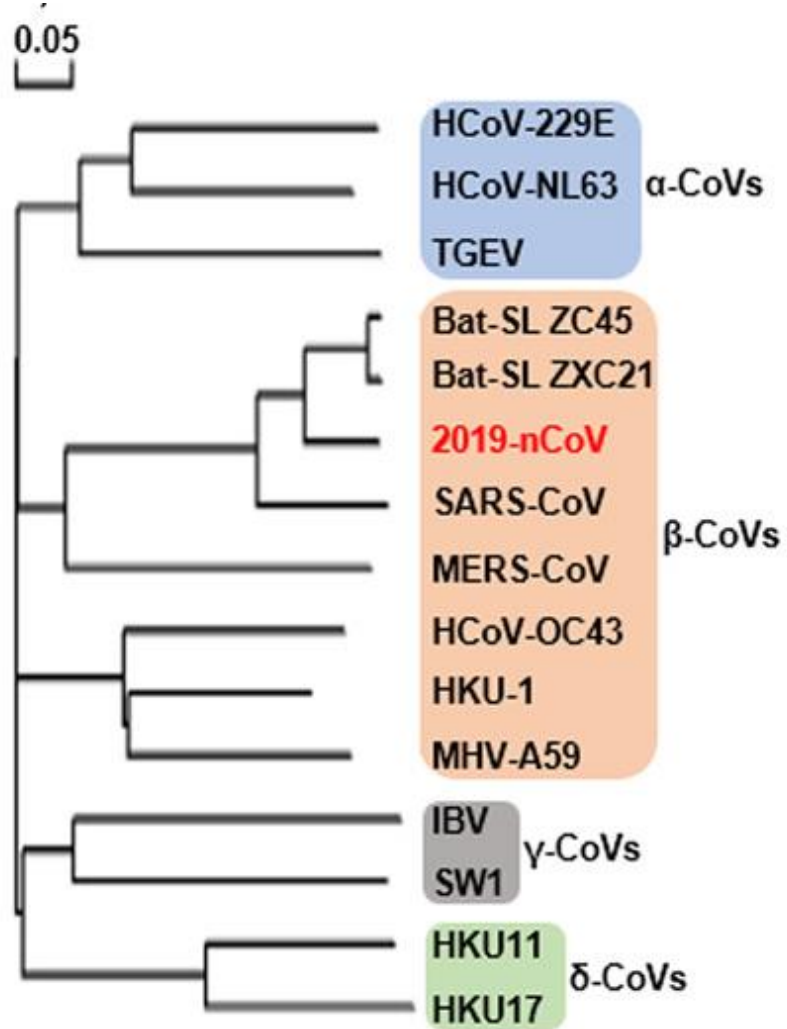


The first ORFs (ORF1a/b) of CoV, about two-thirds of the whole genome length, encode 16 nsps (nsp1-16).

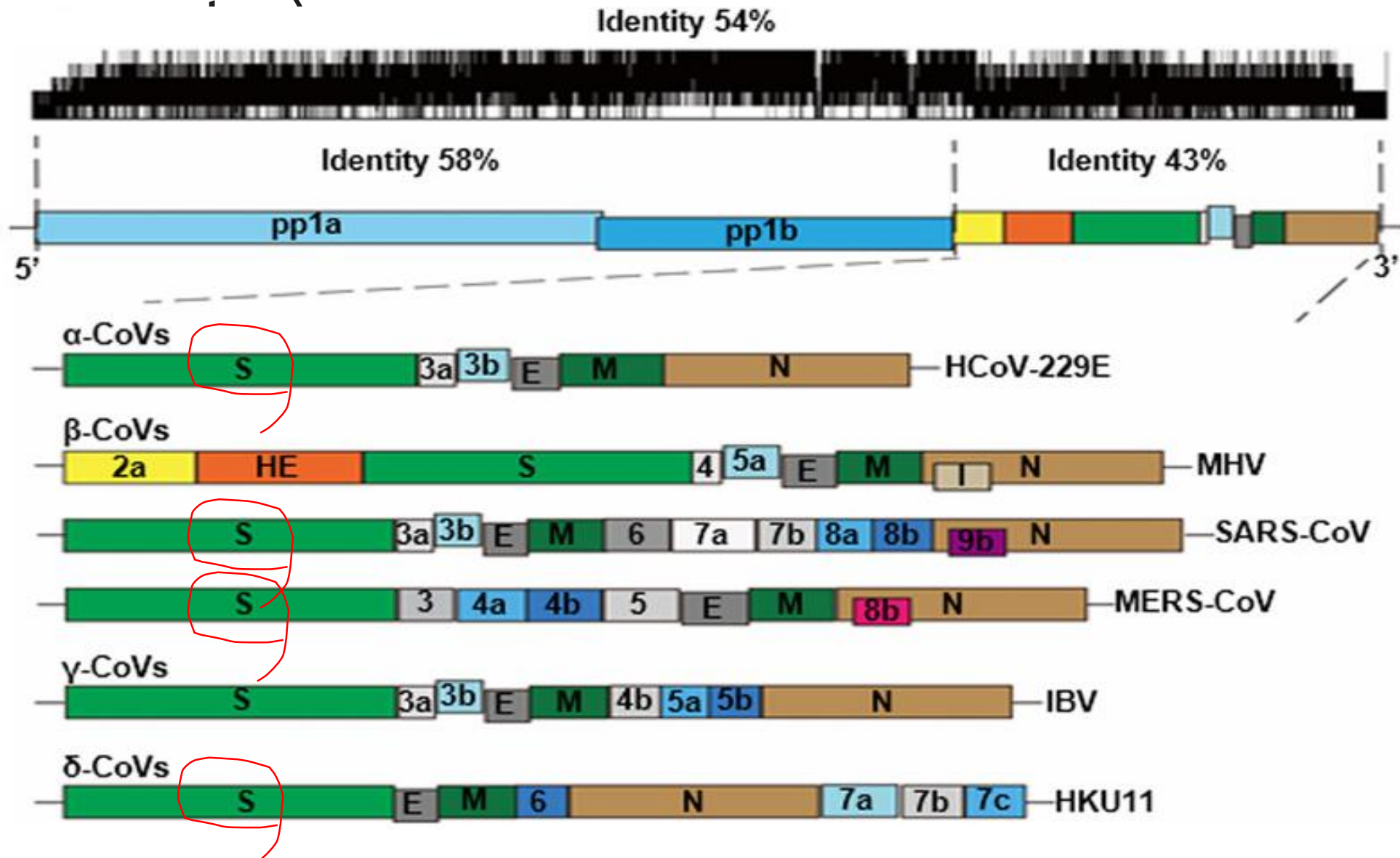
- Replication-transcription complexes (RTCs)
- Double membrane vesicles (DMVs)



Cong, Verlhac and Reggiori_Figure 2



S gene → spike protein (binds to host)



Outline

1. Introduction to coronavirus (CoV)
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A	Strain	Complete genome (%)	Gene region (%)												
			1ab	1a	1b	S	3	E	M	7	8	10b	N	13	14
Nucleotide sequences	Bat-SL-CoVZC45	87.6	88.9	90.7	86.0	75.2	87.8	98.7	93.4	95.2	88.8	88.5	91.1	89.1	96.7
	Bat-SL-CoVZXC21	87.5	88.7	90.3	86.1	74.7	88.9	98.7	93.4	95.2	89.1	88.5	91.2	89.5	96.7
	SARS-CoVGZ02	79.0	79.5	75.4	86.3	72.7	75.6	93.5	85.1	74.5	82.1	..	88.1	..	..
Amino acid sequences	Bat-SL-CoVZC45	..	95.6	95.6	95.8	80.2	90.9	100.0	98.6	93.4	87.6	94.2	94.3	73.2	92.9
	Bat-SL-CoVZXC21	..	95.2	95.1	95.5	79.6	92.0	100.0	98.6	93.4	88.4	94.2	94.3	73.2	92.9
	SARS-CoVGZ02	..	86.2	80.5	95.6	76.2	73.1	94.7	90.1	68.9	85.2	..	90.3	..	..

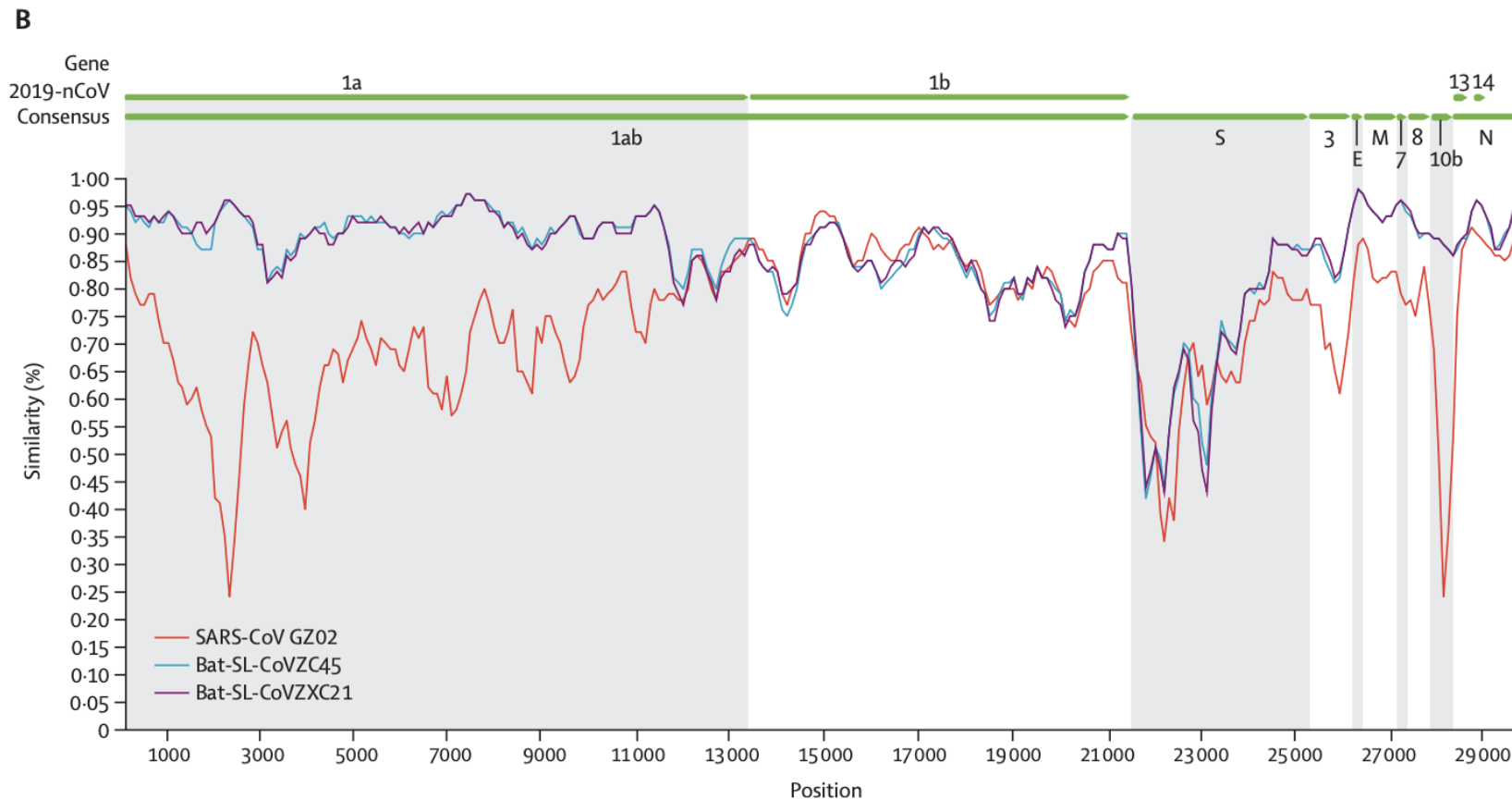
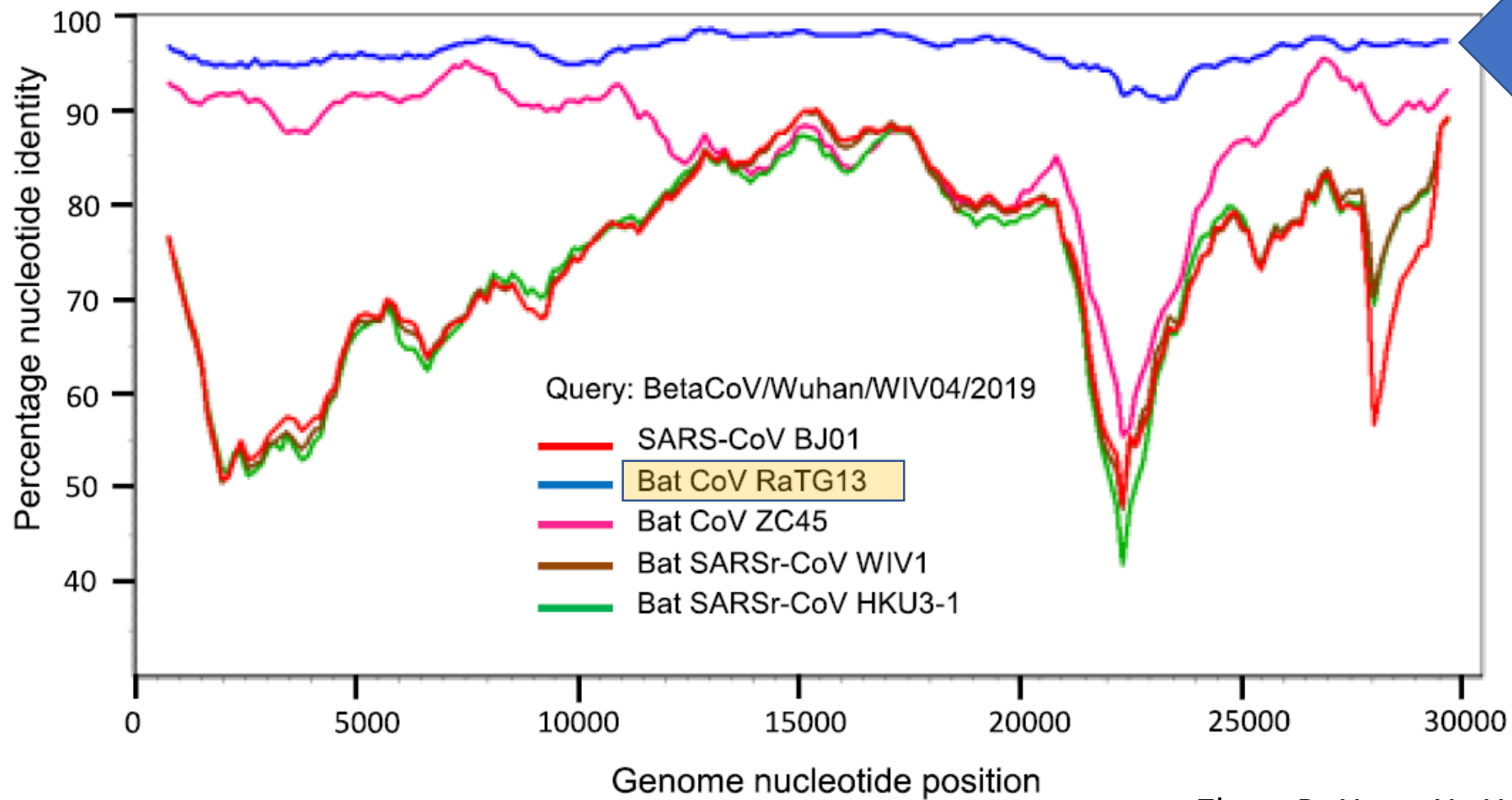
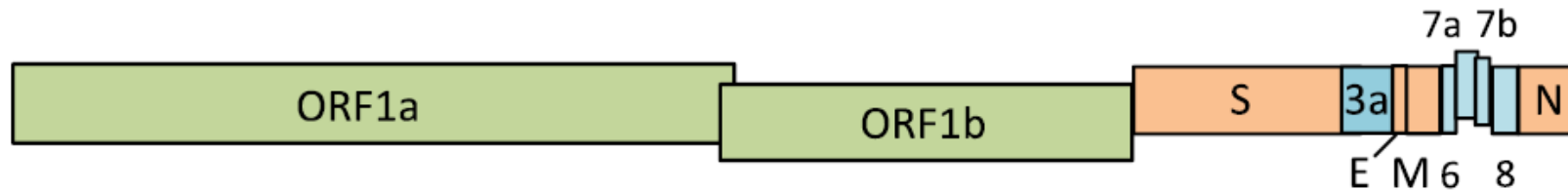
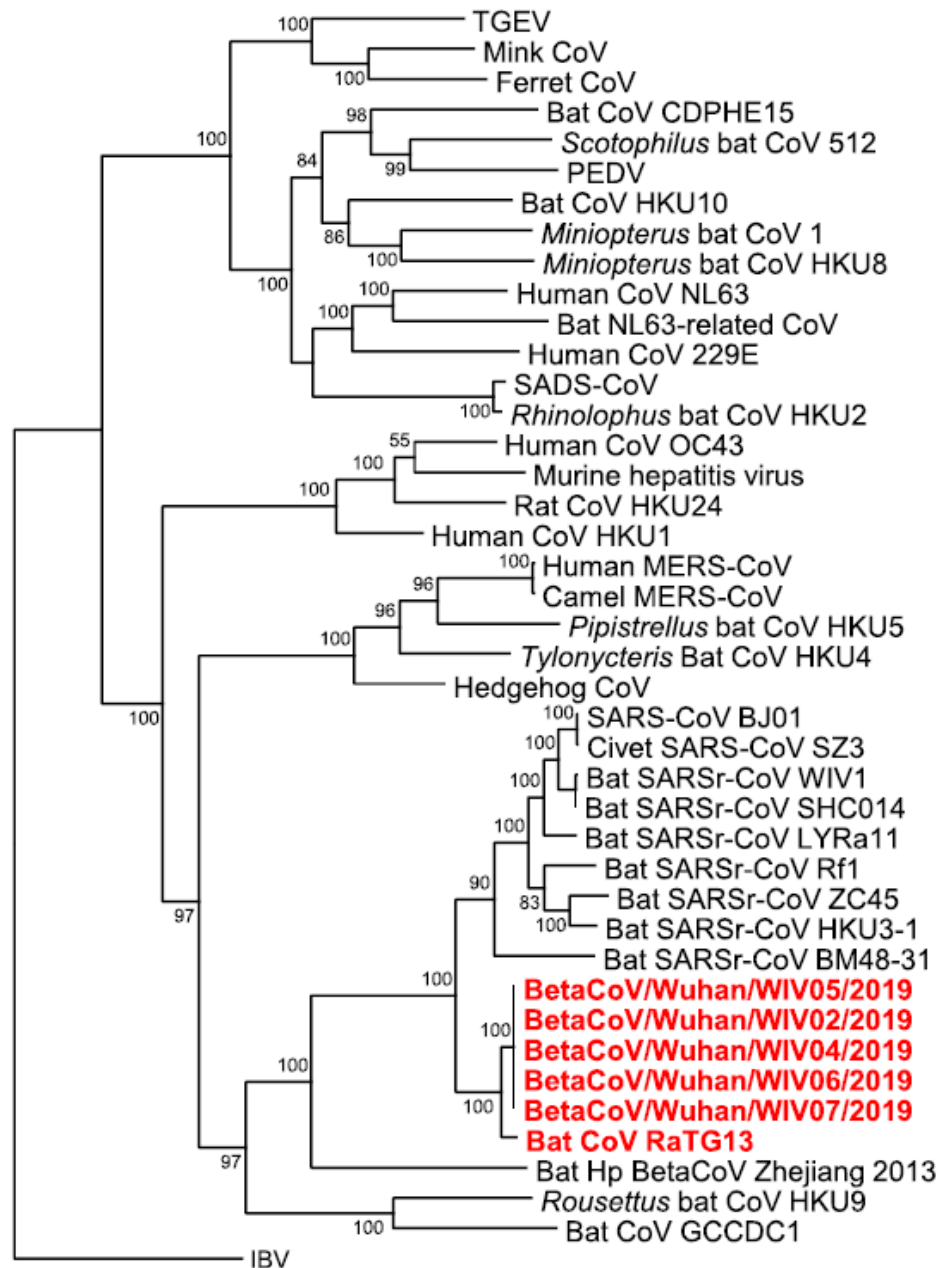


Figure 2: Sequence identity between the consensus of 2019-nCoV and representative betacoronavirus genomes



相似度96.2%!



Alpha-CoV

Beta-CoV

Full-genome evolutionary analysis of the novel corona virus (2019-nCoV) rejects the hypothesis of emergence as a result of a recent recombination event.



?

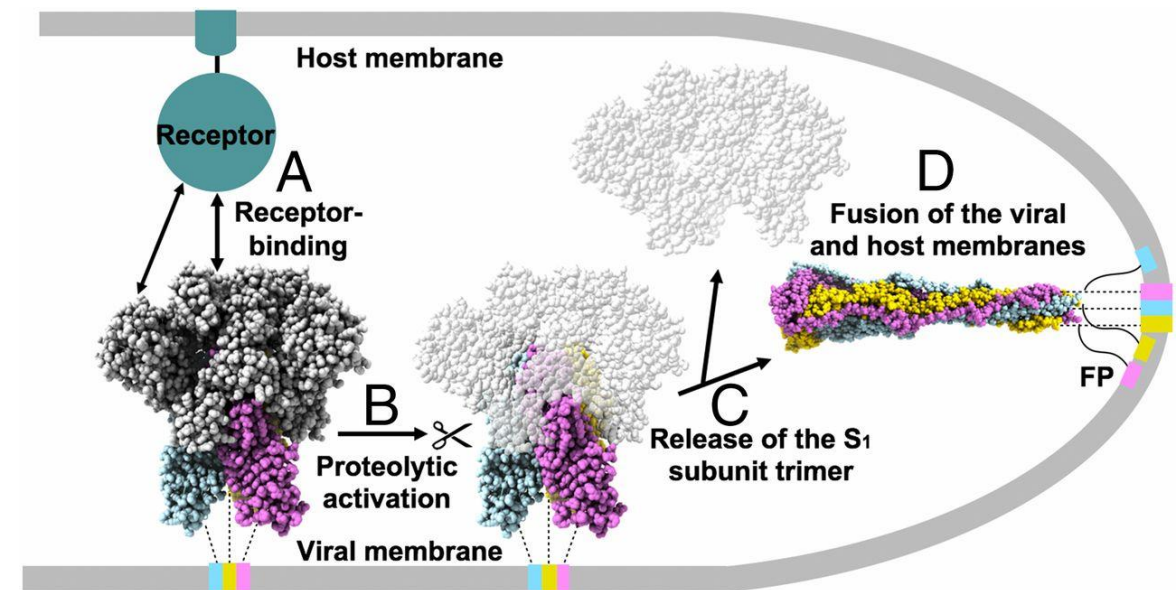
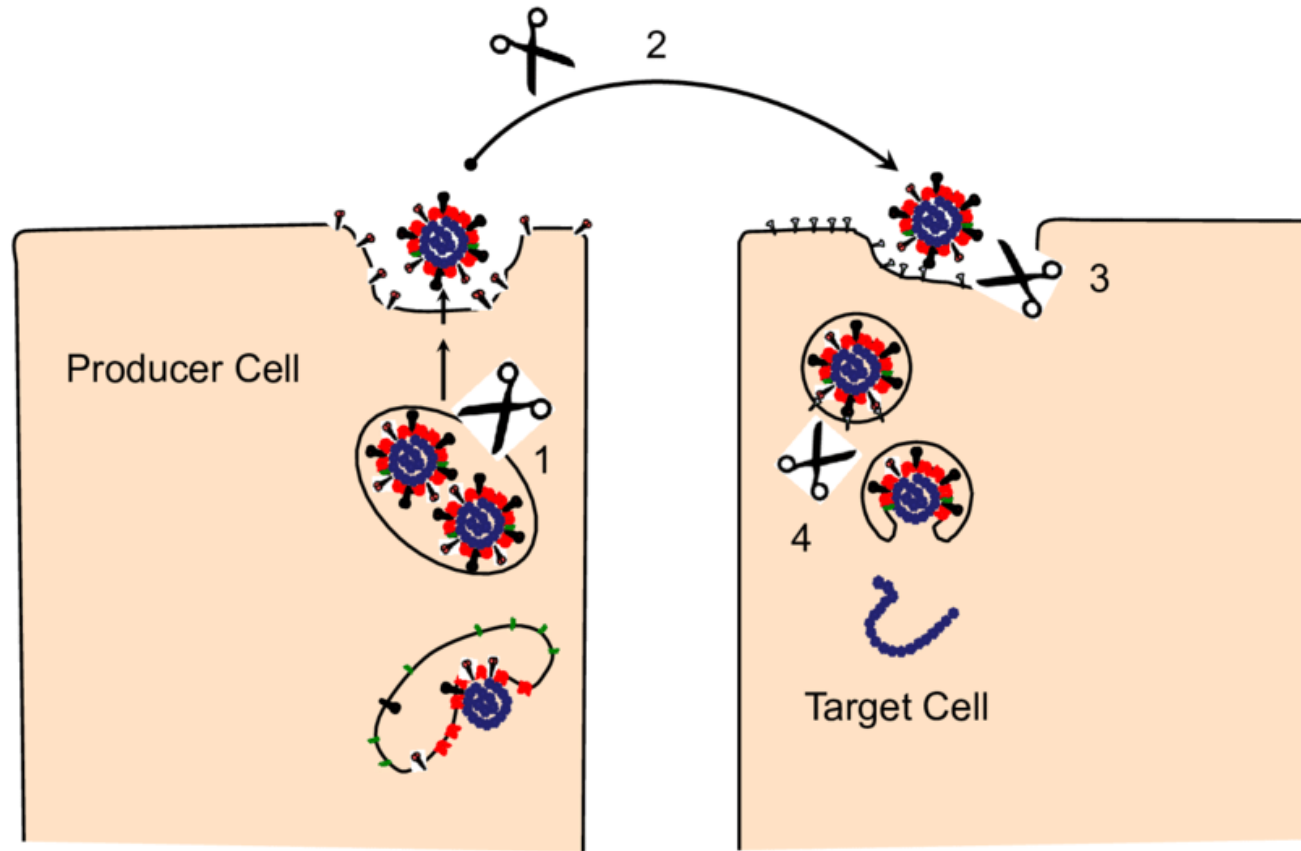


SARS-CoV-2

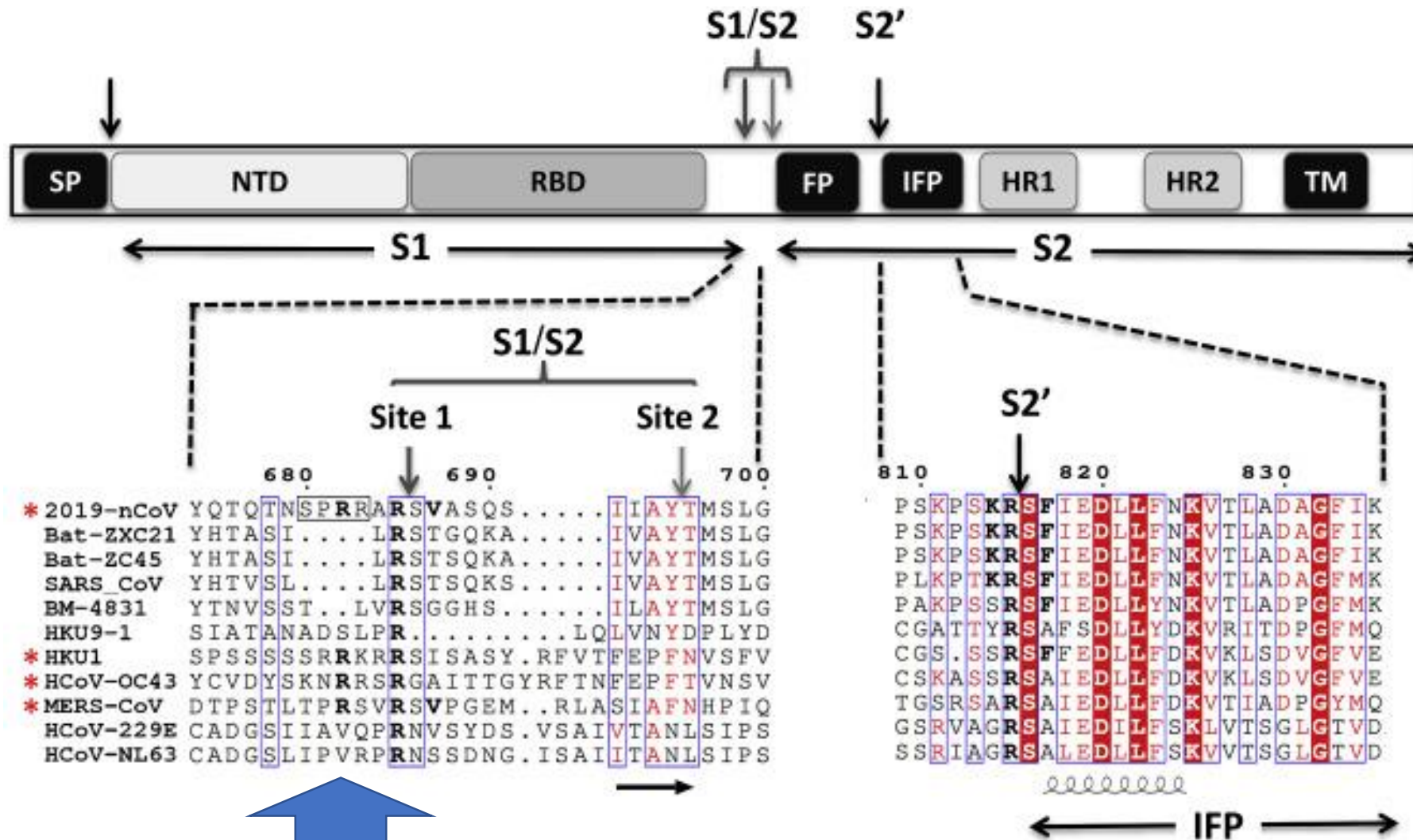
Extended Data Table 3 | Genomic comparison of 2019-nCoV WIV04 with SARS-CoVs and bat SARSr-CoVs

Sequence identities with SARS-CoVs & bat SARSr-CoVs (nt/aa %)												
	Full-length genome	ORF1a	ORF1b	S	ORF3a	E	M	ORF6	ORF7a	ORF7b	ORF8	N
SARS-CoV GZ02	79.6	76.0/80.9	86.2/95.7	73.4/77.0	75.6/73.4	94.7/96.0	85.4/90.5	76.3/68.9	82.8/86.0	84.8/81.4	52.0/31.6	87.7/91.2
SARS-CoV BJ01	79.6	76.0/80.8	86.2/95.7	73.4/76.9	75.3/72.6	94.7/96.0	85.6/90.5	75.8/67.2	82.8/86.0	84.8/81.4	51.1/-	88.8/91.2
SARS-CoV Tor2	79.6	76.0/80.9	86.2/95.8	73.4/76.7	75.4/72.6	94.7/96.0	85.6/90.5	76.3/68.9	82.8/86.0	84.8/81.4	51.1/-	88.8/91.2
SARS-CoV SZ3	79.6	76.0/81.0	86.2/95.8	73.4/76.9	75.4/72.6	94.7/96.0	85.3/90.0	76.3/68.9	82.8/86.0	84.8/81.4	52.3/31.6	88.8/91.2
SARS-CoV PC4-227	79.5	76.0/80.8	86.1/95.6	73.4/76.7	75.5/72.6	94.7/96.0	85.1/90.0	75.8/68.9	82.8/86.0	84.8/81.4	52.3/-	88.5/90.7
Bat SARSr-CoV RaTG13	96.2	96.0/98.0	97.3/99.3	93.1/97.7	96.3/97.8	99.6/100	95.5/99.6	98.4/100	95.6/97.5	99.2/97.7	97.0/95.0	96.9/99.0
Bat SARSr-CoV WIV1	79.7	76.0/80.7	85.9/95.8	73.4/77.6	76.1/74.5	95.6/96.0	84.8/90.0	78.0/73.8	85.0/88.4	85.6/83.7	65.8/57.9	88.5/90.9
Bat SARSr-CoV WIV16	79.7	75.9/81.0	86.1/95.6	73.1/77.8	76.1/74.5	95.6/96.0	84.8/90.0	77.4/72.1	85.0/88.4	85.6/83.7	65.3/57.9	88.6/90.9
Bat SARSr-CoV SHC014	79.6	75.9/80.9	85.9/95.8	73.3/77.7	76.1/74.5	95.6/96.0	84.8/90.0	78.0/70.5	84.4/88.4	85.6/83.7	65.8/58.7	88.6/90.9
Bat SARSr-CoV Rs4231	79.7	76.0/81.0	86.2/95.8	72.9/77.5	75.8/74.1	94.3/94.7	84.4/90.0	76.9/67.2	85.0/88.4	85.6/83.7	65.3/57.9	88.8/91.4
Bat SARSr-CoV YNLF31C	79.0	75.7/80.6	85.8/95.7	71.4/75.5	75.0/71.2	94.3/96.0	84.7/89.6	76.9/70.5	83.1/87.6	86.4/83.7	50.3/31.3	88.3/90.5
Bat SARSr-CoV LYRa11	79.6	75.8/80.6	85.7/95.6	73.9/77.3	77.2/76.3	94.7/94.7	85.1/90.0	78.5/70.5	82.0/85.1	81.1/81.4	66.7/57.9	89.0/91.6
Bat SARSr-CoV ZC45	88.1	91.0/95.7	86.1/96.0	77.8/82.3	87.8/90.9	98.7/100	93.4/98.6	95.2/93.4	88.8/87.6	94.7/93.0	88.5/94.2	91.1/94.3
Bat SARSr-CoV ZXC21	88.0	90.9/95.7	86.2/95.8	77.1/81.7	88.9/92.0	98.7/100	93.4/98.6	95.2/93.4	89.1/88.4	95.5/93.0	88.5/94.2	91.2/94.3
Bat SARSr-CoV HuB2013	79.6	76.3/81.2	85.3/95.7	73.1/76.8	75.4/75.5	95.2/94.7	85.3/91.0	76.3/68.9	84.2/87.6	85.6/83.7	62.0/49.6	88.9/91.6
Bat SARSr-CoV GX2013	79.1	75.9/80.8	86.0/95.9	73.1/77.1	75.6/73.0	94.7/96.0	84.8/91.4	77.4/68.9	85.0/86.8	84.1/79.1	51.4/31.6	87.9/90.2
Bat SARSr-CoV SX2013	78.9	76.2/80.6	85.1/95.5	71.2/75.5	74.7/71.2	94.3/93.3	83.0/89.6	77.4/68.9	84.2/86.8	85.6/83.7	49.7/30.4	86.9/90.2
Bat SARSr-CoV SC2018	79.4	75.8/80.7	85.5/95.2	72.7/76.4	75.0/71.2	94.3/96.0	84.7/90.0	80.0/71.8	85.2/87.6	84.8/83.7	66.1/55.4	88.2/91.2
Bat SARSr-CoV Rs672	79.6	76.0/80.9	85.9/95.8	72.8/76.2	75.2/71.9	95.2/96.0	84.8/89.6	78.5/70.5	84.7/88.4	85.6/83.7	65.8/58.7	87.9/91.2
Bat SARSr-CoV Rp3	79.5	75.9/80.5	86.0/95.7	73.1/77.2	74.9/74.8	95.2/96.0	85.1/90.0	76.9/68.9	83.9/89.3	84.8/83.7	66.4/56.2	88.4/90.7
Bat SARSr-CoV Rfl	78.8	76.2/80.6	84.8/95.3	71.1/75.7	74.3/69.0	94.3/94.7	83.3/89.6	79.0/68.9	84.2/86.8	84.1/83.7	50.6/31.3	86.8/89.5
Bat SARSr-CoV HKU3-1	79.4	76.1/80.9	84.9/95.1	73.4/77.9	75.8/73.4	95.2/96.0	84.7/91.0	75.3/67.2	85.0/89.3	84.1/79.1	66.4/57.0	88.3/90.0

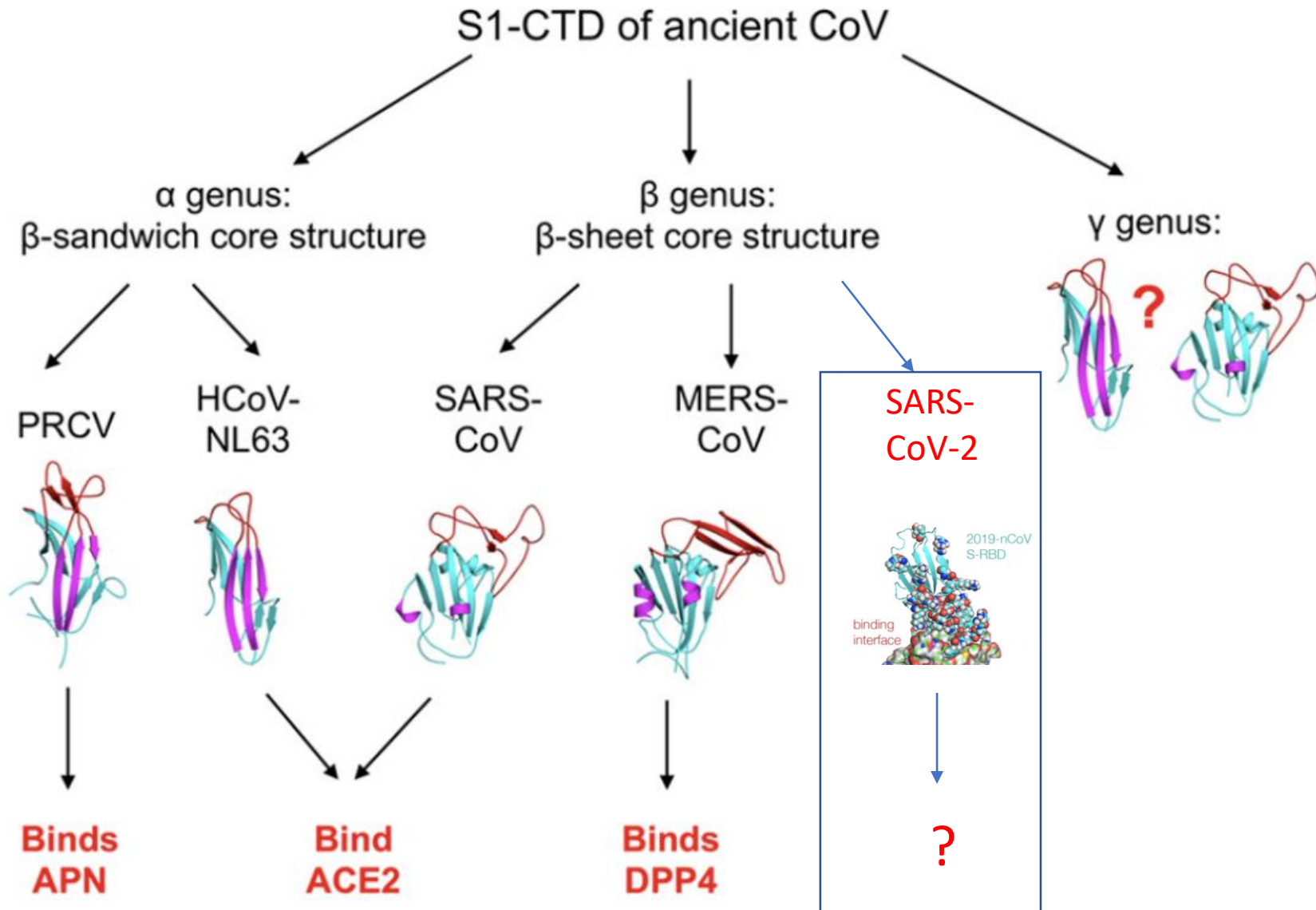
Class I viral fusion: influenza virus, coronavirus, and HIV-1



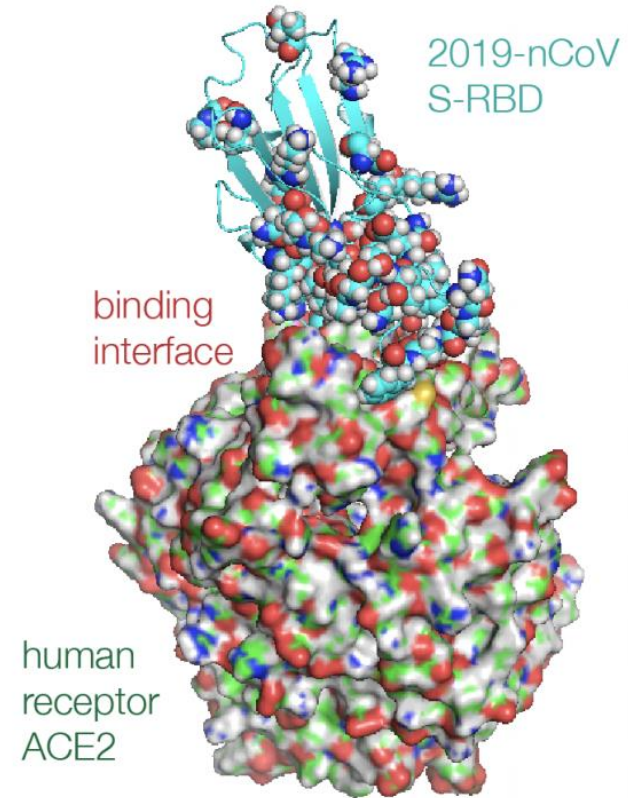
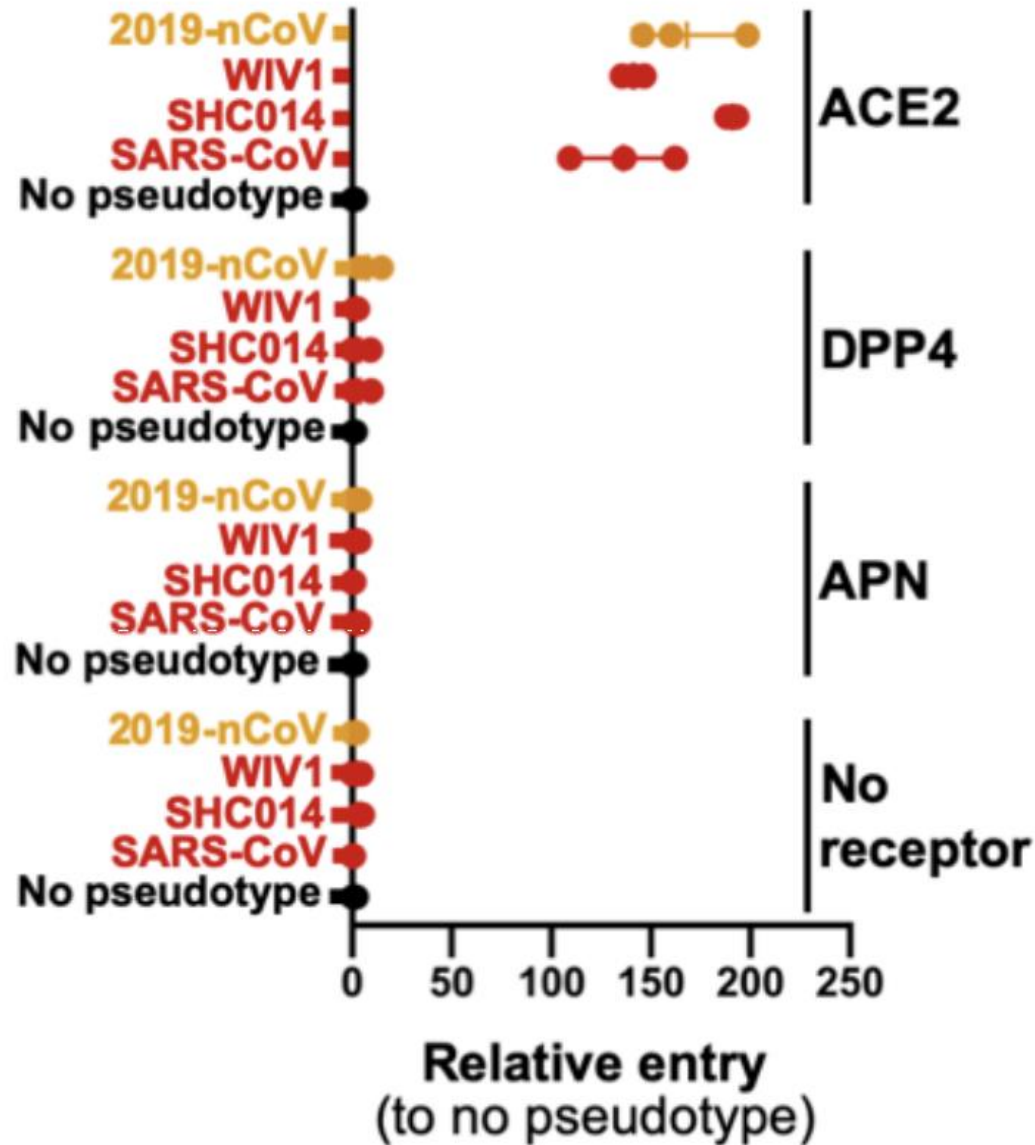
The S protein contains two functional domains: a receptor binding domain, and a second domain which contains sequences that mediate fusion of the viral and cell membranes.



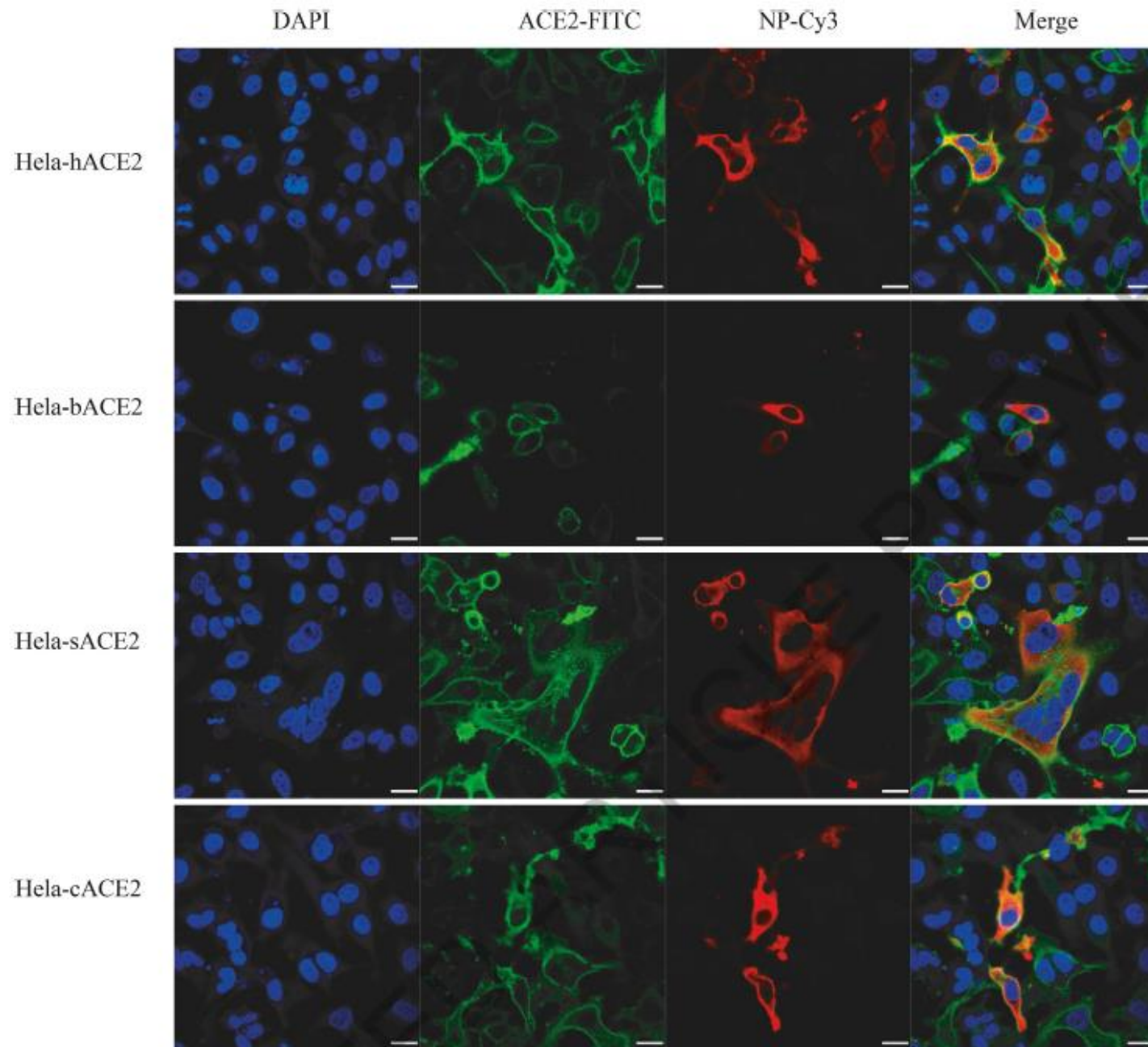
2019-nCoV S-protein sequence has a specific **furin-like cleavage site** absent in lineage b CoV including SARS-CoV sequences.



SARS spike with 2019-nCoV RBD



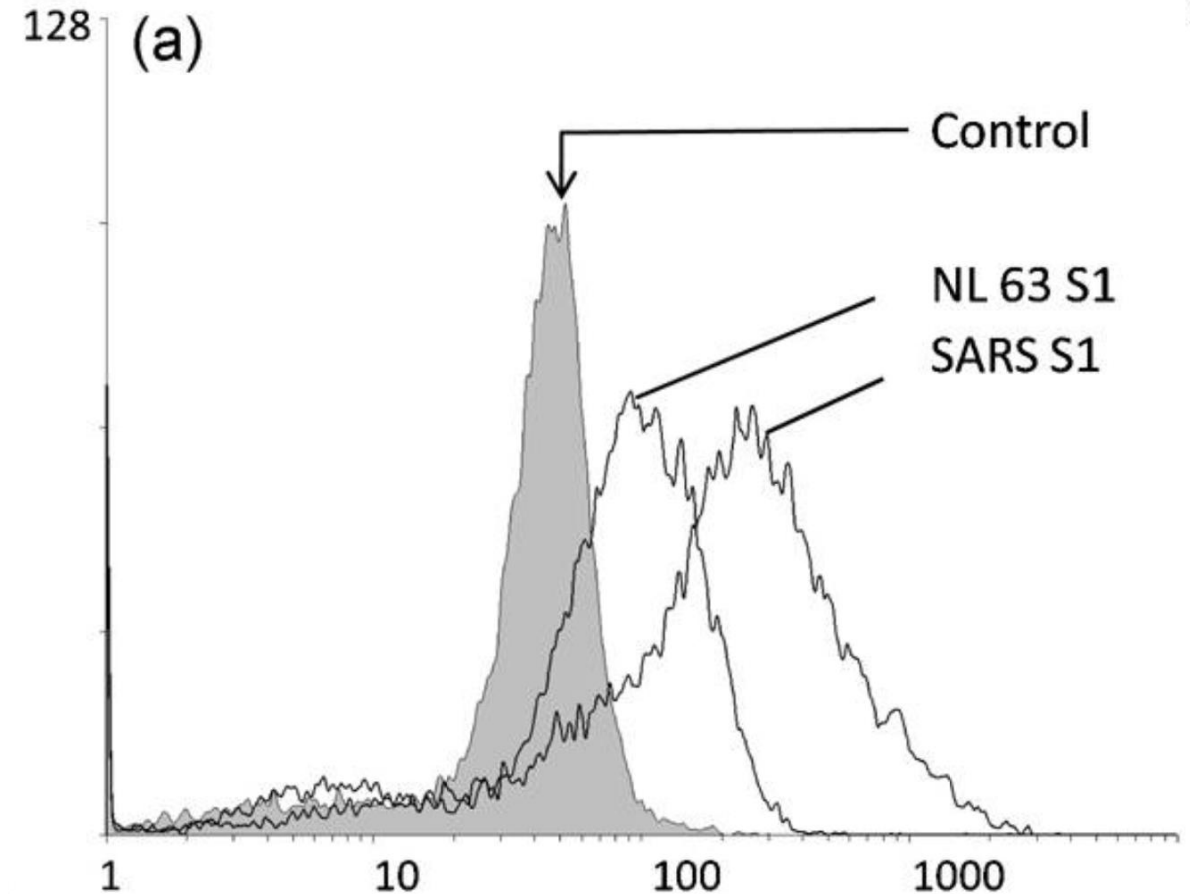
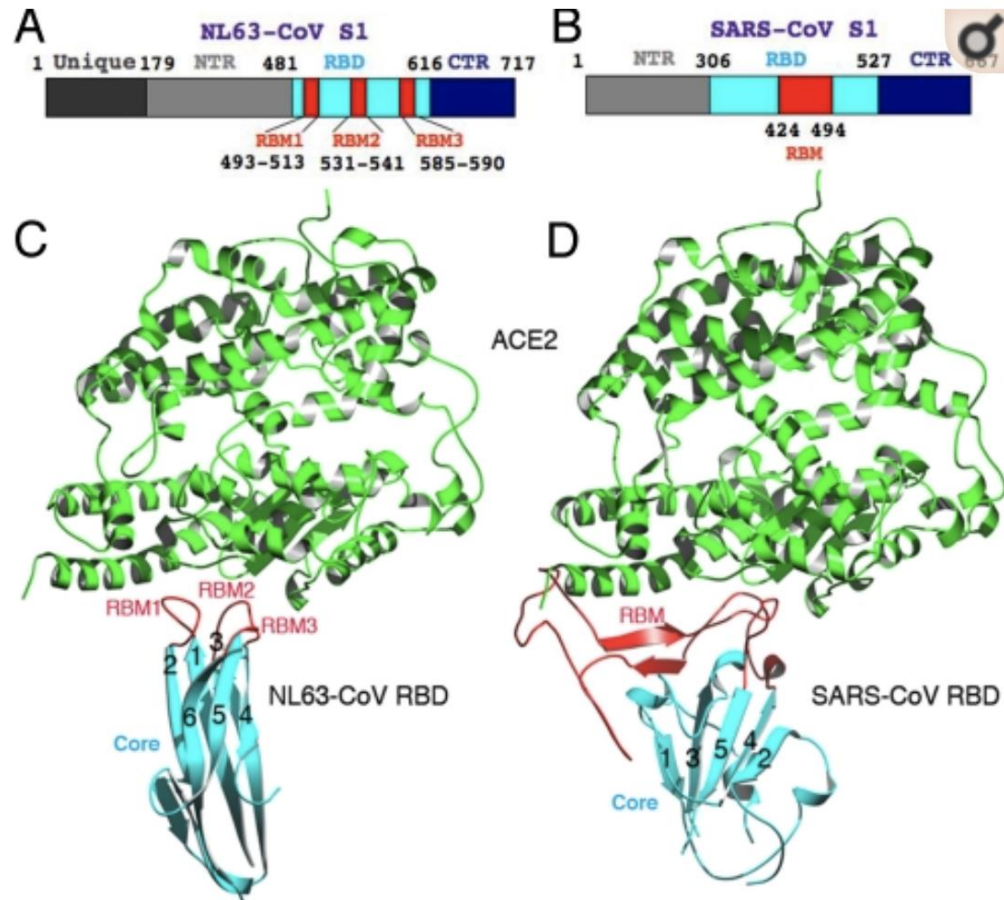
Functional assessment of cell entry and receptor usage for lineage B β -coronaviruses, including 2019-nCoV.



SARS-COV-2 is able to use all but mouse ACE2 as an entry receptor (human, bat, swine, and civet), indicating which is likely the cell receptor of SARS-COV-2.

Zhou, P., Yang, X., Wang, X. *et al.* *Nature* (2020).

A lower-affinity interaction with ACE-2 might partly explain the different pathological consequences of infection by SARS-CoV and NL63.



[J Gen Virol.](#) 2008 Nov; 89(Pt 11): 2741–2745.

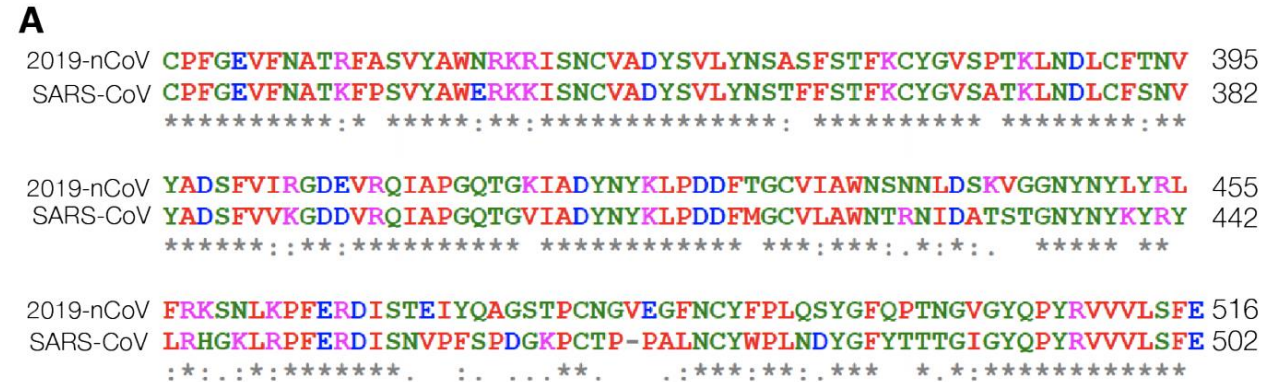
[Proc Natl Acad Sci U S A.](#) 2009 Nov 24; 106(47): 19970–19974.

The binding strength of 2019-nCoV S-RBD vs. SARS-CoV S-RBD to ACE2:

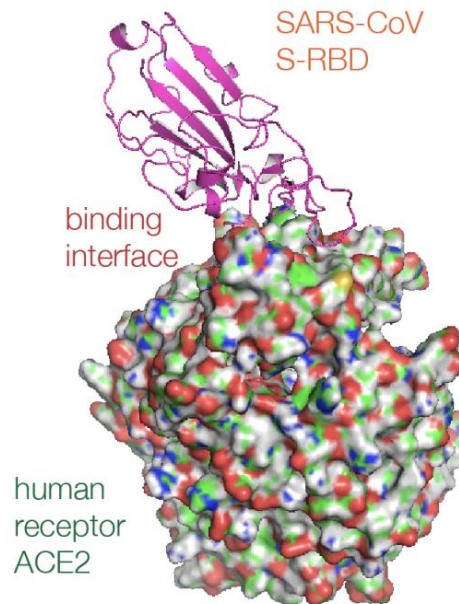
- ~73% (Qiang Huang et al.)
- ~65% (Xu et al.)
- 或許能解釋為什麼 COVID19的症狀較SARS更偏輕症，和NL63類似。

$$\langle \Delta G^{SARS} \rangle \approx -36.6 \text{ kcal} \cdot \text{mol}^{-1}$$

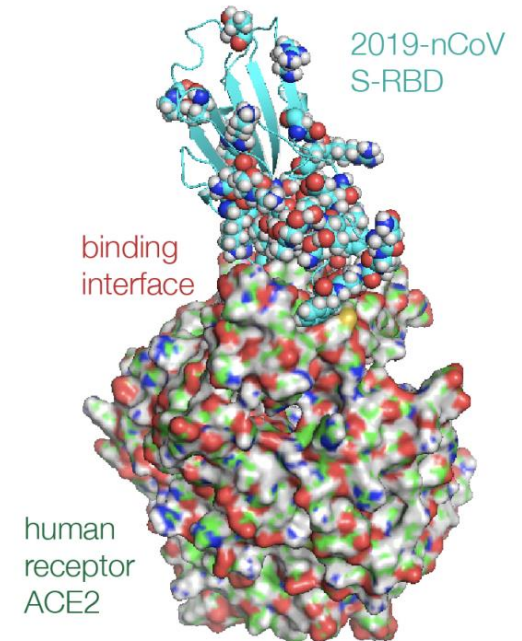
$$\langle \Delta G^{2019} \rangle \approx -27.2 \text{ kcal} \cdot \text{mol}^{-1}$$



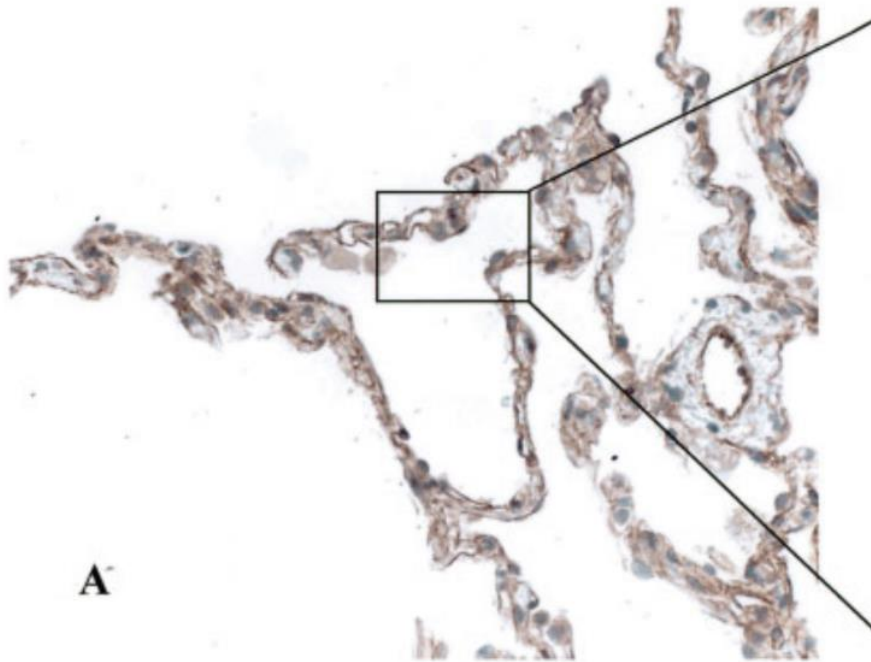
B



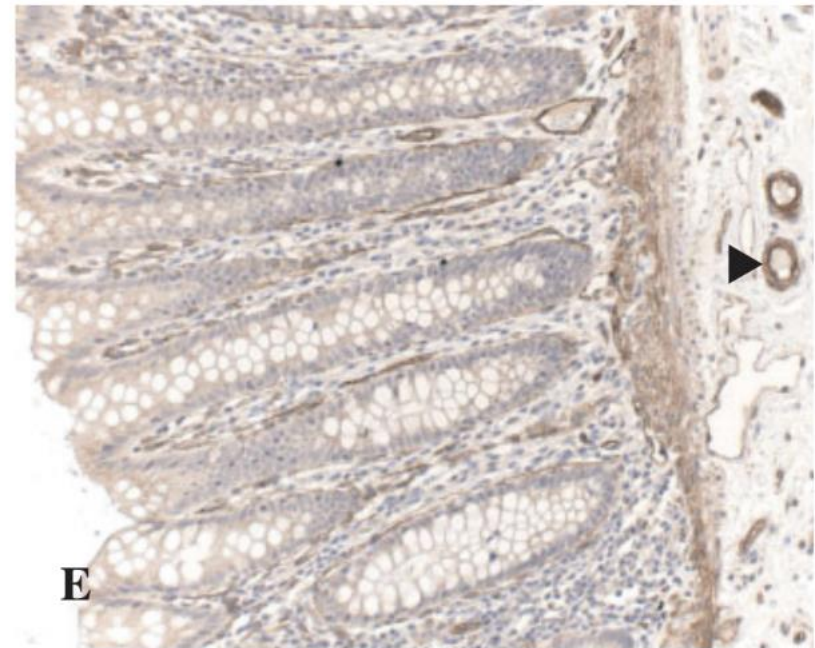
C



ACE2不僅在肺部細胞存在，在腸胃道中的血管內皮細胞與平滑肌細胞也都存在。

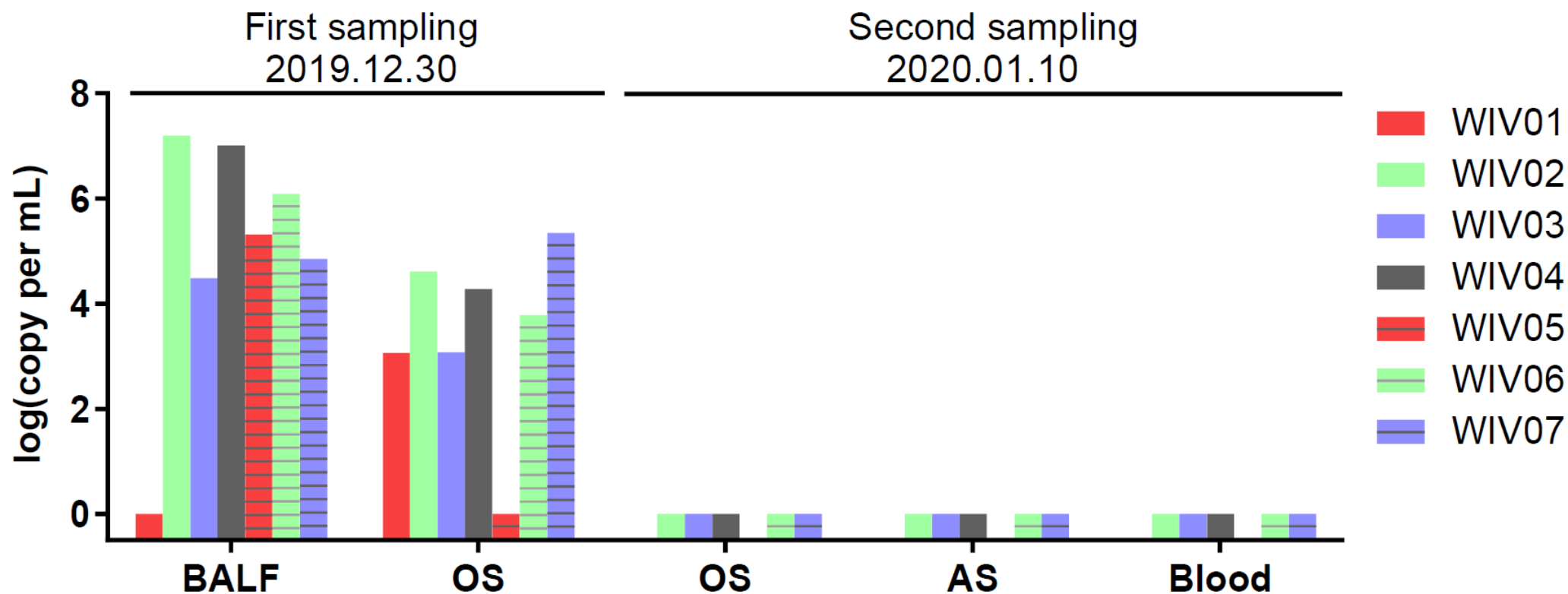


Positive staining for ACE2 is clearly present on alveolar epithelial cells and capillary endothelium.



In the colon, ACE2 staining is present in endothelium and vascular smooth muscle cells from the blood vessels (arrow-head) and in the muscular layers.

在肛門拭子可找到病毒RNA，不等於可以糞口傳染



Molecular detection of 2019-nCoV in seven patients during two times of sampling.
BALF, bronchoalveolar lavage fluid; OS, oral swab; AS, anal swab.

Concentration and detection of SARS coronavirus in sewage from Xiao Tang Shan Hospital and the 309th Hospital

Xiao Tang Shan Hospital
Zhong Wei
Fa

Journal of Clinical Virology 48 (2010) 27–30

Contents lists available at ScienceDirect



ELSEVIER

Journal of Clinical Virology

journal homepage: www.elsevier.com/locate/jcv



Detection of human coronaviruses in children with acute gastroenteritis

Minna Risku

Enteric Involvement of Severe Acute Respiratory Syndrome-Associated Coronavirus Infection

WAI K. LEUNG,* KA-FAI TO,† PAUL K. S. CHAN,§ HENRY L. Y. CHAN,* ALAN K. L. WU,* NELSON LEE,* KWOK Y. YUEN,|| and JOSEPH J. Y. SUNG*

Departments of *Medicine and Therapeutics, †Anatomical and Cellular Pathology, and §Microbiology, The Chinese University of Hong Kong, Prince of Wales Hospital, Shatin, Hong Kong; and ||Department of Microbiology, University of Hong Kong, Hong Kong

Clinical characteristics and intrauterine vertical transmission potential of COVID-19 infection in nine pregnant women: a retrospective review of medical records

Huijun Chen, Juanjuan Guo*, Chen Wang*, Fan Luo, Xuechen Yu, Wei Zhang, Jiafu Li, Dongchi Zhao, Dan Xu, Qing Gong, Jing Liao, Huixia Yang, Wei Hou, Yuanzhen Zhang*

Amniotic fluid, cord blood, neonatal throat swab, and breastmilk samples from six patients were tested for SARS-CoV-2, and all samples tested negative for the virus.

→目前沒有證據顯示有垂直傳染的可能。

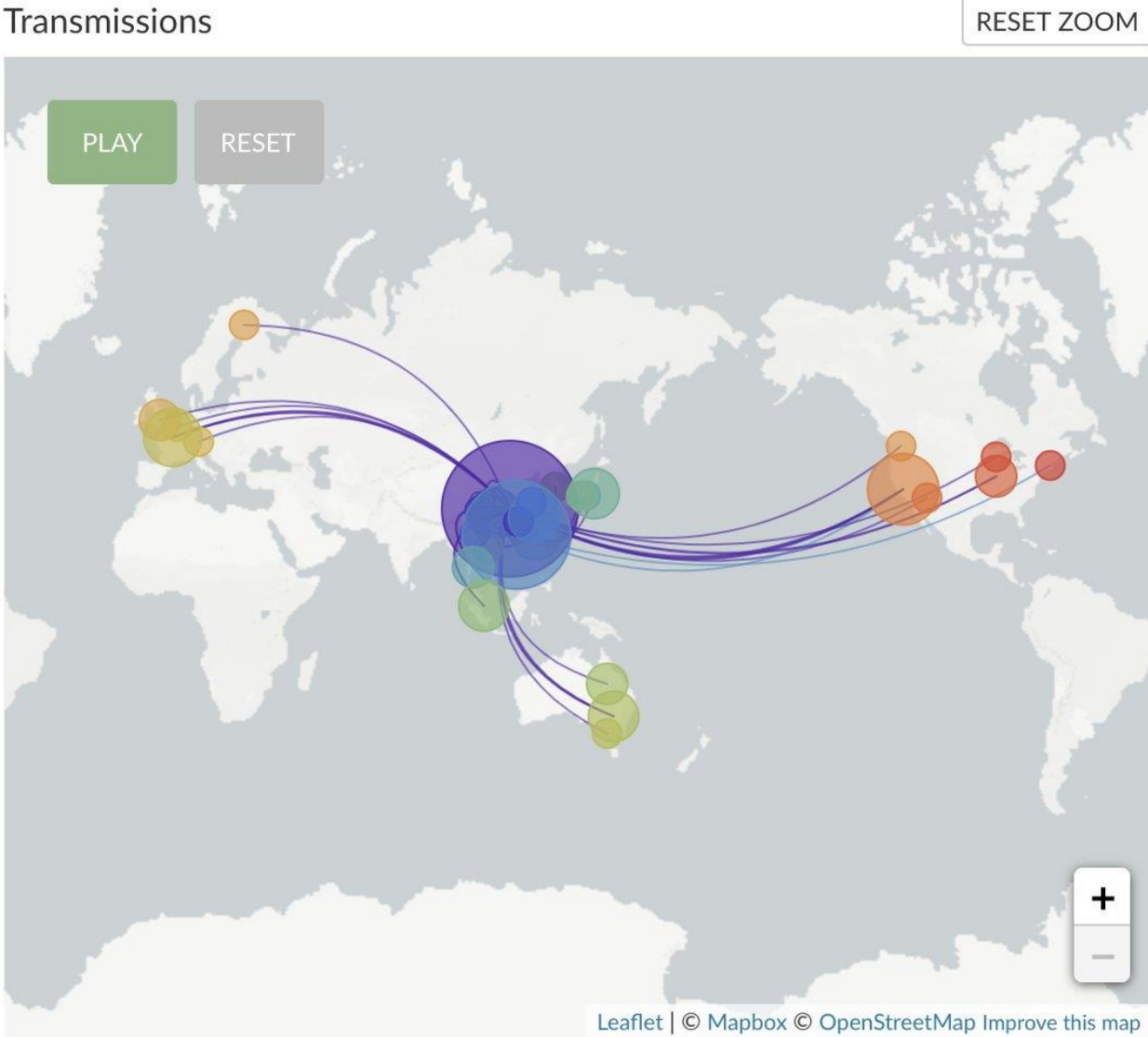
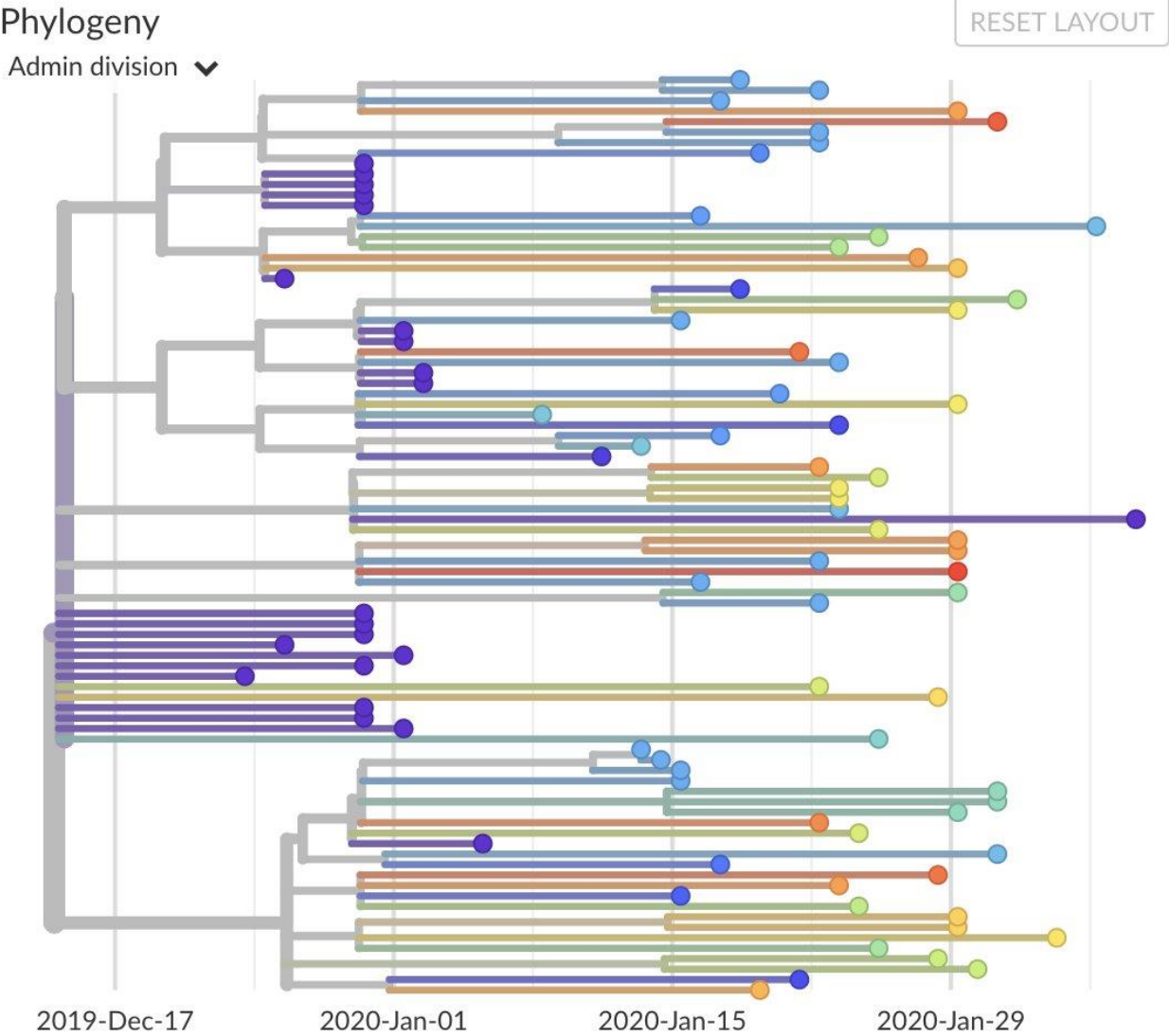
Outline

1. Introduction to coronavirus (CoV)
2. Virology of SARS-CoV-2
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Genomic epidemiology of novel coronavirus (nCoV)

Built with github.com/nextstrain/ncov using data from .

Showing 89 of 89 genomes sampled between Dec 2019 and Feb 2020.

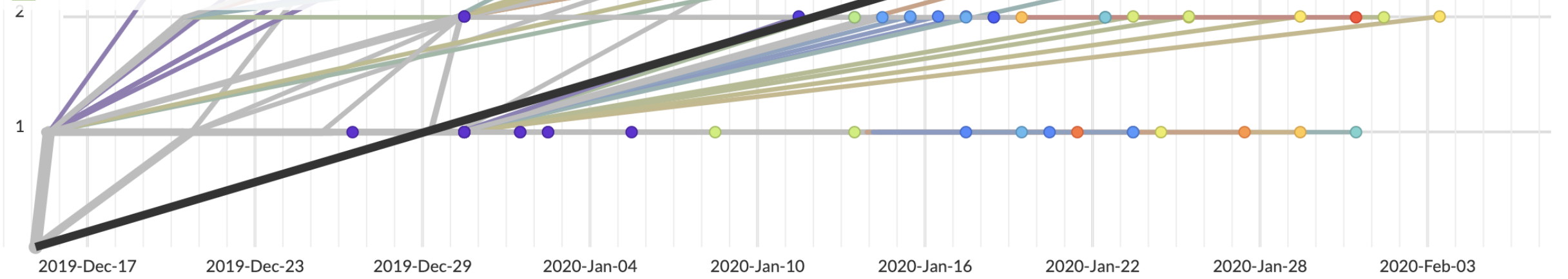


Phylogeny

RESET LAYOUT

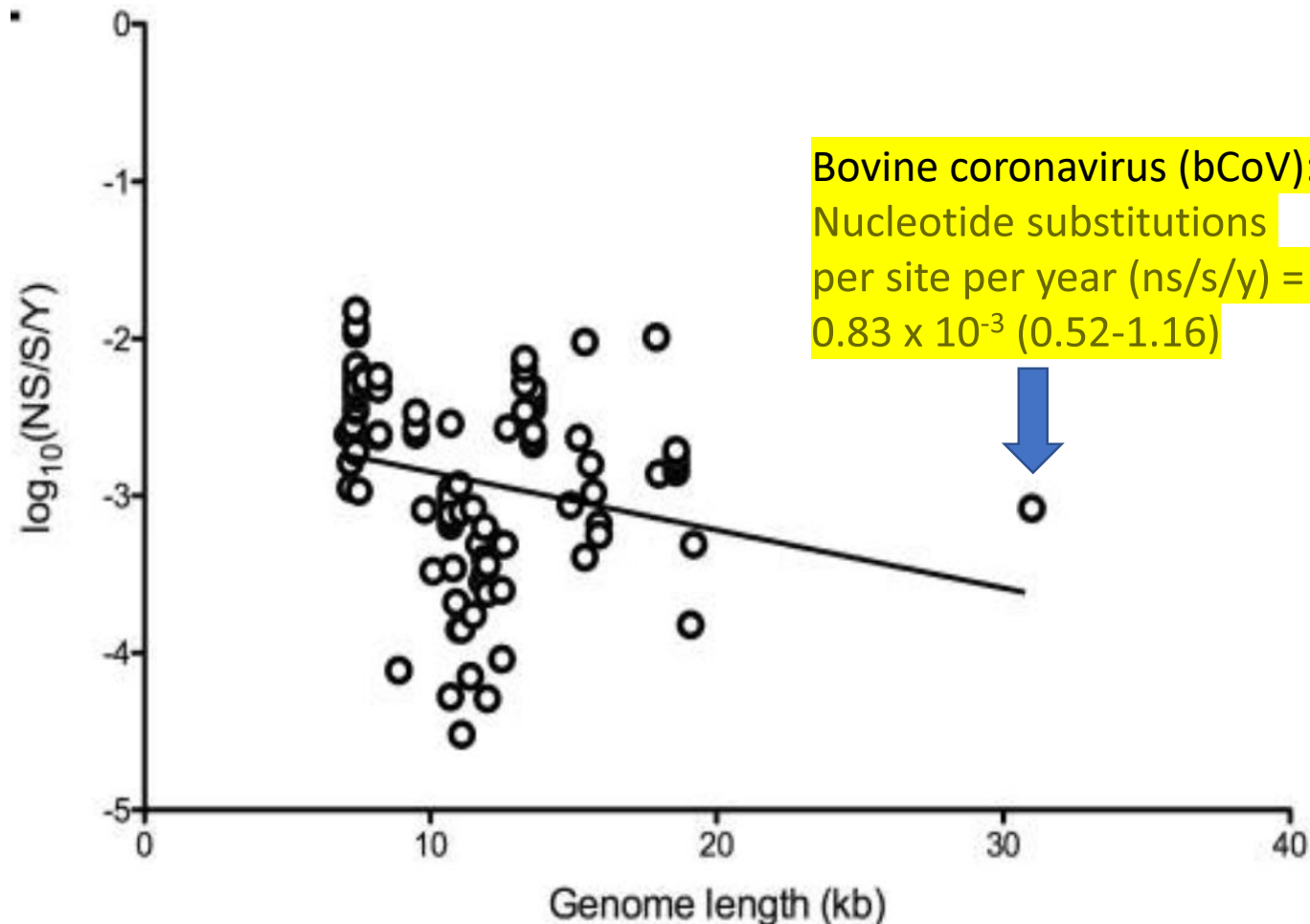
Location ^

- Wuhan
- Pingxiang
- Zhongxian
- Yongchuan
- Chongqing
- Chengdu
- Kunming
- Hangzhou
- Guangdong
- Shenzhen
- Zhuhai
- Huaian
- Guangzhou
- Foshan
- Taipei
- Kaohsiung
- Aichi
- Tokyo
- Kyoto
- Gyeonggi
- Kathmandu

Thanh HoaBangkokSingaporeGold CoastSydneyClaytonParisLeuvenStarnbergEnglandRovaniemiSeattleOrange CountyLos AngelesCaliforniaPhoenixChicagoIllinoisWisconsinBoston

Cell Tropism Predicts Long-term Nucleotide Substitution Rates of Mammalian RNA Viruses

Allison L. Hicks, Siobain Duffy*



$$0.83 \times 10^{-3} \times 30000 = 24.9 \text{ ns/s/y}$$

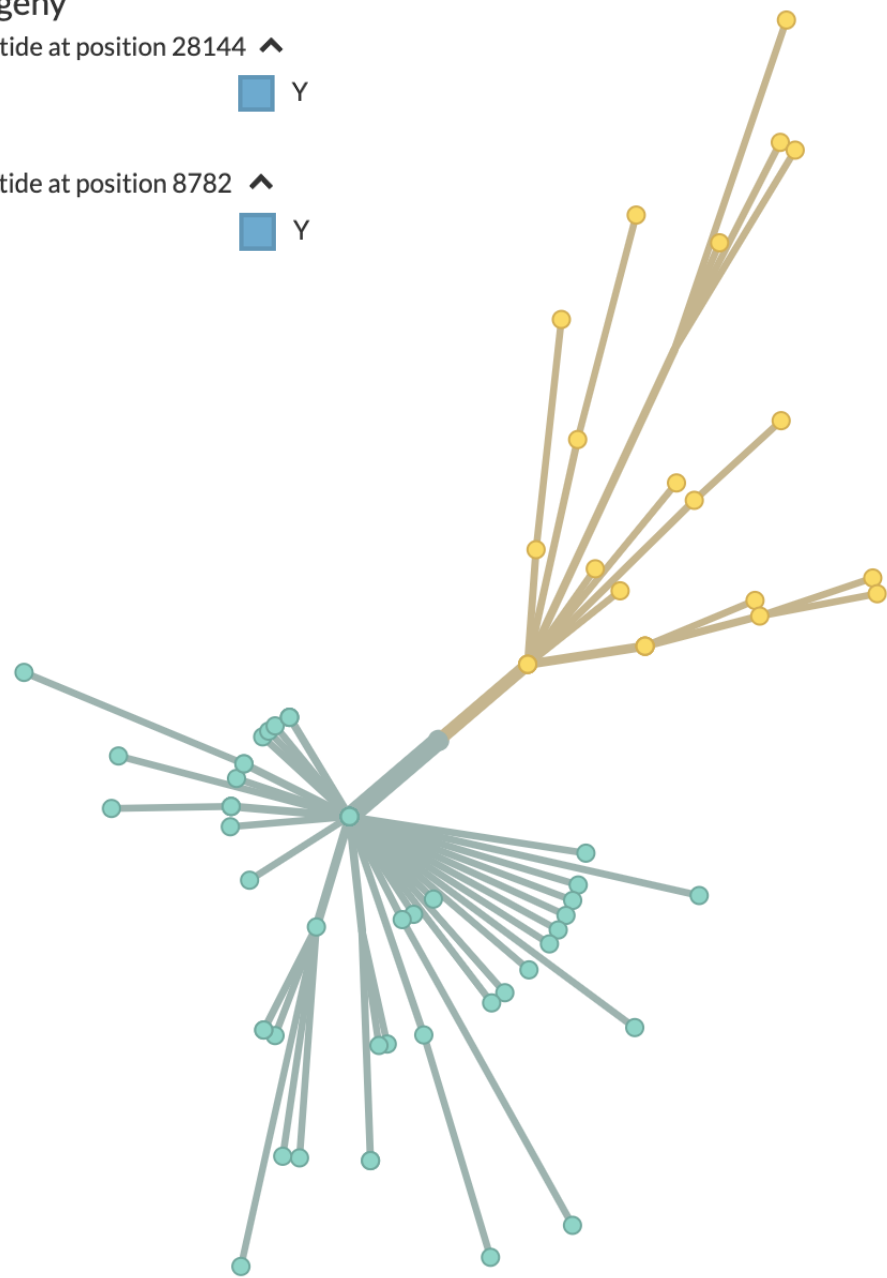
和目前SARS-CoV-2的突變速度相近。

Phylogeny

Nucleotide at position 28144 ^

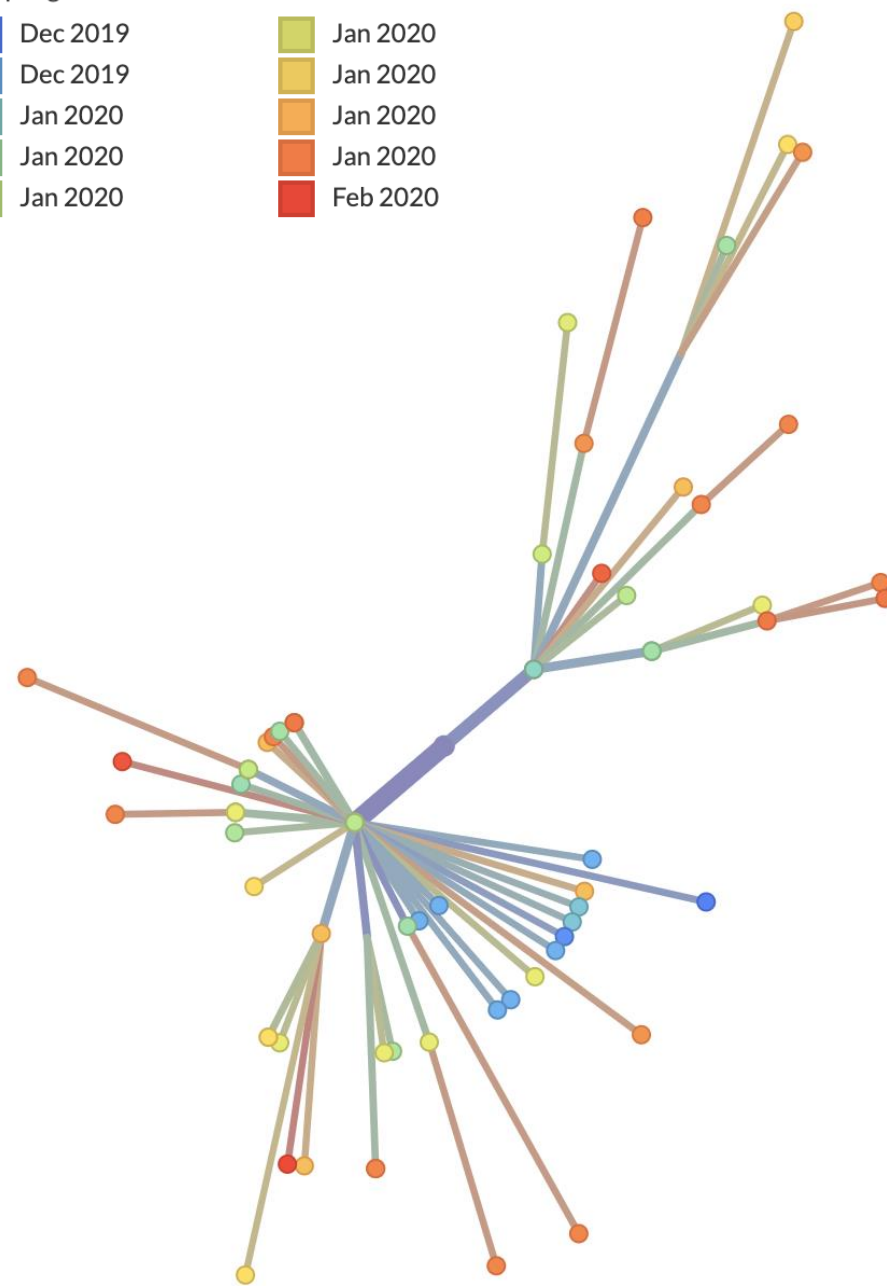
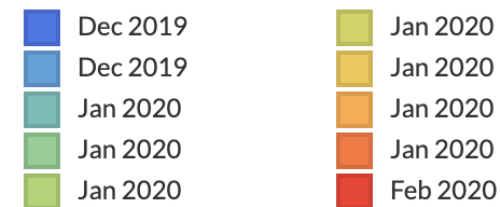


Nucleotide at position 8782 ^



Phylogeny

Sampling date ^



Phylogeny

Genotype at ORF8 site 84 ^



L (Leucine)



X

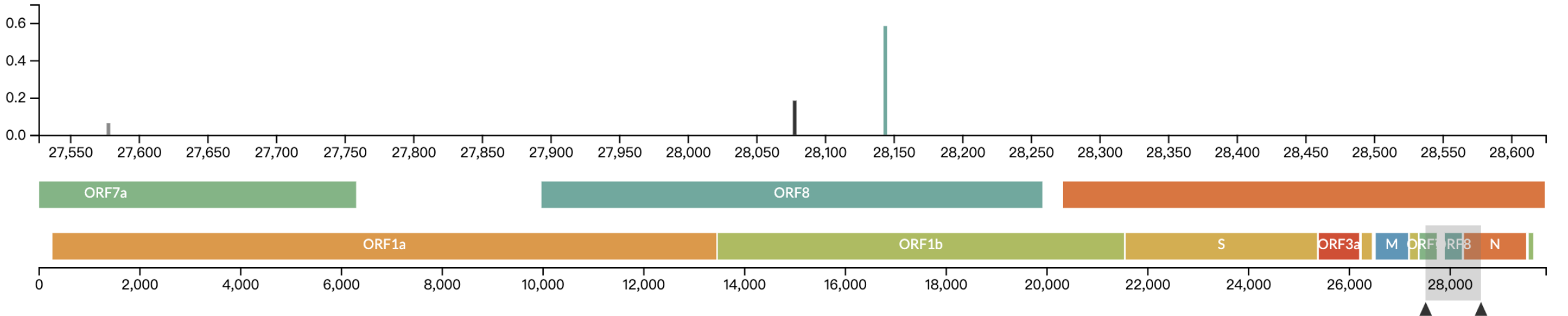


S (Serine)



ENTROPY EVENTS AA NT

Diversity



Outline

1. Introduction to coronavirus (CoV)
2. Virology of SARS-CoV-2
3. Genomic epidemiology of SARS-CoV-2
- 4. Clinical manifestations of COVID19**
5. Possible explanations for some crucial questions
6. Future perspectives

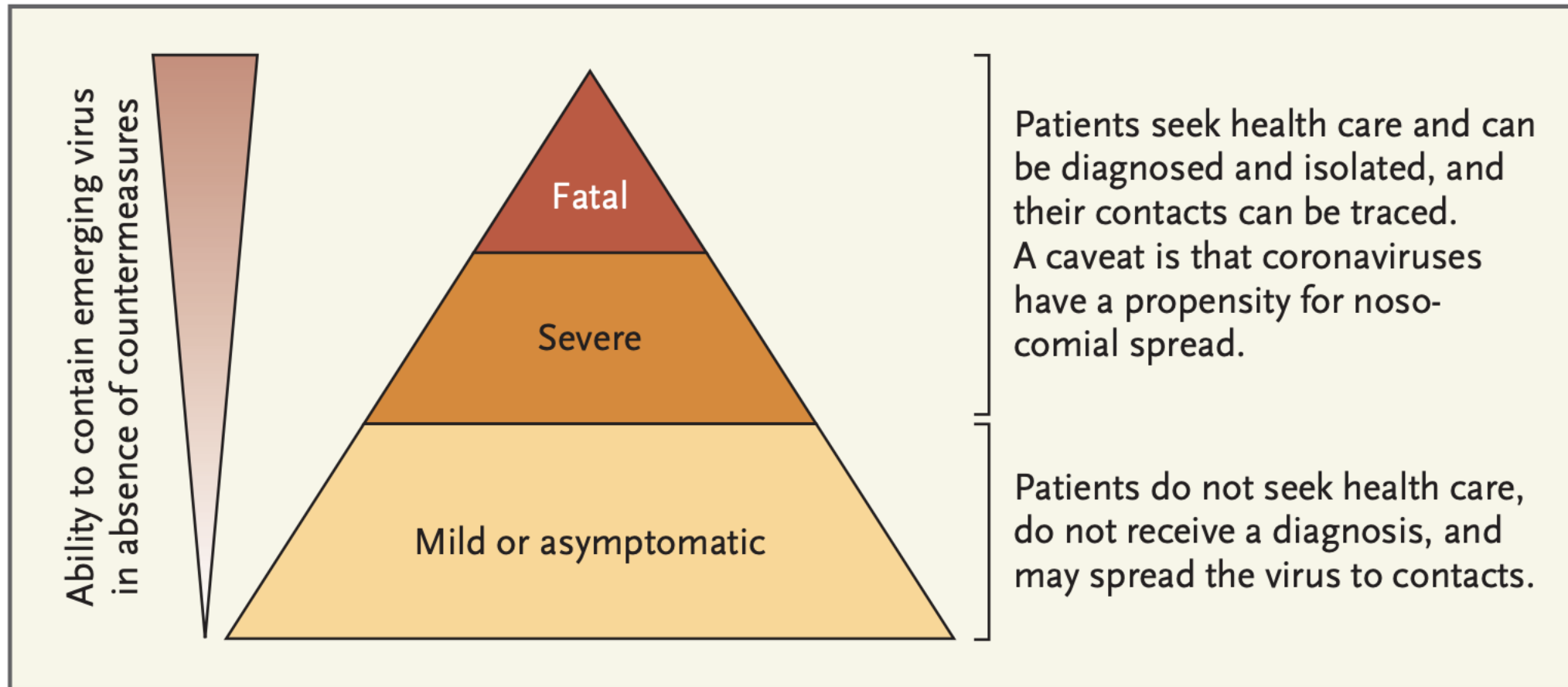


Figure 1. Surveillance Pyramid and Its Relation to Outbreak Containment.

The proportion of mild and asymptomatic cases versus severe and fatal cases is currently unknown for 2019-nCoV — a knowledge gap that hampers realistic assessment of the virus's epidemic potential and complicates the outbreak response.

華南市場41例新型冠狀病毒患者



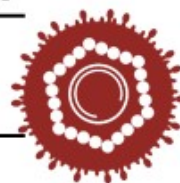
患者背景	所有病人 (N=41)	重症ICU (N=13)	輕症非ICU (N=28)
	中位數 (四分位距) / 比例		
年齡 (歲)	49 (41-58)	49 (41-61)	49 (41-57.5)
男性	73%	85%	68%
體溫	70.6%	70%	71.4%
<37.3	2%	0%	4%
37.3-38.0	20%	23%	18%
> 38.0	78%	77%	78%
咳嗽	76%	85%	71%
有痰	28%	38%	23%
喘	55%	92%	37%
肌肉痠痛或疲倦	44%	54%	71%
共病症	32%	38%	29%

資料來源：Huang C, Wang Y, Li X, et al. Lancet 2020; published online Jan 24.

胸腔重症 蘇一峰醫師

武漢金銀潭醫院99例新型冠狀病毒患者

患者背景	所有病人 (N=99)	患者背景	所有病人 (N=99)
年齡 (平均, 歲)	55.5 (21-82)	胸痛	2%
男性	68%	腹瀉	2%
發燒	83%	噁心嘔吐	1%
咳嗽	82%	慢性病	51%
喘	31%	心血管腦血管疾病	40%
發燒+咳嗽+喘	15%	消化道疾病	11%
肌肉痠痛	11%	內分泌疾病	13%
意識混亂	9%	癌症	1%
喉嚨痛	5%	神經系統	1%
流鼻水	4%	呼吸道	1%



資料來源：Chen N, et al. Lancet 2020; published online Jan 29.

胸腔重症 蘇一峰醫師

138 patients

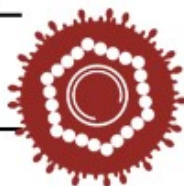
Table 1. Baseline Characteristics of Patients Infected With 2019-nCoV

	No. (%)			P Value ^a
	Total (N = 138)	ICU (n = 36)	Non-ICU (n = 102)	
Age, median (IQR), y	56 (42-68)	66 (57-78)	51 (37-62)	<.001
Sex				
Female	63 (45.7)	14 (38.9)	51 (37-62)	.34
Male	75 (54.3)	22 (61.1)	53 (52.0)	
Huanan Seafood Wholesale Market exposure	12 (8.7)	5 (13.9)	7 (6.9)	.30
Infected				
Hospitalized patients	17 (12.3)	9 (25.0)	8 (7.8)	.02
Medical staff	40 (29)	1 (2.8)	39 (38.2)	<.001
Comorbidities	64 (46.4)	26 (72.2)	38 (37.3)	<.001
Hypertension	43 (31.2)	21 (58.3)	22 (21.6)	<.001
Cardiovascular disease	20 (14.5)	9 (25.0)	11 (10.8)	.04
Diabetes	14 (10.1)	8 (22.2)	6 (5.9)	.009
Malignancy	10 (7.2)	4 (11.1)	6 (5.9)	.29
Cerebrovascular disease	7 (5.1)	6 (16.7)	1 (1.0)	.001
COPD	4 (2.9)	3 (8.3)	1 (1.0)	.054
Chronic kidney disease	4 (2.9)	2 (5.6)	2 (2.0)	.28
Chronic liver disease	4 (2.9)	0	4 (3.9)	.57
HIV infection	2 (1.4)	0	2 (2.0)	>.99
Signs and symptoms				
Fever	136 (98.6)	36 (100)	100 (98.0)	>.99
Fatigue	96 (69.6)	29 (80.6)	67 (65.7)	.10
Dry cough	82 (59.4)	21 (58.3)	61 (59.8)	.88
Anorexia	55 (39.9)	24 (66.7)	31 (30.4)	<.001
Myalgia	48 (34.8)	12 (33.3)	36 (35.3)	.83
Dyspnea	43 (31.2)	23 (63.9)	20 (19.6)	<.001
Expectoration	37 (26.8)	8 (22.2)	29 (28.4)	.35
Pharyngalgia	24 (17.4)	12 (33.3)	12 (11.8)	.003
Diarrhea	14 (10.1)	6 (16.7)	8 (7.8)	.20
Nausea	14 (10.1)	4 (11.1)	10 (9.8)	>.99
Dizziness	13 (9.4)	8 (22.2)	5 (4.9)	.007
Headache	9 (6.5)	3 (8.3)	6 (5.9)	.70
Vomiting	5 (3.6)	3 (8.3)	2 (2.0)	.13
Abdominal pain	3 (2.2)	3 (8.3)	0 (0)	.02
Onset of symptom to, median (IQR), d				
Hospital admission	7.0 (4.0-8.0)	8.0 (4.5-10.0)	6.0 (3.0-7.0)	.009
Dyspnea	5.0 (1.0-10.0)	6.5 (3.0-10.8)	2.5 (0.0-7.3)	.02
ARDS	8.0 (6.0-12.0)	8.0 (6.0-12.0)	8.0 (6.3-11.3)	.97
Heart rate, median (IQR), bpm	88 (78-97)	89 (81-101)	86 (77-96)	.14
Respiratory rate, median (IQR)	20 (19-21)	20 (16-25)	20 (19-21)	.57
Mean arterial pressure, median (IQR), mm Hg	90 (84-97)	91 (78-96)	90 (85-98)	.33

Abbreviations: ARDS, acute respiratory distress syndrome; bpm, beats per minute; COPD, chronic obstructive pulmonary disease; ICU, intensive care unit; IQR, interquartile range; 2019-nCoV, 2019 novel coronavirus.

^a P values indicate differences between ICU and non-ICU patients. P < .05 was considered statistically significant.

1,099例新型冠狀病毒急性呼吸道疾病

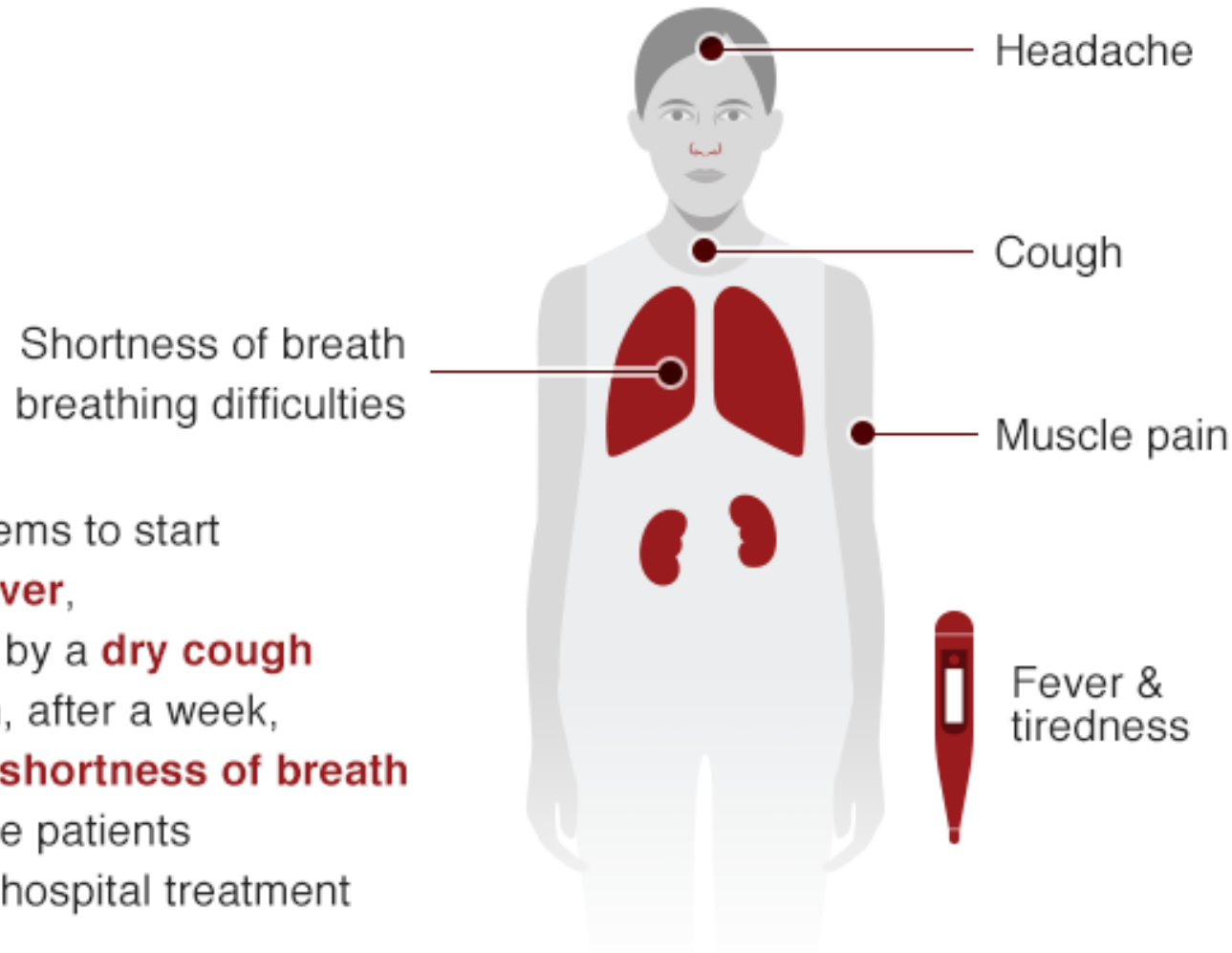


患者背景	所有病人	患者背景	所有病人
	1099		1099
年齡 (中位數、歲)	47	咳嗽	67.7%
男性	58.2%	痰	33.4%
住院前發燒	43.1%	疲勞	38.1%
住院前體溫>38	21.4%	喘	18.6%
住院後發燒	87.9%	噁心嘔吐	5%
結膜充血	0.8%	腹瀉	3.7%
鼻充血	4.8%	肌肉痠痛關節痛	14.8%
頭痛	13.6%	發冷	11.4%
喉嚨痛	13.9%	咳血	0.9%
喉嚨充血	1.7%	紅疹	0.2%

資料來源：Zhong NS, et al. medRxiv preprint first posted online Feb. 9, 2020.

胸腔重症 蘇一峰醫師

Symptoms of China coronavirus



Virus seems to start with a **fever**, followed by a **dry cough** and then, after a week, leads to **shortness of breath** and some patients needing hospital treatment

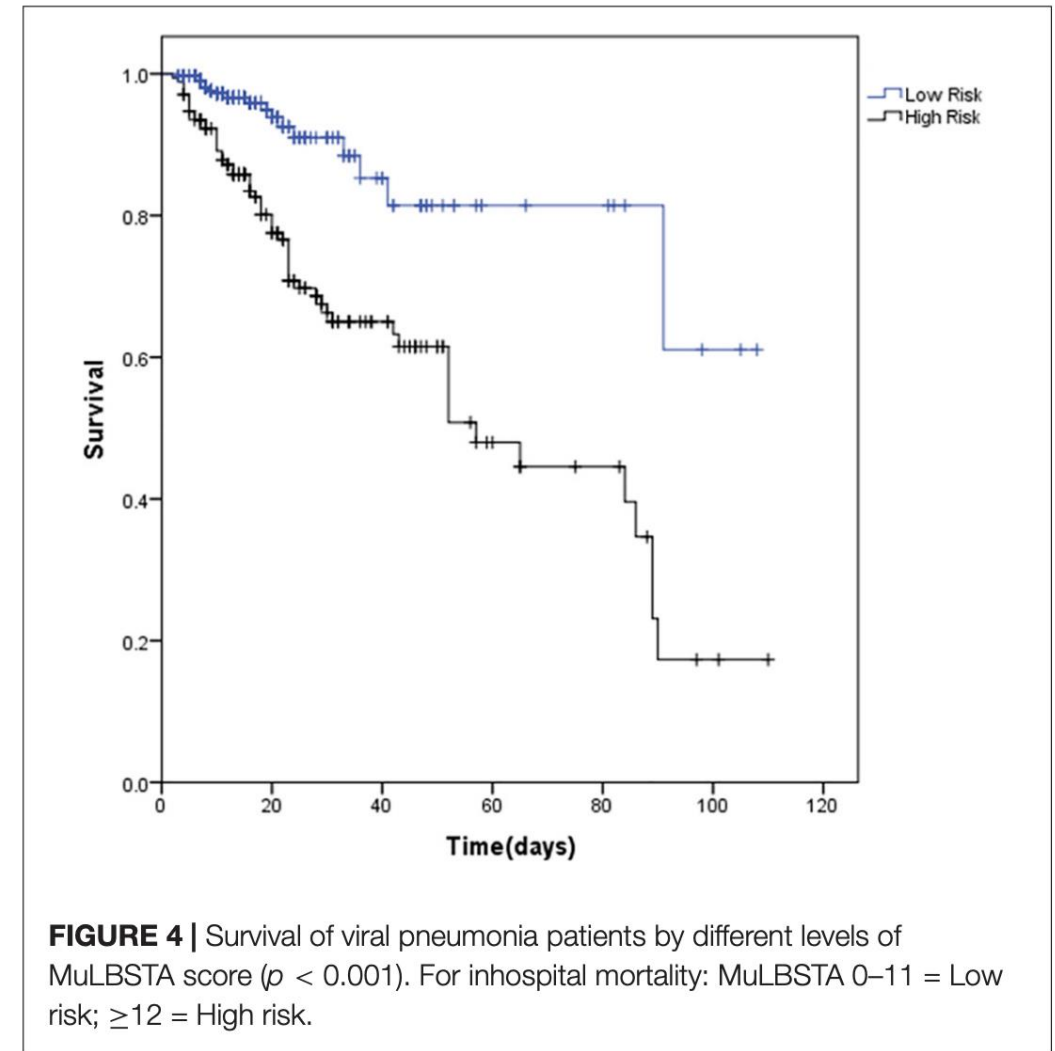
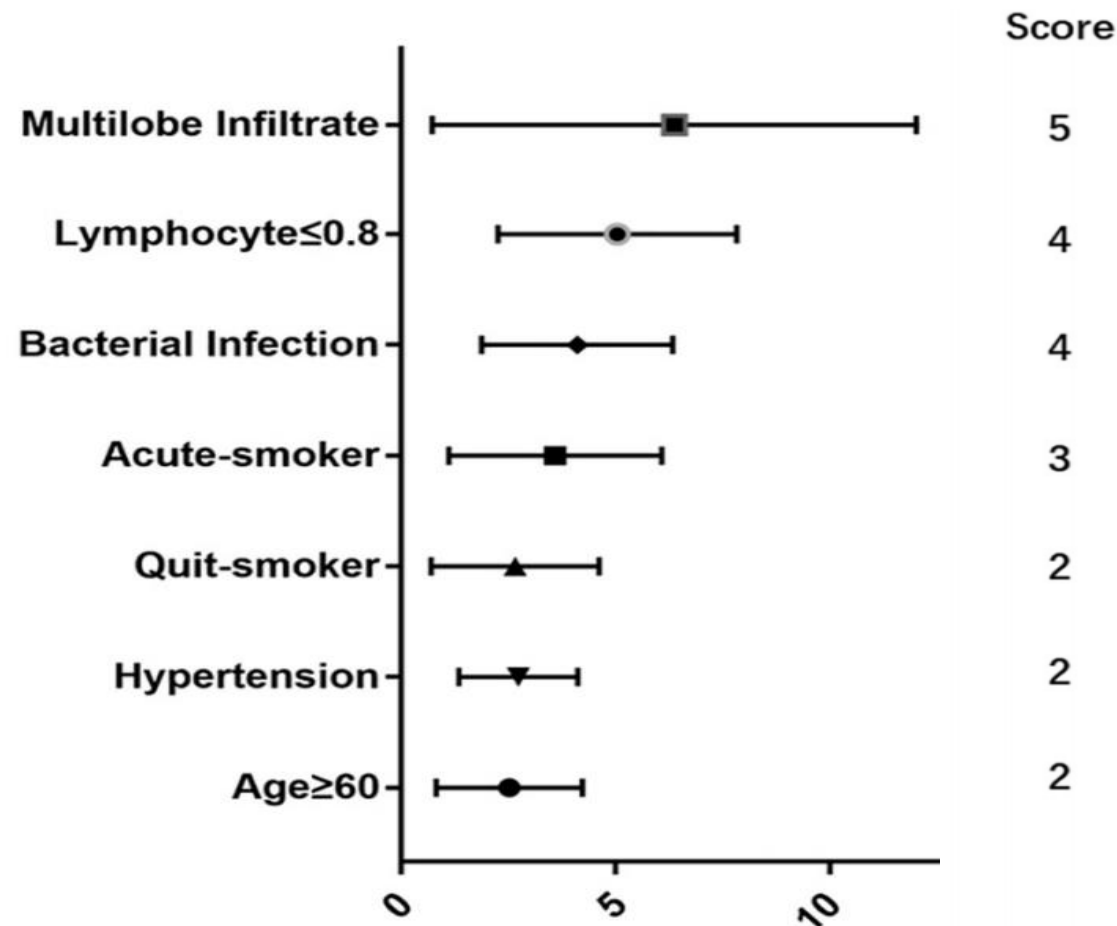


World Health Organization (WHO) 
@WHO

- 82% develop mild symptoms
- 15% develop severe symptoms
- 3% become critically ill

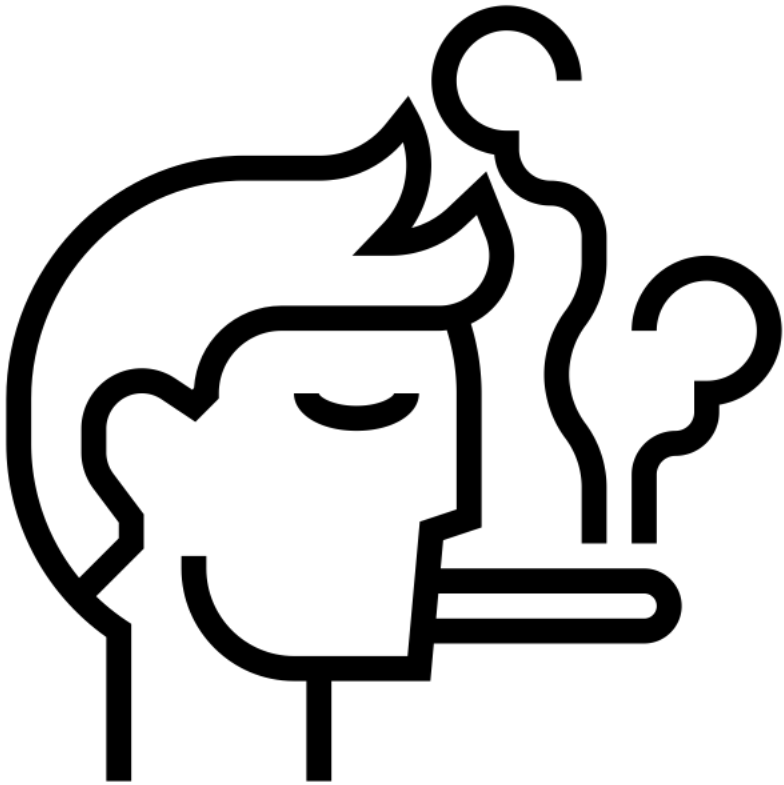
MuLBSTA Score

Multilobular infiltration, hypo-Lymphocytosis, Bacterial coinfection, Smoking history, hyper-Tension and Age

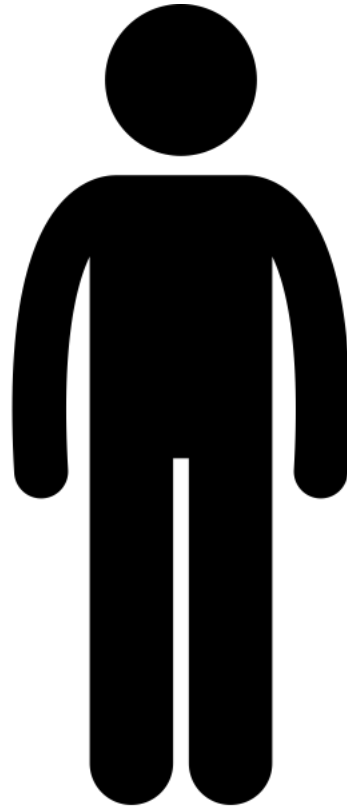


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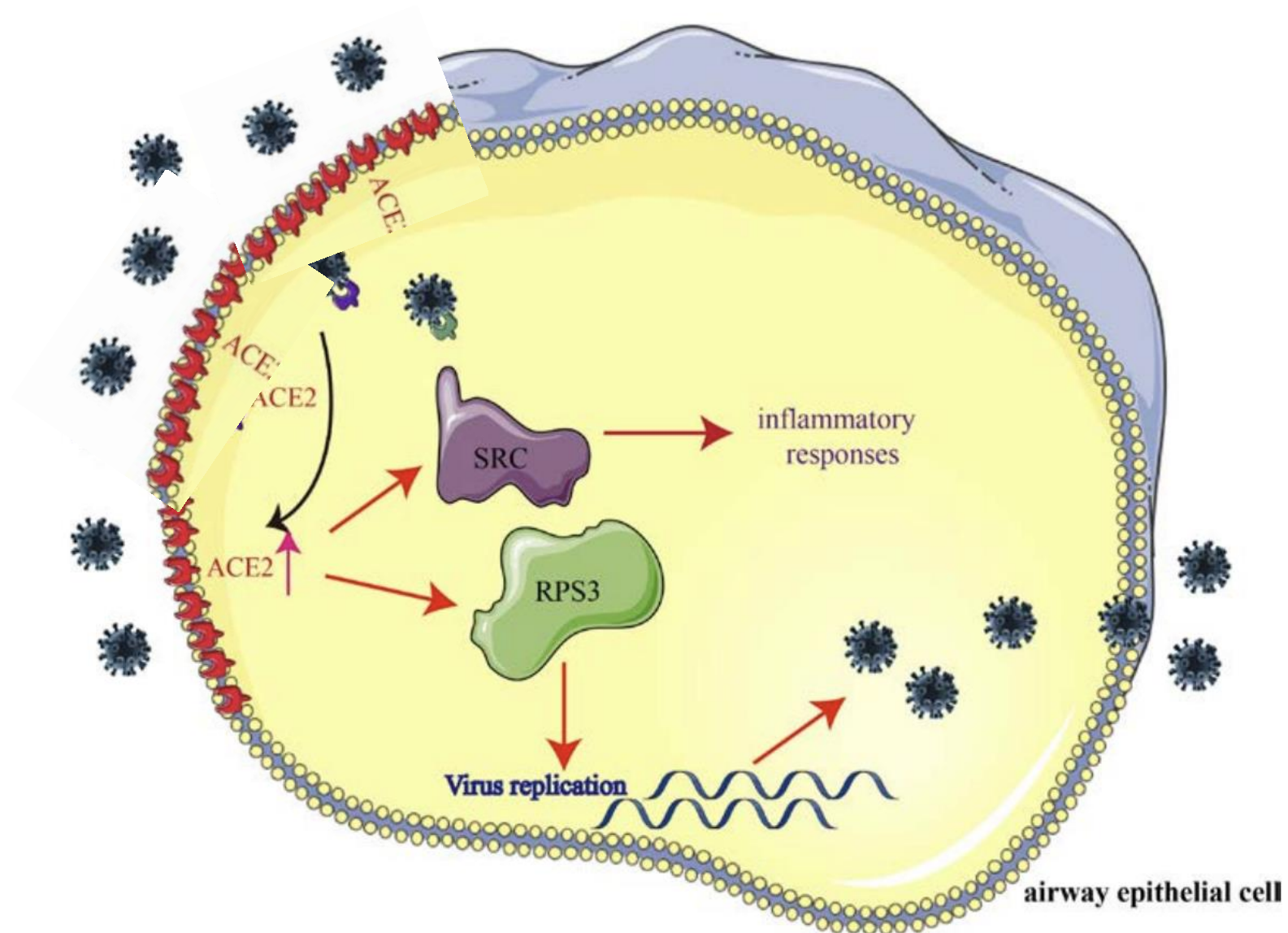
Smoking history



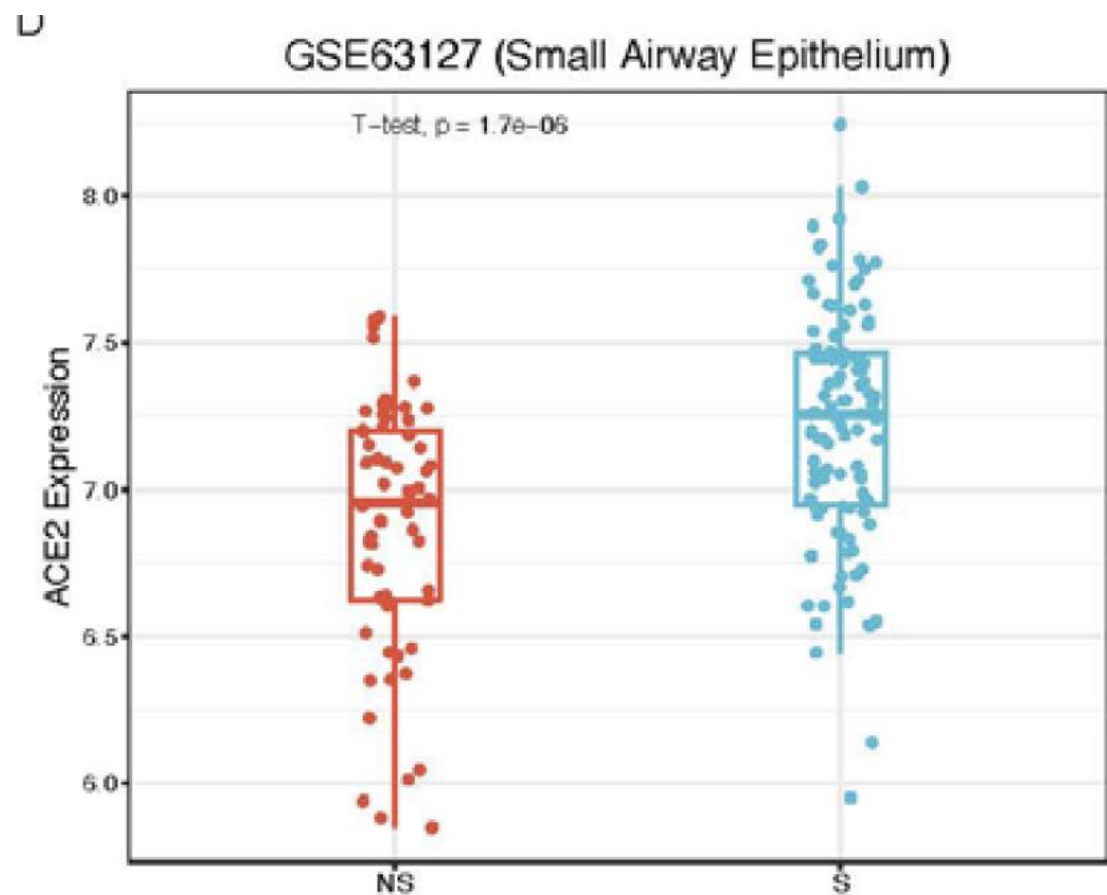
Male gender



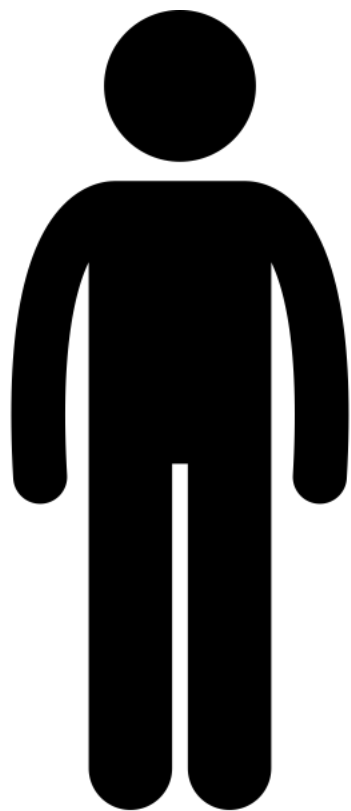
Mild symptoms in
children



Significantly higher ACE2 gene expression in smokers compared to non-smokers.



Variable	Beta	P-value
Platform: RNA-seq	-5.940	<2e-16
Race: Caucasian	0.088	0.359
Age: >60	-0.012	0.900
Gender: Male	0.105	0.352
Smoking: Smoker	0.313	0.008

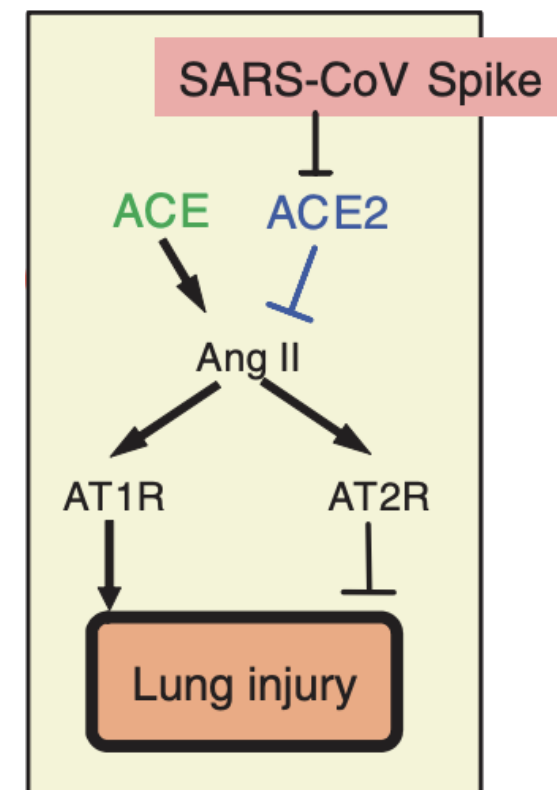
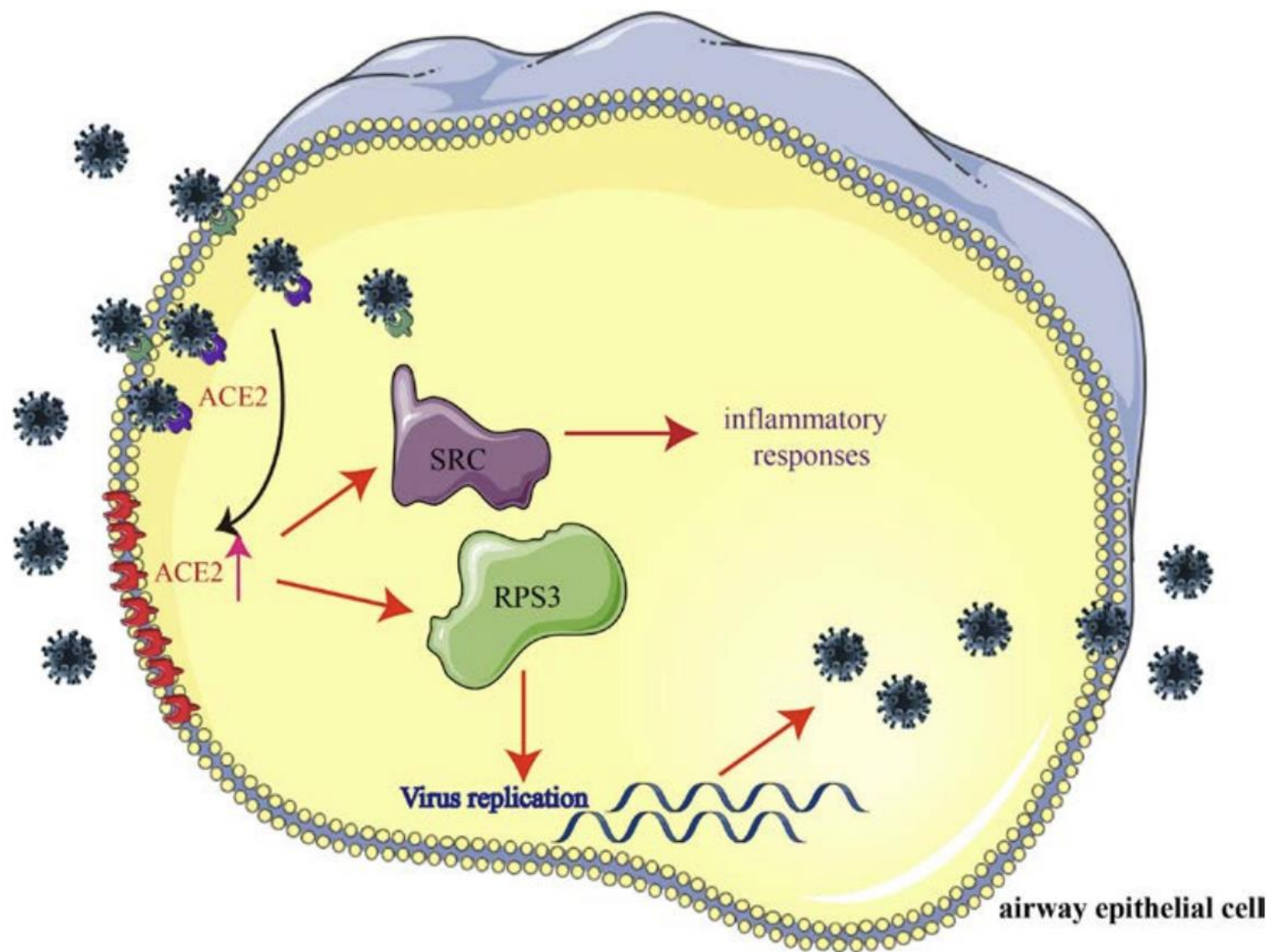


Male gender



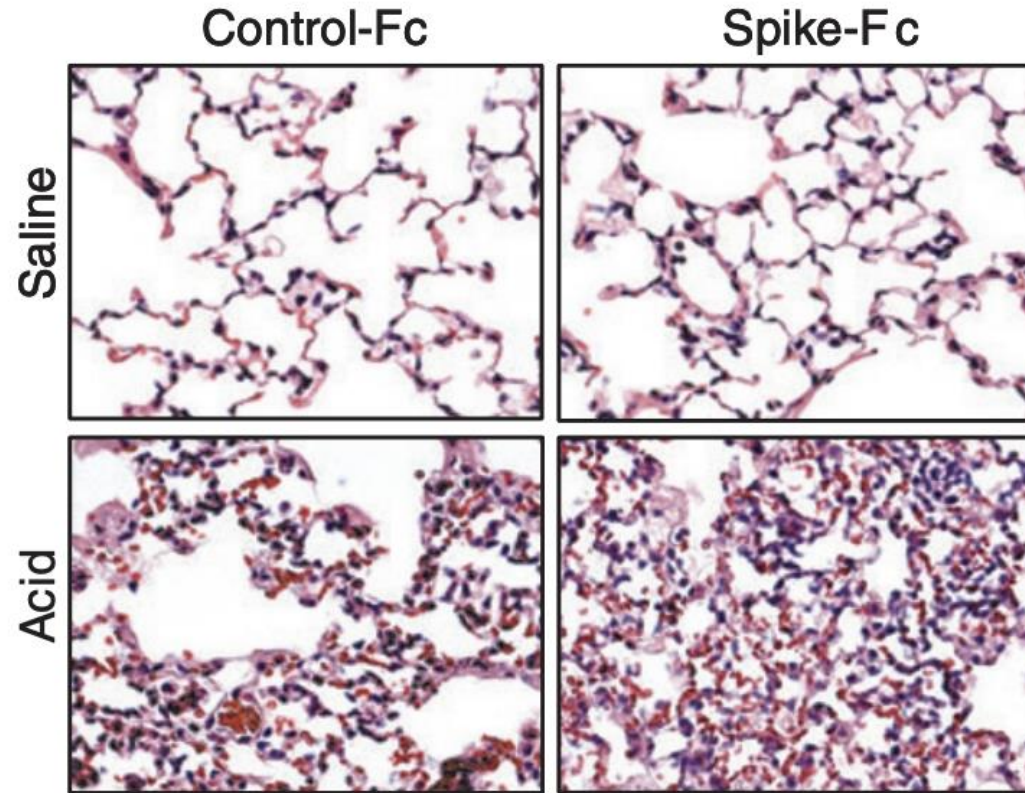
Smoking history

= 48%

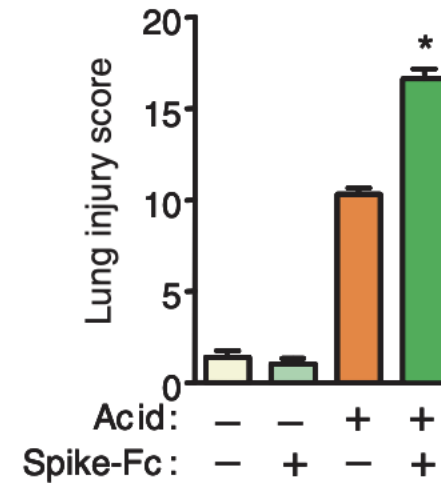


The SARS-CoV Spike protein enhances the severity of acute lung injury.

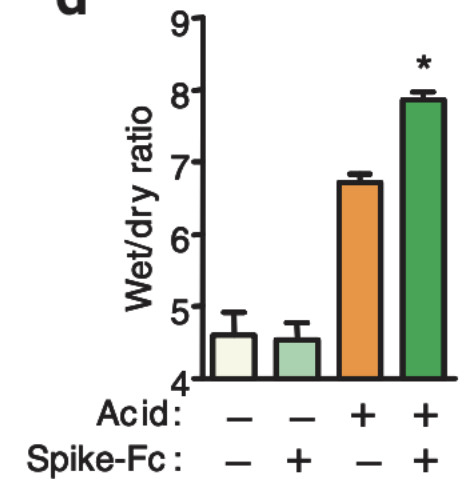
b



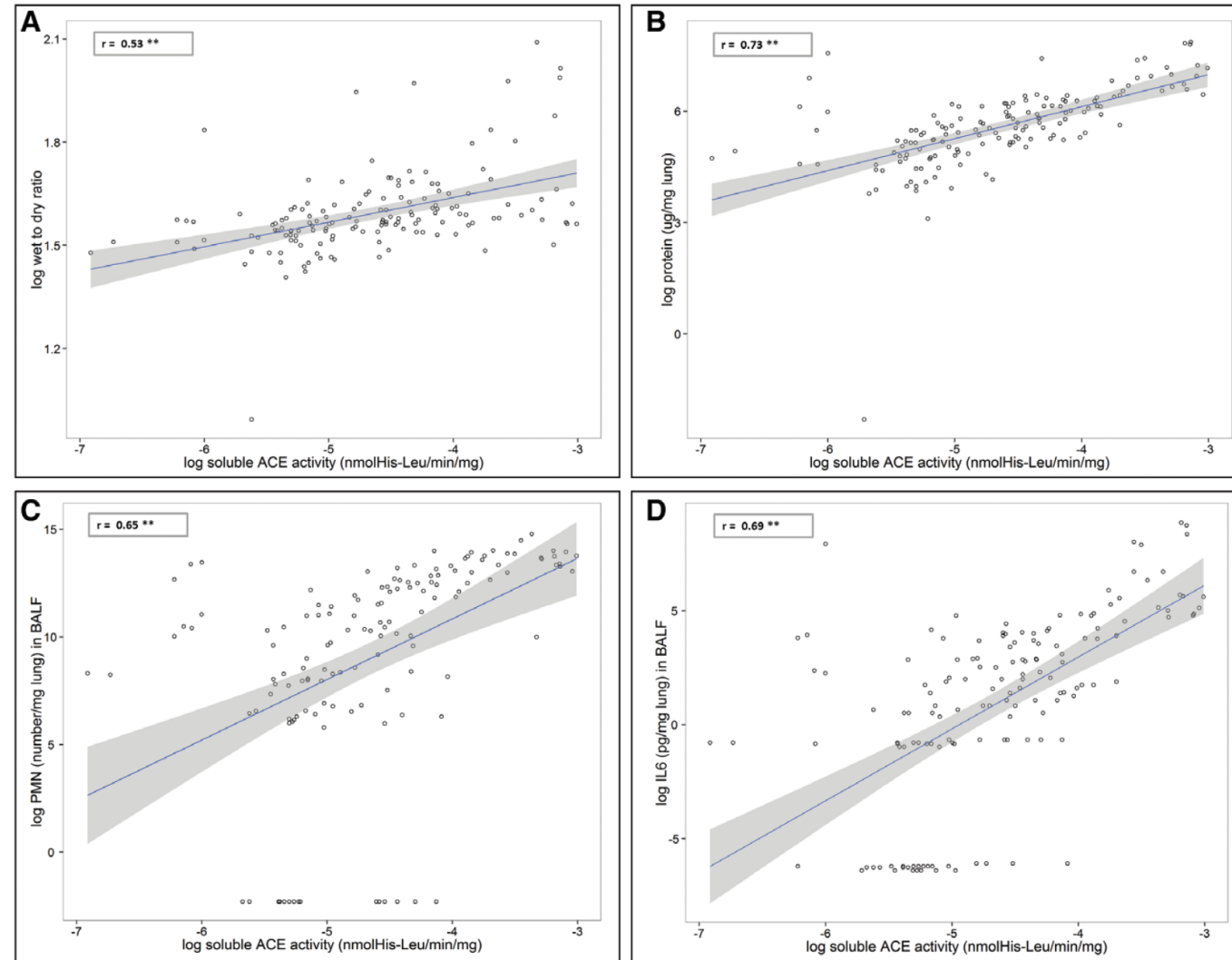
c



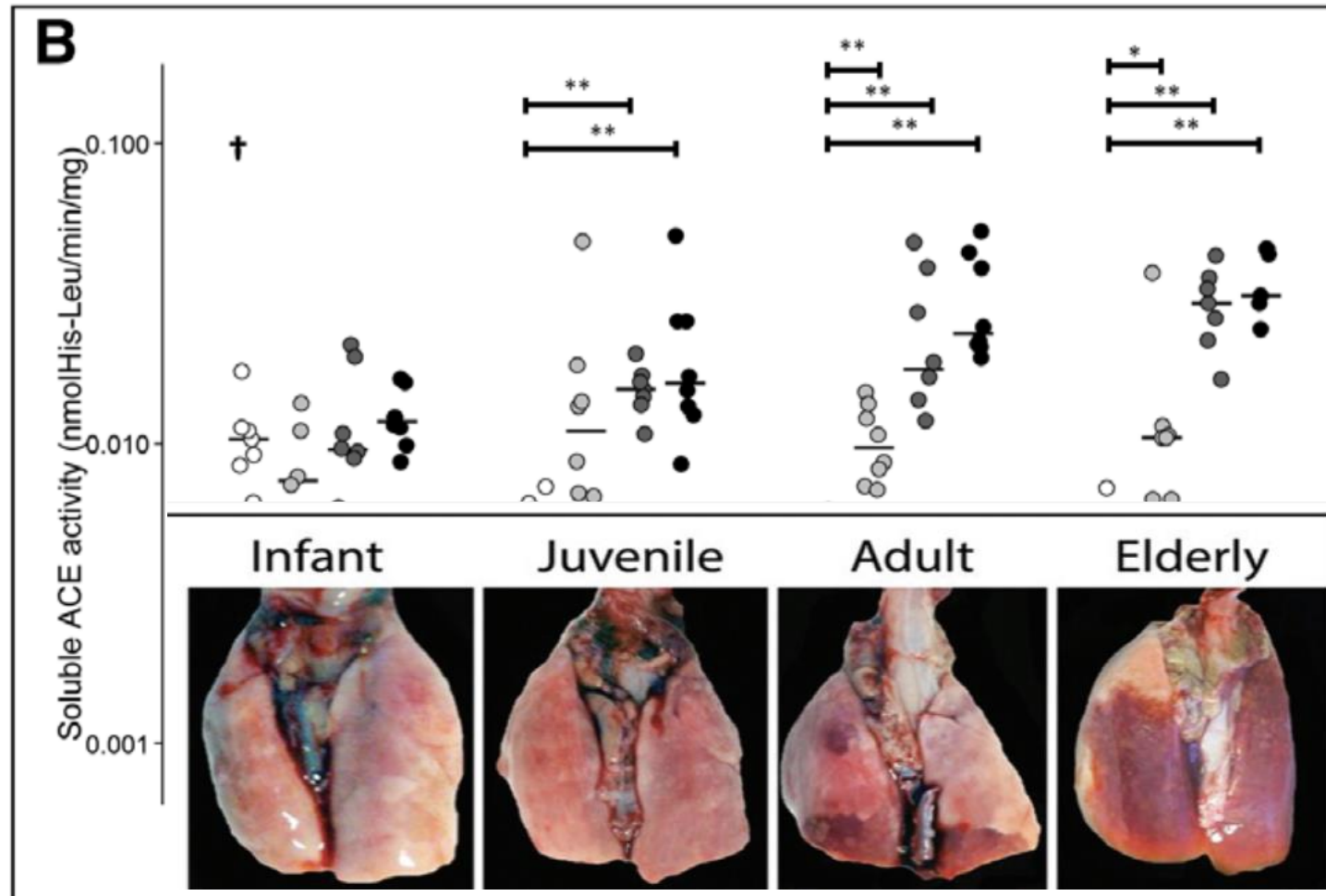
d



Correlation between soluble ACE activity and lung injury and inflammation.



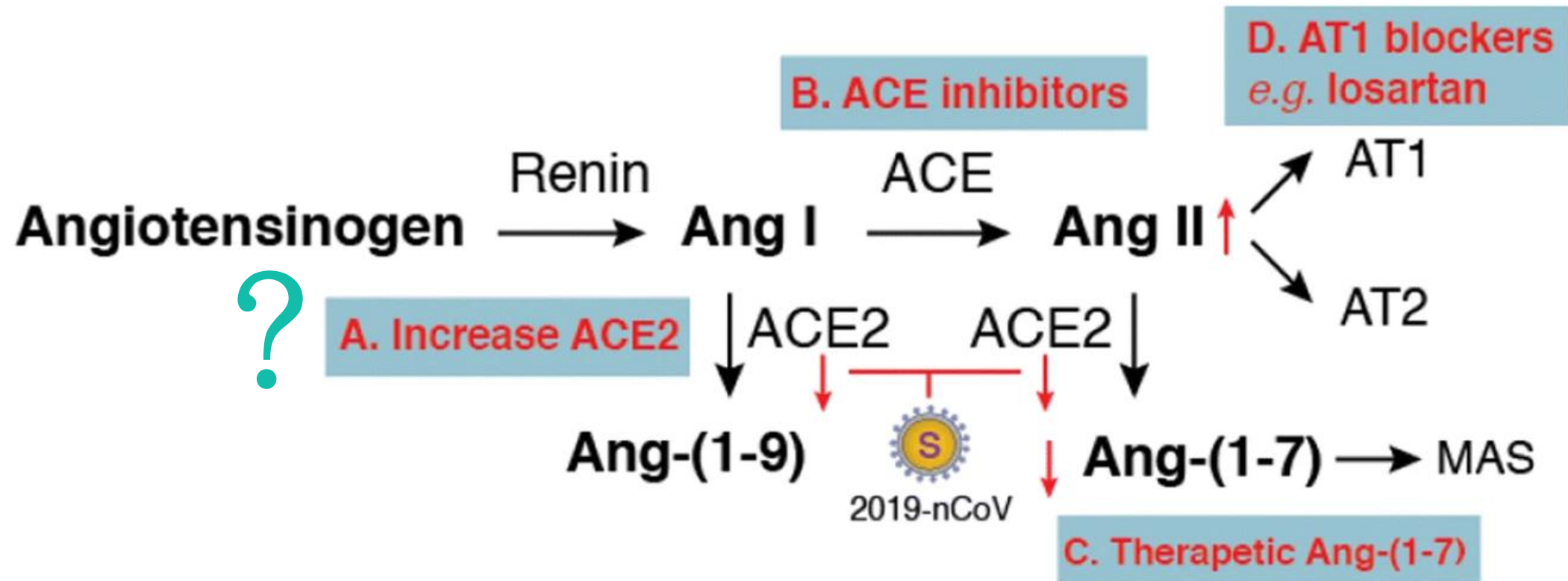
Age Is Associated With Differences in the ACE Activity in Response to Injury in Mice





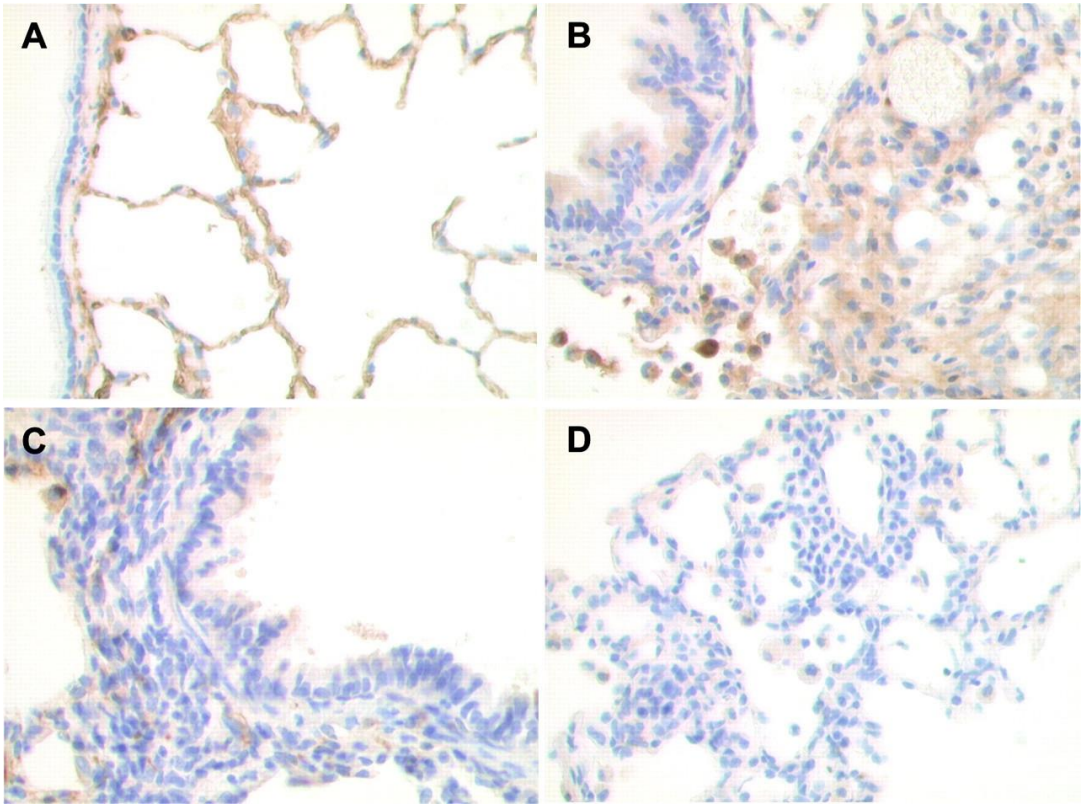
**Mild symptoms in
Children?**

Potential therapeutics for 2019-nCoV-induced lung injury based on balancing the renin–angiotensin system (RAS).

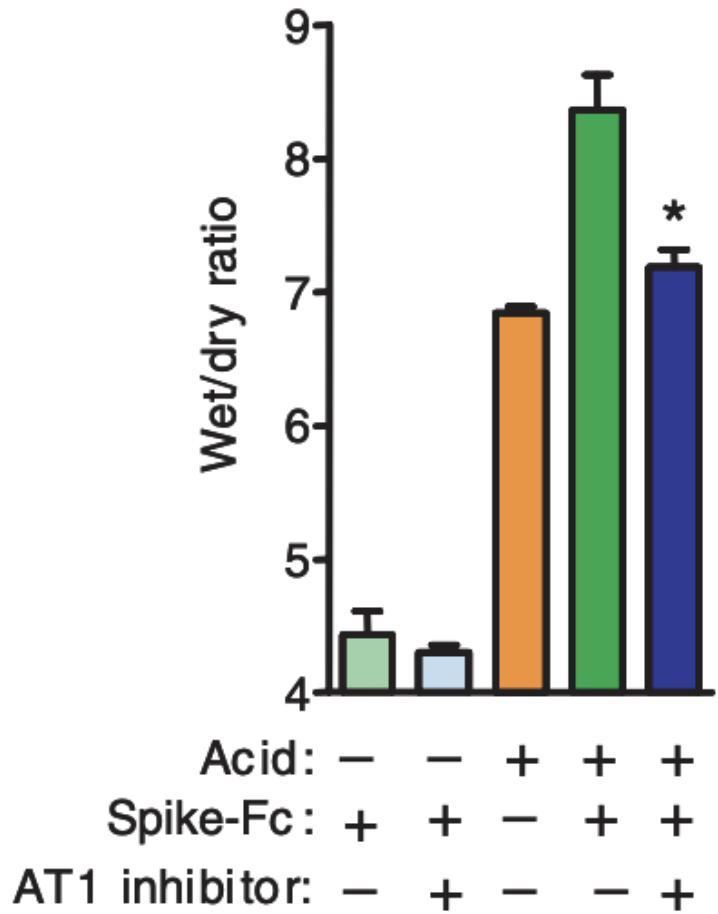


TGF-β immunohistochemistry in bleomycin-induced lung injury:

- A: saline alone; B: saline + bleomycin;
C: losartan + bleomycin;
D: ramipril + bleomycin.

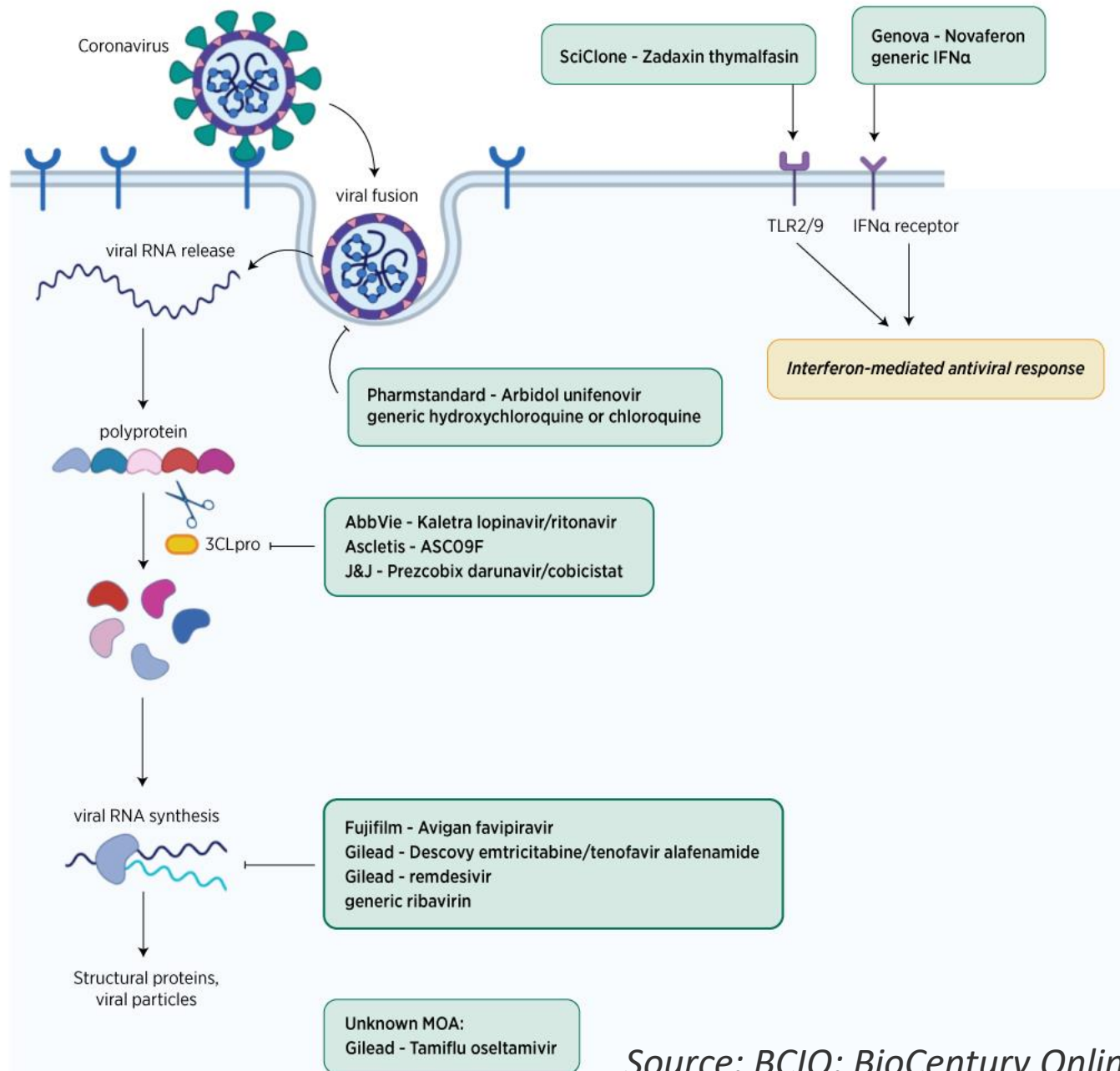


Wet to dry weight ratios of lungs of acid and Spike(S1190)-challenged mice in the presence or absence of losartan (15 mg/kg).



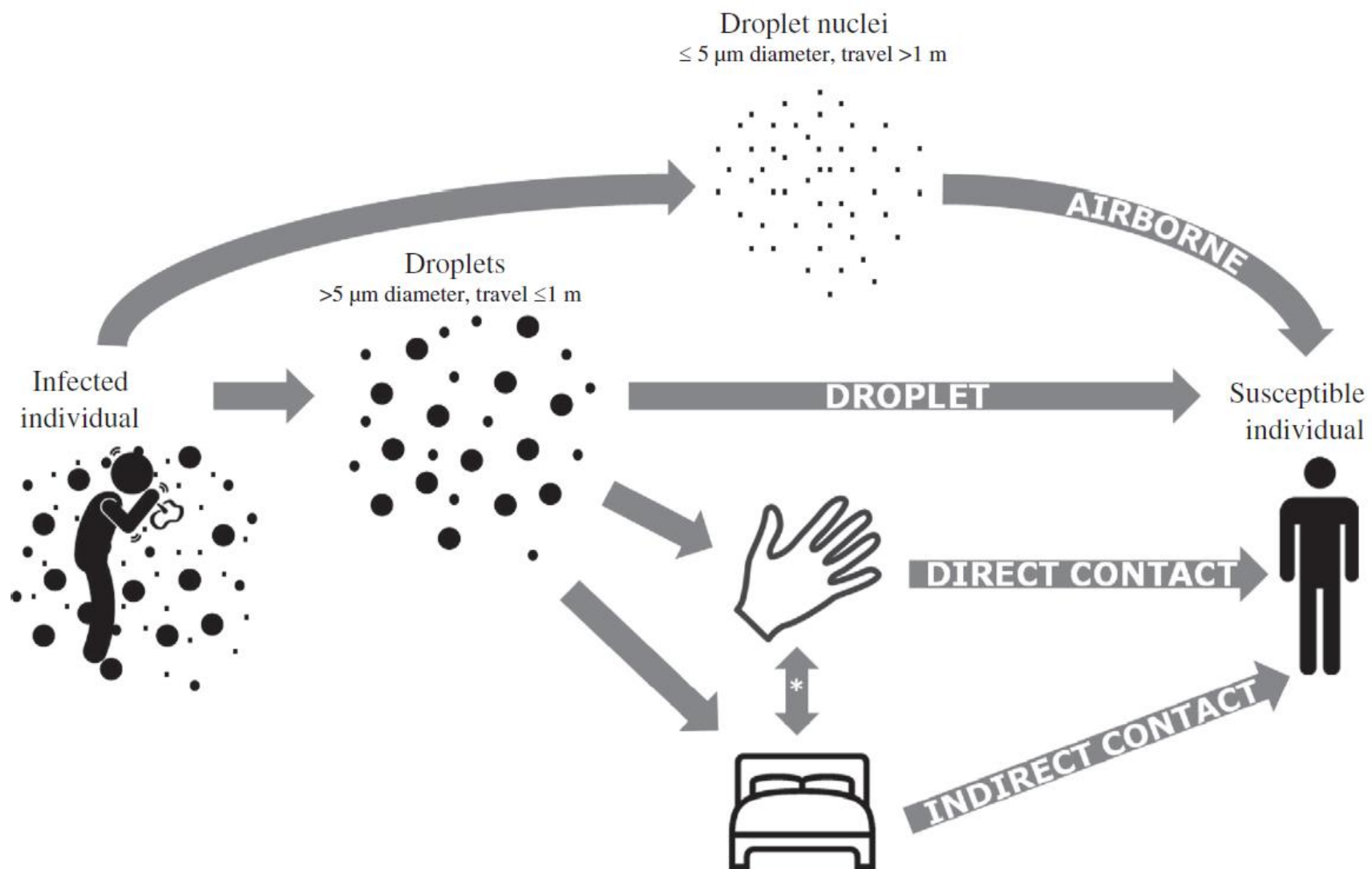
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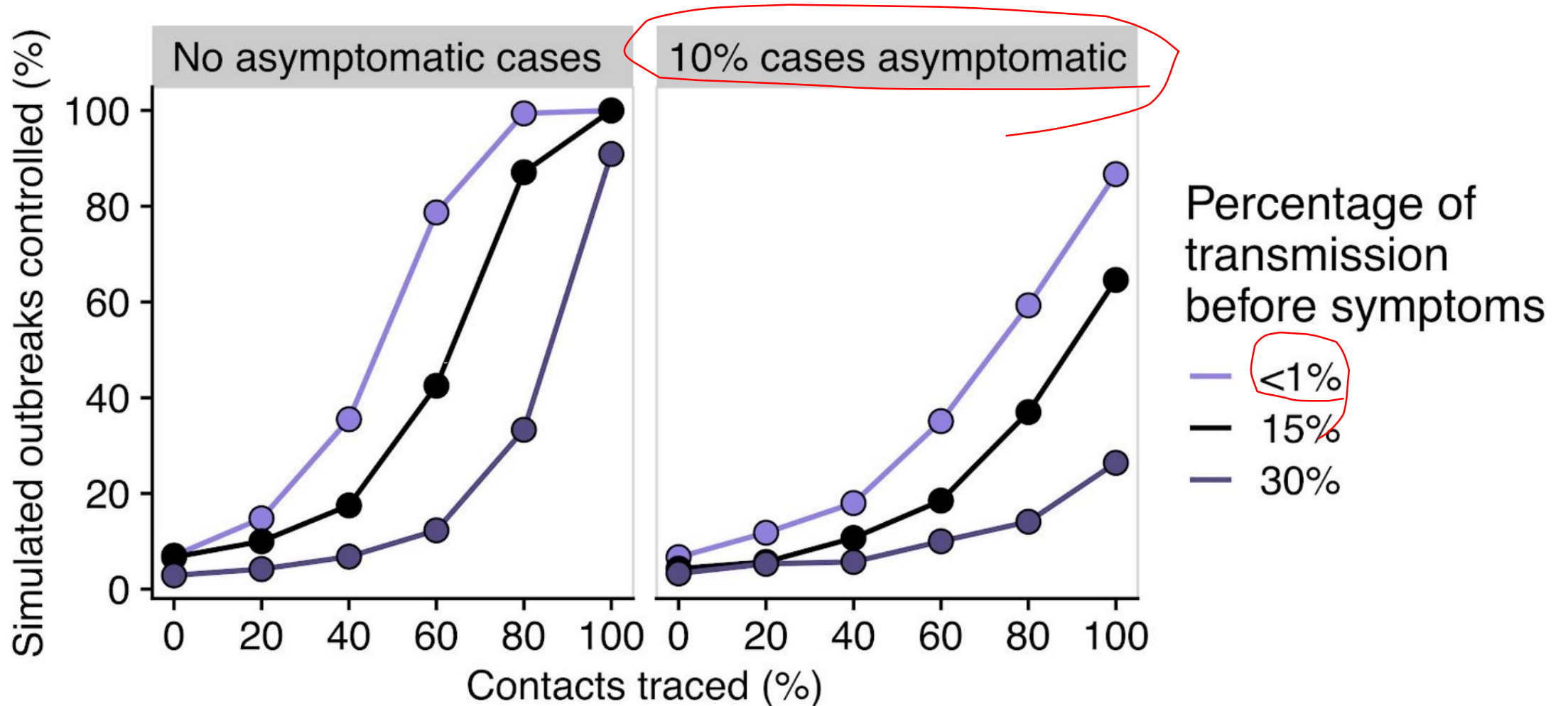
- Lopinavir/Ritonavir (200mg+50mg/tablet) 2# PO BID
- Interferon-β1b 0.25 mg SC QOD5
- Remdesivir ?
- Chloroquine ?

Source: BCIQ: BioCentury Online Intelligence, company websites, scientific literature

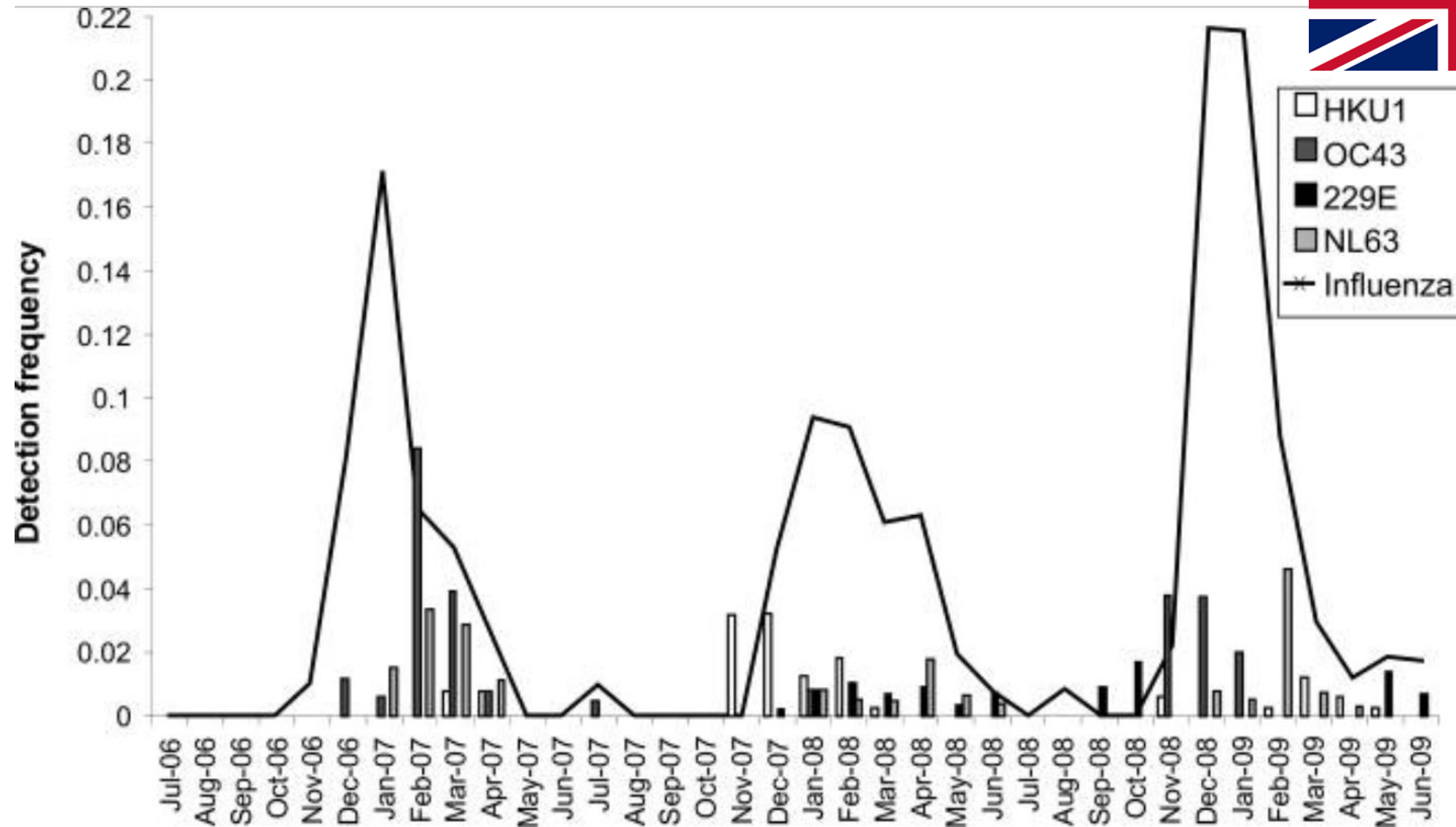


* Transmission routes involving a combination of hand & surface = indirect contact.

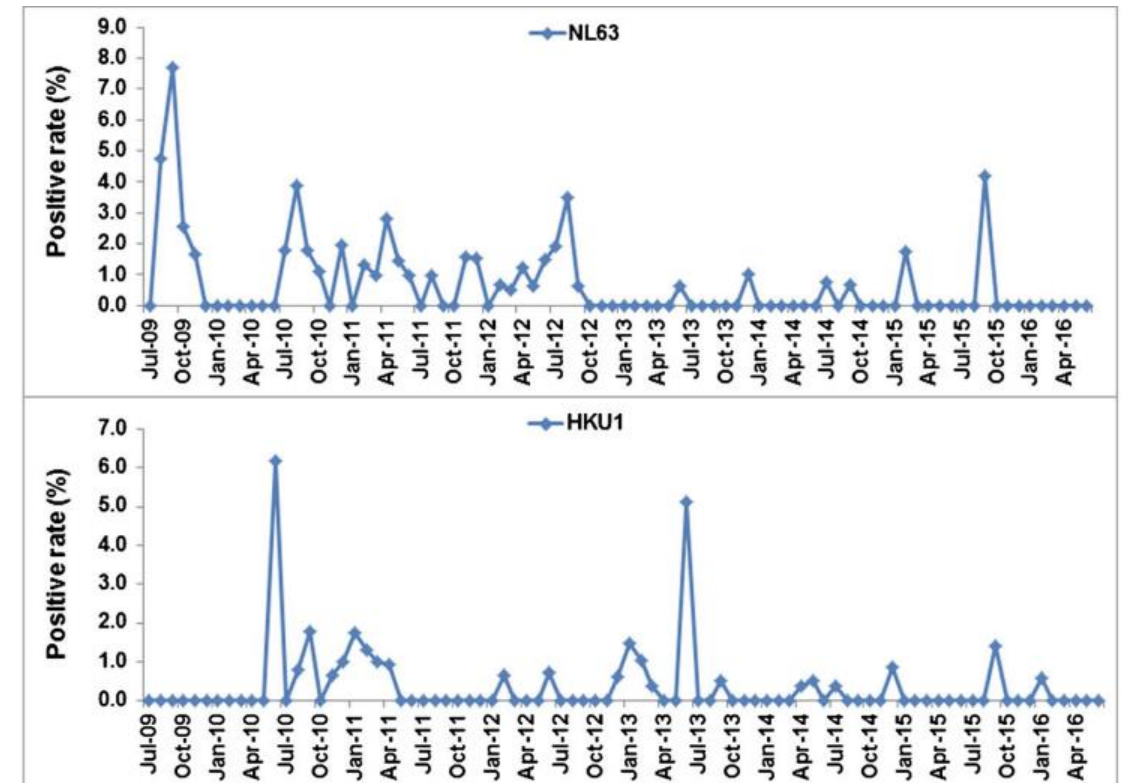
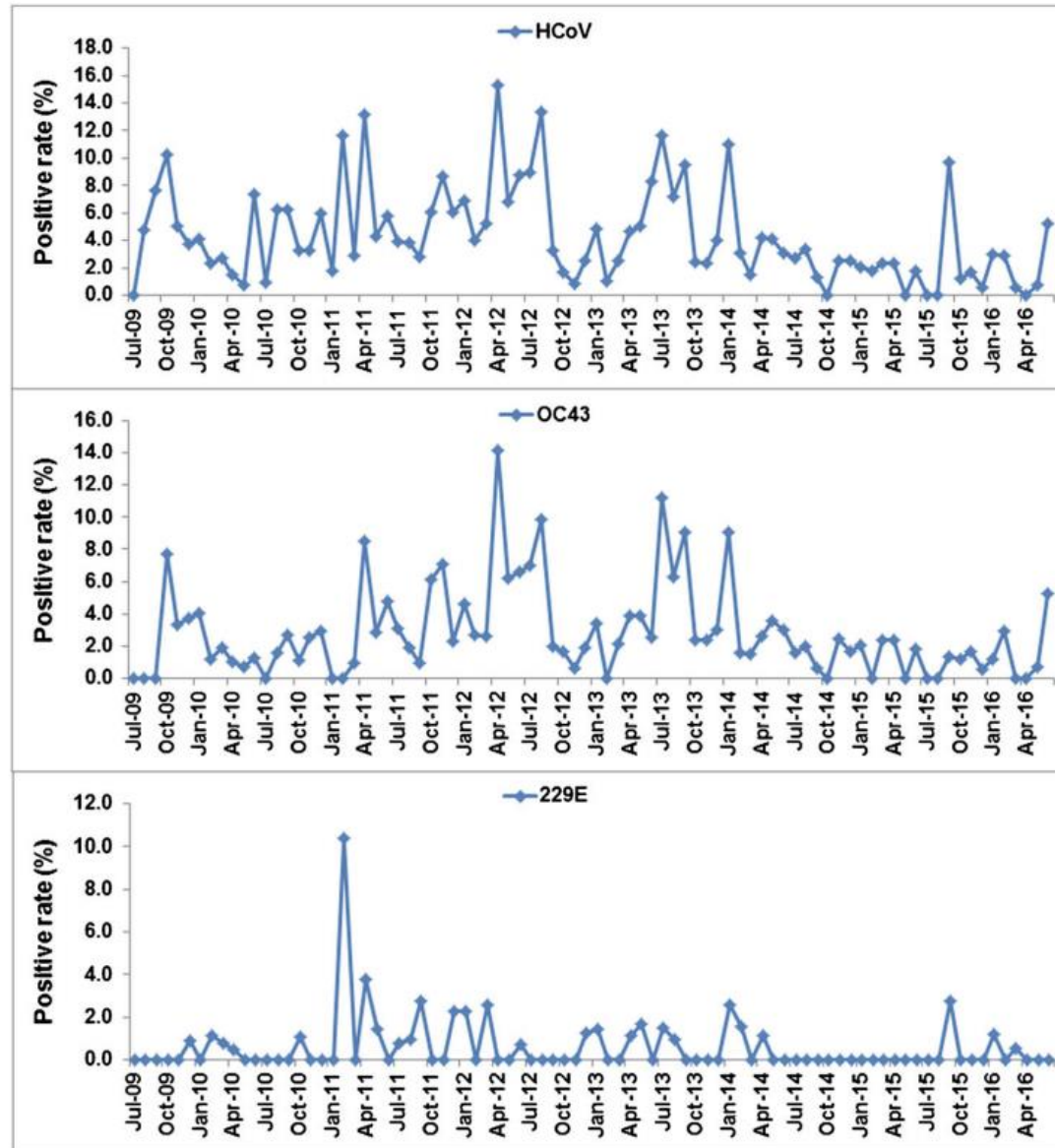
Contact tracing and case isolation alone is unlikely to control a new outbreak of 2019-nCoV within three months.



Seasonality of human coronaviruses: United Kingdom



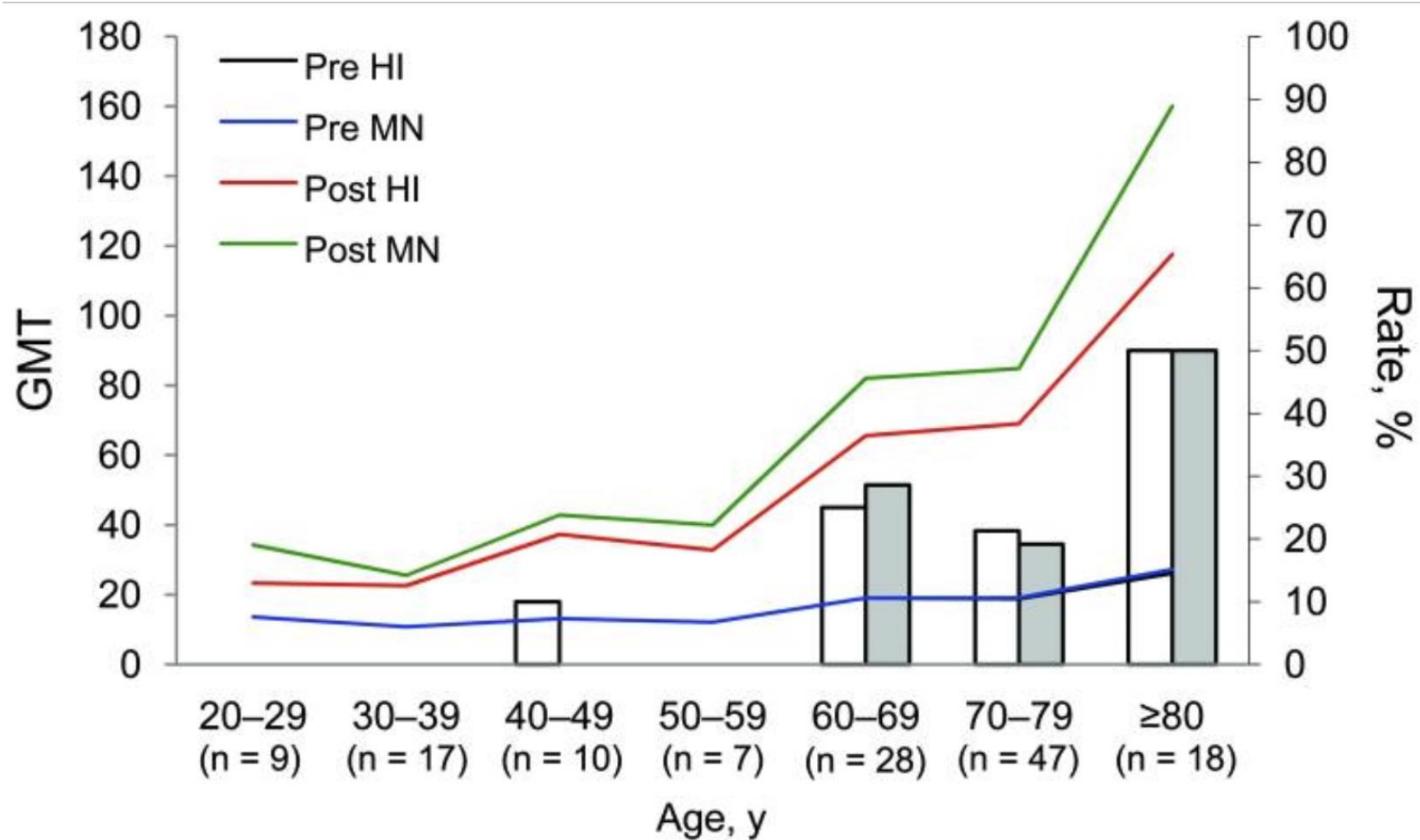
Seasonality of human coronaviruses: 廣州市



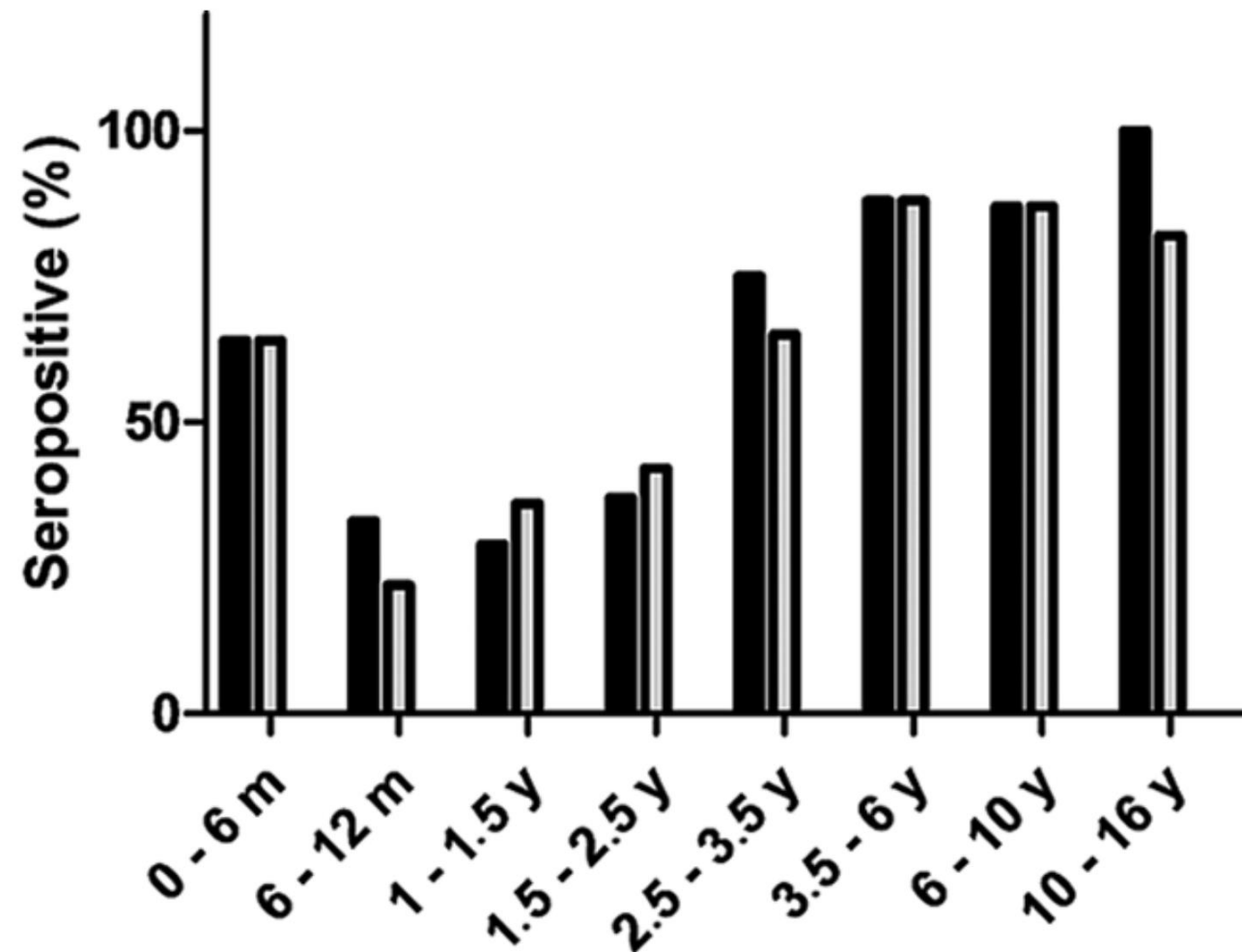
2019新型冠狀病毒與其他傳染病比較



Serologic Status for Pandemic (H1N1) 2009 Virus, Taiwan



Percentages of HCoV-NL63- and HCoV-229E-seropositive results in different age groups.



Genetically diverse
coronaviruses

Natural host

Intermediate host

Human host



?



HCoV-NL63

~800 years ago



HCoV-229E

~200 years ago



HCoV-OC43

~100 years ago



?



HCoV-HKU1



SARS-CoV

~18 years ago



MERS-CoV

~ 8 years ago



?



SARS-CoV-2

NOW

已有的事，後必再有，
日光之下並無新事。
(聖經傳道書1:9)

聞子由瘦（宋·蘇軾）

五日一見花豬肉，十日一遇黃雞粥。
土人頓頓食諸芋，薦以薰鼠**燒蝙蝠**。



- 宋朝三百餘年間，發生大規模疫病近四十次；1075年「南方大疫，兩浙無貧富皆病，死者十有五六」；1131年浙江大疫；1142、1146、1151、1156年臨安幾乎是接連暴發疫情。



THANK YOU FOR
LISTENING!

