Nosocomial Outbreak of 2019 Novel Coronavirus Pneumonia in Wuhan, China

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Contents of Supplements

Supplement 1 Detailed information of exposure history, the symptoms at onset of illness of 9 transmission chains and other sporadic cases as showed in figure 1A and 1B

We found two clusters in the Department of Neurosurgery.

Cluster 1: The first hospitalized man (index patient A) in the Department of Neurosurgery had a fever on the Jan 6, 2020. He was diagnosed as laboratory-confirmed COVID-19 on Jan 16 by Wuhan Center for Disease Control & Prevention. Nurse C who took care of him felt slight malaise on Jan 9, and developed slight dry cough two days later, but his chest roentgenography showed no abnormalities, and was confirmed as COVID-19 on Jan 18 until RT-PCR assays to test for the 2019-nCov be available in hospital then. He was found to be co-infected with A/H1N1 influenza virus after admission. Nurse H took care of the patient A between Jan 9 and Jan 11, she developed symptoms on Jan 13, and was diagnosed on Jan 18. Nurse F was likely to contact with the patient under certain conditions.

Cluster 2: The second patient (index patient B) was admitted to the hospital on Jan 7. Nurse M, Q, O all had close contact with patient, which could be the reason of their infections with 2019-nCoV. Two confirmed patients with five HCWs in close contact with them, acting as a source of infection, spread the virus among the colleagues in the department through daily work and gathering activities. Nurse E wasn't exposed to them but went to a fever clinic without a mask on about Jan 8. At last, 12 HCWs in Department of Neurosurgery were laboratory confirmed COVID-19 cases. Nurse O as probable case had negative viral nucleic acid tests but had COVID-19-like symptoms and imaging findings (Figure S5). And another doctor Z as probable case presented the similar clinical manifestation except for negative viral assay. By far, expect Nurse F, all HCWs in Department of Neurosurgery were recovered and discharged.

We found seven family clusters among HCWs.

Cluster 3: Nurse U developed symptoms on Jan 17 with nasal congestion and rhinorrhea. She lives with her husband and her parents in law, and her parents are in another building but in the same neighborhood. They ate dinner together every night. Then her mother in law f and her mother i and grandmother j developed symptoms successively on Jan 19, Jan 28 and Jan 29, separately.

Cluster 4: Nurse P in Department of Neurology had no clear exposure to any relative patients, but she expressed symptoms of fever on the night of Jan 15, her husband c had fever successively on Jan 18.

Cluster 5: Nurse F developed mild symptoms on Jan 12, but she didn't pay much attention to it and attended Neurosurgery department gala. She lives in the same room with her husband g, her son is in another. Her husband developed symptoms on Jan 21, but her son was fine. Her colleague (doctor S) who had close contact with her on the gala developed symptoms on Jan 16 as well. She suffered severe diarrhea during hospitalization. Even the nucleic acid test of nasopharynx swabs has turned negative and lung CT images got better, the nucleic acid test of stool is still positive one month after onset.

Cluster 6: Nurse R developed symptom of sore throat on Jan 16, later her husband e developed symptoms on Jan 19 immediately.

Cluster 7: Nurse A who treated a child with infectious disease developed symptoms on Jan 5, her husband a and daughter b developed symptoms on Jan 7 and Jan 8. Both of them didn't take much attention until her husband's symptoms worsened with fever and chest tightness on Jan 13. Nurse A was diagnosed on Jan 18 with typical imaging findings of 2019-nCoV pneumonia.

Cluster 8: Nurse B developed symptoms of sore throat, nasal congestion, and intermittent low fever since Jan 8. She met her boyfriend d on Jan 15. Three days later, her boyfriend had headache, later was

diagnosed with 2019-nCoV infection.

Cluster 9: Doctor X was neurological physician who had no clear exposure history. She only had mild symptoms of the upper respiratory tract, and the CT images has no typical infection during hospitalization. Her mother h had cough and fever on Jan 24. Her father k developed myalgia and fever on Jan 26, they went to the hospital and were confirmed with 2019-nCoV infection. Doctor X was confirmed last.

Regarding to HCWs with COVID-19 in other departments in the same hospital, Doctor D who was mainly responsible for gastroscopy fell ill on Jan 11 and did not wear a mask at work. Nurse G in Department of Cardiology and Nurse I in Department of Cardiac Surgery had no clear exposure history but developed symptoms on Jan 12 and 14, 2020, respectively. Staff L in Finance Department had fever on Jan 14, 2020. Doctor T as the director of fever clinic was infected since exposing to many COVID-19 frequently. Nurse V in Department of Laboratory is responsible for the daily delivery clinical specimen of both inpatients and outpatients. Doctor Y in Department of Neurology get fever on Jan 22, who has been exposed to confirmed cases on Jan 19 and Jan 20, 2020.

Supplement 2 Difference between active consultation vs not-active consultation

We compare the difference of clinical symptoms between patients who seek medical treatment actively and those who passively went to see the doctor. We found that mild symptoms are most likely to be ignored, such as nasal congestion and rhinorrhea, which could lead to further spread of the virus. In contrast, symptoms such as fever and poor appetite are more likely to attract people's attention.

Supplement 3 Details of isolation measures

14 HCWs didn't have family members infected. Most of them wearing a mask came home or lived alone in a room. But among the 7(A, B, F, P, R, U, X) family clusters, the HCWs did not pay much attention at the early stage of illness and conduct self-isolation in time. Through investigation, we found that these families were not exposed to other suspected cases. Thus, there is a clear evidence of the transmission between the HCWs and their family members. So timely and effective isolation measures in the early stage of onset may greatly reduce the risk of disease transmission. In contrast, any kind of aggregation activities can greatly increase the likelihood of disease spreading.

Supplementary 4 RNA extraction and real-time RT-PCR assay

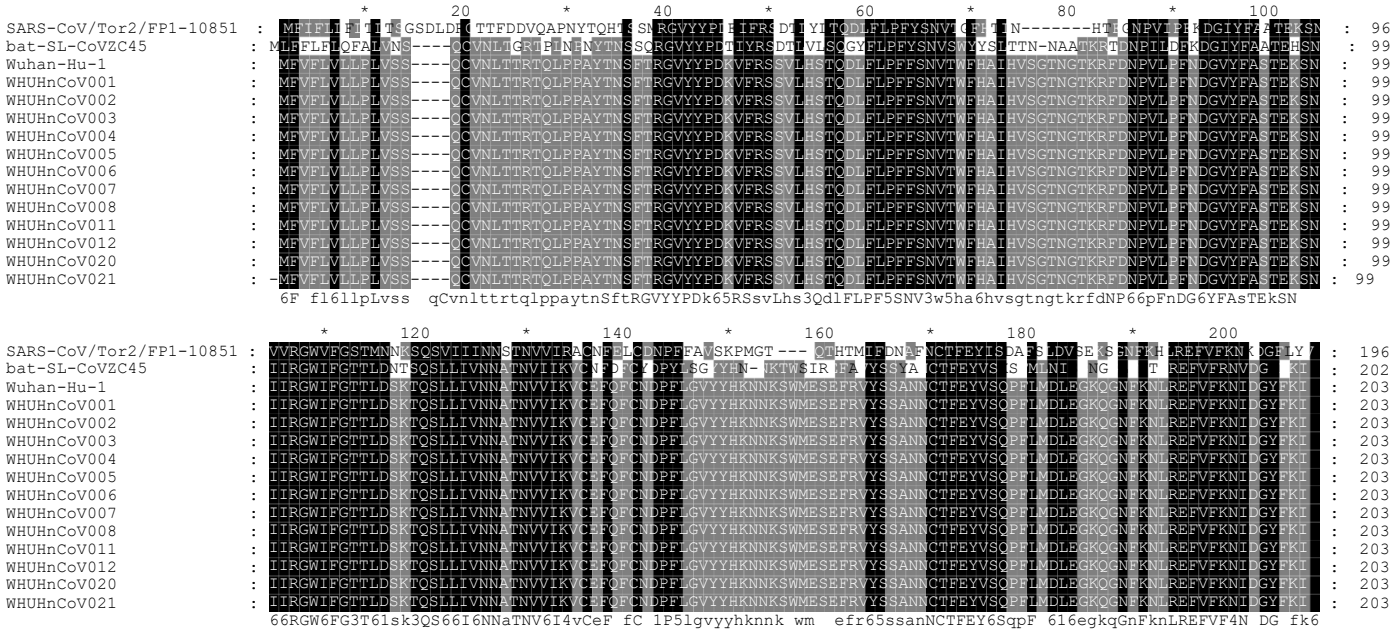
Total RNA was extracted from nasopharynx swabs samples of patients suspected of having 2019-nCoV infection within 2 hours using the respiratory sample RNA isolation kit. In brief, 40 μL of cell lysates were transferred into a collection tube followed by vortex for 10 seconds. After standing at room temperature for 10 minutes, the collection tube was centrifugated at 1000rpm/min for 5minutes. The suspension was used for real-time RT-PCR assay of 2019-nCoV RNA. Two target genes, including open reading frame1ab (ORF1ab) and nucleocapsid protein(N), were simultaneously amplified and tested during the real-time RT-PCR assay. Target 1 (ORF1ab): forward primer CCCTGTGGGTTTTACACTTAA; reverse primer ACGATTGTGCATCAGCTGA. Target2 (N): forward primer GGGGAACTTCTCC TGCTAGAAT; reverse primer CAGACATTTTGCTCTCAAGCTG. RT-PCR assay was performed under the following conditions: incubation at 50 °C for 15 minutes and 95 °C for 2 minutes, 45 cycles of denaturation at 95°C for 3

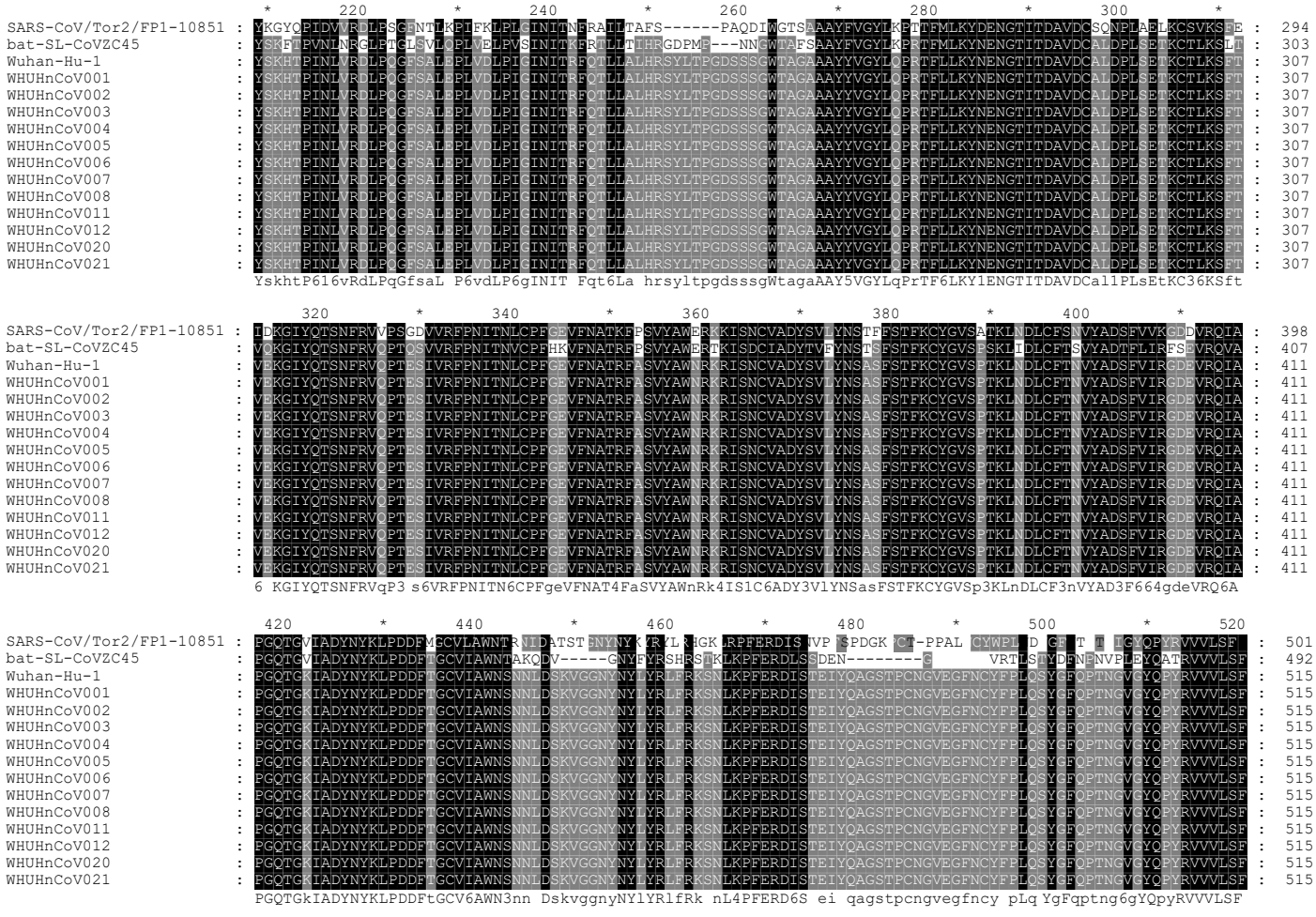
seconds, then annealing, extending and collecting fluorescence signal at 55 °C for 30 seconds[1]. A cycle threshold value (Ct-value) less than 37was defined as a positive test result, and a Ct-value of 40 or more was defined as a negative test. These diagnostic criteria were based on the recommendation by the National Institute for Viral Disease Control and Prevention (China)[2]. A medium load, defined as a Ct-value of 37 to less than 40, required confirmation by retesting.

Supplementary Figures

Figure S1 Comparison of amino acid sequence of Spike protein between 2019-nCoV from our 12 samples, Wuhan-Hu-1 (NC_045512.2), bat-SL-CoVZC45 (MG772933.1) and SARS coronavirus isolate Tor2/FP1-10851 (JX163927.1)

There is no obvious difference between different 2019-nCoVs. Compared with bat-SL-CoVZC45 and SARS coronavirus isolate Tor2/FP1-10851, 2019-nCoV has 4 insertion regions (257th-261th, 449th-454th, 479th-495th, 685th-690th site) and 3 insertion regions (74th-85th, 252th -259th, 685th-690th site) respectively.

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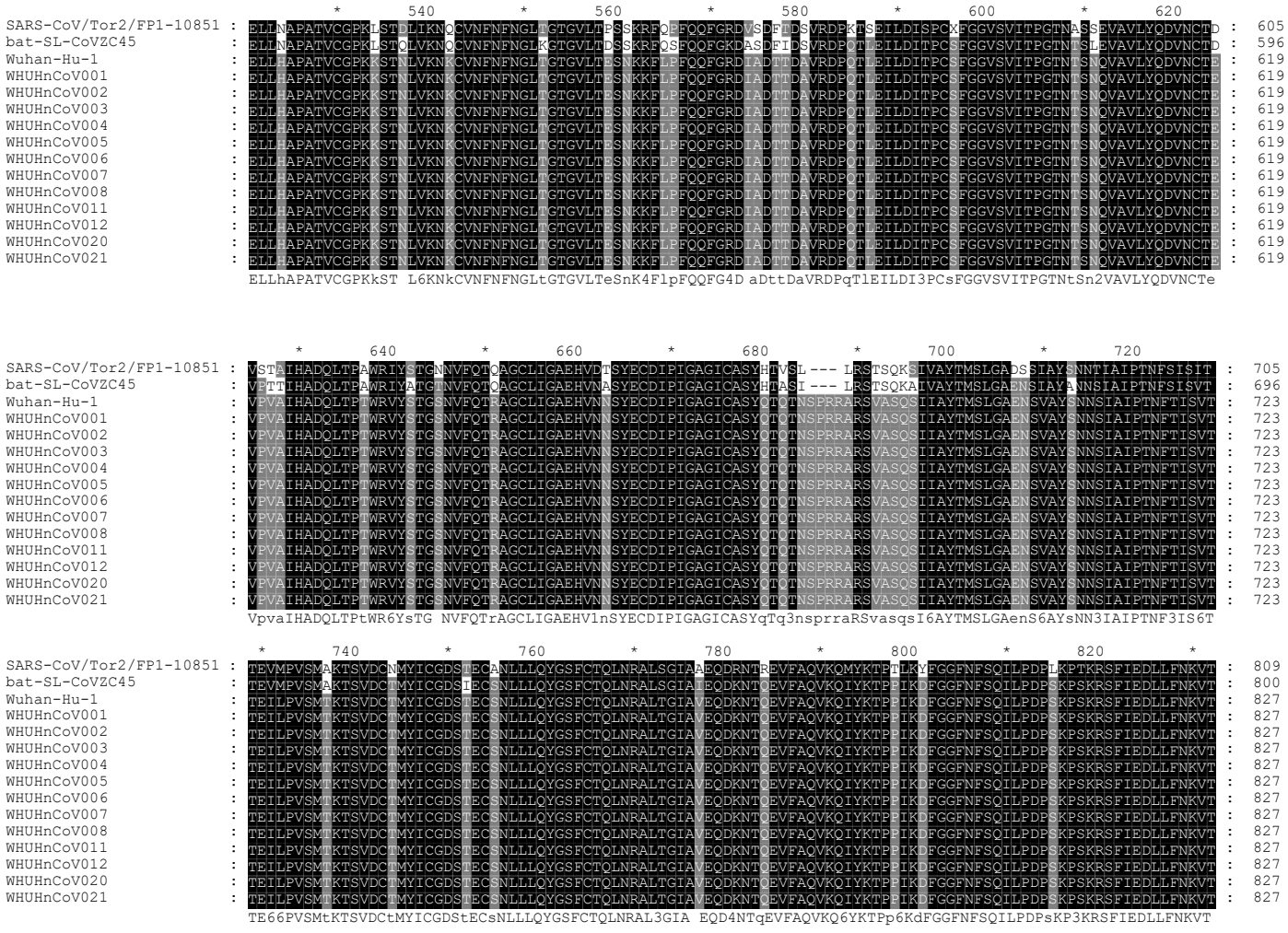
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WHUHnCoV011
WHUHnCoV012
WHUHnCoV020
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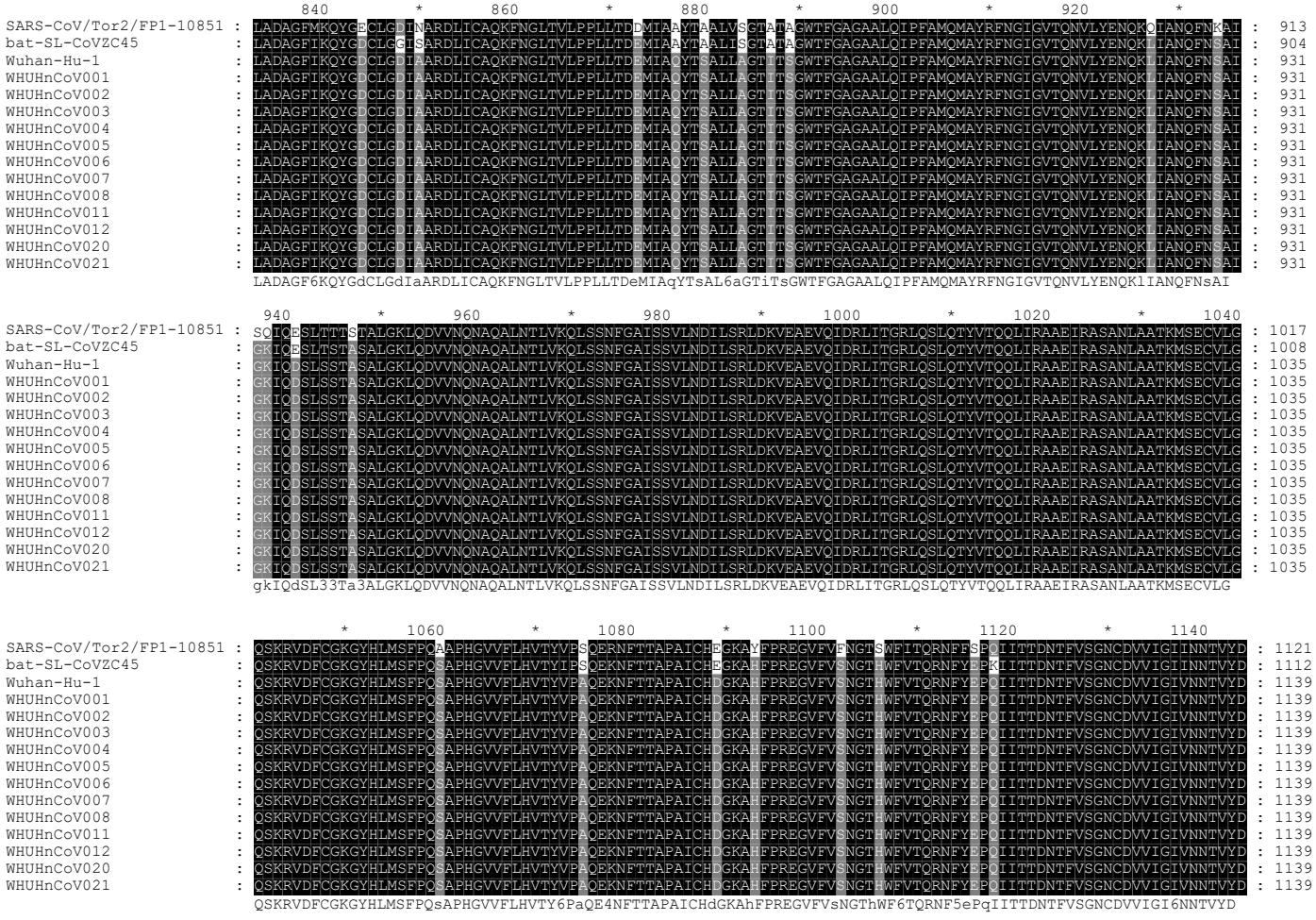
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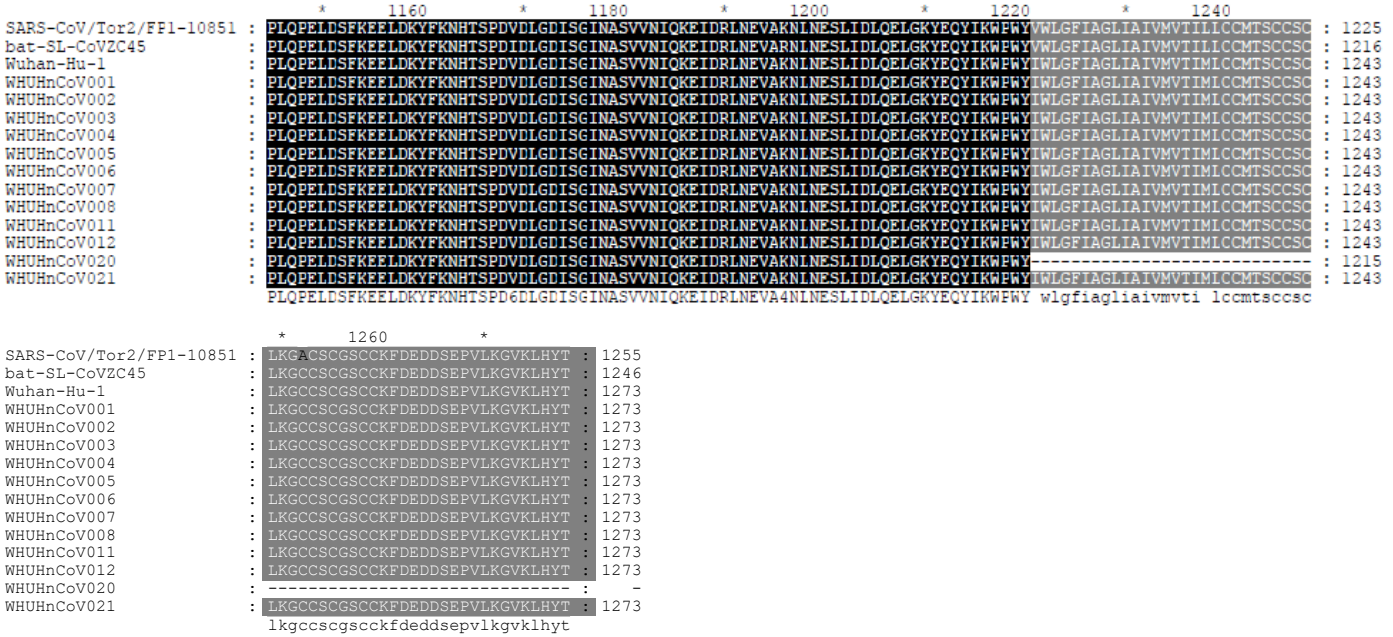
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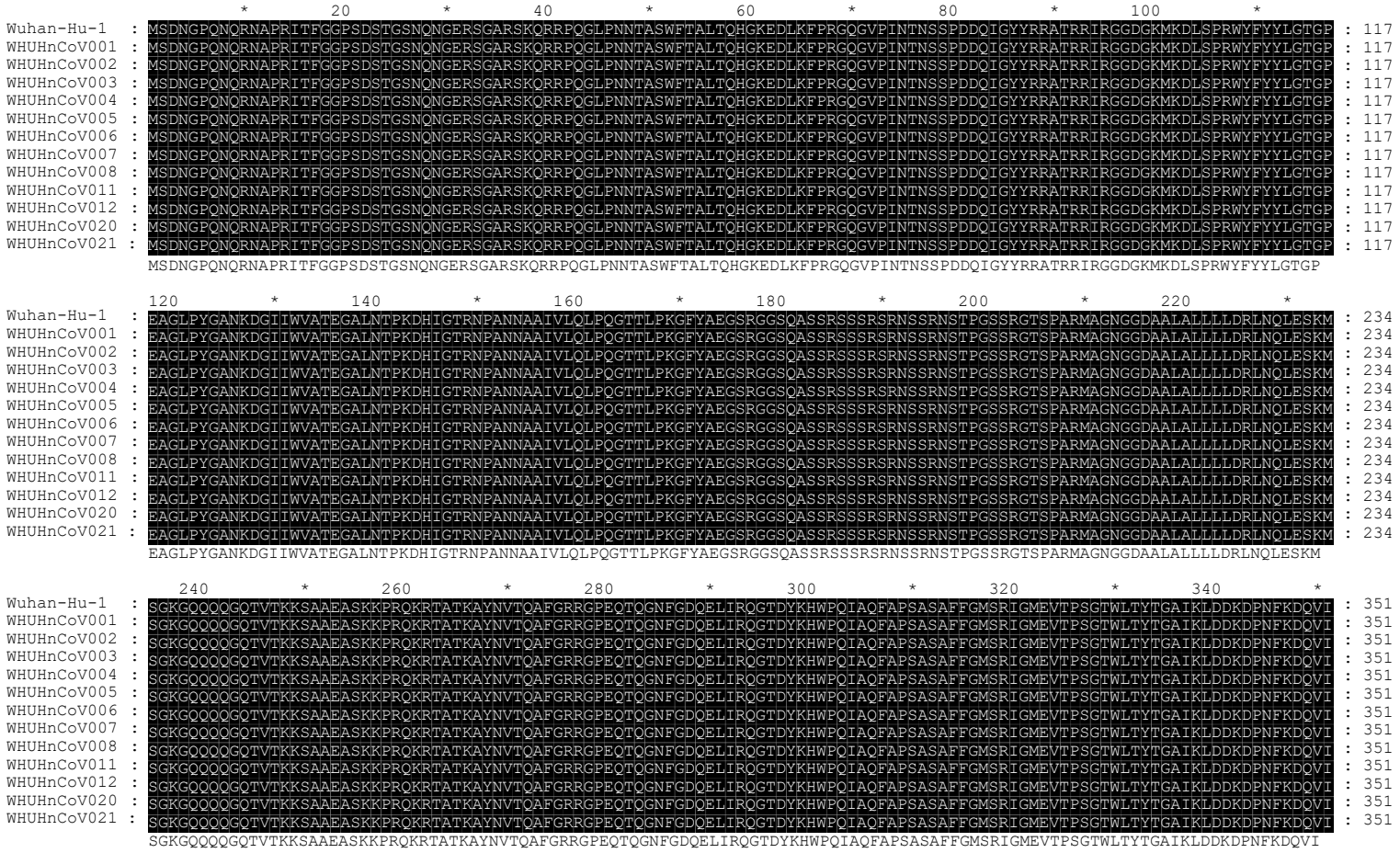
WHUHnCoV020 : PLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWY---------------------------- : 1215
WHUHnCoV021 : PLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSC : 1243
PLQPELDSFKEELDKYFKNHTSPD6DLGDISGINASVVNIQKEIDRLNEVA4NLNESLIDLQELGKYEQYIKWPWY wlgfiagliaivmvti lccmtsccsc
1260
SARS-CoV/Tor2/FP1-10851 : LKGACSCGSCCKFDEDDSEPVLKGVKLHYT : 1255
bat-SL-CoVZC45 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1246
Wuhan-Hu-1 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1273
WHUHnCoV001 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1273
WHUHnCoV002 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1273
WHUHnCoV003 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1273
WHUHnCoV004 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1273
WHUHnCoV005 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1273
WHUHnCoV006 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1273
WHUHnCoV007 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1273
WHUHnCoV008 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1273
WHUHnCoV011 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1273
WHUHnCoV012 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1273
WHUHnCoV020 : ---------------------------- : -
WHUHnCoV021 : LKGCCSCGSCCKFDEDDSEPVLKGVKLHYT : 1273
lkgccscgscckfdeddsepvlkgvklhyt

Figure S2 Comparison of amino acid sequence of N protein between 2019-nCoV from our 12 samples and Wuhan-Hu-1 (NC_045512.2)

The structure of N protein is stable and conserved.



```
                  360         *       380         *       400         *
Wuhan-Hu-1  : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
WHUHnCoV001 : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
WHUHnCoV002 : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
WHUHnCoV003 : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
WHUHnCoV004 : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
WHUHnCoV005 : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
WHUHnCoV006 : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
WHUHnCoV007 : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
WHUHnCoV008 : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
WHUHnCoV011 : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
WHUHnCoV012 : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
WHUHnCoV020 : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
WHUHnCoV021 : LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA : 419
              LLNKHIDAYKTFPPTEPKKDKKKKADETQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA
```

Figure S3 The phylogenetic tree of full-genome of 2019-nCoV from our 12 samples,10 previously identified 2019-nCoV and other coronavirus

The phylogenetic tree was aligned with the use of FFT-NS-2 model. Maximum-likelihood phylogenies were inferred under a generalized-time-reversal (GTR)+ Gamma substitution model and bootstrapped 1000 times to assess confidence. 2019-nCoVs form a monophyletic clade with a bootstrap support of 100%. The most closely related sequence to this clade is bat-SL-CoV.

Figure S4 The phylogenetic tree of Spike protein between 2019-nCoV from our 12 samples,10 previously identified 2019-nCoV and other coronavirus

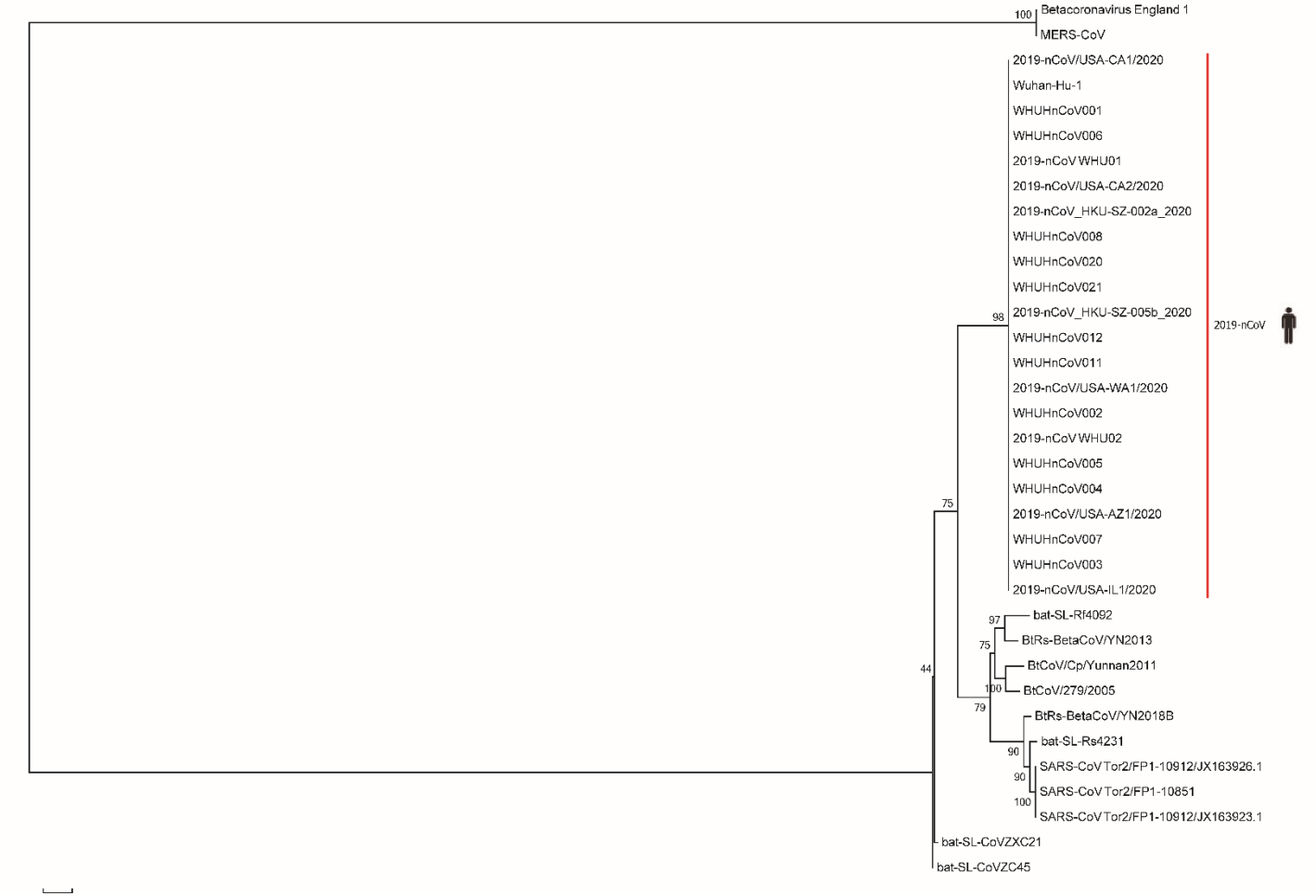
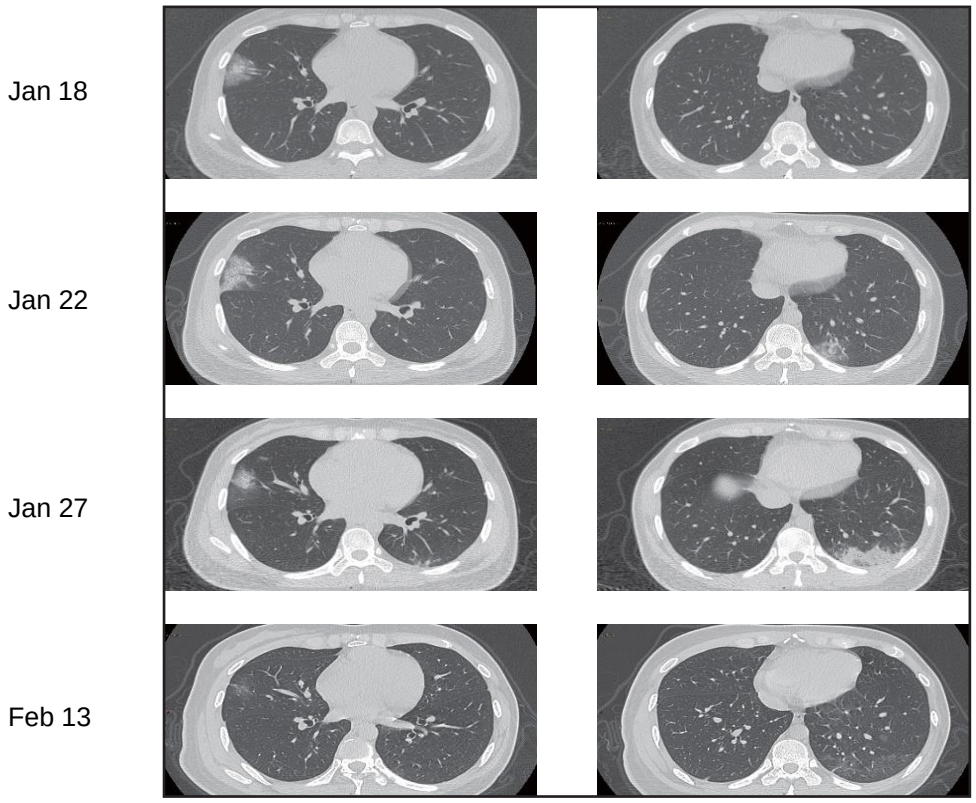


Figure S5 Chest radiographs and computed tomography (CT) of HCW O

Nurse O who was a highly suspected case had negative viral nucleic acid tests but had COVID-19-like symptoms and imaging findings. There is a flaky GGO under the pleura in the middle lobe of right lung on Jan 18, 2020. The density of lesion increased, and the interlobular septum thickened, showing paving stones sign as well as interpleural pleura traction, and a GGO appear in the posterior basal segment of the left lung on Jan 22, 2020. The range and the density of lesions in the right middle lobe reduced, and the lesion in the posterior basal and outer basal segments of the lower lobe of the left lung is enlarged and the density increased on Jan 27, 2020. Most of the lesions disappeared, leaving a few GGO and fiber cable shadows on Feb 13, 2020, 29 days after the onset of illness. The infiltrated can be waning.



Supplementary Tables

Table S1 Clinical Characteristics and Treatments in Patients with Laboratory-Confirmed Novel Coronavirus Pneumonia

Variable	Value
Signs and symptoms on admission	N*=35
Fever	
Any — no. (%)	30(85.7)
Maximal temperature — °C	38.8±1.4
37.3–38.0°C	7(23.3)
38.1–39.0°C	12(40)
>39.0°C	4(13.3)
N/A	7(23.3)
Cough — no. (%)	19(54.3)
Chest tightness — no. (%)	14(40)
Myalgia — no. (%)	16(45.7)
Malaise — no. (%)	26(74.3)
Headache — no. (%)	13(37.1)
Sore throat — no. (%)	17(48.6)
Rhinorrhoea — no. (%)	6(17.1)
Poor appetite — no. (%)	22(62.9)
Nausea and vomiting — no. (%)	3(8.6)
Diarrhoea — no. (%)	9(25.7)
Palpitation — no. (%)	4(11.4)
Chest pain — no. (%)	4(11.4)
Night sweat — no. (%)	1(2.9)
Rash — no. (%)	1(2.9)
Hypoxemia — no. (%)	3(8.6)
Treatment— no. (%)	
Glucocorticoids	0
Oxygen therapy	6(17.1%)

*N represents the number of included patients.

Table S2 Laboratory results of Patients with Laboratory-Confirmed Novel Coronavirus Pneumonia

Characteristic	Value
Laboratory exams on admission	
Blood routine	N*=31
WBC count (G/L)	
Median	4.5
Interquartile range	4.12-6.34
Subgroup — no. (%)	
<3.5	4(12.9)
3.5-9.5	27(87.1)
>9.5	0
Neutrophil count (G/L)	
Median	2.95
Interquartile range	2.17-4.31
Subgroup — no. (%)	
<1.8	5(16.1)
1.8-6.3	25(80.6)
>6.3	1(3.2)
Lymphocyte count (G/L)	
Median	1.13
Interquartile range	0.815-1.515
Subgroup — no. (%)	
<1.1	13(43.3)
1.1-3.2	17(56.7)
>3.2	0
Hemoglobin (g/L)	
Median	136
Interquartile range	125.5-151
Platelet count (G/L)	
Median	170
Interquartile range	148.5-202.5
Subgroup — no. (%)	
<125	2(6.9)
125-350	27(93.1)
>350	0
Blood biochemistry	N=26
Alanine aminotransferase (U/L)	
Median	18
Interquartile range	13-28.5
Subgroup — no. (%)	
≤ 40	22(84.6)
> 40	4(15.4)
Aspartate aminotransferase (U/L)	

Median	22.5
Interquartile range	19-28
Subgroup — no. (%)	
≤ 40	25(96.2)
> 40	1(3.8)
Albumin (g/L)	
Median	41.6
Interquartile range	38.6-44.125
Total bilirubin (μmol/L)	
Median	8.75
Interquartile range	6.9-10.1
Direct bilirubin(μmol/L)	
Median	3.4
Interquartile range	2.225-4
Creatinine (μmol/L)	
Median	64.65
Interquartile range	55.6-77.85
Subgroup — no. (%)	
≤133	26(100)
> 133	0
Blood urea nitrogen (mmol/L)	
Median	3.76
Interquartile range	2.85-4.23
Creatine kinase (U/L)	
Median	55.5
Interquartile range	45-88.75
Subgroup — no. (%)	
≤174	23(95.8)
> 174	1(4.2)
Lactate dehydrogenase (U/L)	
Median	187
Interquartile range	165-262
Subgroup — no. (%)	
≤245	16(69.6)
> 245	7(30.4)
Infection-related biomarkers	N=22
C-reactive protein(mg/L)	
Subgroup — no. (%)	
< 8	11(50)
≥8	11(50)

Procalcitonin (μg/ml)	
Subgroup — no. (%)	
< 0.5	21(95.5)
≥0.5	1(4.5)
Erythrocyte sedimentation rate(mm/h)	
Median	10.5
Interquartile range	6-23.5
Interleukin-6(pg/ml)	
Median	4.68
Interquartile range	3.06-7.17
Chest x-ray and CT findings on admission— no. (%)	
Ground-glass opacity (GGO) dominating	29(82.9)
Consolidation dominating	4(11.4)
GGO and consolidation integrating	1(2.9)
Normal	1(2.9)

*N represents the number of included patients.

Blood routine:

WBC count (G/L) Normal Range: 3.5-9.5

Neutrophil count (G/L) Normal Range: 1.8-6.3

Lymphocyte count (G/L) Normal Range: 1.1-3.2

Hemoglobin (g/L) Normal Range: 130-175

Platelet count (G/L) Normal Range: 125-350

Blood biochemistry:

Alanine aminotransferase (U/L) Normal Range: 5-40

Aspartate aminotransferase (U/L) Normal Range: 8-40

Albumin (g/L) Normal Range: 35-55

Total bilirubin (μmol/L) Normal Range: 5.1-19

Direct bilirubin(μmol/L) Normal Range: 1.7-6.8

Creatinine (μmol/L) Normal Range: 44-133

Blood urea nitrogen (mmol/L) Normal Range: 2.9-8.2

Creatine kinase (U/L) Normal Range: 38-174

Lactate dehydrogenase (U/L) Normal Range: 109-245

Infection-related biomarkers

C-reactive protein(mg/L) Normal Range: < 8

Procalcitonin (μg/ml) Normal Range: < 0.5

Erythrocyte sedimentation rate(mm/h) Normal Range: < 20

Interleukin-6(pg/ml) Normal Range: 0.1-2.9

Table S3 Corresponding sequencing sample ids and patient ids

Sample ID	Patient ID
WHUHnCoV001	J
WHUHnCoV002	Q
WHUHnCoV003	H
WHUHnCoV004	M
WHUHnCoV005	C
WHUHnCoV006	F
WHUHnCoV007	E
WHUHnCoV008	R
WHUHnCoV011	B
WHUHnCoV012	G
WHUHnCoV020	e
WHUHnCoV021	V

Table S4 The detailed mutation information of our 12 samples.

Sample ID	Pos	Ref	Alt
WHUHnCoV001	2536	C	T
WHUHnCoV001	8782	C	T
WHUHnCoV001	8886	T	C
WHUHnCoV001	28144	T	C
WHUHnCoV002	2536	C	T
WHUHnCoV002	8782	C	T
WHUHnCoV002	8886	T	C
WHUHnCoV002	28144	T	C
WHUHnCoV003	8782	C	T
WHUHnCoV003	18996	T	C
WHUHnCoV003	24370	C	T
WHUHnCoV003	28144	T	C
WHUHnCoV003	29029	T	C
WHUHnCoV004	2536	C	T
WHUHnCoV004	8782	C	T
WHUHnCoV004	8886	T	C
WHUHnCoV004	28144	T	C
WHUHnCoV005	8782	C	T
WHUHnCoV005	10626	C	T
WHUHnCoV005	28144	T	C
WHUHnCoV006	8782	C	T
WHUHnCoV006	28144	T	C
WHUHnCoV007	8782	C	T
WHUHnCoV007	16325	G	C
WHUHnCoV007	28144	T	C
WHUHnCoV008	2536	C	T
WHUHnCoV008	8782	C	T
WHUHnCoV008	8886	T	C
WHUHnCoV008	28144	T	C
WHUHnCoV011	8782	C	T
WHUHnCoV011	28144	T	C
WHUHnCoV012	8782	C	T
WHUHnCoV012	28144	T	C
WHUHnCoV020	2536	C	T
WHUHnCoV020	8782	C	T
WHUHnCoV020	8886	T	C
WHUHnCoV020	28144	T	C
WHUHnCoV021	17249	C	T
WHUHnCoV021	17894	C	T

The reference genomes we used was Wuhan-Hu-1 (GenBank accession number, NC_045512.2)

Table S5 The integrated introduction of all 61 published 2019-nCoV

Strain	Gisaid_epi_isl	Genbank_accession	Date	Country	Location	Segment	Host	Originating_lab	Submitting_lab	Authors
2019-nCoV WHU01	EPI_ISL_406716	MN988668	2020/1/2	China	Wuhan	genome	human	State Key Laboratory of Virology, Wuhan University	State Key Laboratory of Virology, Wuhan University	Chen et al
2019-nCoV WHU02	EPI_ISL_406717	MN988669	2020/1/2	China	Wuhan	genome	human	State Key Laboratory of Virology, Wuhan University	State Key Laboratory of Virology, Wuhan University	Chen et al
2019-nCoV/USA-AZ1/2020	EPI_ISL_406223	MN997409	2020/1/22	USA	Phoenix	genome	human	Arizona Department of Health Services, Phoenix, AZ, USA	Pathogen Discovery, Respiratory Viruses Branch, Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA	Tao et al
2019-nCoV/USA-CA1/2020	EPI_ISL_406034	MN994467	2020/1/23	USA	Los Angeles	genome	human	California Department of Public Health, Richmond CA, USA	Pathogen Discovery, Respiratory Viruses Branch, Division of Viral Diseases, Centers for Dieases Control and Prevention, Atlanta GA, USA	Uehara et al
2019-nCoV/USA-CA2/2020	EPI_ISL_40603	MN994468	2020/1/22	USA	Orange	genome	huma	California	Pathogen Discovery,	Uehara

	6				County		n	Department of Public Health, Richmond CA, USA	Respiratory Viruses Branch, Division of Viral Diseases, Centers for Dieases Control and Prevention, Atlanta GA, USA	et al
2019-nCoV/USA-IL1/2020	EPI_ISL_404253	MN988713	2020/1/21	USA	Chicago	genome	human	IL Department of Public Health Chicago Laboratory, Chicago, IL	Pathogen Discovery, Respiratory Viruses Branch, Division of Viral Diseases, Centers for Dieases Control and Prevention, Atlanta, GA	Tao et al
2019-nCoV/USA-WA1/2020	EPI_ISL_404895	MN985325	2020/1/19	USA	Seattle	genome	human	Providence Regional Medical Center	Division of Viral Diseases, Centers for Disease Control and Prevention	Queen et al
2019-nCoV_HKU-SZ-002a_2020	EPI_ISL_406030	MN938384	2020/01/XX	China	Shenzhen	genome	human	University of Hong Kong-Shenzhen Hospital	University of Hong Kong-Shenzhen Hospital	Chan et al
2019-nCoV_HKU-SZ-005b_2020	EPI_ISL_405839	MN975262	2020/01/XX	China	Shenzhen	genome	human	University of Hong Kong-Shenzhen Hospital	University of Hong Kong-Shenzhen Hospital	Chan et al
BetaCoV/Australia/NSW01/2020	EPI_ISL_407893	/	2020/1/24	Australia	Sydney	genome	human	Centre for Infectious Diseases and Microbiology Laboratory	NSW Health Pathology - Institute of Clinical Pathology and Medical Research; Westmead	Eden et al

								Services, Westmead, Australia	Hospital; University of Sydney, Westmead, Australia	
BetaCoV/Australia/VIC01/2020	EPI_ISL_406844	/	2020/1/25	Australia	Clayton	genome	human	Monash Medical Centre, Melbourne, Australia	Collaboration between the University of Melbourne at The Peter Doherty Institute for Infection and Immunity, and the Victorian Infectious Disease Reference Laboratory, Melbourne, Australia	Caly et al
BetaCoV/England/01/2020	EPI_ISL_407071	/	2020/1/29	United Kingdom	England	genome	human	Respiratory Virus Unit, Microbiology Services Colindale, Public Health England, London, United Kingdom	Respiratory Virus Unit, Microbiology Services Colindale, Public Health England, London, United Kingdom	Galiano et al
BetaCoV/England/02/2020	EPI_ISL_407073	/	2020/1/29	United Kingdom	England	genome	human	Respiratory Virus Unit, Microbiology Services Colindale, Public Health England, London, United Kingdom	Respiratory Virus Unit, Microbiology Services Colindale, Public Health England, London, United Kingdom	Galiano et al
BetaCoV/Finland/1/2020	EPI_ISL_407079	MT020781	2020/1/29	Finland	Rovaniemi	genome	human	Lapland Central Hospital, Finland	Department of Virology, University of Helsinki	Smura et al

									and Helsinki University Hospital, Helsinki, Finland	
BetaCoV/Foshan/20SF207/2020	EPI_ISL_406534	/	2020/1/22	China	Foshan	genome	human	Guangdong Provincial Institute of Public Health, Guangzhou, China	Guangdong Provincial Center for Diseases Control and Prevention, Guangzhou, China	Kang et al
BetaCoV/Foshan/20SF210/2020	EPI_ISL_406535	/	2020/1/22	China	Foshan	genome	human	Guangdong Provincial Institute of Public Health, Guangzhou, China	Guangdong Provincial Center for Diseases Control and Prevention, Guangzhou, China	Kang et al
BetaCoV/Foshan/20SF211/2020	EPI_ISL_406536	/	2020/1/22	China	Foshan	genome	human	Guangdong Provincial Institute of Public Health, Guangzhou, China	Guangdong Provincial Center for Diseases Control and Prevention, Guangzhou, China	Kang et al
BetaCoV/France/IDF0372/2020	EPI_ISL_406596	/	2020/1/23	France	Paris	genome	human	Department of Infectious and Tropical Diseases, Bichat Claude Bernard Hospital, Paris, France	National Reference Center for Viruses of Respiratory Infections, Institut Pasteur, Paris, France	Albert et al
BetaCoV/France/IDF0373/2020	EPI_ISL_406597	/	2020/1/23	France	Paris	genome	human	Department of Infectious and Tropical Diseases, Bichat Claude Bernard Hospital,	National Reference Center for Viruses of Respiratory Infections, Institut Pasteur, Paris, France	Albert et al

								Paris, France		
BetaCoV/Germany/BavPat1/2020	EPI_ISL_406862	/	2020/1/28	Germany	Starnberg	genome	human	Charite Universitaetsmedizin Berlin, Institute of Virology; Institut fuer Mikrobiologie der Bundeswehr, Munich, Germany	Charite Universitaetsmedizin Berlin, Institute of Virology, Berlin, Germany	Corman et al
BetaCoV/Guangdong/20SF012/2020	EPI_ISL_403932	/	2020/1/14	China	Shenzhen	genome	human	Guangdong Provincial Center for Diseases Control and Prevention; Guangdong Provinical Public Health, Guangzhou, China	Department of Microbiology, Guangdong Provincial Center for Diseases Control and Prevention; Guangdong Provinical Public Health, Guangzhou, China	Kang et al
BetaCoV/Guangdong/20SF013/2020	EPI_ISL_403933	/	2020/1/15	China	Shenzhen	genome	human	Guangdong Provincial Center for Diseases Control and Prevention; Guangdong Provinical Public Health, Guangzhou, China	Department of Microbiology, Guangdong Provincial Center for Diseases Control and Prevention; Guangdong Provinical Public Health, Guangzhou, China	Kang et al
BetaCoV/Guangdong/20SF014/2020	EPI_ISL_403934	/	2020/1/15	China	Shenzhen	genome	human	Guangdong Provincial Center	Department of Microbiology,	Kang et al

								for Diseases Control and Prevention; Guangdong Provinical Public Health, Guangzhou, China	Guangdong Provincial Center for Diseases Control and Prevention; Guangdong Provinical Public Health, Guangzhou, China	
BetaCoV/Guangdong/20SF025/2020	EPI_ISL_403935	/	2020/1/15	China	Shenzhen	genome	human	Guangdong Provincial Center for Diseases Control and Prevention; Guangdong Provinical Public Health, Guangzhou, China	Department of Microbiology, Guangdong Provincial Center for Diseases Control and Prevention; Guangdong Provinical Public Health, Guangzhou, China	Kang et al
BetaCoV/Guangdong/20SF028/2020	EPI_ISL_403936	/	2020/1/17	China	Zhuhai	genome	human	Guangdong Provincial Center for Diseases Control and Prevention; Guangdong Provinical Public Health, Guangzhou, China	Department of Microbiology, Guangdong Provincial Center for Diseases Control and Prevention; Guangdong Provinical Public Health, Guangzhou, China	Kang et al
BetaCoV/Guangdong/20SF040/2020	EPI_ISL_403937	/	2020/1/18	China	Zhuhai	genome	human	Guangdong Provincial Center for Diseases Control and Prevention;	Department of Microbiology, Guangdong Provincial Center for Diseases	Kang et al

								Guangdong Provinical Public Health, Guangzhou, China	Control and Prevention; Guangdong Provinical Public Health, Guangzhou, China	
BetaCoV/Guangdong/20SF174/2020	EPI_ISL_406531	/	2020/1/22	China	Zhuhai	genome	human	Guangdong Provincial Institute of Public Health, Guangzhou, China	Guangdong Provincial Center for Diseases Control and Prevention, Guangzhou, China	Kang et al
BetaCoV/Guangdong/20SF201/2020	EPI_ISL_406538	/	2020/1/23	China	Guangdong	genome	human	Guangdong Provincial Institute of Public Health, Guangzhou, China	Guangdong Provincial Center for Diseases Control and Prevention, Guangzhou, China	Kang et al
BetaCoV/Guangzhou/20SF206/2020	EPI_ISL_406533	/	2020/1/22	China	Guangzhou	genome	human	Guangdong Provincial Institute of Public Health, Guangzhou, China	Guangdong Provincial Center for Diseases Control and Prevention, Guangzhou, China	Kang et al
BetaCoV/Hangzhou/HZCDC0001/2020	EPI_ISL_407313	/	2020/1/19	China	Hangzhou	genome	human	Hangzhou Center for Disease Control and Prevention	Hangzhou Center for Disease Control and Prevention	/
BetaCoV/Japan/AI/I-004/2020	EPI_ISL_407084	LC521925	2020/1/25	Japan	Aichi	genome	human	Department of Virology III, National Institute of Infectious Diseases, Tokyo, Japan	Pathogen Genomics Center, National Institute of Infectious Diseases, Tokyo, Japan	Sekizuka et al
BetaCoV/Korea/KCDC03/2020	EPI_ISL_407193	/	2020/1/25	South Korea	Gyeonggi	genome	human	Korea Centers for Disease Control &	Korea Centers for Disease Control &	Kim et al

								Prevention (KCDC), Center for Laboratory Control of Infectious Diseases, Division of Viral Diseases, Cheongju, Korea	Prevention (KCDC), Center for Laboratory Control of Infectious Diseases, Division of Viral Diseases, Cheongju, Korea	
BetaCoV/Nonthaburi/61/2020	EPI_ISL_403962	/	2020/1/8	Thailand	Bangkok	genome	human	Bamrasnaradura Hospital, Nonthaburi, Thailand	Department of Medical Sciences, National Institute of Health, Nonthaburi, Thailand	Pilailuk et al
BetaCoV/Nonthaburi/74/2020	EPI_ISL_403963	/	2020/1/13	Thailand	Bangkok	genome	human	Bamrasnaradura Hospital, Nonthaburi, Thailand	Department of Medical Sciences, National Institute of Health, Nonthaburi, Thailand	Pilailuk et al
BetaCoV/Shenzhen/SZTH-001/2020	EPI_ISL_406592	/	2020/1/13	China	Shenzhen	genome	human	Shenzhen Third People's Hospital, Shenzhen, China	Shenzhen Key Laboratory of Pathogen and Immunity, National Clinical Research Center for Infectious Disease, Shenzhen, China	Yang et al
BetaCoV/Shenzhen/SZTH-002/2020	EPI_ISL_406593	/	2020/1/13	China	Shenzhen	genome	human	Shenzhen Third People's Hospital, Shenzhen, China	Shenzhen Key Laboratory of Pathogen and Immunity, National Clinical Research	Yang et al

									Center for Infectious Disease, Shenzhen, China	
BetaCoV/Shenzhen/SZTH-003/2020	EPI_ISL_406594	/	2020/1/16	China	Shenzhen	genome	human	Shenzhen Third People's Hospital, Shenzhen, China	Shenzhen Key Laboratory of Pathogen and Immunity, National Clinical Research Center for Infectious Disease, Shenzhen, China	Yang et al
BetaCoV/Shenzhen/SZTH-004/2020	EPI_ISL_406595	/	2020/1/16	China	Shenzhen	genome	human	Shenzhen Third People's Hospital, Shenzhen, China	Shenzhen Key Laboratory of Pathogen and Immunity, National Clinical Research Center for Infectious Disease, Shenzhen, China	Yang et al
BetaCoV/Singapore/1/2020	EPI_ISL_406973	/	2020/1/23	Singapore	Singapore	genome	human	Singapore General Hospital, Singapore	National Public Health Laboratory, Singapore	Mak et al
BetaCoV/Taiwan/2/2020	EPI_ISL_406031	/	2020/1/23	Taiwan	Kaohsiung	genome	human	Centers for Disease Control, R.O.C., Taipei, Taiwan	Centers for Disease Control, R.O.C., Taipei, Taiwan	Yang et al
BetaCoV/USA/WA1-A12/2020	EPI_ISL_407214	MT020880	2020/1/25	USA	/	genome	human	WA State Department of Health	Pathogen Discovery, Respiratory Viruses Branch, Division of Viral Diseases, Centers	/

									for Dieases Control and Prevention	
BetaCoV/USA/WA1-F6/2020	EPI_ISL_407215	MT020881	2020/1/25	USA	/	genome	human	WA State Department of Health	Pathogen Discovery, Respiratory Viruses Branch, Division of Viral Diseases, Centers for Dieases Control and Prevention	/
BetaCoV/Wuhan/HBCDC-HB-01/2019	EPI_ISL_402132	/	2019/12/30	China	Wuhan	genome	human	Wuhan Jinyintan Hospital, Wuhan, China	Hubei Provincial Center for Disease Control and Prevention, Wuhan, China	Fang et al
BetaCoV/Wuhan/IPBCAMS-WH-01/2019	EPI_ISL_402123	MT019529	2019/12/23	China	Wuhan	genome	human	Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China	Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China	Ren et al
BetaCoV/Wuhan/IPBCAMS-WH-02/2019	EPI_ISL_403931	MT019530	2020/2/4	China	Wuhan	genome	human	NHC Key Laboratory of Systems Biology of Pathogens and Christophe Merieux Laboratory	National Genomics Data Center	Ren,L et al
BetaCoV/Wuhan/IPBCAMS-WH-	EPI_ISL_40393	MT019531	2019/12/30	China	Wuhan	genome	huma	Institute of	Institute of Pathogen	Ren et al

03/2019	0						n	Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China	Biology, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China	
BetaCoV/Wuhan/IPBCAMS-WH-04/2019	EPI_ISL_403929	MT019532	2019/12/30	China	Wuhan	genome	human	Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China	Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China	Ren et al
BetaCoV/Wuhan/IPBCAMS-WH-05/2020	EPI_ISL_403928	MT019533	2020/2/4	China	Wuhan	genome	human	NHC Key Laboratory of Systems Biology of Pathogens and Christophe Merieux Laboratory	National Genomics Data Center	Ren,L et al
BetaCoV/Wuhan/IVDC-HB-01/2019	EPI_ISL_402119	/	2019/12/30	China	Wuhan	genome	human	National Institute for Viral Disease Control and Prevention, China CDC, Beijing, China	National Institute for Viral Disease Control and Prevention, China CDC, Beijing, China	Tan et al
BetaCoV/Wuhan/WH-01/2019	EPI_ISL_40679	/	2019/12/26	China	Wuhan	genome	huma	General Hospital of	BGI & Institute of	Chen et

	8						n	Central Theater Command of People's Liberation Army of China, Wuhan, China	Microbiology, Chinese Academy of Sciences & Shandong First Medical University & Shandong Academy of Medical Sciences	al
BetaCoV/Wuhan/WH-03/2019	EPI_ISL_406800	/	2020/1/1	China	Wuhan	genome	human	General Hospital of Central Theater Command of People's Liberation Army of China, Wuhan, China	BGI & Institute of Microbiology, Chinese Academy of Sciences & Shandong First Medical University & Shandong Academy of Medical Sciences	Chen et al
BetaCoV/Wuhan/WH-04/2019	EPI_ISL_406801	/	2020/1/5	China	Wuhan	genome	human	General Hospital of Central Theater Command of People's Liberation Army of China, Wuhan, China	BGI & Institute of Microbiology, Chinese Academy of Sciences & Shandong First Medical University & Shandong Academy of Medical Sciences	Chen et al
BetaCoV/Zhejiang/WZ-01/2020	EPI_ISL_404227	/	2020/1/16	China	Hangzhou	genome	human	Zhejiang Provincial Center for Disease Control and Prevention, Hangzhou, China	Department of Microbiology, Zhejiang Provincial Center for Disease Control and Prevention, Hangzhou, China	Chen et al

BetaCoV/Zhejiang/WZ-02/2020	EPI_ISL_404228	/	2020/1/17	China	Hangzhou	genome	human	Zhejiang Provincial Center for Disease Control and Prevention, Hangzhou, China	Department of Microbiology, Zhejiang Provincial Center for Disease Control and Prevention, Hangzhou, China	Zhang et al
Wuhan/WIV02/2019	EPI_ISL_402127	MN996527	2019/12/30	China	Wuhan	genome	human	Wuhan Jinyintan Hospital, Wuhan, China	Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China	Zhou et al
Wuhan/WIV04/2019	EPI_ISL_402124	MN996528	2019/12/30	China	Wuhan	genome	human	Wuhan Jinyintan Hospital, Wuhan, China	Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China	Zhou et al
Wuhan/WIV05/2019	EPI_ISL_402128	MN996529	2019/12/30	China	Wuhan	genome	human	Wuhan Jinyintan Hospital, Wuhan, China	Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China	Zhou et al
Wuhan/WIV06/2019	EPI_ISL_402129	MN996530	2019/12/30	China	Wuhan	genome	human	Wuhan Jinyintan Hospital, Wuhan, China	Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China	Zhou et al
Wuhan/WIV07/2019	EPI_ISL_402130	MN996531	2019/12/30	China	Wuhan	genome	human	Wuhan Jinyintan Hospital, Wuhan, China	Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, China	Zhou et al

Wuhan-Hu-1/2019	EPI_ISL_402125	MN908947	2019/12/26	China	Wuhan	genome	human	unknown	National Institute for Communicable Disease Control and Prevention (ICDC), China CDC, Beijing, China	Zhang et al
Zhejiang/Hangzhou-1/2020	EPI_ISL_406970	MT039873	2020/1/20	China	Hangzhou	genome	human	Hangzhou Center for Disease and Control Microbiology Lab, Zhejiang, China	Hangzhou Center for Disease and Control Microbiology Lab, Zhejiang, China	Hua et al

Table S6 The integrated mutation information of all 67 published 2019-nCoV

Gisaid_epi_isl	Pos	Ref	Alt
EPI_ISL_402123	3778	A	G
EPI_ISL_402123	8388	A	G
EPI_ISL_402123	8987	T	A
EPI_ISL_402127	21316	G	A
EPI_ISL_402127	24325	A	G
EPI_ISL_402128	7016	G	A
EPI_ISL_402128	21137	A	G
EPI_ISL_402130	8001	A	C
EPI_ISL_402130	9534	C	T
EPI_ISL_402132	21656	T	A
EPI_ISL_403930	6996	T	C
EPI_ISL_403932	8782	C	T
EPI_ISL_403932	28144	T	C
EPI_ISL_403932	29095	C	T
EPI_ISL_403933	8782	C	T
EPI_ISL_403933	28144	T	C
EPI_ISL_403933	29095	C	T
EPI_ISL_403934	23569	T	C
EPI_ISL_403935	8782	C	T
EPI_ISL_403935	28144	T	C
EPI_ISL_403935	29095	C	T
EPI_ISL_403936	21707	C	T

EPI_ISL_403937	21707	C	T
EPI_ISL_404227	31	A	G
EPI_ISL_404227	583	C	T
EPI_ISL_406030	8782	C	T
EPI_ISL_406030	28144	T	C
EPI_ISL_406030	29095	C	T
EPI_ISL_406031	16188	G	T
EPI_ISL_406031	25964	A	G
EPI_ISL_406031	26144	G	T
EPI_ISL_406031	29877	A	T
EPI_ISL_406531	21707	C	T
EPI_ISL_406533	15324	C	T
EPI_ISL_406533	29303	C	T
EPI_ISL_406534	28291	C	T
EPI_ISL_406534	28854	C	T
EPI_ISL_406535	17373	C	T
EPI_ISL_406536	17373	C	T
EPI_ISL_406592	1648	C	T
EPI_ISL_406592	2169	T	C
EPI_ISL_406592	3801	A	C
EPI_ISL_406592	4643	GAAGAAGCTGCTCG	GGAGAAGCTGCTCC
EPI_ISL_406592	4727	GGTTATCTTACTT	GTATATCTTACTC
EPI_ISL_406592	5464	T	C
EPI_ISL_406592	6308	A	G
EPI_ISL_406592	6786	C	G

EPI_ISL_406592	6833	ATTAAA	AGTAAG
EPI_ISL_406592	8091	T	A
EPI_ISL_406592	8455	T	C
EPI_ISL_406592	12597	T	A
EPI_ISL_406592	15636	T	A
EPI_ISL_406592	19269	C	T
EPI_ISL_406592	20315	T	A
EPI_ISL_406592	24947	G	C
EPI_ISL_406592	25347	A	G
EPI_ISL_406592	26108	A	T
EPI_ISL_406592	26141	A	T
EPI_ISL_406592	26754	GGTGGA	GCTGGT
EPI_ISL_406592	28144	T	C
EPI_ISL_406592	29095	C	T
EPI_ISL_406593	8782	C	T
EPI_ISL_406593	28144	T	C
EPI_ISL_406593	29095	C	T
EPI_ISL_406594	27577	C	T
EPI_ISL_406594	28854	C	T
EPI_ISL_406595	709	G	A
EPI_ISL_406595	6846	T	C
EPI_ISL_406595	11707	A	G
EPI_ISL_406595	19959	A	C
EPI_ISL_406595	22621	GAACAGGAAGAGAATCAGCAACTGTGTTGCTG	GGACAGGAAGAGAATCAGCAACTGTGTTGCTT
EPI_ISL_406595	23569	T	C

EPI_ISL_406595	25645	T	C
EPI_ISL_406595	28716	C	T
EPI_ISL_406596	22661	G	T
EPI_ISL_406596	26144	G	T
EPI_ISL_406597	22661	G	T
EPI_ISL_406597	26144	G	T
EPI_ISL_406798	6968	C	A
EPI_ISL_406798	11764	T	A
EPI_ISL_406801	8782	C	T
EPI_ISL_406801	28144	T	C
EPI_ISL_406844	19065	T	C
EPI_ISL_406844	22303	T	G
EPI_ISL_406844	26144	G	T
EPI_ISL_406844	29749	ACGATCGAGTG	A
EPI_ISL_406862	241	C	T
EPI_ISL_406862	3037	C	T
EPI_ISL_406862	23403	A	G
EPI_ISL_406973	25060	A	G
EPI_ISL_407071	8782	C	T
EPI_ISL_407071	18488	T	C
EPI_ISL_407071	23605	T	G
EPI_ISL_407071	28144	T	C
EPI_ISL_407073	8782	C	T
EPI_ISL_407073	18488	T	C
EPI_ISL_407073	23605	T	G

EPI_ISL_407073	28144	T	C
EPI_ISL_407073	29596	A	G
EPI_ISL_407084	358	TGGAGACTCCGTGGAGGAGGTCTTA	T
EPI_ISL_407084	1912	C	T
EPI_ISL_407084	18512	C	T
EPI_ISL_407193	4402	T	C
EPI_ISL_407193	5062	G	T
EPI_ISL_407193	8782	C	T
EPI_ISL_407193	28144	T	C
EPI_ISL_407214	8782	C	T
EPI_ISL_407214	18060	C	T
EPI_ISL_407214	28144	T	C
EPI_ISL_407215	8782	C	T
EPI_ISL_407215	18060	C	T
EPI_ISL_407215	28144	T	C
EPI_ISL_407893	8782	C	T
EPI_ISL_407893	28144	T	C
MN975262	8782	C	T
MN975262	9561	C	T
MN975262	15607	T	C
MN975262	28144	T	C
MN975262	29095	C	T
MN985325	8782	C	T
MN985325	18060	C	T
MN985325	28144	T	C

MN994467	1548	G	A
MN994467	8782	C	T
MN994467	24034	C	T
MN994467	26729	T	C
MN994467	28077	G	C
MN994467	28144	T	C
MN994467	28792	A	T
MN994468	17000	C	T
MN994468	26144	G	T
MN997409	8782	C	T
MN997409	11083	G	T
MN997409	28144	T	C
MN997409	29095	C	T
MT019530	103	CTGCATGCTTAGTGCACTCACG	CAGCATGCCGAGTGCAGCCACA
MT019533	7866	G	T

The reference genomes we used was Wuhan-Hu-1 (GenBank accession number, NC_045512.2).

Reference

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2 Laboratory diagnostics for novel coronavirus. WHO 2020; (https://www .who .int/health -topics/coronavirus/ laboratory-diagnostics-for-novel-coronavirus).