

Supplementary table 1. Comparison of SARS-CoV-2 positive rate by mNGS and RT-PCR

Time	mNGS				RT-PCR			
	Sample size	Positive number	Positive (%)	rate	Sample size	Positive number	Positive (%)	rate
2023/3	608	4	0.66		59573	309	0.52	
2023/4	758	7	0.92		39429	274	0.69	
2023/5	801	56	6.97		37918	3807	10.04	
2023/6	980	71	7.24		37146	2690	7.24	
2023/7	1032	44	4.26		33232	1478	4.45	
2023/8	1237	60	4.84		32769	1535	4.68	
2023/9	269	12	4.46		10587	294	2.78	
Total	5686	254	4.47		250654	10387	4.14	

Supplementary table 2. Detail information of patients with blood positive for SARS-CoV-2

Patients	Gender	Age	Pneumonia	Comorbidity	WBC (E9/L)	NE (E9/L)	LYM (E9/L)	ct (ORF1ab/ N)	outcome
P1	female	43	severe	Lymphoma	2.76	2.54	0.12	30/32	discharge
P2	male	84	severe	Sepsis; ventricular dysfunction	15.51	13.48	1.74	19/19	death
P3	male	75	severe	Tracheotomy; hypertension; diabetes melitus; dementia; parkinsonism	3.63	2.71	0.68	27/27	discharge
P4	female	78	severe	Hypertension	9.45	9.03	0.12	20/21	discharge
P5	male	47	severe	Hypertension	15.39	14.02	0.96	34/35	discharge
P6	male	71	severe	Hypertension; diabetes melitus; Chronic obstructive pulmonary disease	15.07	13.74	0.93	30/30	discharge
P7	male	85	severe	Hypertension; diabetes melitus; lymphoma	1.65	0	0	20/19	discharge
P8	female	29	non-severe	Wegener's granulomatosis on lungs	9.94	8.89	0.53	28/29	discharge
P9	male	88	non-severe	Hypertension	3.45	2.47	0.77	23/22	discharge
P10	male	93	non-severe	Hypertension; diabetes melitus	3.44	2.47	0.6	27/27	discharge
P11	male	44	non-severe	Lymphoma	2.03	1.16	0.65	30/31	discharge

Supplementary table 3. Sub-lineages of SARS-CoV-2 in COVID-19 patients

Sub-lineages	Non-severe pneumonia (n=77)	Severe pneumonia (n=45)	Total
FU.1	16 (20.78%)	9 (20.00%)	25 (20.50%)
EG.5.1.1	14 (18.18%)	7 (15.56%)	21 (17.21)
FY.3	13 (16.89%)	1 (2.22%)	14 (11.48%)
XBB.1.16.1	9 (11.69%)	5 (11.11%)	14 (11.48%)
XBB.1.16	4 (5.19%)	3 (6.67%)	7 (5.74%)
HK.3	3 (3.90%)	1 (2.22%)	4 (3.28%)
FL.2	0	3 (6.67%)	3 (2.46%)
XBB.1.5.24	3 (3.90%)	0	3 (2.46%)
XBB.2.3	3 (3.90%)	0	3 (2.46%)
BF.7.14	2 (2.60%)	0	2 (1.64%)
BN.1.2	1 (1.30%)	1 (2.22%)	2 (1.64%)
EG.5.1	0	2	2 (1.64%)
FE.1.1	2 (2.60%)	0	2 (1.64%)
FL.4	0	2	2 (1.64%)
FR.1.1	0	2	2 (1.64%)
FY.3.1	2 (2.60%)	0	2 (1.64%)
XBB.1.5	0	2	2 (1.64%)
XBB.1.9.1	1 (1.30%)	1 (2.22%)	2 (1.64%)
XBB.1.9.2	1 (1.30%)	1 (2.22%)	2 (1.64%)
BF.7.14.4	1 (1.30%)	0	1 (0.82%)
EG.4	0	1 (2.22%)	1 (0.82%)
EU.1.1	0	1 (2.22%)	1 (0.82%)
FE.1	1 (1.30%)	0	1 (0.82%)
FL.13	0	1 (2.22%)	1 (0.82%)
FL.3	0	1 (2.22%)	1 (0.82%)
FR.1	0	1 (2.22%)	1 (0.82%)
XBB.1	1 (1.30%)	0	1 (0.82%)

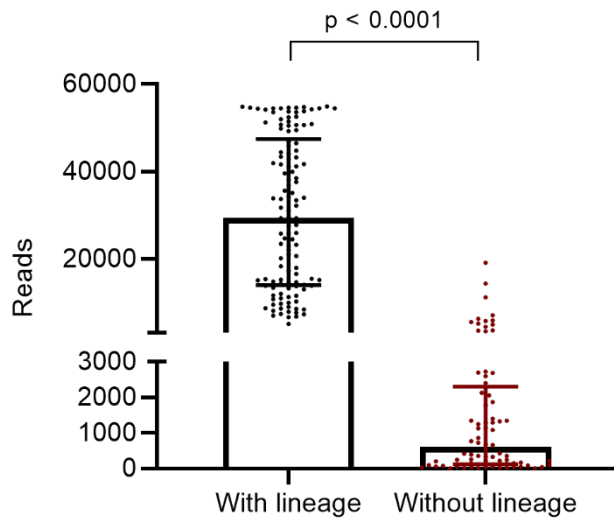


Figure S1. Reads of SARS-CoV-2 sequences typable with lineage. The more SARS-CoV-2 sequences can be obtained in a sample, the greater the coverage of the genome, and the more accurate the lineage information. A total of 122 (61%) patients had sufficient sequences for accurate lineage typing.