

THE LANCET

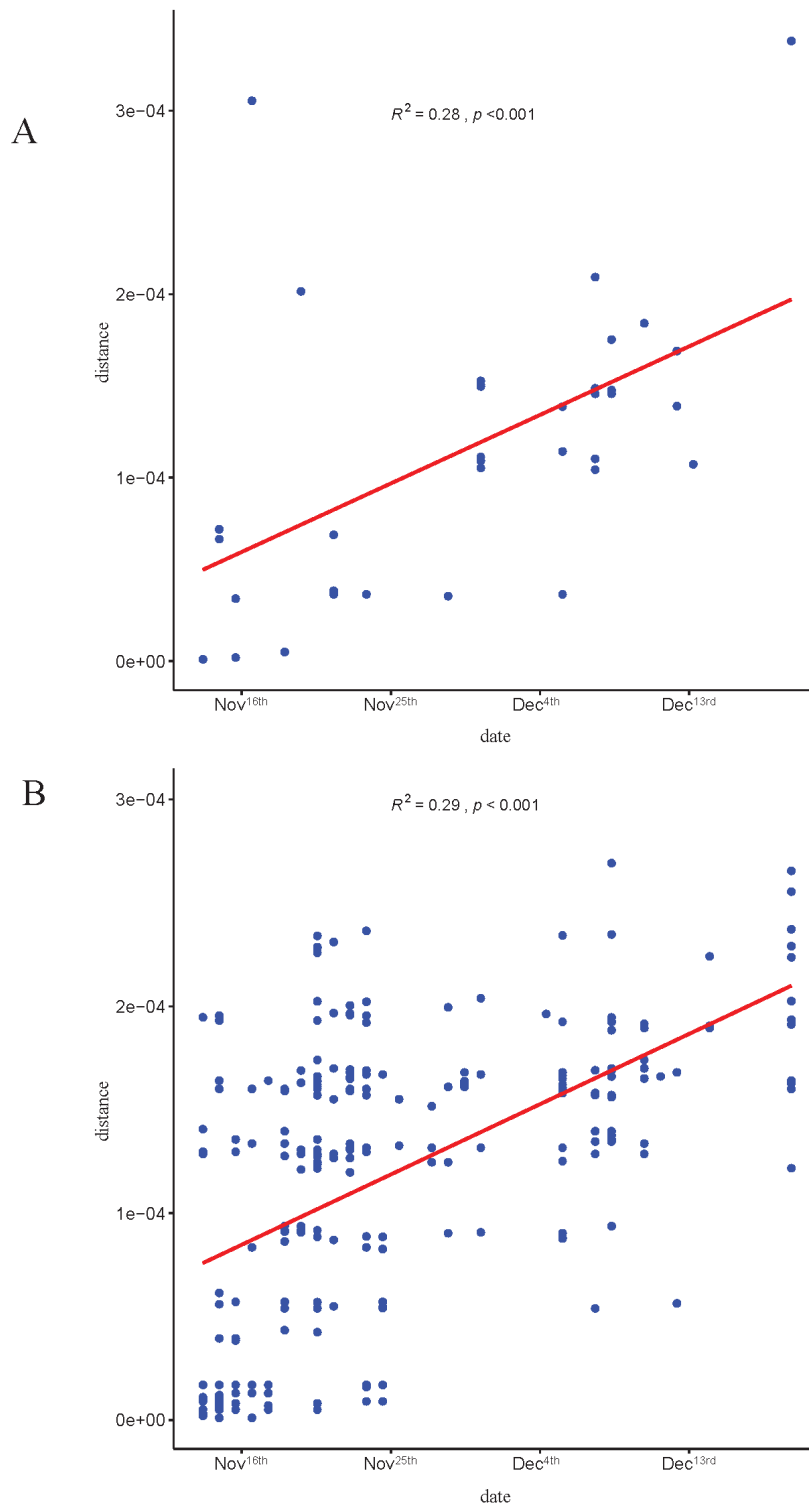
Supplementary appendix 2

This appendix formed part of the original submission and has been peer reviewed. We post it as supplied by the authors.

Supplement to: Pan Y, Wang L, Feng Z, et al. Characterisation of SARS-CoV-2 variants in Beijing during 2022: an epidemiological and phylogenetic analysis. *Lancet* 2023; published online Feb 8. [https://doi.org/10.1016/S0140-6736\(23\)00129-0](https://doi.org/10.1016/S0140-6736(23)00129-0).

Supplemental Results

Supplemental Figure 1

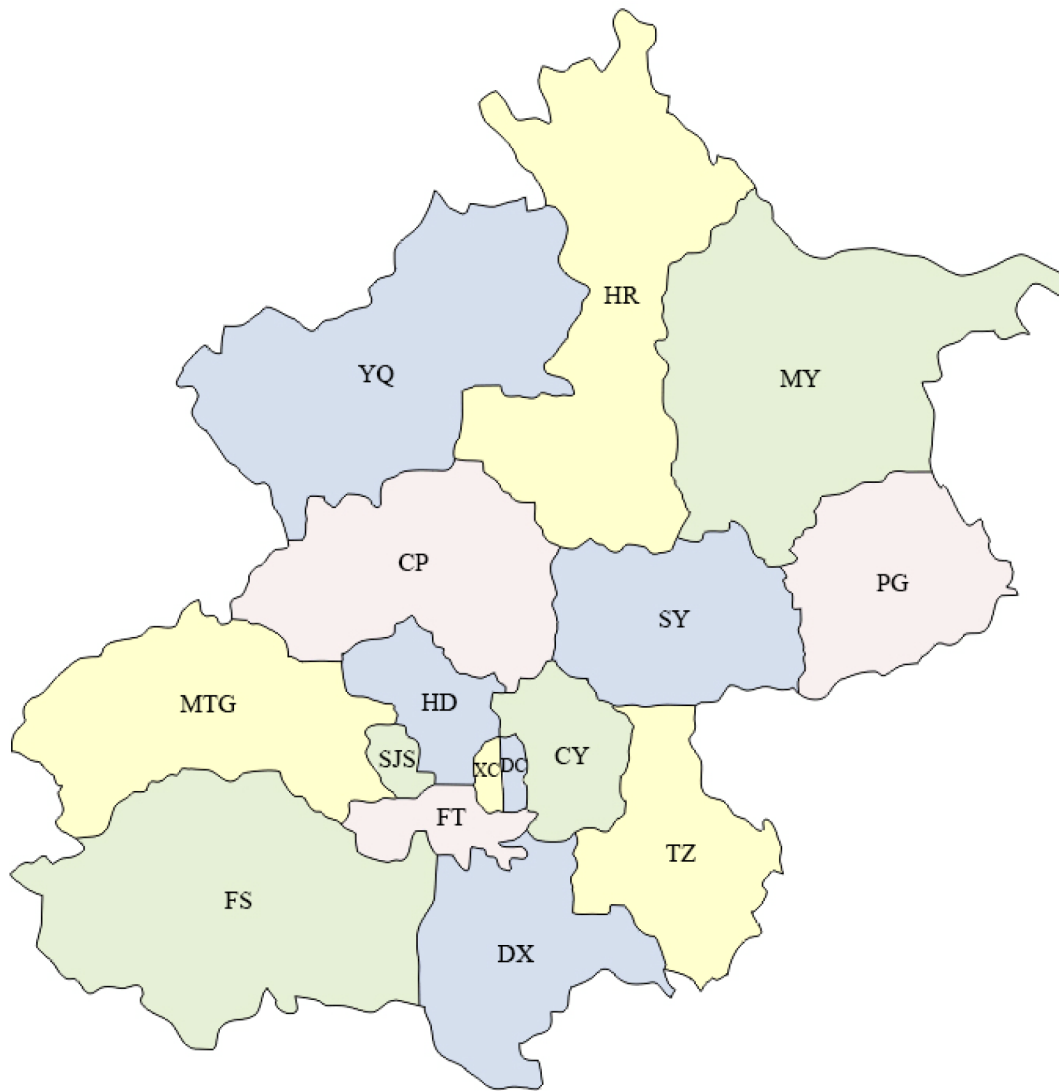


The temporal molecular evolutionary signal in our datasets.

A. Regression of root-to-tip divergence and sampling date for BA.5.2 genomic data used in this study

B. Regression of root-to-tip divergence and sampling date for BF.7 genomic data used in this study

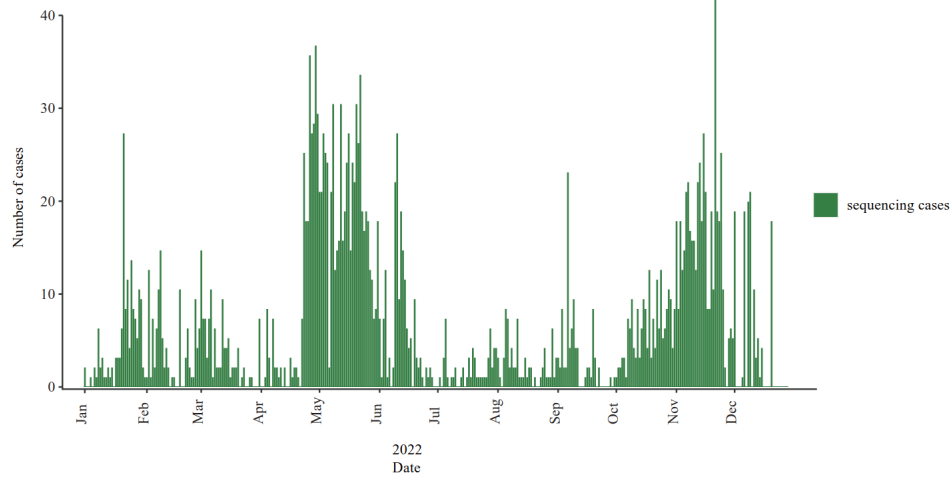
Supplemental Figure 2



Supplemental Figure 2. The map of Beijing Municipality

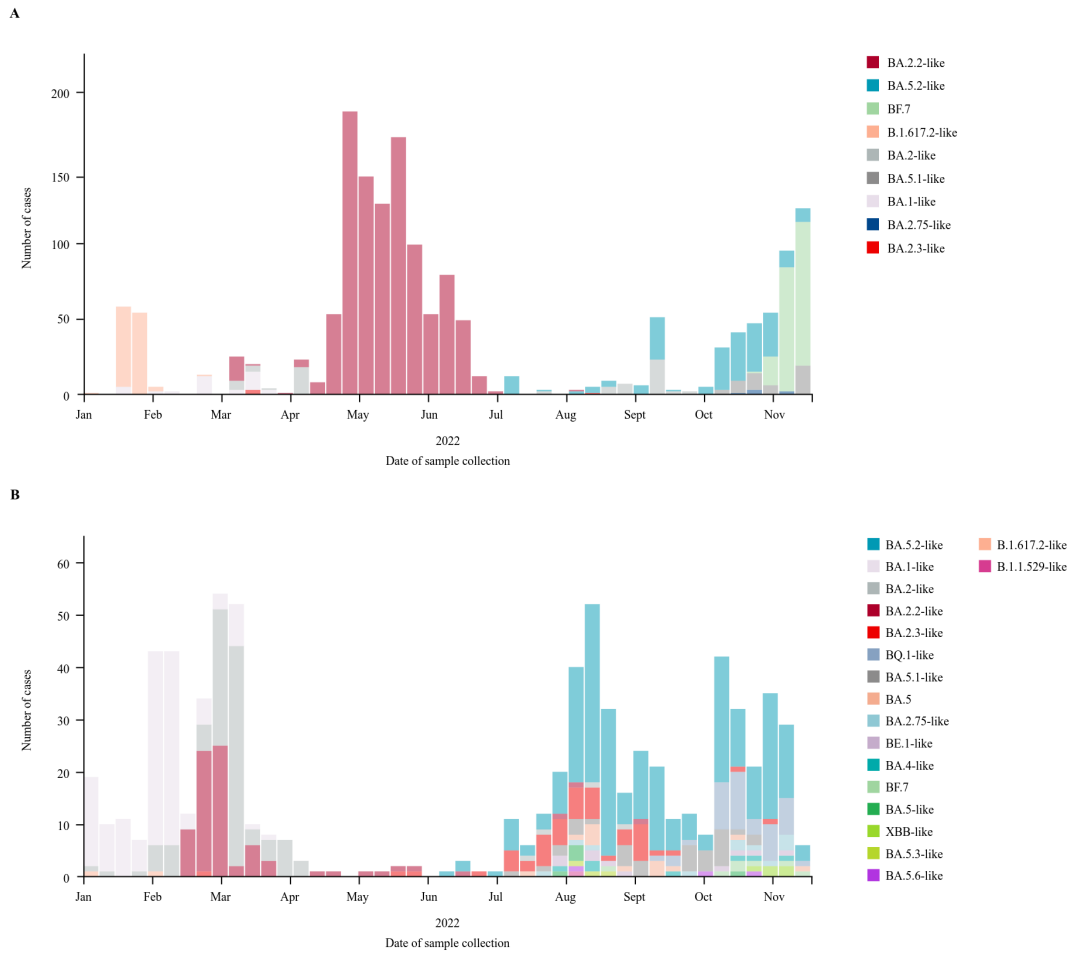
The Jingkai (JK) District locates in Daxing (DX) District, and was not shown in the map.

Supplemental Figure 3



Supplemental Figure 3. Distribution of sequences analyzed in this study in Beijing from January 2022 to 13 November 2022

Supplemental Figure 4



Supplemental Figure 4. Distribution of SARS-CoV-2 subvariants identified in Beijing from January 2022 to 13 November 2022.

A. Distribution of local SARS-CoV-2 subvariants identified in Beijing from January 2022 to 13 November 2022.

B. Distribution of imported SARS-CoV-2 subvariants identified in Beijing from January 2022 to 13 November 2022.

Supplemental Table

Supplemental Table 1 Log-marginal likelihood estimates from model selection by using the path-sampling (PS) and stepping-stone (SS) approaches for both datasets.

Dataset	Coalescent model	Log marginal likelihood	
		path-sampling (PS)	stepping-stone (SS)
BA.5.2	Constant	-41018.62609	-41018.47585
	Exponential	-41018.6987	-41018.72858
	Skyline	-41011.92666	-41011.78615
BF.7	Constant	-42483.07814	-42483.6583
	Exponential	-42477.17172	-42477.82076
	Skyline	-42455.09033	-42455.99873

Supplemental Table 2 The spatial distribution of sequencing samples in Beijing in 2022

	District	Abbreviation	Number of sequences (%)
Urban	Chaoyang	CY	467 (33.5%)
	Fengtai	FT	309 (22.17%)
	Haidian	HD	222 (15.93%)
	Dongcheng	DC	116 (8.32%)
	Xicheng	XC	104 (7.46%)
	Shijingshan	SJS	21 (1.51%)
Suburban	Fangshan	FS	165 (11.84%)
	Changping	CP	114 (8.18%)
	Tongzhou	TZ	71 (5.09%)
	Daxing	DX	55 (3.95%)
	Shunyi	SY	40 (2.87%)
	Huairou	HR	27 (1.94%)
	Mentougou	MTG	25 (1.79%)
	Pinggu	PG	15 (1.08%)
	Jingkai	JK	10 (0.72%)
	Miyun	MY	8 (0.57%)
	Yanqing	YQ	9 (0.65%)
	Total		

*, Among all 2,033 sequences obtained from local infections, 1778 sequences with geographic information were shown.

Supplemental Table 3. The countries and regions of origin of imported cases identified in Beijing in 2022

Countries and regions	Number of sequences (%)
Hong Kong, SAR, China	160 (21.86%)
Russia	108 (14.75%)
Taiwan, China	95 (12.98%)
Germany	70 (9.56%)
Republic of Korea	53 (7.24%)
United Arab Emirates	41 (5.6%)
France	38 (5.19%)
The United Kingdom	24 (3.28%)
Japan	20 (2.73%)
United States of America	10 (1.37%)
Italy	9 (1.23%)
Austria	7 (0.96%)
Turkey	6 (0.82%)
Guinea	5 (0.68%)
Angola	4 (0.55%)
Denmark	4 (0.55%)
Kazakhstan	4 (0.55%)
Switzerland	4 (0.55%)
Sweden	3 (0.41%)
Senegal	3 (0.41%)
Ukraine	3 (0.41%)
Spain	3 (0.41%)
Indonesia	3 (0.41%)
Ethiopia	2 (0.27%)
Ireland	2 (0.27%)
Australia	2 (0.27%)
Bahamas	2 (0.27%)
Bulgaria	2 (0.27%)
Congo	2 (0.27%)
Romania	2 (0.27%)
Mongolia	2 (0.27%)
South Africa	2 (0.27%)

Cyprus	2 (0.27%)
Slovakia	2 (0.27%)
Thailand	2 (0.27%)
Greece	2 (0.27%)
Singapore	2 (0.27%)
Zambia	2 (0.27%)
Albania	1 (0.14%)
Estonia	1 (0.14%)
Pakistan	1 (0.14%)
Brazil	1 (0.14%)
Belarus	1 (0.14%)
Equatorial Guinea	1 (0.14%)
Dominican Republic	1 (0.14%)
Democratic Republic of the Congo	1 (0.14%)
Netherlands	1 (0.14%)
Guinea-Bissau	1 (0.14%)
Canada	1 (0.14%)
Cameroon	1 (0.14%)
Latvia	1 (0.14%)
Lithuania	1 (0.14%)
Madagascar	1 (0.14%)
Mauritius	1 (0.14%)
Namibia	1 (0.14%)
Portugal	1 (0.14%)
Saudi Arabia	1 (0.14%)
Sudan	1 (0.14%)
Tajikistan	1 (0.14%)
Uzbekistan	1 (0.14%)
Hungary	1 (0.14%)
Iraq	1 (0.14%)
Israel	1 (0.14%)
Total	732 (100%)

Supplemental Table 4. The distribution of imported sub-variants identified in Beijing from Nov 14th to Dec 20th

Lineage	Number of sequences (%)
BQ.1	20 (31.7%)
BA.5.2	14 (22.2%)
XBB.1	6 (9.5%)
BF.7	5 (7.9%)
BA.5.9	5 (7.9%)
BA.5.1	3 (4.8%)
CM.8	1 (1.6%)
CL.1	1 (1.6%)
BW.1	1 (1.6%)
BR.2.1	1 (1.6%)
BN.1.4	1 (1.6%)
BF.28	1 (1.6%)
BE.4	1 (1.6%)
BA.5	1 (1.6%)
BA.4	1 (1.6%)
BA.2	1 (1.6%)
Total	63 (100%)