

Supplementary Table 1, related to Fig. 1. Surveillance of wild birds in China between February 2003 and February 2023.

Year	Province	Samples	Influenza isolation numbers	Isolation rates (%)	HPAIV numbers	Numbers of samples positive for HPAIV			
						H5N1	H5N6	H5N8	H5N2
2003	Heilongjiang	26	—						
2004	Heilongjiang	241	1	0.41					
2005	Heilongjiang	235	—						
2006	Heilongjiang	148	22	14.86					
2007	Heilongjiang	156	16	10.26					
2008	Heilongjiang	337	6	1.78					
2009	Heilongjiang	447	3	0.67					
2010	Heilongjiang	254	1	0.39					
	Hunan	30	3	10					
	Jilin	249	17	6.83					
	Subtotal	533	21	3.94					
2011	Jilin	602	160	26.58					
2012	Hebei	387	5	1.29					
	Heilongjiang	479	—						
	Jilin	269	—						
	Subtotal	1135	5	0.44					
2013	Gansu	19	—						
	Hebei	3177	30	0.94					

	Heilongjiang	405	2	0.49		
	Jiangxi	238	—			
	Jilin	456	1	0.22		
	Subtotal	4295	33	0.77		
2014	Anhui	5034	74	1.47		
	Hebei	1283	—			
	Heilongjiang	1647	13	0.79		
	Henan	140	3	2.14	3	3
	Hubei	961	6	0.62		
	Hunan	97	1	1.03		
	Inner Mongolia	1847	8	0.44		
	Jiangxi	110	—			
	Jilin	472	9	1.91		
	Liaoning	318	—			
	Ningxia	175	7	4		
	Qinghai	387	—			
	Sichuan	26	1	0.85		
	Tibet	943	—			
	Yunnan	498	—			
	Subtotal	13938	122	0.88	3	3
2015	Anhui	380	4	1.05		
	Hebei	3597	1	0.03	1	1

	Heilongjiang	1925	2	0.1			
	Henan	820	24	2.93	15	15	
	Hubei	724	3	0.41			
	Inner Mongolia	3687	14	0.38	13		13
	Liaoning	1131	3	0.27			
	Ningxia	136	—				
	Shaanxi	324	1	0.31	1	1	
	Shandong	368	19	5.16			
	Shanxi	3	2	66.67	2	2	
	Tibet	195	19	9.74	19	19	
	Subtotal	13290	92	0.69	51	38	13
2016	Beijing	1	1	100	1		1
	Anhui	5070	2	0.04			
	Hebei	2205	2	0.09			
	Heilongjiang	336	12	3.57	12		12
	Henan	815	67	8.22	67		67
	Hubei	2528	19	0.75	8		8
	Inner Mongolia	1112	4	0.36	1		1
	Jiangxi	187	—				
	Liaoning	3017	6	0.2			
	Ningxia	202	8	0.96	7		7
	Qinghai	5818	1	0.02	1		1

	Tibet	3318	30	0.9	30	1		29
	Subtotal	24609	152	0.62	127	1	12	114
2017	Tianjin	51	3	5.88				
	Anhui	1267	7	0.55	4			4
	Fujian	2610	10	0.38				
	Hebei	2293	—					
	Heilongjiang	2749	5	0.18	1			1
	Henan	1042	1	0.1				
	Hubei	2823	23	0.81				
	Inner Mongolia	3344	7	0.21				
	Jiangsu	1207	10	0.83	2			2
	Liaoning	7488	14	0.19				
	Ningxia	1291	29	2.25				
	Qinghai	5891	—					
	Shaanxi	429	1	0.23				
	Shandong	867	—					
	Tibet	2037	3	0.15	2			2
	Xinjiang	497	3	0.6				
	Subtotal	35886	116	0.32	9			9
2018	Beijing	29	—					
	Chongqing	38	—					
	Anhui	50	—					

	Fujian	1029	1	0.1
	Guizhou	3204	1	0.03
	Hainan	228	—	
	Hebei	2214	10	0.45
	Heilongjiang	2874	—	
	Henan	1049	2	0.19
	Hubei	4710	2	0.04
	Inner Mongolia	1624	2	0.12
	Liaoning	5051	12	0.24
	Ningxia	328	47	14.33
	Qinghai	2634	3	0.11
	Shandong	182	—	
	Tibet	2225	1	0.04
	Xinjiang	326	—	
	Subtotal	27795	81	0.29
2019	Anhui	1164	1	0.09
	Guizhou	14	—	
	Hebei	2187	—	
	Heilongjiang	2769	2	0.07
	Henan	1684	4	0.24
	Hubei	4704	77	1.64
	Inner Mongolia	742	11	1.48

	Liaoning	4559	23	0.5					
	Ningxia	1960	4	0.2					
	Qinghai	2575	1	0.04					
	Tibet	3728	1	0.03					
	Subtotal	26086	124	0.48					
2020	Shanghai	168	20	11.9					
	Anhui	692	31	4.48					
	Gansu	41	—						
	Hebei	2159	—						
	Heilongjiang	1664	1	0.06					
	Henan	180	14	7.78	14			14	
	Hubei	2341	25	1.07	21		1	20	
	Inner Mongolia	229	2	0.87	2			2	
	Jiangsu	188	2	1.06					
	Liaoning	4350	7	0.16					
	Ningxia	571	17	2.98	13			13	
	Shaanxi	108	4	3.7	4			4	
	Shanxi	399	18	4.51	17			16	1
	Subtotal	13090	141	1.08	71		1	69	1
2021	Anhui	1164	1	0.09	1	1			
	Gansu	259	—						
	Guizhou	1041	—						

	Hebei	2374	10	0.42				
	Heilongjiang	1711	—					
	Henan	1050	10	0.95	9	9		
	Hubei	6437	46	0.71	32	31		1
	Inner Mongolia	884	21	2.38	16	12		4
	Jiangxi	1	—					
	Liaoning	6078	39	0.64				
	Ningxia	920	17	1.85	8	2		6
	Qinghai	1499	—					
	Sichuan	387	—					
	Tibet	1804	19	1.05	19	2		17
	Subtotal	25609	163	0.64	85	57		28
2022	Tianjin	2	—					
	Guizhou	949	—					
	Hebei	2156	1	0.05				
	Heilongjiang	3399	58	1.71	4	4		
	Henan	5	1	20	1	1		
	Hubei	5507	1	0.02	1	1		
	Hunan	92	—					
	Inner Mongolia	6	—					
	Jiangxi	916	—					
	Jilin	429	—					

	Liaoning	858	1	0.12	1	1			
	Ningxia	446	—						
	Qinghai	2838	8	0.28	7	7			
	Sichuan	1137	4	0.35	1	1			
	Tibet	3314	3	0.09					
	Subtotal	22054	77	0.35	15	15			
2023	Anhui	1447	2	0.14	1	1			
	Guizhou	906	1	0.11	1	1			
	Henan	968	2	0.21	2	2			
	Hubei	1420	1	0.07					
	Ningxia	2	2	100	2	2			
	Shandong	197	—						
	Sichuan	617	—						
	Tibet	1817	1	0.06	1	1			
	Yunnan	1559	—						
	Subtotal	8933	9	0.1	7	7			
Total		219445	1344	0.61	368	121	26	220	1

Supplementary Table 2, related to Supplementary Fig. 1. H5Nx HPAIV detection events.

Event No.	Period	Province	Subtype	Surveillance strategies
1	Dec. 2014–Jan. 2015	Henan	H5N1	Passive
2	Jan. 2015	Shanxi	H5N1	Passive
3	Mar. 2015	Shaanxi	H5N1	Passive
4	May. 2015	Tibet	H5N1	Passive
5	May. 2015	Hebei	H5N1	Passive
6	Nov. 2015	Inner Mongolia	H5N6	Active
7	Jan. 2016	Tibet	H5N1	Active
8	May. 2016	Tibet	H5N8	Passive
9	Oct.–Dec. 2016	Ningxia	H5N8	Passive
10	Nov.–Dec. 2016	Henan	H5N8	Passive
11	Nov.–Dec. 2016	Hubei	H5N8	Passive
12	Nov. 2016	Beijing	H5N8	Passive
13	Nov. 2016	Qinghai	H5N8	Active
14	Nov. 2016	Inner Mongolia	H5N8	Passive
15	Nov. 2016	Heilongjiang	H5N6	Active
16	Dec. 2016	Tibet	H5N8	Active
17	Jan. 2017	Jiangsu	H5N8	Active
18	Feb. 2017	Anhui	H5N8	Active
19	Feb. 2017	Heilongjiang	H5N8	Active
20	May. 2017	Tibet	H5N8	Active
21	Oct. 2020	Inner Mongolia	H5N8	Passive
22	Oct. 2020	Ningxia	H5N8	Active
23	Nov. 2020	Shanxi	H5N2, H5N8	Active
24	Nov. 2020	Henan	H5N8	Passive
25	Nov. 2020	Hubei	H5N6, H5N8	Passive
26	Nov. 2020	Shaanxi	H5N8	Passive
27	Jan. 2021	Hubei	H5N8	Passive

28	May. 2021	Inner Mongolia	H5N8	Passive
29	May. 2021	Tibet	H5N1, H5N8	Passive
30	Jun. 2021	Ningxia	H5N8	Passive
31	Jul. 2021	Tibet	H5N1	Active
32	Oct.–Dec. 2021	Inner Mongolia	H5N1	Passive
33	Oct. 2021	Ningxia	H5N1	Active
34	Nov.–Dec. 2021	Henan	H5N1	Passive
35	Nov.–Dec. 2021	Hubei	H5N1	Passive
36	Dec. 2021	Anhui	H5N1	Active
37	Jul.–Aug. 2022	Qinghai	H5N1	Passive
38	Sep.–Oct. 2022	Heilongjiang	H5N1	Active
39	Nov. 2022	Liaoning	H5N1	Active
40	Nov. 2022	Sichuan	H5N1	Active
41	Dec. 2022	Hubei	H5N1	Passive
42	Jan. 2023	Tibet	H5N1	Passive
43	Jan.–Feb. 2023	Ningxia	H5N1	Passive
44	Feb. 2023	Henan	H5N1	Active
45	Feb. 2023	Anhui	H5N1	Active
46	Feb. 2023	Guizhou	H5N1	Active

Supplementary Table 3, related to Fig. 4a. Statistically supported epidemiological diffusion links between geographic locations for clade 2.3.2.1c.

From	To	Bayes factor	Posterior probability
China	Southeast Asia	60784.688	1
North Asia	China	60784.688	1
Southeast Asia	China	60784.688	1
China	North Asia	3034.223	0.998
North Asia	Southeast Asia	194.036	0.974
Southeast Asia	Europe	63.414	0.923
North Asia	Middle East	34.587	0.868
North Asia	Africa	28.724	0.845
Southeast Asia	East Asia	16.062	0.753
North Asia	East Asia	11.696	0.689
China	East Asia	8.604	0.620
Middle East	North Asia	5.532	0.512
Europe	East Asia	4.743	0.473
North Asia	Europe	4.582	0.465

Supplementary Table 4, related to Fig. 4b. Statistically supported epidemiological diffusion links between geographic locations for clade 2.3.4.4e.

From	To	Bayes factor	Posterior probability
Japan	Vietnam	287.673	0.989
Japan	Southern China	201.331	0.984
Japan	Northern China	18.238	0.848
Japan	South Korea	17.922	0.846
Southern China	Japan	16.472	0.835
Southern China	Northern China	8.419	0.721
South Korea	Southern China	6.676	0.672
South Korea	Japan	6.185	0.655
Southern China	Vietnam	3.926	0.546

Supplementary Table 5, related to Fig. 4c. Statistically supported epidemiological diffusion links between geographic locations for clade 2.3.4.4b0, b1, and b2.

From	To	Bayes factor	Posterior probability
Clade 2.3.4.4b0			
Europe	North Asia	5123.680	0.999
Europe	Middle East	140.849	0.964
China	East Asia	33.3188	0.863
Europe	East Asia	31.360	0.856
China	Africa	24.0836	0.820
Middle East	Southeast Asia	15.945	0.751
Africa	Middle East	12.906	0.710
East Asia	China	12.399	0.7022
Europe	Africa	9.493	0.6433
Africa	North Asia	7.330	0.582
China	North Asia	7.057	0.572
China	Middle East	5.276	0.500
Africa	China	4.588	0.465
Europe	China	4.235	0.445
North Asia	Europe	3.714	0.413
Clade 2.3.4.4b1			
East Asia	China	476.318	0.997
Europe	East Asia	9.163	0.8822
Clade 2.3.4.4b2			
China	East Asia	610351.342	1
East Asia	North Asia	610351.342	1
North Asia	Europe	610351.342	1
North Asia	China	76288.423	1
East Asia	America	35897.110	1
North Asia	Middle East	32117.806	1
China	Southeast Asia	21040.535	1
America	East Asia	9999.583	0.999
America	Middle East	33.897	0.844

Europe	Middle East	30.7899	0.8311
Europe	Africa	23.981	0.792
Europe	America	15.473	0.711

Supplementary Table 6. Statistically supported epidemiological diffusion links between geographic locations for clade 2.3.4.4b (baseline European cap of 10).

From	To	Bayes factor	Posterior probability
China	East Asia	169588.785	1
North Asia	Europe	169588.785	1
America	East Asia	56525.409	1
North Asia	Middle East	56525.409	1
China	Southeast Asia	42392.487	1
East Asia	America	16953.227	1
Europe	Middle East	12107.654	0.999
North Asia	China	7367.419	0.999
East Asia	China	5464.529	0.999
East Asia	North Asia	3762.500	0.998
Europe	East Asia	1034.181	0.994
Africa	North Asia	930.710	0.993
America	Middle East	392.768	0.984
Europe	Africa	119.440	0.950
China	North Asia	54.924	0.897
China	Africa	29.179	0.823
Middle East	Southeast Asia	22.291	0.780
Africa	Middle East	12.403	0.664
Europe	North Asia	10.527	0.626
Southeast Asia	Middle East	4.375	0.411

Supplementary Table 7. Statistically supported epidemiological diffusion links between geographic locations for clade 2.3.4.4b (baseline European cap of 5).

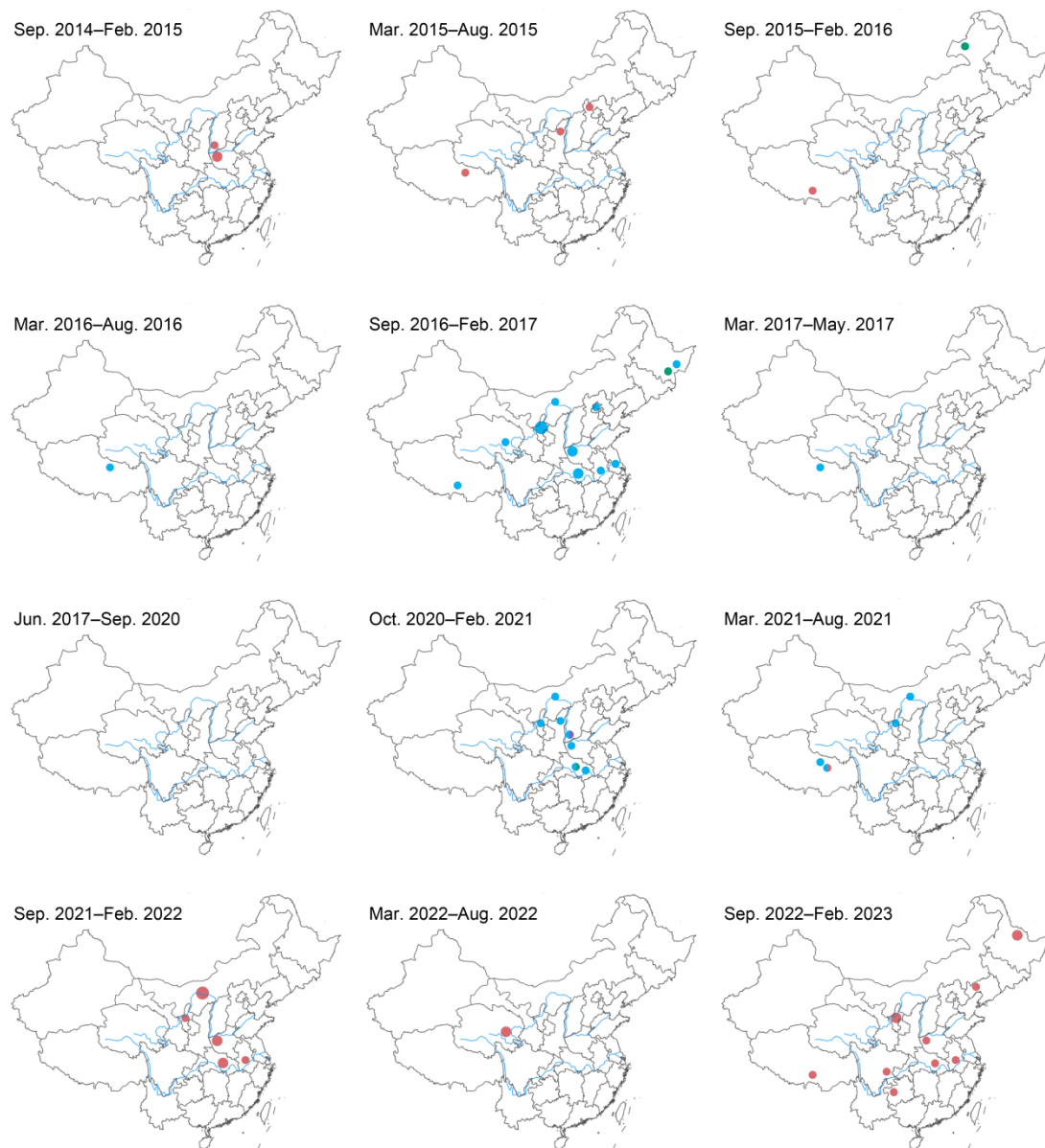
From	To	Bayes factor	Posterior probability
China	East Asia	22605.140	1
North Asia	Europe	22605.140	1
America	East Asia	22605.140	1
North Asia	Middle East	22605.140	0.999
China	Southeast Asia	22605.140	1
East Asia	America	22605.140	1
Europe	Middle East	22605.140	1
North Asia	China	3762.291	0.998
East Asia	China	22605.140	1
East Asia	North Asia	22605.140	0.999
Europe	East Asia	1878.00	0.996
Africa	North Asia	445.949	0.986
America	Middle East	3762.291	0.998
Europe	Africa	67.134	0.914
China	North Asia	295.206	0.979
Middle East	Southeast Asia	4516.005	0.998
Africa	Middle East	9.689	0.606
Europe	North Asia	195.608	0.968
Africa	China	45.227	0.878
Europe	America	4.437	0.414

Supplementary Table 8. Statistically supported epidemiological diffusion links between geographic locations for clade 2.3.4.4b (baseline European cap of 20).

From	To	Bayes factor	Posterior probability
China	East Asia	22605.140	1
North Asia	Europe	22605.140	1
America	East Asia	22605.140	1
North Asia	Middle East	22605.140	1
China	Southeast Asia	22605.140	0.999
East Asia	America	22605.140	1
Europe	Middle East	22605.140	1
North Asia	China	22605.140	0.999
East Asia	China	22605.140	1
East Asia	North Asia	22605.140	1
Europe	East Asia	3223.924	0.998
Africa	North Asia	573.501	0.989
America	Middle East	4516.005	0.998
Europe	Africa	831.181	0.992
China	North Asia	215.401	0.972
China	Africa	33.600	0.842
Middle East	Southeast Asia	39.217	0.861
Africa	Middle East	17.956	0.741
Europe	North Asia	700.328	0.991

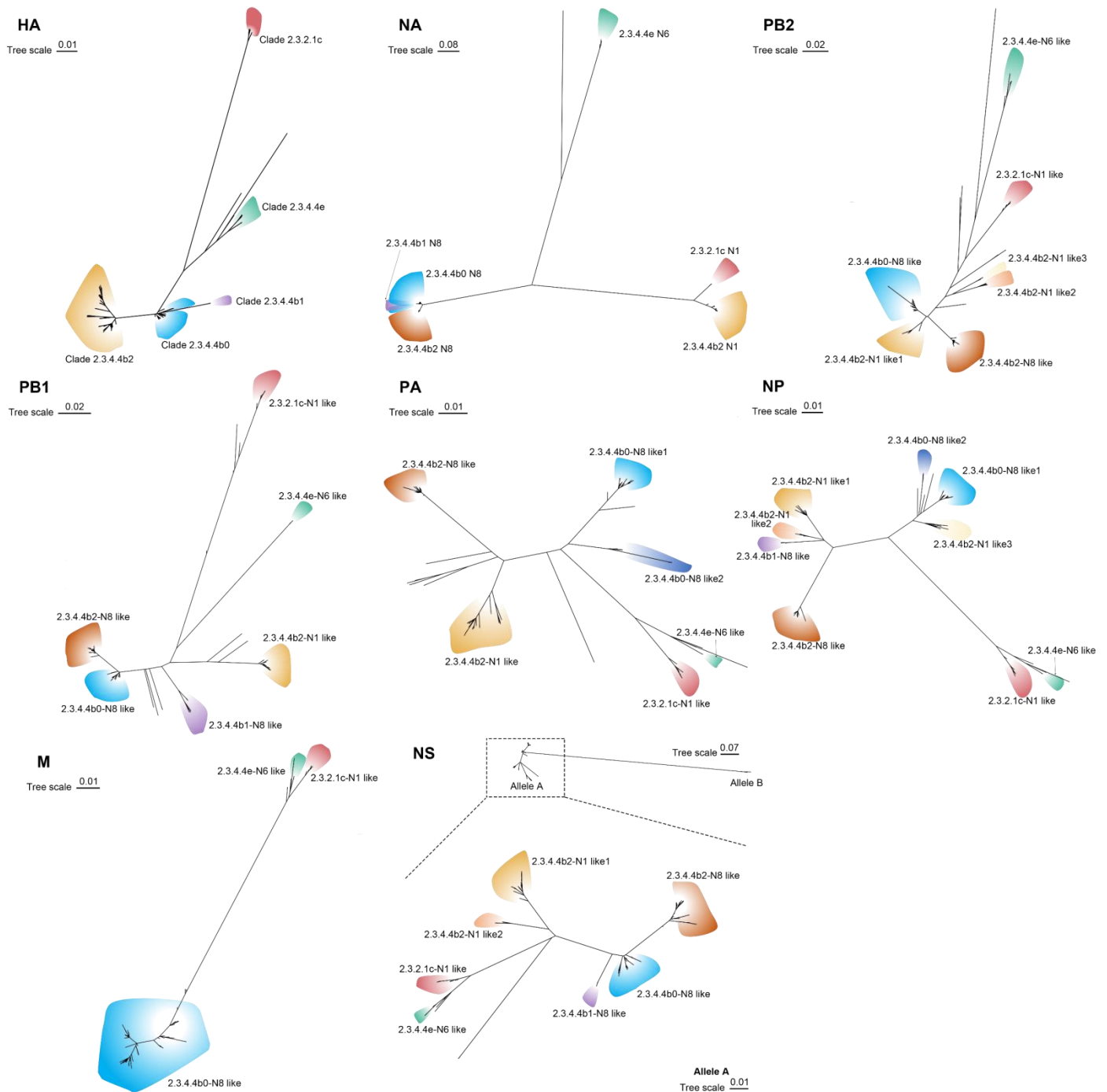
Supplementary Table 9. Primer sequences used for AIV genome amplification and sequencing.

Primer name	Primer sequence (5'-, -3')
Uni12	AgCAAAAgCAgg
H5-F	gCAggggTATAATCTgTCAA
H5-R	TTggAgCACATgCATAAAgATA
N1-F	CTACTTgTCAATggTgAATg
N1-F	TgAATCCAAATCAAAAgATAAT
N2-F	TgATgARYgARYTgggTgT
N2-F	TgTCDCCMACAAgYCCTgA
N6-F	TgAAgATgAATCCAAATCAgAA
N6-R	TTCCAAAATCTTTTTCTACTTA
N8-F	AgCAAAAgCAggAgTTTAAATgAA
N8-R	gTAgAAACAAggAgTTTTTTCgTAA
MF	AgCAAAARCAggTAgATRTTgAA
MR	ACAAGgTAgTTTTTTAYTCCARC
NSF	AAgCAgggTgACAAAAACA
NSR	TAgAAACAAGggTgTTTTTTATCA
NP-F	AAAAGCAgggTAgATAATCACTC
NP-R	TTCTYYAATTgTCATAYTCCTCTgA
PA1-F	AgCAggTACTgATCCAAAATggAgg
PA1-R	AATgTgTTCAATTggTgCAACgTCT
PA2-F	AATTCAACAAAgCATgCgAATTgAC
PA2-R	gCRAATAgTAgCATTgCCACAAYTA
PB11-F	CATTTgAATggATgTCAATCCgA
PB11-R	AARTCATCAgAggATTggAgTCCg
PB12-F	AggACAAAAGAggTACACCAAAAC
PB12-R	TTCATgAAggACAAGCTAAATTCAC
PB21-F	gCAggTCAAATATATTCAATATggA
PB21-R	gCTCTATTgACAAARTTCAgATCRC
PB22-F	CATggTRTTTTCACAAgAggATTgC
PB22-R	ACAATTCgACACTAATTgATggC



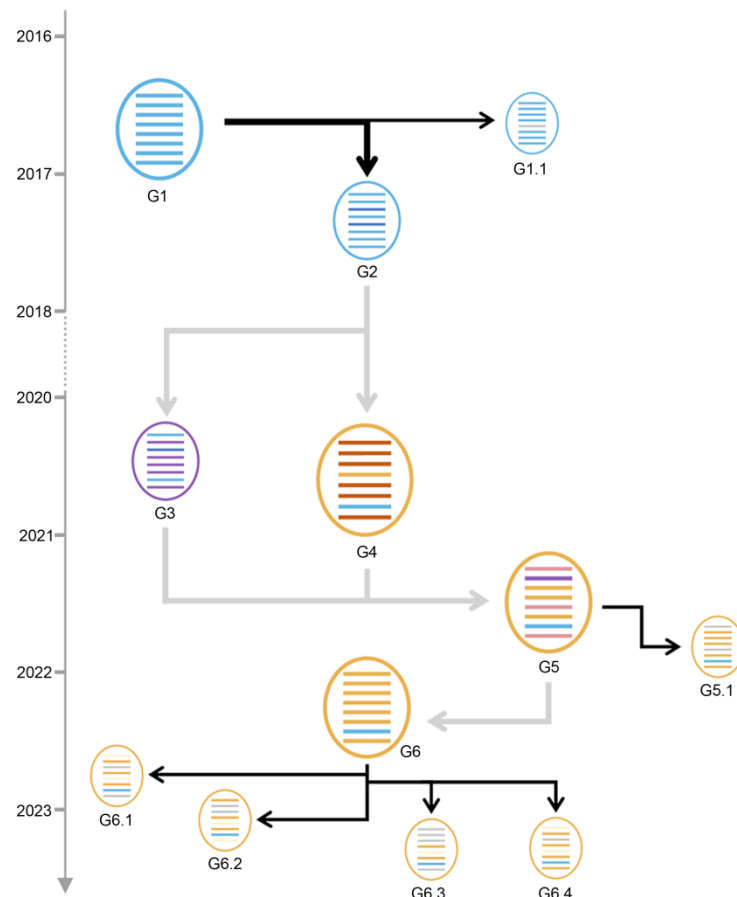
Supplementary Fig. 1 | Spatiotemporal patterns of H5Nx HPAIV detection events.

Geographic distribution of H5Nx HPAIV detections, stratified by subtype and temporal continuity. Detection events were marked by circles with different colors (H5N1, red; H5N2, purple; H5N6, green; H5N8, blue). Co-detection of ≥ 2 subtypes within a single surveillance event were marked by multicolored circles. Circle diameter scales linearly with monthly continuity of detection events (range: 1–3 months), reflecting sustained viral activity at a given location. Blue lines indicate the Yangtze and Yellow Rivers. The maps were generated by the authors using ArcGIS v10.2 from administrative boundary vector data and cropped to show the surveillance regions included in this study.



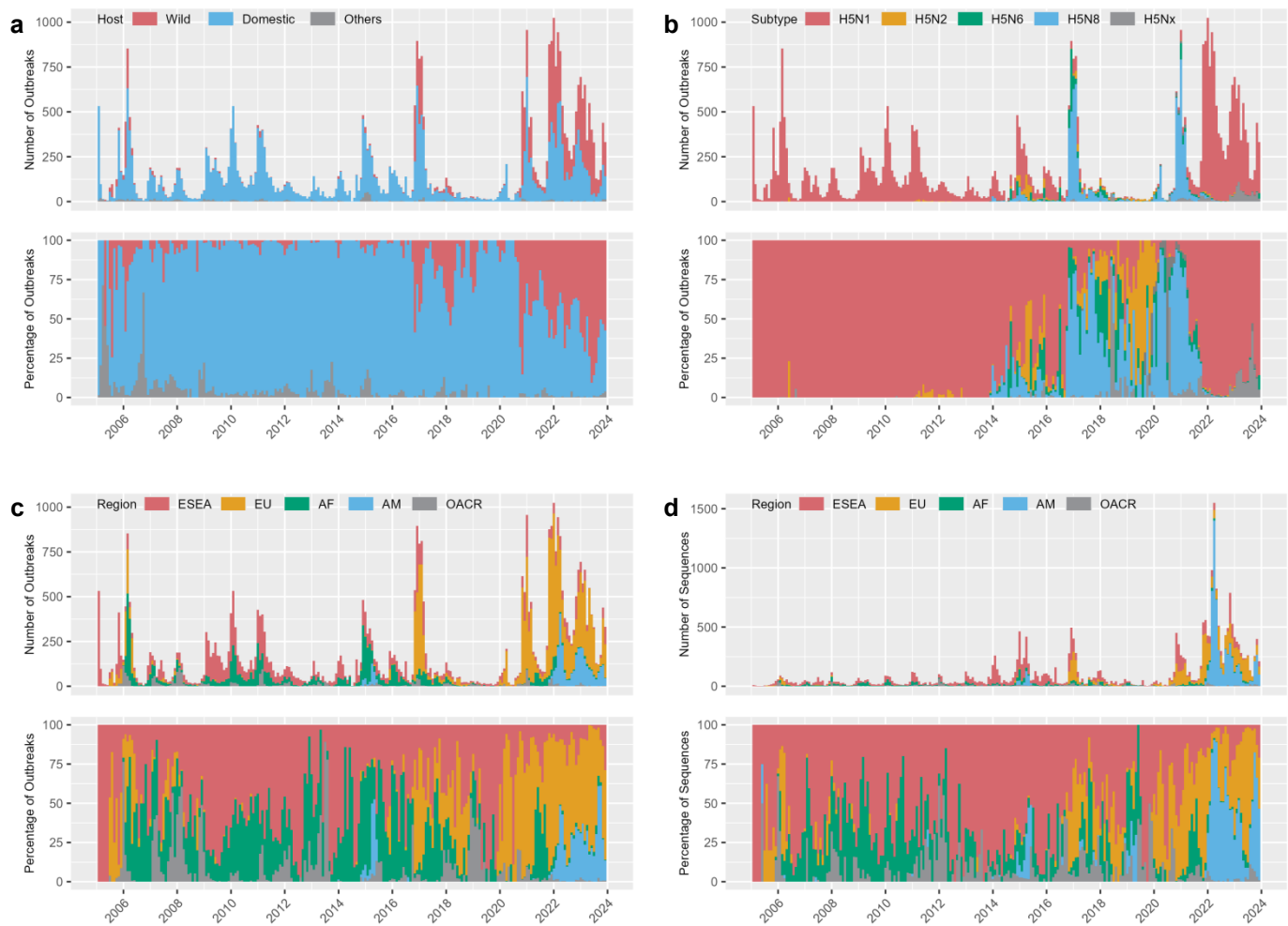
Supplementary Fig. 2 | Maximum-likelihood phylogenetic trees.

Phylogenetic reconstruction based on segment topology, subtype, and bootstrap support grouped viruses into distinct lineages. See also Supplementary data 1.



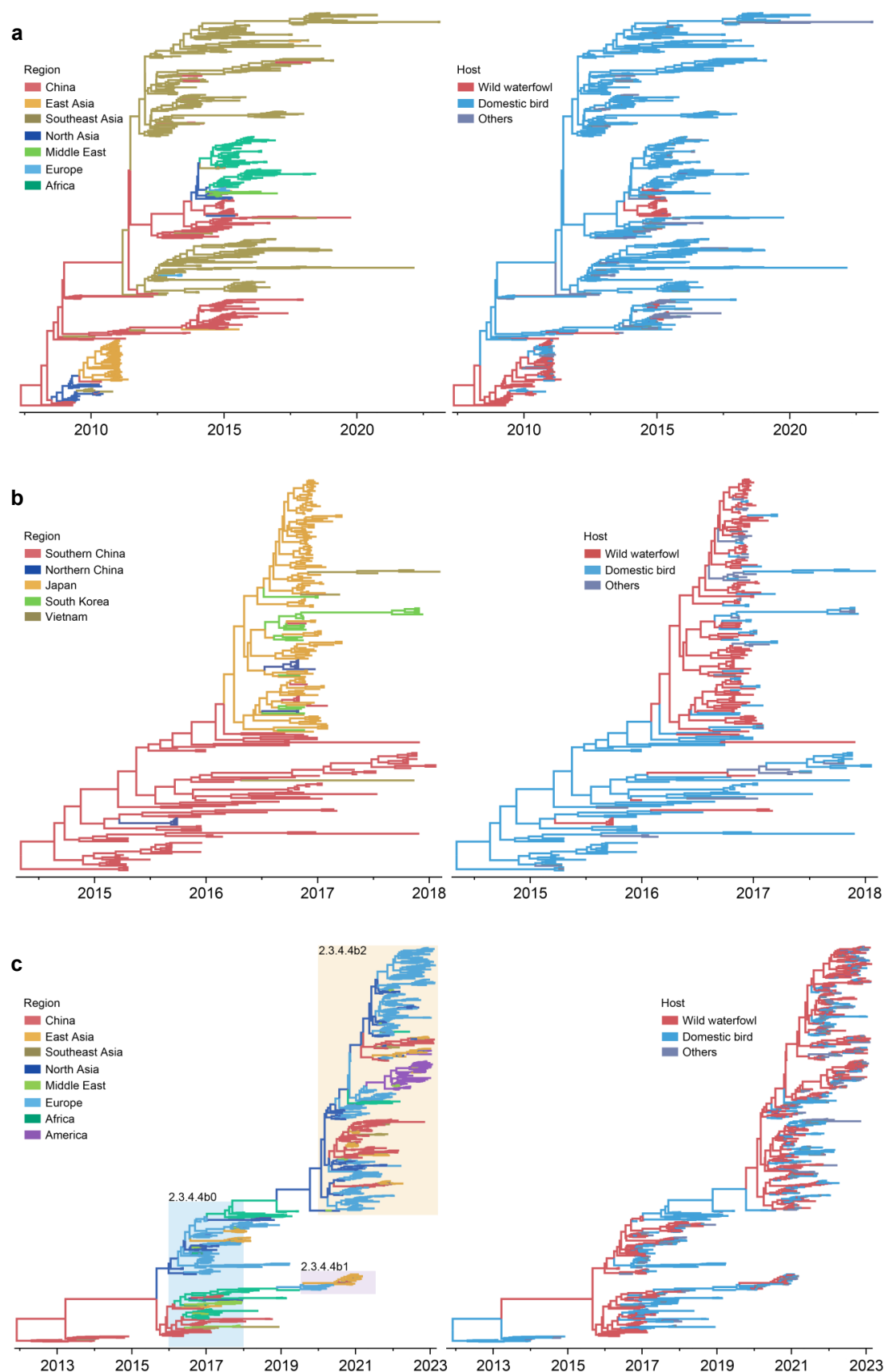
Supplementary Fig. 3 | Schematic of the clade 2.3.4.4b H5Nx HPAIV evolutionary pathway.

Diversity of major genotypes of H5Nx isolates in this study. The group of each gene segment are indicated by different colored bars. The gray arrows indicate "genetic discontinuities" in the HA phylogenetic tree. Detailed information is available in Supplementary Fig. 2 and Supplementary data 1.



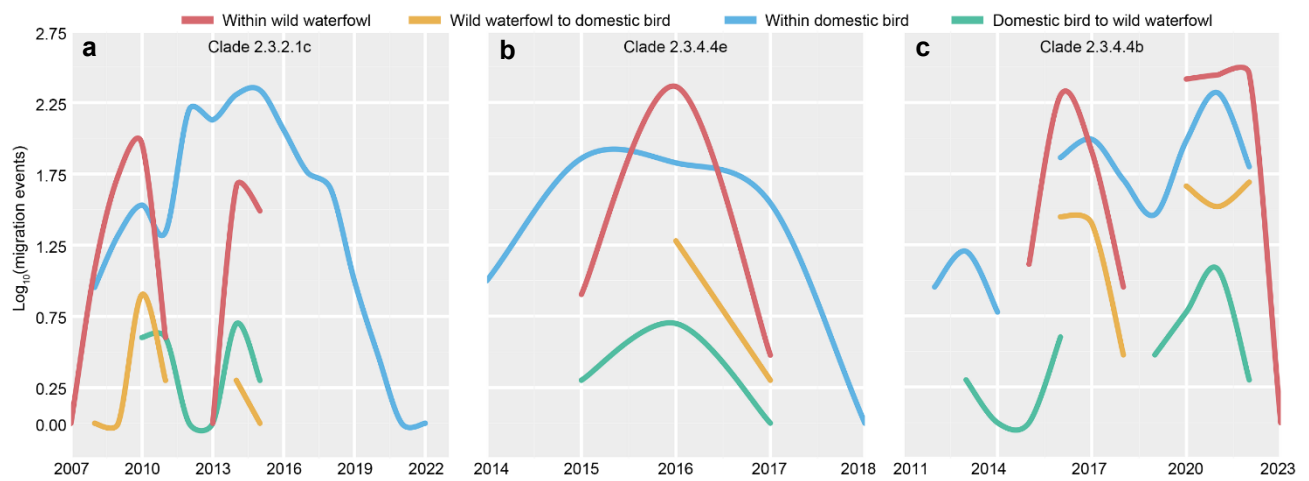
Supplementary Fig. 4 | Epidemiological of global H5Nx HPAI monthly outbreaks and viral sequences, 2005–2023.

(a) Host distribution and proportion of H5Nx HPAI outbreaks, (b) Subtype distribution and proportion of H5Nx HPAI outbreaks, (c) Geographic distribution and proportion of H5Nx HPAI outbreaks, and (d) Geographic distribution and proportion of H5Nx HPAIV HA sequences. H5Nx HPAI outbreaks were obtained from the EMPRESS-i+ Global Animal Disease Information System, Food and Agriculture Organization of the United Nations (FAO) (<https://empres-i.apps.fao.org/>). H5Nx HPAIV HA sequences were obtained from GISAID and NCBI. ESEA, East and South-east Asia; EU, Europe; AF, Africa; AM, Americas; OACR, Other Asian countries and regions.



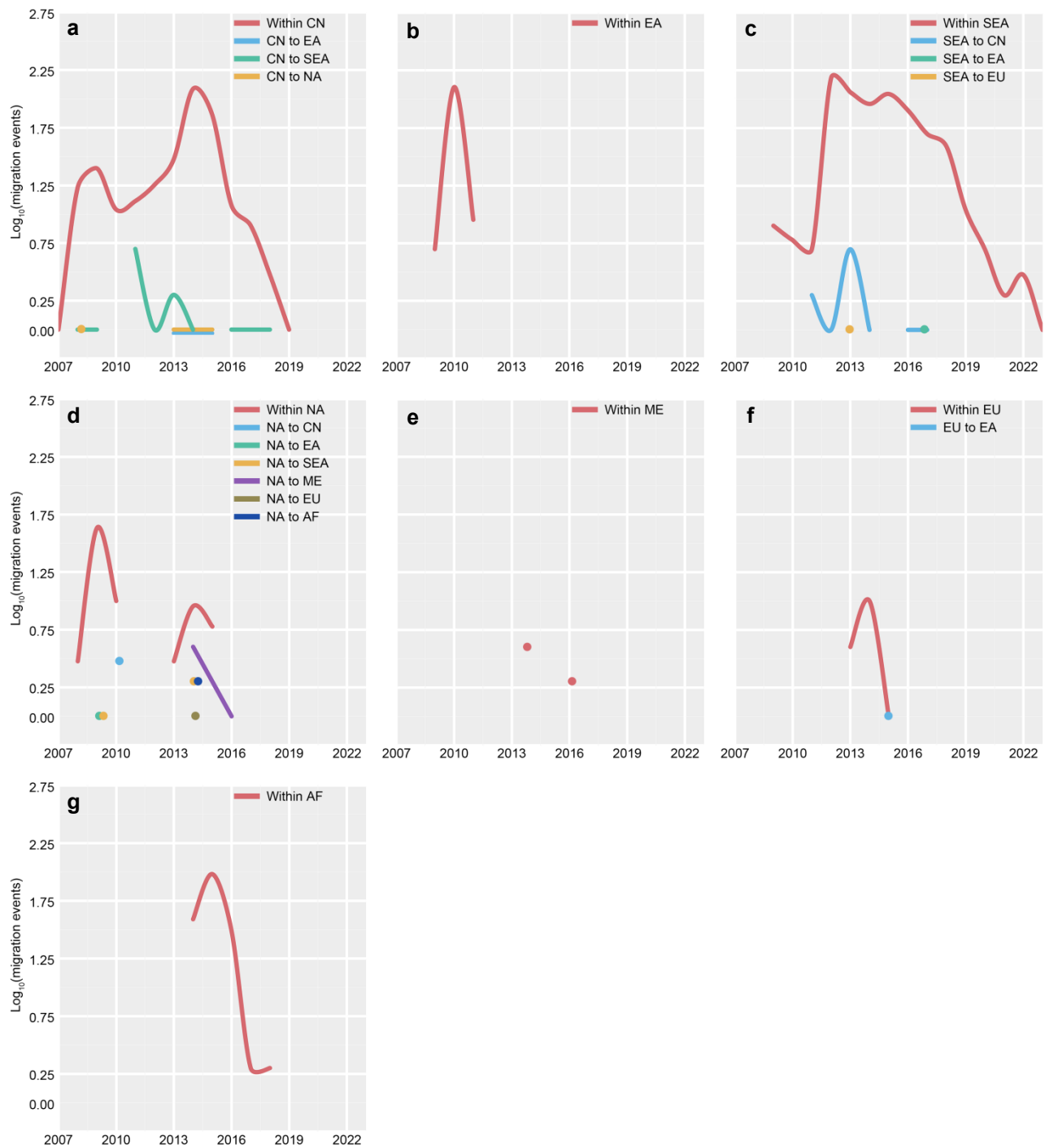
Supplementary Fig. 5 | Maximum clade credibility trees.

(a) Clade 2.3.2.1c, (b) Clade 2.3.4.4e, and (c) Clade 2.3.4.4b. Branches were colored by discrete geographic regions (left) and host types (right).



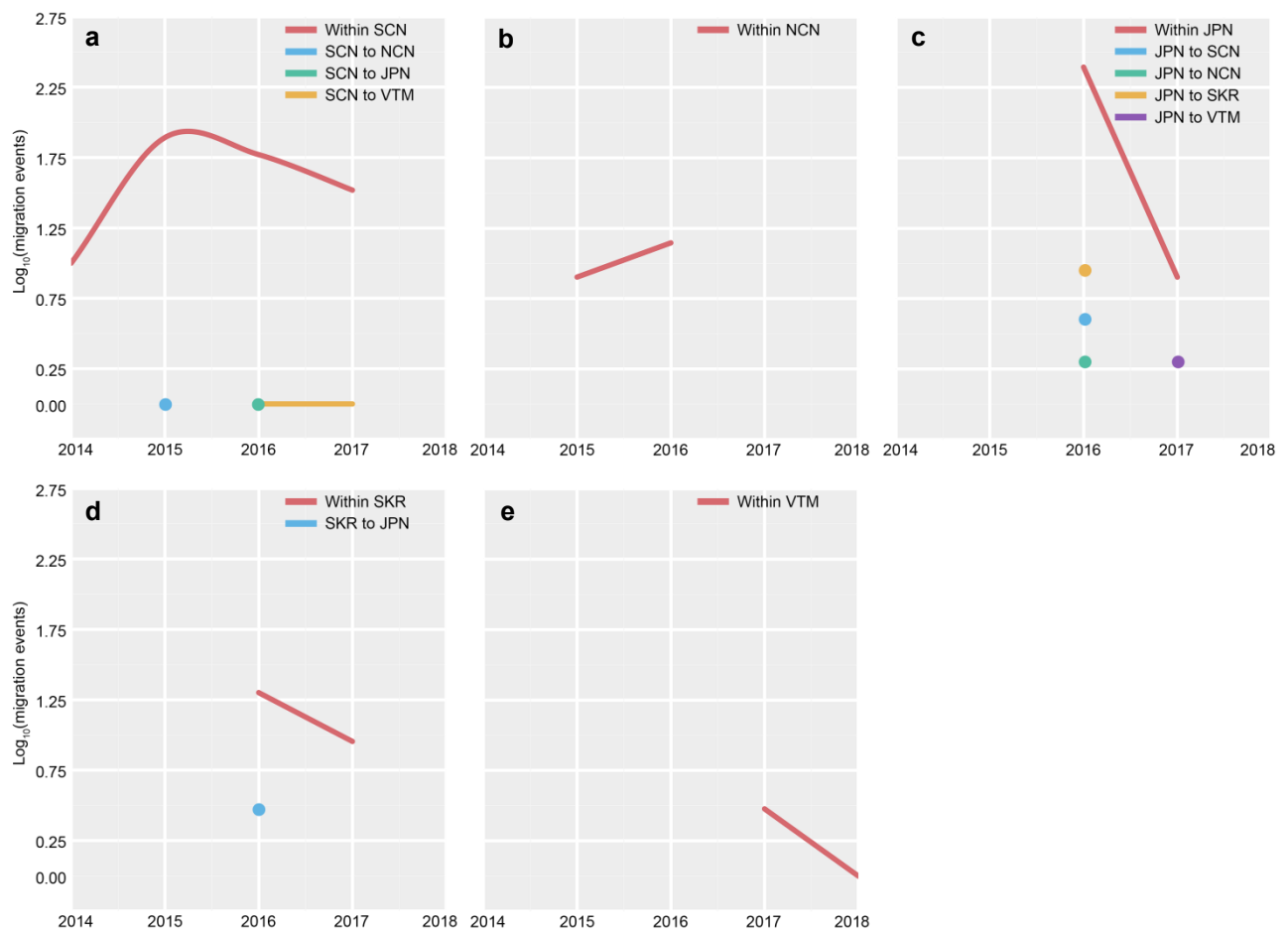
Supplementary Fig. 6 | Virial migration over time in different hosts.

(a) Clade 2.3.2.1c, (b) Clade 2.3.4.4e, and (c) Clade 2.3.4.4b. These plots summarize transition-bearing branches on the maximum clade credibility tree and are provided as descriptive visualizations; they should not be interpreted as posterior estimates of the exact timing of migration events.



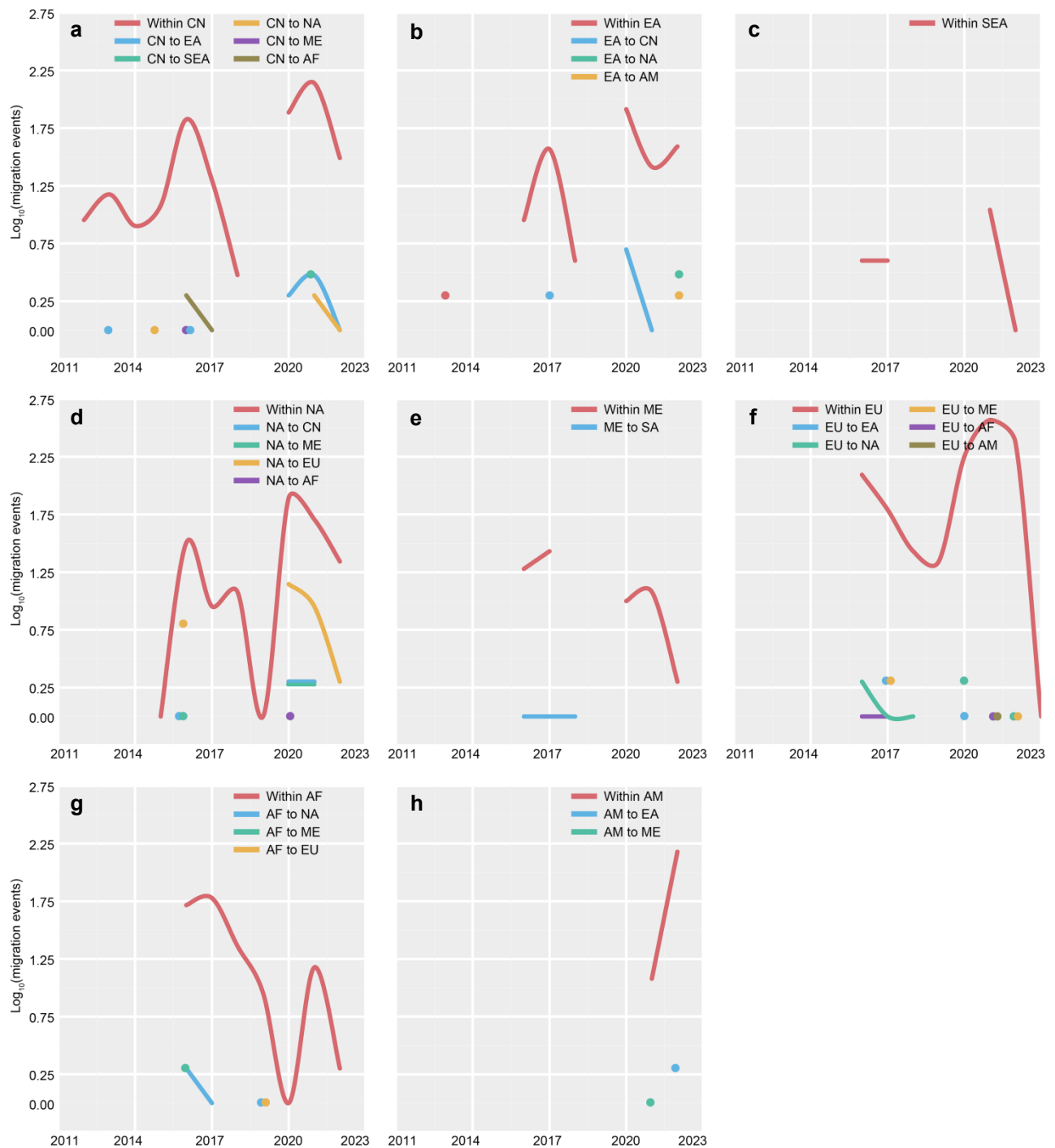
Supplementary Fig. 7 | Virial migration over time in different regions, Clade 2.3.2.1c.

CN, China; EA, East Asia; SEA, Southeast Asia; NA, North Asia; ME, Middle East; EU, Europe; AF, Africa. These plots summarize transition-bearing branches on the maximum clade credibility tree and are provided as descriptive visualizations; they should not be interpreted as posterior estimates of the exact timing of migration events.



Supplementary Fig. 8 | Virial migration over time in different regions, Clade 2.3.4.4e.

SCN, Southern China; NCN, Northern China; JP, Japan; SKR, South Korea; VTM, Vietnam. These plots summarize transition-bearing branches on the maximum clade credibility tree and are provided as descriptive visualizations; they should not be interpreted as posterior estimates of the exact timing of migration events.



Supplementary Fig. 9 | Virial migration over time in different regions, Clade 2.3.4.4b.

CN, China; EA, East Asia; SEA, Southeast Asia; NA, North Asia; ME, Middle East (including West Asia); EU, Europe; AF, Africa; AM, America. These plots summarize transition-bearing branches on the maximum clade credibility tree and are provided as descriptive visualizations; they should not be interpreted as posterior estimates of the exact timing of migration events.