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Human Infection with Avian Influenza A(H10N3) Virus, China, 2024

Appendix

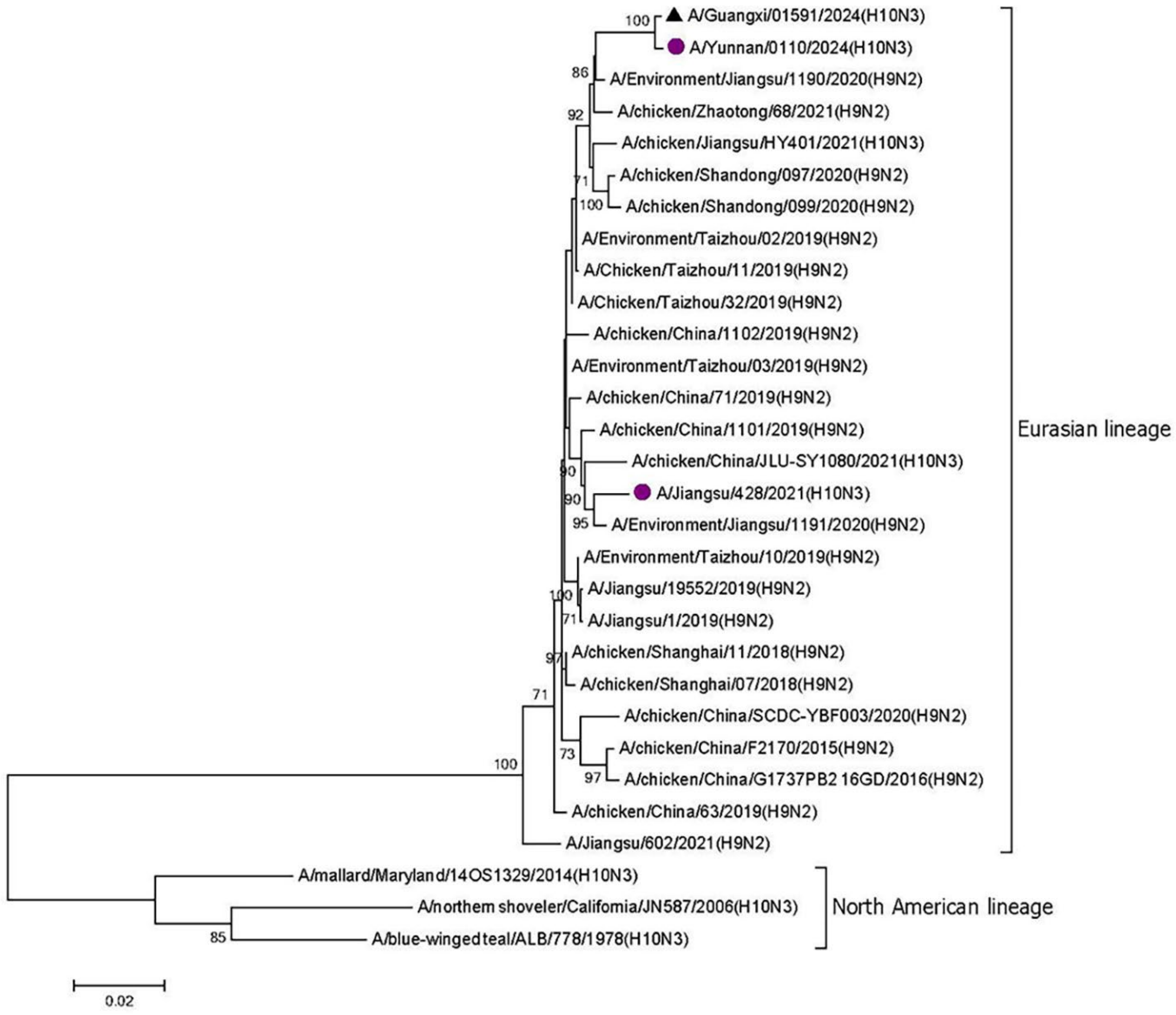
Appendix Table. Clinical blood cell and biochemistry test results from hospital admission to H10N3 positive test*

Tests	19 Dec†	21 Dec	22 Dec‡	23 Dec	24 Dec	Reference range
Leukocytes, cells × 10^9/L	5.52	5.71	5.85	9.81	8.09	3.5–9.5
Lymphocyte, cells × 10^9/L	1.5	1.27	1.15	2.18	1.19	1.1–3.2
Hemoglobin, g/L	140	126	95	101	92	115–150
Neutrophils, %	69.1	74.2	76.8	73.1	77.2	40–75
Lymphocytes, %	27.1	22.2	19.7	22.2	14.7	20–50
Monocyte, %	3.7	3.6	3.3	4.7	8.1	3–10
Eosinophils, %	0	0	0.1	0	0	0.4–8
Basophils, %	0.1	0	0.1	0	0	0.0–1.0
Direct bilirubin, µmol/L	2.2	ND	2.1	5	ND	0–6.8
Indirect bilirubin, µmol/L	3.8	ND	2.2	6.6	ND	2–16.2
Total protein, g/L	66.9	ND	44.8	53.2	ND	65–85
Albumin, g/L	36.3	ND	21.4	34.6	ND	40–55
Globin, g/L	30.6	ND	23.4	18.6	ND	20–40
C-reactive protein, mg/L	75.8	ND	ND	60.7	ND	0.5–10

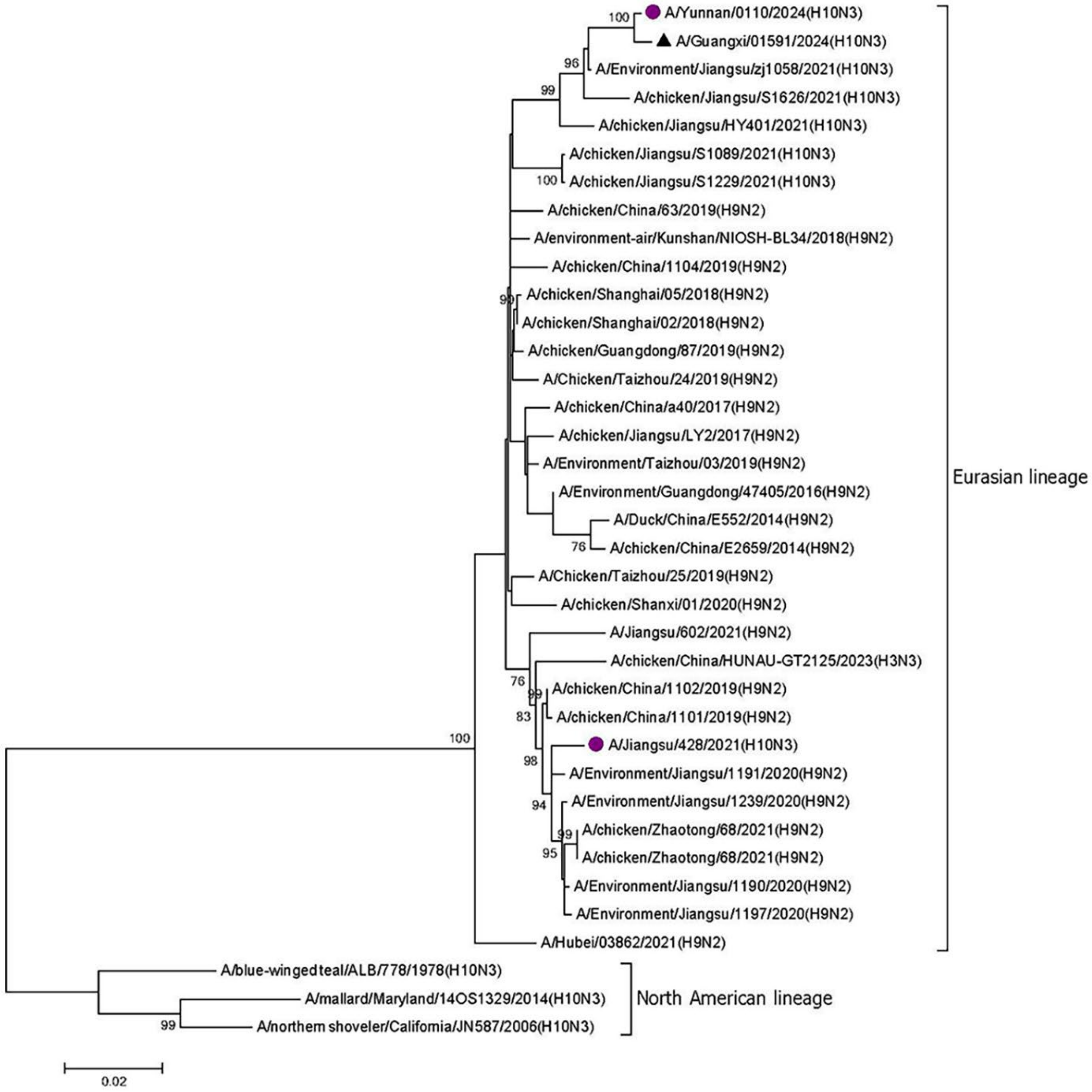
*ND, not done.

†The patient was admitted to hospital.

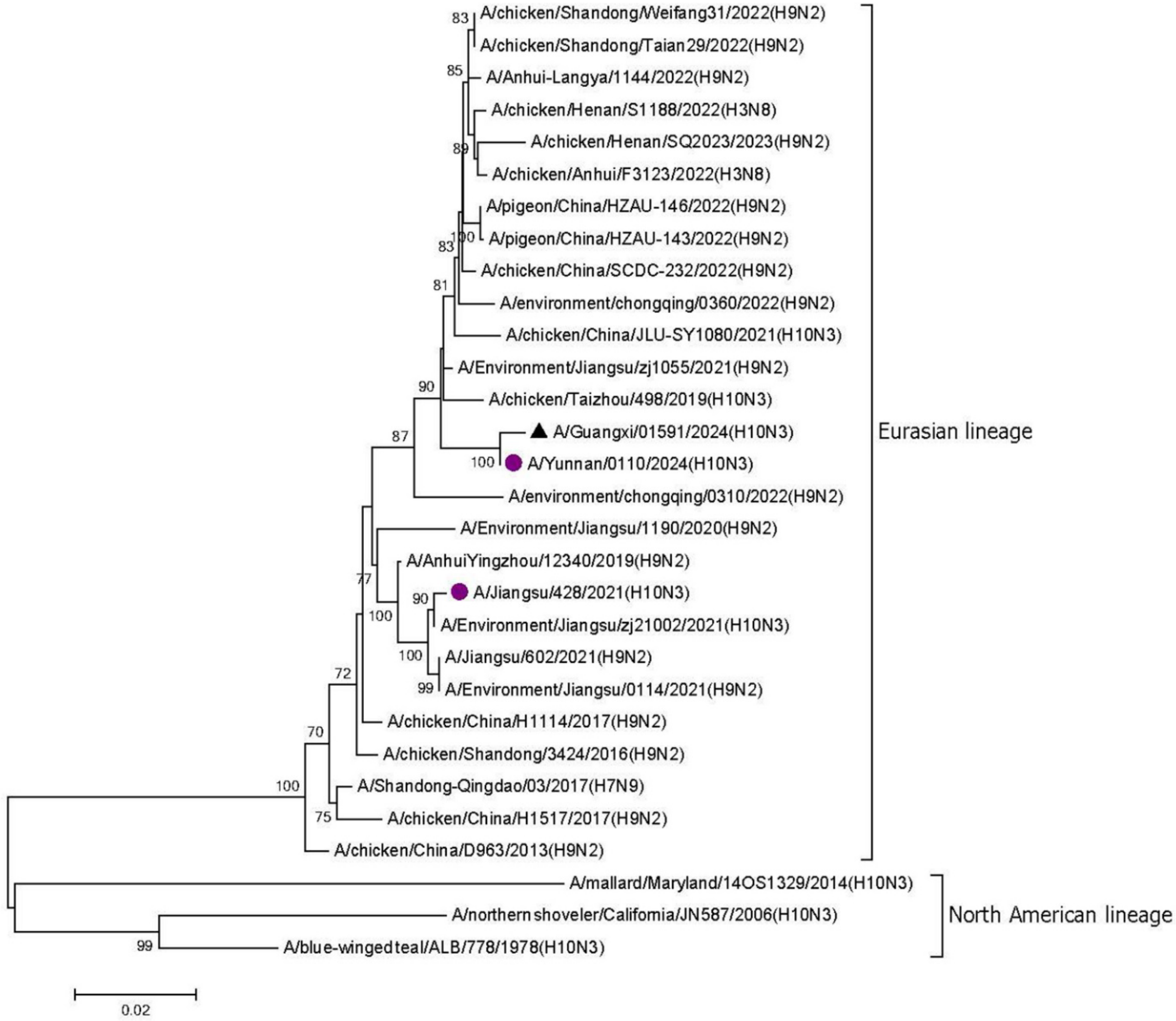
‡The patient was transferred to the Respiratory Intensive Care Unit (RICU).



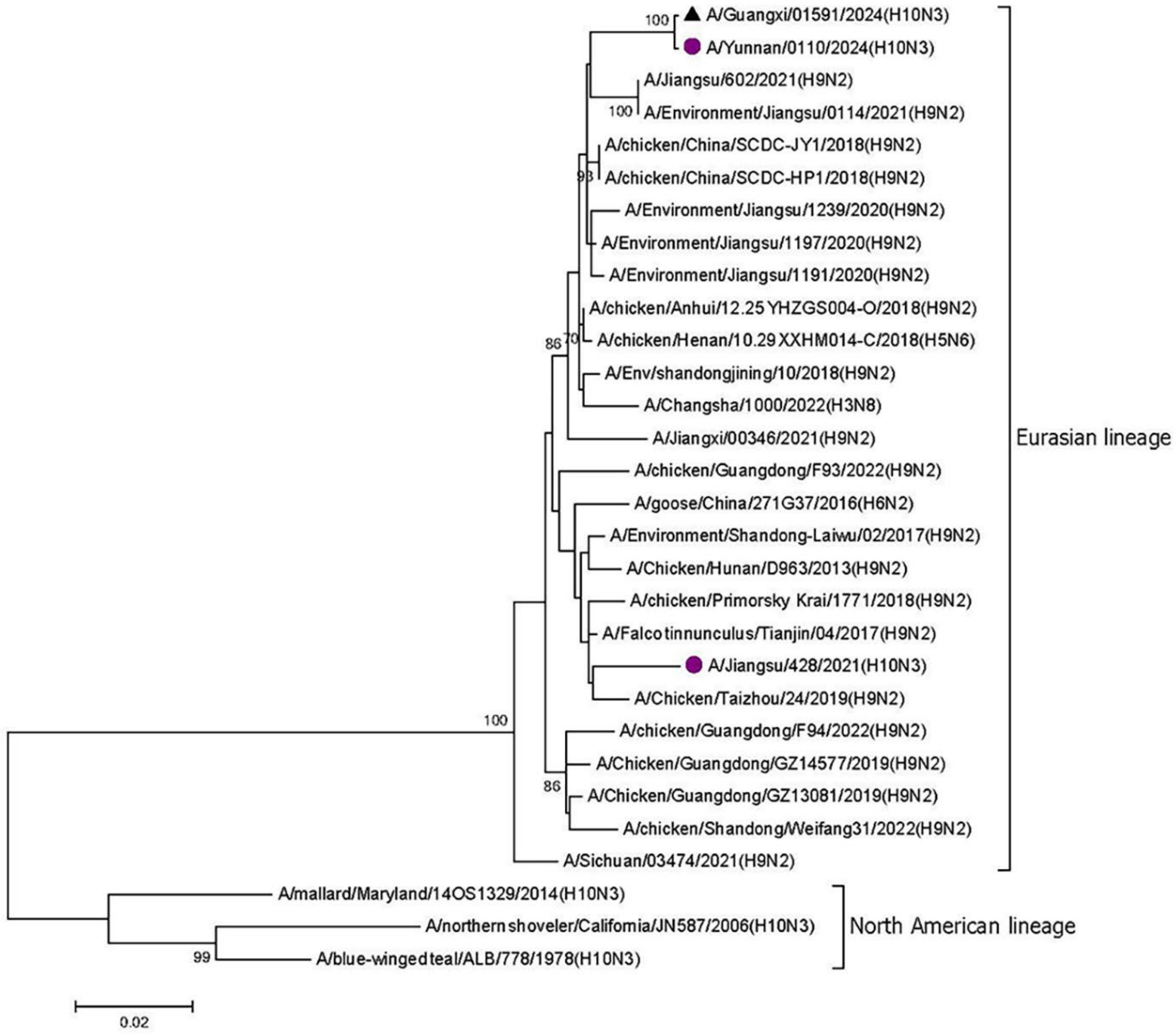
Appendix Figure 1. Phylogenetic tree PB2 gene of the A/Guangxi/01591/2024(H10N3). The phylogenetic trees were constructed with MEGA7.0 software using the maximum likelihood (ML) method. Bootstrap analysis was performed with 1000 replicates. The virus A/Guangxi/01591/2024(H10N3) reported in Guangxi is marked with black triangles. The other 2 viruses isolated from human in People's Republic of China were marked with purple circle. Scale bar indicates nucleotide substitutions per site.



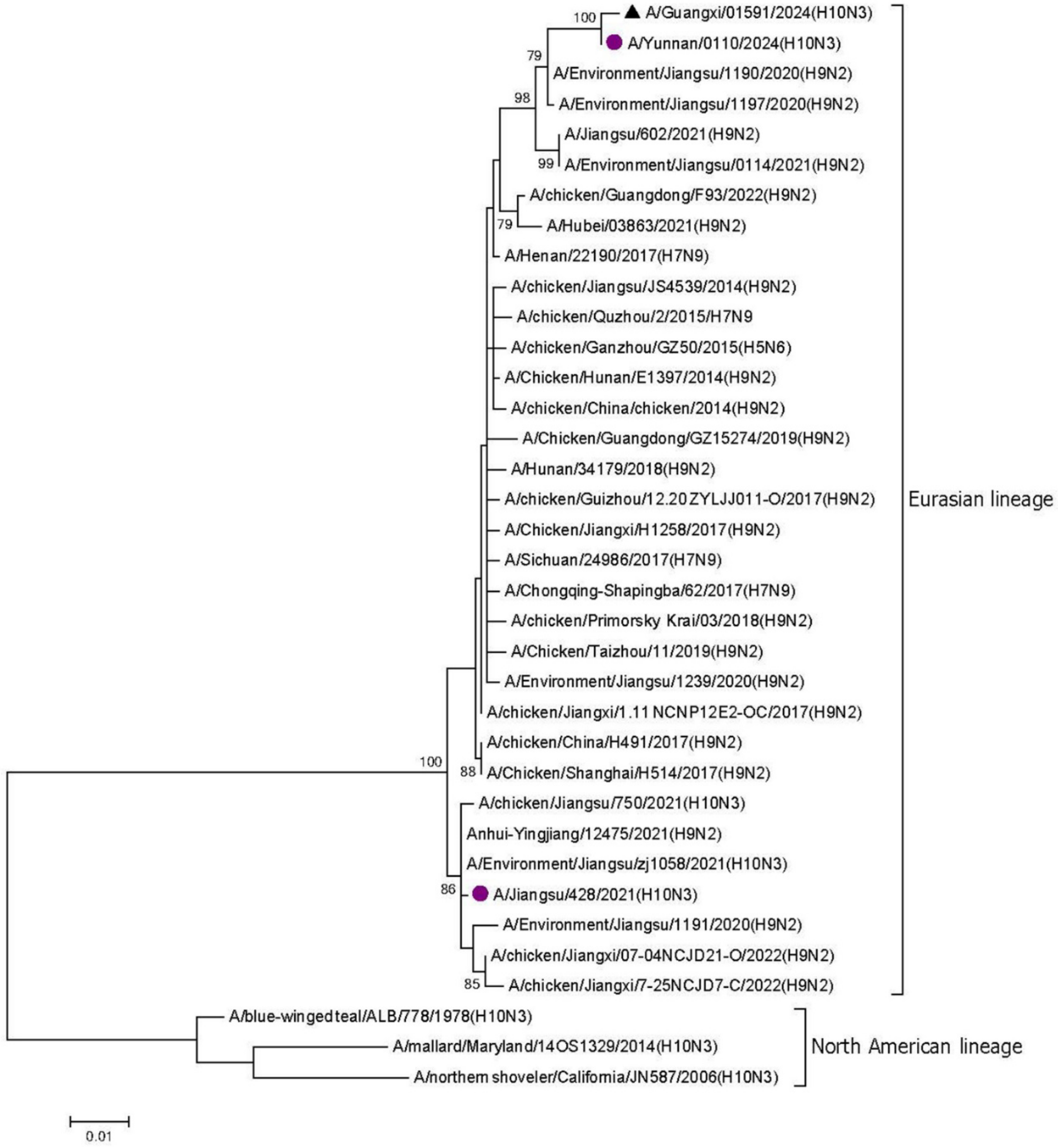
Appendix Figure 2. Phylogenetic tree PB1 gene of the A/Guangxi/01591/2024(H10N3). The phylogenetic trees were constructed with MEGA7.0 software using the maximum likelihood (ML) method. Bootstrap analysis was performed with 1000 replicates. The virus A/Guangxi/01591/2024(H10N3) reported in Guangxi is marked with black triangles. The other 2 viruses isolated from human in People's Republic of China were marked with purple circle. Scale bar indicates nucleotide substitutions per site.



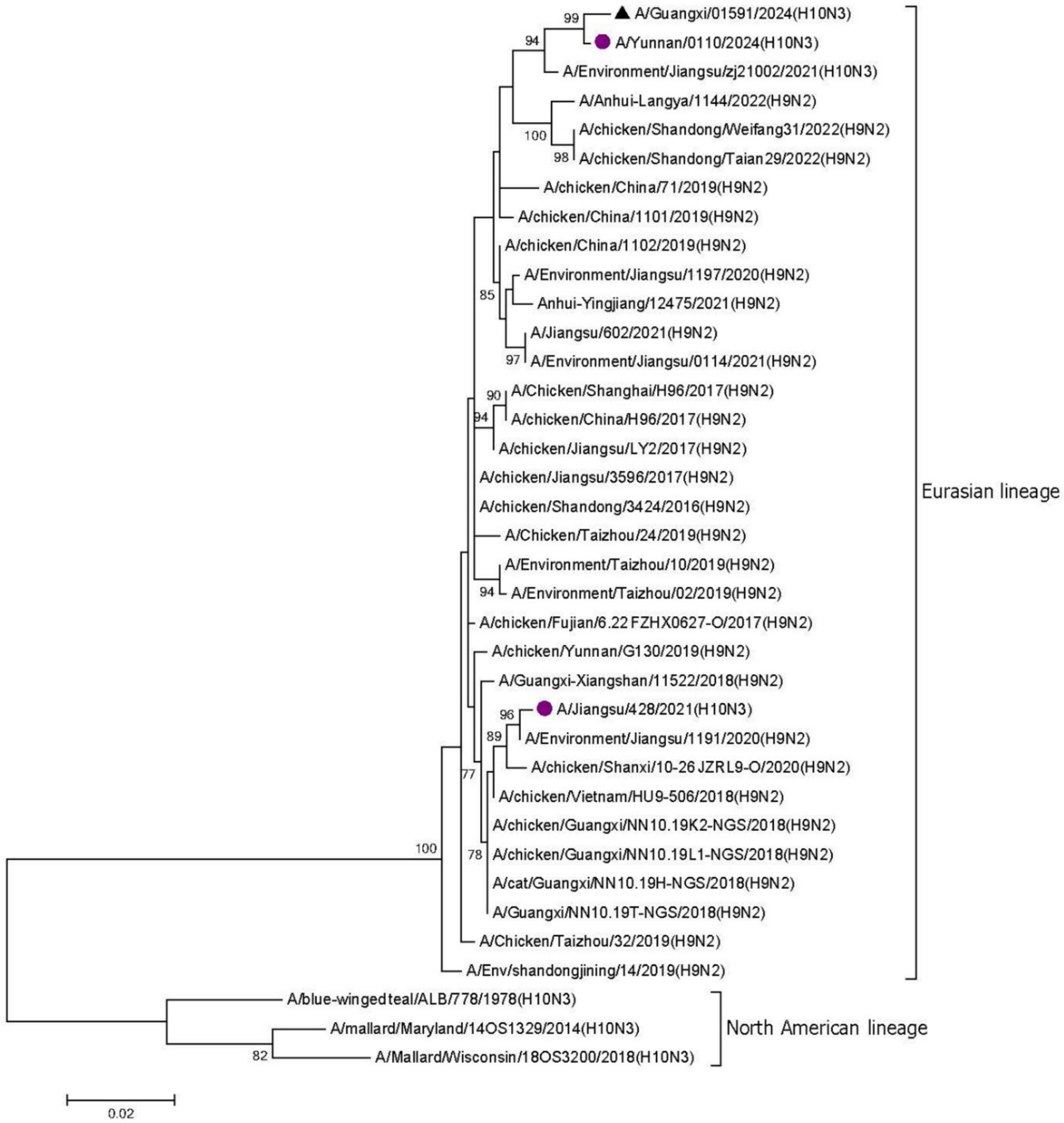
Appendix Figure 3. Phylogenetic tree PA gene of the A/Guangxi/01591/2024(H10N3). The phylogenetic trees were constructed with MEGA7.0 software using the maximum likelihood (ML) method. Bootstrap analysis was performed with 1000 replicates. The virus A/Guangxi/01591/2024(H10N3) reported in Guangxi is marked with black triangles. The other 2 viruses isolated from human in People’s Republic of China were marked with purple circle. Scale bar indicates nucleotide substitutions per site.



Appendix Figure 4. Phylogenetic tree NP gene of the A/Guangxi/01591/2024(H10N3). The phylogenetic trees were constructed with MEGA7.0 software using the maximum likelihood (ML) method. Bootstrap analysis was performed with 1000 replicates. The virus A/Guangxi/01591/2024(H10N3) reported in Guangxi is marked with black triangles. The other 2 viruses isolated from human in People’s Republic of China were marked with purple circle. Scale bar indicates nucleotide substitutions per site.



Appendix Figure 5. Phylogenetic tree MP gene of the A/Guangxi/01591/2024(H10N3). The phylogenetic trees were constructed with MEGA7.0 software using the maximum likelihood (ML) method. Bootstrap analysis was performed with 1000 replicates. The virus A/Guangxi/01591/2024(H10N3) reported in Guangxi is marked with black triangles. The other 2 viruses isolated from human in People's Republic of China were marked with purple circle. Scale bar indicates nucleotide substitutions per site.



Appendix Figure 6. Phylogenetic tree NS gene of the A/Guangxi/01591/2024(H10N3). The phylogenetic trees were constructed with MEGA7.0 software using the maximum likelihood (ML) method. Bootstrap analysis was performed with 1000 replicates. The virus A/Guangxi/01591/2024(H10N3) reported in Guangxi is marked with black triangles. The other 2 viruses isolated from human in People's Republic of China were marked with purple circle. Scale bar indicates nucleotide substitutions per site.