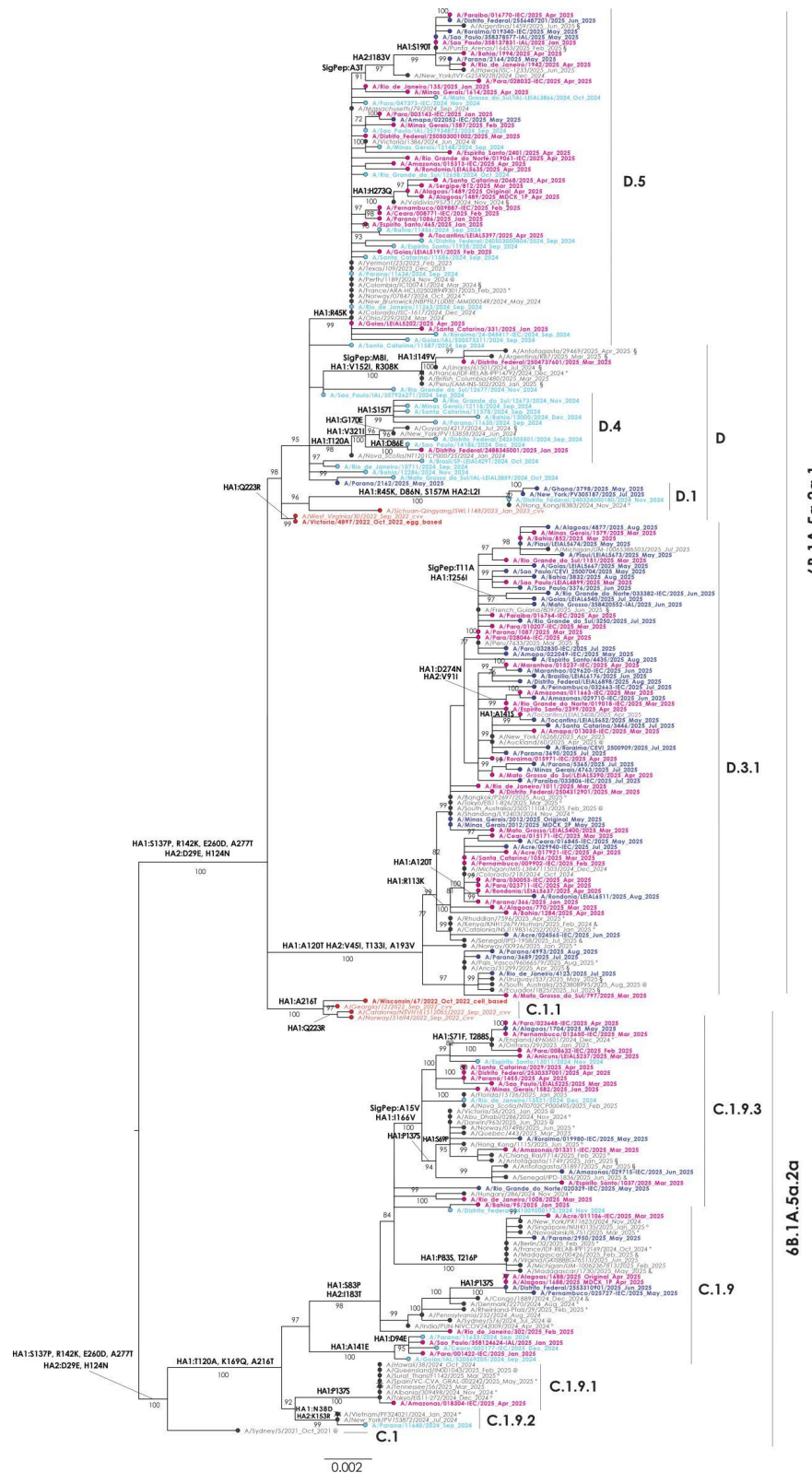
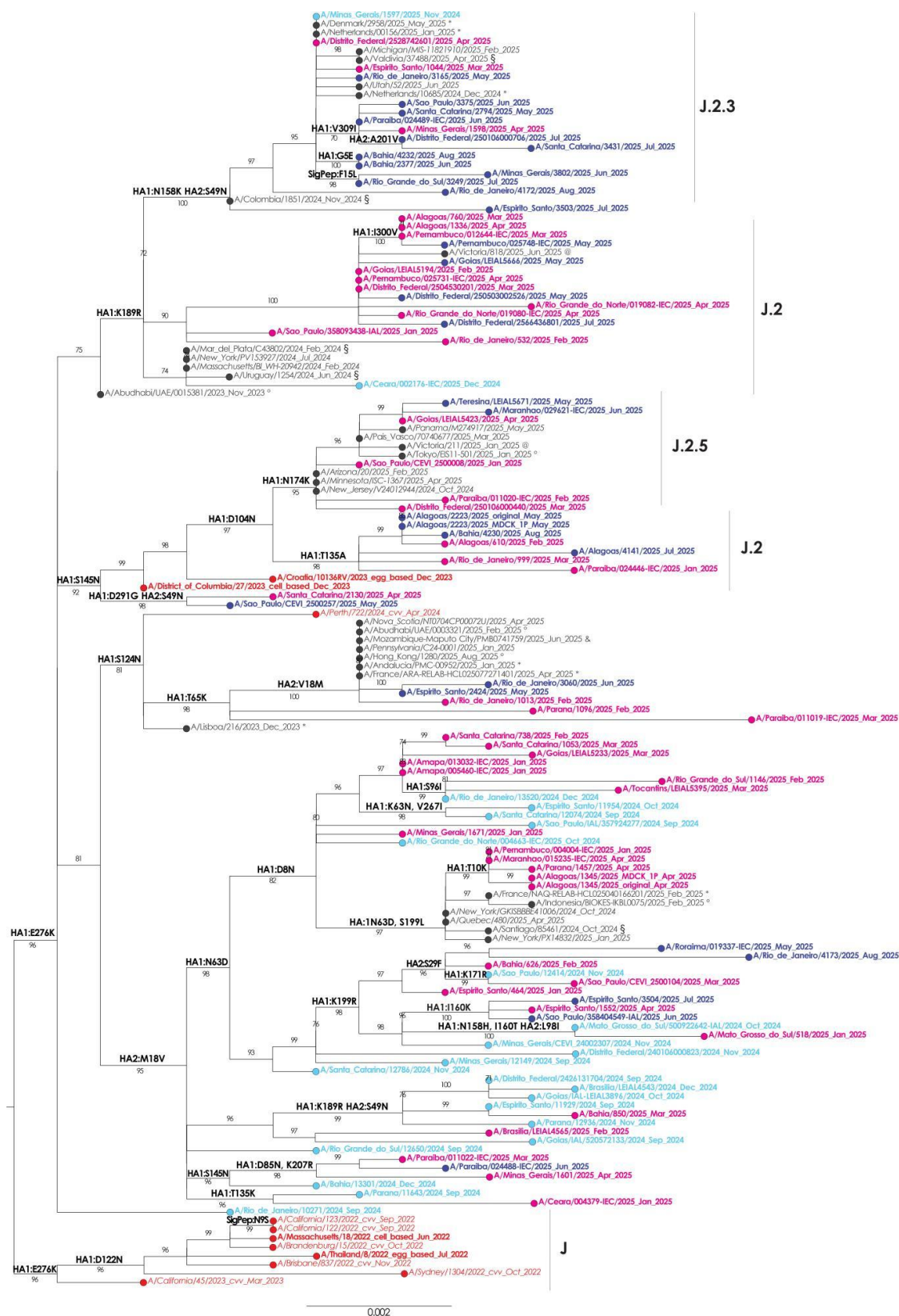
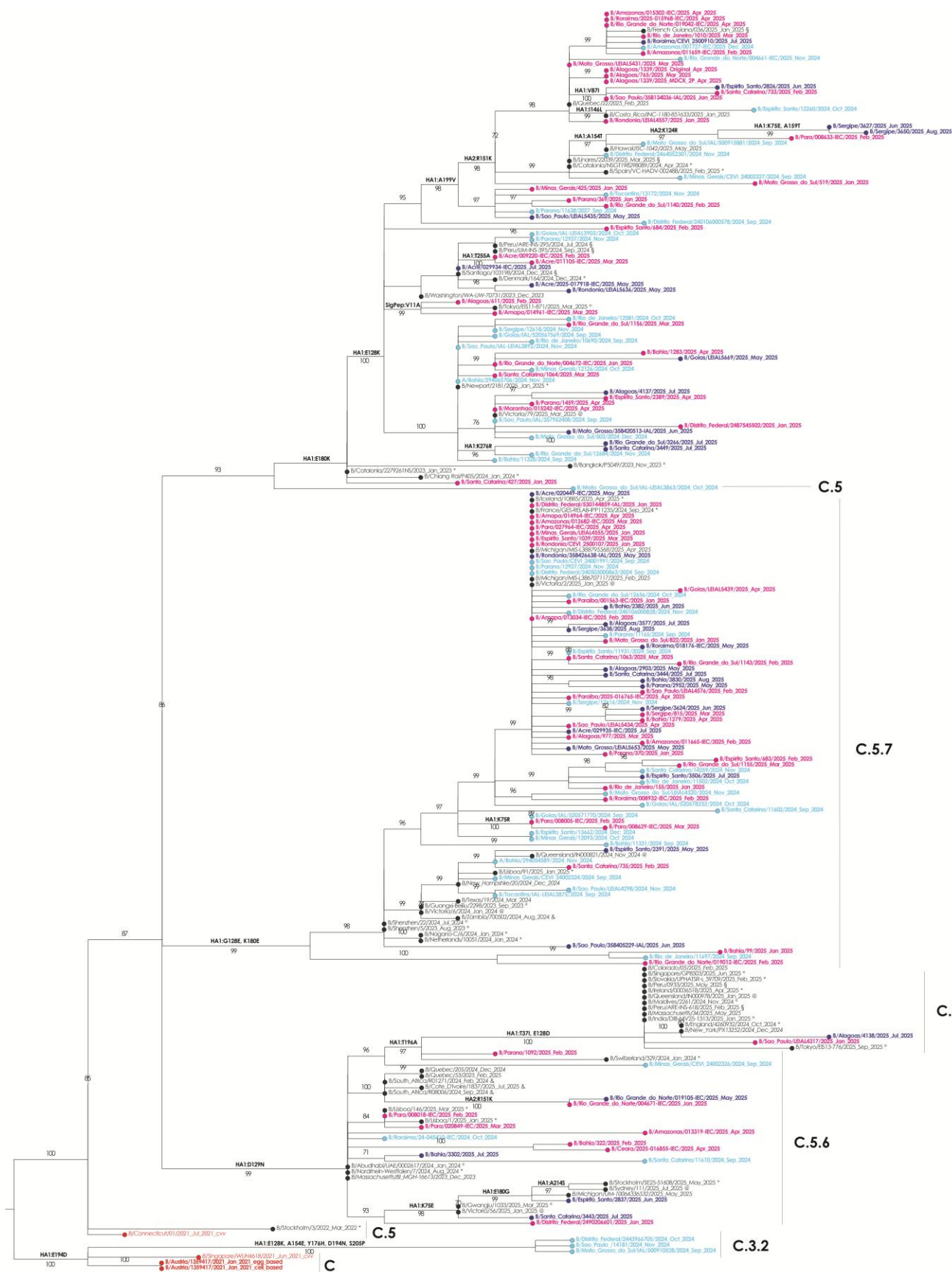




Supplementary Figure 1. Phylogenetic reconstruction of influenza A(H1N1)pdm09 hemagglutinin (HA) sequences collected in Brazil between EW35/2024 and EW35/2025 (Brazilian sequences shown in bold). The phylogenetic tree was inferred using 5,000 bootstrap replicates. The dataset includes reference strains, vaccine strains (bold red), candidate vaccine viruses (CVVs; red), and representative global sequences categorized by geographic region (black). Sequence origin is indicated by the following symbols: § South America (SH), * Europe (NH), ° Asia (NH), & Africa (SH), and @ Oceania (SH). Temporal information based on sample collection dates is indicated by colors: September–December 2024 (light blue), January–April 2025 (pink), and May–August 2025 (blue). Amino acid substitutions are annotated on the branches. Influenza clades and subclades are indicated.



Supplementary Figure 2. Phylogenetic reconstruction of influenza A(H3N2) hemagglutinin (HA) sequences collected in Brazil between EW35/2024 and EW35/2025 (Brazilian sequences shown in bold). The phylogenetic tree was inferred using 5,000 bootstrap replicates. The dataset includes reference strains, vaccine strains (bold red), candidate vaccine viruses (CVVs; red), and representative global sequences categorized by geographic region (black). Sequence origin is indicated by the following symbols: § South America (SH), * Europe (NH), ° Asia (NH), & Africa (SH), and @ Oceania (SH). Temporal information based on sample collection dates is indicated by colors: September–December 2024 (light blue), January–April 2025 (pink), and May–August 2025 (blue). Amino acid substitutions are annotated on the branches. Influenza clades and subclades are indicated.



C.5.1

C.5

C.5.7

C.5.6.1

C.5.6

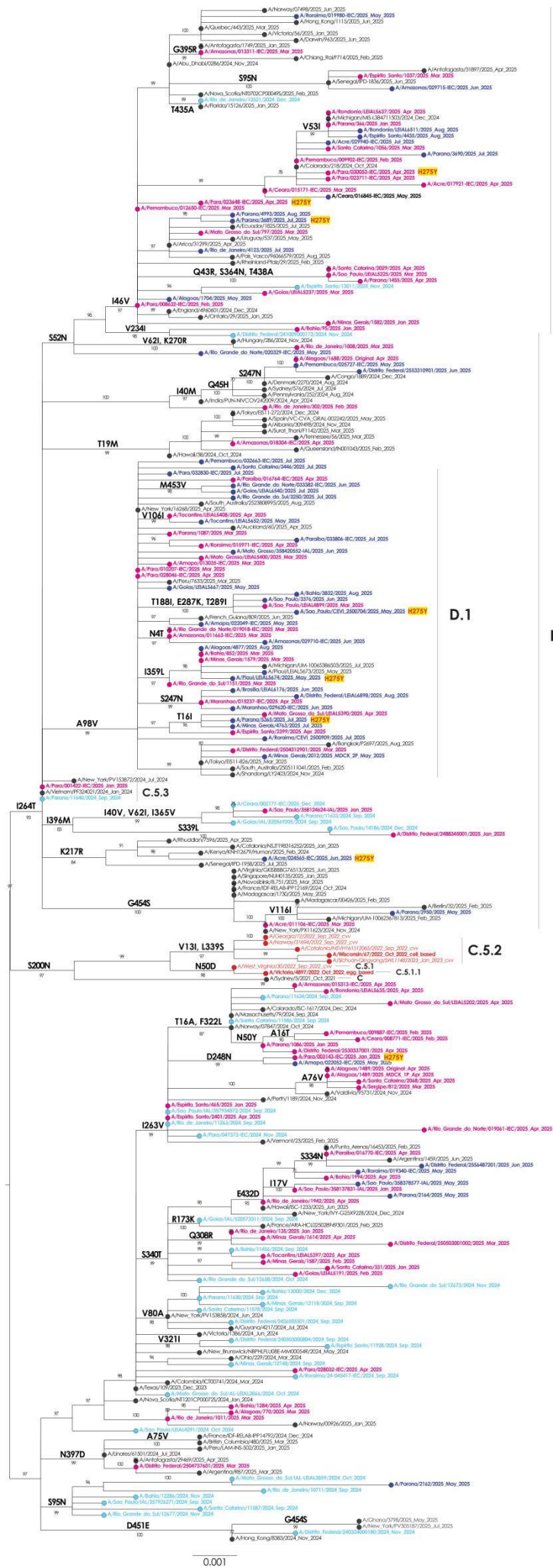
C.3.2

C

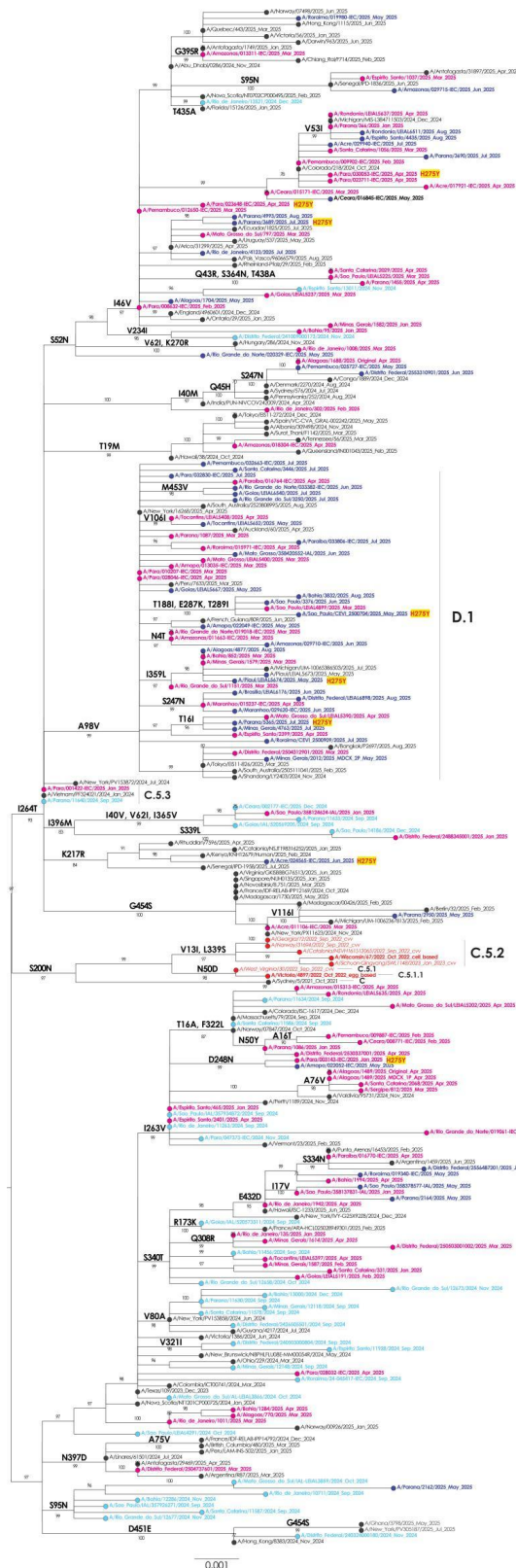
0.002



Supplementary Figure 3. Phylogenetic reconstruction of influenza B Victoria hemagglutinin (HA) sequences collected in Brazil between EW35/2024 and EW35/2025 (Brazilian sequences shown in bold). The phylogenetic tree was inferred using 5,000 bootstrap replicates. The dataset includes reference strains, vaccine strains (bold red), candidate vaccine viruses (CVVs; red), and representative global sequences categorized by geographic region (black). Sequence origin is indicated by the following symbols: § South America (SH), * Europe (NH), ° Asia (NH), & Africa (SH), and @ Oceania (SH). Temporal information based on sample collection dates is indicated by colors: September–December 2024 (light blue), January–April 2025 (pink), and May–August 2025 (blue). Amino acid substitutions are annotated on the branches. Influenza clades and subclades are indicated.



0,001



D.2

D.1

D

C.5.2

C.5.3

Supplementary Figure 4. Phylogenetic reconstruction of influenza A(H1N1)pdm09 neuraminidase (NA) sequences collected in Brazil between EW35/2024 and EW35/2025 (Brazilian sequences shown in bold), highlighting the H275Y resistance marker, which is associated with high-level resistance to oseltamivir phosphate. The phylogenetic tree was inferred using 5,000 bootstrap replicates. The dataset includes reference strains, vaccine strains (bold red), candidate vaccine viruses (CVVs; red), and representative global sequences categorized by geographic region (black). Sequence origin is indicated by the following symbols: § South America (SH), * Europe (NH), ° Asia (NH), & Africa (SH), and @ Oceania (SH). Temporal information based on sample collection dates is indicated by colors: September–December 2024 (light blue), January–April 2025 (pink), and May–August 2025 (blue). Amino acid substitutions are annotated on the branches. Influenza clades and subclades are indicated.

Supplementary Table 1. Clinical, epidemiological, and laboratory characteristics of influenza cases detected in Brazil from epidemiological week (EW) 35/2024 to EW 35/2025.

		A(H1N1)pdm09												A(H3N2)					B Victoria							
N total		2132												726					945							
		5a.2a.1 (D.3.1)	5a.2a.1 (D.5)	5a.2a (C.1.9.3)	5a.2a.1 (D)	5a.2a.1 (D.4)	5a.2a (C.1.9)	5a.2a (C.1.9.1)	5a.2a (C.1.9.2)	5a.2a (C.1.9.4)	5a.2a (C.1)	5a.2a.1 (C.1.1)	5a.2a.1 (D.1)	2a.3a.1 (J.2)	2a.3a.1 (J.2.3)	2a.3a.1 (J.2.2)	2a.3a.1 (J.2.5)	2a.3a.1 (J)	V1A.3a.2 (C.5.7)	V1A.3a.2 (C.5.1)	V1A.3a.2 (C.5.6)	V1A.3a.2 (C.5.6.1)	V1A.3a.2 (C.3)	V1A.3a.2 (C.3.2)	V1A.3a.2 (C.5)	
Geographical Region	Brazilian State	70,8%	16,2%	7,9%	2,9%	1,0%	0,7%	0,2%	0,0%	0,0%	0,0%	0,0%	0,0%	76,2%	22,2%	0,8%	0,6%	0,3%	52,1%	42,5%	3,6%	0,8%	0,4%	0,3%	0,2%	
		1509	345	169	62	22	15	5	1	1	1	1	1	553	161	6	4	2	492	402	34	8	4	3	2	
Midwest 583	Federal District	29					2												20	28						
	Goiás	33	1												2				6	1						
Northeast 777	Mato Grosso	40	3	30					1										12	7	3					
	Mato Grosso do Sul	133	42	68			1												117	1	3					
	Alagoas	12	11	1					4						2				18	6						
	Bahia	60	2	2											1				3	4	6					
	Ceara	9	2												3				2	1						
	Maranhao	53	3	17			1								77				16	13		7				
	Paraiba	40	7	2	1	1									9	6		1	65	34	2					
	Pernambuco	37	1	1			1								4				2	1	2					
	Piaui	10													6			1		2						
	Rio Grande do Norte	59	1												59	2	1			3						
North 796	Sergipe	36	1	7										35						1						
	Acre	7																2								
	Amapa	86	2	4											5	1			1	7	3					
	Amazonas		4																11	7						
	Para	135	30	4	9	2							1	170	72		1		33	22	4	1	1	3		
	Rondonia	11	5	1	1		2								15	4			5	9						
	Roraima	17													1				4	7	1					
Southeast 1137	Tocantins	40	5		3										5	1			6	23			1		1	
	Espirito Santo	42	26	3	1									30	12	1			47	19	2					
	Minas Gerais	82	43	7	2	1						1		14	20				11	16	1					
	Rio de Janeiro	87	25	5	3							1		27	14	3			14	12	1					
	Sao Paulo	222	78	8	9	12	6			1			1	62	9				43	110	2		2			
South 510	Parana	130	23	3	17	2	2		1					8	7	1			16	24	1					
	Rio Grande do Sul	13	3		3	1								4	3			1	13	15						
	Santa Catarina	86	27	6	13	3								14	10				24	32	3				1	
Host Gender																										
	Not informed	85	7	7	4	2	1	3						27	7				52	61						
	Female	741	171	93	21	10	6	1	1	1	1			285	79	6	2	1	221	183	15	4	3	2	1	
	Male	686	158	69	32	10	8	1				1	1	228	95		2	1	210	144	21	4	1	1	1	
Age groups (years)																										
	< 2	94	21	8	4	1						1		53	23	1			17	16	1	1	1			
	2 a 4	68	10	6	5		3							45	15	1	1		10	14	1		1			
	5 a 14	199	35	24	5	2	2	2						88	35		1		79	88	6				1	
	15 a 49	562	158	72	26	10	5		1	1		1		247	56	2	2		276	180	20	5	2	1		
	50 a 64	228	52	27	7	4	2	1					1	46	11				26	20	1					
	> 65	318	57	26	6	3	3							53	21	2		2	19	13	2				1	
	Not informed	40	12	6	9	2		2						21					65	71	3					
Patient Status																										
	Deceased	12	1											1					1							
	In-patient	147	17	3	6	2	1		1					21	22	2			19	18	2	1	1			
	Out-patient	118	18	13	1		1							29	6	2			25	28	1		1			
	Not informed	1232	309	153	55	20	13	5		1	1	1	1	502	133	2	4	2	447	356	31	7	2	3	2	
Laboratory																										
	NIC FIOCRUZ	554	143	43	24	9	3		1		1	1		178	80	5		2	172	143	9	7	2		1	
	NIC FIOCRUZ (WHOCC)		7		6									4					10	11	2					
	NIC IAL*	129	47	3	6	4	3							58	28		2		34	54	3		1		1	
	NIC IAL (WHOCC)	19	9	2	1		2							11	2				8	24						
	NIC IEC	511	53	112			4	1						108	2	1	1		159	50	17					
	NIC IEC (WHOCC)	11												4	1				5							
	FIOCRUZ-MS	25	2											2					3	19						
	LACEN-BA																		31	20						
	LACEN-DF	130	27	4	9	2							1	158	68		1		29	20	4	1	1	3		
	LACEN-MG				1															1						
	LACEN-RO		3					2											4							
	Outros	133	45	5	10	7	3	2		1				17					28	46	1					

* NIC IAL, represented by the Strategic Laboratory of the Rapid Response Center of the Adolfo Lutz Institute

Supplementary Table 2: Antigenic analysis of A(H1N1)pdm09 isolates by hemagglutination inhibition assay (HI) with ferret immune serum.

<i>Viruses</i>	<i>Other information</i>			<i>HI titre with ferret immune serum</i>	
<i>Reference isolates</i>	<i>Type of isolate</i>		<i>Genetic group</i>	<i>A/Wisconsin/67/2022</i>	<i>A/Victoria/4897/2022</i>
A/Victoria/4897/2022	Vaccine virus – egg isolate		5a.2a.1	1280	2560
A/Wisconsin/67/2022	Vaccine virus – cell isolate		5a.2a.1	1280	640
<i>Clinical isolates</i>	<i>Type of isolate</i>	<i>EpiFlu ID</i>	<i>Genetic group</i>	<i>A/Wisconsin/67/2022</i>	<i>A/Victoria/4897/2022</i>
A/Alagoas/1489/2025	MDCK-1P	EPI_ISL_20160196	5a.2a.1 (D.5)	2560	2560
A/Alagoas/1502/2025	MDCK-1P	EPI_ISL_20160197	5a.2a.1 (D.3.1)	2560	2560
A/Alagoas/1503/2025	MDCK-1P	EPI_ISL_20160198	5a.2a.1 (D.3.1)	2560	2560
A/Alagoas/1687/2025	MDCK-1P	EPI_ISL_20160199	5a.2a.1 (D.3.1)	2560	2560
A/Alagoas/1688/2025	MDCK-1P	EPI_ISL_20160200	5a.2a (C.1.9.3)	2560	2560
A/Alagoas/1690/2025	MDCK-1P	EPI_ISL_20160201	5a.2a (C.1.9.3)	2560	2560
A/Alagoas/1698/2025	MDCK-1P	EPI_ISL_20160202	5a.2a.1 (D.3.1)	2560	2560
A/Alagoas/1703/2025	MDCK-2P	EPI_ISL_20160203	5a.2a.1 (D.3.1)	2560	2560
A/Alagoas/1704/2025	MDCK-1P	EPI_ISL_20160204	5a.2a (C.1.9.3)	2560	2560
A/Alagoas/1707/2025	MDCK-2P	EPI_ISL_20160205	5a.2a.1 (D.3.1)	2560	2560
A/Alagoas/1708/2025	MDCK-1P	Not sequenced	5a.2a.1 (*)	2560	2560
A/Alagoas/1709/2025	MDCK-1P	Not sequenced	5a.2a.1 (*)	2560	2560
A/Alagoas/1717/2025	MDCK-2P	EPI_ISL_20160208	5a.2a.1 (D.3.1)	2560	2560
A/Alagoas/1726/2025	MDCK-2P	Not sequenced	5a.2a.1 (*)	2560	2560
A/Alagoas/1729/2025	MDCK-2P	EPI_ISL_20155356	5a.2a.1 (D.3.1)	2560	2560
A/Alagoas/2222/2025	MDCK-2P	Not sequenced	5a.2a (*)	2560	2560
A/Alagoas/2226/2025	MDCK-1P	EPI_ISL_20160211	5a.2a.1 (D.3.1)	2560	2560
A/Bahia/1291/2025	MDCK-2P	EPI_ISL_20160215	5a.2a.1 (D.3.1)	2560	2560
A/Bahia/211/2025	MDCK-2P	EPI_ISL_20160217	5a.2a (C.1.9.3)	2560	2560
A/Bahia/2196/2025	MDCK-1P	EPI_ISL_20160218	5a.2a.1 (D.3.1)	2560	2560
A/Bahia/2197/2025	MDCK-2P	Not sequenced	5a.2a.1 (*)	2560	2560

<i>Clinical isolates</i>	<i>Type of isolate</i>	<i>EpiFlu ID</i>	<i>Genetic group</i>	<i>HI: A/Wisconsin/67/2022</i>	<i>HI: A/Victoria/4897/2022</i>
A/Bahia/2260/2025	MDCK-1P	EPI_ISL_20160220	5a.2a.1 (D.3.1)	2560	2560
A/Espirito Santo/1537/2025	MDCK-1P	EPI_ISL_20160221	5a.2a.1 (D.3.1)	2560	2560
A/Espirito Santo/1549/2025	MDCK-1P	EPI_ISL_20160222	5a.2a.1 (D.3.1)	2560	2560
A/Espirito Santo/1551/2025	MDCK-1P	EPI_ISL_20160223	5a.2a.1 (D.3.1)	1280	640
A/Minas Gerais/1577/2025	MDCK-1P	EPI_ISL_20164454	5a.2a.1	2560	2560
A/Minas Gerais/1578/2025	MDCK-2P	EPI_ISL_20160225	5a.2a.1 (D.5)	2560	2560
A/Minas Gerais/1580/2025	MDCK-1P	EPI_ISL_20160226	5a.2a.1 (D)	2560	2560
A/Minas Gerais/1581/2025	MDCK-1P	EPI_ISL_20160227	5a.2a (C.1.9.3)	2560	2560
A/Minas Gerais/1585/2025	MDCK-1P	EPI_ISL_20160229	5a.2a.1 (D.5)	2560	2560
A/Minas Gerais/1587/2025	MDCK-1P	EPI_ISL_20164456	5a.2a.1	2560	2560
A/Minas Gerais/1589/2025	MDCK-1P	EPI_ISL_20164457	5a.2a.1	2560	2560
A/Minas Gerais/1590/2025	MDCK-1P	EPI_ISL_20164458	5a.2a.1	2560	2560
A/Minas Gerais/1595/2025	MDCK-2P	EPI_ISL_20160231	5a.2a.1 (D.5)	2560	2560
A/Minas Gerais/1602/2025	MDCK-1P	EPI_ISL_20164461	5a.2a.1	2560	2560
A/Minas Gerais/1603/2025	MDCK-1P	EPI_ISL_20160232	5a.2a.1 (D.3.1)	2560	2560
A/Minas Gerais/1604/2025	MDCK-1P	EPI_ISL_20160233	5a.2a.1 (D.3.1)	2560	2560
A/Minas Gerais/1606/2025	MDCK-1P	Not sequenced	5a.2a.1 (*)	2560	2560
A/Minas Gerais/1607/2025	MDCK-1P	EPI_ISL_20164462	5a.2a.1	2560	2560
A/Minas Gerais/1608/2025	MDCK-2P	EPI_ISL_20160234	5a.2a.1 (D.3.1)	2560	2560
A/Minas Gerais/1613/2025	MDCK-2P	EPI_ISL_20160236	5a.2a.1 (D.3.1)	2560	2560
A/Minas Gerais/1614/2025	MDCK-1P	EPI_ISL_20164463	5a.2a.1	2560	2560
A/Minas Gerais/2013/2025	MDCK-1P	Not sequenced	5a.2a.1 (*)	2560	2560
A/Minas Gerais/2015/2025	MDCK-2P	EPI_ISL_20155290	5a.2a.1 (D.3.1)	2560	2560
A/Minas Gerais/2018/2025	MDCK-1P	EPI_ISL_20160237	5a.2a.1 (D.3.1)	2560	2560
A/Minas Gerais/2020/2025	MDCK-2P	EPI_ISL_20160238	5a.2a.1 (D.3.1)	1280	1280
A/Minas Gerais/2021/2025	MDCK-2P	EPI_ISL_20160239	5a.2a.1 (D.3.1)	1280	1280
A/Minas Gerais/2022/2025	MDCK-2P	EPI_ISL_20160240	5a.2a.1 (D.3.1)	2560	2560
A/Minas Gerais/2023/2025	MDCK-2P	EPI_ISL_20160241	5a.2a.1 (D.3.1)	2560	2560

<i>Clinical isolates</i>	<i>Type of isolate</i>	<i>EpiFlu ID</i>	<i>Genetic group</i>	<i>HI: A/Wisconsin/67/2022</i>	<i>HI: A/Victoria/4897/2022</i>
A/Minas Gerais/2024/2025	MDCK-2P	EPI_ISL_20155291	5a.2a.1 (D.3.1)	2560	2560
A/Parana/2161/2025	MDCK-2P	Not sequenced	5a.2a.1 (*)	1280	1280
A/Rio de Janeiro/1308/2025	MDCK-1P	EPI_ISL_20160249	5a.2a.1 (D.3.1)	640	640
A/Rio de Janeiro/1512/2025	MDCK-1P	EPI_ISL_20160250	5a.2a.1 (D.3.1)	2560	2560
A/Rio de Janeiro/1973/2025	MDCK-2P	EPI_ISL_20155299	5a.2a.1 (D.3.1)	2560	2560
A/Rio de Janeiro/2146/2025	MDCK-1P	EPI_ISL_20155295	5a.2a.1 (D.3.1)	2560	2560
A/Rio de Janeiro/2168/2025	MDCK-1P	EPI_ISL_20155296	5a.2a.1 (D.3.1)	2560	2560
A/Rio de Janeiro/2173/2025	MDCK-1P	"EPI_ISL_20155297	5a.2a.1 (D.3.1)	2560	2560
A/Rio de Janeiro/2176/2025	MDCK-1P	Not sequenced	5a.2a.1 (*)	2560	2560
A/Rio de Janeiro/2334/2025	MDCK-1P	EPI_ISL_20155298	5a.2a.1 (D.3.1)	2560	2560
A/Rio de Janeiro/302/2025	MDCK-1P	Not sequenced	5a.2a (*)	2560	2560
A/Rio Grande do Sul/1163/2025	MDCK-1P	EPI_ISL_20160253	5a.2a.1 (D.3.1)	2560	2560
A/Santa Catarina/2074/2025	MDCK-1P	Not sequenced	Not determined	2560	2560
A/Santa Catarina/2120/2025	MDCK-1P	Not sequenced	Not determined	2560	2560
A/Santa Catarina/2129/2025	MDCK-2P	Not sequenced	Not determined	1280	1280
A/Santa Catarina/2132/2025	MDCK-2P	Not sequenced	Not determined	2560	2560
A/Santa Catarina/2290/2025	MDCK-2P	Not sequenced	Not determined	2560	2560
A/Santa Catarina/2306/2025	MDCK-2P	Not sequenced	Not determined	2560	2560
A/Santa Catarina/2307/2025	MDCK-2P	Not sequenced	Not determined	2560	2560
A/Sao Paulo/1627/2025	MDCK-2P	Not sequenced	Not determined	2560	2560
A/Sao Paulo/1628/2025	MDCK-2P	Not sequenced	5a.2a.1 (*)	2560	2560

The vaccine viral isolates A/Wisconsin/67/2022 (passage MDCK3) and A/Victoria/4897/2022 (passage E3/D6/E2d) and corresponding ferret immune sera were provided by the Worldwide Influenza Centre, WHO CC for Reference and Research on Influenza, at the Francis Crick Institute, London, UK. (*) For those isolates that could not be sequenced, the definition of the genetic group was based on the sequence of the original clinical sample. MDCK-nP, number of passages in cell culture.

Supplementary Table 3: Antigenic analysis of A(H3N2) isolates by hemagglutination inhibition assay (HI) with ferret immune serum.

<i>Viruses</i>	<i>Other information</i>		<i>HI titre with ferret immune serum</i>		
<i>Reference viruses</i>	<i>Type of isolate</i>		<i>Genetic group</i>	<i>A/Croatia/10136RV/2023</i>	<i>A/District of Columbia/27/2023</i>
A/Croatia/10136RV/2023	Vaccine virus - Egg isolate		2a.3a.1	1280	1280
A/District of Columbia/27/2023	Vaccine virus - Cell isolate		2a.3a.1	640	640
<i>Clinical isolates</i>	<i>Type of isolate</i>	<i>EpiFlu ID</i>	<i>Genetic group</i>	<i>A/Croatia/10136RV/2023</i>	<i>A/District of Columbia/27/2023</i>
A/Alagoas/1338/2025	MDCK-1P	EPI_ISL_20155444	2a.3a.1 (J.2)	1280	1280
A/Alagoas/1341/2025	MDCK-1P	EPI_ISL_20155445	2a.3a.1 (J.2)	160	320
A/Alagoas/1344/2025	MDCK-1P	EPI_ISL_20155391	2a.3a.1 (J.2)	1280	640
A/Alagoas/1345/2025	MDCK-1P	EPI_ISL_20155446	2a.3a.1 (J.2)	1280	1280
A/Alagoas/1701/2025	MDCK-1P	EPI_ISL_20155447	2a.3a.1 (J.2)	1280	1280
A/Alagoas/1711/2025	MDCK-1P	EPI_ISL_20155385	2a.3a.1 (J.2)	1280	1280
A/Alagoas/1712/2025	MDCK-1P	EPI_ISL_20155448	2a.3a.1 (J.2)	640	640
A/Alagoas/2223/2025	MDCK-1P	EPI_ISL_20155408	2a.3a.1 (J.2)	1280	1280
A/Alagoas/2902/2025	MDCK-1P	EPI_ISL_20155355	2a.3a.1 (J.2)	1280	1280
A/Alagoas/2923/2025	MDCK-1P	EPI_ISL_20155449	2a.3a.1 (J.2)	1280	1280
A/Alagoas/768/2025	MDCK-1P	EPI_ISL_20155519	2a.3a.1 (J.2)	160	320
A/Alagoas/978/2025	MDCK-2P	EPI_ISL_20155394	2a.3a.1 (J.2)	1280	640
A/Santa Catarina/332/2025	MDCK-2P	Not sequenced	2a.3a.1 (J.2)*	320	320

The vaccine viral isolates A/Croatia/10136RV/2023 (passage E3/E3) and A/District of Columbia/27/2023 (passage SIAT2/SIAT2), and the corresponding ferret immune sera were provided by the Worldwide Influenza Centre, WHO CC for Reference and Research on Influenza at the Frances Crick Institute, London, UK. (*) For those isolates that could not be sequenced, the definition of the genetic group was based on the sequence of the original clinical sample. MDCK-nP, number of passages in cell culture.

Supplementary Table 4: Antigenic analysis of B Victoria isolates by hemagglutination inhibition assay (HI) with ferret immune serum.

<i>Viruses</i>	<i>Other information</i>			<i>HI with ferret immune serum</i>	
<i>Reference isolates</i>	<i>Type of isolate</i>	<i>Genetic group</i>	<i>B/Austria/1359417/2021-cell</i>	<i>B/Austria/1359417/2021-egg</i>	
B/Austria/1359417/2021	Vaccine virus – cell isolate	V1A.3a.2 (C.5.7)	1280	640	
B/Austria/1359417/2021	Vaccine virus – egg isolate	V1A.3a.2 (C.5.7)	640	1280	
<i>Clinical isolates</i>	<i>Type of isolate</i>	<i>EpiFlu ID</i>	<i>Genetic group</i>	<i>B/Austria/1359417/2021-cell</i>	<i>B/Austria/1359417/2021-egg</i>
B/Bahia/99/2025	MDCK-1P	EPI_ISL_20084240	V1A.3a.2 (C.5.7)	1280	1280
B/Espirito Santo/461/2025	MDCK-2P	EPI_ISL_20084140	V1A.3a.2 (C.5.7)	640	320
B/Espirito Santo/466/2025	MDCK-1P	EPI_ISL_20084242	V1A.3a.2 (C.5.7)	1280	640
B/Espirito Santo/467/2025	MDCK-2P	EPI_ISL_20084244	V1A.3a.2 (C.5.7)	640	320
B/Espirito Santo/469/2025	MDCK-1P	EPI_ISL_20084245	V1A.3a.2 (C.5.1)	1280	1280
B/Espirito Santo/472/2025	MDCK-1P	EPI_ISL_20084247	V1A.3a.2 (C.5.7)	1280	640
B/Santa Catarina/420/2025	MDCK-1P	EPI_ISL_20084248	V1A.3a.2 (C.5.1)	1280	640
B/Santa Catarina/422/2025	MDCK-1P	EPI_ISL_20084250	V1A.3a.2 (C.5.7)	1280	640
B/Santa Catarina/424/2025	MDCK-1P	EPI_ISL_20084252	V1A.3a.2 (C.5.1)	640	640
B/Santa Catarina/427/2025	MDCK-1P	EPI_ISL_20084254	V1A.3a.2 (C.5.1)	1280	640
B/Santa Catarina/428/2025	MDCK-2P	Not sequenced	Not available	1280	640

The B/Austria/1359417/2021 isolates propagated in both cells (SIAT1/MDCK4) and eggs (E3/E5 ISL2) and the corresponding ferret immune sera were provided by the Worldwide Influenza Centre, WHO CC for Reference and Research on Influenza, at the Frances Crick Institute, London, UK. MDCK-nP, number of passages in cell culture.