

SUPPLEMENTARY TABLE 2. Genetic characteristics of sequenced influenza A(H3N2) viruses (N = 286) and A(H1N1)pdm09 viruses (N = 158) — three vaccine effectiveness networks, United States, 2024–2025 influenza season

Network	Total sequenced A(H3N2) viruses		Total sequenced A(H1N1)pdm09 viruses		
	No.	Clade, No. (%)	No.	Clade, No. (%)	
		HA clade 2.3a.1*		HA clade 5a.2a	HA clade 5a.2a.1 [†]
IVY	26	26 (100)	5	3 (60)	2 (40)
U.S. Flu VE	200	200 (100)	80	55 (69)	25 (31)
NVSN	60	60 (100)	73	46 (63)	27 (37)
TOTAL	286	286 (100)	158	104 (66)	54 (34)

Abbreviations: HA = hemagglutinin; IVY = Investigating Respiratory Viruses in the Acutely Ill; NVSN = New Vaccine Surveillance Network; U.S. Flu VE = U.S. Flu Vaccine Effectiveness.

* Includes the A(H3N2) strain selected for the 2024–2025 cell-grown influenza vaccine (A/Massachusetts/18/2022)

[†] Includes the A(H1N1)pdm09 strain selected for the 2024–2025 cell-grown influenza vaccine (A/Wisconsin/67/2022)