SUPPLEMENTARY TABLE 2. Genetic characteristics of sequenced influenza A(H3N2) viruses (n = 572), A(H1N1)pdm09 viruses (n = 47), and influenza B viruses (n = 108) — U.S. Flu Vaccine Effectiveness Network and New Vaccine Surveillance Network, United States, 2025–26 influenza season

	Surveillance network, No. (%)		
Genetic Type/Subclade	**U.S. Flu VE**	**NVSN**	**Total**
All A(H3N2)	**287 (100)**	**285 (100)**	**572 (100)**
K	263 (92)	211 (74)	474 (83)
J.2	2 (1)	0 (0)	2 (<1)
J.2.3	2 (1)	35 (12)	37 (6)
J.2.4	20 (7)	39 (14)	59 (10)
All A(H1N1)pdm09	**32 (100)**	**15 (100)**	**47 (100)**
D.3.1	16 (50)	8 (53)	24 (51)
D.3.1.1	16 (50)	7 (47)	23 (49)
All B	**95 (100)**	**13 (100)**	**108 (100)**
C.3	2 (2)	0 (0)	2 (2)
C.3.1	80 (84)	7 (54)	87 (81)
C.5.1	0 (0)	1 (8)	1 (1)
C.5.6	13 (14)	0 (0)	13 (12)
C.5.6.1	0 (0)	4 (31)	4 (4)
C.5.7	0 (0)	1 (8)	1 (1)

Abbreviations: NVSN = New Vaccine Surveillance Network; U.S. Flu VE = U.S. Flu Vaccine Effectiveness Network.