Table S3. Amino acid substitutions in the HA and NA segments of influenza A and B samples (2024–2025 season).
(Only missense (non-synonymous) substitutions with allele frequency ⩾80% are listed. Samples are grouped by subtype and confirmed Nextclade HA clade. Substitution notation follows [Reference AA][Position][Variant AA] convention - H1 numbering for H1N1 HA, N1 numbering for H1N1 NA; H3 numbering for H3N2 HA, N2 numbering for H3N2 NA; B numbering for influenza B HA and NA.)

Sample	Clade (HA)	HA amino acid substitutions	NA amino acid substitutions
Influenza A(H1N1) pdm09			
A/Athens/SENT11007/2025	C.1.9.3	A15V, S100P, T137A, S154P, R159K, V169I, I183V, K186Q, R222K, A233T, E277D, A294T, D373E, H468N, I527T	I46V, D50N, S52N, S200N, I264T, E382G
A/Athens/21c/2025 [1]	C.1.9.3	A15V, S100P, T137A, S160G, I183V, K186Q, A233T, E277D, A294T, D373E, H468N, I527T	I46V, D50N, S52N, S200N, I264T, H275Y, E382G
A/Athens/21/2025 [1]	C.1.9.3	A15V, S100P, T137A, S160G, I183V, K186Q, A233T, E277D, A294T, D373E, H468N, I527T	I46V, D50N, S52N, S200N, I264T, H275Y, E382G
A/Athens/ILI1600/2024	C.1.9.3	S100P, T137A, S154P, R159K, K186Q, A233T, E277G, A294T, D373E, H468N, I527T	D50N, S52N, S200N, I264T, E382G
A/Athens/SENT11007/2025	C.1.9.3	A15V, S100P, T137A, S154P, R159K, V169I, I183V, K186Q, R222K, A233T, E277D, A294T, D373E, H468N, I527T	I46V, D50N, S52N, S200N, I264T, E382G
A/Athens/SENT10789/2025	D.3.1	T137E, I389V, I477T, V537A	D50N, S200N, I211V, K217R, I264T, E382G
A/Athens/63/2025 [2]	D.3.1	T137E, I389V, I477T, V537A	D50N, S200N, I211V, K217R, I264T, E382G
Influenza A(H3N2)			
A/Athens/ILI1563/2024	J.1.1	I41V, R49Q, D138N, V198I, I230T, E292K, V363M	E83G
A/Athens/SENT11220/2025	J.1.1	I41V, I41M, R49Q, D138N, V198I, I230T, E292K, V363M	E83G, H336N
A/Athens/ILI180/2025	J.1.1	I41V, R49Q, D138N, V198I, I230T, E292K, V363M	E83G, H150Y
A/Athens/SARI12258/2025	J.2.2	H34Y, T81K, S140N, N161S, V363M	S181A, P386S
Influenza B (Victoria lineage)			
B/Athens/ILI89/20	C.5.1	E143G, E195K, D209E	L52S, K152R, G378E, I459V
B/Athens/ILI186/2025 [2]	C.5.1	V11A, E143K, E195K, D209E, F566S	D35G, L52S, G378E, I459V
B/Athens/SENT11109/2025	C.5.1	V11A, E143K, E195K, D209E	L52S, G378E, I459V
B/Athens/SENT11017/2025	C.5.6	D144N, D209E	I45T, R65H, S397N, I459V
B/Athens/SENT11012_MDCK/2025 [3]	C.5.6.1	T52I, T136I, ED143DN, D209E, T211A	I45T, D53N, S397N, K404R, I459V
B/Phthiotis.GR/SENT11772/2025	C.5.7	E143G, E195K, D209E	A47V, G378E, I459V

B/Athens/SENT10797/2025	C.5.7	E143G, E195K, D209E	A47V, P48S, T91I, T334A, G378E, I459V
B/Athens/ILI204/2025	C.5.7	E143G, E195K, D209E	A47V, P48S, T334A, G378E, I459V
B/Athens/SENT10773/2025	C.5.7	E143G, E195K, E196G, D209E	A47V, P48S, T334A, G378E, I459V
B/Athens/ILI81/2025	C.5.7	E143G, E195K, D209E	A47V, P48S, G378E, I459V
B/Athens/SENT10804/2025	C.5.7	E143G, E195K, D209E	A47V, P48S, T334A, G378E, I459V

[1] H275Y in NA (N1 numbering) is the primary marker of reduced oseltamivir susceptibility in A(H1N1)pdm09

[2] Partial genome - HA and NA fully assembled and included, polymerase segments partially covered

[3] ED143DN denotes a simultaneous dinucleotide substitution at positions 143–144; additional changes at positions 52, 136, and 211 may reflect in vitro adaptation.