Genomic Analysis Report

Influenza Surveillance

Report Date: 15/05/2026

1. Analysis Summary

Influenza A/H3N2 remains the predominant subtype detected through genomic surveillance. 98% of the A/H3N2 sequences characterised during this reporting period were assigned to subclade 2a.3a.1-K.

The total number of influenza virus sequences analysed for this reporting period was 69 including 51 type A and 18 type B. Sequences were sampled from specimens collected in the period 21/03/2026 to 19/04/2026.

Influenza A virus sequenced during this reporting period included HA sequences for H1N1, subclade 5a.2a.1 (n=6) and H3N2 subclades 2a.3a.1 (n=1) and 2a.3a.1-K (n= 44). Influenza B virus sequenced during this reporting period included HA sequences for subclade V1A.3a.2 (n= 18).

Mean percentage amino acid divergence from the current 2026 Southern Hemisphere vaccine strains was 0.88% (95% CI, 0.76–1.01) for A/H1N1, 1.59% (95% CI, 1.34–1.85) for A/H3N2, and 1.42% (95% CI, 0.57–2.28) for influenza B. Queensland influenza virus A/H1N1 sequences phylogenetically clustered within HA subclade 5a.2a.1 (Figure 3.2), which contains the 2026 Southern Hemisphere A/H1N1 vaccine strain, A/Missouri/11/2025. Queensland influenza virus A/H3N2 sequences clustered within HA subclade 2a.3a.1 (Figure 3.3), which contains the 2026 Southern Hemisphere A/H3N2 vaccine strains A/Singapore/GP20238/2024 and A/Sydney/1359/2024.

Of note, whilst influenza A/H3N2 viruses belonging to subclade 2a.3a.1-K phylogenetically cluster within HA subclade 2a.3a.1, antigenic characterisation has demonstrated these viruses to be antigenically distinct from the 2026 Southern Hemisphere vaccine-like strains A/Singapore/GP20238/2024 and A/Sydney/1359/2024.

No sequences were identified with mutations which are known to be implicated in conferring resistance to the neuraminidase drug inhibitors Oseltamivir, Zanamivir, Peramivir or Laninamivir during this reporting period. Similarly, there was no evidence of the potential I38T resistance mutation associated with the drug Baloxavir identified in sequences analysed.

The WHO provides regular updates on the levels of influenza activity globally. Based on the Week 18, 3rd of April 2026 update; Globally, influenza activity remained low with influenza B viruses predominant among influenza detections. In the southern hemisphere, influenza activity remained low overall although elevated positivity (>10%) was reported in some countries.

2. Background

The Public and Environmental Health Reference Laboratories (PEHRL), Pathology Queensland perform genomic surveillance on representative seasonal influenza viral strains sampled from mainland and Torres Strait regions throughout Queensland (QLD). This surveillance aims to provide an overview of the genetic diversity among circulating human influenza virus A and B populations and monitor genetic viral changes which may suggest resistance to anti-influenza viral therapies or notable diversion from vaccine strains. For each reporting period, a selection of submitted influenza A and B virus positive samples is made based on risk factor stratification, potential viral load and geographical distribution. These are further processed and extracted influenza nucleic acid is subjected to whole genome sequencing (WGS) and phylogenetic analyses.

Genomic resistance mutation analysis cannot replace phenotypic or antigenic assessment of influenza virus strains which are required to further determine if identified mutations lead to evasion of prescribed treatments or vaccines.

3. Results

3.1 Genomic Surveillance

For this reporting period, 69 of 85 samples passed quality control (QC) for the HA gene. For detailed description of QC see section 5, Methods.

Table 3.1.1 Summary of influenza virus positive samples with a sequenced HA gene. This reporting period covers collections dates between 21/03/2026 to 19/04/2026.

Influenza virus type	Influenza virus subtype	Count of current reporting period (%)	Count of previous 12 months (%)
Type A	H1N1	6 (9%)	357 (42%)
Type A	H3N2	45 (65%)	245 (29%)
Type B	-	18 (26%)	249 (29%)
Total		69	851

Table 3.2 Proportion of HA gene sequences represented by each Hospital and Health Services (HHS) area. This reporting period covers collections dates between 21/03/2026 to 19/04/2026.

Region	Hospital and Health Service (HHS)	Sequences in current reporting period	Sequences in previous 12 months
Central	Wide Bay	4%	6%
Central	South West	3%	3%
Central	Central Queensland	13%	4%
Central	Central West	-	1%
North	Townsville	12%	6%
North	Cairns and Hinterland	6%	5%
North	Mackay	7%	6%
North	Torres and Cape	1%	1%
North	North West	-	1%
South East	Metro South	13%	18%
South East	Metro North	15%	16%
South East	Gold Coast	14%	12%
South East	Sunshine Coast	3%	6%
South East	West Moreton	4%	7%
South East	Darling Downs	3%	7%
Overseas	Overseas	1%	1%
Interstate	Interstate	1%	-

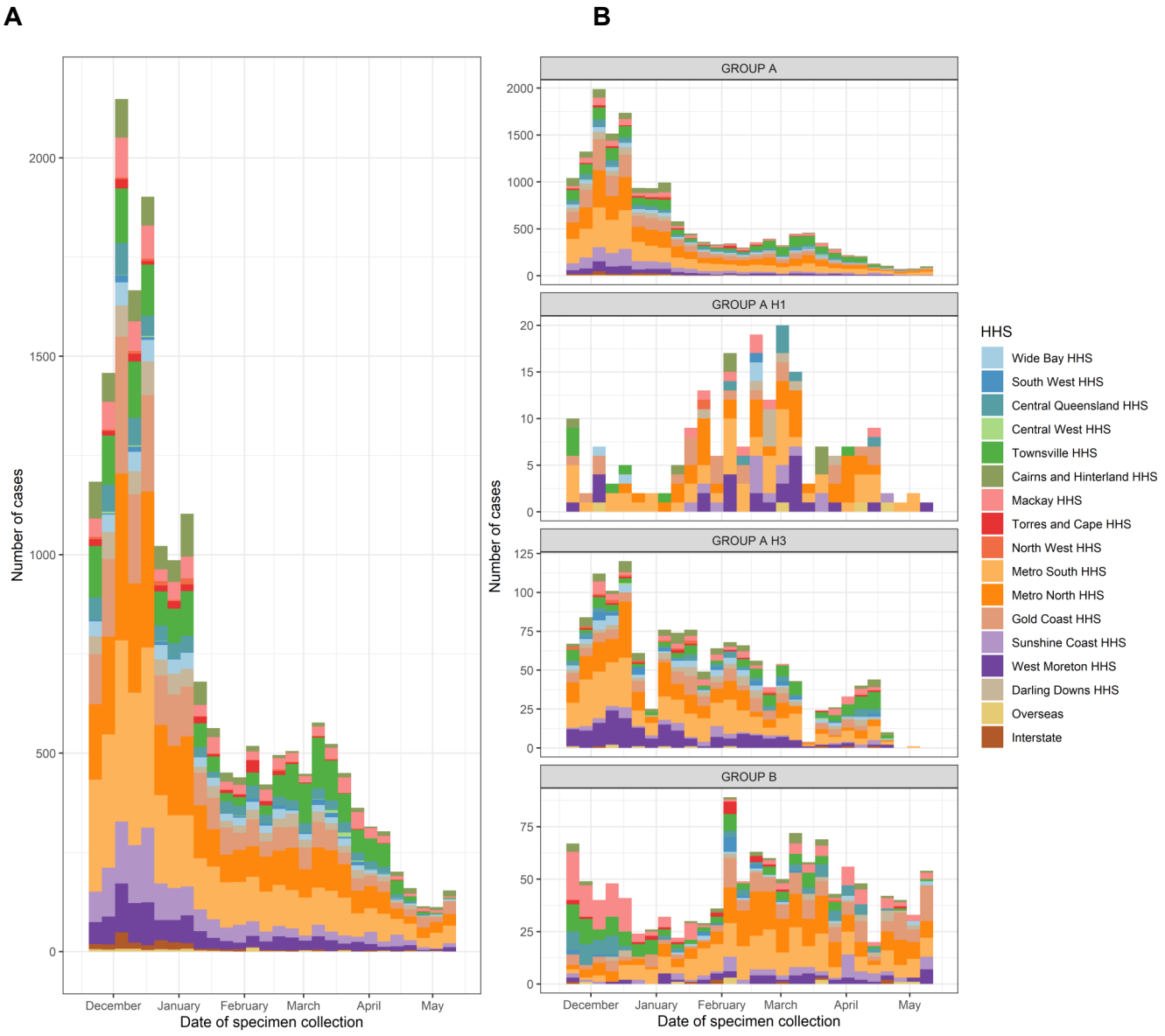

Figure 3.1 Counts of laboratory confirmed influenza virus positive cases by HHS in Queensland over the last 180 days. **A)** All laboratory confirmed influenza virus positive cases. **B)** Influenza virus positive cases by type and subtype. Please note the different y axis scales in this figure.

Data provided from the Queensland Notifiable Conditions System (NOCS).

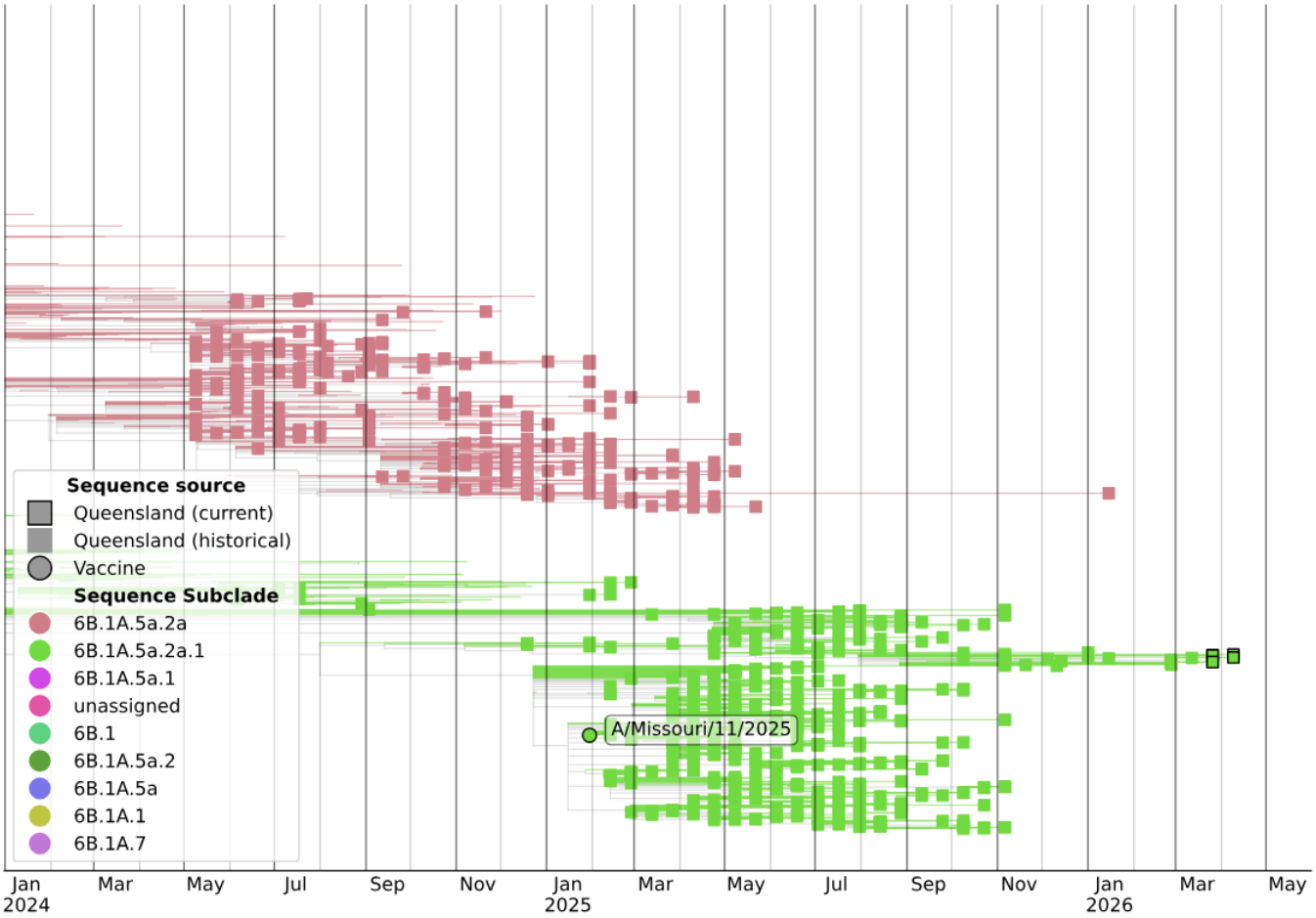

Figure 3.2 Approximately maximum likelihood phylogenetic tree of local Queensland influenza virus A/H1N1 HA sequences in the context of global publicly available genomic sequences shared via GISAID, the global data science initiative[1] (https://gisaid.org), and vaccine strains.

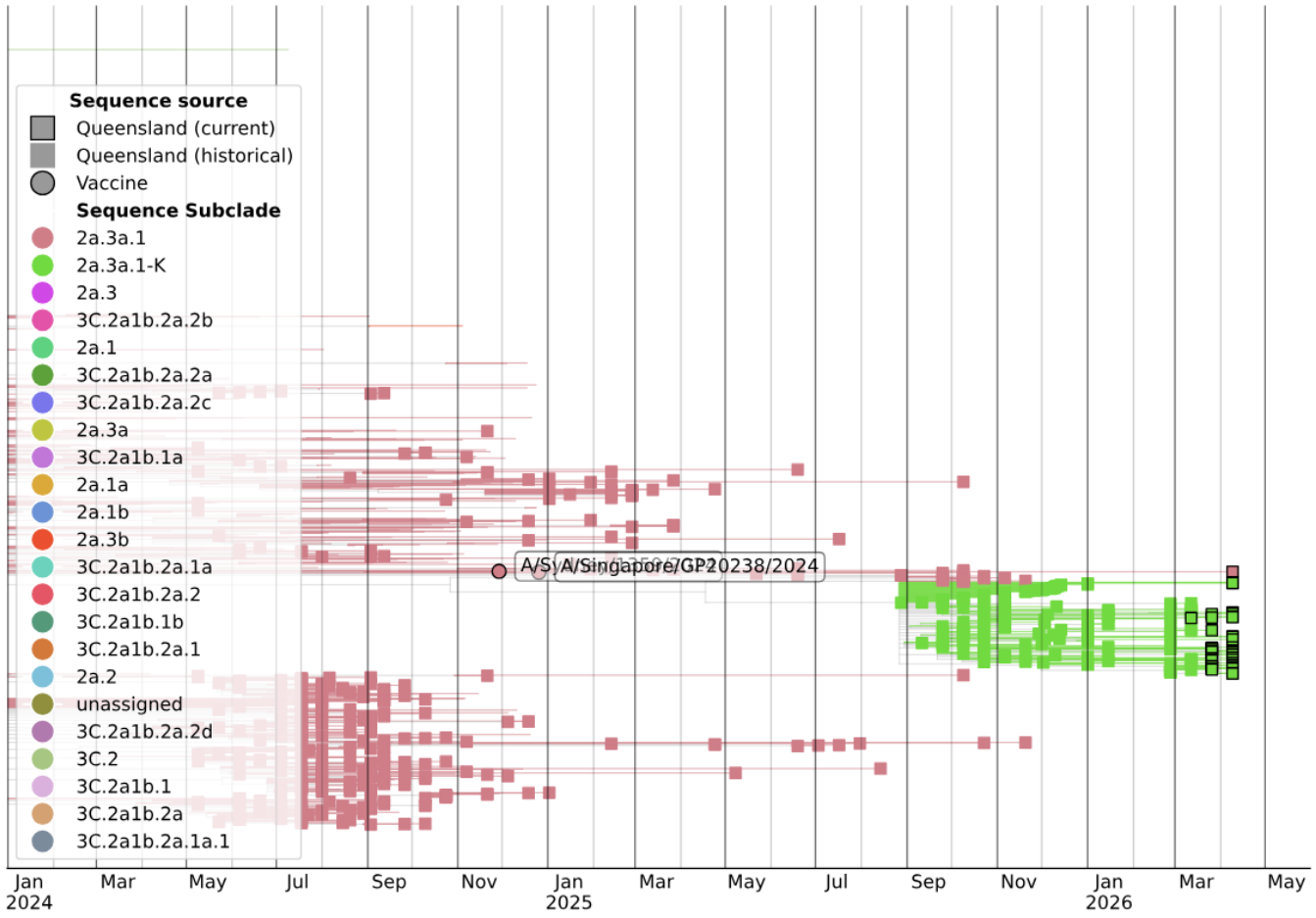

Figure 3.3 Approximately maximum likelihood phylogenetic tree of local Queensland influenza virus A/H3N2 HA sequences in the context of global publicly available genomic sequences shared via GISAID, the global data science initiative[1] (https://gisaid.org), and vaccine strains.

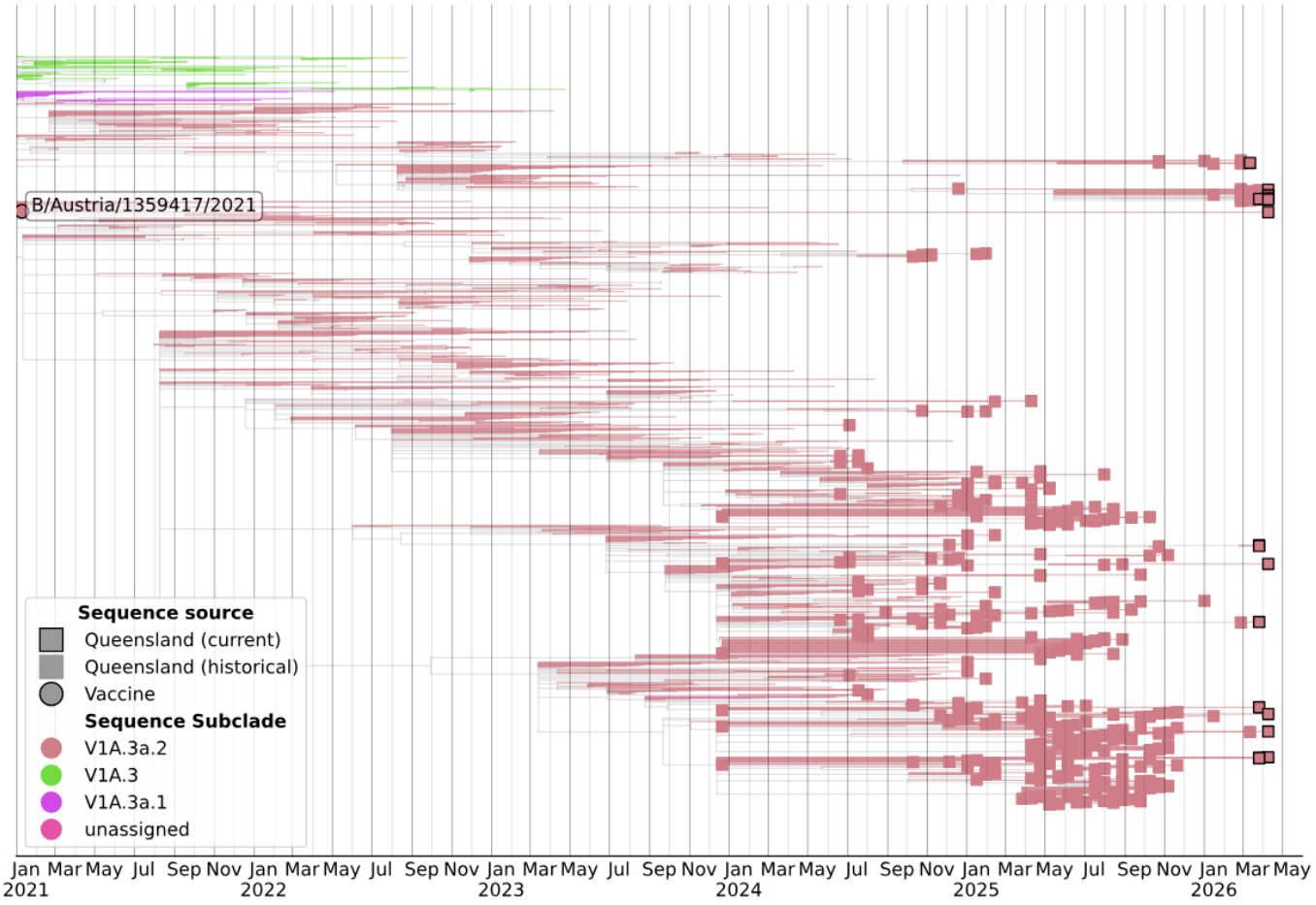

Figure 3.4 Approximately maximum likelihood phylogenetic tree of local Queensland influenza B virus HA sequences in the context of global publicly available genomic sequences shared via GISAID, the global data science initiative[1] (https://gisaid.org), and vaccine strains.

Table 3.3 Mean amino acid divergence of QLD influenza viral sequences from the 2026 Southern Hemisphere vaccine sequences.

Influenza virus type	Vaccine strain	Mean amino acid divergence (95% CI)
Influenza A H1N1	A/Missouri/11/2025	0.88% (0.76 – 1.01)
Influenza A H3N2	A/Singapore/GP20238/2024 A/Sydney/1359/2024	1.59% (1.34 – 1.85)
Influenza B	B/Austria/1359417/2021	1.42% (0.57 – 2.28)

3.2 Resistance mutation analyses

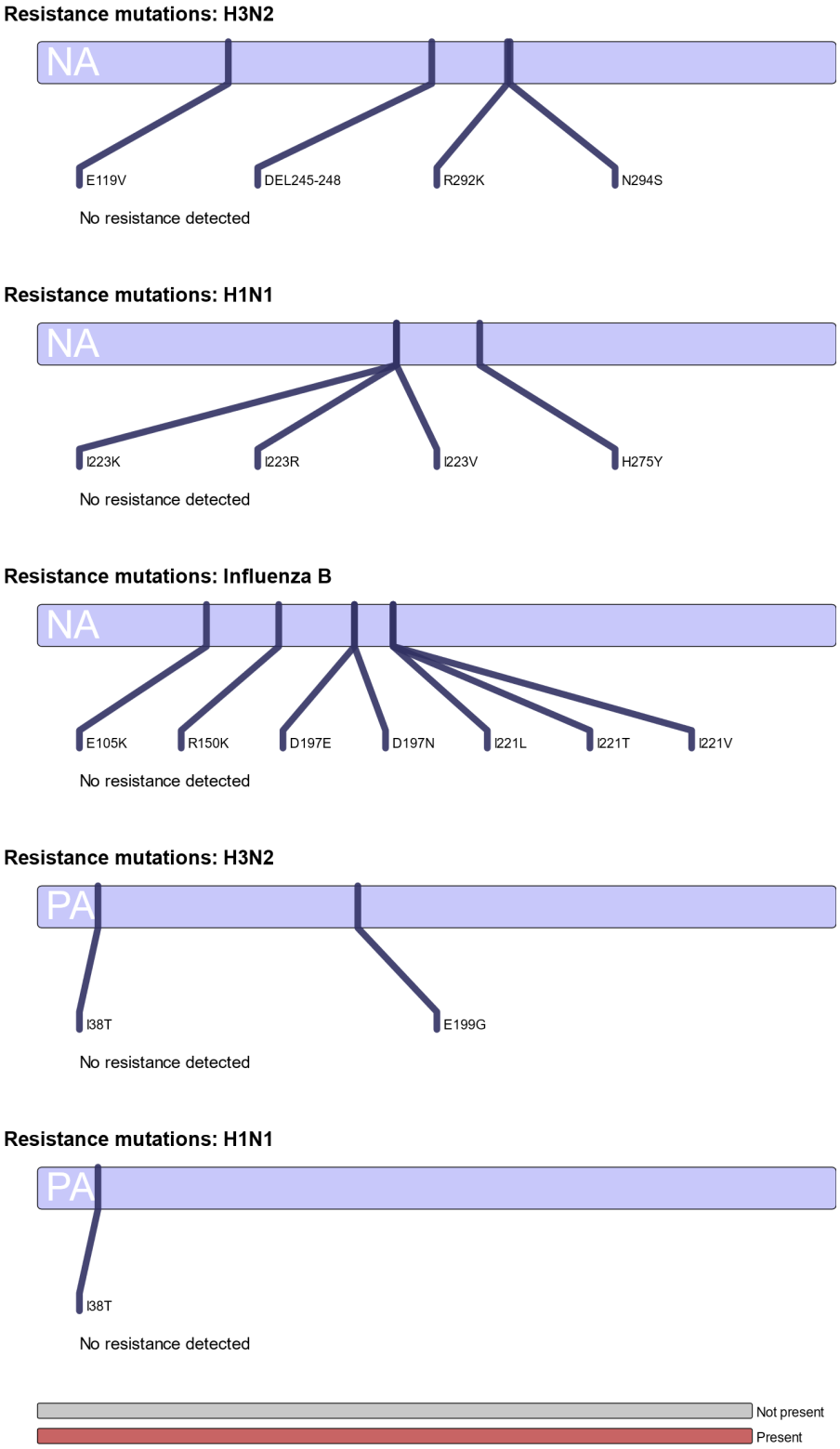

Figure 3.5 Resistance mutation analysis of sequences presented during this reporting period. Sequences are assessed for mutations that confer resistance to anti-influenza virus drugs Oseltamivir, Zanamivir, Peramivir, Laninamivir and Baloxavir. For a list of the mutations assessed in the Neuraminidase (NA) gene, see Table 5.1 in the appendices. For Baloxavir, sequences pertaining to the polymerase acidic (PA) gene were assessed for the potential resistance mutation, I38T.

4. Data caveats

The test has not been fully validated to the current NPAAC Requirements because the assay is still under development therefore, results should be interpreted accordingly. For further information please contact the laboratory.

The samples sequenced in this reporting period have collection dates from approximately 2 weeks prior to the report date and may not reflect current cases.

Reference and genomic interpretation of epidemiological association with genomic relatedness is based on the epidemiological information available to the Public and Environmental Health Reference Laboratories at the time of this report, and this should be taken into consideration when the report is read. It is the responsibility of the Communicable Diseases and Public Health teams to ensure interpretation in view of most up-to-date epidemiological information. Such information can be updated in future reports if provided to PEHRL.

Resistance mutation genomic analysis cannot replace phenotypic or antigenic assessment of influenza virus strains which are required to further determine if identified mutations lead to evasion of prescribed treatments or vaccines. Phenotypic and antigenic testing of representative QLD influenza strains is performed at the WHO Collaborating Centre for Reference and Research on Influenza or the Peter Doherty Institute for Infection and Immunity, Melbourne, Victoria.

5. Methods

Nucleic acids were extracted using the Qiagen EZ1 Mini kit v 2.0 or Roche MagNA Pure 96 DNA and Viral NA Small Volume kit. Influenza A virus whole genome sequencing (WGS) was primarily performed following amplification of viral gene segments using previously published primers (Zhou, B. et. al., 2009; Zhou, B. et. al., 2014) and DNA libraries were constructed using the Illumina Microbial Amplicon Prep-Influenza A/B v1.0 (Illumina). Prepared DNA libraries were sequenced on the Illumina NextSeq550, MiniSeq or iSeq100 platform which generated between 30-50 million, up to 16 million or up to 4 million total paired reads (2 x 150 nt) respectively. The sequences were then assembled with IRMA and flagged as failing QC if more than 10% of the genome could not be assigned a base. Influenza virus types and subtypes were determined from the IRMA output and lineages were assigned using Nextclade. Amino acid changes listed by Nextclade were then compared to a list of known antiviral resistance mutations. Haemagglutinin gene (HA) segments passing QC were combined with a subsampled set of sequences deposited on GISAID since January 2021 and Augur was used to generate a timed tree. The tree was then visualised with Baltic. Average nucleotide identity to the HA segment of the vaccine strains was calculated using BLAST+.

Table 5.1 Bioinformatic tools used to perform analysis.

Tool name	Version number	Description
IRMA	v1.1.4	Assembly, variant calling, and phasing of highly variable RNA viruses.
Augur	v24.4.0	Pipeline components for real-time phylodynamic analysis
Nextclade	v3.3.1	Genetic sequence alignment, clade assignment, mutation calling, phylogenetic placement, and quality checks
Baltic	v0.2.2	A Python library for parsing and visualising phylogenetic trees.
Blast+	v2.14.1	Alignment-free computation of whole-genome Average Nucleotide Identity (ANI).

6. Appendices

Table 6.1 List of Neuraminidase (NA) gene amino acid substitutions assessed for their effects on anti-influenza NA inhibitor drugs for which QLD sequences are screened and reported in section 3.2

Amino Acid Change	Oseltamivir	Zanamivir	Peramivir	Laninamivir
A(H1N1)pdm09				
H275Y	**R**	**S**	**R**	**S**
I223K/R/V	RS	S/RS	UNK	UNK
A(H3N2)				
E119V	**R**	**S**	**S**	**S**
DEL 245-248	R	S	S	UNK
R292K	**R**	**R**	**R**	**UNK**
N294S	**R**	**S**	**S**	**UNK**
Influenza B (Victoria and Yamagata Lineages)				
E105K	S	RS	R	RS
R150K	**R**	**R**	**R**	**UNK**
D197/N/E	**RS**	**RS**	**RS**	**UNK**
I221L/T/V/I	**R**	**RS**	**RS**	**S**

RS= Reduced susceptibility, R=Resistance, S=Susceptible

Table referenced from The Public Health England 2018 Surveillance and laboratory testing of influenza neuraminidase inhibitor resistance,

https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/757445/surveillance_and_laboratory_testing_of_influenza_neuraminidase_inhibitor_resistance.pdf

Table 6.2 Vaccine strains used in analysis

Accession	Name	Flu type	Subclade	Vaccine information*
EPI_ISL_2233238	A/Darwin/6/2021	A / H3N2	2a.2a	Historical
EPI_ISL_16998756	A/Massachusetts/18/2022	A / H3N2	2a.3a.1	Cell-based trivalent
EPI_ISL_19194107	A/Thailand/8/2022	A / H3N2	2a.3a.1	Egg-based trivalent, Cell-based trivalent
EPI_ISL_18856647	A/Croatia/10136RV/2023	A / H3N2	2a.3a.1	Egg-based trivalent
EPI_ISL_18862356	A/District of Columbia/27/2023	A / H3N2	2a.3a.1	Cell-based trivalent
EPI_ISL_15907696	A/Victoria/2570/2019	A / H1N1	5a.2	Historical
EPI_ISL_17830834	A/Victoria/4897/2022	A / H1N1	5a.2a.1	Egg-based trivalent
EPI_ISL_15397632	A/Wisconsin/588/2019	A / H1N1	5a.2	Historical
EPI_ISL_15928563	A/Wisconsin/67/2022	A / H1N1	5a.2a.1	Cell-based trivalent
EPI_ISL_1519459	B/Austria/1359417/2021	B	V1A.3a.2	Egg-based trivalent
EPI_ISL_517766	B/Phuket/3073/2013	B	Unknown	Egg-based quadrivalent
EPI_ISL_20077100	A/Missouri/11/2025	A / H1N1	6B.1A.5a.2a.1	Egg-based trivalent
EPI_ISL_19871656	A/Singapore/GP20238/2024	A / H3N2	3C.2a1b.2a.2a.3a.1	Egg-based trivalent
EPI_ISL_19711425	A/Sydney/1359/2024	A / H3N2	3C.2a1b.2a.2a.3a.1	Cell-based trivalent

* This indicates if the strain is currently included in a vaccine approved by the Therapeutic Goods Administration (TGA). All “Egg-based trivalent” strains are also included in the “Egg-based quadrivalent” vaccine. Historical strains are not currently in use.

Acknowledgements

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References

[1]Shu, Y. and McCauley, J. (2017) GISAID: from vision to reality. *EuroSurveillance*, 22(13) doi: 10.2807/1560-7917.ES.2017.22.13.30494

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