

# Online tools (Nextstrain, Nextclade, FluSurver, RSVsurver)



WHO Collaborating Centre  
for Reference and  
Research on Influenza  
**VIDRL**



A joint venture between The University of Melbourne and The Royal Melbourne Hospital

# Objective

- To familiarise with online tools, Nextstrain  
Nextclade

https://nextstrain.org

Nextstrain

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# Nextstrain

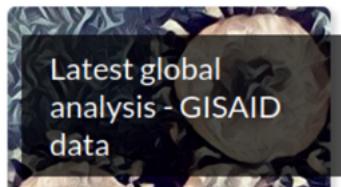
## Real-time tracking of pathogen evolution

Nextstrain is an open-source project to harness the scientific and public health potential of pathogen genome data. We provide a continually-updated view of publicly available data alongside powerful analytic and visualization tools for use by the community. Our goal is to aid epidemiological understanding and improve outbreak response. If you have any questions, or simply want to say hi, please give us a shout at [hello@nextstrain.org](mailto:hello@nextstrain.org).

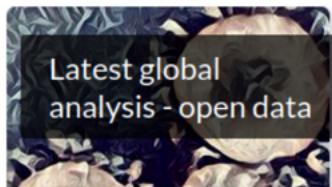
[READ MORE](#)

## SARS-CoV-2 (COVID-19)

We are incorporating SARS-CoV-2 genomes as soon as they are shared and providing analyses and situation reports. In addition we have developed a number of resources and tools, and are facilitating independent groups to run their own analyses.



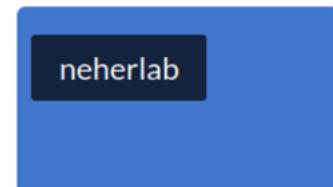
Latest global  
analysis - GISAID  
data



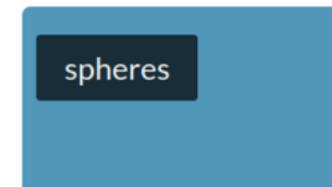
Latest global  
analysis - open data

## Nextstrain Groups

We want to enable research labs, public health entities and others to share their datasets and narratives through Nextstrain with complete control of their data and audience.



neherlab

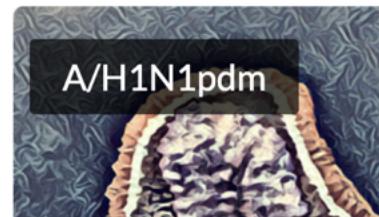
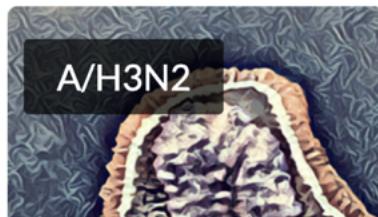


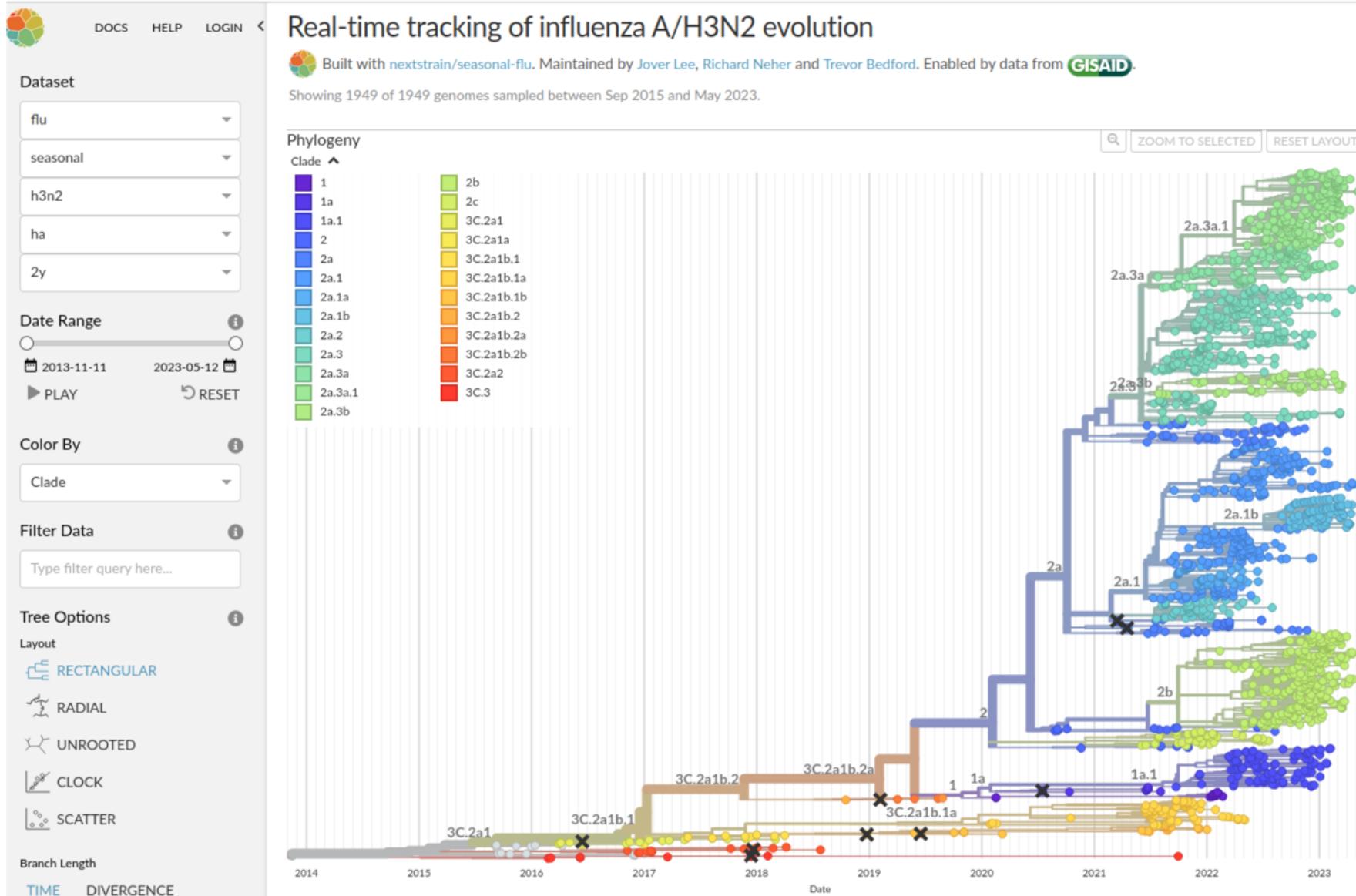
spheres

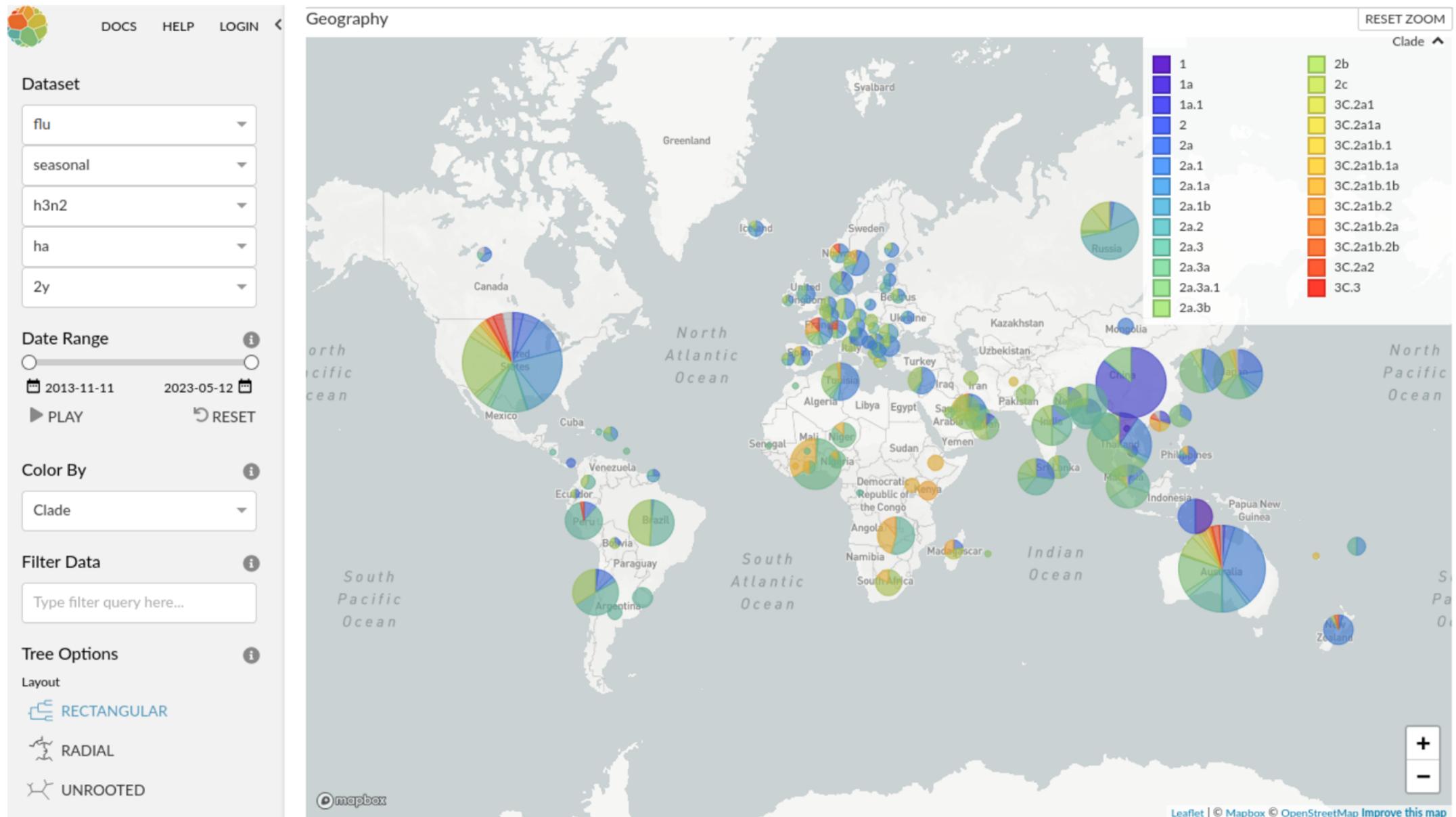


## Influenza resources

The Nextstrain team maintains datasets and other tools for analyzing a variety of influenza viruses. We track the evolution of seasonal influenza viruses (A/H3N2, A/H1N1pdm, B/Victoria, and B/Yamagata) and use these analyses to inform recommendations for the World Health Organization's influenza vaccine composition meetings. We also maintain datasets for a subset of avian influenza viruses that have caused recurrent outbreaks in humans and domestic birds, including novel reassortant H5 viruses.









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ENTROPY EVENTS AA NT

## Dataset

flu

seasonal

h3n2

ha

2y

## Date Range

2013-11-11 2023-05-12

▶ PLAY 🔍 RESET

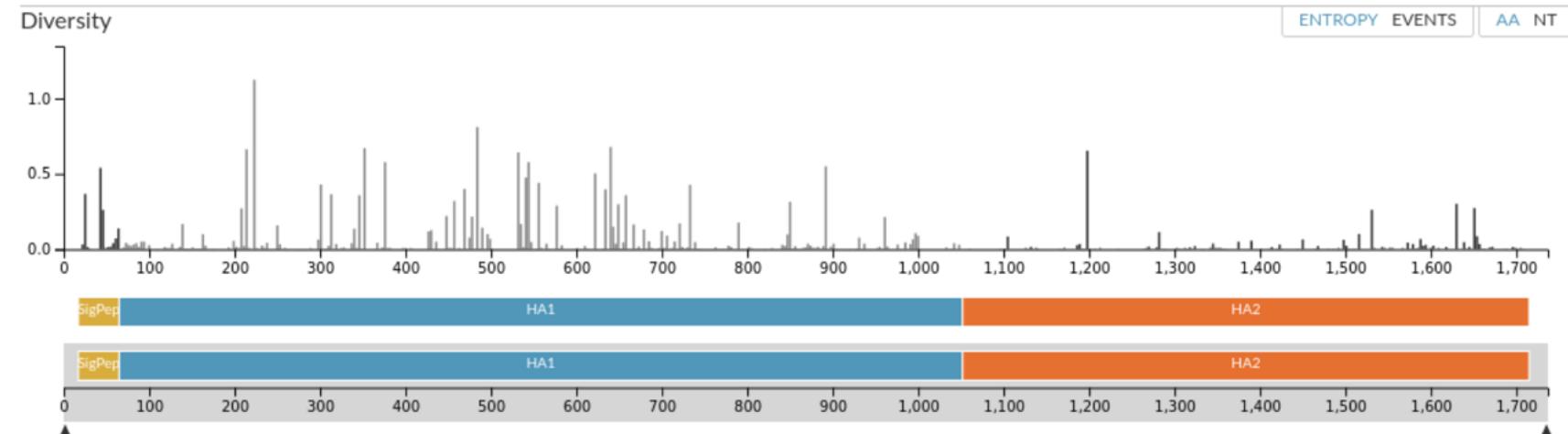
## Color By

Clade

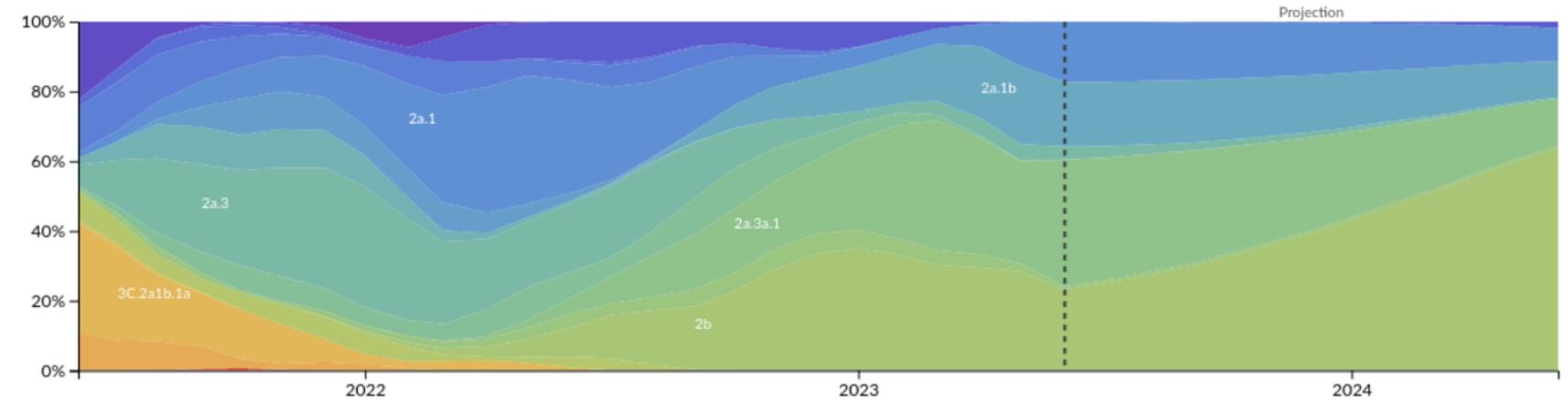
## Filter Data

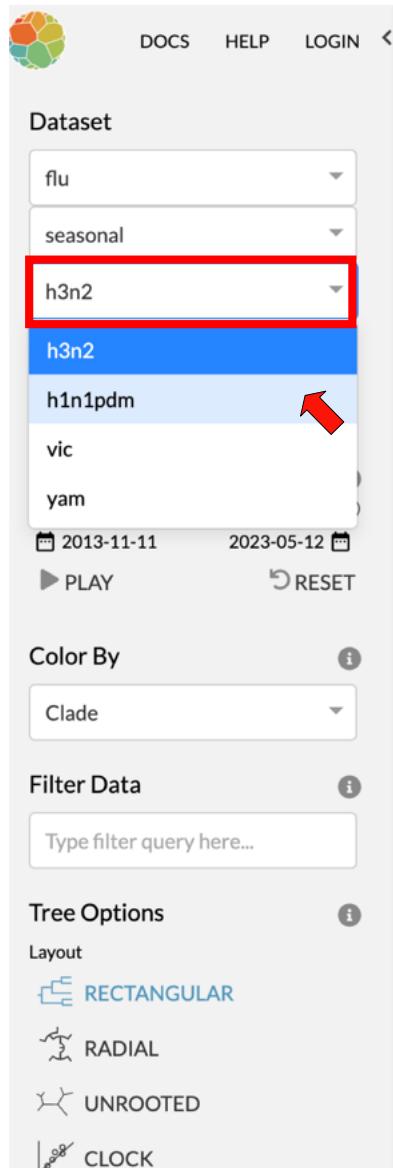
Type filter query here...

## Tree Options



## Frequencies (colored by Clade)

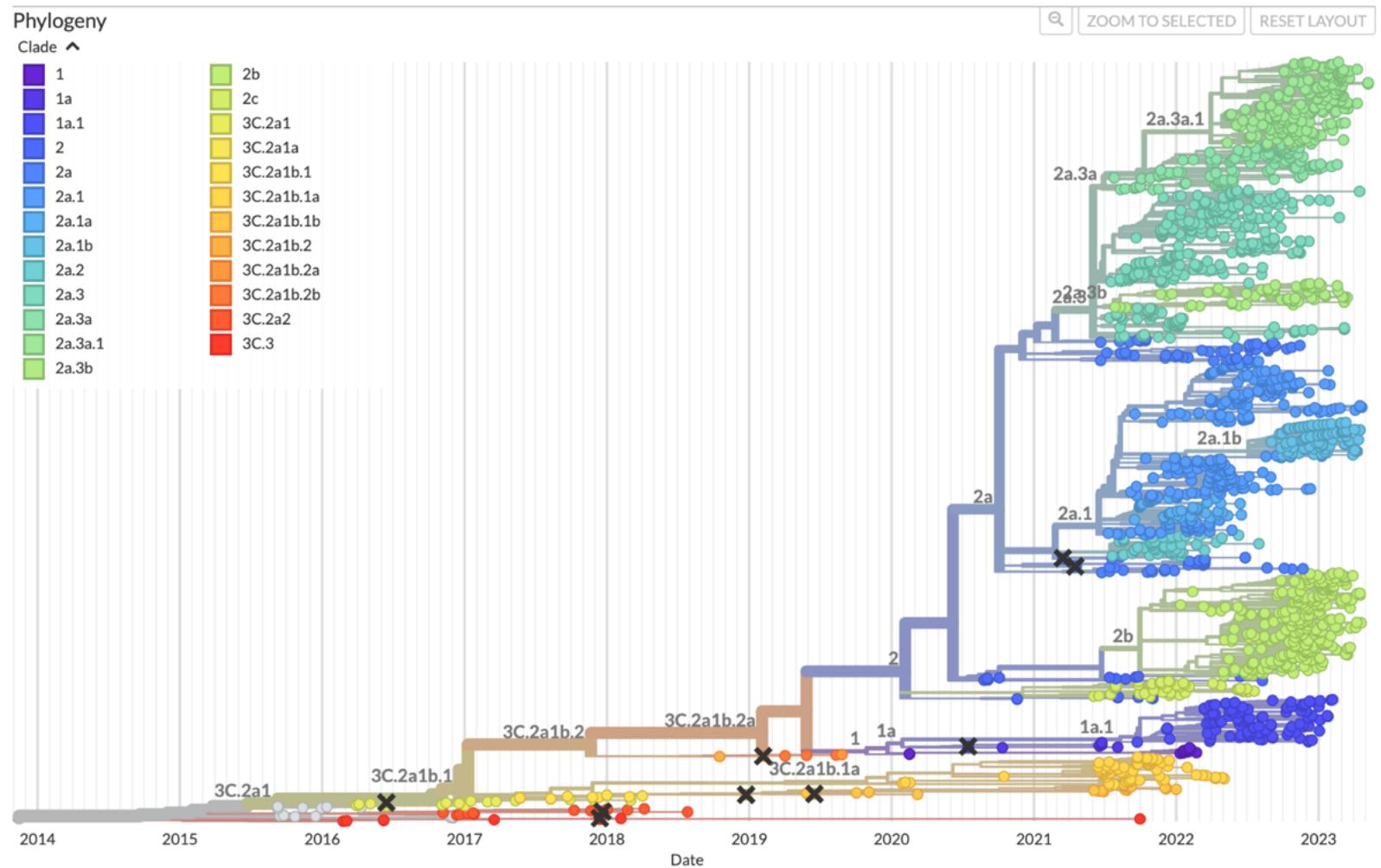




## Real-time tracking of influenza A/H3N2 evolution

Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAYD](#)

Showing 1949 of 1949 genomes sampled between Sep 2015 and May 2023.





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## Dataset

flu

seasonal

h1n1pdm

ha

ha

na

2012-05-19 2023-05-25

▶ PLAY ⏪ RESET

## Color By

Clade

## Filter Data

Type filter query here...

## Tree Options

### Layout

RECTANGULAR

RADIAL

UNROOTED

CLOCK

# Real-time tracking of influenza A/H1N1pdm evolution

Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAID](#).

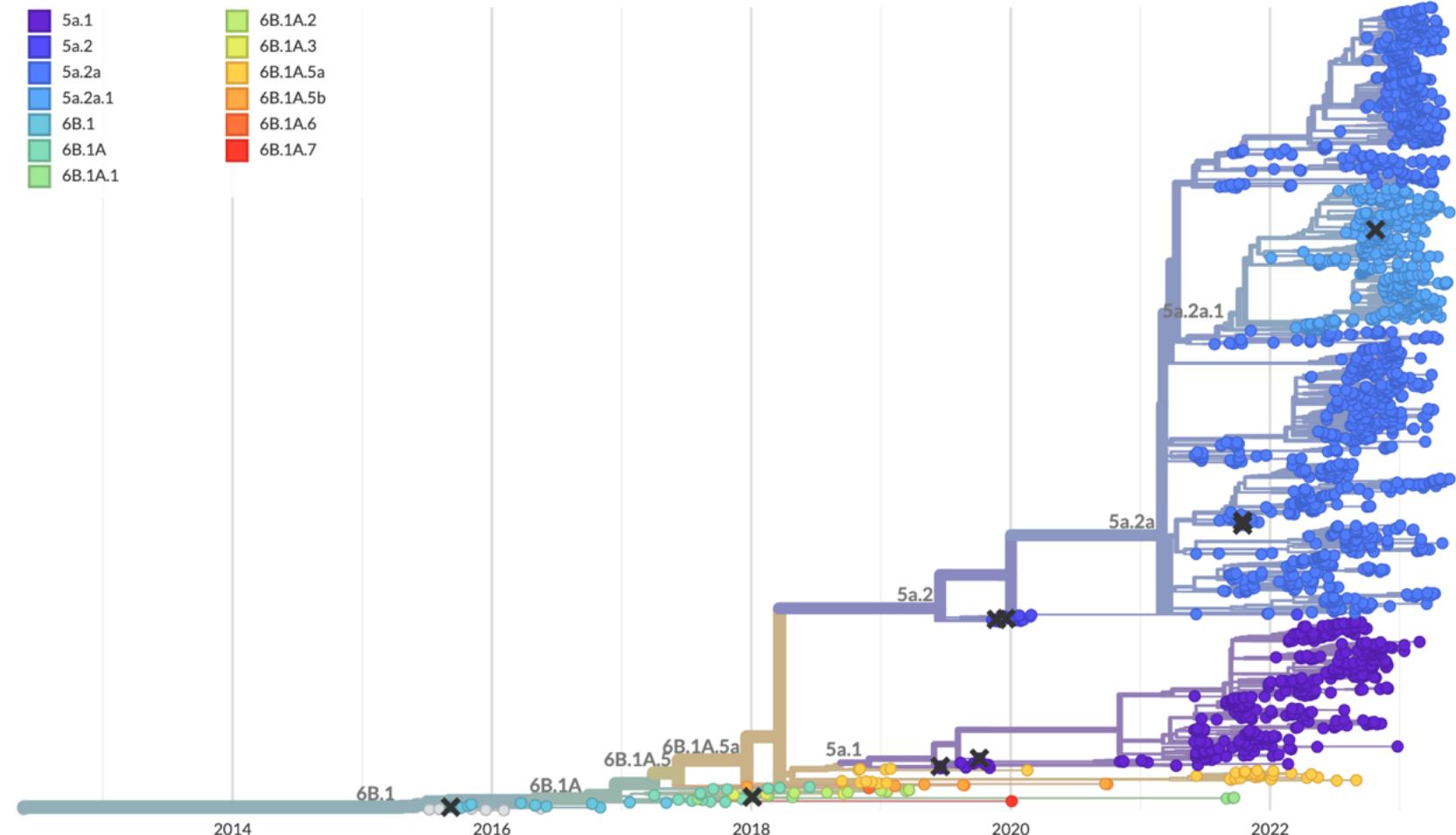
Showing 2027 of 2027 genomes sampled between Jul 2015 and May 2023.

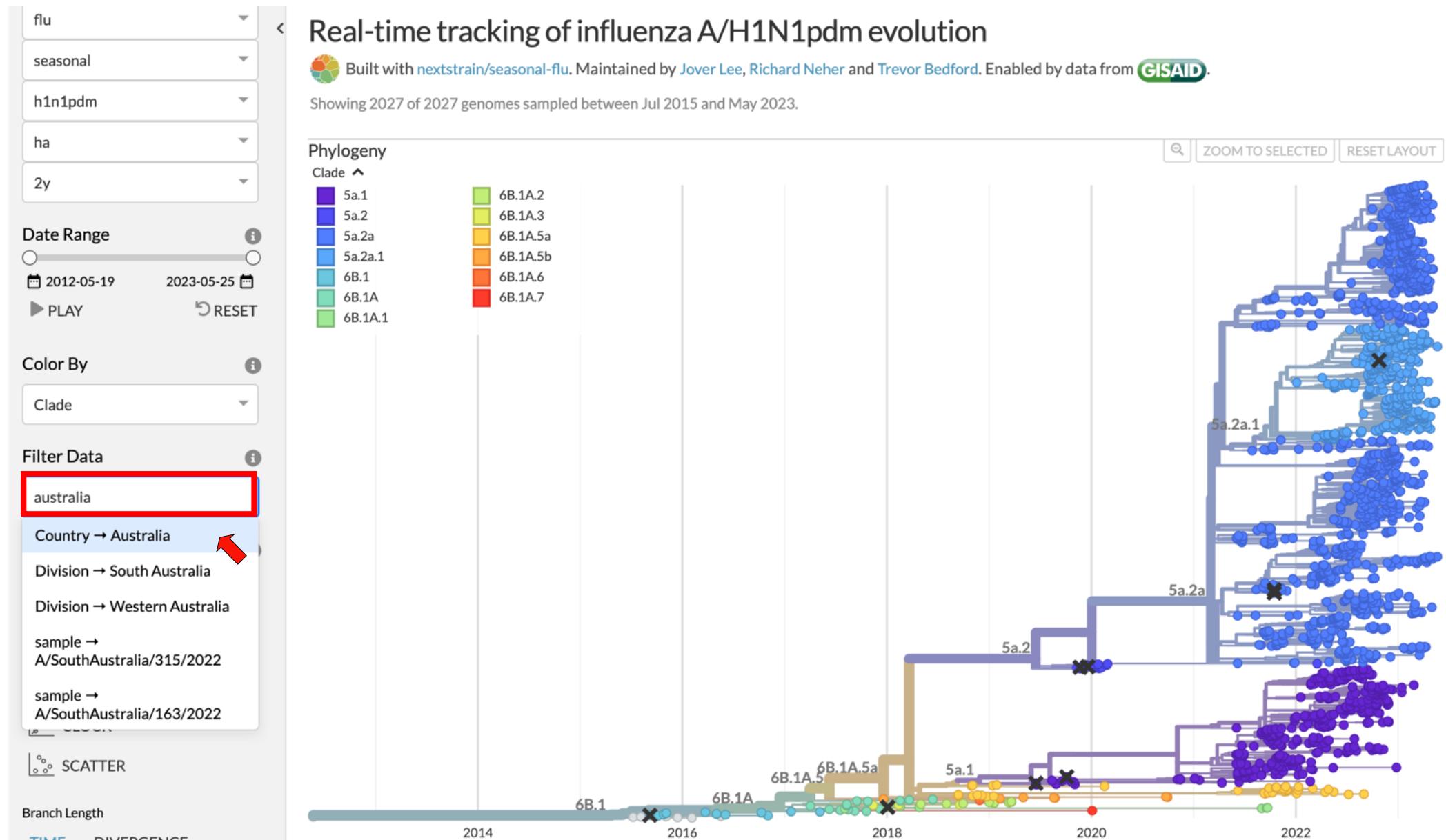
## Phylogeny

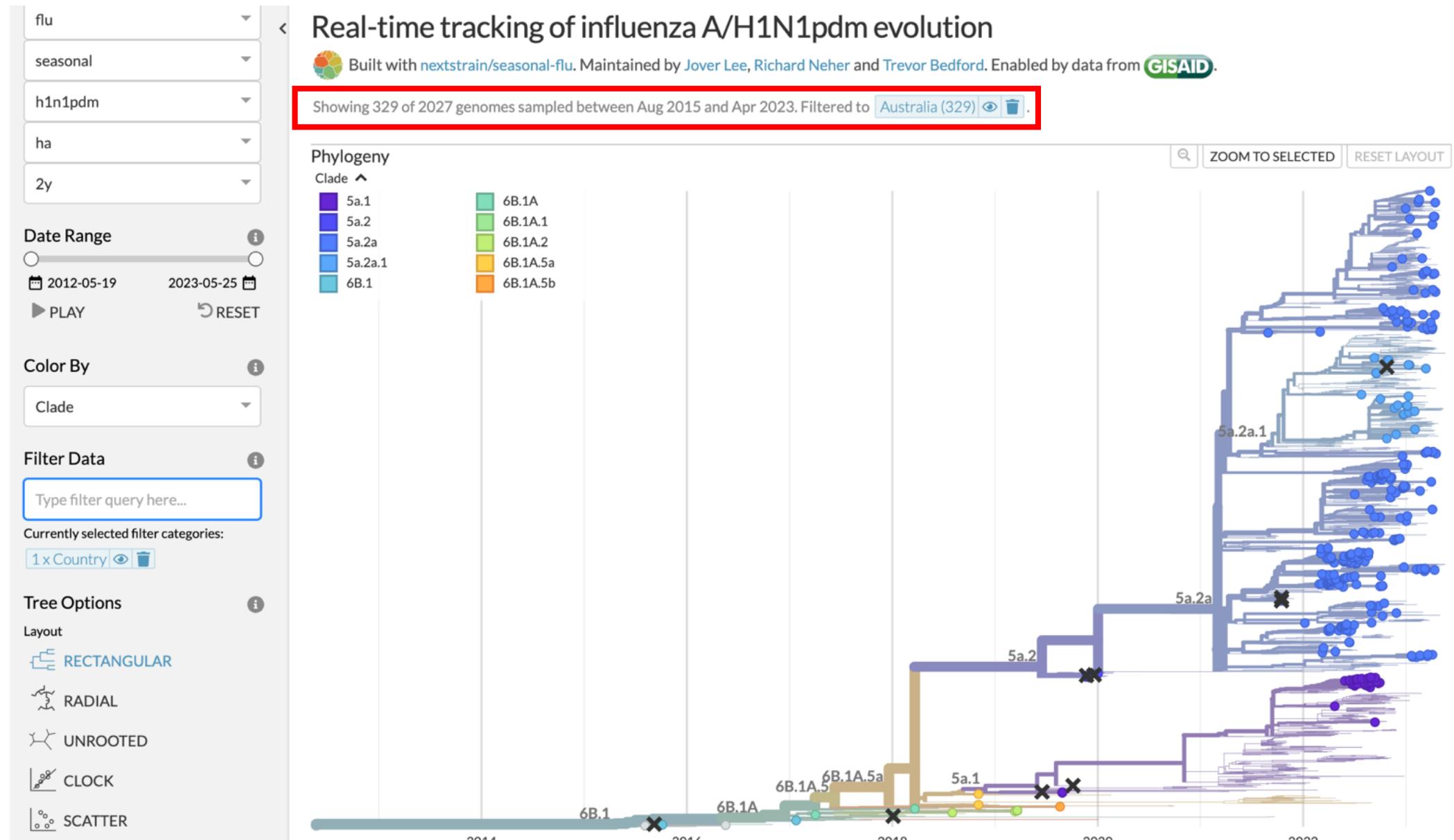
### Clade ^

- 5a.1
- 5a.2
- 5a.2a
- 5a.2a.1
- 6B.1
- 6B.1A
- 6B.1A.1
- 6B.1A.2
- 6B.1A.3
- 6B.1A.5a
- 6B.1A.5b
- 6B.1A.6
- 6B.1A.7

ZOOM TO SELECTED RESET LAYOUT







flu

seasonal

h1n1pdm

ha

2y

Date Range

2012-05-19  2023-05-25

▶ PLAY ⏪ RESET

Color By

Clade

Filter Data

Type filter query here...

- Year/month → 2023-01
- Year/month → 2023-02
- Year/month → 2023-03
- Year/month → 2023-04
- Year/month → 2023-05
- genotype HA1 104Q
- genotype HA1 104R
- genotype HA1 105L
- genotype HA1 105M

## Real-time tracking of influenza A/H1N1pdm evolution



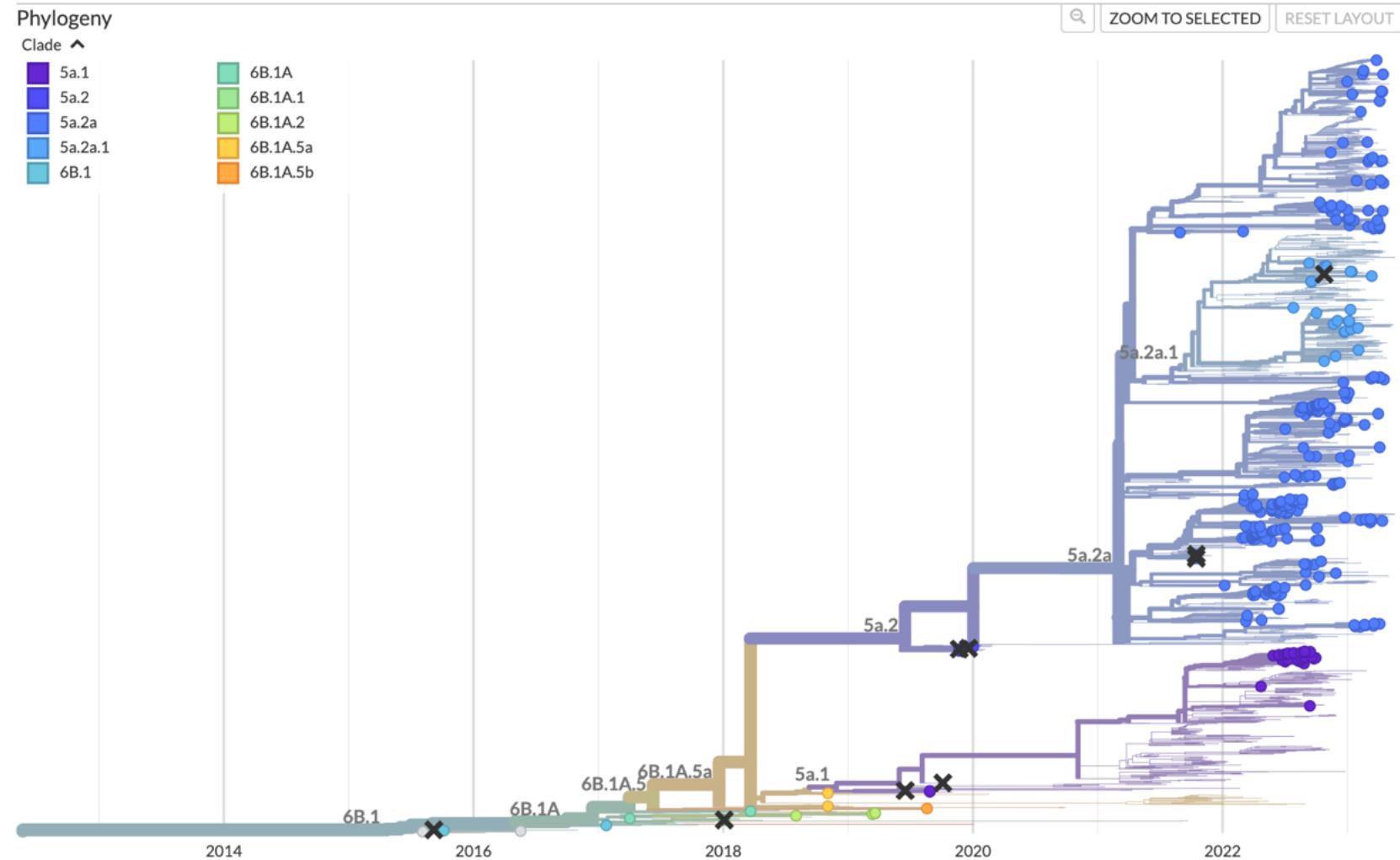
Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAID](#).

Showing 329 of 2027 genomes sampled between Aug 2015 and Apr 2023. Filtered to [Australia \(329\)](#) .

### Phylogeny

#### Clade ^

5a.1	6B.1A
5a.2	6B.1A.1
5a.2a	6B.1A.2
5a.2a.1	6B.1A.5a
6B.1	6B.1A.5b



flu

seasonal

h1n1pdm

ha

2y

Date Range

2012-05-19 2023-05-25

PLAY RESET

Color By

Clade

Filter Data

Type filter query here...

Currently selected filter categories:

- 1 x Country
- 1 x Year/month

Tree Options

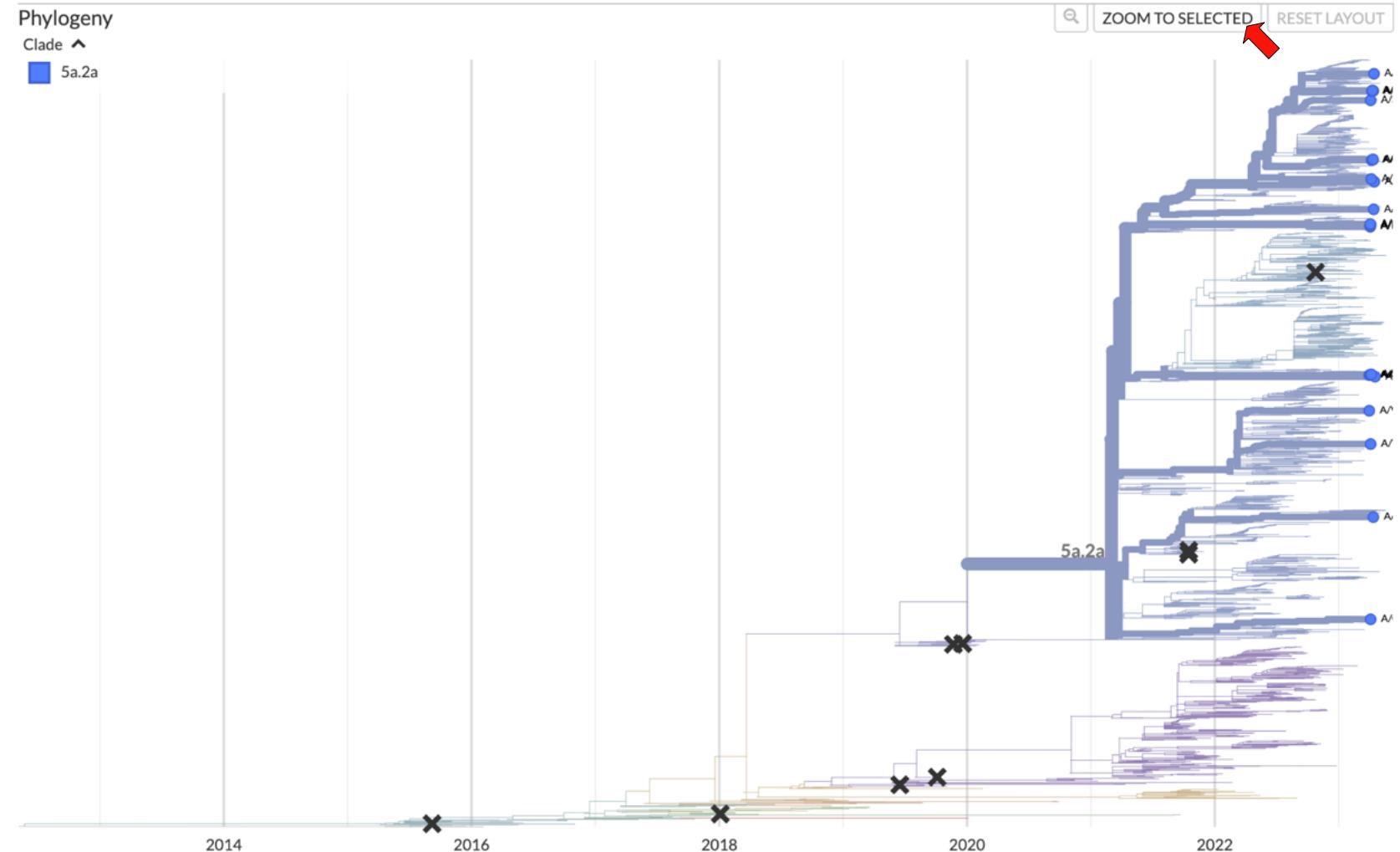
Layout

- RECTANGULAR
- RADIAL
- UNROOTED
- CLOCK
- SCATTERED

## Real-time tracking of influenza A/H1N1pdm evolution

Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISaid](#).

Showing 23 of 2027 genomes sampled between Apr 2023 and Apr 2023. Filtered to [Australia \(329\)](#)  $\cap$  [2023-04 \(82\)](#) .



flu

seasonal

h1n1pdm

ha

2y

Date Range

2012-05-19 2023-05-25

PLAY RESET

Color By

Clade

Filter Data

Type filter query here...

Currently selected filter categories:

1 x Country 1 x Year/month

Tree Options

Layout

RECTANGULAR

RADIAL

UNROOTED

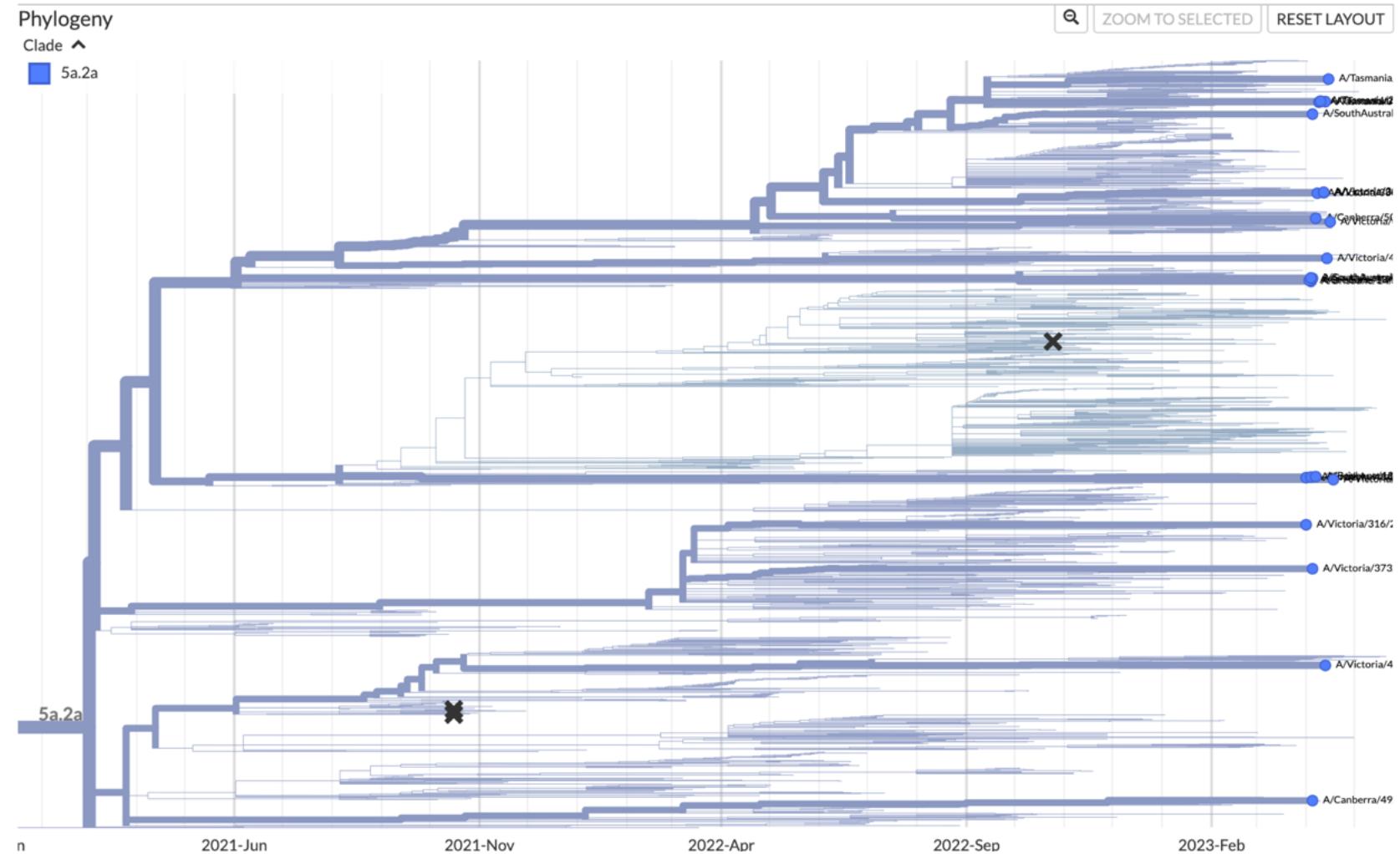
CLOCK

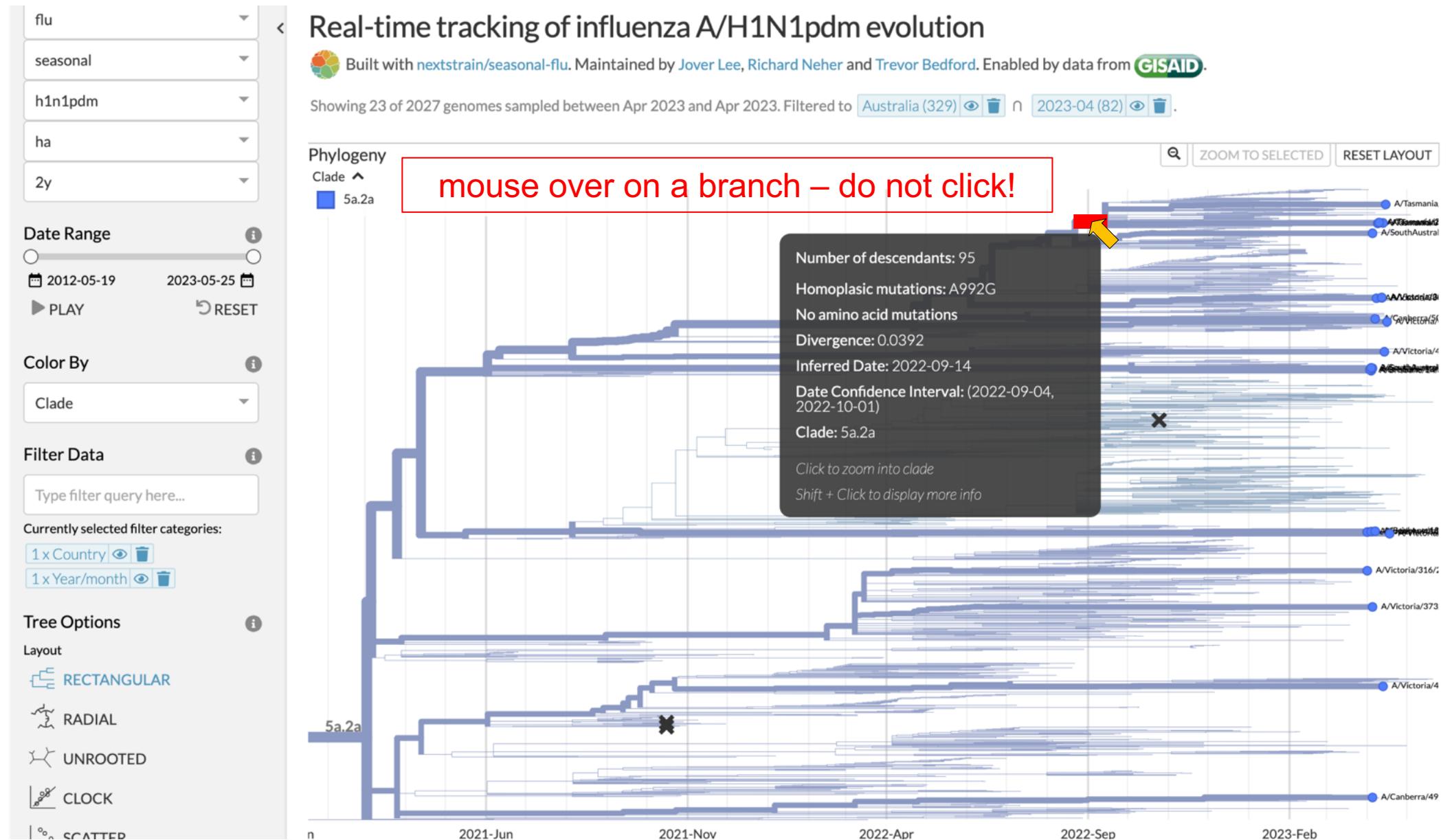
SCATTERED

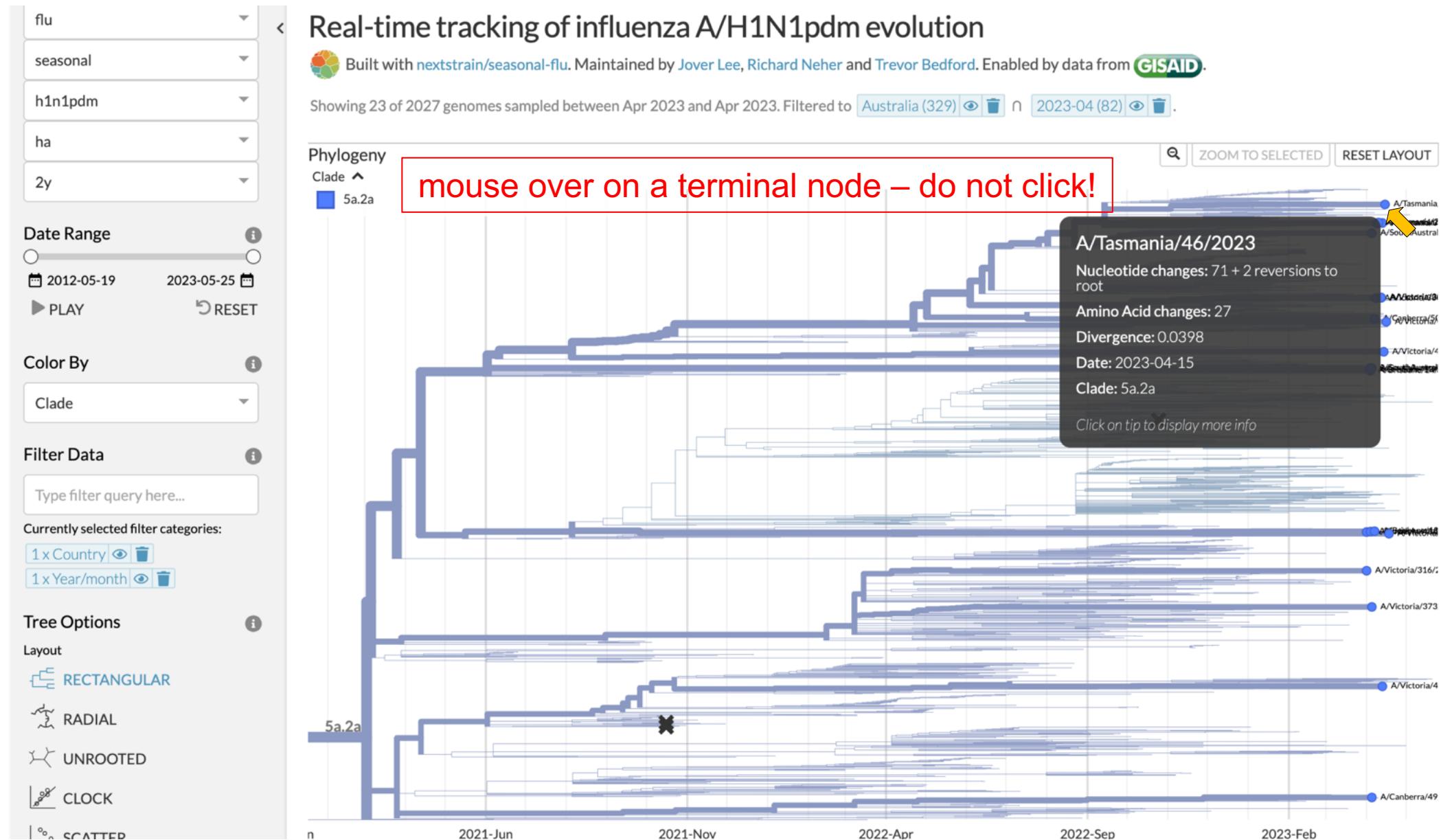
## Real-time tracking of influenza A/H1N1pdm evolution

Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAYD](#).

Showing 23 of 2027 genomes sampled between Apr 2023 and Apr 2023. Filtered to [Australia \(329\)](#)   [∩](#) [2023-04 \(82\)](#)  .







flu

seasonal

h1n1pdm

ha

2y

Date Range

2012-05-19 2023-05-25

PLAY RESET

Color By

Clade

Filter Data

Type filter query here...

Currently selected filter categories:

1 x Country

1 x Year/month

Tree Options

Layout

- RECTANGULAR
- RADIAL (arrow)
- UNROOTED
- CLOCK
- SCATTERED

## Real-time tracking of influenza A/H1N1pdm evolution

Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISaid](#).

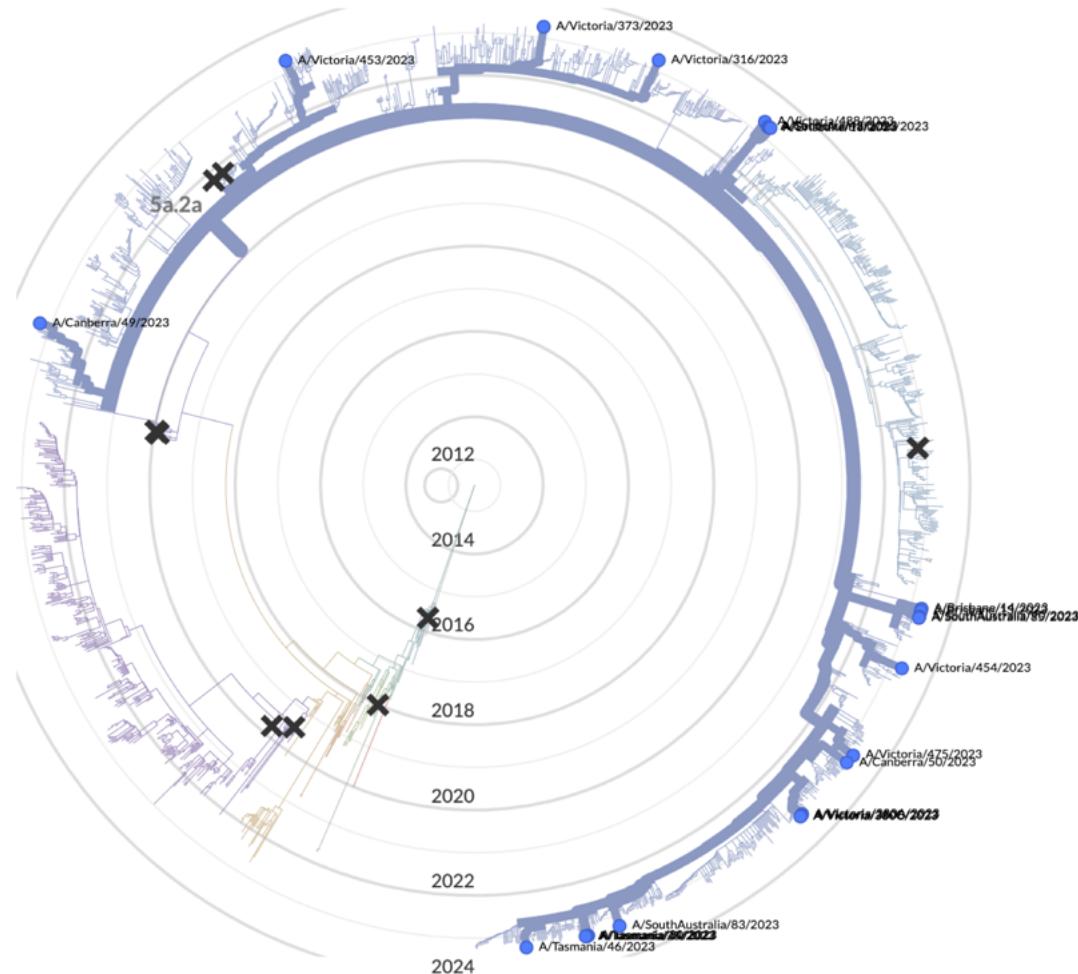
Showing 23 of 2027 genomes sampled between Apr 2023 and Apr 2023. Filtered to [Australia \(329\)](#) [2023-04 \(82\)](#) .

### Phylogeny

Clade ^

5a.2a

ZOOM TO SELECTED RESET LAYOUT



flu

seasonal

h1n1pdm

ha

2y

Date Range

2012-05-19 2023-05-25

PLAY RESET

Color By

Clade

Filter Data

Type filter query here...

Currently selected filter categories:

1 x Country

1 x Year/month

Tree Options

Layout

- RECTANGULAR
- RADIAL
- UNROOTED (arrow)
- CLOCK
- SCATTERED

## Real-time tracking of influenza A/H1N1pdm evolution

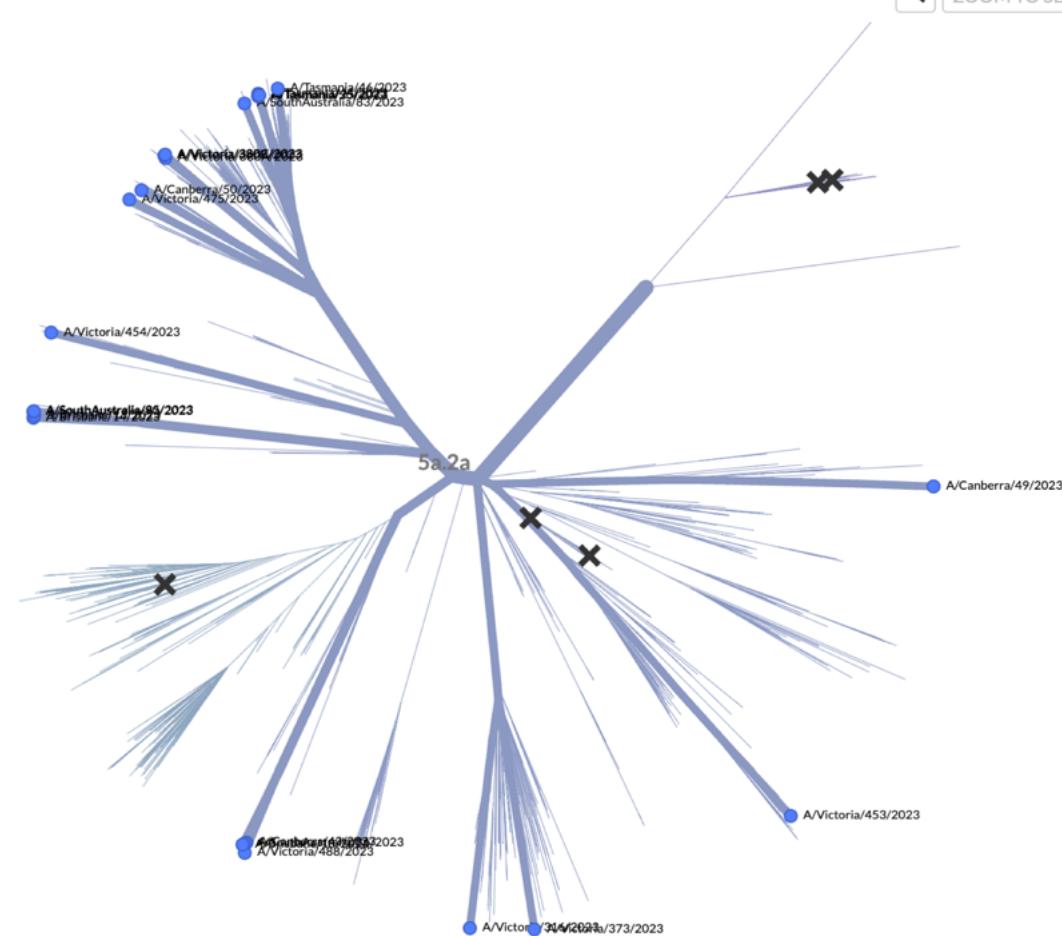
Built with [nextstrain/seasonal-flu](#). Maintained by [Jover Lee](#), [Richard Neher](#) and [Trevor Bedford](#). Enabled by data from [GISAYD](#).

Showing 23 of 2027 genomes sampled between Apr 2023 and Apr 2023. Filtered to [Australia \(329\)](#)    $\cap$  [2023-04 \(82\)](#)  .

### Phylogeny

Clade ^

5a.2a



ZOOM TO SELECTED

RESET LAYOUT



# Nextclade: analysis of viral genetic sequences

Nextclade is an open-source project for viral genome alignment, mutation calling, clade assignment, quality checks and phylogenetic placement.

Nextclade consists of a set of related tools:

- Nextclade Web - a web application available online at [clades.nextstrain.org](https://clades.nextstrain.org)
- Nextclade CLI - a command-line tool

Both tools are powered by the same algorithms, they consume the same inputs and produce the same outputs, but they differ in the user interface, the features included, and the degree of customization. It is recommended to start with Nextclade Web and later proceed to CLI tools if you have more advanced use-cases (for example, repeated batch processing, bioinformatics pipelines).



Nextclade

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# Nextclade<sup>v3.6.0</sup>

Clade assignment, mutation calling, and sequence quality checks

## Provide sequence data

File

Link

Text

Example ▾



Drag & drop files  
or folders

Select files

## Select reference dataset i



Suggest automatically

Reset

Suggest

Select reference dataset



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# Nextclade<sup>v3.6.0</sup>

Clade assignment, mutation calling, and sequence quality checks

## Provide sequence data

File

Link

Text

Example ▾



Drag & drop files  
or folders

Select files



## Select reference dataset i



Suggest automatically

Reset

Suggest

Select reference dataset



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# Nextclade<sup>v3.6.0</sup>

Clade assignment, mutation calling, and sequence quality checks

## Add more sequence data

File

Link

Text

Example ▾



Drag & drop files  
or folders

Select files

## Sequence data you've added

Remove all

gisaid\_epiflu\_sequence\_Australia.fasta (42.4 KB)

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## Selected reference dataset ⓘ



Suggest automatically

Reset

Re-suggest

### Influenza A H1N1pdm HA

official

Reference: A/Wisconsin/588/2019 (MW626062)

Updated at: 2024-04-19 07:50:39 (UTC)

Dataset name: nextstrain/flu/h1n1pdm/ha/MW626062

Load example

Change reference dataset

Run

# Nextclade quality metrics

- **Individual Scores**

- **Missing data (N):** If your sequence misses more than 3000 sites (N characters), it will be flagged as bad
- **Mixed sites (M):** Ambiguous nucleotides are often indicative of contamination
- **Private mutations (P):** As a by-product of the phylogenetic placement method of assigning lineages, Nextclade identifies the mutations, called “private mutations”, that differ between the query sequence and the nearest neighbor sequence.
- **Mutation clusters (C):** To be more sensitive for quality problems in a narrow area of a genome, the mutation cluster rule counts the number of private within all possible 100-nucleotide windows
- **Stop codons (S):** Premature stops
- **Frame shifts (F):** Wrong grouping of codons

- **Overall QC score**

- multiple mildly concerning scores don't result in a bad overall score, but a single bad score guarantees a bad overall score.
- lower value means better quality, higher value means worse quality



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#	i	Sequence name	QC	Clade	short-clade	Subclade	Glyc.	Mut.	non-ACGTN	Ns	Cov.	Gaps	Ins.	FS	SC
?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
0	0	✓ A/Victoria/380B/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	22	0	0	97.1%	0	0	0	0
1	1	✓ A/Victoria/380C/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	22	0	0	97.1%	0	0	0	0
2	2	✓ A/Victoria/453/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1.7	7(+0-0 0)	28	0	0	97.1%	0	0	0	0
3	5	✓ A/Victoria/373/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1.2	7(+0-0 0)	22	0	0	97.1%	0	0	0	0
4	3	✓ A/Victoria/454/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1	6(+0-1 0)	24	0	0	97.1%	0	0	0	0
5	4	✓ A/Victoria/488/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	27	0	0	97.1%	0	0	0	0
6	6	✓ A/Victoria/475/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	21	0	0	97.1%	0	0	0	0
7	8	✓ A/Brisbane/14/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1.6	7(+0-0 0)	26	0	0	97.1%	0	0	0	0
8	7	✓ A/Victoria/316/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1.2	7(+0-0 0)	26	0	0	97.1%	0	0	0	0
9	9	✓ A/Brisbane/18/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	25	0	0	97.1%	0	0	0	0
10	12	✓ A/Tasmania/30/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	23	0	0	97.1%	0	0	0	0
11	10	✓ A/Tasmania/46/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	19	0	0	97.1%	0	0	0	0
12	11	✓ A/Tasmania/44/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	21	0	0	97.1%	0	0	0	0
13	13	✓ A/Brisbane/13/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1.6	7(+0-0 0)	25	0	0	97.1%	0	0	0	0
14	14	✓ A/South_Australia/85/2023	M P F S	6B.1A.5a.2a	5a.2a	C.1.6	7(+0-0 0)	25	0	0	97.1%	0	0	0	0

Genome annotation ?





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de ?	short- clade ?	Subclade ?	Glyc. ?	Mut. ?	non- ACGTN ?	Ns ?	Cov. ?	Gaps ?	Ins. ?	FS ?	SC ?	Filter ?	Gene	CDS	HA1	?
5a.2a	5a.2a	C.1	7(+0-0 0)	22	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1	7(+0-0 0)	22	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1.7	7(+0-0 0)	28	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1.2	7(+0-0 0)	22	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1	6(+0-1 0)	24	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1	7(+0-0 0)	27	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1	7(+0-0 0)	21	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1.6	7(+0-0 0)	26	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1.2	7(+0-0 0)	26	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1	7(+0-0 0)	25	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1	7(+0-0 0)	23	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1	7(+0-0 0)	19	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1	7(+0-0 0)	21	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1.6	7(+0-0 0)	25	0	0	97.1%	0	0	0	0					
5a.2a	5a.2a	C.1.6	7(+0-0 0)	25	0	0	97.1%	0	0	0	0					

Genome annotation ?



50 100 150 200 250 300



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#	i	Sequence name	QC	Clade	short-clade	Subclade	Glyc.	Mut.	non-ACGTN	Ns	Cov.	Gaps	Ins.	FS	SC
?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
0	0	✓ A/Victoria/380B/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>	Overall QC score: 0 Overall QC status: good Detailed QC assessment:  <span>M</span> Mixed Sites: good No issues  <span>P</span> Private Mutations: good No issues  <span>F</span> Frame shifts: good  <span>S</span> Stop codons: good No issues	22	0	0	97.1%	0	0	0	0	0	0	
1	1	✓ A/Victoria/380C/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>		22	0	0	97.1%	0	0	0	0	0	0	
2	2	✓ A/Victoria/453/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>		28	0	0	97.1%	0	0	0	0	0	0	
3	5	✓ A/Victoria/373/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>		22	0	0	97.1%	0	0	0	0	0	0	
4	3	✓ A/Victoria/454/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>		24	0	0	97.1%	0	0	0	0	0	0	
5	4	✓ A/Victoria/488/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>		27	0	0	97.1%	0	0	0	0	0	0	
6	6	✓ A/Victoria/475/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>		21	0	0	97.1%	0	0	0	0	0	0	
7	8	✓ A/Brisbane/14/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>		26	0	0	97.1%	0	0	0	0	0	0	
8	7	✓ A/Victoria/316/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>		26	0	0	97.1%	0	0	0	0	0	0	
9	9	✓ A/Brisbane/18/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	25	0	0	97.1%	0	0	0	0
10	12	✓ A/Tasmania/30/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	23	0	0	97.1%	0	0	0	0
11	10	✓ A/Tasmania/46/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	19	0	0	97.1%	0	0	0	0
12	11	✓ A/Tasmania/44/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	21	0	0	97.1%	0	0	0	0
13	13	✓ A/Brisbane/13/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>	6B.1A.5a.2a	5a.2a	C.1.6	7(+0-0 0)	25	0	0	97.1%	0	0	0	0
14	14	✓ A/South_Australia/85/2023	<span>M</span> <span>P</span> <span>F</span> <span>S</span>	6B.1A.5a.2a	5a.2a	C.1.6	7(+0-0 0)	25	0	0	97.1%	0	0	0	0

Genome annotation ?





#	i	Sequence	short-clade	Subclade	Glyc.	Mut.	non-ACGTN	Ns	Cov.	Gaps	Ins.	FS	SC
0	0	✓ A/Victoria/38/2023	5a.2a	C.1	7(+0-0 0)	22	0	0	97.1%	0	0	0	0
1	1	✓ A/Victoria/38/2023	5a.2a	C.1	7(+0-0 0)	22	0	0	97.1%	0	0	0	0
2	2	✓ A/Victoria/454/2023	5a.2a	C.1.7	7(+0-0 0)	28	0	0	97.1%	0	0	0	0
3	5	✓ A/Victoria/37/2023	5a.2a	C.1.2	7(+0-0 0)	22	0	0	97.1%	0	0	0	0
4	3	✓ A/Victoria/454/2023	5a.2a	C.1	6(+0-1 0)	24	0	0	97.1%	0	0	0	0
5	4	✓ A/Victoria/488/2023	5a.2a	C.1	7(+0-0 0)	27	0	0	97.1%	0	0	0	0
6	6	✓ A/Victoria/475/2023	5a.2a	C.1	7(+0-0 0)	21	0	0	97.1%	0	0	0	0
7	8	✓ A/Brisbane/14/2023	5a.2a	C.1.6	7(+0-0 0)	26	0	0	97.1%	0	0	0	0
8	7	✓ A/Victoria/316/2023	5a.2a	C.1.2	7(+0-0 0)	26	0	0	97.1%	0	0	0	0
9	9	✓ A/Brisbane/18/2023	5a.2a	C.1	7(+0-0 0)	25	0	0	97.1%	0	0	0	0
10	12	✓ A/Tasmania/30/2023	5a.2a	C.1	7(+0-0 0)	23	0	0	97.1%	0	0	0	0
11	10	✓ A/Tasmania/46/2023	5a.2a	C.1	7(+0-0 0)	19	0	0	97.1%	0	0	0	0
12	11	✓ A/Tasmania/44/2023	5a.2a	C.1	7(+0-0 0)	21	0	0	97.1%	0	0	0	0
13	13	✓ A/Brisbane/13/2023	5a.2a	C.1.6	7(+0-0 0)	25	0	0	97.1%	0	0	0	0
14	14	✓ A/South_Australia/85/2023	5a.2a	C.1.6	7(+0-0 0)	25	0	0	97.1%	0	0	0	0

Genome annotation ?



Nextclade   Start ▶ Dataset ▶ **Results** ▶ Tree ▶ Export    Done... Settings About Citation Docs CLI X D S EN

#	i	Sequence name	QC	Clade	short-clade	Subclade	Glyc.	Mut.	non-ACGTN	Ns	Cov.	Gaps	Ins.	FS	SC
?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
0	0	✓ A/Victoria/380B/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)								
1	1	✓ A/Victoria/380C/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)								
2	2	✓ A/Victoria/453/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1.7	7(+0-0 0)								
3	5	✓ A/Victoria/373/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1.2	7(+0-0 0)								
4	3	✓ A/Victoria/454/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1	6(+0-1 0)								
5	4	✓ A/Victoria/488/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)								
6	6	✓ A/Victoria/475/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)								
7	8	✓ A/Brisbane/14/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1.6	7(+0-0 0)								
8	7	✓ A/Victoria/316/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1.2	7(+0-0 0)								
9	9	✓ A/Brisbane/18/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)								
10	12	✓ A/Tasmania/30/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	23	0	0	97.1%	0	0	0	0
11	10	✓ A/Tasmania/46/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	19	0	0	97.1%	0	0	0	0
12	11	✓ A/Tasmania/44/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	21	0	0	97.1%	0	0	0	0
13	13	✓ A/Brisbane/13/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1.6	7(+0-0 0)	25	0	0	97.1%	0	0	0	0
14	14	✓ A/South_Australia/85/2023	(M P F S)	6B.1A.5a.2a	5a.2a	C.1.6	7(+0-0 0)	25	0	0	97.1%	0	0	0	0

### Glycosylation

Note that motifs are detected after insertions are stripped.

Total: 7

Preserved: 7

Motifs carried from reference sequence (sometimes mutated)

Gene	Ref pos.	Motif
HA1	10	N N S
HA1	23	N V T
HA1	87	N G T
HA1	162	N Q T
HA1	276	N T T
HA1	287	N T S
HA2	154	N G T

Genome annotation ?





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EN

#	i	Sequence name	QC	Clade	short-clade	Subclade	Glyc.	Mut.	non-ACGTN	Ns	Cov.	Gaps	Ins.	FS	SC
?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
0	0	✓ A/Victoria/						22	0	0	97.1%	0	0	0	0
1	1	✓ A/Victoria/3						22	0	0	97.1%	0	0	0	0
2	2	✓ A/Victoria/4						28	0	0	97.1%	0	0	0	0
3	5	✓ A/Victoria/3						22	0	0	97.1%	0	0	0	0
4	3	✓ A/Victoria/4						24	0	0	97.1%	0	0	0	0
5	4	✓ A/Victoria/4						27	0	0	97.1%	0	0	0	0
6	6	✓ A/Victoria/4						21	0	0	97.1%	0	0	0	0
7	8	✓ A/Brisbane/1						26	0	0	97.1%	0	0	0	0
8	7	✓ A/Victoria/3						26	0	0	97.1%	0	0	0	0
9	9	✓ A/Brisbane/1						25	0	0	97.1%	0	0	0	0
10	12	✓ A/Tasmania/2						23	0	0	97.1%	0	0	0	0
11	10	✓ A/Tasmania/4						19	0	0	97.1%	0	0	0	0
12	11	✓ A/Tasmania/44/2023		M P F S	6B.1A.5a.2a	5a.2a	C.1	7(+0-0 0)	21	0	0	97.1%	0	0	0
13	13	✓ A/Brisbane/13/2023		M P F S	6B.1A.5a.2a	5a.2a	C.1.6	7(+0-0 0)	25	0	0	97.1%	0	0	0
14	14	✓ A/South_Australia/85/2023		M P F S	6B.1A.5a.2a	5a.2a	C.1.6	7(+0-0 0)	25	0	0	97.1%	0	0	0

Genome annotation ?





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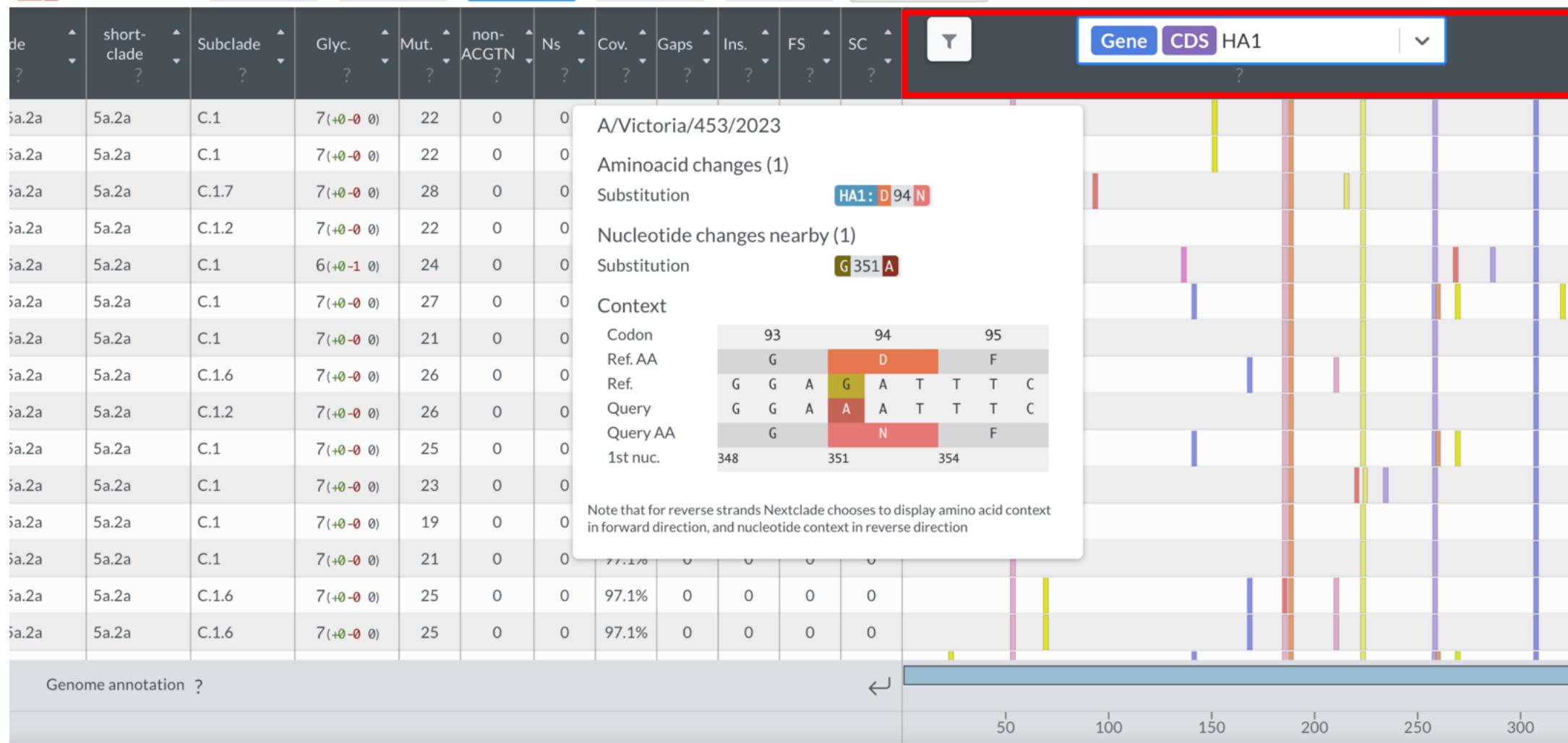
Citation

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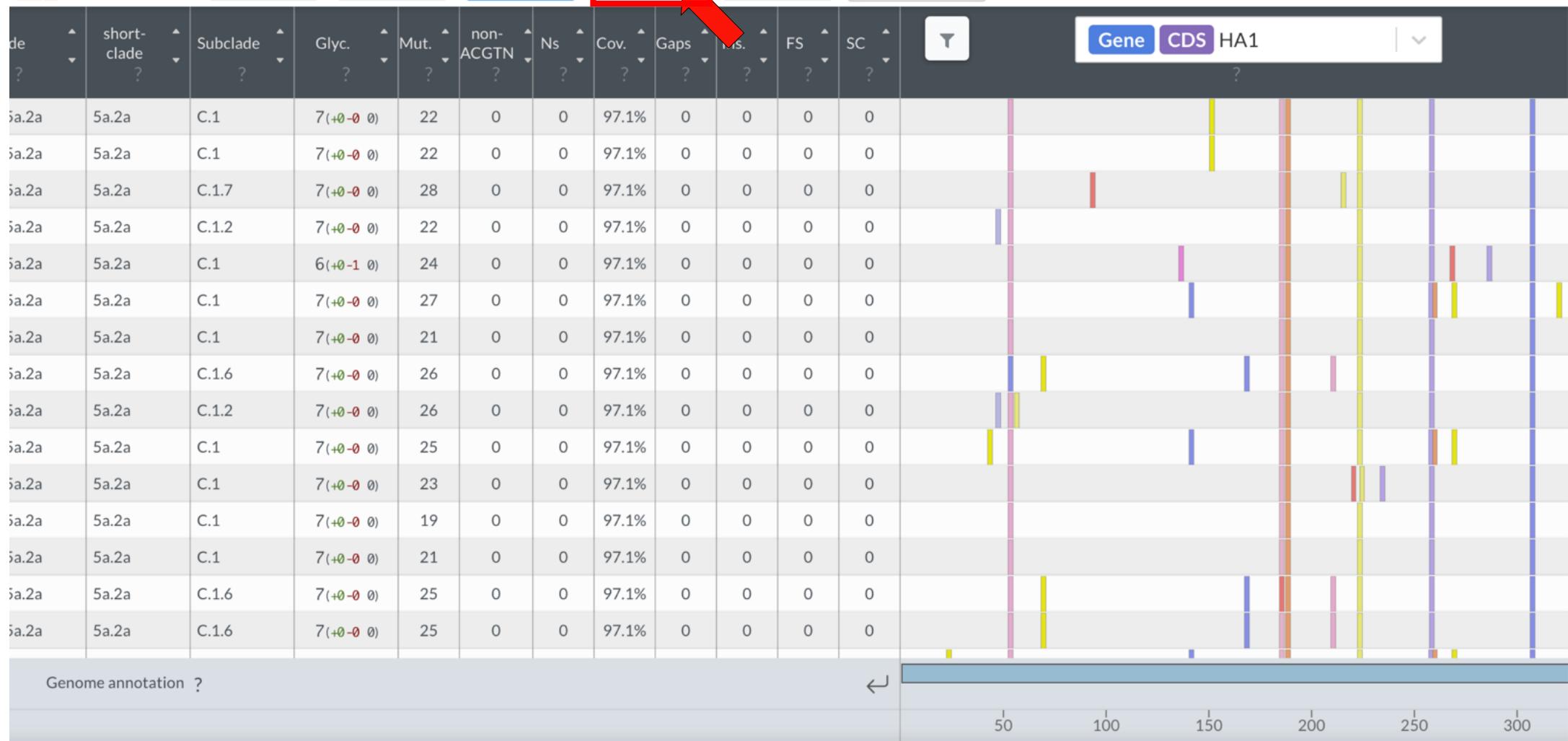
Export

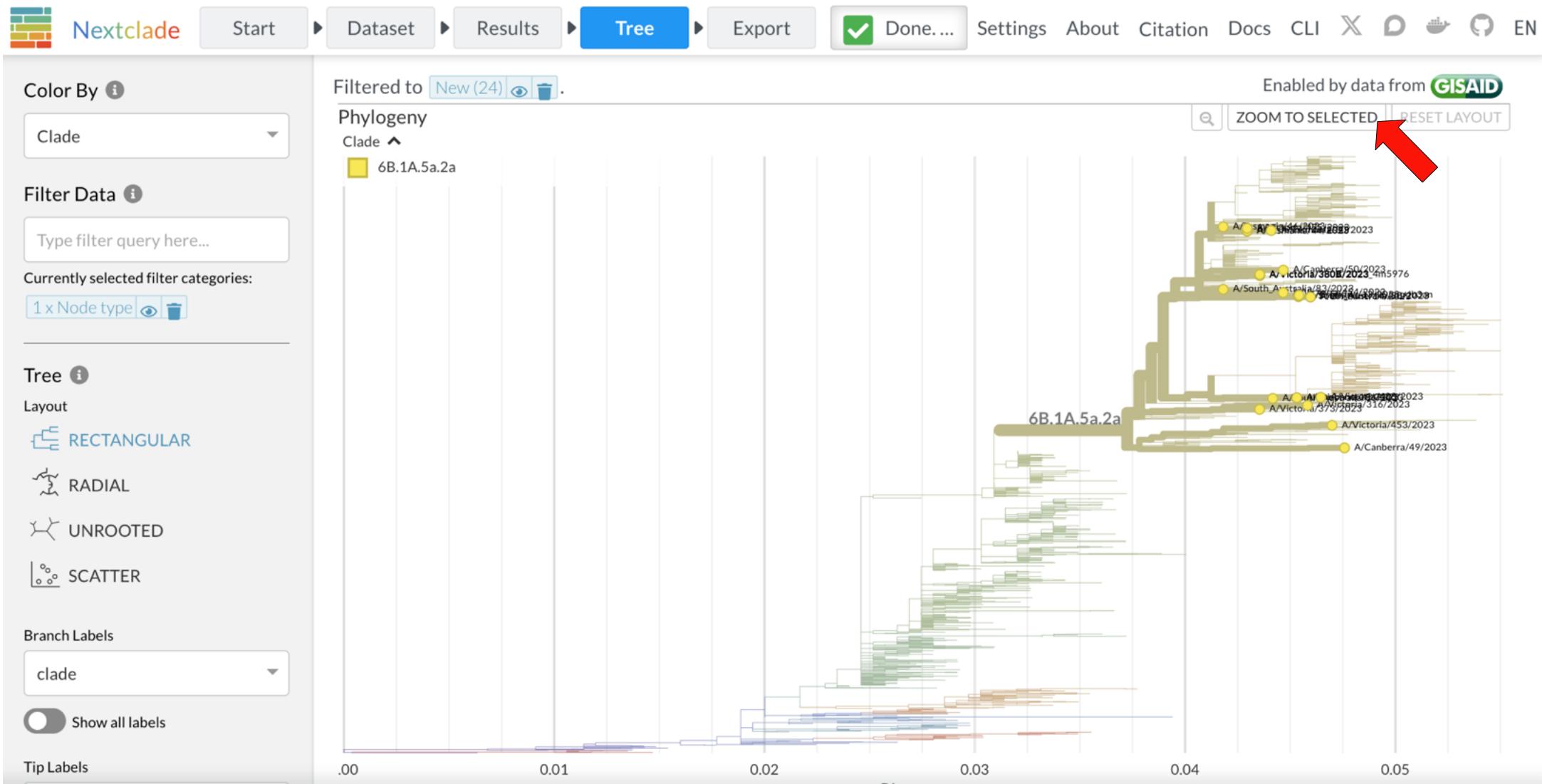
Done....

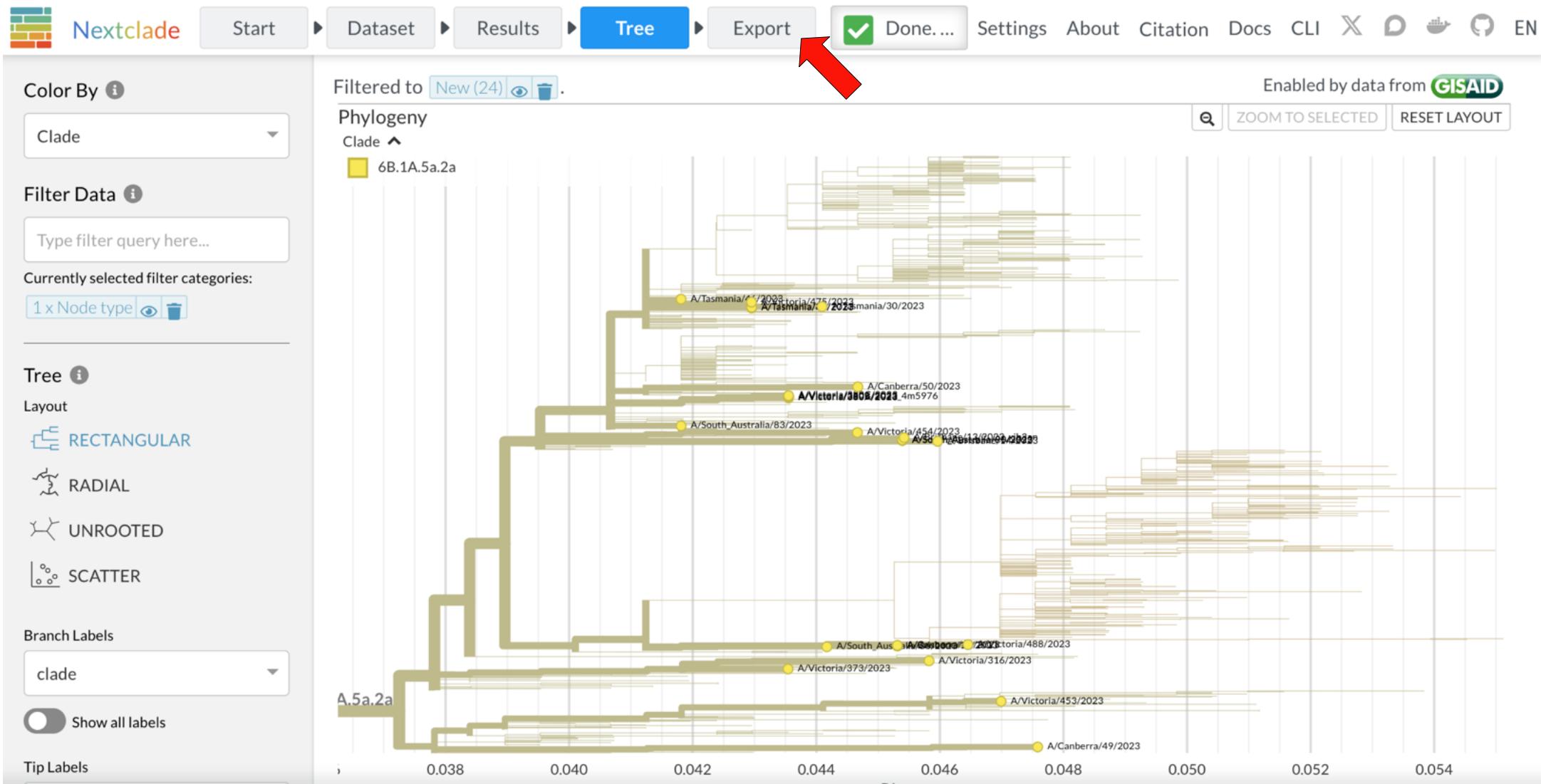
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## Download output files

Files

Column config



nextclade.json

Results of the analysis in JSON format.  
Contains detailed results of the analysis, such as clades, mutations, QC metrics etc., in JSON format. Convenient for further automated processing. Note that this format is unstable and can change without notice.



nextclade.ndjson

Results of the analysis in NDJSON format.  
Contains detailed results of the analysis, such as clades, mutations, QC metrics etc., in NDJSON format (newline-delimited JSON). Convenient for further automated processing. Note that this format is unstable and can change without notice.



nextclade.csv

Summarized results of the analysis in CSV format.  
Contains summarized results of the analysis, such as clades, mutations, QC metrics etc., in tabular format. Convenient for further review and processing using spreadsheets or data-science tools.

[Configure columns](#)

nextclade.tsv

Summarized results of the analysis in TSV format.  
Contains summarized results of the analysis, such as clades, mutations, QC metrics etc., in tabular format. Convenient for further review and processing using spreadsheets or data-science tools.



Office Update To keep up-to-date with security updates, fixes, and improvements, choose Check for Updates.

E28

Check for Updates

	A	B	C	D	E	F	G	H	I
1	index	seqName	clade	short-clade	subclade	glycosylation	qc.overallScc	qc.overallSta	totalSub:
2		0 A/Victoria/380B/2023	6B.1A.5a.2a	5a.2a	C.1	HA1:10:NNS;	0	good	
3		1 A/Victoria/380C/2023	6B.1A.5a.2a	5a.2a	C.1	HA1:10:NNS;	0	good	
4		2 A/Victoria/453/2023	6B.1A.5a.2a	5a.2a	C.1.7	HA1:10:NNS;	0	good	
5		3 A/Victoria/454/2023	6B.1A.5a.2a	5a.2a	C.1	HA1:10:NNS;	0	good	
6		4 A/Victoria/488/2023	6B.1A.5a.2a	5a.2a	C.1	HA1:10:NNS;	0	good	
7		5 A/Victoria/373/2023	6B.1A.5a.2a	5a.2a	C.1.2	HA1:10:NNS;	0	good	
8		6 A/Victoria/475/2023	6B.1A.5a.2a	5a.2a	C.1	HA1:10:NNS;	0	good	
9		7 A/Victoria/316/2023	6B.1A.5a.2a	5a.2a	C.1.2	HA1:10:NNS;	0	good	
10		8 A/Brisbane/14/2023	6B.1A.5a.2a	5a.2a	C.1.6	HA1:10:NNS;	0	good	
11		9 A/Brisbane/18/2023	6B.1A.5a.2a	5a.2a	C.1	HA1:10:NNS;	0	good	
12		10 A/Tasmania/46/2023	6B.1A.5a.2a	5a.2a	C.1	HA1:10:NNS;	0	good	
13		11 A/Tasmania/44/2023	6B.1A.5a.2a	5a.2a	C.1	HA1:10:NNS;	0	good	
14		12 A/Tasmania/30/2023	6B.1A.5a.2a	5a.2a	C.1	HA1:10:NNS;	0	good	
15		13 A/Brisbane/13/2023	6B.1A.5a.2a	5a.2a	C.1.6	HA1:10:NNS;	0	good	

nextclade

Ready

191%

# FluSurver & RSVsurver

# Objective

- To identify mutations using FluSurver

# rsvsurver.bii.a-star.edu.sg

Enabled by

## RSVsurer



Paste your protein or nucleotide FASTA sequence(s) into the text area below. ([Sample FASTA sequence: Example hCoV-19 genome](#))

OR upload your protein or nucleotide sequences in a FASTA file

No file chosen

The server can **automatically** determine the type of input (either protein or nucleotide) and the closest reference sequence among current strains to compare.

To compare with more remotely related sequences/strains, it is possible to select a specific reference strain by choosing below.

Compare with:

(estimated time needed: ~10 seconds per sequence in automatic mode)

# flusurver.bii.a-star.edu.sg



#### Important usage notes:

The main application scenario for FluSurver is to highlight phenotypically or epidemiologically interesting candidate mutations for further research and should ideally be combined with experimental testing and verification of any predicted phenotypes. Importantly, any direct diagnostic use, assumed severity or recommendation on patient treatment should not be based solely on these computational predictions. Our curated reference sequences used for annotation transfer of equivalent mutations are mainly comprised of strains that recently infected humans. Therefore, the **usage scenario that will give the most fruitful and reliable results are current surveillance sequences with very close relation to used vaccine strains, including some candidates for avian flu (including H5N1, H5N6, H5N8 and H7N9) and novel reassortant swine flu H3N2v.**

Please take a look at the [Frequently Asked Questions](#) and [Tutorial](#) if you are new to FluSurver. You could also look at this [NA drug susceptibility example analysis walkthrough starting from GISAID](#) and the [GISAID access summary poster](#)

Paste your protein or nucleotide FASTA sequence(s) into the text area below. ([Sample FASTA sequences: 2009 H1N1 NA and HA](#))

OR upload your protein or nucleotide sequences in a FASTA file

No file chosen



## To screen for mutations associated with drug resistance

### Important usage notes:

The main application scenario for FluSurver is to highlight phenotypically or epidemiologically interesting candidate mutations for further research and should ideally be combined with experimental testing and verification of any predicted phenotypes. Importantly, any direct diagnostic use, assumed severity or recommendation on patient treatment should not be based solely on these computational predictions. Our curated reference sequences used for annotation transfer of equivalent mutations are mainly comprised of strains that recently infected humans. Therefore, the **usage scenario that will give the most fruitful and reliable results are current surveillance sequences with very close relation to used vaccine strains, including some candidates for avian flu (including H5N1, H5N6, H5N8 and H7N9) and novel reassortant swine flu H3N2v.**

Please take a look at the [Frequently Asked Questions](#) and [Tutorial](#) if you are new to FluSurver. You could also look at this [NA drug susceptibility example analysis walkthrough starting from GISAID](#) and the [GISAID access summary poster](#)

Paste your protein or nucleotide FASTA sequence(s) into the text area below. ([Sample FASTA sequences: 2009 H1N1 NA and HA](#))

```
>A/Victoria/3035/2023|NA
atgaatccaaaccaaagataataaccattggtctatctgtalgacaattggaaacggctaacttaataattacaaaattgg
aaacataatctcaaatggtagccactcaatcaaattggaaatcaaaggccagatggaaacatgcataaaaagcgtca
ttacttatggaaaacaacacttggtaaatcagacattgttaacatcagcaacactaactctgtctgtacataatcagtg
gcttcgtgaaattagcggcaattccctctcgccctgttagtggatggctatacatcagaataagacaacagtgtaa
aatcgggtccaaggggatgttgtgtataagggaaccattcatgcgtccctggaaatgcagaacccttctt
tgactcaaggggcttgcataatggaaacattcaatggaaacattaaagacaacagaacccatatcgaaccctaatgg
tgccatattggtaagtccctccatcaaactcaagatttgactgtcgtccgttgcagaactgtgtcatgtgg
cacaatggctacaatggaaattctggccagacaatggggcagtggctgtttaataatcaatggcataataacag
```

OR upload your protein or nucleotide sequences in a FASTA file

Choose file No file chosen

The server can **automatically** determine the type of input (either protein or nucleotide) and the closest reference sequence among current vaccine strains to compare. Also mixtures of genes/proteins (e.g. HA and NA or all genes of the same patient) can be provided as input. To compare with more remotely related sequences/strains, it is possible to select a specific reference strain by choosing below.

Paste your protein or nucleotide FASTA sequence(s) into the text area below. ([Sample FASTA sequences: 2009 H1N1 NA and HA](#))

```
>A/Victoria/3035/2023|NA
atgaatccaaacaaaaagataataaccattggtttatctgtatgacaattggAACGGCTAACTTAATTACAAATTGG
AACACATAATCTCAATATGGGTTAGCCACTCAATTGGAATCAAAGGCCAGATTGAAACATGCAATAAAAGCGTCA
TTACTTATGAAAACAACACTGGGTTAAATCAGACATTGTTAACATCAGCAACACTAATCTGCTGTAGACAATCAGTG
GCTTCGTTGAAATTAGCGGGCAATTCTCTCGCCCTGTTAGTGGATGGCTATATAACAGTAAAGACAACAGTGTAAAG
AACTGGTTCCAAGGGGGATGTGTTGTCTAAAGGGACCATTCAATCATGCTCTCCCTGGAATGCGAGAACCTCTCT
TGACTCAAGGGGCTTGCTAAATGACAACATTCAATGGAACAATTAAAGACAAGGCCATATCGAACCCATAATGAGC
TGTCTATTGGTGAAGTCCCTCTCCATAACTCAAGATTGAGTCAGTCGCTGGTCAGCAAGTGCTGTGATGATGG
CACCAATTGGCTAACATTGAAATTCTGGCCAGACAATGGGCAGTGGCTGTGTTAAACATGGCATAATAACAG
```

OR upload your protein or nucleotide sequences in a FASTA file

No file chosen

The server can **automatically** determine the type of input (either protein or nucleotide) and the closest reference sequence among current vaccine strains to compare. Also mixtures of genes/proteins (e.g. HA and NA or all genes of the same patient) can be provided as input. To compare with more remotely related sequences/strains, it is possible to select a specific reference strain by choosing below.

Compare with:

Automatic detection of closest reference (larger selection of strains, not always full genomes)

Additional settings:

ignore low quality bases for nucleotide input (indicated by lower case, except for all lower case sequences)



Bioinformatics  
Institute

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Result for comparison with reference selection: autorefall

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Query	Clade	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a.2a)	HA A/Sydney/5/2021(H1N1)	98.763	<a href="#">100.000</a>	7	<a href="#">V7A</a> , <a href="#">V36I</a> , <a href="#">N111D</a> , <a href="#">A233T</a> , <a href="#">R240Q</a> , <a href="#">E422D</a> , <a href="#">I435V</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 MP	-	M1 A/Victoria/4897/2022(H1N1)	100.000	<a href="#">100.000</a>	0	no mutations
A/Victoria/3035/2023 MP	-	M2 A/Victoria/2570/2019(H1N1)	95.652	<a href="#">94.845</a>	4	<a href="#">E6K</a> , <a href="#">V7I</a> , <a href="#">E8Y</a> , <a href="#">T9R</a> <a href="#">show in structure</a> M2 drug sensitivity positions: <a href="#">17</a> , <a href="#">0</a> , <a href="#">1</a> Reduced sensitivity or resistance!
A/Victoria/3035/2023 NA	-	NA A/Sydney/5/2021(H1N1)	99.359	<a href="#">99.787</a>	3	NA drug sensitivity positions: <a href="#">35</a> , <a href="#">0</a> , <a href="#">1</a> Reduced sensitivity or resistance!
A/Victoria/3035/2023 NP	-	NP A/Michigan/45/2015(H1N1)	98.795	<a href="#">100.000</a>	6	<a href="#">E14D</a> , <a href="#">T22A</a> , <a href="#">I33V</a> , <a href="#">I136L</a> , <a href="#">V217I</a> , <a href="#">V425I</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 NS	-	NS1 A/Victoria/2570/2019(H1N1)	99.543	<a href="#">100.000</a>	1	<a href="#">V84I</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 NS	-	NS2 A/Michigan/45/2015(H1N1)	100.000	<a href="#">93.388</a>	0	no mutations
A/Victoria/3035/2023 PA	-	PA A/Sydney/5/2021(H1N1)	98.883	<a href="#">100.000</a>	8	<a href="#">I30V</a> , <a href="#">L63I</a> , <a href="#">I226L</a> , <a href="#">R262K</a> , <a href="#">I330V</a> , <a href="#">A343S</a> , <a href="#">I438V</a> , <a href="#">K626R</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 PB1	-	PB1 A/Victoria/2570/2019(H1N1)	99.868	<a href="#">100.000</a>	1	<a href="#">K757R</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 PB2	-	PB2 A/Victoria/2570/2019(H1N1)	99.868	<a href="#">100.000</a>	1	<a href="#">L475M</a> <a href="#">show in structure</a>

[Right-click here to save/download detailed mutation report table for archiving or import to Excel \(Tab-separated, one mutation per line\)](#)[Right-click here to save/download query summary report table for archiving or import to Excel \(Comma-separated, one query per line\)](#)[Right-click here to save/download query clade report table for archiving or import to Excel \(Tab-separated, one query per line\)](#)



Result for comparison with reference selection: **autorefall**

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Query	Clade	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a.2a)	HAA/Sydney/5/2021(H1N1)	98.763	<u>100.000</u>	7	<u>V7A</u> , <u>V36I</u> , <u>N111D</u> , <u>A233T</u> , <u>R240Q</u> , <u>E422D</u> , <u>I435V</u> show in structure
A/Victoria/3035/2023 MP	-	M1 A/Victoria/4897/2022(H1N1)	100.000	<u>100.000</u>	0	no mutations
A/Victoria/3035/2023 MP	-	M2 A/Victoria/2570/2019(H1N1)	95.652	<u>94.845</u>	4	<u>E6K</u> , <u>V7I</u> , <u>E8Y</u> , <u>T9R</u> show in structure M2 drug sensitivity positions: <u>17</u> , <u>0</u> , <u>1</u> Reduced sensitivity or resistance!
A/Victoria/3035/2023 NA	-	NA A/Sydney/5/2021(H1N1)	99.359	<u>99.787</u>	3	<u>S200N</u> , <u>H275Y</u> , <u>N434S</u> show in structure NA drug sensitivity positions: <u>35</u> , <u>0</u> , <u>1</u> Reduced sensitivity or resistance!
A/Victoria/3035/2023 NP	-	NP A/Michigan/45/2015(H1N1)	98.795	<u>100.000</u>	6	<u>E14D</u> , <u>T22A</u> , <u>I33V</u> , <u>I136L</u> , <u>V217I</u> , <u>V425I</u> show in structure
A/Victoria/3035/2023 NS	-	NS1 A/Victoria/2570/2019(H1N1)	99.543	<u>100.000</u>	1	<u>V84I</u> show in structure
A/Victoria/3035/2023 NS	-	NS2 A/Michigan/45/2015(H1N1)	100.000	<u>93.388</u>	0	no mutations



Result for comparison with reference selection: autorefall

[Back to Reference Selection](#)

Query	Clade	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a.2a)	HA A/Sydney/5/2021(H1N1)	98.763	<a href="#">100.000</a>	7	<a href="#">V7A</a> , <a href="#">V36I</a> , <a href="#">N111D</a> , <a href="#">A233T</a> , <a href="#">R240Q</a> , <a href="#">E422D</a> , <a href="#">I435V</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 MP	-	M1 A/Victoria/4897/2022(H1N1)	100.000	<a href="#">100.000</a>	0	no mutations
A/Victoria/3035/2023 MP	-	M2 A/Victoria/2570/2019(H1N1)	95.652	<a href="#">94.845</a>	4	M2 drug sensitivity positions: <a href="#">17</a> , <a href="#">0</a> , <a href="#">1</a> Reduced sensitivity or resistance!
A/Victoria/3035/2023 NA	-	NA A/Sydney/5/2021(H1N1)	99.359	<a href="#">99.787</a>	3	NA drug sensitivity positions: <a href="#">35</a> , <a href="#">0</a> , <a href="#">1</a> Reduced sensitivity or resistance!
A/Victoria/3035/2023 NP	-	NP A/Michigan/45/2015(H1N1)	98.795	<a href="#">100.000</a>	6	<a href="#">E14D</a> , <a href="#">T22A</a> , <a href="#">I33V</a> , <a href="#">I136L</a> , <a href="#">V217I</a> , <a href="#">V425I</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 NS	-	NS1 A/Victoria/2570/2019(H1N1)	99.543	<a href="#">100.000</a>	1	<a href="#">V84I</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 NS	-	NS2 A/Michigan/45/2015(H1N1)	100.000	<a href="#">93.388</a>	0	no mutations
A/Victoria/3035/2023 PA	-	PA A/Sydney/5/2021(H1N1)	98.883	<a href="#">100.000</a>	8	<a href="#">I30V</a> , <a href="#">L63I</a> , <a href="#">I226L</a> , <a href="#">R262K</a> , <a href="#">I330V</a> , <a href="#">A343S</a> , <a href="#">I438V</a> , <a href="#">K626R</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 PB1	-	PB1 A/Victoria/2570/2019(H1N1)	99.868	<a href="#">100.000</a>	1	<a href="#">K757R</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 PB2	-	PB2 A/Victoria/2570/2019(H1N1)	99.868	<a href="#">100.000</a>	1	<a href="#">L475M</a> <a href="#">show in structure</a>

[Right-click here to save/download detailed mutation report table for archiving or import to Excel \(Tab-separated, one mutation per line\)](#)[Right-click here to save/download query summary report table for archiving or import to Excel \(Comma-separated, one query per line\)](#)[Right-click here to save/download query clade report table for archiving or import to Excel \(Tab-separated, one query per line\)](#)



flusurver.bii.a-star.edu.sg/tmp/tmpblastout.15517\_aln.html#1

flusurver.bii.a-star.edu.sg/tmp/tmpblastout.15517\_aln.html#1

Query= A/Victoria/3035/2023|HA

>HA\_H1N1\_Human\_2021\_Sydney5

HA|A/Sydney/5/2021|2021-10-16|EPI\_ISL\_12109632|E3/E1|A /  
H1N1|WHO Collaborating Centre for Reference and Research  
on Influenza|Centers for Disease Control and  
Prevention|DaSilva Juliana

|A/SYDNEY/5/2021|3000822336|EPI2020621

Length = 566

Score = 1162 bits (3006), Expect = 0.0

Identities = 559/566 (98%), Positives = 564/566 (99%)

Frame = +1

Query: 1 MKAILVAMLYTFTTANADTLCIGYHANNSTDVTILEKNVTVHSVNLLLEDKHNGKLCK 180  
MKAILV MLYTFTTANADTLCIGYHANNSTDVT+LEKNVTVHSVNLLLEDKHNGKLCK

Sbjct: 1 MKAILVVMLYTFITANADTLCIGYHANNSTDVTILEKNVTVHSVNLLLEDKHNGKLCK 60

Query: 181 LRGVAPLHLGQCNIAGWILGNPECESLSTARWSYIVETSNSDNGTCYPGDFINYEELRE 360  
LRGVAPLHLGQCNIAGWILGNPECESLSTARWSYIVETSNSDNGTCYPG+FINYEELRE

Sbjct: 61 LRGVAPLHLGQCNIAGWILGNPECESLSTARWSYIVETSNSDNGTCYPGNFINYEELRE 120

Query: 361 QLSSVSSFERFEIFPKTSSWPNHSDSDNGVTAACPHAGAKSFYKNLIWLVKKGKSYKPINQ 540  
QLSSVSSFERFEIFPKTSSWPNHSDSDNGVTAACPHAGAKSFYKNLIWLVKKGKSYKPINQ

Sbjct: 121 QLSSVSSFERFEIFPKTSSWPNHSDSDNGVTAACPHAGAKSFYKNLIWLVKKGKSYKPINQ 180

Query: 541 TYINDKGKEVLVLWGIHHPPITIDQESLYQNADAYVFVGTSRYSKKFKPEIATRPKVRDQ 720  
TYINDKGKEVLVLWGIHHPPITIDQESLYQNADAYVFVGTSRYSKKFKPEIA RPKVRD+

Sbjct: 181 TYINDKGKEVLVLWGIHHPPITIDQESLYQNADAYVFVGTSRYSKKFKPEIAARPKVRDR 240

Query: 721 AGRMNYWTLVEPGDKITFEATGNLVAPRYAFTMEKDAGSGIIISDTPVHDCTTCQTPE 900  
AGRMNYWTLVEPGDKITFEATGNLVAPRYAFTMEKDAGSGIIISDTPVHDCTTCQTPE

Sbjct: 241 AGRMNYWTLVEPGDKITFEATGNLVAPRYAFTMEKDAGSGIIISDTPVHDCTTCQTPE 300

Query: 901 GAINSTSLPFQNVHPITIGKCPKYVRSTKLRLATGLRNVPsiQSRGLFGAIAGFIEGGWTG 1080  
GAINSTSLPFQNVHPITIGKCPKYVRSTKLRLATGLRNVPsiQSRGLFGAIAGFIEGGWTG

Sbjct: 301 GAINSTSLPFQNVHPITIGKCPKYVRSTKLRLATGLRNVPsiQSRGLFGAIAGFIEGGWTG 360

Query: 1081 MVDGWYGYHHQNEQGSGYAADLKSTQNAIDKITNKVNSVIEKMNTQFTAVGKEFNHLEKR 1260  
MVDGWYGYHHQNEQGSGYAADLKSTQNAIDKITNKVNSVIEKMNTQFTAVGKEFNHLEKR

Sbjct: 361 MVDGWYGYHHQNEQGSGYAADLKSTQNAIDKITNKVNSVIEKMNTQFTAVGKEFNHLEKR 420



Result for comparison with reference selection: autorefall

[Back to Reference Selection](#)

Query	Clade	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a.2a)	HA A/Sydney/5/2021(H1N1)	98.763	<a href="#">100.000</a>	7	<a href="#">V7A</a> , <a href="#">V36I</a> , <a href="#">N111D</a> , <a href="#">A233T</a> , <a href="#">R240Q</a> , <a href="#">E422D</a> , <a href="#">I435V</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 MP	-	M1 A/Victoria/4897/2022(H1N1)	100.000	<a href="#">100.000</a>	0	no mutations
A/Victoria/3035/2023 MP	-	M2 A/Victoria/2570/2019(H1N1)	95.652	<a href="#">94.845</a>	4	<a href="#">E6K</a> , <a href="#">V7I</a> , <a href="#">E8Y</a> , <a href="#">T9R</a> <a href="#">show in structure</a> M2 drug sensitivity positions: <a href="#">17</a> , <a href="#">0</a> , <a href="#">1</a> Reduced sensitivity or resistance!
A/Victoria/3035/2023 NA	-	NA A/Sydney/5/2021(H1N1)	99.359	<a href="#">99.787</a>	3	<a href="#">S200N</a> , <a href="#">H275Y</a> , <a href="#">N434S</a> <a href="#">show in structure</a> NA drug sensitivity positions: <a href="#">35</a> , <a href="#">0</a> , <a href="#">1</a> Reduced sensitivity or resistance!
A/Victoria/3035/2023 NP	-	NP A/Michigan/45/2015(H1N1)	98.795	<a href="#">100.000</a>	6	<a href="#">E14D</a> , <a href="#">T22A</a> , <a href="#">I33V</a> , <a href="#">I136L</a> , <a href="#">V217I</a> , <a href="#">V425I</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 NS	-	NS1 A/Victoria/2570/2019(H1N1)	99.543	<a href="#">100.000</a>	1	<a href="#">V84I</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 NS	-	NS2 A/Michigan/45/2015(H1N1)	100.000	<a href="#">93.388</a>	0	no mutations
A/Victoria/3035/2023 PA	-	PA A/Sydney/5/2021(H1N1)	98.883	<a href="#">100.000</a>	8	<a href="#">I30V</a> , <a href="#">L63I</a> , <a href="#">I226L</a> , <a href="#">R262K</a> , <a href="#">I330V</a> , <a href="#">A343S</a> , <a href="#">I438V</a> , <a href="#">K626R</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 PB1	-	PB1 A/Victoria/2570/2019(H1N1)	99.868	<a href="#">100.000</a>	1	<a href="#">K757R</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 PB2	-	PB2 A/Victoria/2570/2019(H1N1)	99.868	<a href="#">100.000</a>	1	<a href="#">L475M</a> <a href="#">show in structure</a>

[Right-click here to save/download detailed mutation report table for archiving or import to Excel \(Tab-separated, one mutation per line\)](#)[Right-click here to save/download query summary report table for archiving or import to Excel \(Comma-separated, one query per line\)](#)[Right-click here to save/download query clade report table for archiving or import to Excel \(Tab-separated, one query per line\)](#)

Query	Clade
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a)
A/Victoria/3035/2023 MP	-
A/Victoria/3035/2023 MP	-
A/Victoria/3035/2023 NA	-
A/Victoria/3035/2023 NP	-
A/Victoria/3035/2023 NS	-
A/Victoria/3035/2023 NS	-
A/Victoria/3035/2023 PA	-
A/Victoria/3035/2023 PB1	-
A/Victoria/3035/2023 PB2	-

X

## NA H275Y

Key to alternative position numbering:

275                    FluSurver numbering  
                          (absolute as in 2009 H1N1 pandemic)

274                    Classical H3N2 strain numbering

275                    Classical H1N1 strain numbering

Chosen reference: NA\_H1N1\_Human\_2021\_Sydney5

Position in reference: 275

AA in reference: H

AA in query: Y

Mutation occurrence statistics are not available for this strain at the moment, please contact flusurver.org if you would like it to be included in future.

A mutation at the position equivalent to **NA 275** has been reported in the literature to be related to [strong drug resistance and mild drug resistance](#).

A combination of mutations including the position equivalent to **NA 275** has been reported in the literature to be related to [strong drug resistance](#).

As seen in resolved structures of proteins from related strains, the NA position equivalent to your mutation is involved in:

- [drug binding](#)

[See all interactions for this position](#)

[PubMed search for this mutation \(including alternative numbering\)](#)

PB2 A/Victoria/2570/2019(H1N1) 99.868 100.000

1

L475M

[show in structure](#)

K757R

[show in structure](#)

I0V, L63I, I226L, R262K, I330V, A343S, I438V, K626R

[show in structure](#)

V84I

[show in structure](#)

no mutations

S200N, H275Y, N434S

[show in structure](#)

NA drug sensitivity positions:  
17, 0, 1

Reduced sensitivity or resistance!

E14D, T22A, I33V, I136L, V217I, V425I

[show in structure](#)

no mutations

V7A, V36I, N111D, A233T, R240Q, E422D, I435V

[show in structure](#)

no mutations

E6K, V7I, E8Y, T9R

[show in structure](#)

M2 drug sensitivity positions:  
17, 0, 1

Reduced sensitivity or resistance!

S200N, H275Y, N434S

[show in structure](#)

NA drug sensitivity positions:  
35, 0, 1

Reduced sensitivity or resistance!

E14D, T22A, I33V, I136L, V217I, V425I

[show in structure](#)

I0V, L63I, I226L, R262K, I330V, A343S, I438V, K626R

[show in structure](#)

Right-click here to save/download [detailed mutation report](#) table for archiving or import to Excel (Tab-separated, one mutation per line)

Right-click here to save/download [query summary report](#) table for archiving or import to Excel (Comma-separated, one query per line)

Right-click here to save/download [query clade report](#) table for archiving or import to Excel (Tab-separated, one query per line)

FluSurver

Result for comparison with reference selection: autorefall Back to Reference Selection

**NA H275Y**

Key to alternative position numbering:  
 FluSurver numbering  
 (absolute as in 2009 H1N1 pandemic)  
 Classical H3N2 strain numbering  
 Classical H1N1 strain numbering  
 NA\_H1N1\_Human\_2021\_Sydney5

Position:	275
Residue:	H
Effect:	Y

no mutations

M2 drug sensitivity positions:  
 17, 0, 1  
 Reduced sensitivity or resistance!

S200N, H275Y, N434S  
[show in structure](#)

NA drug sensitivity positions:  
 35, 0, 1  
 Reduced sensitivity or resistance!

E14D, T22A, I33V, I136L, V217I, V425I  
[show in structure](#)

V84I  
[show in structure](#)

no mutations

L60V, L63I, I226L, R262K, I330V, A343S, I438V, K626R  
[show in structure](#)

K757R  
[show in structure](#)

L475M  
[show in structure](#)

A/Victoria/3035/2023|PB2 - PB2 A/Victoria/2570/2019(H1N1) 99.868 100.000 1

Right-click here to save/download detailed mutation report table for archiving or import to Excel (Tab-separated, one mutation per line)  
 Right-click here to save/download query summary report table for archiving or import to Excel (Comma-separated, one query per line)  
 Right-click here to save/download query clade report table for archiving or import to Excel (Tab-separated, one query per line)



> *Antimicrob Agents Chemother.* 2008 Sep;52(9):3284-92. doi: 10.1128/AAC.00555-08.

Epub 2008 Jul 14.

# Surveillance for neuraminidase inhibitor resistance among human influenza A and B viruses circulating worldwide from 2004 to 2008

Tiffany G Sheu <sup>1</sup>, Varough M Deyde, Margaret Okomo-Adhiambo, Rebecca J Garten, Xiyan Xu, Rick A Bright, Ebeneé N Butler, Teresa R Wallis, Alexander I Klimov, Larisa V Gubareva

Affiliations + expand

PMID: 18625765 PMCID: PMC2533500 DOI: 10.1128/AAC.00555-08

## Abstract

The surveillance of seasonal influenza virus susceptibility to neuraminidase (NA) inhibitors was conducted using an NA inhibition assay. The 50% inhibitory concentration values (IC<sub>50</sub>s) of 4,570 viruses collected globally from October 2004 to March 2008 were determined. Based on mean IC<sub>50</sub>s, A(H3N2) viruses (0.44 nM) were more sensitive to oseltamivir than A(H1N1) viruses (0.91 nM). The opposite trend was observed with zanamivir: 1.06 nM for A(H1N1) and 2.54 nM for A(H3N2). Influenza B viruses exhibited the least susceptibility to oseltamivir (3.42 nM) and to zanamivir (3.87 nM). To identify potentially resistant viruses (outliers), a threshold of a mean IC<sub>50</sub> value + 3 standard deviations was defined for type/subtype and drug. Sequence analysis of outliers was performed to identify NA changes that might be associated with reduced susceptibility. Molecular markers of oseltamivir resistance were found in six A(H1N1) viruses (H274Y) and one A(H3N2) virus (E119V) collected between 2004 and 2007. Some outliers contained previously

<https://pubmed.ncbi.nlm.nih.gov/18625765/#similar> I222T in the B viruses), while other mutations (e.g., R371K and H274Y in B

Query	Clade
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a)
A/Victoria/3035/2023 MP	-
A/Victoria/3035/2023 MP	-
A/Victoria/3035/2023 NA	-
A/Victoria/3035/2023 NP	-
A/Victoria/3035/2023 NS	-
A/Victoria/3035/2023 NS	-
A/Victoria/3035/2023 PA	-
A/Victoria/3035/2023 PB1	-
A/Victoria/3035/2023 PB2	-

X

**NA H275Y**

Key to alternative position numbering:

FluSurver numbering  
 (absolute as in 2009 H1N1 pandemic)

275      FluSurver numbering

274      Classical H3N2 strain numbering

275      Classical H1N1 strain numbering

Chosen reference: NA\_H1N1\_Human\_2021\_Sydney5

Position in reference: 275

AA in reference: H

AA in query: Y

Mutation occurrence statistics are not available for this strain at the moment, please contact flusurver.org if you would like it to be included in future.

A mutation at the position equivalent to **NA 275** has been reported in the literature to be related to [strong drug resistance](#) and [mild drug resistance](#).

A combination of mutations including the position equivalent to **NA 275** has been reported in the literature to be related to [strong drug resistance](#).

As seen in resolved structures of proteins from related strains, the NA position equivalent to your mutation is involved in:

- [drug binding](#)[See all interactions at this position](#)[PubMed search for this mutation \(including alternative numbering\)](#)

PB2 A/Victoria/2570/2019(H1N1) 99.868 100.000

1

[L475M](#)[show in structure](#)[K757R](#)[show in structure](#)[V84I](#)[show in structure](#)[S200N, H275Y, N434S](#)[show in structure](#)

NA drug sensitivity positions:

[35, 0, 1](#)

Reduced sensitivity or resistance!

M2 drug sensitivity positions:

[17, 0, 1](#)

Reduced sensitivity or resistance!

[E14D, T22A, I33V, I136L, V217I, V425I](#)[show in structure](#)[I10V, L63I, I226L, R262K, I330V, A343S, I438V, K626R](#)[show in structure](#)[I10V, L63I, I226L, R262K, I330V, A343S, I438V, K626R](#)[show in structure](#)[Right-click here to save/download detailed mutation report table for archiving or import to Excel \(Tab-separated, one mutation per line\)](#)[Right-click here to save/download query summary report table for archiving or import to Excel \(Comma-separated, one query per line\)](#)[Right-click here to save/download query clade report table for archiving or import to Excel \(Tab-separated, one query per line\)](#)

**FluSurver**

Result for comparison with reference selection: autorefall

Query	Clade
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a)
A/Victoria/3035/2023 MP	-
A/Victoria/3035/2023 MP	-
A/Victoria/3035/2023 NA	-
A/Victoria/3035/2023 NP	-
A/Victoria/3035/2023 NS	-
A/Victoria/3035/2023 NS	-
A/Victoria/3035/2023 PA	-
A/Victoria/3035/2023 PB1	-
A/Victoria/3035/2023 PB2	-

PB2 A/Victoria/2570/2019(H1N1) 99.868

Right-click here to save/download detailed mutation report table for archiving.  
 Right-click here to save/download query summary report table for archiving or  
 Right-click here to save/download query clade report table for archiving or

X

### NA H275Y

Key to alternative position numbers:

- 275 FluSurver number (absolute as in 2009)
- 274 Classical H3N2 strain
- 275 Classical H1N1 strain
- NA\_H1N1\_Human Chosen reference:

Position in reference: 275

AA in reference: H

AA in query: Y

Mutation occurrence statistics are not available for this structure. Contact flusurver.org if you would like it to be included.

A mutation at the position equivalent to **NA 275** has been reported in literature to be related to [strong drug resistance](#) and [mild drug binding](#).

A combination of mutations including the position equivalent to **NA 275** has been reported in the literature to be related to [strong drug resistance](#) and [mild drug binding](#).

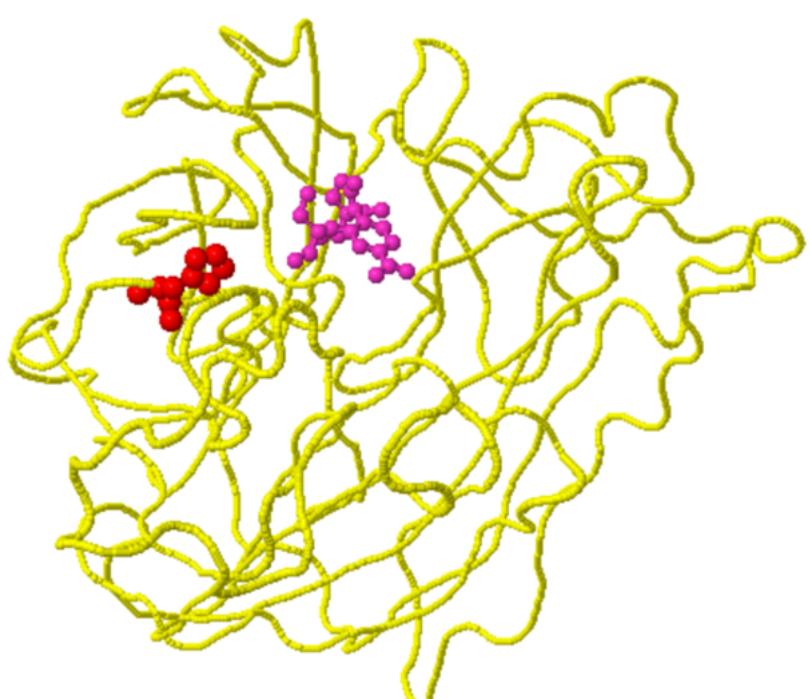
As seen in resolved structures of protein chains from related strains, the NA position equivalent to your mutation is located near [drug binding](#).

[See all interactions for this position](#)

[PubMed search for this mutation \(including alternative positions\)](#)

NA\_275\_1B9V\_A\_273

flusurver.bii.a-star.edu.sg/INTERACTIONS/NA/275/NA\_275\_1B9V\_A\_2...



JSmol

Spin ON Spin OFF Save IMAGE

Description:  
The mutation position (**red atoms**) corresponds to position 273 on viral chain A (**yellow backbone**) and is within 5 Å from drug RA2 (**pink atoms**).  
[See all 18 interactions for this position](#)



Result for comparison with reference selection: autorefall

[Back to Reference Selection](#)

Query	Clade	Best reference hit	% AA identity	% length coverage	# mutations	List of mutations
A/Victoria/3035/2023 HA	6B.1A.5a.2a (5a.2a)	HA A/Sydney/5/2021(H1N1)	98.763	<a href="#">100.000</a>	7	<a href="#">V7A</a> , <a href="#">V36I</a> , <a href="#">N111D</a> , <a href="#">A233T</a> , <a href="#">R240Q</a> , <a href="#">E422D</a> , <a href="#">I435V</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 MP	-	M1 A/Victoria/4897/2022(H1N1)	100.000	<a href="#">100.000</a>	0	no mutations
A/Victoria/3035/2023 MP	-	M2 A/Victoria/2570/2019(H1N1)	95.652	<a href="#">94.845</a>	4	<a href="#">E6K</a> , <a href="#">V7I</a> , <a href="#">E8Y</a> , <a href="#">T9R</a> <a href="#">show in structure</a> M2 drug sensitivity positions: <a href="#">17</a> , <a href="#">0</a> , <a href="#">1</a> Reduced sensitivity or resistance!
A/Victoria/3035/2023 NA	-	NA A/Sydney/5/2021(H1N1)	99.359	<a href="#">99.787</a>	3	NA drug sensitivity positions: <a href="#">35</a> , <a href="#">0</a> , <a href="#">1</a> Reduced sensitivity or resistance!
A/Victoria/3035/2023 NP	-	NP A/Michigan/45/2015(H1N1)	98.795	<a href="#">100.000</a>	6	<a href="#">E14D</a> , <a href="#">T22A</a> , <a href="#">I33V</a> , <a href="#">I136L</a> , <a href="#">V217I</a> , <a href="#">V425I</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 NS	-	NS1 A/Victoria/2570/2019(H1N1)	99.543	<a href="#">100.000</a>	1	<a href="#">V84I</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 NS	-	NS2 A/Michigan/45/2015(H1N1)	100.000	<a href="#">93.388</a>	0	no mutations
A/Victoria/3035/2023 PA	-	PA A/Sydney/5/2021(H1N1)	98.883	<a href="#">100.000</a>	8	<a href="#">I30V</a> , <a href="#">L63I</a> , <a href="#">I226L</a> , <a href="#">R262K</a> , <a href="#">I330V</a> , <a href="#">A343S</a> , <a href="#">I438V</a> , <a href="#">K626R</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 PB1	-	PB1 A/Victoria/2570/2019(H1N1)	99.868	<a href="#">100.000</a>	1	<a href="#">K757R</a> <a href="#">show in structure</a>
A/Victoria/3035/2023 PB2	-	PB2 A/Victoria/2570/2019(H1N1)	99.868	<a href="#">100.000</a>	1	<a href="#">L475M</a> <a href="#">show in structure</a>

Right-click here to save/download **detailed mutation report** table for archiving or import to Excel (Tab-separated, one mutation per line)Right-click here to save/download **query summary report** table for archiving or import to Excel (Comma-separated, one query per line)Right-click here to save/download **query clade report** table for archiving or import to Excel (Tab-separated, one query per line)

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	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	Reference	Query	% AA identity	% length cove	HA vacc.	eff.	total # mutat	Mutation	Interestlevel	Subtype mark	# global occ	# country occ	Prev. reporte	Multiple posit	Structural int	Effect on glycosylation
2	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	V7A	0	-	0	0	-	-	-	-
3	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	V36I	1	-	0	0	-	-	viral oligomer	
4	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	N111D	0	-	0	0	host specificit	-	viral oligomer	
5	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	A233T	1	-	0	0	-	-	viral oligomer	
6	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	R240Q	0	-	0	0	host specificit	host specificit	host cell rece	-
7	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	E422D	1	-	0	0	-	-	viral oligomer	
8	HA_H1N1_HtA/Victoria/30		98.763	100	-		566	I435V	1	-	0	0	-	-	viral oligomer	
9	M1_H1N1_HtA/Victoria/30		100	100	-		252	no mutations	0	-	-	-	-	-	-	-
10	M2_H1N1_HtA/Victoria/30		95.652	94.845	-		92	E6K	0	-	0	0	-	-	-	-
11	M2_H1N1_HtA/Victoria/30		95.652	94.845	-		92	V7I	2	-	0	0	host specificit	-	-	-
12	M2_H1N1_HtA/Victoria/30		95.652	94.845	-		92	E8Y	0	-	0	0	-	-	-	-
13	M2_H1N1_HtA/Victoria/30		95.652	94.845	-		92	T9R	0	-	0	0	-	-	-	-
14	NA_H1N1_HtA/Victoria/30		99.359	99.787	-		468	S200N	2	-	0	0	antigenic drift	antigenic drift	binding small	-
15	NA_H1N1_HtA/Victoria/30		99.359	99.787	-		468	H275Y	3	-	0	0	strong drug r	strong drug r	drug binding	-
16	NA_H1N1_HtA/Victoria/30		99.359	99.787	-		468	N434S	1	-	0	0	-	-	viral oligomer	
17	NP_H1N1_HtA/Victoria/30		98.795	100	-		498	E14D	0	-	121	4	-	-	-	-
18	NP_H1N1_HtA/Victoria/30		98.795	100	-		498	T22A	0	-	236	12	-	-	-	-
19	NP_H1N1_HtA/Victoria/30		98.795	100	-		498	I33V	0	-	13	1	host specificit	-	-	-
20	NP_H1N1_HtA/Victoria/30		98.795	100	-		498	I136L	0	-	8	2	-	-	-	-
21	NP_H1N1_HtA/Victoria/30		98.795	100	-		498	V217I	1	-	46	5	-	-	viral oligomer	
22	NP_H1N1_HtA/Victoria/30		98.795	100	-		498	V425I	1	-	1042	18	-	-	viral oligomer	
23	NS1_H1N1_HtA/Victoria/30		99.543	100	-		219	V84I	1	-	0	0	-	-	viral oligomer	
24	NS2_H1N1_HtA/Victoria/30		100	93.388	-		113	no mutations	0	-	-	-	-	-	-	-
25	PA_H1N1_HtA/Victoria/30		98.883	100	-		716	I30V	1	-	0	0	-	-	viral oligomer	
26	PA_H1N1_HtA/Victoria/30		98.883	100	-		716	L63I	1	-	0	0	-	-	viral oligomer	
27	PA_H1N1_HtA/Victoria/30		98.883	100	-		716	I226L	1	-	0	0	-	-	a T-cell epitop	-
28	PA_H1N1_HtA/Victoria/30		98.883	100	-		716	P269K	0	-	0	0	-	-	-	-

# Thank you !

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