

# Influenza Surveillance Report

[www.infectiousdisease.dhh.la.gov](http://www.infectiousdisease.dhh.la.gov)

Week 49: 12/3/17-12/9/17

**Influenza activity remains high in Louisiana. The majority of positive influenza specimens from the state public health laboratory are influenza A/H3. The most commonly reported other respiratory viruses are RSV and Rhino/Enterovirus.**

**The Influenza Surveillance Summary Report describes the results of the tracking done by the Louisiana Office of Public Health Infectious Disease Epidemiology Section (IDEpi). This report relies on data supplied by sentinel surveillance sites, including hospital emergency departments (ED), laboratories and physicians' offices. Sentinel sites provide weekly data on Influenza Like Illness (ILI) and/or laboratory confirmed cases.**

Taken together, ILI surveillance and laboratory surveillance provide a clear picture of the influenza activity occurring in Louisiana each week. If you have any questions about our surveillance system or would like more information, please contact Julie Hand at 504-568-8298 or [julie.hand@la.gov](mailto:julie.hand@la.gov).

**ILI** is defined as an illness characterized by cough and/or cold symptoms and a fever of 100° F or greater in the absence of a known cause. While not every case of ILI is a case of influenza, the CDC has found that trends in ILI from sentinel sites are a good proxy measure of the amount of influenza activity in an area. For this reason, all states and territories participating in the national surveillance program monitor weekly ILI ratios from their sentinel surveillance sites.

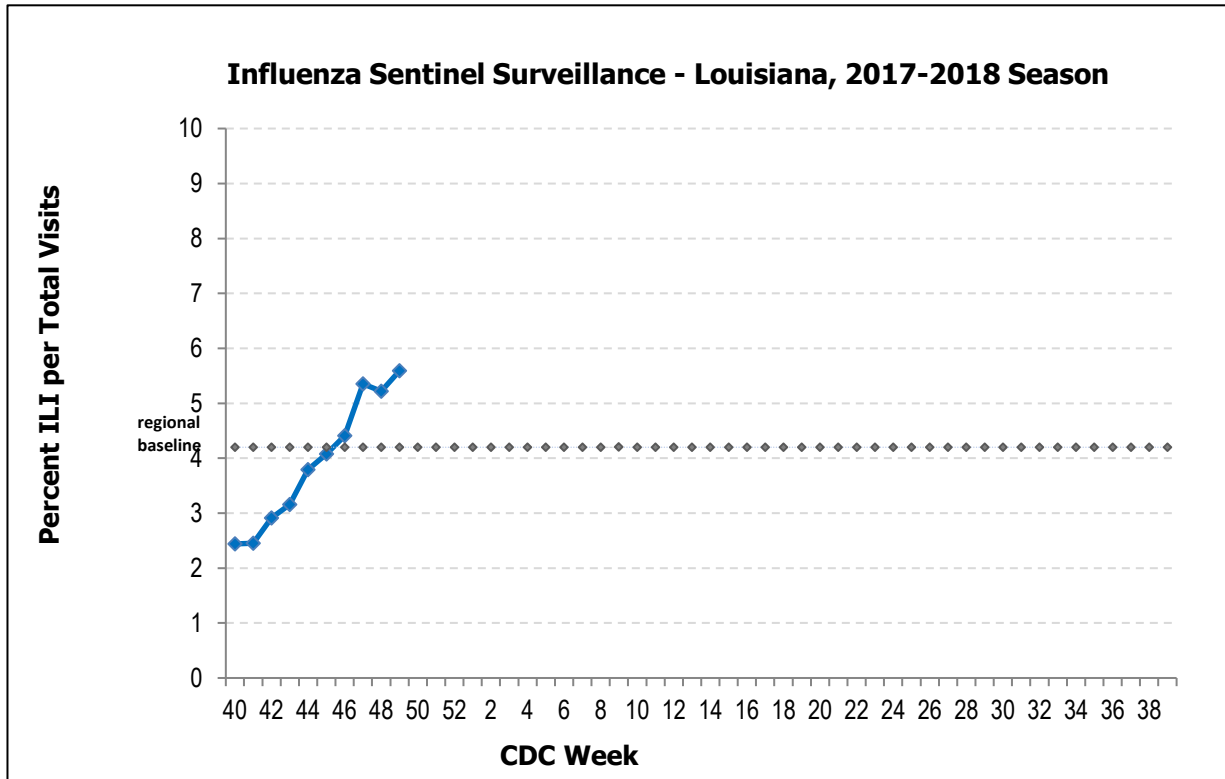


**Laboratory testing:** Not all sentinel sites have access to laboratory testing. However, many hospitals and physicians' offices do perform some influenza testing. Sites that test for influenza report the number of positive tests each week and the total number of tests performed each week. This information is included on page 3 of this report.

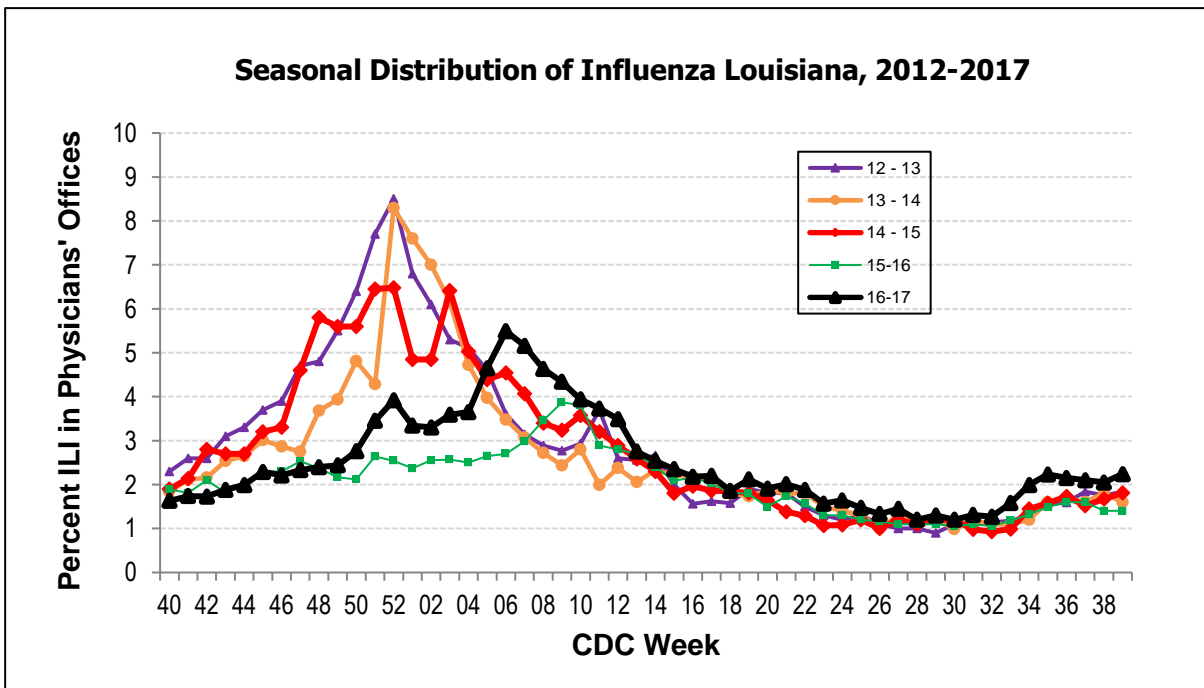
Page 2 : ILI Activity  
Page 3: Virologic Surveillance  
Page 4: Geographic Distribution  
Page 5 & 6: Regional & National Data

## 2017-2018 Season

This graph shows the percentage of visits for ILI over the total number of visits for sentinel surveillance sites. This is the best approach to estimate the magnitude of influenza transmission. ILI counts do include some viral infections other than influenza, but experience over the last 50 years has shown that this approach is a reliable method to estimate influenza transmission. It does not show which strain of influenza virus is responsible. The page on lab surveillance does show the proportion of specimens attributable to each virus strain.

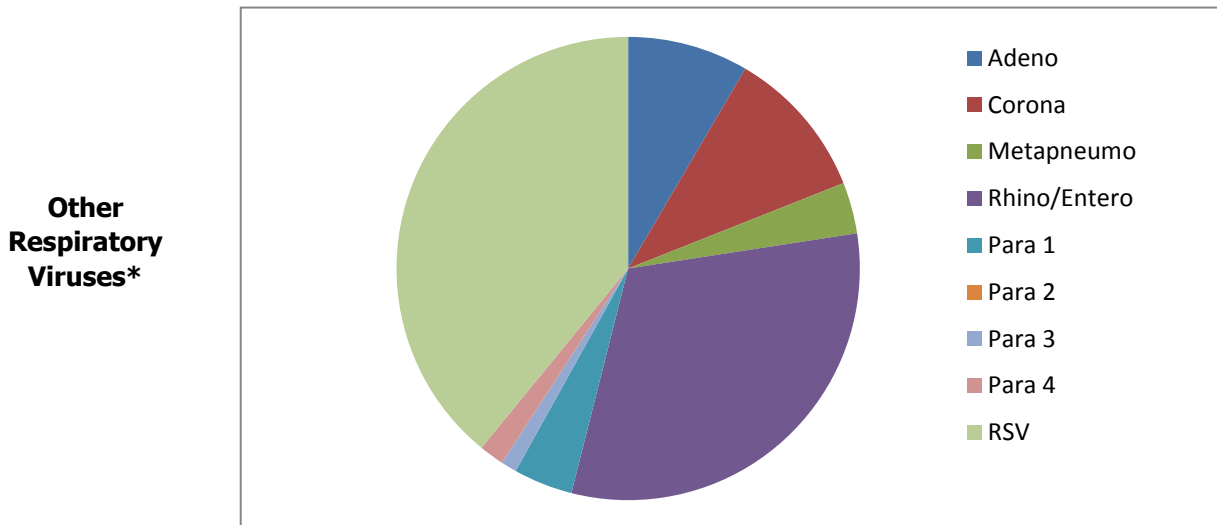
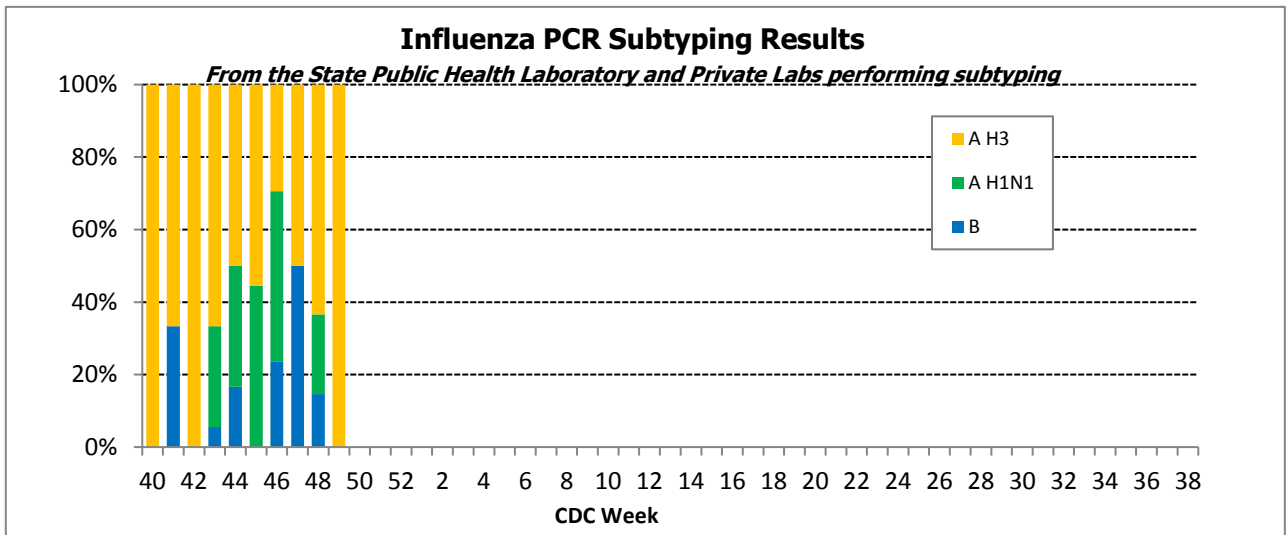
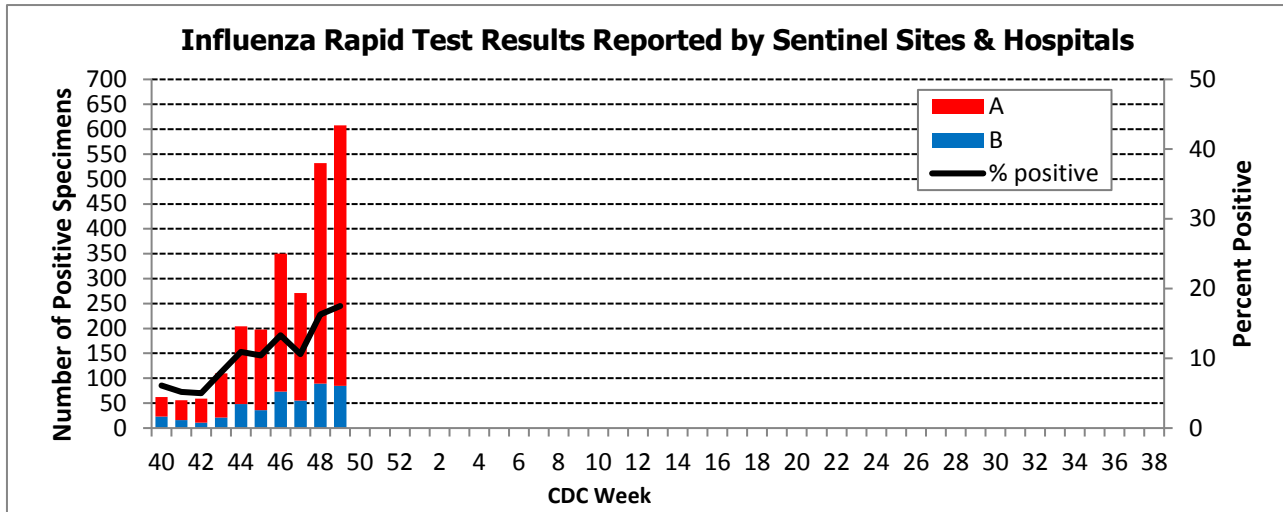


This graph shows the data on ILI surveillance among sentinel physicians' over the past 5 seasons to enable comparisons with previous years and better estimate the amplitude of this season's influenza transmission.



# 2017-2018 Season

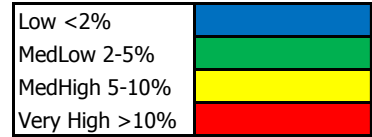
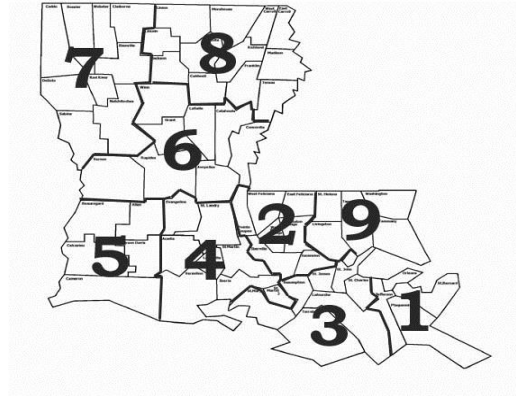
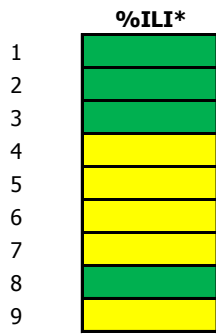
## Virologic Surveillance



\*Based on results from the State Public Health Laboratory Respiratory Virus Panel (RVP) Testing and other labs reporting RVP results over the last 4 weeks.

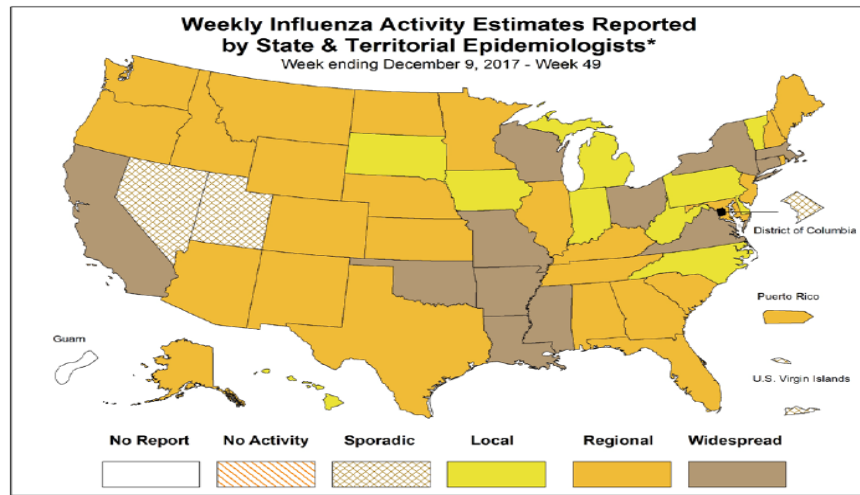
# 2017-2018 Season

## Geographical Distribution of ILI



\* %ILI over the last 4 weeks based on sentinel surveillance data

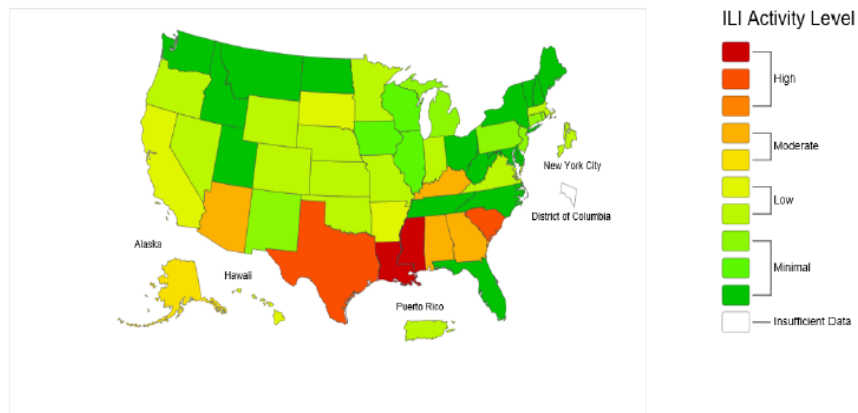
## Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists



\* This map indicates geographic spread & does not measure the severity of influenza activity

## Influenza-Like Illness (ILI) Activity Level Indicator Determined by Data Reported to ILINet 2017-18 Influenza Season Week 49 ending Dec 09, 2017

## ILINet Activity Indicator Map



## 2017-2018 Season

### National Surveillance

During week 49, overall influenza activity increased in the United States.

The proportion of deaths attributed to pneumonia and influenza (P&I) was below the system-specific epidemic threshold.

One influenza-associated pediatric deaths were reported.

The proportion of outpatient visits for influenza-like illness (ILI) was 2.7%, which is above the national baseline of 2.2%.

### Clinical Laboratory Data

	Week 49	Data Cumulative since October 1, 2017 (Week 40)
<b>No. of specimens tested</b>	19,326	195,339
<b>No. of positive specimens (%)</b>	1,633 (8.4%)	9,446 (4.8%)
<b>Positive specimens by type</b>		
<b>Influenza A</b>	1,343 (82.2%)	7,218 (76.4%)
<b>Influenza B</b>	290 (17.8%)	2,228 (23.6%)

### Public Health Laboratory Data

	Week 49	Data Cumulative since October 1, 2017 (Week 40)
<b>No. of specimens tested</b>	1,411	13,393
<b>No. of positive specimens*</b>	562	3,711
<b>Positive specimens by type/subtype</b>		
<b>Influenza A</b>	500 (89.0%)	3,228 (87.0%)
(H1N1)pdm09	26 (5.2%)	276 (8.6%)
H3N2	464 (92.8%)	2,916 (90.3%)
Subtyping not performed	10 (2.0%)	36 (1.1%)
<b>Influenza B</b>	62 (11.0%)	483 (13.0%)
Yamagata lineage	34 (54.8%)	318 (65.8%)
Victoria lineage	1 (1.6%)	22 (4.6%)
Lineage not performed	27 (43.5%)	143 (29.6%)

### HHS Surveillance Region Data:

**U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet) 2017-2018 Influenza Season**  
**HHS Region 6 (AR, LA, NM, OK, and TX) (Baseline: 4.2%) Data as of Friday, December 15, 2017**

CDC Week	# Sites Reporting	ILI 0-4 years	ILI 5-24 years	ILI 25-49 years	ILI 50-64 years	ILI 65 years and older	Total ILI	Total Patient Visits	% Unweighted ILI	% Weighted ILI
201746	277	1298	1563	915	374	259	4409	127901	3.4	4.0
201747	272	1333	1097	853	353	257	3893	93996	4.1	4.2
201748	276	1351	1477	1324	526	394	5072	117829	4.3	4.7
201749	254	1206	1547	1119	473	312	4657	99894	4.7	5.3

### Region 6 (AR, LA, NM, OK, TX)

CDC Week	Public Health Labs	Public Health Specimens Tested	AUNK_POS	AH1N1 pdm09	AH3N2	AH3N2v	B	BvC	BYam	Clinical Labs	Clinical Specimens Tested	Clinical Flu Positive	% Positive	A	B
201746	9	185	0	22	34	0	6	1	5	25	4194	351	8.37	264	87
201747	8	70	0	12	19	0	1	0	3	25	3967	356	8.97	286	70
201748	8	196	0	14	63	0	6	0	4	23	4133	428	10.36	346	82
201749	8	64	0	6	15	0	4	0	2	19	2632	398	15.12	349	49

## 2017-2018 Season

### Antiviral Resistance:

Neuraminidase Inhibitor Resistance Testing Results on Samples Collected  
Since October 1, 2017

	Oseltamivir		Zanamivir		Peramivir	
	Virus Samples tested (n)	Resistant Viruses, Number (%)	Virus Samples tested (n)	Resistant Viruses, Number (%)	Virus Samples tested (n)	Resistant Viruses, Number (%)
Influenza A (H1N1)pdm09	58	0 (0.0)	50	0 (0.0)	58	0 (0.0)
Influenza A (H3N2)	314	0 (0.0)	314	0 (0.0)	236	0 (0.0)
Influenza B	61	0 (0.0)	61	0 (0.0)	61	0 (0.0)

### Antigenic & Genetic Characterization:

CDC has antigenically or genetically characterized 400 influenza viruses collected during October 1 – December 9, 2017, and submitted by U.S. laboratories, including 58 influenza A(H1N1)pdm09 viruses, 256 influenza A(H3N2) viruses, and 86 influenza B viruses.

#### Influenza A Viruses

- A(H1N1)pdm09:** Phylogenetic analysis of the HA genes from 58 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. 41 A(H1N1)pdm09 viruses were antigenically characterized, and all were antigenically similar (analyzed using HI with ferret antisera) to the reference 6B.1 virus A/Michigan/45/2015, representing the recommended influenza A(H1N1)pdm09 reference virus for the 2017–18 Northern Hemisphere influenza vaccines.
- A(H3N2):** Phylogenetic analysis of the HA genes from 256 A(H3N2) viruses revealed extensive genetic diversity with multiple clades/subclades co-circulating. The HA genes of circulating viruses belonged to clade 3C.2a (n=198), subclade 3C.2a1 (n=56) or clade 3C.3a (n=2). 68 influenza A(H3N2) viruses were antigenically characterized, and 67 (98.5%) A(H3N2) viruses tested were well-inhibited (reacting at titers that were within fourfold of the homologous virus titer) by ferret antisera raised against A/Michigan/15/2014 (3C.2a), a cell propagated A/Hong Kong/4801/2014-like reference virus representing the A(H3N2) component of 2017–18 Northern Hemisphere influenza vaccines.

#### Influenza B Viruses

- B/Victoria:** Phylogenetic analysis of five B/Victoria-lineage viruses indicate that all HA genes belonged to genetic clade V1A, the same genetic clade as the vaccine reference virus, B/Brisbane/60/2008. However, a small number of viruses identified in 2017 had a 6-nucleotide deletion (encoding amino acids 162 and 163) in the HA (abbreviated as V1A-2Del). One (50%) of two B/Victoria lineage viruses were well-inhibited by ferret antisera raised against cell-propagated B/Brisbane/60/2008 reference virus, representing a recommended B virus component of 2017–18 Northern Hemisphere influenza vaccines. One B/Victoria lineage virus reacted poorly (at titers that were 8-fold or greater reduced compared with the homologous virus titer) with ferret antisera raised against cell-propagated B/Brisbane/60/2008, and this virus had the two amino acid deletion in the HA of the V1A-2Del viruses.
- B/Yamagata:** Phylogenetic analysis of 81 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 57 influenza B/Yamagata-lineage viruses were antigenically characterized, and all were antigenically similar to cell propagated B/Phuket/3073/2013, the reference vaccine virus representing the influenza B/Yamagata-lineage component of the 2017–18 Northern Hemisphere quadrivalent vaccines.