Table S1. Avian influenza viruses (excluding H7N9) isolated during the surveillance between February 2017 and January 2018 (related to Table 1).

Time period	Location	Total number of markets or farms investigated	Number of samples collected	Avian influenza virus								
				H1N1/N2/N3/N8	H3N1/N2/N8	H4N2/N6/N8	H5N1/N2/N3/N6	H6N1/N6/N2/N8	H9N2	H10N3/N8	H11N2/N3/N8/N9	H12N5
Feb. 2017–May. 2017	Market	379	12,504	22 (H1N2=21, H1N8=1)	61 (H3N1=2, H3N2=58, H3N8=1)	11 (H4N2=4, H4N6=1, H4N8=6)	51 (H5N1=3, H5N2=4, H5N6=44)	89 (H6N2=13, H6N6=74, H6N8=2)	215	0	2 (H11N8=1, H11N9=1)	1
	Farm	665	17,697	0	12 (H3N2=9, H3N8=3)	1 (H4N6)	6 (H5N2=1， H5N3=1, H5N6=4)	36 (H6N1=2, H6N2=4, H6N6=25, H6N8=5)	28	1 (H10N8)	1 (H11N2)	0
Oct. 2017–Jan. 2018	Market	204	12,967	21 (H1N1=2, H1N2=6， H1N3=13)	100 (H3N2=93, H3N8=7)	16 (H4N2=5, H4N3=1, H4N6=5, H4N8=5)	222 (H5N1=5, H5N2=1, H5N3=2, H5N6=214)	105 (H6N2=9, H6N6=94, H6N8=2)	404	9 (H10N3=7, H10N8=2)	2 (H11N2=1, H11N3=1)	0
	Farm	374	10,716	0	7 (H3N2)	0	3 (H5N6=3)	6 (H6N2=3, H6N6=3)	20	1 (H10N8)	0	0
Total		1,622	53,884	43	180	28	282	236	667	11	5	1

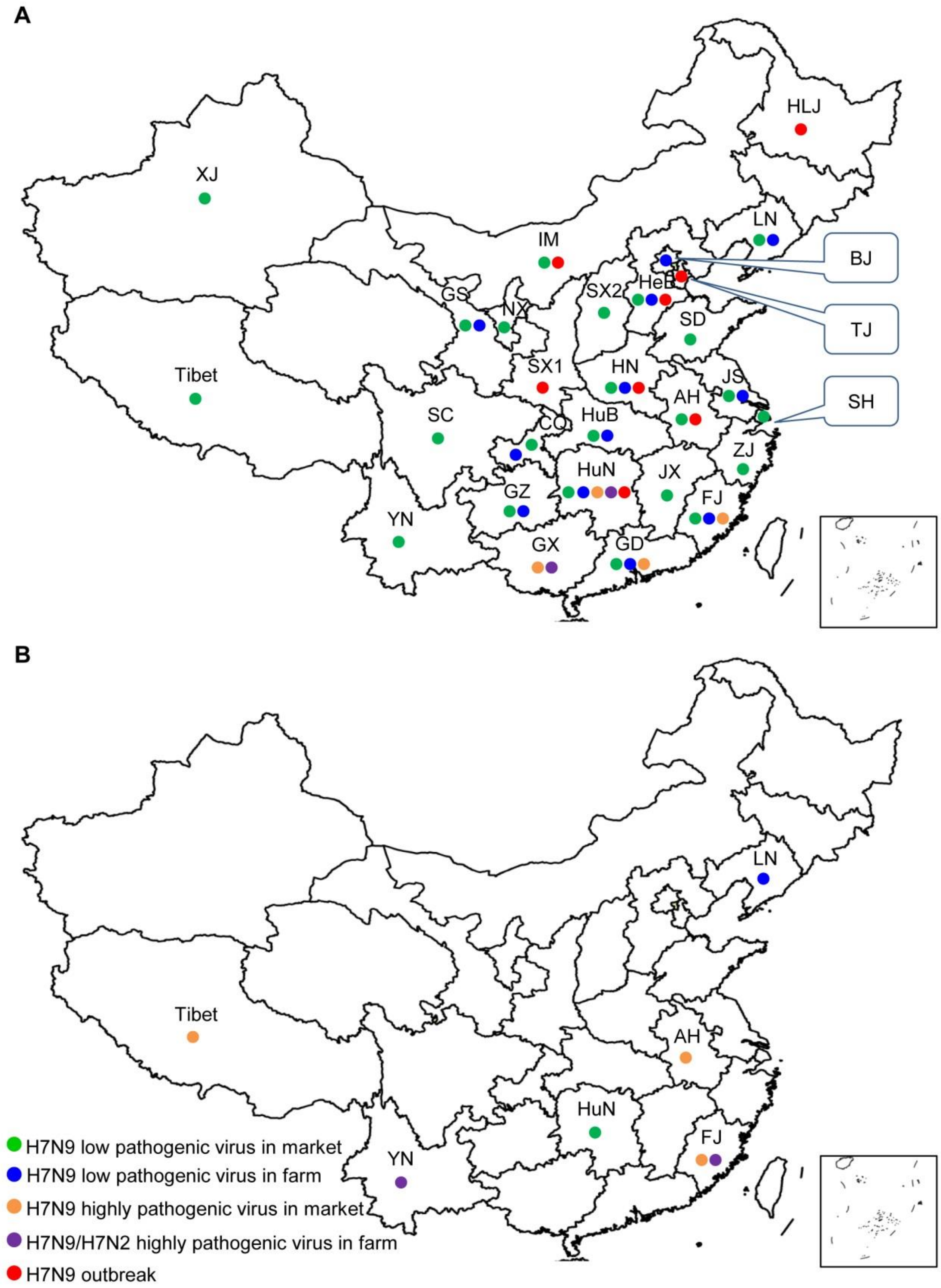

Figure S1. Geographic distribution of the H7N9 viruses detected in this study (related to Table 1). (A) Provinces where the H7N9 viruses were detected in the first round of surveillance and where disease outbreaks occurred. (B) Provinces where the H7N2 and H7N9 viruses were detected in the second surveillance.

Table S2. HA gene of the H7N9 low pathogenic viruses isolated in 2017 and sequenced in this study (related to Figure 1A).

No.	Viruses	Accession number in GenBank
1	A/chicken/Anhui/S2351/2017(H7N9)	MH209256
2	A/chicken/Beijing/SD147/2017(H7N9)	MH209257
3	A/chicken/Chongqing/SD057/2017(H7N9)	MH209258
4	A/chicken/Guangdong/SD004/2017(H7N9)	MH209259
5	A/chicken/Gansu/SD162/2017(H7N9)	MH209260
6	A/chicken/Guizhou/SD106/2017(H7N9)	MH209261
7	A/chicken/Henan/SD181/2017(H7N9)	MH209262
8	A/chicken/Hubei/SD095/2017(H7N9)	MH209263
9	A/chicken/Jiangsu/S10428/2017(H7N9)	MH209264
10	A/chicken/Ningxia/S1215/2017(H7N9)	MH209265
11	A/chicken/Sichuan/S1267/2017(H7N9)	MH209266
12	A/chicken/Shandong/S1174/2017(H7N9)	MH209267
13	A/chicken/Shanxi/SD179/2017(H7N9)	MH209268
14	A/chicken/Tibet/SD143/2017(H7N9)	MH209269
15	A/chicken/Zhejiang/SD036/2017(H7N9)	MH209270
16	A/chicken/Fujian/SD180/2017(H7N9)	MH209271
17	A/chicken/Hebei/SD167/2017(H7N9)	MH209272
18	A/duck/Fujian/S10998/2017(H7N9)	MH209273
19	A/duck/Hunan/S2760/2017(H7N9)	MH209274
20	A/duck/Jiangsu/S12863/2017(H7N9)	MH209275
21	A/chicken/Hunan/S31330/2017(H7N9)	MH209276
22	A/chicken/Liaoning/SD207/2017(H7N9)	MH209277
23	A/chicken/Xinjiang/SD192/2017(H7N9)	MH209278
24	A/chicken/Yunnan/SD193/2017(H7N9)	MH209279

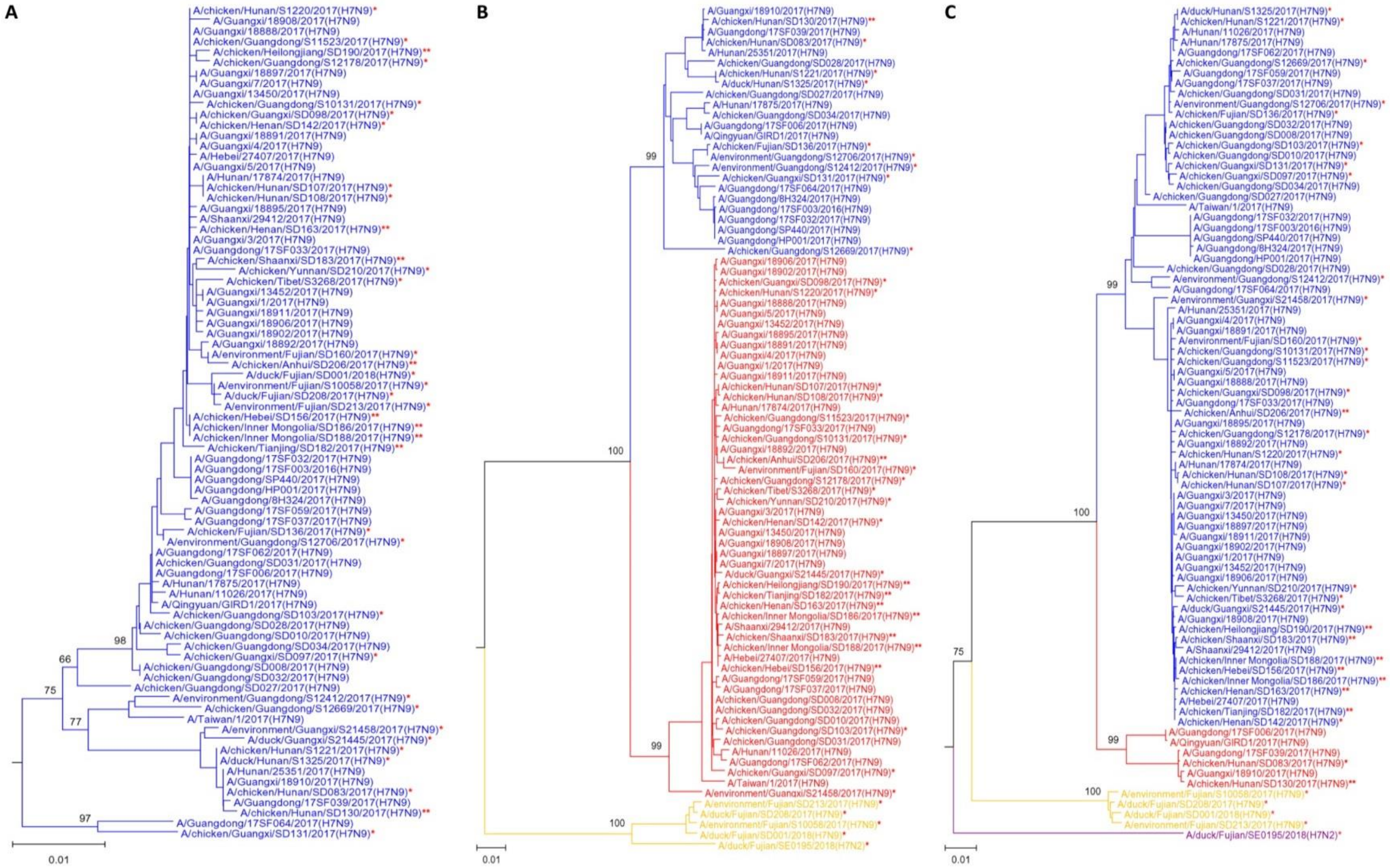

Figure S2. The phylogenetic trees of the NA, PB2, and PB1 of H7N9 highly pathogenic viruses (related to Figure 1). (A) NA, (B) PB2, and (C) PB1. H7N9 highly pathogenic viruses sequenced in this study are labeled with single asterisk or double asterisks; double asterisks denote the viruses that have caused disease outbreaks in poultry farms. The color coding is the same as Figure 1B.

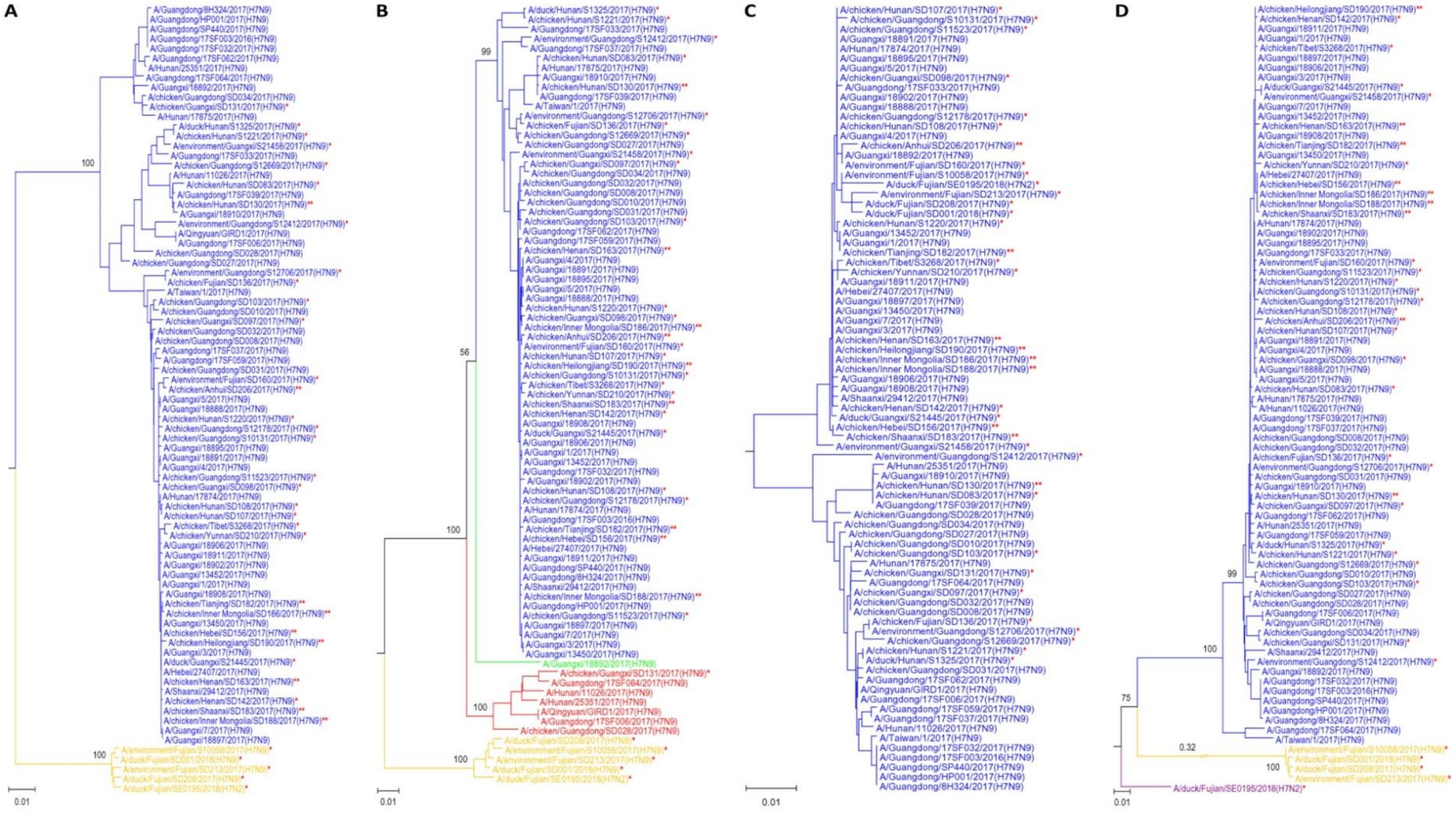

Figure S3. The phylogenetic trees of the PA, NP, M, and NS genes of H7N9 highly pathogenic viruses (related to Figure 1). (A) PA, (B) NP, (C) M, and (D) NS. H7N9 highly pathogenic viruses sequenced in this study are labeled with single asterisk or double asterisks; double asterisks denote the viruses that have caused disease outbreaks in poultry farms. The color coding is the same as Figure 1B.

Table S3. Amplification primers (related to the STAR Methods).

REAGENT or RESOURCE	**SOURCE**	**IDENTIFIER**
Oligonucleotides		
Amplification primers		
H7N9-PB2-F: 5'-AGCRAAAGCAGGTCAAATATATTCAAT-3'	This study	N/A
H7N9-PB2-R: 5'-AGTAGAAACAAGGTCGTTTTAAAACTATT-3'	This study	N/A
H7N9-PB1-F: 5'-AGCAAAAGCAGGCAAACCATT-3'	This study	N/A
H7N9-PB1-R: 5'-AGTAGAAACAAGGCATTTTTTCATG-3'	This study	N/A
H7N9-PA-F: 5'-AGCAAAAGCAGGTACTGATCC-3'	This study	N/A
H7N9-PA-R: 5'-AGTAGAAAGAAGGTACCTTTTTGGA-3'	This study	N/A
H7N9-NP-F: 5'-GCAGGGTAGATAATCACTCAC-3'	This study	N/A
H7N9-NP-R: 5'-AGTAGAAACAAGGGTATTTTTTC-3'	This study	N/A
H7N9-M-F: 5'-AGCAGGTAGATATTGAAAAATGA-3'	This study	N/A
H7N9-M-R: 5'-GTAGAAACAAGGTAGTTTTTTAC-3'	This study	N/A
H7N9-NS-F: 5'-AGCAAAAGCAGGGTGACAAA-3'	This study	N/A
H7N9-NS-R: 5'-AGAAACAAGGGTGTTTTTTA-3'	This study	N/A

Table S4. Sequencing primers (related to the STAR Methods).

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Oligonucleotides		
Portion of the NA gene sequencing primers:		
M13-F: 5'-GTAAAACGACGGCCAGT-3'	Alvarez et al., 2010	N/A
M13-R: 5'-CAGGAAACAGCTATGAC-3'	Alvarez et al., 2010	N/A
H7N9 virus sequencing primers:		
PB2-F279: 5'-TCTGGCTGTGACGTGGTG-3'	This study	N/A
PB2-F652: 5'-CTACCAGTAGCTGGAGGGACA-3'	This study	N/A
PB2-R526: 5'-TTCTGGCTCCAACTTCGT-3'	This study	N/A
PB2-F1234: 5'-GTATTCTCACAAGAGGATTGCATG-3'	This study	N/A
PB2-F1736: 5'-CCTTTCAATCCCTAGTGCC-3'	This study	N/A
PB2-R1872: 5'-GGCTGCTGCAAATGGTAATAG-3'	This study	N/A
PB1-F202: 5'-GAGACTGGAGCACCCCAACT-3'	This study	N/A
PB1-F931: 5'-ACTGGAGACAATACCAAGCGGA-3'	This study	N/A
PB1-R772: 5'-GCTCCTCGCTAATGCTTCTA-3'	This study	N/A
PB1-R1243: 5'-TTGAACATACCCATCATCAT-3'	This study	N/A
PB1-F1613: 5'-ATCTTGGACCAGCGACAGC-3'	This study	N/A
PB1-R1845: 5'-CAATTCCCATTTCAAGCAG-3'	This study	N/A
PA-F259: 5'-GCCTGGACAGTGGTGAATAG-3'	This study	N/A
PA-F876: 5'-TGAGGACCCGAGCCACGA-3'	This study	N/A
PA-R660: 5'-TTTGGTCGGCAAGCCTG-3'	This study	N/A
PA-F1400: 5'-AATGAAGGGAGTGTACATAA-3'	This study	N/A
PA-F1794: 5'-ACAGATTGAAAGCATGATTG-3'	This study	N/A
PA-R2020: 5'-GTTCCAGGTTCCAGGTT-3'	This study	N/A
HA-R697: 5'-TAACTTGTGGTCTCGCTCC-3'	This study	N/A
HA-F507: 5'-GTTCCCGCAGATGACTA-3'	This study	N/A
HA-R1566: 5'-AACCAAAGTATCACATCT-3'	This study	N/A
HA-F1222: 5'-GAATTCAATGAGGTAGAG-3'	This study	N/A
NP-F247: 5'-CTCTCTGCATTTGATGAAAG-3'	This study	N/A
NP-R500: 5'-GGAGAGTTGATCCTTGCAT-3'	This study	N/A
NP-R1370: 5'-AAGACTCCCCGCCCCTGGAA-3'	This study	N/A
NP-F953: 5'-CAAATGAGAACCCAGCACA-3'	This study	N/A
N9-F299: 5'-ATGCAGTAAGAATTGGAGA-3'	This study	N/A
N9-R515: 5'-TACTTGACCACCCAATGC-3'	This study	N/A
N9-F650: 5'-RAAACATACTAAGAACACA-3'	This study	N/A
N9-F1070: 5'-GGCTAGGGAGGACAATAAG-3'	This study	N/A
N2-F332: 5'-TCTGGGTRACAAGAGAAC-3'	This study	N/A
N2-F543: 5'-TGATGGRAAAGCATGGTT-3'	This study	N/A
N2-R730: 5'-ACAAGTYCCATTGATGCA-3'	This study	N/A
N2-F1060: 5'-GGGAATGATGTTTGGATG-3'	This study	N/A
M-F239: 5'-CGAGGACTGCAGCGTAGACG-3'	This study	N/A
M-R462: 5'-ATCTGCTCACAAGTGGCACA-3'	This study	N/A
NS-R595: 5'-TTCTCCAAGCGAATCTC-3'	This study	N/A
NS-F129: 5'-CGGCTTCGCCGAGATCAGAA-3'	This study	N/A
HA Cleavage site sequencing primer:		
HA-F869: 5'-GCTATCATAGTGGAGGGAC-3'	This study	N/A