

Supplementary Table S1 – Primer pairs used in sequencing HA and NA genes

Primer	Sequence(5'→3')	Positions	Size
¹ HA1 Forward	<u>TG</u> TAAAACGACGGCCAGTATACGACTAGCAAAAGCAGGGG	–41 ~ –19	943 bp
¹ HA943 Reverse	CAGGAAACAGCTATGACCGAAAKGGGAGRCTGGTGTTTA	928 ~ 908	
¹ HA736 Forward	<u>TG</u> TAAAACGACGGCCAGTAGRATGRACTATTACTGGAC	727 ~ 746	564 bp
HA1300 Reverse	CCAGGAAACCATCATCAAC	1300 ~ 1282	
¹ HA1204 Forward	<u>TG</u> TAAAACGACGGCCAGTAAGATGAAYACRCARTTCACAG	1202 ~ 1225	574 bp
¹ HA1778 Reverse	<u>CAG</u> GAAACAGCTATGACCGTGTCAGTAGAAACAAGGGTGTTT	1750 ~ 1727	
NA0 Forward	TTAAAATGAATCCAAACCAAAAGA	–5 ~ 19	630 bp
NA630 Reverse	TGTACTTTAACACAGCCACTGCCC	625 ~ 620	
NA536 Forward	GGTCAGCAAGCGCATGYCATGA	536 ~ 557	527 bp
NA1063 Reverse	ACCATTGCCGTATTTGAATGAAAA	1068 ~ 1045	
NA941 Forward	ATAGGATACATATGCAGTGGA	940 ~ 961	511 bp
NA1452 Reverse	AGTAGAAACAAGGAGTTTTT	1438 ~ 1418	

¹Extended from WHO primers (http://www.who.int/csr/resources/publications/swineflu/sequencing_primers/en/index.html) by adding underlined nucleotides.