

Table S1. General sequencing information and statistics

Run	Influenza A H1N1 DNA sample	Fragmentation method	Sequencing platform	Variant1* : Variant2#	Number of reads	Total bases	Length in bp (Mean ± SD)	Quality score (Mean ± SD)	Average depth of coverage
1	NS Segment	Enzymatic Shearing	Ion PGM Sequencer	50 : 50	31,160	1,379,139	44± 30	16± 5	420
2	NS Segment	Enzymatic Shearing	Ion PGM Sequencer	50 : 50	55,806	8,958,397	161± 66	24± 6	2,800
3	NS Segment	Enzymatic Shearing	Ion PGM Sequencer	90 : 10	17,021	743,200	44± 31	16± 5	230
4	NS Segment	Enzymatic Shearing	Ion PGM Sequencer	90 : 10	65,915	12,093,134	183± 68	23± 6	3,770
5	NS Segment	Enzymatic Shearing	Ion PGM Sequencer	75 : 25	36,295	1,674,023	46± 29	16± 5	520
6	NS Segment	Enzymatic Shearing	Ion PGM Sequencer	75 : 25	30,977	5,705,874	184± 66	23± 5	1,780
7	NS Segment	Enzymatic Shearing	Ion PGM Sequencer	25 : 75	56,713	9,898,011	175± 68	23± 6	3,100
8	NS Segment	Enzymatic Shearing	Ion PGM Sequencer	25 : 75	39,973	7,258,889	182± 65	23± 6	2,270
9	NS Segment	Enzymatic Shearing	Ion PGM Sequencer	10 : 90	32,105	5,989,430	187± 66	23± 6	1,870
10	NS Segment	Enzymatic Shearing	Ion PGM Sequencer	10 : 90	27,361	5,205,112	190± 65	23± 6	1,620
11	Whole genome‡	Enzymatic Shearing	Ion PGM Sequencer	N/A	67,699	6,405,499	95± 22	18± 7	470
12	Whole genome	Enzymatic Shearing	Ion PGM Sequencer	N/A	360,161	43,519,129	121± 23	21± 7	3,200
13	Whole genome	Sonication	Ion PGM Sequencer	N/A	378,491	38,897,823	103± 32	21± 7	2,870
14	Whole genome	Nebulization	Roche GS Junior	N/A	8,277	2,757,743	333± 170	31± 7	200

\* Variant1: 173C-435G-575G

# Variant2: 173T-435A-575A

‡ Amplified by 8 gene specific primers