S2 Table. Prevalence of the clade 2.2.1 virus polymerase and NP mutations identified in the database search in this study.

			% of strains with mutation (no. of strains)	
Gene (no. of mutations)	Category of mutation	Mutation	Human viruses[a]	Bird viruses[a]
PB2 (14)	Only in human viruses	Q257L	4.9 (3)	0 (0)
		R299K	4.9 (3)	0 (0)
		N456D	4.9 (3)	0 (0)
		I463M	8.2 (5)	0 (0)
		K617E	4.9 (3)	0 (0)
		T637I	4.9 (3)	0 (0)
		T683I	4.9 (3)	0 (0)
	More prevalent in human viruses than in avian viruses	K80R	68.9 (42)	20.9 (19)
		T129N	67.2 (41)	20.9 (19)
		D195N	8.2 (5)	1.1 (1)
		I292M	59.0 (36)	20.9 (19)
		R389K	9.8 (6)	1.1 (1)
		M473V	13.1 (8)	3.3 (3)
		M570I	72.1 (44)	47.3 (43)
PB1 (13)	Only in human viruses	K54R	4.9 (3)	0 (0)
		D175N	4.9 (3)	0 (0)
		K198R	23.0 (14)	0 (0)
		A374T	9.8 (6)	0 (0)
		M616R	11.5 (7)	0 (0)
		E618D	8.2 (5)	0 (0)
		P627L	11.5 (7)	0 (0)
		N642K	11.5 (7)	0 (0)
		P756S	9.8 (6)	0 (0)
	More prevalent in human viruses than in avian viruses	T182I	85.2 (52)	28.2 (22)
		K214R	85.2 (52)	28.2 (22)
		L384S	65.5 (40)	24.4 (19)
		K386R	6.6 (4)	1.3 (1)
PA (17)	Only in human viruses	D55N	8.2 (5)	0 (0)
		N321I	4.9 (3)	0 (0)
		E327K	6.6 (4)	0 (0)
		V341L	4.9 (3)	0 (0)
		E382D	6.6 (4)	0 (0)
		T608S	4.9 (3)	0 (0)
		E629H	9.8 (6)	0 (0)
		G631C	11.5 (7)	0 (0)
		L641P	11.5 (7)	0 (0)
		S644F	8.2 (5)	0 (0)
		L649I	4.9 (3)	0 (0)
		A669V	11.5 (7)	0 (0)
		F681L	9.8 (6)	0 (0)
	More prevalent in human viruses than in avian viruses	N321S	80.3 (49)	29.5 (23)
		S400T	57.4 (35)	25.6 (20)
		K615R	60.7 (37)	24.4 (19)
		K716N	67.2 (41)	28.2 (22)
NP (2)	More prevalent in human viruses than in avian viruses	G287S	73.8 (45)	24.7 (20)
		T371M	16.4 (10)	2.5 (2)

[a] For human viruses there were 61 PB2, PB1, PA and NP sequences, and for avian viruses there were 91 PB2, 78 PB1, 78 PA and 81 NP sequences.