

Supplementary information

Table S1. Summary of GS144 and GS148 Potential glycosylation site

Segments	Amino acid position	Virus	
		GS144	GS148
	Stalk		
HA1	26	NNST	NNST
	27	NSTE	NSTE
	39	NVTV	NVTV
	181	NNTN	NNTN
	302	NSSM	NSSM
HA2	500	NGTY	NGTY
	559	NGSL	NGSL
NA	59	NITN	NITN
	146	NGTI	NGTI
	190	NASA	NASA
	391	NWSG	NWSG
	402	NWSG	NWSG

^a For an asparagine (N) to be glycosylated, it requires the context of the amino acid pattern N(X)S/T, where X can be any amino acid (X cannot be Proline), followed by a Serine (S) or Threonine (T).

Table S2. Amino-acid differences between AIVs GS144 and GS148

Gene	Amino acid position	GS144	GS148
PB2	81	T	I
	109	V	I
	117	P	T
	125	L	V
	409	R	C
	490	K	N
	590	W	G
PB1	178	I	V
HA (H5 - numbering)	179	I	T
	190	M	V
	209	P	S
	242	T	A
	243	N	T
	257	Y	F
	386	E	Q
NP	50	S	G
	61	I	M
	84	N	S
	408	I	V
NA (N6 - numbering)	27	T	A
	76	M	V
	137	S	G
	174	V	I
	387	T	A
M	261	Y	H
NS1	100	I	L

Table S3. Summary of signature amino acid Mutations in GS144 and GS148

Virus	Segment	Summary of Amino acid residues Mutation							
		PB1	HA(H5)	NP			M1		NS1
		L13P	D190E	M61I	S319N	L479F	N30D	T215A	D92E
GS144		P	E	I	N	F	D	A	E
GS148		P	E	M	N	F	D	A	E

^a Amino acids sites HA segment was located by taking A/goose/Guangdong/1/1996 (H5N1)