

Supplementary Table S2 Molecular characterization of influenza strains based on amino acid sequences.

Virus Name	HA ^a									NA ^b		PB2					PB1-F2	M2	NS1	
	Cleavage Site	158	193	222	224	226	227	228	318	274	292	158	271	591	627	701	66S	31	Deletion ^c	C-terminal
En/W149(H5N1)	GERRRKKR/GLF	N	K	K	N	Q	S	G	T	H	R	E	T	Q	K	D	N	S	YES	ESKV
Dk/k1203/10(H5N8)	REKRR_KR/GLF	N	N	Q	N	Q	R	G	T	H	R	E	T	Q	E	D	S	N	YES	EPEV
En/W401(H5N1)	RERRR_KR/GLF	D	R	K	N	Q	S	G	T	H	R	E	T	Q	E	D	N	S	YES	ESEV
Dk/1111(H5N2)	REKRR_KR/GLF	N	N	Q	N	Q	R	G	T	H	R	E	T	Q	E	D	S	N	NO	ESEV
Dk1-15(H4N2)	PEKA__SR/GLF	D	N	W	R	Q	S	G	T	H	R	E	T	Q	E	D	S	N	NO	ESEV
MDk/W452(H5N8)	REKRR_KR/GLF	N	N	Q	N	Q	R	G	T	H	R	E	T	Q	E	D	S	N	NO	ESEVRGNKMAD
BDk/Gochang1(H5N8)	REKRR_KR/GLF	N	N	Q	N	Q	R	G	T	H	R	E	T	Q	E	D	No	N	NO	ESEV
BTI/Donglim3/14(H5N8)	REKRR_KR/GLF	N	N	Q	N	Q	R	G	T	H	R	E	T	Q	E	D	S	N	NO	ESEVRGNKMAD

Deduced amino sequences were used to compare and examine known virulence markers and pathogenicity determinants.

^aH3 numbering.

^bN2 numbering.

^cPresence or absence of deletion at positions 80-84.