

Identification, Genetic Analysis and Pathogenicity of Classical Swine H1N1 and Human-Swine Reassortant H1N1 Influenza Viruses from Pigs in China

Yafen Song¹, Yong Zhang¹, Bing Zhang¹, Ling Chen¹, Min Zhang¹, Jingwen Wang¹, Ying Jiang¹, Chenghuai Yang¹, Taozhen Jiang^{1*}

¹ China Institute of Veterinary Drug Control, Beijing 100081, China

* Taozhen Jiang is the Corresponding author:

Dr. Taozhen Jiang, China Institute of Veterinary Drug Control, 8 Nandajie, Zhongguancun, Haidian District, Beijing, 100081, China.

Tel: (+86) 010-62103518; Fax: (+86) 010-61255380; E-mail:

taozhen_jiang@163.com

Table S1. The nucleotide homology between the AV1522 virus and the A/swine/Hubei/02/2008(H1N1) virus, when analyzing each gene fragment.

virus	gene	virus with similarity	Homology (%)
A/swine/Shandong/AV1522/2011(H1N1)	HA	A/swine/Hubei/02/2008(H1N1)	99.5
	NA	A/swine/Hubei/02/2008(H1N1)	100
	PB2	A/swine/Hubei/02/2008(H1N1)	99.7
	PB1	A/swine/Hubei/02/2008(H1N1)	99.9
	PA	A/swine/Hubei/02/2008(H1N1)	99.6
	NP	A/swine/Hubei/02/2008(H1N1)	99.5
	M	A/swine/Hubei/02/2008(H1N1)	99.9
	NS	A/swine/Hubei/02/2008(H1N1)	100

Figure S1. Phylogenetic analysis of the NA(A), PB2 (B), PB1 (C), PA (D), NP (E), M (F), and NS (G)genes. The trees were constructed by using the neighbor-joining method with the Maximum Composite Likelihood model and MEGA version 4.0 with 1,000 bootstrap replicates. Our viruses were indicated by triangle marker “▲”.

Figure S1A



Figure S1B

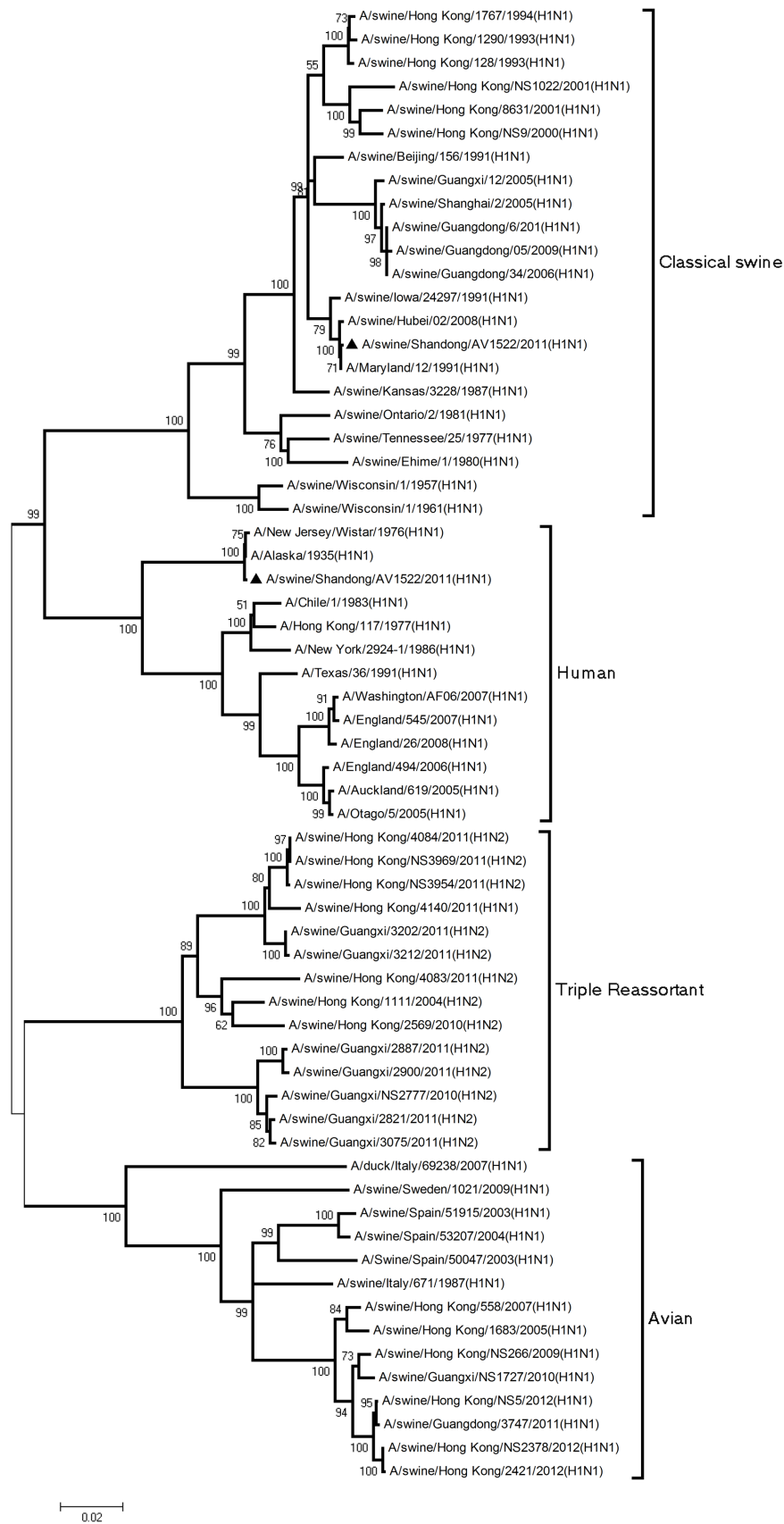


Figure S1C

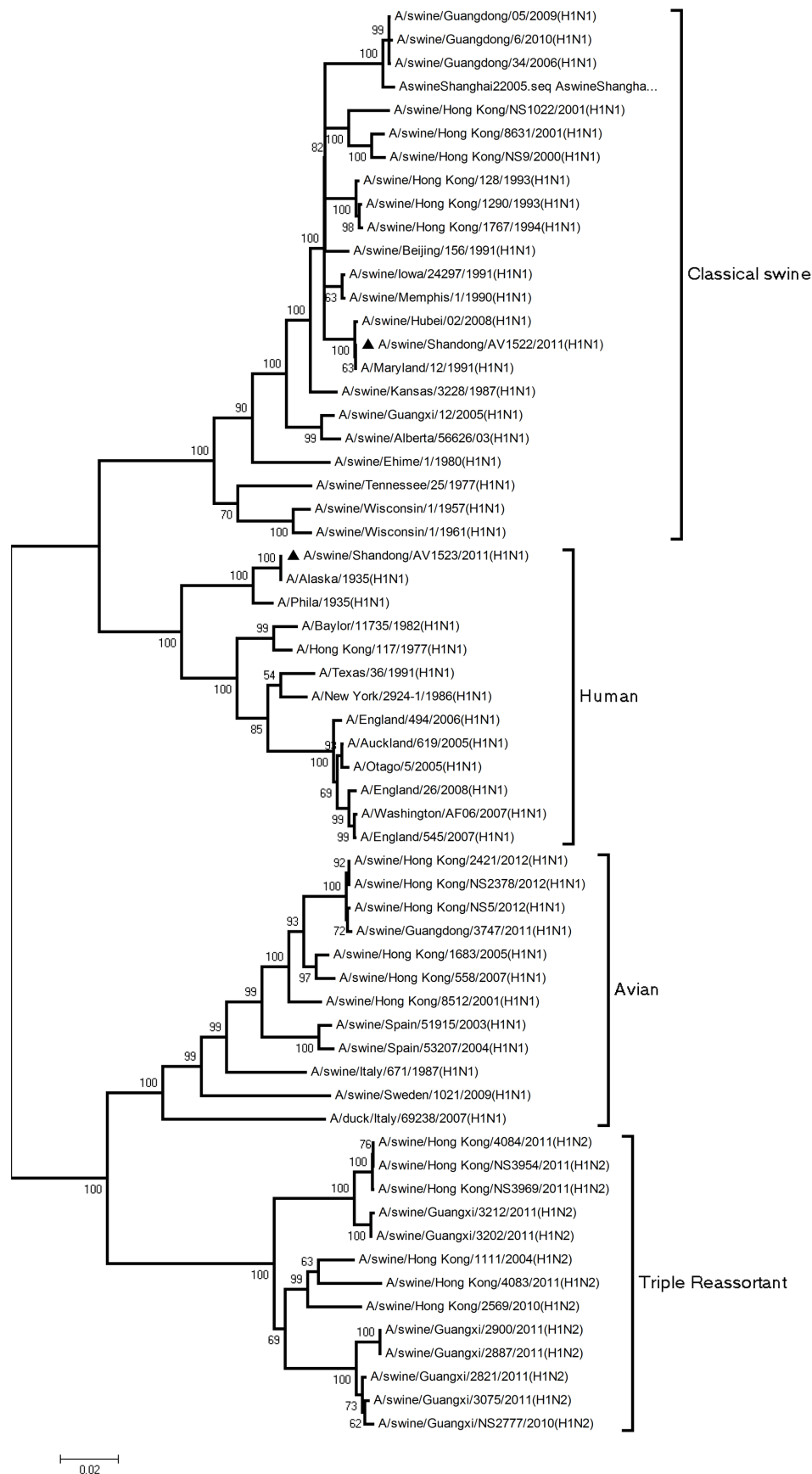


Figure S1D

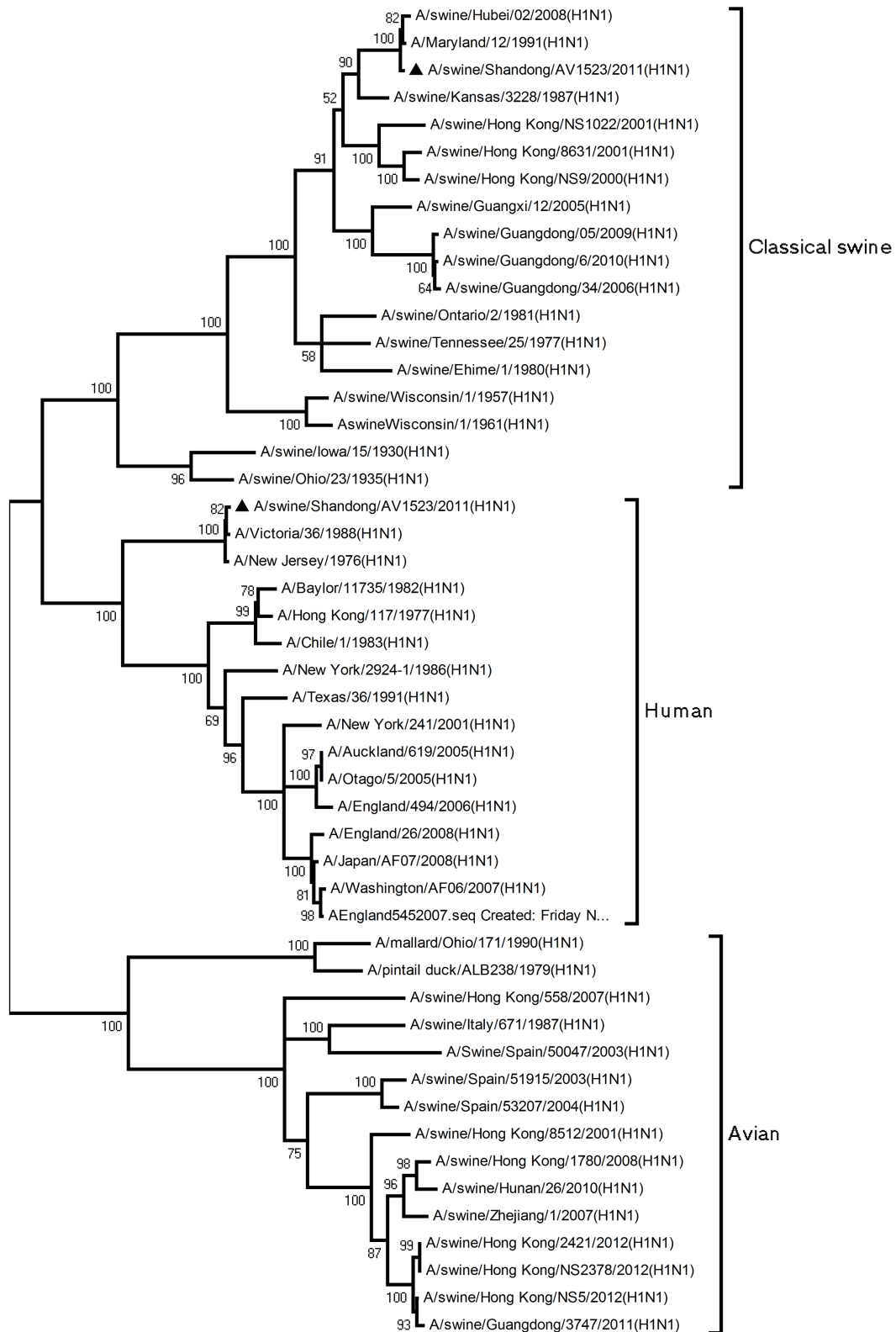


Figure S1E

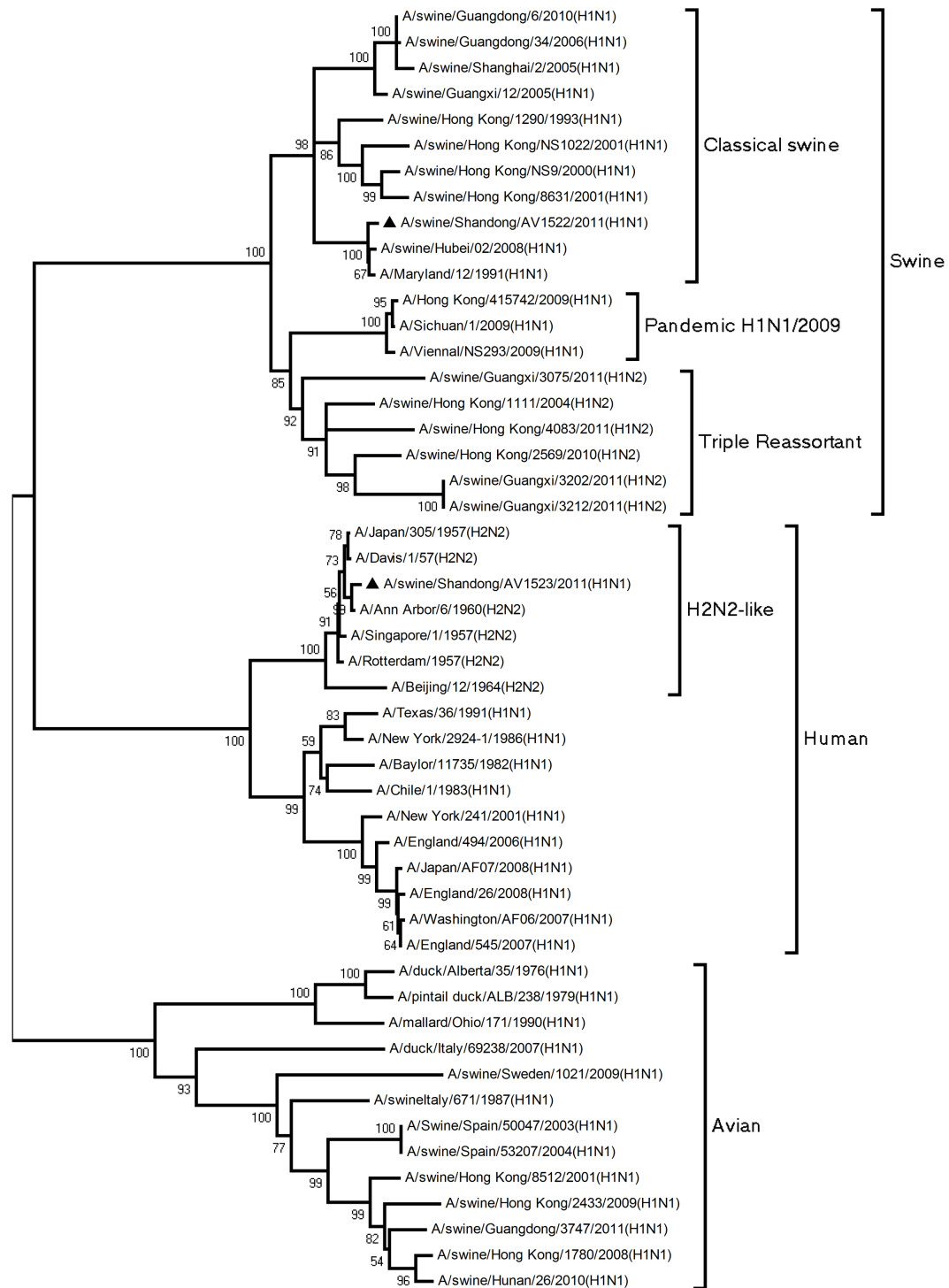


Figure S1F

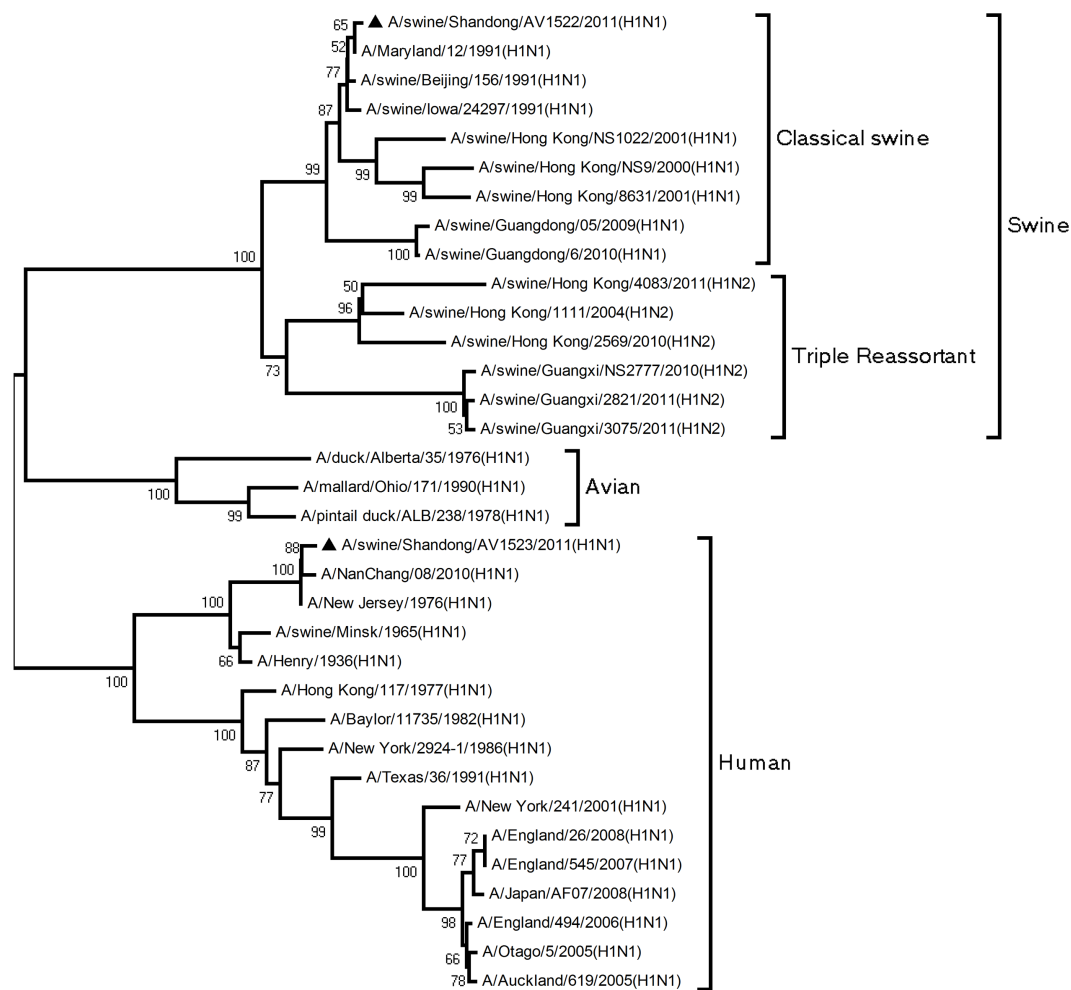


Figure S1G

