

Natural Reassortment of Eurasian Avian-like Swine H1N1 and Avian H9N2 Influenza Viruses in Pigs, China

Appendix

Appendix Table. Viral sequences used in this study

Segment	Strain name	Accession number
PB2	A/swine/Fujian/204/2007	FJ536816
PB2	A/swine/Wisconsin/30954/1976	CY036806
PB2	A/swine/Shanghai/2/2005	FJ789824
PB2	A/swine/Hong Kong/915/2004	GQ229273
PB2	A/swine/Hong Kong/78/2003	GQ229313
PB2	A/swine/Hong Kong/1562/2005	GQ229337
PB2	A/swine/Hong Kong/1110/2006	GQ229377
PB2	A/swine/Hong Kong/1435/2009	CY061650
PB2	A/swine/Hong Kong/NS1583/2009	CY061722
PB2	A/swine/Hong Kong/2299/2009	CY061730
PB2	A/swine/Hong Kong/2314/2009	CY061738
PB2	A/swine/Hong Kong/NS1809/2009	CY061746
PB2	A/swine/Hong Kong/NS1810/2009	CY061754
PB2	A/swine/Hong Kong/2885/2009	CY061762
PB2	A/swine/Hong Kong/2886/2009	CY061770
PB2	A/swine/Hong Kong/2974/2009	CY061786
PB2	A/swine/Hong Kong/189/2010	CY061802
PB2	A/swine/Hong Kong/1795/1994	CY085102
PB2	A/swine/Hong Kong/8278/2001	CY085371
PB2	A/swine/Hong Kong/227/2002	CY085491
PB2	A/swine/Hong Kong/1248/2002	CY085523
PB2	A/swine/Hong Kong/1578/2003	CY085603
PB2	A/swine/Hong Kong/1111/2004	CY085659
PB2	A/swine/Hong Kong/729/2005	CY085731
PB2	A/swine/Hong Kong/72/2007	CY085811
PB2	A/swine/Hong Kong/NS252/2009	CY085995
PB2	A/swine/Guangdong/1605/2010	JN375017
PB2	A/swine/Guangdong/1623/2010	JN375023
PB2	A/swine/Shaanxi/s2/2012	JX963608
PB2	A/Jiangsu/1/2011	KF057091
PB2	A/swine/Guangdong/109/2013	KP404209
PB2	A/swine/Hunan/30/2013	KP404289
PB2	A/swine/Hong Kong/299/1993	CY084982
PB2	A/swine/Hong Kong/1223/1993	CY085054
PB2	A/swine/Hebei/0116/2017	MN416337
PB2	A/swine/Henan/SN13/2018	MN416362
PB2	A/swine/Jiangsu/J004/2018	MN416364
PB2	A/swine/Shandong/1207/2016	MN416383
PB1	A/Chicken/Hong Kong/G9/97	AF156416
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PB1	A/Duck/Hong Kong/Y280/97	AF156419
PB1	A/Quail/Hong Kong/G1/97	AF156421
PB1	A/Chicken/Hong Kong/739/94	AF156422
PB1	A/Chicken/Beijing/1/94	AF156423
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PB1*	A/Jiangxi/1/2013	EPI_ISL_174265

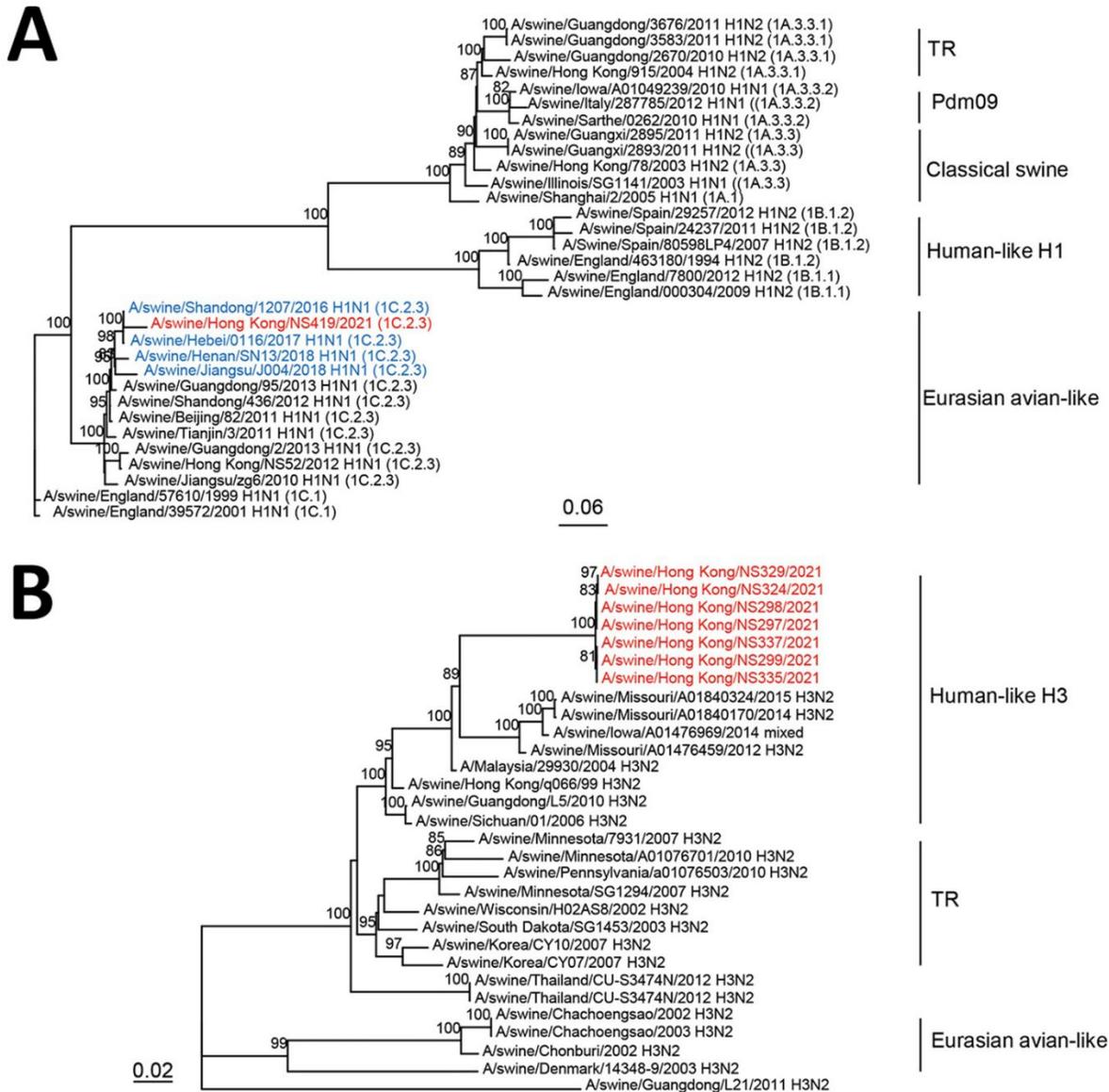
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PB1	A/swine/Hong Kong/1435/2009	CY061651
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PB1	A/swine/Guangxi/9/2007	CY075044
PB1	A/Jiangsu/1/2011	KF057098
PB1	A/chicken/Hong Kong/YU214/2010	KF260616
PB1	A/Jiangxi/IPB13/2013	KJ406535
PB1	A/swine/Tianjin/42/2011	KP404402
PB1	A/chicken/Ningbo/2929/2013	KP415347
PB1	A/Guangdong/W1/2004	KX867847
PB1	A/swine/Hebei/0116/2017	MN416424
PB1	A/swine/Hebei/T37/2013	MN416433
PB1	A/swine/Henan/08/2011	MN416437
PB1	A/swine/Henan/SN13/2018	MN416449
PB1	A/swine/Shandong/1207/2016	MN416470
PB1	A/chicken/ShanXi/1807/2019	MN780833
PB1	A/swine/Shanghai/2/2005	FJ789825
PB1	A/swine/Jiangsu/J004/2018	MN416451
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PA	A/swine/Shanghai/2/2005	FJ789826
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PA	A/swine/Hong Kong/2299/2009	CY061732
PA	A/swine/Hong Kong/2314/2009	CY061740
PA	A/swine/Hong Kong/NS1809/2009	CY061748
PA	A/swine/Hong Kong/NS1810/2009	CY061756
PA	A/swine/Hong Kong/2885/2009	CY061764
PA	A/swine/Hong Kong/2886/2009	CY061772
PA	A/swine/Hong Kong/2974/2009	CY061788
PA	A/swine/Hong Kong/189/2010	CY061804
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HA	A/swine/England/39572/2001	CY116151
HA	A/swine/England/57610/1999	CY116222
HA	A/swine/Sarthe/0262/2010	FR871195
HA	A/Swine/Spain/80598LP4/2007	HF674912
HA	A/swine/Tianjin/3/2011	KJ725064
HA	A/swine/Italy/287785/2012	KJ847624
HA	A/swine/Guangdong/3583/2011	KM027639
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HA	A/swine/Guangxi/2893/2011	KM028095
HA	A/swine/Guangxi/2895/2011	KM028103
HA	A/swine/Hong Kong/NS52/2012	KM029159
HA	A/swine/Guangdong/2/2013	KP404164
HA	A/swine/Guangdong/95/2013	KP404204
HA	A/swine/Spain/24237/2011	KR700161
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HA	A/swine/Hebei/0116/2017	MN416597
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HA	A/swine/Chachoengsao/2003	AB434344
HA	A/swine/Minnesota/7931/2007	FJ519977
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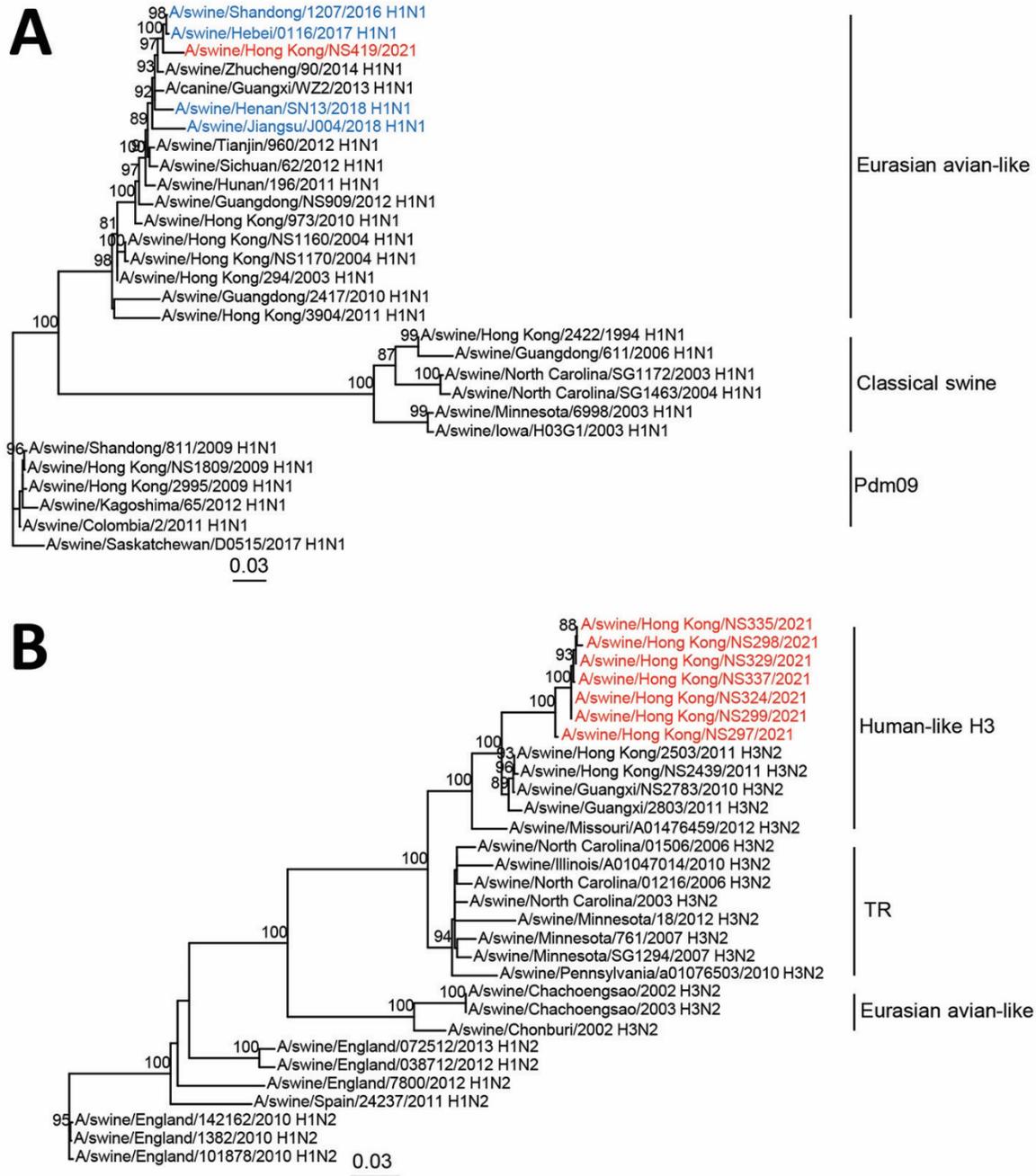
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Segment	Strain name	Accession number
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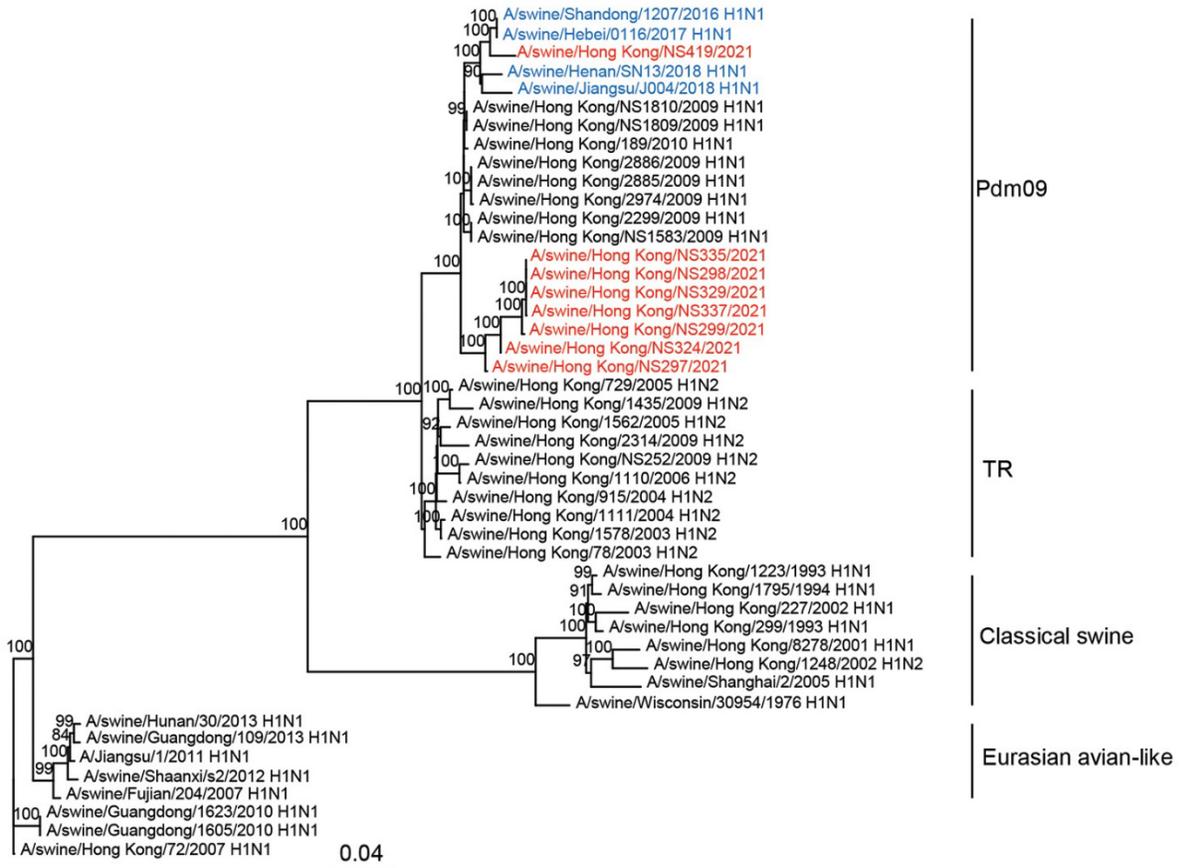
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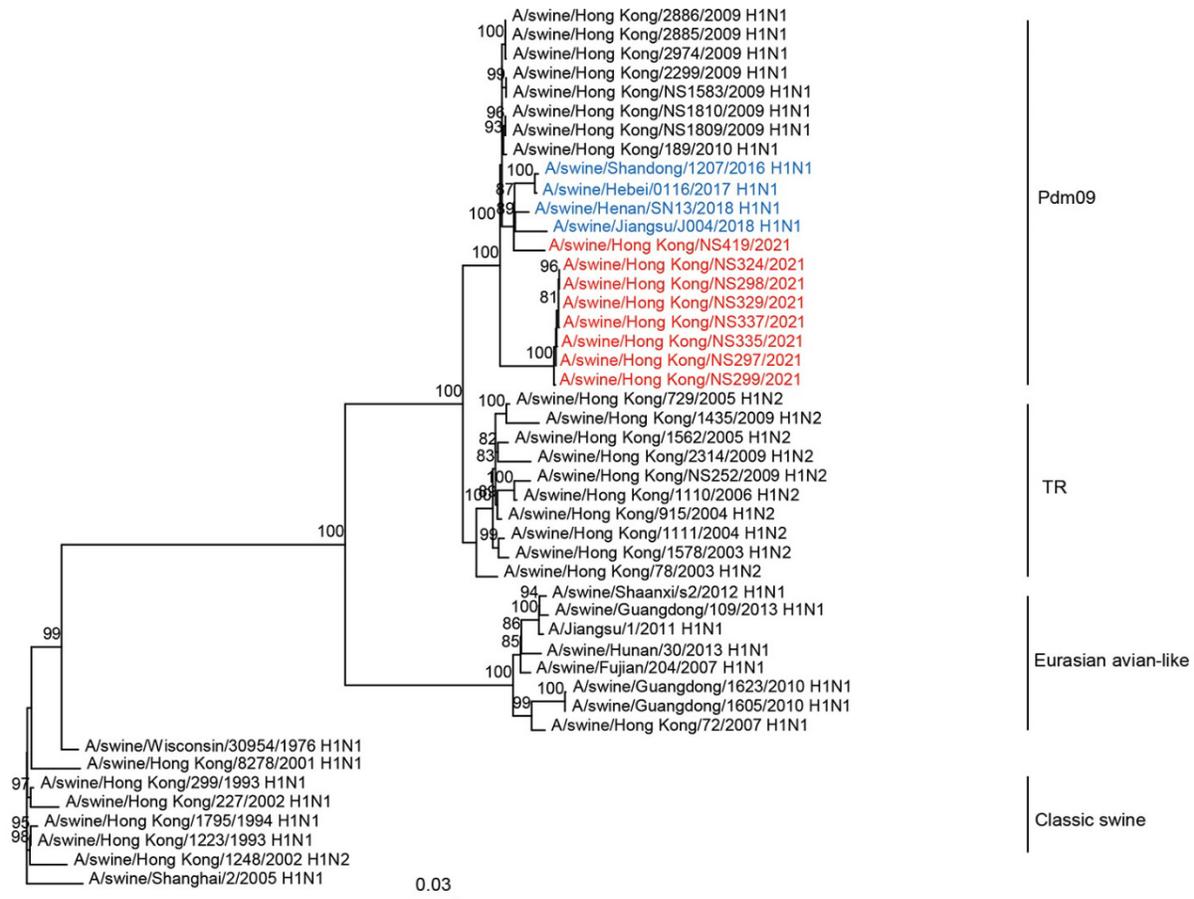
Appendix Figure 1. Phylogenetic tree of H1 (A) or H3 (B) gene sequences. Viral sequences generated from this study (red) and those downloaded from public domains (Appendix Table) were aligned using muscle v3.8 (<http://www.drive5.com/muscle/>). Virus sequences from G4 swine viruses (Main text) are highlighted in blue. Phylogenetic trees were then constructed by IQ-tree v1.6.12 (<http://www.iqtree.org/release/v1.6.12>) using the GTR+G model. Major animal viral lineages are as shown. The phylogenetic clades of the studied H1 sequences are shown in brackets (Anderson et al., mSphere 2016; <https://doi.org/10.1128/mSphere.00275-16>). Bootstrap values $\geq 80\%$ are shown. Scale bar indicates estimated genetic distance.



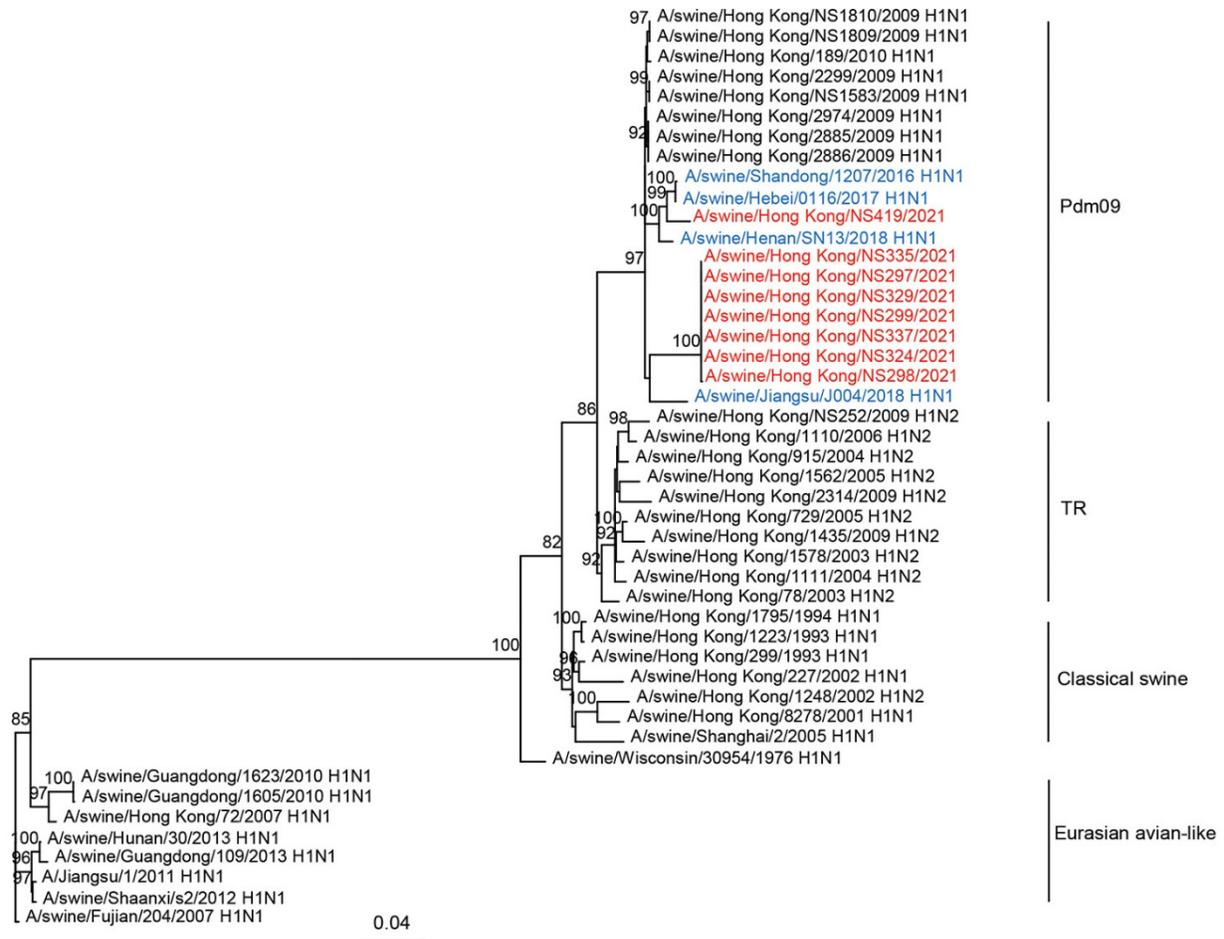
Appendix Figure 2. Phylogenetic tree of N1 (A) or N2 (B) gene sequences. Viral sequences generated from this study (red) and those downloaded from public domains (Appendix Table) were aligned using muscle v3.8 (<http://www.drive5.com/muscle/>). Virus sequences from G4 swine viruses (Main text) are highlighted in blue. Phylogenetic trees were then constructed by IQ-tree v1.6.12 (<http://www.iqtree.org/release/v1.6.12>) using the GTR+G model. Major animal viral lineages are as shown. Bootstrap values $\geq 80\%$ are shown. Scale bar indicates estimated genetic distance.



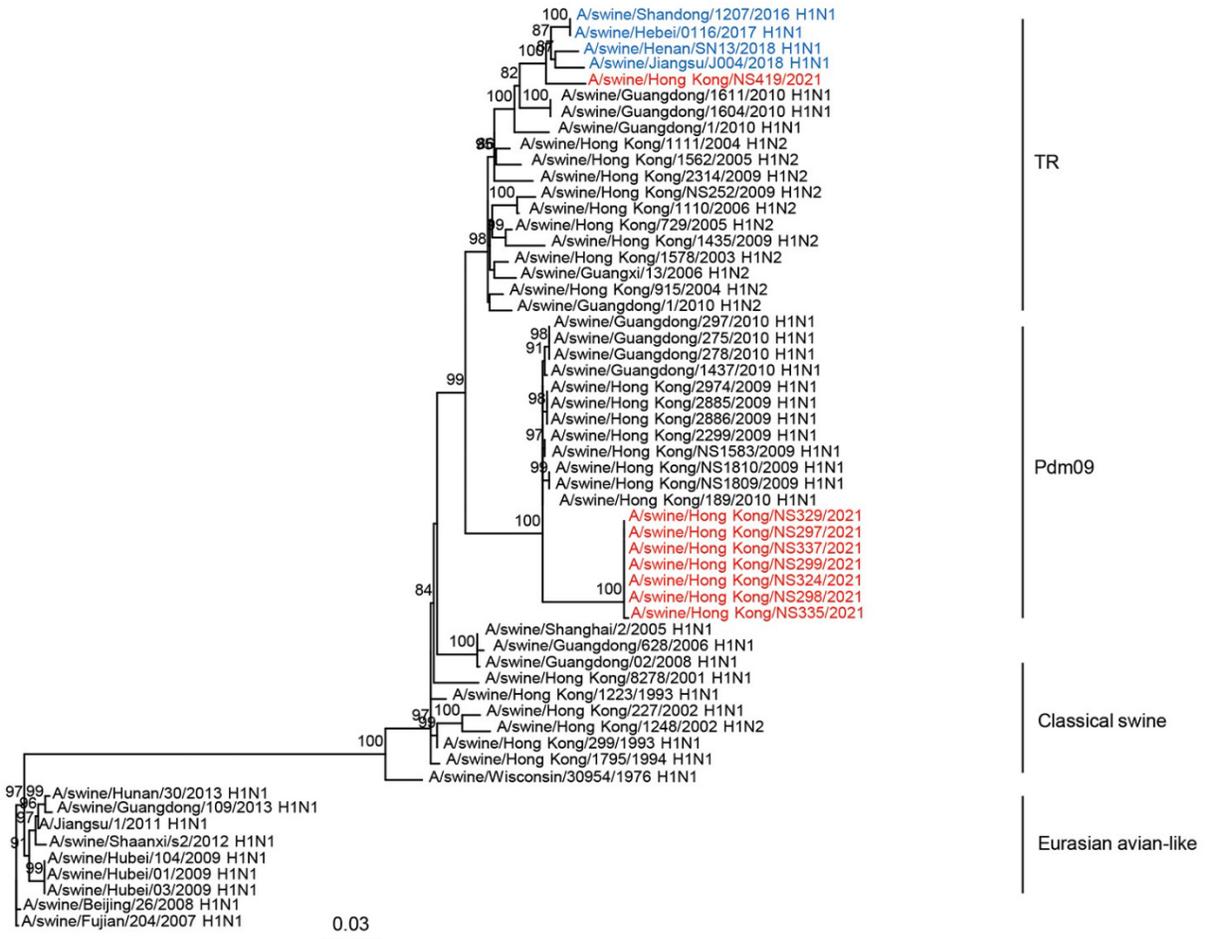
Appendix Figure 3. Phylogenetic tree of PB2 gene sequences. Viral sequences generated from this study (red) and those downloaded from public domains (Appendix Table) were aligned using muscle v3.8 (<http://www.drive5.com/muscle/>). Virus sequences from G4 swine viruses (Main text) are highlighted in blue. Phylogenetic trees were then constructed by IQ-tree v1.6.12 (<http://www.iqtree.org/release/v1.6.12>) using the GTR+G model. Major animal viral lineages are as shown. Bootstrap values $\geq 80\%$ are shown. Scale bar indicates estimated genetic distance.



Appendix Figure 4. Phylogenetic tree of PA gene sequences. Viral sequences generated from this study (red) and those downloaded from public domains (Appendix Table) were aligned using muscle v3.8 (<http://www.drive5.com/muscle/>). Virus sequences from G4 swine viruses (Main text) are highlighted in blue. Phylogenetic trees were then constructed by IQ-tree v1.6.12 (<http://www.iqtree.org/release/v1.6.12>) using the GTR+G model. Major animal viral lineages are as shown. Bootstrap values $\geq 80\%$ are shown. Scale bar indicates estimated genetic distance.



Appendix Figure 5. Phylogenetic tree of M gene sequences. Viral sequences generated from this study (red) and those downloaded from public domains (Appendix Table) were aligned using muscle v3.8 (<http://www.drive5.com/muscle/>). Virus sequences from G4 swine viruses (Main text) are highlighted in blue. Phylogenetic trees were then constructed by IQ-tree v1.6.12 (<http://www.iqtree.org/release/v1.6.12>) using the GTR+G model. Major animal viral lineages are as shown. Bootstrap values $\geq 80\%$ are shown. Scale bar indicates estimated genetic distance.



Appendix Figure 6. Phylogenetic tree of NS gene sequences. Viral sequences generated from this study (red) and those downloaded from public domains (Appendix Table) were aligned using muscle v3.8 (<http://www.drive5.com/muscle/>). Virus sequences from G4 swine viruses (Main text) are highlighted in blue. Phylogenetic trees were then constructed by IQ-tree v1.6.12 (<http://www.iqtree.org/release/v1.6.12>) using the GTR+G model. Major animal viral lineages are as shown. Bootstrap values $\geq 80\%$ are shown. Scale bar indicates estimated genetic distance.