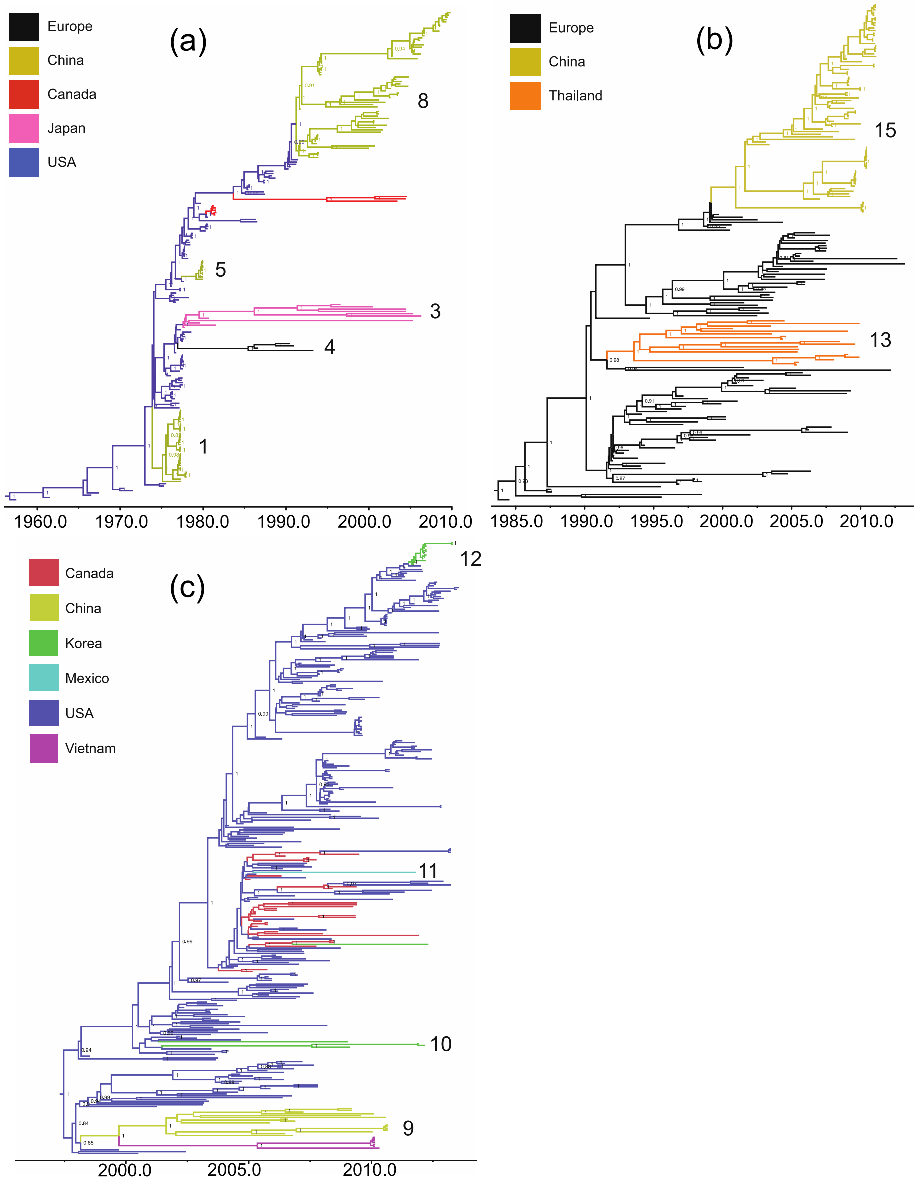
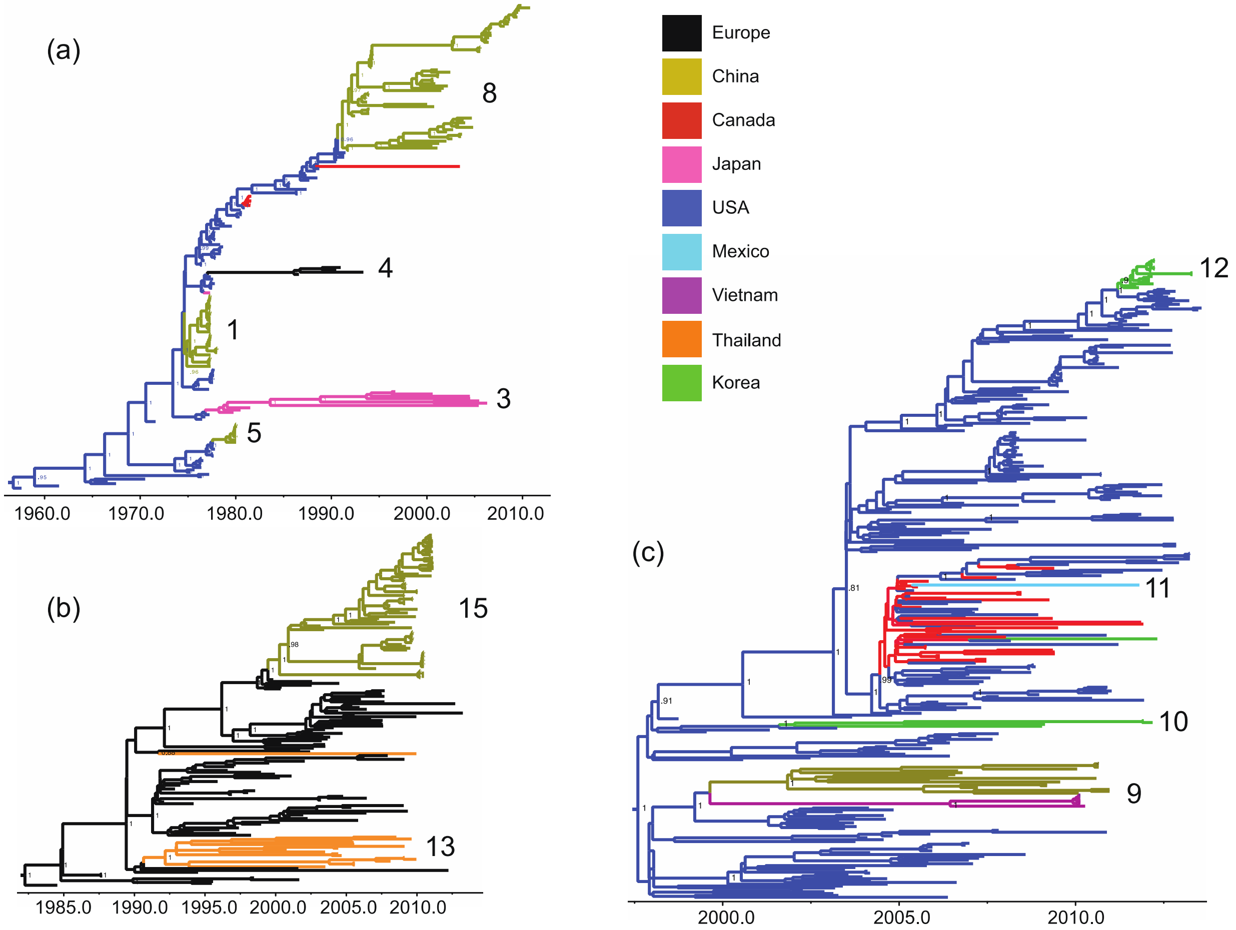
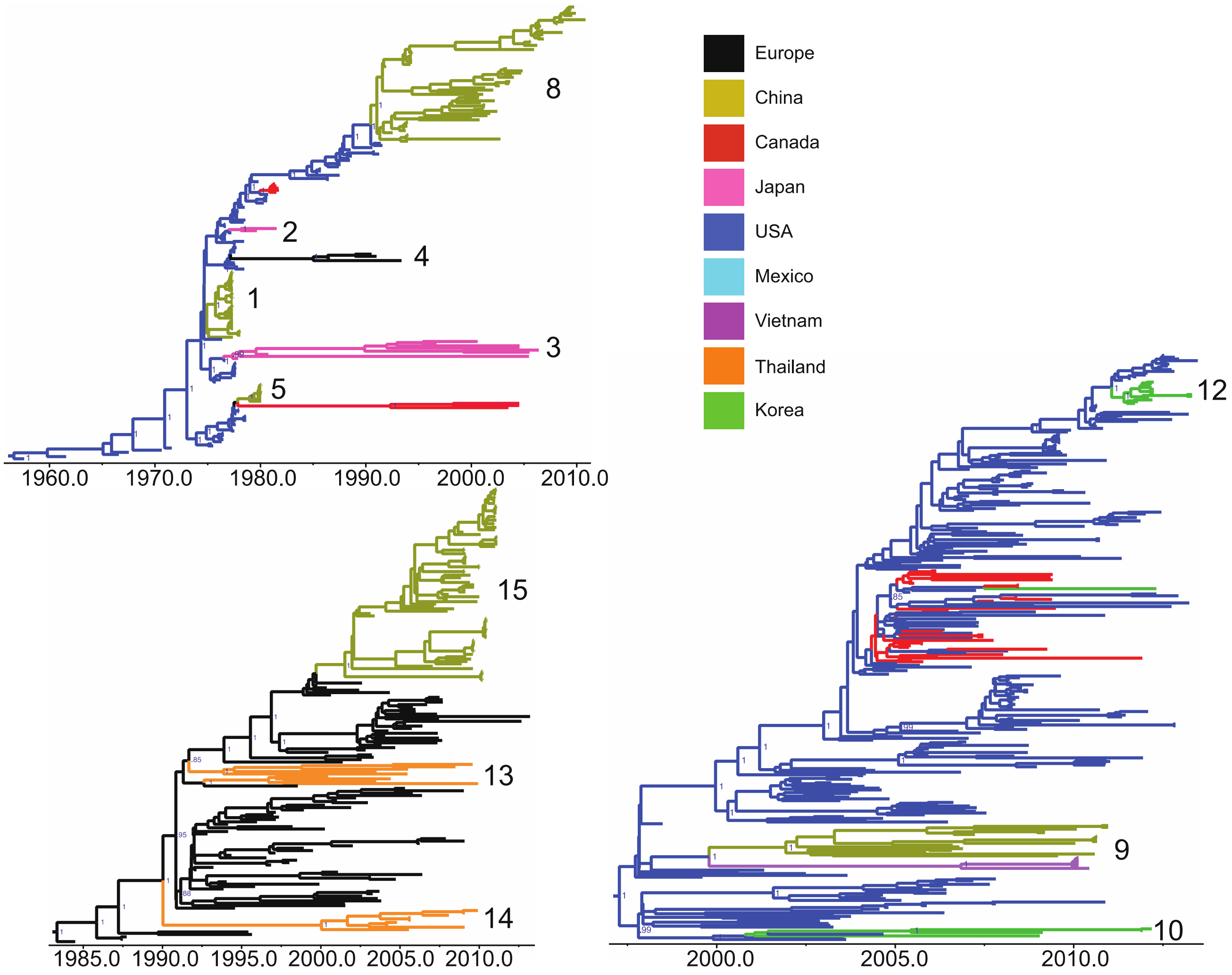


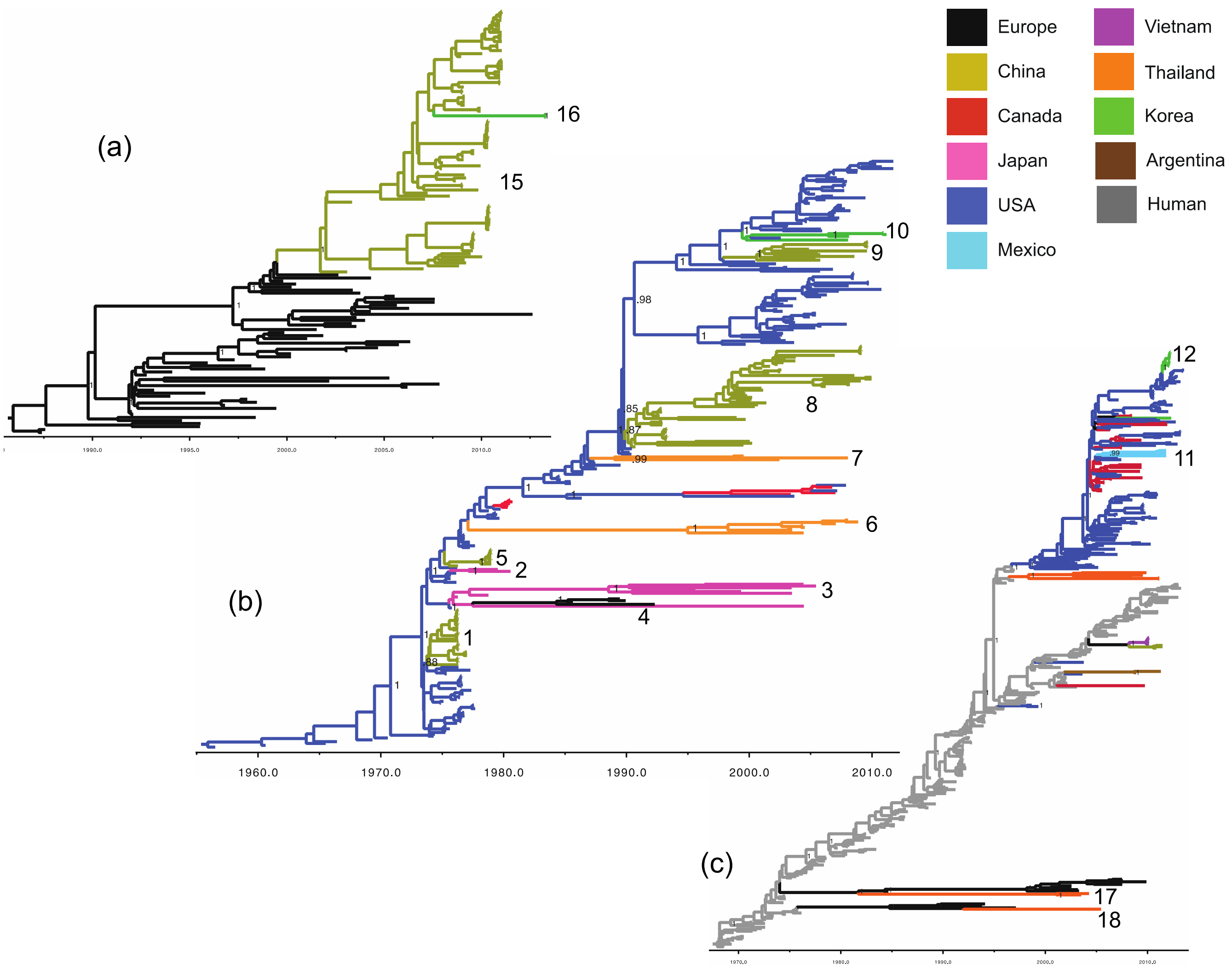
Supplementary Fig. 1. MCC trees of the PB2 lineages in swine. Time-scaled Bayesian MCC trees inferred for the PB2 segment for the three major swine virus lineages: (a) classical swIAV lineage, (b) avian-origin Eurasian swIAV lineage, and (c) triple reassortant (trig) swIAV lineage. Shading and labeling is identical to Fig. 3.



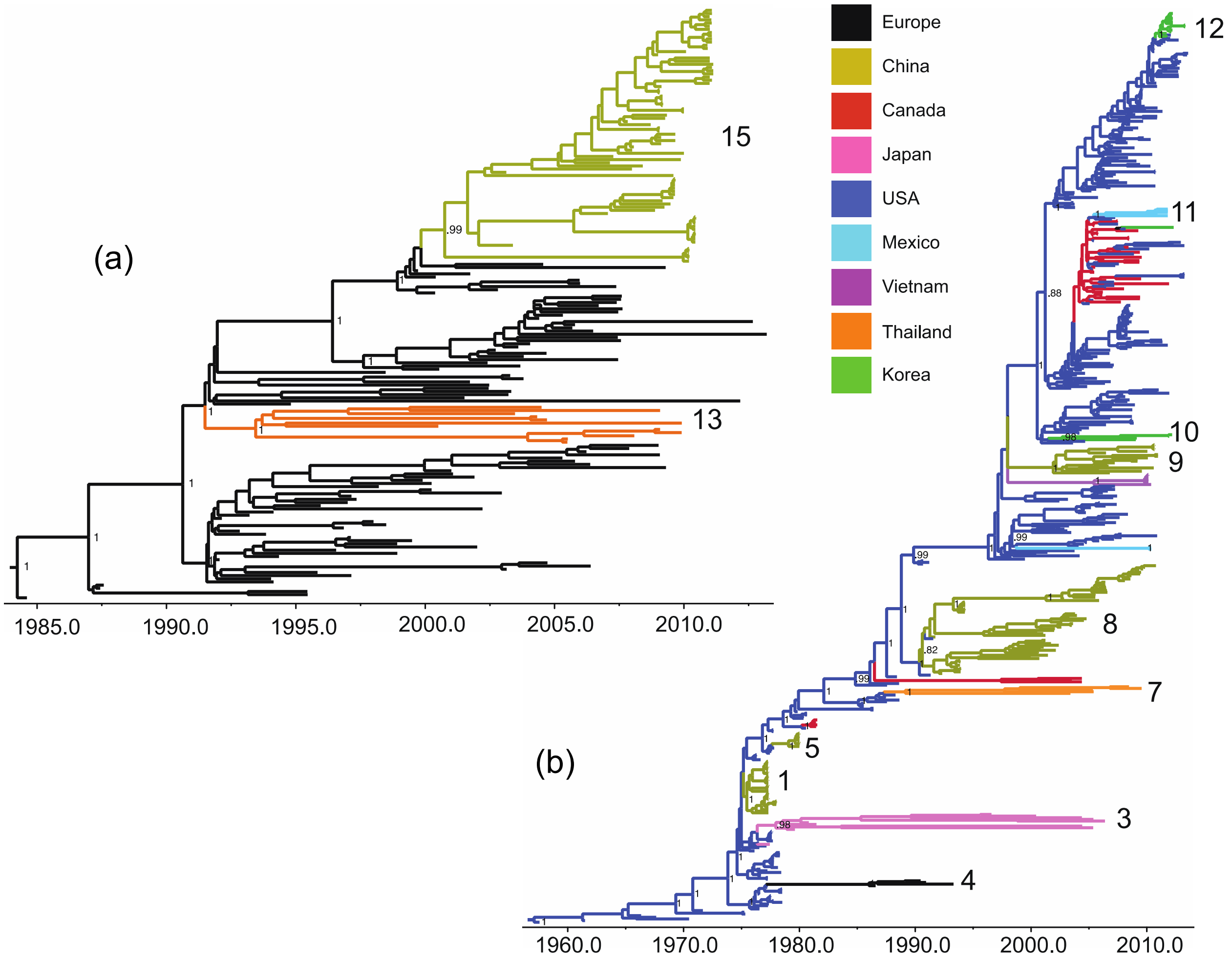
Supplementary Fig. 2. MCC trees of the PB1 lineages in swine. Time-scaled Bayesian MCC trees inferred for the PB1 segment for the three major swine virus lineages: (a) classical swIAV lineage, (b) avian-origin Eurasian swIAV lineage, and (c) triple reassortant (trig) swIAV lineage. Shading and labeling is identical to Fig. 3.



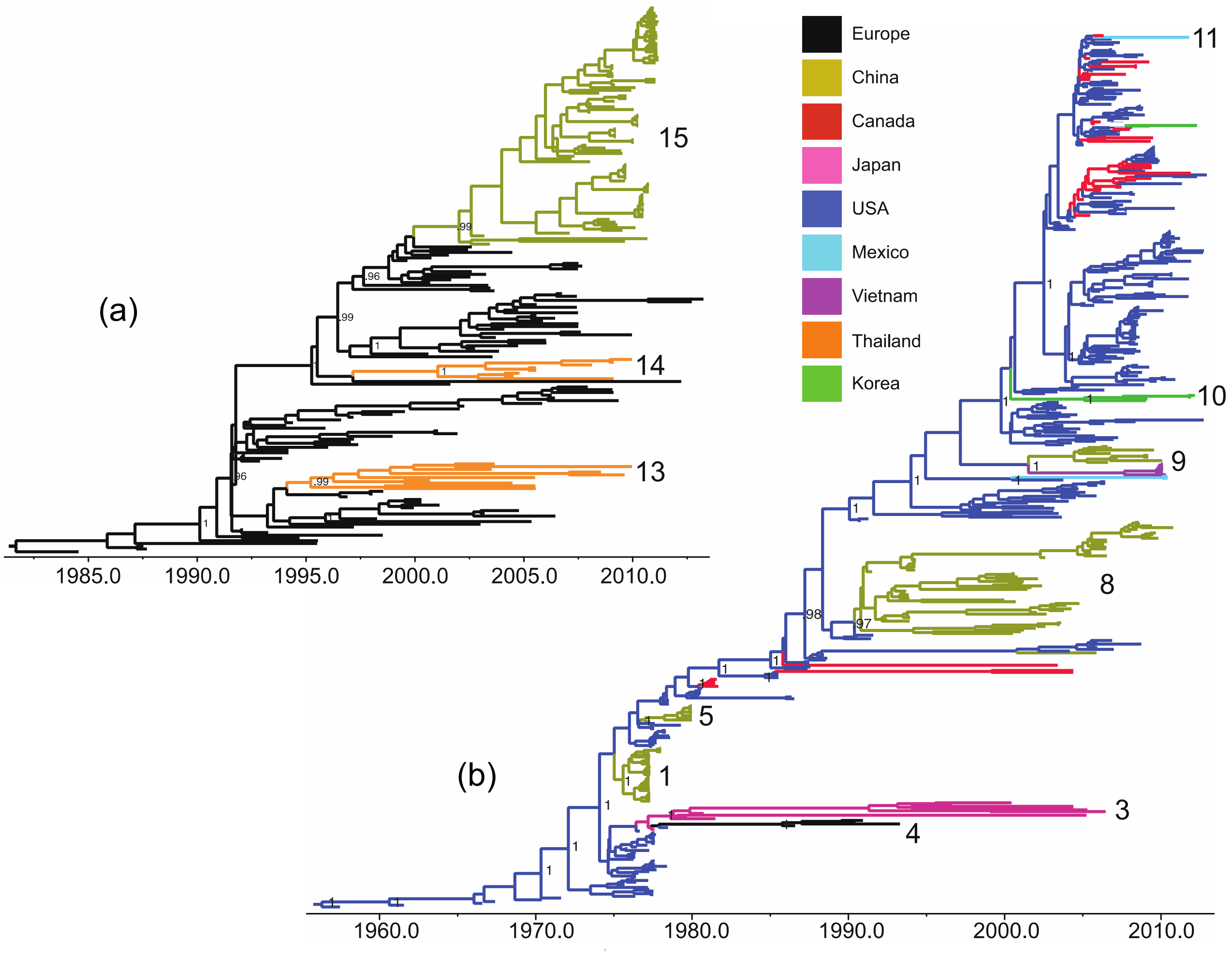
Supplementary Fig. 3. MCC trees of the PA lineages in swine. Time-scaled Bayesian MCC trees inferred for the PA segment for the three major swine virus lineages: (a) classical swIAV lineage, (b) avian-origin Eurasian swIAV lineage, and (c) triple reassortant (trig) swIAV lineage. Shading and labeling is identical to Fig. 3.



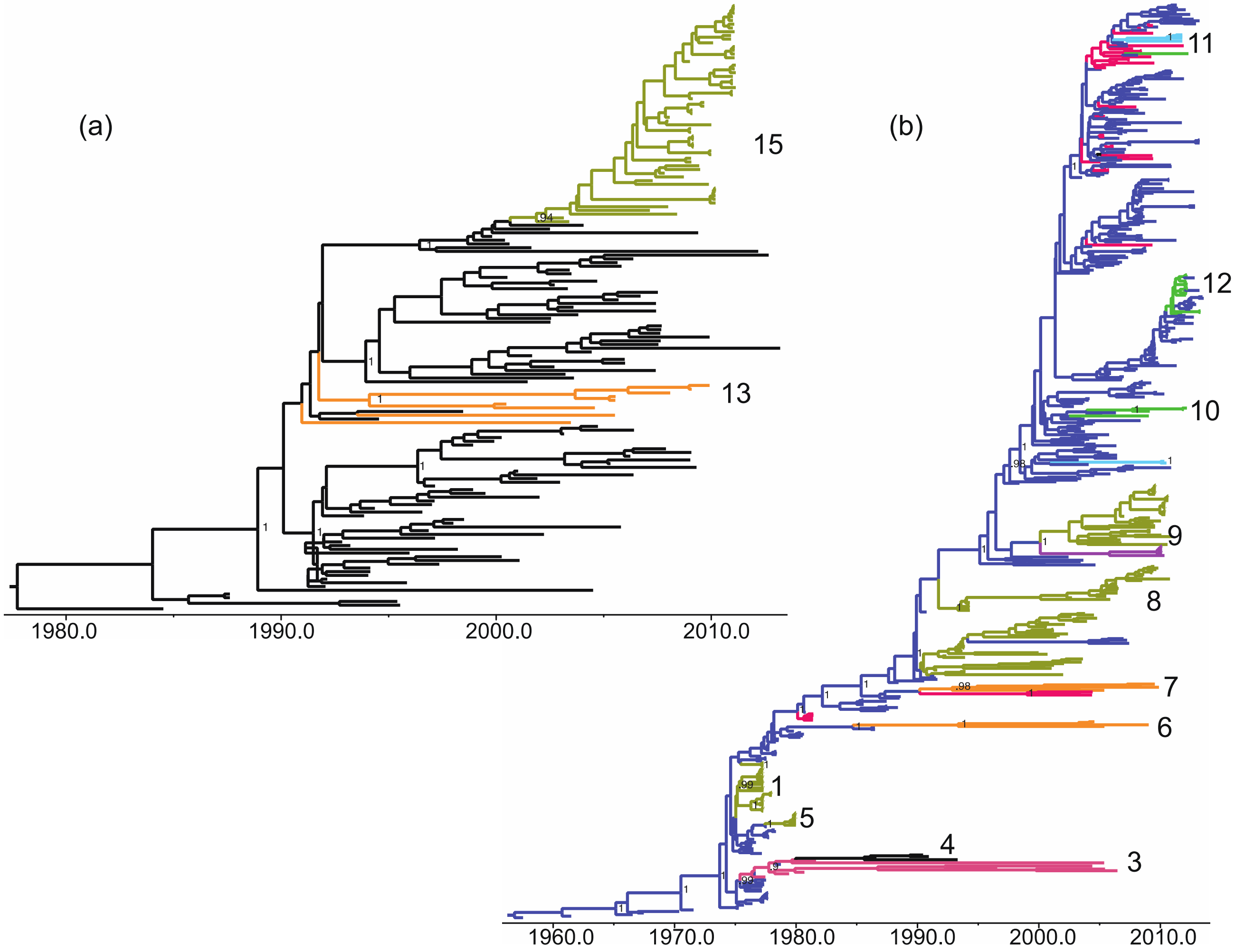
Supplementary Fig. 4. MCC trees of the HA lineages in swine. Time-scaled Bayesian MCC trees inferred for the HA segment for the three major swine virus lineages: (a) avian-origin Eurasian H1 swIAV lineage, (b) classical H1 swIAV lineage, and (c) multiple human seasonal virus-origin H3 swIAV lineages circulating in swine. Shading and labeling is identical to Fig. 3.



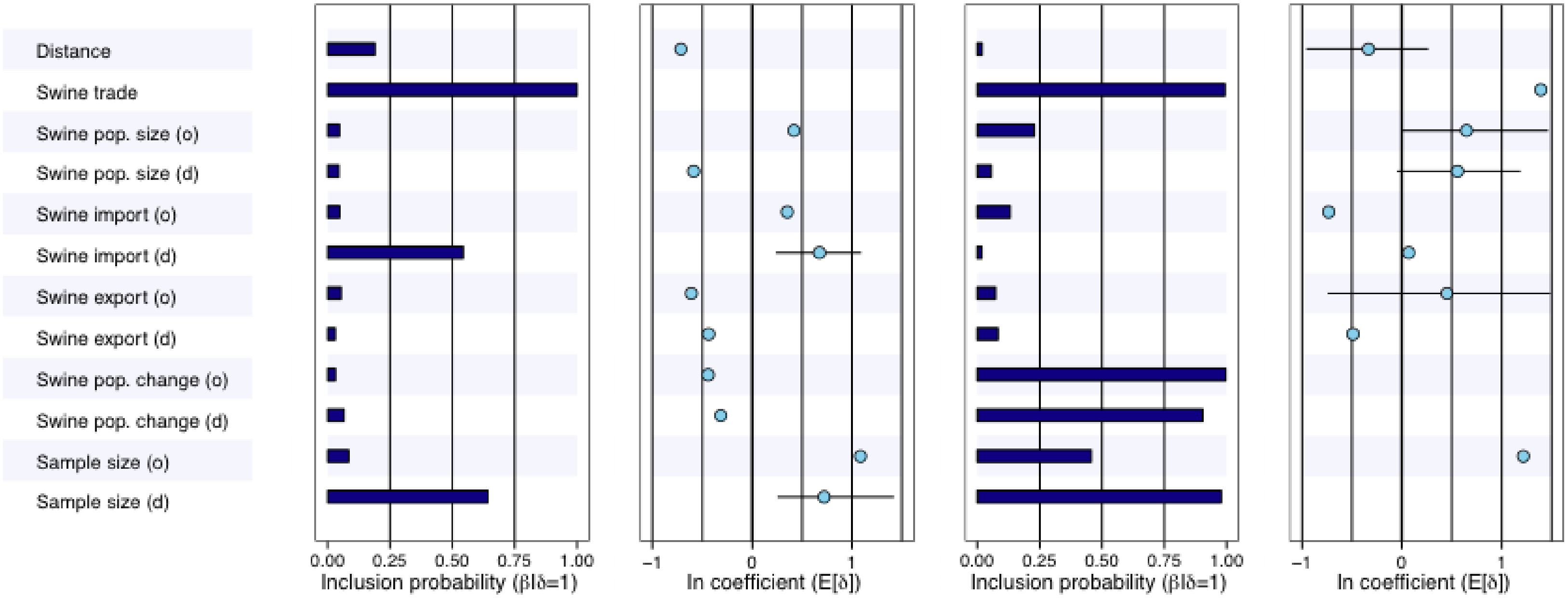
Supplementary Fig. 5. MCC trees of the NP lineages in swine. Time-scaled Bayesian MCC trees inferred for the NP segment for the two major swine virus lineages: (a) avian-origin Eurasian swIAV lineage, and (b) classical swIAV lineage. Shading and labeling is identical to Fig. 3.



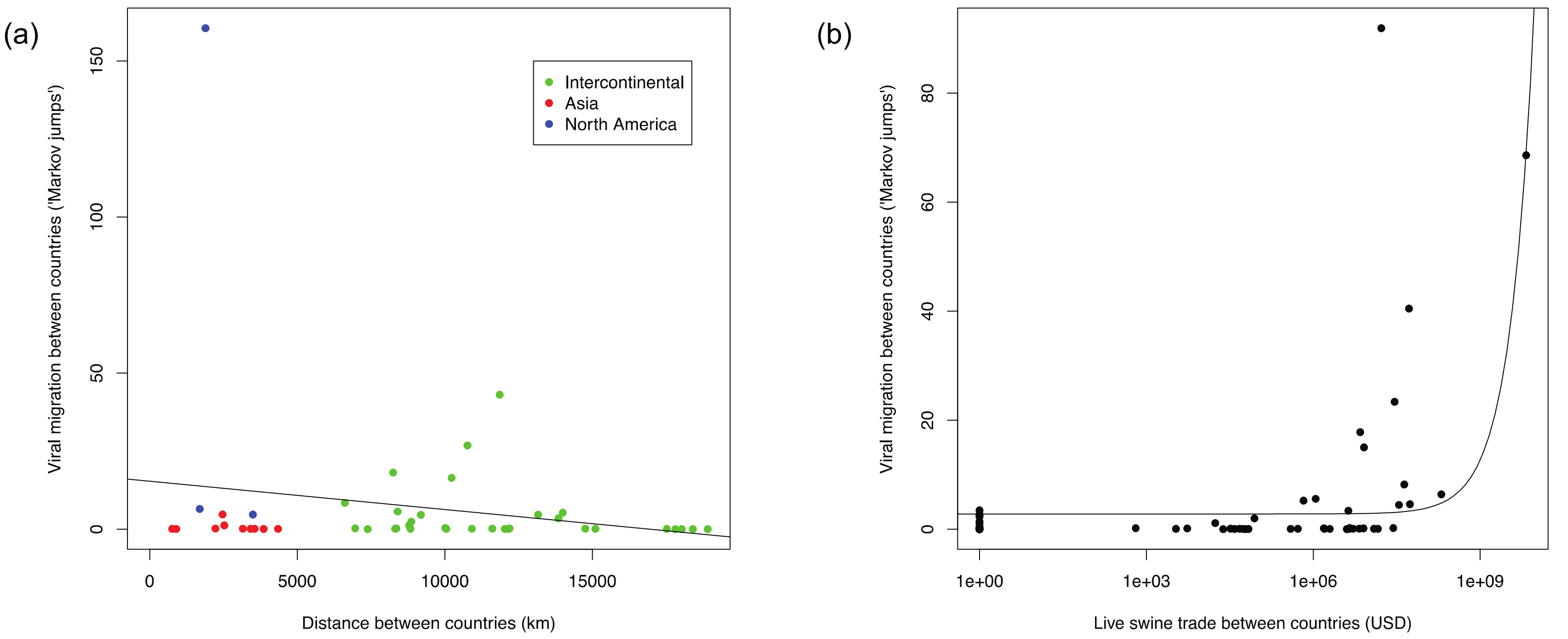
Supplementary Fig. 6. MCC trees of the MP lineages in swine. Time-scaled Bayesian MCC trees inferred for the MP segment for the two major swine virus lineages: (a) avian-origin Eurasian swIAV lineage, and (b) classical swIAV lineage. Shading and labeling is identical to Fig. 3.



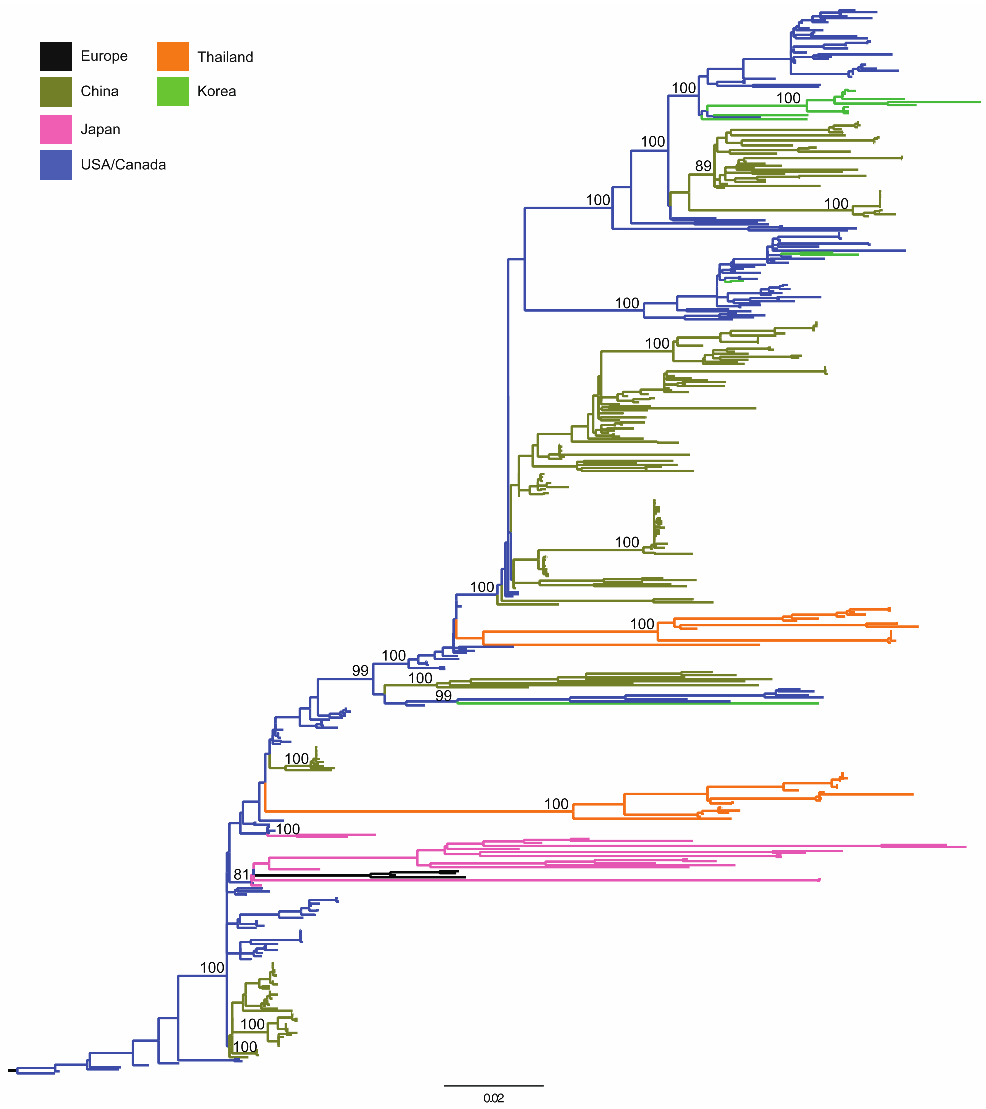
Supplementary Fig. 7. MCC trees of the NS lineages in swine. Time-scaled Bayesian MCC trees inferred for the NS segment for the two major swine virus lineages: (a) avian-origin Eurasian swIAV lineage, and (b) classical swIAV lineage. Shading and labeling is identical to Fig. 3.



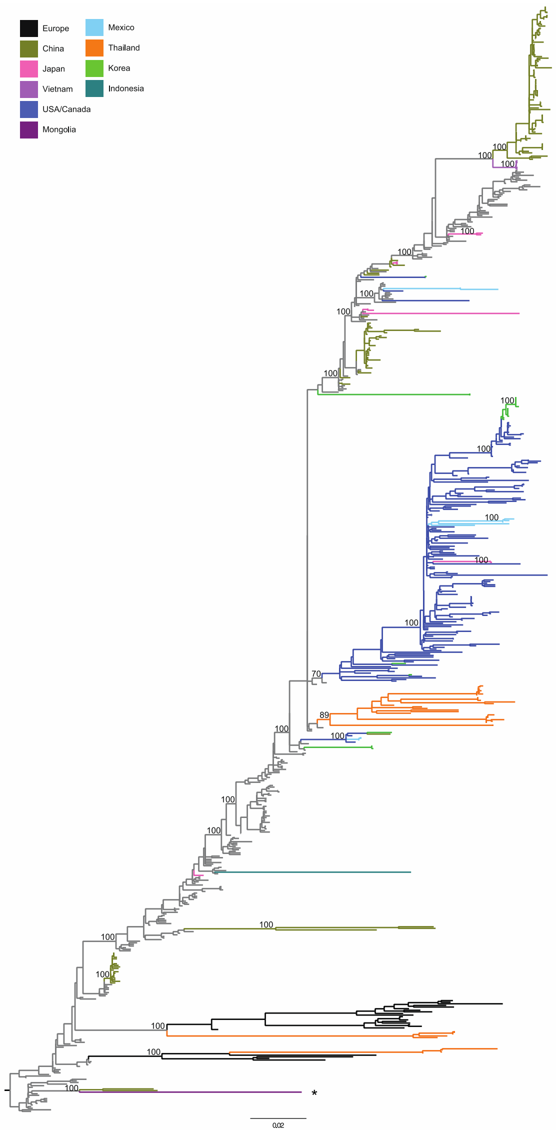
Supplementary Fig. 8. **The support and contribution of predictors of swIAV diffusion among 9 countries for the MP and NS segments**. Twelve predictors were considered: geographical distance (km), volume of live swine trade, 1996-2012 (USD), swine population size for the years 1969-2010, the total number of imports of live swine during 1969-2010, the total number of swine exports during 1969-2010, the percent change in swine population size from 1969-2010, and the number of sequences available from a given country for our analysis. (O) refers to the swine population of origin, and (d) refers to the swine population of destination. Support for each predictor is represented by an inclusion probability that is estimated as the posterior expectation for the indicator variable associated with each predictor (E[δ]). The contribution of each predictor is represented by the mean and credible intervals of the GLM coefficients (β) on a log scale conditional on the predictor being included in the model (β|δ=1).



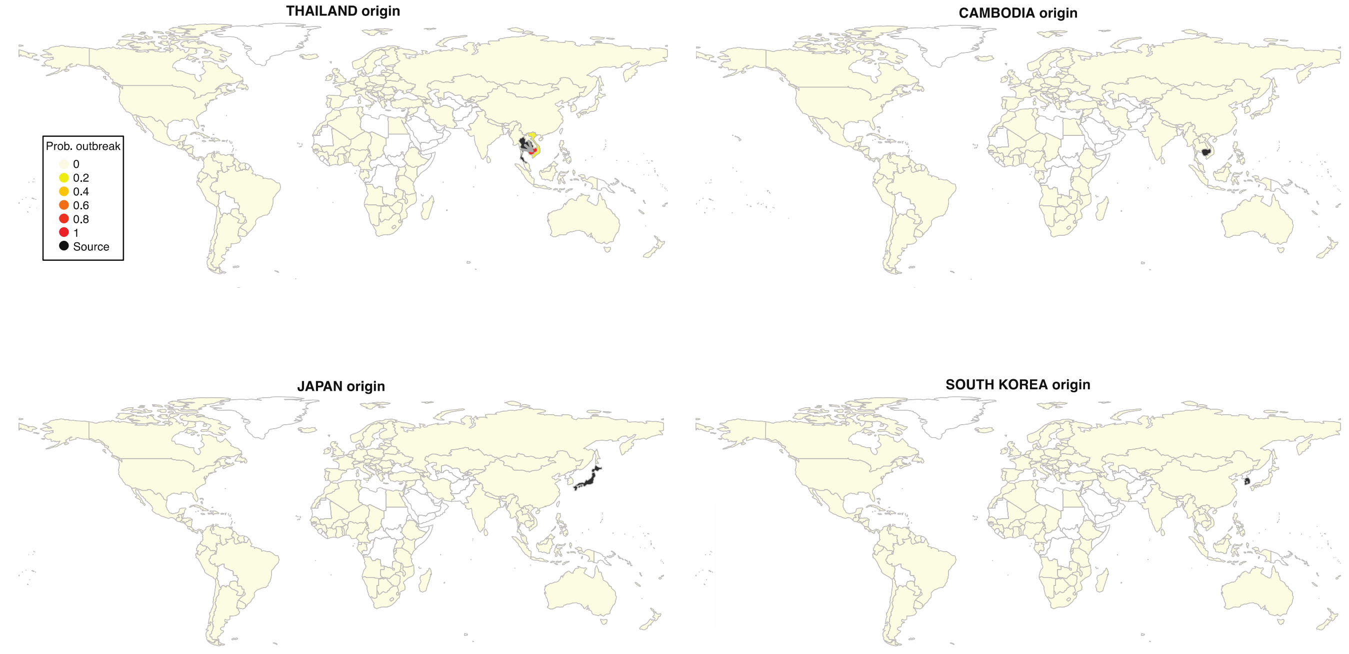
Supplementary Fig. 9. **Plots of viral migration, distance, and live swine trade.** (a) Viral migration between pairwise countries (represented by the number of 'Markov jump' counts, symmetrical) is plotted against geographical distance (km) between countries, which are shaded by region (connections between countries in North America are blue, connections between Asian countries are red, and intercontinental links are green). (b) Viral migration (asymmetrical) is plotted against the volume of live swine trade from one country to another (asymmetrical), which is presented on a log scale.



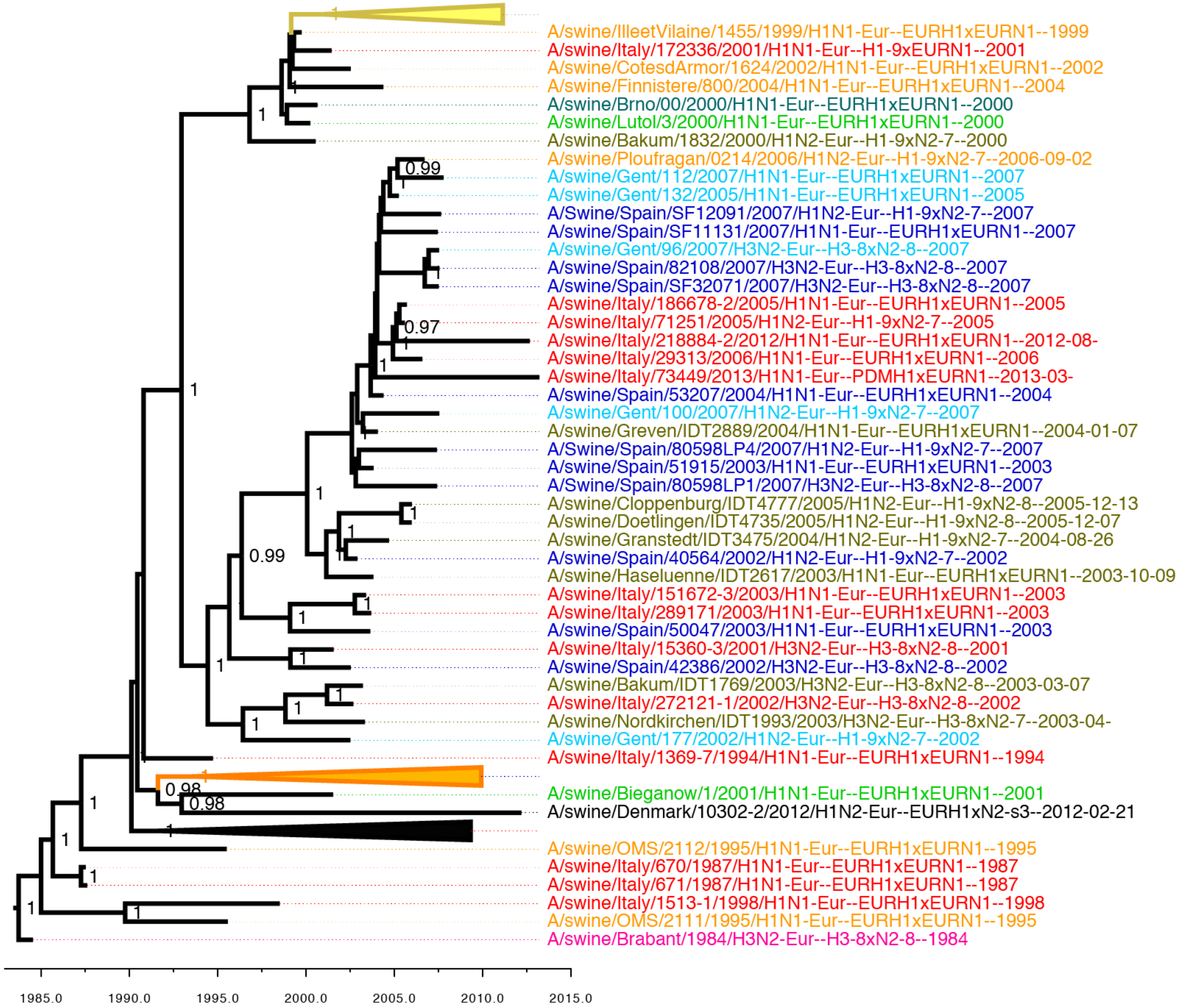
Supplementary Fig. 10. **Maximum likelihood phylogeny of classical swine H1 sequences.** Phylogenetic relationships of H1 sequences from 527 influenza viruses collected globally in swine during 1957-2013, including all full-length H1 sequences from Asian swine, estimated using a maximum likelihood method. Branch lengths are drawn to scale, and bootstrap values > 70% are provided for key nodes.



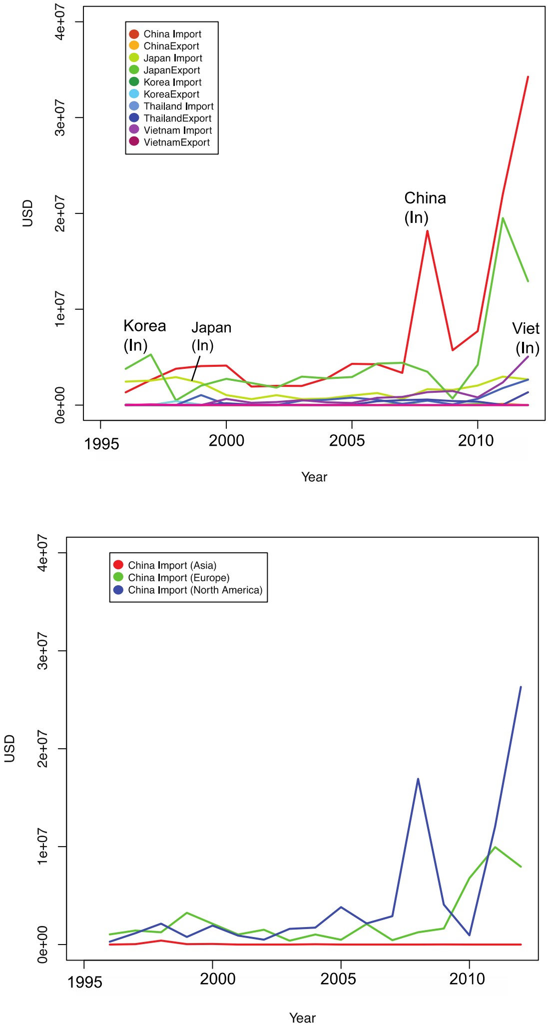
Supplementary Fig. 11. **Maximum likelihood phylogeny of human and swine H3 sequences.** Phylogenetic relationships of full-length H3 sequences from 689 influenza viruses collected globally from humans and swine during 1968-2013, including all data from Asian swine, estimated using a maximum likelihood method. Branch lengths are drawn to scale, and bootstrap values > 70% are provided for key nodes. The asterisk denotes a new putative viral migration event between Asian countries, not evident in the analysis of whole-genome sequence data. However, only three sequences associated with this clade are available: A/sw/Hong Kong/81/1978(H3N2), A/sw/Hong Kong/126/1982(H3N2), and A/sw/Inner Mongolia/547/2001(H3N2).



Supplementary Fig. 12. **Maps of simulated spread of influenza viruses via live swine trade flows.** Simulated spread of an influenza virus from a seed country (shaded in black) to 146 countries for which live swine trade is available from the United Nations Commodity Trade Statistics Database (available at http://comtrade.un.org). Probability of an outbreak is shaded from light yellow (probability of 0) to red (probability of 1).



Supplementary Fig. 13. **Time-scaled MCC tree of PB2 segments from Eurasian swine.** Viruses from European countries have been shaded by color: Belgium = light blue, Czech Republic = dark green, Denmark = black, France = yellow, Germany = gold, Italy = red, Netherlands = pink, Poland = light green, and Spain = dark blue. For clarity a clade of viruses from England has been collapsed (black triangle). Viruses from China and Thailand have also been collapse (yellow and orange triangles, respectively).



Supplementary Fig. 14. **Trends in live swine trade volume (USD) during 1996-2012 for (a) Asian countries and (b) China.**

Supplementary Table 1. Times to the Most Recent Common Ancestor (tMRCA). Estimates for the timing of the spatial movements associated with introductions 1-18 (Fig. 2), summarized across the eight genome segments of the influenza A virus. The mean of the estimates across the genome segments is provided, as well as the range representing the highest and lowest estimates across the segments, for the two nodes representing the estimated temporal range for spatial movement in swine (e.g., introduction 1 is estimated to have spread from the US to China during 1974.44 - 1974.94) and the most recently sampled virus from a given introduction (e.g., 1978.02 for intro 1). Introduction 16 was only evident for one segment (H1) and therefore does not have a range.

Intro	**Mean**			**Range**		
1	1974.44	1974.94	1978.02	1973.42; 1975.16	1973.91; 1975.59	1978.02; 1978.02
2	1976.32	1977.65	1981.0	1975.66; 1976.99	1977.16; 1978.15	1981; 1981
3	1976.44	1977.52	2005.87	1975.55; 1976.84	1975.88; 1978.27	2005; 2006
4	1976.98	1985.49	1993.31	1975.66; 1977.89	1984.3; 1986.12	1993.31; 1993.31
5	1977.16	1978.34	1979.99	1975.17; 1977.84	1975.56; 1979.16	1979.99; 1979.99
6	1980.87	1994.14	2009.48	1977.1; 1984.64	1993.3; 1994.98	2009.04; 2009.92
7	1988.14	1990.32	2009.5	1987.0; 1990.13	1989.02; 1992.8	2009.04; 2009.88
8	1990.36	1990.85	2010.25	1989.84; 1990.68	1990.12; 1991.27	2009.84; 2010.83
9	1998.01	2000.15	2010.63	1997.17; 1999.34	1997.97; 2001.77	2010.17; 2010.95
10	2001.49	2004.87	2012.32	2000.16; 2004.03	2001.94; 2007.76	2012.18; 2013.32
11	2005.50	2006.52	2011.83	2004.81; 2006.45	2005.34; 2006.45	2011.81; 2006.45
12	2011.11	2011.3	2013.00	2010.6; 2011.51	2010.69; 2011.65	2012.24; 2013.31
13	1991.82	1993.81	2009.90	1990.65; 1994.33	1992.18; 1995.43	2009.88, 2009.92
14	1993.61	2000.565	2009.91	1990.07; 1997.15	2000.08; 2001.05	2009.91; 2009.92
15	1999.68	2001.22	2011.1	1999.15; 2000.69	2000.28; 2002.03	2011.1; 2011.1
16	2007.54	2013.26	2013.31	-	-	-
17	1981.25	1999.17	2004	1981.02; 1981.48	1997.51; 2000.83	2004; 2004
18	1986.56	2000.84	2005	1982.37; 1990.76	1999.07; 2002.61	2005; 2005

Supplementary Table 2. 'Markov jump' counts between countries. Expected number of location state transitions along the branches of the inferred phylogenies, from which the heat-map presented in Fig. 4 was generated.

	Arg	Can	Chi	Eur	Jap	Kor	Mex	Thai	USA	Viet	Total
Arg	-	0.04	0.02	0.04	0.01	0.01	0.01	0.06	0.03	0.01	0.24
Can	0.09	-	0.22	0.17	0.10	**4.47**	**4.60**	0.18	**68.61**	0.24	78.69
Chi	0.02	0.19	-	0.21	0.07	**1.13**	0.12	0.16	**2.59**	**2.75**	7.25
Eur	0.06	0.12	**8.22**	-	0.09	0.09	0.10	**17.83**	0.09	0.07	26.67
Jap	0.01	**1.10**	0.08	**2.33**	-	0.07	0.08	0.09	**1.43**	0.06	5.25
Kor	0.02	0.14	0.10	0.08	0.04	-	0.12	0.10	**3.47**	0.13	4.19
Mex	0.02	0.09	0.06	0.07	0.03	0.08	-	0.08	0.09	0.09	0.61
Thai	0.02	0.07	0.05	0.33	0.03	0.04	0.05	-	0.04	0.04	0.66
USA	0.23	**91.92**	**40.49**	**5.59**	**15.02**	**23.38**	**6.42**	**5.25**	-	**3.41**	191.7
Viet	0.03	0.08	**2.00**	0.07	0.03	0.11	0.12	0.09	0.08	-	2.62
Tot	0.50	93.76	51.25	8.88	15.42	29.39	11.61	23.84	76.44	6.80	

Supplementary Table 3. Viruses sequenced for this study. Swine influenza A viruses from North America (Canada, Mexico, and United States) that were sequenced for this study at the J Craig Venter Institute, Rockville, MD (n = 240). GenBank accession numbers provided for PB2 segment.

Virus name	Country	Year	Accession
A/swine/Alberta/00805/2005(H3N2)	Canada	10/10/05	AHB22080
A/swine/Alberta/SG1405/2005(H3N2)	Canada	10/7/05	AHB22068
A/swine/Alberta/SG1415/2006(H1N1)	Canada	3/13/06	AHB22507
A/swine/Arkansas/01460/2007(H1N1)	USA	1/31/07	AHB21170
A/swine/Arkansas/02598/2009(H3N2)	USA	2/12/09	AHB23070
A/swine/Arkansas/02720/2009(H1N2)	USA	4/6/09	AHB23809
A/swine/Arkansas/02863/2009(H3N2)	USA	6/26/09	AHB23094
A/swine/Arkansas/02927/2009(H1N2)	USA	12/2/09	AHB23082
A/swine/Arkansas/SG1241/2006(H1N1)	USA	5/2/06	AHB21014
A/swine/Arkansas/SG1295/2008(H3N2)	USA	5/15/08	AHB21376
A/swine/Arkansas/SG1297/2008(H3N2)	USA	10/15/08	AHB21388
A/swine/Arkansas/SG1298/2008(H3N2)	USA	12/30/08	AHB21400
A/swine/Arkansas/SG1319/2009(H3N2)	USA	1/14/09	AHB23798
A/swine/Arkansas/SG1323/2009(H1N1)	USA	10/12/09	AHB21579
A/swine/Arkansas/SG1327/2009(H1N1)	USA	10/30/09	AHB23833
A/swine/Arkansas/SG1327/2009(H1N1)	USA	10/30/09	AHB22389
A/swine/Arkansas/SG1375/2011(H1N2)	USA	8/17/11	AHB21840
A/swine/Arkansas/SG1376/2011(H1N2)	USA	1/26/11	AHB21852
A/swine/Arkansas/SG1377/2011(H1N2)	USA	4/29/11	AHB21864
A/swine/Arkansas/SG1378/2011(H1N2)	USA	6/16/11	AHB21876
A/swine/Arkansas/SG1381/2011(H1N2)	USA	9/1/11	AHB24574
A/swine/Arkansas/SG1382/2011(H1N2)	USA	6/14/11	AHB24586
A/swine/Arkansas/SG1383/2011(H1N2)	USA	9/1/11	AHB21888
A/swine/Arkansas/SG1384/2011(H1N2)	USA	7/13/11	AHB21900

A/swine/Arkansas/SG1499/2010(H1N1)	USA	8/11/10	AHB23116
A/swine/British Columbia/00633/2005(H3N2)	Canada	5/19/05	AHB22056
A/swine/Colorado/02875/2009(H1N2)	USA	7/21/09	AHB23105
A/swine/Colorado/SG1322/2009(H1N1)	USA	8/26/09	AHB21567
A/swine/Georgia/02604/2009(H3N2)	USA	2/20/09	AHB21603
A/swine/Georgia/SG1251/2006(H1N1)	USA	5/12/06	AHB22329
A/swine/Illinois/00303/2004(H3N2)	USA	5/18/04	AHB20891
A/swine/Illinois/01131/2006(H3N2)	USA	5/5/06	AHB21158
A/swine/Illinois/02166/2008(H1N1)	USA	5/1/08	AHB22377
A/swine/Illinois/02166/2008(H1N1)	USA	5/1/08	AHB21543
A/swine/Illinois/02626/2009(H1N1)	USA	1/29/09	AHB21699
A/swine/Illinois/02757/2009(H1N1)	USA	4/28/09	AHB21711
A/swine/Illinois/02957/2010(H1N1)	USA	1/26/10	AHB21804
A/swine/Illinois/SG1398/2011(H1N2)	USA	8/26/11	AHB24645
A/swine/Indiana/04254/2011(H1N2)	USA	3/31/11	AHB21996
A/swine/Iowa/00186/2003(H3N2)	USA	10/2/03	AHB22578
A/swine/Iowa/00250/2004(H1N1)	USA	2/19/04	AHB22758
A/swine/Iowa/02204/2008(H3N2)	USA	6/11/08	AHB23784
A/swine/Iowa/03734/2011(H3N2)	USA	1/24/11	AHB21984
A/swine/Iowa/13B093/2013(H1N2)	USA	2/26/13	AHA98542
A/swine/Iowa/13C019/2013(H3N2)	USA	3/26/13	AHA98565
A/swine/Iowa/13C020/2013(H3N2)	USA	3/26/13	AHA98576
A/swine/Iowa/13C029/2013(H3N2)	USA	3/26/13	AHA98587
A/swine/Iowa/13C038/2013(H3N2)	USA	3/26/13	AHA98554
A/swine/Iowa/13C040/2013(H3N2)	USA	3/26/13	AHA98598
A/swine/Iowa/SG1368/2010(H1N1)	USA	8/3/10	AHB24523
A/swine/Iowa/SG1401/2011(H1N1)	USA	10/5/11	AHB22008
A/swine/Iowa/SG1469/2004(H3N2)	USA	10/14/04	AHB22794

A/swine/Kansas/00246/2004(H1N2)	USA	2/5/04	AHB22293
A/swine/Kansas/00246/2004(H1N2)	USA	2/5/04	AHB20879
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A/swine/Kentucky/02573/2009(H1N2)	USA	2/10/09	AHB21627
A/swine/Kentucky/SG1277/2007(H1N1)	USA	3/16/07	AHB21254
A/swine/Manitoba/00446/2005(H3N2)	Canada	1/25/05	AHB22495
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A/swine/Manitoba/01093/2006)	Canada	4/12/06	AHB24732
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A/swine/Manitoba/01642/2007(H3N2)	Canada	6/20/07	AHB22128
A/swine/Manitoba/01643/2007(H3N2)	Canada	6/20/07	AHB22140
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A/swine/Manitoba/02182/2008(H3N2)	Canada	5/30/08	AHB22176
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A/swine/Manitoba/02862/2009(H3N2)	Canada	7/1/09	AHB22212
A/swine/Manitoba/SG1431/2008(H3N2)	Canada	6/17/08	AHB22188
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A/swine/Mexico/3146/2010(H1N1)	Mexico	9/16/10	AHB22554
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A/swine/Mexico/SG1450/2011(H1N1)	Mexico	11/9/11	AHB24797
A/swine/Minnesota/00352/2004(H1N1)	USA	7/23/04	AHB22770
A/swine/Minnesota/00401/2004(H1N1)	USA	9/9/04	AHB22782
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A/swine/Minnesota/SG1238/2005(H3N2)	USA	6/2/05	AHB20990
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A/swine/Minnesota/SG1454/2003(H1N1)	USA	10/2/03	AHB22614
A/swine/Minnesota/SG1470/2004(H1N1)	USA	8/13/04	AHB22806
A/swine/Nebraska/00178/2003(H1N1)	USA	8/29/03	AHB22590
A/swine/Nebraska/00188/2003(H3N2)	USA	10/3/03	AHB22626
A/swine/Nebraska/00386/2004(H3N2)	USA	8/13/04	AHB23228
A/swine/Nebraska/01711/2007(H3N2)	USA	7/31/07	AHB21328
A/swine/North Carolina/00371/2004(H1N1)	USA	10/7/04	AHB22698
A/swine/North Carolina/00378/2004(H1N1)	USA	8/3/04	AHB22746
A/swine/North Carolina/00850/2005(H1N1)	USA	11/8/05	AHB24809
A/swine/North Carolina/00925/2005(H1N1)	USA	12/13/05	AHB22914
A/swine/North Carolina/00950/2006(H3N2)	USA	9/27/06	AHB24821
A/swine/North Carolina/01052/2006(H3N2)	USA	3/14/06	AHB22962
A/swine/North Carolina/01169/2006(H1N2)	USA	6/22/06	AHB21086
A/swine/North Carolina/01216/2006(H3N2)	USA	8/16/06	AHB22986
A/swine/North Carolina/01312/2006(H3N2)	USA	11/16/06	AHB21098
A/swine/North Carolina/01469/2007(H3N2)	USA	2/21/07	AHB23010
A/swine/North Carolina/01484/2006(H3N2)	USA	11/3/06	AHB21110
A/swine/North Carolina/01506/2006(H3N2)	USA	10/31/06	AHB22950
A/swine/North Carolina/01514/2007(H1N1)	USA	1/26/07	AHB23034
A/swine/North Carolina/01550/2007(H1N1)	USA	4/4/07	AHB23046
A/swine/North Carolina/01591/2007(H1N1)	USA	4/24/07	AHB22998
A/swine/North Carolina/01855/2007(H1N1)	USA	11/14/07	AHB23022
A/swine/North Carolina/01930/2007(H3N2)	USA	7/27/07	AHB21292
A/swine/North Carolina/02249/2008(H1N2)	USA	7/30/08	AHB21471
A/swine/North Carolina/02403/2008(H1N1)	USA	9/12/08	AHB21507
A/swine/North Carolina/03289/2011(H3N2)	USA	1/7/11	AHB21912

A/swine/North Carolina/SG1197/2004(H3N2)	USA	12/30/04	AHB20855
A/swine/North Carolina/SG1199/2004(H3N2)	USA	12/2/04	AHB82076
A/swine/North Carolina/SG1229/2005(H1N1)	USA	12/6/05	AHB23675
A/swine/North Carolina/SG1230/2005(H3N2)	USA	3/16/05	AHB20966
A/swine/North Carolina/SG1255/2006(H1N1)	USA	5/18/06	AHB23713
A/swine/North Carolina/SG1278/2007(H1N1)	USA	11/20/07	AHB21266
A/swine/North Carolina/SG1279/2007(H1N1)	USA	10/23/07	AHB23755
A/swine/North Carolina/SG1281/2007(H1N1)	USA	2/1/07	AHB22353
A/swine/North Carolina/SG1282/2007(mixed)	USA	10/25/07	AHB21280
A/swine/North Carolina/SG1306/2008(H3N2)	USA	7/3/08	AHB21447
A/swine/North Carolina/SG1307/2008(H1N1)	USA	9/16/08	AHB22365
A/swine/North Carolina/SG1307/2008(H1N1)	USA	9/16/08	AHB21459
A/swine/North Carolina/SG1309/2008(H1N1)	USA	10/23/08	AHB21483
A/swine/North Carolina/SG1310/2008(H1N1)	USA	11/11/08	AHB21495
A/swine/North Carolina/SG1313/2008(H1N1)	USA	9/26/08	AHB21519
A/swine/North Carolina/SG1314/2008(H1N1)	USA	9/16/08	AHB21531
A/swine/North Carolina/SG1334/2009(H1N1)	USA	1/20/09	AHB21639
A/swine/North Carolina/SG1335/2009(H1N2)	USA	1/20/09	AHB22401
A/swine/North Carolina/SG1335/2009(H1N2)	USA	1/20/09	AHB21651
A/swine/North Carolina/SG1338/2009(H3N2)	USA	2/6/09	AHB21663
A/swine/North Carolina/SG1357/2010(H1N2)	USA	1/13/10	AHB21746
A/swine/North Carolina/SG1358/2010(H3N2)	USA	9/24/10	AHB21758
A/swine/North Carolina/SG1359/2010(H1N2)	USA	2/19/10	AHB24464
A/swine/North Carolina/SG1360/2010(H1N2)	USA	4/21/10	AHB21769
A/swine/North Carolina/SG1361/2010(H1N1)	USA	6/18/10	AHB21781
A/swine/North Carolina/SG1363/2010(H1)	USA	4/1/10	AHB82082
A/swine/North Carolina/SG1364/2010(H3N2)	USA	11/24/10	AHB24501
A/swine/North Carolina/SG1364/2010(H3N2)	USA	11/24/10	AHB22437

A/swine/North Carolina/SG1365/2010(H1N2)	USA	10/29/10	AHB21793
A/swine/North Carolina/SG1387/2011(H1N1)	USA	9/30/11	AHB21936
A/swine/North Carolina/SG1388/2011(H1N2)	USA	3/25/11	AHB21948
A/swine/North Carolina/SG1389/2011(H1N2)	USA	3/18/11	AHB21960
A/swine/North Carolina/SG1391/2011(H1N2)	USA	3/30/11	AHB21972
A/swine/North Carolina/SG1394/2011(H1N2)	USA	9/28/11	AHB22471
A/swine/North Carolina/SG1462/2004(H3N2)	USA	3/3/04	AHB22710
A/swine/North Carolina/SG1463/2004(H1N1)	USA	8/27/04	AHB22722
A/swine/North Carolina/SG1464/2004(H3N2)	USA	3/10/04	AHB22734
A/swine/North Carolina/SG1477/2005(H1N1)	USA	10/20/05	AHB22878
A/swine/North Carolina/SG1478/2005(H1N1)	USA	5/5/05	AHB22890
A/swine/North Carolina/SG1479/2005(H1N1)	USA	12/8/05	AHB22902
A/swine/Oklahoma/00130/2003(H1N1)	USA	8/12/03	AHB23166
A/swine/Oklahoma/00259/2004(H1N2)	USA	3/3/04	AHB22674
A/swine/Oklahoma/00518/2005(H3N2)	USA	3/1/05	AHB22305
A/swine/Oklahoma/00518/2005(H3N2)	USA	3/1/05	AHB20930
A/swine/Oklahoma/00606/2005(H3N2)	USA	5/4/05	AHB23243
A/swine/Oklahoma/00790/2005(H1N1)	USA	9/23/05	AHB22830
A/swine/Oklahoma/00801/2005(H1N1)	USA	10/4/05	AHB22854
A/swine/Oklahoma/01117/2006(H1N2)	USA	5/2/06	AHB22317
A/swine/Oklahoma/01139/2006(H1N1)	USA	5/17/06	AHB22926
A/swine/Oklahoma/01382/2006(H1N2)	USA	12/6/06	AHB22938
A/swine/Oklahoma/01741/2007(H1N2)	USA	8/23/07	AHB21242
A/swine/Oklahoma/02056/2008(H1N2)	USA	2/29/08	AHB21424
A/swine/Oklahoma/02107/2008(H1N2)	USA	4/2/08	AHB21412
A/swine/Oklahoma/02530/2009(H3N2)	USA	1/9/09	AHB23821
A/swine/Oklahoma/02722/2009(H1N2)	USA	4/10/09	AHB23058
A/swine/Oklahoma/02985/2010(H3N2)	USA	3/10/10	AHB24441

A/swine/Oklahoma/02989/2010(H1N1)	USA	3/12/10	AHB24452
A/swine/Oklahoma/SG1216/2005(H3N2)	USA	3/3/05	AHB20942
A/swine/Oklahoma/SG1217/2005(H1N1)	USA	12/6/05	AHB20954
A/swine/Oklahoma/SG1243/2006(H1N1)	USA	10/6/06	AHB21026
A/swine/Oklahoma/SG1244/2006(H1N1)	USA	6/7/06	AHB21038
A/swine/Oklahoma/SG1249/2006(H1N1)	USA	6/7/06	AHB23687
A/swine/Oklahoma/SG1251/2010(H1N1)	USA	9/24/10	AHB21723
A/swine/Oklahoma/SG1325/2009(H1N1)	USA	2/4/09	AHB21591
A/swine/Oklahoma/SG1349/2010(H1N1)	USA	9/24/10	AHB22425
A/swine/Oklahoma/SG1349/2010(H1N2)	USA	11/10/10	AHB24429
A/swine/Oklahoma/SG1457/2004(H1N1)	USA	9/23/04	AHB22650
A/swine/Oklahoma/SG1458/2004(H1N1)	USA	9/1/04	AHB22662
A/swine/Oklahoma/SG1460/2004(H1N1)	USA	8/26/04	AHB22686
A/swine/Oklahoma/SG1473/2005(H3N2)	USA	9/23/05	AHB22842
A/swine/Oklahoma/SG1498/2010(H3N2)	USA	11/11/10	AHB24833
A/swine/Oklahoma/SG1500/2010(H1N1)	USA	10/19/10	AHB23128
A/swine/Oklahoma/SG1501/2010(mixed)	USA	11/18/10	AHB23141
A/swine/Oklahoma/SG1501/2010(mixed)	USA	11/18/10	AHB23142
A/swine/Quebec/00686/2005(H3N2)	Canada	9/14/05	AHB24669
A/swine/Quebec/01000/2006(H3N2)	Canada	2/23/06	AHB82085
A/swine/Quebec/01001/2006(H3N2)	Canada	2/23/06	AHB22092
A/swine/Quebec/01002/2006(H3N2)	Canada	2/23/06	AHB24707
A/swine/Saskatchewan/01114/2006(H3N2)	Canada	5/1/06	AHB22104
A/swine/Saskatchewan/01974/2008(H1N1)	Canada	1/8/08	AHB24744
A/swine/Saskatchewan/01974/2008(H1N1)	Canada	1/8/08	AHB22531
A/swine/Saskatchewan/02903/2009(H3N2)	Canada	9/24/09	AHB22224
A/swine/Saskatchewan/SD0001/2011(H3N2)	Canada	12/1/11	AHB22543
A/swine/South Carolina/01414/2006(H1N1)	USA	12/19/06	AHB22974

A/swine/South Dakota/SG1453/2003(H3N2)	USA	4/10/03	AHB22602
A/swine/Tennessee/00264/2004(H1N1)	USA	3/11/04	AHB20867
A/swine/Texas/00244/2004(H1N1)	USA	2/4/04	AHB22638
A/swine/Texas/00376/2004(H3N2)	USA	7/22/04	AHB23193
A/swine/Texas/00816/2005(H3N2)	USA	10/12/05	AHB22866
A/swine/Texas/00867/2005(H1N1)	USA	11/17/05	AHB22818
A/swine/Texas/01308/2006(H1N2)	USA	11/2/06	AHB21050
A/swine/Texas/01492/2007(H1N2)	USA	3/8/07	AHB21230
A/swine/Texas/01522/2007(H1N1)	USA	3/13/07	AHB21182
A/swine/Texas/01657/2007(H1N1)	USA	6/21/07	AHB21218
A/swine/Texas/01822/2007(H3N1)	USA	10/25/07	AHB21206
A/swine/Texas/03042/2010(H3N2)	USA	7/2/10	AHB21735
A/swine/Texas/SG1186/2004(H3N2)	USA	10/22/04	AHB20833
A/swine/Texas/SG1250/2006(H1N2)	USA	6/21/06	AHB21062
A/swine/Texas/SG1270/2007(H3N2)	USA	3/1/07	AHB23744
A/swine/Texas/SG1271/2007(H1N1)	USA	10/25/07	AHB21194
A/swine/Texas/SG1380/2011(H1N1)	USA	10/6/11	AHB22460
A/swine/Texas/SG1501/2010(H3N2)	USA	4/20/10	AHB23154
A/swine/Virginia/01359/2006(H1N1)	USA	11/28/06	AHB21074
A/swine/Virginia/SG1386/2011(H1N2)	USA	11/4/11	AHB21924

Supplementary Table 4. Sensitivity analysis for GLM model for 1990-2013 and 2000-2013 using an 'epoch extension'. Live swine trade was still found to be the only well-supported predictor of viral migration.

Predictor	Inclusion probability (1990-2013)	Ln coefficient (1990-2013)	Inclusion probability (2000-2013)	Ln coefficient (2000-2013)
Distance	0.014	-0.143	2.109E-02	-9.933E-02
Swine trade	1.000	4.918	1.000	4.972
Swine pop size (origin)	6.659E-3	0.047	1.443E-02	-9.978E-02
Swine pop size (destination)	0.017	-0.035	1.665E-02	-3.479E-02
Swine import (o)	0.021	-0.024	2.775E-02	2.293E-02
Swine import (d)	0.021	-0.036	1.887E-02	-8.445E-02
Swine export (o)	7.770E-3	0.114	1.443E-02	-8.251E-02
Swine export (d)	7.770E-3	0.098	5.549E-03	3.037E-02
Swine pop change (o)	0.014	-0.073	2.109E-02	-8.834E-02
Swine pop change (d)	0.019	0.015	3.108E-02	3.520E-02
Sample size (o)	0.012	-0.097	2.331E-02	-2.975E-02
Sample size (d)	8.879E-3	-0.113	7.769E-03	1.030E-01

Supplementary Table 5. Probabilities of viral invasion estimated from simulation model. Probabilities of viral invasion for five seed countries (USA, Canada, China, Mexico, United Kingdom, and France) and for co-invasion by North American (USA and Canada) and European viruses, as visualized in Fig. 6.

Country	P(invasion)
USA source	
China	0.912
Hong Kong	0.912
Mexico	0.912
Russian Federation	0.912
South Korea	0.912
Canada	0.911
Venezuela	0.867
Cuba	0.796
Japan	0.796
Chile	0.755
Cambodia	0.73
Vietnam	0.683
Brazil	0.625
Guatemala	0.5
Philippines	0.496
Panama	0.453
Thailand	0.449
Ukraine	0.355
Costa Rica	0.323
Belarus	0.315
Kazakhstan	0.315

Country	P(invasion)
Canada source	
USA	0.911
China	0.909
Cuba	0.909
Hong Kong	0.909
Mexico	0.909
Russian Federation	0.909
South Korea	0.909
Venezuela	0.875
Japan	0.798
Chile	0.769
Cambodia	0.745
Vietnam	0.685
Brazil	0.625
Philippines	0.516
Guatemala	0.5
Thailand	0.485
Panama	0.424
Ukraine	0.368
Belarus	0.342
Costa Rica	0.326
Czech Republic	0.324

Country	P(invasion)
China source	
Hong Kong	0.913
Cambodia	0.693
Japan	0.06
South Korea	0.039
Indonesia	0.038
Mongolia	0.016
Singapore	0.015
Russian Federation	0.009
Austria	0.003
Albania	0.002
Belarus	0.002
Belgium	0.002
Bosnia and Herzegovina	0.002
Croatia	0.002
Czech Republic	0.002
France	0.002
Georgia	0.002
Germany	0.002
Greece	0.002
Hungary	0.002
Italy	0.002

Country	P(invasion)
Mexico source	
Costa Rica	0.087
Guatemala	0.016
Cuba	0.012
Japan	0.004

Czech Republic	0.304
Singapore	0.302
Poland	0.284
United Kingdom	0.278
Colombia	0.277
Ecuador	0.271
Lithuania	0.264
Germany	0.262
Georgia	0.25
Croatia	0.249
Belgium	0.248
France	0.247
Spain	0.242
Netherlands	0.241
Romania	0.241
Austria	0.24
Italy	0.24
Hungary	0.239
Latvia	0.238
Slovakia	0.238
Argentina	0.235
Portugal	0.233
Bosnia and Herzegovina	0.232
Luxembourg	0.232
Montenegro	0.231
Malaysia	0.211
Slovenia	0.207
Bulgaria	0.202

Kazakhstan	0.307
Poland	0.29
Singapore	0.289
Ecuador	0.285
Germany	0.282
United Kingdom	0.27
Lithuania	0.264
Belgium	0.263
Georgia	0.26
Colombia	0.254
Croatia	0.253
Spain	0.251
France	0.25
Austria	0.248
Netherlands	0.248
Italy	0.247
Romania	0.247
Hungary	0.244
Slovakia	0.244
Bosnia and Herzegovina	0.242
Latvia	0.242
Luxembourg	0.241
Portugal	0.241
Montenegro	0.24
Slovenia	0.227
Argentina	0.218
Greece	0.206
Peru	0.202

Latvia	0.002
Lebanon	0.002
Lithuania	0.002
Luxembourg	0.002
Montenegro	0.002
Netherlands	0.002
Poland	0.002
Portugal	0.002
Romania	0.002
Serbia	0.002
Slovakia	0.002
Spain	0.002
Thailand	0.002
Ukraine	0.002
Bulgaria	0.001
Colombia	0.001
Denmark	0.001
Kazakhstan	0.001
Mozambique	0.001
Slovenia	0.001

Greece	0.188
Albania	0.186
Serbia	0.186
Peru	0.185
India	0.16
Dominican Republic	0.116
Indonesia	0.081
Denmark	0.068
El Salvador	0.066
Honduras	0.057
Switzerland	0.034
Paraguay	0.033
Ireland	0.032
Armenia	0.026
Jamaica	0.025
Malta	0.025
Netherlands Antilles	0.025
Syria	0.023
South Africa	0.022
Guyana	0.02
Australia	0.017
Belize	0.017
Saint Lucia	0.017
Cyprus	0.016
Kyrgyzstan	0.013
Mongolia	0.013
Uruguay	0.013
Sweden	0.011
Estonia	0.009
Aruba	0.006

Malaysia	0.198
Albania	0.187
Bulgaria	0.181
Serbia	0.181
India	0.167
Dominican Republic	0.133
Indonesia	0.094
El Salvador	0.081
Denmark	0.077
Honduras	0.05
Paraguay	0.045
Ireland	0.037
Switzerland	0.034
Syria	0.032
Australia	0.028
Jamaica	0.025
Netherlands Antilles	0.023
South Africa	0.022
Armenia	0.019
Kyrgyzstan	0.019
Cyprus	0.018
Malta	0.018
Estonia	0.017
Sweden	0.017
Belize	0.016
Guyana	0.016
Mongolia	0.014
Uruguay	0.012
Saint Lucia	0.01
Tunisia	0.008

Bahamas	0.005
Tunisia	0.004
Israel	0.003
Kenya	0.003
Cote d Ivoire	0.002
Lebanon	0.001
Mozambique	0.001
Norway	0.001
Seychelles	0.001

Kenya	0.006
Aruba	0.005
Bahamas	0.004
Seychelles	0.003
Grenada	0.002
Israel	0.002
Lebanon	0.002
Norway	0.002
Suriname	0.002
Cote d Ivoire	0.001
Rwanda	0.001
Tanzania	0.001

Country	P(invasion)
United Kingdom source	
Russian Federation	0.877
Germany	0.863
China	0.852
Spain	0.801
Ukraine	0.795
Netherlands	0.794
Belgium	0.791
Italy	0.79
France	0.784

Country	P(invasion)
France source	
Austria	0.904
Belgium	0.904
Croatia	0.904
Czech Republic	0.904
Germany	0.904
Hungary	0.904
Italy	0.904
Lithuania	0.904
Luxembourg	0.904

Country	P(invasion)
North America and Europe sources (co-invasion)	
Russian Federation	0.824
China	0.801
South Korea	0.698
Hong Kong	0.602
Cambodia	0.375
Ukraine	0.321
Czech Republic	0.275
Poland	0.257
France	0.247

Romania	0.78
Croatia	0.762
Czech Republic	0.759
Austria	0.757
Hungary	0.757
Poland	0.755
Slovakia	0.755
Luxembourg	0.752
Portugal	0.752
Lithuania	0.751
Montenegro	0.748
Bosnia and Herzegovina	0.745
Georgia	0.745
Latvia	0.732
Hong Kong	0.691
South Korea	0.69
Slovenia	0.667
Belarus	0.65
Greece	0.642
Serbia	0.614
Bulgaria	0.592
Cambodia	0.59
Albania	0.576
Kazakhstan	0.546
Japan	0.449
Vietnam	0.203
Philippines	0.198
Malta	0.159

Netherlands	0.904
Poland	0.904
Portugal	0.904
Romania	0.904
Russian Federation	0.904
Slovakia	0.904
Spain	0.904
Ukraine	0.904
Montenegro	0.894
Bosnia and Herzegovina	0.886
Latvia	0.883
China	0.878
Georgia	0.867
Slovenia	0.778
Belarus	0.772
South Korea	0.765
Albania	0.707
Serbia	0.705
Greece	0.701
Bulgaria	0.678
Hong Kong	0.66
Kazakhstan	0.642
Cambodia	0.514
Vietnam	0.189
Japan	0.163
Denmark	0.146
Brazil	0.143
Philippines	0.142

Belarus	0.243
Lithuania	0.239
Germany	0.237
Croatia	0.225
Belgium	0.224
Spain	0.219
Netherlands	0.218
Romania	0.218
Austria	0.217
Italy	0.217
Georgia	0.217
Hungary	0.216
Slovakia	0.215
Portugal	0.211
Latvia	0.210
Luxembourg	0.210
Montenegro	0.207
Bosnia and Herzegovina	0.206
Kazakhstan	0.202
Slovenia	0.161
Bulgaria	0.137
Greece	0.132
Albania	0.132
Serbia	0.131
Japan	0.130
Vietnam	0.129
Brazil	0.089
Philippines	0.070

Mexico	0.143
Denmark	0.134
Canada	0.13
Brazil	0.115
Chile	0.108
Thailand	0.106
Switzerland	0.1
Ireland	0.083
Syria	0.083
Armenia	0.08
USA	0.076
Venezuela	0.074
Cuba	0.063
Cyprus	0.058
Singapore	0.051
Colombia	0.045
Malaysia	0.044
Indonesia	0.039
Sweden	0.038
Costa Rica	0.033
Panama	0.033
Argentina	0.031
Guatemala	0.03
Ecuador	0.021
Peru	0.015
Dominican Republic	0.014
Kenya	0.013
Kyrgyzstan	0.013
Uruguay	0.013
India	0.011

Switzerland	0.135
Armenia	0.099
Cyprus	0.077
Syria	0.07
Chile	0.062
United Kingdom	0.058
Thailand	0.053
Canada	0.046
Sweden	0.045
Indonesia	0.038
Argentina	0.035
Venezuela	0.035
Mexico	0.032
USA	0.03
Singapore	0.029
Colombia	0.026
Cuba	0.025
Costa Rica	0.022
Malaysia	0.017
Tunisia	0.016
Guatemala	0.015
Panama	0.014
Uruguay	0.013
Kyrgyzstan	0.012
Mongolia	0.012
Kenya	0.011
Norway	0.008
Estonia	0.007
Ireland	0.006
South Africa	0.006

Chile	0.047
Canada	0.042
Venezuela	0.030
USA	0.030
Mexico	0.029
Thailand	0.024
Cuba	0.020
United Kingdom	0.016
Denmark	0.010
Singapore	0.009
Argentina	0.008
Guatemala	0.008
Colombia	0.007
Costa Rica	0.007
Panama	0.006
Switzerland	0.005
Malaysia	0.004
Indonesia	0.003
Armenia	0.003
Syria	0.002
Ecuador	0.001
Cyprus	0.001

Mongolia	0.009
Paraguay	0.008
Turkey	0.008
South Africa	0.007
Tunisia	0.007
Norway	0.006
Seychelles	0.006
Lebanon	0.005
Estonia	0.004
Netherlands Antilles	0.004
Nigeria	0.004
El Salvador	0.003
Honduras	0.003
Jamaica	0.003
Saint Lucia	0.002
Antigua and Barbuda	0.001
Australia	0.001
Cote d Ivoire	0.001
Gabon	0.001
Guyana	0.001
Mozambique	0.001
Senegal	0.001
Suriname	0.001

Ecuador	0.005
Gabon	0.005
Turkey	0.005
Dominican Republic	0.004
Paraguay	0.004
India	0.003
Mozambique	0.003
Australia	0.002
Cote d Ivoire	0.002
Malta	0.002
Netherlands Antilles	0.002
Peru	0.002
Bahamas	0.001
Belize	0.001
Honduras	0.001
Lebanon	0.001
Seychelles	0.001
Suriname	0.001

Supplementary Table 6. Data sets used in this study. The 22 segment- and lineage-specific data sets of swine influenza A viruses collected globally that were used in the spatial analysis. For each data set, the number of sequences and the countries for which sequence data were available are listed (Arg = Argentina; Can = Canada; Chi = China; Eur = European countries; Kor = South Korea; Jap = Japan; Mex = Mexico; Thai = Thailand; USA = United States; Viet = Vietnam).

Segment		**Classical**	**TRIG**	**Eurasian**	**Human seasonal**
PB2	No. sequences	213	340	192	
	Countries	Can Chi Eur Jap USA	Can Chi Kor Mex USA Viet	Chi Eur Thai	
PB1	No. sequences	211	344	190	
	Countries	Can Chi Eur Jap USA	Can Chi Kor Mex USA Viet	Chi Eur Thai	
PA	No. sequences	213	329	190	
	Countries	Can Chi Eur Jap USA	Can Chi Kor USA Viet	Chi Eur Thai	
H1	No. sequences	321		140	192
	Countries	Can Chi Eur Jap Kor Thai USA		Chi Eur Kor	Arg Eur USA Viet
H3	No. sequences				459

	Countries			Arg Can Chi Eur Kor Mex Thai USA Viet
NP	No. sequences	549	186	
	Countries	Can Chi Eur Jap Kor Mex Thai USA Viet	Chi Eur Thai	
N1	No. sequences	286	150	
	Countries	Can Chi Eur Jap USA	Chi Eur Thai	
N2	No. sequences			675
	Countries			Arg Can Chi Eur Jap Kor Mex Thai USA Viet
MP	No. sequences	495	199	
	Countries	Can Chi Eur Jap Kor Mex USA Viet	Chi Eur Thai	
NS	No. sequences	583	163	
	Countries	Can,Chi,Eur,Jap,Kor,Mex,Thai,USA,Viet	Chi, Eur, Thai	

Supplementary Table 7. Pig population sizes by country. Data for the year 2010 is provided. Data from previous years (1969-2009) is available at http://data.fao.org/datasets).

Country	Pig population in 2010
Albania	164,000
Algeria	5,500
American Samoa	10,500
Angola	1,934,764
Antigua and Barbuda	3,000
Argentina	2,300,000
Armenia	112,608
Australia	2,289,292
Austria	3,136,967
Azerbaijan	5,347
Bahamas	5,000
Barbados	21,500
Belarus	3,781,500
Belgium	6,430,000
Belize	17,400
Benin	368,000
Bermuda	800
Bhutan	19,711
Bolivia (Plurinational State of)	2,640,616
Bosnia and Herzegovina	590,431
Botswana	12,950
Brazil	39,000,000
British Virgin Islands	1,500
Brunei Darussalam	1,300
Bulgaria	729,798

Burkina Faso	2,167,245
Burundi	244,362
Cabo Verde	238,600
Cambodia	2,057,431
Cameroon	2,150,000
Canada	12,700,000
Cayman Islands	1,063
Central African Republic	1,087,000
Chad	30,400
Chile	2,706,148
China	476,000,000
China, Hong Kong SAR	170,000
China, Taiwan Province of	6,130,003
China, mainland	470,000,000
Colombia	5,161,804
Congo	88,000
Cook Islands	32,200
Costa Rica	438,000
Croatia	1,231,000
Cuba	1,591,000
Cyprus	463,729
Czech Republic	1,909,000
CÌ«te d'Ivoire	348,590
Democratic People's Republic of Korea	2,248,000
Democratic Republic of the Congo	977,379
Denmark	13,200,000
Dominica	5,000
Dominican Republic	620,000

Ecuador	1,489,761
Egypt	10,500
El Salvador	427,000
Equatorial Guinea	6,400
Estonia	365,100
Ethiopia	31,000
Falkland Islands (Malvinas)	40
Fiji	145,700
Finland	1,366,932
France	14,300,000
French Guiana	9,900
French Polynesia	30,000
Gabon	215,000
Gambia	28,500
Georgia	135,200
Germany	26,500,000
Ghana	536,000
Greece	1,087,000
Grenada	3,000
Guadeloupe	16,319
Guam	5,200
Guatemala	2,733,280
Guinea	95,187
Guinea-Bissau	394,147
Guyana	13,600
Haiti	1,001,000
Honduras	469,635
Hungary	3,247,000

Iceland	40,016
India	9,630,000
Indonesia	7,477,000
Ireland	1,516,300
Israel	223,000
Italy	9,157,100
Jamaica	197,400
Japan	9,800,000
Kazakhstan	1,326,300
Kenya	347,413
Kiribati	13,000
Kyrgyzstan	59,791
Lao People's Democratic Republic	2,752,000
Latvia	376,500
Lebanon	7,735
Lesotho	83,976
Liberia	265,300
Liechtenstein	1,690
Lithuania	928,200
Luxembourg	83,774
Madagascar	1,380,250
Malawi	1,861,503
Malaysia	1,922,321
Mali	75,089
Malta	70,583
Martinique	11,193
Mauritius	22,327
Mexico	15,400,000

Micronesia (Federated States of)	33,000
Mongolia	24,842
Montenegro	11,205
Montserrat	1,200
Morocco	8,500
Mozambique	1,340,712
Myanmar	9,416,208
Namibia	65,000
Nauru	3,000
Nepal	1,064,858
Netherlands	12,300,000
Netherlands Antilles	2,710
New Caledonia	37,000
New Zealand	335,114
Nicaragua	480,000
Niger	40,000
Nigeria	7,471,730
Niue	2,100
Norway	850,383
Panama	276,400
Papua New Guinea	1,950,000
Paraguay	1,181,930
Peru	3,254,413
Philippines	13,400,000
Poland	14,900,000
Portugal	1,917,000
Puerto Rico	50,000
Republic of Korea	9,880,632

Republic of Moldova	377,142
Romania	5,793,400
Russian Federation	17,200,000
Rwanda	684,708
Saint Kitts and Nevis	6,000
Saint Lucia	20,000
Saint Vincent and the Grenadines	8,000
Samoa	203,000
Sao Tome and Principe	2,850
Senegal	354,474
Serbia	3,488,738
Seychelles	4,470
Sierra Leone	47,364
Singapore	270,000
Slovakia	740,862
Slovenia	415,230
Solomon Islands	54,000
Somalia	4,000
South Africa	1,594,494
Spain	25,700,000
Sri Lanka	83,790
Suriname	32,125
Swaziland	32,000
Sweden	1,519,900
Switzerland	1,588,998
Syrian Arab Republic	0
Tajikistan	418
Thailand	7,623,730

Macedonia	190,552
Timor-Leste	415,315
Togo	564,900
Tokelau (Associate Member)	1,000
Tonga	81,200
Trinidad and Tobago	34,799
Tunisia	5,800
Turkey	1,896
Turkmenistan	30,000
Tuvalu	13,600
Uganda	2,297,000
Ukraine	7,576,600
United Kingdom	4,460,000
United Republic of Tanzania	495,000
United States Virgin Islands	2,650
United States of America	64,900,000
Uruguay	210,000
Uzbekistan	92,000
Vanuatu	90,000
Venezuela (Bolivarian Republic of)	3,385,000
Viet Nam	27,400,000
Wallis and Futuna Islands	25,000
Zambia	715,000
Zimbabwe	635,000