Supplementary Material

Supplementary Figure 1. Maximum likelihood tree of the HA1 domain of influenza B virus. Bootstrap values >70% are shown next to appropriate nodes. The major 'Vic87' and 'Yam88' lineages are also shown. The tree is mid-pointed rooted for purposes of clarity only, and all horizontal branch lengths are drawn to a scale of nucleotide substitutions per site. Branches are color-coded according to Figure 1.

Supplementary Figure 2. Maximum likelihood tree of the NA gene segment of influenza B virus. Bootstrap values >70% are shown next to appropriate nodes. Two major viral lineages – I and II – are indicated. Because of frequent reassortment, their correspondence to the Vic87 and Yam88 cannot be assigned with certainty. The tree is mid-pointed rooted for purposes of clarity only, and all horizontal branch lengths are drawn to a scale of nucleotide substitutions per site. Branches are color-coded according to Figure 1.

Supplementary Figure 3. Maximum likelihood tree of the PB2 gene segment of influenza B virus. Bootstrap values >70% are shown next to appropriate nodes. Two major viral lineages – I and II – are indicated. Because of frequent reassortment, their correspondence to the Vic87 and Yam88 cannot be assigned with certainty. The tree is mid-pointed rooted for purposes of clarity only, and all horizontal branch lengths are drawn to a scale of nucleotide substitutions per site. Branches are color-coded according to Figure 1.

Supplementary Figure 4. Maximum likelihood tree of the PB1 gene segment of influenza B virus. Bootstrap values >70% are shown next to appropriate nodes. Two major viral lineages – I and II – are indicated. Because of frequent reassortment, their correspondence to the Vic87 and Yam88 cannot be assigned with certainty. The tree is mid-pointed rooted for purposes of clarity only, and all horizontal branch lengths are drawn to a scale of nucleotide substitutions per site. Branches are color-coded according to Figure 1.

Supplementary Figure 5. Maximum likelihood tree of the PA gene segment of influenza B virus. Bootstrap values >70% are shown next to appropriate nodes. Two major viral lineages – I and II – are indicated. Because of frequent reassortment, their correspondence to the Vic87 and Yam88 cannot be assigned with certainty. The tree is mid-pointed rooted for purposes of clarity only, and all horizontal branch lengths are drawn to a scale of nucleotide substitutions per site. Branches are color-coded according to Figure 1.

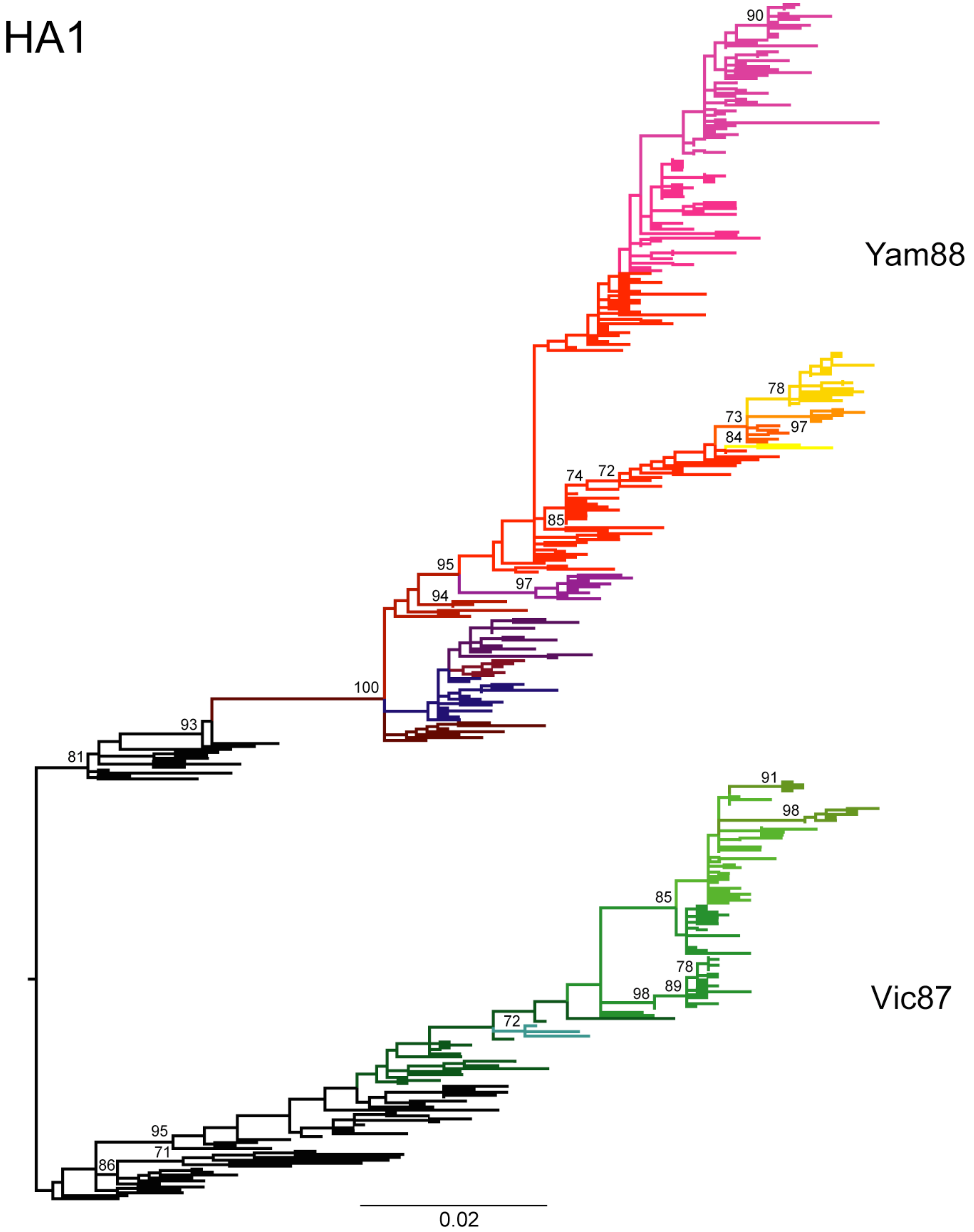
Supplementary Figure 6. Maximum likelihood tree of the NP gene segment of influenza B virus. Bootstrap values >70% are shown next to appropriate nodes. Two major viral lineages – I and II – are indicated. Because of frequent reassortment, their correspondence to the Vic87 and Yam88 cannot be assigned with certainty. The tree is mid-pointed rooted for purposes of clarity only, and all horizontal branch lengths are drawn to a scale of nucleotide substitutions per site. Branches are color-coded according to Figure 1.

Supplementary Figure 7. Maximum likelihood tree of the M1 gene of influenza B virus. Bootstrap values >70% are shown next to appropriate nodes. Two major viral lineages – I and II – are indicated. Because of frequent reassortment, their correspondence to the Vic87 and Yam88 cannot be assigned with certainty. The tree is mid-pointed rooted for purposes of clarity only, and all horizontal branch lengths are drawn to a scale of nucleotide substitutions per site. Branches are color-coded according to Figure 1.

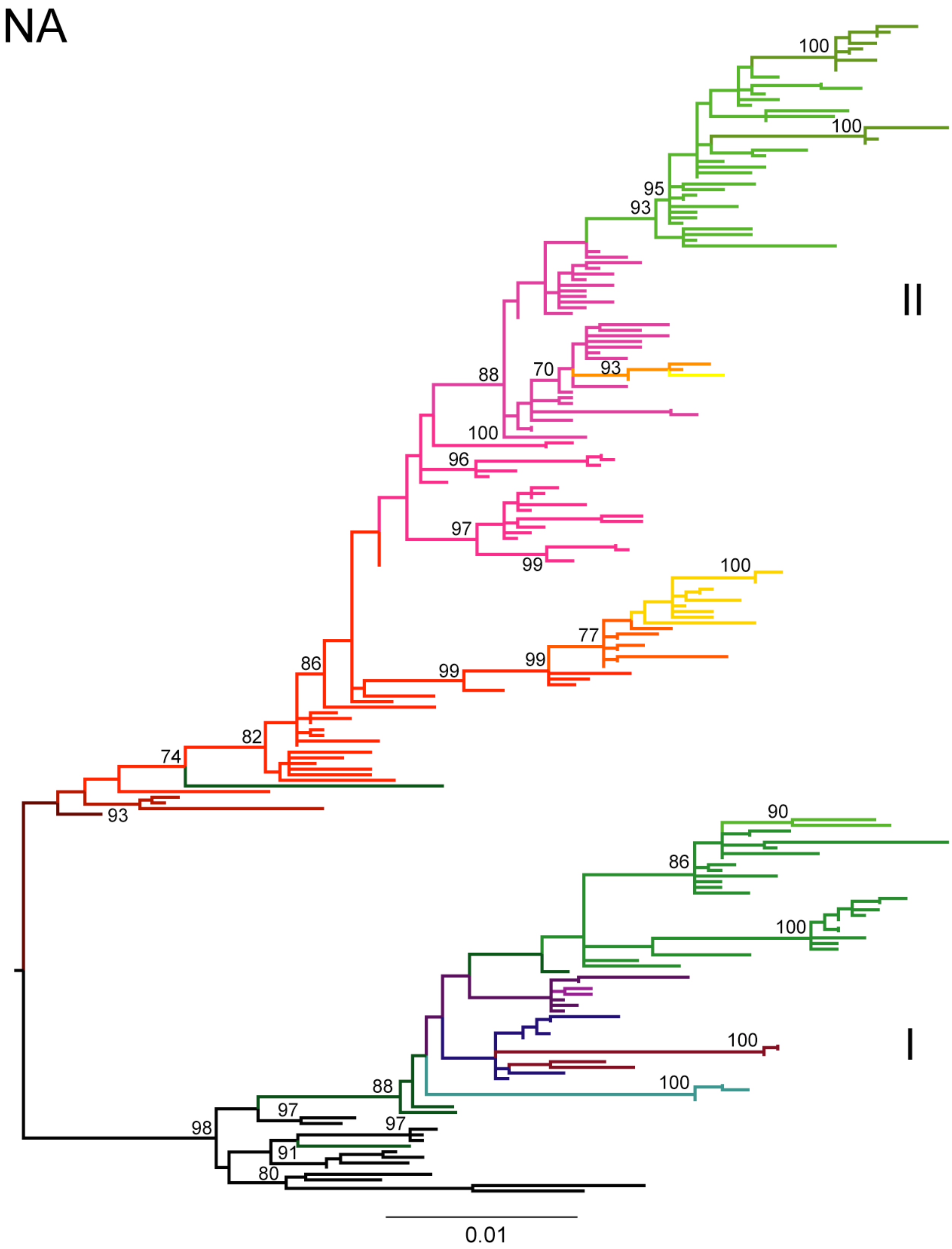
Supplementary Figure 8. Maximum likelihood tree of the NS1 gene of influenza B virus. Bootstrap values >70% are shown next to appropriate nodes. Two major viral lineages – I and

II – are indicated. Because of frequent reassortment, their correspondence to the Vic87 and Yam88 cannot be assigned with certainty. The tree is mid-pointed rooted for purposes of clarity only, and all horizontal branch lengths are drawn to a scale of nucleotide substitutions per site. Branches are color-coded according to Figure 1.

Supplementary Figure 1

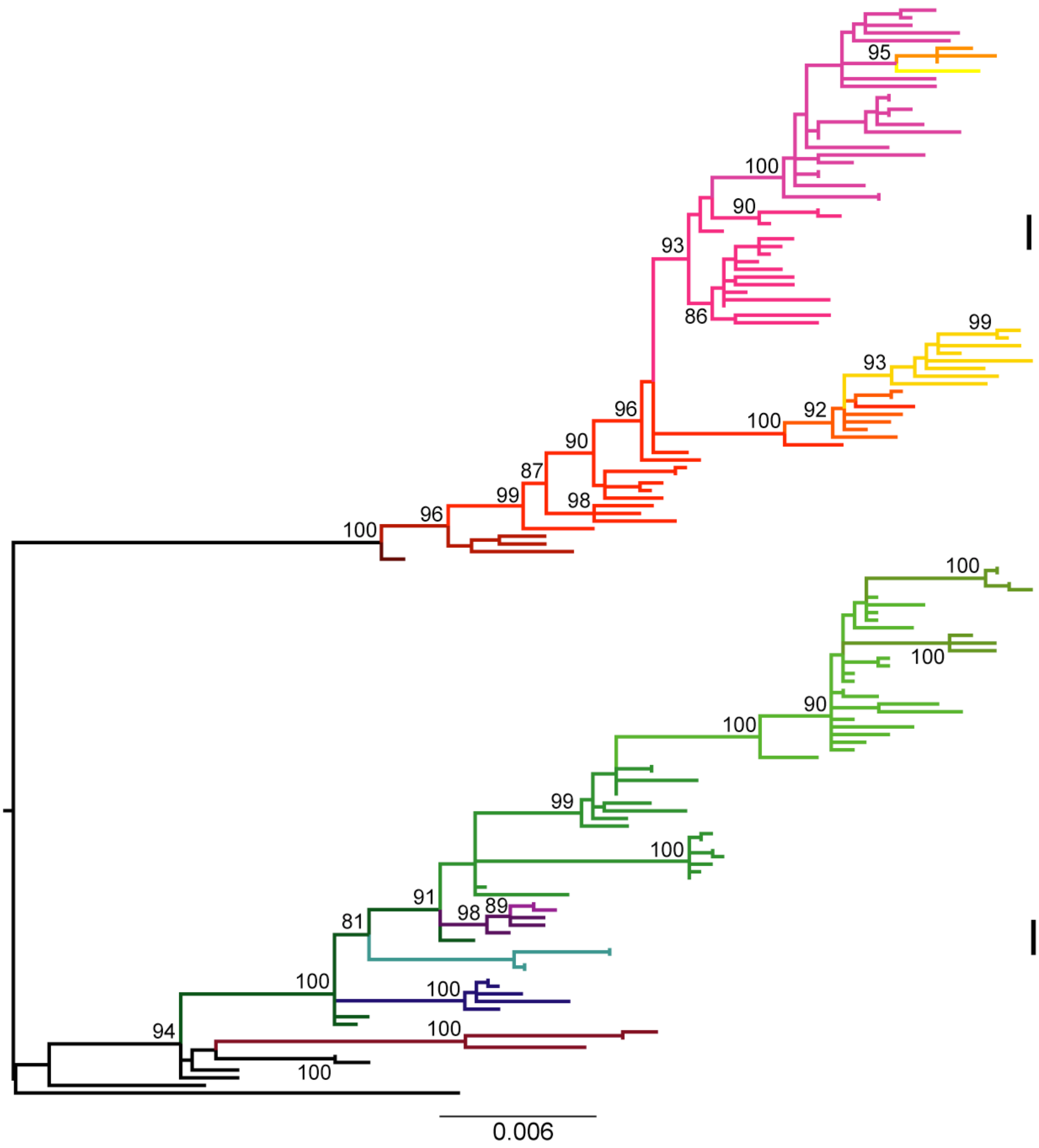


Supplementary Figure 2

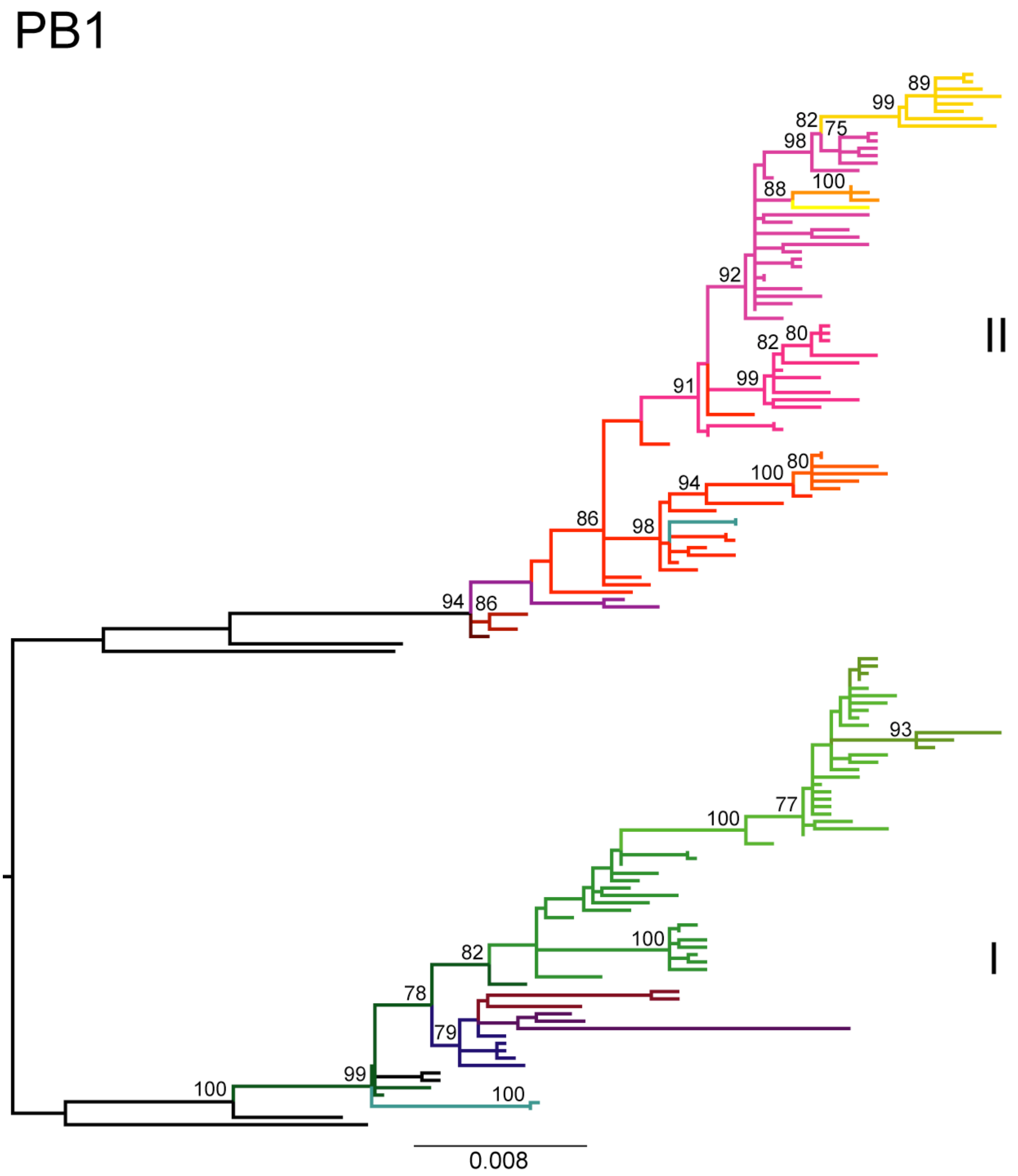


Supplementary Figure 3

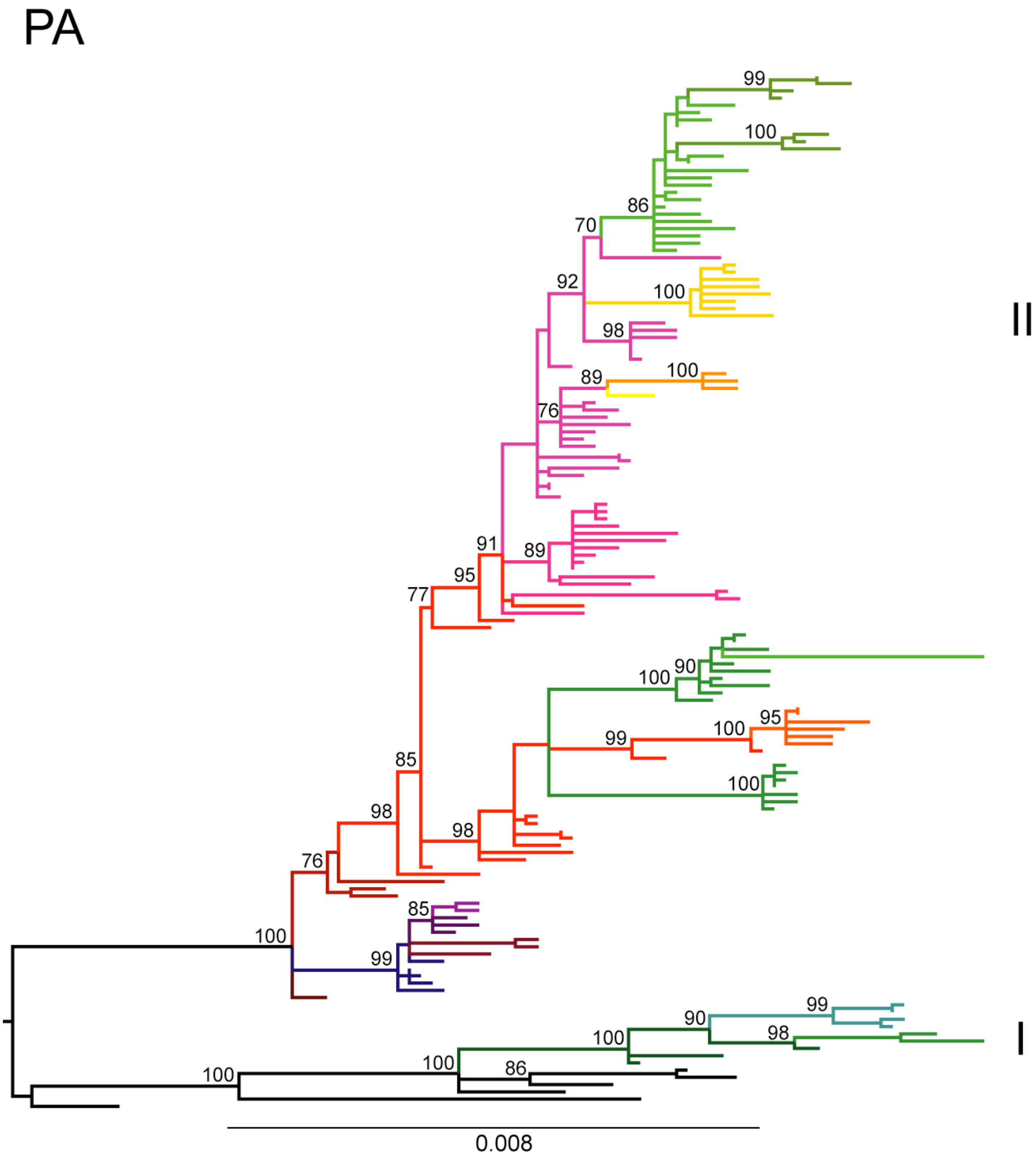
PB2



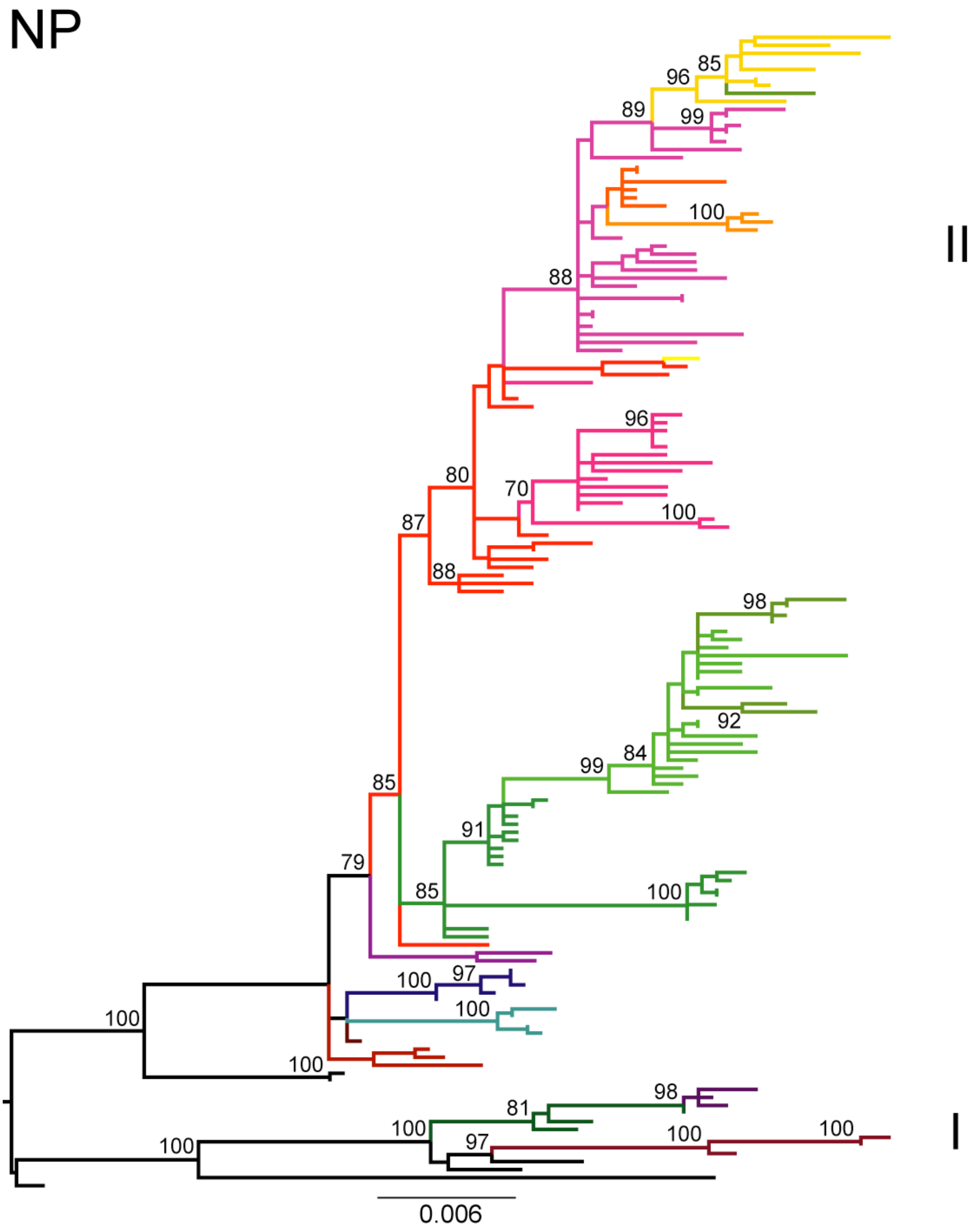
Supplementary Figure 4



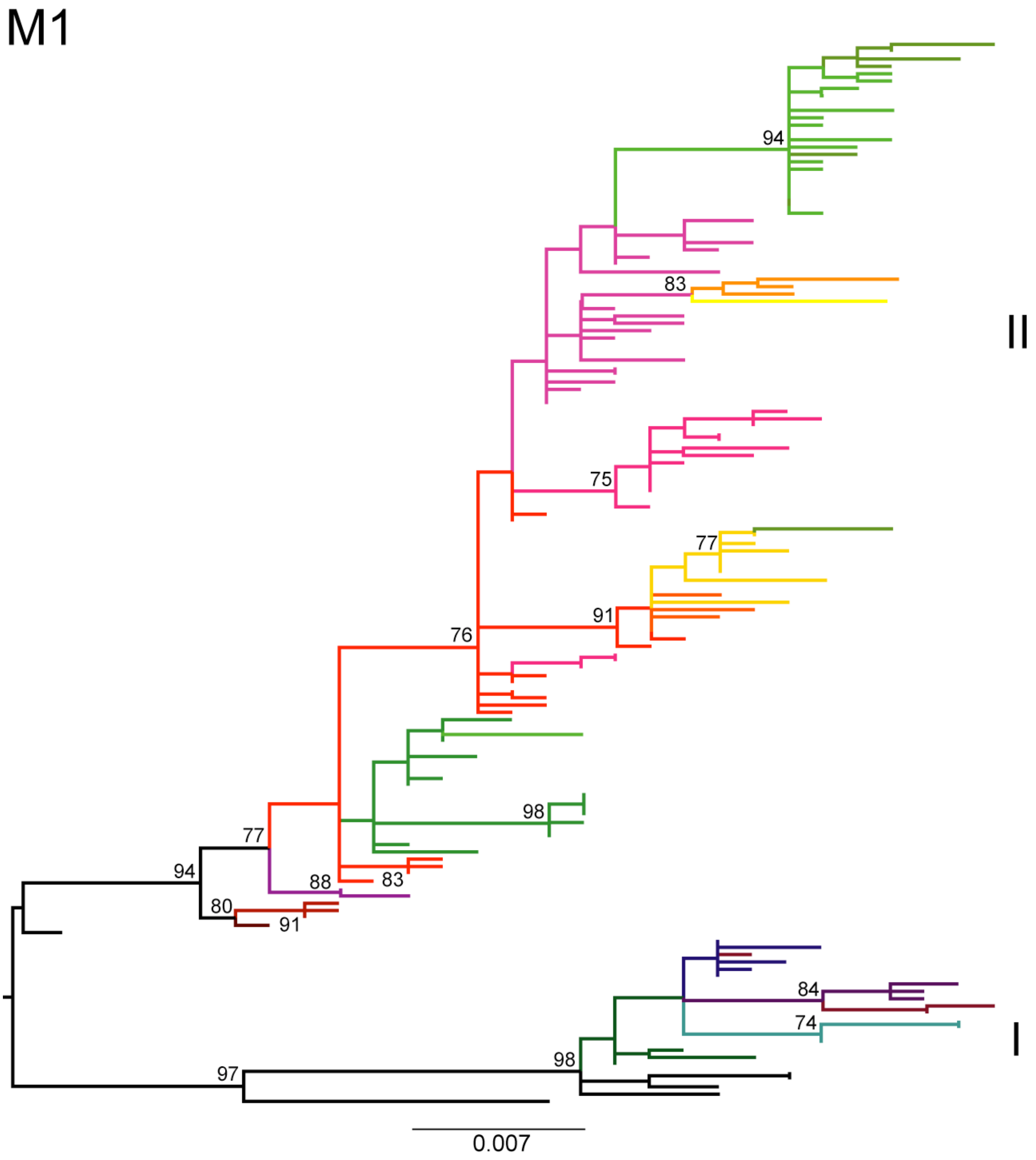
Supplementary Figure 5



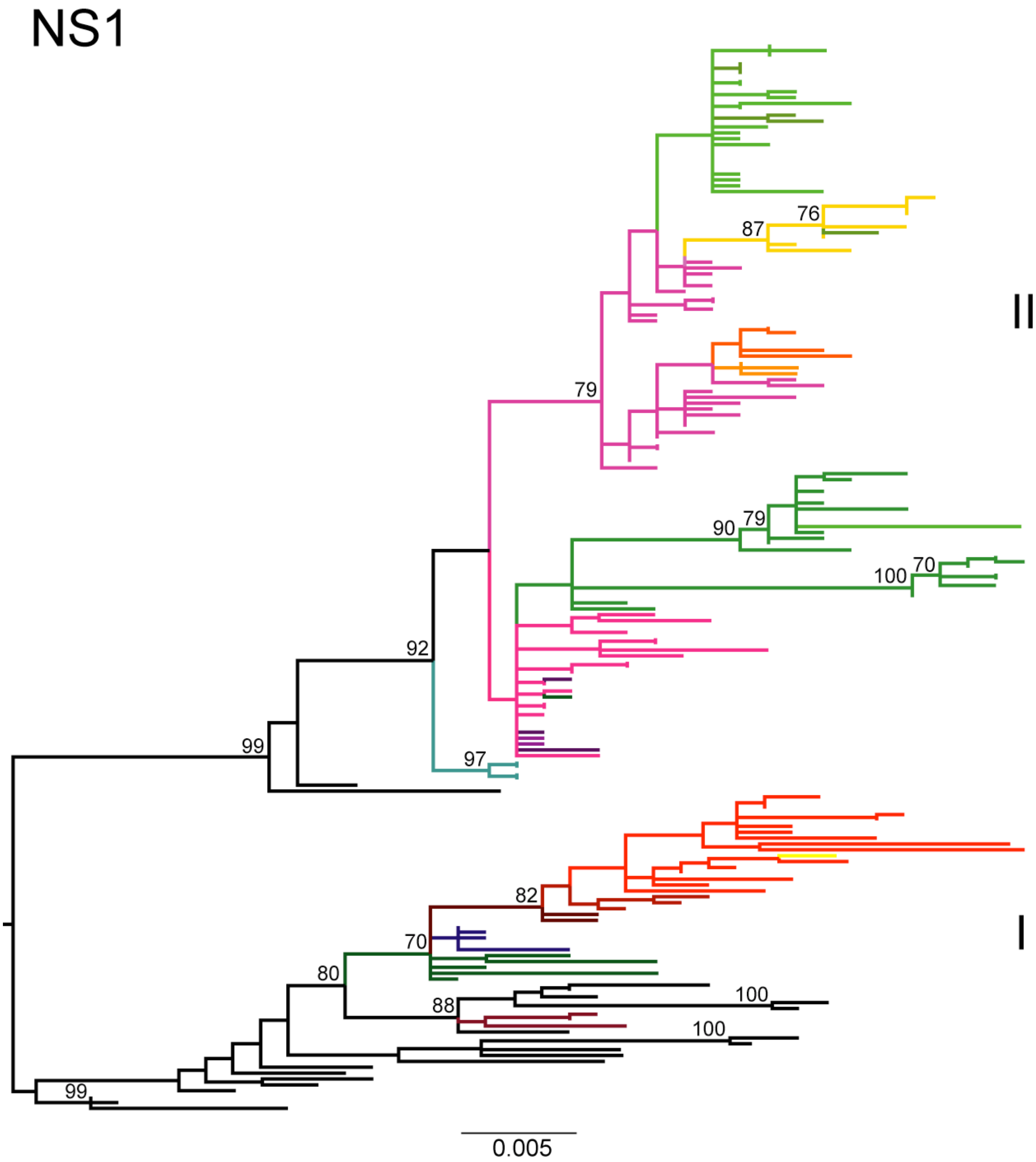
Supplementary Figure 6



Supplementary Figure 7



Supplementary Figure 8



Supplementary Table 1. Influenza activity in USA[a]

Season	No. specimens tested	No. H1N1/H1N2	No. H3N2	No. B	Prevalence H1N1/H1N2	Prevalence H3N2	Prevalence B	Overall %
1976-77	17,600	3	212	633	0.00%	1.20%	3.60%	0.048
1977-78	18,727	311	1617	5	1.70%	8.60%	0.00%	0.103
1978-79	13,275	1140	1	21	8.60%	0.00%	0.20%	0.088
1979-80	15,195	20	17	1298	0.10%	0.10%	8.50%	0.088
1980-81	16,128	315	1125	1	2.00%	7.00%	0.00%	0.089
1981-82	14,804	143	0	461	1.00%	0.00%	3.10%	0.041
1982-83	16,929	165	1263	160	1.00%	7.50%	0.90%	0.094
1983-84	16,111	1059	79	937	6.60%	0.50%	5.80%	0.129
1984-85	15,355	2	1977	53	0.00%	12.90%	0.30%	0.132
1985-86	20,234	2	554	1789	0.00%	2.70%	8.80%	0.116
1986-87	22,056	2206	5	11	10.00%	0.00%	0.00%	0.101
1987-88	26,258	167	1776	354	0.60%	6.80%	1.30%	0.087
1988-89	29,357	2234	359	2530	7.60%	1.20%	8.60%	0.175
1989-90	29,956	46	3342	13	0.20%	11.20%	0.00%	0.114
1990-91	32,420	179	271	2732	0.60%	0.80%	8.40%	0.098
1991-92	38,557	1055	4854	47	2.70%	12.60%	0.10%	0.154
1992-93	36,233	132	1126	3081	0.40%	3.10%	8.50%	0.12
1993-94	35,597	22	4193	35	0.10%	11.80%	0.10%	0.119
1994-95	38,705	62	2819	1005	0.20%	7.30%	2.60%	0.1
1995-96	37,612	2357	1650	716	6.30%	4.40%	1.90%	0.126
1996-97	39,183	0	5047	1449	0.00%	12.90%	3.70%	0.166
1997-98	99,072	6	3241	102	0.01%	3.27%	0.10%	0.131
1998-99	102,105	30	2607	3370	0.03%	2.55%	3.30%	0.142
1999-00	106,768	153	3715	97	0.14%	3.48%	0.09%	0.138
2000-01	86,534	2028	95	4583	2.34%	0.11%	5.30%	0.114

2001-02	98,570	83	3996	1705	0.08%	4.05%	1.73%	0.155
2002-03	94,966	2534	847	4703	2.67%	0.89%	4.95%	0.116
2003-04	127,316	2	7188	232	0.00%	5.65%	0.18%	0.193
2004-05	149,131	16	5780	5591	0.01%	3.88%	3.75%	0.154
2005-06	135,973	420	5228	3,211	0.31%	3.84%	2.36%	0.126
2006-07	170,452	3847	2188	4753	2.26%	1.28%	2.79%	0.135

[a] Data from 1976-77 season to 1996-97 season were taken from: Viboud C, Bjørnstad ON, Smith DL, Simonsen L, Miller MA, Grenfell BT. 2006. Synchrony, waves, and spatial hierarchies in the spread of influenza. Science. 312:447-451.
Data from 1997-1998 season until present were taken from CDC website http://www.cdc.gov/flu/weekly/fluactivity.htm.