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Supplementary material

Phylogenetic analysis of avian influenza viruses from migratory waterfowl at Pacific wetlands

Supplementary material

Table S1. Number of reads obtained

Sample	all reads	unique reads[1]	influenza reads
A/green winged teal/Mexico-Sonora/1116/2009 (H10N7)	5 260 599	548 112	382 955
A/green winged teal/Mexico-Sonora/1132/2009 (H10N3)	7 318 431	2 106 937	192 033
A/green winged teal/Mexico-Sonora/266/2008 (H6N1)	8 990 438	813 130	122 616
A/redhead/Mexico-Sonora/408/2008 (H5N2)	7 011 978	834 433	235 457
A/green winged teal/Mexico-Sonora/701/2008 (H11N3)	7 561 429	832 664	224 200
A/northern shoveler/Mexico-Sonora/738/2008 (H6N1)	6 081 579	503 531	302 830
A/American wigeon/Mexico-Sonora/769/2008 (H9N2)	10 008 629	1 910 239	580 907
A/northern shoveler/Mexico-Sonora/797/2008 H5N3)	10 902 300	2 589 322	582 465
A/green winged teal/Mexico-Sonora/829/2009 (H6N5)	7 855 551	1 928 906	310 219

[1] Low quality reads were eliminated and duplicated reads were colapsed.

Table S2. Number of sequences used in phylogenetic analyses

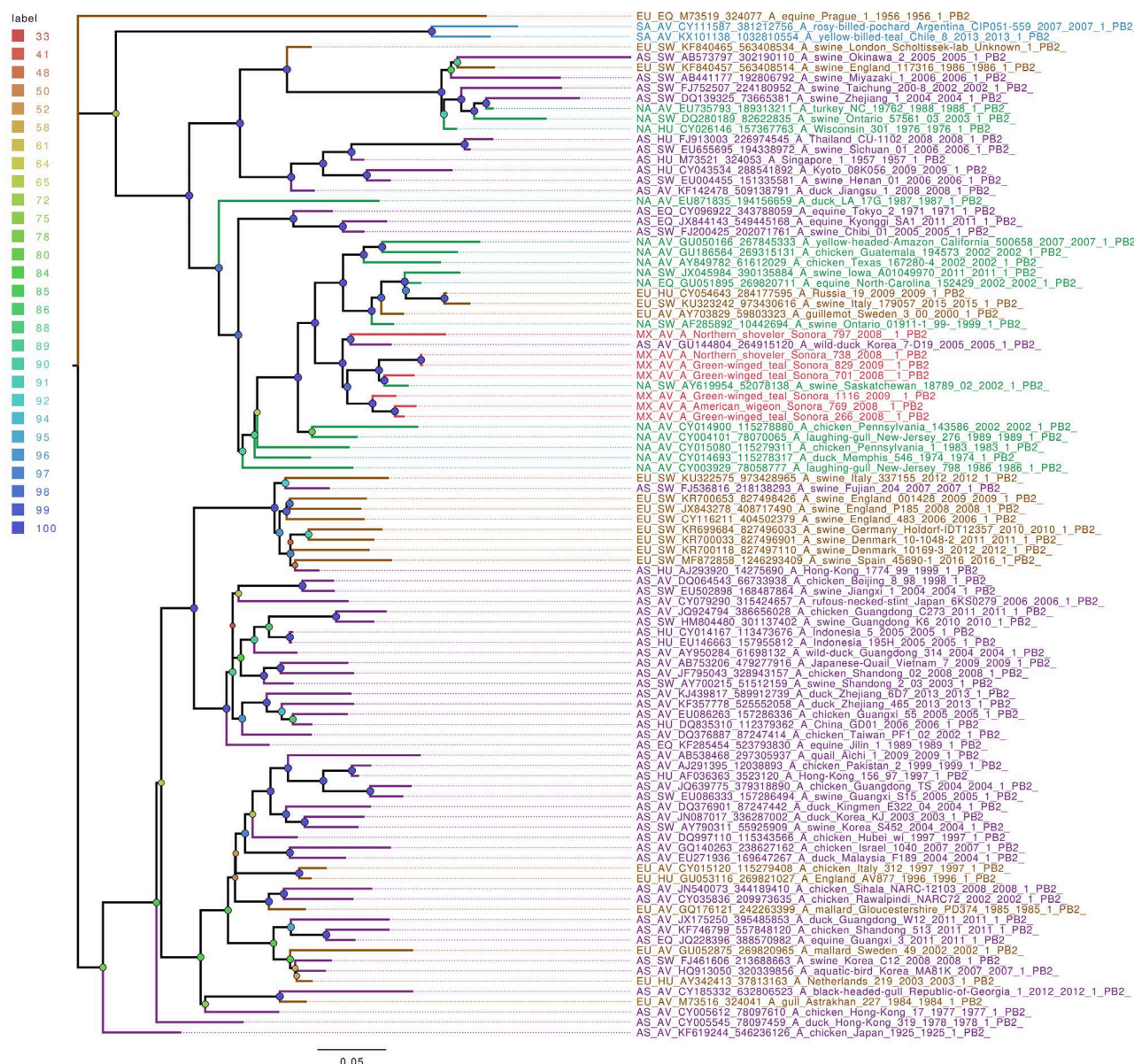| Segment	Number of selected sequences	This study sequences	Total sequences
PB1	95	5	100
PB2	78	6	84
PA	67	5	72
NP	89	7	96
M	49	5	54
NS	98	6	104
H5	81	1	82
H6	62	3	65
H9	96	1	97
H10	30	1	31
H11	22	1	23
N1	177	2	179
N2	297	1	298
N3	41	2	43
N5	42	1	43
N7	32	1	33

Supplementary material

Figure S1. The phylogenetic tree for the PB2 gene segment of avian influenza viruses analyzed in this work. For used sequences the name was changed as follows: continent of origin, source, gi and accession number, virus name, segment number and segment name. In phylogenetic trees, following area code was used: Europe (EU), North America (NA), South America (SA), Asia (AS) and Mexico-this work (MX). The bootstrap value for each split is shown in a circle with the intensity color code indicating its value as a percentage. Color code of continent of origin is as follows: green North America (NA), blue South America (SA), brown Europe (EU) purple Asia (AS), red samples sequences in this work (MX).
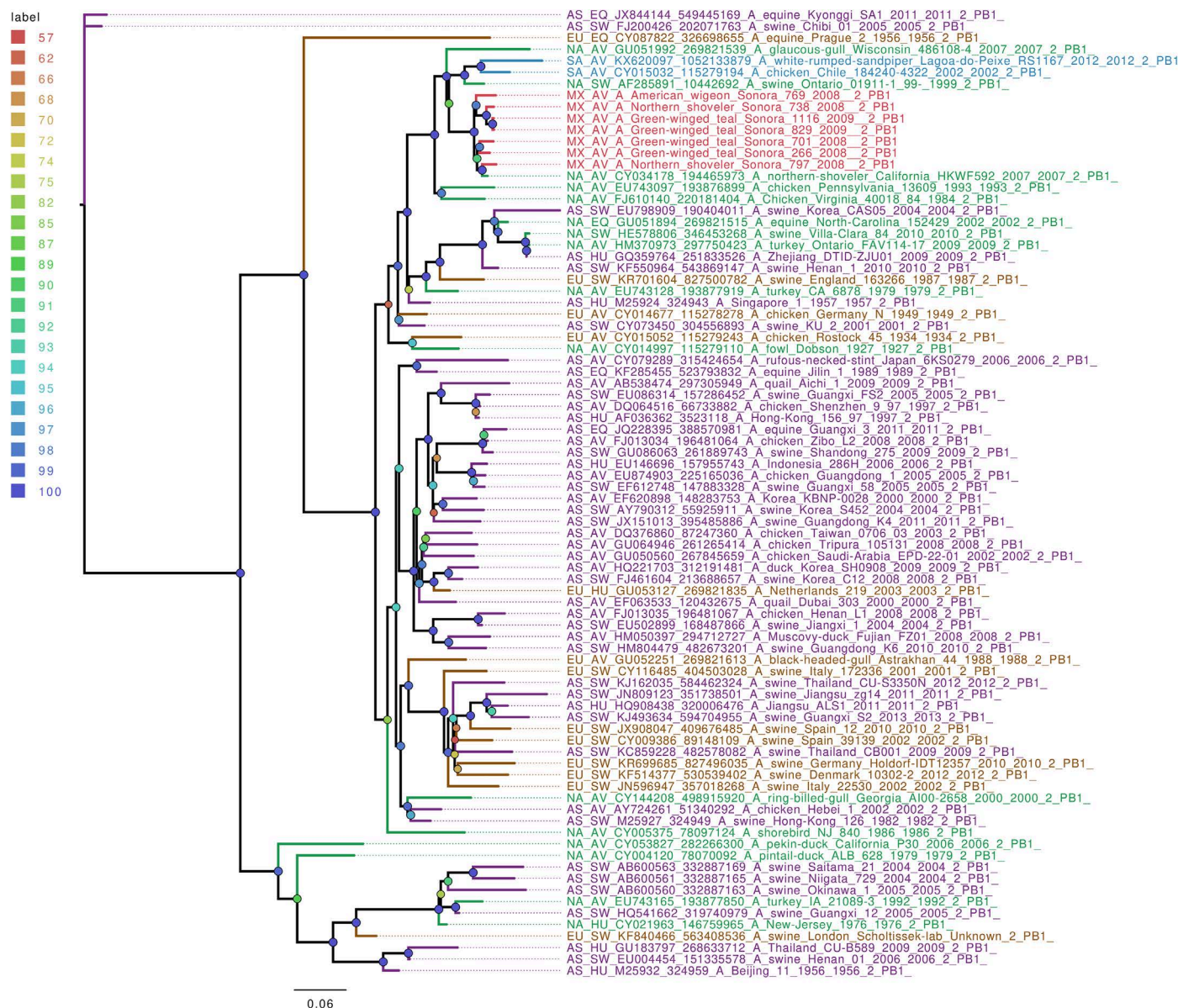
Supplementary material

Figure S2. The phylogenetic tree for the PB1 gene segment of avian influenza viruses analyzed in this work. For used sequences the name was changed as follows: continent of origin, source, gi and accession number, virus name, segment number and segment name. In phylogenetic trees, following area code was used: Europe (EU), North America (NA), South America (SA), Asia (AS) and Mexico-this work (MX). The bootstrap value for each split is shown in a circle with the intensity color code indicating its value as a percentage. Color code of continent of origin is as follows: green North America (NA), blue South America (SA), brown Europe (EU) purple Asia (AS), red samples sequences in this work (MX).
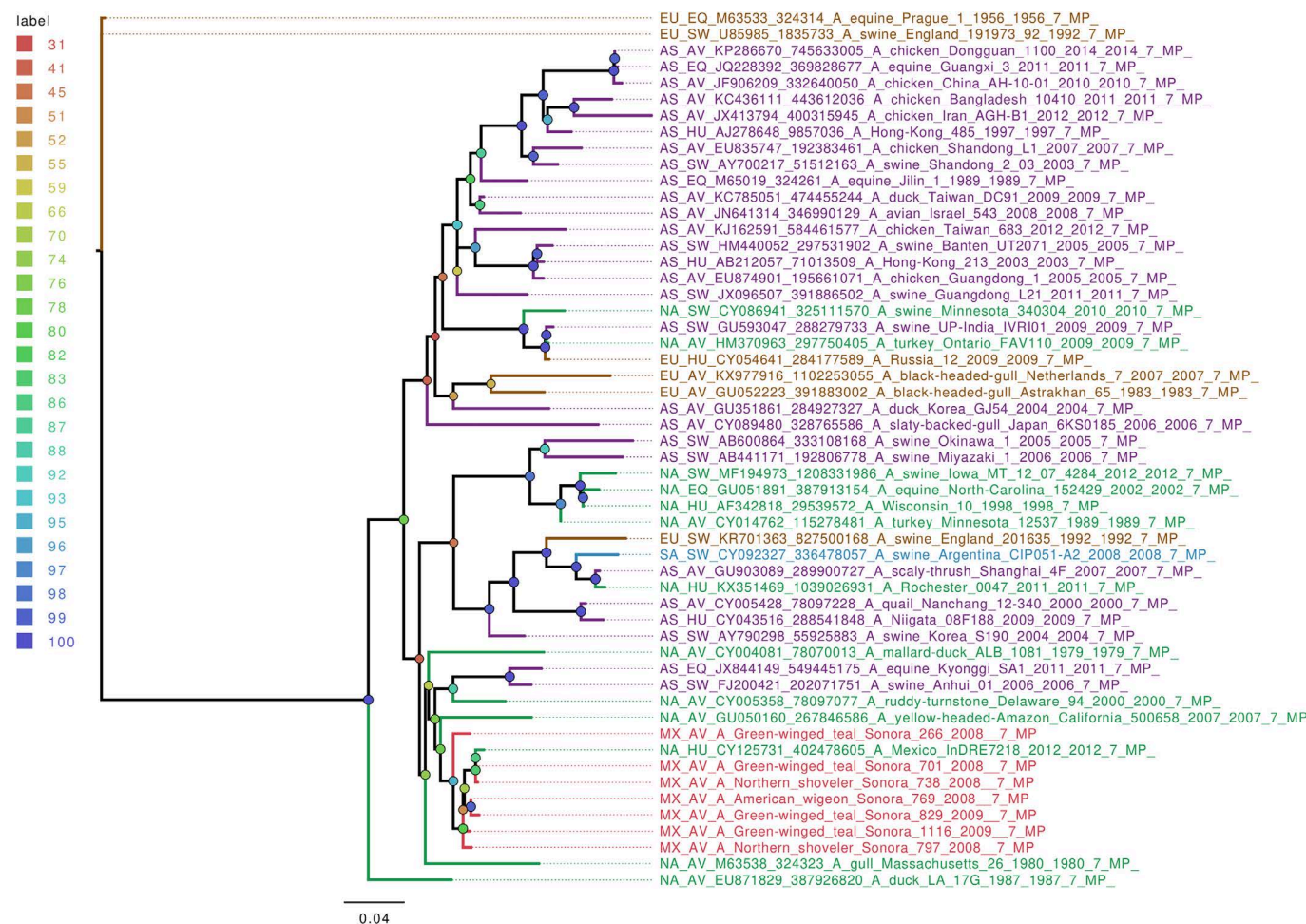
Supplementary material

Figure S3. The phylogenetic tree for the M gene segment of avian influenza viruses analyzed in this work. For used sequences the name was changed as follows: continent of origin, source, gi and accession number, virus name, segment number and segment name. In phylogenetic trees, following area code was used: Europe (EU), North America (NA), South America (SA), Asia (AS) and Mexico-this work (MX). The bootstrap value for each split is shown in a circle with the intensity color code indicating its value as a percentage. Color code of continent of origin is as follows: green North America (NA), blue South America (SA), brown Europe (EU) purple Asia (AS), red samples sequences in this work (MX).
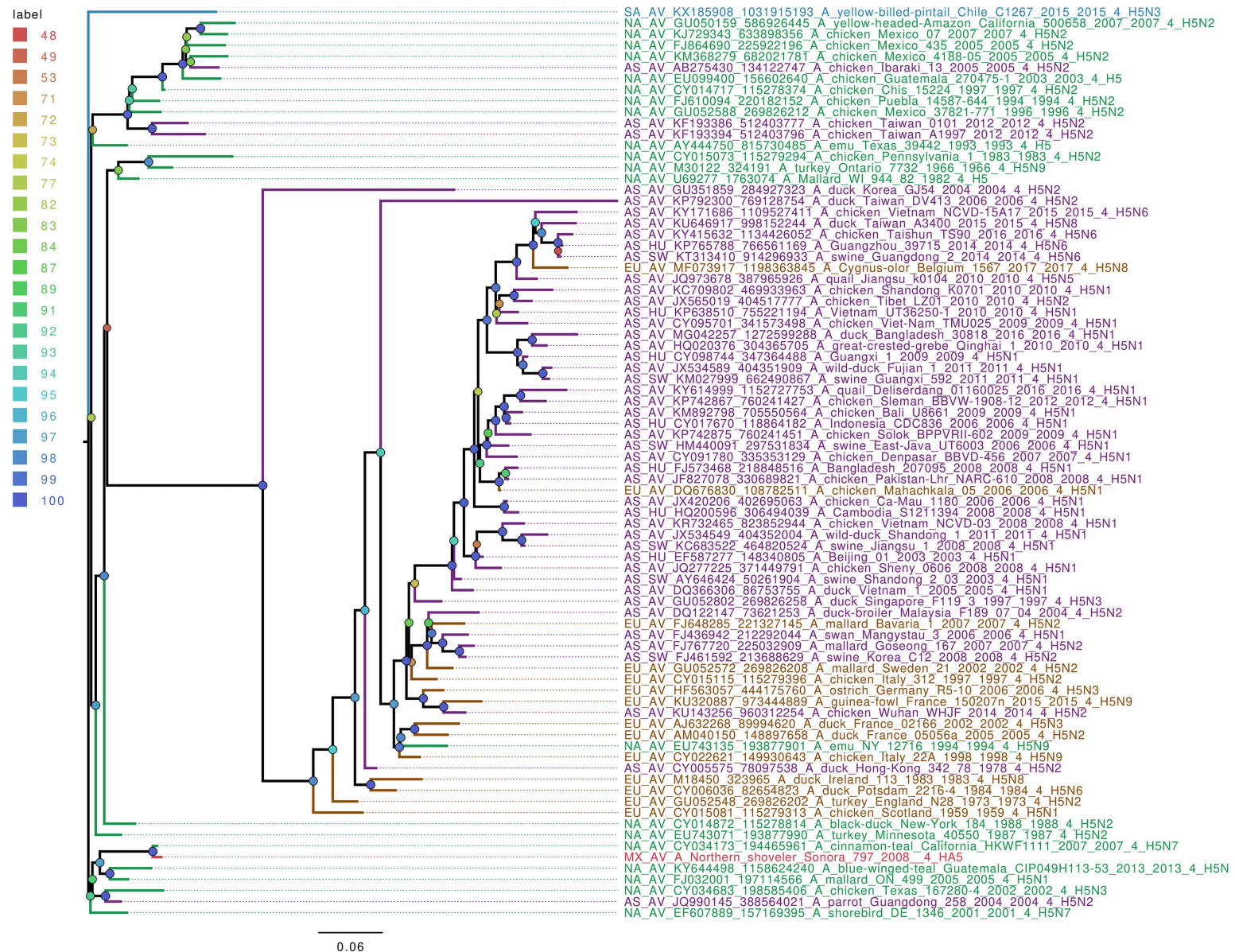
Supplementary material

Figure S4. The phylogenetic tree for the H5 gene segment of avian influenza viruses analyzed in this work. For used sequences the name was changed as follows: continent of origin, source, gi and accession number, virus name, segment number and segment name. In phylogenetic trees, following area code was used: Europe (EU), North America (NA), South America (SA), Asia (AS) and Mexico-this work (MX). The bootstrap value for each split is shown in a circle with the intensity color code indicating its value as a percentage. Color code of continent of origin is as follows: green North America (NA), blue South America (SA), brown Europe (EU) purple Asia (AS), red samples sequences in this work (MX).
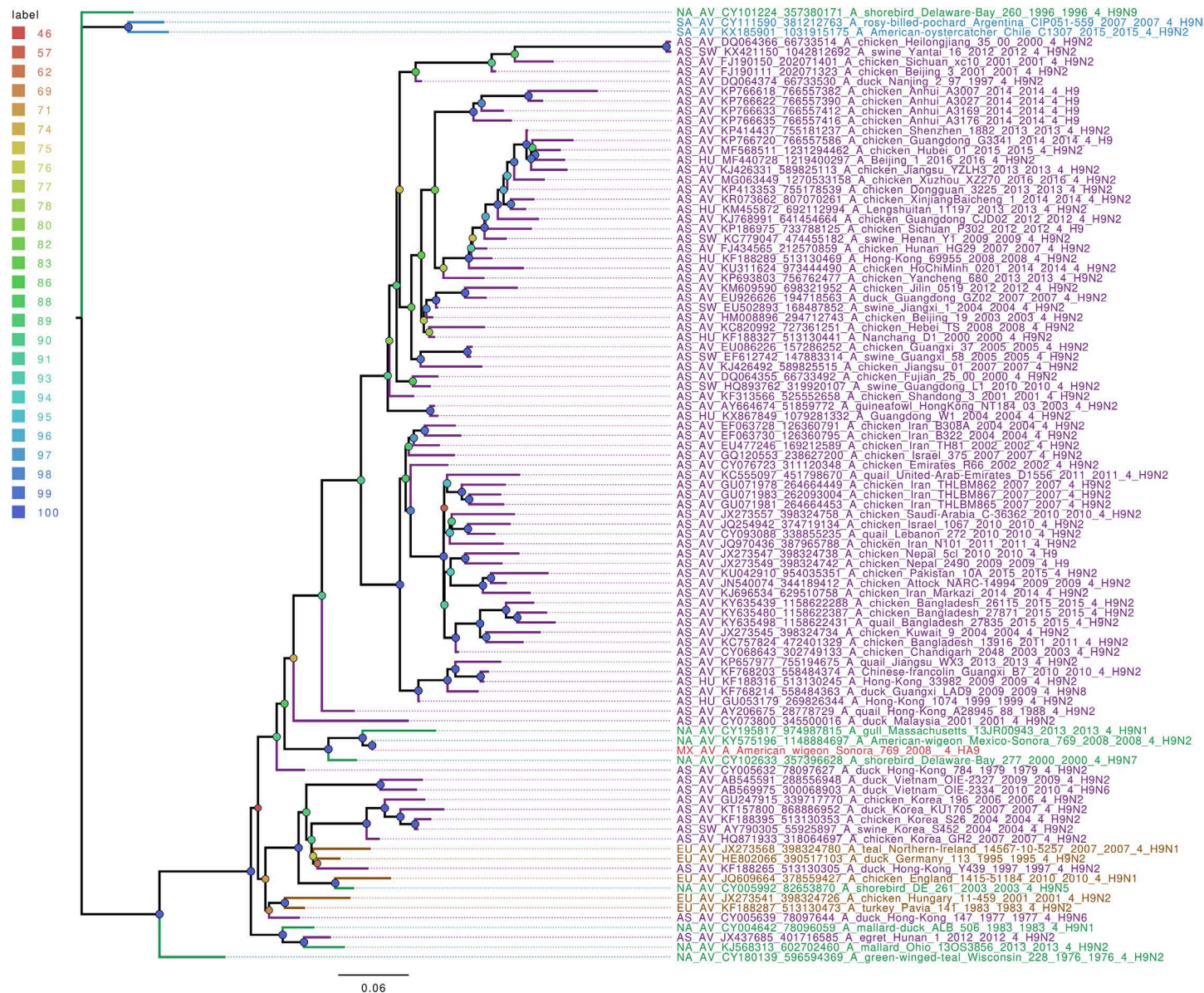
Supplementary material

Figure S5. The phylogenetic tree for the H9 gene segment of avian influenza viruses analyzed in this work. For used sequences the name was changed as follows: continent of origin, source, gi and accession number, virus name, segment number and segment name. In phylogenetic trees, following area code was used: Europe (EU), North America (NA), South America (SA), Asia (AS) and Mexico-this work (MX). The bootstrap value for each split is shown in a circle with the intensity color code indicating its value as a percentage. Color code of continent of origin is as follows: green North America (NA), blue South America (SA), brown Europe (EU) purple Asia (AS), red samples sequences in this work (MX).
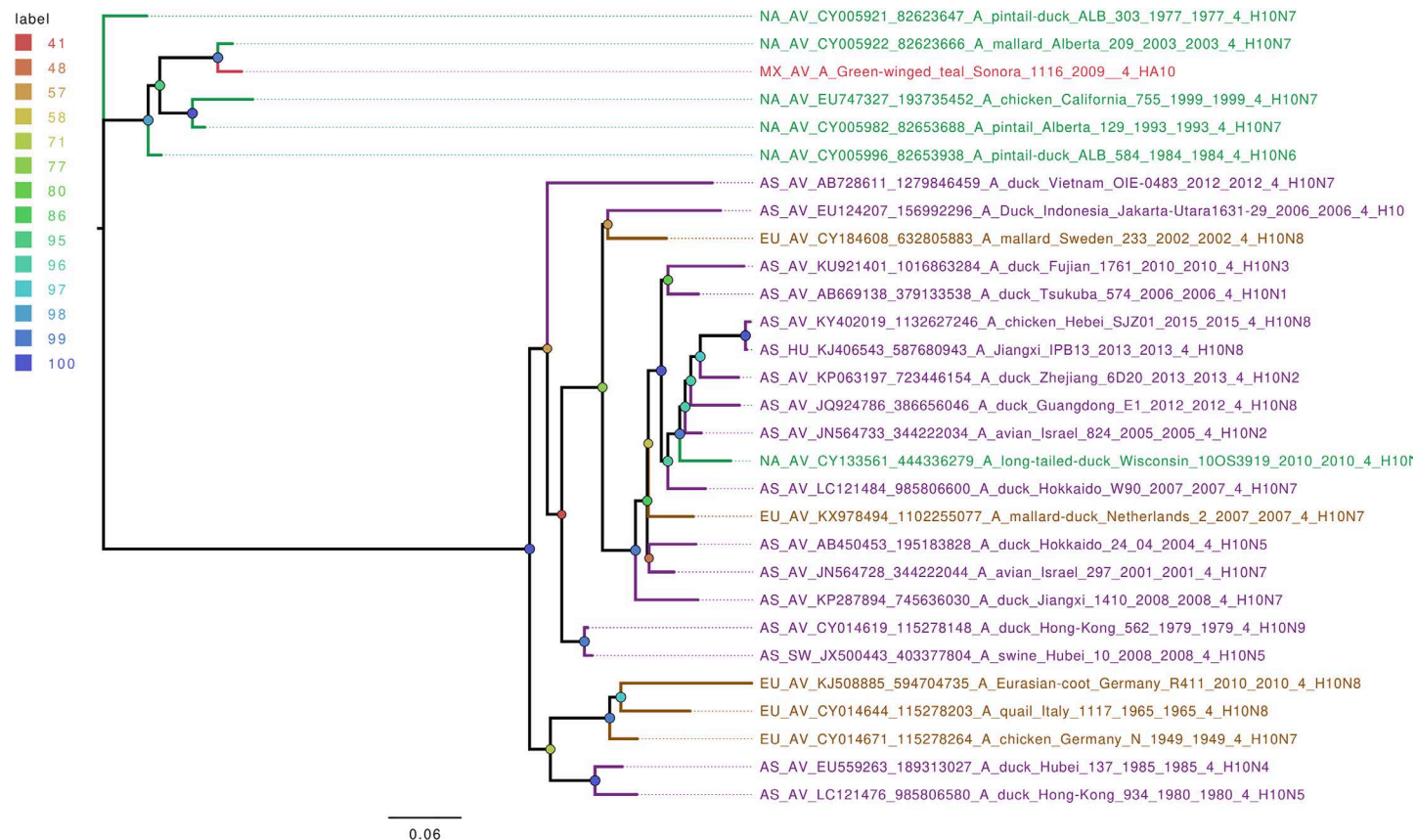
Supplementary material

Figure S6. The phylogenetic tree for the H10 gene segment of avian influenza viruses analyzed in this work. For used sequences the name was changed as follows: continent of origin, source, gi and accession number, virus name, segment number and segment name. In phylogenetic trees, following area code was used: Europe (EU), North America (NA), South America (SA), Asia (AS) and Mexico-this work (MX). The bootstrap value for each split is shown in a circle with the intensity color code indicating its value as a percentage. Color code of continent of origin is as follows: green North America (NA), blue South America (SA), brown Europe (EU) purple Asia (AS), red samples sequences in this work (MX).

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Phylogenetic analysis of avian influenza viruses
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Original Research

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Figure S7. The phylogenetic tree for the N1 gene segment of avian influenza viruses analyzed in this work. For used sequences the name was changed as follows: continent of origin, source, gi and accession number, virus name, segment number and segment name. In phylogenetic trees, following area code was used: Europe (EU), North America (NA), South America (SA), Asia (AS) and Mexico-this work (MX). The bootstrap value for each split is shown in a circle with the intensity color code indicating its value as a percentage. Color code of continent of origin is as follows: green North America (NA), blue South America (SA), brown Europe (EU) purple Asia (AS), red samples sequences in this work (MX).

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Original Research
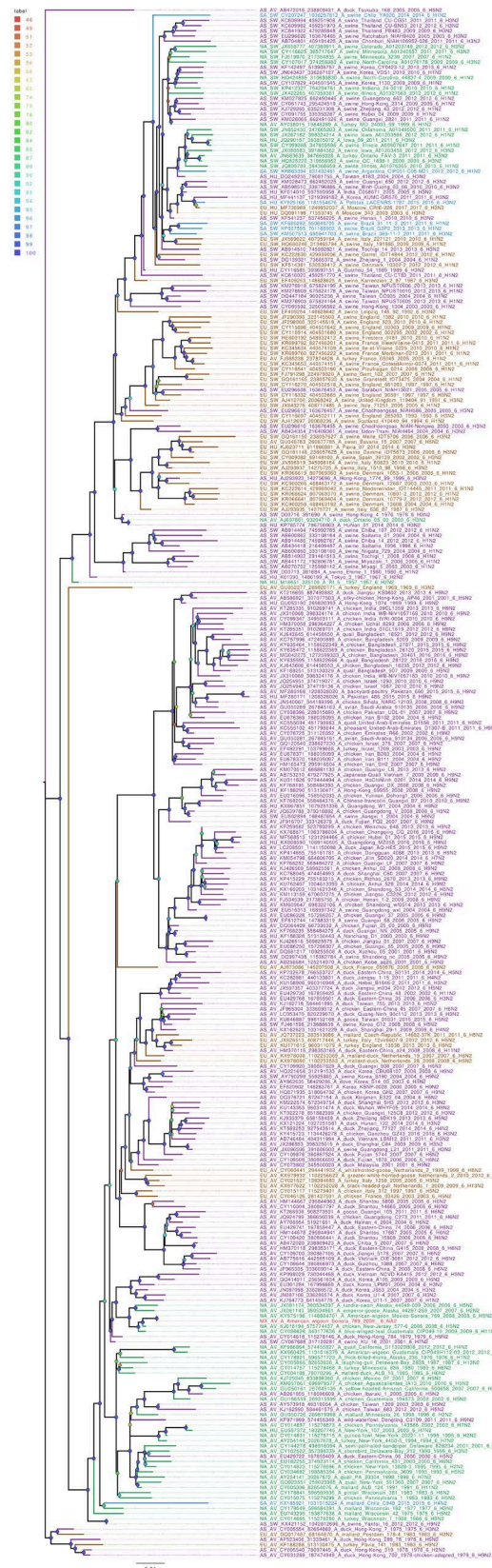
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Supplementary material

Figure S8. The phylogenetic tree for the N2 gene segment of avian influenza viruses analyzed in this work. For used sequences the name was changed as follows: continent of origin, source, gi and accession number, virus name, segment number and segment name. In phylogenetic trees, following area code was used: Europe (EU), North America (NA), South America (SA), Asia (AS) and Mexico-this work (MX). The bootstrap value for each split is shown in a circle with the intensity color code indicating its value as a percentage. Color code of continent of origin is as follows: green North America (NA), blue South America (SA), brown Europe (EU) purple Asia (AS), red samples sequences in this work (MX).
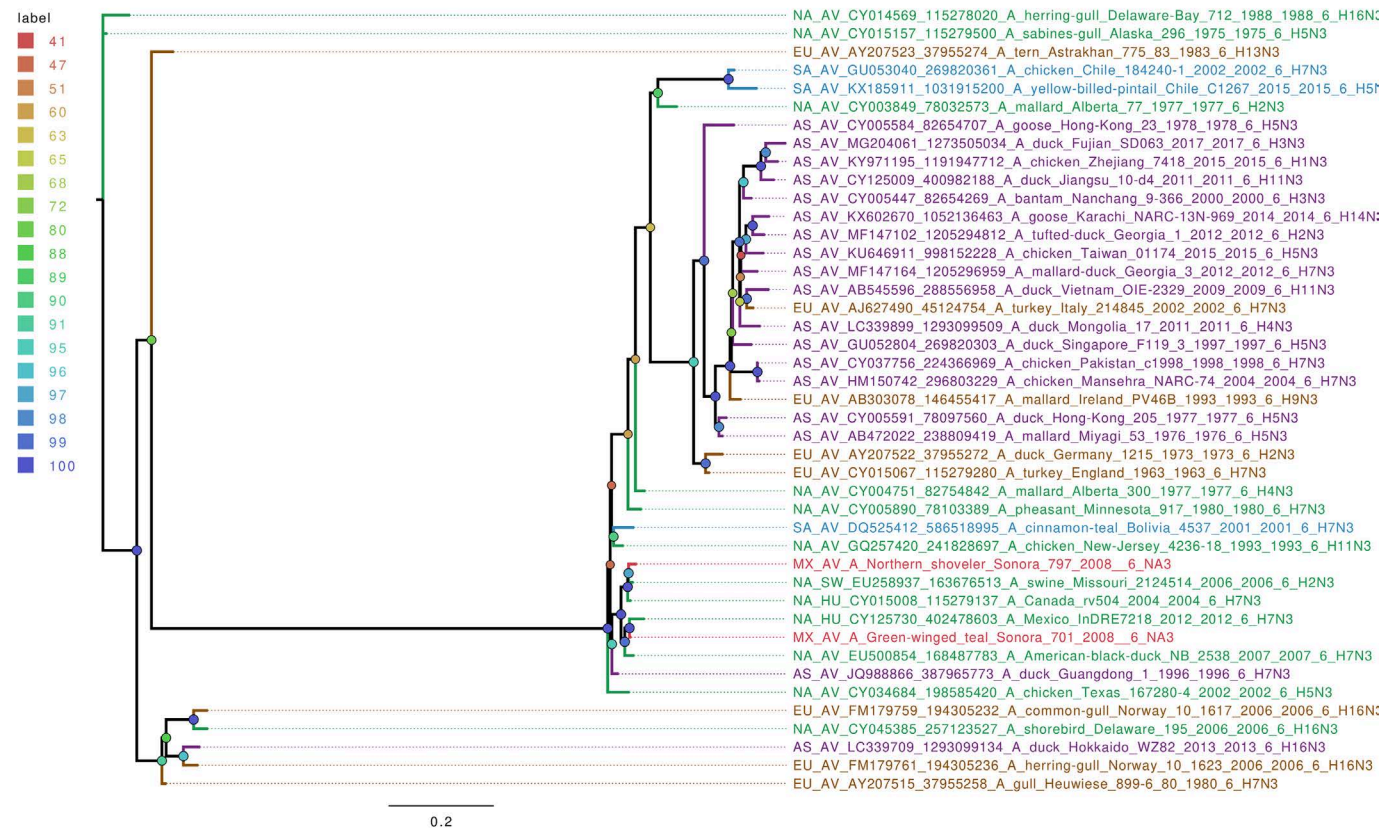
Supplementary material

Figure S9. The phylogenetic tree for the N3 gene segment of avian influenza viruses analyzed in this work. For used sequences the name was changed as follows: continent of origin, source, gi and accession number, virus name, segment number and segment name. In phylogenetic trees, following area code was used: Europe (EU), North America (NA), South America (SA), Asia (AS) and Mexico-this work (MX). The bootstrap value for each split is shown in a circle with the intensity color code indicating its value as a percentage. Color code of continent of origin is as follows: green North America (NA), blue South America (SA), brown Europe (EU) purple Asia (AS), red samples sequences in this work (MX).
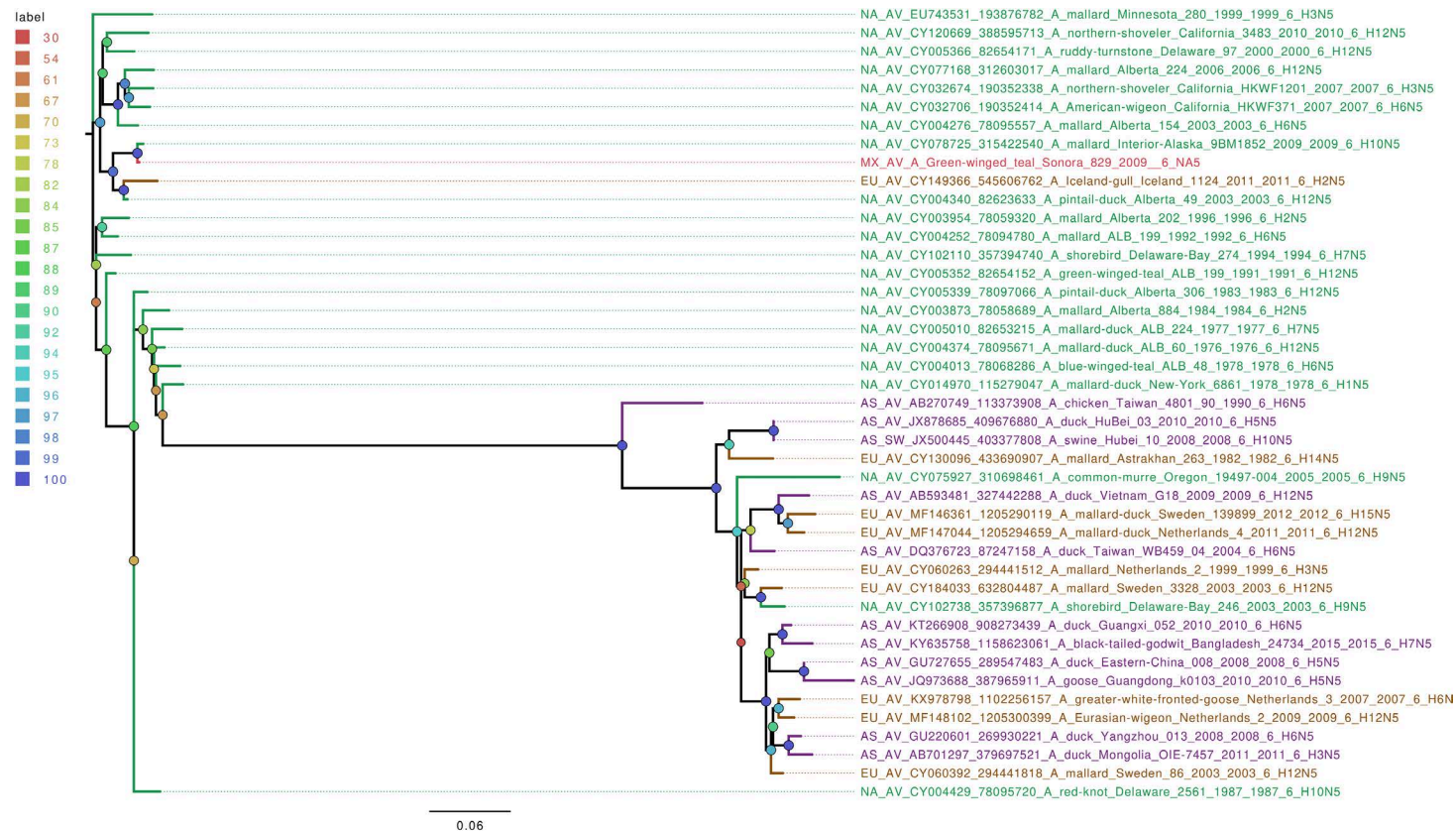
Supplementary material

Figure S10. The phylogenetic tree for the N5 gene segment of avian influenza viruses analyzed in this work. For used sequences the name was changed as follows: continent of origin, source, gi and accession number, virus name, segment number and segment name. In phylogenetic trees, following area code was used: Europe (EU), North America (NA), South America (SA), Asia (AS) and Mexico-this work (MX). The bootstrap value for each split is shown in a circle with the intensity color code indicating its value as a percentage. Color code of continent of origin is as follows: green North America (NA), blue South America (SA), brown Europe (EU) purple Asia (AS), red samples sequences in this work (MX).
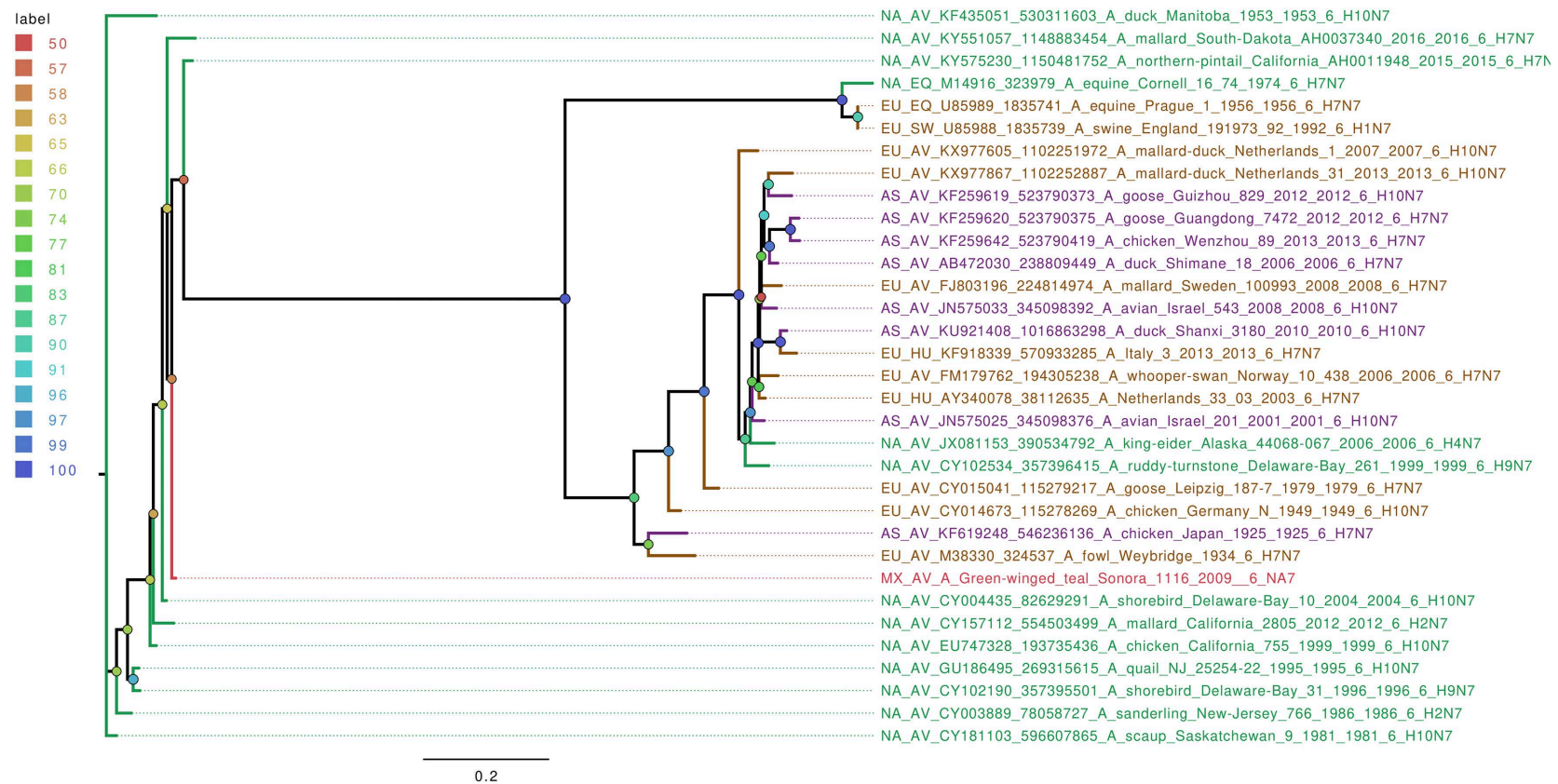
Supplementary material

Figure S11. The phylogenetic tree for the N7 gene segment of avian influenza viruses analyzed in this work. For used sequences the name was changed as follows: continent of origin, source, gi and accession number, virus name, segment number and segment name. In phylogenetic trees, following area code was used: Europe (EU), North America (NA), South America (SA), Asia (AS) and Mexico-this work (MX). The bootstrap value for each split is shown in a circle with the intensity color code indicating its value as a percentage. Color code of continent of origin is as follows: green North America (NA), blue South America (SA), brown Europe (EU) purple Asia (AS), red samples sequences in this work (MX).