

1 **Supplementary Figure Legends**

2 SFig. 1. Maximum clade credibility tree inferred under a host-specific local clock model
3 for IAVs internal gene segment PB2 (435 sequences). Color-coded annotations are
4 shown by colored rectangles: South American (light red), Eurasian (light green) and
5 North American (light blue). Viruses isolated from avian species are shown in colors
6 depending on region of origin: South America (red), Eurasian (green), North America
7 (blue), and Antarctica (violet). IAVs isolated from non-avian hosts are also shown in
8 color depending on the host: Human (black), swine (pink), equine (brown) and bat
9 (grey). Please note that IAV strains from avian hosts obtained from various South
10 American countries are shown in red irrespective of their lineage. Posterior probabilities
11 are shown. The asterisks (*) indicate the 15 IAVs isolates from Argentina analyzed in
12 this study.

13 SFig. 2. Maximum clade credibility tree inferred under a host-specific local clock model
14 for IAVs internal gene segment PB1 (413 sequences). Color-coded annotations are the
15 same as described in SFig. 1. Posterior probabilities are shown. *IAVs isolates from
16 Argentina obtained from this study.

17 SFig. 3. Maximum clade credibility tree inferred under a host-specific local clock model
18 for IAVs internal gene segment PA (462 sequences). Color-coded annotations are the
19 same as described in SFig. 1. Posterior probabilities are shown. *IAVs isolates from
20 Argentina obtained from this study.

21 SFig. 4. Maximum clade credibility tree inferred under a host-specific local clock model
22 for IAVs internal gene segment NP (508 sequences). Color-coded annotations are the
23 same as described in SFig. 1. Posterior probabilities are shown. *IAVs isolates from
24 Argentina obtained from this study.

25 SFig. 5. Maximum clade credibility tree inferred under a host-specific local clock model
26 for IAVs internal gene segment M (519 sequences). Color-coded annotations are the
27 same as described in SFig. 1. Posterior probabilities are shown. *IAVs isolates from
28 Argentina obtained from this study.

29 SFig. 6. Maximum clade credibility tree inferred under a host-specific local clock model
30 for IAVs internal gene segment NS (442 sequences). Color-coded annotations are the
31 same as described in SFig. 1. Posterior probabilities are shown. *IAVs isolates from
32 Argentina obtained from this study.

33 SFig. 7. Maximum likelihood phylogenetic tree of H1 gene segment (172 sequences).
34 Color-coded annotations are the same as described in SFig. 1. Bootstrap values from
35 1000 replicates are shown. *IAVs isolates from Argentina obtained from this study.

36 SFig. 8. Maximum likelihood phylogenetic tree of H5 gene segment (183 sequences).
37 Color-coded annotations are the same as described in SFig. 1. Bootstrap values from
38 1000 replicates are shown. *IAVs isolates from Argentina obtained from this study.

39 SFig. 9. **Maximum likelihood** phylogenetic tree of H7 gene segment (**173 sequences**).
 40 Color-coded annotations are the same as described in SFig. 1. Bootstrap values from
 41 1000 replicates are shown. *IAVs isolates from Argentina obtained from this study.

42 SFig. 10. Maximum clade credibility tree inferred under an uncorrelated lognormal clock
 43 model for H10 gene segment (**258 sequences**). Color-coded annotations are the same
 44 as described in SFig. 1. **Posterior probabilities are shown**. *IAVs isolates from Argentina
 45 obtained from this study.

46 SFig. 11. Maximum clade credibility tree inferred under a host-specific local clock model
 47 for H4 gene segment (**264 sequences**). Color-coded annotations are the same as
 48 described in SFig. 1. **Posterior probabilities are shown**. *IAVs isolates from Argentina
 49 obtained from this study.

50 SFig. 12. Maximum clade credibility tree inferred under a host-specific local clock model
 51 for H6 gene segment (**469 sequences**). Color-coded annotations are the same as
 52 described in SFig. 1. **The two clades containing viruses from Argentina are denoted as 1**
 53 **and 2. Posterior probabilities are shown**. *IAVs isolates from Argentina obtained from
 54 this study.

55 SFig. 13. **Maximum likelihood** phylogenetic tree of N1 gene segment (**339 sequences**).
 56 Color-coded annotations are the same as described in SFig. 1. Bootstrap values from
 57 1000 replicates are shown. *IAVs isolates from Argentina obtained from this study.

58 SFig. 14. **Maximum likelihood** phylogenetic tree of N2 gene segment (**637 sequences**).
 59 Color-coded annotations are the same as described in SFig. 1. Bootstrap values from
 60 1000 replicates are shown. *IAVs isolates from Argentina obtained from this study.

61 SFig. 15. **Maximum likelihood** phylogenetic tree of N3 gene segment (**379 sequences**).
 62 Color-coded annotations are the same as described in SFig. 1. Bootstrap values from
 63 1000 replicates are shown. *IAVs isolates from Argentina obtained from this study.

64 SFig. 16. **Maximum likelihood** phylogenetic tree of N6 gene segment (**264 sequences**).
 65 Color-coded annotations are the same as described in SFig. 1. Bootstrap values from
 66 1000 replicates are shown. *IAVs isolates from Argentina obtained from this study.

67 SFig. 17. **Maximum likelihood** phylogenetic tree of N9 gene segment (**297 sequences**).
 68 Color-coded annotations are the same as described in SFig. 1. Bootstrap values from
 69 1000 replicates are shown. *IAVs isolates from Argentina obtained from this study.

70 SFig. 18. Maximum clade credibility tree inferred under a host-specific local clock model
 71 for N7 gene segment (**213 sequences**). Color-coded annotations are the same as
 72 described in SFig. 1. **Posterior probabilities are shown**. *IAVs isolates from Argentina
 73 obtained from this study.

74 SFig. 19. Maximum clade credibility trees inferred under a host-specific local clock
 75 model for N8 gene segment (**463 sequences**). Color-coded annotations are the same as
 76 described in SFig. 1. **Posterior probabilities are shown**. *IAVs isolates from Argentina
 77 obtained from this study.

78 SFig. 20. Alignment of PB1-F2 predicted amino acid sequences from Argentinean LPAIV
79 isolated from 2006 to 2016.

80 SFig. 21. Alignment of PA-X predicted amino acid sequences from Argentinean LPAIV
81 isolated from 2006 to 2016.