

TITLE: Global phylodynamic analysis of avian paramyxovirus-1 provides evidence of inter-host transmission and intercontinental spatial diffusion

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Please find below descriptions and figures for Additional File 2.

Supplemental Figures

Supplemental Figure S1. Global Distribution of Newcastle Disease (ND), 2005 - 2016 (A). Countries with at least one ND outbreak are indicated by blue circles. Blue crosses indicate suspected, but unconfirmed Newcastle Disease cases. APMV-1 complete fusion gene sequences collected between 2006 and 2016 and included in this analysis originated from the shaded countries. Base map was used with permission from OpenStreetMap (<https://www.openstreetmap.org/copyright>). For comparison, the distribution of common hosts, domestic chickens (B) and domestic ducks (C), are provided from the Gridded Livestock of the World database (GLW v3.1) of the Food and Agriculture Organization of the United Nations (FAO) (B: Gilbert, Marius; Nicolas, Gaëlle; Cinardi, Giusepina; Van Boeckel, Thomas P.; Vanwambeke, Sophie; Wint, G. R. William; Robinson, Timothy P., 2018, "Global chickens distribution in 2010 (5 minutes of arc)", <https://doi.org/10.7910/DVN/SUFASB>, Harvard Dataverse, V3; C: Gilbert, Marius; Nicolas, Gaëlle; Cinardi, Giusepina; Van Boeckel, Thomas P.; Vanwambeke, Sophie; Wint, William G. R.; Robinson, Timothy P., 2018, "Global ducks distribution in 2010 (5 minutes of arc)", <https://doi.org/10.7910/DVN/ICHCBH>, Harvard Dataverse, V3). **(Page 4)**

Supplemental Figure S2. Class I Host Transition Heat Map, 2005 - 2016. Darkness of each cell color is proportional to the absolute number of transitions from the first column into the second column. The maximum transition count is 6.0 transitions (Domestic chickens to Anseriformes, 2009). (ANS – Anseriformes, CHA – Charadriiformes, CHI – domestic chicken) **(Page 5)**

Supplemental Figure S3. Class II Host Transition Heat Map, 2005-2016. Darkness of each cell color is proportional to the absolute number of transitions from the first column into the second column. The maximum transition count is 9.6 transitions (Domestic chickens to Anseriformes, 2009). (ANS – Anseriformes, CHI – domestic chicken, COL – Columbiformes, GAL – other Galliformes, PSI - Psittaciformes) **(Page 6)**

Supplemental Figure S4. Class I World Migration Heat Map, 2005-2016. Darkness of each cell color is proportional to the absolute number of transitions from the first column into the second column. The maximum migration count is 0.92 migrations (East Asia to Europe, 2006). **(Page 7)**

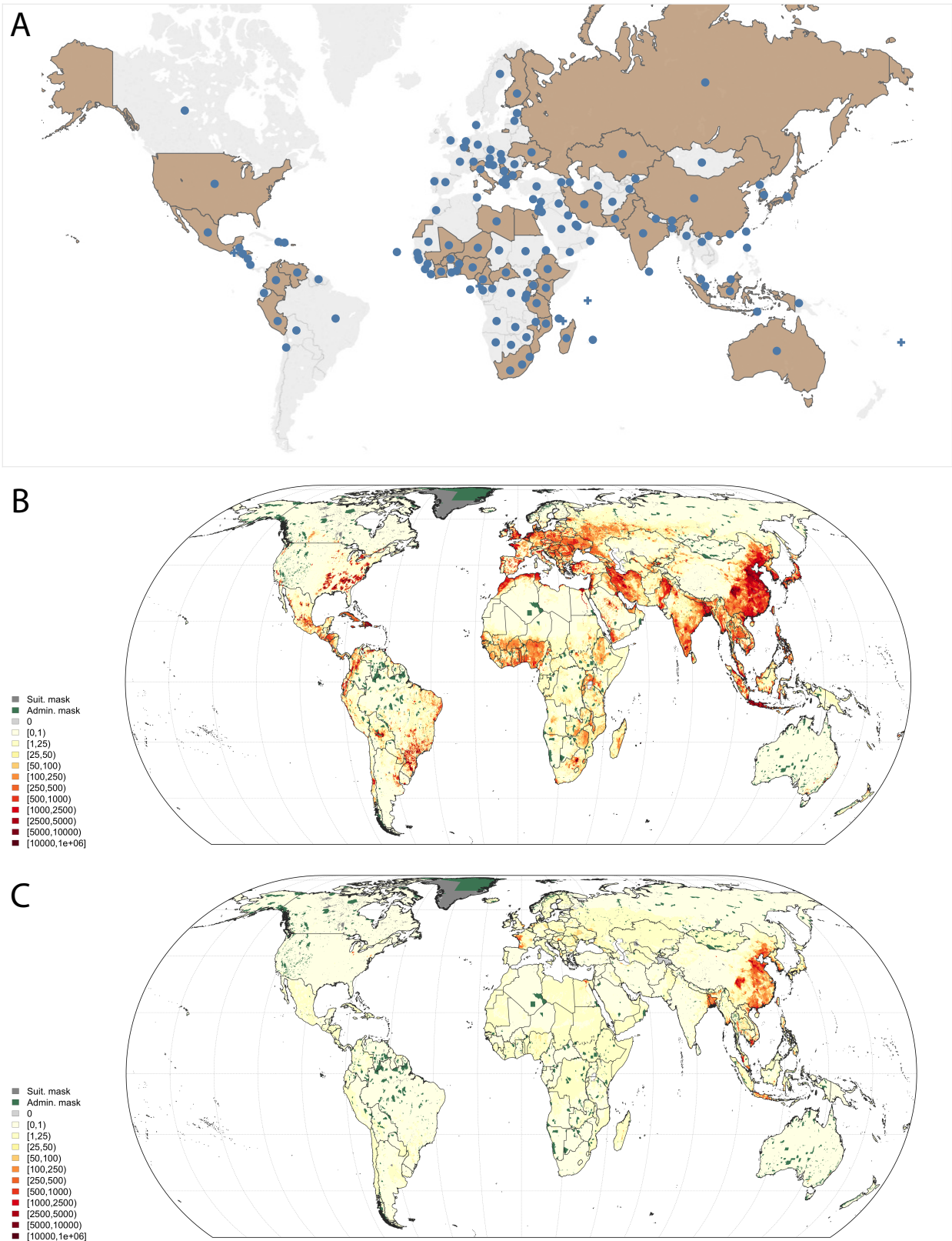
Supplemental Figure S5. Class II World Migration Heat Map, 2005-2016. Darkness of each cell color is proportional to the absolute number of transitions from the first column into the second column. The maximum migration count is 1.3 migrations (South Asia to Middle East, 2011). **(Page 8)**

Supplemental Figure S6. Tip Swap Analysis Host Transition Rates. Blue circles indicate the median transition rate per year from the host source (top axis label) to the sink (bottom axis label). Gray bars represent the 95% highest posterior density of the estimate. The “Older” category represents sequences collected before 2006 of any host. (ANS – Anseriformes, CHA – Charadriiformes, CHI – domestic chicken, COL – Columbiformes, GAL – other Galliformes, PSI - Psittaciformes) **(Page 9)**

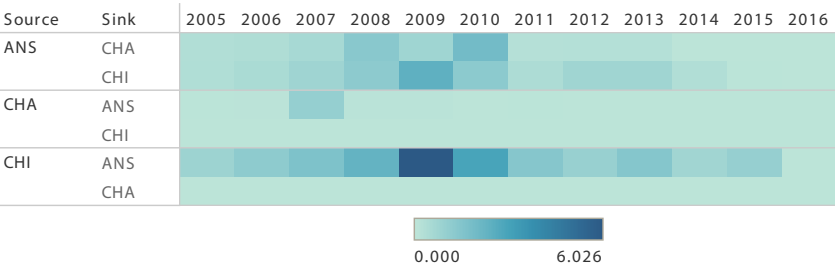
Supplemental Figure S7. Tip Swap Analysis World Region Transition Rates. Blue circles indicate the median transition rate per year from the world region source (top axis label) to the sink (bottom axis label). Gray bars represent the 95% highest posterior density of the estimate. The “Older/UN” category represents sequences collected before 2006 of any host. **(Page 10)**

Supplemental Figure S8. Tip Swap Analysis United States Transition Rates. Blue circles indicate the median transition rate per year from the United States region source (top axis label) to the sink (bottom axis label). Gray bars represent the 95% highest posterior density of the estimate. The “Older/UN” category represents sequences collected before 2006 of any host. (AK – Alaska, MW – Midwest, NE – Northeast, P – Plains, S – South, W- West, X – Outside United States) **(Page 11)**

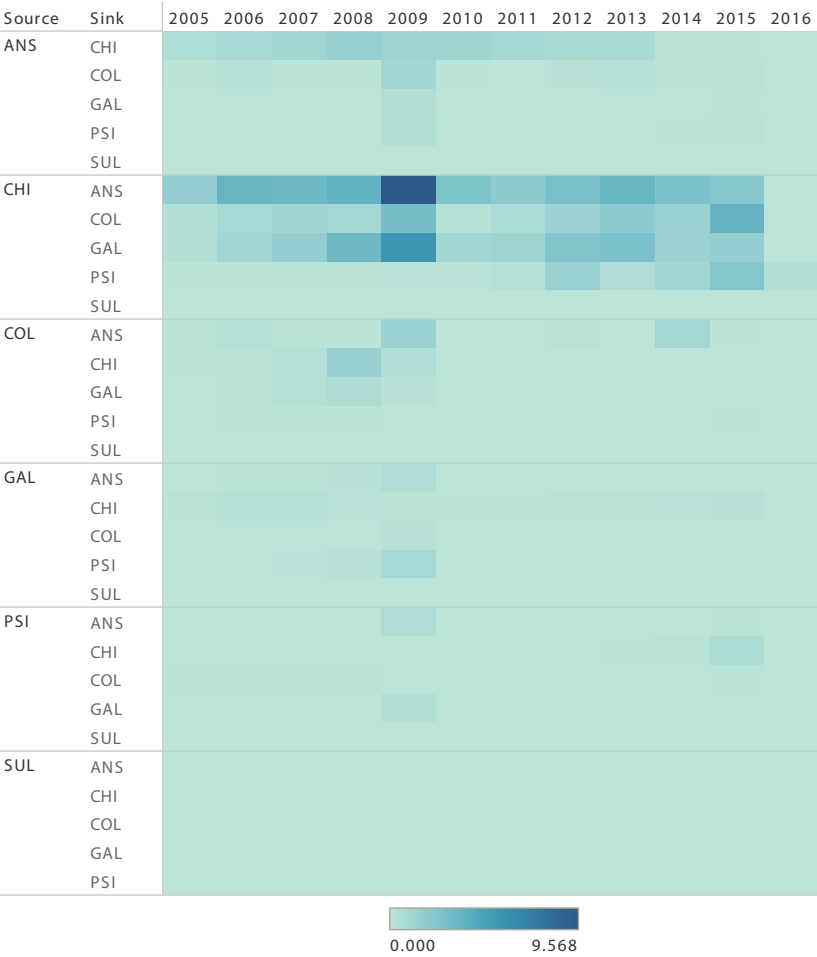
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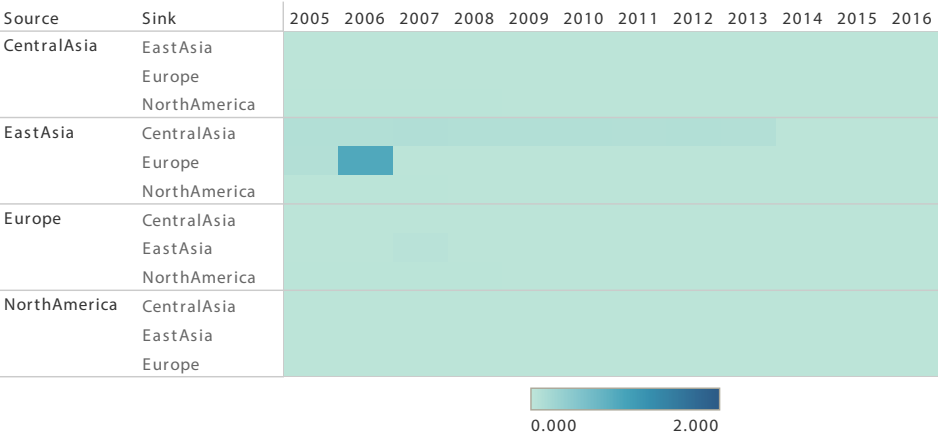
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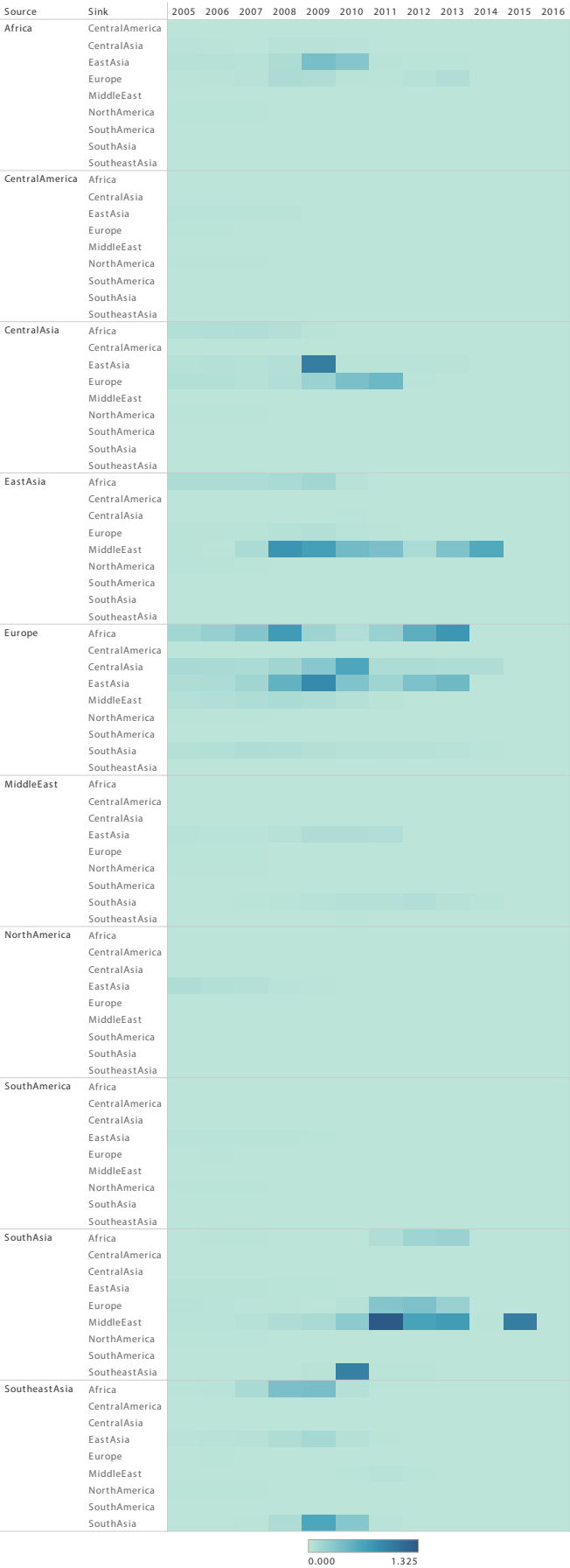
Supplemental Figure S3. Class II Host Transition Heat Map, 2005-2016. Darkness of each cell color is proportional to the absolute number of transitions from the first column into the second column. The maximum transition count is 9.6 transitions (Domestic chickens to Anseriformes, 2009). (ANS – Anseriformes, CHI – domestic chicken, COL – Columbiformes, GAL – other Galliformes, PSI – Psittaciformes)



Supplemental Figure S4. Class I World Migration Heat Map, 2005-2016. Darkness of each cell color is proportional to the absolute number of transitions from the first column into the second column. The maximum migration count is 0.92 migrations (East Asia to Europe, 2006).

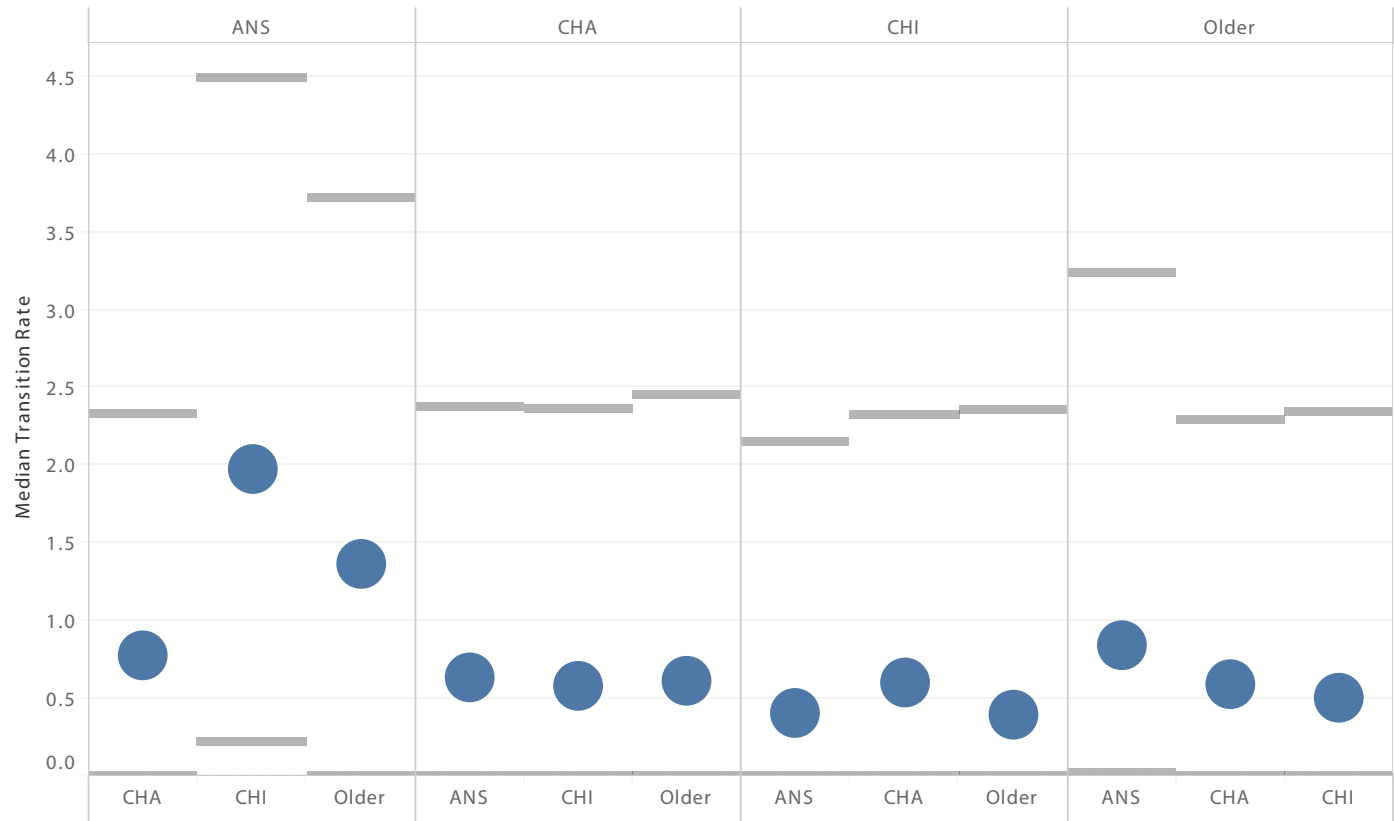


Supplemental Figure S5. Class II World Migration Heat Map, 2005-2016. Darkness of each cell color is proportional to the absolute number of transitions from the first column into the second column. The maximum migration count is 1.3 migrations (South Asia to Middle East, 2011).

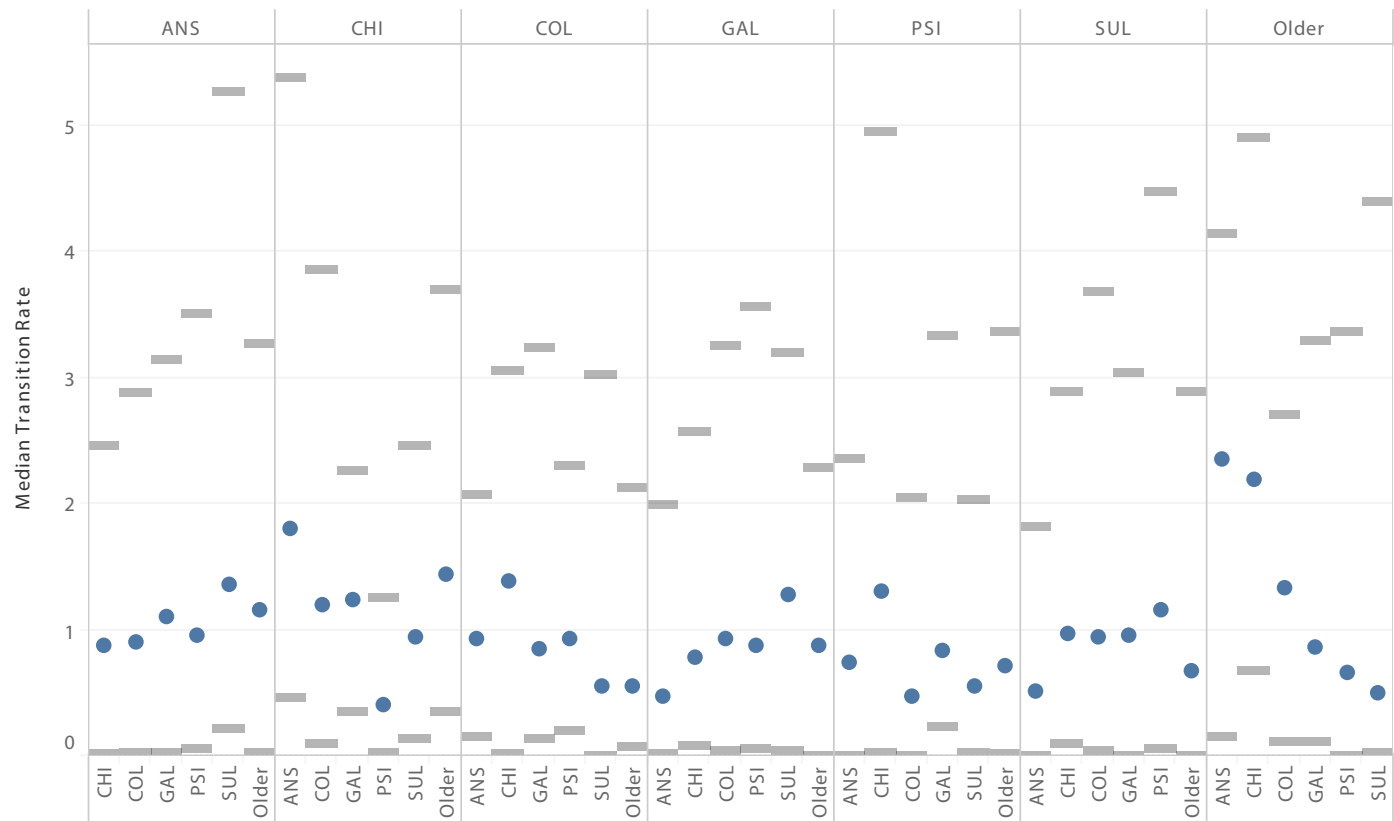


Supplemental Figure S6. Tip Swap Analysis Host Transition Rates. Blue circles indicate the median transition rate per year from the host source (top axis label) to the sink (bottom axis label). Gray bars represent the 95% highest posterior density of the estimate. The “Older” category represents sequences collected before 2006 of any host. (ANS – Anseriformes, CHA – Charadriiformes, CHI – domestic chicken, COL – Columbiformes, GAL – other Galliformes, PSI – Psittaciformes)

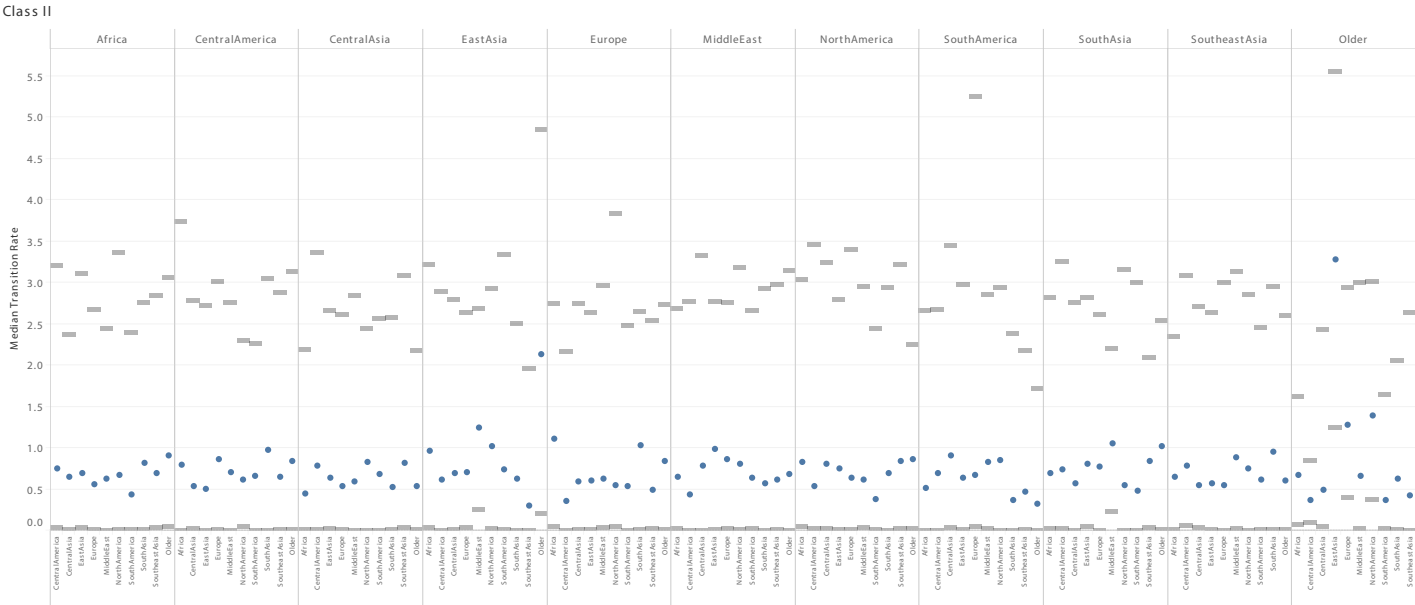
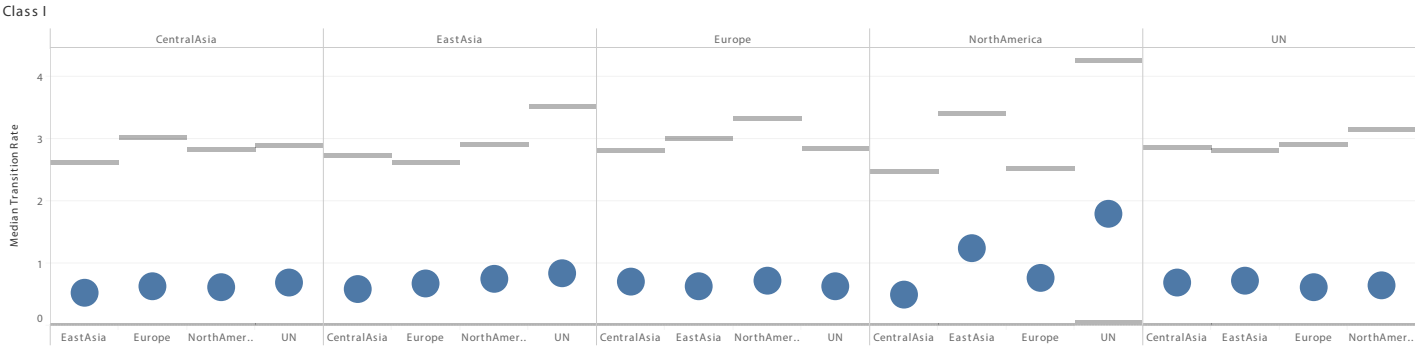
Class I



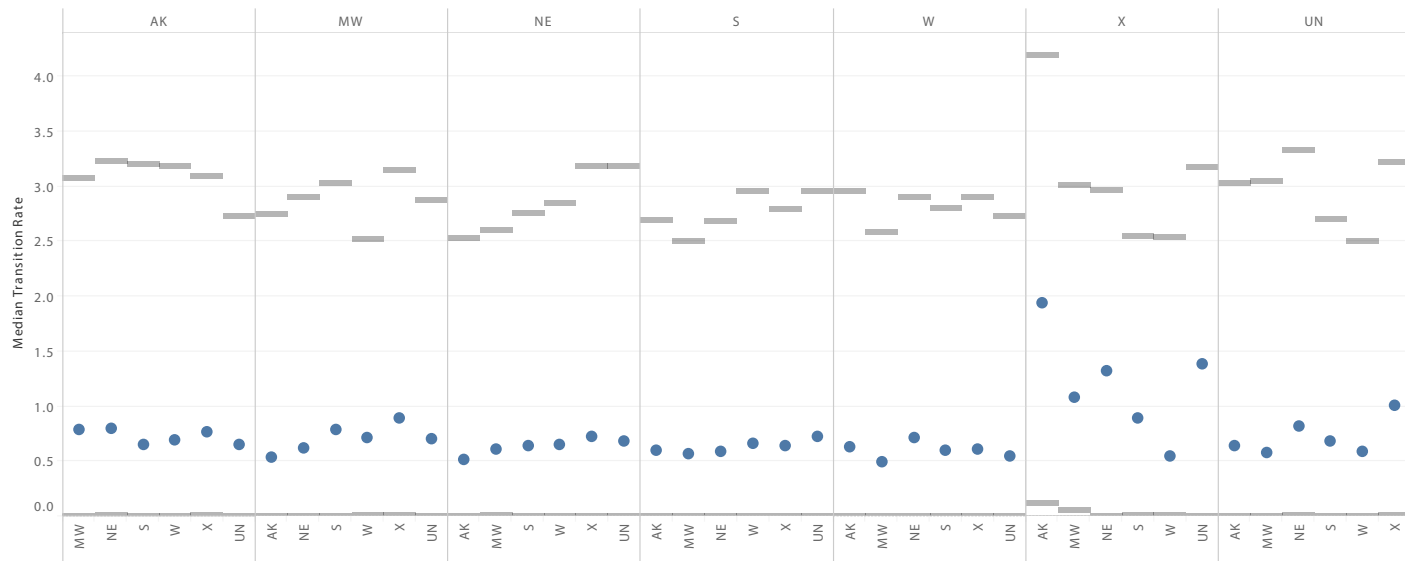
Class II



Supplemental Figure S7. Tip Swap Analysis World Region Transition Rates. Blue circles indicate the median transition rate per year from the world region source (top axis label) to the sink (bottom axis label). Gray bars represent the 95% highest posterior density of the estimate. The “Older/UN” category represents sequences collected before 2006 of any host.



Class I



Class II

