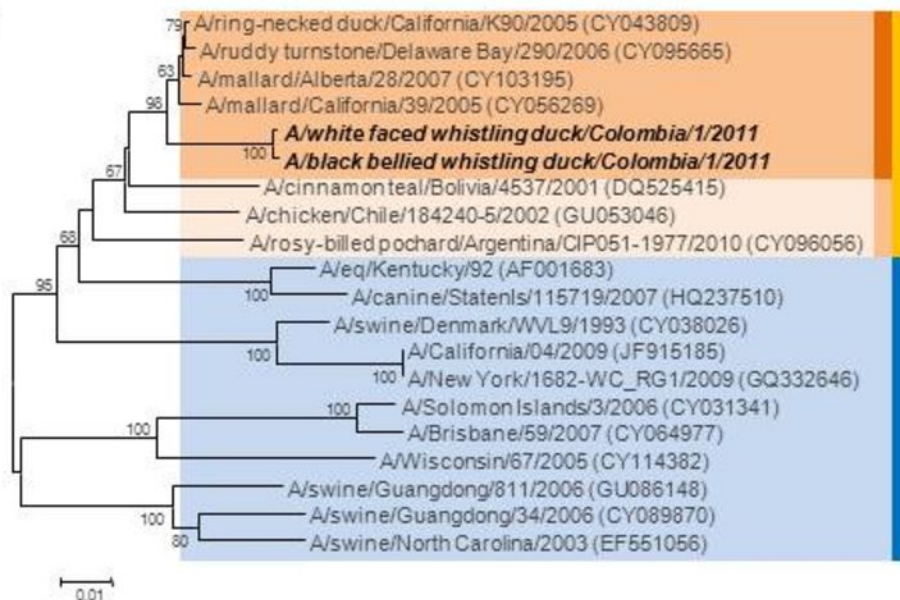
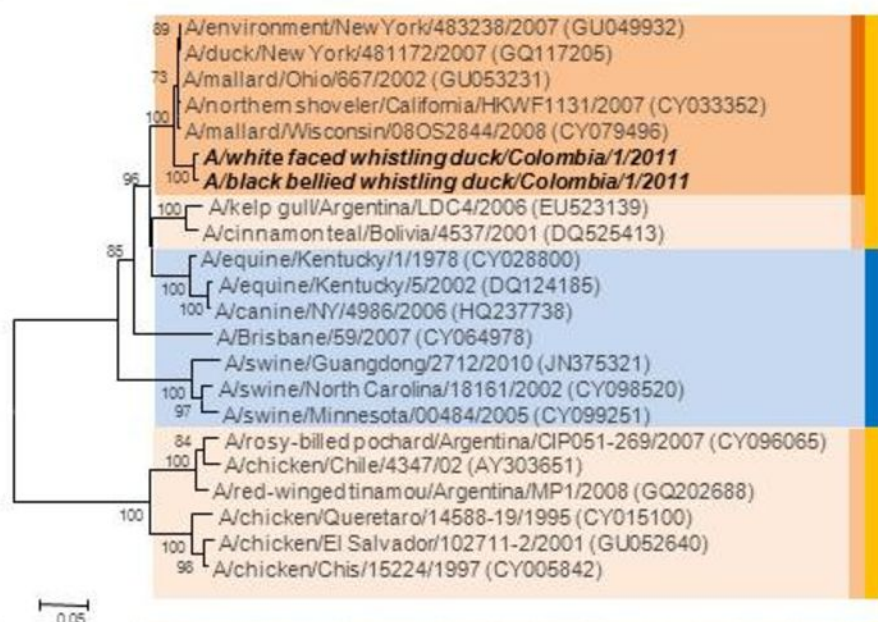


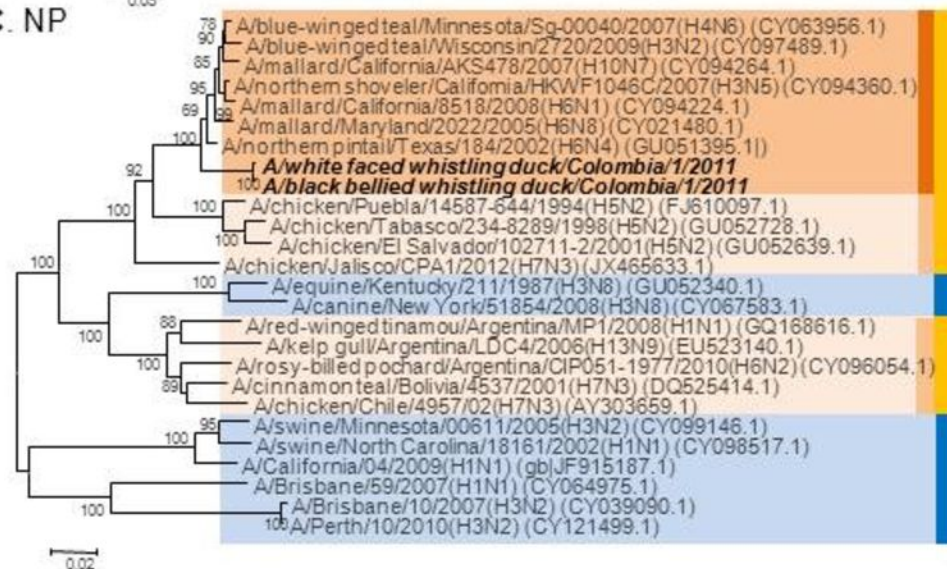
A. M



B. NS

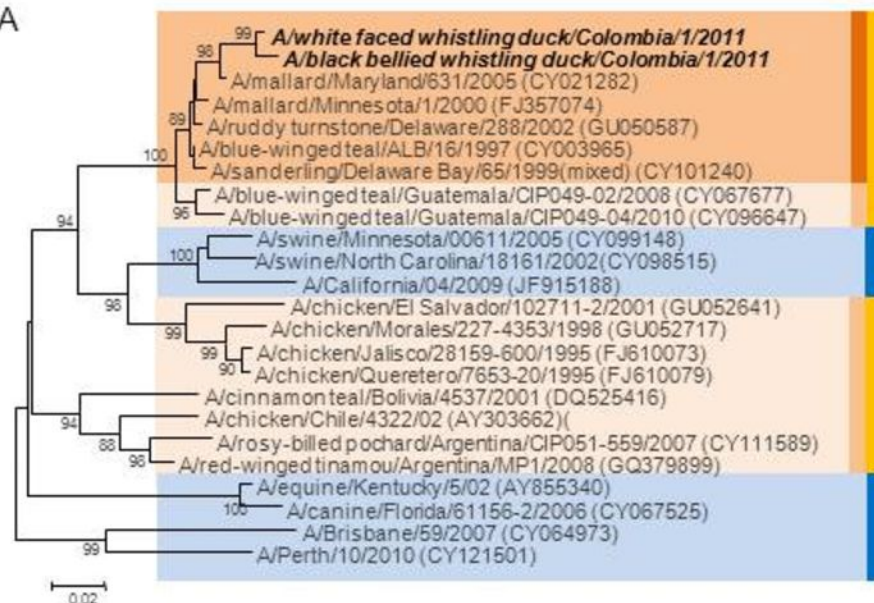


C. NP

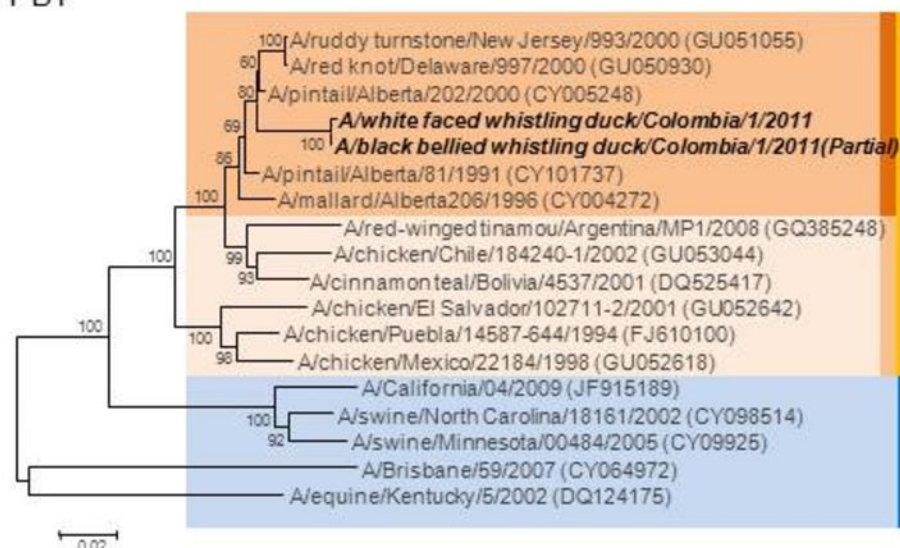


Supplementary Figure 2: Phylogenetic trees of the M (A), NS (B), NP (C), PA (D), PB1 (E), PB2 (F) genes of influenza viruses isolated from Whistling duck in the Llanos region of Colombia. Trees were generated using the neighbor-joining method in MEGA. Numbers next to branches indicate neighbor-joining bootstrap values. Only bootstrap values above 60 were included in the tree for clarity. Trees are based on full genetic sequence for M, NS, NP, PB1 and PB2 and on ~520 nucleotides for PA from HxNx viruses from Central/South American avian (light orange), North America avian (dark orange) and Mammalian (blue) strains. Strains under characterization in this study are highlighted in black italics. Scale bars represent number of substitutions per site.

D. PA

Supplementary Figure 2
Whistling duck (con't)

E. PB1



F. PB2

