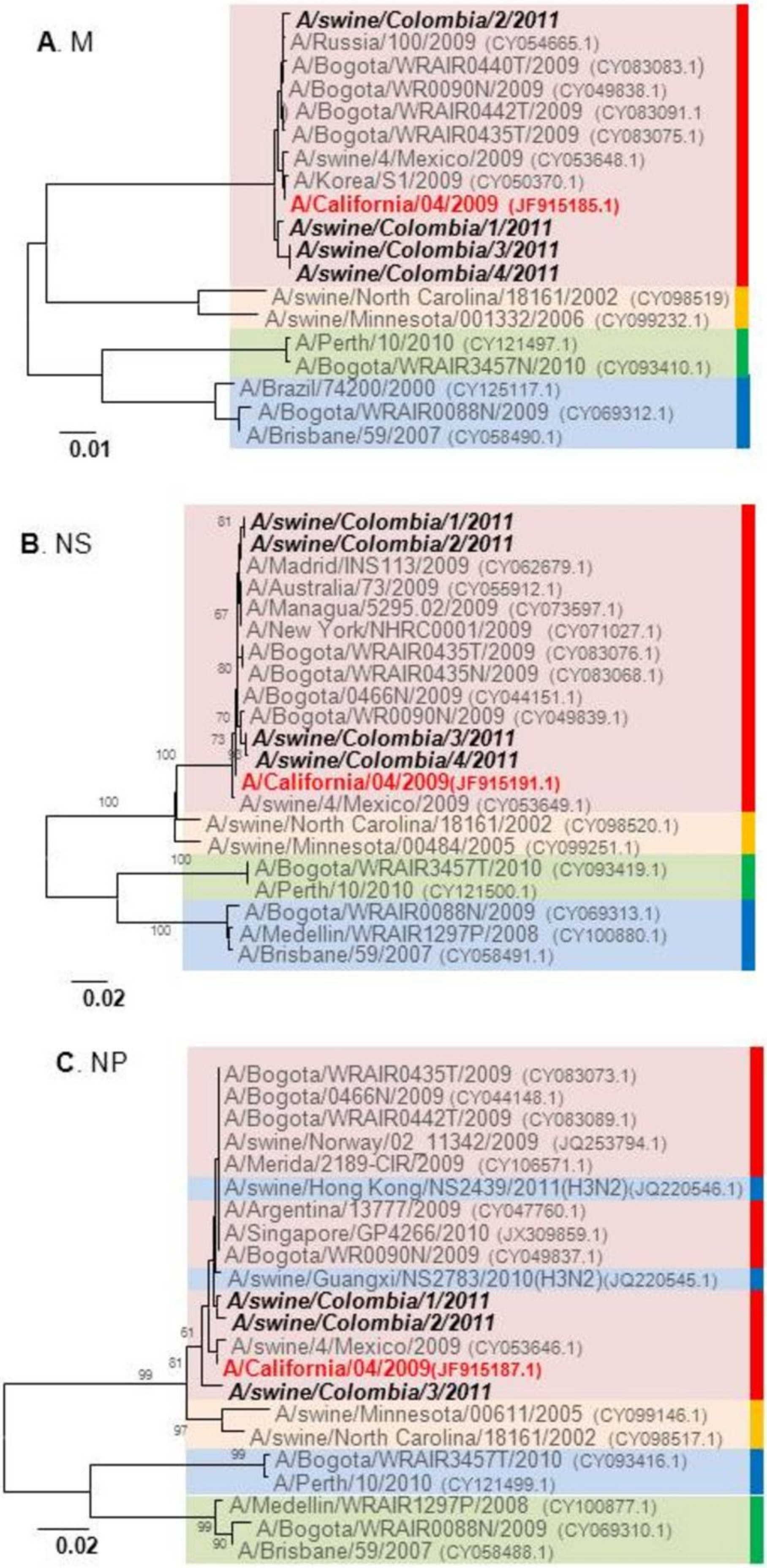

Supplementary Figure 1: Phylogenetic trees of the M (A), NS (B), NP (C), PA (D), PB1 (E), PB2 (F) genes of influenza viruses isolated from swine in the Llanos region of Colombia. Trees were generated using the neighbor-joining method in MEGA. Numbers next to branches indicate neighbor-joining bootstrap values. Only bootstrap values above 60 were included in the tree for clarity. Sequences from pandemic H1N1 (red), classical swine H1N1 (yellow), seasonal human N1N1 (green) and both seasonal human and swine H3N2 viruses (blue) are represented. Trees are based on full genetic sequence for M and NS genes and on ~330. ~820, ~120 and ~330 nucleotides for NP, PA, PB1 and PB2 respectively. Swine isolates are in black italics. An archetypal 2009 pandemic H1N1 strain (A/California/04/2009) is highlighted in red. Scale bars represent number of substitutions per site.

Supplementary Figure 1
Swine con't