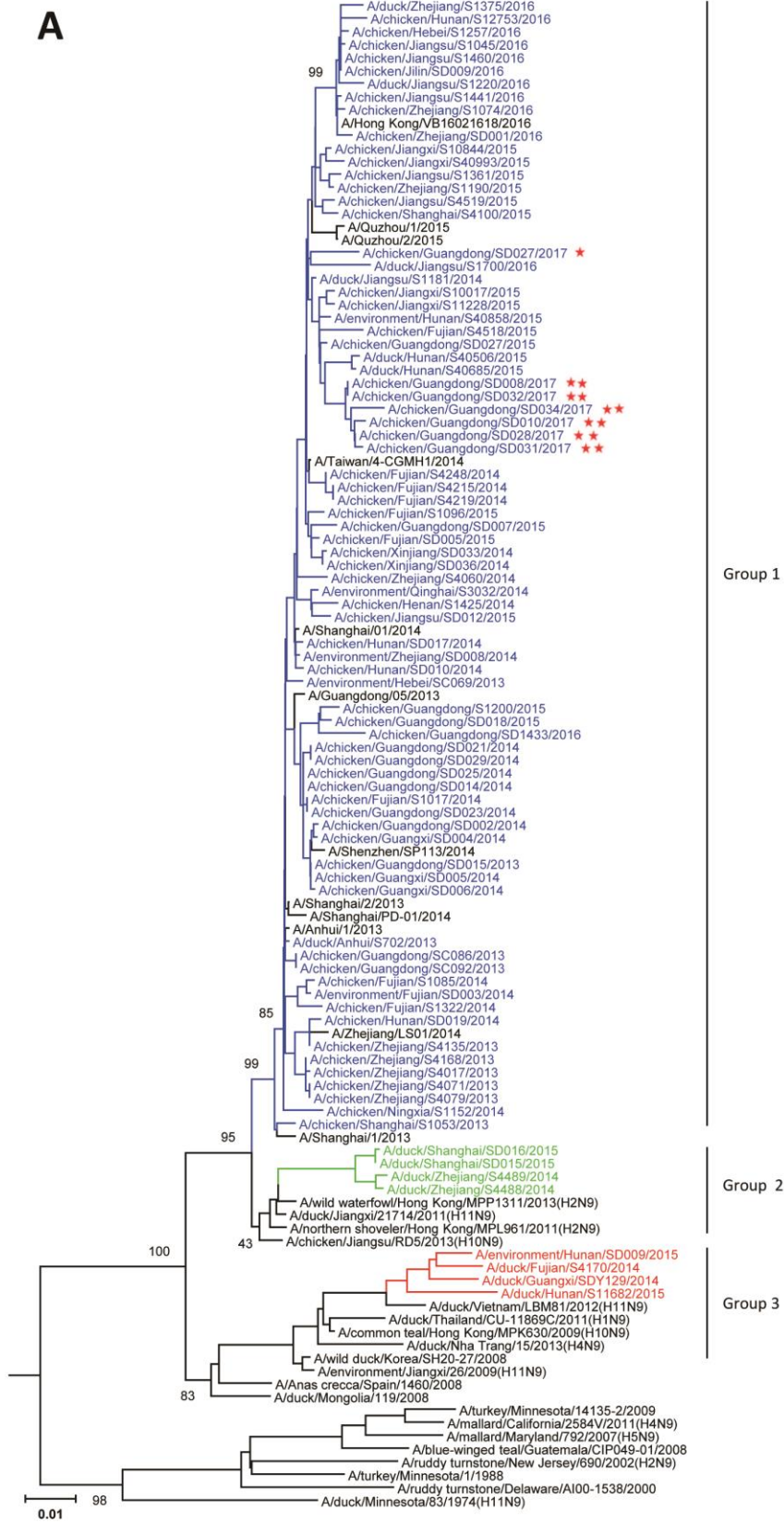
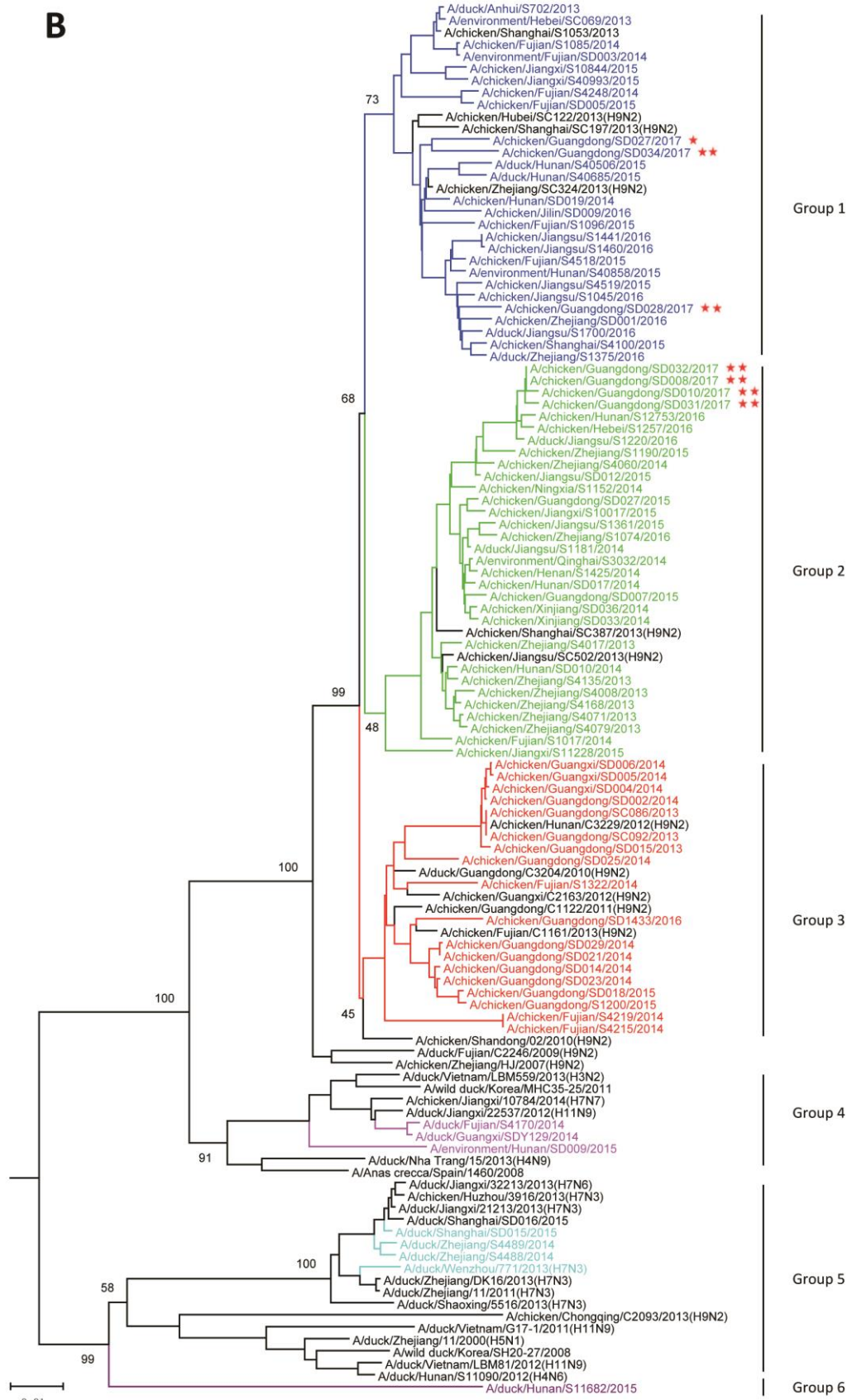


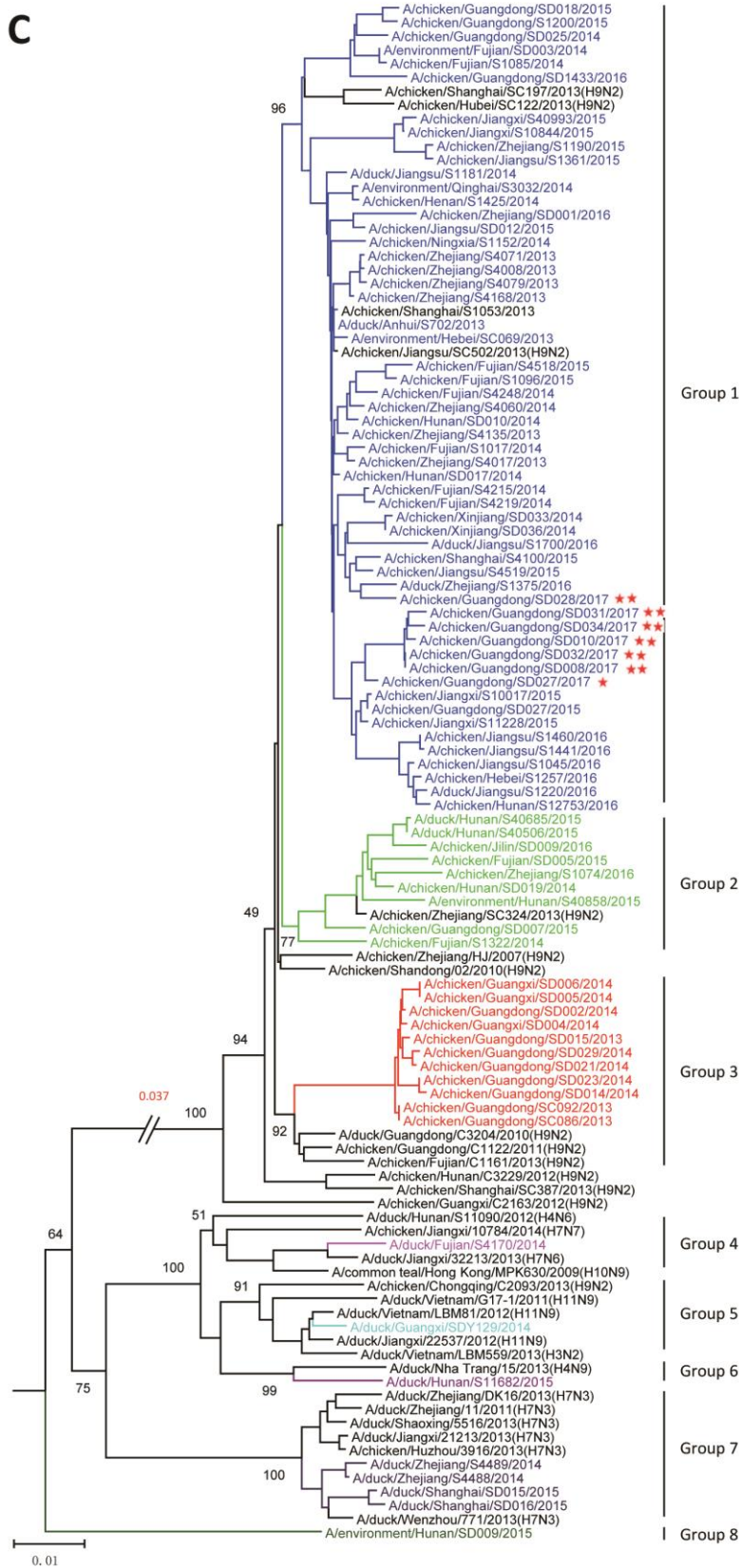
Figure S1



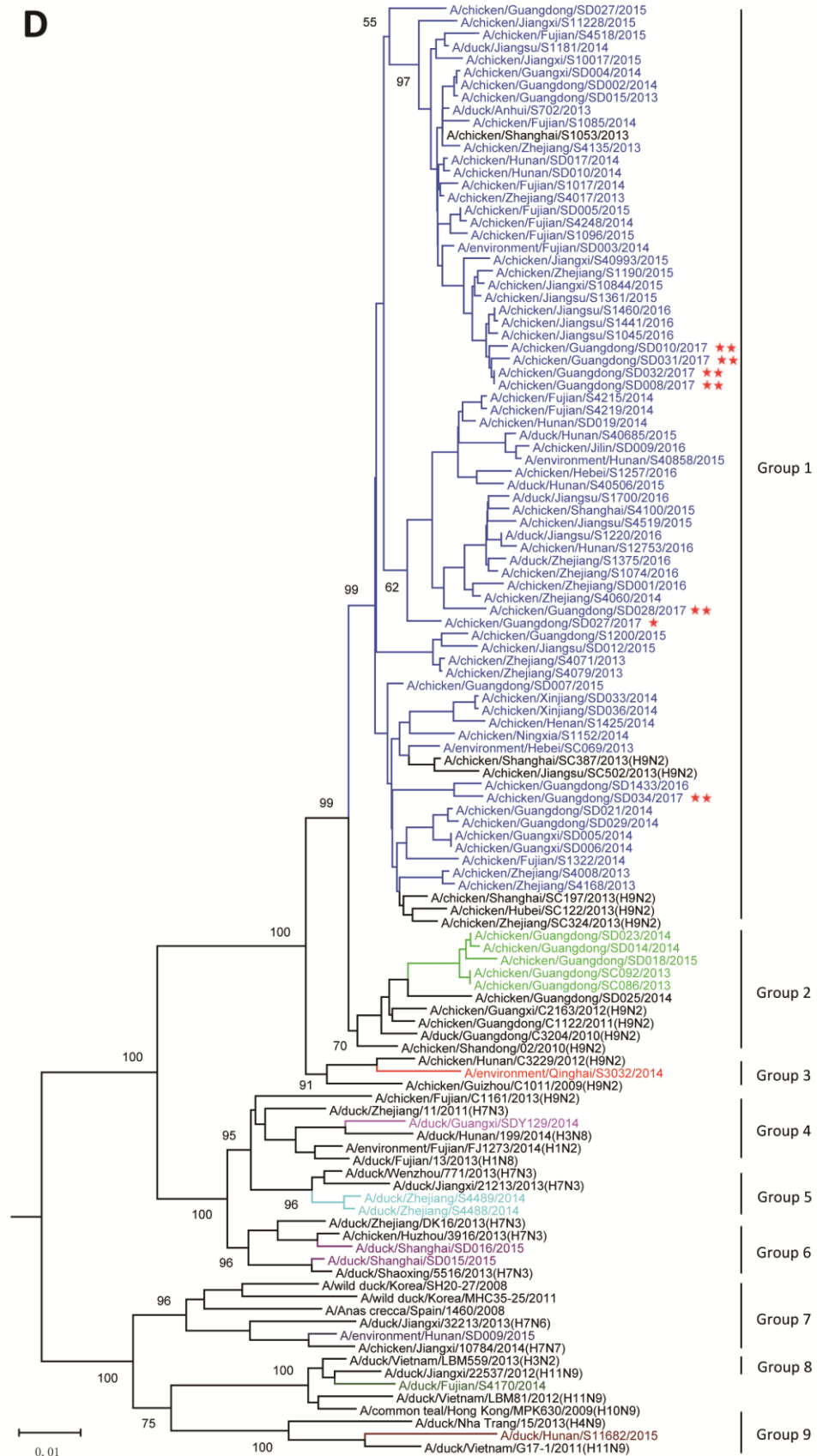
**B**



C

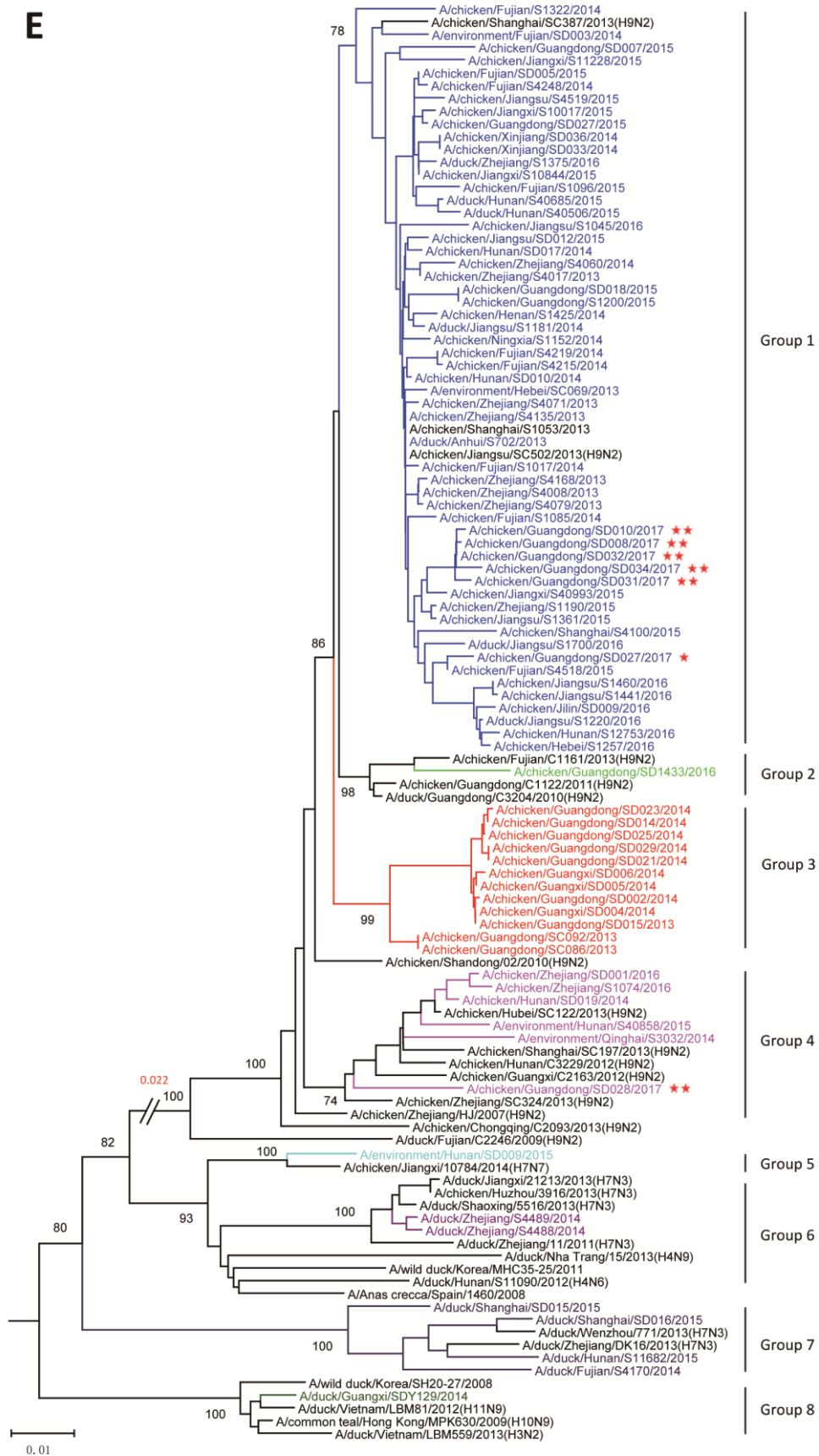


D

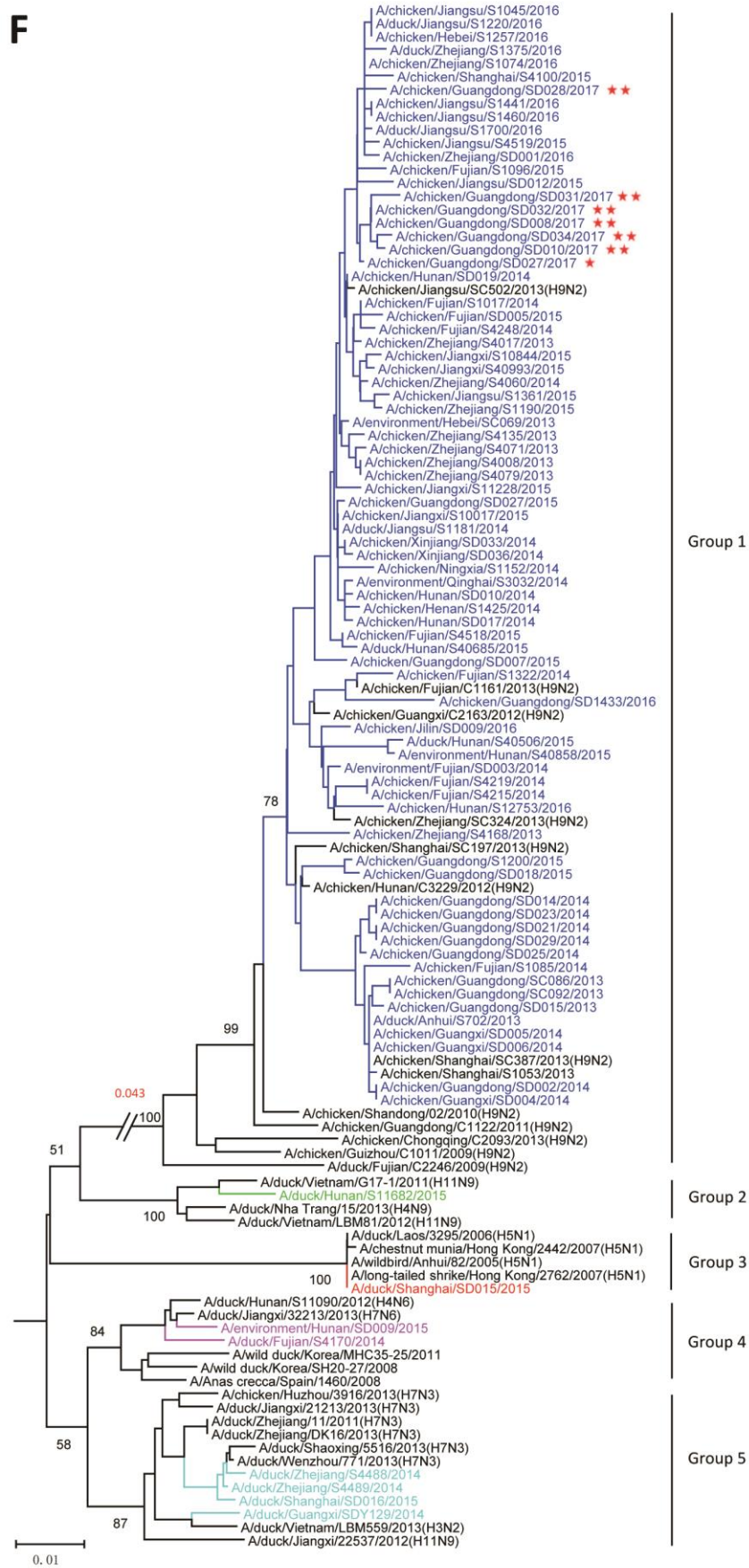




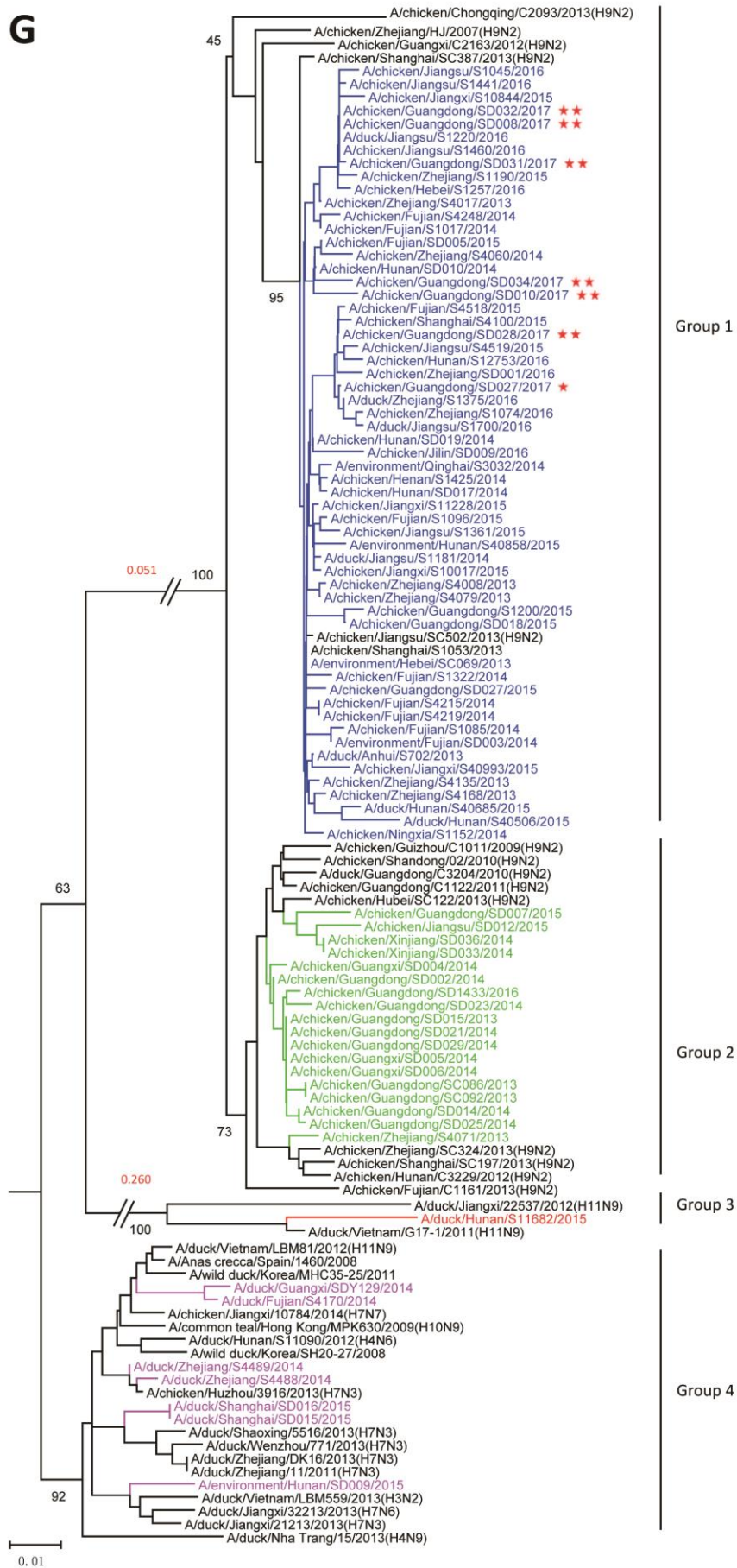
E



F



G



**Figure S1. Phylogenetic trees of the NA and internal genes of H7N9 influenza viruses.**

(A) Phylogenetic tree of NA. The tree was rooted to A/chicken/Italy/22A/1998(H5N9) virus and based on nucleotides (nt) 19 to 1416. The phylogenetic trees of PB2 (B), PB1(C), PA (D), NP (E), M (F), and NS (G) were based on nt 28–2307, 25–2298, 25–2175, 46–1542, 26–1007, and 27–864, respectively, and rooted to A/chicken/Rostock/45/1934(H7N1) virus. Sequences of viruses with names in black were downloaded from available databases; viruses with names in colors were sequenced in this study. Viruses labelled with stars contain the four amino acid (-KRTA-) insertion in their HA gene cleavage sites.