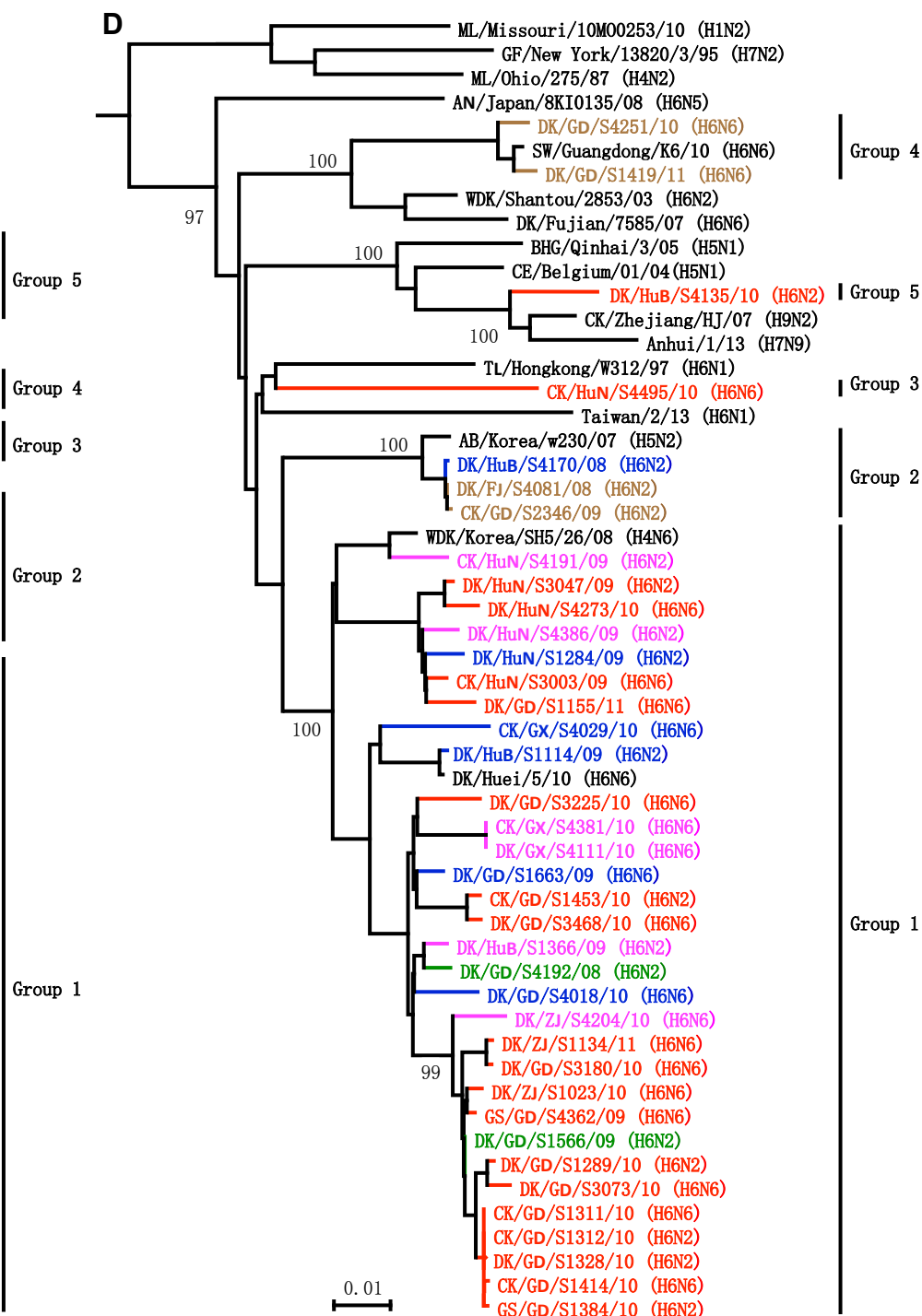
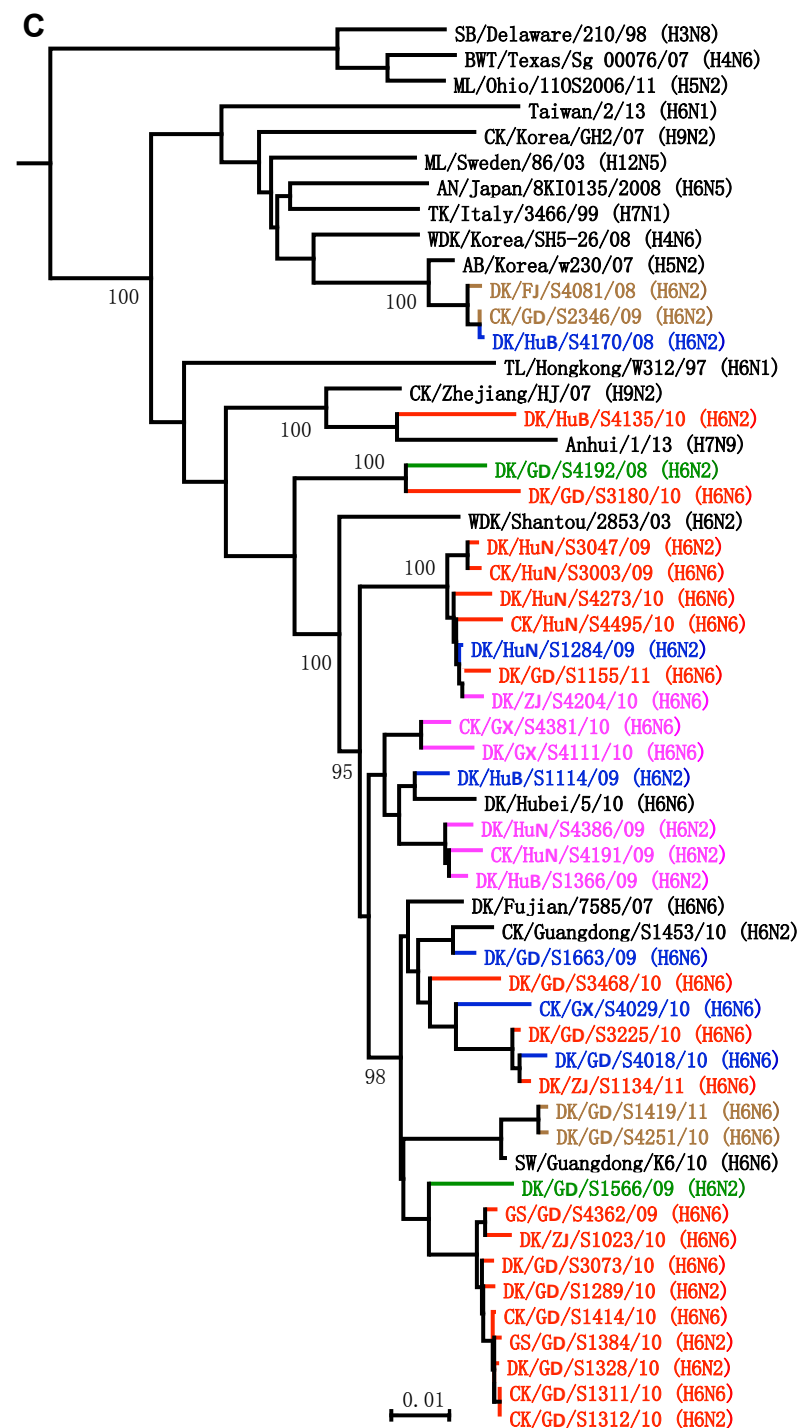


Figure S1A-F



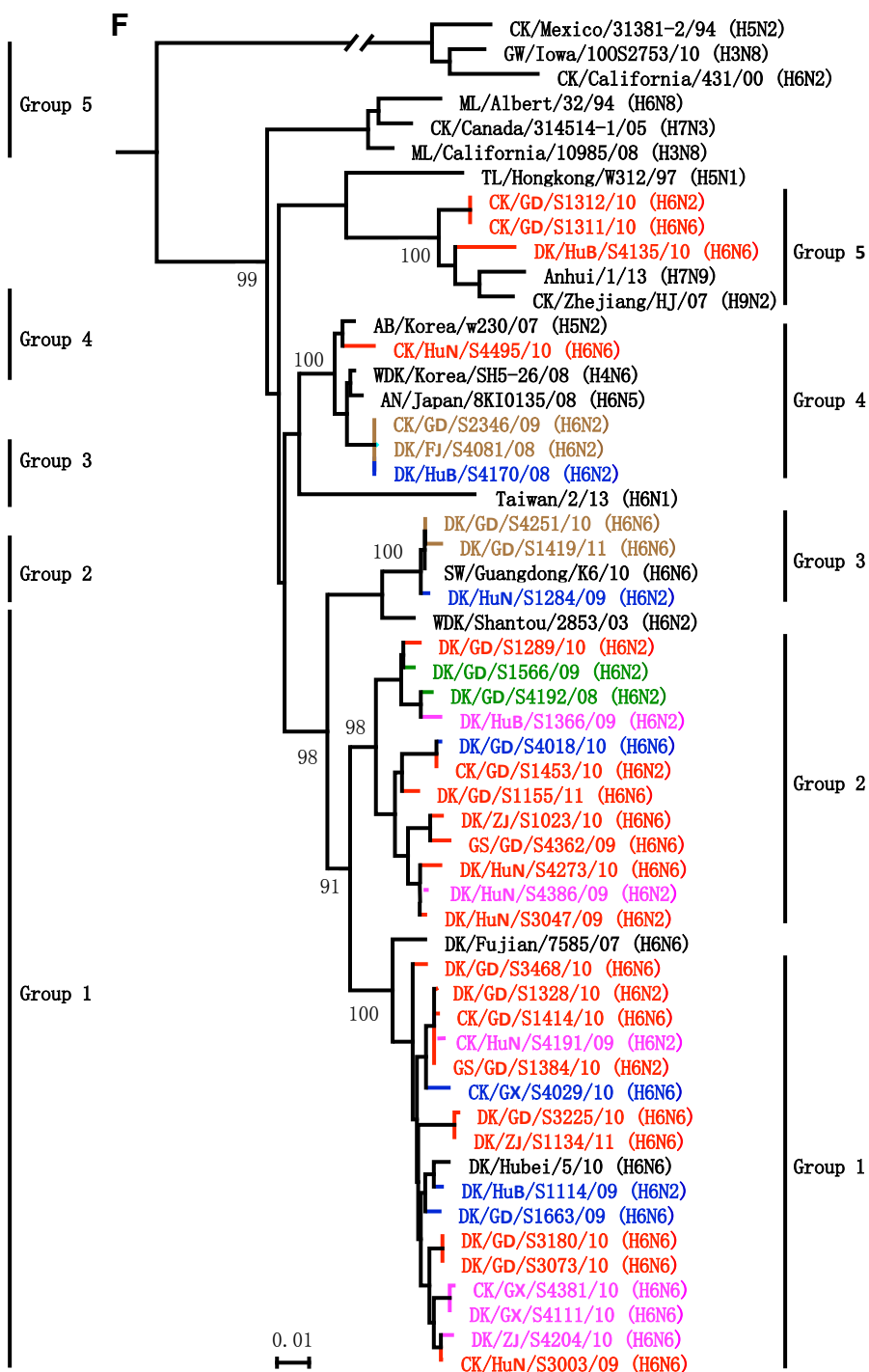
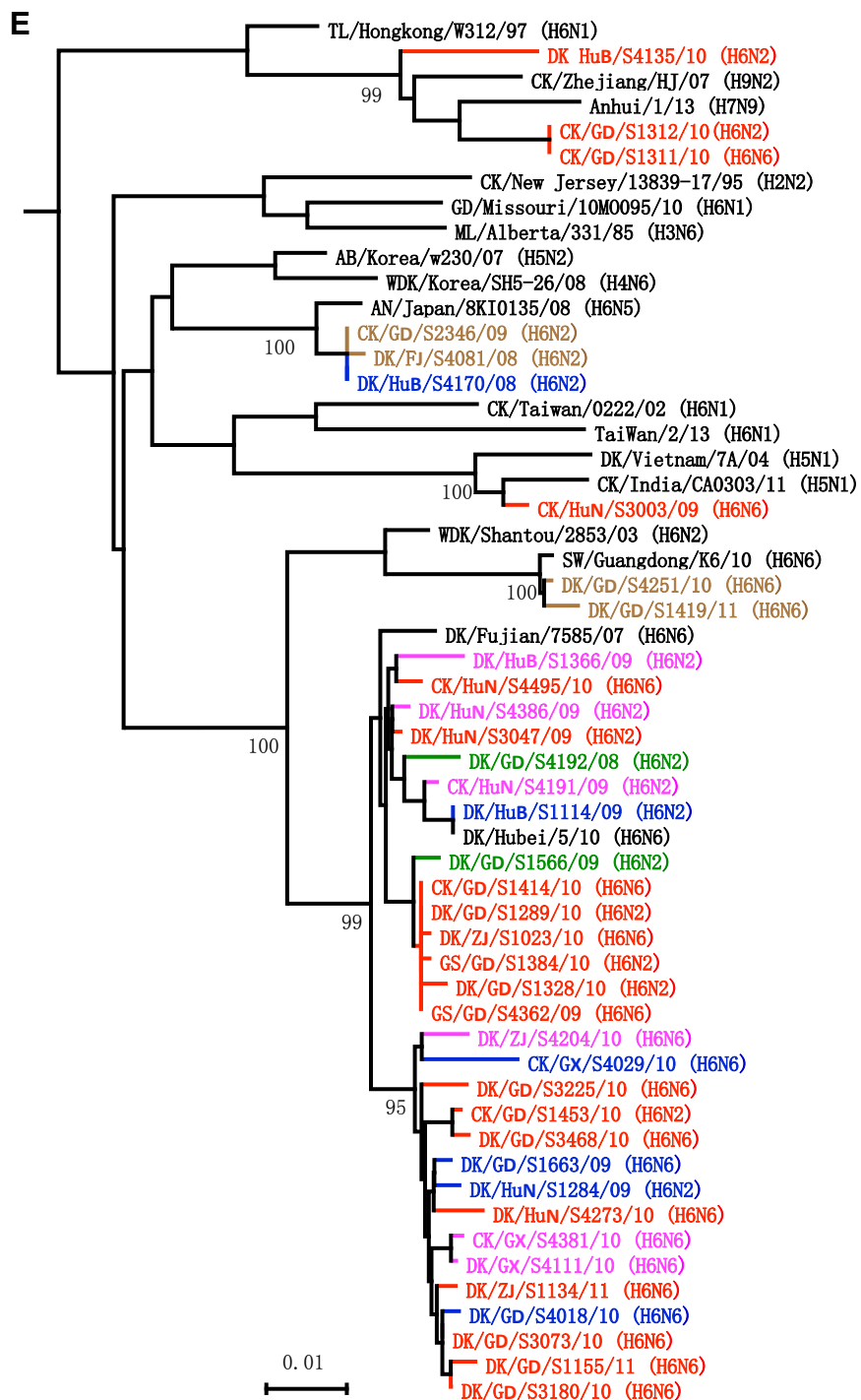


Figure S1. Phylogenetic analyses of the H6 viruses isolated from 2008 to 2011 in China. Phylogenetic analyses of the H6 viruses isolated from 2008 to 2011 in China. The phylogenetic trees were generated with the PHYLIP program of the CLUSTALX software package (version 1.81). The six trees were generated based on the following sequences: PB2 nt 28–2307, PB1 nt 25–2298, PA nt 25–2175, NP nt 46–1542, M nt 26–1007, and NS nt 27–864. The phylogenetic trees of PB2 (A), PB1 (B), PA (C), NP (D), M (E), and NS (F) were rooted to A/EQ/Prague/1/56 (H7N7). Viruses shown in black were downloaded from available databases; viruses in other colors were sequenced in this study. The colors of the viruses in the PB2, PB1, PA, NP, M and, NS trees match with those used in the HA tree. Abbreviations: AB, aquatic bird; ABD, American black duck; AN, avian; BHG, bar headed goose; BWT, blue winged teal; CE, crested eagle; CK, chicken; DK, duck; FJ, Fujian; GD, Guangdong; GF, guinea fowl; GS, goose; GW, gadwall; GX, Guangxi; GY, Guiyang; HuB, Hubei; HK, Hongkong; HuN, Hunan; MDK, muscovy duck; ML, mallard; TL, teal; RT, ruddy turnstone; SB, shorebird; SW, swine; TK, turkey; WDK, wild duck; ZJ, Zhejiang.