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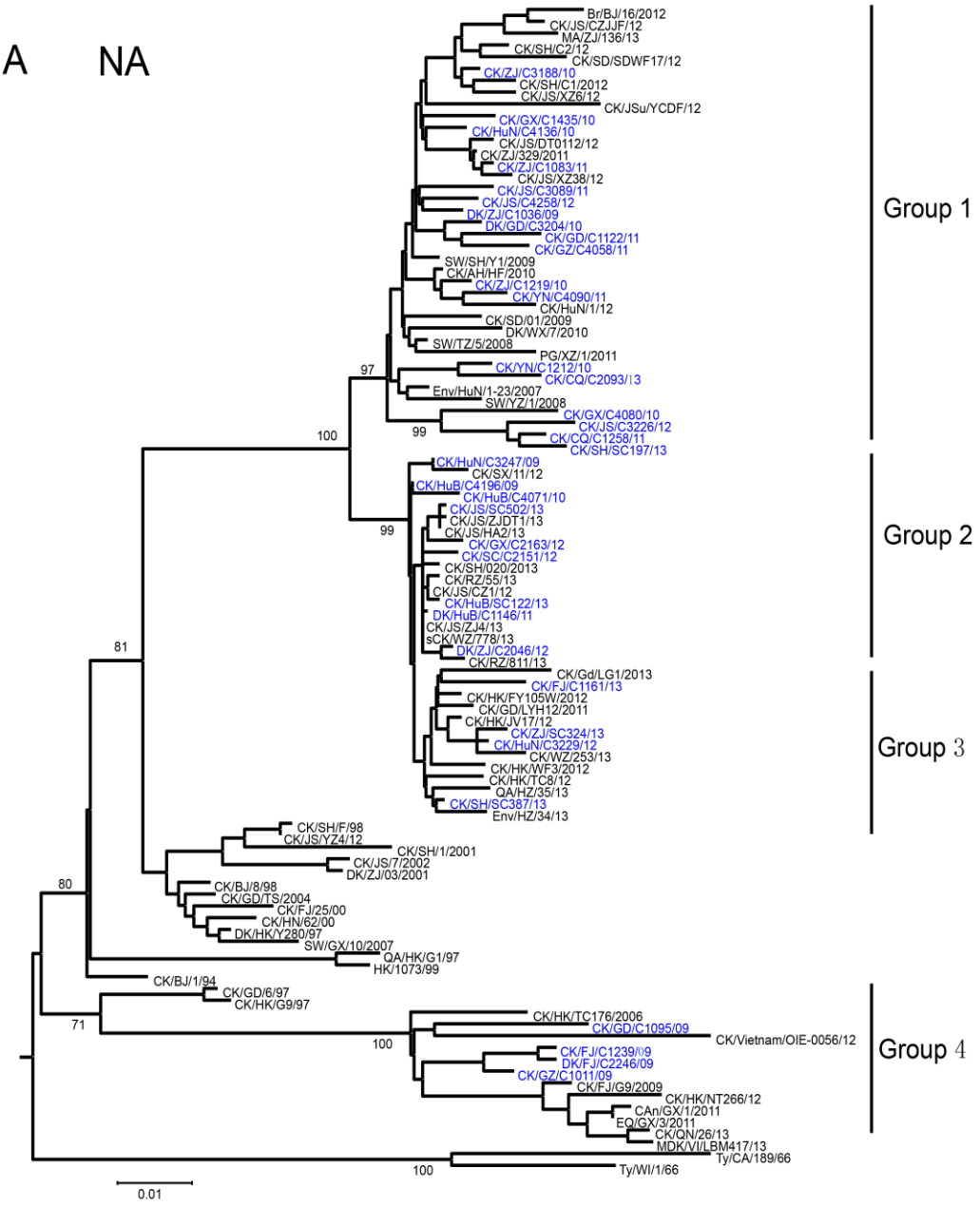
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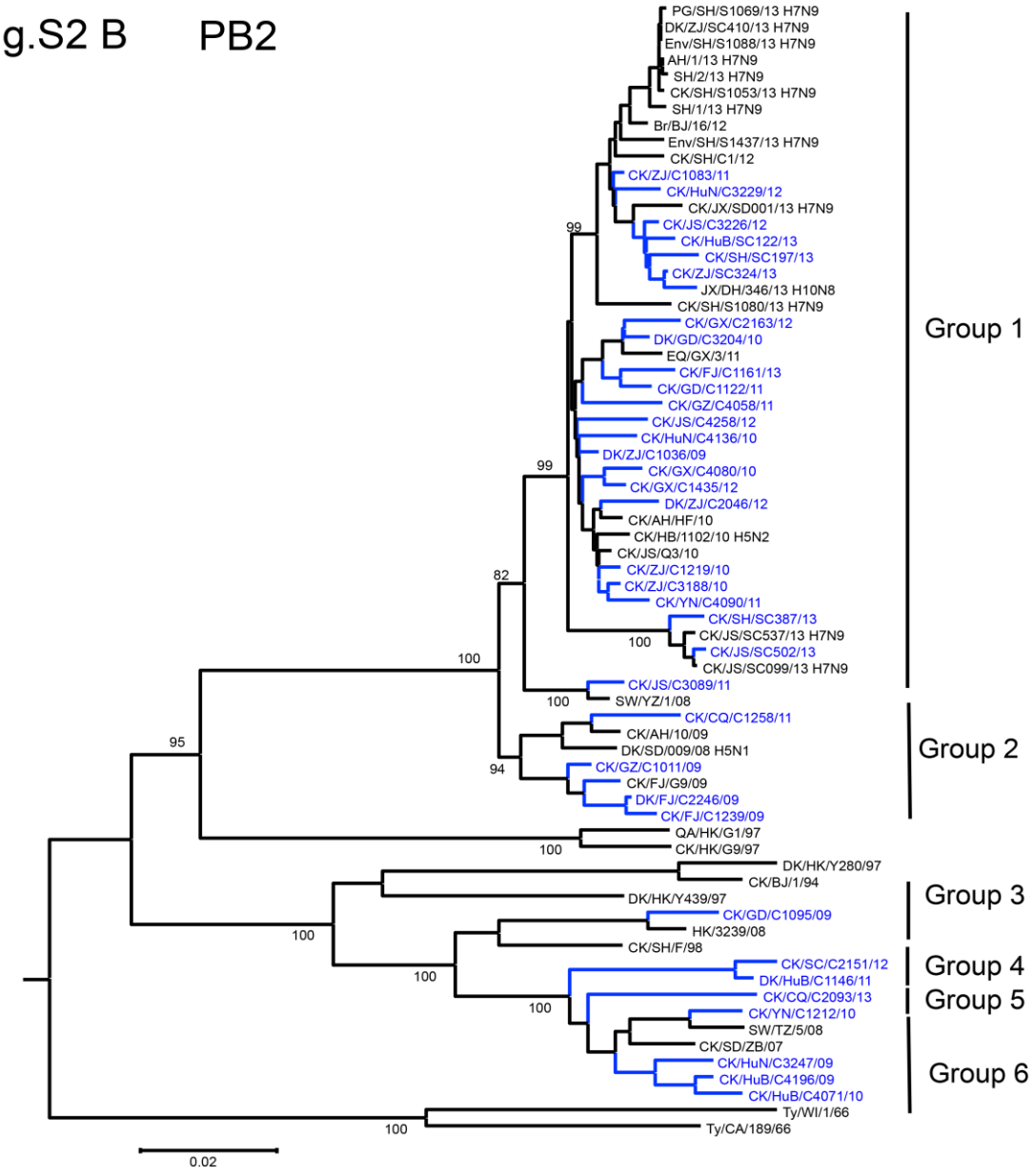
Group 2
Group 3
Group 4

Fig.S2 B PB2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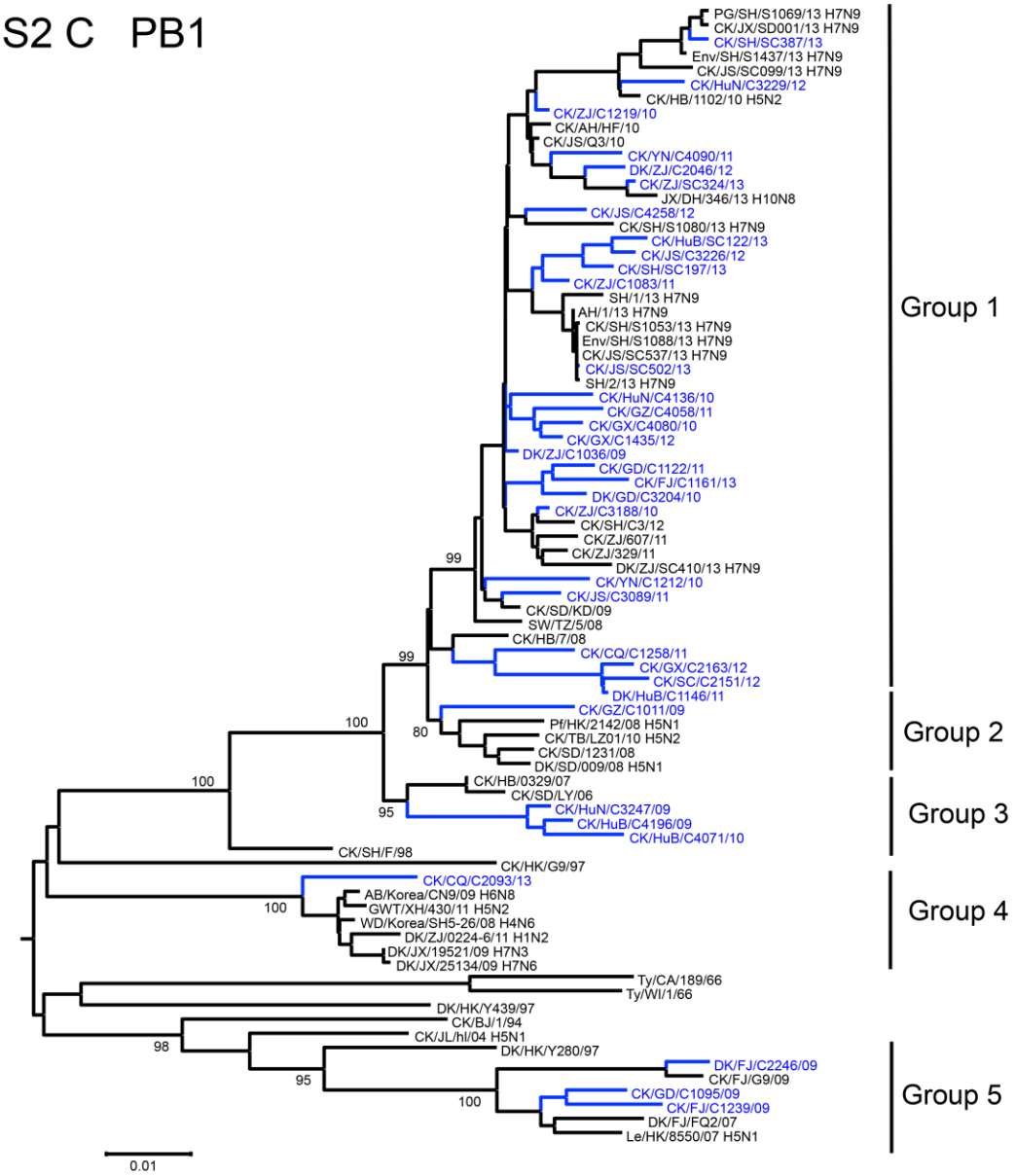
Group 3
Group 4
Group 5
Group 6

Fig.S2 C PB1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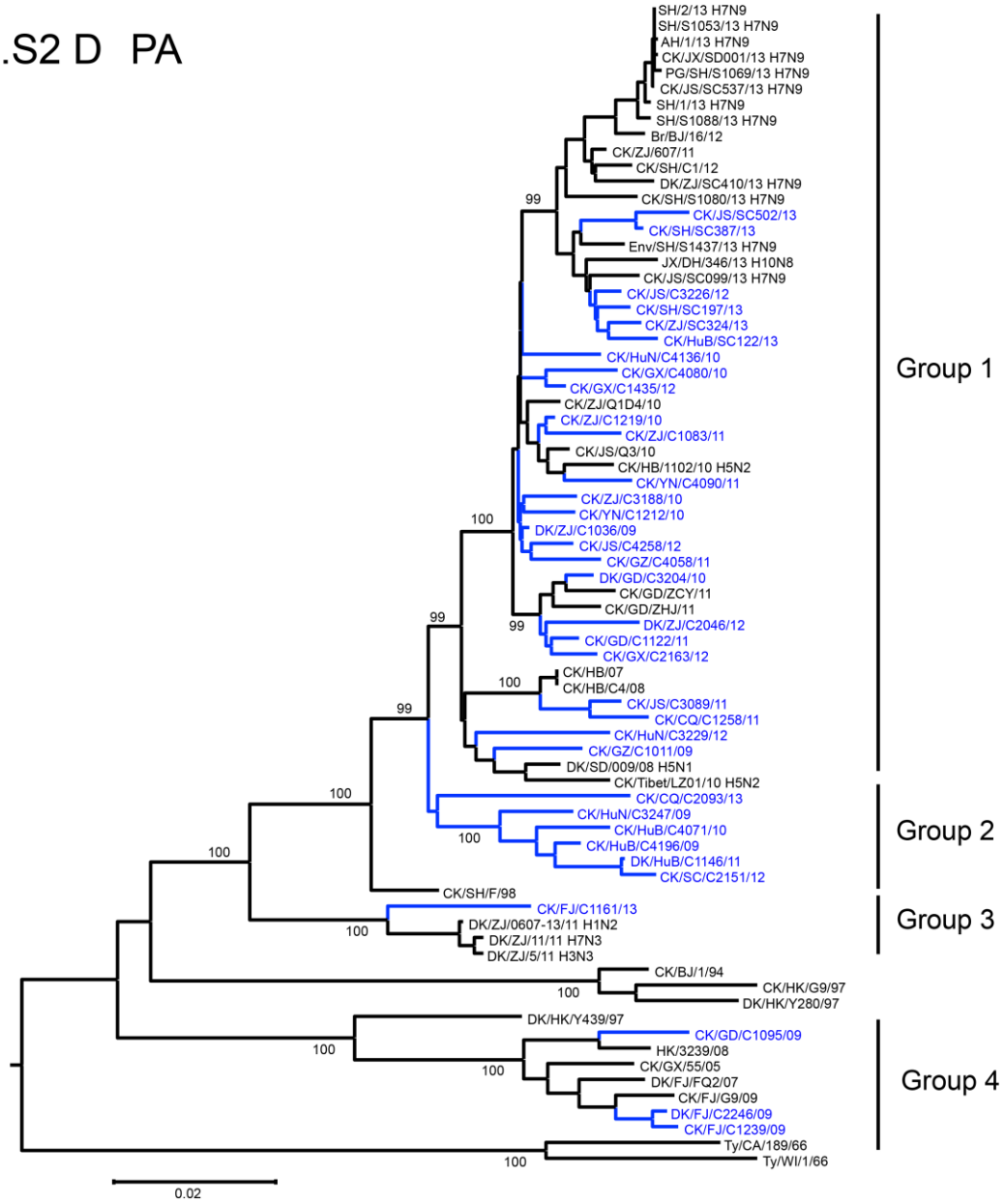
Group 2
Group 3
Group 4
Group 5

Fig.S2 D PA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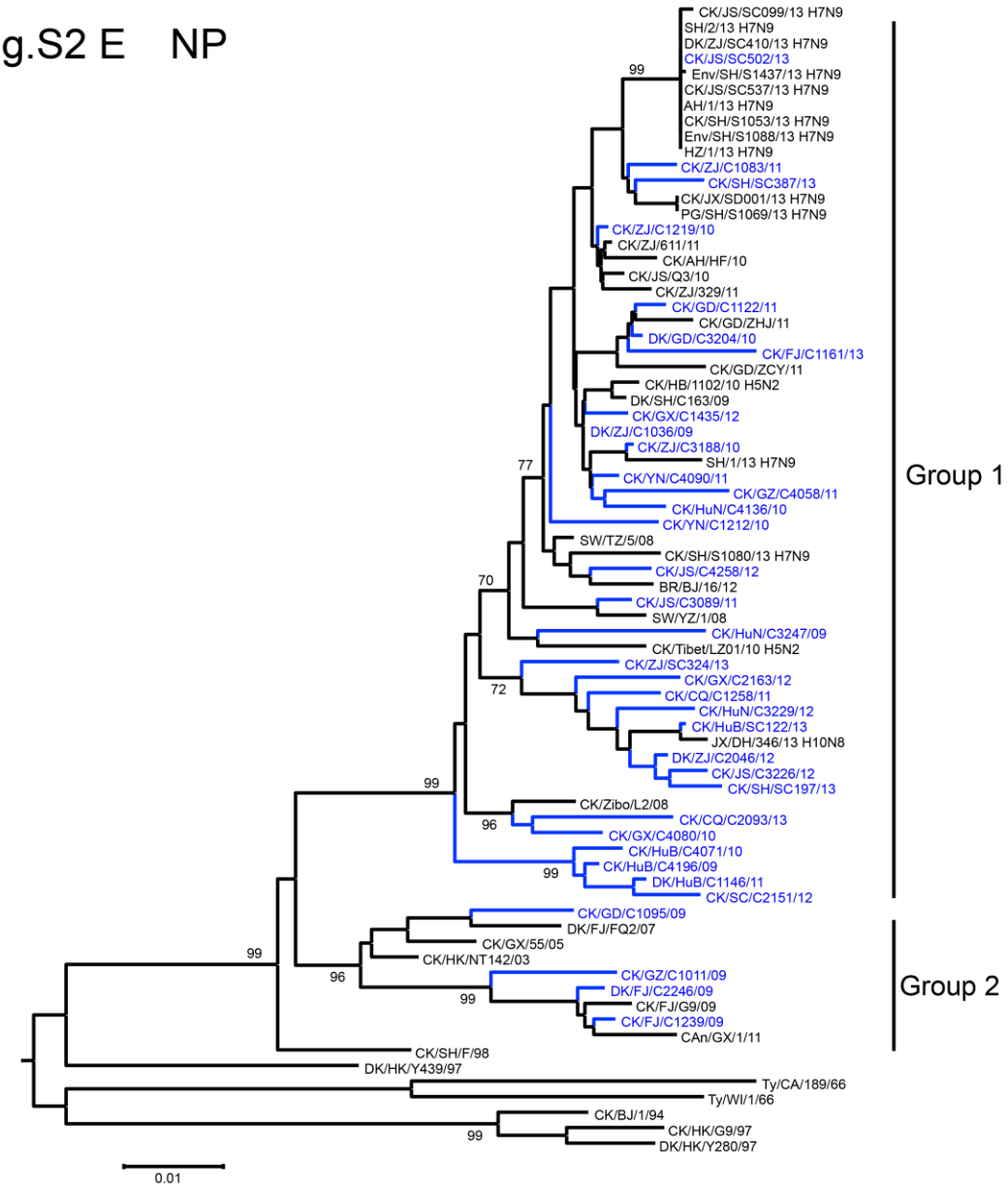
Group 2
Group 3
Group 4

Fig.S2 E NP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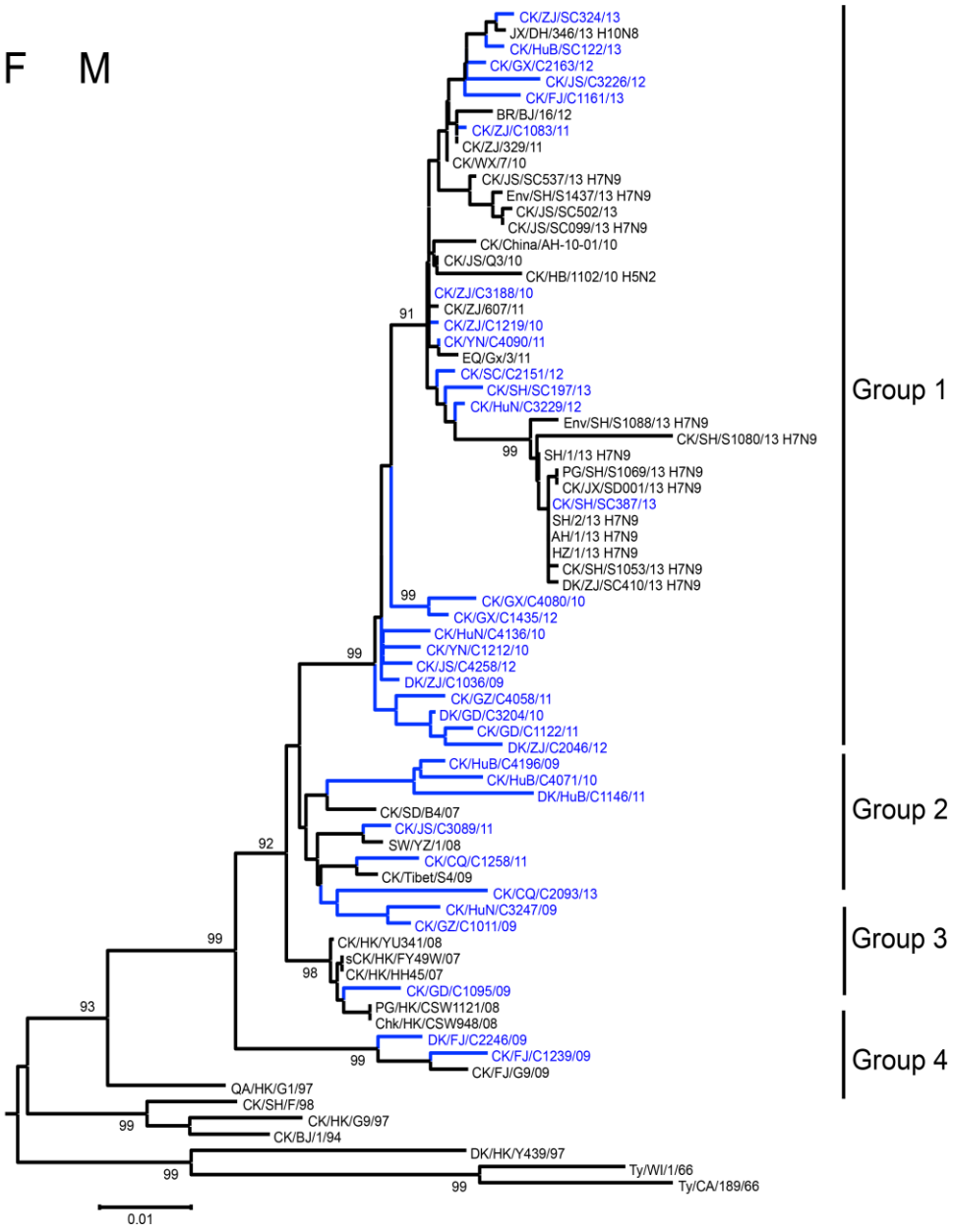
Group 2

Fig.S2 F M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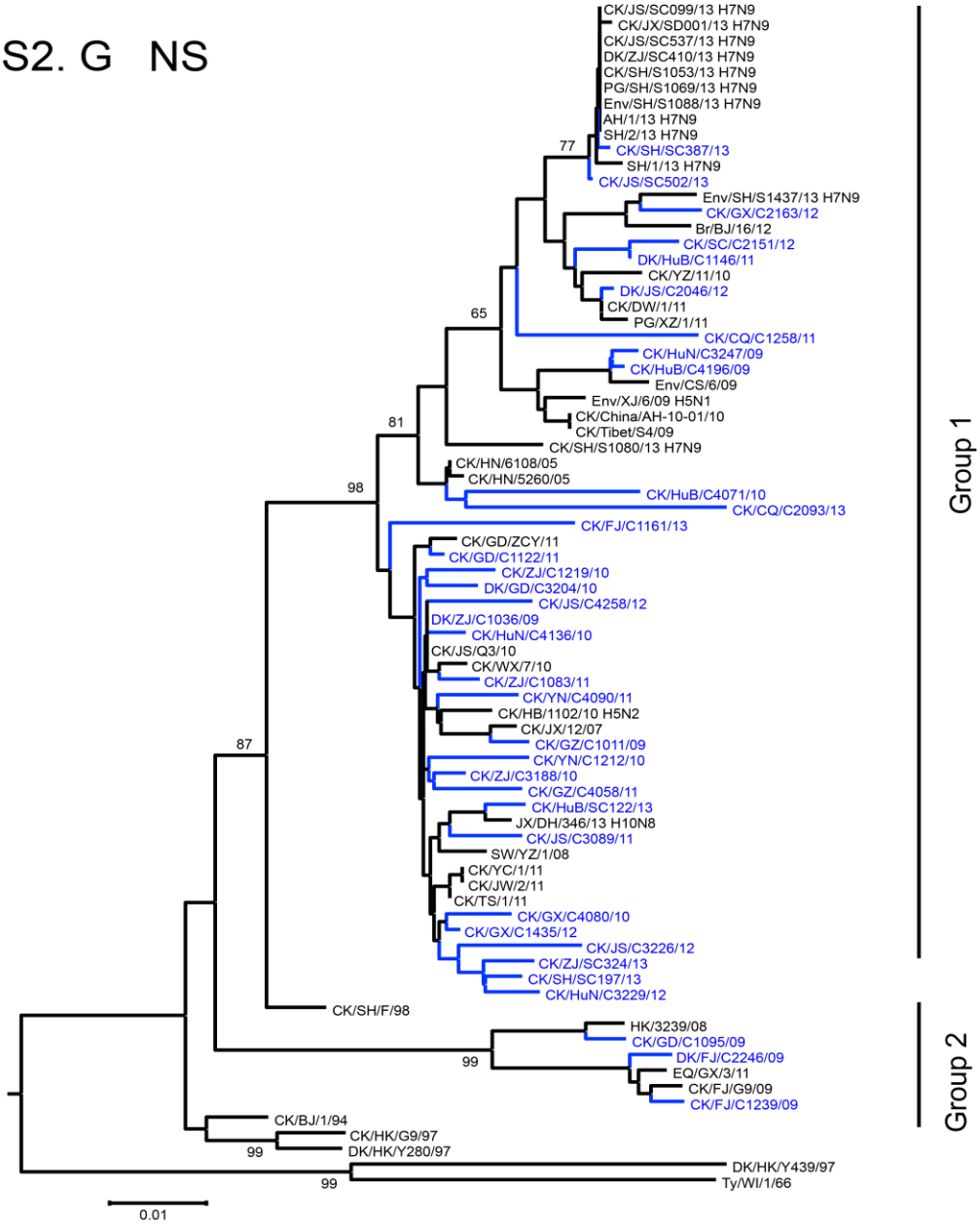
Group 2
Group 3
Group 4

Fig.S2. G NS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Group 1
Group 2

Figure S2. Phylogenetic analyses of the seven genes of H9N2 viruses. Phylogenetic analyses of the seven genes of the avian H9N2 influenza viruses isolated between 2009 and 2013.Trees were generated by using the neighbor-joining method (N-J Method) with the MEGA 5.0 program, and the tree topology was evaluated by means of 1000 bootstrap analyses. (**A**) NA gene tree. (**B**) PB2 gene tree. (**C**) PB1 gene tree. (**D**) PA gene tree. (**E**) NP gene tree. (**F**) M gene tree. (**G**) NS gene tree. The trees of NA, PB2, NP, M, and NS were rooted to A/Equine/Prague/1/56(H7N7), the PB1 and PA trees were rooted to A/Equine/London/1416/73(H7N7). The regions of the nucleotide sequences used for the phylogenetic analysis were: NA, 87 to 1263; PB2, 185 to 2290; PB1, 31 to 2233; PA, 25 to 2129; NP, 35 to 1457; M, 56 to 960; and NS, 75 to 800. Sequences of viruses with names in black were downloaded from available databases; viruses with names in blue were sequenced in this study. Abbreviations are as follows: Br, Brambling; CAn, Canine; CK, Chicken; DK, Duck; Env, Environment; GS, Goose; Pf, Peregrine falcon; Pg, Pigeon; QA, Quail ; SW, Swine; Ty , Turkey; AH, Anhui; BJ, Beijing; CA, California; CS, Chang Sha ; CQ, Chongqing ; DH, Donghu; FJ, Fujian; GD, Guangdong ; GX, Guangxi ; GZ, Guangzhou; HB, Hebei ; HZ, Hangzhou; HN, Henan; HK, Hong Kong ; HuB, Hubei ; HuN, Hunan; JL, Jilin; JS, Jiangsu ; SD, Shandong ; SH, Shanghai; TZ, Taizhou; WI, Wisconsin ; XJ, Xinjiang; XZ, Xuzhou; YZ, Yangzhou ; YN, Yunnan; ZJ, Zhejiang.