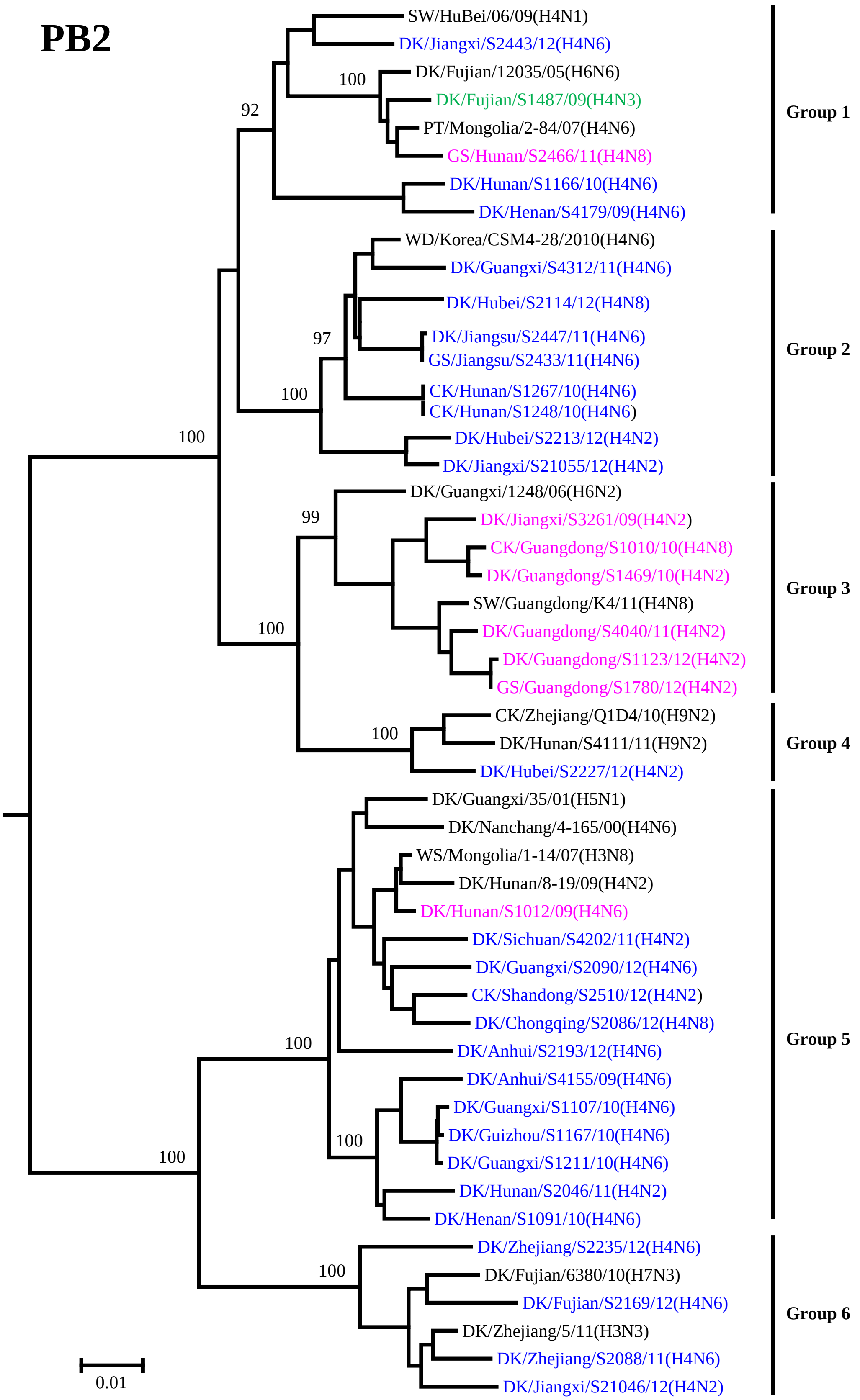
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92
97
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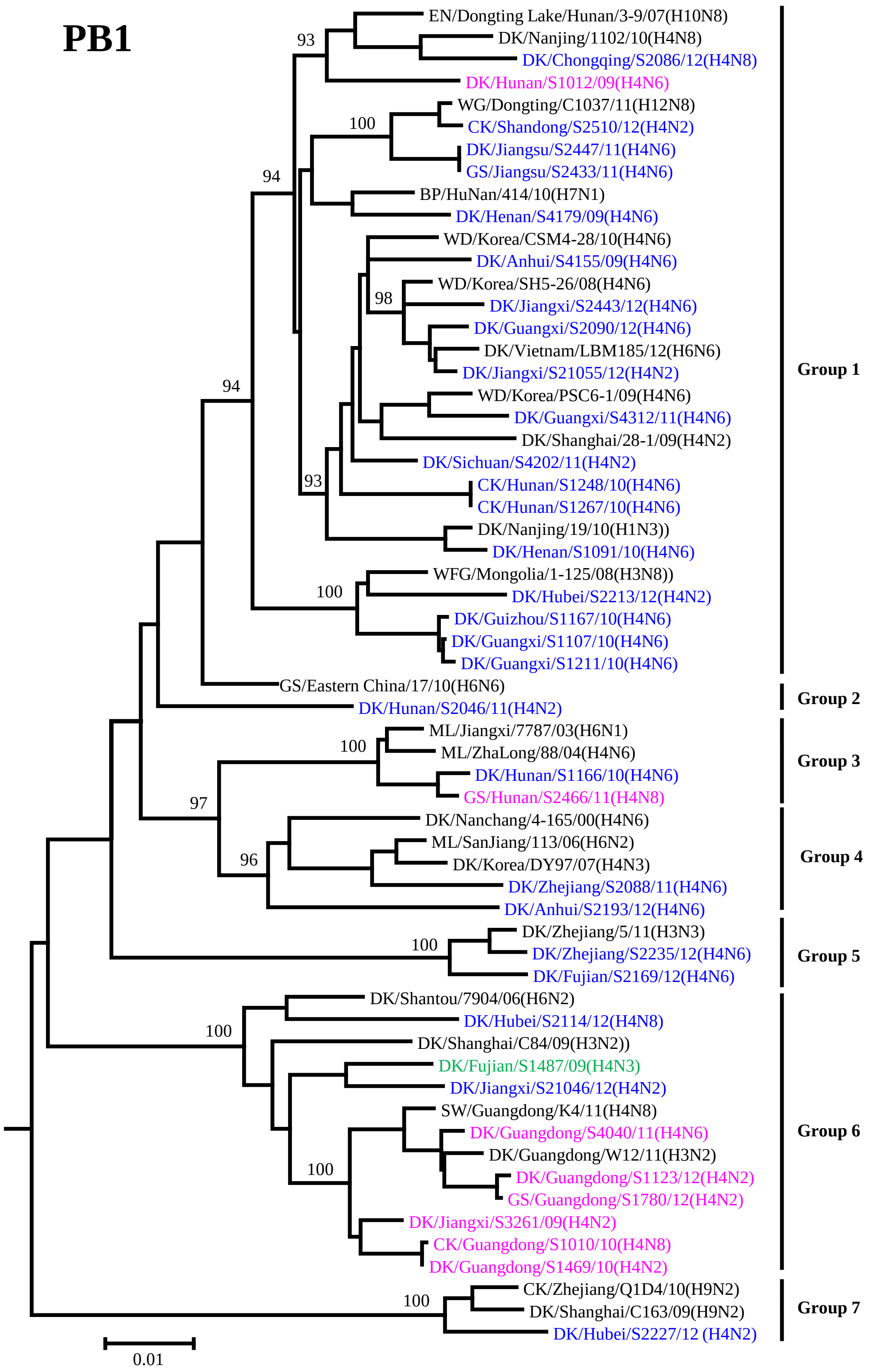
Group 3
Group 4
Group 5
Group 6

Fig. S1A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WD/Korea/SH5-26/08(H4N6)
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DK/Jiangxi/S21055/12(H4N2)
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WFG/Mongolia/1-125/08(H3N8))
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ML/SanJiang/113/06(H6N2)
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DK/Zhejiang/5/11(H3N3)
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DK/Shantou/7904/06(H6N2)
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DK/Shanghai/C84/09(H3N2))
DK/Fujian/S1487/09(H4N3)
DK/Jiangxi/S21046/12(H4N2)
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DK/Guangdong/S4040/11(H4N6)
DK/Guangdong/W12/11(H3N2)
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DK/Guangdong/S1123/12(H4N2)
GS/Guangdong/S1780/12(H4N2)
DK/Jiangxi/S3261/09(H4N2)
CK/Guangdong/S1010/10(H4N8)
DK/Guangdong/S1469/10(H4N2)
CK/Zhejiang/Q1D4/10(H9N2)
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DK/Shanghai/C163/09(H9N2)
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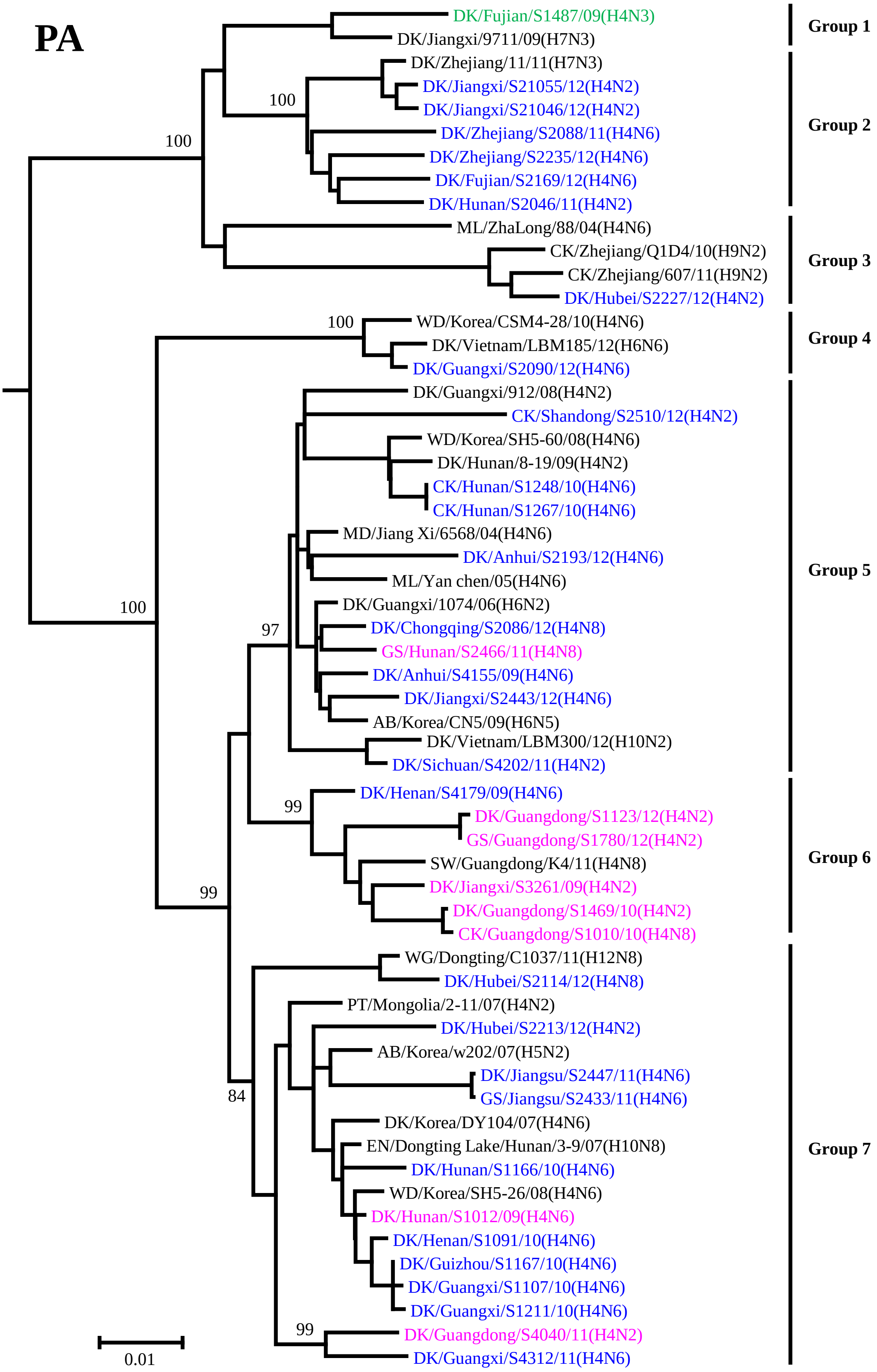
Group 1
Group 2
Group 3
Group 4
Group 5
Group 6
Group 7

Fig. S1B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DK/Jiangxi/S3261/09(H4N2)
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CK/Guangdong/S1010/10(H4N8)
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PT/Mongolia/2-11/07(H4N2)
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100
100
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99
84
99
Group 1
Group 2
Group 3
Group 4
Group 5
Group 6
Group 7
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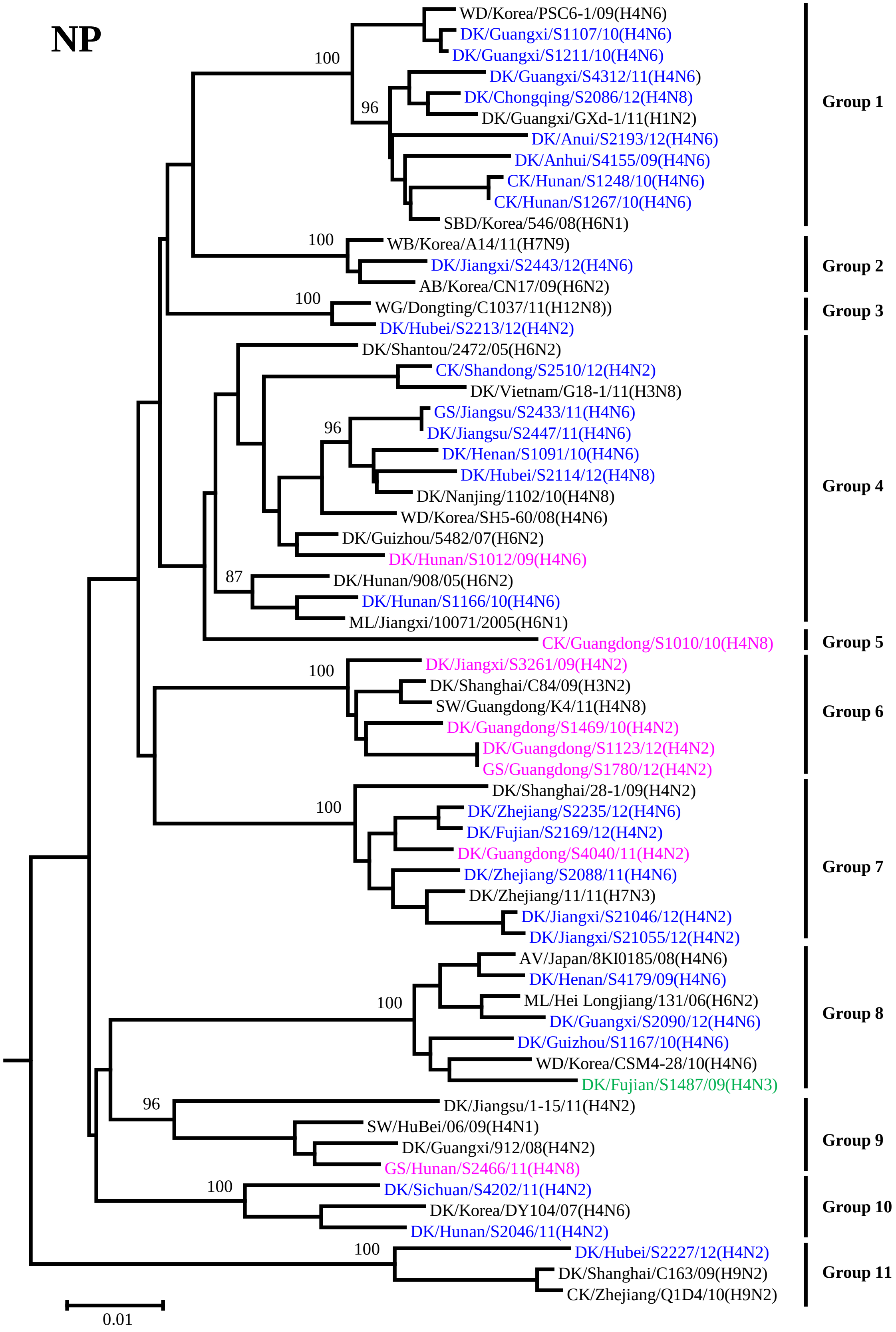
Fig. S1C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96
DK/Guangxi/GXd-1/11(H1N2)
DK/Anui/S2193/12(H4N6)
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CK/Hunan/S1248/10(H4N6)
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Group 1
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Group 2
100
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Group 3
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DK/Vietnam/G18-1/11(H3N8)
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96
DK/Jiangsu/S2447/11(H4N6)
DK/Henan/S1091/10(H4N6)
DK/Hubei/S2114/12(H4N8)
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87
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Group 5
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DK/Guangdong/S1123/12(H4N2)
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DK/Guangxi/912/08(H4N2)
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Group 9
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DK/Korea/DY104/07(H4N6)
DK/Hunan/S2046/11(H4N2)
Group 10
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Group 11
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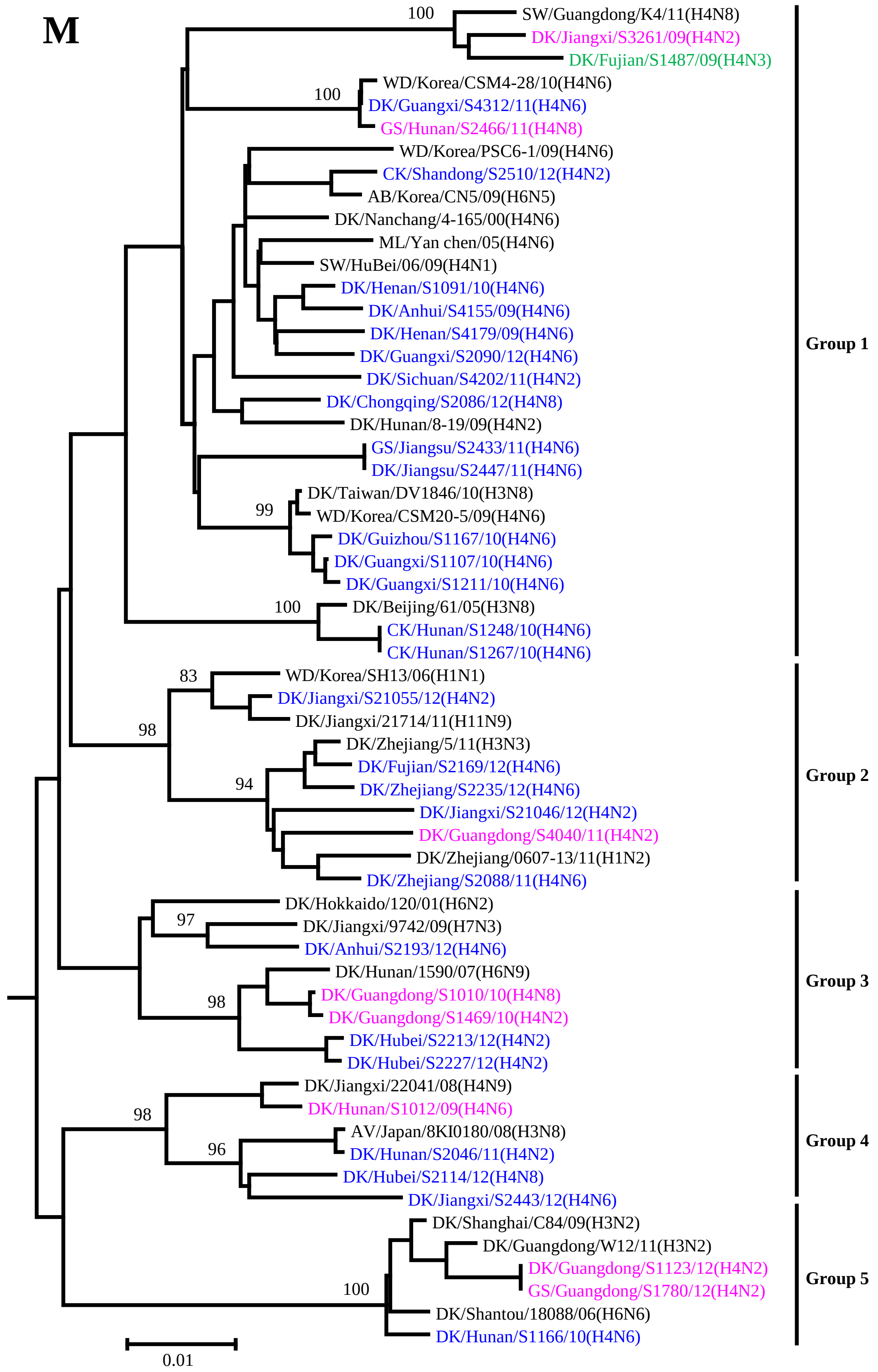
Fig. S1D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WD/Korea/PSC6-1/09(H4N6)
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ML/Yan chen/05(H4N6)
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DK/Guangxi/S2090/12(H4N6)
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DK/Chongqing/S2086/12(H4N8)
DK/Hunan/8-19/09(H4N2)
GS/Jiangsu/S2433/11(H4N6)
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99
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DK/Guangxi/S1211/10(H4N6)
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CK/Hunan/S1267/10(H4N6)
Group 1
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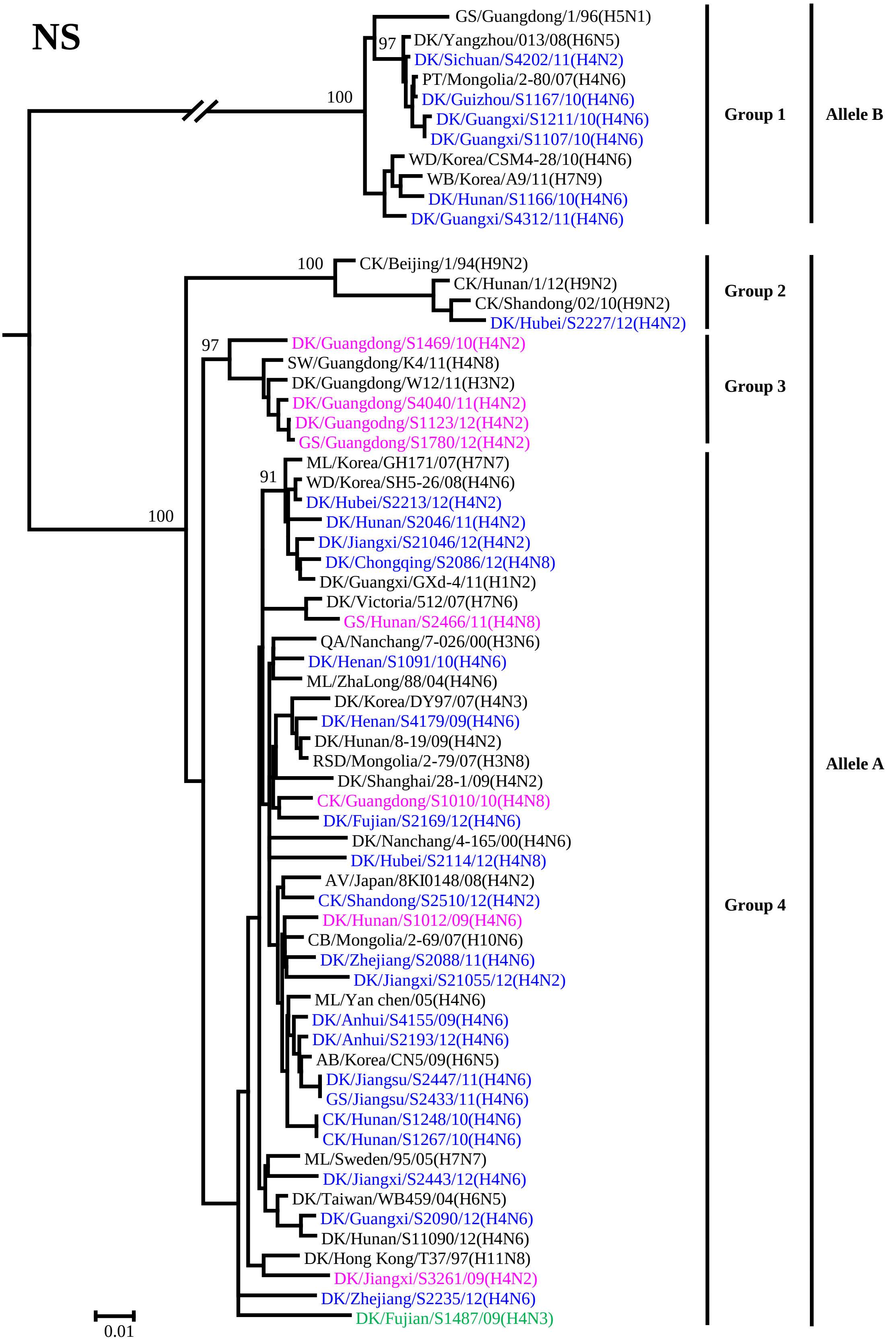
Fig. S1E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PT/Mongolia/2-80/07(H4N6)
100
DK/Guizhou/S1167/10(H4N6)
DK/Guangxi/S1211/10(H4N6)
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WB/Korea/A9/11(H7N9)
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DK/Guangxi/S4312/11(H4N6)
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Allele B
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CK/Hunan/1/12(H9N2)
CK/Shandong/02/10(H9N2)
DK/Hubei/S2227/12(H4N2)
Group 2
97
DK/Guangdong/S1469/10(H4N2)
SW/Guangdong/K4/11(H4N8)
DK/Guangdong/W12/11(H3N2)
DK/Guangdong/S4040/11(H4N2)
DK/Guangodng/S1123/12(H4N2)
GS/Guangdong/S1780/12(H4N2)
Group 3
91
ML/Korea/GH171/07(H7N7)
WD/Korea/SH5-26/08(H4N6)
DK/Hubei/S2213/12(H4N2)
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DK/Hunan/S2046/11(H4N2)
DK/Jiangxi/S21046/12(H4N2)
DK/Chongqing/S2086/12(H4N8)
DK/Guangxi/GXd-4/11(H1N2)
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DK/Jiangxi/S21055/12(H4N2)
ML/Yan chen/05(H4N6)
DK/Anhui/S4155/09(H4N6)
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DK/Hunan/S11090/12(H4N6)
DK/Hong Kong/T37/97(H11N8)
DK/Jiangxi/S3261/09(H4N2)
DK/Zhejiang/S2235/12(H4N6)
DK/Fujian/S1487/09(H4N3)
Group 4
Allele A
0.01

Fig. S1F

Fig. S1 Phylogenetic analyses of the six internal genes of H4 avian influenza viruses isolated from live poultry markets in China between 2009 and 2012. Phylogenetic trees were generated by using the neighbor-joining method of the MEGA5.0 software package. The regions of nucleotide sequence used for the phylogenetic analyses were: PB2, 37-2289; PB1, 25-2233; PA, 25-2167; NP, 46-1526; M, 26-1007; and NS, 27-859. The phylogenetic trees of PB2 (A), PB1 (B), PA (C), NP (D), M (E), and NS (F) were rooted to A/equine/Prague/1/1956 (H7N7). The colors of the virus names in the phylogenetic trees match with the colors of their HA genes. Abbreviations: AB, aquatic bird; AV, avian; BP, baer's pochard; CB, canvasback; CK, chicken; DK, duck; EN, environment; GS, goose; MD, migratory duck; ML, mallard; PT, pintail; QA, quail; RSD, ruddy shelduck; SBD, spot-billed duck; SW, swine; WB, wild bird; WD, wild duck; WFG, white-fronted goose; WG, wild goose; WS, whooper swan.