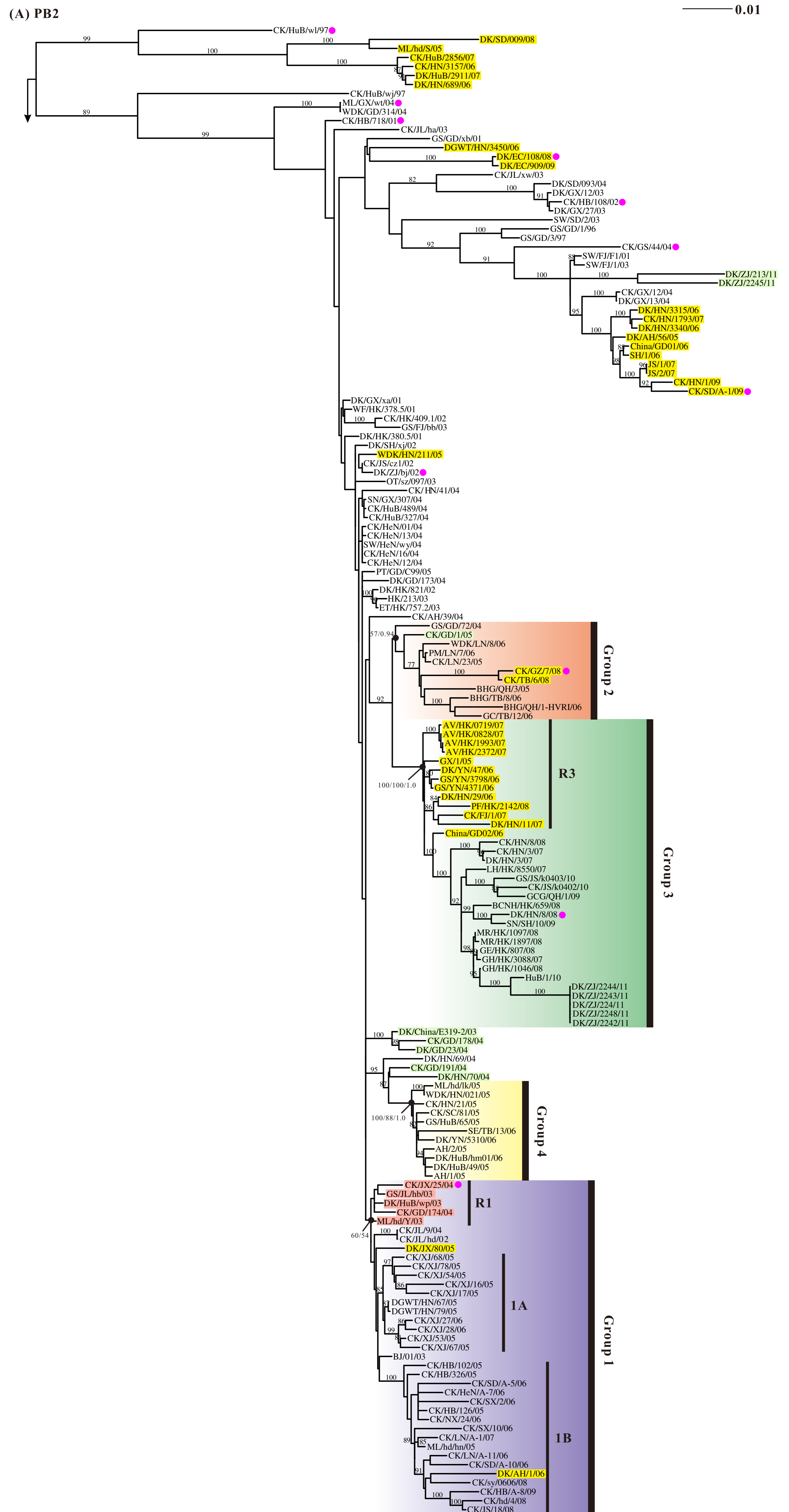
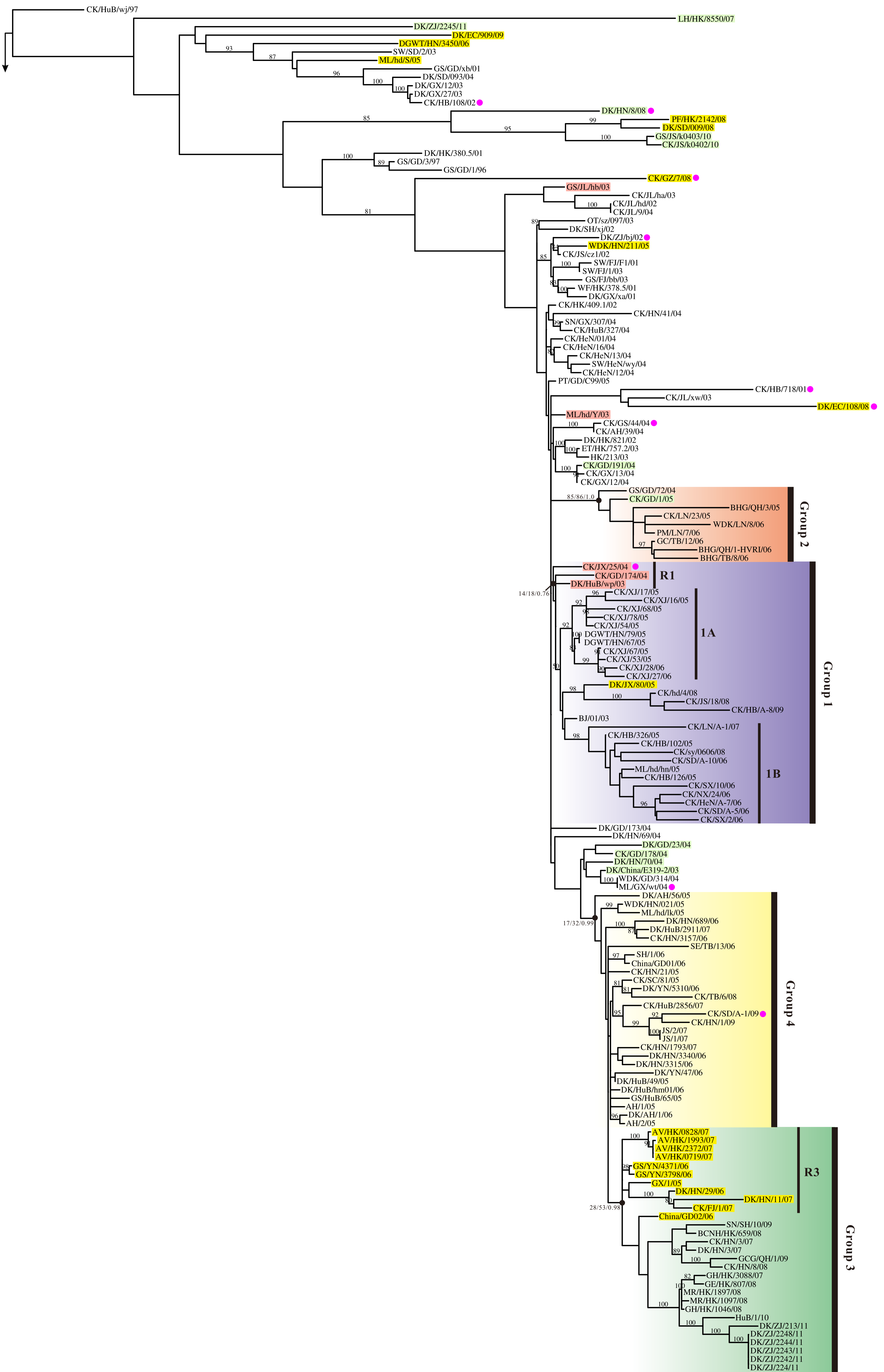
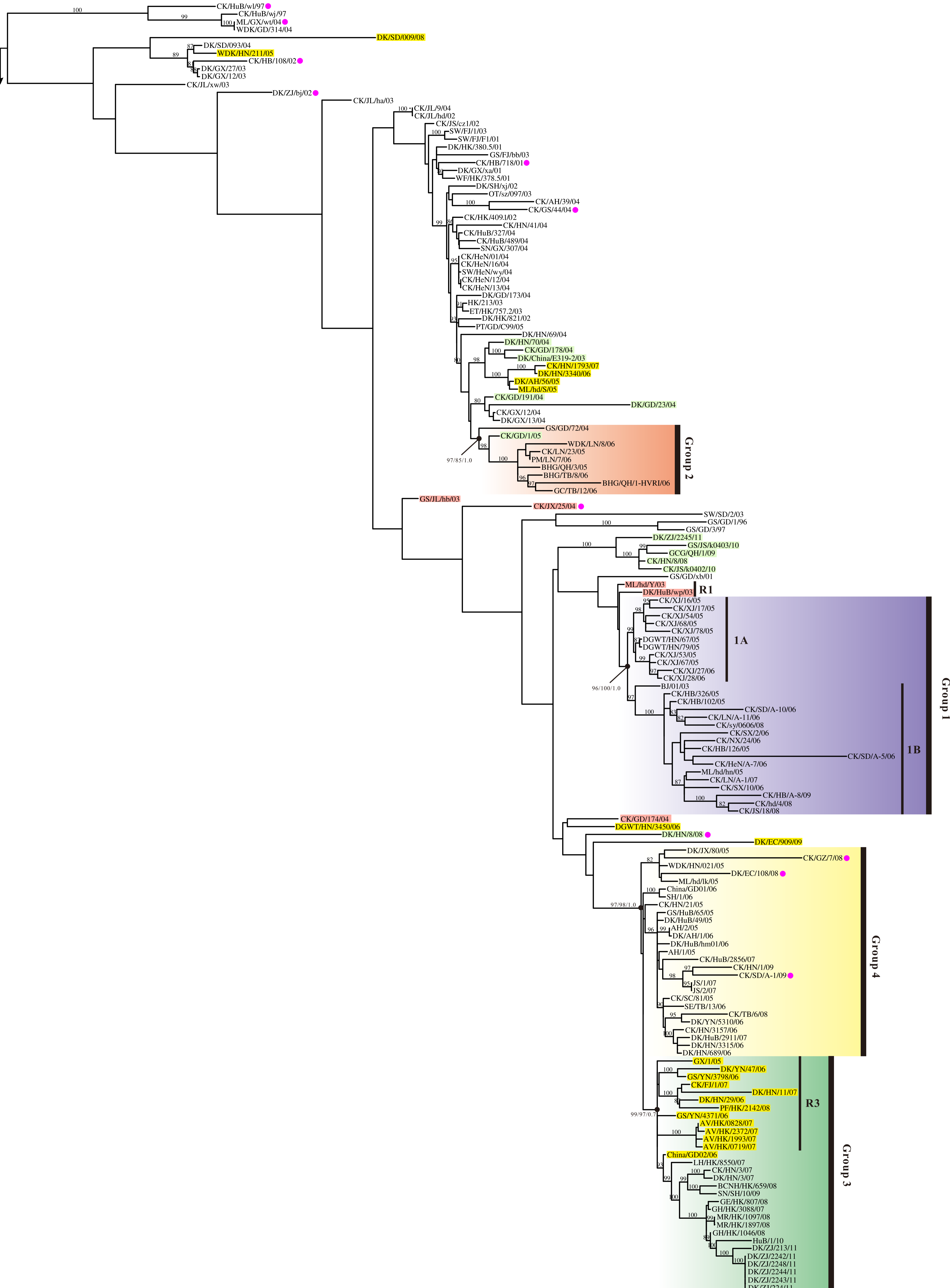


**Figure S1 Phylogenetic trees of H5N1 influenza viruses sampled from 1996-2012.** ML phylogenies reconstructed from (A) PB2 gene; (B) PB1 gene; (C) PA gene; (D) HA gene; (E) NP gene; (F) NA gene; (G) MP gene; (H) M1 gene; (I) M2 gene; (J) NS gene; (K) NS1 gene; (L) NS2 gene. Topology supports summarized from 100 ML bootstrap replications are shown. For major lineages, NJ bootstrap (100 replications) and posterior probability from BMCMC analyses (5000 tree) are shown for key nodes (ML/NJ/BMCMC). Putative recombinant viruses are designated by magenta circles. Reassortant subgroups (R1, R2 and R3) are indicated with solid lines. Arrows indicate the roots, and scale bars represent nucleotide substitutions per site.

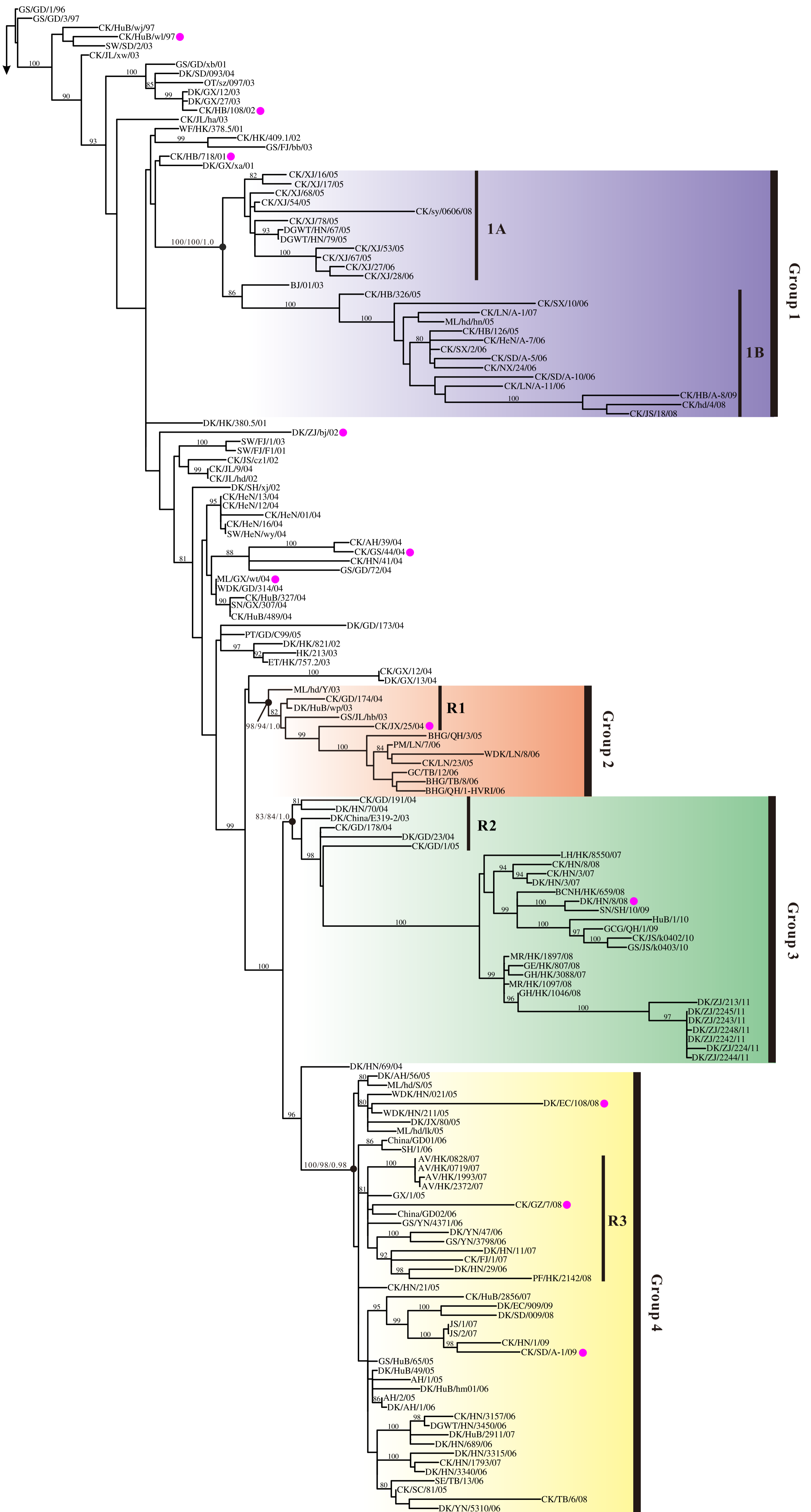


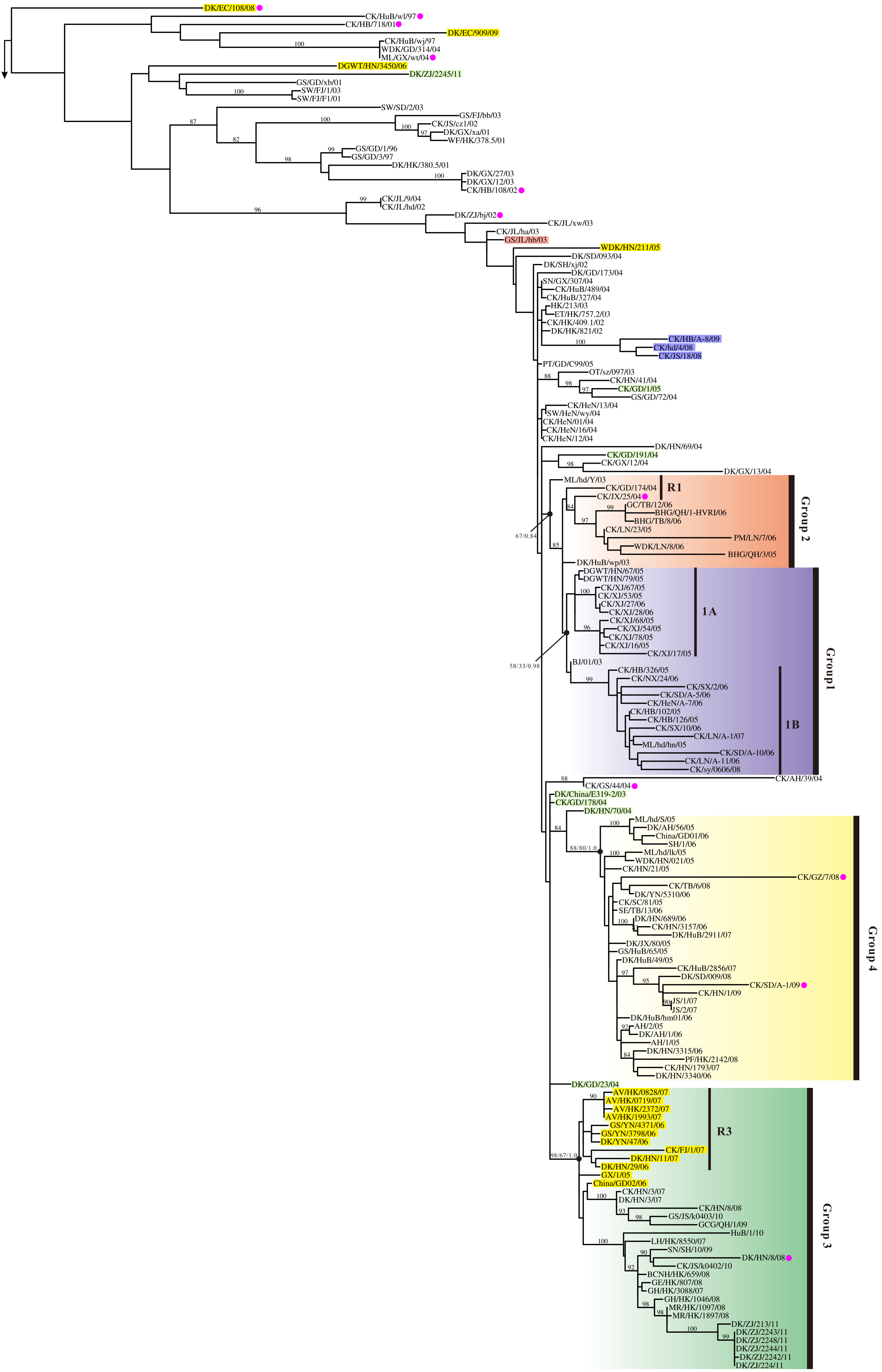




(D) HA

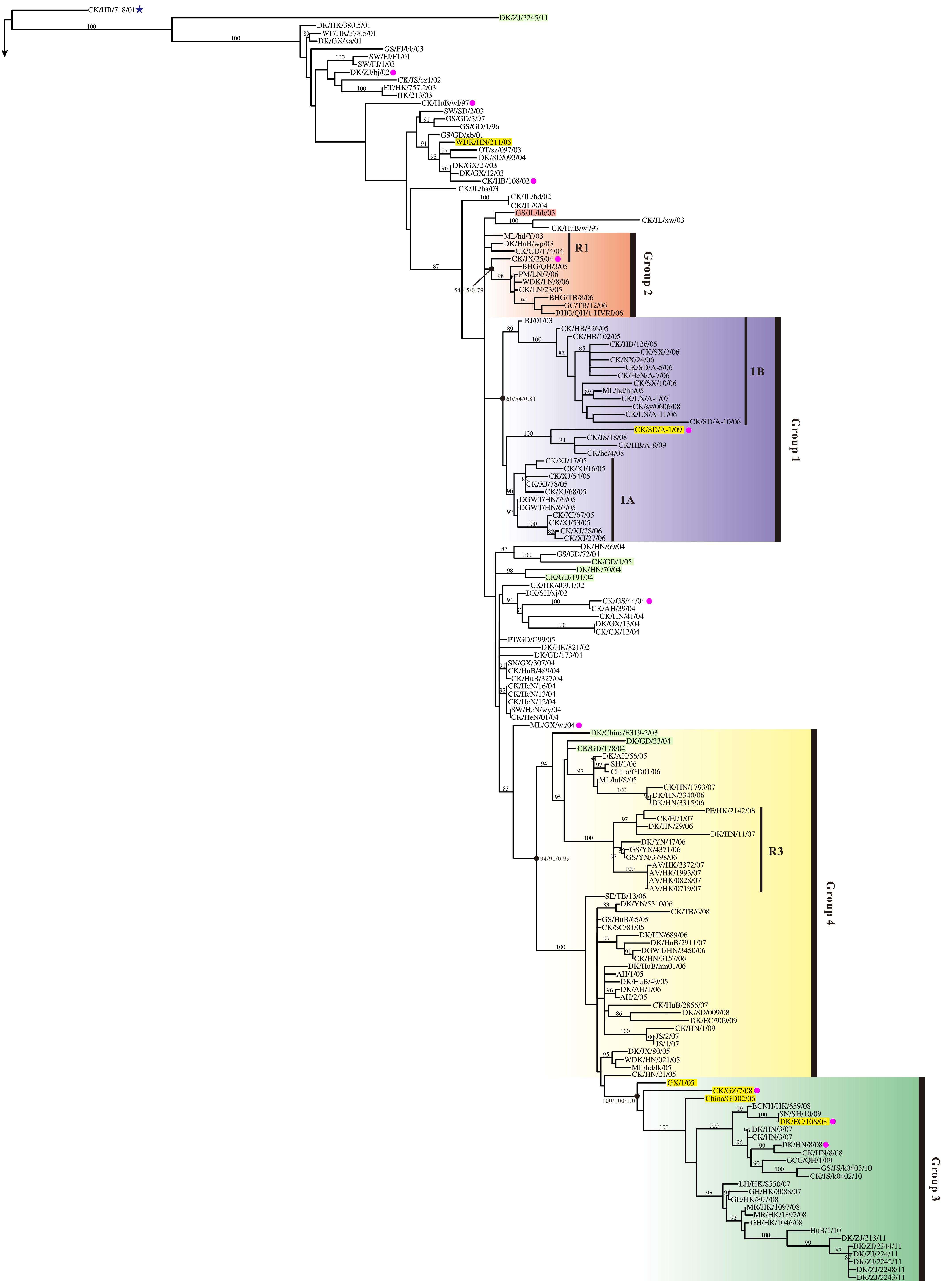
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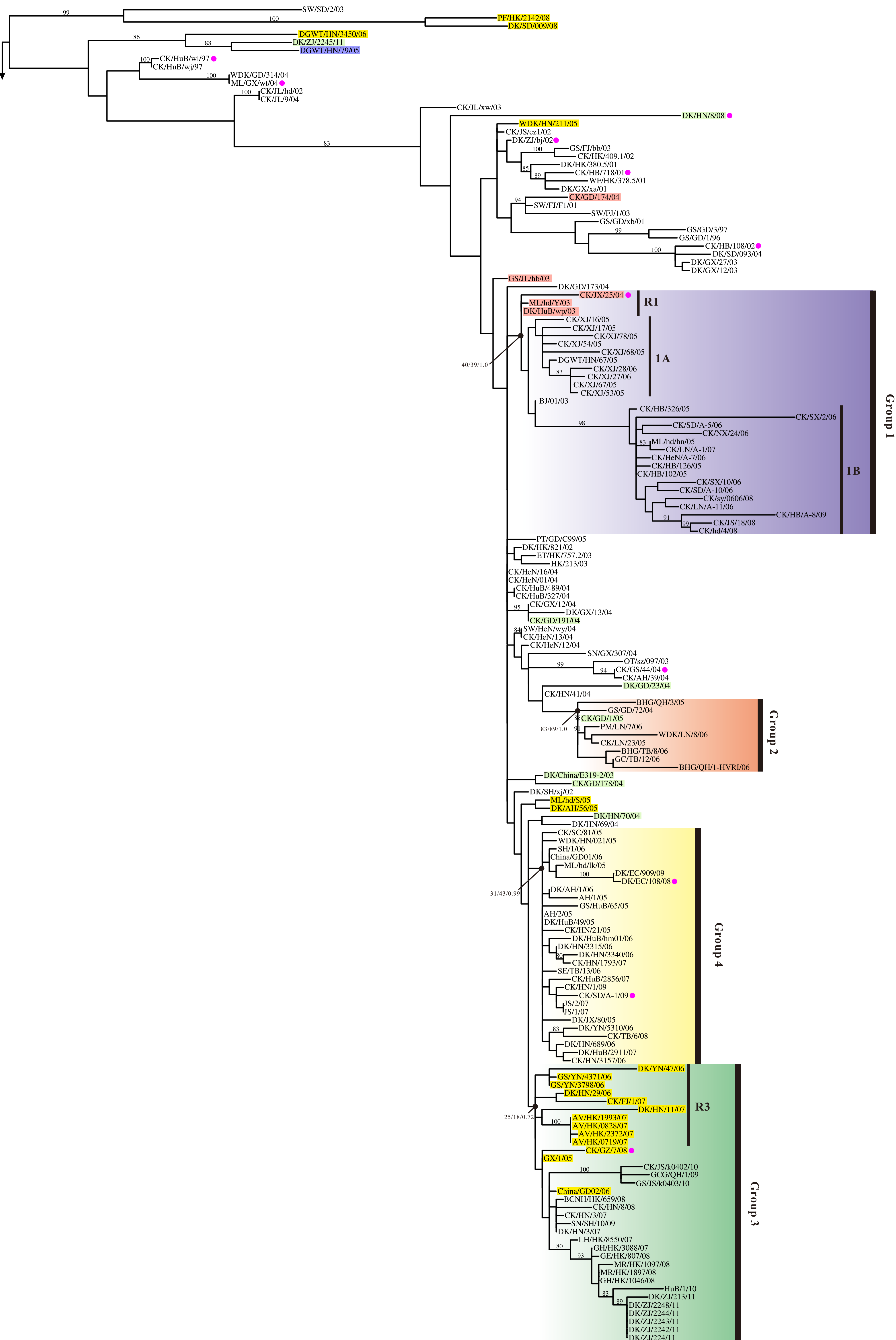




(F) NA

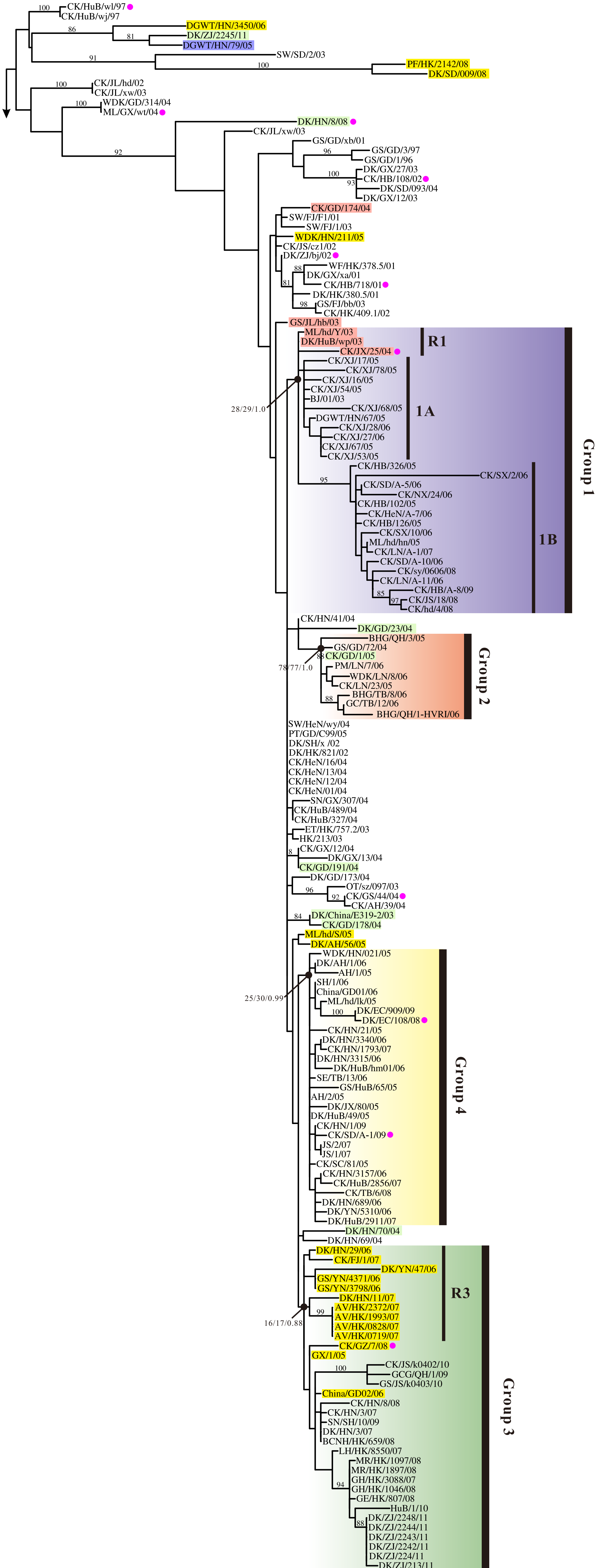
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(H) M1

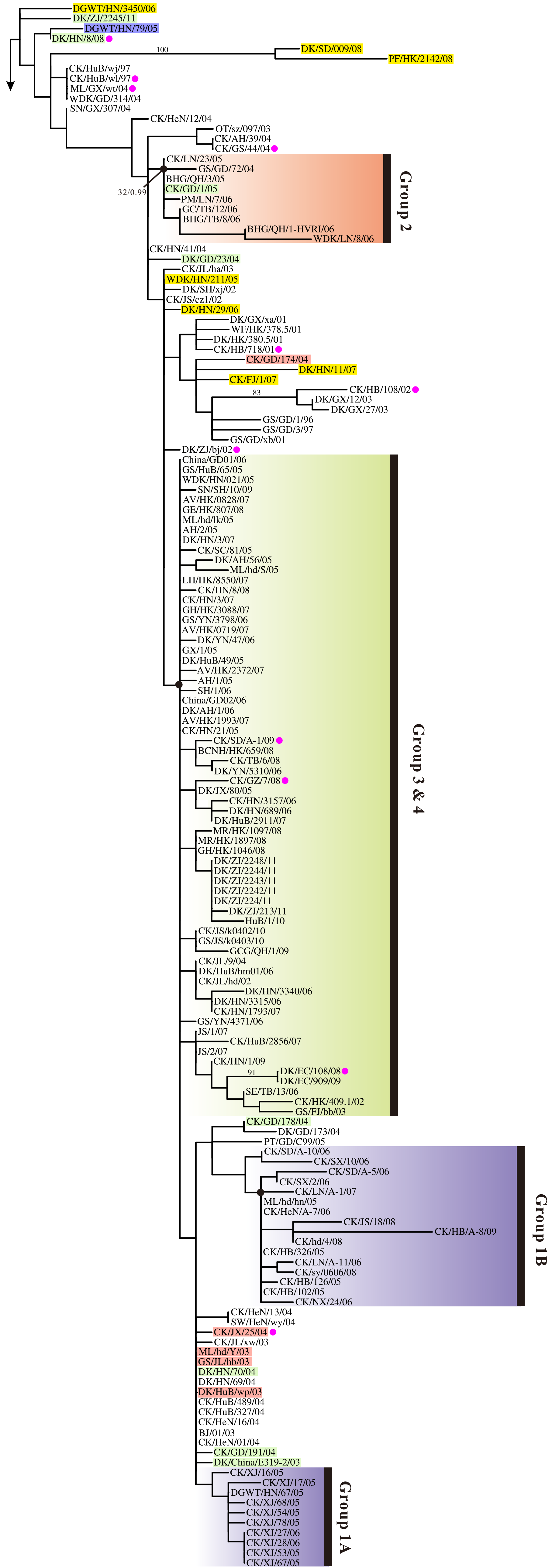
0.01





(I) M2

0.01



(J) NS

0.01

