Figure S2

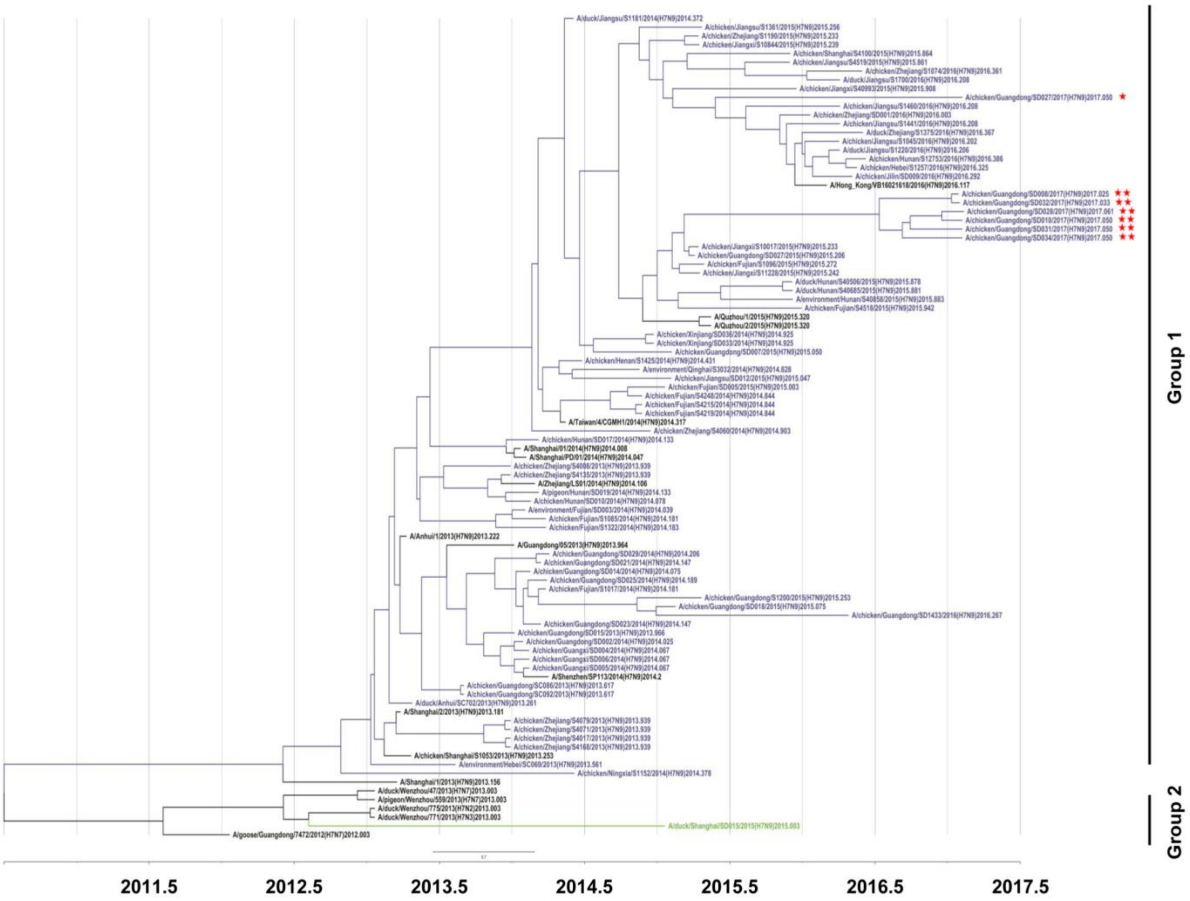

Figure S2. Bayesian time-resolved phylogenetic tree of the HA gene of H7N9 viruses. The tree was created using BEAST 1.8 with the SRD06 nucleotide substitution model, an uncorrelated relaxed clock with a log-normal distribution, and skygrid flexible effective population size tree prior. The tree was viewed in Figtree 1.4.3.