



Supplemental Figure 1. Phylogenetic analysis of the PB2, PB1, PA, NP, MP, and NS genes of H5N1 highly pathogenic avian influenza viruses isolated from 31 patients in China. The phylogenetic trees were generated using the maximum likelihood method implemented in Garli version 0.95, and the bootstrap values were generated using neighbor-joining methods implemented in PAUP* version 4.0 beta. Viruses of human origin are shown in red and those of environmental origin in blue. Genotype nomenclature is designated as defined by Duan et al. (2008). Genotypes V5, V6, and V7 are new genotypes identified in this study. Abbreviations: chicken, Ck; duck, Dk; environment, Env; goose, Gs.