Supplemental Fig. 2: Maximum likelihood tree (nucleotide sequences; GTR+gamma; 10,000 local support bootstraps; FastTree2) for 581 H5 hemagglutinin genes of highly pathogenic avian influenza H5N1. Virus names along with annotations in curly brackets are shown. The tree is rooted to an early highly pathogenic virus, A/goose/Guangdong/96, from clade *0*.