



Supplemental Fig. 5: Maximum likelihood tree (nucleotide sequences; GTR+gamma; 10,000 local support bootstraps; FastTree2) for the H5 hemagglutinin genes of highly pathogenic avian influenza A(H5N1). Clades 3 and 4 along with the 3-like group are indicated. The tree is rooted to an early highly pathogenic virus, A/goose/Guangdong/96, from clade 0.