

Supplemental Fig. 4: Maximum likelihood tree (nucleotide sequences; GTR+gamma; 10,000 local support bootstraps; FastTree2) for the hemagglutinin genes of highly pathogenic avian influenza A(H5N1). Clades 1 and 1.1 along with the 1.1-like group are indicated. The tree is rooted to an early highly pathogenic virus, A/goose/Guangdong/96, from clade 0.

