Supplemental Fig. 3: Maximum likelihood tree (nucleotide sequences; GTR+gamma; 10,000 local support bootstraps; FastTree2) for 606 H9 hemagglutinin genes of low pathogenicity avian influenza A, mostly comprised of H9N2. Virus names preceded by GISAID accession numbers and followed by subtype and clade annotations in curly brackets are shown. The tree is rooted to the *WI66* clade.