

Title: Isolation and characterization of H9N2 influenza virus isolates from poultry respiratory disease outbreak

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Additional file 1- Phylogenetic trees of all eight genes of H9N2 avian influenza

Phylogenetic relationships for HA (A), NA (B), PB2 (C), PB1 (D), PA (E), NP (F), MP (G) and NS (H) genes of the 223 analyzed H9N2 influenza viruses along with 2 isolates from present study. Genome sequences of 223 H9N2 viruses from Asian strains and reference lineage strains were selected from the NCBI Influenza Virus Resource Database. Neighbor-joining trees were constructed using MEGA and bootstrap values are shown for the key nodes. Clade labelled using different color indicate viruses clustered as Indian isolates together with isolates from this study. Representative viruses for each lineage and isolates from this study are presented in blue color.

Fig S1A HA



Fig S1B NA



G1-like

Fig S1C PB2

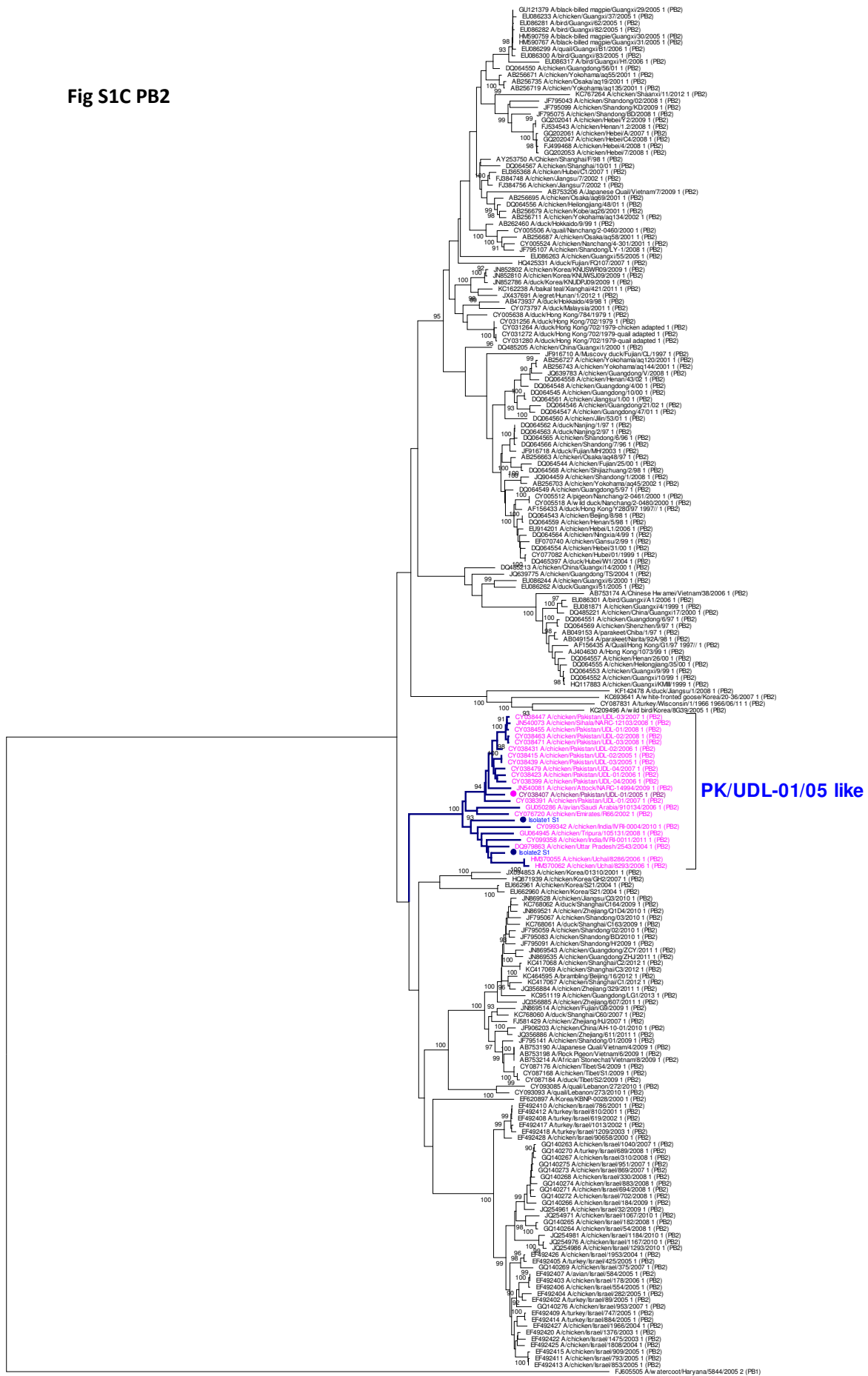


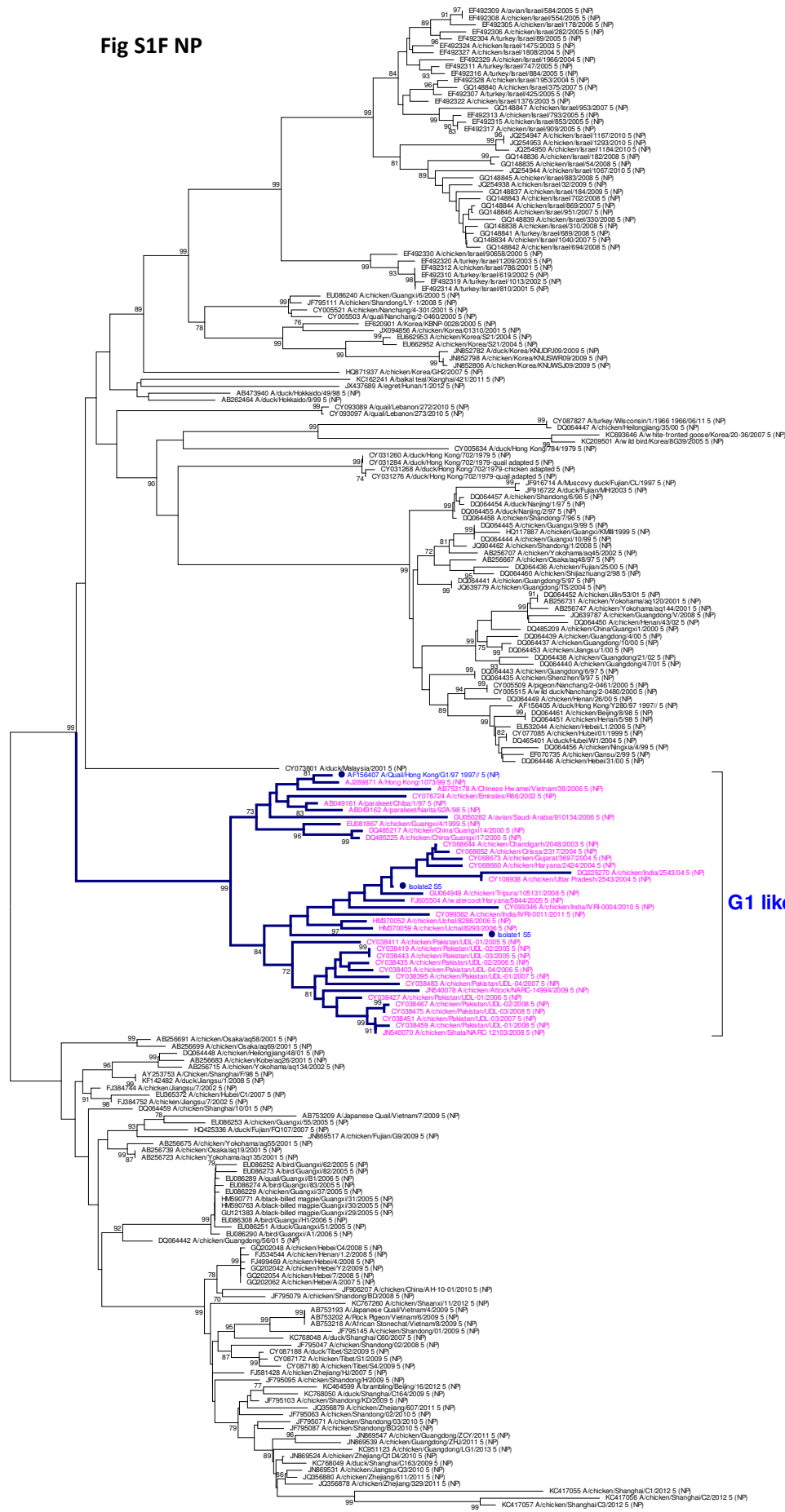
Fig S1E PA



Hok/49/98 like

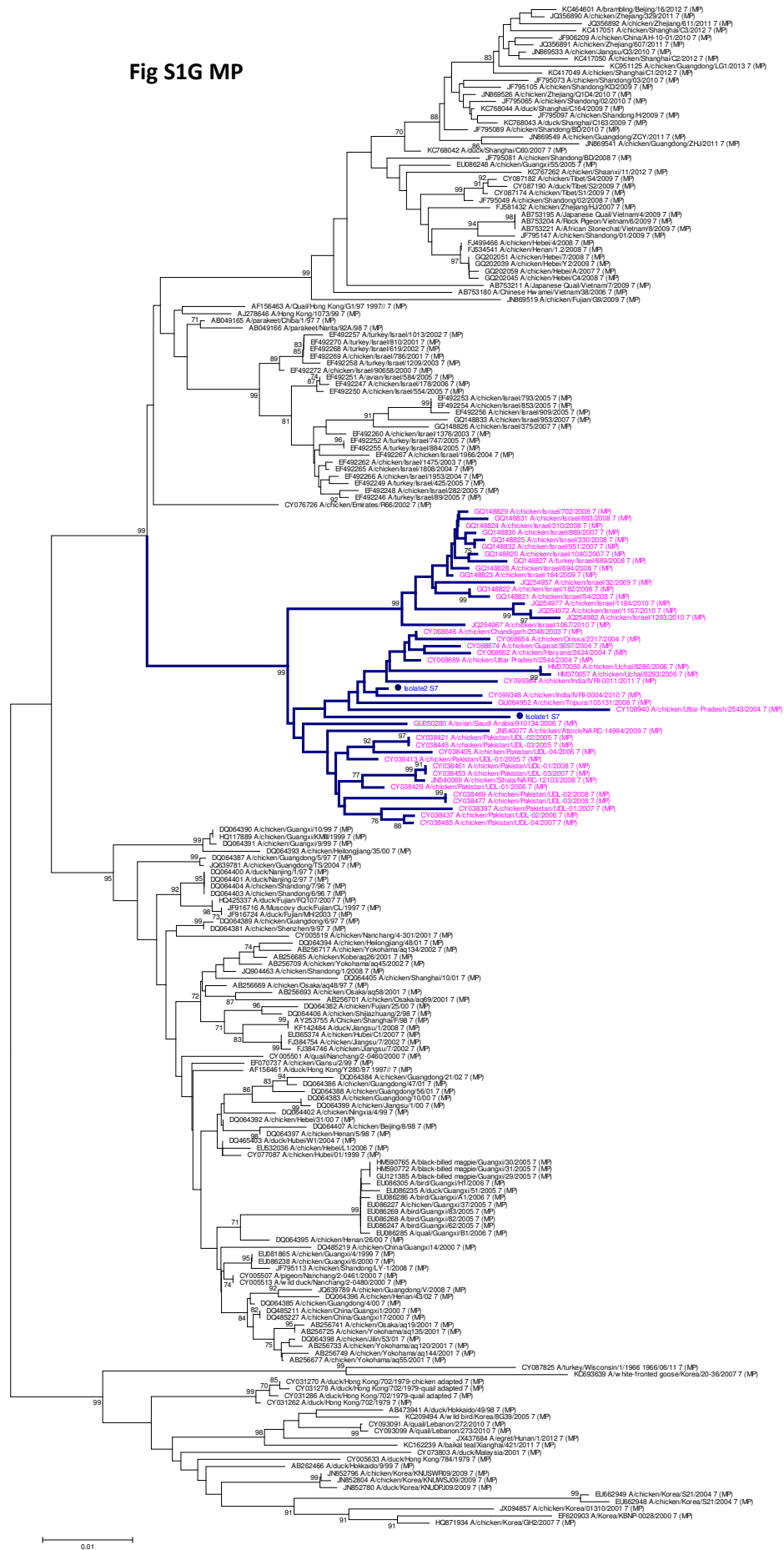
CY087829 A.turkey/Wisconsin/1966/196/06/11 3 (PA)

Fig S1F NP



G1 like

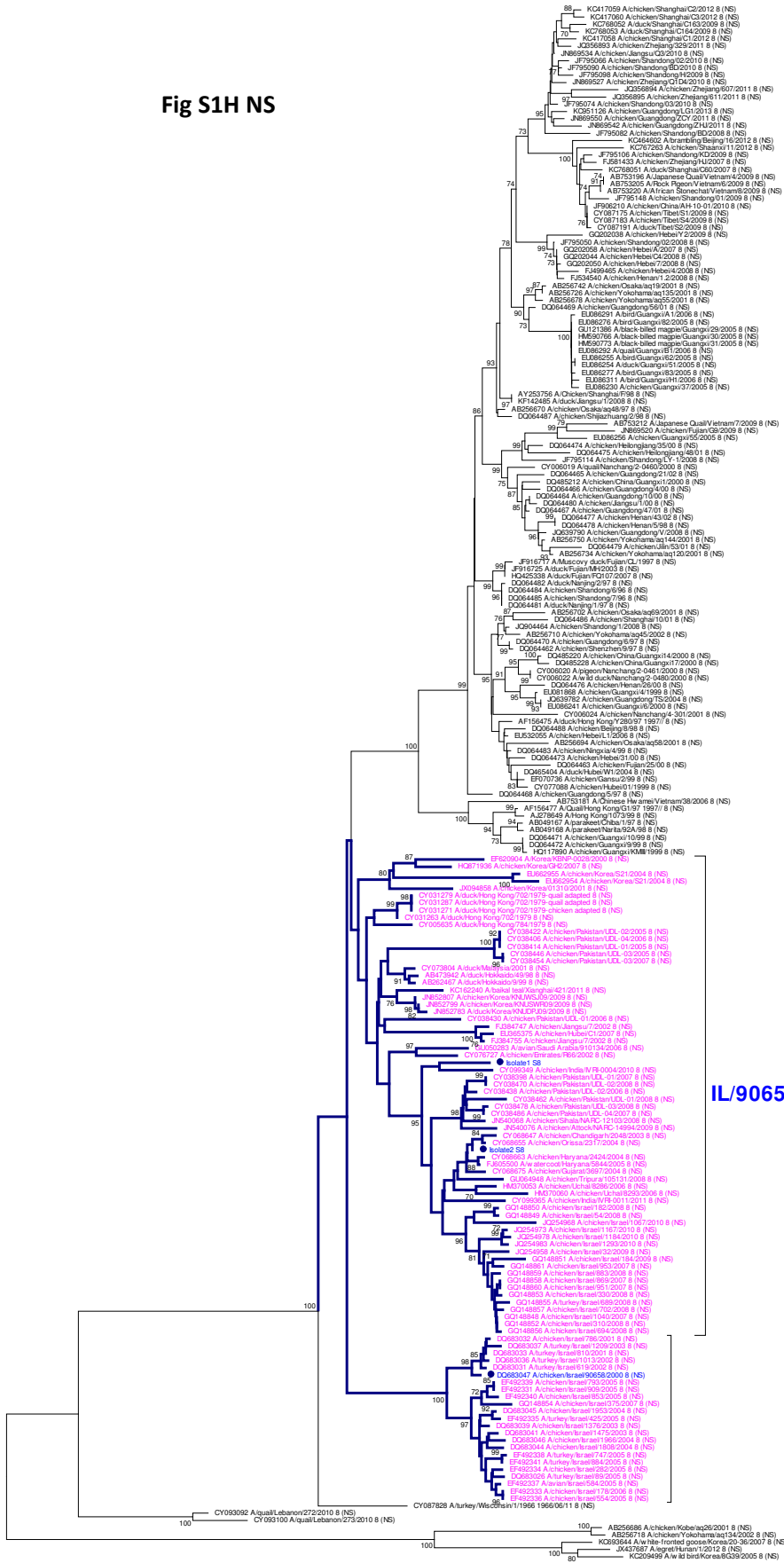
Fig S1G MP



Unknown

0.01

Fig S1H NS



IL/90658/00 like