# Towards a better understanding of the novel avian-origin H7N9 influenza A virus in China

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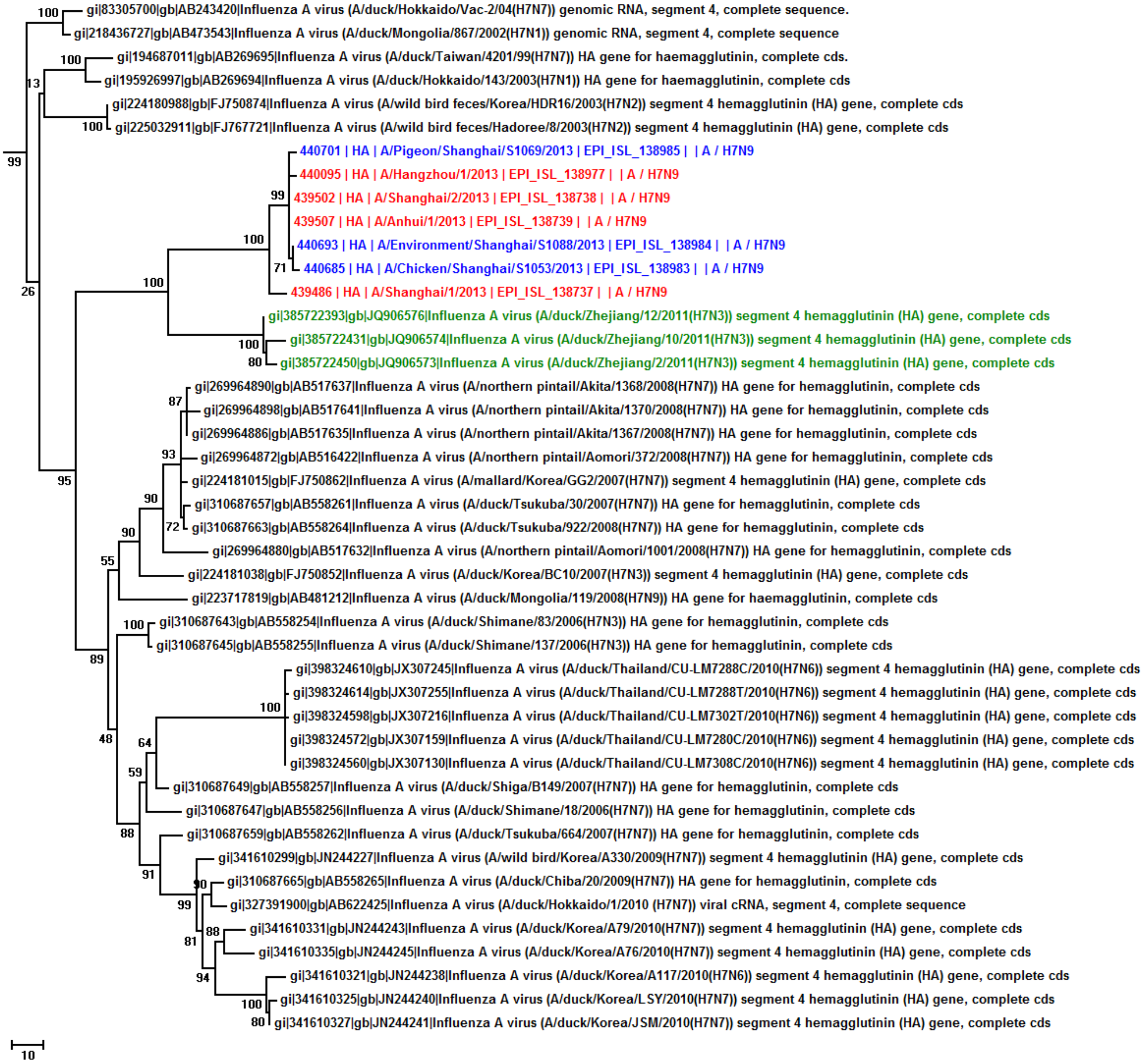
## Supplementary information

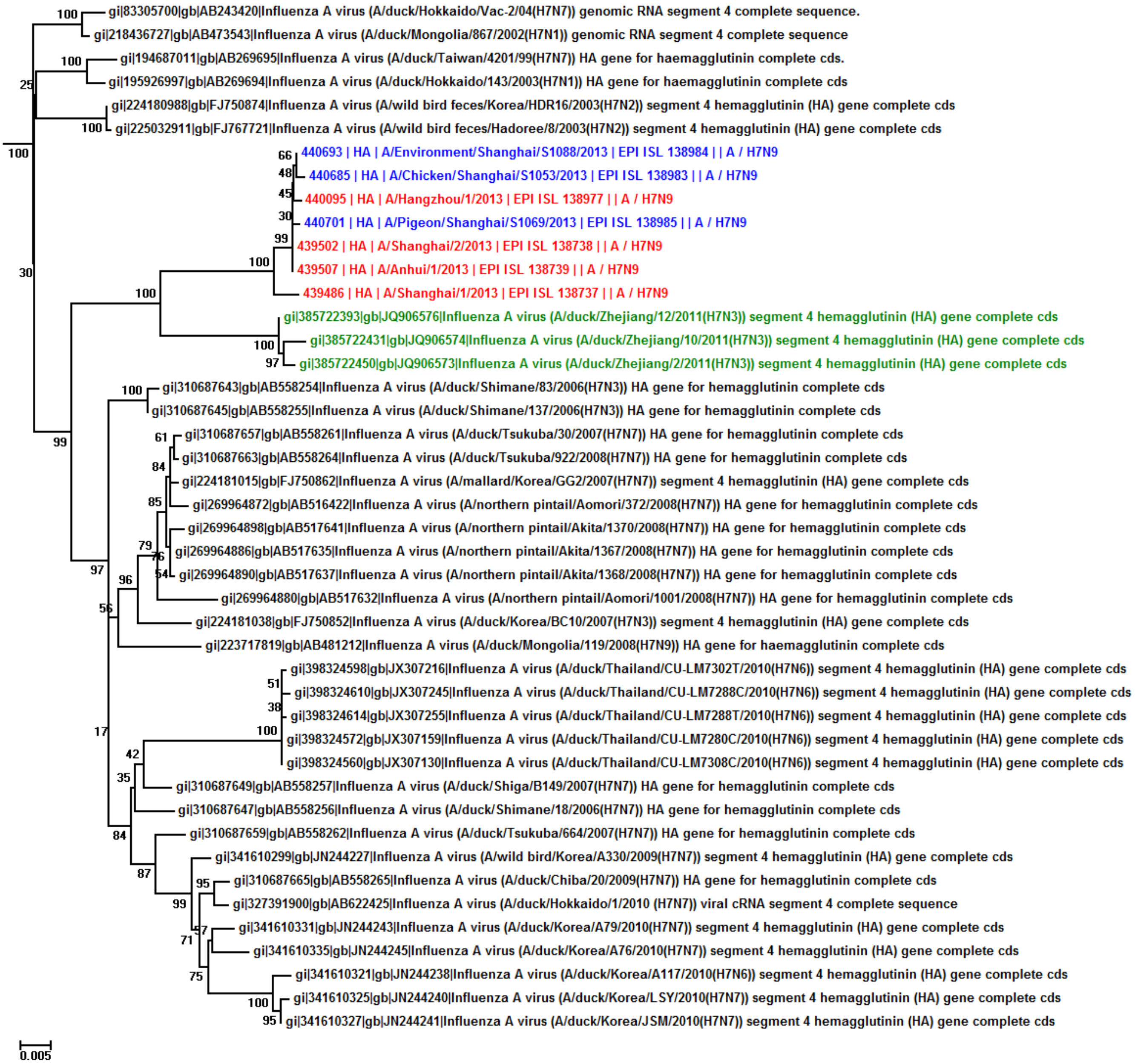
**Supplementary Fig. S1** – Phylogenetic analyses of H7N9 virus genes. The detailed MP trees for (a) HA and (b) were presented, while the NJ trees were also constructed for (c) HA and (d) NA. The NJ trees were also shown for (e) PB1, (f) PB2, (g) PA, (h) NP, (i) M and (j) NS. The HPAI viruses in patients were marked in red, while HPAI viruses from non-human samples were marked in blue. The nearest genes from LPAI viruses were shown in green.

# Supplementary Figure 1a



# Supplementary Figure 1b

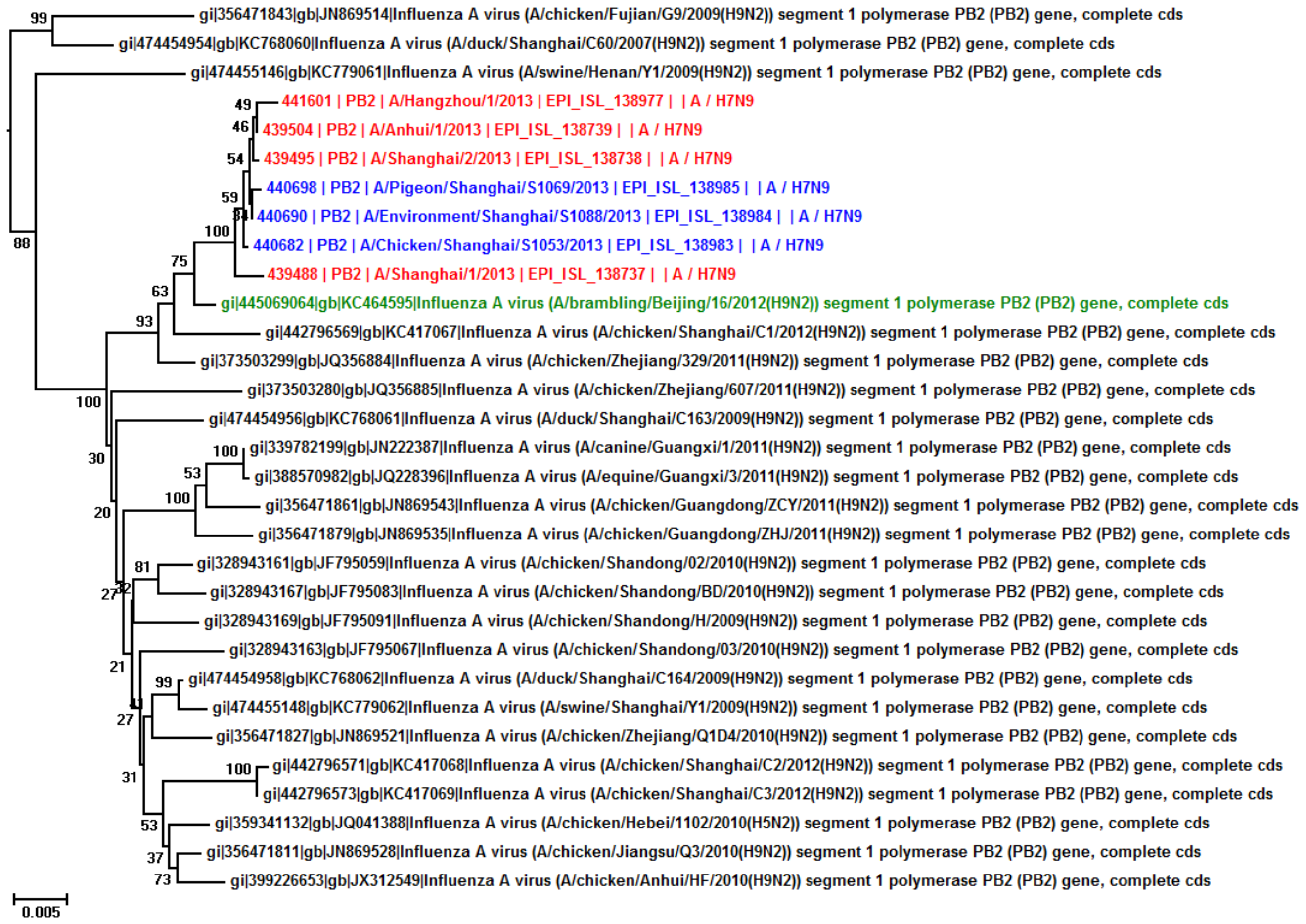
# Supplementary Figure 1c



# Supplementary Figure 1d

# Supplementary Figure 1e

# Supplementary Figure 1f



# Supplementary Figure 1g

# Supplementary Figure 1h

# Supplementary Figure 1i

# Supplementary Figure 1j