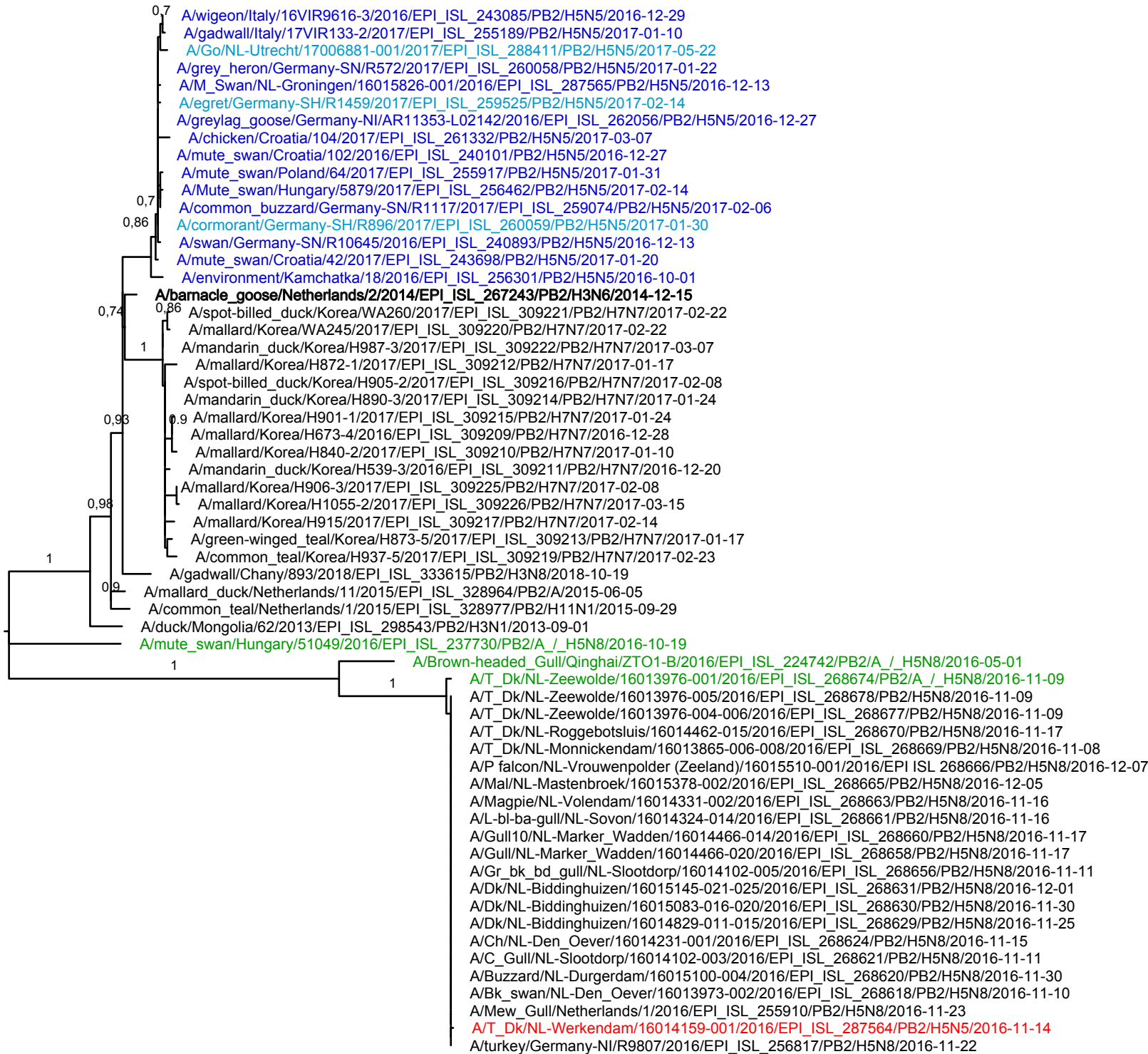


Figure S1. Phylogenetic analysis of H5N5 viruses. Phylogenetic trees of individual gene segments of highly pathogenic avian influenza (HPAI) H5N5 viruses isolated during the HPAI H5 2016-2017 epizootic, including the top 20 sequence matches of other subtypes identified by BLAST in the GISAID's EpiFlu™ Database (<http://www.gisaid.org>) on 10 May 2019. The H5N5 virus sequences are coloured according to their genotype (H5N5-GT1, red; H5N5-GT2, dark blue; H5N5-GT3, light blue). As a reference, HPAI H5N8 cluster representatives were included (green). Detailed information on the HPAI H5N5 and H5N8 virus sequences is provided in Table S2 and Table S3, respectively. The most closely related low pathogenic avian influenza (LPAI) ancestor viruses of the reassortant genes, as listed in Table S5, are depicted in bold. Phylogenetic analysis was performed using the maximum likelihood (ML) method within the MEGA7 software package. PB2, polymerase basic 2; PB1, polymerase basic 1; PA, polymerase acidic; HA, hemagglutinin; NP, nucleoprotein; NA, neuraminidase; MP, matrix protein; NS, nonstructural protein.

PB2

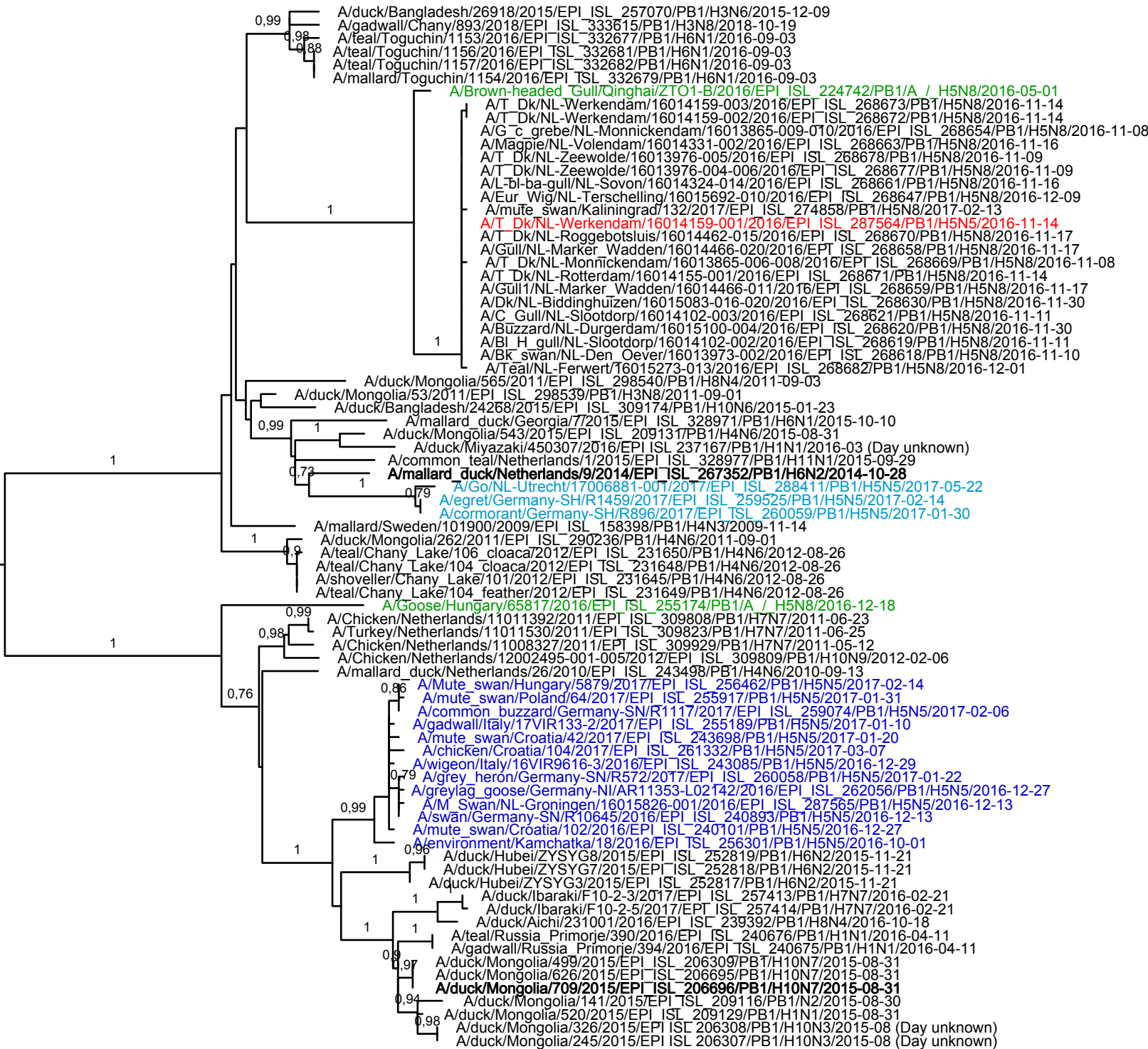
- H5N5-GT1
- H5N5-GT2
- H5N5-GT3
- H5N8 cluster representative



0.009

PB1

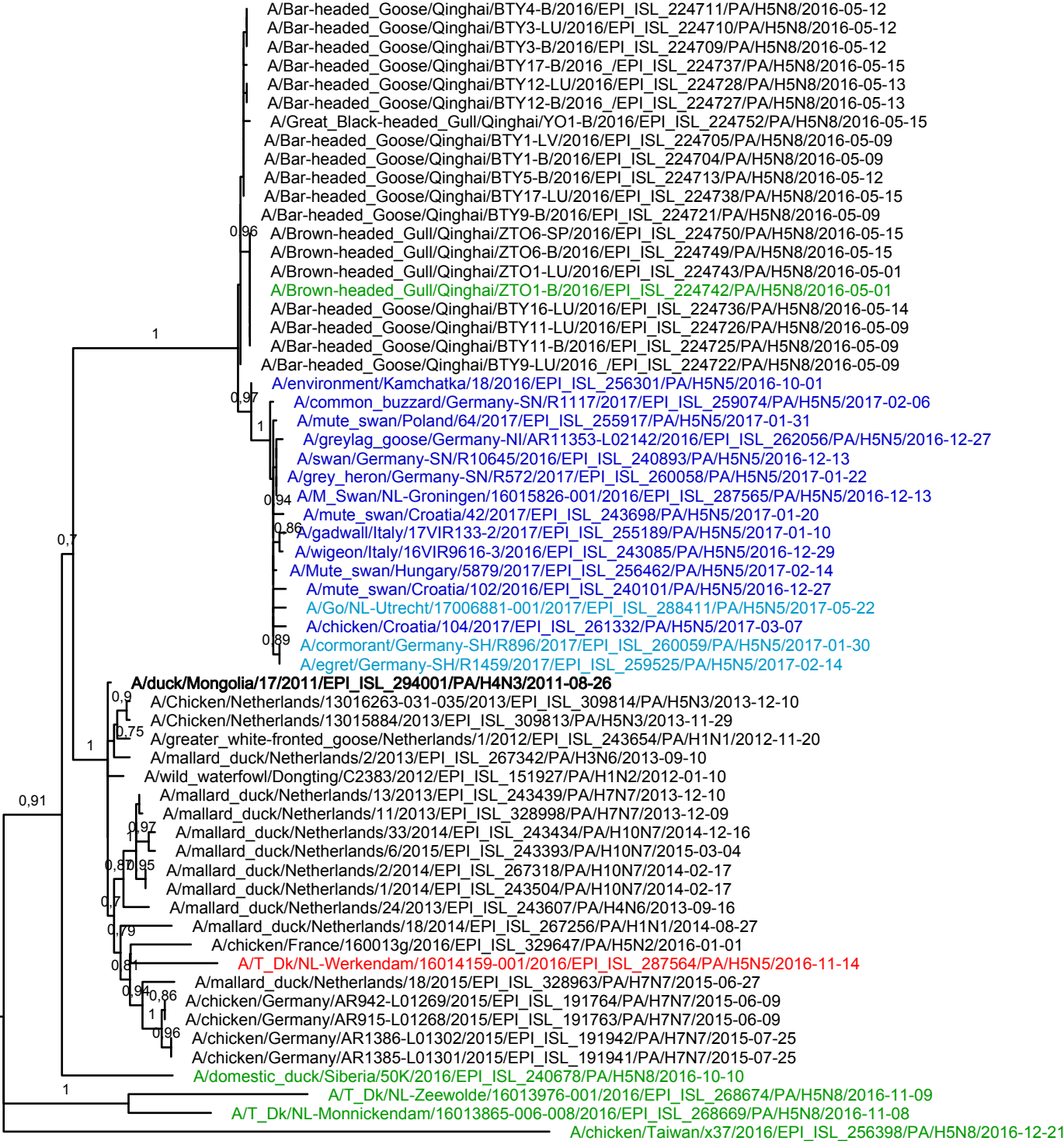
- H5N5-GT1
- H5N5-GT2
- H5N5-GT3
- H5N8 cluster representative



0.005

PA

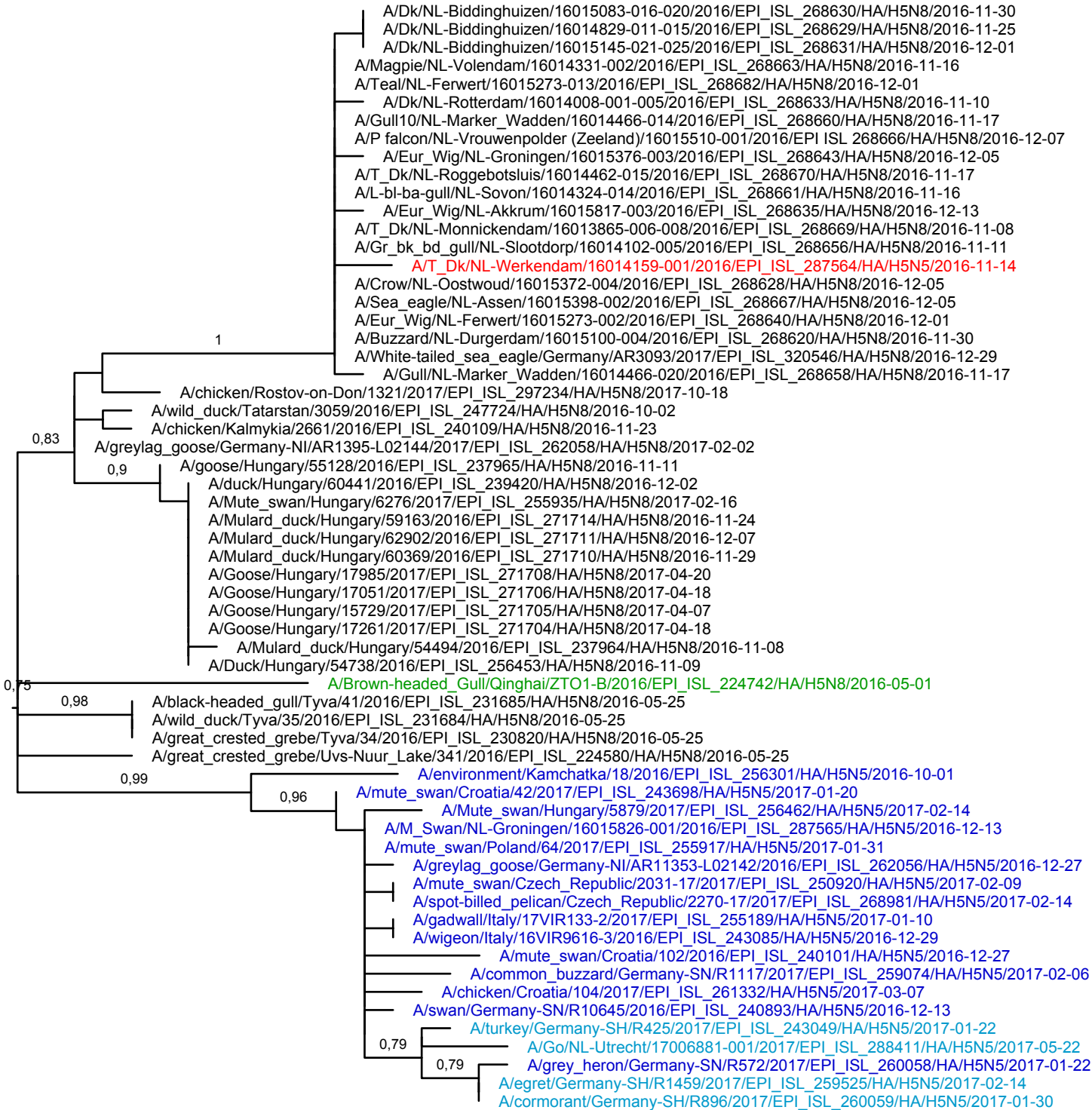
- H5N5-GT1
- H5N5-GT2
- H5N5-GT3
- H5N8 cluster representative



0.009

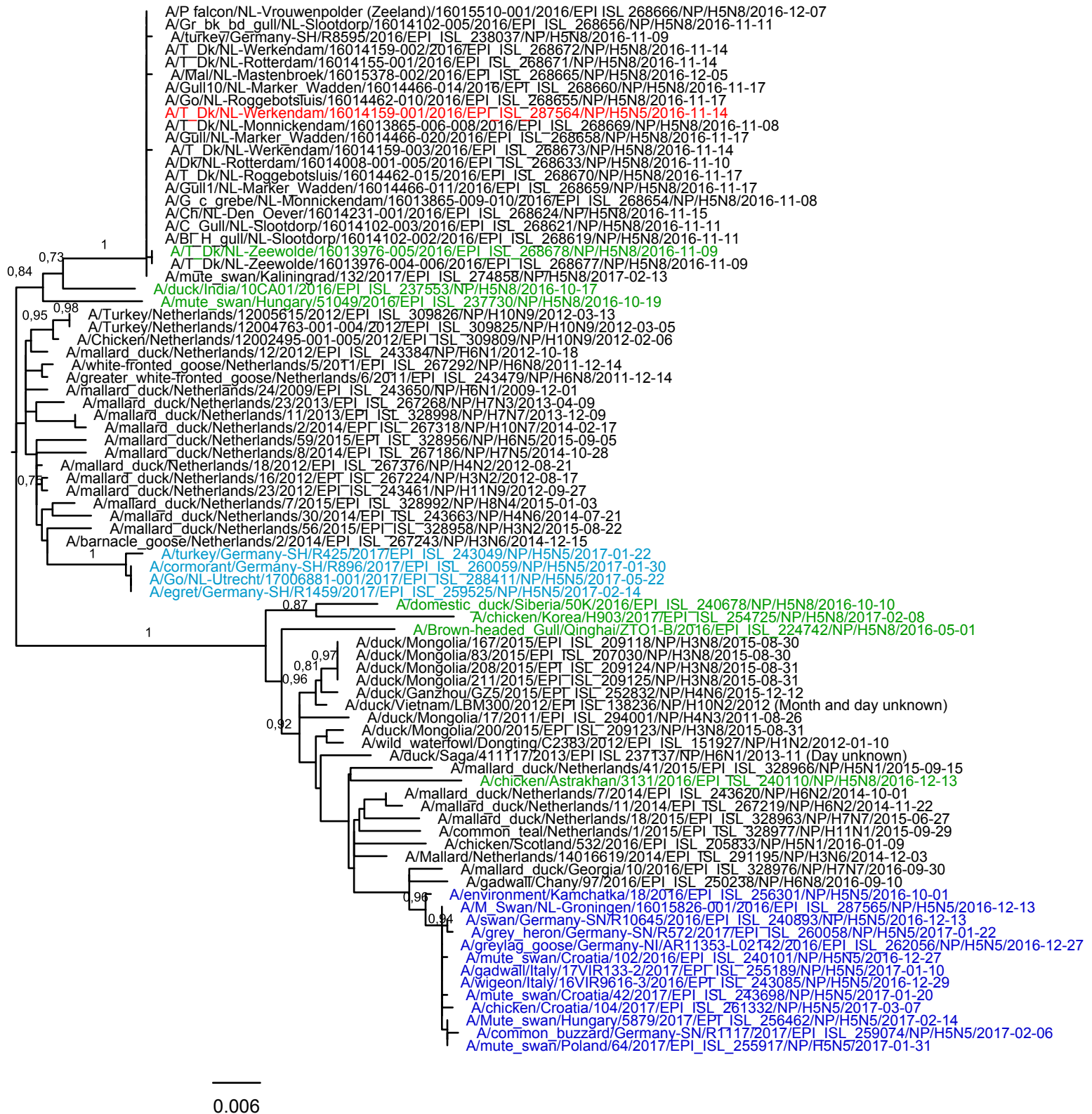
HA

- H5N5-GT1
- H5N5-GT2
- H5N5-GT3
- H5N8 cluster representative



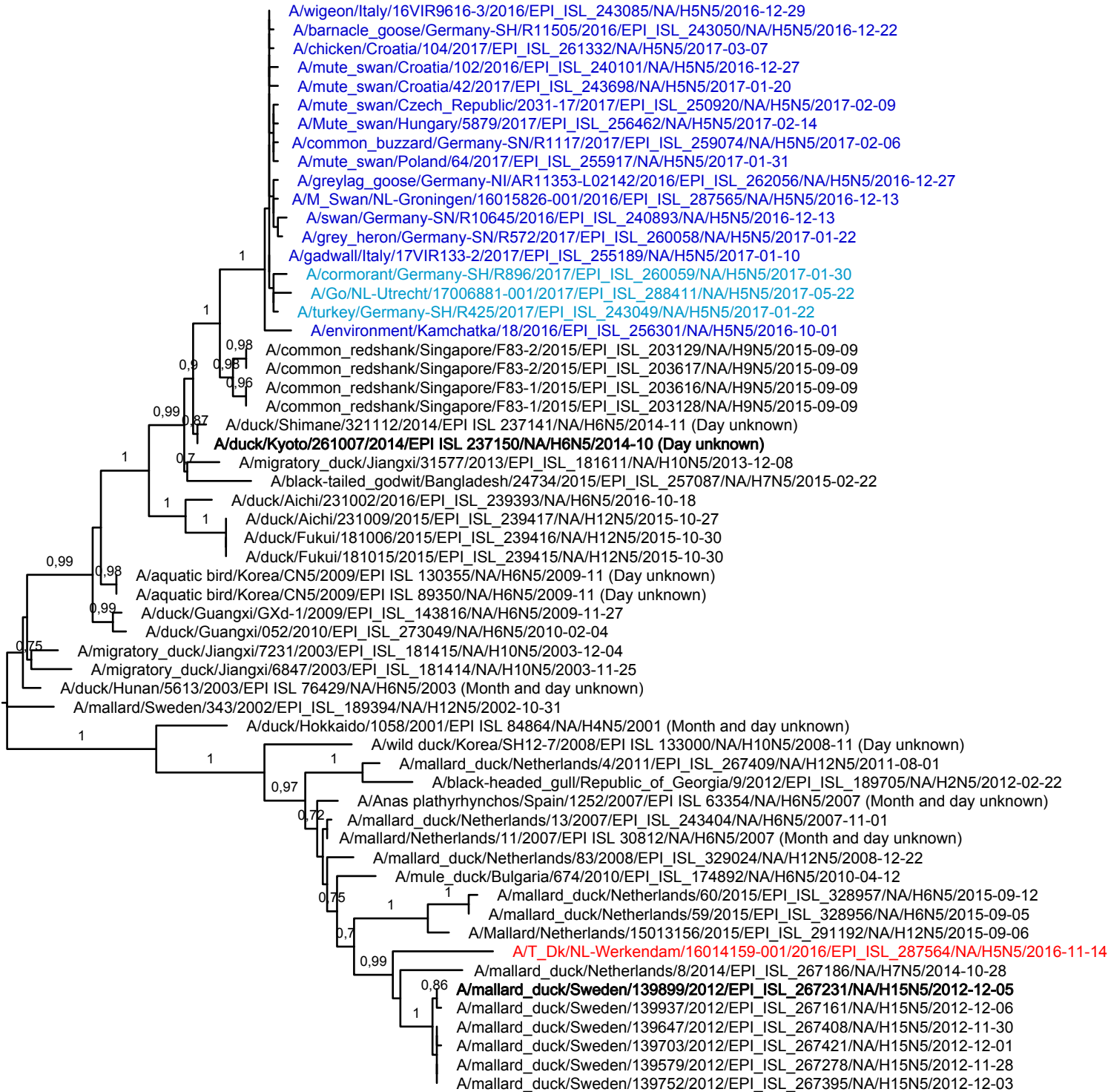
0.002

- H5N5-GT1
- H5N5-GT2
- H5N5-GT3
- H5N8 cluster representative



NA

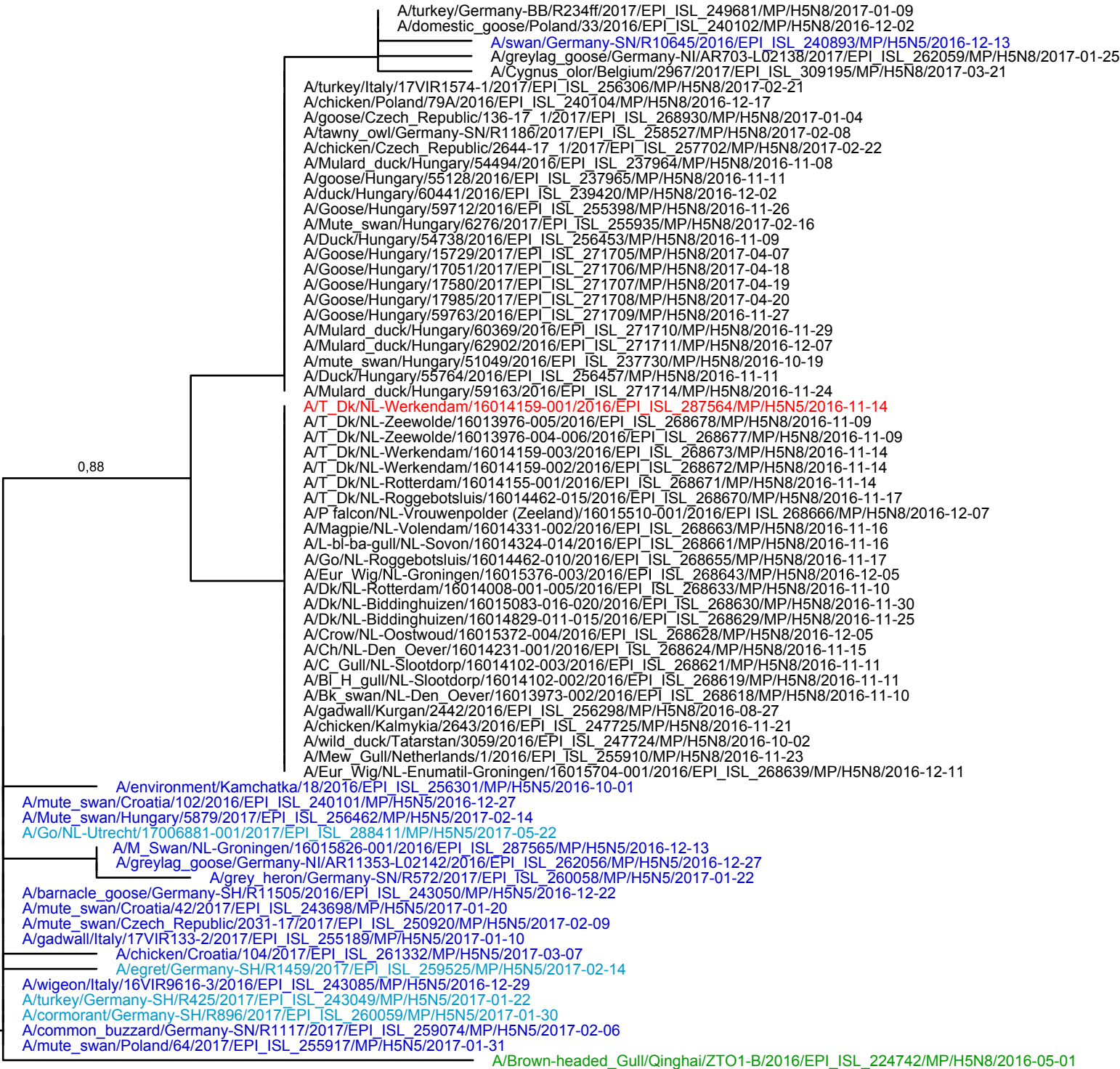
- H5N5-GT1
- H5N5-GT2
- H5N5-GT3
- H5N8 cluster representative



0.009

MP

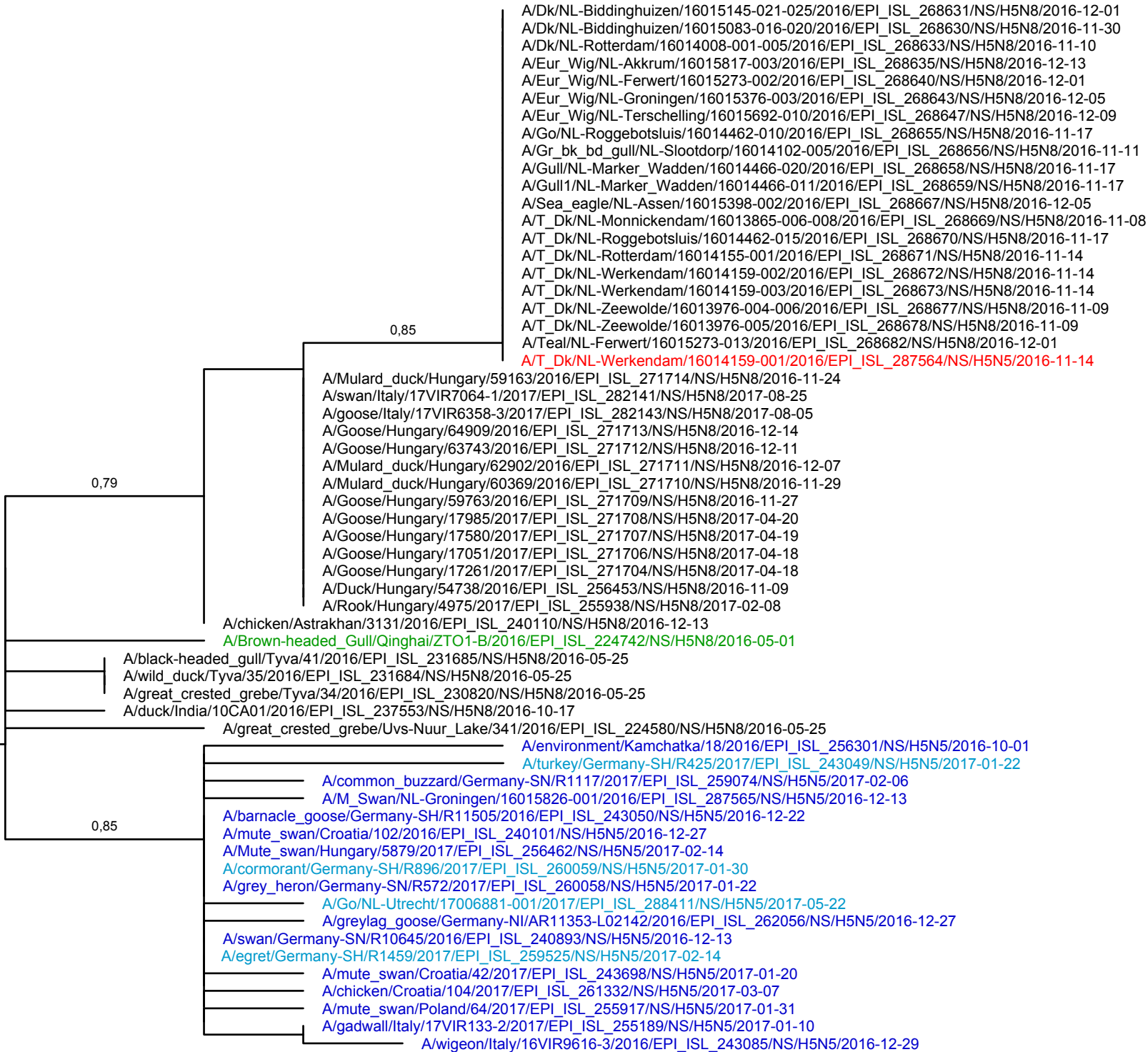
- H5N5-GT1
- H5N5-GT2
- H5N5-GT3
- H5N8 cluster representative



7.0E-4

NS

- H5N5-GT1
- H5N5-GT2
- H5N5-GT3
- H5N8 cluster representative



7.0E-4