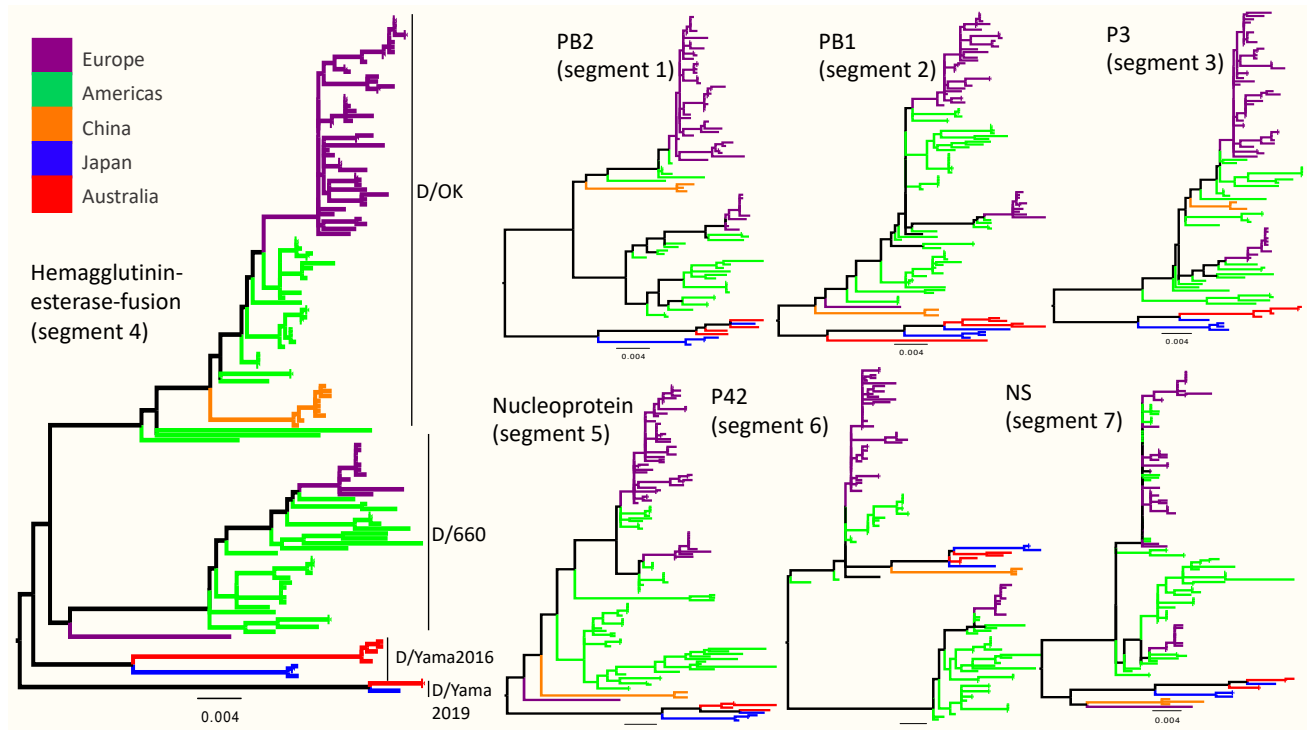


Additional file 5. Overview of Influenza D virus' segments phylogenies

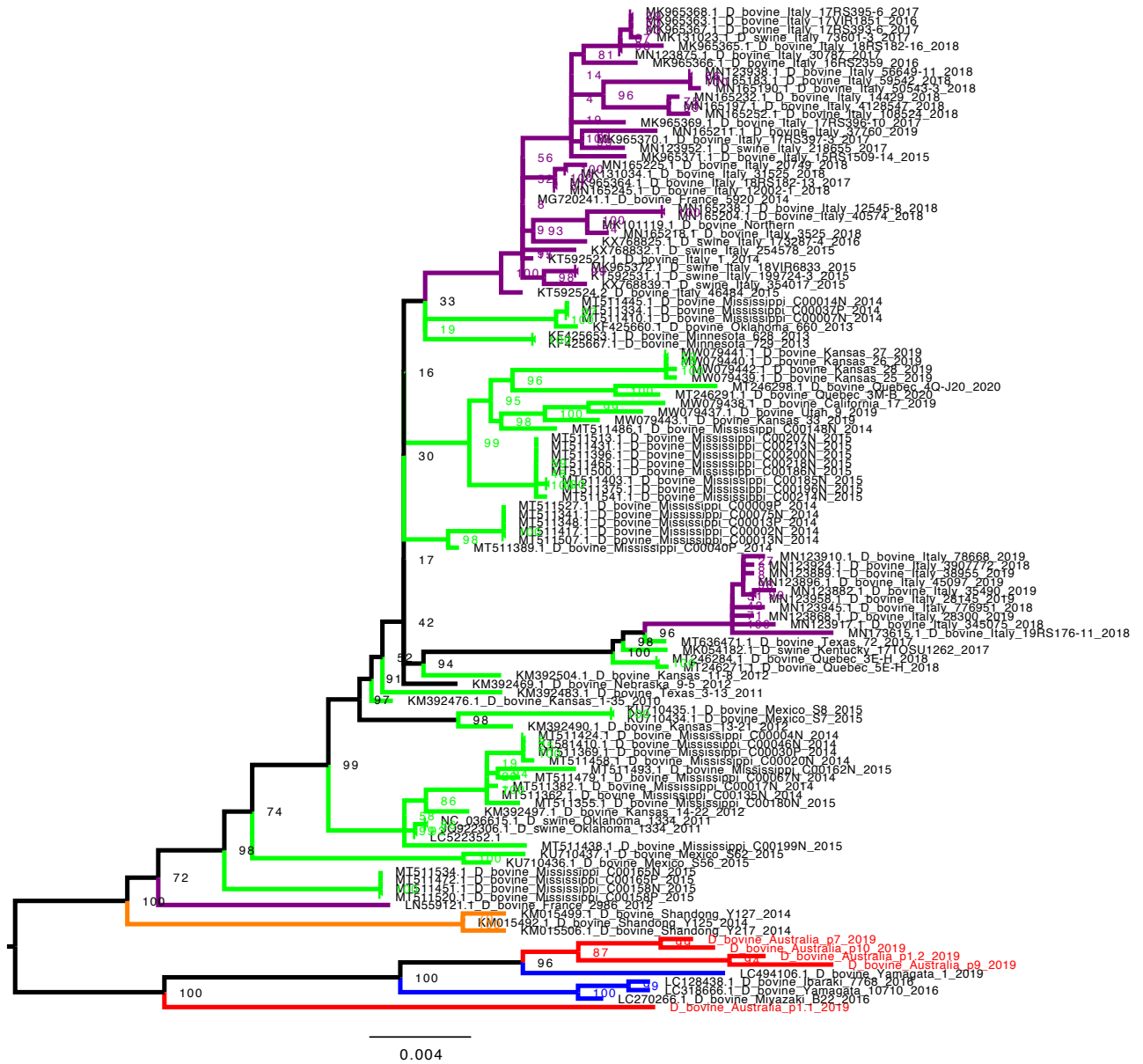


Additional fig 5.1. Maximum likelihood phylogenies of the seven segments of Influenza D virus. The colours of the tips in the trees indicate the geographic area. Trees are midpoint rooted. Branch length indicate nucleotide substitutions per nucleotide site. The four different IDV lineages are indicated in the HEF phylogeny. Australian viruses from this study belong to the Japanese lineages D/Yama2016 and D/Yama2019.

5.2- Influenza D virus- segment 1



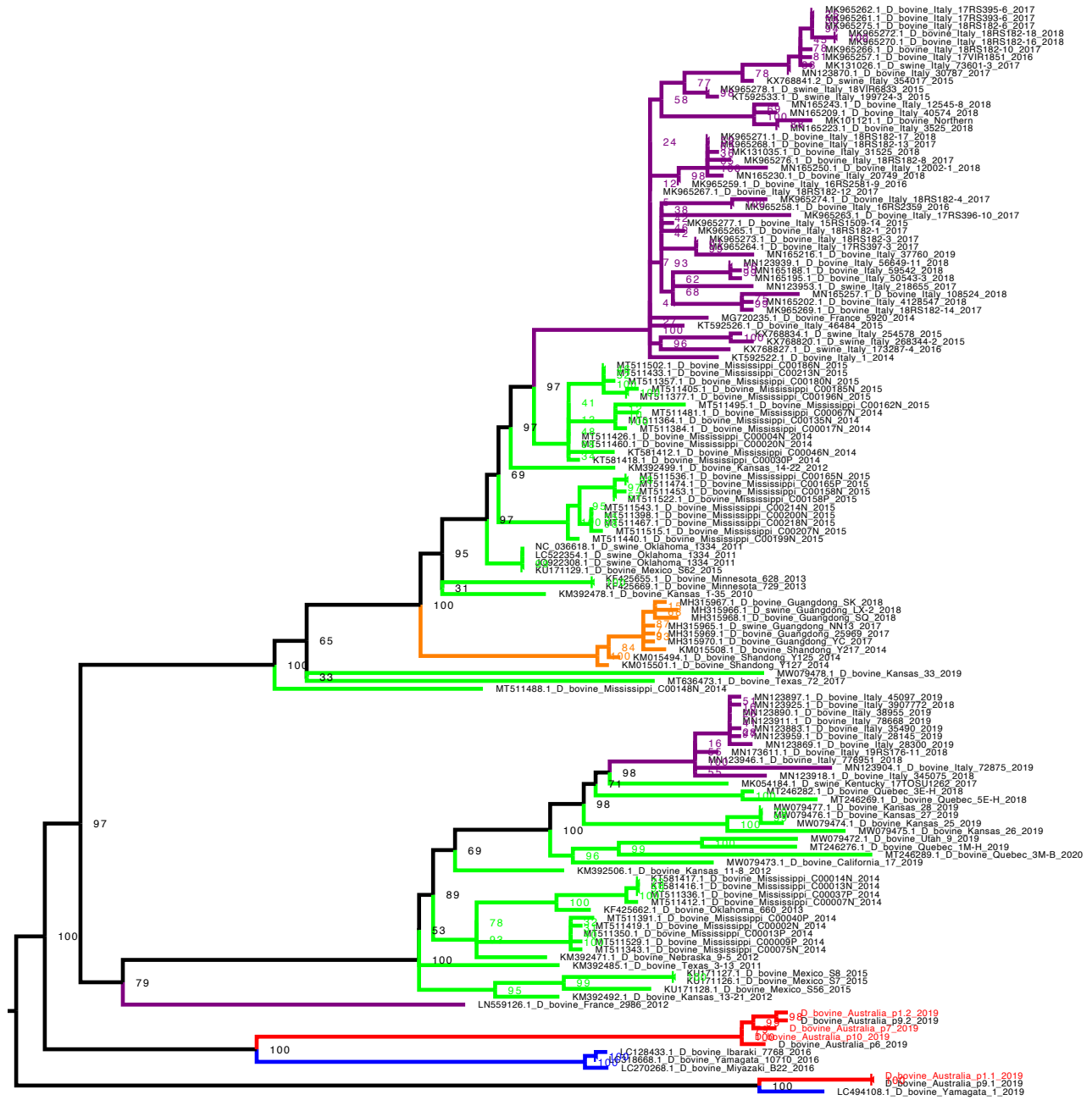
5.3- Influenza D virus- segment 2



5.4- Influenza D virus- segment 3

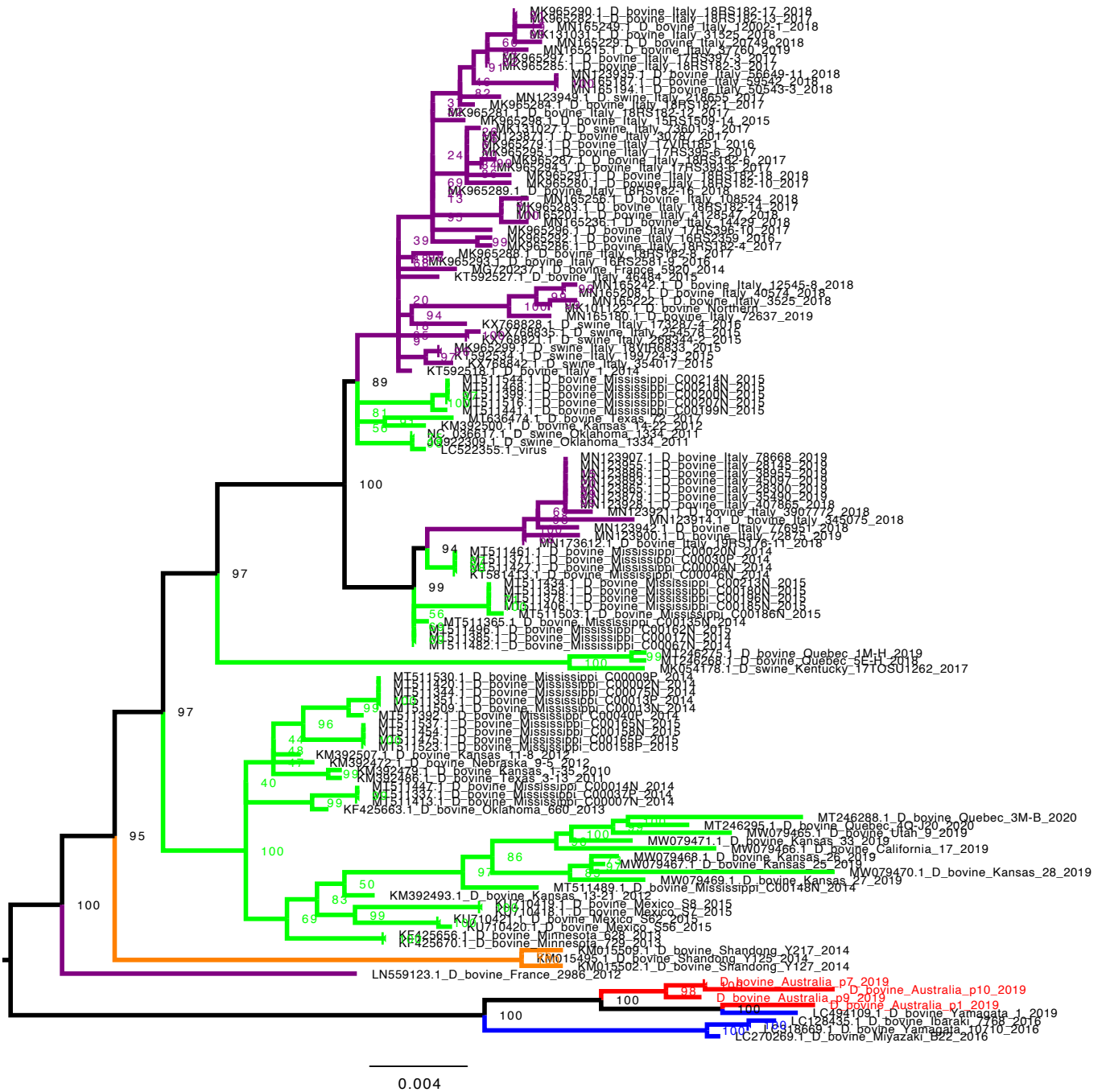


5.5- Influenza D virus- segment 4



0.004

5.6- Influenza D virus - segment 5



5.8- Influenza D virus – segment 7

