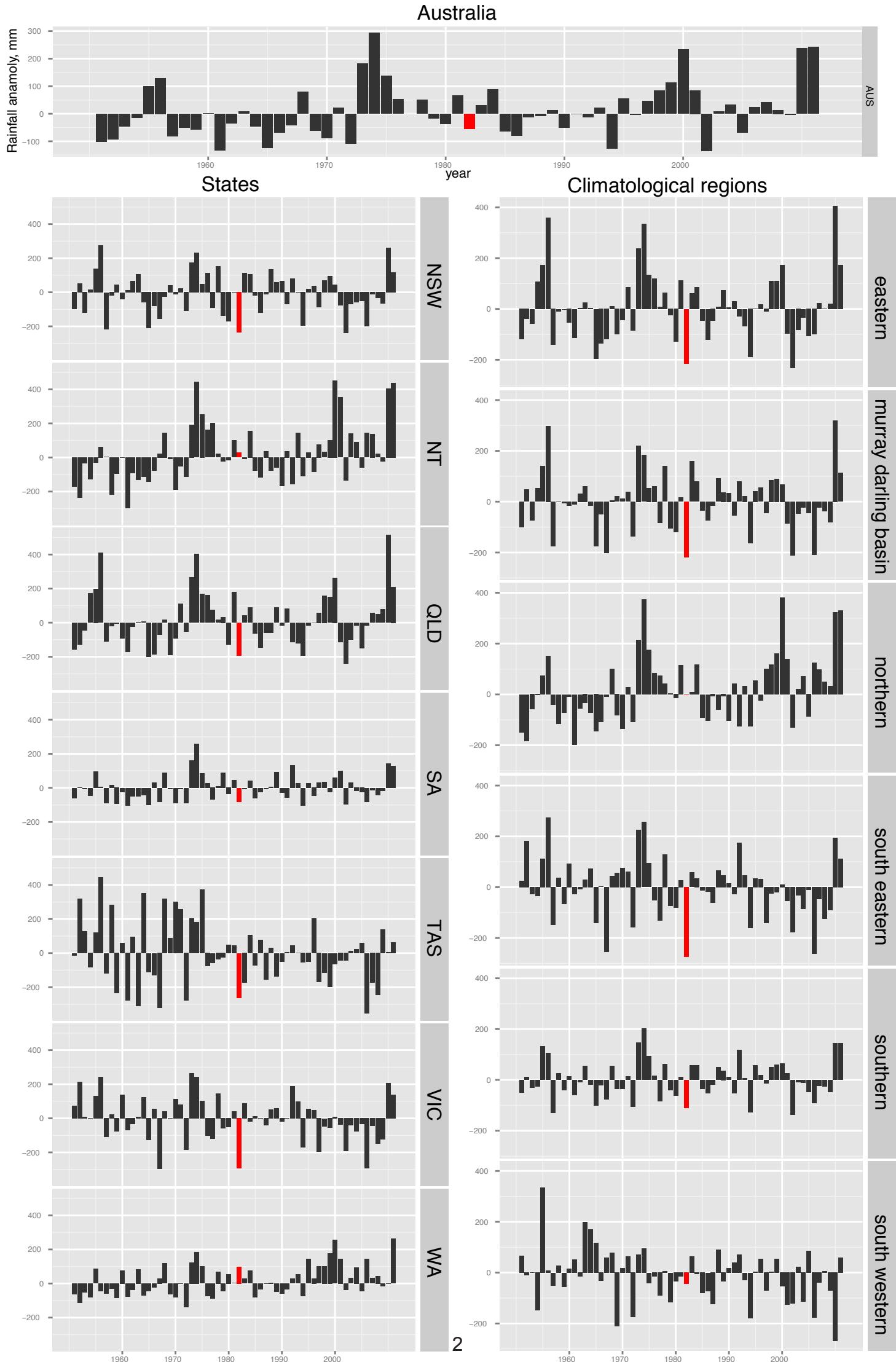


Fig S1. Distribution of full genome sequences of avian influenza A viruses from New Zealand and all states of Australia. Viruses for which state locations are unknown are listed under Australia in red.

Fig S2. (see page 2) Annual anomaly in average rainfall during 1950–2011 in Australia. Average anomaly in rainfall for all seven states, including New South Wales, Northern Territory, Queensland, South Australia, Tasmania, Victoria and Western Australia and also six major climatological regions as listed by the Bureau of Meteorology, Australian Government are presented. Red highlights the lowest rainfall observed during 1982 across several regions in Australia.



PB2

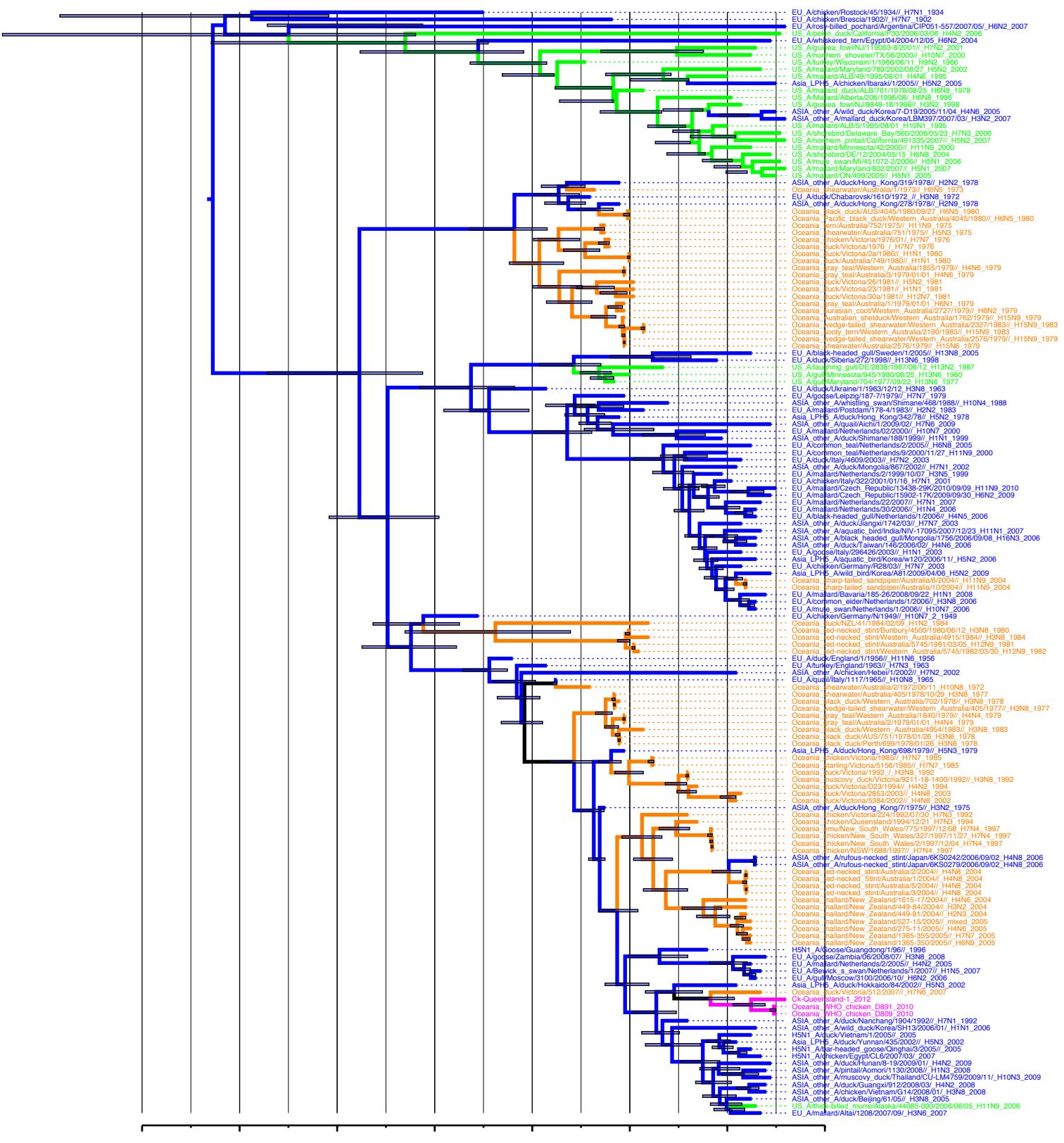
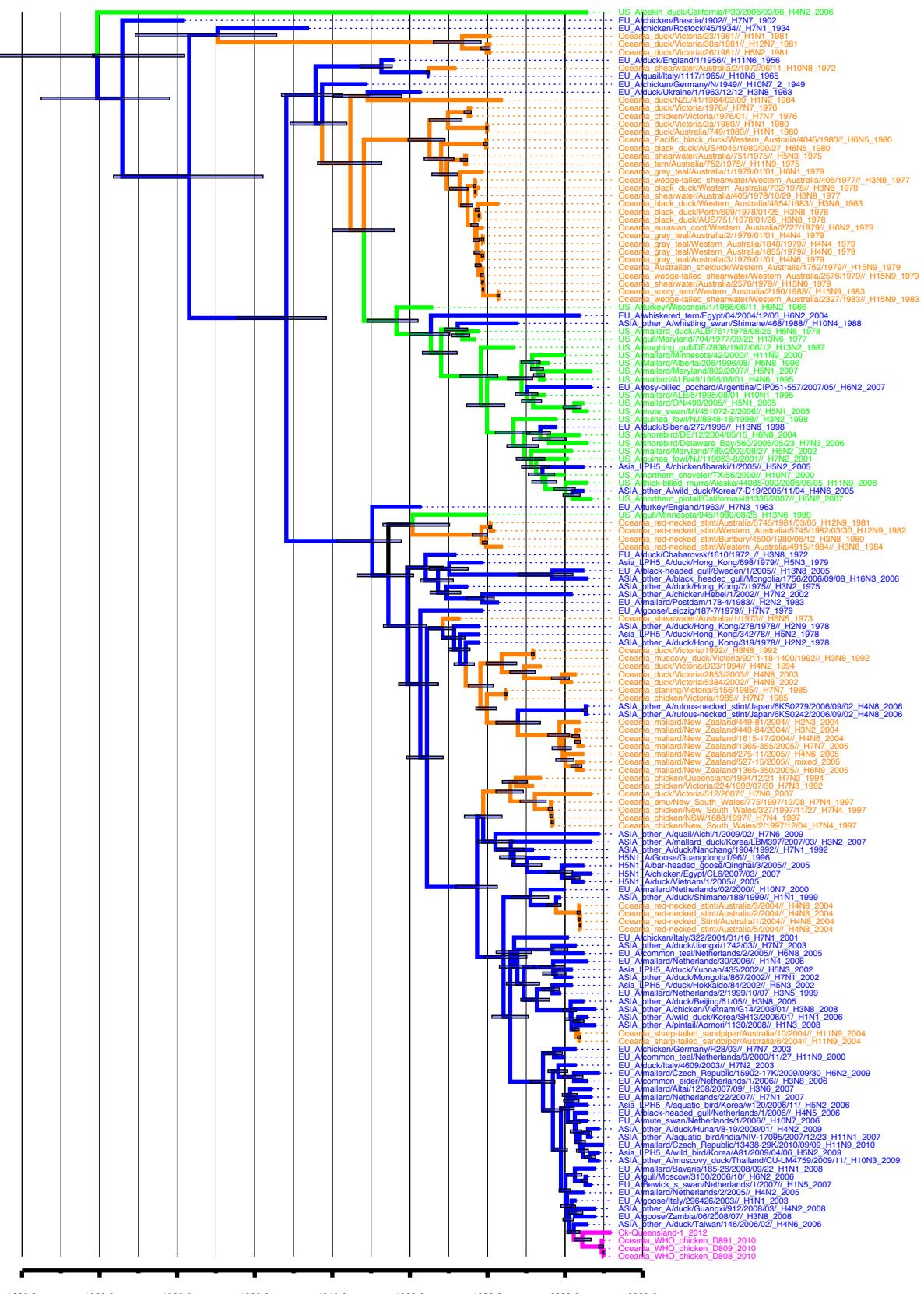
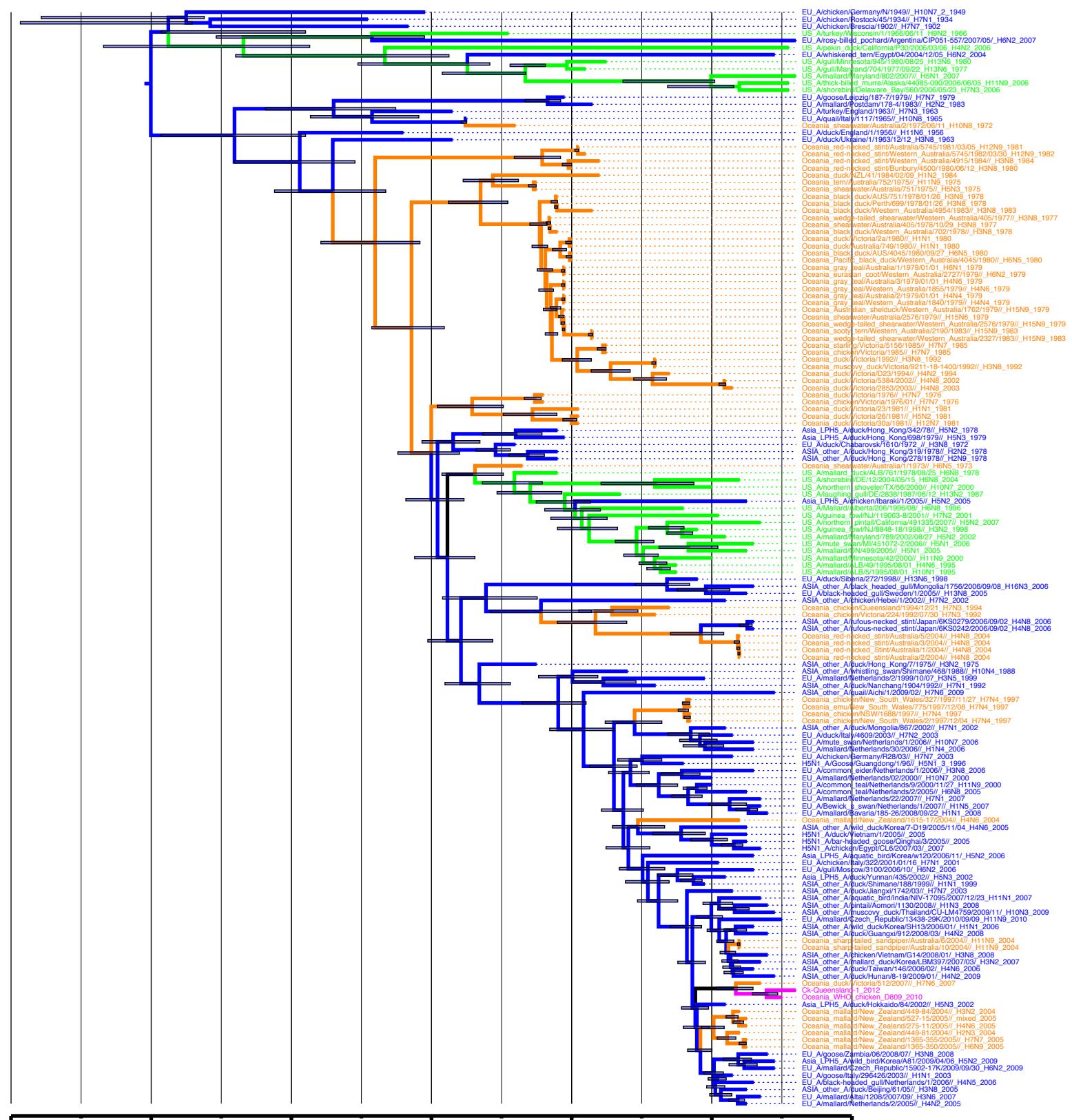


Fig S3. Phylogenies presented in Fig 3 of the main text are shown here with virus names. Phylogenetic relationship of the (a) polymerase basic 2 (PB2), (b) polymerase basic 1 (PB1), (c) polymerase acidic (PA), (d) nucleoprotein (NP), (e) matrix (M) and (f) non-structural (NS) protein genes of avian influenza viruses isolated from Oceania (orange), Eurasia (blue) and America (green) of all subtypes. Influenza A H10N7 subtype viruses isolated from Australia during 2009-2012 are highlighted in pink. The 95% credible intervals of the age of internal nodes are represented by blue bars

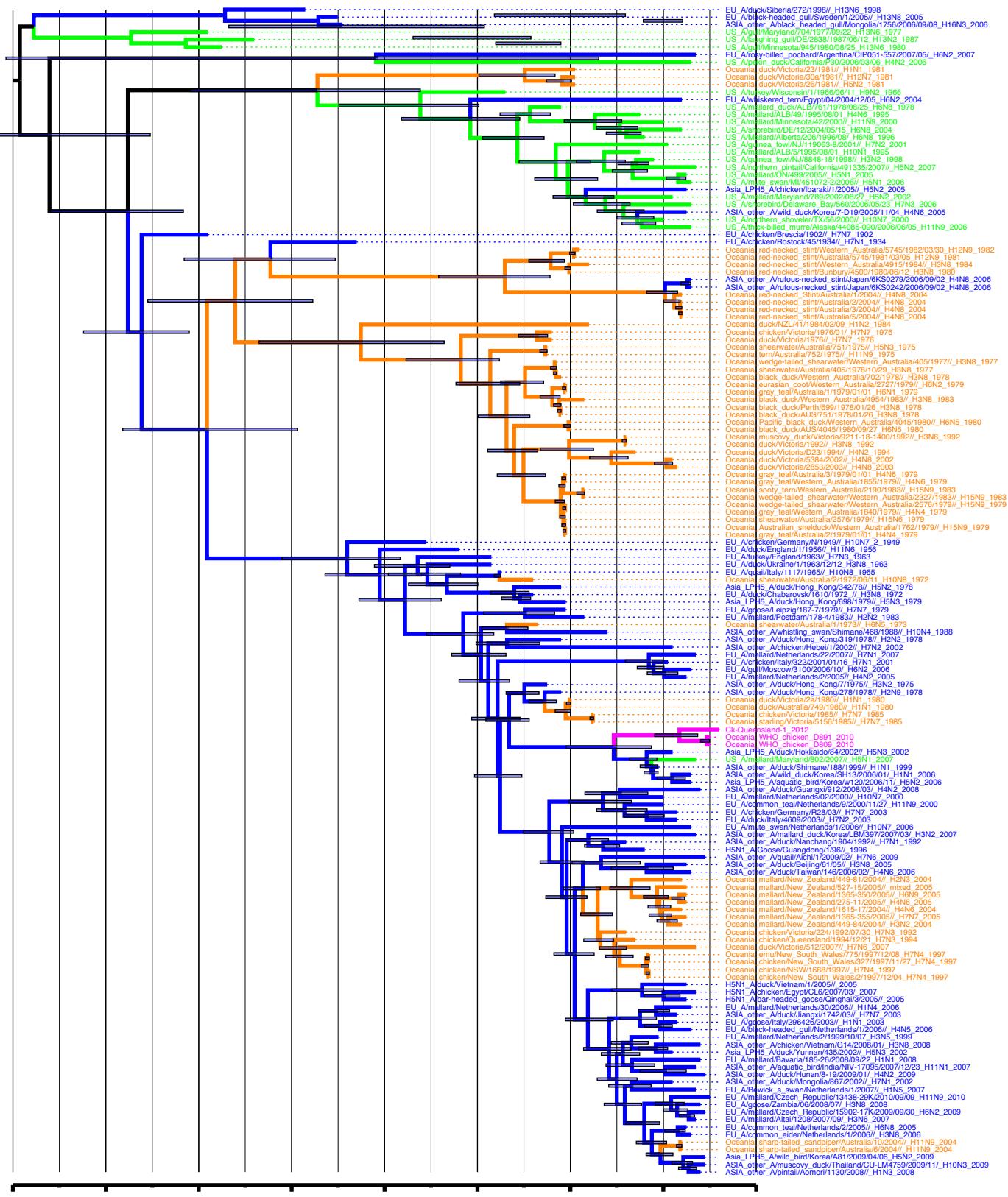
PB1



PA



NP



M



NS

