



Supplementary Figure 1: Maximum clade credibility tree of avian influenza sequences for H5 clade 2.3.4.4. NA sequences were used to inform the structure of the starred Eurasian clade, where available. Tips are labelled with isolate name and accession number (refer to Supplementary Figure 1 for accession number details). Posterior support is given at nodes where >0.7. Tree is equivalent to Figure 3 (main text). Note that whilst all branches are coloured according to the inferred ancestral location based on asymmetric trait reconstruction using BSSVS, branch locations in some parts of the tree may not accurately reflect the true dynamics of the virus. Refer to the main text for discussion.