



Supplementary data 3: Maximum likelihood phylogenetic trees of HA and NA segment pairings of H1 viruses circulating in European pigs where sequence data were available for both segments (n=1424). Identical tips are connected with lines coloured according to HA genetic lineage as per figure 1 in order to visualise the diversity of HA and NA gene segment pairings among H1 European viruses. Parallel lines indicate genetically stable pairings and crossed lines indicate heterogeneity in gene pairings.