Figure 4 - figure supplement 1. Bayesian phylogenetic tree of the M sequences of the Danish swIAV surveillance 2011-2018. A/sw/Denmark/12687/2003(H1N2) accession number: KC900267 was used as the outgroup. A blue taxon indicates that the M gene of the sample is of avian-like origin, whereas a black taxon indicates that the M gene of the sample is of H1N1pmd09 origin. Sequences are named according to their sequence ID and lineage.

