



Figure 5 - figure supplement 5. Networks determined from pairwise tree distances. Overall vRNA relationships corresponding to H1N1 viruses from 2010-2018 were assessed with UPGMA trees derived from the mean RF corresponding to Figures 5A (**A**) or the CID corresponding to Figure 5 - figure supplement 2A (**B**). Scale bar corresponds to either RF or CID. The point at which edges merge is equivalent to 1/2 RF or 1/2 CID.