Figure 2 - figure supplement 4. Networks determined from pairwise tree distances. Overall vRNA relationships corresponding to H3N2 viruses from 2005-2014 were assessed with UPGMA trees derived from the mean RF corresponding to Figure 2C **(A)** or the mean CID corresponding to Figure 2 - 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.