



**Figure 6 - figure supplement 1. Parallel evolution between proteins in H3N2 viruses from 2005-2014.** H3N2 virus vRNA gene sequence alignments were translated into the corresponding amino acid alignments. Neighbor-joining trees were reconstructed from these alignments and the Robinson-Foulds distance (RF) was tabulated for all protein tree pairs. An RF network was constructed using a UPGMA tree. Scale bar corresponds to RF.