

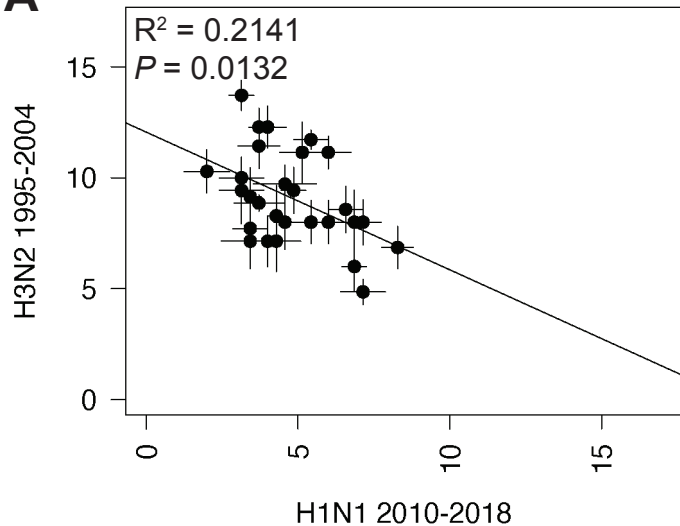
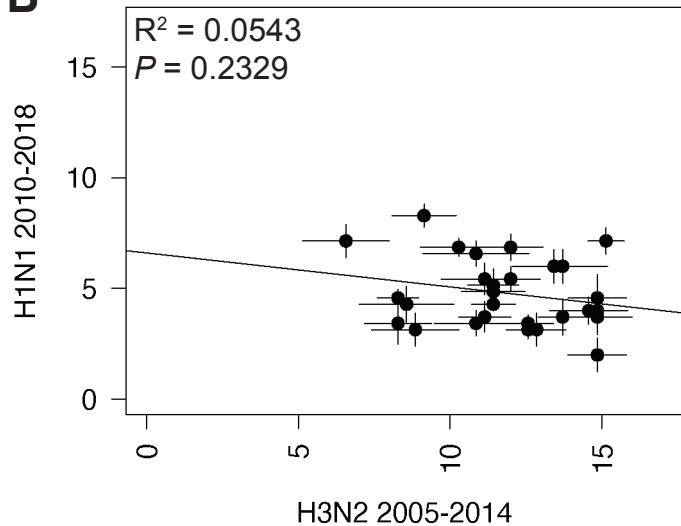
A**B**

Figure 5 - figure supplement 3. Linear regression of tree distances determined by Robinson-Foulds distance (RF). Mean RF distances of replicate trees from H1N1 viruses from 2010-2018 were plotted against those from H3N2 viruses from 1995-2004 (**A**) and H3N2 viruses from 2005-2014 (**B**). The line of best fit was determined by linear regression (solid line). The R^2 and P -value are indicated. Error bars indicate the SEM of all replicates.