

## Supplementary Figure S7

**Predictors of global H3N2 diffusion among the 14 air communities and the 15 & 26 geographic locations using equal prior probability on the inclusion and exclusion of each predictor.** The inclusion probabilities are defined by the indicator expectations  $E[\delta]$  because they reflect the frequency at which the predictor is included in the model and therefore represent the support for the predictor. As opposed the analysis reported in main manuscript (Fig. 2), which specifies a prior probability of 0.019 on each predictor's inclusion, we here specify a prior probability of 0.5 on the inclusion of each predictor. Indicator expectations corresponding to Bayes factor support values of 3 and 20 are shown as a thin and thick vertical line respectively in these bar plots. The contribution of each predictor, when included in the model ( $\beta|\delta = 1$ ), where  $\beta$  is the coefficient or effect size, is represented by the mean and credible intervals of the GLM coefficients on a log scale. NA<sup>1</sup>: no conditional effect size available because the effect was never included in the model. We tested different population size and density measures, different incidence-based measures and different seasonal measures (*Supplementary Text S1*), but only list the estimates for a representative predictor for the sake of clarity. NA<sup>2</sup>: no indicator expectation or conditional effect size available because the predictor was not available for this discretization of the sequence data. A comparison with the analysis reported in main manuscript (Fig. 2) indicates that our results are robust to the prior specification for the inclusion probabilities; only the scale of the Bayes factor support shifts to lower values because of the higher prior odds (1:1 as opposed to 0.019:0.981) in this case.

