

## Supplementary Figure S5

**Predictors of global H3N2 diffusion among the 14 air communities for three different sub-samples of the sequence data.** Each combination of inclusion probability bar plot and corresponding coefficient plot represents the GLM results for one of the three different sub-samples of the H3N2 sequence data. These sub-samples were obtained by randomly down-sampling the four locations with the highest number of samples relative to their population size for each sampling year. 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. Indicator expectations corresponding to Bayes factor support values of 10 and 100 are represented by 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. 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.

