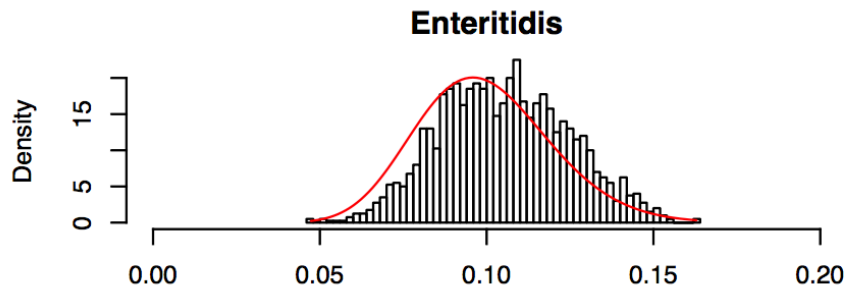
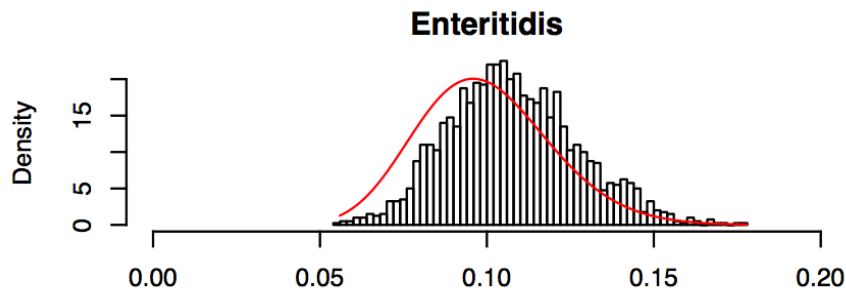


**Supporting information - Inferring source attribution from a multi-year multi-source dataset of Salmonella in Minnesota**

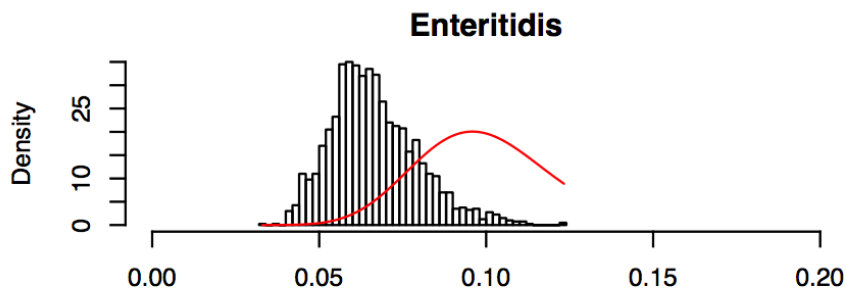
A) Single attribution, including only sampled sources



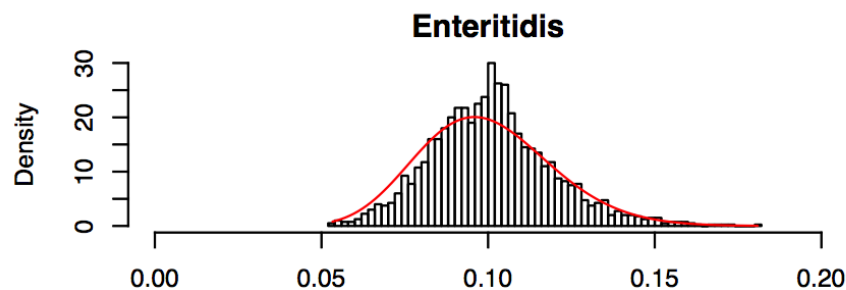
B) Single attribution, including non-sampled sources



C) Temporal attribution, including only sampled sources

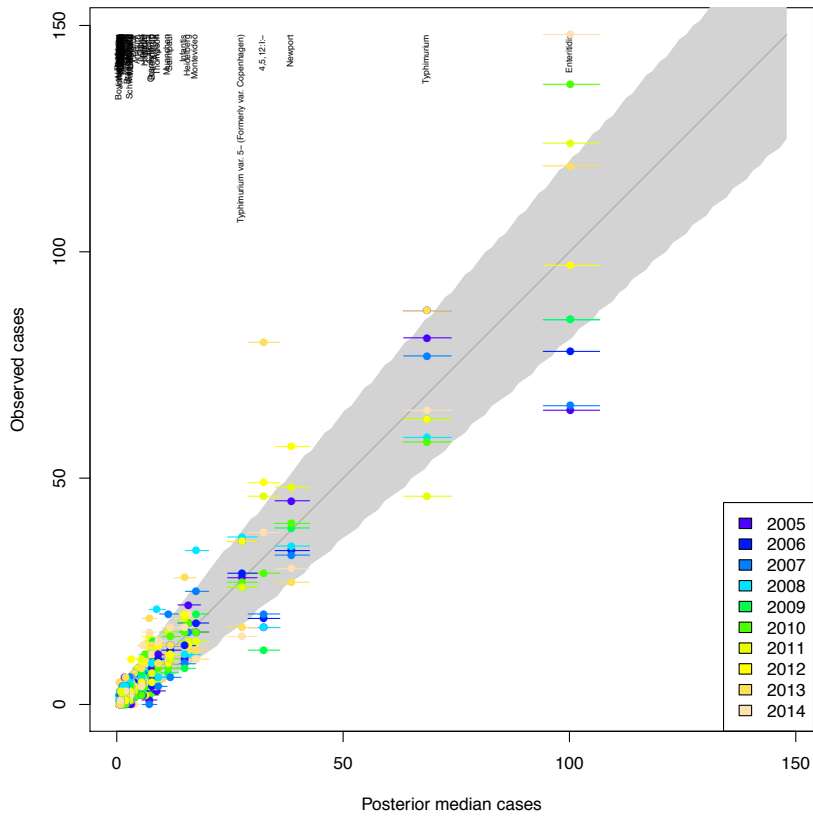


D) Temporal attribution, including non-sampled sources

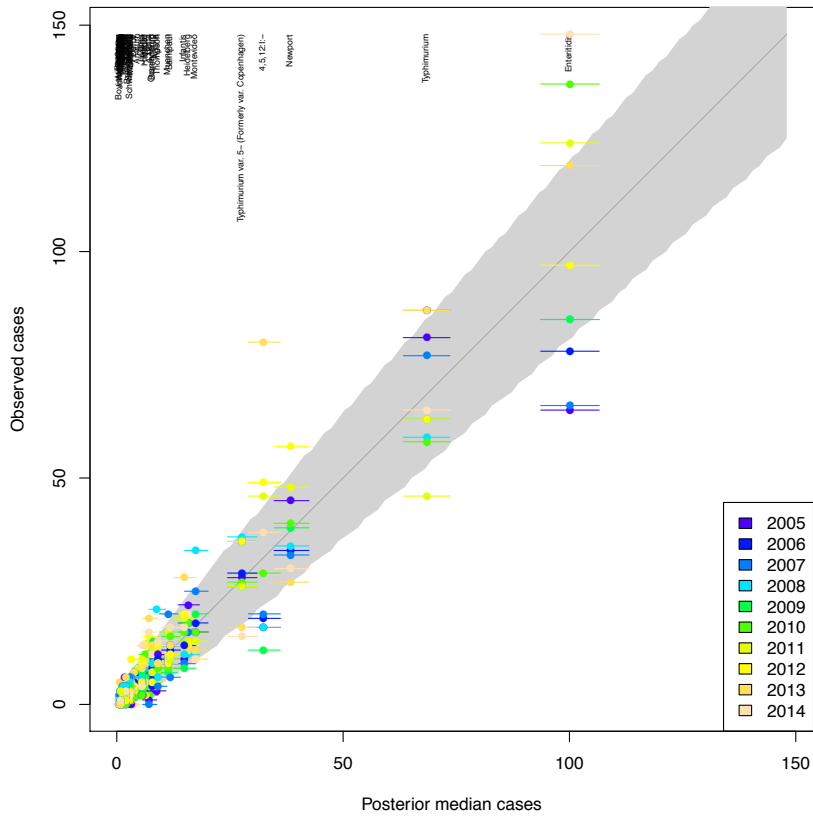


Supporting Figure 1. Posterior distribution of relative prevalence of *S. Enteritidis* in chicken with informative prior density (based on source typing data) shown in red for four different models – A) Single attribution including only sampled sources, B) Single attribution including non-sampled sources, C) Temporal attribution including only sampled sources, and D) Temporal attribution including non-sampled sources.

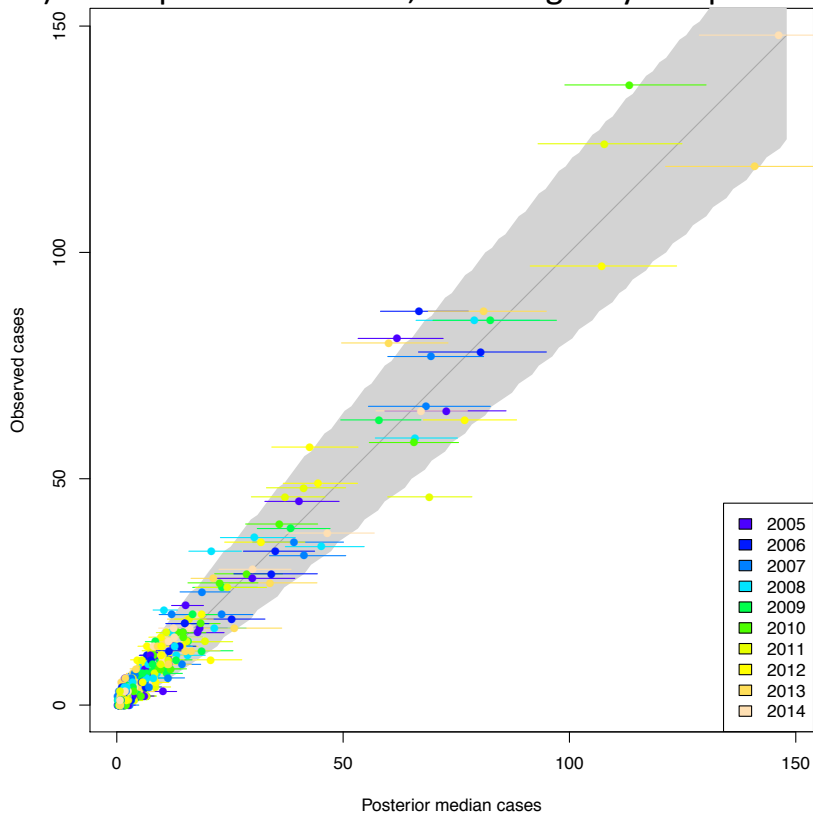
A) Single attribution, including only sampled sources



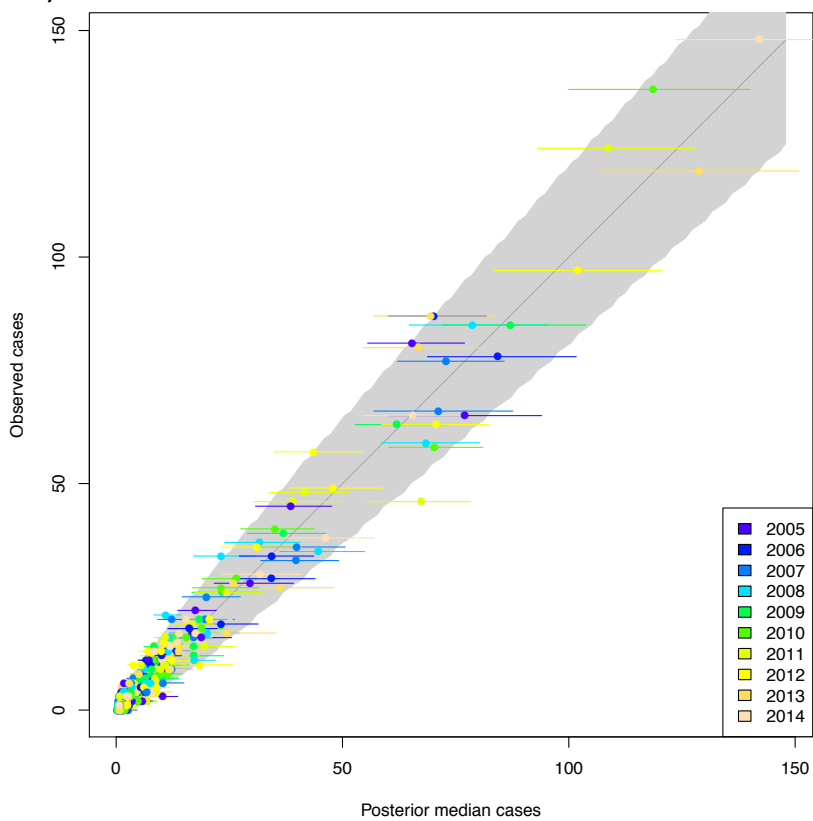
B) Single attribution, including non-sampled sources



C) Temporal attribution, including only sampled sources



D) Temporal attribution, including non-sampled sources



Supporting Figure 2 Plots of the observed and expected cases for individual *Salmonella* serotypes in the A) Single attribution model including only sampled sources, B) Single attribution including non-sampled sources, C) Temporal attribution including only sampled sources, and D) Temporal attribution including non-sampled sources.