



Figure S2. A simulated outbreak. 24 individuals are infected in a simulated SIR outbreak, of which 18 have sampled genotypes. Each individual has an infectious period shown as a gray bar, with genotypes shown as colored circles, the color denoting the genetic distance from the first sample (top). One randomly sampled genome for each individual is used to assess the likelihood of direct transmission from each other sampled individual. The pairwise genetic distances are shown (bottom right), with black boxes denoting the true source of infection, and gray boxes denoting presence at the time of infection. The relative likelihood of direct transmission using the geometric-Poisson approximation is shown for each pair (bottom left, green and red indicating high and low relative likelihood respectively). Crosses indicate the maximum likelihood estimate, while circles indicate the genetically closest isolate to each sample.