

Table S3. Proportion of correct transmission routes identified using the geometric Poisson likelihood, as well as with the ‘outbreaker’ and ‘seqTrack’ functions. A total of 25 outbreaks with 30 susceptible individuals were simulated for each scenario, with outbreaks terminating with fewer than 20 infections excluded. R_0 was set to be 2, with a within-population size 5000. In outbreaker, no spatial model was defined, importation identification was suppressed, and the infectivity distribution was specified to be uniform. In seqTrack, the mutation rate was provided.

^a If the true source and other hosts are genetically equidistant, the true host is assumed to be identified with probability $1/(\# \text{ equidistant closest hosts})$.

Parameters		Network identification method			
Mutation rate	Inoculum size	ML estimate	outbreaker	seqTrack	Closest genotype ^a
0.002	1	0.28	0.20	0.14	0.21
0.002	5	0.26	0.19	0.13	0.17
0.002	10	0.24	0.19	0.14	0.16
0.005	1	0.28	0.20	0.13	0.22
0.005	5	0.22	0.18	0.12	0.18
0.005	10	0.21	0.21	0.13	0.17