



Supplementary Fig. 8. Excess genetic variability during outbreaks. This figure shows the distribution of the difference in genetic diversity (mean pair-wise genetic distances) between 50 replicates taken ten generations apart for each simulation. The main figure uses a reduced scale, whereas the full range is shown in the inset. Boxplots in the main figure and the inset indicate the ranges of the two central 25% quantiles of mean values. Colored curves (below) show the densities of the respective distributions. Numbers on the left indicate outbreaks at the indicated  $R_0$  values (1.1: yellow; 1.5: red; 2.0: blue) whereas equilibrium populations (equ) are indicated in grey.