Supplementary Fig. 9. Distribution of allele frequencies during outbreaks. For the equilibrium control population (a), the histogram was obtained by pooling 1,000 randomly chosen generations. The bar on the far right (allele frequencies = 1.0) represents the relative frequency of derived mutations having reached fixation. Panels b-d show the distribution of allele frequencies pooled over the last 10 generations for outbreak simulations based on 50 replicates (b: R0=1.1; c: R0=1.5; d: R0=2), overlayed with the frequency distribution of the equilibrium control simulation (grey).