We model transmission using a two-group SIR model, where the two groups are the majority population (group 1) and the minority population (group 2). The model tracks the number of individuals who are susceptible (*S*), infectious (*I*), and removed (*R*) over time in each of the two groups, where the group number is indicated by the subscript. The removed population includes individuals who have either recovered or died from a prior infection.

The following differential equations govern the number of individuals in each of the six compartments over time (*t*):

The parameter is a per-capita rate of transition from the infectious state to the removed state, such that 1 / is the average time of remaining infectious, assumed to be the same for both groups. The four are transmission rates from infectious members of group *j* to susceptible members of group *i*. These four transmission rates are calculated as follows:

The values and are the overall contact rates for members of each group, i.e. the total number of people (of either group) contacted per unit time, while and are the fraction of each group’s contacts that are exclusively within-group. The values and quantify the susceptibility to infection of members of each group for a given amount of contact with infectious individuals. The population sizes of each group are and .

The basic reproduction number, , the expected number of transmissions from an infectious individual in a fully susceptible population, is the quotient of the dominant eigenvalue of the two-by-two matrix of values and :

For our analyses, we make assumptions for the values of , , , , , , and the ratios and . From these assumptions, the values of the four can be uniquely determined, as follows. The four can be expressed:

The four quantities in square brackets can be calculated directly from our assumptions for , , , , , and . Then, the product acts as a scaling coefficient on all four values, and we can calculate the value of this scaling coefficient using our assumed values of and and the above formula:

Next, we use a formula to calculate the final sizes, and , of an outbreak in a population with the assumed parameter values and with a given initial condition, including the number of individuals initially immunized against infection by vaccination, and . Mathematically, the final size for the system of differential equations is defined as in the limit as , i.e. the number of initially susceptible individuals who are no longer susceptible after the there are no more infectious individuals remaining to transmit. We assume that , i.e. that vaccinated individuals are immunized at time 0 and all remaining individuals are initially susceptible. Formulas for the values of have been derived for an equivalent model [Cui et al. 2019], and are expressed as follows for our notation:

We calculated the values of the coefficients for a given set of assumptions, using the formulas above, and then numerically solved for and to produce the results in the main text.