

## Supplemental Figures and Tables

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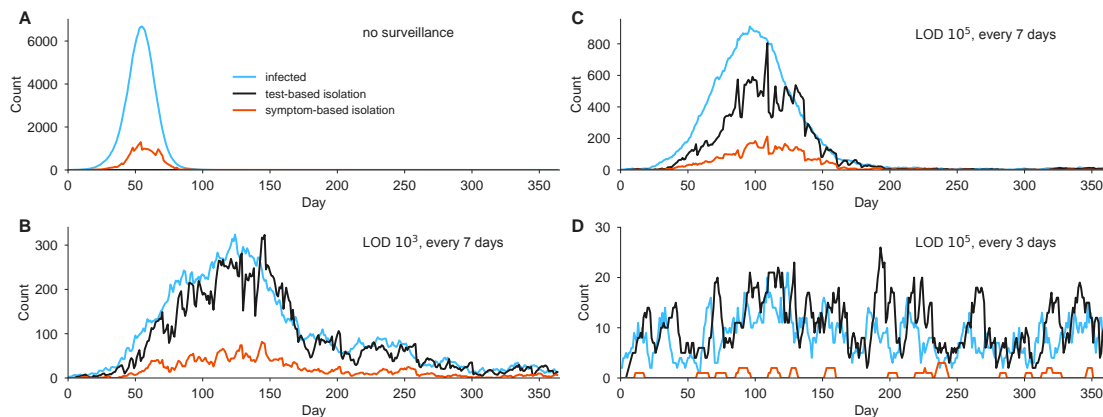
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**Figure S1: Sample simulation trajectories from fully mixed model.** Simulation trajectories show the number of infected individuals in a population of  $N = 20,000$  with a constant rate of external infection set to  $1/N$  per person per day, i.e. around 1 imported case per day. Infections (blue), test-based isolation (black), and symptom-based isolation (red) are shown for four scenarios, with  $R_0 = 2.5$ . (A) No surveillance. (B) Weekly testing at LOD  $10^3$ . (C) Weekly testing at LOD  $10^5$ . (D) Testing every 3 days with LOD  $10^5$ . Note the variation in the vertical axis scales. The model is fully described in Methods.

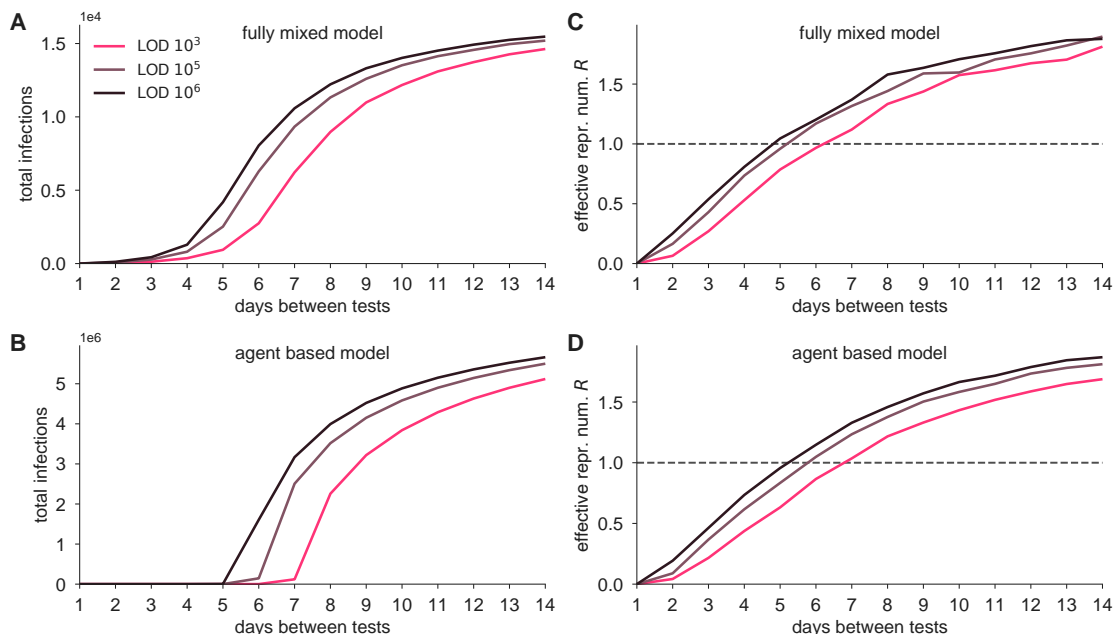


Figure S2: **Epidemiological model outcomes for various test LODs and frequencies.** The fully mixed model (top row) and agent based model (bottom row) were simulated (Methods) with various test frequencies, ranging from daily to once every 14 days, and with LODs of  $10^3$ ,  $10^5$ , and  $10^6$ . Modeling results show mean outcomes from 50 independent simulations at each point, expressed as (A, B) total infections and (C, D) effective reproductive number  $R$ , from a baseline of  $R_0 = 2.5$ . For the fully mixed model, only secondary infections are shown, excluding imported infections. Total population sizes were  $N = 2 \times 10^4$  for the fully mixed model and  $8.4 \times 10^6$  for the agent based model. Dashed lines indicate  $R = 1$  for reference.

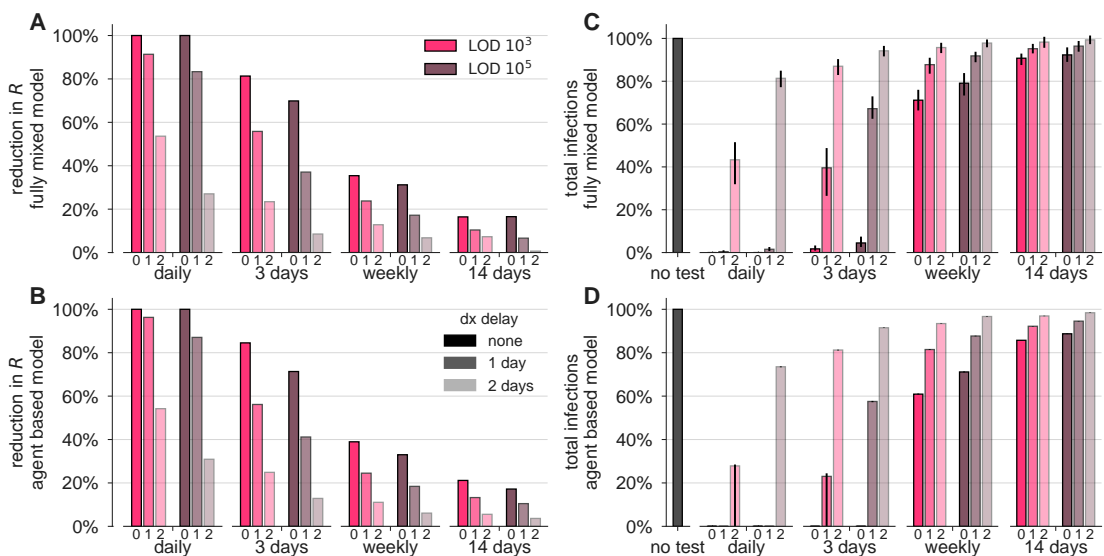
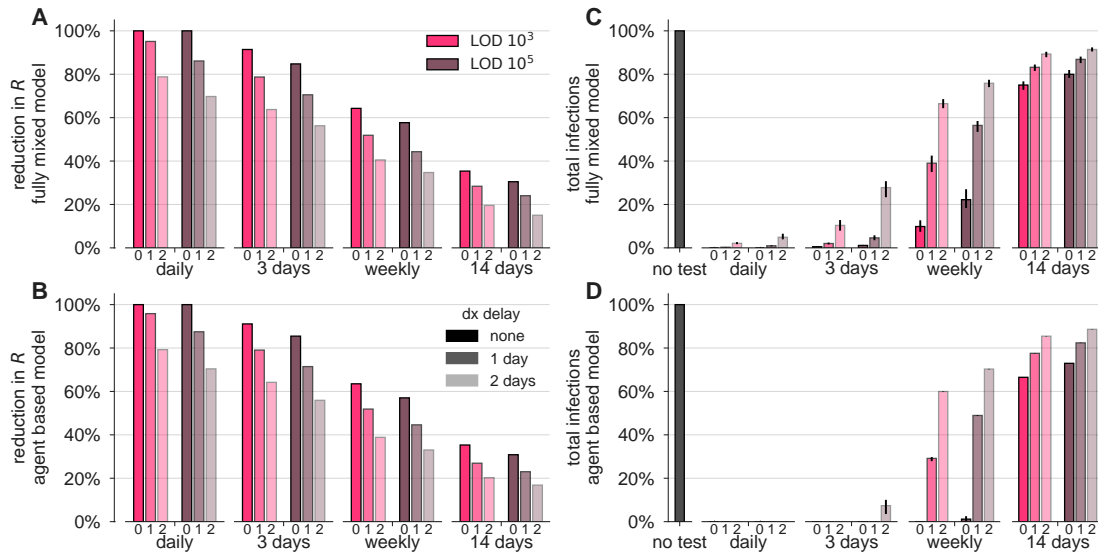
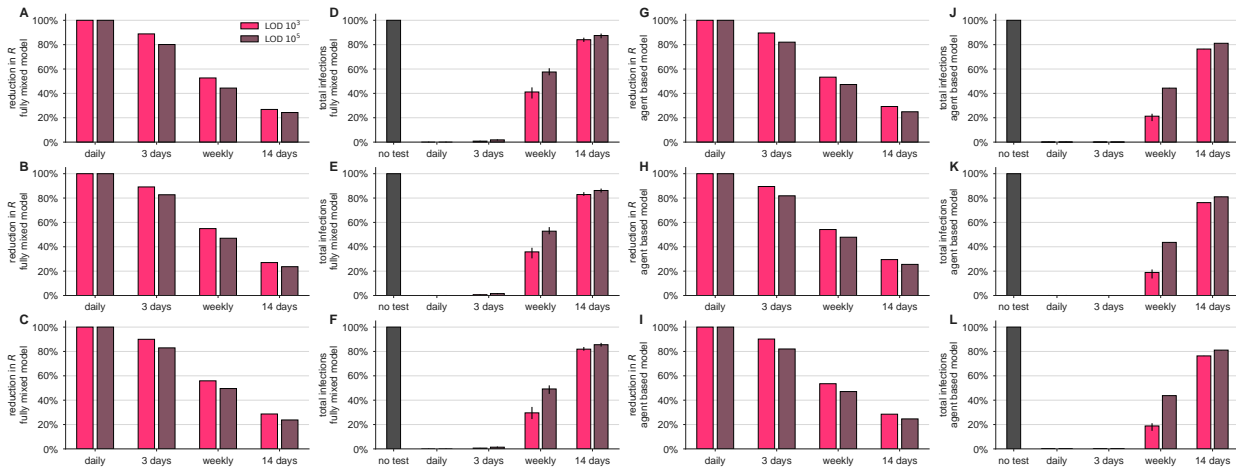


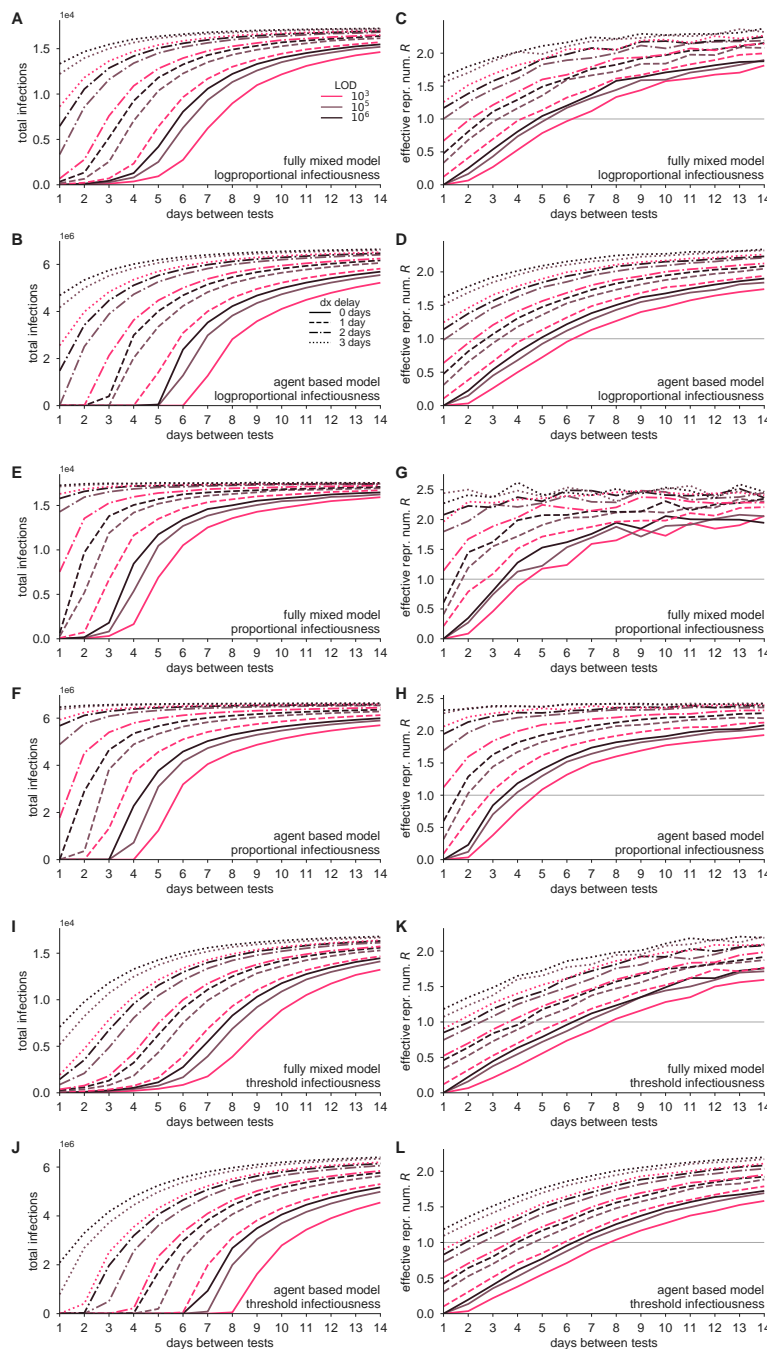
Figure S3: **Delays in reporting decrease the epidemiological impact of surveillance-driven isolation (proportional infectiousness).** This figure presents results from simulations which were identical to those shown in the main text Figure 4, but in which infectiousness was assumed to be *directly proportional* to viral load. Compare with threshold (binary) infectiousness in Fig. S4 and log-proportional infectiousness in Fig 4. See Methods.



**Figure S4: Delays in reporting decrease the epidemiological impact of surveillance-driven isolation (threshold infectiousness).** This figure presents results from simulations which were identical to those shown in the main text Figure 4, but in which infectiousness was assumed to be *binary*, i.e. no infectiousness below 10<sup>6</sup> and equal infectiousness for any viral load above 10<sup>6</sup>. Compare with proportional infectiousness in Fig. S3 and log-proportional infectiousness in Fig 4. See Methods.



**Figure S5: Robustness of surveillance effectiveness to the fraction of individuals who are symptomatic.** (A-F) Results from fully-mixed simulations and (G-L) agent-based simulations using an asymptomatic rate of 50% (top row), 65% (middle row; identical to main text Fig 2), and 80% (bottom row).



**Figure S6: Epidemiological model outcomes for various test LODs, frequencies, infectiousness functions, and with reporting delays.** The fully mixed model and agent based model were simulated (Methods) with various test frequencies, ranging from daily to once every 14 days, with LODs of  $10^3$ ,  $10^5$ , and  $10^6$ , and with delays of 0, 1, 2, or 3 days, for log-proportional, proportional, and threshold infectiousness functions (see Methods). Legends in panels A and B indicate LODs and delays, and in-plot annotations describe various conditions. Modeling results show mean outcomes from 50 independent simulations at each point, expressed as total infections and effective reproductive number  $R$ , from a baseline of  $R_0 = 2.5$ . For the fully mixed model, only secondary infections are shown, excluding imported infections. Total population sizes were  $N = 2 \times 10^4$  for the fully mixed model and  $8.4 \times 10^6$  for the agent based model. A horizontal line indicates  $R = 1$  for reference.

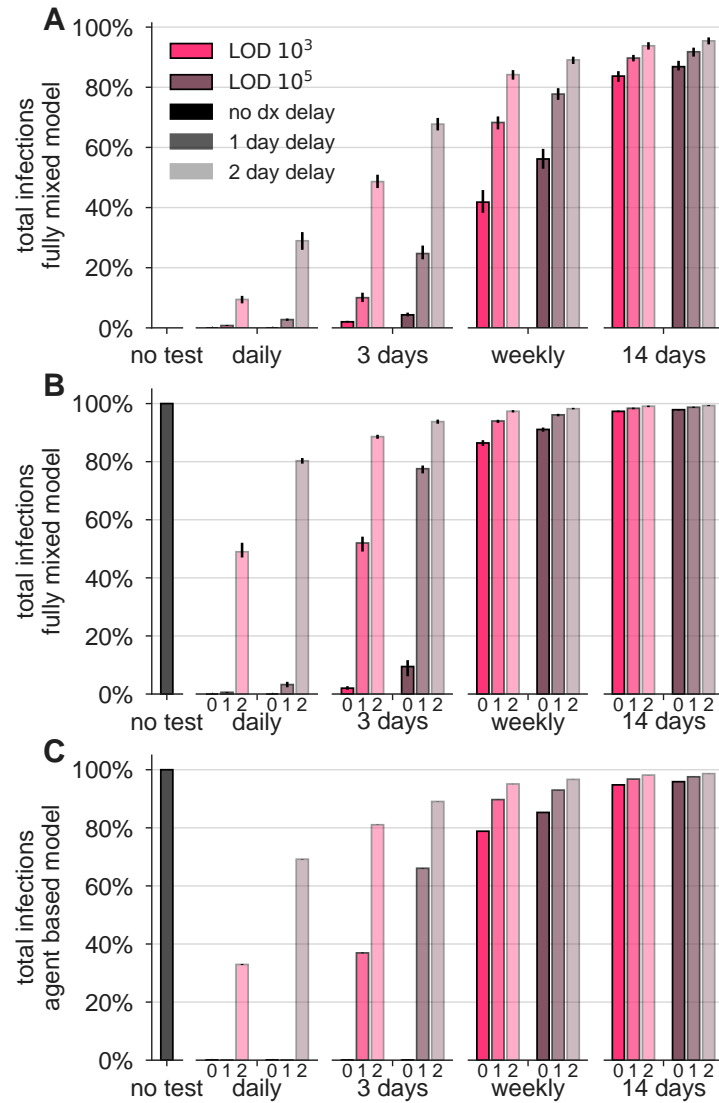


Figure S7: **Robustness of surveillance effectiveness to epidemiological model parameters.** (A) Results from the fully-mixed simulation with a tripled rate of external infection, i.e.  $3/N$  per person per day. (B) Results from the fully mixed simulation with  $R_0$  doubled, i.e.  $R_0 = 5$ . (C) Results from the agent-based simulation with  $R_0$  doubled, i.e.  $R_0 = 5$ .

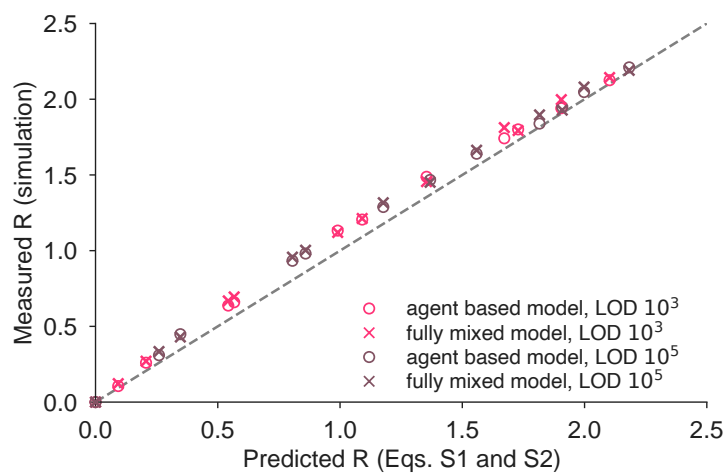


Figure S8: **Predicted and simulated impact of surveillance on the reproductive number  $R$ .** Mathematical predictions of the reproductive number  $R$  (see Equation (S1) in Supplemental Text S1) are scattered against their empirical measurements for the simulations shown in the main text (Figs. 2 and 4). Pearson's  $r = 0.998$ ,  $p < 10^{-6}$ .

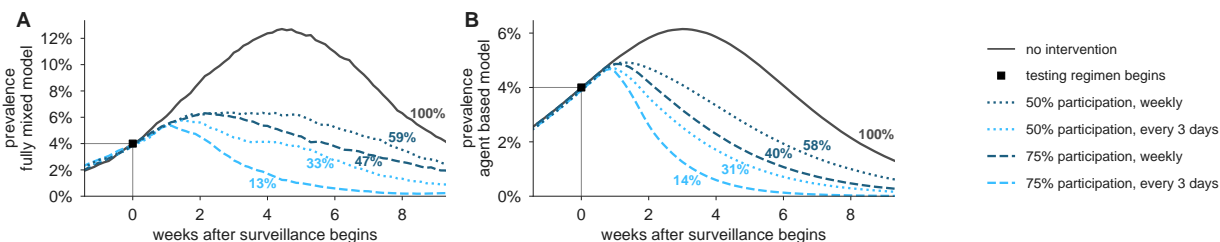


Figure S9: **Surveillance testing suppresses an ongoing epidemic using a test with  $LOD 10^6$ .** Widespread testing and isolation of infected individuals drives prevalence downward for both (A) the fully-mixed compartmental model and (B) the agent based model. Time-series of prevalence, measured as the total number of infectious individuals, are shown for no intervention (solid) and surveillance testing scenarios (various dashed; see legend). Surveillance testing began only when prevalence reached 4% (box), and time series are shifted such that testing begins at  $t = 0$ . Scenarios show the impact of a test with  $LOD 10^6$ , no delay in results, and with 10% of samples assumed to be incorrectly collected (and therefore negative) to reflect decreased sensitivity incurred at sample collection in a mass testing scenario. Annotations show total number of post-intervention infections, as a percentage of the no-intervention scenario, labeled as 100%. See Fig. 5 for identical simulations using a test with  $LOD 10^5$ .

## Supplemental Text

### S1 Predicting the impact of surveillance testing on $R$

The impact of surveillance on the reproductive number can be estimated by considering the ratio of population infectiousness with surveillance testing to population infectiousness with no surveillance testing. However, note that the impact of a surveillance testing policy may depend on two additional factors.

First, not all individuals may wish to participate in a testing program. Let the fraction of individuals who participate be given by  $\phi$ .

Second, a test may produce a false negative result *unrelated* to its limit of detection—for instance due to an improperly collected sample. Let  $se$  be the test sensitivity, in the particular sense of the probability of correctly diagnosing an individual as positive when that person’s viral load should, in principle, have provided a sufficiently high RNA concentration to be detectable.

Let  $f_0$  be the total infectiousness removed with no testing policy, i.e. due to symptom-driven self isolation. Let  $f_{\text{test}}(se)$  be the fraction of total infectiousness removed with a chosen testing policy, inclusive of symptom-driven self isolation, as well as the test sensitivity  $se$  introduced above.

Both  $f_0$  and  $f_{\text{test}}(se)$  can be estimated rapidly via Monte Carlo by drawing trajectories and applying a surveillance policy to them in which a fraction  $1 - se$  positive tests are discarded uniformly at random. In the main text, we found that estimating these values using 10,000 randomly drawn trajectories was sufficient to produce stable estimates.

Under the assumption of statistical independence between an individual’s participation or refusal, viral load, and  $se$ , we can approximate the reproductive number as

$$R \approx \left[ \phi \frac{1 - f_{\text{test}}(se)}{1 - f_0} + 1 - \phi \right] R_0, \quad (\text{S1})$$

which simply expresses a weighted combination of removed infectiousness via surveillance testing participation and no test. Intuitively, note that if there is complete refusal to participate ( $\phi = 0$ ) or an entirely ineffective test ( $f_{\text{test}}(se) = f_0$ ), then  $R \approx R_0$ , as expected.