Supplementary Material
Lipsitch et al.
Transmission Dynamics and Control of Severe Acute Respiratory Syndrome
Revised 4 June 2003 for *Science*

1. Estimation of *R*: Deterministic. In the main text (Fig. 2), we estimated R from the mean serial interval V and the exponential growth rate of the cumulative number of cases in the epidemic $\lambda(t) = \dfrac{\ln(Y(t))}{t}$ using the formula $R = 1 + V\lambda + f(1-f)(V\lambda)^2$, where f is the ratio of the infectious period to the serial interval. For clarity in Fig. 2 we used a single value of f=0.7 (equivalent to f=0.3). This formula, a generalization of the more commonly used formula $R = 1 + V\lambda$ (*10*) from the SIR model, is obtained by linearizing the SEIR model (*11*) by assuming no depletion of susceptibles, and obtaining the larger eigenvalue of the linearized system $\begin{pmatrix} \dot{E} \\ \dot{I} \end{pmatrix} = \begin{pmatrix} -1/L & R/D \\ 1/L & 1/D \end{pmatrix}\begin{pmatrix} E \\ I \end{pmatrix}$ where E and I are the number of infected but not yet infectious and infectious persons respectively, L is the duration of the latent period, D is the duration of the infectious period, and the mean serial interval is the sum of the mean infectious and mean latent periods, $V=L+D$. R is the reproductive number. This eigenvalue can be rewritten as

$\lambda = \dfrac{-1 + \sqrt{(1-2f)^2 + 4f(1-f)R}}{2Vf(1-f)}$, where f=D/V is the ratio of the infectious period to the serial interval. The formula for R above is given by rearranging this equation.

Under this equation, the particular second-order dependence of the estimate of R on the relative contributions of latent and infectious period depends on the exponentially distributed sojourn times assumed in the simple, deterministic *SEIR* model. Fig. S1 below shows that the correction factor is relatively unimportant except for large Rs and long serial intervals.
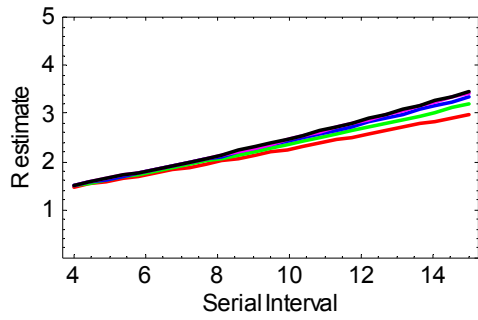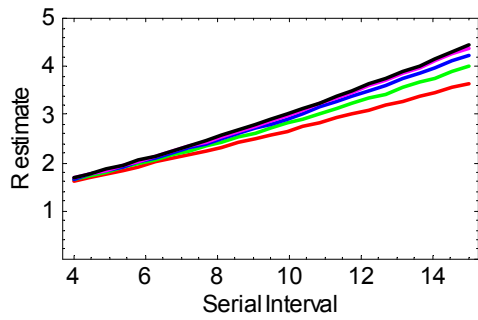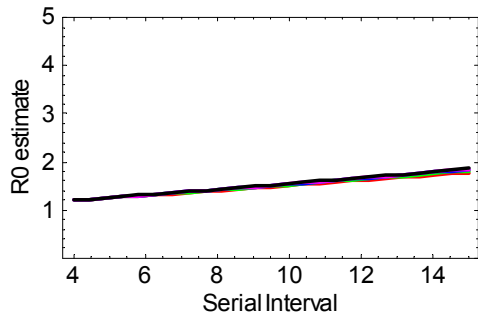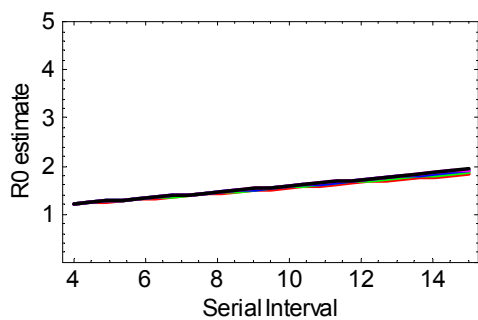
FIGURE S1: Sensitivity of deterministic estimates of R to varying values of f, the ratio of the infectious period to the serial interval. Dependence is on the product $f(1-f)$; hence the results are symmetric. Values of f range from 0 or 1 (red) to 0.5 (black). (a) $Y(t)=1358$ cases at $t=63$ days; (b) $Y(t)=425$ cases at $t=41$ days; (c) $Y(t)=7919$ cases at $t=185$ days; (d) $Y(t)=15,000$ cases at $t=185$ days.

2. Transmission model for the effect of quarantine

The model depicted in Fig. 5 consists of the following ordinary differential equations.

$$dS/dt = -kbI_U X/N_0 + r_Q S_Q$$
$$dS_Q/dt = qk(1-b)I_U S/N_0 - r_Q S_Q$$
$$dE/dt = -pE + kb(1-q)I_U S/N_0$$
$$dE_Q/dt = qkbI_U S/N_0 - pE_Q$$
$$dI_U/dt = pE - (v+m+w)I_U$$
$$dI_D/dt = w(I_U + I_Q) - (v+m)I_D$$
$$dI_Q/dt = pE_Q - (v+m+w)I_Q$$
$$dR/dt = v(I_U + I_D + I_Q)$$
$$d(dead)/dt = m(I_U + I_D + I_Q)$$

The model is a modification of the standard SEIR model ([10]), tracking susceptible, infected but not yet infectious, infectious, and recovered/immune individuals in compartments S, E, I and R respectively. At time $t=0$, there are N_0 people in the population, of whom one is exposed but not yet infectious (E), and all the rest are susceptible (S). In our model, the I compartment is composed of cases who are not yet isolated (I_U) and those who have been isolated (I_D). k is the baseline daily number of contacts per capita, and b is the probability of transmission per contact between a susceptible and an infectious person. We have separated the parameters k and b, rather than use the more conventional composite transmission parameter, β. We thus assume that each infectious person makes k contacts per day, of whom a proportion b are infected if the infectious person is undetected. The number of actual contacts per day is assumed to be linearly related to the population size (standard for models of directly transmitted infectious diseases); hence, N_0 appears in the denominator of the transmission term. $1/p$ is the mean time for progression from latently infected to infectious. v is the per capita recovery rate, m the per capita death rate, and w the mean daily rate at which infectious cases (who are not in quarantine) are detected and isolated. We make the simplifying assumption that isolated cases (I_D) do not infect anyone; clearly this is an optimistic assumption, and the rate of isolation w should be thought of as a rate of "effective" isolation. Under these assumptions, the mean duration of infectiousness is $1/(v+m+w)$.

We model quarantine as follows. A fraction q of all persons infected by an infectious person are successfully quarantined, moving to E_Q. A fraction q of all persons contacted but not infected by an infectious person are also quarantined, moving to S_Q.

These assumptions involve several simplifications. We make the simplification that for each infectious case, the fraction of uninfected contacts who are quarantined is the same as the fraction of infected contacts who are quarantined before they become infectious; both are given by q. In actuality, for each infectious case, the fraction of infected contacts quarantined before becoming infectious will be determined by the fraction of

contacts who can be traced and by the fraction of those who are still in the latent phase (not yet infectious) at the time they are traced. This may be best seen by an example. Suppose a particular infectious individual has 60 contacts, and 4 of these 50 are infected. Further, suppose that authorities are able to track down 75% of the individual's contacts; then we expect they will find (on average) 45 contacts, 42 uninfected and 3 infected. Of the infected ones, some will be found too late as they are already infectious. Thus, the fraction of susceptible contacts quarantined will be 75%, but the fraction of infected contacts quarantined before they are infectious will be less than that. By defining q as the fraction of infected contacts quarantined before they become infectious, and assuming the same fraction of noninfected contacts of infectious persons are quarantined, we are underestimating the total number of noninfected persons quarantined. We also assume that if a latently infected person is quarantined, s/he will not transmit infection to others in quarantine, and will be detected before infecting anyone else: thus, rather than a duration of infectiousness of $1/(v+m+w)$, a quarantined person has zero duration of infectiousness. Like our assumptions about isolation, this is clearly optimistic, and q should be thought of as an "effective" proportion: the proportion of contacts of cases effectively quarantined fast enough and with adequate detection so that if they become infectious, they are isolated before they can transmit. We assume that susceptible (non-infected) contacts remain quarantined for an average of $1/r_Q$ days.

In the absence of quarantine, the reproductive number for this model is given by:

$R = \dfrac{kb}{v+m+w}$. The effect of quarantining a fraction q of contacts of infectious persons is to multiply this expression by (1-q).

Parameter values for this simulation are given below in Table S1.

| Parameter	Symbol	Baseline Value	Range Tested	Reference
Reproductive number	R	3.0		main text
Contact rate	k	10 per day	5 – 20 per day	unknown
Average time of progression from latent infection to infectious	$1/p$	5 days		(1)
Average duration of infectiousness	$1/(w+m+v)$	5 days	1-5 days	(1)
Duration of quarantine	$1/r_q$	10 days		WHO recommendation

Table S1. Parameters used in the quarantine simulations

3. Sensitivity of person-days in quarantine to assumed number of daily contacts _k_.

One model parameter that is largely unknown is the average number of daily contacts made by an individual, k. Our estimate of R depends only on the product of this number and the probability of transmission per contact, β. However, the logistics of quarantine depends on the separate values of these parameters because the daily number of contacts quarantined for each infectious person is equal to $q\,k$, the proportion of contacts quarantied times the daily number of contacts. Thus we expect that the number of person-days in quarantine will be approximately linearly related to k for a given q and a given R_0, though not exactly so because larger values of k result in more susceptible persons quarantined, thereby slightly reducing transmission. This is borne out by simulations with varying values of k shown below in Fig. S2. Because k is unknown, the actual numbers in Fig. 6b and Fig. S2 should be seen as illustrative. However, the key point is that if an epidemic with an R of 3 is allowed to proceed in a population, even under the relatively modest assumption that an individual has 25 contacts during a 5 day infectious period, enormous numbers of people would be quarantined unless the quarantine, combined with isolation measures, were effective enough to check the spread of the epidemic.

k=5

k=20
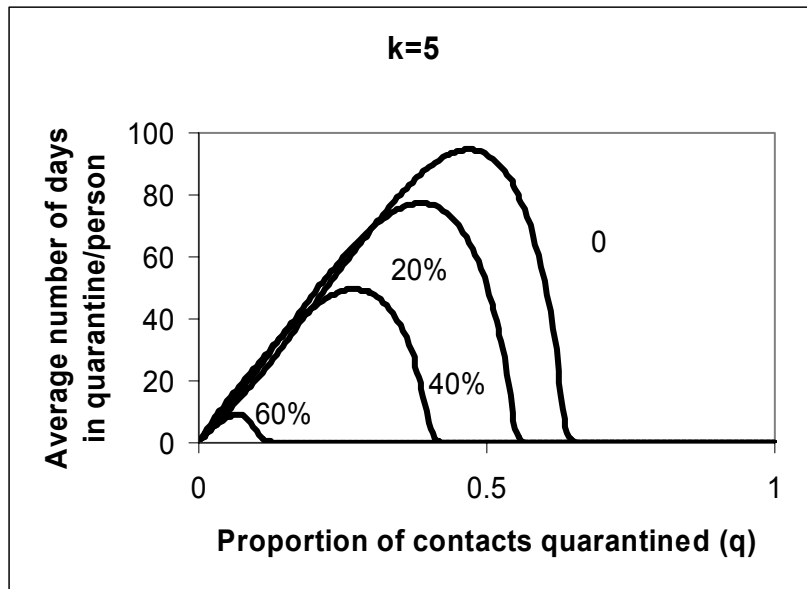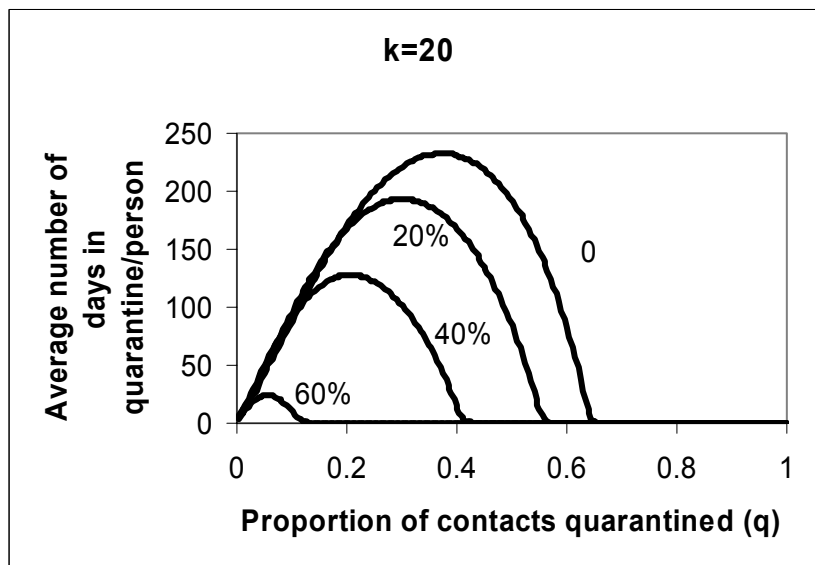
FIGURE S2: Sensitivity of average days in quarantine to the number of daily contacts assumed per infectious person: (a) $k=5$; (b): $k=20$. These figures correspond to Fig. 6b in the main text, for which it is assumed $k=10$.