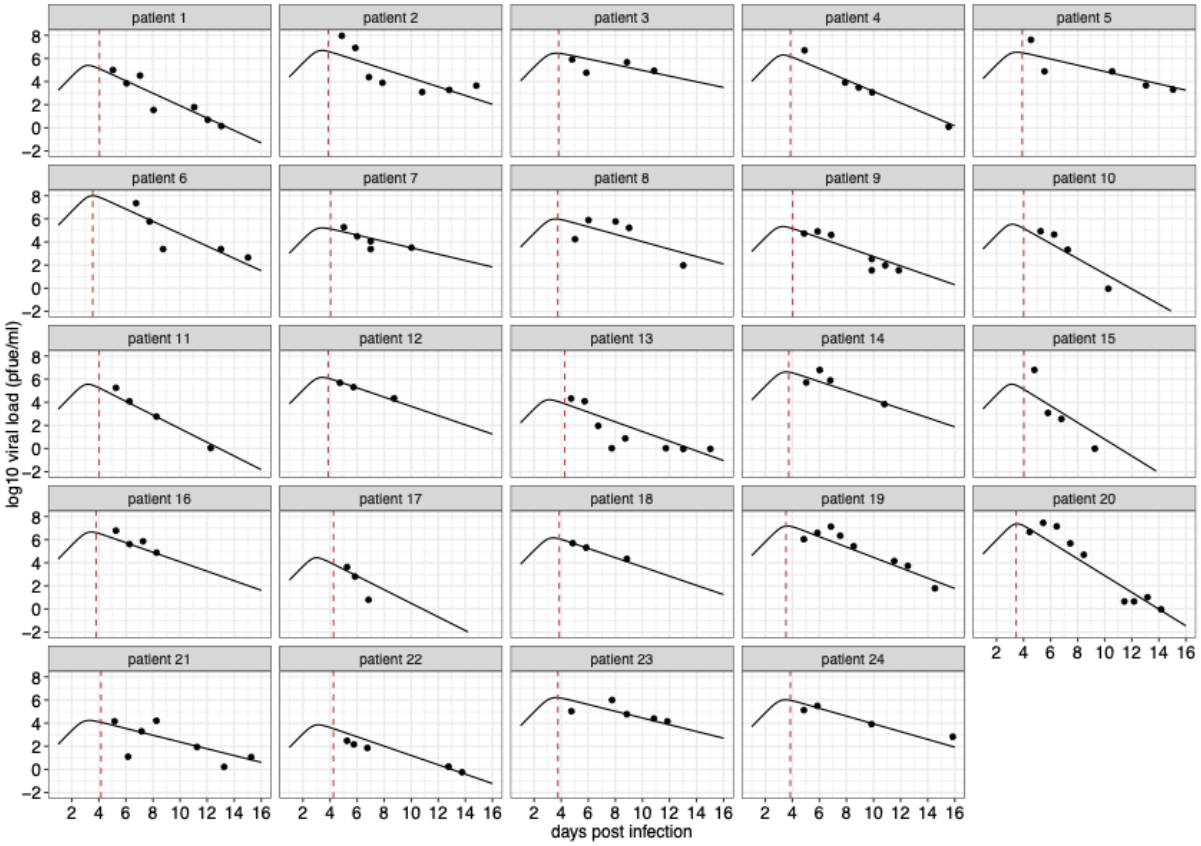
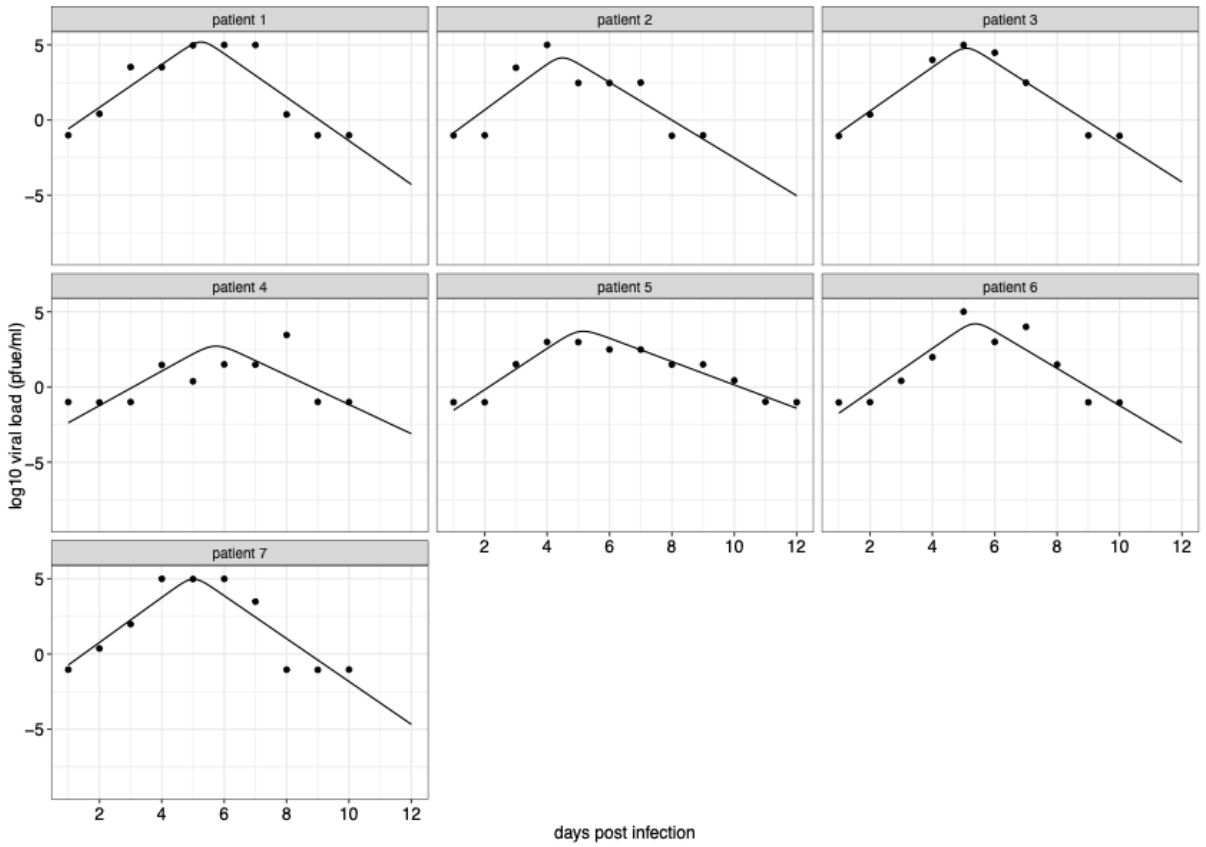
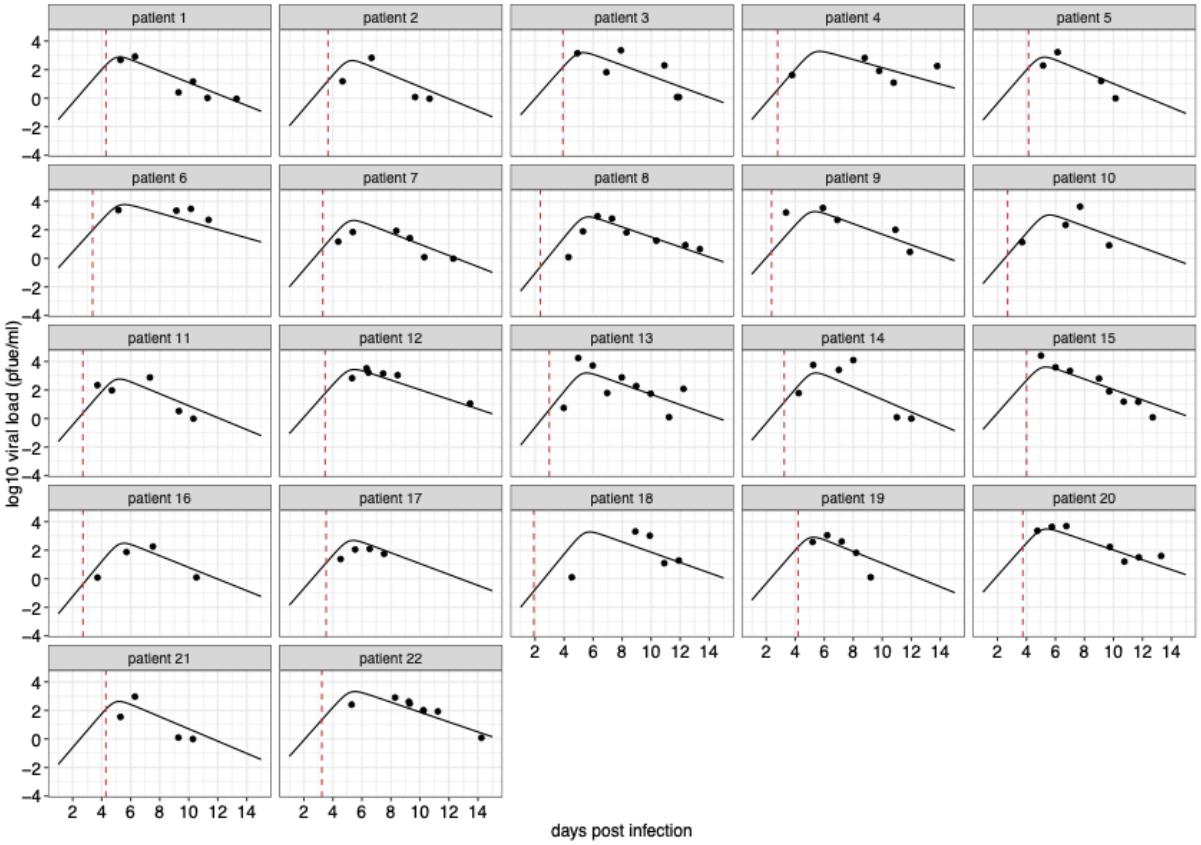
Supplementary Figures



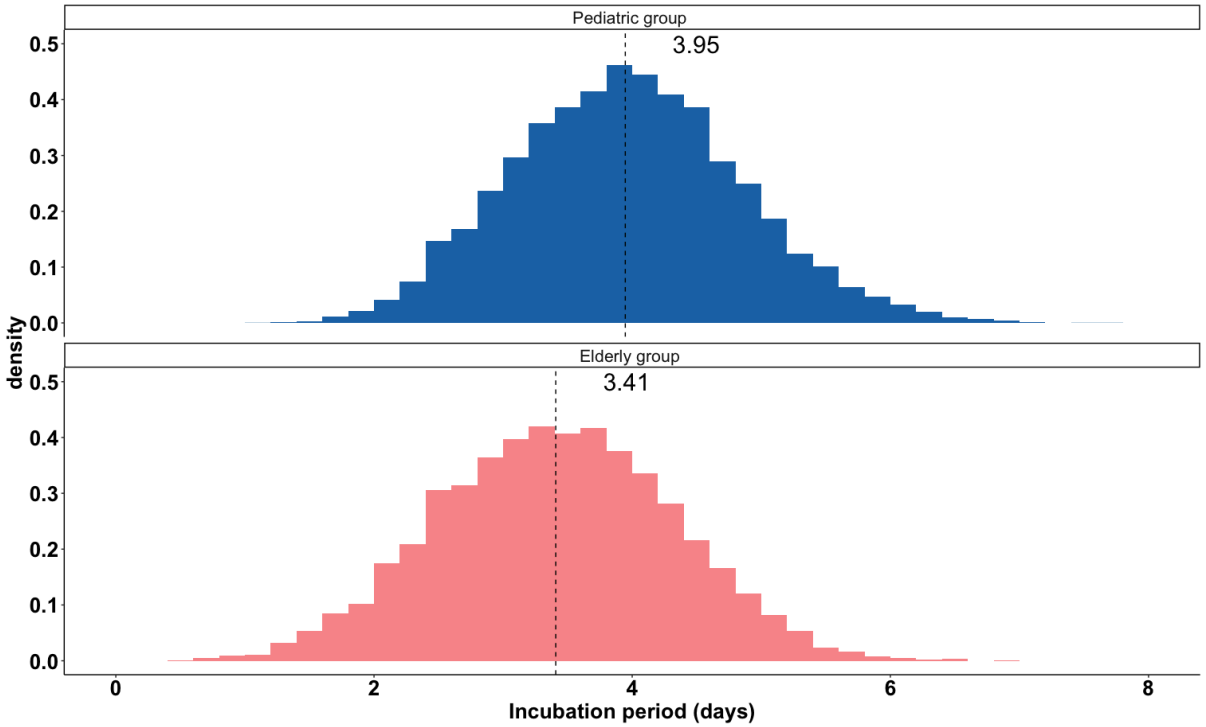
Supplements Figure 1 Model fits to viral kinetic data of RSV infections in the pediatric group. Data are presented with solid circles, and solid lines are median predictions of viral load. The dashed red lines indicate the median estimates of the time of symptom onset. Note that the median predictions of viral load are calculated using estimated parameters for each individual. Viral load data of patient 1-16 were from [14], and the data of patient 17-24 were from [13].



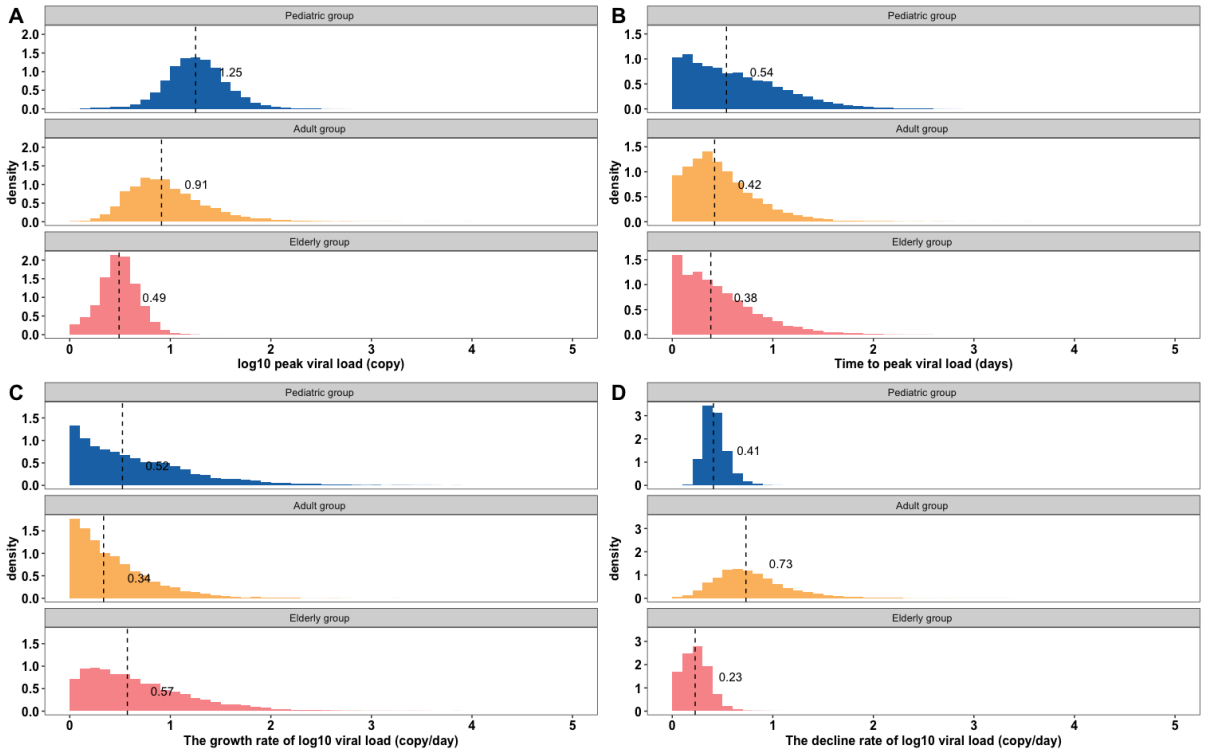
Supplements Figure 2 Model fits to viral kinetic data of RSV infections in the adult group. Data are presented with solid circles, and solid lines are median predictions of viral load. Note that the median predictions of viral load are calculated using estimated parameters for each individual.



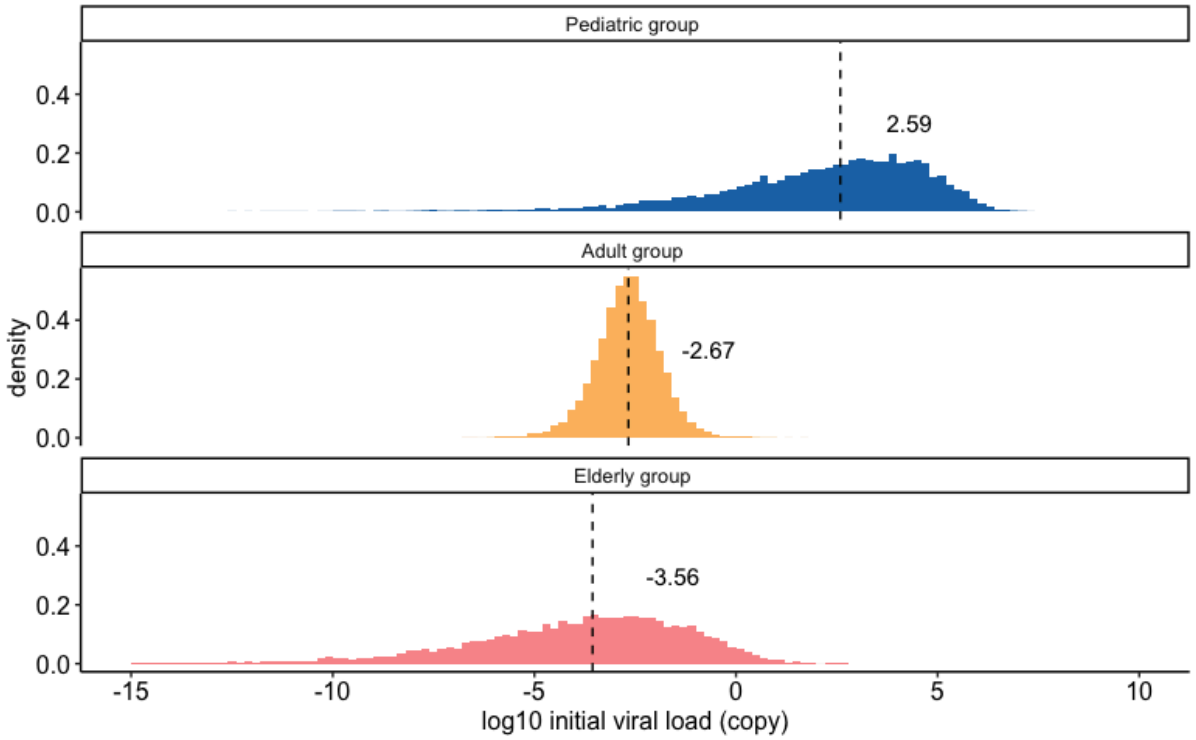
Supplements Figure 3 Model fits to viral kinetic data of RSV infections in the elderly group. Data are presented with solid circles, and solid lines are median predictions of viral load. The dashed red lines indicate the median estimates of the time of symptom onset. Note that the median predictions of viral load are calculated using estimated parameters for each individual.



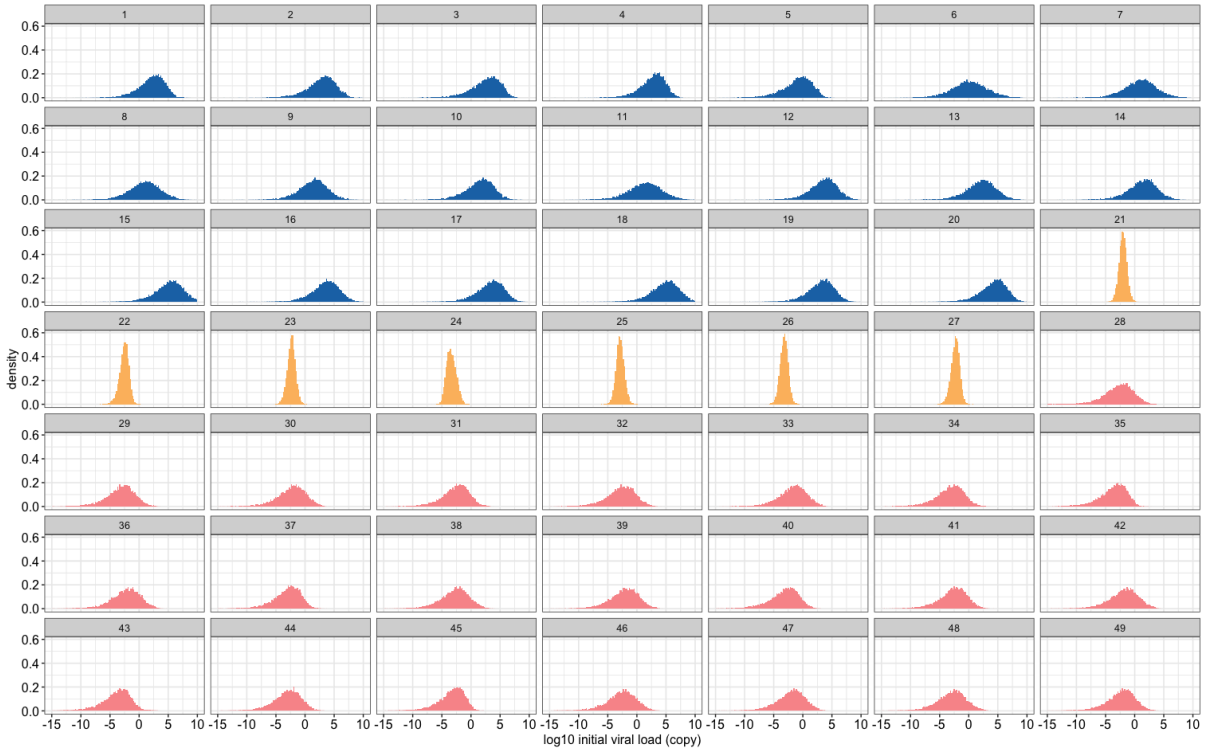
Supplements Figure 4 Posteriors distributions of incubation periods. 12,500 samples are drawn from the posterior distributions of incubation periods for the pediatric group (the upper panel) and the elderly group (the lower panel). Dashed lines indicate the median estimates.



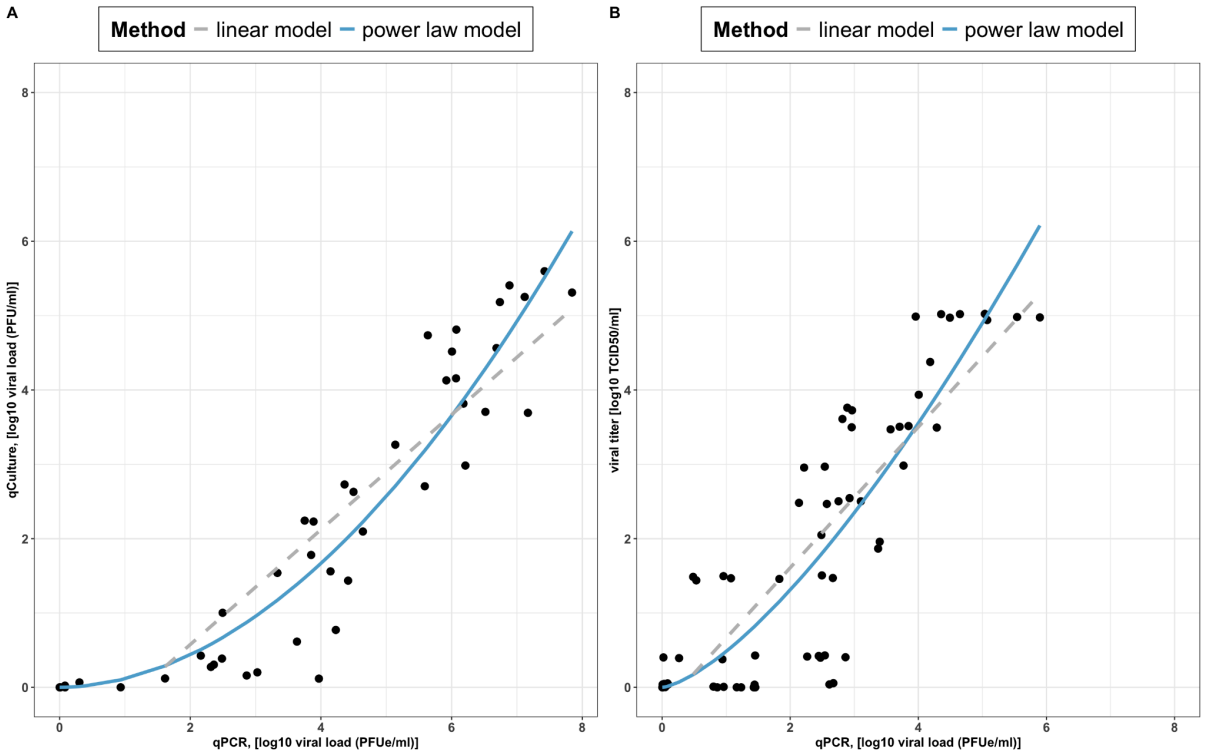
Supplements Figure 5 Posterior distributions showing the level of uncertainty (posterior standard deviations) of estimated model parameters. 12,500 samples are drawn from the posterior distributions of **(A)** peak viral load, **(B)** time to peak viral load, **(C)** the growth rate of viral load, and **(D)** the decline rate of viral load in the three age groups. Dashed lines indicated the median value of the posterior distributions.



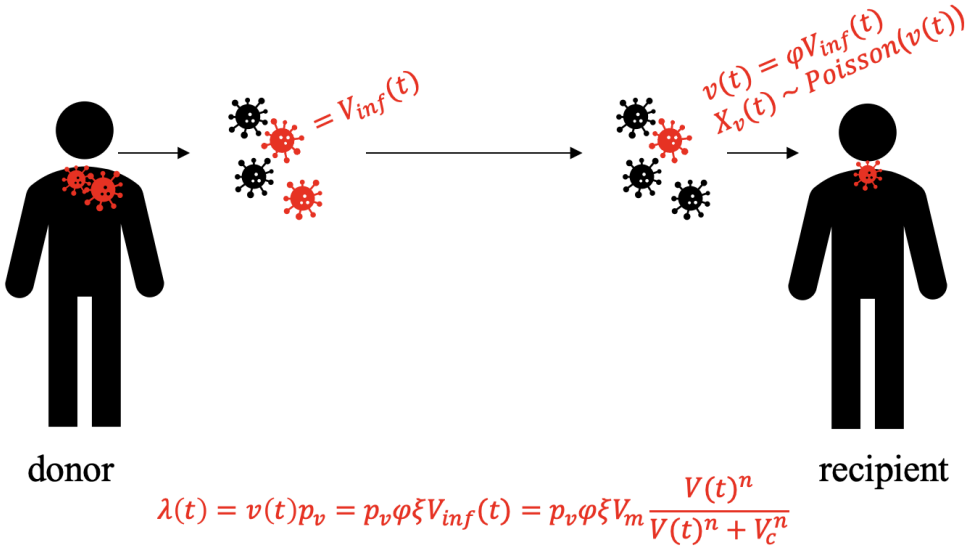
Supplements Figure 6 Distributions of initial viral load based on the population-level parameters. 12,500 samples are drawn from the posterior distributions to calculate the initial viral load for the pediatric group (the upper panel), the adult group (middle panel), and the elderly group (the lower panel). Dashed lines indicate the median estimates.



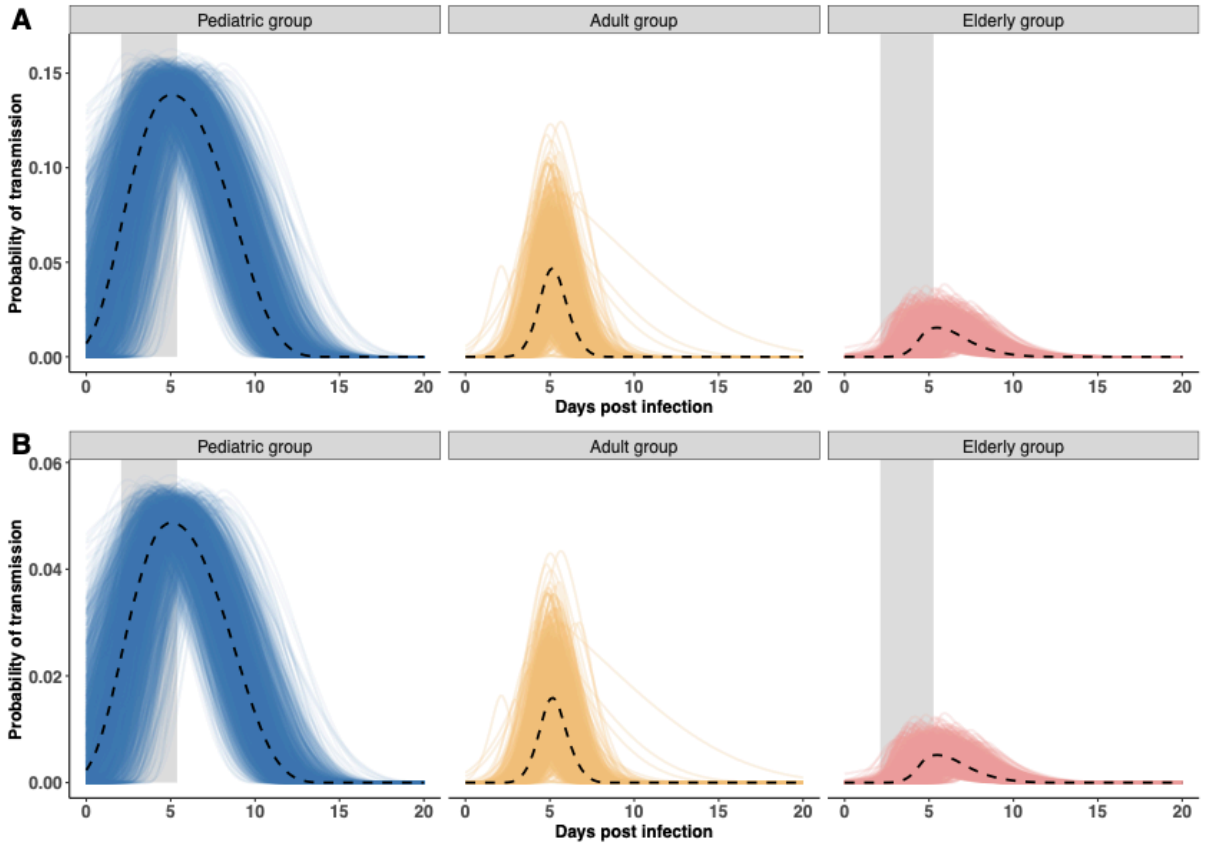
Supplements Figure 7 Distributions of initial viral load based on individual-level posteriors. 12,500 samples are drawn from the posterior distributions to calculate the initial viral load for the pediatric group (blue), the adult group (yellow), and the elderly group (red).



Supplements Figure 8 Characterization of total viral load with cell culture infectivity and transmission probability. (A-B) The model fits of using linear (in a form of $qCulture(t) = a + bV(t)$, where $V(t)$ is viral laid measured by qPCR) or power-law models ($qCulture(t) = cV^h(t)$) to the viral loads measured by qPCR (horizontal axis) and cell culture (vertical axis) are based on the data from DeVincenzo et al. ($a = -0.97,\ b = 0.77,\ c = 0.11, h = 1.93$) and Falsey et al. ($a = -0.28,\ b = 0.95,\ c = 0.48, h = 1.43$), respectively.



Supplements Figure 9 Illustrative model for transmission probability. To estimate the likelihood of transmission during a short contact duration τ, we assumed the total number of infectious viruses at time t is $V_{inf}(t)$, and a proportion (φ) of of the viruses are transmitted to the recipient, such that $v(t) = \varphi V_{inf}(t)$. We also assumed that the number of infectious viruses reaching the recipient during a contact at time t is a random variable $X_v(t)$ that is Poisson distributed with the parameter $v(t)$. We further assumed that each infectious virus has a probability p_v to establish infection in a recipient. Since X_v follows a Poisson distribution, we can show that the distribution of the number of viruses that successfully establish an infection follows a Poisson distribution with parameter $\lambda = v(t)p_v = \varphi p_v \xi V_{inf}(t) = p_v \xi \varphi f(V(t))$, where f is a saturation function characterizing the relationship between total viral load and infectious viral load. The parameter ξ is a parameter that accounts for the number of infectious particles derived from the measured viral concentration (i.e., PFU/ml). We assumed the proportion $\varphi = 1$ in our analysis.



Supplements Figure 10 Probability of transmission in different age groups. 12,500 population-level samples are drawn from the posterior distribution to calculate the probability of transmission as time-series in different age groups, given the median estimates of infection probability from the household transmission studies **(A)** [20] and **(B)** [18]. Dashed lines indicate the median trajectory, and shaded areas indicate estimated incubation period in the pediatric and elderly group.