Supplementary Information

A. Model dynamics. (HG*).

theoremf $I_0 > 0$ or $A_0 > 0$, then the pathogen (within-the host) eventually clears ($\lim_{\tau\to\infty} P(\tau) = 0$), and subsequently the innate immune response antibodies decay and the adaptive immune response antibodies increase to a steady-state, respectively; i.e. $\lim_{\tau\to\infty} I(\tau) = \Lambda/d$ and $\lim_{\tau\to\infty} A(\tau) = A^+$, where $A^+ > 0$ depends on the initial condition; i.e. $A^+ = z(P_0, I_0, A_0)$.

Proof. Let $P_0 > 0$. By the second equation in (**??**), we obtain

$$P(\tau) \leq P_0 e^{\int_0^\tau [r-\delta A(\tau)]ds}. \qquad [1]$$

Without loss of generality, assume that $I_0 > 0$. Then $\exists \tilde{\tau} : A'(\tau) \geq 0$ for all $\tau \geq \tilde{\tau}$. Therefore $A(\tau)$ increases for all $\tau \geq \tilde{\tau}$.

Case (i) Assume $A(\tilde{\tau}) > \frac{r}{\delta}$. Then, we obtain $A(\tau) > \frac{r}{\delta}$, for all $\tau > \tilde{\tau}$. Therefore as $\tau \to \infty$, the RHS of the inequality (1) goes to zero. Then by comparison principle, we obtain $\lim_{\tau\to\infty} P(\tau) = 0$. Thus $\lim_{\tau\to\infty} I(\tau) = \Lambda/d$. Then $A(\tau)$ saturates as $\tau \to \infty$; i.e $\lim_{\tau\to\infty} A(\tau) = \bar{A}$, for some $\bar{A} > 0$, depending on the initial condition (P_0, I_0, A_0).

Case (ii)Now suppose that $A(\tilde{\tau}) < \frac{r}{\delta}$. Assume that there exists $\hat{\tau}$: $P(\hat{\tau}) = 0$. Then we obtain that $P(\tau) = 0$, for all $\tau > \hat{\tau}$ and $\lim_{\tau\to\infty} I(\tau) = \Lambda/d$ and $\lim_{\tau\to\infty} A(\tau) = \bar{A}$, for some $\bar{A} > 0$. Now assume that $P(\tau) > 0$, for all $\tau > 0$. Then $A'(\tau) > 0$, for all $\tau > 0$. Hence there exists $\tau^+ > 0 :\ A(\tau^+) > \frac{r}{\delta}$. The rest of the proof follows the argument in case (i), completing the proof. □

B. Model Fitting (CM, HG). In this section we denote pathogen data for host j as $X_P^{(j)}$ and the data for host j collectively as $\mathbf{X}_j$. All program files and data generated by the fitting process are available on GitHub and are archived together in citeable format in the Zenodo repository (done upon submission). Data was collected for *contact infected hosts* on infection days $\tau = \{0, 2, 4, 6, 9, 12, 28\}$ and for *needle infected hosts* on infection days $\tau = \{0, 2, 4, 6, 8, 11, 14, 30\}$. For our data fitting we first obtain initial estimates for *initial viral load*, P_0, and *viral growth rate*, r, assuming a simple exponential growth model up to time τ^*:

$$P(\tau) = P_0 e^{\tilde{r}\tau} \qquad \tau \leq \tau^*_{i,j}, \qquad [2]$$

where $\tilde{r}$ is the net viral growth rate (in presence of innate immune response). There are two implicit biological assumptions inherent to this fitting. First, that since the innate immune response is always present estimating r is this way will account for killing of the pathogen by the innate response (thus providing a lower bound for r), and second that prior to the presence of sufficient adaptive immune response pathogen growth will be exponential (instead of logistic). The second is a common assumption in the literature when estimating viral growth rates (**? ?**). This estimate of P_0 was retained and fixed, while this estimate for viral growth rate was used for a lower bound and initial estimate for viral growth rate when simultaneously fit with other model parameters when we consider the following immunological model (obtained by setting $\theta, a = 0$):

$$\begin{cases} \dfrac{dI}{d\tau} = \Lambda + \dfrac{kP(\tau)}{\gamma + P(\tau)} I(\tau) - dI(\tau) \\ \dfrac{dP}{d\tau} = \left[r\left(1 - \dfrac{P(\tau)}{K}\right) - \delta A(\tau) \right] P(\tau), \\ \dfrac{dA}{d\tau} = bA(\tau)P(\tau), \end{cases} \qquad [3]$$

This simplification is numerically justified in that when fit these quantities were approximately $\mathcal{O}(1 \times 10^{-10})$ (see program files on GitHub). The following parameters were fixed: *innate response maintenance level*, $\Lambda = d \cdot \min_\tau X_I$, and $d = 1/11.18$ $days^{-1}$, $d = 1/21.23$ $days^{-1}$ when using SAA and Haptoglobin as measures of innate immunity. For BKA data d was fit separately to an exponential decay curve for each individual host, and in across all measures of innate immune response remaining parameters in Eqn. Eq. (3) were fit.

For each measurement of innate response considered (SAA, Haptoglobin, and BKA) we take m (viral load and adaptive response data, as described in section, and either SAA, Haptoglobin, or BKA data as appropriate) time-series

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for host j: $\left\{\left(\tau_{i,k}^{(j)}, X_{i,k}^{(j)}\right)\right\}_{i=0}^{N_{j,k}}$, $1 \leq k \leq m$, $1 \leq j \leq 23$ and model Eq. (3):

$$\begin{cases} \frac{d\mathbf{u}}{d\tau} = f(\tau, \mathbf{u}(\tau, \mathbf{p})) & \mathbf{u}(\tau) \in \mathbb{R}_+^n, \mathbf{p} \in \mathcal{D} \subseteq \mathbb{R}_+^\ell \\ \mathbf{u}(0) = \mathbf{u}_0 \in \mathbb{R}_+^n \end{cases} \quad [4]$$

where $\mathcal{D}$ is the parameter space. Define

$$\begin{aligned} \mathbf{X_j} &:= \left[X_{0,1}^{(j)}, \ldots, X_{N_{j,1},1}^{(j)}, \ldots, X_{0,m}^{(j)}, \ldots, X_{N_{j,m},m}^{(j)}\right] \in \mathbb{R}_+ \times \mathbb{R}_+^{(M_j+1)} \\ \mathbf{u}_j &:= \left[u_{0,1}^{(j)}, \ldots, u_{N_{j,1},1}^{(j)}, \ldots, u_{0,m}^{(j)}, \ldots, u_{N_{j,m},m}^{(j)}\right] \in \mathbb{R}_+ \times \mathbb{R}_+^{(M_j+1)} \end{aligned} \quad [5]$$

We seek to find $\hat{\mathbf{p}} \in \mathcal{D}$ such that for

$$S_j(\mathbf{p}) = \sum_{s=0}^{M_j} \left[w_s(\mathbf{X}_j^{(s)} - \mathbf{u}_j^{(s)}(\tau, \mathbf{p}))\right]^2 \quad [6]$$

$$S_j(\mathbf{p}) \geq S_j(\hat{\mathbf{p}}) \quad [7]$$

for all $\mathbf{p} \in \mathcal{D}$.

To obtain these fit parameter point estimates we numerically solve these two non-linear least squares problems in sequence using the interior-reflexive Newton method as implemented by MatLab's lsqcurvefit function,

where

$$w_s = \begin{cases} \left[\max_\tau X_I^{(j)}\right]^{-1} & 0 \leq s \leq N_{j,1} \\ \left[\max_\tau X_P^{(j)}\right]^{-1} & N_{j,1} + 1 \leq s \leq \sum_{k=1}^2 N_{j,k} \\ \left[\max_\tau X_A^{(j)}\right]^{-1} & \left(\sum_{k=1}^2 N_{j,k}\right) + 1 \leq s \leq \sum_{k=1}^3 N_{j,k} \end{cases} \quad [8]$$

for BKA data and $w_s = 1$ when fitting $\log_{10}$ of SAA and Haptoglobin data, in order to account for the different scales of the data. We were unable to obtain quality fits for BKA data (see program files on GitHub) and use fits obtained from SAA and Haptoglobin as measures of innate response for comparative analysis across route of infection, individual host variation, and sample mean parameter values and related quantities.

C. Practical Identifiability Analysis and Uncertainty Quantification. (CM*, HG). Code to generate data-sets and generate all figures and statistical analyses is available on GitHub and is archived in citeable format in Zenodo repository. In order to assess identifiability, confidence in our fitting procedure, and differences in both sample mean and standard deviation *across innate response measurement and across serotype* we conducted uncertainty analysis. This analysis was carried out in the following manner (see (**?**) for detailed review of identifiability analysis for non-linear ODE models). Under the assumption that the measurement error is independently and normally distributed with variation relative in magnitude to the measured total at each data point, $X_{i,k}^{(j)}$:

$$X_{i,k}^{(j)} = g(u_{i,k}^{(j)}, \hat{\mathbf{p}}) + \epsilon_i^{(j)} \qquad \epsilon_i^{(j)} \sim n(0, X_{i,k}^{(j)} \cdot s^2),$$

where g is the true set of values at each time and $\hat{\mathbf{p}}$ the set of true parameter values, generate M data sets (M = $40,000$ for SAT 1 & SAT 2, $M = 30,000$ for SAT 3, *contact infected hosts* , $M = 40,000$ for all serotypes with *needle infected hosts* $M = 10,000$ for individual hosts as well as sample mean and sample standard deviation, calculated for each block of 3 or 4 generated data-sets at each iteration). The model was then refit to each of these generated data-sets. The results of this analysis both indicate that the key model parameters and associated quantities are all practically identifiable assuming the 40% noise level in measurement error as indicated by average relative error (ARE) for all parameters, p_ξ, $1 \leq \xi \leq \ell$,

$$ARE_\xi = \left[\frac{100}{M} \sum_{j=1}^{M} \frac{|p_\xi^{(j)} - \hat{p}_\xi|}{\hat{p}_\xi}\right] \leq 40\%. \quad [9]$$

(see figure and tables (add refs))

1. for both SAA and Haptoglobin data fit model Eq. (3), as described above for each host

DRAFT

2. under the assumption that the measurement error is independently and normally distributed with variation relative in magnitude to the measured total at each data point, $X_{i,k}^{(j)}$:

$$X_{i,k}^{(j)} = g(u_{i,k}^{(j)}, \hat{\mathbf{p}}) + \epsilon_i^{(j)} \qquad \epsilon_i^{(j)} \sim n(0, X_{i,k}^{(j)} \cdot s^2),$$

   where g is the true set of values at each time and $\hat{\mathbf{p}}$ the set of true parameter values, generate M data sets (M = $40,000$ for SAT 1 & SAT 2, $M = 30,000$ for SAT 3, *contact infected hosts* , $M = 40,000$ for all serotypes with *needle infected hosts* $M = 10,000$ for individual hosts as well as sample mean and sample standard deviation, calculated for each block of 3 or 4 generated data-sets at each iteration)

3. refit the model to each of these blocks of simulated host data allowing us to generate interval estimates for sample mean parameter values by serotype as well interval estimates for fit parameters of each host

4. Arrange the generated values in increasing order and remove the top and bottom 2.5% in order to obtain the desired approximate 95% confidence intervals.

5. If average relative error (ARE) for all parameters, p_ξ, $1 \leq \xi \leq \ell$,

$$ARE_\xi = \left[\frac{100}{M} \sum_{j=1}^{M} \frac{|p_\xi^{(j)} - \hat{p}_\xi|}{\hat{p}_\xi} \right] \%, \qquad [10]$$

   is less or close to introduced noise level conclude that parameters are practically identifiable

6. to asses robustness of results across measures of innate response and compare across sereotypes and individual hosts conduct both paired sample analysis between measures of innate response and analysis of variance both within host and within serotype.

7. fit log normal distribution to relative frequency histograms of all fit model parameters for each host

8. generate summary figures [ref figures and tables]

The results of this analysis both indicate that the key model parameters and associated quantities such as means, standard deviations, peak and cumulative viral load are all practically identifiable assuming the 40% noise level in measurement error (see figures and tables). and have biological implications. We discuss these implications in the results section.

D. Effect of route of infection on within-host viral and immune dynamics. There is significant difference in viral and immune dynamic parameters between needle and contact infected hosts within serotype (see supplementary table S12). The strain of SAT1 used has the least differentiation between these routes of infection with only two parameters differing. For these hosts needle infected individuals had greater sample mean adaptive clearance rate than contact infected hosts [1.85 vs. 2.72 *95% confidence intervals* 1.6758-2.0546 vs. 2.5052-2.9291]. This difference may attributable to their initial viral loads [0.009 vs 0.016 *CI* 0.0076-0.0095 for contact infected vs. 0.0138-0.0181 for needle infected]. Among all three serotypes viral carrying capacity in absence of adaptive response, model parameter K, and maximum viral load (as calculated from time trajectory) were not greatly affected by route of transmission. While distinguishable from one another SAT1 carrying capacity [6.80 vs 9.23, *CIs* 5.8326-7.7683 contact vs 7.8492-10.3055 needle] remained relatively similar across route of infection. SAT2 and SAT3 in turn were not distinct across route of infection with sample means [5.70, *CIs* 4.6555-6.8801 contact vs 6.26, 5.4082-7.2638 needle SAT2; 8.93, 7.768-10.4041 contact vs. 7.30, 6.0295-8.6165 SAT3]. All other model parameters show significant difference across transmission route. Differences in viral and immune dynamic parameters among serotypes are less detectable in needle infected hosts (see Supplementary Figures S6 and S7, S13 and Supplementary Table Table S2). All viral and immune parameters varied among serotypes in contact infected hosts except initial innate response, as expected, since this quantity is the level of innate immune markers present in the buffalo *at time of* initial exposure to any virus (see figure **??**, Supplementary table S1) For needle infected hosts, differences among serotypes remain detectable for viral carrying capacity, K, maximum viral load, EAR, cumulative viral load, and adaptive activation and clearance rates. However these detected differences do not always line up with those detected in contact infected buffalo (see supplementary figures S6-S7). Because of these differences in viral and immune dynamics between needle and contact infected hosts, we focus on contact infected hosts only for the remainder of this work.

Serotypes 1,2 and 3 displayed contrasting life histories in contact infected hosts. SAT1 has the lowest infectious dose and so high transmissibility, but attains its maximum load rapidly [3.69 (*CI* 3.4335-3.8525) *days*] due to a high

DRAFT

viral growth rate [3.48 *CI* 3.2654-4.0188]. SAT2 has a similarly low initial viral load to SAT1 [0.01, *CI* 0.00868-0.0114]. Its viral growth rate [2.23, *CI* 2.084-2.4007], and time until max viral load [4.58, *CI* 4.39-4.79 *days*] are intermediate compared to the other two strains. SAT3 in contrast has a much higher infectious dose, and so lower transmissibility [0.015, *CI* 0.0123-0.0172] (see figure **??**). Despite this, it attains its maximum viral load more slowly than SAT1 [6.24 *CI* 6.0467-6.5833 *days*], due to a lower viral growth rate [1.47, *CI* 1.3725-1.5676].

Table S1. Point estimates and confidence intervals for differences between sample means and sample means, *contact infected* hosts using *haptoglobin* as measure of innate immune response. Asterisk indicates difference between means is statistically significant

Feature	SAT1-SAT2	SAT1-SAT3	SAT2-SAT3
Difference			
Initial viral load	-0.002, (-0.003, 0.0001)	-0.006, (-0.009, -0.004)*	-0.005, (-0.008, -0.002)*
Viral growth rte	1.25, (0.96, 1.82)*	2.00, (1.76, 2.56)*	0.76, (0.58, 0.96)*
Time to maximum viral load (days)	-0.89, (-1.21, -0.63)*	-2.55, (-2.90, -2.29)*	-1.66, (-1.97, -1.38)*
Viral carrying capacity	1.12, (-0.42, 2.57)	-2.12, (-3.93, -0.16)*	-3.25, (-5.09, -1.15)*
Max viral load	1.61, (0.33,2.85)*	-0.73, (-2.17,0.79)	-2.34, (-3.70,-0.89)*
EAR (%)	8.48, (3.97, 14.07)*	15.28, (8.30, 20.68)*	6.82, (-1.66, 14.05)
Cum. viral load	14.8, (11.1, 18.2)*	5.55, (1.17, 9.78)*	-9.22, (-12.98, -5.50)*
Initial innate response	0.23, (-0.27, 0.71)	-0.19, (-0.72, 0.35)	-0.42, (-0.92, 0.11)
Innate response activation rate	-0.041, (-0.084,0.002)	0.046, (0.009, 0.081)*	0.088, (0.045, 0.130)*
Adaptive response activation rate	-0.39, (-0.48,-0.30)*	-0.10, (-0.18,-0.03)*	0.29, (0.18, 0.40)*
Adaptive response clearance rate	-0.69, (-0.99, -0.35)*	-0.11, (-0.45, 0.27)	0.58, (0.19, 0.98)*
Feature	SAT1	SAT2	SAT3
Means			
Initial viral load	0.009, (0.008, 0.010)	0.010, (0.009, 0.011)	0.015 (0.012, 0.017)
viral growth rate	3.48, (3.27, 4.02)	2.23, (2.08, 2.40)	1.47, (1.37, 1.57)
Time to max. viral load (days)	3.69, (3.42, 3.85)	4.58, (4.39, 4.79)	6.24, (6.05, 6.58)
Viral carrying capacity	6.80, (5.83, 7.77)	5.70, (4.66, 6.88)	8.93, (7.77 ,10.40)
Max viral load	6.76, (5.80,7.71)	5.15, (4.38,5.99)	7.49, (6.30,8.58)
EAR (%)	-0.07, (-0.90, -0.50)	-9.18, (-14.78, -4.70)	-15.99, (-21.36, -8.99)
Cum. viral load.	28.96, (25.98, 31.92)	14.19, (12.43, 16.30)	23.41, (20.29, 26.70)
Initial innate response	2.62, (2.26, 2.98)	2.39, (2.06, 2.73)	2.81, (2.40, 3.19)
Innate response activation rate	0.114, (0.089, 0.141)	0.155, (0.123, 0.191)	0.068, (0.046, 0.095)
Adaptive response activation rate	0.33, (0.30, 0.37)	0.72, (0.64, 0.80)	0.43, (0.36, 0.50)
Adaptive response clearance rate	1.85, (1.68, 2.05)	2.53, (2.26, 2.77)	1.96, (1.63, 2.25)

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E. Supplementary Tables.

Table S2. Confidence Intervals for differences between means and means, both needle and contact infected hosts. Grey highlight indicates difference between means is not statistically significant

Feature	SAT1-SAT2	SAT1-SAT3	SAT2-SAT3	SAT1	SAT2	SAT3
Contact SAA						
Initial pathogen	(-0.0032,0.0001)	(-0.009,-0.0037)	(-0.0076,-0.002)	(0.0076,0.0095)	(0.0088,0.0115)	(0.0124,0.0173)
Viral growth rate	(0.9753,1.8143)	(1.7961,2.586)	(0.609,0.9652)	(3.2763,4.0313)	(2.0958,2.3911)	(1.3608,1.5476)
Time max viral (days)	(-1.2075,-0.65)	(-2.8475,-2.2825)	(-1.8833,-1.38)	(3.44,3.8775)	(4.4325,4.795)	(6.0733,6.4167)
Viral carry c.	(-0.3296,2.4358)	(-4.4299,-0.812)	(-5.5017,-1.8557)	(5.7893,7.7135)	(4.7584,6.7302)	(7.85,10.9611)
Max viral load	(0.3224,2.7388)	(-2.5236,0.3747)	(-3.9266,-1.2285)	(5.76,7.6598)	(4.4579,5.9535)	(6.6485,8.8655)
EAR (%)	(4.3395,12.7007)	(11.2493,21.7305)	(1.9077,14.9914)	(-0.8126,-0.4439)	(-13.3111,-4.968)	(-22.3551,-11.909)
Cum. viral load	(11.3065,18.2202)	(1.4398,9.7756)	(-12.6533,-5.6557)	(26.0487,31.9377)	(12.5051,16.1247)	(20.3386,26.3826)
Initial innate res.	(-0.2083,0.5129)	(-1.3548,-0.3231)	(-1.4959,-0.4776)	(1.6604,2.1931)	(1.5323,2.0236)	(2.3157,3.205)
Innate activation rate	(-0.0941,-0.0117)	(-0.0312,0.0481)	(0.0175,0.1045)	(0.1094,0.1618)	(0.1564,0.2209)	(0.0978,0.157)
Adaptive activation rate	(-0.4791,-0.3045)	(-0.1733,-0.0262)	(0.1941,0.3969)	(0.3081,0.38)	(0.6541,0.8135)	(0.3786,0.5045)
Adaptive clearance rate	(-0.9875,-0.3743)	(-0.5062,0.1759)	(0.1518,0.8844)	(1.7003,2.0795)	(2.3182,2.7917)	(1.7572,2.3226)
Contact Haptoglobin						
Initial pathogen	(-0.0032,0.0001)	(-0.0089,-0.0037)	(-0.0075,-0.002)	(0.0076,0.0095)	(0.0088,0.0114)	(0.0123,0.0172)
Viral growth rate	(0.9593,1.8184)	(1.7619,2.5605)	(0.5790,0.9555)	(3.2654,4.0188)	(2.084,2.4007)	(1.3725,1.5676)
Time max viral (days)	(-1.21,-0.63)	(-2.8950,-2.2875)	(-1.9683,-1.3800)	(3.4225,3.8525)	(4.39,4.79)	(6.0467,6.5833)
Viral carry c.	(-0.4178,2.5704)	(-3.9335,-0.1572)	(-5.0891,-1.1501)	(5.8326,7.7683)	(4.6555,6.8801)	(7.768,10.4041)
Max viral load	(0.3338,2.8468)	(-2.1712,0.7877)	(-3.7034,-0.8917)	(5.8005,7.706)	(4.3779,5.9867)	(6.2993,8.5833)
EAR (%)	(3.9728,14.0705)	(8.3001,20.6816)	(-1.6574,14.0495)	(-0.9043,-0.5049)	(-14.7802,-4.6959)	(-21.3619,-8.9929)
Cum. Viral load	(11.0961,18.2067)	(1.1690,9.7829)	(-12.9777,-5.4969)	(25.9838,31.923)	(12.4325,16.3)	(20.2886,26.7023)
Initial innate res.	(-0.2666,0.7146)	(-0.7160,0.3488)	(-0.9162,0.1115)	(2.2605,2.9779)	(2.0611,2.7313)	(2.4019,3.1890)
Innate activation rate	(-0.0838,0.0017)	(0.0086,0.0813)	(0.0452,0.1296)	(0.0888,0.1407)	(0.1225,0.1906)	(0.0455,0.0954)
Adaptive activation rate	(-0.48,-0.2994)	(-0.1799,-0.0258)	(0.1810,0.3960)	(0.2978,0.3678)	(0.6363,0.8028)	(0.3647,0.5036)
Adaptive clearance rate	(-0.9929,-0.3502)	(-0.4519,0.2667)	(0.1859,0.9752)	(1.6758,2.0546)	(2.259,2.7737)	(1.6347,2.2452)
Needle SAA						
Initial pathogen	(-0.0008,0.0047)	(-0.0004,0.0053)	(-0.002,0.003)	(0.0138,0.0181)	(0.0123,0.0157)	(0.0117,0.0153)
Viral growth rate	(-1.7057,0.6122)	(-1.0391,0.9726)	(-0.6347,1.6676)	(3.5869,4.9323)	(3.8624,5.6675)	(3.6557,5.0002)
Time max viral (days)	(-0.415,0.61)	(-0.255,0.58)	(-0.4125,0.5525)	(2.6175,3.2275)	(2.435,3.2375)	(2.485,3.0075)
Viral carry c.	(1.2028,3.9003)	(0.1445,3.2265)	(-2.264,0.5109)	(7.6766,9.8327)	(5.4481,7.0745)	(6.0344,8.2226)
Max. viral load	(1.152,3.7617)	(0.1905,3.1359)	(-2.1411,0.5333)	(7.5879,9.6708)	(5.4277,7.0196)	(5.9713,8.0642)
EAR (%)	(-1.8401,-0.0934)	(-1.163,1.0433)	(-0.0568,1.9072)	(-2.2545,-0.8247)	(-1.1872,-0.183)	(-2.3379,-0.6933)
Cum. viral load	(-1.9539,5.9091)	(6.027,13.2882)	(4.2817,11.1208)	(25.3305,31.1799)	(23.6787,28.9278)	(16.455,20.7974)
Initial innate res.	(-0.0236,0.7217)	(-0.2118,0.5904)	(-0.5222,0.1949)	(1.6764,2.2674)	(1.3888,1.854)	(1.517,2.0608)
Innate activation rate	(-0.0321,0.056)	(-0.064,0.0369)	(-0.0756,0.0243)	(0.1518,0.2154)	(0.141,0.2015)	(0.1583,0.236)
Adaptive activation rate	(-0.1043,0.0148)	(-0.2538,-0.1032)	(-0.2128,-0.0547)	(0.3231,0.4016)	(0.3612,0.4495)	(0.4735,0.6025)
Adaptive clearance rate	(-0.0952,0.6487)	(-0.4383,0.1613)	(-0.7498,-0.0795)	(2.4379,2.9164)	(2.1174,2.6816)	(2.631,2.9826)
Needle Haptoglobin						
Initial pathogen	(-0.0008,0.0047)	(-0.0003,0.0052)	(-0.002,0.003)	(0.0138,0.0181)	(0.0122,0.0158)	(0.0117,0.0153)
Viral growth rate	(-1.8792,0.4719)	(-1.227,0.8595)	(-0.6862,1.7324)	(3.5209,4.8563)	(3.8619,5.7439)	(3.6083,5.0776)
Time max viral load	(-0.395,0.5975)	(-0.2575,0.56)	(-0.4375,0.5425)	(2.59,3.1575)	(2.395,3.1975)	(2.4425,3.0075)
Viral carry c.	(1.3105,4.4098)	(0.0669,3.6636)	(-2.6364,0.5565)	(7.8492,10.3055)	(5.4082,7.2638)	(6.0295,8.6165)
Max. viral load	(1.2585,4.2028)	(0.1265,3.4988)	(-2.4559,0.5681)	(7.7458,10.0735)	(5.3896,7.1767)	(5.9717,8.3983)
EAR (%)	(-2.3782,-0.0787)	(-1.5294,1.3406)	(-0.1283,2.437)	(-2.8372,-0.976)	(-1.515,-0.1958)	(-2.9017,-0.7478)
Cum. viral load	(-4.0935,3.404)	(3.7558,10.5361)	(4.1111,10.923)	(23.3126,28.5862)	(23.713,29.0666)	(16.6663,21.053)
Initial innate res.	(-0.2696,0.7446)	(-0.3862,0.6667)	(-0.5958,0.3756)	(2.2664,3.0221)	(2.0705,2.7289)	(2.1448,2.8554)
Innate activation rate	(-0.0407,0.054)	(-0.0651,0.0411)	(-0.0658,0.0312)	(0.1188,0.1913)	(0.1194,0.1786)	(0.128,0.2058)
Adaptive activation rate	(-0.0728,0.0438)	(-0.2168,-0.0704)	(-0.2042,-0.0522)	(0.3323,0.4097)	(0.3414,0.4269)	(0.4499,0.5744)
Adaptive clearance rate	(-0.0085,0.7032)	(-0.3563,0.209)	(-0.76,-0.0846)	(2.5052,2.9291)	(2.0907,2.6487)	(2.5952,2.9688)

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Table S3. Percent average relative error (ARE) for *needle infected hosts*. Parameters are said to be practically identifiable if ARE is less than or similar to introduced noise level of 40%

ID	k	K	δ	b	I_0	r	γ	P_0	Max viral	Time max (days)	Cum. Viral
SAA											
7	11.7	10.9	10.9	8.9	11.7	17.4	32.8	44.0	10.8	13.4	8.8
10	16.4	8.7	3.6	8.7	12.4	8.0	23.6	31.7	8.6	4.8	7.8
11	12.8	9.0	3.9	9.1	11.8	5.8	18.4	22.9	9.0	3.5	7.8
13	18.5	10.7	12.1	8.2	11.3	19.0	24.0	30.2	10.6	12.5	8.5
8	13.1	15.7	4.2	9.8	13.0	14.8	17.7	24.4	15.1	9.6	10.2
20	23.7	10.4	12.8	8.7	11.4	15.7	13.8	17.0	10.9	16.6	8.0
28	13.2	9.4	12.0	7.7	10.9	17.9	13.2	16.7	9.3	15.9	7.6
32	22.2	10.0	12.6	7.8	11.2	18.7	16.8	23.6	9.9	14.6	7.9
26	14.8	13.3	2.1	10.3	18.3	12.3	21.2	31.1	13.2	7.1	10.2
27	21.0	12.7	7.3	9.7	11.5	13.7	28.9	40.7	12.3	7.9	10.4
34	13.6	13.6	3.6	9.5	11.9	10.9	21.9	28.5	13.1	6.6	10.0
35	22.4	14.6	6.8	9.9	12.0	16.2	19.3	25.9	14.1	11.2	10.1
Haptoglobin											
7	21.0	8.9	7.0	8.6	11.9	10.5	33.6	45.1	8.8	6.1	8.4
10	19.0	10.1	4.4	8.2	11.9	12.1	22.6	31.2	9.9	6.6	7.4
11	21.4	11.5	5.1	9.0	11.9	9.5	17.2	22.8	11.3	5.0	7.7
13	21.9	10.8	12.1	8.3	11.5	19.2	21.2	29.8	10.7	12.2	8.6
8	18.1	17.3	5.5	10.3	12.1	16.8	17.2	24.5	16.6	10.2	11.4
20	17.7	10.4	12.5	8.9	11.6	15.6	13.8	17.0	10.3	16.0	8.1
28	20.5	9.3	12.0	7.9	11.4	17.9	13.3	16.9	9.2	15.3	7.7
32	16.7	10.0	12.5	8.0	11.4	18.8	17.2	23.4	10.6	13.5	8.2
26	21.2	17.0	3.9	10.0	11.9	15.7	21.5	31.0	16.1	9.0	11.0
27	21.5	15.0	7.5	9.7	11.7	12.3	30.5	39.7	14.9	7.0	10.0
34	19.0	16.5	3.8	9.7	11.7	13.9	21.0	28.1	15.9	7.5	9.4
35	22.5	15.4	7.2	10.4	11.8	17.7	19.0	26.4	14.9	10.9	11.6

Table S4. Percent average relative error (ARE) for *contact infected hosts*. Parameters are said to be practically identifiable if ARE is less than or similar to introduced noise level of 40%

ID	k	K	δ	b	I_0	r	γ	P_0	Max viral	Time max (days)	Cum viral
SAA											
2	18.2	10.9	8.1	8.4	11.2	4.3	34.1	20.9	11.6	3.2	8.4
4	16.0	11.2	7.8	8.4	11.3	4.1	20.1	25.7	11.2	2.7	8.2
19	19.0	11.4	9.4	8.0	11.3	11.3	26.5	37.6	11.3	7.0	8.0
33	19.5	12.2	7.0	9.5	11.8	4.5	20.1	27.5	12.0	2.8	8.9
5	17.3	7.6	3.6	6.2	11.6	6.0	23.9	34.9	7.3	3.7	8.4
9	12.1	16.7	10.8	9.6	11.4	7.0	26.5	37.2	13.7	2.8	9.7
22	21.4	16.6	12.2	11.5	11.4	5.2	15.9	22.5	13.0	2.9	12.4
29	12.5	14.0	2.4	8.6	11.5	6.2	48.0	32.2	11.0	3.2	9.2
12	20.1	8.5	10.0	8.7	10.7	4.0	21.6	12.8	10.5	1.5	8.1
16	16.5	7.8	9.2	9.8	11.4	2.9	34.8	21.9	8.7	1.3	9.3
17	18.6	17.3	11.1	9.5	11.3	6.9	17.5	17.6	14.1	3.4	9.2
Haptoglobin											
2	19.8	11.0	8.0	8.4	11.4	4.1	14.8	20.0	10.9	3.1	8.3
4	21.8	11.3	7.9	8.5	11.2	4.1	17.4	25.1	11.2	2.8	8.4
19	19.7	11.6	9.3	8.1	11.5	10.9	27.4	37.0	11.5	6.6	8.0
33	21.1	12.2	7.1	9.6	11.6	4.5	18.6	27.3	12.1	2.9	9.0
5	20.5	8.8	3.6	6.7	11.8	5.6	20.8	30.7	8.4	3.6	9.3
9	19.4	19.2	12.3	10.1	11.5	7.9	24.7	37.1	15.4	3.3	10.7
22	18.7	19.8	13.7	12.1	11.5	5.5	15.4	22.4	14.6	3.1	13.6
29	22.6	13.1	3.6	9.6	11.7	6.7	45.4	32.3	10.2	3.9	10.0
12	28.4	14.4	11.3	8.8	9.7	4.2	14.4	12.7	12.3	1.8	8.7
16	24.6	9.5	10.8	10.6	11.3	3.0	33.8	21.5	9.4	1.8	10.7
17	15.7	14.8	9.9	9.5	7.6	6.6	16.1	17.6	13.2	3.4	9.2

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Table S5. 95% Confidence Intervals for Log-nomral distribution parameters, *SAT1 contact infected hosts*

Feature	μ, ID2	σ, ID2	μ, ID4	σ, ID4	μ, ID19	σ, ID19	μ, ID33	σ, ID33
SAA								
P_0	(-4.8013,-4.7968)	(0.1132,0.1164)	(-5.0257,-5.0212)	(0.1128,0.116)	(-4.6395,-4.6349)	(0.1163,0.1196)	(-4.666,-4.6617)	(0.1084,0.1115)
r	(1.2119,1.2139)	(0.0512,0.0527)	(1.1924,1.194)	(0.0403,0.0415)	(1.356,1.3619)	(0.1481,0.1523)	(1.2148,1.2167)	(0.0488,0.0502)
Time max	(1.3505,1.3522)	(0.0428,0.044)	(1.3622,1.3635)	(0.033,0.0339)	(1.2091,1.2135)	(0.112,0.1152)	(1.3037,1.3052)	(0.0382,0.0393)
K	(1.86,1.8653)	(0.1336,0.1374)	(1.7807,1.7862)	(0.1384,0.1423)	(1.774,1.7796)	(0.1401,0.1441)	(2.1336,2.1397)	(0.1535,0.1578)
Max viral	(1.8553,1.8608)	(0.1394,0.1434)	(1.7746,1.7801)	(0.1374,0.1413)	(1.7701,1.7756)	(0.139,0.1429)	(2.1251,2.1311)	(0.1521,0.1564)
Cum. viral	(3.4145,3.4186)	(0.1016,0.1045)	(3.2606,3.2647)	(0.1013,0.1042)	(3.2734,3.2772)	(0.0965,0.0992)	(3.4773,3.4817)	(0.1118,0.1149)
I_0	(0.6503,0.6558)	(0.1385,0.1423)	(0.6114,0.617)	(0.1402,0.1442)	(0.4864,0.4919)	(0.1395,0.1434)	(0.7913,0.7972)	(0.1489,0.1531)
k	(-2.0381,-2.0296)	(0.2148,0.2209)	(-1.9054,-1.8994)	(0.1511,0.1554)	(-2.033,-2.024)	(0.2261,0.2324)	(-2.2544,-2.2437)	(0.2701,0.2777)
b	(-1.152,-1.1479)	(0.1036,0.1065)	(-0.9909,-0.9868)	(0.1033,0.1062)	(-0.985,-0.981)	(0.0987,0.1014)	(-1.2286,-1.2241)	(0.1137,0.1169)
δ	(0.5852,0.5891)	(0.099,0.1018)	(0.5613,0.5652)	(0.0977,0.1004)	(0.615,0.6196)	(0.1152,0.1185)	(0.6596,0.6631)	(0.0873,0.0897)
Haptoglobin								
P_0	(-4.8093,-4.8048)	(0.1124,0.1155)	(-5.0308,-5.0263)	(0.1127,0.1158)	(-4.6439,-4.6392)	(0.1167,0.1199)	(-4.667,-4.6628)	(0.1074,0.1104)
r	(1.206,1.2079)	(0.0476,0.0489)	(1.1914,1.193)	(0.0411,0.0423)	(1.3479,1.3536)	(0.1445,0.1485)	(1.2137,1.2158)	(0.0516,0.053)
Time max	(1.3442,1.3457)	(0.0386,0.0397)	(1.357,1.3583)	(0.0337,0.0347)	(1.2016,1.2059)	(0.108,0.111)	(1.3008,1.3024)	(0.0401,0.0413)
K	(1.8733,1.8787)	(0.1363,0.1401)	(1.7802,1.7857)	(0.1399,0.1438)	(1.7802,1.7859)	(0.1421,0.1461)	(2.138,2.1441)	(0.1537,0.158)
Max viral	(1.8553,1.8608)	(0.1394,0.1434)	(1.7746,1.7801)	(0.1374,0.1413)	(1.7701,1.7756)	(0.139,0.1429)	(2.1251,2.1311)	(0.1521,0.1564)
Cum. viral	(3.4025,3.4065)	(0.1017,0.1045)	(3.2704,3.2744)	(0.1025,0.1054)	(3.2679,3.2718)	(0.0983,0.1011)	(3.4766,3.4811)	(0.1123,0.1154)
I_0	(0.9279,0.9336)	(0.142,0.146)	(0.9804,0.986)	(0.1404,0.1443)	(0.9777,0.9833)	(0.1413,0.1453)	(0.9157,0.9215)	(0.1456,0.1497)
k	(-2.1745,-2.1654)	(0.2296,0.236)	(-2.2653,-2.2554)	(0.2506,0.2576)	(-2.2516,-2.2414)	(0.2556,0.2628)	(-2.1242,-2.1148)	(0.2378,0.2444)
b	(-1.1686,-1.1645)	(0.1035,0.1065)	(-1.039,-1.0349)	(0.1048,0.1077)	(-1.0305,-1.0266)	(0.1003,0.1031)	(-1.2411,-1.2365)	(0.1146,0.1179)
δ	(0.5852,0.5891)	(0.099,0.1018)	(0.5613,0.5652)	(0.0977,0.1004)	(0.615,0.6196)	(0.1152,0.1185)	(0.6596,0.6631)	(0.0873,0.0897)

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Table S6. 95% Confidence Intervals for Log-nomral distribution parameters, *SAT2 contact infected hosts*

Feature	μ, ID5	σ, ID5	μ, ID9	σ, ID9	μ, ID 22	σ, ID22	μ, ID29	σ, ID29
SAA								
P_0	(-5.0993,-5.0947)	(0.1159,0.1191)	(-4.2256,-4.2201)	(0.138,0.1418)	(-4.7036,-4.6993)	(0.109,0.112)	(-4.6048,-4.5999)	(0.1246,0.1281)
r	(1.2782,1.2807)	(0.0626,0.0644)	(0.5772,0.5799)	(0.0674,0.0693)	(0.4971,0.4994)	(0.0587,0.0604)	(0.6377,0.6406)	(0.0729,0.0749)
Time max	(1.1319,1.1336)	(0.0451,0.0463)	(1.639,1.6403)	(0.0333,0.0342)	(1.7096,1.7112)	(0.0391,0.0402)	(1.5306,1.5322)	(0.0397,0.0408)
K	(1.3889,1.3924)	(0.0888,0.0913)	(2.0729,2.08)	(0.1788,0.1838)	(1.7492,1.7569)	(0.1943,0.1997)	(1.5265,1.5325)	(0.1527,0.157)
Max viral	(1.3694,1.3727)	(0.0838,0.0862)	(1.9838,1.9899)	(0.1527,0.157)	(1.6337,1.6399)	(0.1565,0.1609)	(1.4151,1.4201)	(0.1257,0.1292)
Cum. viral	(2.3275,2.3308)	(0.083,0.0854)	(3.0299,3.0346)	(0.116,0.1192)	(2.703,2.7088)	(0.1458,0.1499)	(2.3333,2.3375)	(0.1049,0.1078)
I_0	(0.5399,0.5456)	(0.1439,0.1479)	(0.3936,0.3991)	(0.1374,0.1413)	(0.6892,0.6948)	(0.1426,0.1466)	(0.605,0.6108)	(0.1457,0.1498)
k	(-1.575,-1.5672)	(0.1966,0.2021)	(-1.557,-1.552)	(0.1277,0.1313)	(-2.1704,-2.1572)	(0.3311,0.3404)	(-1.5929,-1.5871)	(0.1459,0.15)
b	(-0.0686,-0.0653)	(0.0834,0.0857)	(-0.7447,-0.74)	(0.1177,0.121)	(-0.484,-0.4782)	(0.1478,0.1519)	(-0.106,-0.1018)	(0.1058,0.1087)
δ	(1.0591,1.0614)	(0.0573,0.0589)	(0.6459,0.651)	(0.1281,0.1317)	(0.9003,0.9062)	(0.1483,0.1525)	(1.072,1.074)	(0.05,0.0515)
Haptoglobin								
P_0	(-5.1313,-5.1268)	(0.1128,0.116)	(-4.226,-4.2205)	(0.1377,0.1416)	(-4.704,-4.6997)	(0.1081,0.1112)	(-4.6043,-4.5994)	(0.1234,0.1269)
r	(1.2584,1.2607)	(0.0587,0.0603)	(0.5928,0.5961)	(0.0832,0.0855)	(0.4901,0.4925)	(0.0608,0.0625)	(0.655,0.6583)	(0.0834,0.0858)
Time max	(1.134,1.1357)	(0.0418,0.0429)	(1.6339,1.6355)	(0.0392,0.0403)	(1.7125,1.7141)	(0.0406,0.0417)	(1.51,1.5119)	(0.0481,0.0495)
K	(1.3988,1.4027)	(0.0994,0.1022)	(2.0396,2.048)	(0.2096,0.2154)	(1.7861,1.795)	(0.2222,0.2285)	(1.5113,1.5174)	(0.1535,0.1578)
Max viral	(1.3741,1.3778)	(0.0925,0.0951)	(1.9532,1.9602)	(0.1742,0.1791)	(1.6586,1.6654)	(0.1712,0.176)	(1.3952,1.4001)	(0.123,0.1265)
Cum. viral	(2.2956,2.2991)	(0.0898,0.0923)	(3.0496,3.0546)	(0.1243,0.1278)	(2.7132,2.7194)	(0.1548,0.1591)	(2.3081,2.3126)	(0.1127,0.1159)
I0	(0.893,0.8989)	(0.1472,0.1513)	(0.8183,0.8239)	(0.1417,0.1457)	(0.7554,0.7611)	(0.1424,0.1464)	(0.9596,0.9654)	(0.1451,0.1492)
k	(-1.7825,-1.7732)	(0.2336,0.2402)	(-1.9341,-1.9257)	(0.2122,0.2181)	(-1.9042,-1.8956)	(0.2158,0.2218)	(-1.9563,-1.9465)	(0.2469,0.2538)
b	(-0.0752,-0.0716)	(0.0905,0.093)	(-0.8084,-0.8034)	(0.1254,0.1289)	(-0.5014,-0.4951)	(0.1572,0.1616)	(-0.12,-0.1154)	(0.1148,0.1181)
δ	(1.0587,1.0611)	(0.0599,0.0616)	(0.59,0.5959)	(0.1488,0.1529)	(0.9052,0.9118)	(0.1652,0.1699)	(1.0584,1.0608)	(0.0621,0.0638)

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Table S7. 95% Confidence Intervals for Log-nomral distribution parameters, *SAT3 contact infected hosts*

Feature	μ, ID12	σ, ID12	μ, ID16	σ, ID16	μ, ID17	σ, ID17
SAA						
P_0	(-3.9739,-3.9679)	(0.1504,0.1546)	(-4.8787,-4.8745)	(0.1064,0.1094)	(-4.0268,-4.0218)	(0.1261,0.1296)
r	(0.0476,0.0496)	(0.0487,0.0501)	(0.4113,0.4124)	(0.0277,0.0285)	(0.5854,0.5883)	(0.0732,0.0753)
Time max	(2.0761,2.0769)	(0.0187,0.0193)	(1.731,1.7318)	(0.0187,0.0193)	(1.6247,1.6262)	(0.0377,0.0388)
K	(2.2975,2.303)	(0.137,0.1409)	(2.3022,2.3083)	(0.1539,0.1582)	(2.1068,2.1135)	(0.1677,0.1724)
Max viral	(2.1293,2.1345)	(0.1316,0.1353)	(1.9897,1.9944)	(0.1196,0.123)	(2.0227,2.0285)	(0.1456,0.1497)
Cum. viral	(3.4611,3.4652)	(0.1033,0.1062)	(2.6978,2.7025)	(0.1194,0.1227)	(3.1333,3.1379)	(0.1147,0.1179)
I_0	(0.9599,0.9653)	(0.1377,0.1416)	(0.9824,0.9882)	(0.1464,0.1505)	(1.0694,1.0751)	(0.144,0.1481)
k	(-2.2349,-2.2275)	(0.1845,0.1897)	(-1.9167,-1.9089)	(0.1952,0.2007)	(-2.1624,-2.1528)	(0.2415,0.2483)
b	(-1.2568,-1.2526)	(0.1051,0.1081)	(-0.4824,-0.4775)	(0.1217,0.1251)	(-0.93,-0.9254)	(0.1166,0.1199)
δ	(0.4644,0.4692)	(0.1205,0.1239)	(0.9378,0.9424)	(0.1158,0.1191)	(0.6537,0.6586)	(0.1221,0.1256)
Haptoglobin						
P_0	(-3.9962,-3.99)	(0.1558,0.1602)	(-4.882,-4.8777)	(0.1078,0.1108)	(-4.0269,-4.0219)	(0.1255,0.129)
r	(0.0733,0.0754)	(0.0516,0.0531)	(0.412,0.4132)	(0.0301,0.031)	(0.602,0.6049)	(0.0739,0.076)
Time max	(2.075,2.0759)	(0.023,0.0236)	(1.7356,1.7368)	(0.0288,0.0296)	(1.6215,1.623)	(0.0393,0.0404)
K	(2.1657,2.1727)	(0.1777,0.1827)	(2.2793,2.2864)	(0.179,0.184)	(2.0572,2.0633)	(0.1526,0.1569)
Max viral	(2.0348,2.0409)	(0.1531,0.1574)	(1.9743,1.9794)	(0.1274,0.1309)	(1.9859,1.9915)	(0.1428,0.1468)
Cum. viral	(3.4532,3.4574)	(0.1067,0.1097)	(2.7112,2.7167)	(0.1394,0.1433)	(3.1325,3.1372)	(0.116,0.1193)
I_0	(0.9839,0.9885)	(0.1168,0.12)	(1.1413,1.1471)	(0.1451,0.1491)	(0.9318,0.9361)	(0.1061,0.1091)
k	(-3.0121,-3.0017)	(0.2604,0.2677)	(-2.3005,-2.2879)	(0.3161,0.325)	(-3.1097,-3.1006)	(0.2283,0.2348)
b	(-1.2487,-1.2444)	(0.1087,0.1118)	(-0.5138,-0.5082)	(0.1412,0.1452)	(-0.9137,-0.909)	(0.117,0.1203)
δ	(0.3727,0.3782)	(0.1381,0.142)	(0.8999,0.9057)	(0.1473,0.1515)	(0.6364,0.6409)	(0.1143,0.1175)

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Table S8. 95% Confidence Intervals for Log-nomral distribution parameters, *SAT1 needle infected hosts*

Feature	μ, ID7	σ, ID7	μ, ID 10	σ, ID 10	μ, ID11	σ, ID11	μ, ID13	σ, ID13
SAA								
P_0	(-4.1074,-4.1017)	(0.143,0.147)	(-4.0937,-4.0883)	(0.1357,0.1396)	(-4.2097,-4.2046)	(0.1274,0.131)	(-4.2211,-4.2158)	(0.1345,0.1383)
r	(1.5495,1.5571)	(0.1917,0.1971)	(1.3311,1.3354)	(0.1093,0.1124)	(1.2704,1.2738)	(0.0867,0.0891)	(1.5068,1.5148)	(0.2014,0.2071)
Time max	(1.0416,1.0473)	(0.1436,0.1476)	(1.0617,1.0645)	(0.0705,0.0725)	(1.1023,1.1045)	(0.0556,0.0572)	(1.055,1.0609)	(0.146,0.1501)
K	(2.0837,2.0886)	(0.1238,0.1273)	(2.2975,2.3024)	(0.1222,0.1256)	(2.2919,2.2972)	(0.1326,0.1363)	(1.9689,1.9739)	(0.1274,0.131)
Max viral	(2.081,2.0858)	(0.123,0.1264)	(2.2763,2.281)	(0.1183,0.1216)	(2.2641,2.2692)	(0.1278,0.1314)	(1.9648,1.9698)	(0.1262,0.1298)
Cum. viral	(3.5652,3.5696)	(0.1109,0.114)	(3.1459,3.15)	(0.1012,0.1041)	(3.094,3.098)	(0.0999,0.1027)	(3.4628,3.4667)	(0.099,0.1018)
I_0	(0.2491,0.2545)	(0.136,0.1398)	(0.4754,0.4813)	(0.1492,0.1534)	(0.6539,0.6599)	(0.1502,0.1544)	(1.0873,1.093)	(0.1454,0.1495)
k	(-1.6898,-1.6842)	(0.142,0.146)	(-1.6247,-1.6164)	(0.2086,0.2144)	(-1.4666,-1.4605)	(0.1534,0.1577)	(-2.287,-2.2779)	(0.2285,0.2349)
b	(-1.2699,-1.2654)	(0.112,0.1151)	(-0.8727,-0.8686)	(0.1026,0.1055)	(-0.8405,-0.8365)	(0.1013,0.1041)	(-1.2507,-1.2467)	(0.1007,0.1035)
δ	(-1.2699,-1.2654)	(0.112,0.1151)	(-0.8727,-0.8686)	(0.1026,0.1055)	(-0.8405,-0.8365)	(0.1013,0.1041)	(-1.2507,-1.2467)	(0.1007,0.1035)
Haptoglobin								
P_0	(-4.1,-4.0942)	(0.1447,0.1487)	(-4.0977,-4.0923)	(0.1348,0.1386)	(-4.2101,-4.2051)	(0.1256,0.1292)	(-4.2245,-4.2192)	(0.1332,0.137)
r	(1.3677,1.3732)	(0.1366,0.1404)	(1.3636,1.3698)	(0.1553,0.1596)	(1.3004,1.3059)	(0.1388,0.1427)	(1.4972,1.5053)	(0.2023,0.208)
Time max	(1.056,1.0597)	(0.0913,0.0938)	(1.0333,1.0372)	(0.099,0.1017)	(1.0784,1.0819)	(0.0875,0.09)	(1.0631,1.0689)	(0.1461,0.1502)
K	(2.2943,2.2994)	(0.1275,0.1311)	(2.2777,2.2838)	(0.1521,0.1563)	(2.258,2.265)	(0.175,0.1799)	(1.9735,1.9787)	(0.1316,0.1353)
Max viral	(2.277,2.2819)	(0.1228,0.1263)	(2.2556,2.2613)	(0.1451,0.1492)	(2.23,2.2367)	(0.1664,0.1711)	(1.9694,1.9746)	(0.1304,0.134)
Cum. viral	(3.2662,3.2704)	(0.1056,0.1086)	(3.1531,3.1569)	(0.0976,0.1004)	(3.0961,3.1)	(0.0999,0.1027)	(3.4531,3.457)	(0.0997,0.1025)
I_0	(0.9553,0.9612)	(0.1487,0.1529)	(0.9231,0.9291)	(0.1517,0.1559)	(1.0075,1.0135)	(0.1506,0.1548)	(0.9413,0.9471)	(0.1448,0.1488)
k	(-1.8834,-1.8734)	(0.2496,0.2566)	(-1.7351,-1.7261)	(0.2278,0.2342)	(-1.8722,-1.8617)	(0.265,0.2724)	(-2.1984,-2.1887)	(0.2439,0.2507)
b	(-1.0466,-1.0424)	(0.1071,0.1101)	(-0.9271,-0.9232)	(0.0991,0.1019)	(-0.8808,-0.8768)	(0.1014,0.1042)	(-1.226,-1.2219)	(0.1015,0.1044)
δ	(1.0217,1.0244)	(0.0697,0.0716)	(1.0483,1.0505)	(0.055,0.0565)	(1.0435,1.0459)	(0.0591,0.0607)	(0.8486,0.8539)	(0.1322,0.136)

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Table S9. 95% Confidence Intervals for Log-nomral distribution parameters, *SAT2 needle infected hosts*

Feature	μ, ID8	σ, ID8	μ, ID20	σ, ID20	μ, ID28	σ, ID28	μ, ID32	σ, ID32
SAA								
P_0	(-4.2296,-4.2245)	(0.128,0.1316)	(-4.0893,-4.0844)	(0.1226,0.126)	(-4.5812,-4.5769)	(0.1087,0.1118)	(-4.2972,-4.2921)	(0.129,0.1327)
r	(1.4592,1.4655)	(0.1596,0.1641)	(1.5946,1.603)	(0.2112,0.2172)	(1.555,1.563)	(0.2026,0.2083)	(1.546,1.554)	(0.2017,0.2074)
Time max	(0.9801,0.9842)	(0.1018,0.1047)	(0.9988,1.0048)	(0.1516,0.1559)	(1.0569,1.063)	(0.1541,0.1584)	(1.0622,1.0684)	(0.156,0.1603)
K	(1.957,1.9631)	(0.1552,0.1595)	(1.9407,1.9455)	(0.1205,0.1239)	(1.4784,1.4825)	(0.1031,0.106)	(1.8243,1.8289)	(0.1153,0.1185)
Max viral	(1.9446,1.9506)	(0.1512,0.1554)	(1.9384,1.9434)	(0.1265,0.1301)	(1.4766,1.4806)	(0.1026,0.1055)	(1.8222,1.8267)	(0.1147,0.1179)
Cum viral	(2.9241,2.9289)	(0.1201,0.1235)	(3.48,3.484)	(0.0998,0.1026)	(3.0907,3.0945)	(0.0933,0.0959)	(3.447,3.4508)	(0.094,0.0967)
I_0	(0.3501,0.3562)	(0.1544,0.1588)	(0.629,0.6347)	(0.1441,0.1481)	(0.2103,0.2154)	(0.1279,0.1315)	(0.6302,0.6358)	(0.1415,0.1455)
k	(-1.4071,-1.4007)	(0.1611,0.1657)	(-2.2643,-2.2463)	(0.452,0.4647)	(-1.5932,-1.5891)	(0.1033,0.1062)	(-2.1649,-2.1551)	(0.2464,0.2534)
b	(-0.6366,-0.6318)	(0.1206,0.124)	(-1.2135,-1.2095)	(0.1011,0.1039)	(-0.7801,-0.7763)	(0.0944,0.0971)	(-1.1732,-1.1694)	(0.0958,0.0985)
δ	(1.0558,1.0579)	(0.0547,0.0563)	(0.8475,0.8531)	(0.1426,0.1466)	(0.795,0.8006)	(0.1414,0.1453)	(0.7196,0.7253)	(0.1452,0.1493)
Haptoglobin								
P_0	(-4.2284,-4.2233)	(0.1279,0.1314)	(-4.0886,-4.0837)	(0.1228,0.1263)	(-4.5789,-4.5746)	(0.11,0.1131)	(-4.299,-4.2938)	(0.1291,0.1327)
r	(1.485,1.4924)	(0.1863,0.1915)	(1.5972,1.6053)	(0.2056,0.2114)	(1.5654,1.5735)	(0.2048,0.2105)	(1.5274,1.5354)	(0.2007,0.2063)
Time max	(0.9543,0.959)	(0.1185,0.1218)	(0.9896,0.9954)	(0.1459,0.15)	(1.0322,1.0382)	(0.1506,0.1549)	(1.0696,1.0756)	(0.1525,0.1568)
K	(1.9622,1.9697)	(0.189,0.1943)	(1.941,1.9459)	(0.1216,0.125)	(1.4795,1.4836)	(0.1028,0.1057)	(1.8297,1.8344)	(0.1178,0.1211)
Max viral	(1.9483,1.9556)	(0.1823,0.1874)	(1.9382,1.943)	(0.1208,0.1242)	(1.477,1.4811)	(0.1022,0.1051)	(1.8274,1.8324)	(0.1245,0.128)
Cum. viral	(2.9452,2.95)	(0.1217,0.1251)	(3.4739,3.4779)	(0.1007,0.1035)	(3.1055,3.1093)	(0.0949,0.0976)	(3.435,3.4389)	(0.0964,0.0991)
I_0	(0.8004,0.8063)	(0.1489,0.1531)	(0.8827,0.8884)	(0.1437,0.1477)	(0.9459,0.9516)	(0.142,0.146)	(0.8114,0.817)	(0.1408,0.1448)
k	(-1.5932,-1.5855)	(0.196,0.2015)	(-2.0635,-2.0551)	(0.2097,0.2156)	(-2.1709,-2.1623)	(0.2164,0.2225)	(-2.0058,-1.9985)	(0.1834,0.1885)
b	(-0.7046,-0.6997)	(0.1225,0.1259)	(-1.2341,-1.23)	(0.1023,0.1052)	(-0.8698,-0.866)	(0.0966,0.0994)	(-1.1803,-1.1764)	(0.0983,0.1011)
δ	(1.0493,1.0518)	(0.0617,0.0635)	(0.8447,0.8502)	(0.1379,0.1418)	(0.7709,0.7766)	(0.1441,0.1482)	(0.7088,0.7145)	(0.1418,0.1457)

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Table S10. 95% Confidence Intervals for Log-nomral distribution parameters, *SAT3 needle infected hosts*

Feature	μ, ID26	σ, ID26	μ, ID27	σ, ID27	μ, ID34	σ, ID34	μ, ID35	σ,ID35
SAA								
P_0	(-4.0874,-4.082)	(0.136,0.1398)	(-4.4409,-4.4353)	(0.1407,0.1446)	(-4.4557,-4.4505)	(0.1302,0.1339)	(-4.3593,-4.3541)	(0.1316,0.1353)
r	(1.423,1.4288)	(0.1452,0.1492)	(1.4079,1.4144)	(0.1638,0.1684)	(1.3927,1.3979)	(0.1307,0.1343)	(1.4901,1.4971)	(0.177,0.182)
Time max	(0.9882,0.9919)	(0.0913,0.0938)	(1.0497,1.054)	(0.1096,0.1127)	(1.0352,1.0385)	(0.0839,0.0862)	(0.9626,0.9673)	(0.1187,0.122)
K	(2.1668,2.1733)	(0.1624,0.1669)	(1.9119,1.9181)	(0.1556,0.16)	(1.8313,1.8374)	(0.154,0.1583)	(1.8257,1.8314)	(0.1455,0.1496)
Max viral	(2.1506,2.157)	(0.1613,0.1658)	(1.8997,1.9057)	(0.151,0.1553)	(1.8166,1.8225)	(0.1497,0.1539)	(1.8142,1.8198)	(0.142,0.146)
Cum. viral	(3.0235,3.0283)	(0.1222,0.1257)	(2.9572,2.9617)	(0.1155,0.1188)	(2.7986,2.8032)	(0.1151,0.1184)	(2.8633,2.8682)	(0.1212,0.1246)
I_0	(0.1826,0.1895)	(0.173,0.1778)	(0.5293,0.535)	(0.1442,0.1482)	(0.5376,0.5436)	(0.1501,0.1543)	(0.8812,0.8873)	(0.153,0.1573)
k	(-1.2987,-1.2917)	(0.177,0.182)	(-1.7936,-1.7842)	(0.2376,0.2443)	(-1.5815,-1.5747)	(0.171,0.1758)	(-2.122,-2.1097)	(0.3095,0.3182)
b	(-0.717,-0.7121)	(0.1233,0.1267)	(-0.6865,-0.6818)	(0.1165,0.1198)	(-0.5359,-0.5313)	(0.1163,0.1195)	(-0.6305,-0.6257)	(0.1222,0.1256)
δ	(1.076,1.0776)	(0.0379,0.039)	(0.9725,0.976)	(0.0863,0.0887)	(1.0634,1.0653)	(0.0492,0.0506)	(1.0126,1.0158)	(0.0798,0.082)
Haptoglobin								
P_0	(-4.0877,-4.0823)	(0.134,0.1378)	(-4.4483,-4.4428)	(0.1401,0.144)	(-4.4585,-4.4534)	(0.1285,0.1321)	(-4.3556,-4.3503)	(0.1332,0.1369)
r	(1.43,1.4369)	(0.1759,0.1808)	(1.3744,1.3806)	(0.1557,0.1601)	(1.4002,1.4063)	(0.1526,0.1569)	(1.5009,1.5085)	(0.1924,0.1978)
Time max	(0.9682,0.9726)	(0.1118,0.115)	(1.0623,1.0665)	(0.1041,0.1071)	(1.0254,1.0292)	(0.0967,0.0994)	(0.9527,0.9577)	(0.1258,0.1293)
K	(2.1958,2.203)	(0.1804,0.1855)	(1.955,1.962)	(0.1749,0.1798)	(1.8401,1.8472)	(0.1783,0.1833)	(1.8363,1.8433)	(0.1745,0.1794)
Max viral	(2.1746,2.1814)	(0.172,0.1769)	(1.9394,1.9463)	(0.1726,0.1775)	(1.8239,1.8307)	(0.1719,0.1768)	(1.8239,1.8306)	(0.1686,0.1733)
Cum. viral	(3.04,3.0446)	(0.1151,0.1183)	(2.9614,2.9661)	(0.1181,0.1214)	(2.8117,2.8164)	(0.1184,0.1217)	(2.8797,2.8846)	(0.1237,0.1271)
I_0	(0.9256,0.9315)	(0.1501,0.1543)	(0.8847,0.8905)	(0.1471,0.1512)	(0.7989,0.8048)	(0.1478,0.152)	(0.9973,1.0032)	(0.1462,0.1503)
k	(-1.7382,-1.7288)	(0.2353,0.242)	(-1.9124,-1.9022)	(0.257,0.2642)	(-1.7992,-1.7898)	(0.2361,0.2428)	(-1.9025,-1.8923)	(0.2566,0.2638)
b	(-0.8106,-0.806)	(0.116,0.1192)	(-0.7282,-0.7234)	(0.119,0.1224)	(-0.5768,-0.572)	(0.1187,0.1221)	(-0.6596,-0.6546)	(0.1245,0.128)
δ	(1.0597,1.0617)	(0.0504,0.0518)	(0.9571,0.9606)	(0.0885,0.091)	(1.0579,1.06)	(0.0542,0.0557)	(1.0165,1.0196)	(0.0792,0.0814)

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Table S11. Spearman rank coefficients for correlation between key model quantities for both individual and mean values from generated data-sets.

	Across Individual	serotype means	SAT1 individual	means	SAT2 individual	means	SAT3 individual	means
Viral growth vs. time max	-0.97	-0.97	-0.89	-0.93	-0.93	-0.69	-0.96	-0.7
Viral growth vs. Initial viral load	-0.4	-0.85	0.57	0.44	-0.41	-0.35	-0.41	-0.06
Initial viral load vs time max	0.4	0.83	-0.75	-0.53	0.44	-0.35	0.04	-0.12
Initial innate response vs innate activation rate	-0.69	-0.87	-0.87	-0.87	-0.69	-0.85	0.13	-0.8
Adaptive activation rate vs adaptive clearance rate	0.73	0.79	-0.21	-0.07	0.78	0.3	0.8	0.14
Adaptive activation rate vs cum. viral load	-0.99	-0.99	-0.99	-0.96	-0.99	-0.84	-0.99	-0.82

Table S12. 95% confidence intervals for difference between sample means within serotype and across route of infection. The results indicate needle infected hosts are not useful for understanding contact transmission. Negative values indicate parameter value for needle hosts is greater, positive that contact infected value is greater.

parameter	SAT1	SAT2	SAT3
Initial pathogen	(-0.00975, -0.00513)	(-0.00611,-0.00175)	(-0.00162,0.00443)
Viral growth rate	(-1.438, 0.165)	(-3.522,-1.621)	(-3.609,-2.126)
Time max viral (days)	(0.433, 1.150)	(1.345, 2.230)	(3.158, 3.870)
Viral carry c.	(-3.929,-0.759)	(-2.002, 0.902)	(-0.505,3.630)
Max viral load	(-3.740, -0.696)	(-2.268, 0.102)	(-1.367, 1.958)
Cum. Viral load	(-0.947,6.902)	(-15.396,-8.837)	(0.761, 8.537)
Initial innate res.	(-0.543, 0.506)	(-0.478, 0.476)	(-0.221, 0.832)
Adaptive activation rate	(-0.090, 0.015)	(0.246, 0.433)	(-0.167, 0.015)
Adaptive clearence rate	(-1.150,-0.579)	(-0.229, 0.539)	(-1.197, -0.487)

F. Supplementary Figures. Figures not appearing in the primary text. These figures provide in-depth visualization of relationships between parameters, both within and between serotypes, across all fitting exercises.

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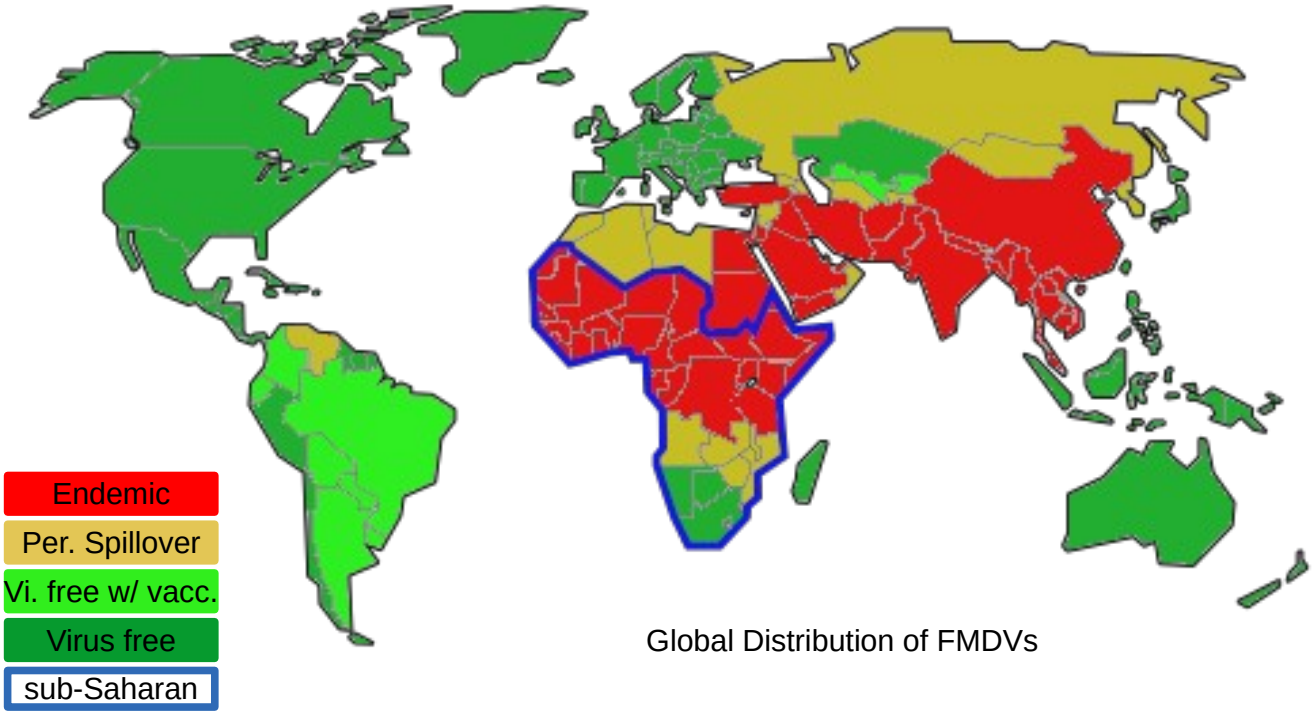

Fig. S1. Global Distribution of FMDVs based upon https://www.wrlfmd.org/foot-and-mouth-disease/occurrence

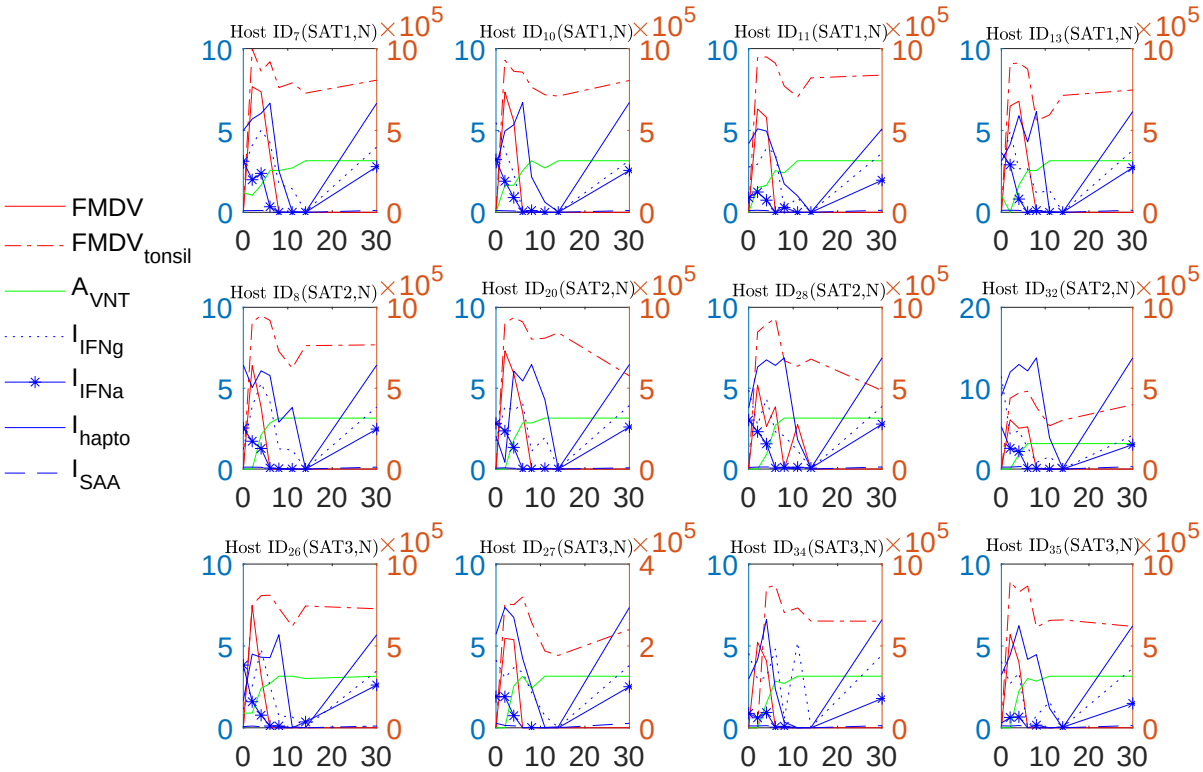

Fig. S2. FMD virus and immune data, obtained from *needle infected hosts*. The right y-axis (orange axis) displays the concentration of innate immune responses I_{hapto}, and I_{SAA}. The rest of the virus-immune response concentrations is presented at the left y-axis (blue axis).

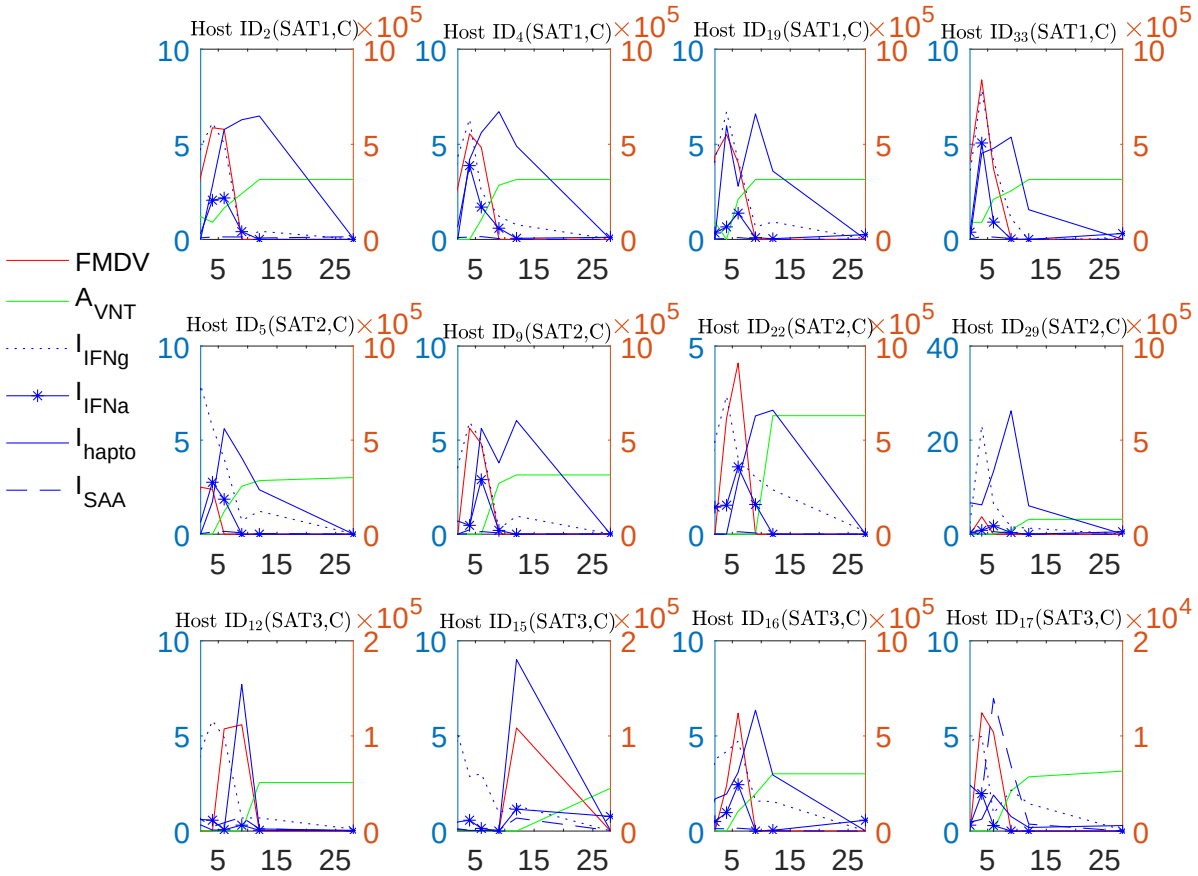

Fig. S3. FMD virus and immune data obtained from *infected hosts via contact*. The right y-axis displays the concentration of innate immune responses I_{hapto}, and I_{SAA}. The rest of the virus-immune response concentrations is presented at the left y-axis.

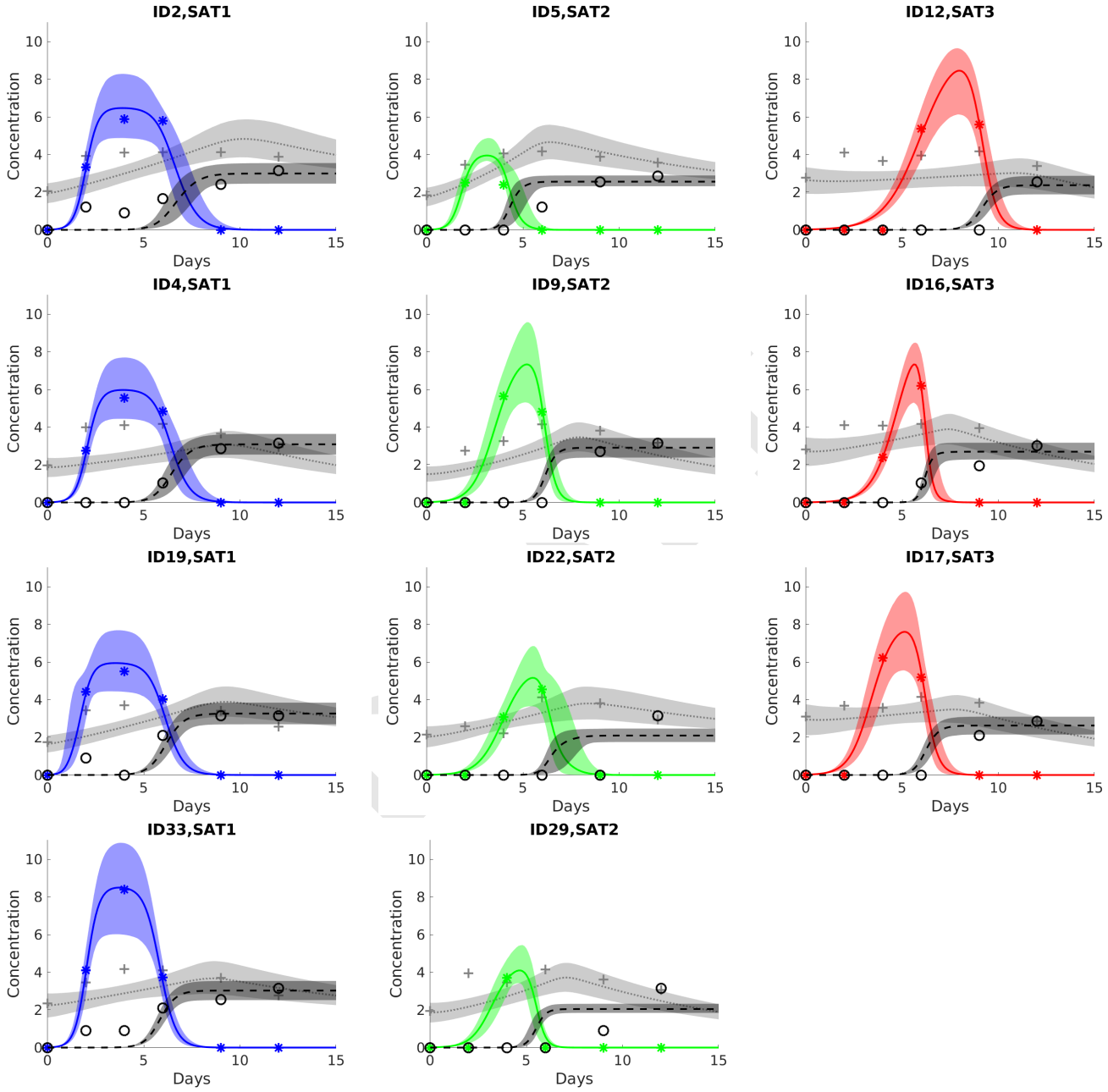

Fig. S4. Mean time trajectories (lines) and 95% confidence intervals (shaded regions) for *contact infected hosts*. Blue indicates SAT1, green SAT2, red SAT3. $\log_{10}(I_{SAA})$ used as measure of innate response (dark shade, dotted line), FMDV viral data (light shade, solid line), and VNT used as measure of adaptive response (intermediate shade, dashed line)

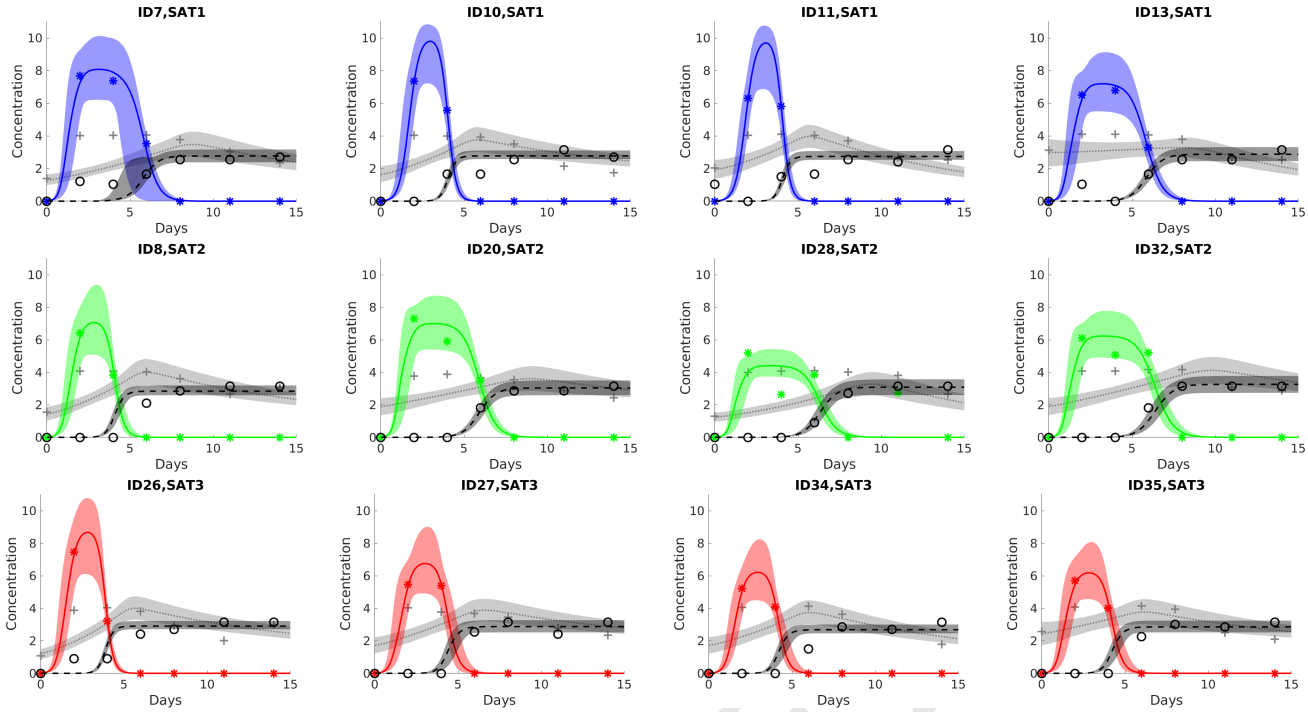

Fig. S5. Mean time trajectories (lines) and 95% confidence intervals (shaded regions) for *needle infected hosts*. Blue indicates SAT1, green SAT2, red SAT3. $\log_{10}(I_{SAA})$ used as measure of innate response (dark shade, dotted line), FMDV viral data (light shade, solid line), and VNT used as measure of adaptive response (intermediate shade, dashed line)

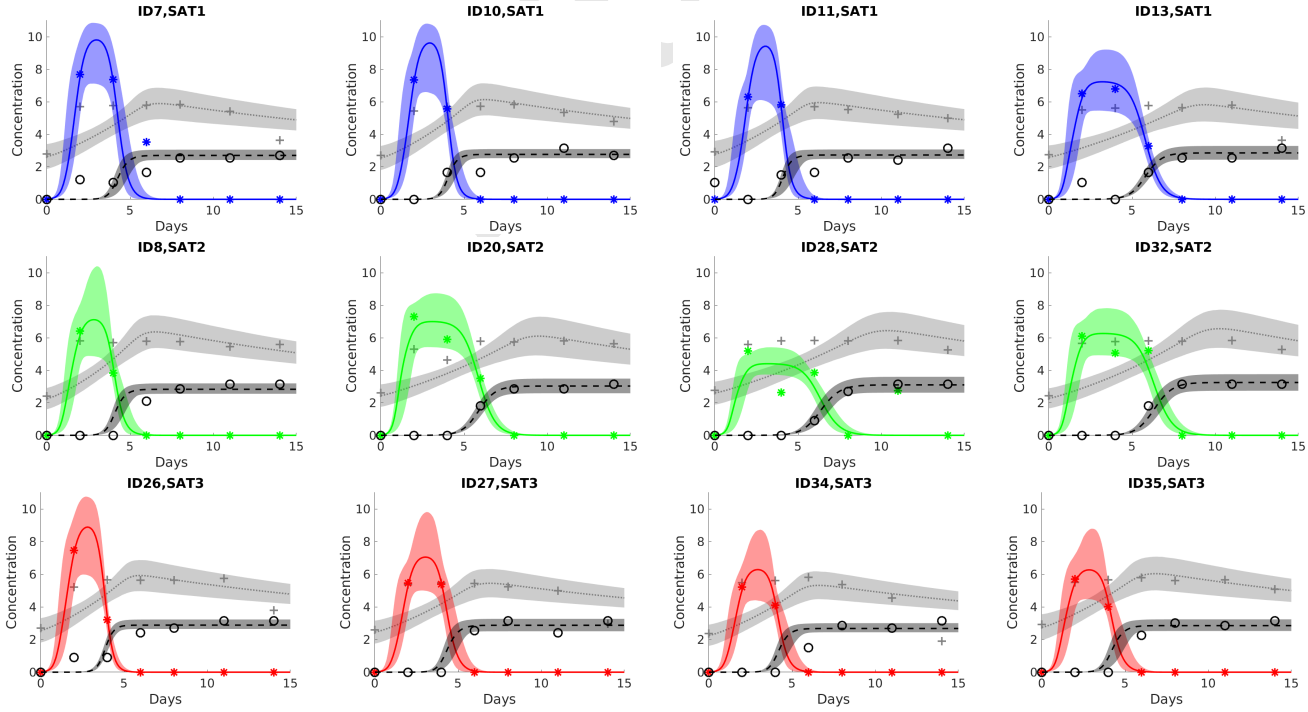

Fig. S6. Mean time trajectories (lines) and 95% confidence intervals (shaded regions) for *needle infected hosts*. Blue indicates SAT1, green SAT2, red SAT3. $\log_{10}(I_{Hapto})$ used as measure of innate response (dark shade, dotted line), FMDV viral data (light shade, solid line), and VNT used as measure of adaptive response (intermediate shade, dashed line)

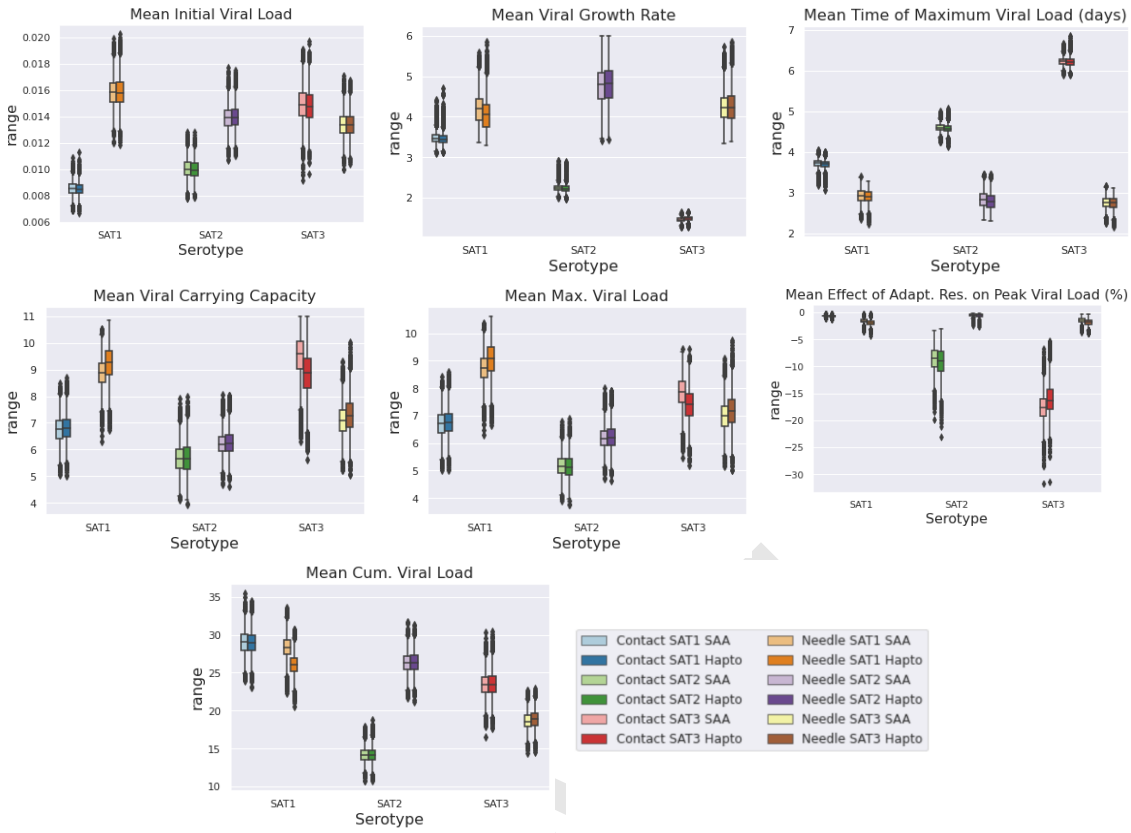

Fig. S7. box-plots for fit serotype sample mean *viral* parameters and quantities inferred from model time trajectories, both *contact infected* hosts and *needle infected* hosts. Viral Carrying capacity, K, represents maximum obtainable viral load *in absence of adaptive response* and is a fit model parameter, max viral load is obtained from model *time trajectory*. Their difference quantifies the effect of adaptive immune response on maximum viral load. (see sub-figure in row 2 column 3). See also Tab. A1.

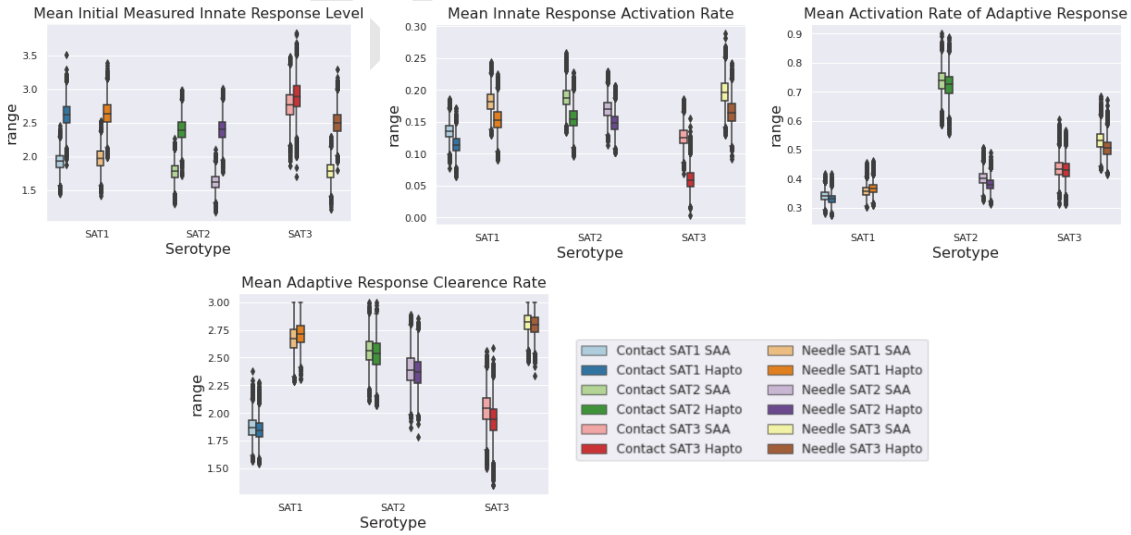

Fig. S8. box-plots for fit serotype sample mean *immune* parameters. See also Tab. A1.

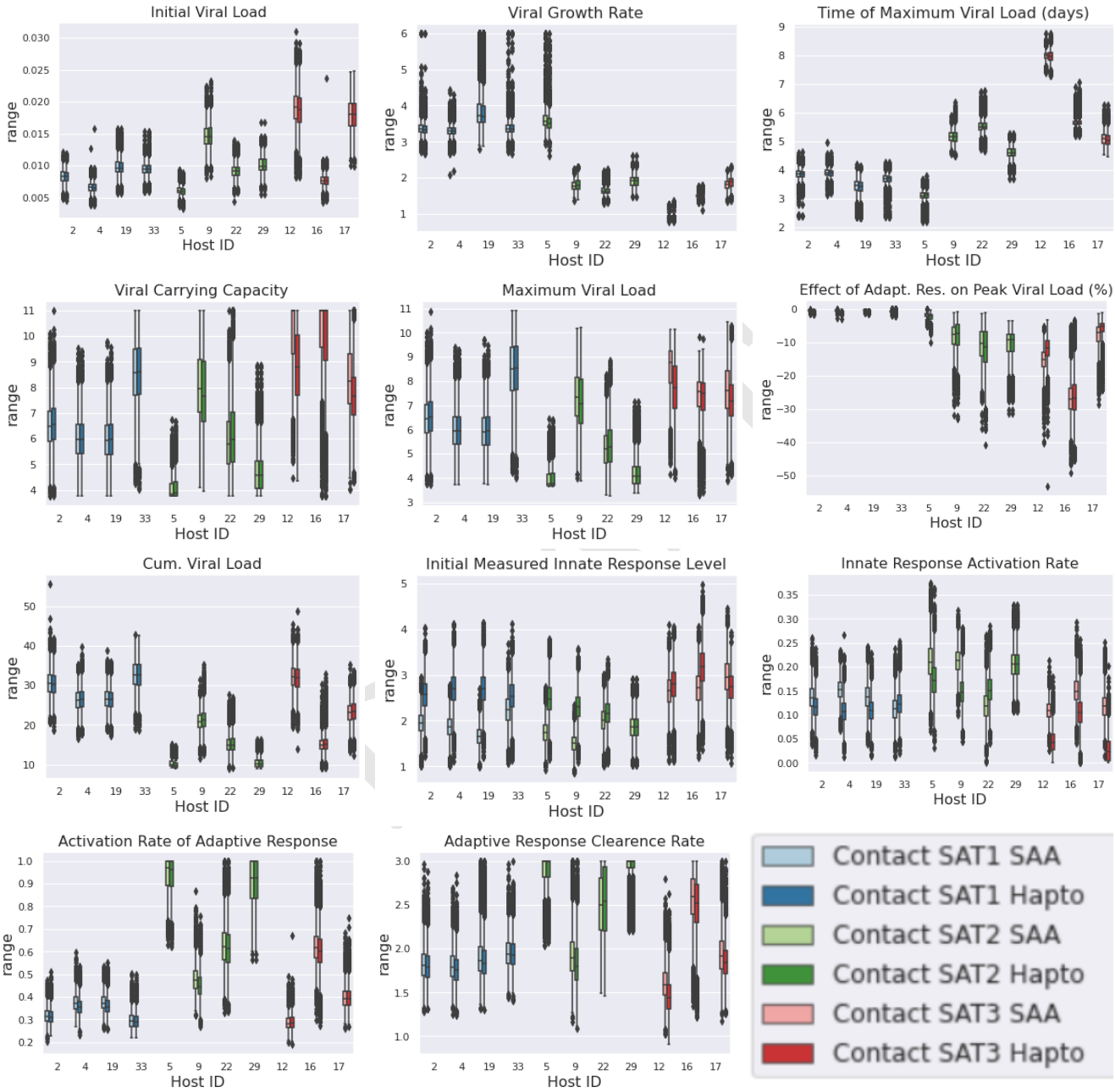

Fig. S9. box-plots for fit parameters, individual *contact infected* hosts.

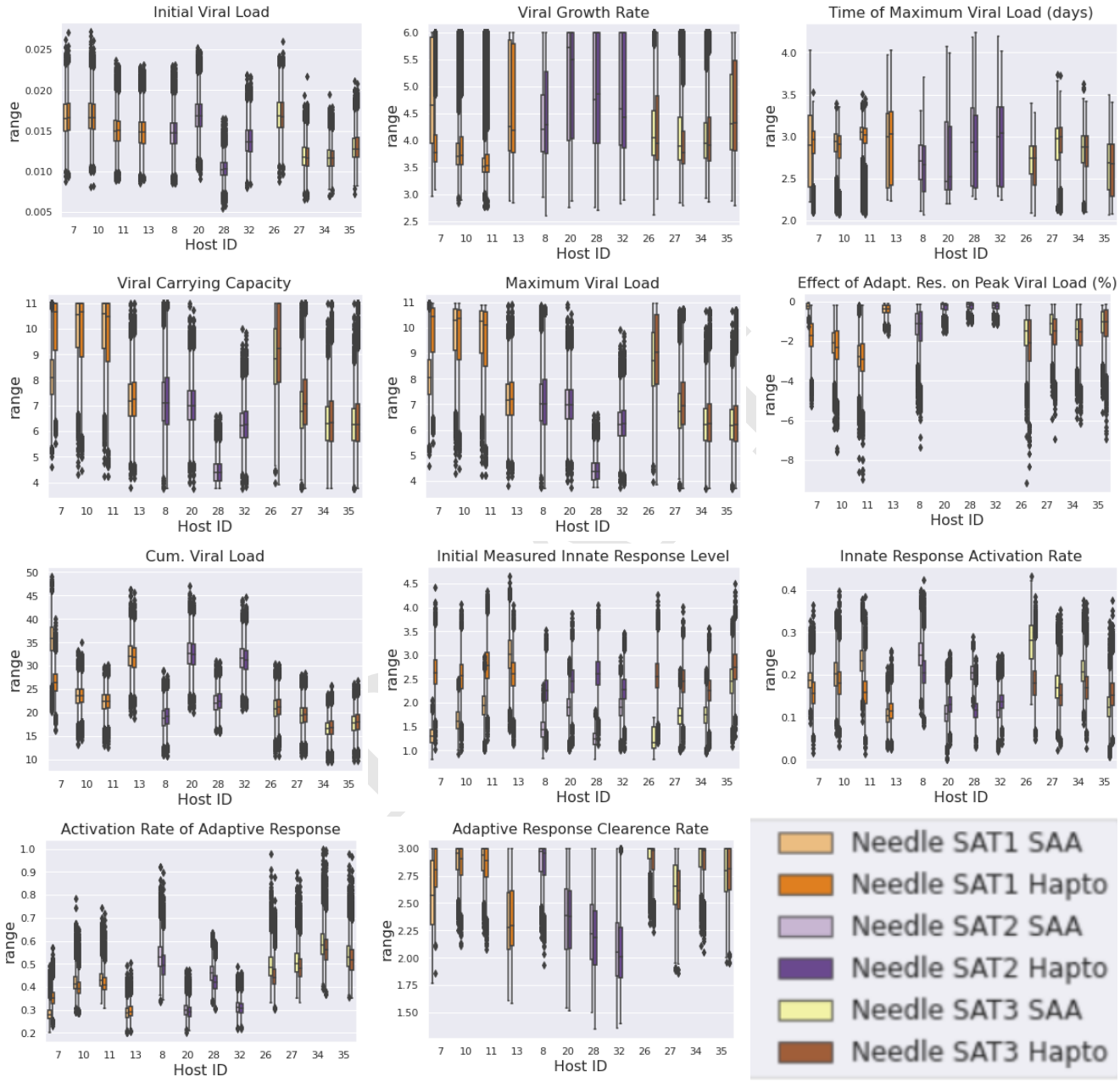

Fig. S10. box-plots for fit parameters, individual *needle infected* hosts.

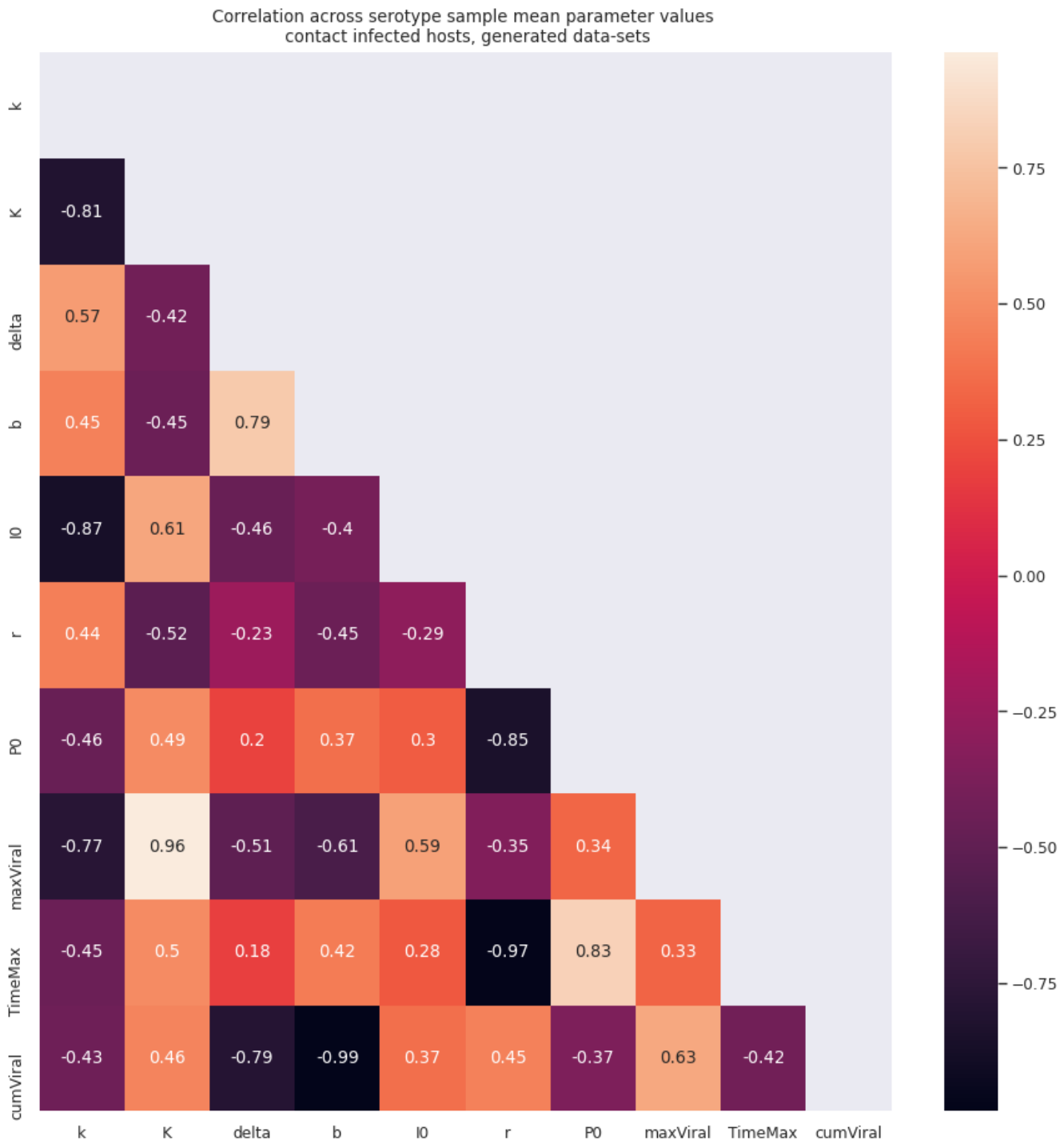

Fig. S11. Correlation values between generated contact infected host sample means across serotype

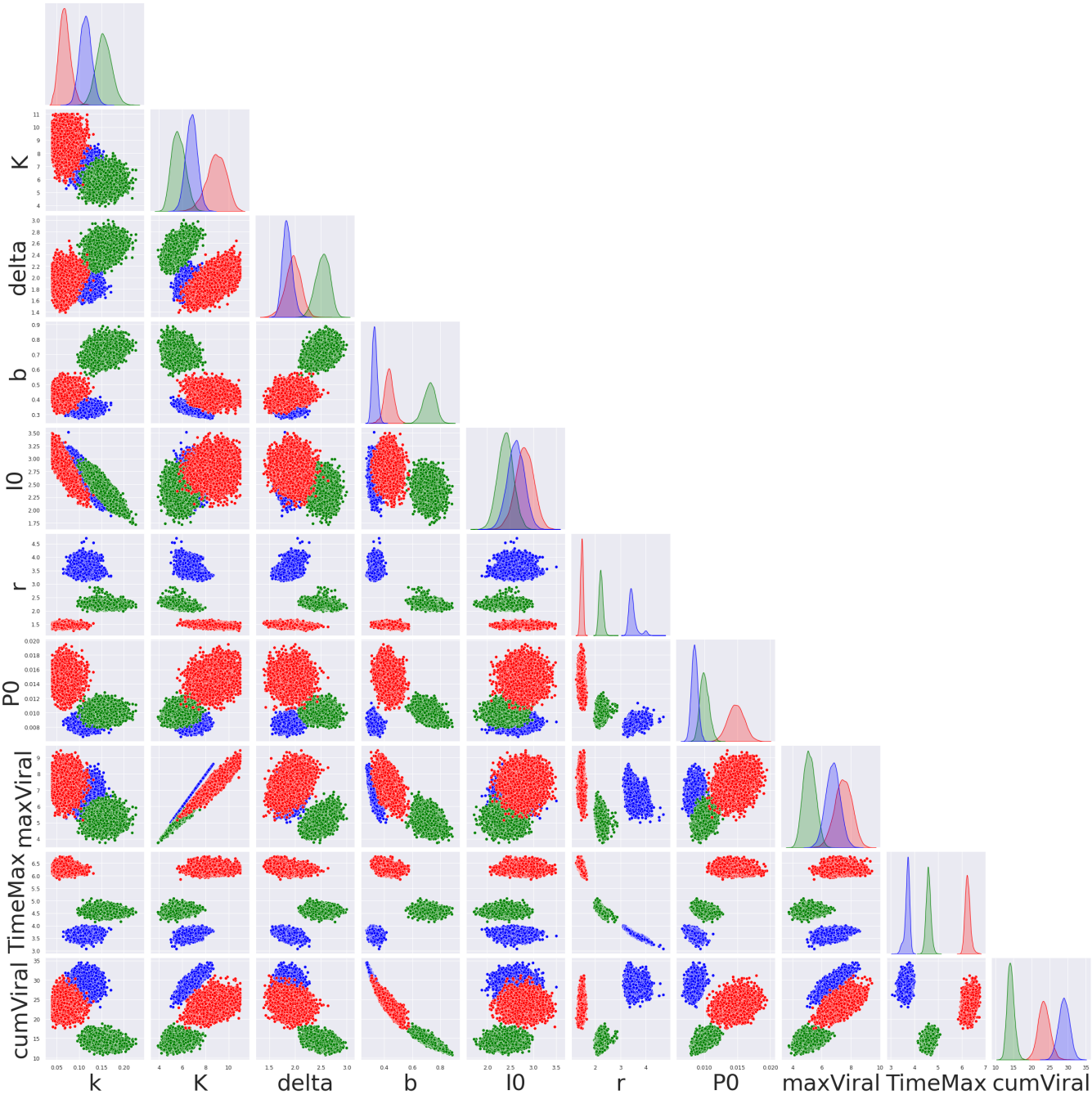

Fig. S12. Scatter plots for generated sample mean model parameters for *Contact infected hosts* using haptoglobin as measure of innate immune response. Blue indicates SAT1, green SAT2, red SAT3. Of particular note is the negative relationship between innate response activation rate, k, and Initial measured innate response level, I_0; the positive relationship between viral carrying capacity, K, and max viral load; the negative relationships between viral growth rate, r, and initial viral load, P_0, time to max viral load; the negative relationship between adaptive response activation rate, b and cumulative viral load, and the negative relationship between clearance rate of pathogen by adaptive response, δ and cumulative viral load.

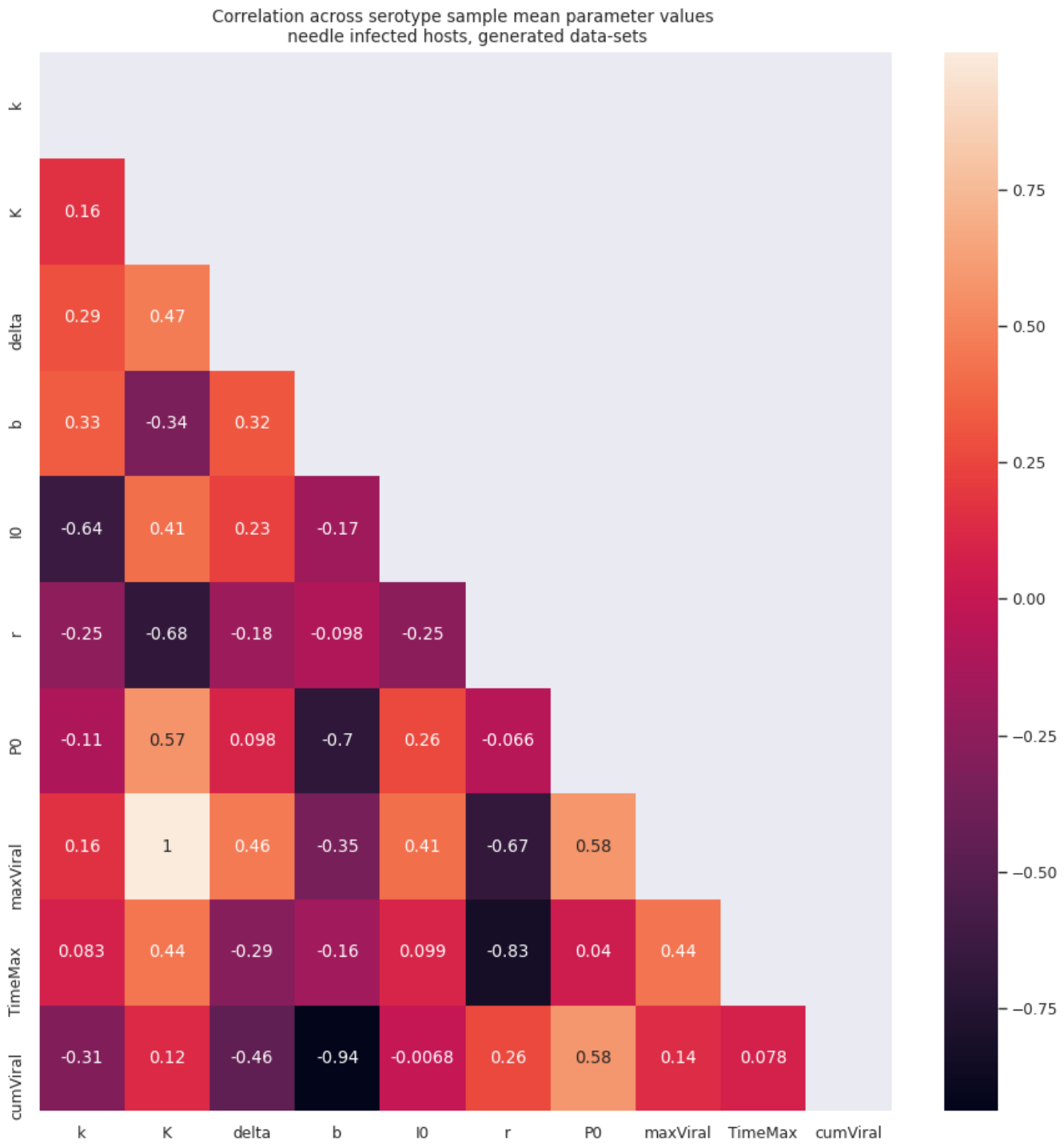

Fig. S13. Correlation values between generated needle infected host sample means across serotype

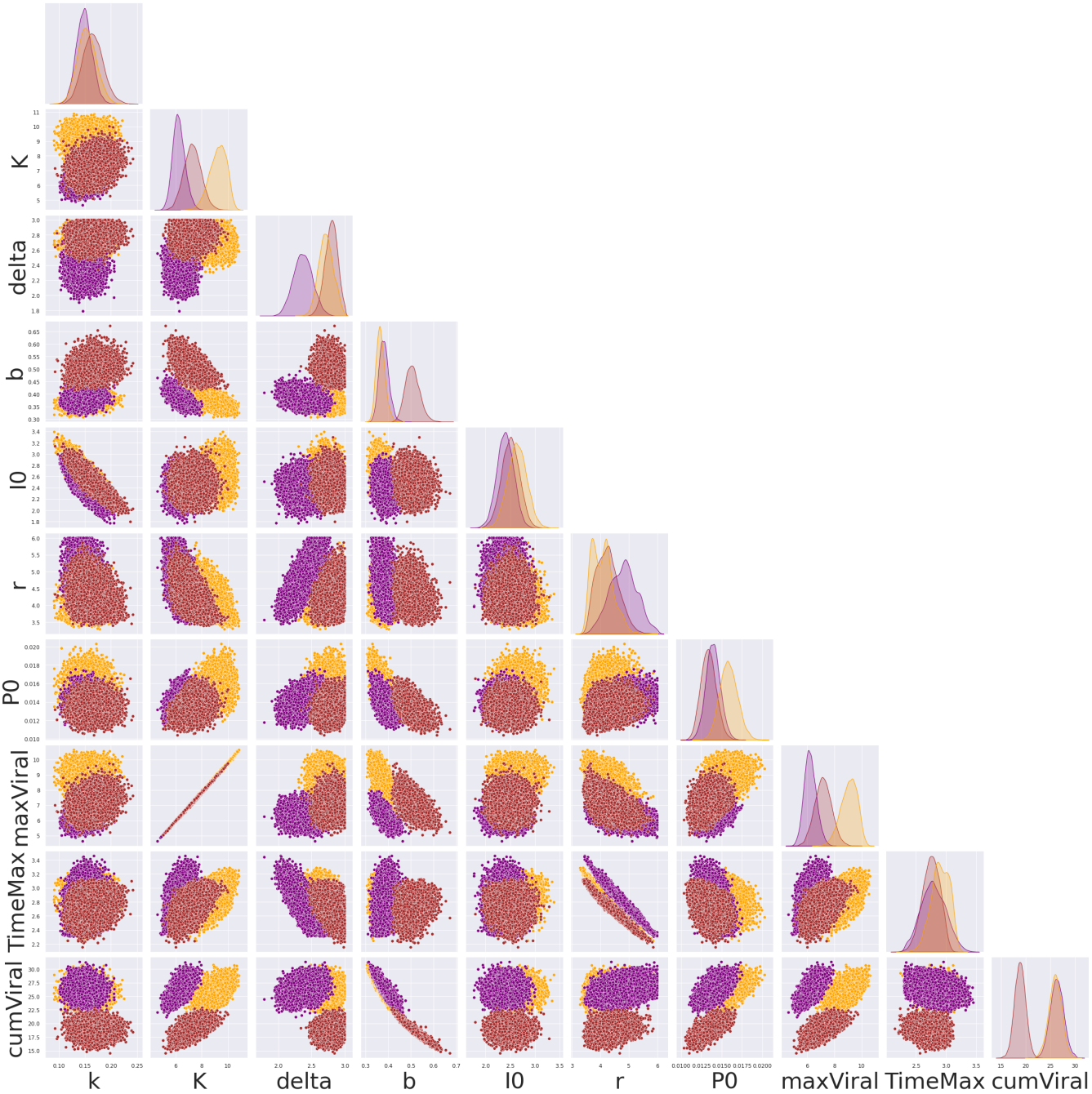

Fig. S14. Scatter plots for generated sample mean model parameters for *needle infected hosts.* Of particular note is the negative relationship between innate response activation rate, k, and Initial measured innate response level, I_0; the positive relationship between viral carrying capacity, K, and max viral load; the negative relationships between viral growth rate, r, and initial viral load, P_0, time to max viral load; the negative relationship between adaptive response activation rate, b and cumulative viral load, and the negative relationship between clearance rate of pathogen by adaptive response, δ and cumulative viral load.

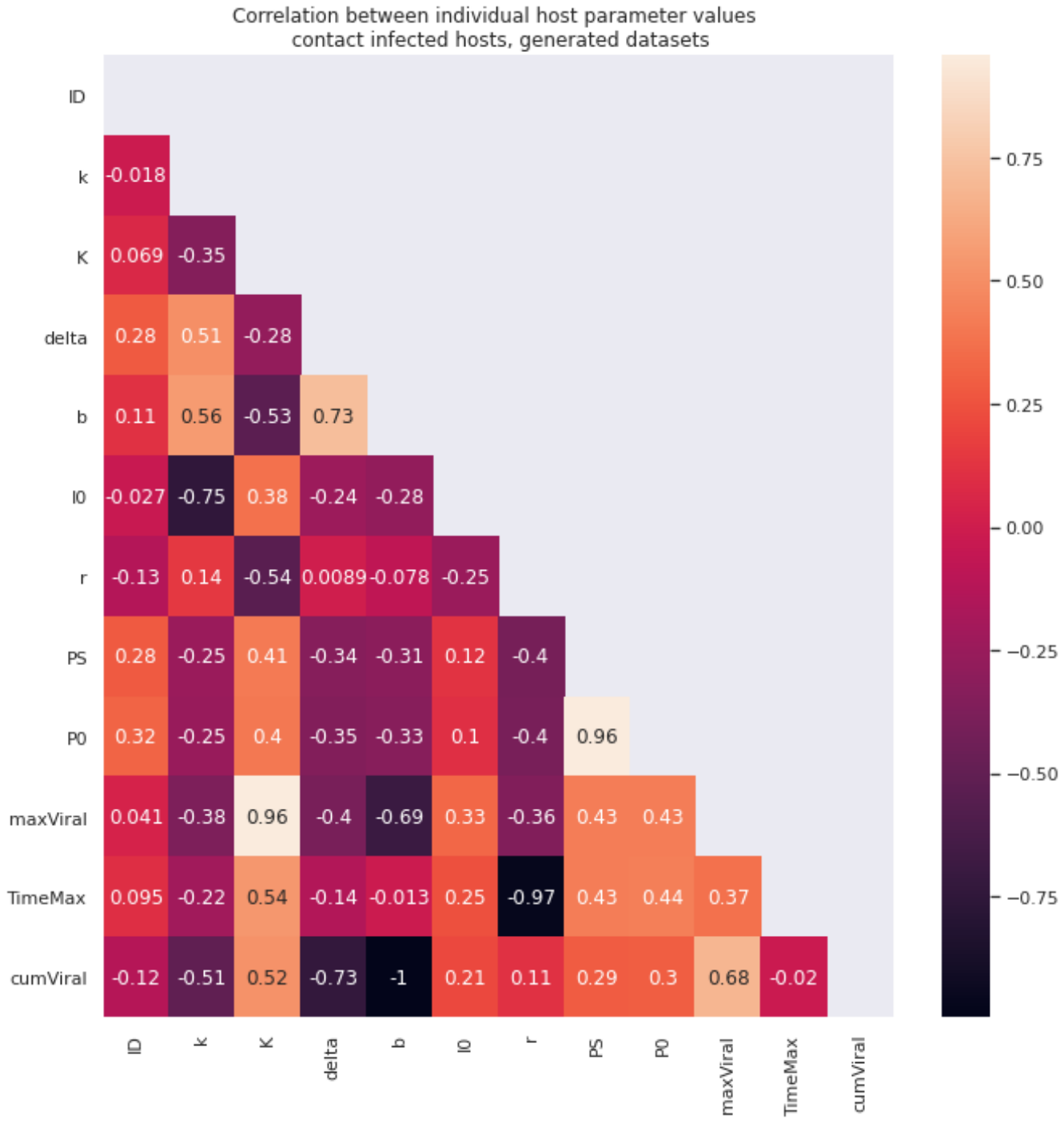

Fig. S15. Correlation values for fit parameters and derived quantities across 220,000 generated *contact infected* individual host datasets

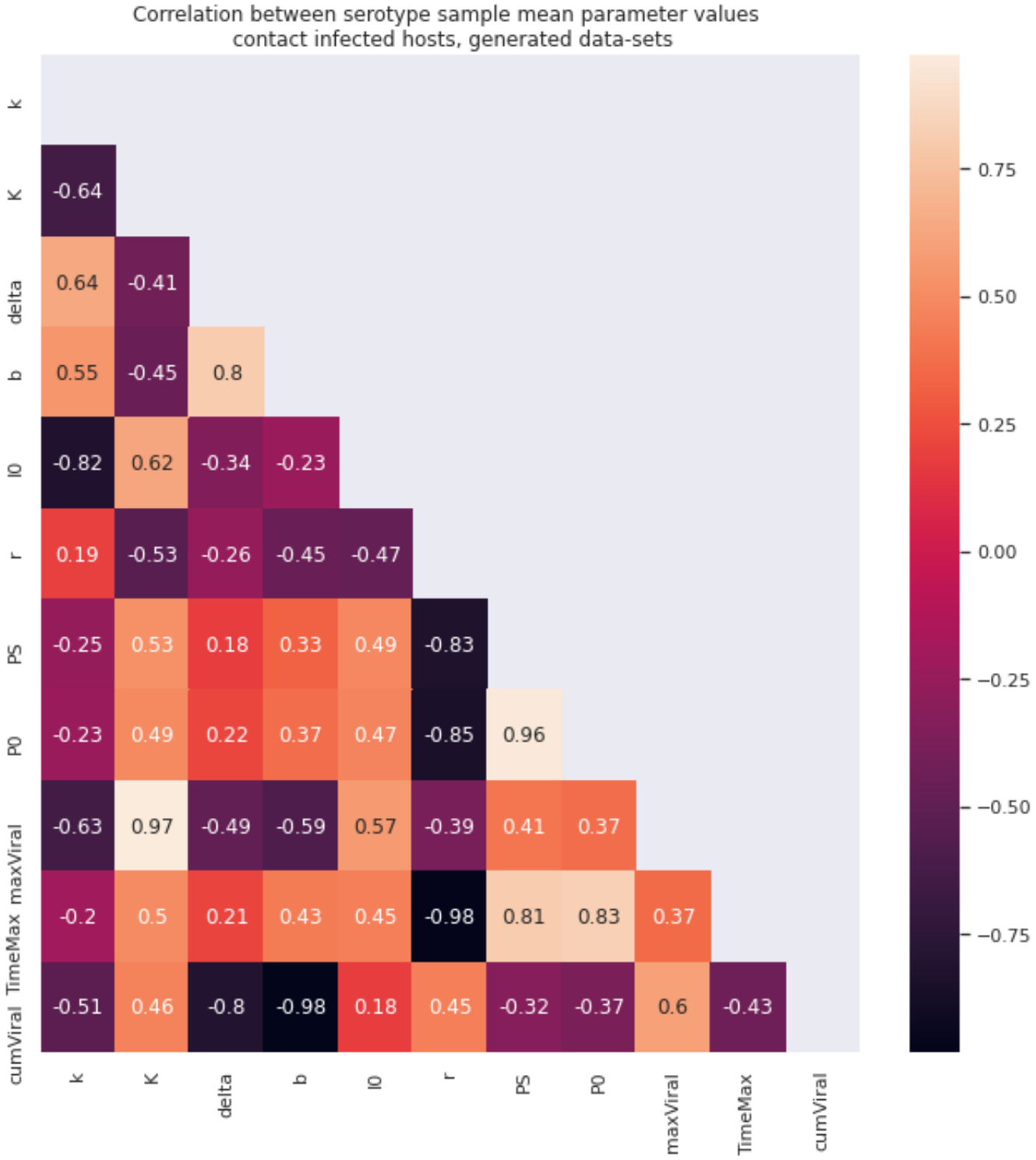

Fig. S16. Correlation values for fit parameters and derived quantities across 60,000 generated serotype sample means for *contact infected* hosts

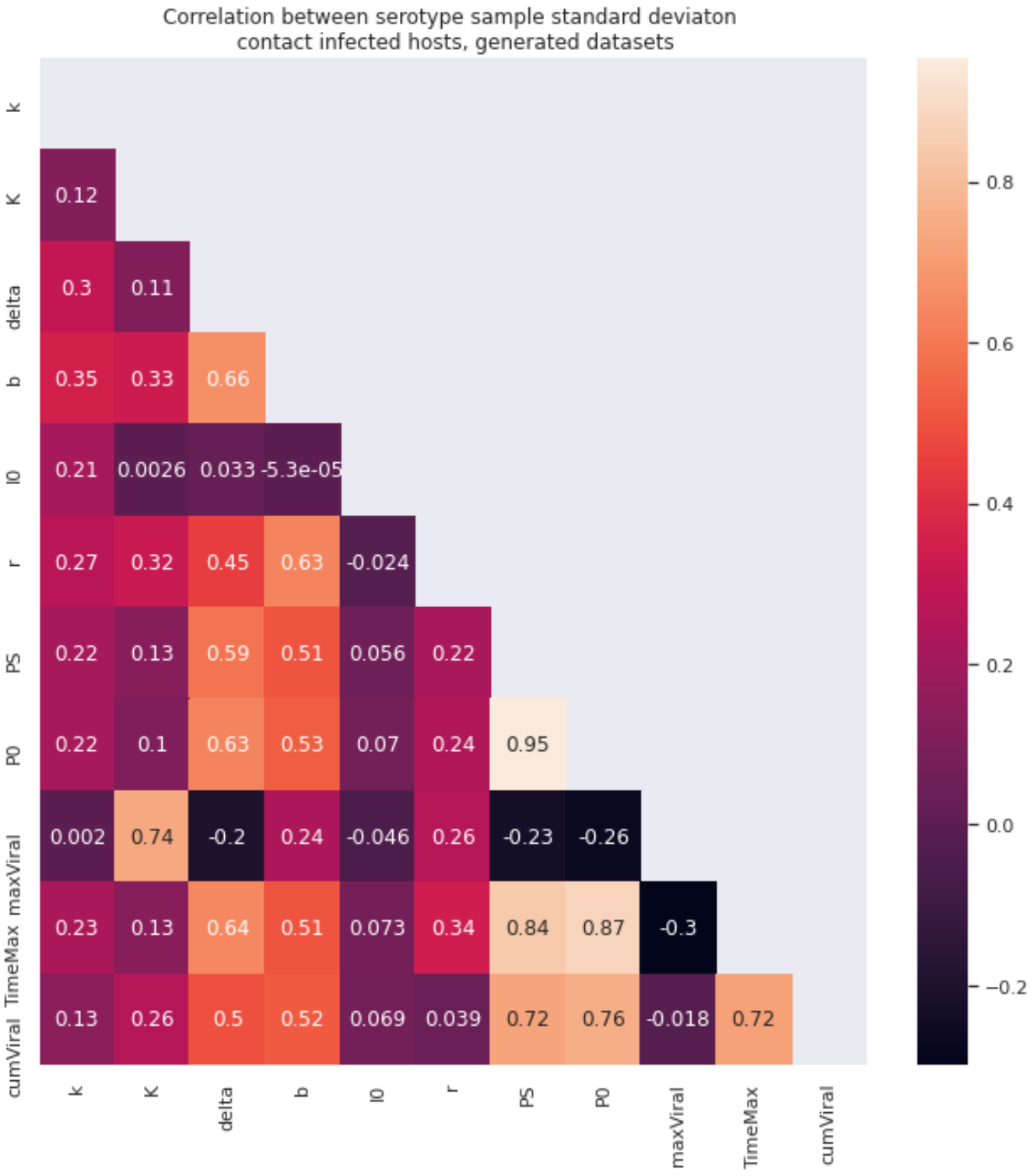

Fig. S17. Correlation values for fit parameters and derived quantities across 60,000 generated serotype sample standard deviations for *contact infected* hosts

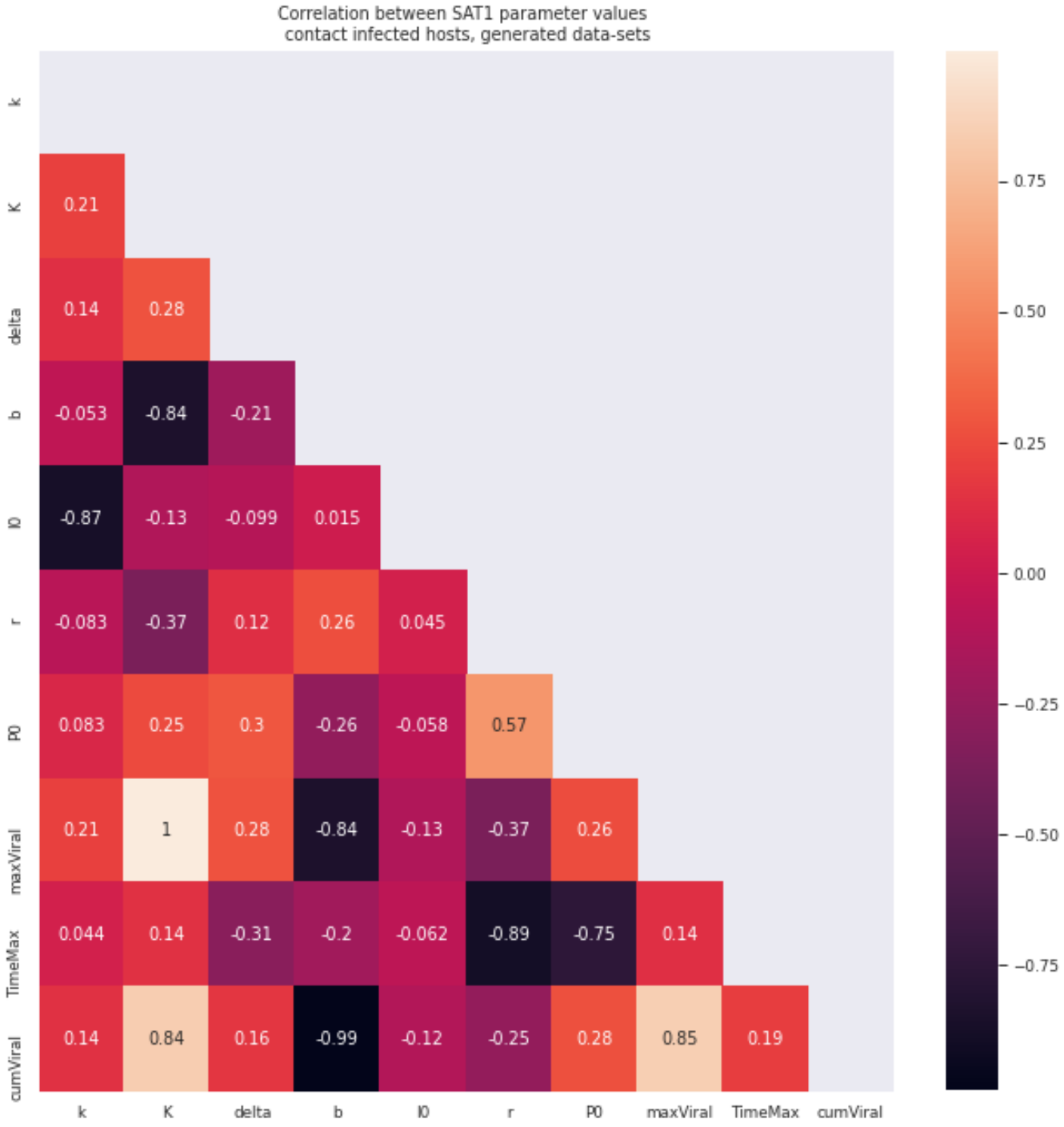

Fig. S18. Correlation values for fit parameters and derived quantities across 40,000 generated SAT1 data-sets for *contact infected* hosts

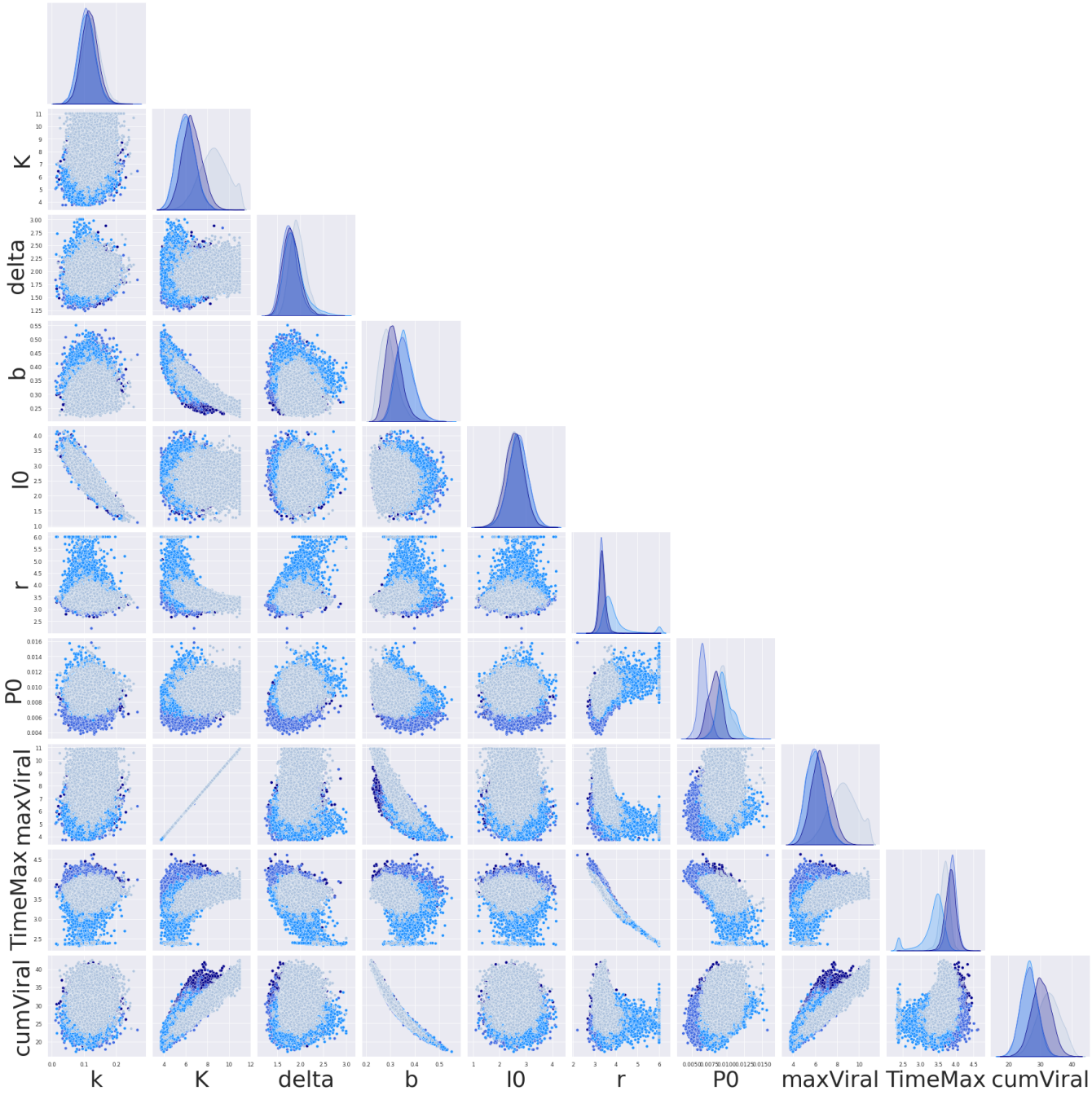

Fig. S19. Scatter plots for fit parameters and derived quantities across 40,000 generated SAT1 data-sets for *contact infected* hosts

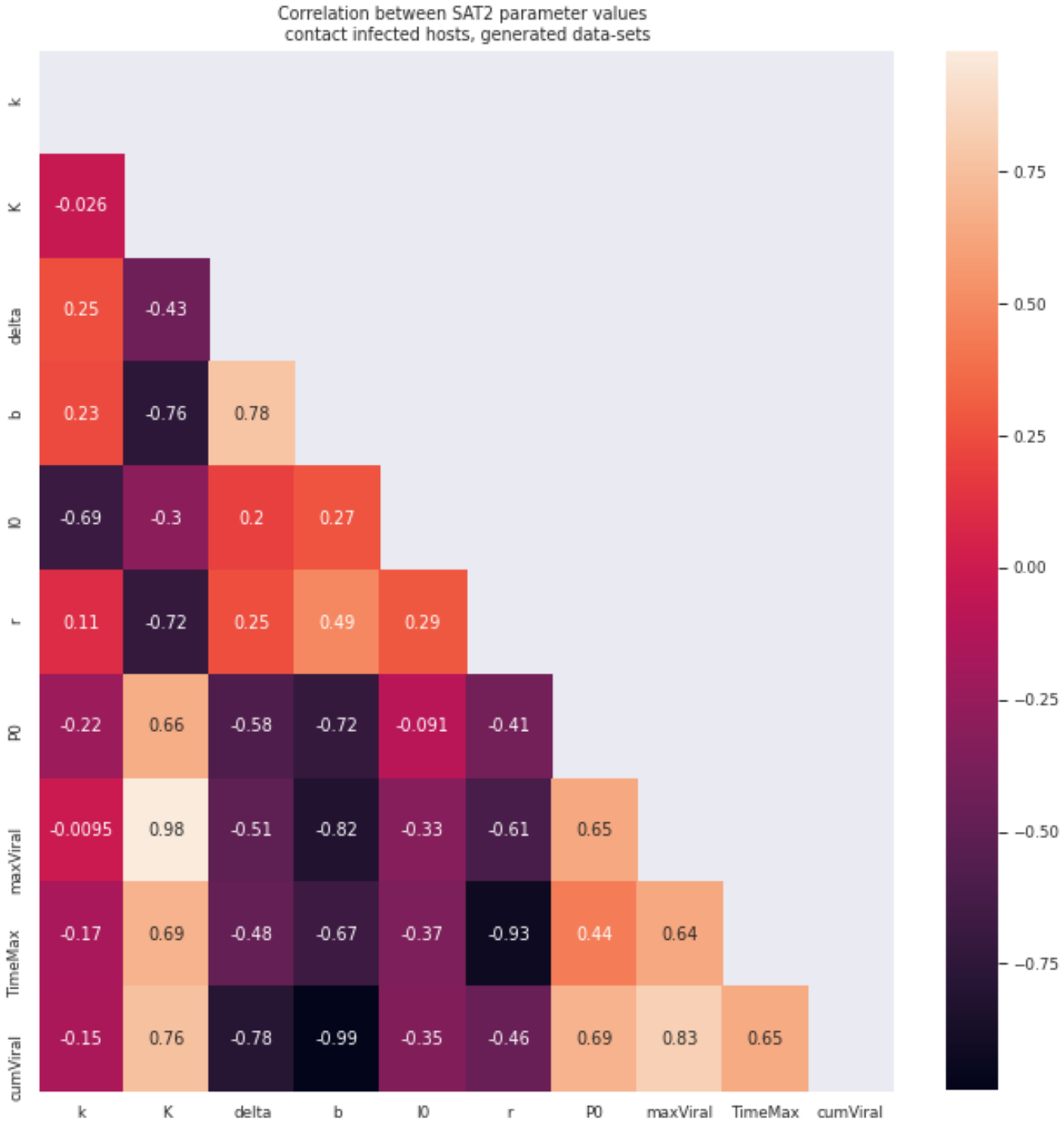

Fig. S20. Correlation values for fit parameters and derived quantities across 40,000 generated SAT2 data-sets for *contact infected* hosts

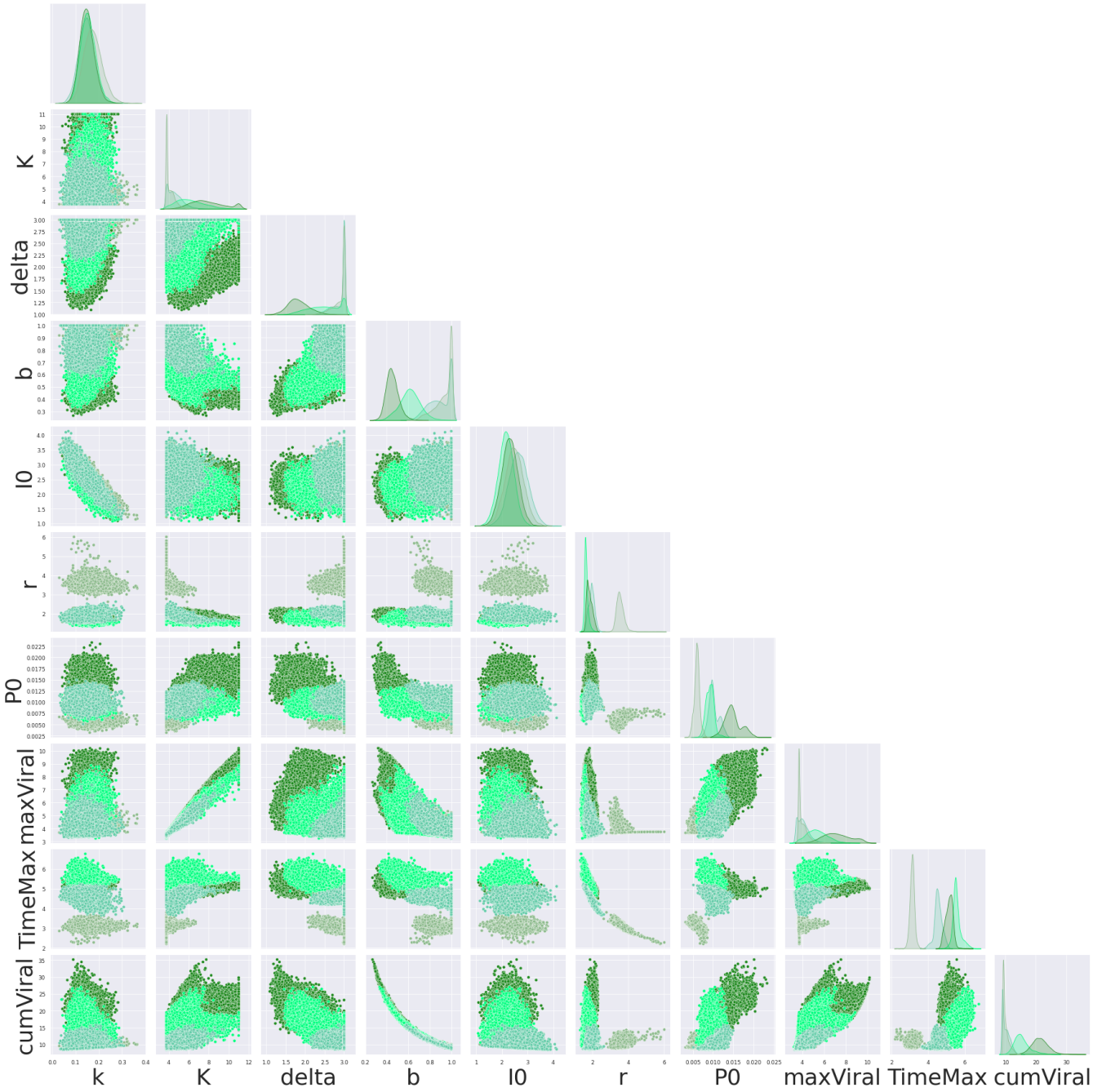

Fig. S21. Scatter plots for fit parameters and derived quantities across 40,000 generated SAT2 data-sets for *contact infected* hosts

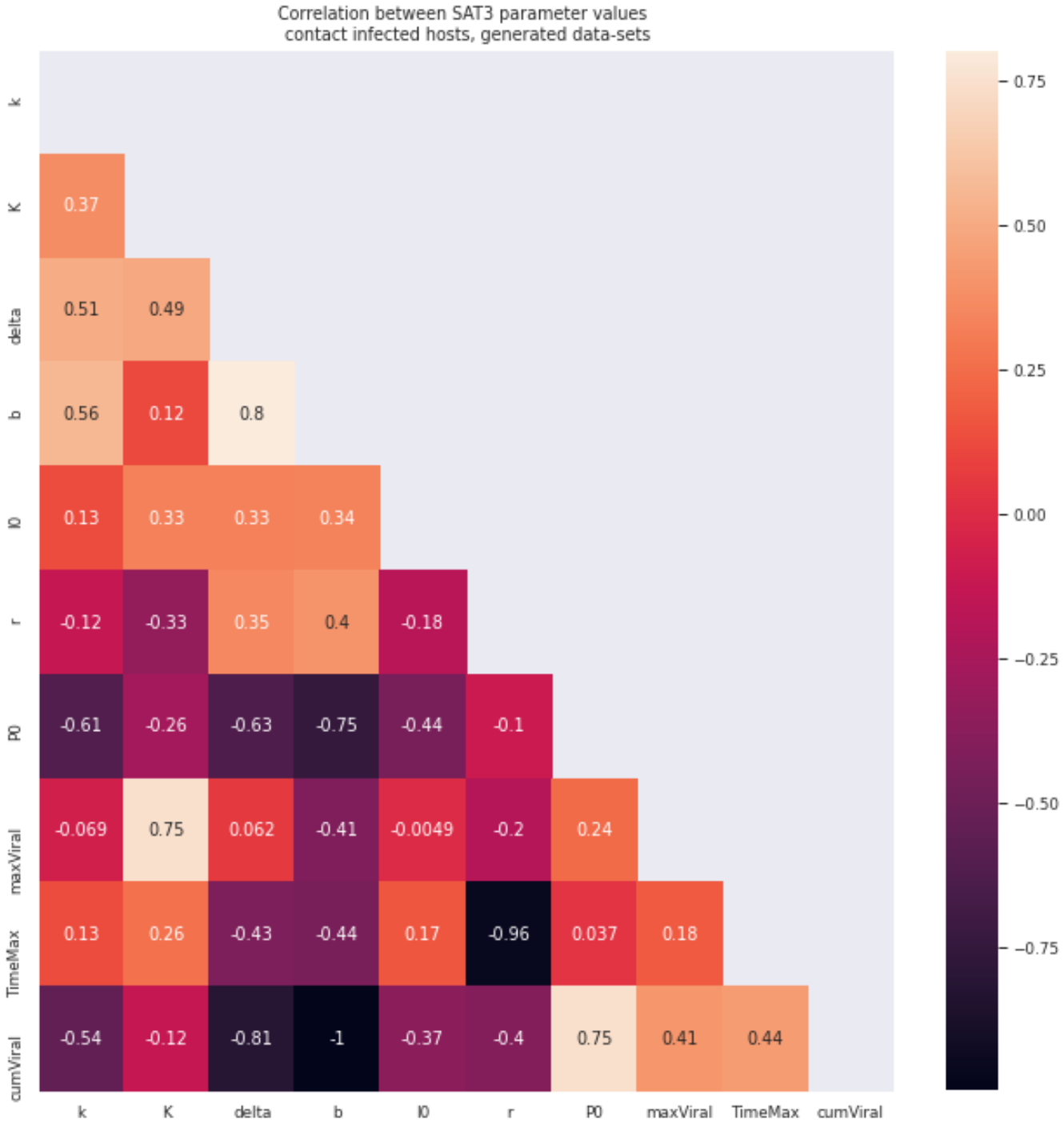

Fig. S22. Correlation values for fit parameters and derived quantities across 30,000 generated SAT3 data-sets for *contact infected* hosts

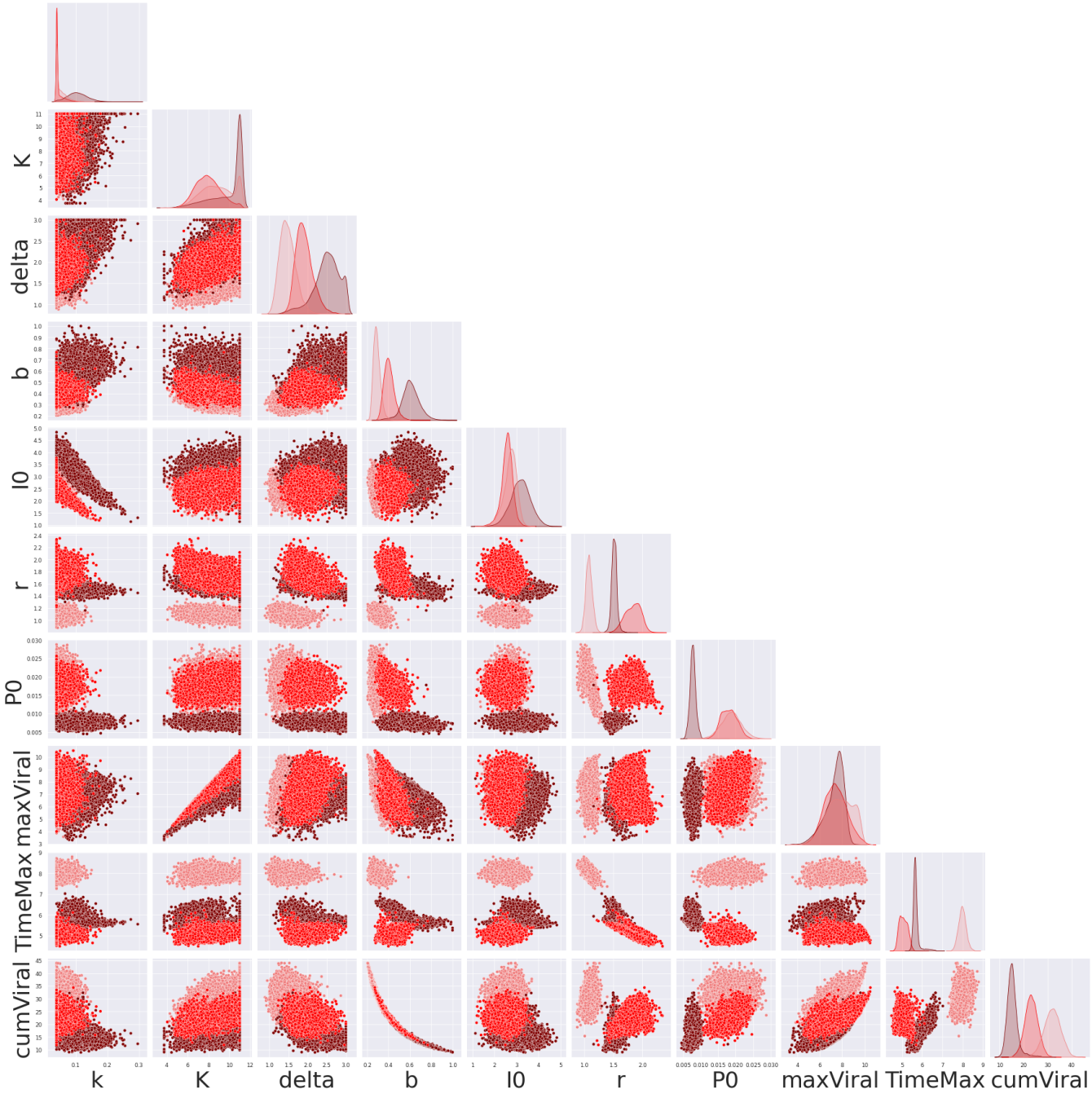

Fig. S23. Scatter plots for fit parameters and derived quantities across 30,000 generated SAT3 data-sets for *contact infected* hosts

Fig. S24. Correlation values for fit parameters and derived quantities across 40,000 generated SAT1 data-sets for *needle infected* hosts

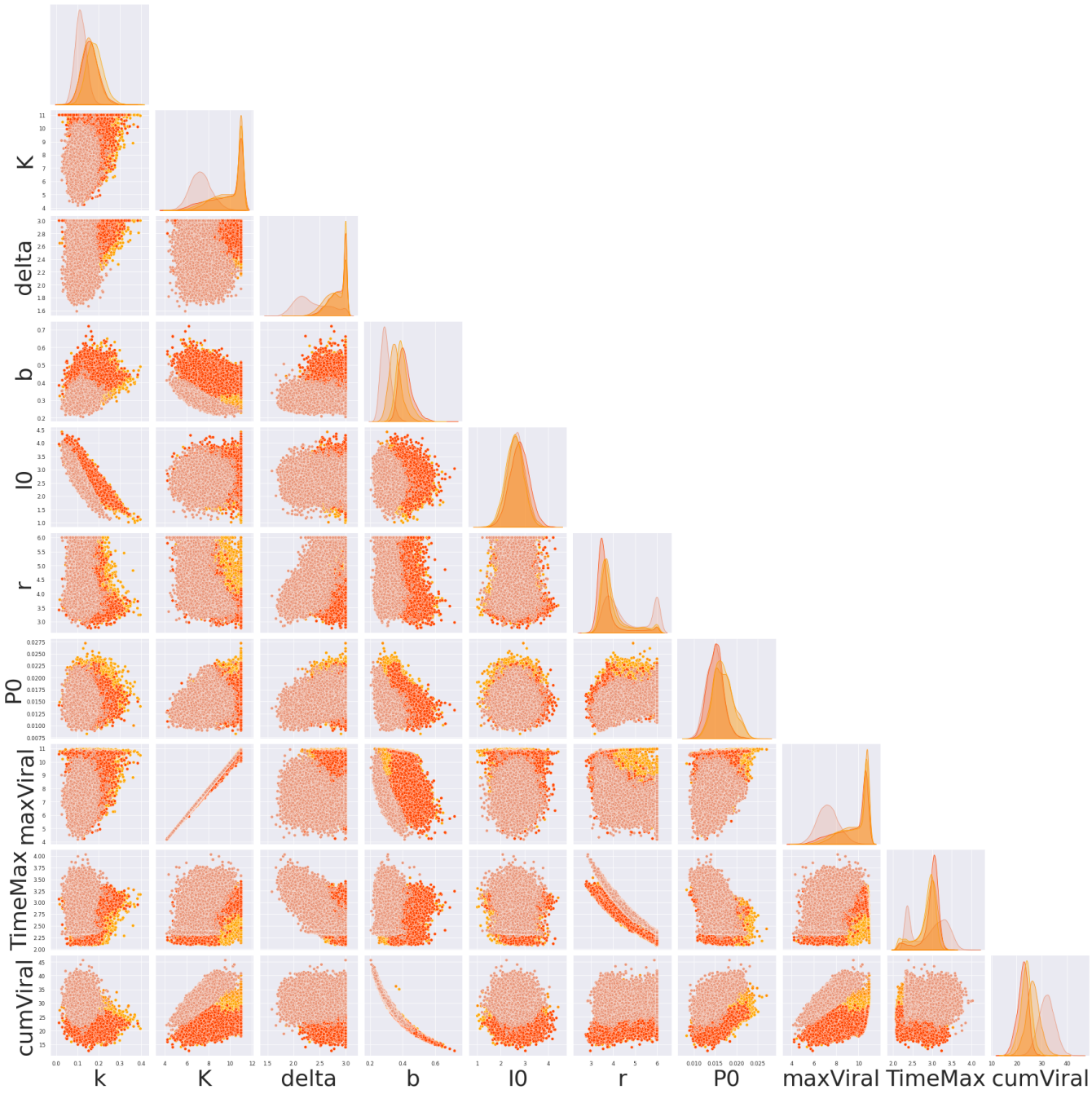

Fig. S25. Scatter plots for fit parameters and derived quantities across 40,000 generated SAT1 data-sets for *needle infected* hosts

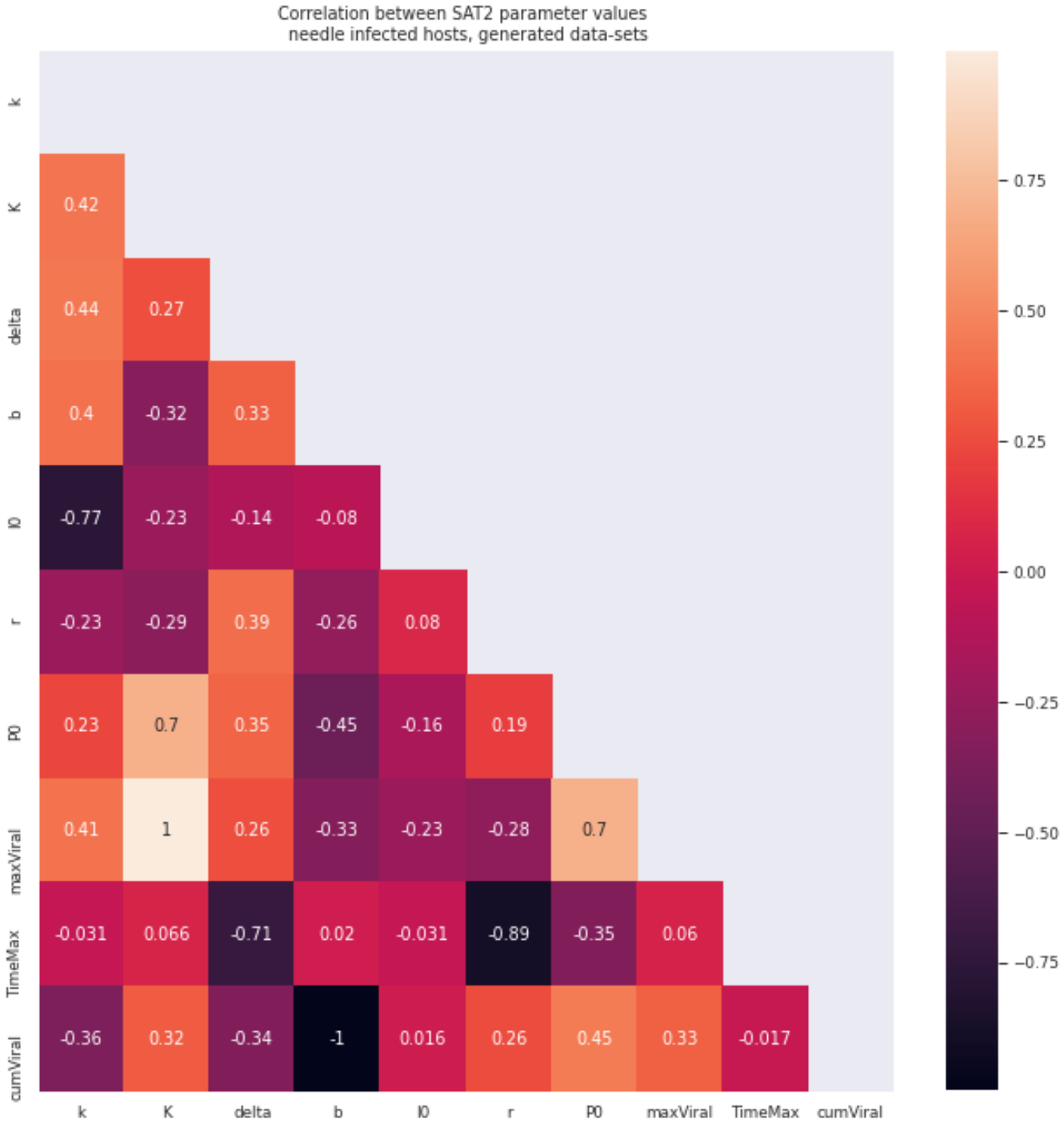

Fig. S26. Correlation values for fit parameters and derived quantities across 40,000 generated SAT2 data-sets for *needle infected* hosts

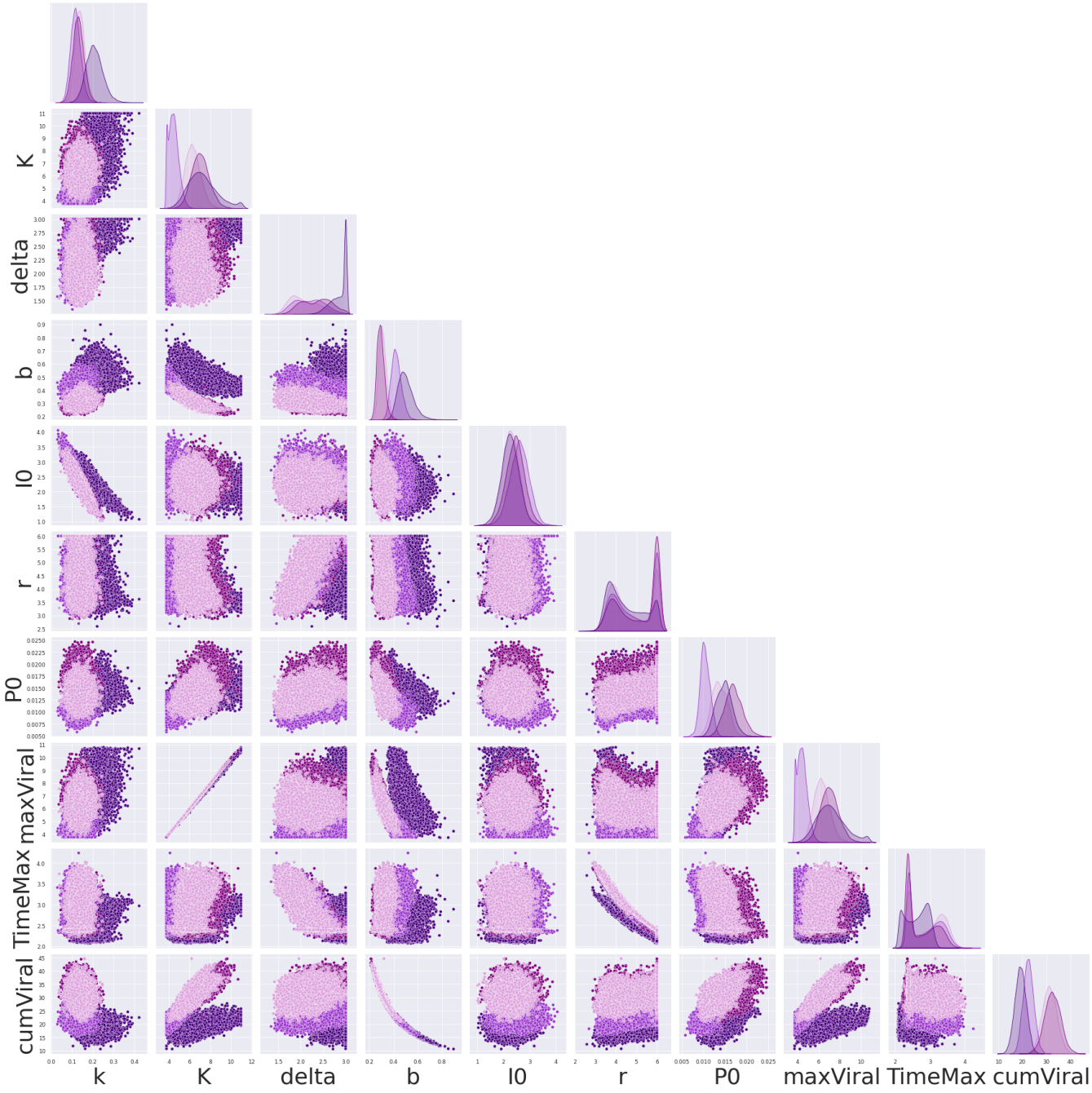

Fig. S27. Scatter plots for fit parameters and derived quantities across 40,000 generated SAT2 data-sets for *needle infected* hosts

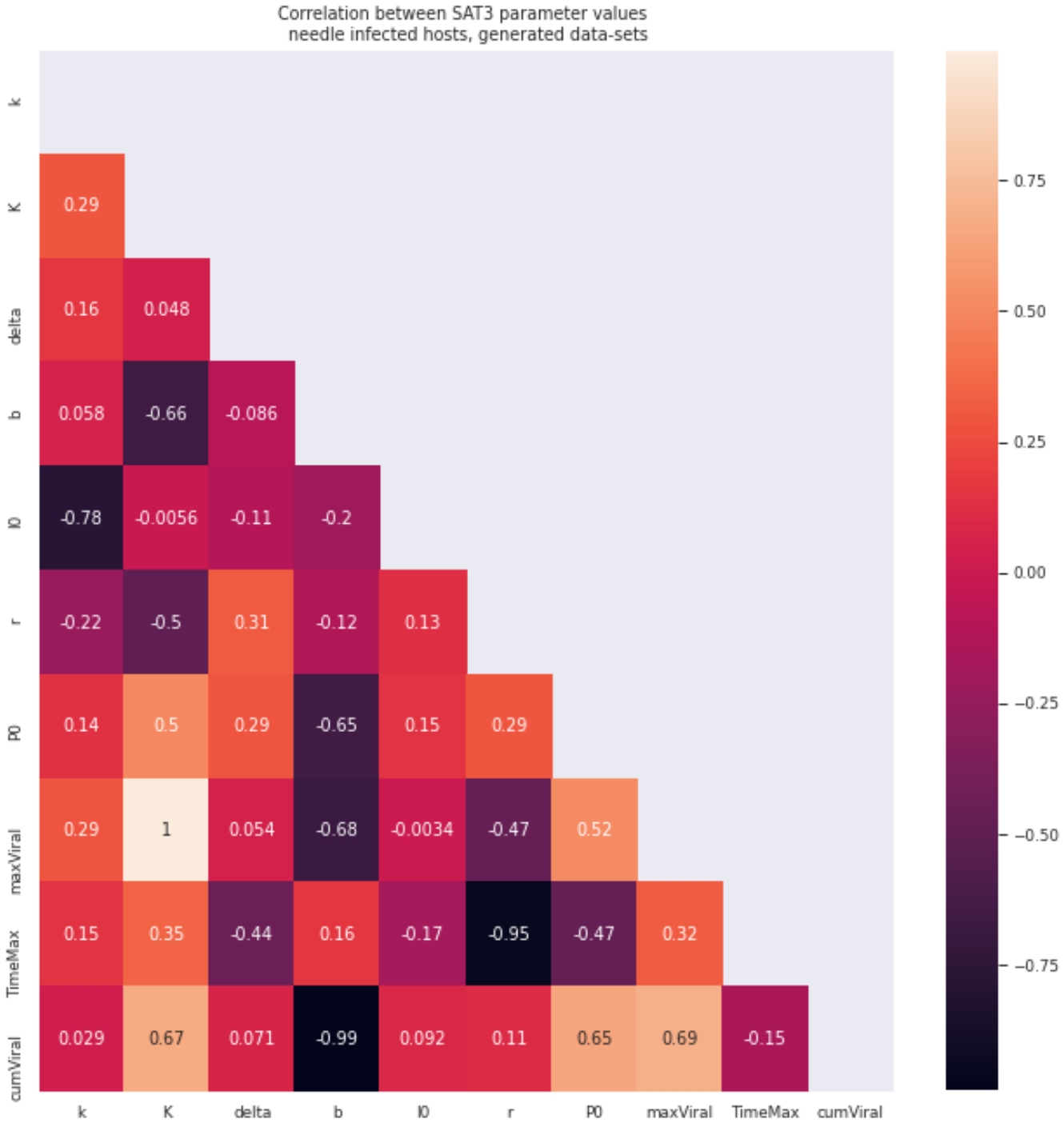

Fig. S28. Correlation values for fit parameters and derived quantities across 40,000 generated SAT3 data-sets for *needle infected* hosts

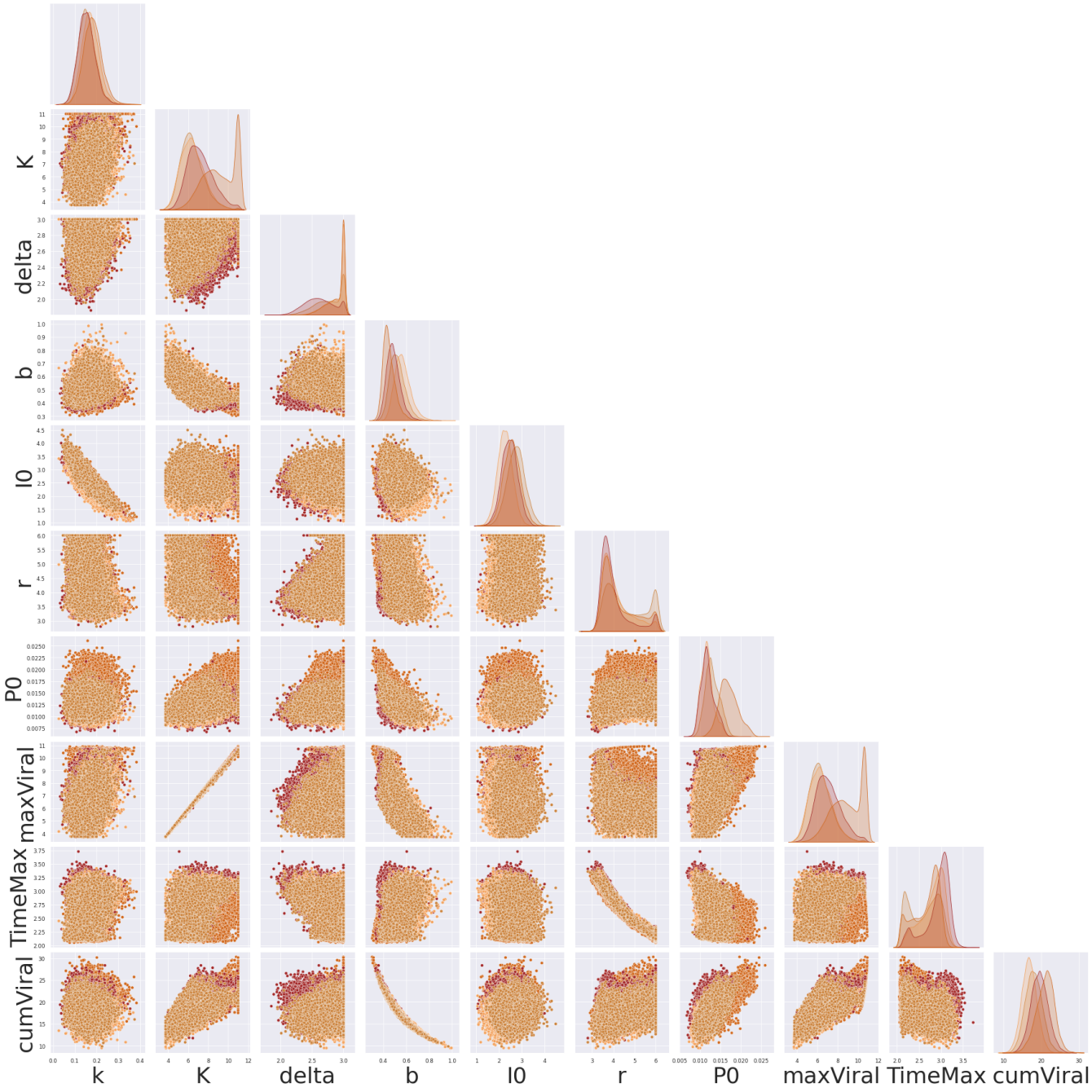

Fig. S29. Scatter plots for fit parameters and derived quantities across 40,000 generated SAT3 data-sets for *needle infected* hosts

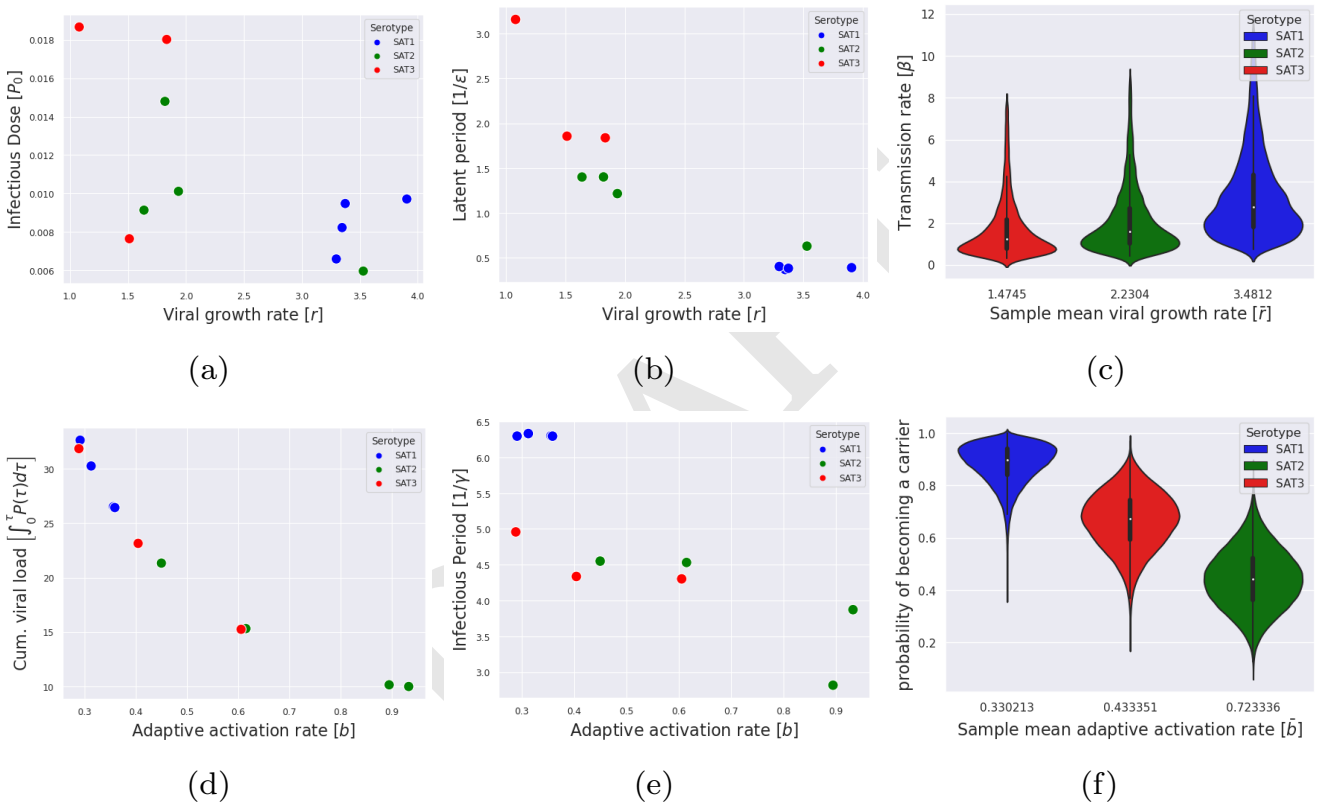

Fig. S30. Biological Relationships across scales

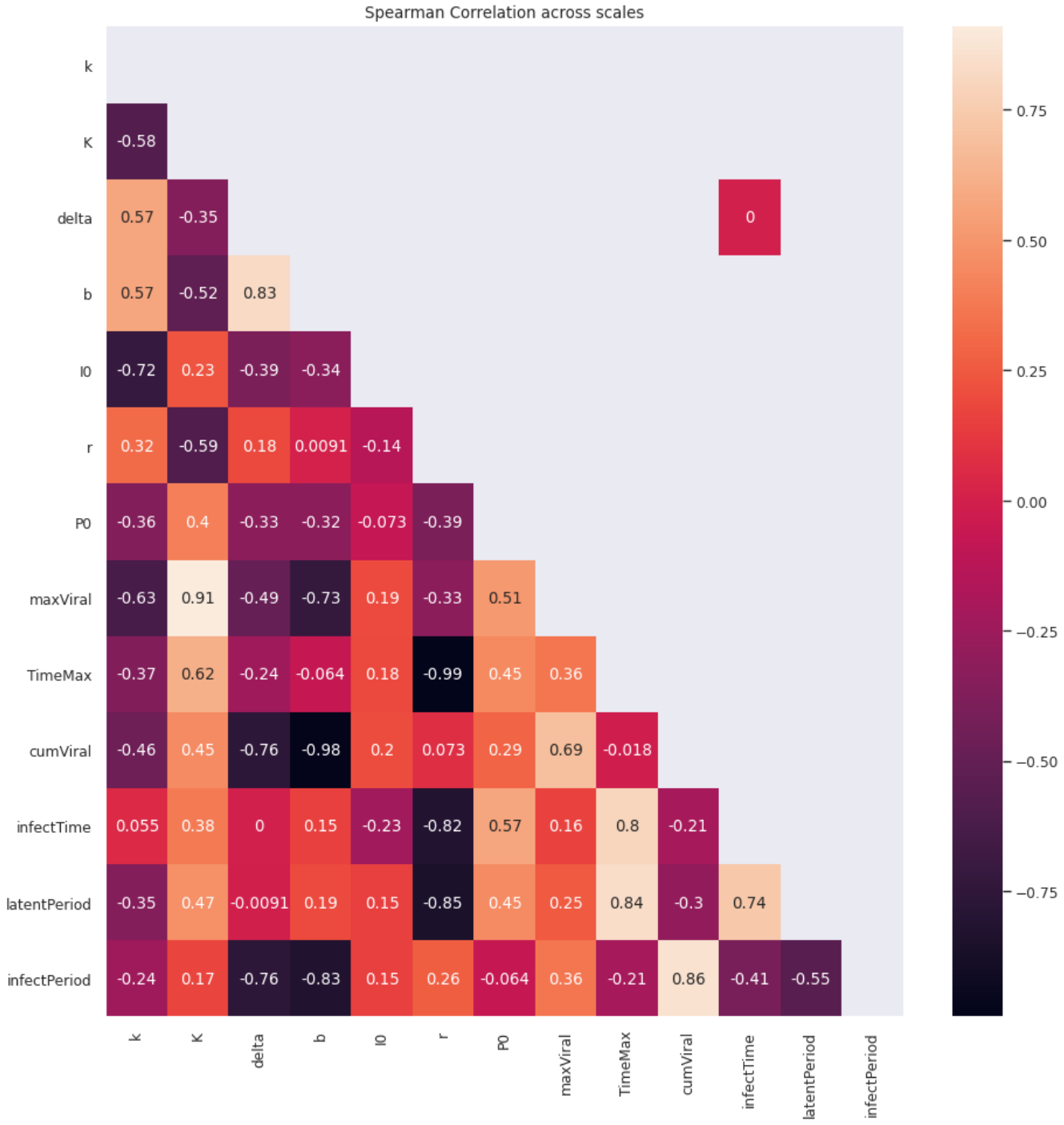

Fig. S31. correlation across biological scales