Supplementary Information S1 Text:

Fits of models (1) and (2) to patient data

We fit parameters p, β and c in model (1) to the data of [1, 2]. The best fits show that model (1) cannot describe the dynamics of SARS-CoV-2 infection. Model (1) can only generate two stages during infection. In the initial stage, viral load grows rapidly to the peak level. After that, it starts to decline as the availability of target cells decreases. This is not consistent with the observations in many patients who showed a viral plateau or even viral rebound. The best fits of model (1) to the viral load data in refs. [1, 2] are shown in Figs. S1-S3. Parameter estimates are listed in Tables S1-S3.

We also fit parameters p, k, β and c in model (2) to the same viral load data. The fitting has the same problem with model (1). The viral dynamics predicted by model (2) is very similar to that by model (1). The best fits using model (2) are shown in Figs. S4-S6 with parameter estimates listed in Tables S4-S6.

Reference

1. Wölfel R, Corman VM, Guggemos W, Seilmaier M, Zange S, Müller MA, et al. Virological assessment of hospitalized patients with COVID-2019. Nature. 2020. doi: 10.1038/s41586-020-2196-x.

2. Pan Y, Zhang D, Yang P, Poon LLM, Wang Q. Viral load of SARS-CoV-2 in clinical samples. The Lancet Infectious diseases. 2020:S1473-3099(20)30113-4. doi: 10.1016/S1473-3099(20)30113-4. PubMed PMID: 32105638.

3. Böhmer MM, Buchholz U, Corman VM, Hoch M, Katz K, Marosevic DV, et al. Outbreak of COVID-19 in Germany resulting from a single travel-associated primary case. <https://ssrn.com/abstract=3551335> 2020.

Table S1. Best fits of model (1) to the LRT viral load data in patients from Germany

Patient	β (ml/virus/day)	p (day^{-1})	c (day^{-1})	$V(0)$ RNA/ml	AIC value
#1	9.8×10^{-7}	9.7×10^{2}	6.7×10^{-1}	10^{-4}	7.890298
#2	1.8×10^{-6}	6.25×10^{2}	6.5×10^{-1}	10^{-4}	0.06341452
#3	5×10^{-4}	19	0.3	10^{-4}	-12.76443
#4	6.5×10^{-4}	2.2×10^{3}	1	10^{-4}	7.098075
#7	1.9×10^{-6}	4.3×10^{2}	0.6	10^{-4}	9.350209
#8	9.1×10^{-5}	5.8×10^{3}	0.6	10^{-4}	10.45424
#10	9.7×10^{-7}	9.4×10^{2}	0.5	10^{-4}	15.19438
#14	4.7×10^{-5}	1.2×10^{2}	2	10^{-4}	-0.409692

Table S2. Best fits of model (1) to the URT viral load data in patients from Germany

Patient	β (ml/virus/day)	p (day^{-1})	c (day^{-1})	$V(0)$ RNA/ml	AIC value
#1	10^{-2}	50	9.3×10^{-1}	10^{-4}	14.20882
#2	10^{-2}	1.1×10^{3}	1.3	10^{-4}	3.264037
#3	10^{-2}	2	0.6	10^{-4}	2.384303
#4	10^{-2}	20	1	10^{-4}	6.476089
#7	10^{-2}	4.8×10^{2}	0.9	10^{-4}	12.31662
#8	9.1×10^{-4}	2	0.6	10^{-4}	7.213507
#10	1.9×10^{-5}	45	0.6	10^{-4}	11.02112
#14	9.1×10^{-6}	1.53×10^{2}	2	10^{-4}	-0.6889368

Table S3. Best fits of model (1) to the viral load data in a patient from China

	β (ml/virus/day)	p (day^{-1})	c (day^{-1})	$V(0)$ RNA/ml	AIC value
URT	2.6×10^{-5}	4.97×10^{2}	78	10^{-4}	12.35573
LRT	5.4×10^{-7}	3.3×10^{3}	5	10^{-4}	6.341917

Table S4. Best fits of model (2) to the LRT viral load data in patients from Germany

Patient	β (ml/virus/day)	p (day^{-1})	k (day^{-1})	c (day^{-1})	V(0) RNA/ml	AIC value
#1	1.9×10^{-6}	5.9×10^{2}	33	0.6	10^{-4}	9.615257
#2	3.6×10^{-6}	1.5×10^{4}	0.6	20	10^{-4}	2.23195
#3	6×10^{-4}	5×10^{3}	0.3	82	10^{-3}	-10.92767
#4	5.1×10^{-6}	1.2×10^{2}	2	2	10^{-4}	4.329506
#7	7.7×10^{-6}	7×10^{2}	1	0.8	10^{-3}	10.38379
#8	5.9×10^{-6}	4×10^{3}	97	0.6	10^{-4}	12.4546
#10	4.7×10^{-5}	7.23×10^{2}	0.5	0.6	10^{-4}	16.78154
#14	5.9×10^{-5}	5×10^{3}	2	80	10^{-3}	1.590262

Table S5. Best fits of model (2) to the URT viral load data in patients from Germany

Patient	β (ml/virus/day)	p (day^{-1})	k (day^{-1})	c (day^{-1})	V(0) RNA/ml	AIC value
#1	10^{-2}	10^{3}	0.9	39	10^{-4}	16.23456
#2	10^{-2}	10^{4}	1	94	10^{-4}	7.645712
#3	10^{-3}	9×10^{2}	0.6	3×10^{2}	10^{-4}	4.557492
#4	5.8×10^{-4}	10	90	1	10^{-4}	5.980355
#7	9×10^{-5}	3×10^{2}	10^{2}	0.9	10^{-4}	14.33665
#8	9.9×10^{-4}	2	10^{2}	0.6	10^{-4}	-5.213483
#10	5.2×10^{-5}	2.96×10^{2}	0.6	4	10^{-4}	13.78441
#14	3.9×10^{-5}	1.3×10^{2}	3	2	10^{-4}	0.2970936

Table S6. Best fits of model (2) to the viral load data from a patient in China

	β (ml/virus/day)	p (day^{-1})	k (day^{-1})	c (day^{-1})	V(0) RNA/ml	AIC value
URT	2.6×10^{-5}	1.2×10^{3}	2.4×10^{2}	1.9×10^{2}	10^{-3}	14.35748
LRT	5.6×10^{-7}	3.3×10^{3}	1.7×10^{2}	5	10^{-4}	8.34129

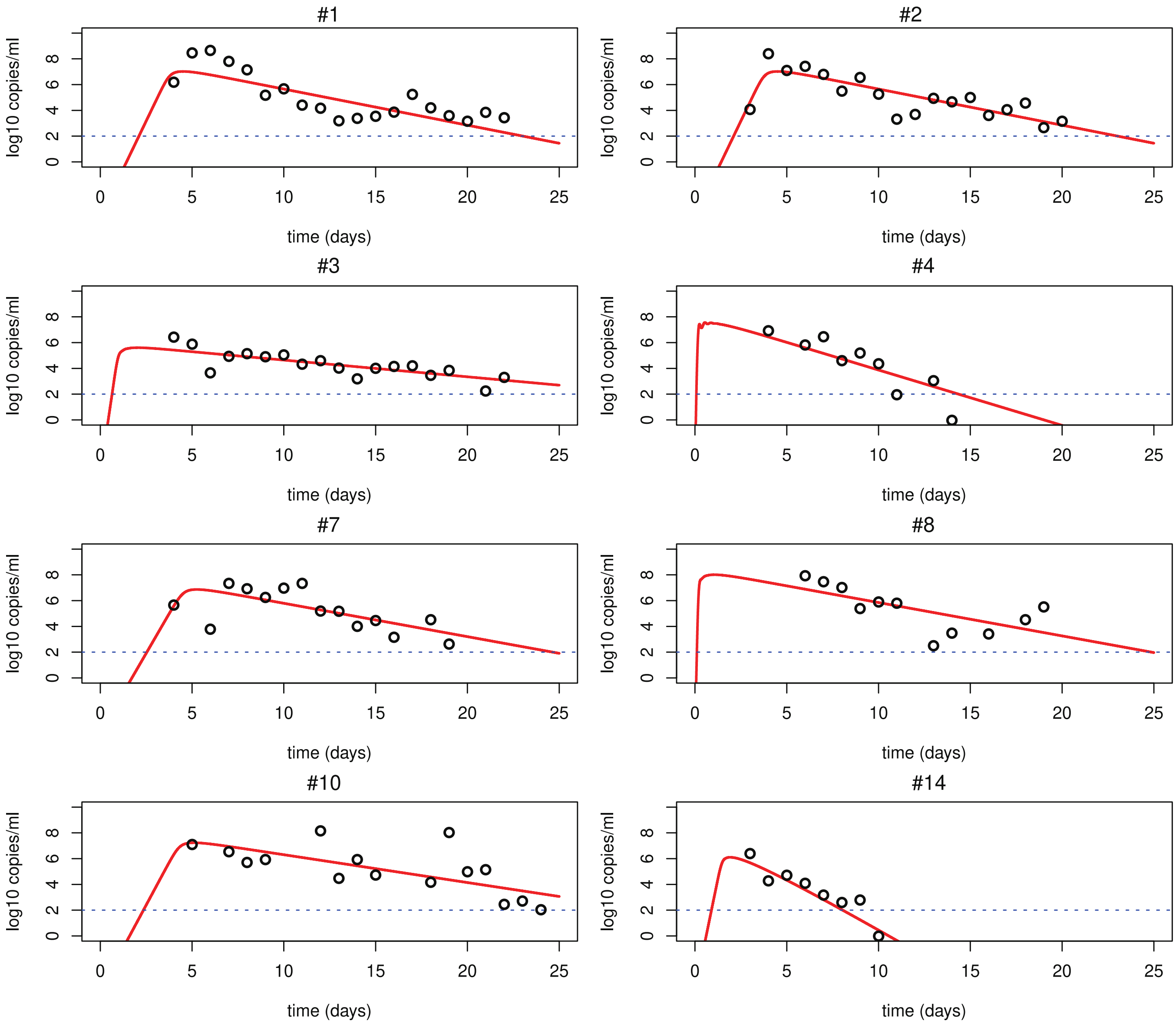

Figure S1. Best fits of model (1) to the LRT viral load data in ref. [1]. Patients #1, #2, #3, #4, #7, #8, #10 and #14 are the cases in refs. [1, 3].

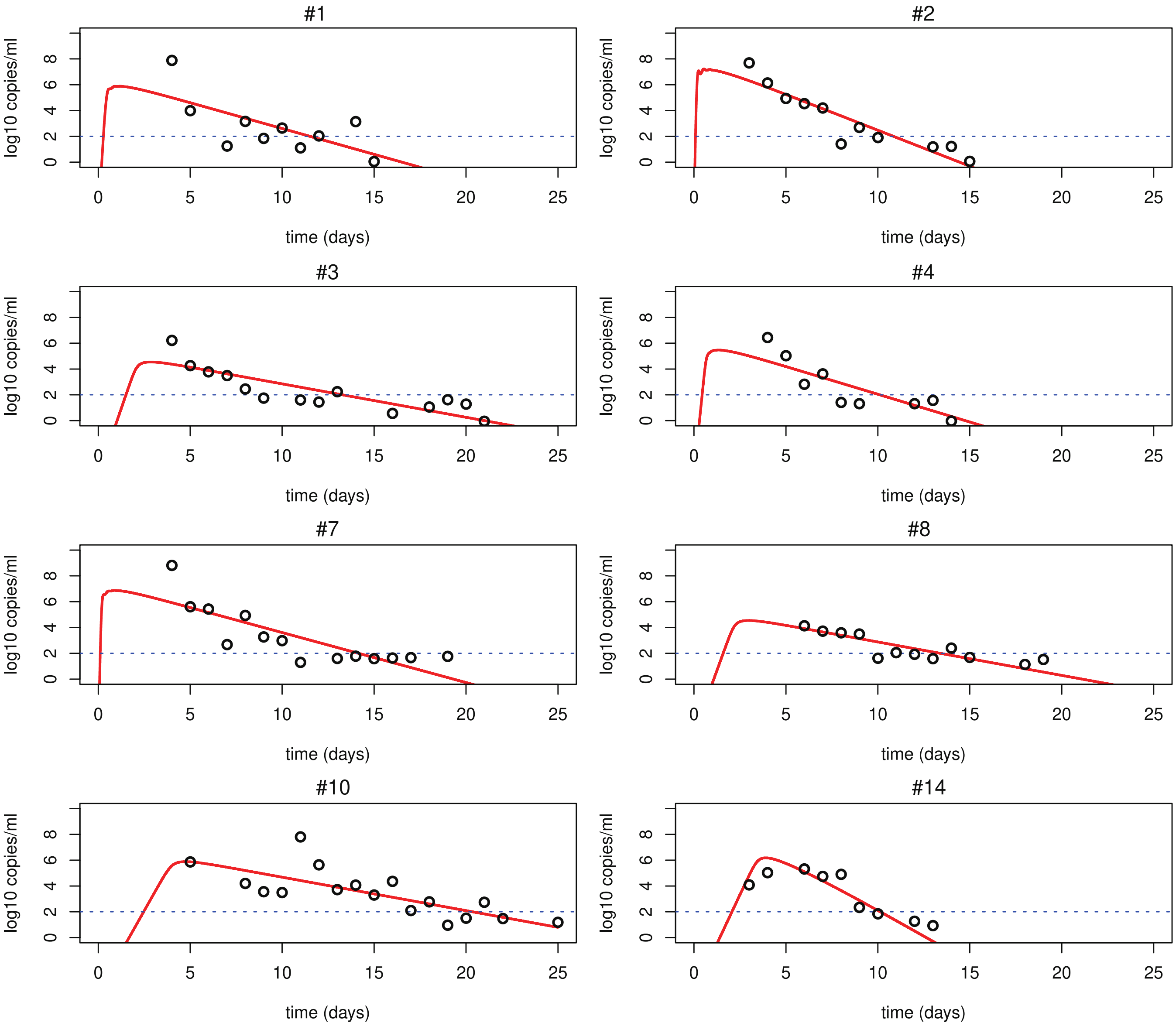

Figure S2. Best fits of model (1) to the URT viral load data of ref. [1]. Patients #1, #2, #3, #4, #7, #8, #10 and #14 are the cases in refs. [1, 3].

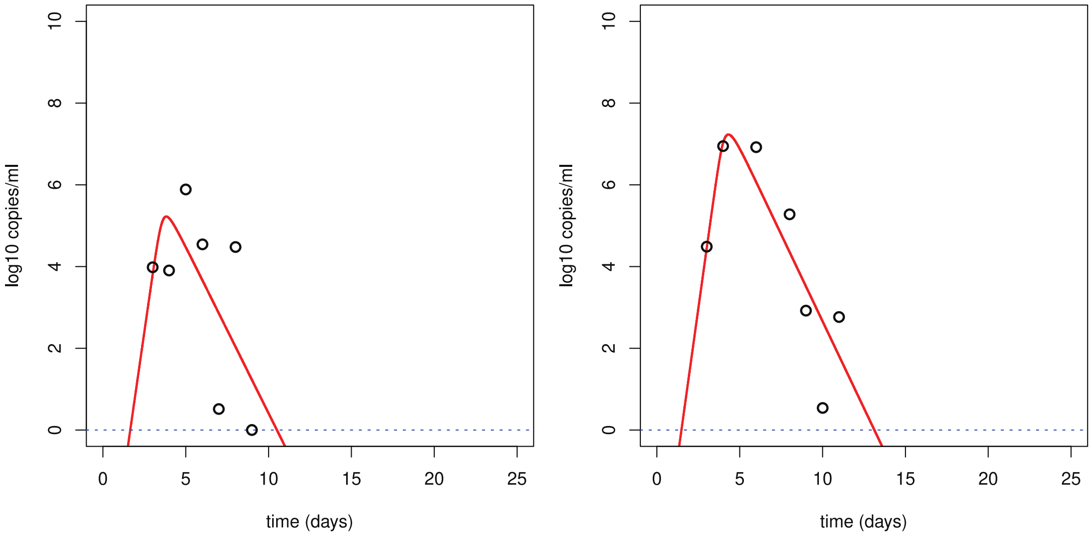

Figure S3. Best fits of model (1) to the URT (left) and LRT (right) viral load data of ref. [2].

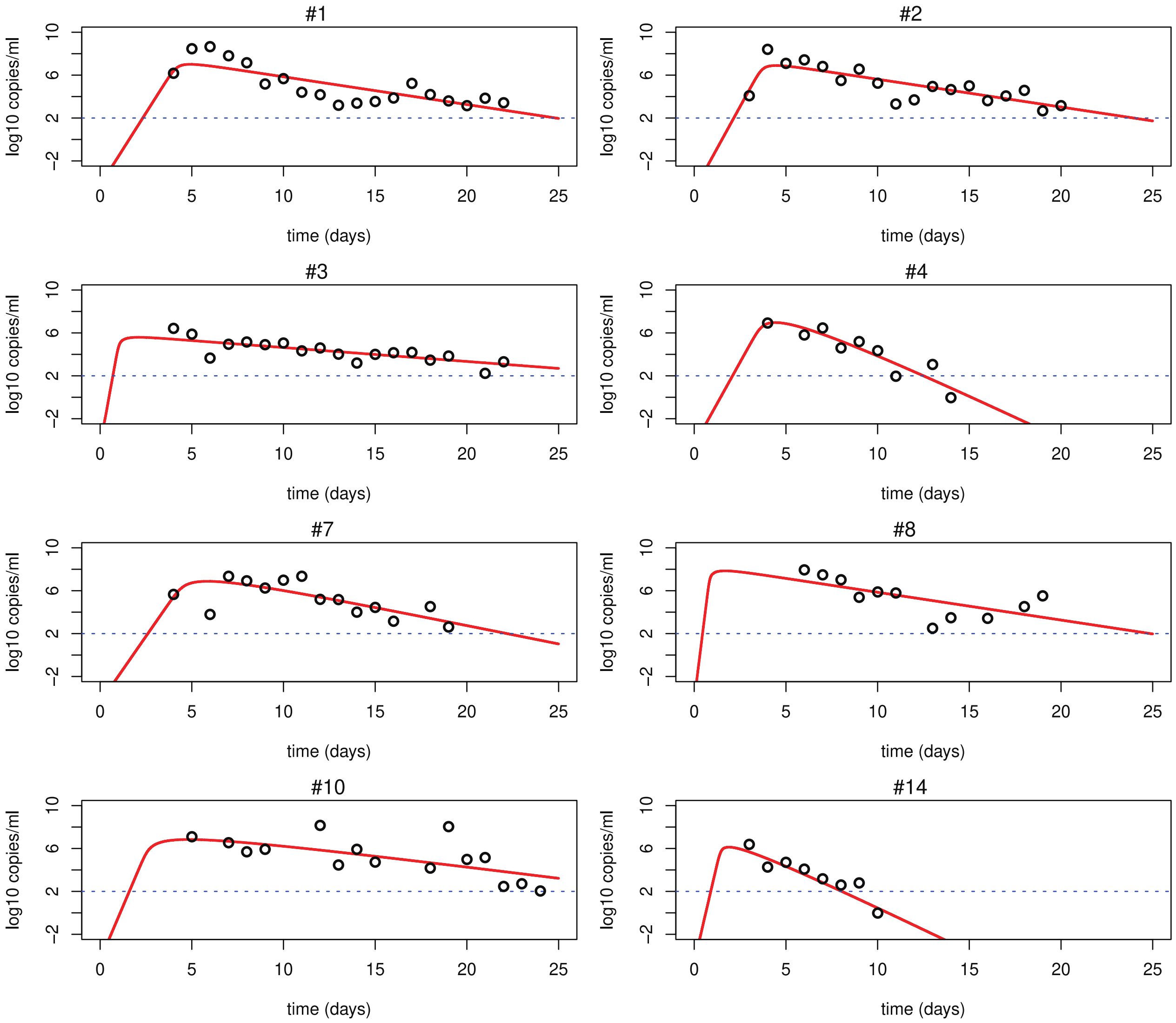

Figure S4. Best fits of model (2) to the LRT viral load data of ref. [1].

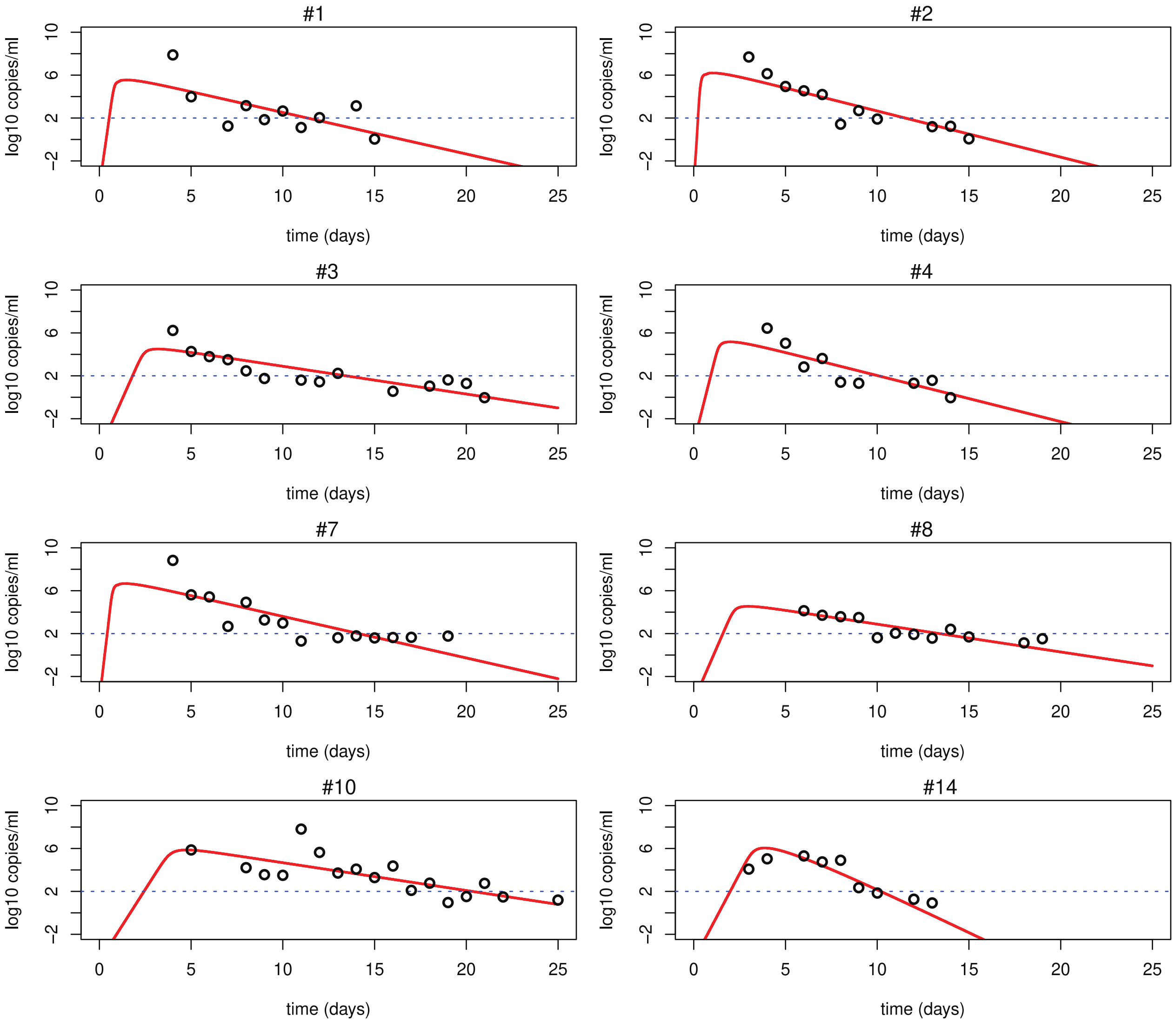

Figure S5. Best fits of model (2) to the URT viral load data of ref. [1].

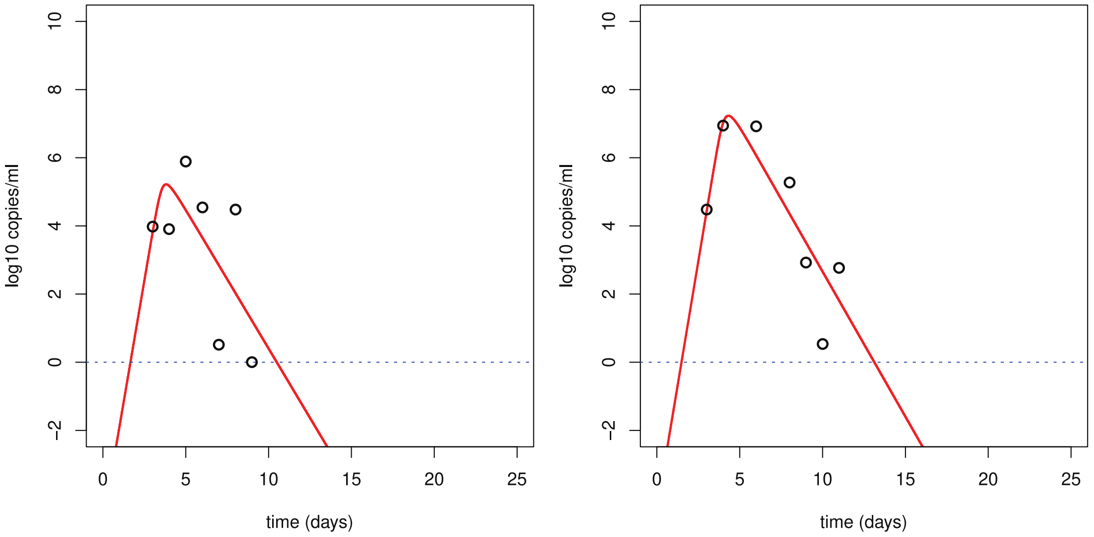

Figure S6. Best fits of model (2) to the URT (left) and LRT (right) viral load data of ref. [2].