

Supplementary Information

Modelling virus and antibody dynamics during dengue infection suggests a role for antibody in virus clearance

Short title: Modelling dengue virus and antibody dynamics

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Figure S1A: Fit of the model to virus and IgG measurements for only secondary DENV1-infected subjects for the model variant in which antibody removed infected cells. Each plot shows an individual patient. Virus data is shown in black and IgG data in red. Parameters z_0 , η_1 , η_2 , IP and SF fitted as patient specific, other parameters fitted per group. Pink, grey and blue curves show 100 samples from the posterior distributions of antibody, virus and target cell trajectories, respectively. Median fits are shown as bold lines (red shows IgG, black

shows virus). Parameter estimates are shown in Table S4A.

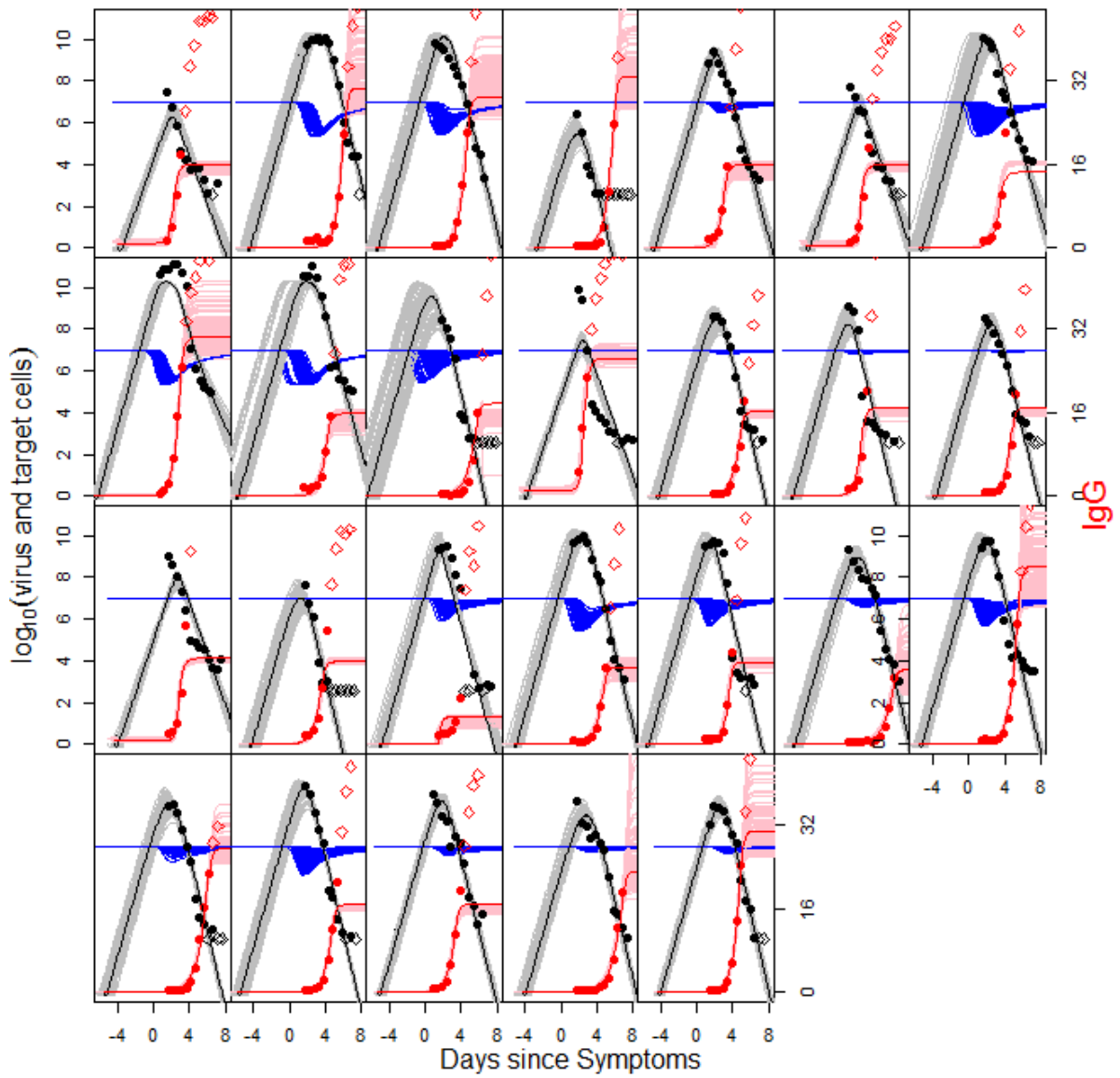


Figure S2B: Fit of the model to virus and IgG measurements for DENV2-infected subjects for the model variant in which antibody removes infected cells. Each plot shows an individual patient. Virus data is shown in black and IgG data in red. Parameters z_0 , η_1 , η_2 , IP and SF fitted as patient specific, other parameters fitted per group. Pink, grey and blue curves show 100 samples from the posterior distributions of antibody, virus and target cell trajectories, respectively. Median fits are shown as bold lines (red shows IgG, black shows virus). Parameter estimates are shown in Table S1A.

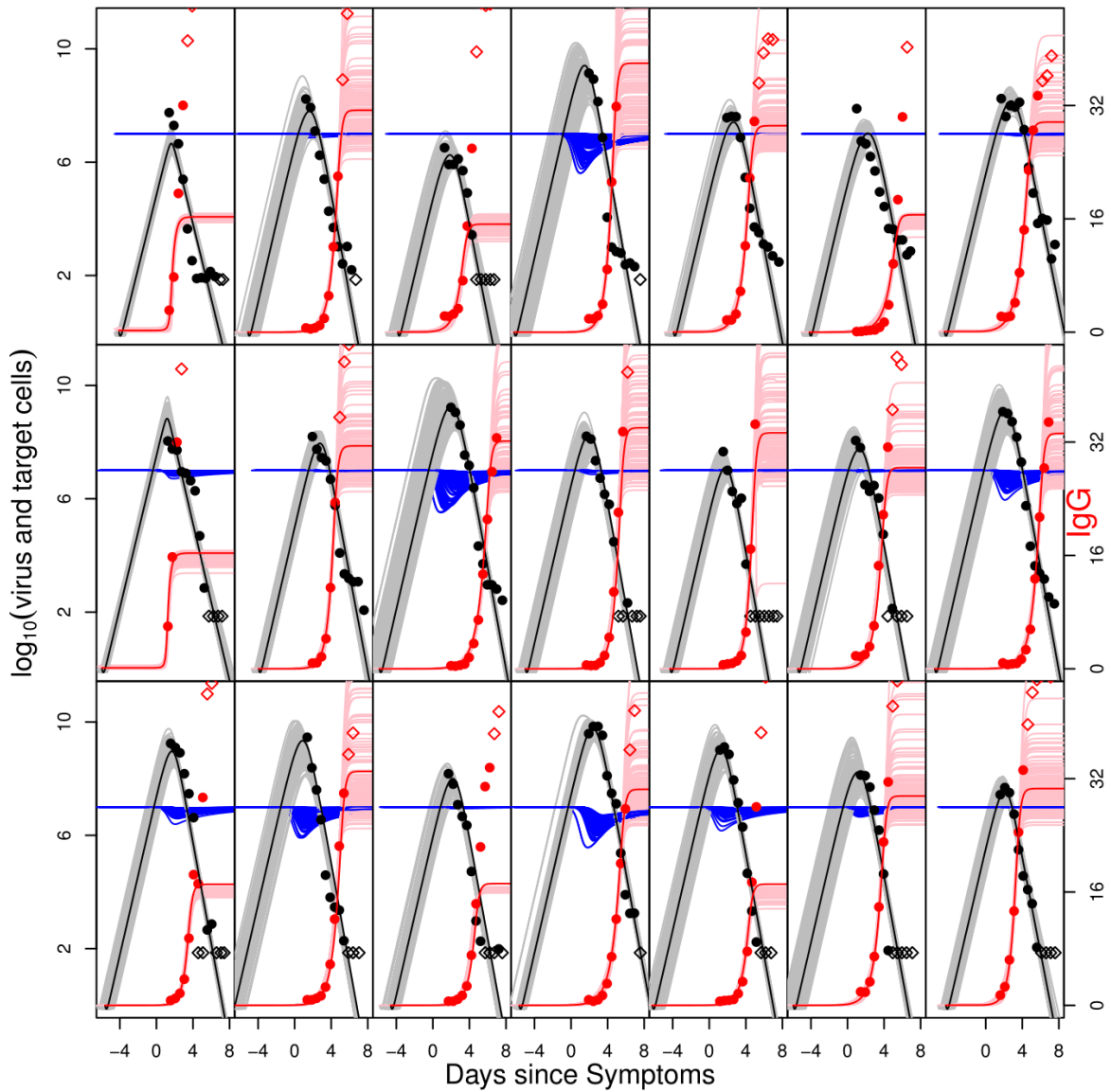


Figure S3C: Fit of the model to virus and IgG measurements for only secondary DENV1-infected subjects for the model variant in which antibody removes virus. Each plot shows an individual patient. Virus data is shown in black and IgG data in red. Parameters z_0 , η_1 , η_2 , IP and SF fitted as patient specific, other parameters fitted per group. Pink, grey and blue curves show 100 samples from the posterior distributions of antibody, virus and target cell trajectories, respectively. Median fits are shown as bold lines (red shows IgG, black shows virus). Parameter estimates are shown in Table S2B.

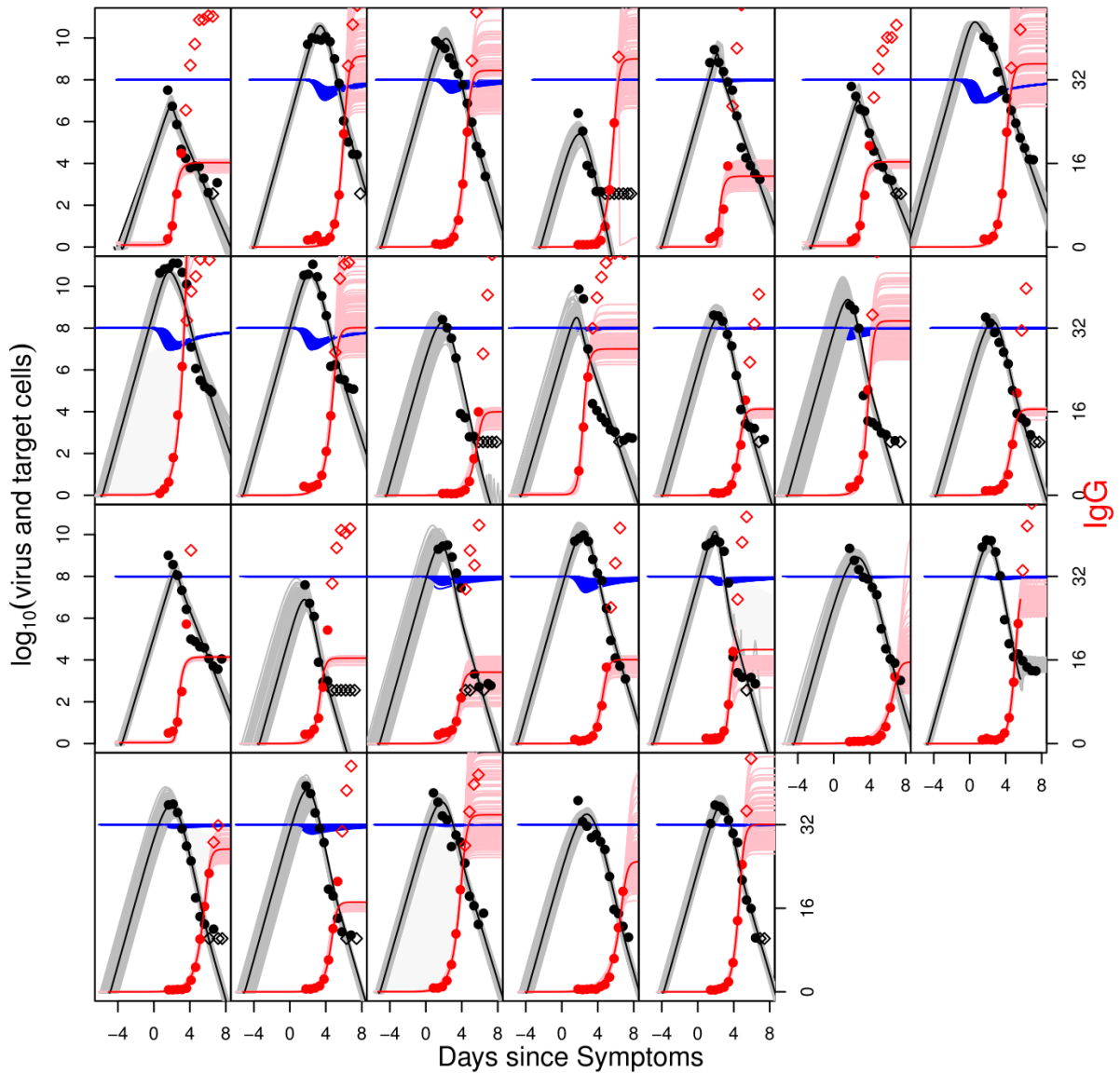


Figure S4D: Fit of the model to virus and IgG measurements for DENV2-infected subjects for the model variant in which antibody removes virus. Each plot shows an individual patient. Virus data is shown in black and IgG data in red. Parameters z_0 , η_1 , η_2 , IP and SF fitted as patient specific, other parameters fitted per group. Pink, grey and blue curves show 100 samples from the posterior distributions of antibody, virus and target cell trajectories, respectively. Median fits are shown as bold lines (red shows IgG, black shows virus). Parameter estimates are shown in Table S2B.

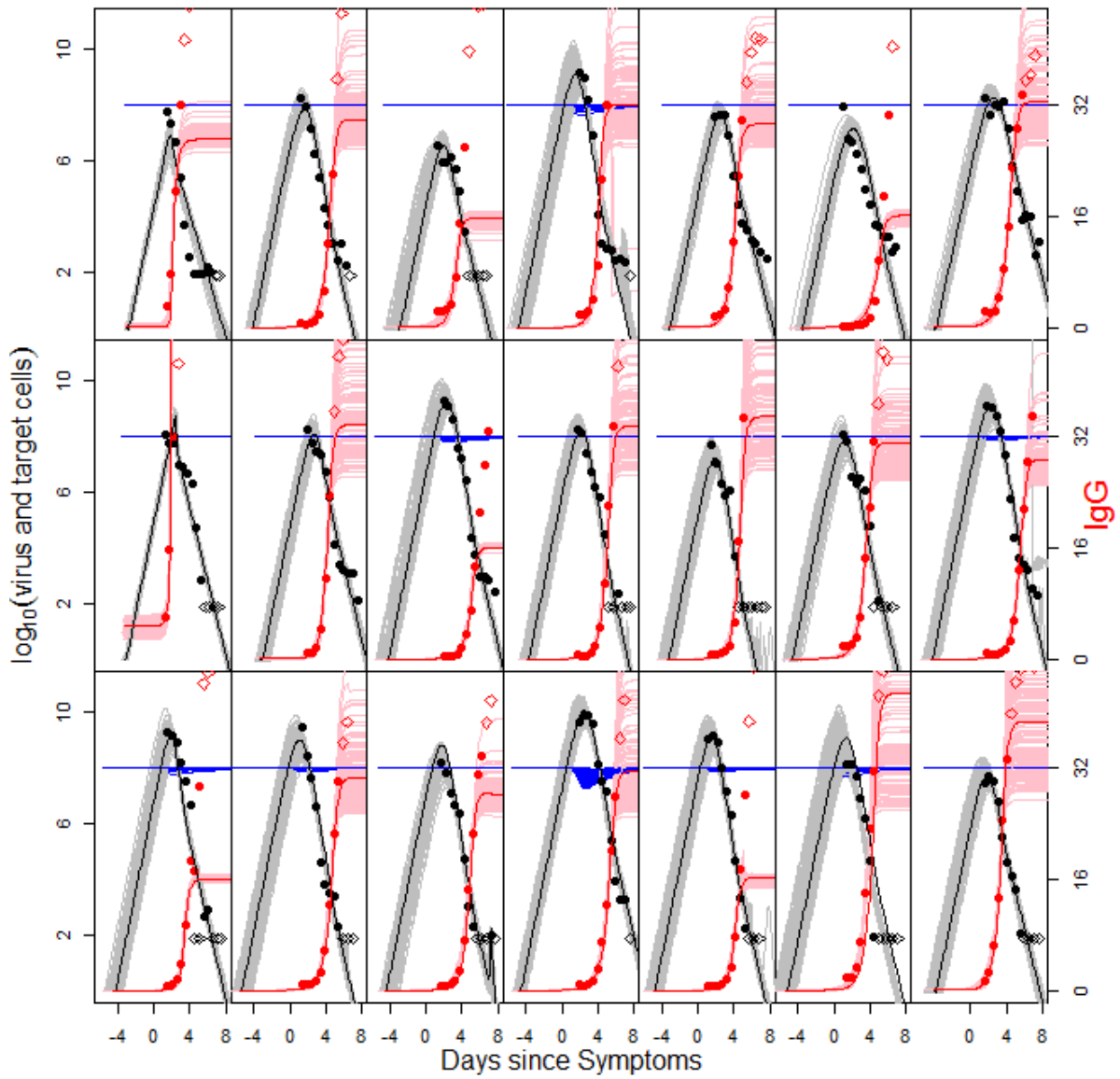


Figure S5E: Fit of the model to virus and IgM measurements for DENV1-infected subjects for the model variant in which antibody removed virus, but with the scaling factor parameter estimated as common to all subjects, compared to being patient specific in the main paper. Each plot shows an individual patient. Virus data is shown in black and IgM data in purple. Parameters z_0 , η_1 , η_2 , and IP fitted as patient specific, other parameters fitted per group. Mauve, grey and blue curves show 100 samples from the posterior distributions of antibody, virus and target cell trajectories, respectively. Median fits are shown as bold lines (purple shows IgM, black shows virus). Subjects classified as primary infections highlighted with green outline. **The loglikelihood of this model is -759, and the estimate of the scaling factor parameter is 0.093 and 95% CI (0.080, 0.111). This model fits the data fairly well, but not as well as the model with the patient level scaling factor (loglikelihood: -539).**

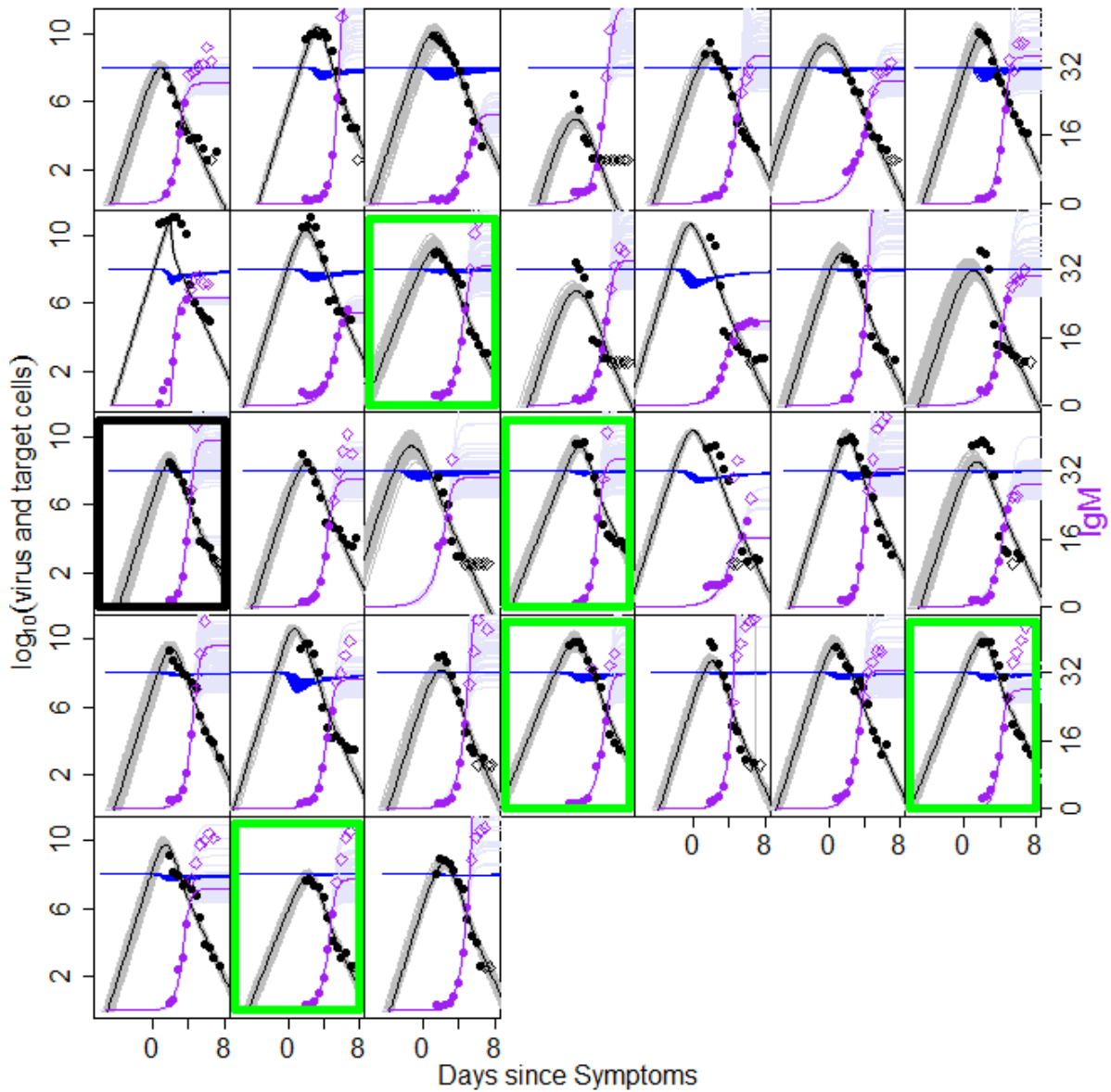


Figure S6F: Fit of the model to virus and IgM measurements for DENV2-infected subjects for the model variant in which antibody removed virus, but with the scaling factor parameter estimated as common to all subjects, compared to being patient specific in the main paper. Each plot shows an individual patient. Virus data is shown in black and IgM data in purple. Parameters z_0 , η_1 , η_2 , and IP fitted as patient specific, other parameters fitted per group. Mauve, grey and blue curves show 100 samples from the posterior distributions of antibody, virus and target cell trajectories, respectively. Median fits are shown as bold lines (purple shows IgM, black shows virus). **The loglikelihood of this model is -757, and the estimate of the scaling factor parameter is 0.086 (95% CI: 0.078, 0.110). This model fits the data fairly well, but not as well as the model with the patient level scaling factor (loglikelihood: -647).**

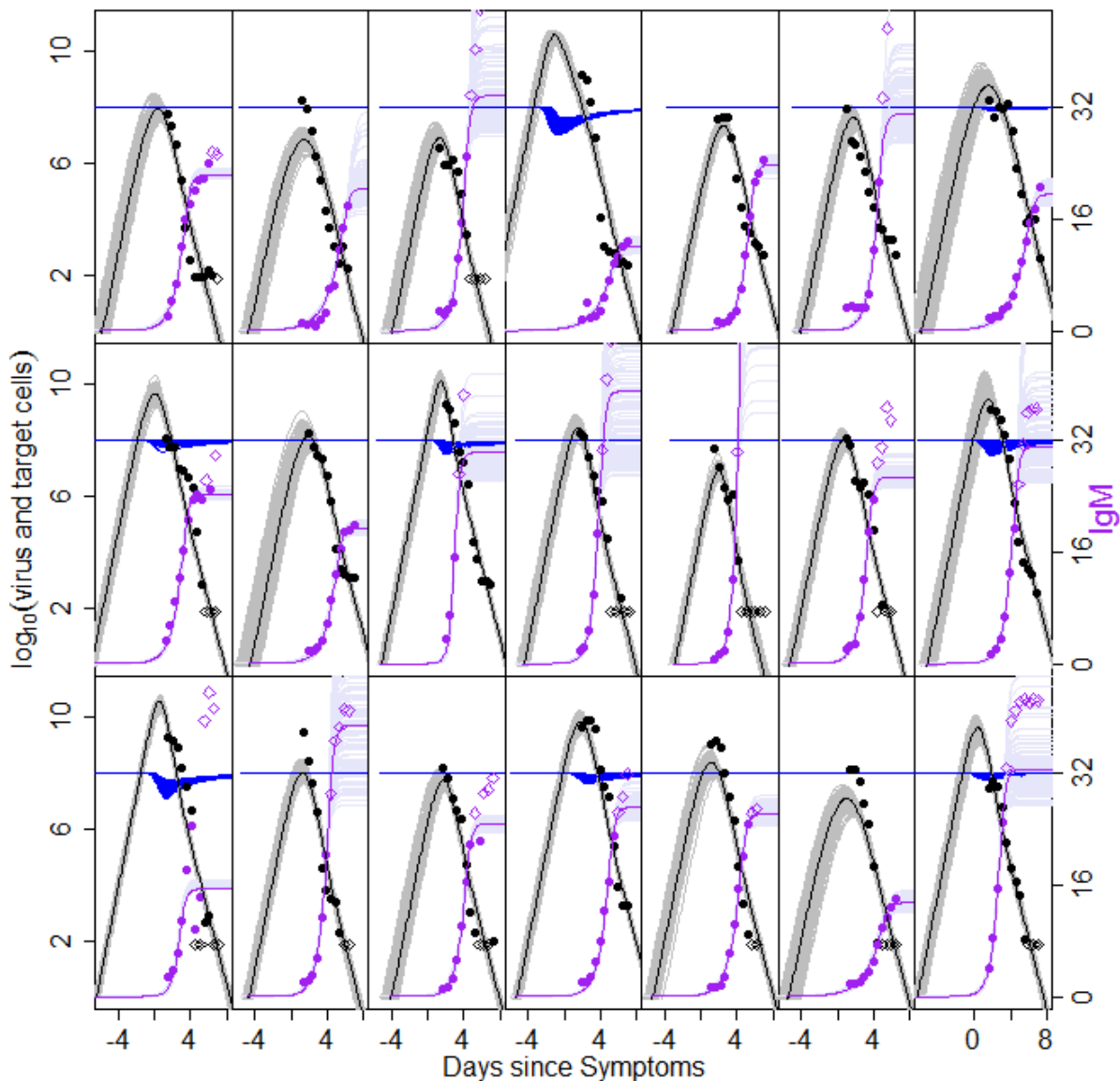


Table S1A: Parameter estimates for the model with ADCC, in which antibody removes infected cells. The model was separately fitted to IgG data for DENV1 and DENV2 infections. For patient specific parameters (i.e. the immune response parameters and the incubation period, IP), median [IQR] and {minimum, maximum} estimates across subjects are reported. For parameters assumed to be the same for all infections with the same serotype (β and κ), the median posterior estimate and 95% CI are reported. Parameters z_0 , η_1 , η_2 , IP and SF were fitted as patient-specific and others as common to all patients in the fitted group.

Serotype	Parameter	Parameter Estimates
DENV1	z_0	0.0134 [3.27x10 ⁻³ , 0.0341] {7.42x10 ⁻⁴ , 1.11}
	η_1	1.54 [1.40, 1.84] {1.00, 8.64x10 ²⁰⁰ }
	IP	4.86 [4.30, 5.49] {2.93, 6.74}
	κ	4.33 (4.23, 4.42)
	SF	0.139 [0.0507, 0.647] {0.0135, 3.69}
	η_2	3.53 [1.39e-01, 1.38e+04] {1.83e-07, 7.58e+203}
	<i>Log likelihood</i>	-720
DENV2	z_0	6.46x10 ⁻³ [1.43 x10 ⁻³ , 0.0692] {2.54x10 ⁻⁴ , 0.367}
	η_1	1.38 [1.29, 1.70] {1.08, 2.11x10 ¹⁵ }
	IP	5.11 [4.29, 5.85] {3.83, 6.89}
	κ	4.17 (4.08, 4.26)
	SF	0.083 [0.041, 0.244] {0.0160, 0.648}
	η_2	0.196 [7.67x10 ⁻³ , 16.6] {4.68x10 ⁻⁴ , 9.69x10 ¹⁷ }
	<i>Log likelihood</i>	-482

Table S2B: Parameter estimates for the model with virus neutralisation, in which antibody removes virus. The model was separately fitted to IgG data for DENV1 and DENV2 infections. For immune response parameters and the incubation period which are patient specific parameters, median (IQR) and min and max are reported. For the group-level parameters, β and κ the median and (95% CI) are reported. Parameters z_0 , η_1 , η_2 , IP and SF were fitted as patient specific and others as common to all patients in the fitted group.

Serotype	Parameter	Parameter Estimates
DENV1	z_0	4.72x10 ⁻² [1.67x10 ⁻² , 8.88x10 ⁻²] {1.59 x10 ⁻⁴ , 0.996}
	η_1	1.59 [1.37, 2.00] {0.916, 7.75x10 ²³³ }
	IP	4.64 [3.99, 5.18] {2.55, 7.06}
	δ	3.50 (3.49, 3.52)
	SF	7.17x10 ⁻² [2.96x10 ⁻² , 0.297] {7.23x10 ⁻³ , 4.48}
	η_2	8.19x10 ⁵ [1.78x10 ⁴ , 9.81x10 ⁶] {0.0384, 1.13x10 ²³⁰ }
	<i>Log likelihood</i>	-557
DENV2	z_0	3.45x10 ⁻² [1.24x10 ⁻² , 0.192] {4.96x10 ⁻⁶ , 0.556}
	η_1	1.62 [1.40, 1.82] {1.07, 2.45x10 ⁵ }
	IP	4.28 [3.45, 4.75] {2.96, 5.52}
	δ	3.28 (3.19, 3.28)
	SF	4.39 x10 ⁻² [1.65x10 ⁻² , 0.140] {9.15x10 ⁻³ , 9.56x10 ⁵ }
	η_2	2.37x10 ⁴ [1.34x10 ³ , 2.10x10 ⁵] {1.17x10 ² , 1.45x10 ¹² }
	<i>Log likelihood</i>	-414