##### **Supplementary File 2. Population-wide parameter estimates for the within-host model.** The table provides population-wide fixed and random effects estimates for the viral dynamic parameters, whereas Supplementary File 1 provides the estimated median and variation across individuals for each parameter. The values assume that antiviral efficacy follows a logit-normal distribution and all other parameters follow log normal distributions\*. Values in parentheses are relative standard errors (RSE) as a percent.

| **Parameter** | **Fixed effect** | **Random effect SD** |
| --- | --- | --- |
| Cell infection ratein 10-9 mL/Copies in days-1 ($β$) | 17.26 (12) | 0.49 (29) |
| Rate in log10 for the interferon-induced conversion of target cells to refractory cells (Φ) | -9.37 (110) | 0.81 (17) |
| Rate in 10-3 at which refractory cells become target cells again (𝜌) | 5.24 (28) | 0.46 (86) |
| Infected cell clearance rate in days-1 ($δ$) | 0.49 (5) | 0.61 (7) |
| Virus production rate inCopies/ mL in days-1 (𝜋) | 68.58 (10) | 0.38 (26) |
| Maximum antiviral efficacy ($ϵ\_{max}$) | 0.91 (1) | 0.32 (43) |

\* The estimation model is of the form $Y\_{i}(t)=log\_{10}(V\_{i}(t,ψ\_{i}))+e\_{i}(t)$, where $Y\_{i}(t)$ is the measured viral load of patient $i$ at time $t$, $V\_{i}(t,ψ\_{i})$ is the actual viral load given viral dynamic parameters $ψ\_{i}$ for patient $i$, and $e\_{i}(t)$ is the residual term. For parameters $ψ\_{i}$ following a log-normal distribution or logit-normal distribution, $ψ\_{i}=γ×e^{η\_{i}}$ or $logit(ψ\_{i})=logit(γ)+η\_{i}$, respectively, where $γ$ are fixed effects and $η\_{i}$ are random effects.