SUPPORTING FIGURES

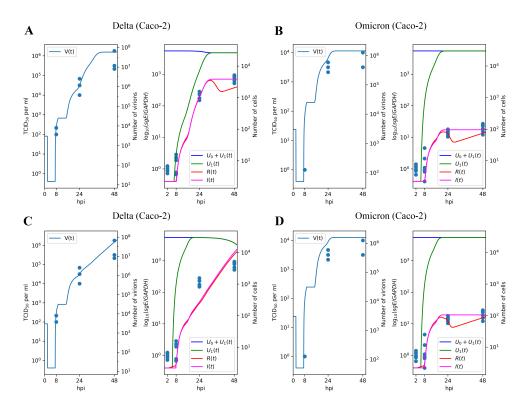


Figure S1. Results of parameter fitting for Caco-2 cell line. The top row shows the results for Delta (A) and Omicron (B) variants with a single variant-specific parameter (the cytokine generation rate p_c). The bottom row shows the results for Delta (C) and Omicron (D) variants with a single variant-specific parameter (the infectivity reduction rate k). The left parts of panels (A), (B), (C), and (D) show TCID₅₀ assay values (infectious virus titers); the right parts show RT-qPCR results for subgenomic envelope viral RNA (sgE), normalized by the human housekeeping gene GAPDH. The following parameter values were inferred for the top row: $\beta = 9.23736 \cdot 10^{-9}$, $k = 3.46004 \cdot 10^{7}$, $p_c = 12389.2$ (Delta), $p_c = 573035$ (Omicron). The following parameter values were inferred for the bottom row: $\beta = 1.14462 \cdot 10^{-8}$, k = 10.001 (Delta), $k = 1.\cdot 10^9$ (Omicron), $p_c = 626586$.

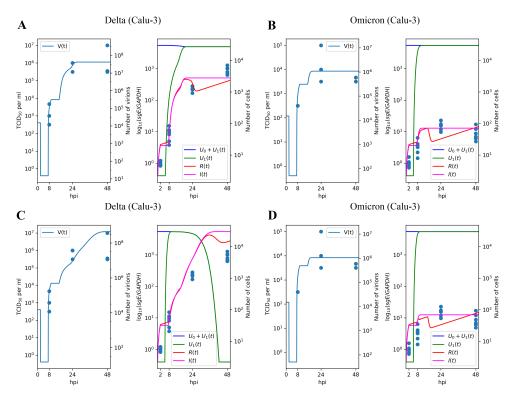


Figure S2. Results of parameter fitting for Calu-3 cell line. The top row shows the results for Delta (A) and Omicron (B) variants with a single variant-specific parameter (the cytokine generation rate p_c). The bottom row shows the results for Delta (C) and Omicron (D) variants with a single variant-specific parameter (the infectivity reduction rate k). The left parts of panels (A), (B), (C), and (D) show TCID₅₀ assay values (infectious virus titers); the right parts show RT-qPCR results for subgenomic envelope viral RNA (sgE), normalized by the human housekeeping gene GAPDH. The following parameter values were inferred for the top row: $\beta = 2.29588 \cdot 10^{-8}$, $k = 9.48894 \cdot 10^{8}$, $p_c = 40612.4$ (Delta), $p_c = 1.86387 \cdot 10^{6}$ (Omicron). The following parameter values were inferred for the bottom row: $\beta = 3.61456 \cdot 10^{-8}$, k = 10.0223 (Delta), $k = 1.\cdot 10^{9}$ (Omicron), $p_c = 2.12825 \cdot 10^{6}$.