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Supplemental information

B.1.617.2 enters and fuses lung cells with increased efficiency and evades antibodies induced by infection and vaccination

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Figure S1

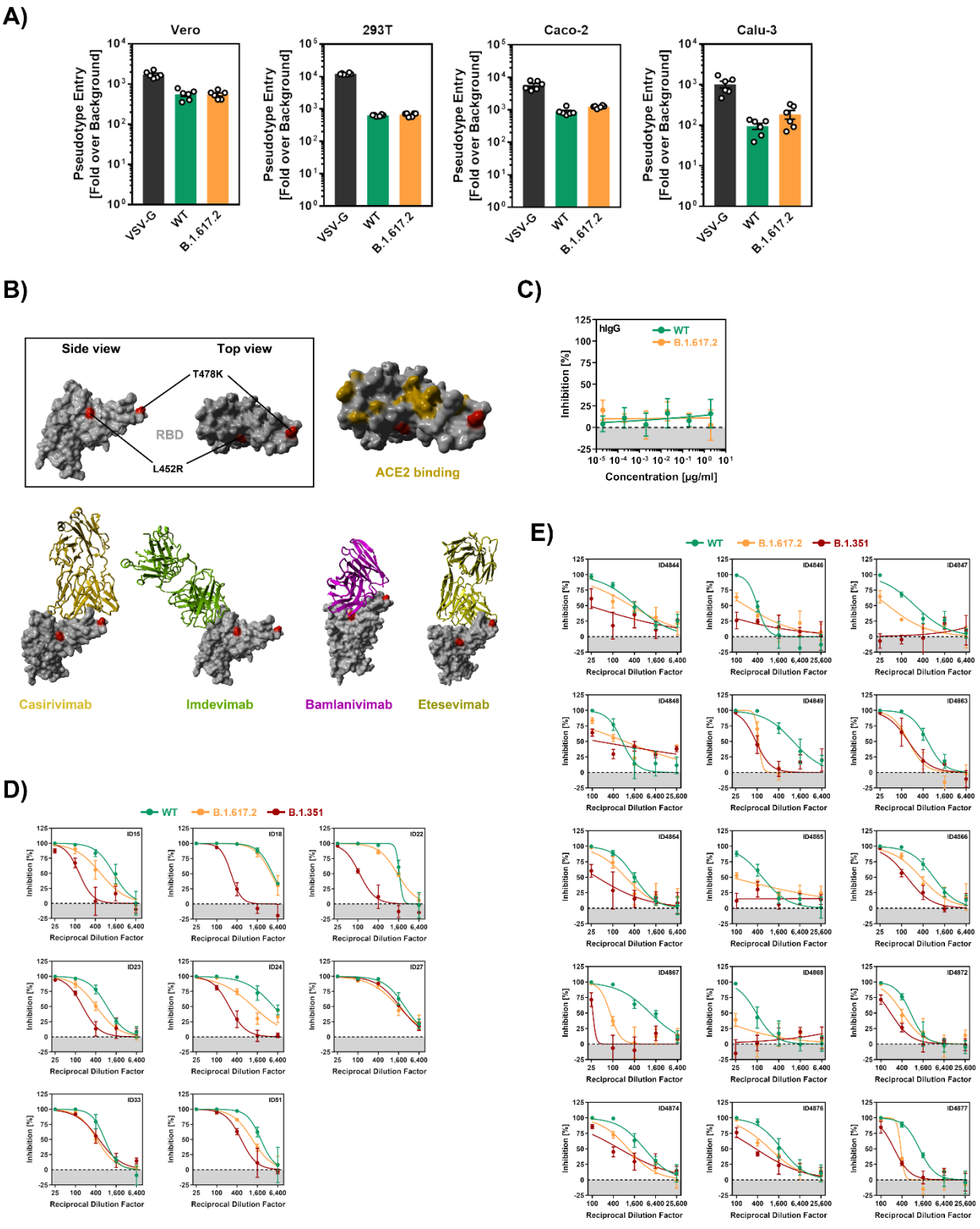

Figure S1: Cell entry and evasion of antibody-mediated neutralization by the spike protein of SARS-CoV-2 B.1.617.2 (related to Figure 1).

(A) Transduction data normalized against the assay background (related to Figure 1C). The experiment was performed as described in the legend of Figure 1C. Presented are the average (mean) data from the same six biological replicates (each conducted with technical quadruplicates) as presented in Figure 1C with the difference that transduction was normalized against signals obtained from cells inoculated with particles bearing no viral glycoprotein (background, set as 1). In addition, transduction data of particles bearing VSV-G are included. Error bars indicate the SEM.

(B) Location of the receptor binding domain (grey) mutations L452R and T478K (both red) of SARS-CoV-2 variant B.1.617.2 in the context of the interfaces for ACE2 binding (orange) and binding of monoclonal antibodies used for COVID-19 therapy.

(C) An unrelated control antibody does not affect cell entry of particles pseudotyped with SARS-CoV-2 WT, B.1.351 or B.1.617.2 S (related to Figure 1E). The experiment was performed as described in the legend of Figure 1F.

(D) Individual neutralization data for convalescent plasma (related to Figure 1G). Particles pseudotyped with the indicated S proteins were incubated (30 min, 37 °C) with different dilutions of convalescent plasma before being inoculated onto Vero cells. Transduction efficiency was quantified by measuring virus-encoded luciferase activity in cell lysates at 16-18 h posttransduction. Presented are the data from a single representative experiment conducted with technical quadruplicates. For normalization, inhibition of S protein-driven entry in the absence of plasma was set as 0%. Error bars indicate the SD. The data were further used to calculate the plasma dilution that leads to 50% reduction in S protein-driven cell entry (neutralizing titer 50, NT50; shown in Figure 1G).

(E) Individual neutralization data for vaccinee serum (related to Figure 1H). Particles pseudotyped with the indicated S proteins were incubated (30 min, 37 °C) with different dilutions of serum from individuals vaccinated with the Pfizer/BioNTech vaccine Comirnaty/BNT162b2 before being inoculated onto Vero cells. Transduction efficiency was quantified by measuring virus-encoded luciferase activity in cell lysates at 16-18 h posttransduction. Presented are the data from a single representative experiment conducted with technical quadruplicates. For normalization, inhibition of S protein-driven entry in the absence of serum was set as 0%. Error bars indicate the SD. The data were further used to calculate the NT50 (shown in Figure 1H).