

Sensitivity of SARS-CoV-2 B.1.1.7 to mRNA vaccine-elicited antibodies

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Transmission of SARS-CoV-2 is uncontrolled in many parts of the world; control is compounded in some areas by the higher transmission potential of the B.1.1.7 variant¹, which has now been reported in 94 countries. It is unclear whether the response of the virus to vaccines against SARS-CoV-2 on the basis of the prototypic strain will be affected by the mutations found in B.1.1.7. Here we assess the immune responses of individuals after vaccination with the mRNA-based vaccine BNT162b2². We measured neutralizing antibody responses after the first and second immunizations using pseudoviruses that expressed the wild-type spike protein or a mutated spike protein that contained the eight amino acid changes found in the B.1.1.7 variant. The sera from individuals who received the vaccine exhibited a broad range of neutralizing titres against the wild-type pseudoviruses that were modestly reduced against the B.1.1.7 variant. This reduction was also evident in sera from some patients who had recovered from COVID-19. Decreased neutralization of the B.1.1.7 variant was also observed for monoclonal antibodies that target the N-terminal domain (9 out of 10) and the receptor-binding motif (5 out of 31), but not for monoclonal antibodies that recognize the receptor-binding domain that bind outside the receptor-binding motif. Introduction of the mutation that encodes the E484K substitution in the B.1.1.7 background to reflect a newly emerged variant of concern (VOC 202102/02) led to a more-substantial loss of neutralizing activity by vaccine-elicited antibodies and monoclonal antibodies (19 out of 31) compared with the loss of neutralizing activity conferred by the mutations in B.1.1.7 alone. The emergence of the E484K substitution in a B.1.1.7 background represents a threat to the efficacy of the BNT162b2 vaccine.

The BNT162b2 mRNA vaccine encodes the full-length trimerized spike protein of SARS-CoV-2² and was designed against the Wuhan-1 isolate. Concerns have been raised as to whether vaccines will be effective against newly emergent SARS-CoV-2 variants, such as B.1.1.7 (N501Y.V1)³. In clinical studies of BNT162b2, the geometric mean titre (GMT) of neutralizing antibodies associated with 50% neutralization increased after the first dose and the vaccine provided high levels of protection against infection and severe disease after the second dose⁴.

Activity of vaccine and convalescent sera against B.1.1.7

Participants ($n = 37$) received the first dose of the BNT162b2 mRNA vaccine 3 weeks before blood was drawn for the collection of serum and

peripheral blood mononuclear cells. The median age was 62 years (interquartile range, 47–84 years) and 35% of participants were female. Of these participants, 21 individuals also had a blood draw 3 weeks after receiving the second dose of the BNT162b2 mRNA vaccine. Serum IgG titres against nucleocapsid protein, the spike protein and the receptor-binding domain (RBD) of the spike protein were assayed (Extended Data Fig. 1a).

Using lentiviral pseudotyping, we studied the wild-type (wild-type spike bearing D614G) and mutant B.1.1.7 spike proteins (Fig. 1a) to measure the neutralization activity of vaccine-elicited sera. The vaccine sera exhibited a range of inhibitory dilutions that provided 50% neutralization (ID_{50}) (Fig. 1b, c). The GMT against the wild-type spike protein after the second dose of vaccine was substantially higher than after the first dose (318 compared with 77) (Fig. 1b, e). There was correlation between total

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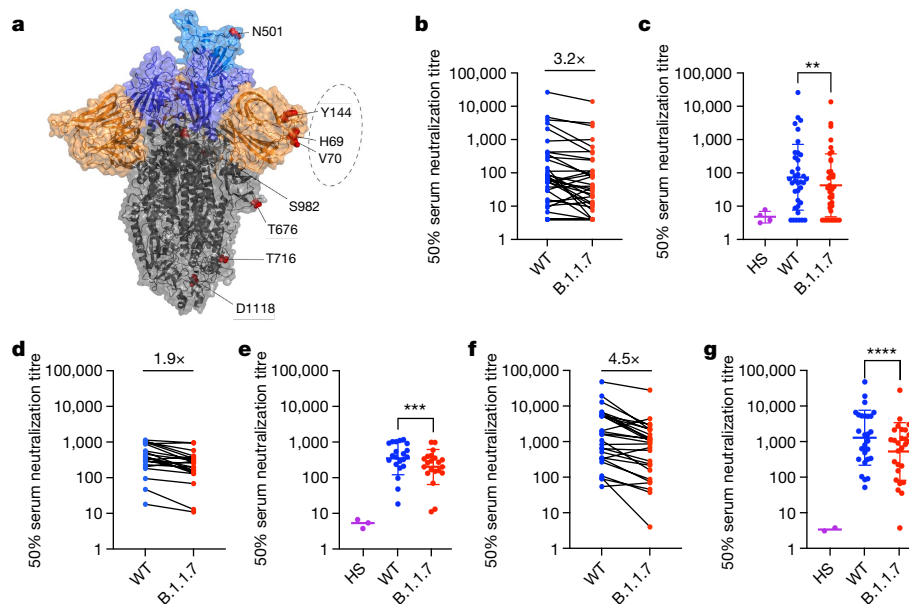


Fig. 1 | Neutralization by sera from the first and second dose of the BNT162b2 mRNA vaccine against wild-type and B.1.1.7 spike mutant SARS-CoV-2-pseudotyped viruses. a, Spike in the open conformation with a single erect RBD (Protein Data Bank (PDB): 6ZGG) is shown in the vertical view of the trimer axis. The locations of mutated residues are shown as red spheres, with deletions indicated in a dashed outline, and are labelled on the monomer with an erect RBD. **b–g**, The 50% serum neutralization titres of the first dose of the vaccine (**b, c**, $n = 37$), the second dose of the vaccine (**d, e**, $n = 21$) and convalescent sera

(**f, g**, $n = 27$) against the wild-type (WT) spike protein and the spike protein of the variant B.1.1.7 (containing the N501Y, A570D, Δ H69/ Δ V70, Δ Y144, P681H, T716I, S982A and D1118H mutations). HS, human serum control. **b, d, f**, Mean fold changes in ID_{50} are indicated above the graphs. Data points of the same individual are connected by lines. Data are GMT \pm s.d. and individual values of two independent experiments each with two technical repeats. Two-tailed Wilcoxon matched-pairs signed-rank test with no adjustment for multiple comparisons; ** $P < 0.01$, **** $P < 0.0001$. The cut-off for 50% neutralization was set to 4.

spike IgG titres and serum neutralization titres (Extended Data Fig. 1b). A broad range of T cell responses was measured by IFN γ FluoroSpot against SARS-CoV-2 peptides in samples from individuals who received the vaccine after the first dose. These cellular responses did not correlate with serum neutralization titres or IgG spike antibody titres (Extended Data Fig. 1c, d).

We then generated mutated pseudoviruses carrying the spike protein with the N501Y and A570D substitutions and the H69/V70 deletion (Δ H69/ Δ V70). We observed a small increase in the ability of sera from individuals who were vaccinated or had recovered from COVID-19 to inhibit this triple-mutant virus (Extended Data Fig. 2a–c). We next included the full set of eight mutations in the spike protein that is present in the B.1.1.7 variant (Fig. 1a). Of the 29 sera with neutralization activity after the first dose, 20 showed evidence of a reduction in neutralization titres against the B.1.1.7 variant (Fig. 1b, c and Extended Data Fig. 3), with a fold change of 3.2 ± 5.7 (mean \pm s.d.). After the second dose, the GMT was markedly increased compared with the first-dose titres, with a fold change of 1.9 ± 0.9 (mean \pm s.d.) (Fig. 1d, e). Among sera from 27 individuals who had recovered from COVID-19, the GMT at 50% neutralization was 1,334 for the wild-type spike protein, which is significantly higher than the GMT after the second dose of the vaccine (Fig. 1f, g). The fold change in ID_{50} for neutralization of the B.1.1.7 compared with wild-type (D614G) spike protein was 4.5 ± 8.7 (Fig. 1f, g and Extended Data Fig. 4).

The E484K substitution (Fig. 2a) has been reported as an escape mutation for several monoclonal antibodies⁵, and is present in the B.1.351 (501Y.V2) and P.1 (501Y.V3) lineages. As of 11 February 2021, 30 B.1.1.7 sequences also had the E484K substitution (Fig. 2c). Phylogenetic analysis suggests that there have been multiple independent acquisitions, with one lineage appearing to expand over time, indicating active transmission (Fig. 2b). This has resulted in Public Health England naming this a variant of concern (VOC 202102/02)⁶. We therefore generated pseudoviruses that carried the B.1.1.7 spike mutations with or without the additional E484K substitution and tested these against sera obtained after the first and second dose of the BNT162b2 mRNA vaccine as well as against convalescent sera. After the second vaccine dose, we observed

a considerable loss of neutralizing activity for the pseudovirus with the B.1.1.7 spike mutations and E484K (Fig. 3d, e). The mean fold change for the E484K-containing B.1.1.7 spike variant was 6.7 compared with 1.9 for the B.1.1.7 variant, relative to the wild-type spike protein (Fig. 3a–c and Extended Data Fig. 5). Similarly, when we tested a panel of convalescent sera with a range of neutralization titres (Fig. 1f, g and Extended Data Fig. 5), we observed additional loss of activity against the mutant B.1.1.7 spike with E484K, with fold change of 11.4 relative to the wild-type spike protein (Fig. 3f, g and Extended Data Fig. 5).

Monoclonal antibody activity against B.1.1.7

We tested 60 monoclonal antibodies isolated from 15 individuals who had recovered from SARS-CoV-2 infection in early 2020 with an in vitro pseudotyped neutralization assay against the B.1.1.7 spike protein (Supplementary Table 1). Out of 60 monoclonal antibodies, 20 (33.3%) showed a greater than twofold loss of neutralizing activity against the B.1.1.7 variant compared to wild-type SARS-CoV-2 (Fig. 4a, b and Extended Data Fig. 6). The B.1.1.7 mutant virus fully escaped neutralization by 8 out of 10 monoclonal antibodies (80%) that target the N-terminal domain (NTD) (Fig. 4c). Of the 31 monoclonal antibodies that target the receptor-binding motif (RBM), 5 (16.1%) showed more than 100-fold decrease in B.1.1.7 neutralization, and additional 6 monoclonal antibodies (19.4%) had a partial 2–10-fold reduction (Fig. 4d). Finally, all RBM-specific non-RBM-targeting monoclonal antibodies that were tested fully retained neutralizing activity against B.1.1.7 (Fig. 4e).

To address the role of the N501Y substitution in B.1.1.7 in the neutralization escape from RBM-specific antibodies, we tested the binding of 50 RBM-specific monoclonal antibodies to the wild-type and N501Y-mutant RBD by biolayer interferometry (Fig. 4f and Extended Data Fig. 7). The 5 RBM-specific monoclonal antibodies that did not neutralize the B.1.1.7 variant (Fig. 4d) showed a complete loss of binding to the N501Y-mutant RBD (Fig. 4g, h), demonstrating a role for this mutation as an escape mechanism for certain RBM-targeting monoclonal antibodies.

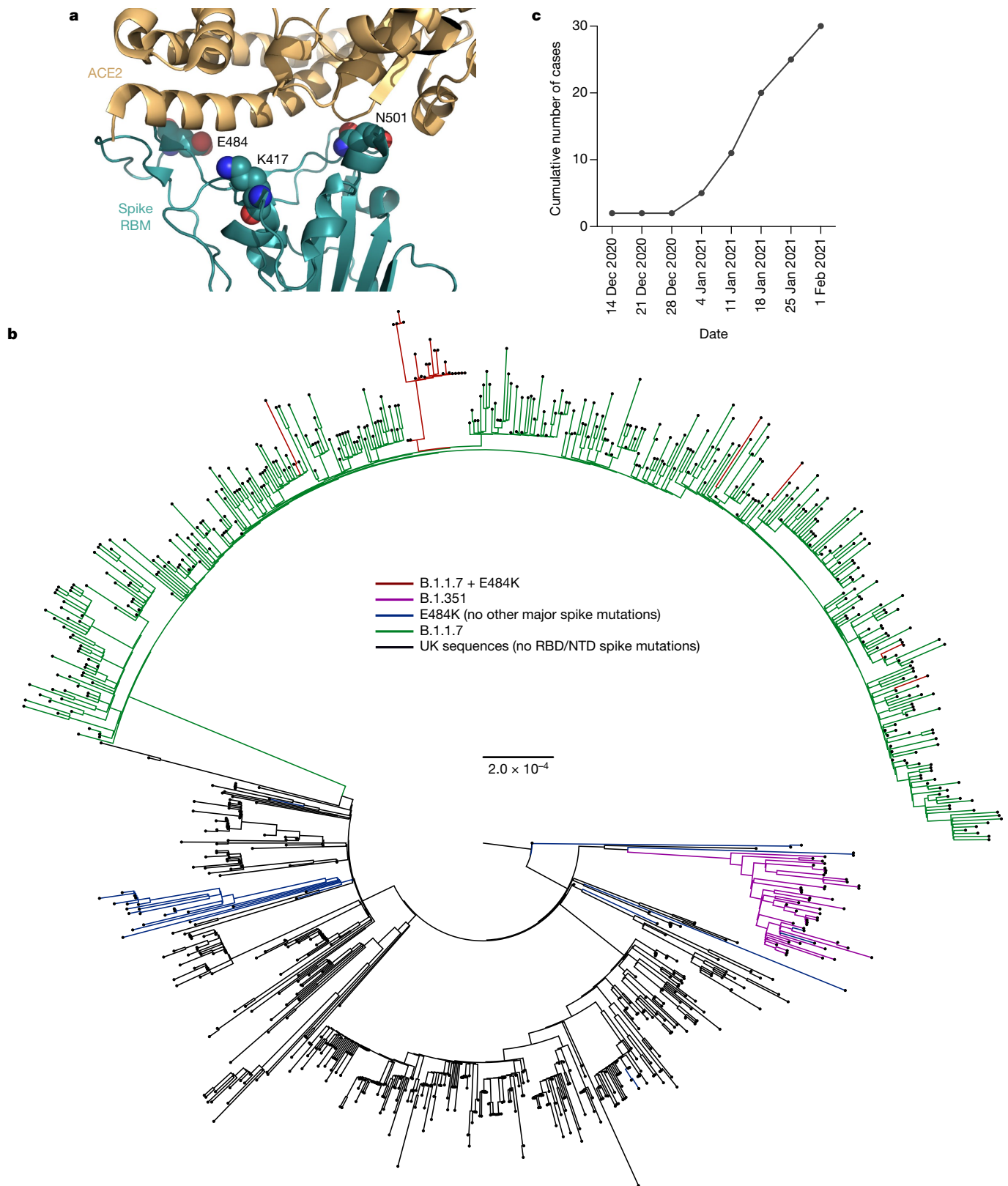


Fig. 2 | The E484K substitution was found in the background of B.1.1.7 and showed evidence of transmission. a, Representation of the spike RBM:ACE2 interface (PDB: 6M0J) with residues E484, N501 and K417 highlighted as spheres coloured by element. **b**, Maximum likelihood phylogeny of a subset of sequences from the UK with the E484K mutation (blue) and the B.1.1.7 lineage

To assess the effect of E484K on this panel of monoclonal antibodies, we generated a triple-mutant SARS-CoV-2 pseudotype virus carrying the K417N, E484K and N501Y mutations (spike(N501Y, E484K, K417N)).

(green), with background sequences from the UK without RBD mutations shown in black. As of 11 February 2021, 30 sequences from the B.1.1.7 lineage (one cluster of 25 at the top of the phylogenetic tree) have acquired the E484K substitution (red). **c**, Sequence accumulation over time in GISAID for UK sequences of the B.1.1.7 and other variants with or without E484K.

The inclusion of the K417N substitution was prompted by the observation that substitutions at this position have been found in five sequences from recent viral isolates within the B.1.1.7 lineage (K417 to

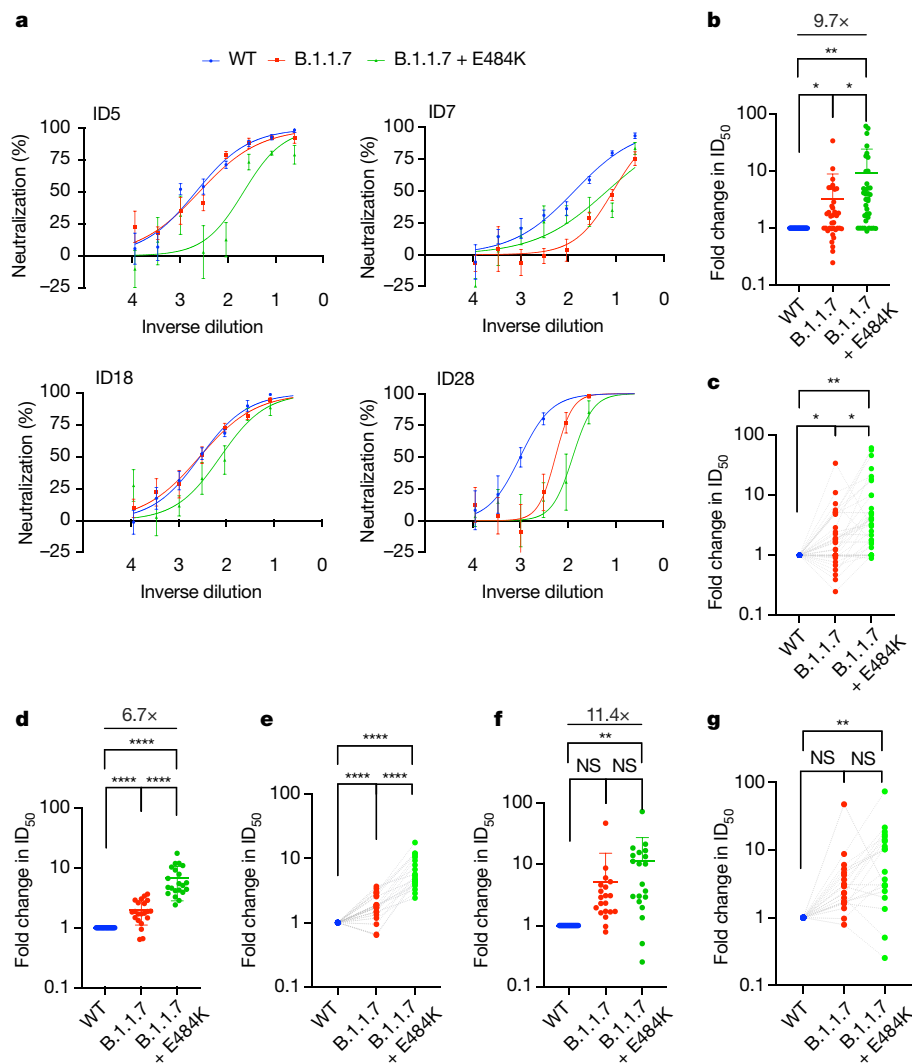


Fig. 3 | Neutralization potency of mRNA vaccine sera and convalescent sera (before SARS-CoV-2 B.1.1.7) against a pseudotyped virus with the spike mutations of the B.1.1.7 lineage with or without E484K. All virus variants were in a spike(D614G) background. **a**, Example neutralization curves of vaccinated individuals (ID 5, 7, 18, 28). The inverse dilution is shown on a log scale. Data are mean \pm s.e.m. representative of two independent experiments each with two technical replicates. **b–g**, The 50% neutralization titres of each virus against sera derived after the first vaccine dose (**b, c**, $n = 37$), the second vaccine dose (**d, e**, $n = 21$) and for convalescent sera (**f, g**, $n = 20$) expressed as fold change relative to the wild-type virus. **b, d, f**, Mean fold changes in ID_{50} are indicated above the graphs. Data are mean \pm s.d. and individual values; error bars for negative values are not shown. **c, e, g**, Data are the mean fold change of two technical replicates and are representative of two independent experiments. Data points of the same individual are connected by lines. **b, d, f**, Two-tailed paired Student's t -test; * $P < 0.05$, ** $P < 0.01$, **** $P < 0.0001$; NS, not significant. The cut-off for 50% neutralization was set to 4.

Asn, Glu or Arg). This is in keeping with the convergent evolution of the virus to an RBD containing N501Y, E484K and K417N or K417T as evidenced by the B.1.351 and P.1 lineages. Notably, mutations at K417 are reported to escape neutralization by monoclonal antibodies, including the recently approved monoclonal antibody LY-CoV016^{5,7}. Out of the 60 monoclonal antibodies tested, 20 (33.3%) showed a loss of neutralizing activity against the spike(N501Y, E484K, K417N) mutant of more than 10-fold compared to wild-type SARS-CoV-2 (Fig. 4a, b and Extended Data Fig. 6), and of these 19 are RBM-specific monoclonal antibodies. As above, we addressed the role of the E484K substitution in the escape from RBM-specific antibodies by testing the binding of 50 RBD-specific monoclonal antibodies to the RBD of the wild-type and E484K-mutant spike protein by biolayer interferometry (Fig. 4f and Extended Data Fig. 8). Out of the 19 RBM-specific monoclonal antibodies that showed reduced or loss of neutralization of the spike(N501Y, E484K, K417N) mutant (Fig. 4d), 16 showed a complete or partial loss of binding to the RBD of the E484K mutant (Fig. 4g, h), which is consistent with findings that E484K is an important mutation for viral escape^{8–10}. In addition, 3 of these 16 monoclonal antibodies also lost the ability to bind to an RBD containing the N501Y substitution, indicating that a fraction of RBM-specific antibodies are sensitive to both the N501Y and E484K substitutions. Similarly, 3 of the 19 monoclonal antibodies that lost neutralization against the spike(N501Y, E484K, K417N) mutant (S2D8, S2H7 and S2X128) were previously shown to lose binding and neutralization to the K417V mutant, and are here shown to be sensitive to either the N501Y or the E484K substitution.

Binding of the RBD of the B.1.1.7 variant to ACE2

Using biolayer interferometry, we found that human ACE2 bound to the RBD of the B.1.1.7 variant with an affinity of 22 nM compared to an affinity of 133 nM for the wild-type RBD (Extended Data Fig. 9), in agreement with our previous deep-mutational scanning measurements using dimeric ACE2²¹. Although ACE2 bound with comparable on rates to both RBDs, the observed dissociation rate constant was slower for B.1.1.7 than for the wild-type RBD (Extended Data Table 1). These findings could explain the efficient ongoing transmission of this newly emergent SARS-CoV-2 lineage and the possibly reduced opportunity for antibody binding. To understand the effect of the mutations in the triple mutant (K417N, E484K and N501Y), we evaluated the binding of ACE2 to the immobilized RBD of spike(N501Y, E484K, K417N). We determined an ACE2-binding affinity of 64 nM for the RBD of spike(N501Y, E484K, K417N), driven by a faster off rate than observed for the RBD of the B.1.1.7 variant but slower than for the wild-type RBD. We propose that the K417N mutation is slightly detrimental to ACE2 binding, which explains the intermediate affinity determined for the RBD of spike(N501Y, E484K, K417N) compared to the B.1.1.7 and wild-type RBDs, probably as a result of disrupting the salt bridge formed with ACE2 residue D30.

Discussion

Serum neutralizing activity is a correlate of protection for other respiratory viruses, including influenza¹² and respiratory syncytial virus, for which

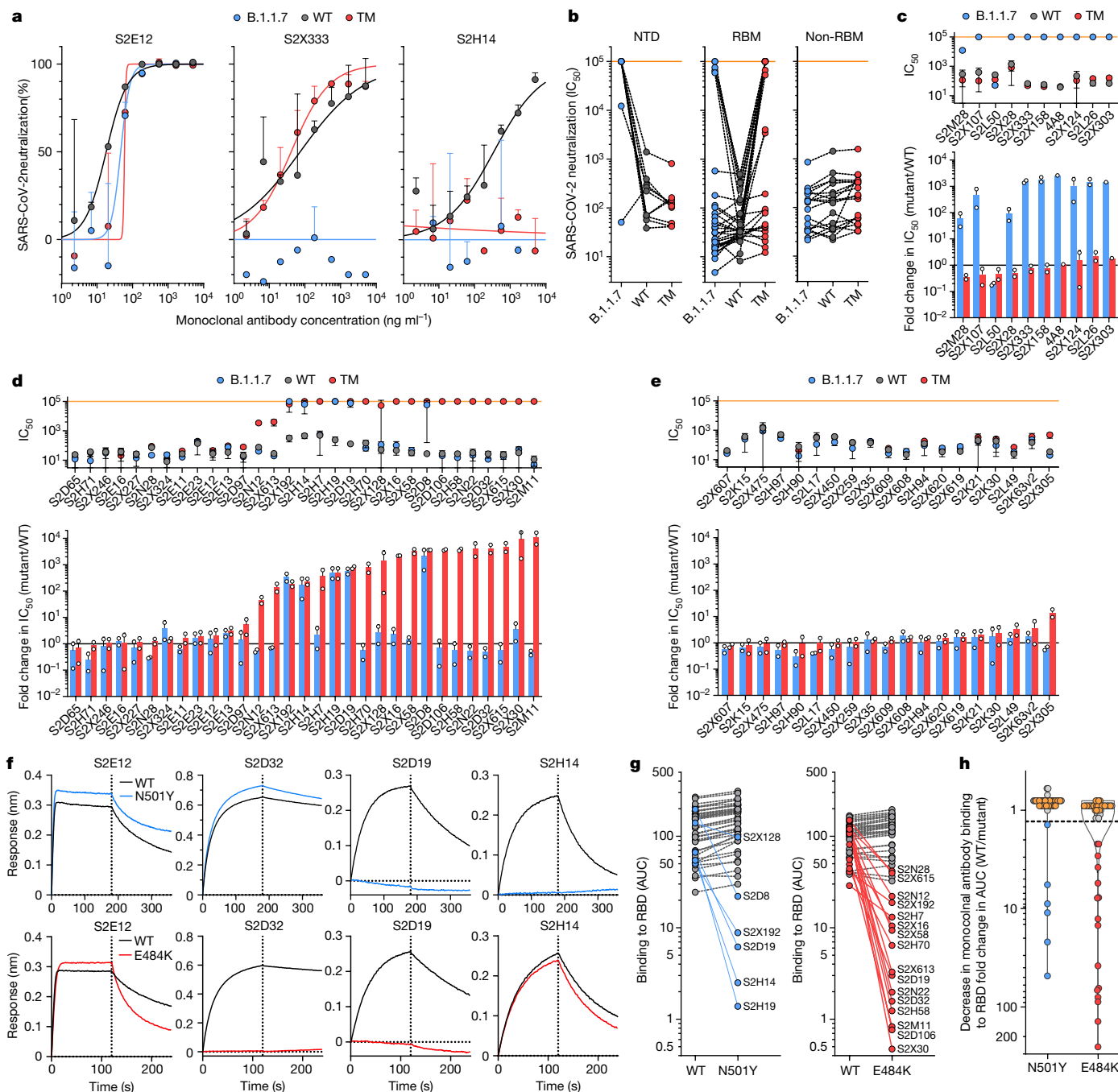


Fig. 4 | Neutralization and binding by a panel of NTD- and RBD-specific monoclonal antibodies against wild-type, B.1.1.7 and RBD-mutant SARS-CoV-2 viruses. **a**, Neutralization of pseudotyped SARS-CoV-2–murine leukemia virus (MLV) carrying wild-type spike (spike(D614G)) (grey), spike from B.1.1.7 (blue) or a triple-mutant spike protein (TM, carrying RBD mutations K417N, E484K and N501Y) (red) by three selected monoclonal antibodies (S2E12, S2X333 and S2H14) from one representative experiment. Data are mean \pm s.d. of two technical replicates. **b**, Neutralization of SARS-CoV-2–MLVs carrying wild-type spike (spike(D614G)), spike from B.1.1.7 or a triple-mutant spike protein (spike(N501Y, E484K, K417N)) by 60 monoclonal antibodies targeting the NTD ($n = 10$), RBM ($n = 31$) or non-RBM sites in the RBD ($n = 19$). Data are the mean 50% inhibitory concentration (IC_{50}) values ($ng\ ml^{-1}$) of $n = 2$ independent experiments. **c–e**, Neutralization by NTD-specific (**c**), RBM-specific (**d**) and non-RBM-specific (**e**) monoclonal antibodies is shown as

the mean IC_{50} values (top) and mean fold change in B.1.1.7 (blue) or the triple mutant (spike(N501Y, E484K, K417N)) (red) relative to the wild-type virus (bottom). The orange line shows the threshold for non-neutralizing titres. Top, data are mean \pm s.d. IC_{50} values from two independent experiments. Bottom, data are mean \pm s.d. fold change from two independent experiments. **f–h**, The kinetics of the binding of monoclonal antibodies to wild-type (black), N501Y (blue) or E484K (red) RBD as measured by biolayer interferometry. **f**, The four RBM-targeting monoclonal antibodies with no reduced binding to the RBD with N501Y or E484K are shown. **g**, Area under the curve (AUC) (**g**) and the fold change in the area under the curve (**h**) of 50 monoclonal antibodies tested against the wild-type, N501Y and E484K RBD. Monoclonal antibodies with a more than 1.3-fold (cut-off indicated by the orange line) change in area under the curve are shown in blue and red; orange dots show non-RBM-specific monoclonal antibodies.

prophylaxis with monoclonal antibodies has been used in at-risk groups^{13,14}. Neutralizing antibody titres seemed to be highly correlated with vaccine protection against SARS-CoV-2 rechallenge in nonhuman primates^{15,16}.

This study reports on neutralization by sera collected after both the first and second doses of the BNT162b2 vaccine. The participants of this study were older adults, in line with the targeting of this age

group in the initial rollout of the vaccination campaign in the UK. We demonstrate that neutralization of a pseudovirus containing the spike protein with the full set of mutations that is present in the B.1.1.7 variant showed a small reduction using sera from individuals who received the BNT162b2 vaccine that was more marked after the first dose than the second dose. This could be related to the increased breadth, potency and/or concentration of antibodies after the boost dose. Other studies have reported a small reduction in neutralization against the B.1.1.7 variant in individuals vaccinated with two doses of BNT162b2¹⁷ and mRNA-1273¹⁸. The reduced neutralizing activity observed with polyclonal antibodies elicited by mRNA vaccines observed in this study is further supported by the loss of neutralizing activity observed with human monoclonal antibodies directed against both the RBD and, to a major extent, the NTD.

Multiple variants, including the 501Y.V2 and B.1.1.7 lineages, have multiple mutations as well as deletions in the NTD, most of which are located in a site of vulnerability that is targeted by all known NTD-specific neutralizing antibodies^{19,20}. The role of NTD-specific neutralizing antibodies might be underestimated, in part by the use of neutralization assays based on target cells that overexpress ACE2 receptors. NTD-specific monoclonal antibodies were suggested to interfere with viral entry based on other accessory receptors, such as DC-SIGN and L-SIGN²¹, and their neutralization potency was found to be dependent on different in vitro culture conditions¹⁹. The observation that 9 out of 10 NTD-specific neutralizing antibodies did not show a complete or near-complete loss of neutralizing activity against B.1.1.7 indicates that this new variant may have also evolved to escape from this class of antibodies, which may have a yet unrecognized role in protective immunity. Taken together, the presence of multiple escape mutations in the NTD is supportive of the hypothesis that this region of the spike, in addition to the RBM, is also under immune pressure.

Worryingly, we have shown that there are multiple B.1.1.7 sequences in the UK that contain the E484K substitution with early evidence of transmission as well as independent acquisitions. We measured a further reduction in neutralization titres by vaccine sera when E484K was present alongside the B.1.1.7 spike mutations. A recent study¹⁸ has also shown that variants carrying the E484K substitution resulted in a 3–6-fold reduction in neutralization by sera from individuals who received the mRNA-1273 vaccine. Consistently, in this study we found that approximately 50% of the RBM-specific monoclonal antibodies tested lost neutralizing activity against SARS-CoV-2 carrying E484K. E484K has been shown to affect neutralization by monoclonal antibodies or convalescent sera, especially in combination with N501Y and K417N^{8,22–24}.

Vaccines are a key part of a long-term strategy to bring SARS-CoV-2 transmission under control. Our data suggest that vaccine escape by the virus of current spike-directed vaccines designed against the Wuhan-1 strain will be inevitable, particularly given that E484K is emerging independently and recurrently on a B.1.1.7 (501Y.V1) background, and given the rapid global spread of B.1.1.7. Other major variants with E484K such as 501Y.V2 and V3 are also spreading regionally. This should be mitigated by designing next-generation vaccines with mutated spike sequences and using alternative viral antigens.

Online content

Any methods, additional references, Nature Research reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at <https://doi.org/10.1038/s41586-021-03412-7>.

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Methods

Data reporting

No statistical methods were used to predetermine sample size. The experiments were not randomized and the investigators were not blinded to allocation during experiments and outcome assessment.

Participant recruitment and ethics

Participants who had received the first dose of the BNT162b2 vaccine and individuals with COVID-19 were consented into the COVID-19 cohort of the NIHR Bioresource. The study was approved by the East of England–Cambridge Central Research Ethics Committee (17/EE/0025).

SARS-CoV-2 serology by multiplex particle-based flow cytometry

Recombinant SARS-CoV-2 nucleocapsid, spike and RBD proteins were covalently coupled to distinct carboxylated bead sets (Luminex) to form a triplex and were analysed as previously described²⁵. Specific binding was reported as the mean fluorescence intensity.

Generation of spike mutants

Amino acid substitutions were introduced into the D614G pCDNA₂-SARS-CoV-2 S plasmid as previously described²⁶ using the QuikChange Lightning Site-Directed Mutagenesis kit, following the manufacturer's instructions (Agilent Technologies). Sequences were checked by Sanger sequencing.

The plasmid encoding the B.1.1.7 or triple-mutant (spike(N501Y, E484K, K417N)) SARS-CoV-2 spike glycoprotein was used to produce SARS-CoV-2-MLVs based on overlap extension PCR as follows. In brief, a modification of the overlap extension PCR protocol²⁷ was used to introduce the eight mutations of the B.1.1.7 lineage or the three mutations of the triple mutant (spike(N501Y, E484K, K417N)) in the SARS-CoV-2 spike gene. In a first step, nine DNA fragments with overlapping sequences were amplified by PCR from a plasmid (pHCMV1, Genlantis) encoding the full-length SARS-CoV-2 spike gene (BetaCoV/Wuhan-Hu-1/2019; accession number, mn908947). The mutations (Δ H69/ Δ V70, Δ I144, N501Y, A570D, D614G, P681H, S982A, T716I and D1118H or K417N, E484K and N501Y) were introduced by amplification with primers with a similar melting temperature. Deletion of the C-terminal 21 amino acids was introduced to increase surface expression of the recombinant spike protein²⁸. Next, three contiguous overlapping fragments were fused by a first overlap PCR using the most external primers of each set, resulting in three larger fragments with overlapping sequences. A final overlap PCR was performed on the three large fragments using the most external primers to amplify the full-length spike gene and the flanking sequences including the restriction sites KpnI and NotI. This fragment was digested and cloned into the expression plasmid pHCMV1. For all PCR reactions the Q5 Hot Start High Fidelity DNA polymerase (New England Biolabs) was used according to the manufacturer's instructions and adapting the elongation time to the size of the amplicon. After each PCR step, the amplified regions were separated on an agarose gel and purified using an Illustra GFX PCR DNA and Gel Band Purification Kit (Merck).

Pseudotype virus preparation

Viral vectors were prepared by transfection of HEK293T cells using the Fugene HD transfection reagent (Promega). HEK293T cells were transfected with a mixture of 11 μ l of Fugene HD, 1 μ g of pCDNAD-19spike-HA, 1 μ g of p8.91 HIV-1 Gag-Pol expression vector^{29,30} and 1.5 μ g of pCSFLW (expressing the firefly luciferase reporter gene with the HIV-1 packaging signal)³¹. Viral supernatants were collected at 48 h and 72 h after transfection, filtered through a 0.45- μ m filter and stored at -80°C . The 50% tissue culture infectious dose of the SARS-CoV-2 pseudovirus was determined using the Steady-Glo Luciferase assay system (Promega).

Serum and plasma pseudotype neutralization assay

Spike pseudotype assays have been shown to have similar characteristics to neutralization tests using fully infectious wild-type SARS-CoV-2³². Virus neutralization assays were performed on HEK293T cells that were transiently transfected with ACE2 and TMPRSS2 using a SARS-CoV-2 spike pseudotyped virus that expressed luciferase³³. Pseudotyped virus was incubated with a serial dilution of heat-inactivated human serum samples or sera from individuals who were vaccinated in duplicate for 1 h at 37°C . Virus-only and cell-only controls were also included. Then, freshly trypsinized HEK293T ACE2- and TMPRSS2-expressing cells were added to each well. After incubation for 48 h in a 5% CO_2 environment at 37°C , luminescence was measured using the Steady-Glo or Bright-Glo Luciferase assay system (Promega). Neutralization was calculated relative to virus-only controls. Dilution curves are shown as the mean \pm s.e.m. neutralization. ID₅₀ values were calculated in GraphPad Prism. The ID₅₀ values within groups were summarized as the GMT and statistical comparisons between groups were made with Wilcoxon ranked-sign tests. In addition, the effects of the mutations on the neutralizing effect of the sera were expressed as fold change in ID₅₀ of the wild-type compared to mutant pseudotyped virus. Statistical difference in the mean fold change between groups was determined using a two-tailed Student's *t*-test.

IFN γ FluoroSpot assays

Frozen peripheral blood mononuclear cells (PBMCs) were rapidly thawed, and the freezing medium was diluted into 10 ml of TexMACS medium (Miltenyi Biotech), centrifuged and resuspended in 10 ml of fresh medium with 10 U ml^{-1} DNase (Benzonase, Merck-Millipore via Sigma-Aldrich), PBMCs were incubated at 37°C for 1 h, followed by centrifugation and resuspension in fresh medium supplemented with 5% human serum (Sigma-Aldrich) before being counted. PBMCs were stained with 2 μ l of each antibody: anti-CD3–fluorescein isothiocyanate (FITC), clone UCHT1; anti-CD4–phycoerythrin (PE), clone RPA-T4; anti-CD8a–peridinin-chlorophyll protein-cyanine 5.5 (PerCP-Cy5.5), clone RPA-8a (all BioLegend, London, UK), LIVE/DEAD Fixable Far Red Dead Cell Stain Kit (Thermo Fisher Scientific). PBMC phenotyping was performed on the BD Accuri C6 flow cytometer. Data were analysed with FlowJo v.10 (Becton Dickinson). In brief, $1.5\text{--}2.5 \times 10^5$ PBMCs were incubated in pre-coated Fluorospot plates (Human IFN γ FLUOROSPOT (Mabtech)) in triplicate with peptide mixes specific to spike, nucleocapsid and membrane proteins of SARS-CoV-2 (final peptide concentration 1 μ g ml^{-1} per peptide, Miltenyi Biotech) and an unstimulated and positive control mix (containing anti-CD3 (Mabtech), *Staphylococcus* Enterotoxin B, phytohaemagglutinin (all Sigma-Aldrich)) at 37°C in a humidified CO_2 atmosphere for 48 h. The cells and medium were decanted from the plate and the assay was developed following the manufacturer's instructions. Developed plates were read using an AID iSpot reader (Oxford Biosystems) and counted using AID EliSpot v.7 software (Autoimmun Diagnostika). All data were then corrected for background cytokine production and expressed as spot-forming units per million PBMCs or CD3⁺ T cells.

Antibody discovery and recombinant expression

Human monoclonal antibodies were isolated from plasma cells or memory B cells of donors who are immune to SARS-CoV or SARS-CoV-2 as previously described^{34–37}. Recombinant antibodies were expressed in ExpiCHO cells at 37°C and 8% CO_2 . Cells were transfected using ExpiFectamine. Transfected cells were supplemented 1 day after transfection with ExpiCHO Feed and ExpiFectamine CHO Enhancer. The cell culture supernatant was collected 8 days after transfection and filtered through a 0.2- μ m filter. Recombinant antibodies were affinity purified on an ÄKTA xpress FPLC device using 5-ml HiTrap MabSelect Prisma columns followed by buffer exchange to histidine buffer (20 mM histidine, 8% sucrose, pH 6) using HiPrep 26/10 desalting columns.

Pseudovirus neutralization assay using monoclonal antibodies

MLV-based SARS-CoV-2 S-glycoprotein-pseudotyped viruses were prepared as previously described³⁵. HEK293T/17 cells were cotransfected with a plasmid encoding the wild-type, B.1.1.7 or triple-mutant (spike(N501Y, E484K, K417N)) SARS-CoV-2 spike glycoprotein, an MLV Gag-Pol packaging construct and the MLV transfer vector encoding a luciferase reporter using X-tremeGENE HP transfection reagent (Roche) according to the manufacturer's instructions. Cells were cultured for 72 h at 37 °C with 5% CO₂ before collection of the supernatant. VeroE6 cells stably expressing human TMPRSS2 were cultured in Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal bovine serum, 1% penicillin-streptomycin (100 IU ml⁻¹ penicillin, 100 µg ml⁻¹), 8 µg ml⁻¹ puromycin and plated into 96-well plates for 16–24 h. Pseudovirus with a serial dilution of monoclonal antibodies was incubated for 1 h at 37 °C and then added to the wells after washing twice with DMEM. After 2–3 h, DMEM containing 20% fetal bovine serum and 2% penicillin-streptomycin was added to the cells. After 48–72 h of infection, Bio-Glo (Promega) was added to the cells and incubated in the dark for 15 min before the the luminescence was read using a Synergy HI microplate reader (BioTek). Measurements were done in duplicate and relative luciferase units were converted to the percentage of neutralization and plotted with a nonlinear regression model to determine the IC₅₀ values using GraphPad Prism software (v.9.0.0).

Antibody binding measurements using biolayer interferometry

Monoclonal antibodies (Supplementary Table 1) were diluted to 3 µg ml⁻¹ in kinetic buffer (PBS supplemented with 0.01% BSA) and immobilized on Protein A Biosensors (FortéBio). Antibody-coated biosensors were incubated for 3 min with a solution containing 5 µg ml⁻¹ of wild-type, N501Y or E484K SARS-CoV-2 RBD in kinetic buffer, followed by a 3-min dissociation step. Changes in the molecules bound to the biosensors caused a shift in the interference pattern that was recorded in real time using an Octet RED96 system (FortéBio). The binding response over time was used to calculate the area under the curve using GraphPad Prism software (v.9.0.0).

Production of SARS-CoV-2 and B.1.1.7 RBDs and human ACE2

The SARS-CoV-2 RBD (BEI NR-52422) construct was synthesized by GenScript into CMVR with an N-terminal mu-phosphatase signal peptide, a C-terminal octa-histidine tag (GHHHHHHHH) and an avi tag. The boundaries of the construct are ₃₂₈RFPN₃₃₁ (N terminus) and ₅₂₈KKST₅₃₁ (C terminus)³⁸. The B.1.1.7 RBD gene was synthesized by GenScript into pCMVR with the same boundaries and construct details with a mutation at N501Y. These plasmids were transiently transfected into Expi293F cells using Expi293F expression medium (Life Technologies) at 37 °C 8% CO₂ while rotating at 150 rpm. The cultures were transfected using PEI cultivated for 5 days. Supernatants were clarified by centrifugation (10 min at 4,000g) before loading onto a nickel-NTA column (GE Healthcare). Purified protein was biotinylated overnight using BirA (Biotin ligase) before size-exclusion chromatography into PBS. Human ACE2-Fc (residues 1–615 with a C-terminal thrombin cleavage site and human Fc tag) was synthesized by Twist. Clarified supernatants were affinity-purified using a Protein A column (GE Life Sciences) that was directly neutralized and buffer exchanged. The Fc tag was removed by thrombin cleavage in a reaction mixture containing 3 mg of recombinant ACE2-Fc ectodomain and 10 µg of thrombin in 20 mM Tris-HCl pH 8.0, 150 mM NaCl and 2.5 mM CaCl₂. The reaction mixture was incubated at 25 °C overnight and reloaded on a Protein A column to remove uncleaved protein and the Fc tag. The cleaved protein was further purified by gel filtration using a Superdex 200 column 10/300 GL (GE Life Sciences) equilibrated in PBS.

Protein affinity measurements using biolayer interferometry

Biotinylated RBDs (from wild-type spike, spike(N501Y) or spike(N501Y, E484K, K417N)) were immobilized at 5 ng µl in undiluted 10× Kinetics

Buffer (Pall) to SA sensors until a load level of 1.1 nm. A dilution series of either monomeric ACE2 or Fab in undiluted kinetics buffer starting at 1,000 to 50 nM was used for 300–600 s to determine protein-protein affinity. The data were baseline subtracted and the plots fitted using the Pall FortéBio/Sartorius analysis software (v.12.0). Data were plotted in Graphpad Prism (v.9.0.2).

Phylogenetic analysis

All complete and low-coverage-excluded SARS-CoV-2 sequences were downloaded from the GISAID database (<http://gisaid.org/>)³⁹ on 11 February 2021. All sequences were realigned to the SARS-CoV-2 reference strain MN908947.3, using MAFFT v.7.475 with automatic flavour selection and the ---keeplength--addfragments options⁴⁰. Sequences were then deduplicated. Major SARS-CoV-2 clade memberships were assigned to all sequences using the Nextclade server v.0.12 (<https://clades.nextstrain.org/>).

Maximum likelihood phylogenetic trees were produced using the above curated dataset using IQ-TREE v.2.1.2⁴¹. Evolutionary model selection for trees was inferred using ModelFinder¹⁰ and trees were estimated using the GTR + F + I model with 1,000 ultrafast bootstrap replicates⁴². All trees were visualized with Figtree v.1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree/>) and manipulated and coloured with ggtree v.2.2.4. Phylogenies were rooted on the SARS-CoV-2 reference sequence (MN908947.3) and nodes arranged in descending order.

Statistical analysis

Linear regression was used to explore the association between the antibody response, T cell response and serum neutralization in Stata 13. The Pearson correlation coefficient was reported.

Neutralization data analysis

Neutralization was calculated relative to virus-only controls. Dilution curves were presented as a mean ± s.e.m. neutralization. IC₅₀ values were calculated in GraphPad Prism. The ID₅₀ values within groups were summarized as a GMT and statistical comparisons between groups were made using Wilcoxon ranked-sign tests. In addition, the effects of the mutations on the neutralizing effect of the sera were expressed as the fold change in ID₅₀ of the wild-type compared to the mutant pseudotyped virus. Statistical difference in the mean fold change between groups was determined using a two-tailed Student's t-test.

IFNγ FluoroSpot assay data analysis

The association between the spike-associated T cell response, spike-specific antibody response and serum neutralization was determined using linear regression. The Pearson correlation coefficients between these variables were determined using Stata 13.

Reporting summary

Further information on research design is available in the Nature Research Reporting Summary linked to this paper.

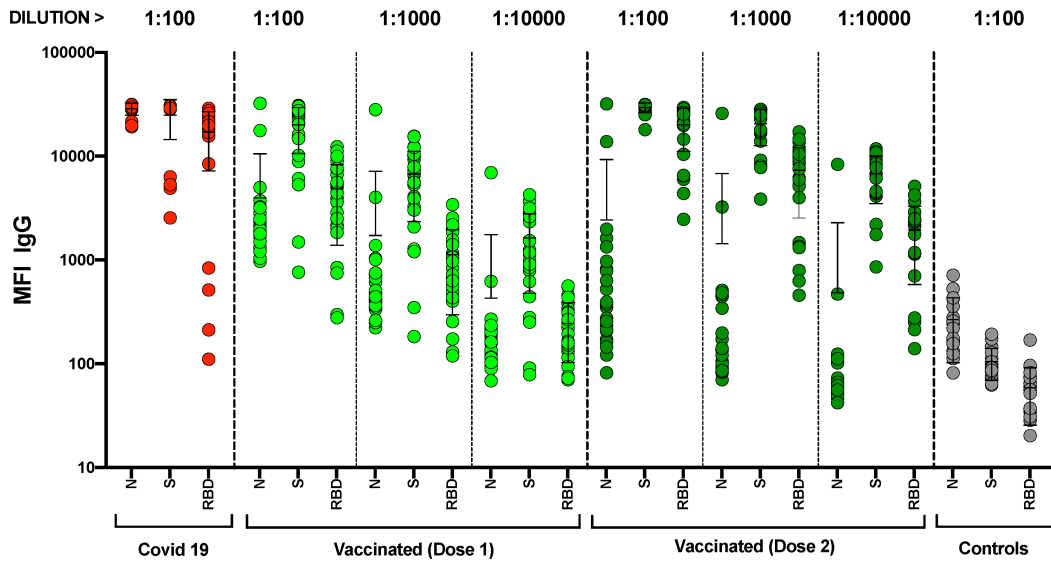
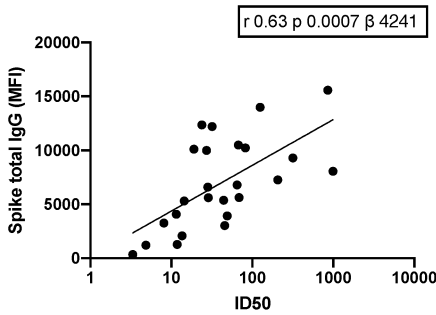
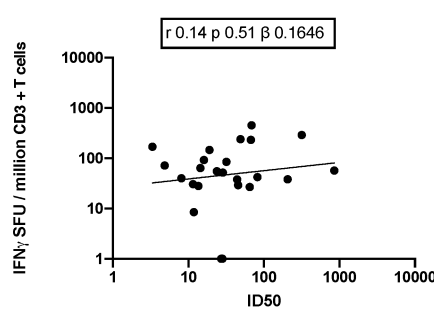
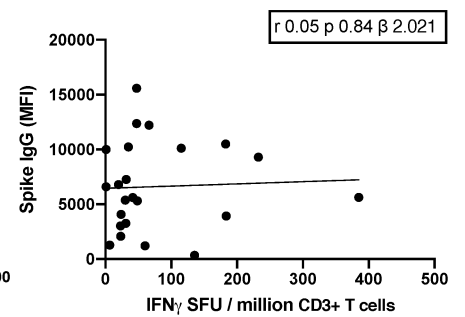
Data availability

The neutralization and biolayer interferometry data shown in Fig. 4 and Extended Data Figs. 6–8 can be found in the Source Data for Fig. 4. All sequences are publicly available and were downloaded from <http://gisaid.org>. Deduplicated and subsampled data are freely available at https://github.com/StevenKemp/sequence_files/blob/main/vaccinepaper/with_background_subsampled_deduped_aligned_UKonly_484_vui.fasta.gz. Other data are available from the corresponding authors on request. Source data are provided with this paper.

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- Author contributions** D.C., R.K.G. and D.A.C. conceived the study. R.K.G., D.A.C., L.E.M., J. Bassi, M.W., L.C.-G., G.B.-M., R.D., B.G., N.K., A.E., M.S.P., D.V., L.P., A.D.M., J.R.B. and D.C. designed the study and experiments. B.M., D.A.C., N.T., R.P.D., I.A.T.M.F., A.C.W., L.C.-G., S.A.K. and G.B.-M. performed experiments. R.K.G., D.A.C., B.M., R.D., I.A.T.M.F., A.C.W., L.E.M., J. Bassi, K.G.C.S. and D.V. interpreted data. A.D.M., and C.S.F. carried out pseudovirus neutralization assays. D.P. produced pseudoviruses. M.S.P., L.P., W.H., D.V. and D.C. designed the experiments. M.A.T., J. Bassi and S.J. expressed and purified the proteins. K.C., S.J. and E.C. sequenced and expressed antibodies. E.C. and K.C. performed mutagenesis to create mutant expression plasmids. A.C.W. and S.B. performed binding assays. A.R., A.F.P. and C.G. contributed to the recruitment of donors and collection of samples related to the isolation of monoclonal antibodies. H.W.V., G.S., A.L., D.V., L.P., D.V. and D.C. analysed the data and prepared the manuscript with input from all authors.
- Competing interests** A.D.M., J. Bassi, D.P., C.S.F., S.B., K.C., N.S., E.C., G.S., S.J., A.L., H.W.V., M.S.P., L.P. and D.C. are employees of Vir Biotechnology and may hold shares in Vir Biotechnology. H.W.V. is a founder of PierianDx and Casma Therapeutics. Neither company provided funding for this work or is performing related work. D.V. is a consultant for Vir Biotechnology. The Veessler laboratory has received a sponsored research agreement from Vir Biotechnology. R.K.G. has received consulting fees from UMOVIS Lab, Gilead and ViiV. The other authors declare no competing interests.
- Additional information**
Supplementary information The online version contains supplementary material available at <https://doi.org/10.1038/s41586-021-03412-7>.
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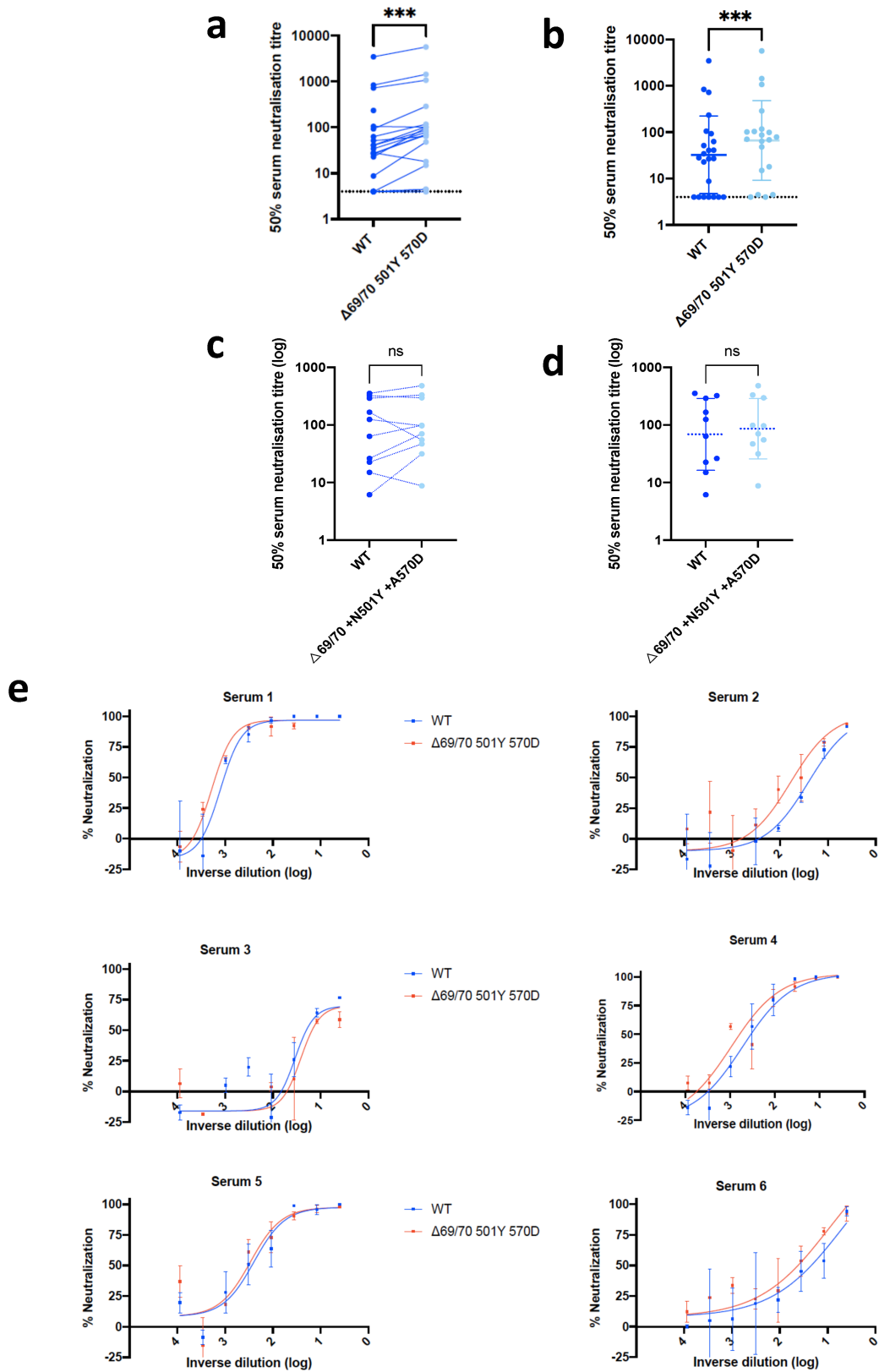
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a**b****c****d**

Extended Data Fig. 1 | Immune responses three weeks after first dose of the BNT162b2 vaccine against SARS-CoV-2. **a**, Serum IgG responses against the N protein, spike protein and the RBD of the spike protein of participants who received one vaccine dose (light green) or two vaccine doses (dark green), patients who had recovered from COVID-19 (red) and healthy control individuals (grey) were measured by a flow-cytometry-based Luminex assay. $n = 25$. MFI, mean fluorescence intensity. Data are GMT \pm s.d. (lines and error

bars) of two technical repeats and individual values (circles).

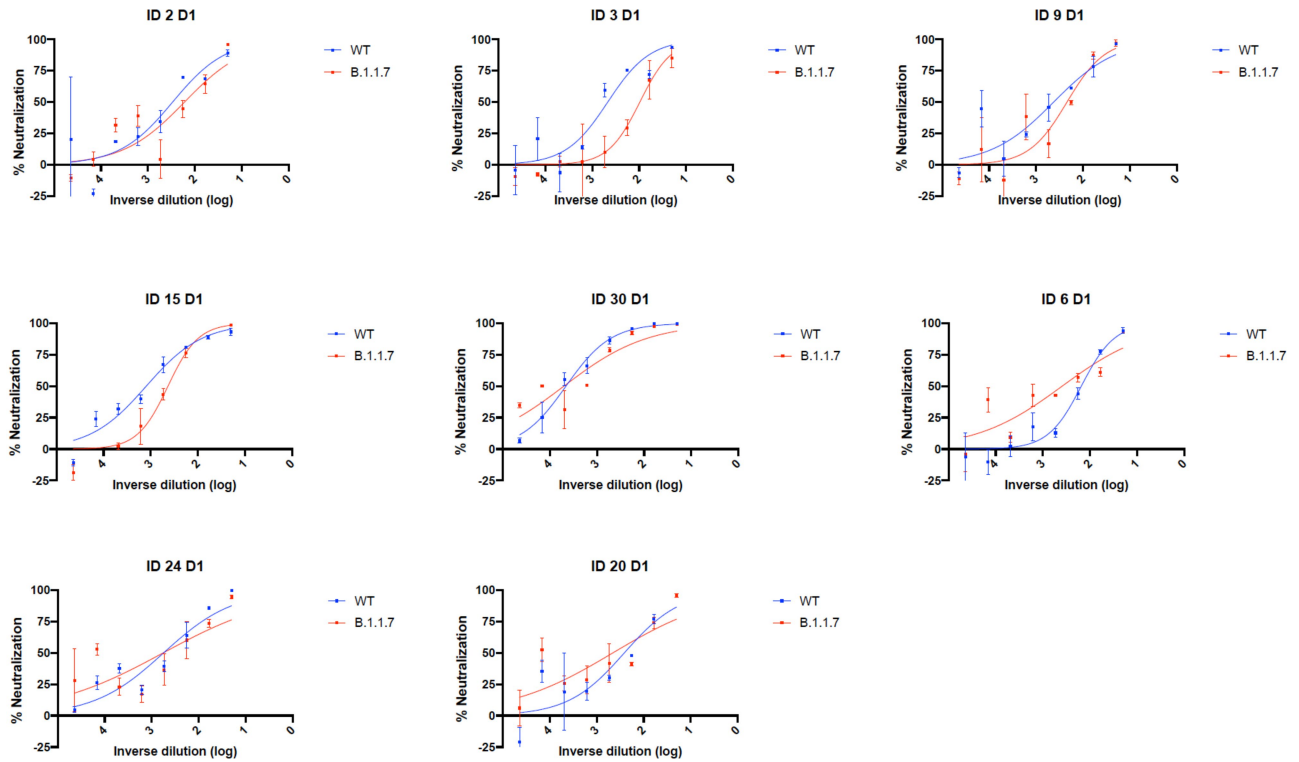
b, Relationship between serum IgG responses, measured by flow cytometry, and serum neutralization ID₅₀. $n = 25$. **c**, Relationship between serum neutralization ID₅₀ and T cell responses against SARS-CoV-2 by IFN γ FluoroSpot. $n = 24$. SFU, spot-forming units. **d**, Relationship between serum IgG responses and T cell responses. $n = 23$. **b-d**, Simple linear regressions are shown with Pearson correlation (r), P value (p) and regression coefficient/slope (β).



Extended Data Fig. 2 | See next page for caption.

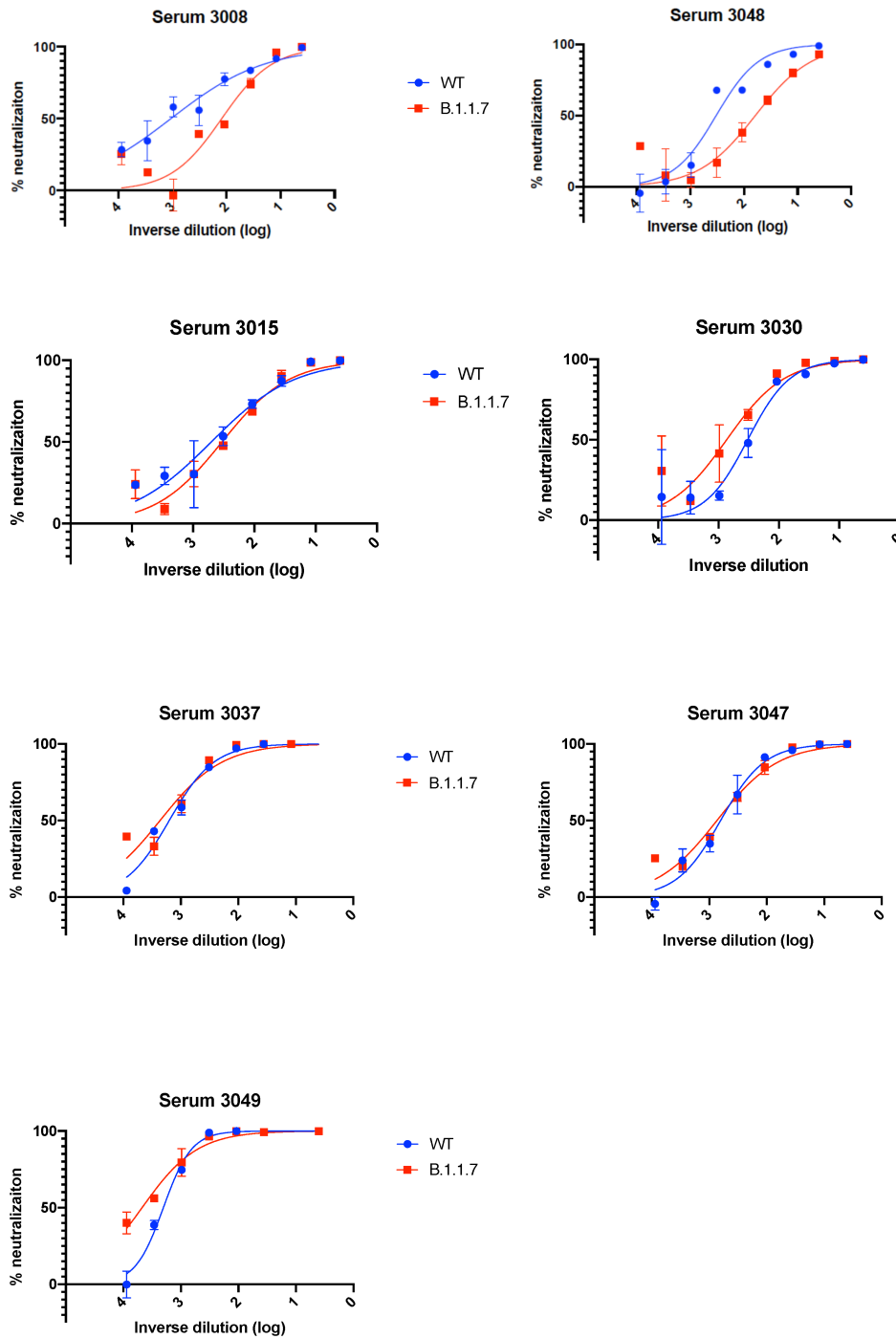
Extended Data Fig. 2 | Neutralization by the first dose of the BNT162b2 vaccine and convalescent sera against the wild-type and mutant (N501Y, A570D, ΔH69/ΔV70) SARS-CoV-2-pseudotyped viruses. **a, b**, Dilution of the vaccine sera for 50% neutralization against the wild-type and spike mutant (N501Y, A570D, ΔH69/ΔV70) viruses. **b**, Data are GMT \pm s.d. (lines and error bars) of two independent experiments with two technical repeats and individual values (circles). Two-tailed Wilcoxon matched-pairs signed-rank test with no adjustment for multiple comparisons; *** $P < 0.001$. **c, d**, Dilution of convalescent sera for 50% neutralization against the wild-type and spike mutant (N501Y, A570D, ΔH69/ΔV70) viruses. Data are GMT \pm s.d. (dotted lines and error bars) of a representative experiment with two technical repeats and

individual values (circles). Two-tailed Wilcoxon matched-pairs signed-rank test with no adjustment for multiple comparisons; ns, not significant. **e**, Representative curves of \log_{10} -transformed inverse dilutions of convalescent sera against the percentage of neutralization for the wild-type and spike mutant (N501Y, A570D, ΔH69/ΔV70) viruses. In cases in which a curve is shifted to the right the virus is less sensitive to the neutralizing antibodies in the serum. Data are mean \pm s.e.m. of two technical replicates. Data are representative of two independent experiments. The cut-off for 50% neutralization was set to 4 (dotted lines in **a, b**). **a, c**, Data points of the same individual are connected by lines.



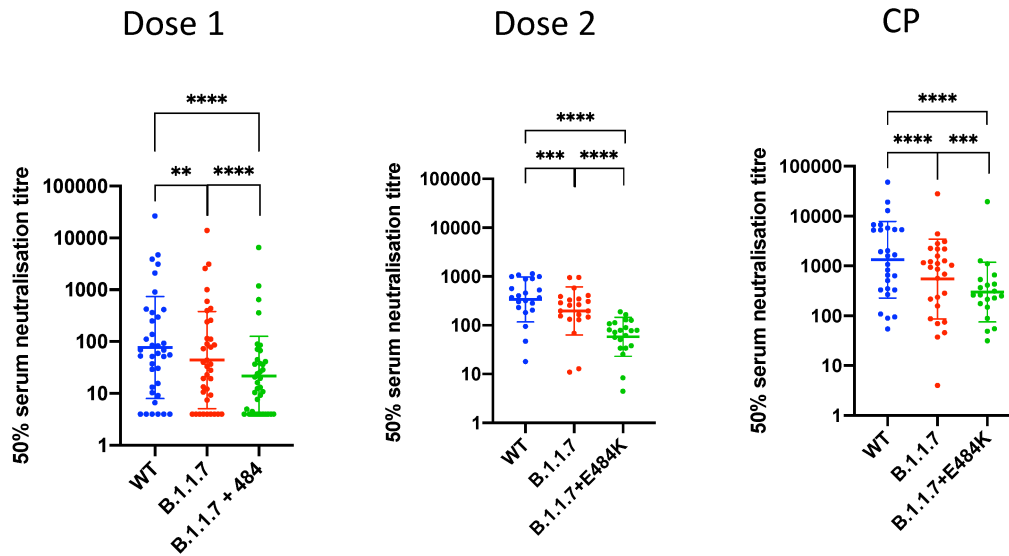
Extended Data Fig. 3 | Representative neutralization curves of sera from individuals vaccinated with the BNT162b2 vaccine against pseudotyped virus bearing eight mutations in the spike protein that are present in the B.1.1.7 variant compared with the wild-type virus. All virus variants were in a spike(D614G) background. The log₁₀-transformed inverse dilutions of the sera

are shown against the percentage of neutralization. In cases in which a curve is shifted to the right the virus is less sensitive to the neutralizing antibodies in the serum. Data are for the first dose of vaccine (D1). Data are mean ± s.e.m. representative of two independent experiments each with two technical replicates.



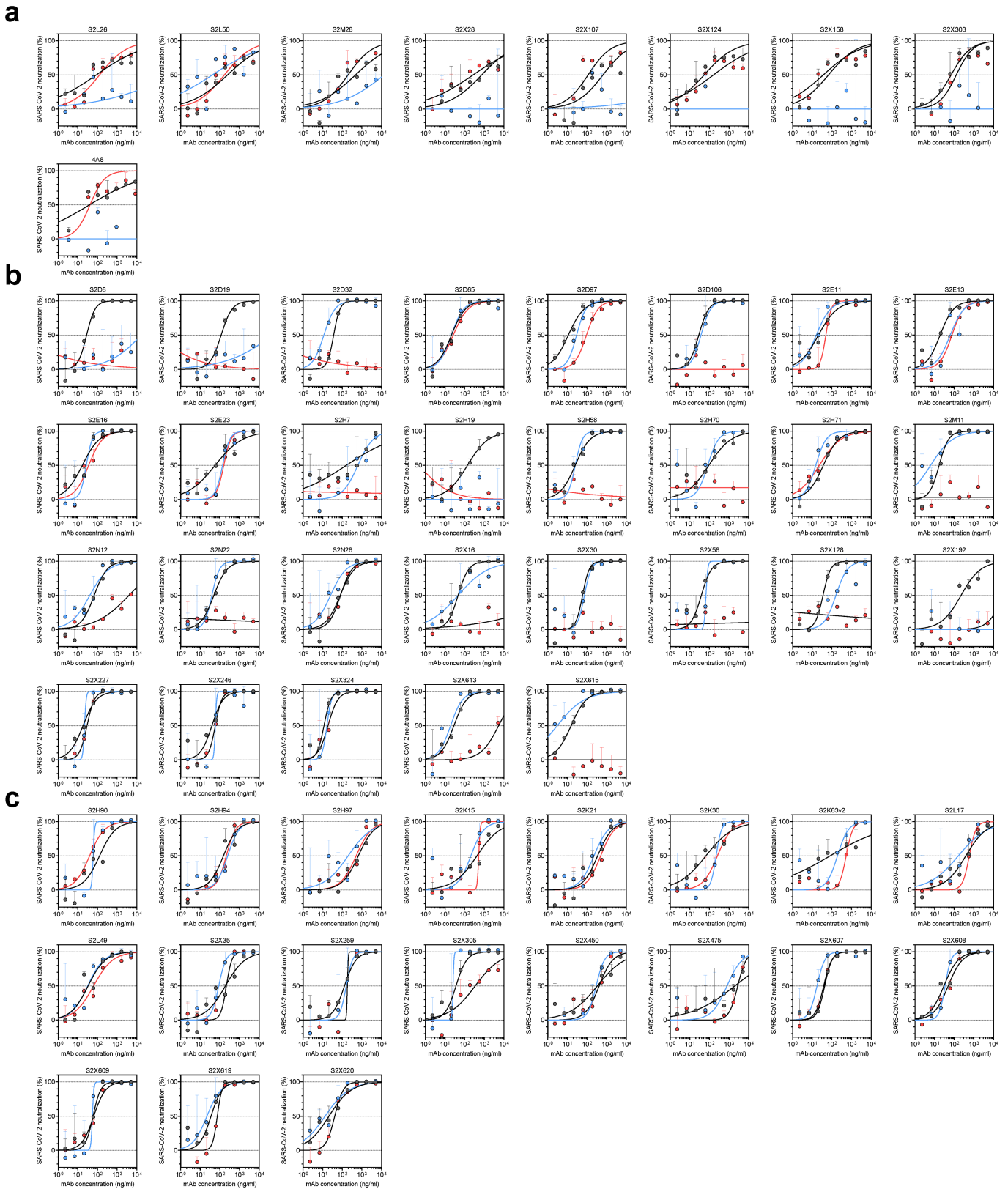
Extended Data Fig. 4 | Representative neutralization curves of convalescent sera against wild-type and B.1.1.7 spike-mutant SARS-CoV-2 pseudotyped viruses. The \log_{10} -transformed inverse dilutions of the sera are shown against the percentage of neutralization. In cases in which a curve is

shifted to the right the virus is less sensitive to the neutralizing antibodies in the serum. Data are mean \pm s.e.m. representative of two independent experiments each with two technical replicates.



Extended Data Fig. 5 | Neutralization potency of mRNA vaccine sera and convalescent sera (before SARS-CoV-2 B.1.1.7) against pseudotyped virus bearing spike mutations in the B.1.1.7 lineage with and without the E484K substitution in the RBD. All virus variants were in a spike(D614G) background. Neutralization potency of the sera from the first (left; $n = 37$) and the second (middle, $n = 21$) vaccine dose and of convalescent plasma (CP) (right; $n = 27$)

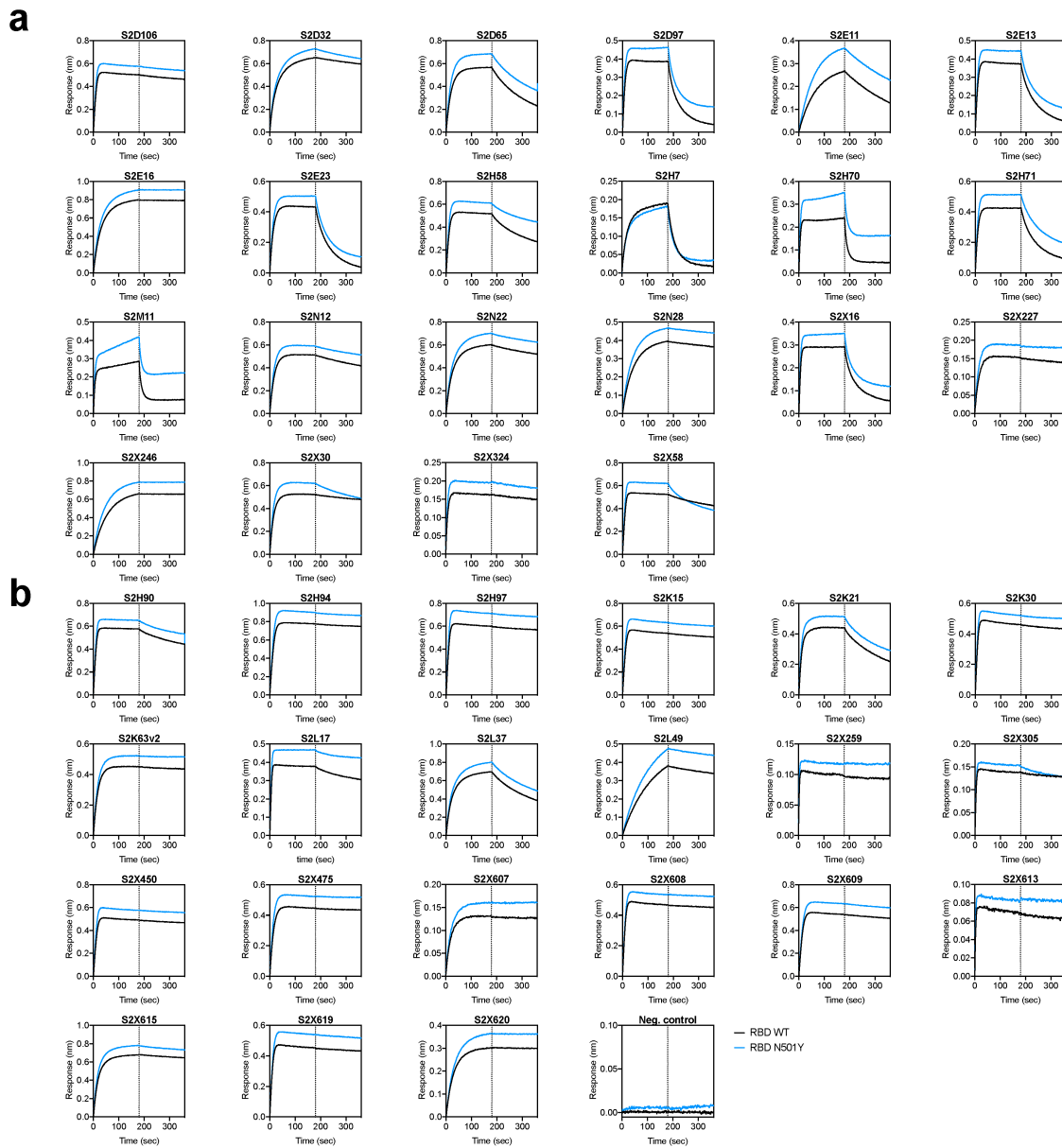
against wild-type SARS-CoV-2, the B.1.1.7 variant with spike(N501Y, A570D, Δ H69/ Δ V70, Δ I144, P681H, T716I, S982A, D1118H) and the B.1.1.7 variant with spike(N501Y, A570D, Δ H69/ Δ V70, Δ I144, P681H, T716I, S982A, D1118H) and the additional E484K substitution. Data are GMT \pm s.d. representative of two independent experiments each with two technical repeats. Wilcoxon matched-pairs signed-rank test; ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$.



Extended Data Fig. 6 | Neutralization of the wild-type spike (D614G), B.1.1.7 spike and spike(N501Y, E484K, K417N) proteins of the SARS-CoV-2-pseudotyped virus by a panel of 57 monoclonal antibodies.

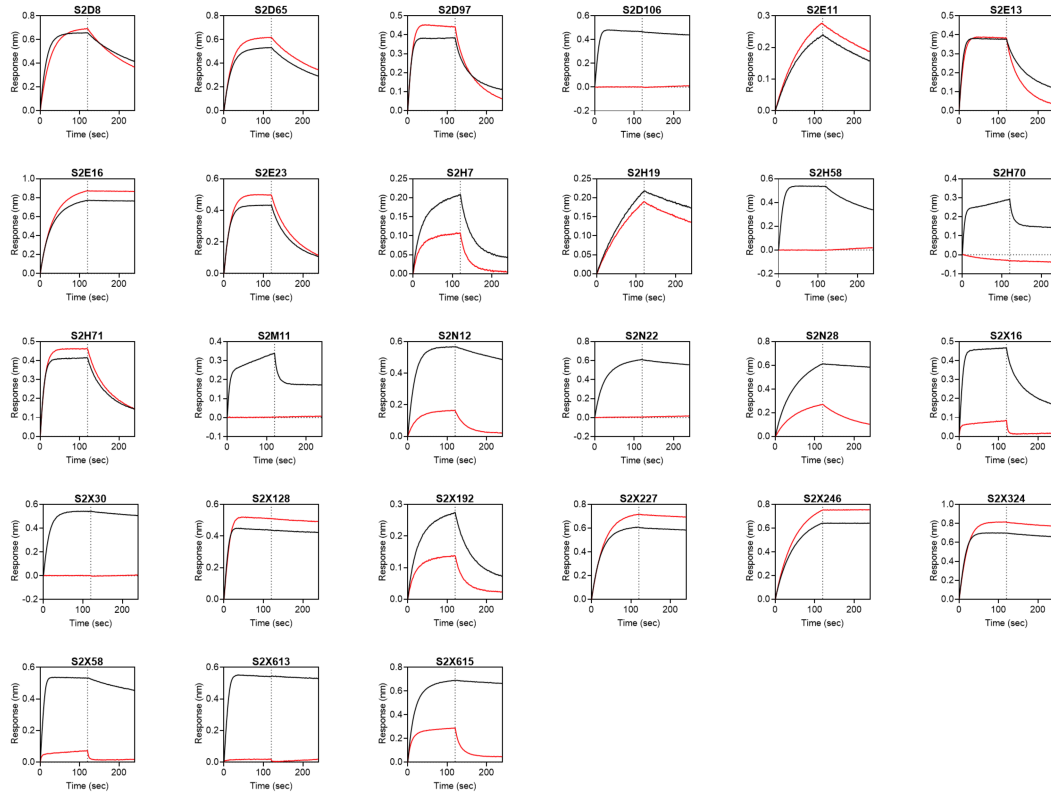
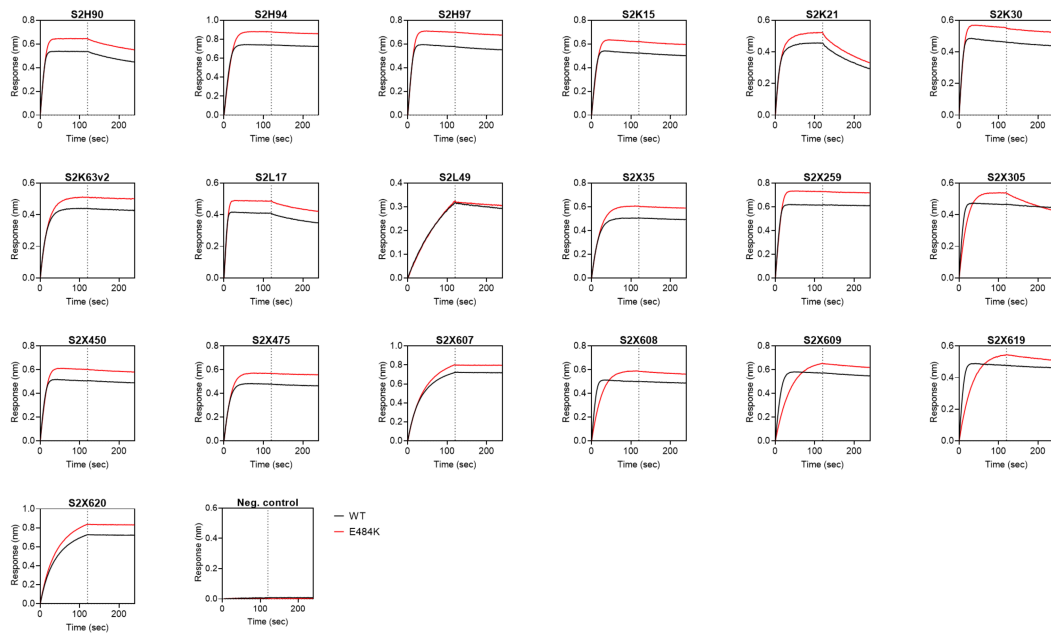
a-c. Neutralization of the wild-type spike (black), B.1.1.7 spike (blue) and

spike(N501Y, E484K, K417N) (TM) (red) SARS-CoV-2-MLV by 9NTD-targeting (a), 29RBM-targeting (b) and 19 non-RBM-targeting (c) monoclonal antibodies. Data are mean \pm s.d. of two technical replicates from one representative experiment.



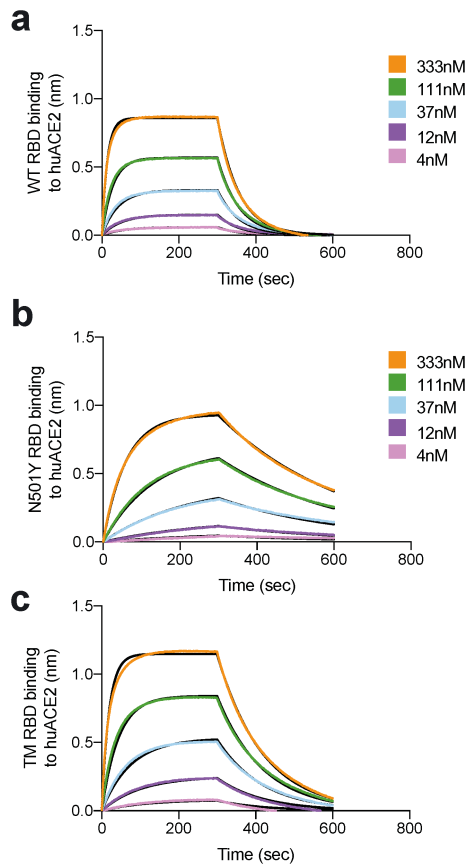
Extended Data Fig. 7 | Kinetics of binding to the RBD of wild-type and spike(N501Y) SARS-CoV-2 for 43 RBD-specific monoclonal antibodies. a-b, a, b, Binding to the RBD of wild-type (black) and spike(N501Y) (blue)

SARS-CoV-2 by 22 RBM-targeting (a) and 21 non-RBM-targeting (b) monoclonal antibodies. An antibody of irrelevant specificity was included as a negative control.

a**b**

Extended Data Fig. 8 | Kinetics of binding to the RBD of wild-type and spike(E484K) SARS-CoV-2 for 46 RBD-specific monoclonal antibodies. a, b, Binding to the RBD of wild-type (black) and spike(E484K) (red) SARS-CoV-2

by 27 RBM-targeting (a) and 19 non-RBM-targeting (b) monoclonal antibodies. An antibody of irrelevant specificity was included as a negative control.



Extended Data Fig. 9 | Binding of human ACE2 to the RBDs of the wild-type SARS-CoV-2 spike, spike(N501Y) and spike(N501Y, E484K, K417N) proteins. a–c, Biolayer interferometry binding analysis of the human ACE2 (huACE2) ectodomain (residues 1–615) to immobilized RBD of wild-type SARS-CoV-2 (a) and the RBD of B.1.1.7 spike(N501Y) (b) and spike (N501Y, E484K, K417N) proteins (c). Black lines correspond to a global fit of the data using a 1:1 binding model.

Extended Data Table 1 | Kinetic analysis of human ACE2 binding to RBDs of SARS-CoV-2

		SARS-CoV-2 RBD WT	SARS-CoV-2 RBD N501Y	SARS-CoV-2 RBD TM
K_D (nM)		133	22	64
k_{on} (M⁻¹.s⁻¹)	hACE2	1.3*10 ⁵	1.4*10 ⁵	1.3*10 ⁵
k_{off} (s⁻¹)		1.8*10 ⁻²	3*10 ⁻³	8.5*10 ⁻³

Kinetic analyses were carried out using biolayer interferometry for the RBDs of the Wuhan-1 spike, spike(N501Y) and spike(N501Y, E484K, K417N) (TM) proteins. Values reported represent the global fit to the data shown in Extended Data Fig. 9.

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Software and code

Policy information about [availability of computer code](#)

Data collection	Sequences were obtained from GISAID using the search parameters defined in the methods section. Monoclonal antibody binding data were collected with Octet RED96 system (FortéBio). Monoclonal antibody neutralization data (luminescence) were collected with Synergy H1 microplate reader (BioTek). Sera neutralising antibody data were read on a Glomax luminometer (Promega).
Data analysis	Graphad Prism v9 for statistical analyses and to produce figures. Monoclonal antibody binding data were analyzed by Pall FortéBio/Sartorius analysis software (version 12.0). Stata V13 for correlation analyses. PyMol v1.4 (Schodinger) to produce figures. Software versions and parameters used for all software are reported in full in the methods section.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

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All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

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- A description of any restrictions on data availability

The data analysed during the current study are available freely online in the GISAID database (<https://gisaid.org>) though specific files may be requested from the corresponding author on reasonable request. Pymol structures were all obtained from PDB and are available using the accession numbers described in the methods.

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Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	n=37. No sample size calculation was performed. The sample size of this study is sufficient to obtain a relevant analysis.
Data exclusions	No exclusions.
Replication	We performed 2 independent experiments and presented representative data with technical replicates. All data were reproducible.
Randomization	This is not relevant to the study as it is not an interventional study.
Blinding	No blinding undertaken as this is not an interventional study.

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We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

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<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Antibodies

Antibodies used	The source of monoclonal antibodies used in this study is described in Extended Data Table 1 and in the Method session.
Validation	The monoclonal antibodies were validated by binding and neutralization assays as described in the references of Extended Data Table 1.

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	HEK 293T and ExpiCHO cells were used for transfection work to produce pseudoviruses and mAbs, respectively.
Authentication	No cell lines used were authenticated. No new cell lines were generated.
Mycoplasma contamination	All cell lines used were tested (by PCR) and were mycoplasma free.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified lines were used in this study.

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics	Individuals receiving the Pfizer BNT162b2 mRNA vaccine were consented for the study. Median age was 62 years (IQR 47-84) and 35% were female.
Recruitment	Participants were consented into the COVID-19 cohort of the NIHR Bioresource. Consecutive individuals were enrolled without exclusion.
Ethics oversight	The study was approved by the East of England – Cambridge Central Research Ethics Committee (17/EE/0025).

Note that full information on the approval of the study protocol must also be provided in the manuscript.