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Supplementary Materials for

SARS-CoV-2 Beta variant infection elicits potent lineage-specific and cross-reactive antibodies

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The PDF file includes:

Other Supplementary Material for this manuscript includes the following:

Materials and Methods

Patient recruitment

All donors have given written informed consent and analyses were approved by the Institutional Review Board of Charité - Universitätsmedizin Berlin, corporate member of Freie Universität Berlin, Humboldt-Universität Berlin, and Berlin Institute of Health, Berlin (study protocol number EA1/258/18), the Institutional Review Board of the Faculty of Medicine at Ludwig-Maximilians-Universität (LMU) Munich, Germany (20-371), as well as the ethics committee of the Innsbruck Medical University (1167/2020). All donors in this study tested positive for SARS-CoV-2 infection by quantitative PCR with reverse transcription (RT-qPCR) from nasopharyngeal swabs. Beta variant infection was confirmed using next-generation sequencing of swab material from the donor or the unequivocal contact person in the chain of infection. All donors were unvaccinated. Patient characteristics are described in table S1.

Patient sample handling and single cell isolation

Peripheral blood mononuclear cells (PBMCs) were isolated by gradient centrifugation and then enriched for B cells by negative selection using a pan-B-cell isolation kit according to the manufacturer's instructions (Miltenyi Biotec, 130-101-638).

His-tagged recombinant RBD Beta protein was produced in HEK cells (ACROBiosystems, SPD-C52Hp) and covalently labeled using CruzFluor488 (Santa Cruz Biotechnology, sc-362617) according to the manufacturer's instructions. Separately, the same protein was labeled using its His-tag by incubating the antigen with an Alexa Fluor 647-conjugated anti-His-antibody (R&D Systems, IC0501R) for 30 minutes at room temperature at a 2:1 ratio (RBD molecules:IgG

molecules). Ovalbumin (Sigma, A5503) was covalently labeled with PE-Cy7 (abcam, ab102903) according to the manufacturer's instructions.

Using fluorescence-activated cell sorting (FACSAriaII SORP, BD Biosciences), we then sorted single RBD-Beta-double-positive $7AAD^{-}Ovalbumin^{-}CD19^{+}CD27^{+}$ memory B cells (MBCs) into 96-well PCR plates. Staining was performed on ice for 25 minutes in PBS with 1 mM EDTA, 1:100 human IgG (1 mg/ml) as FcR block and 2 % FCS using the following staining reagents: 7-AAD 1:400 (Thermo Fisher Scientific), CD19-BV786 1:20 (clone SJ25C1, BD Biosciences, 563326), CD27-PE 1:5 (clone M-T271, BD Biosciences, 555441), Ovalbumin-PECy7 at 2 µg/ml, RBD-Beta-CruzFluor488 at 1 µg/ml (RBD concentration) and RBD-Beta/Anti-His-AF647 at 1 µg/ml (RBD concentration).

Recombinant mAb generation

The mAbs were generated following our established protocols (*19*) with modifications as indicated. We used a nested PCR strategy to amplify the variable domains of the immunoglobulin heavy and light chain genes from single cell cDNA and analyzed their sequences with the aBASE module of Brain Antibody Sequence Evaluation (BASE) software (*32*). For further characterization representative mAbs were selected for cloning and expression based on the following criteria: (a) mAbs that are clonally expanded within one patient, (b) mAbs of clonotypes present in several patients in our dataset to decipher the shared antibody response to RBD Beta, (c) mAbs of clonotypes found both in our and CoV-AbDab datasets to potentially identify cross-reactive mAbs, (d) VH3-53/VH3-66 mAbs to elucidate the unexpected recurrent shared antibody response against RBD Beta, (e) mAbs of VH genes with strongest enrichment in our dataset, including VH4-39 and VH1-58 or (f) randomly selected mAbs of other germline genes and that appeared only once. The criteria-based selection for mAb

expression combined a focused investigation of mAb groups of special interest based on previous reports (e.g. VH3-53/VH3-66 mAbs) or on findings of this study (e.g. VH4-39 and VH1-58 mAbs) together with an unbiased investigation of randomly selected mAbs (category f), however, with the limitation of reducing the unbiased group of mAbs to ~30% of the expressed mAbs. The respective criteria for expression selection are listed in table S2 for each mAb individually. For mAbs selected for expression, pairs of functional Ig genes were PCR-amplified using specific primers with Q5 Polymerase (NEB). PCR-product and linearized vector containing the constant part of IgG1 heavy or kappa/lambda light chain sequences respectively were assembled using Gibson cloning with HiFi DNA Assembly Master Mix (NEB). All variable heavy chains were cloned into an IgG1 vector independent of the isotype of the source cells, where distribution was 70.8% IgG, 6.3% IgA and 22.9% IgM. Cloning was considered successful when sequence identity was >99.5% as verified by the cBASE module of BASE software. For mAb expression, human embryonic kidney cells (HEK293T) were transiently transfected with matching Ig heavy and light chains. The day after transfection, the supernatant was discarded and cells were supplemented with fresh medium. Six days later, mAb containing cell culture supernatant was harvested. Ig concentrations were determined and supernatants were used for reactivity and neutralization screening, if the Ig concentration was higher than 10 µg/ml. For biophysical characterization assays, supernatants were purified using Protein G Sepharose beads (GE Healthcare), dialyzed against PBS, and sterile-filtered using 0.2 µm filter units (GE Healthcare).

mAb sequence analysis, clonotype analysis and data visualization

Sequence analysis, including gene usage, CDR3 length, and number of somatic hypermutations, was performed using our previously published script collection BASE (*32*). To identify

antibodies which share the same V and J genes on both Ig heavy and light chains and thus are considered to be one clonotype, we used an in-house R script. After identification of public clonotypes, they were plotted in a Circos plot using the R package circlize (*33*). Our newly acquired dataset was compared to all previously published RBD mAbs included in the CoV-AbDab database, retrieved on 2021-06-16. As the CoV-AbDab includes SARS-CoV-2 mAbs from other sources than humans, and against other epitopes than the RBD, the following selection criteria were used (nomenclature like in CoV-AbDab): binds to: SARS-CoV-2, Protein + Epitope: RBD, Origin: B-cells (human). 1157 mAbs fulfilled these criteria as human RBD mAbs, none of which were derived from studies of patients where infection with a VOC was reported. All 1037 mAbs for which information on V-J gene usage was available for both heavy and light chain were included in the clonotype analysis and VH gene usage analysis in Fig. 2.

Diagnostic antibody testing

Initial serological testing of patient samples was performed using a solid phase immunoassay (SeraSpot®Anti-SARS-CoV-2 IgG, Seramun Diagnostica GmbH, Heidesee, Germany). Briefly, on the bottom of each well, SARS-CoV-2 recombinant antigens (nucleocapsid, wildtype full spike, wildtype S1 domain, wildtype RBD) and controls are printed in an array format as spots. Serum samples were diluted 1:101 in sample dilution buffer, added to the wells, and incubated for 30 minutes at room temperature. After washing, bound antibodies were detected by incubation with horseradish peroxidase (HRP)-labeled anti-human IgG for 30 minutes at room temperature. After washing again, 3′3,5,5-tetramethylbenzidine (TMB) solution was added to each well and incubated in the dark for 30 minutes at room temperature. Subsequently, the solution was removed, and color intensity of immune complexes formed at the site of each antigen spot was measured using a SpotSight®plate scanner. Color intensity correlates to the

antibody concentration and results were calculated as signal-to-cutoff ratios using the internal cutoff control.

Second, the presence of SARS-CoV-2 S1-specific antibodies was analyzed using a commercially available anti-SARS-CoV-2-S1 IgG ELISA (EUROIMMUN Medizinische Labordiagnostika AG, Lübeck, Germany) according to the manufacturer's instructions. Serum samples were diluted 1:101. The optical density (OD) at 450nm was measured and OD ratios were calculated by dividing this value by the OD of the kit-included calibrator.

Additionally, we applied a modified solid phase immunoassay (Seramun Diagnostica GmbH, Heidesee, Germany) as described above, which additionally contained SARS-CoV-2 RBD-VOCs (InVivo BioTech Services GmbH, Hennigsdorf, Germany).

Surrogate virus neutralization test (ACE2 binding inhibition)

Neutralizing capacity of patients' sera was assessed by a surrogate virus neutralization test (cPass Assay, Medac, Wedel, Germany) according to the manufacturer´s instructions and as described previously (*34*). Similarly, inhibition of ACE2 interaction of mAbs was tested using cell culture supernatants containing 10 µg/ml IgG. Briefly, serum samples or mAbs, positive and negative controls were diluted 1:10 with sample dilution buffer, mixed 1:1 with wildtype HRP-RBD or Beta HRP-RBD (Medac, Wedel, Germany) solution and incubated at 37°C for 30 minutes. Afterwards, the mixture was added to the hACE2-coated plate and incubated at 37°C for 15 minutes. After a washing step, TMB solution was added, and the plate was incubated in the dark at room temperature for 15 minutes. Stop solution was then added and the optical density at 450 nm was measured using a Tecan Infinite 200 PRO plate reader. For calculation of the relative inhibition of ACE2/RBD binding, the following formula was applied: Inhibition score (%) = (1 − OD value sample/OD value negative control) × 100%.

RBD ELISA

Binding of mAbs to SARS-CoV-2 spike RBD or variants thereof was detected by ELISA as previously described (*19*). Briefly, HEK293T cell-secreted RBD-Fc fusion proteins composed of the RBD-SD1 component of the SARS-CoV-2 spike S1 subunit (amino acids 319-591) and the constant region of rabbit IgG1 heavy chain (Fc) were immobilized onto 96-well plates via anti-rabbit IgG (Dianova, 711-005-152). Human mAbs were applied and detected using HRP-conjugated anti-human IgG (Dianova, 709-035-149) and the HRP substrate 1-step Ultra TMB (Thermo Fisher Scientific, Waltham, MA).

All mAbs were initially screened at 10 ng/ml for binding to RBD Beta and wildtype RBD to identify strong binders and to distinguish Beta-selective from cross-reactive antibodies. RBD Beta-selective mAbs were tested at 100 ng/ml for binding to RBD Beta, wildtype RBD as well as RBD variants containing all other combinations of amino-acid differences at positions 417 (N or K), 484 (K or E) and 501 (Y or N). Cross-reactive mAbs that neutralized SARS-CoV-2 Beta were tested at 100 ng/ml for binding to RBD-Fc proteins derived from SARS-CoV-2 variants of concern (VOCs) Alpha (lineage B.1.1.7; RBD N501Y and SD1 A570D), Beta (B.1.351; RBD K417N, E484K and N501Y), Gamma (P.1; RBD K417T, E484K and N501Y) and Delta (B.1.617.2; RBD L452R and T478K) (*35, 36*); from SARS-CoV-2 wildtype; and from SARS-CoV (*19*). For each mAb, the absorbance values at 450 nm based on binding to the RBD variants were normalized to its value on RBD Beta. Means of the relative values were determined from data of at least two independent experiments.

RBD Alpha and RBD Beta were generated based on gene synthesis of the S1 RBD-SD1 regions (Eurofins Genomics). Mutations for single amino-acid changes and for RBD Gamma and RBD

Delta were introduced by overlap extension PCR. All constructs were checked by Sanger sequencing (LGC Genomics).

Plaque reduction neutralization test

To assess the neutralizing activity of serum samples and SARS-CoV-2 mAbs, we performed plaque reduction neutralization tests (PRNT) as described (*37*) using virus of Beta isolate (GISAID accession no: EPI_ISL_862149), wildtype Munich isolate 984 (*37*) and Delta isolate (GISAID accession no EPI_ISL_2500366). In brief, Vero E6 cells (1.6 x105 cells/well) were seeded in 24-well plates and incubated overnight. Serum or mAbs were diluted in OptiPro and mixed 1:1 with 200 µL of the respective virus isolate solution containing 100 plaque forming units. The serum- or mAb-virus solutions were incubated on the Vero E6 cells for 1 hour at 37°C, then discarded, and cells were washed once with PBS and supplemented with 1.2% Avicel solution in DMEM. After three days of incubation, the supernatants were removed, the cells were fixed and inactivated using a 6% formaldehyde in PBS solution and then stained with crystal violet to count plaques. mAbs were diluted to 200 and 2000 ng/ml in mAb-virus solution for screening assays and in further dilutions for the determination of the IC_{50}. Serum samples were serially diluted starting at 1:20. All dilutions were tested in duplicate.

Surface plasmon resonance

Anti-human IgG (Fc) capture antibody was covalenty immobilized on a C1 sensor chip. Purified mAbs were reversibly immobilized via the anti-human IgG capture surface. The RBD Beta protein (Acro Biosystems, SPD-C52Hp) was injected at different concentrations in a buffer consisting of 10 mM HEPES pH 7.4, 150 mM NaCl, 3 mM EDTA, 0.05% Tween 20, 0.1 mg/ml

BSA. Ka, Kd and KD-values were determined using a monovalent analyte model. Recordings were performed on a Biacore T200 instrument at 25°C.

Crystallization and structural determination

The RBD (residues 333-529) of the SARS-CoV-2 spike (S) protein (GenBank: QHD43416.1) and the Beta variant that carries three mutations on the RBD (K417N, E484K, and N501Y) were cloned into a customized pFastBac vector (*38*), and fused with an N-terminal gp67 signal peptide and C-terminal His_6 tag. A recombinant bacmid DNA was generated using the Bac-to-Bac system (Life Technologies). Baculovirus was generated by transfecting purified bacmid DNA into Sf9 cells using FuGENE HD (Promega), and subsequently used to infect suspension cultures of High Five cells (Life Technologies) at an MOI of 5 to 10. Infected High Five cells were incubated at 28 °C with shaking at 110 r.p.m. for 72 h for protein expression. The supernatant was then concentrated using a 10 kDa MW cutoff Centramate cassette (Pall Corporation). The RBD protein was purified by Ni-NTA, followed by size exclusion chromatography, and buffer exchanged into 20 mM Tris-HCl pH 7.4 and 150 mM NaCl.

For expression and purification of the Fabs, heavy and light chains were cloned into phCMV3. The plasmids were transiently co-transfected into ExpiCHO cells at a ratio of 2:1 (HC:LC) using ExpiFectamine™ CHO Reagent (Thermo Fisher Scientific) according to the manufacturer's instructions. The supernatant was collected at 14 days post-transfection. The Fabs were purified with a CaptureSelect™ CH1-XL Affinity Matrix (Thermo Fisher Scientific) followed by size exclusion chromatography.

CS23/B.1.351 RBD, CS44/COVA1-16/B.1.351 RBD, and CV07-287/COVA1-16/wild-type RBD complexes were formed by mixing each of the protein components at an equimolar ratio and incubated overnight at 4°C. COVA1-16 Fab was used to assist with the crystal packing (*39*).

Each complex was screened for crystallization using the 384 conditions of the JCSG Core Suite (Qiagen) and ProPlex screen (Molecular Dimensions) on either our robotic CrystalMation system (Rigaku) or an Oryx8 (Douglas Instruments) at Scripps Research. Crystallization trials were set-up by the vapor diffusion method in sitting drops containing 0.1 μl of protein and 0.1 μl of reservoir solution. Diffraction-quality crystals were obtained in the following conditions:

CS23/B.1.351 RBD (12.5 mg/ml): 1.6 M ammonium sulfate and 0.1 M bicine pH 9.0 at 20°C
CS44/COVA1-16/B.1.351 RBD (12.0 mg/ml): 1.6 M ammonium sulfate and 0.1 M citric acid pH 4.0 at 20°C
CV07-287/COVA1-16/wild-type RBD (12.0 mg/ml): 1.6 M ammonium sulfate and 0.1 M bicine pH 9.0 at 20°C
All crystals appeared on day 3 and were harvested on day 7. Before flash cooling in liquid nitrogen for X-ray diffraction studies, crystals were equilibrated in reservoir solution supplemented the following cryoprotectants:

CS23/B.1.351 RBD: 20% ethylene glycol
CS44/COVA1-16/B.1.351 RBD: 20% glycerol
CV07-287/COVA1-16/wild-type RBD: 20% ethylene glycol

Diffraction data were collected at cryogenic temperature (100 K) at the Advanced Light Source on the beamline 5.0.1 and the Stanford Synchrotron Radiation Lightsource (SSRL) on Scripps/Stanford beamline 12-1, and processed with HKL2000 (*40*) (table S4). Structures were solved by molecular replacement using PHASER (*41*) with PDB 6W41. Iterative model building and refinement were carried out in COOT (*42*) and PHENIX (*43*), respectively (table S4).

Epitope and paratope residues, as well as their interactions, were identified by accessing PISA at the European Bioinformatics Institute (http://www.ebi.ac.uk/pdbe/prot_int/pistart.html) (*44*) (table S5).

Biolayer interferometry (BLI) competition assay

Competition assays were performed by biolayer interferometry (BLI) using an Octet Red instrument (FortéBio). IgGs were diluted with kinetic buffer (1x PBS, pH 7.4, 0.01% BSA and 0.002% Tween 20). After His-tagged RBD Beta was immobilized on anti-Penta His BLI sensors, sensors were first dipped into indicated "first antibodies" (50 µg/ml), and then dipped into indicated "second antibodies" (12.5 µg/ml). Three replicates were performed for each BLI experiment. The response signals each of the bound first antibodies were normalized to 100%, and the additional signals of the secondary antibodies were calculated accordingly. Numbers > 20% indicate different binding sites.

BLI binding assay to VOC RBDs

RBD proteins for the biolayer interferometry (BLI) binding assay were expressed in human cells. RBDs were cloned into phCMV3 vector and fused with a C-terminal His_6 tag. The plasmids were transiently transfected into Expi293F cells using ExpiFectamine 293 Reagent (Thermo Fisher Scientific) according to the manufacturer's instructions. The supernatant was collected at 7 days post-transfection. The His_6-tagged proteins were then purified with Ni Sepharose Excel resin (Cytiva) followed by size exclusion chromatography. The Omicron RBD was purchased from AcroBiosystems Inc. To measure the binding kinetics of anti-SARS-CoV-2 IgGs and RBDs, the IgGs were diluted with kinetic buffer (1x PBS, pH 7.4, 0.01% BSA and 0.002%

Tween 20) into 15 μg/ml. The IgGs were then loaded onto anti-human IgG Fc (AHC) biosensors and interacted with 5-fold gradient dilutions of 500 nM to 4 nM of SARS-CoV-2 RBDs. The assay went through the following steps. 1) baseline: 1 min with 1x kinetic buffer; 2) loading: 90 seconds with IgGs; 3) wash: 15 seconds wash of unbound IgGs with 1x kinetic buffer; 4) baseline: 1 min with 1x kinetic buffer; 5) association: 90 seconds with RBDs; and 6) dissociation: 90 seconds with 1x kinetic buffer. For estimating KD, a 1:1 binding model was used.

Statistical analyses

Area under the curve (AUC) calculations in Fig. 1 and all statistical analyses were performed using GraphPad Prism (9.2.0).

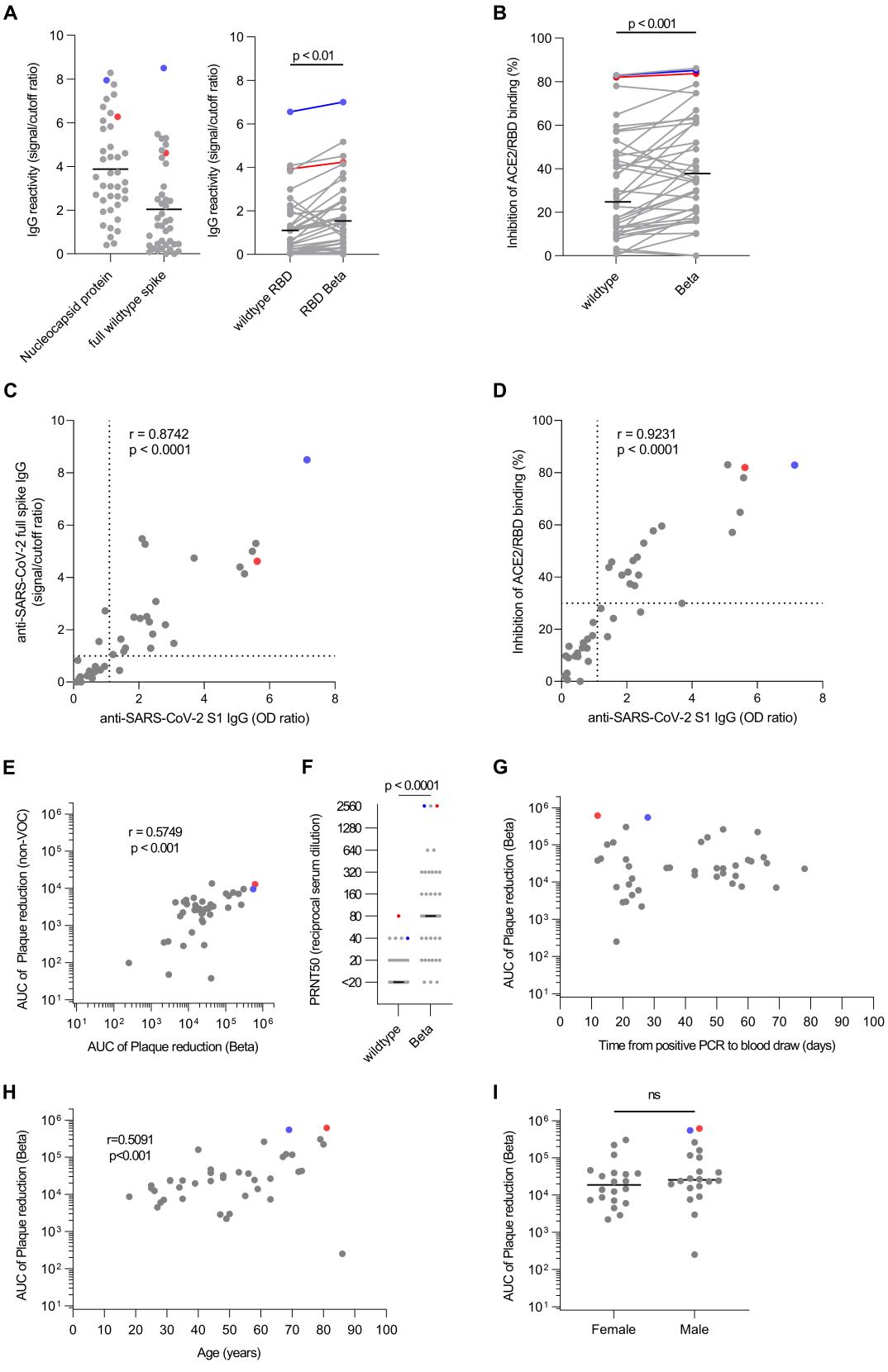
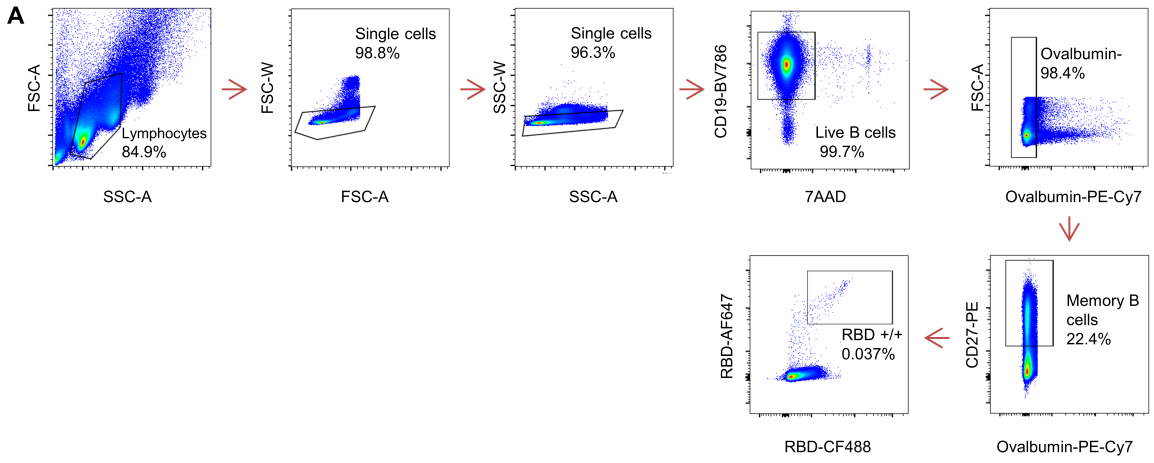

A
IgG reactivity (signal/cutoff ratio)
Nucleocapsid protein
full wildtype spike
p < 0.01
wildtype RBD
RBD Beta
B
Inhibition of ACE2/RBD binding (%)
p < 0.001
wildtype
Beta
C
anti-SARS-CoV-2 full spike IgG (signal/cutoff ratio)
r = 0.8742
p < 0.0001
anti-SARS-CoV-2 S1 IgG (OD ratio)
D
Inhibition of ACE2/RBD binding (%)
r = 0.9231
p < 0.0001
anti-SARS-CoV-2 S1 IgG (OD ratio)
E
AUC of Plaque reduction (non-VOC)
r = 0.5749
p < 0.001
AUC of Plaque reduction (Beta)
F
PRNT50 (reciprocal serum dilution)
p < 0.0001
wildtype
Beta
G
AUC of Plaque reduction (Beta)
Time from positive PCR to blood draw (days)
H
AUC of Plaque reduction (Beta)
r=0.5091
p<0.001
Age (years)
I
AUC of Plaque reduction (Beta)
ns
Female
Male

Fig. S1. Polyclonal antibodies from individuals after infection with SARS-CoV-2 Beta. (A) IgG reactivity against indicated antigens was measured by SeraSpot Anti-SARS-CoV-2 IgG assay. Statistical analysis was performed using a Friedman test and Dunn's multiple comparison test. Only the p-value for comparison of wildtype RBD vs. RBD Beta is shown. Horizontal bars indicate median values. **(B)** ACE2 interaction with indicated RBD was determined using the cPass Surrogate Neutralization Assay. Statistical analysis was performed using a Wilcoxon matched-pairs signed rank test. Horizontal bars indicate median values. Values below zero were set to zero, indicating no inhibition. **(C-D)** Anti-SARS-CoV-2 S1 IgG measured by Euroimmun S1-ELISA is plotted against **(C)** anti-SARS-CoV-2 full wildtype spike IgG measured by SeraSpot IgG assay and against **(D)** inhibition of ACE2/wildtype RBD binding measured by cPass Surrogate Neutralization assay. Statistical analysis was performed by two-tailed Spearman's correlation. Dashed lines indicate cutoffs defined by the assays' manufacturers, which have been validated for wildtype sera. **(E)** Correlation of neutralization activity against SARS-CoV-2 Beta and SARS-CoV-2 wildtype measured as AUC of PRNT is shown. Statistical analysis was performed by two-tailed Spearman's correlations. **(F)** The 50% serum neutralization titers (PRNT50) against indicated authentic virus is shown (from PRNT curves shown in Fig. 1, A and B). Statistical analysis was performed using a Wilcoxon matched-pairs signed rank test. Horizontal bars indicate median. **(G)** Time between first positive PCR test and sample collection in days is plotted against the AUC of PRNT against SARS-CoV-2 Beta. Statistical analysis performed by two-tailed Spearman's correlations showed no statistically significant correlation. **(H)** Patient age is plotted against AUC of PRNT against SARS-CoV-2 Beta. Statistical analysis was performed by two-tailed Spearman's correlations. **(I)** AUC of PRNT is plotted against SARS-CoV-2 Beta for men (n = 20) and women (n = 20) Statistical significance was determined using two-tailed Mann–Whitney U-tests. **(E, G-H)** AUC calculation is based on authentic virus PRNT curves (shown in Fig. 1, A and B). Patients SA1 and SA2 mounted the strongest antibody response, which are highlighted in red and blue, respectively.


A
FSC-A
SSC-A
Lymphocytes
84.9%
FSC-W
FSC-A
Single cells
98.8%
SSC-W
SSC-A
Single cells
96.3%
CD19-BV786
7AAD
Live B cells
99.7%
FSC-A
Ovalbumin-PE-Cy7
Ovalbumin-
98.4%
CD27-PE
Ovalbumin-PE-Cy7
Memory B
cells
22.4%
RBD-AF647
RBD-CF488
RBD +/+
0.037%

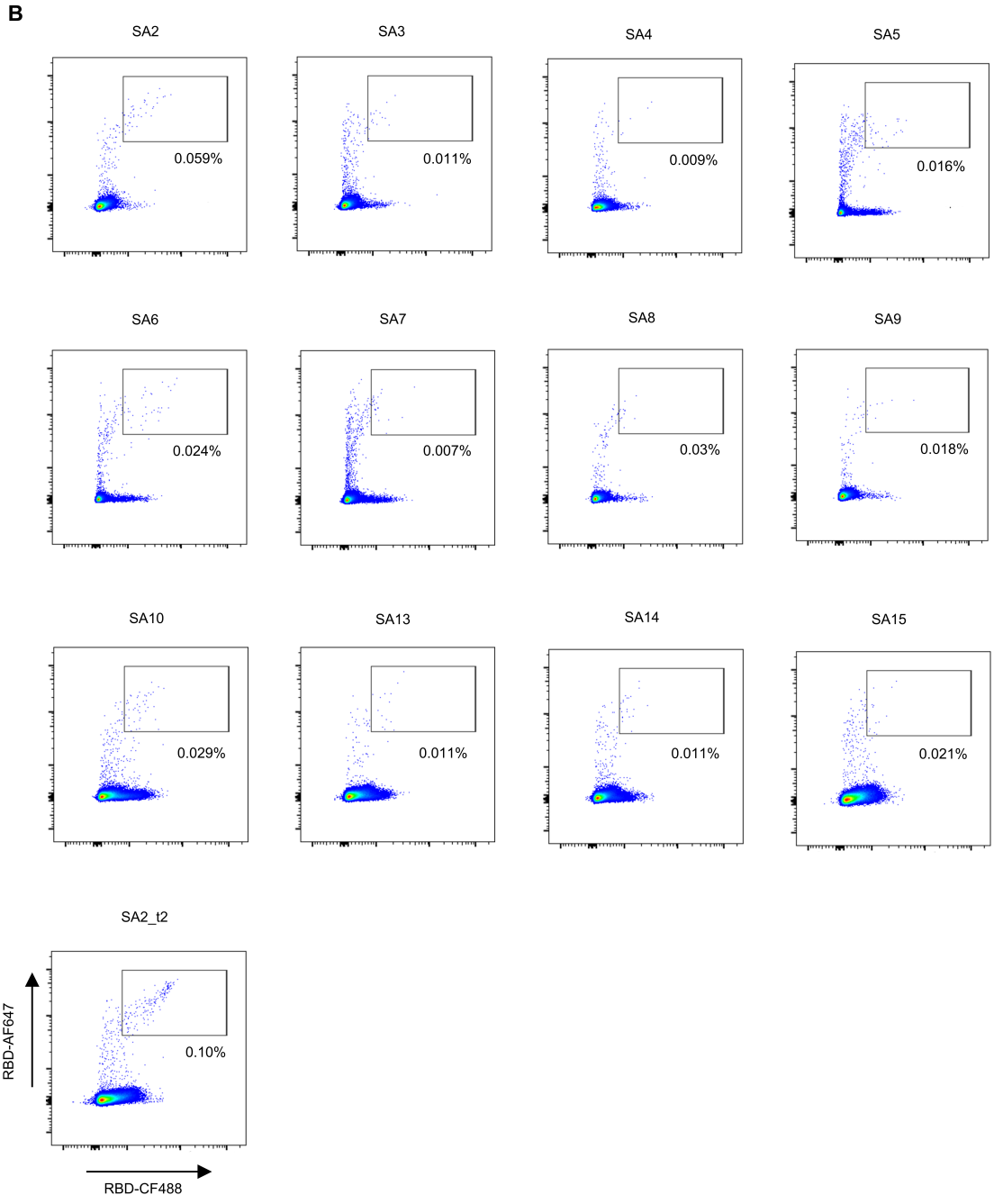

B
SA2
0.059%
SA3
0.011%
SA4
0.009%
SA5
0.016%
SA6
0.024%
SA7
0.007%
SA8
0.03%
SA9
0.018%
SA10
0.029%
SA13
0.011%
SA14
0.011%
SA15
0.021%
SA2_t2
0.10%
RBD-AF647
RBD-CF488

Fig. S2. Gating strategy used for single cell sorting of RBD-reactive memory B cells. (A) Gating was on singlets that were $CD19^{+}7AAD^{-}Ovalbumin^{-}CD27^{+}$. Sorted cells were $RBD\text{-}AF647^{+}/RBD\text{-}CF488^{+}$. **(B)** Flow cytometry showing the percentage of RBD-double-positive memory B cells of indicated patients. Patient SA2 donated blood twice, and the analysis from the second time point is denoted by SA2_t2.

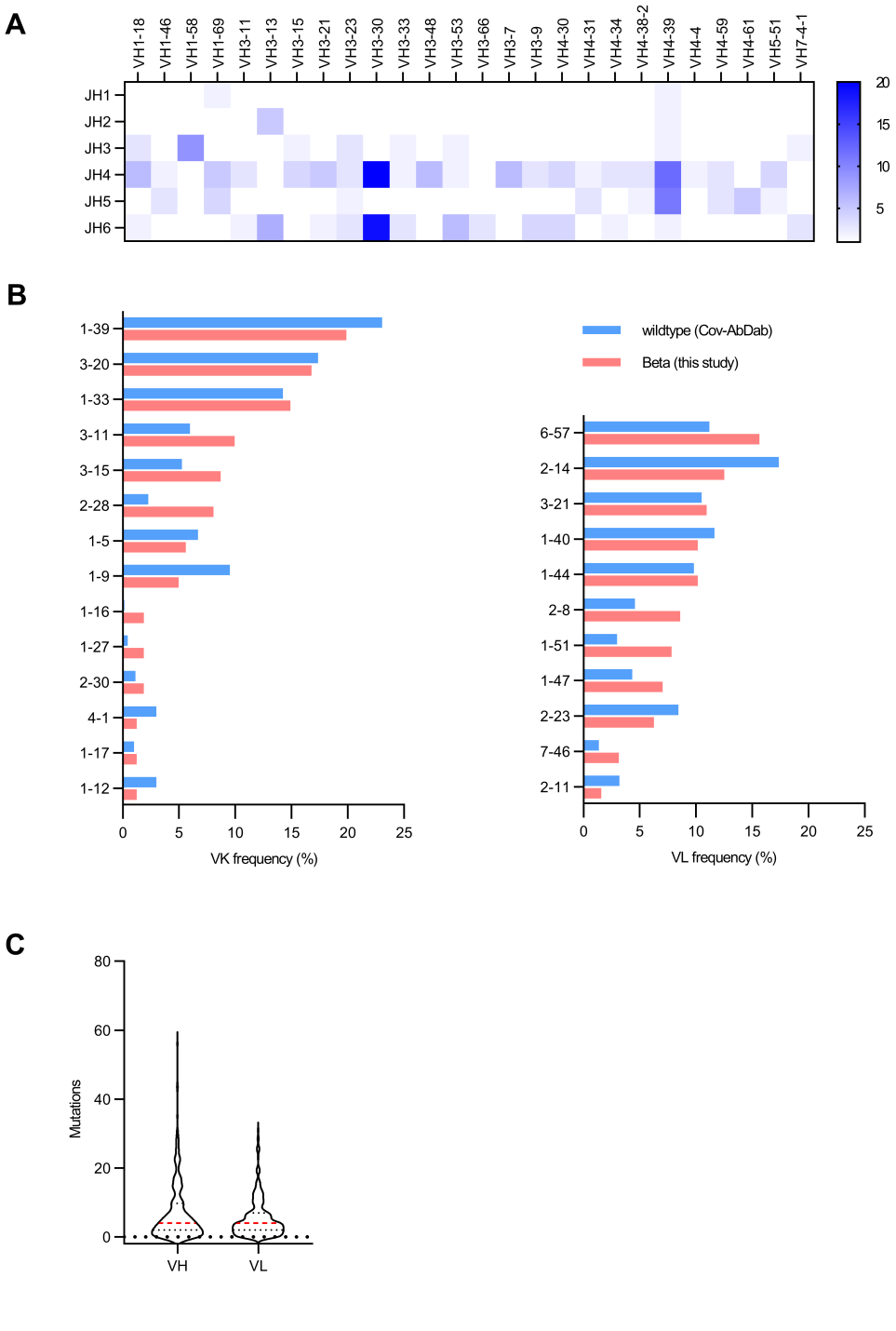


Fig. S3. Sequence characteristics of Beta-elicited monoclonal antibodies in this study. (A) Pairing of indicated VH genes with JH gene families of 289 IgG mAbs are shown in absolute numbers. Only VH genes with 4 or more occurrences are shown. **(B)** VK and VL gene usage of 289 RBD Beta IgG mAbs from this study (red) is compared to 1037 wildtype RBD mAbs from 96 previously published studies

(blue, CoV-AbDab). Frequencies of mAbs encoded by each VK/VL gene are shown as bars. Genes are ordered by frequency in CoV-AbDab. **(C)** Violin plots of somatic nucleotide mutations in the IGVH and IGVL genes in all 289 IgG mAbs obtained from all donors. Red bars indicate mean.

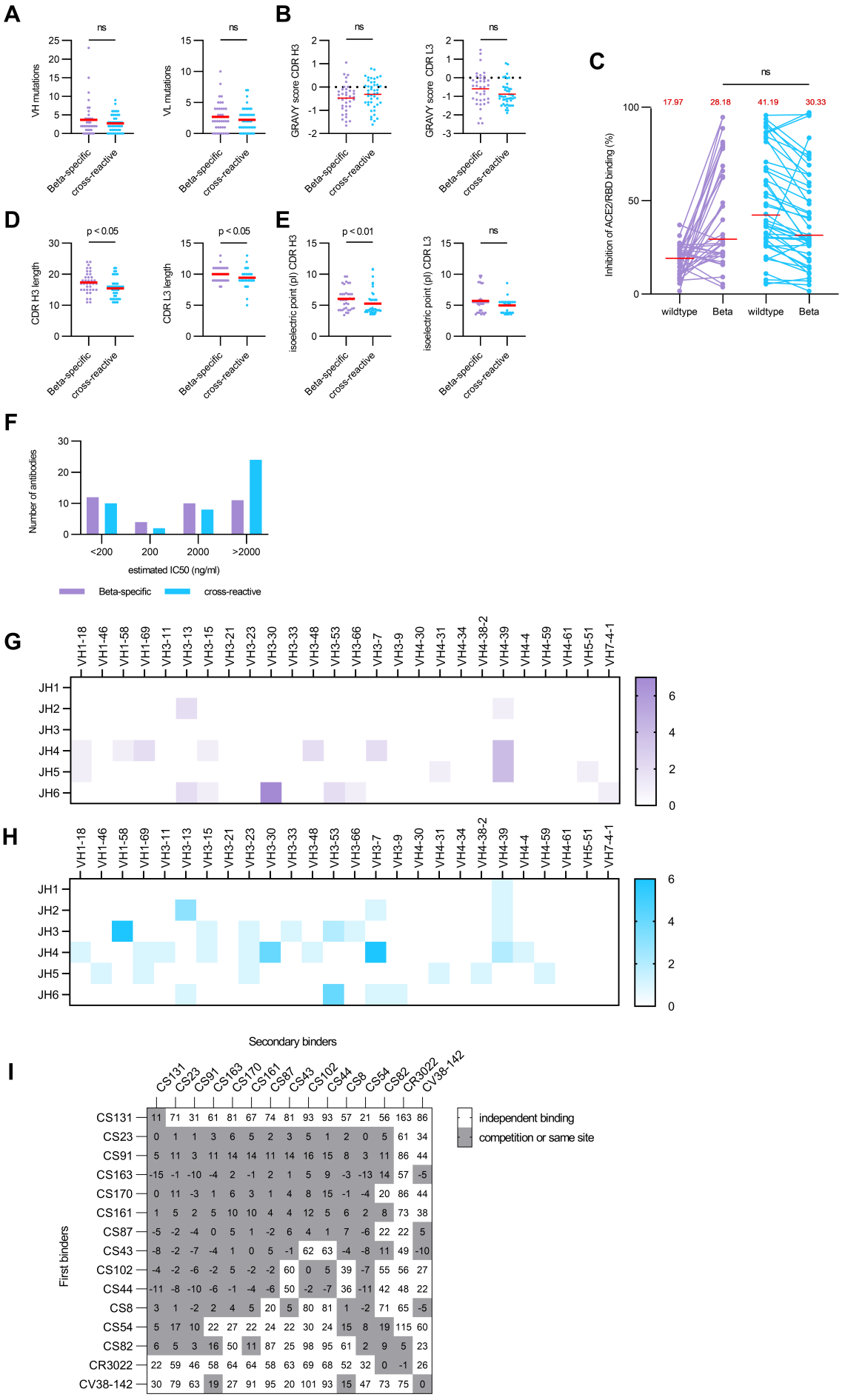
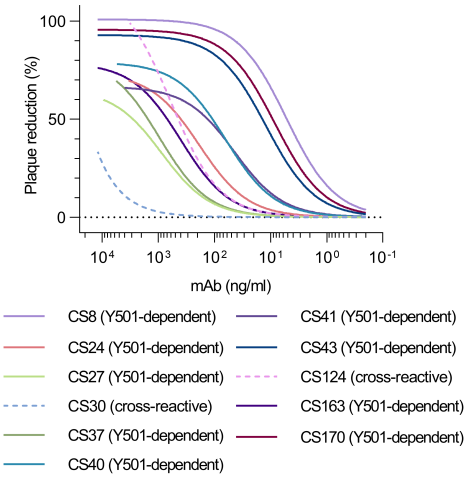

A
VH mutations
VL mutations
ns
Beta-specific
cross-reactive
B
GRAVY score CDR H3
GRAVY score CDR L3
C
Inhibition of ACE2/RBD binding (%)
17.97
28.18
41.19
30.33
wildtype
Beta
D
CDR H3 length
CDR L3 length
p < 0.05
E
isoelectric point (pI) CDR H3
isoelectric point (pI) CDR L3
p < 0.01
F
Number of antibodies
<200
200
2000
>2000
estimated IC50 (ng/ml)
G
H
VH1-18
VH1-46
VH1-58
VH1-69
VH3-11
VH3-13
VH3-15
VH3-21
VH3-23
VH3-30
VH3-33
VH3-48
VH3-53
VH3-66
VH3-7
VH3-9
VH4-30
VH4-31
VH4-34
VH4-38-2
VH4-39
VH4-4
VH4-59
VH4-61
VH5-51
VH7-4-1
JH1
JH2
JH3
JH4
JH5
JH6
I
Secondary binders
First binders
CS131
CS23
CS91
CS163
CS170
CS161
CS87
CS43
CS102
CS44
CS8
CS54
CS82
CR3022
CV38-142
independent binding
competition or same site

Fig. S4. Comparison between cross-reactive and Beta-specific antibodies of this study. All 44 cross-reactive and 37 Beta-specific mAbs that strongly bound the RBD were included in this comparison. **(A)** Number of somatic nucleotide mutations in the IGVH (left) and IGVL (right) genes. Statistical significance was determined using a two-tailed Mann–Whitney U-tests. **(B)** GRAVY score as a measure of hydrophobicity of CDR H3 (left) and CDR L3 (right) regions was calculated using https://www.bioinformatics.org/sms2/protein_gravy.html. Statistical significance was determined using an unpaired t-test, and a Shapiro-Wilk test was used to test for normality. **(C)** ACE2 interaction with indicated RBD was determined using the cPass Surrogate Neutralization Assay. Statistical analysis was performed using a two-tailed Mann–Whitney U-test. Median values are given in red. **(D)** Length of heavy chain (left) or light chain (right) CDR3 regions. Statistical significance was determined using a two-tailed Mann–Whitney U-test. **(E)** Isoelectric point of CDR H3 (left) and CDR L3 (right) regions was calculated using the pI/Mw tool at https://web.expasy.org/compute_pi/. **(A-B)** and **(D-E)** Red bars indicate mean. **(F)** Estimated IC50 in PRNT against Beta isolate is shown for cross-reactive and Beta-specific antibodies. **(G-H)** Pairing of indicated VH genes with JH gene families of all 81 expressed mAbs with strong binding to the RBD Beta with **(G)** showing pairings of 37 Beta-specific antibodies in purple **(H)** showing pairings of 44 cross-reactive antibodies in light blue. **(I)** Competition of mAbs was determined using a biolayer interferometry assay. Shown are additional signals of the secondary antibodies in percent after normalization of the response signals of the indicated bound first antibodies. Positive numbers >20% indicate different binding sites, numbers smaller than 20% suggest competition or same sites.

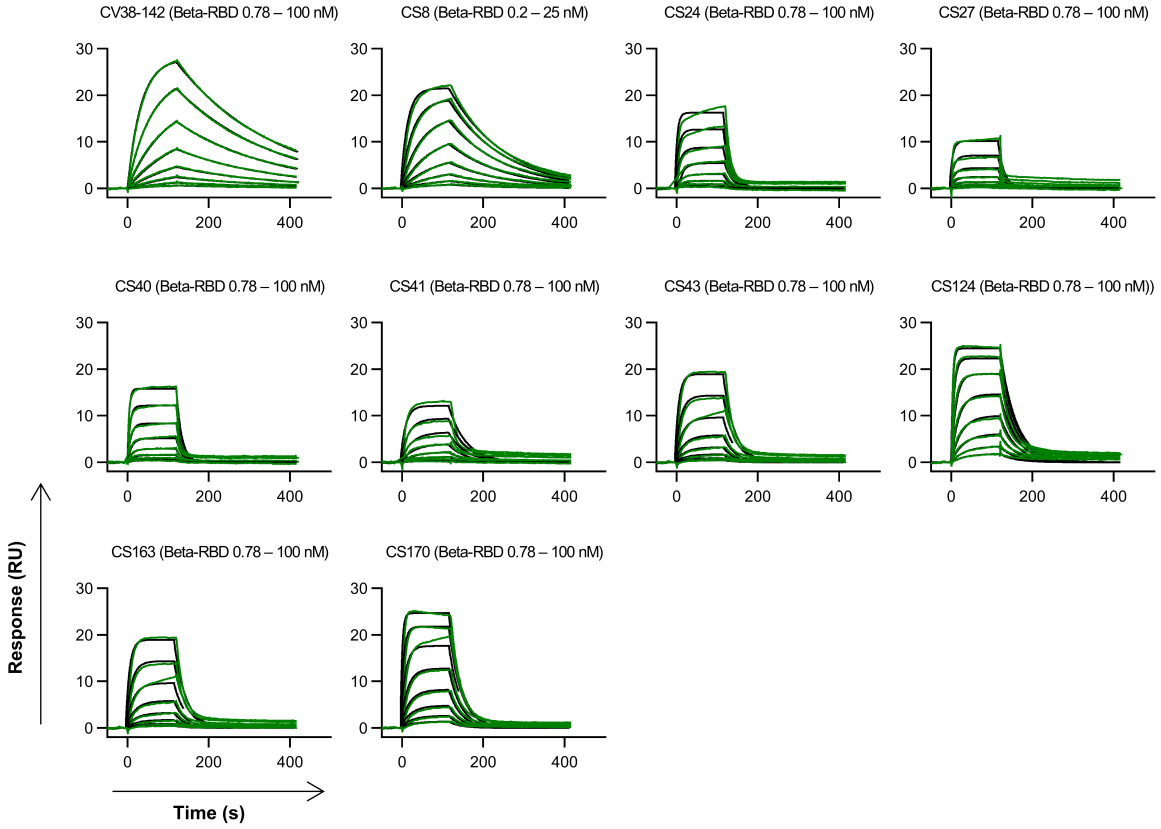
A

mAb		Heavy Chain					Light Chain	
ID	patient	CDR H1	CDR H2	CDR H3	DH	JH	VK/VL	JK/JL
VH4-39 GL		GGSISSSSYY	IYYSGST	AR				
501Y-dependent								
CS8	SA2	||||||||||	|||||||	||HEGSTSPLMV---KNYFDY	3-10	4	K1D-12	K5
CS24	SA5	||||||||||	|||||||	||QFWTRPPS------VWFDP	3-3	5	L1-51	L3
CS27	SA5	||||||||||	|||||||	||GIAARPGD------WHFDL	6-6	2	L1-51	L3
CS37	SA5	||||||||||	|||||||	||HVGPYSGYDK---NNWFDP	5-12	5	K3-11	K4
CS40	SA5	||||||||||	|||||||	||HAAPRPGD------SWFDP	6-6	5	K1-12	K5
CS41	SA5	||||||||||	|H|||||	||HAGPYSSSWI---ANWFDP	6-13	5	K1-9	K4
CS43	SA5	||||||||||	|||||||	||RLGPRGPFDNH--GNHFDY	1-14	4	K1-9	K1
CS163	SA10	||||||R||	|||||||	||QVAWLPRD------DYFDY	6-19	4	L2-8	L2
CS170	SA2	||||||||||	||||G|	||EVAPIKQW--L--VSYFDY	6-19	4	L1-40	L3
cross-reactive								
CS30	SA5	|D||||||||	F||||||	||RGWLRGYF---------DL	3-22	2	L6-57	L2
CS31	SA6	||||||||||	F||||||	|TQLWLRSNF---------DS	5-12	4	L6-57	L2
CS45	SA8	||||||||||	|||||||	||QSSPKLGD------DAFDI	3-10	3	L1-51	L2
CS124	SA7	||||||||||	|H|||||	||HTGYYDSSGYYR-LEYFQH	3-22	1	K1-33	K4
CS167	SA2	||||||||||	|||||||	||FTPFAGL-------YYFDY	2-15	4	L2-8	L2
non-RBD-reactive								
CS97	SA4	||||N|N||	|D|||||	||VNSRDGHSYASGGHEDFQP	3-10	1	L3-27	L3
CS104	SA4	|||N|||||	V|||R|	VTYSS---GW------DNEDY	6-19	4	K3-20	K1

B



C



D

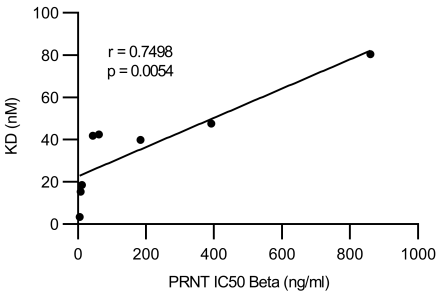


Fig. S5. Neutralization and binding kinetics of Beta-specific VH4-39 antibodies from multiple patients infected with SARS-CoV-2 Beta. (A) Comparison of sequence features of all expressed VH4-39 mAbs in this study. All antibodies which were expressed are shown in this panel. **(B)** Fitted curves of VH4-39 mAbs show dose-dependent neutralization against authentic SARS-CoV-2 Beta variant virus. **(C)** Binding kinetics of Beta-RBD to indicated mAbs were modeled (black) from multi-cycle surface plasmon resonance (SPR) measurements (green). The fitted monovalent analyte model is shown. For CS24, CS27 and CS41, there was a second phase after the fast dissociation impeding the quality of the monovalent analyte model. All measurements are performed using serial 2-fold dilutions of SARS-CoV-2 Beta-RBD-His on immobilized mAbs. **(D)** Correlation of neutralization and affinity of monoclonal VH4-39 Y501-specific antibodies. IC50 was determined from neutralization curves shown in **(B)**. Affinity of monoclonal antibodies to Beta RBD was determined by the fitted analyte model shown in **(A)**. Statistical analysis was performed by a simple linear regression.

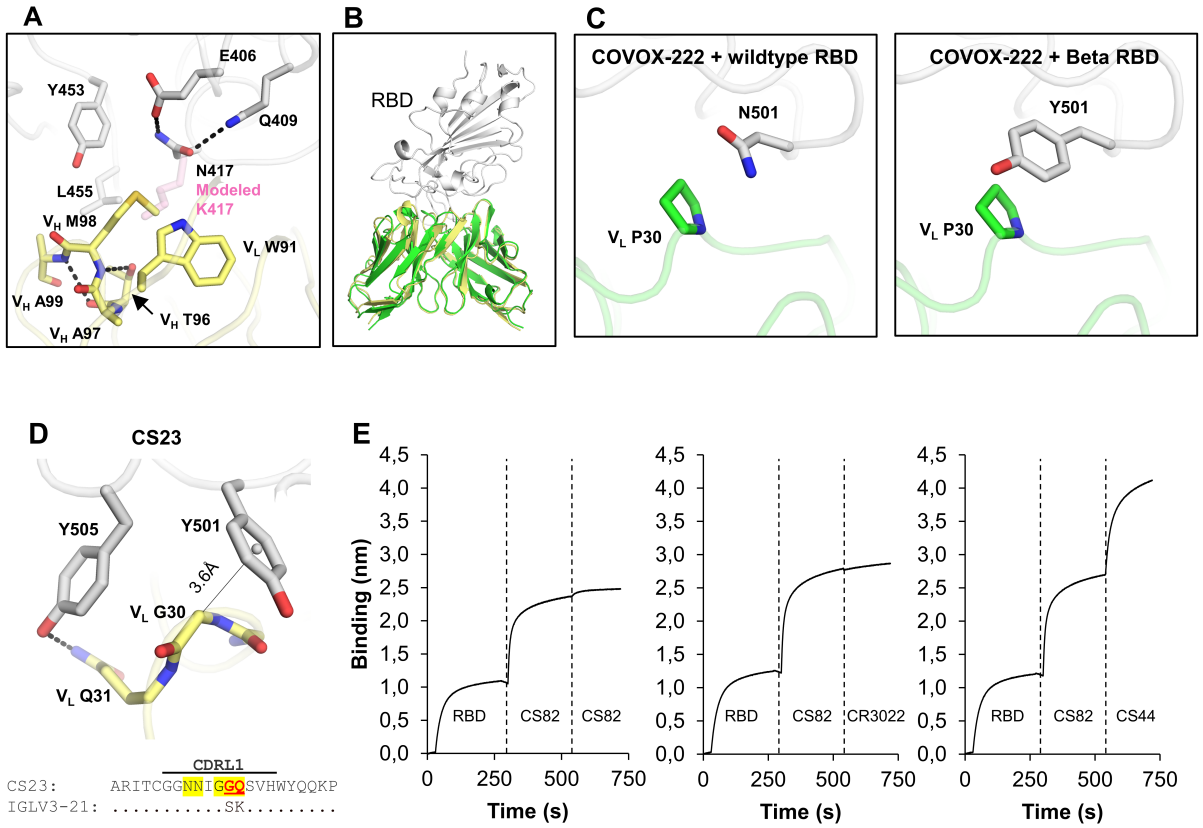


Fig. S6. Structural and binding analysis of VH3-53 mAbs that bind to Beta RBD. The RBD is shown in white. Hydrogen bonds are represented by black dashed lines. **(A)** Structure of the CDR H3 of CS23 (yellow). A modeled side chain of K417 is shown as transparent pink sticks, which would be unfavorable for binding to CS23, where VH M98 occupies this pocket. **(B)** COVOX-222 and CS23 adopt the same binding mode. The crystal structure of COVOX-222 (green) in complex with RBD (Beta) was superimposed onto the structure of CS23 (yellow) in complex with RBD (Beta). Only the variable domains of the antibodies are shown for clarity. **(C)** Structures of COVOX-222 (green) in complex with wildtype RBD (left, PDB 7NX6) and Beta RBD (right, PDB 7NXA). VL P30 and Y501 in the Beta RBD forms a π-π interaction. **(D)** CDR L1 of CS23 (yellow) interacts with the Beta RBD (white). Hydrogen bonds are represented by black dashed lines. The distance between V_L G30-Cα and the benzene ring center of RBD-Y501 (white sphere) is represented by a thin black solid line. Sequence alignment between the light chain of CS23 and its germline sequence is shown at the bottom, where identical residues are

represented by dots. Paratope residues (defined as buried surface area > 0 $Å^2$) are highlighted in yellow, and somatically mutated residues shown in red letters. **(E)** Biolayer interferometry competition assay between antibodies. The biosensor was first loaded with SARS-CoV-2 RBD, followed by two binding events: 1) CS82 IgG; 2) CS82, CR3022, or CS44 IgGs. Representative results of three replicates for each experiment are shown.

Table S1. Clinical characteristics and neutralization of serum by patients included in this study.

Patient	Sex	Age	Date of first positive PCR test	Days from positive PCR to blood draw	Symptoms	Hospitalization	AUC PRNT Beta	AUC PRNT wildtype (Munich isolate)	ACE2/RBD inhibition wildtype (percent)[a]	ACE2/RBD inhibition Beta (percent)[a]
SA1	m	81	22.01.2021	12	yes	yes	614037	12807	82.0	83.7
SA2	m	69	27.01.2021	28	yes	yes	547486	9557	82.9	85.2
SA2_t2[b]	m	69	27.01.2021	50	yes	yes	396551	4861	79,18	83,78
SA3	f	49	29.01.2021	26	yes	no	2210	351,1	7.65	16.4
SA4	f	18	02.02.2021	22	yes	no	8601	4879	47.6	40.9
SA5	f	27	03.02.2021	23	yes	no	4466	4173	53.0	35.3
SA6	f	28	01.02.2021	25	yes	no	6061	1794	40.7	33.7
SA7	f	26	03.02.2021	23	yes	no	12492	654,1	16.2	30.0
SA8	m	63	04.02.2021	22	yes	no	26705	296,6	9.7	10.3
SA9	f	63	08.02.2021	18	yes	no	7399	281,2	9.0	16.0
SA10	m	67	22.02.2021	15	yes	no	101879	7195	78.1	74.8
SA11	m	72	16.02.2021	21	no	no	41076	38	9.5	22.2
SA12	m	86	19.02.2021	18	yes	no	250	98,8	0.6	10.1
SA13	f	79	16.02.2021	21	yes	no	304474	9535	59.5	62.9
SA14	m	50	16.02.2021	21	yes	no	2982	47,5	13.4	17.2
SA15	f	47	17.02.2021	20	yes	no	2879	372,7	3.1	0
SA17	f	68	18.01.2021	45	yes	yes	119883	6225	46.3	74.5
SA19	m	70	16.02.2021	17	yes	yes	117433	3033	57.1	61.0
SA20	f	44	24.02.2021	12	yes	yes	38354	1959	29.9	26.7
SA21	f	59	19.01.2021	50	no	no	13887	5602	37.4	60.9
SA23	f	35	19.01.2021	50	yes	no	23737	4387	17.2	35.7
SA24	f	44	04.01.2021	65	yes	no	46577	3262	57.7	63.7
SA25	m	39	26.01.2021	43	yes	no	19655	2838	12.9	15.3
SA26	m	58	03.02.2021	35	yes	no	24506	1246	40.7	49.0
SA27	m	34	26.01.2021	43	yes	no	15453	3490	22.8	20.6
SA28	m	61	17.01.2021	52	yes	yes	263808	3634	64.8	78.9
SA29	m	55	14.01.2021	55	yes	no	9084	3722	2.0	0
SA30	f	29	31.12.2020	69	yes	no	7079	2242	0	20.2
SA31	m	40	23.01.2021	47	no	no	160344	7747	83.0	86.1
SA32	f	80	07.01.2021	63	yes	yes	223456	7066	45.8	52.0
SA33	f	25	14.01.2021	56	no	no	14762	2588	10.8	16.4
SA34	f	56	09.01.2021	61	yes	no	36553	2994	41.9	39.1
SA35	m	31	18.01.2021	52	yes	no	23301	1388	27.9	38.7
SA36	m	25	18.01.2021	52	yes	no	17300	2663	43.7	34.5
SA37	f	53	11.01.2021	60	yes	no	39374	3673	24.2	51.7
SA38	f	44	27.12.2020	78	yes	no	22795	2083	17.6	29.6

Patient	Sex	Age	Date of first positive PCR test	Days from positive PCR to blood draw	Symptoms	Hospitalization	AUC PRNT Beta	AUC PRNT wildtype (Munich isolate)	ACE2/RBD inhibition wildtype (percent)[a]	ACE2/RBD inhibition Beta (percent)[a]
SA39	m	31	09.02.2021	34	yes	no	24121	2182	12.8	21.8
SA40	m	48	18.01.2021	56	yes	no	27711	2745	36.7	66.9
SA41	f	48	08.01.2021	66	yes	no	32266	2855	26.6	61.8
SA42	m	35	16.01.2021	58	yes	no	7638	4355	14.8	29.4
SA43	m	73	03.03.2021	13	yes	yes	42477	13482	9.8	43.6

[a] Values below zero were set to zero, indicating no inhibition.
[b] SA2_t2 refers to the second timepoint of sampling 50 days post-infection of subject SA2

Table S2. Sequence features of monoclonal antibodies in this study.

mAb expression ID	mAb clone ID	Ig class isotype	VH	JH	CDR H3	SHM VH	light chain	VK/VL	JK/JL	CDR K3/L3	SHM VK/VL	criteria for expression
CS1	SA2-101[(1)]	IgG1	3-30	6	AKDFQYVAATHSPYYYYGMDV	2	K	3-20	3	QQYGSSPGVT	2	a,e
CS2	SA2-125	IgA1	3-15	6	TTDLVDYDFWSGAYGMDV	12	L	2-11	1	SSYAGEYTCYV	14	f
CS3K	SA2-137	IgA1	1-2	6	AREDYYCGGRTCYRPYYYYGLDV	17	K	1-39	4	QQSYSTPRIT	1	f
CS3L	SA2-137	IgA1	1-2	6	AREDYYCGGRTCYRPYYYYGLDV	17	L	1-40	2	QSYDNSLSGVV	14	f
CS4	SA2-149	IgG1	3-30	6	AKDFGSTGTTLGYYGMDV	4	L	1-47	3	AAWDDSLSGWV	1	e
CS5	SA2-158	IgA2	3-15	6	STLGFYGDLIQRTFHYGLDV	45	K	2-30	4	MQGTRWPALS	34	f
CS8	SA2-178	IgG1	4-39	4	ARHEGSTSPLMVKNYFDY	3	K	1D-12	5	QQANSFPIS	0	e
CS9	SA2-193	IgM	3-74	6	ARGGDHDSADYMFRVYRHNGMDV	20	K	3-11	4	HQRNNWPLT	8	f
CS11	SA2-205	IgG1	4-39	6	ARRRGPAAPGGWYYGMDV	0	K	1-9	4	QQLNSYPPT	0	e
CS12	SA2-208	IgG1	3-30	6	AKSGAPAAMRGYYYYGMDV	2	L	7-46	2	LLSYSGAREV	4	e
CS15	SA2-239[(2)]	IgM	3-30	6	AKAPYAYCSSTSCYADYYYGMDV	1	L	2-14	2	SSYTSSSVV	0	a,e
CS18	SA3-137[(3)]	IgM	5-51	6	ARTATGTNHYYYYYYMDV	0	L	1-44	3	AAWDDSLNGPV	0	a,b
CS19	SA3-149[(46)]	IgA1	3-74	4	ARAPALGGRGDY	10	L	1-40	3	QSYDSSLSGWV	4	b
CS20	SA3-185	IgM	3-74	4	ARGSAISPTVLFDY	6	L	2-14	1	SSYTSSSSYV	4	f
CS21	SA3-195[(3)]	IgM	5-51	6	ARTATGTNHYYYYYYMDV	4	L	1-44	2	SSWDDSLNAVL	0	a,b
CS23	SA6-122	IgG1	3-53	6	ARGTAMAYGMDV	2	L	3-21	2	QVWDSSSDHVV	3	d
CS24	SA5-126[(4)]	IgG1	4-39	5	ARQFWTRPPSVWFDP	3	L	1-51	3	GTWDSSLSAGV	6	a,e
CS26	SA5-143	IgG1	3-15	6	TTDPNQQPPRGYYFYYGLDV	3	L	7-46	2	LLSYSGAPVV	5	f
CS27	SA5-160	IgG3	4-39	2	ARGIAARPGDWHFDL	0	L	1-51	3	GTWDSSLSRGV	1	e
CS29	SA5-170	IgG1	3-7	4	ARALSMVRGVIIPPYFDY	4	L	6-57	3	QSYDSSNHWV	2	f
CS30	SA5-176	IgG1	4-39	2	ARRGWLRGYFDL	5	L	6-57	2	QSYDSTNHVV	1	e
CS31	SA5-195	IgG1	4-39	4	ATQLWLRSNFDS	2	L	6-57	2	QSYDSGNVV	1	e
CS34	SA8-123	IgG1	3-7	4	ARSQSTSWHDY	1	L	6-57	2	SLMITTIMW	4	f
CS37	SA5-219	IgG1	4-39	5	ARHVGPYSGYDKNNWFDP	3	K	3-11	4	QQRSNWPLT	0	e
CS38	SA5-233	IgG1	3-13	2	ARDLTQDWYFDL	0	K	1-39	5	QQSYSTPPIT	1	c,e
CS39	SA5-250	IgG1	3-15	3	TTDKARNYYDSSGYEHDAFDI	0	K	1-39	5	QQSYSTLIT	3	f
CS40	SA5-252	IgG1	4-39	5	ARHAAPRPGDSWFDP	0	K	1-12	5	QQANSFPT	2	e
CS41	SA5-259[(5)]	IgG1	4-39	5	ARHAGPYSSSWIANWFDP	4	K	1-9	4	QQLNSYPLT	1	a,e
CS42	SA5-260	IgM	3-15	4	TTDSLDVGGGSYVNFDY	3	K	1-33	4	QQYDNLPLT	2	f
CS43	SA5-263	IgG1	4-39	4	ARRLGPRGPFDNHGNHFDY	2	K	1-9	1	QQLNSYPWT	2	e
CS44	SA5-266[(6)]	IgG1	1-58	3	AAPYCSGGTCHDGFDI	2	K	3-20	1	QQYGSSPWT	1	b,c,e
CS45	SA8-141	IgG1	4-39	3	ARQSSPKLGDDAFDI	0	L	1-51	2	GTWDSSLSVVV	2	e
CS46	SA7-154[(7)]	IgM	3-30	6	AKDRSVGATTSQYNYYYGMDV	11	L	1-51	2	GTWETSLSAEV	5	a,c,e
CS47	SA7-165[(7)]	IgM	3-30	6	AKDRSVGATTSQSHYYYGMDV	5	L	1-51	2	GTWDSSLSTGV	4	a,c,e
CS48	SA4-104[(8)]	IgG2	3-21	4	VRDWYASSGANTRFDY	23	L	1-44	3	ETWDDSLLGPV	13	a
CS49	SA4-110	IgG1	3-53	3	ARGKWLRGAFDI	9	L	6-57	3	QSYDSSDLWV	1	d
CS50	SA4-117	IgG1	3-30	4	AKAGGWVSTRPPFDY	14	L	1-40	1	QSYDSSLSGYV	4	e
CS51	SA4-127	IgG2	3-53	4	ATLITSEY	11	L	1-44	2	ASWDDSLNGPV	10	d
CS52	SA4-138	IgG1	7-4-1	6	ARTSGWSGPSYGMDV	4	L	7-43	1	LLYFGGAQYV	4	f
CS54	SA4-142[(9)]	IgG1	3-53	6	ARDLAVYGMDV	3	K	3-20	5	QQYDSSLIT	3	b,d
CS55	SA4-156	IgG2	3-53	4	ARGRFEH	28	L	7-46	3	LFFFNGPGV	19	d
CS56	SA4-170	IgG1	4-4	4	ASAPGTPWFDY	6	L	2-14	1	SSYTSSSTLYV	4	f
CS57	SA4-178[(10)]	IgM	3-74	4	ARGGVSGEMSNWAY	16	L	7-43	3	LLFFGDAWV	10	a
CS58	SA4-181	IgG3	4-4	3	ARAYYYGSGSYYNRDAFHI	9	K	3-15	5	QQYNNWPPIT	1	f
CS59	SA4-184	IgG1	1-58	3	AAPYCSGGSCFDAYDM	4	K	3-20	3	QQYGSSLFT	0	e
CS60	SA2-102	IgM	4-34	4	ARGKRYYDFWSGYWIYYFDY	0	L	2-14	2	SSYTSSSTRVV	0	f

mAb expression ID	mAb clone ID	Ig class isotype	VH	JH	CDR H3	SHM VH	light chain	VK/VL	JK/JL	CDR K3/L3	SHM VK/VL	criteria for expression
CS61	SA2-119	IgM	3-21	6	ARDSSSSNYYYGMDV	21	K	1-39	4	QQSYNTPRLI	21	f
CS62	SA2-130	IgA1	3-23	4	ATKWGGELINYFDF	19	K	3-11	4	QQRRNWPTT	11	f
CS63	SA2-163[47]	IgM	4-59	4	ARGGWSLDF	17	K	3-20	2	HQYGGSLPYT	17	b,c
CS65	SA2-198[2]	IgG1	3-30	6	AKDLDIVLMVYAIPRGYYGMDV	6	L	2-14	2	SSYTSSSPPVV	6	a,e
CS67K	SA3-290	IgG1	1-8	4	VRGHGSYYDYWSGYYPFDY	17	K	3-20	5	QQYGSSPSIT	13	f
CS67L	SA3-290	IgG1	1-8	4	VRGHGSYYDYWSGYYPFDY	17	L	3-21	3	QVWDRNDHWV	6	f
CS68	SA3-125[11]	IgM	3-23	4	AKRSPVYSWNPEDY	18	K	1-5	1	QQYNTYSRT	12	a,c
CS69	SA3-134	IgM	3-53	2	ARDDVSGGYWYFDL	0	K	3-11	2	QQRSNWPHT	1	d
CS70	SA3-136[12]	IgM	4-59	4	ARNLGRTGGSYYFDY	5	L	1-47	3	AAWDDSLSAWV	22	a
CS71	SA3-145	IgG1	7-4-1	3	ARVSGWGIAALDDAFDI	0	K	4-1	4	QQYYSTPLT	1	f
CS72	SA3-147[13]	IgA2	3-7	4	ARSRGVDY	7	K	2-30	5	MQATHGPIT	4	a
CS73	SA3-148[14]	IgM	3-74	4	ARGGGHKYDH	19	L	2-14	3	SSYRNTVTL	9	a,b
CS74	SA3-151	IgG1	4-31	4	ARDYGGNQNYFGY	5	K	1-33	4	QQYDNLPLT	4	f
CS75	SA3-153	IgA2	3-7	4	ARSRGVDY	7	K	1-39	2	QQSYSTHT	0	f
CS76	SA3-180[15]	IgG3	3-13	6	ARSGLHTSIAARFYYYYYMDV	1	K	1-39	1	QQSYSTPSWT	3	a,b,c,e
CS77	SA3-189[16]	IgM	1-3	4	ARPKRSIAAAGIGNYFEY	11	K	1-39	2	QQSYITPGT	4	a
CS79	SA3-251[17]	IgA2	3-33	4	AKRGDSCTGGVCSYFDY	9	L	8-61	3	VLYMGSGIWV	9	a
CS80	SA3-261[48]	IgM	3-53	6	ARSLAAAGTDGMDV	0	L	3-25	3	QSADSSGTWV	2	b,d
CS81	SA3-263	IgG3	7-4-1	6	ARNYDFWIGHYYYYYMDV	3	L	1-44	2	AAWDDSLNGVV	2	f
CS82	SA6-108	IgG1	3-53	3	ARDLHSSGPFDAFDI	3	K	1-33	4	QQYDI	4	d
CS83	SA6-120	IgG1	3-66	6	VRGPAVHHYGMDV	7	L	2-11	2	CSYAGRYTPVL	9	d
CS84	SA5-127	IgG1	4-38-2	4	ARDDYGDYAVSY	5	L	1-40	1	QSYDSSLSALYV	0	f
CS85	SA5-129	IgG3	3-11	4	ARELLLLGYCSGGSCYPVGPDY	0	L	6-57	3	QSYDSSNHWV	1	f
CS86	SA5-135	IgM	3-9	4	AKAWGGDWTTAVGY	5	L	3-21	2	QVWDSSSDPVI	2	f
CS87	SA5-162[18]	IgM	3-13	6	ARALYGSGSYSTQAGYYYGMDV	1	K	1-39	3	QQSYRAFT	0	a,c,e
CS88	SA5-163	IgG1	1-18	4	ARDYDYVWGSYPSACCY	0	L	2-14	3	SSYTSSTNWV	2	f
CS89	SA5-179[9]	IgG1	3-53	6	ARDLSVAGGMDV	3	K	3-20	5	QQYGSSPPIT	2	b,d
CS90	SA5-189[19]	IgM	3-13	2	ARVRPTMTKGFDWYFDL	2	K	1-39	1	QQSYNTLGT	4	a,c,e
CS91	SA5-191[49]	IgM	3-53	6	ARWAGADGMDV	3	K	3-20	2	QQYGSSQYT	2	b,d
CS92	SA5-256[20]	IgG1	3-23	4	AKDFVVVVAARSHDDYYFDY	4	K	1-5	4	QQYKNFPLT	2	a
CS93	SA5-262[21]	IgM	4-39	5	ARLTPQAPGVVWFDP	0	L	2-23	2	CSYAGSSTYVV	3	a,e
CS97	SA4-153	IgG1	4-39	1	ARVNSRDGHSYASGGHEDFQP	13	L	3-27	3	YSAADNSWV	10	e
CS98	SA4-177	IgG1	1-18	6	ARDSSGWFYYYYGMDV	7	L	2-8	3	SSYAGSNNLV	2	f
CS99	SA4-182	IgM	1-69	4	ATQGGRFYCSGGSCYRYYFDY	1	K	3-20	4	QQYGSSPLT	0	c
CS100	SA4-183[14]	IgM	3-74	4	AKDPFGSGSF	18	L	2-14	3	SSYTSSSTWV	7	a,b
CS101	SA4-188[8]	IgG2	3-21	4	ARLAAVGPGGSPPYYFDY	21	L	1-44	2	VTWDGSLDGWV	11	a
CS102	SA4-216[6]	IgG1	1-58	3	AAPHCGGGSCYDGFDI	1	K	3-20	1	QQYGSSPWT	1	a,b,c,e
CS103	SA4-236[22]	IgG1	3-13	2	ARGGGDGYNLGLWYFDL	3	K	1-39	3	QQSYSNPPPT	3	b,c,e
CS104	SA4-282	IgG1	4-39	4	VTYSSGWDNEDY	15	K	3-20	1	QQYISSPRT	12	e
CS109	SA3-158[47]	IgM	4-59	4	ARGGSRLDY	10	K	3-20	2	QQYGTSPYT	2	b,c
CS110	SA3-193[11]	IgM	3-23	4	AKRSPVYSYNPEDY	17	K	1-5	1	QQYNSYSRA	12	a,c
CS111	SA6-105	IgG1	3-64D	4	VKDVTVDTAMVTIFDN	1	K	1-39	4	QQSYSTPT	0	c
CS112	SA5-134	IgG1	3-15	4	TTDPGYTYSPAY	3	K	1-39	3	QQSYSTLFT	2	c
CS113	SA5-159	IgG1	3-9	6	AKDIGYSSSPHLVNYGMDV	2	L	3-21	2	QVWDSSGDHSVV	2	c
CS114	SA5-165	IgG1	1-69	4	ASSSPLLRYFDWPHEAIFDY	2	K	3-11	5	QQRSNWSGIT	0	c
CS115	SA5-166	IgG1	1-69	4	ACSSGRWGVLGNYFDY	23	K	1-33	4	QQYANLLLT	10	f
CS116	SA5-172[23]	IgG2	3-30	6	AKGDDYGDLFYYGMDV	1	K	2-28	4	MQALQRTLT	1	a,e
CS117	SA5-183	IgG1	3-9	6	AKDAFGDPQGLYGMDV	1	K	1-39	5	QQSYSTPLT	0	f

mAb expression ID	mAb clone ID	Ig class isotype	VH	JH	CDR H3	SHM VH	light chain	VK/VL	JK/JL	CDR K3/L3	SHM VK/VL	criteria for expression
CS120	SA5-204	IgG1	3-30	4	AKVLGSYCSGGSCYGGSFDY	2	K	1-33	4	QQYDNLPS	3	c,e
CS123	SA5-253	IgG1	4-59	5	ARSRGYNYGLGLGWFDP	2	K	1-33	3	QQYDDVPFT	7	f
CS124	SA7-164	IgM	4-39	1	ARHTGYYDSSGYYRLEYFQH	3	K	1-33	4	QQYDNLPLT	4	e
CS125	SA9-204	IgM	1-18	5	ARDGTSHYYDSSGYYGADRNWFDP	0	L	1-40	2	QSYDSSLSGWV	1	c
CS126	SA10-101	IgG1	3-33	6	ARDDYYGSGSYYYYGMDV	0	K	1-17	4	LQHNSYRLT	0	f
CS127	SA10-105[6]	IgG1	1-58	3	AAPNCSGGSWYDAFDI	0	K	3-20	1	QQYGSSPWT	0	a,b,c,e
CS128	SA10-109	IgG1	5-51	4	ARTEYGDPLDY	0	K	1-16	4	QQYNSYPLT	0	f
CS129	SA10-111	IgG1	3-48	4	ARQPREYYDFWSGYRRLFYFDY	0	K	1-33	4	QQYDNLPLT	0	f
CS130	SA10-124	IgG1	4-38-2	3	ARDREATVVRPPDAFDI	1	K	2-28	4	MQALQTPP	0	f
CS131	SA10-126[49]	IgG1	3-53	6	ARWAQQLVPSENLKPYYYYYGMDV	0	K	3-20	2	QQYGSSPGYT	0	b,d
CS133	SA10-130	IgG1	4-61	5	ARGLYYYDSSGYQMGDWFDP	1	K	3-11	4	QQRSNWPLT	0	f
CS134	SA10-134	IgG1	3-23	5	AKGTQPIPDYGDFFDP	0	K	3-20	2	QQYGSSPPCT	1	f
CS135	SA13-138	IgG1	3-30	4	AKGGGWYDYKGYYFDY	0	K	1-33	5	QQYDNLPIT	0	e
CS136	SA14-165[24]	IgG1	3-48	4	VRVGHPDTLFGVDY	15	K	3-15	2	QQYNNWPRYS	2	a
CS138	SA14-176	IgM	3-15	4	STRSFIAADSRIFIDY	0	K	4-1	2	QQYYSTPYS	0	f
CS139	SA14-186[24]	IgG1	3-48	4	ARVGHPDTLFGVEY	9	K	3-15	2	QQYNNWPRYS	5	a
CS140	SA15-191	IgM	3-15	5	TTTIYRSP	0	K	2-30	1	MQTLYGWT	3	f
CS143	SA4-206	IgG3	1-58	4	AAAIIASAAPDY	5	K	3-11	2	QQRSNWPPYT	0	e
CS144	SA4-250	IgG3	3-33	4	ARASMVRGVITGGFDY	0	L	6-57	3	QSYDSSNHWV	1	f
CS145	SA2-206	IgG1	1-46	5	ARGGIVPAATLLFDP	2	K	1-5	2	QQYNSYSCS	0	f
CS146	SA3-288	IgG2	1-3	4	ARDGGVGPPNYFDY	19	K	2-28	2	MQALQTPFT	3	f
CS148	SA3-216	IgG1	4-38-2	4	AKTRQQFIWD	12	L	1-40	3	QSYDRSLNWV	7	f
CS149	SA3-252	IgG2	3-23	5	AKRGNTGPGFPWFDP	20	K	3-11	4	QQRSSWPLT	5	f
CS151	SA3-264	IgG1	3-13	6	VRDGVRGSGRGQYYMDV	17	K	3-11	4	HQHSNWPPLT	13	e
CS152	SA4-311	IgG1	1-46	4	ASTTVAYYFDY	4	L	6-57	3	QSYDSSIANWV	1	f
CS153	SA4-325[6]	IgG1	1-58	3	AAPYCSGSSCLDGFDI	2	K	3-20	1	QQYGSSPWT	3	a,b,c,e
CS154	SA5-155	IgG1	4-31	5	ARVSSPSGGRHWFDP	3	L	1-51	2	GTWDSSLRAPL	3	f
CS155	SA5-177	IgG1	3-23	3	AKDTYYDIFPDVFDI	2	L	2-14	1	SSYTSSSTLPV	6	f
CS156	SA5-184[19]	IgG1	3-13	2	ARVRPTMTKGFDWYFDL	3	K	1-39	1	QQSYNTLGT	3	a,e
CS157	SA5-223	IgM	3-13	6	ARGHFYGLIGYMDV	3	K	1-39	4	QQSYSTPPLT	3	c,e
CS158	SA5-232[15]	IgM	3-13	6	ARAAYDILTGYYRGMDV	0	K	1-39	1	QQSYNIAST	3	a,b,c,e
CS160	SA8-138	IgG1	7-4-1	3	ASGDWNAFDI	0	L	6-57	2	QSYDSSNVV	1	f
CS161	SA8-149[25]	IgG1	3-66	6	ARDLAVYGMDV	2	L	3-21	2	QVWDSSSDHPVV	4	a,d
CS162	SA10-107	IgG1	5-10-1	1	ARHAQGYYDSSGYYTGAEYFQH	0	K	1-33	4	QQYDNLRLT	0	f
CS163	SA10-110[26]	IgG1	4-39	4	ARQVAWLPRDDYFDY	2	L	2-8	2	SSYAGSNNYVV	2	b,e
CS165	SA10-120	IgG1	5-51	5	ARHMSGTHSSGWYERWFDP	0	L	1-44	3	AAWDDSLNGPV	0	f
CS167	SA2t2-105[26]	IgG1	4-39	4	ARFTPFAGLYYFDY	1	L	2-8	2	SSYAGTVL	3	b,e
CS169	SA2t2-107	IgG1	3-33	3	ARDRFYDYSSSGYSLDAFDI	2	L	1-36	3	AAWDDSLNAWV	1	f
CS170	SA2t2-117[50]	IgG1	4-39	4	AREVAPIKQWLVSYFDY	4	L	1-40	3	QSYDSSLSGLV	2	b,e
CS171	SA2t2-127	IgG1	3-30	4	AKDPPQFAVAGTGYFDY	6	L	3-21	3	QVWDSSSDPWV	3	e
CS172	SA2t2-129	IgG1	3-30	4	AKAVYSYAYAVLYFDY	6	L	6-57	2	QSYDYNNHVV	7	e
CS173	SA2t2-130[22]	IgG1	3-13	2	ARGGAVIPVWYFDL	5	K	1-39	3	QQSYSHPGIT	5	b,c,e
CS175	SA2t2-136	IgG1	1-69	5	ARREYSSTDWFDP	4	L	3-21	1	QVWDSTSDHPGYV	3	f
CS176	SA2t2-139	IgG1	3-66	3	ARWGRVGATGLAFDI	6	L	3-21	1	QVWDSSSDHHYV	4	d
CS177	SA2t2-144	IgG1	3-66	6	ARLRPDYHLWSGLMDV	5	K	3-15	4	QQYNNWPPLT	3	d
CS178	SA2t2-161	IgG1	3-30	4	AKKGMEYCGGDCYSGYFDY	7	K	1-39	2	QQSYSTPMCS	3	e
CS179	SA2t2-169[51]	IgG1	4-31	5	ARTTAPRPGSSWFDP	7	L	1-51	3	GTWDNTLSPGRGV	8	b
CS180	SA2t2-174[6]	IgG1	1-58	3	AAPACSSTRCYDGFDI	6	K	3-20	1	QQYGSSPWT	1	a,b,c,e

mAb expression ID	mAb clone ID	Ig class isotype	VH	JH	CDR H3	SHM VH	light chain	VK/VL	JK/JL	CDR K3/L3	SHM VK/VL	criteria for expression
CS181	SA2t2-175	IgG1	1-18	4	ARDGGWTGIVGAINFDY	7	L	1-47	3	ATWDDSLSGWV	4	f
CS182	SA2t2-182	IgG1	3-53	6	ARDLITYGMDV	8	K	1-9	4	QHLLT	4	d
	SA2-105	IgG1	4-38-2	4	AREPFNGPRFLYRGSYFDF	15	K	3-20	1	QQYGSSPPRT	6	
	SA2-114	IgM	3-23	3	AKSLFYGPTAMLYTFDI	11	K	1-27	3	KTITVPRSL	8	
	SA2-115	IgG1	4-30-4	4	ANIAARLPGSYYFDY	2	K	3-15	1	QQYKNWPRT	4	
	SA2-118	IgM	3-23	4	AKAFSTGWGYYFGS	18	K	3-11	2	QQRSNWPMCS	9	
	SA2-122	IgG1	3-49	4	TLVCYYDILTGYYCY	0	K	1-5	2	QQYNSYPYT	0	
	SA2-124	IgM	3-23	3	AKDKYDWRRAFDM	7	K	1-5	1	QQYNSYPWT	1	
	SA2-129[2]	IgG1	3-30	6	AKDLDIVLMVYAIPRGYYGMDV	6	L	2-14	2	SYNSSSCCL	n/d	
	SA2-136	IgG1	3-30	2	AKDHRLTSIIVVLTGPFDF	25	K	1-39	2	QQSYGTPLT	16	
	SA2-138	IgM	1-46	4	ARDLGGSYNDY	17	K	4-1	1	NNIILILDR	11	
	SA2-142	IgM	3-23	3	AITGRNVPDSAFDI	14	K	1-39	1	QQSHSTPRT	10	
	SA2-144	IgG2	1-69	5	ATSGHSSLLNWFDP	22	K	3-11	2	QQRSNWPNT	3	
	SA2-147	IgM	3-30	6	ARVAGSSASPYSYYGMDV	13	K	2-28	2	MQALYPYT	12	
	SA2-148	IgM	4-4	4	ARQGDYTSDY	15	L	2-8	1	SSYAGSLYV	7	
	SA2-150	IgM	3-23	4	ARTPPRPGTDYFDL	40	K	3-15	1	QQYSKWPGT	5	
	SA2-154	IgG1	3-30	6	ARETTETYHEFWSGYNIDYYFYGMDV	16	K	1-39	1	QQSYSAPPWT	19	
	SA2-159	IgM	1-69	4	RRGECITIFGVVTPT	8	K	2-28	2	MQALQTPPDT	0	
	SA2-162	IgM	1-18	4	ARGPIVVLPAARGADANFDY	14	K	1-NL1	4	QQYYSTPLT	1	
	SA2-167	IgG1	4-39	6	ARRQGGYEYYYGLDV	9	K	3-15	2	QQYNDWRSS	12	
	SA2-171	IgM	4-59	6	ARVKRGYSYDLDV	17	K	3-11	1	QQRDNWPQT	12	
	SA2-175	IgG1	3-49	6	TSPGGTMVRGALGDYYGMDV	4	K	2-28	3	MQALQTLFT	0	
	SA2-180	IgM	3-48	4	ARDYNWTPDY	9	K	1-17	4	LQHNSYPSLT	5	
	SA2-183	n/d	1-18	5	LWLLPYGP	36	K	1-33	3	QQYDNLPLT	0	
	SA2-184	IgG1	3-30	6	AKDLDIVLMVYAIPRGYYGMDV	10	K	3-20	4	LHYGSSPT	15	
	SA2-185	IgG1	3-30	4	AKSGGTDPRMVVYYFDY	0	L	2-14	2	SSYTSSSPPVV	6	
	SA2-186	IgG1	4-31	4	ARESQQLVPYFDY	0	L	3-1	3	QAWDSSTFWV	1	
	SA2-190	IgG1	3-23	4	AKDYNWRGELDY	5	L	1-47	2	AAWDDSLSGVV	4	
	SA2-191	IgG1	3-30	4	AKDLGRYCSGTSCYGAGYFDY	1	K	1D-13	4	QQFNNYPPPT	1	
	SA2-195[27]	IgM	1-58	6	GRGYYGVDV	48	K	1-33	3	QQYDNLPLT	0	
	SA2-197	IgM	4-39	6	ARHSSSLGADYYNGLDV	12	K	1-39	2	QQSYSTPMYT	4	
	SA2-204	IgM	3-66	3	ARGGAFDI	16	K	1-5	1	QQYNSYWT	5	
	SA2-209	IgM	3-30	4	AKSYGSSGYTIKALFDY	0	K	3-20	1	QHYGSSFRL	10	
	SA2-210	IgM	4-34	6	ARGYYDFWSGYFPPNYYGMDV	2	K	1D-16	5	QQYNTYPIN	7	
	SA2-214	IgM	3-23	5	AKVSHYYGSGSSAS	33	K	1-33	4	QQYDNLRLT	4	
	SA2-225	IgM	1-3	6	ARPPEFNYYDSSGYLNVPYGMDV	2	K	3-20	4	QQYGSSPPVT	5	
	SA2-230[28]	IgG1	3-30	4	AKGQGVYCSGGSCYSGFCDY	4	K	3-20	4	QQYGSSPPVT	3	
	SA2-238	IgG1	4-39	4	AREVGATTMNYFDY	2	K	3-11	4	QQRSNWPPSLT	7	
	SA2-241	IgG3	5-10-1	6	ARQGLYYDILTGYYRDYYYGMDV	1	K	3-20	3	QQYGSSQGVT	2	
	SA2t2-103	IgG1	4-38-2	5	ARMEYYYDSSGYSRLGWFDP	0	K	1-39	2	QQSYSTPYT	3	
	SA2t2-104	IgG1	5-51	5	ARLATPLQYNWFDP	10	L	2-14	2	SSYTSSSTLVI	4	
	SA2t2-106[29]	IgG1	1-18	4	AREGPDIVLEPVAMGYDH	3	K	3-20	2	QQFGSSRYS	2	
	SA2t2-108[30]	IgG1	3-30	6	AKDSRPLPAAMPGYYYYGMDV	7	K	2-28	1	MQALQTPQT	4	
	SA2t2-112[27]	IgG1	1-58	6	GRGYYGVDV	6	K	1-33	3	QQFDNLPLT	3	
	SA2t2-113	IgG1	3-30-3	4	ARVYNDFSVTPYHYYFDY	12	K	2-28	2	MQALQTPTCS	2	
	SA2t2-114	IgG1	3-48	3	ARTYGDWPDAFDI	3	L	1-51	3	GTWDGSLSAWV	5	
	SA2t2-115	IgG1	4-34	4	ARVYCSGACYFDY	9	L	6-57	3	QSYDSSNWV	6	
	SA2t2-116	IgG1	3-30	6	AKAFFRYCSSTSCGRDYYHGLDV	0	L	1-40	1	QSYDSSLSGCV	6	

mAb expression ID	mAb clone ID	Ig class isotype	VH	JH	CDR H3	SHM VH	light chain	VK/VL	JK/JL	CDR K3/L3	SHM VK/VL	criteria for expression
	SA2t2-119[31]	IgG1	3-30-3	4	ARSGSYGYDY	6	K	1-33	4	QQYDNLPLT	0	
	SA2t2-120	IgG3	4-30-2	3	ARLALWGAFDI	2	K	1-33	2	QQYDNLSWT	3	
	SA2t2-122	IgG1	3-15	5	TTGPPGLIVGPDNWFDP	3	L	1-40	1	QSYDSSLSGYV	7	
	SA2t2-123	IgG1	4-38-2	5	ARHGNRIVYLTSESNWFDP	14	L	6-57	3	QSYDSTNRG	31	
	SA2t2-125	IgG1	1-58	3	AAPHCNRTTCHDGFDI	0	K	1-39	1	QQTYSTPRR	10	
	SA2t2-128	IgG1	1-69	1	ADMTNNYYDSSGPYYFQH	11	L	1-44	3	AVWDDSLNGWV	4	
	SA2t2-132	IgG1	3-30	6	AKDQDIVLMVYGIPRGLYGMDV	1	L	2-8	2	SSYAGSNNFGVV	2	
	SA2t2-134	IgG1	3-30	4	AKGPWYYYASSTFSGARTDFDY	4	L	1-47	2	AAWDDSLSASGCG	6	
	SA2t2-140[32]	IgG1	4-30-4	4	ARTIAARPGDFYFDF	7	L	1-47	2	AAWDDSLSGPV	3	
	SA2t2-141[29]	IgG1	1-18	4	AREGPDIVVVPVAMGYDY	6	K	3-20	2	QQFGSSRYS	5	
	SA2t2-146[28]	IgG1	3-30	4	AKTPLPYCTNGVCYIDY	0	K	3-20	4	QQYGRSPLT	20	
	SA2t2-147	IgG1	3-30	4	AKAVYSYAYGALYFDY	4	K	3-15	1	QQYKNWPRT	4	
	SA2t2-148[1]	IgG1	3-30	6	AKDFQYVAATHSPYYYYGMDV	5	K	3-20	3	QQYGSSPGVT	5	
	SA2t2-149[32]	IgG1	4-30-4	4	ARTIAARPGDFYFDY	10	L	1-47	2	SAWDDSLSGPV	6	
	SA2t2-150	IgG1	4-30-4	4	ARLLAPRPGSYYFDF	7	L	2-23	3	CSYAGCSTFG	7	
	SA2t2-152	IgG1	3-30	4	AKQLGSYYARSSYYFDY	2	K	1-33	3	QQYDNSLVT	3	
	SA2t2-153	IgG1	4-30-4	5	ARLAAPAPSSYWFDP	8	L	1-51	7	GTWDSSLGVAV	6	
	SA2t2-157[33]	IgG1	1-69	4	AREIPQGRYGDYEGAFDY	7	K	1-39	3	QQSYSTPRFT	4	
	SA2t2-162	IgG1	4-30-4	6	ARETTGTTSSIKYHYYGIDV	6	K	3-15	1	QQYNNWPPWT	7	
	SA2t2-163[31]	IgG1	3-30-3	4	ARGGGRGFDY	9	K	1-33	4	QQFDNLPFT	10	
	SA2t2-164	IgG1	3-21	6	ARDREGGAEGMDV	14	K	1-5	1	QQYSSYLRT	10	
	SA2t2-170	IgG1	4-59	3	ARNRWLRGAFDI	10	L	6-57	1	QSYDSSNYV	2	
	SA2t2-172[30]	IgG1	3-30	6	AKDSRPVPAAMPDYYYYGMDV	6	K	2-28	1	MQALQTPQT	1	
	SA2t2-173K	IgG1	4-30-4	6	ARVVRMNYNYGMDV	2	K	2-30	4	MQDTHWPPGLT	4	
	SA2t2-173L	IgG1	4-30-4	6	ARVVRMNYNYGMDV	2	L	2-23	1	CSYAGSYV	3	
	SA2t2-176	IgG1	1-18	4	ARDNYYGDHVPDY	9	L	2-14	1	SSYTRSNTLV	7	
	SA2t2-177	IgG1	3-30	4	AKSGYGYAYNSGYFDY	5	K	1-33	2	QQYDNLPRYT	3	
	SA2t2-178	IgG1	4-31	5	ARETVPAPNSNWFDP	8	L	1-44	2	STWDYSLSVMW	n/d	
	SA2t2-179	IgM	3-48	6	ARDSGIVVVPAAFYGMDV	3	K	3-20	1	QQYGSSPWT	3	
	SA2t2-180[33]	IgG1	1-69	4	ARDTHSGYSYGTFDY	3	K	1-39	3	QQSSSTPRFT	3	
	SA2t2-181[6]	IgG1	1-58	3	AAPACNRTSCYDGFDI	3	K	3-20	1	QQYGTSPWT	4	
	SA3-104	IgG2	3-7	6	ARVRHYQLPFYSYYMDV	11	K	1-39	1	QQSYSTLDT	9	
	SA3-105	IgG2	3-23	3	ANRDWSQGGGFDI	44	K	3-11	5	SSAATGRSP	16	
	SA3-108	IgG1	1-46	6	AREWVPATATSYYYYYMDV	2	K	1-16	4	QQYNSYPRSL	4	
	SA3-114	IgG1	3-33	5	ARDGPDYDSSGYYVSWFDS	3	K	1-39	1	NRVTVPLRGR	7	
	SA3-116	IgG1	4-34	4	ARGGLEDWNDSSFDS	10	K	3-20	2	QQGTSRMYT	14	
	SA3-117	IgG1	3-9	2	AKLLSVGEYFDL	7	K	1-27	3	KSITVPLH	7	
	SA3-122	IgG1	3-33	6	AKGYSSSPYYYYYMDV	2	K	2-28	4	MQALQTPLT	2	
	SA3-124	IgG1	4-34	6	ARGRLYSSSWYYYSYMDV	20	L	1-44	2	ATWDDSLNVV	14	
	SA3-127	IgM	4-39	3	ARDRPSGNWNYDIDAFDI	12	K	3-20	1	QQYGSSPRT	0	
	SA3-130	IgA2	3-74	4	TRLTVGEPAGRDY	10	K	3-11	4	QQRNNWPLT	7	
	SA3-131	IgM	1-18	4	ARTIYEDH	18	K	3-20	1	QQYGNLPRT	10	
	SA3-132	IgM	3-15	2	ITGWYFDL	17	K	3-20	2	LQYGNSPMYT	16	
	SA3-135[15]	IgG1	3-13	6	ARVRESTHYSKDAKPYYYYYMDV	2	K	1-39	1	QQSYTNPLGT	11	
	SA3-141	IgM	3-7	3	ARGYCTGGVCSSDAFDI	15	K	1-12	3	QQANSFPFT	3	
	SA3-157	IgM	5-51	4	ARHDPPGASGALDY	0	K	1-39	2	QQSYSTPYT	8	
	SA3-159	IgM	3-74	4	TSRYILPTTRGSDFDY	3	K	3-20	2	QQYGSSLYT	3	
	SA3-160	IgG1	1-18	3	ARMGRMIVGLWGAFDL	17	L	1-47	3	AAWDDSLSGWV	7	

mAb expression ID	mAb clone ID	Ig class isotype	VH	JH	CDR H3	SHM VH	light chain	VK/VL	JK/JL	CDR K3/L3	SHM VK/VL	criteria for expression
	SA3-163	IgM	3-21	6	ARDPQKTYYDFWSGYASGDGYYYYMDV	0	L	1-44	3	AAWDDSLNGWV	1	
	SA3-165	IgM	3-33	4	AKRGSRWDFDY	11	L	2-8	2	SSHAGNNNLV	6	
	SA3-167[16]	IgM	1-3	4	ARPKRSIAAAGIGNYFEY	11	K	1-39	2	QQSYITPGT	4	
	SA3-168	IgM	4-59	4	ARNLGRTGGSYYFDS	23	K	4-1	4	QQCYSSPH	18	
	SA3-173	IgM	1-3	6	ARVMPYCSGGSCYSPYYYGMDV	4	L	1-44	3	AAWDDSLNVWV	2	
	SA3-174	IgM	3-15	5	TIPGGAGADLKRSGFDP	7	K	4-1	3	QQYYSTPFT	2	
	SA3-176	IgM	3-74	5	ARGCSGVSCYGGP	7	K	3-20	1	QQYGSSPWT	6	
	SA3-181[13]	IgG2	3-7	4	ARKGAWDVDF	15	K	2-30	5	FQGTHWPPT	11	
	SA3-186	IgM	3-7	4	ATYCSGDGCRSFDH	21	K	1-16	5	QQYKSYPII	8	
	SA3-190[34]	IgM	1-18	6	ARDTRITPNGMDV	6	K	3-20	1	QQYGSSPRT	4	
	SA3-191	IgG1	4-34	6	VVIAIPFMSHILHGR	18	K	1-33	3	QQHDNLPFT	2	
	SA3-197	IgG1	3-74	2	AGAGGWHLDL	27	K	1-33	4	QQHDSLPLT	28	
	SA3-199	IgM	3-74	3	ARGQKGVPGAFDI	9	L	2-14	2	SSYTSITSPLV	7	
	SA3-201[14]	IgM	3-73	4	TRHLGTNFDD	3	L	2-14	3	NSYTTTSTWV	11	
	SA3-203	IgM	3-74	3	ARPRSGAFDI	8	K	3-20	1	QQYGSSPWT	8	
	SA3-205	IgM	3-30	4	ARAPSGGGSNMRVYRVFDY	23	L	2-14	1	SSYTSSNNYV	3	
	SA3-209	IgG3	3-30	3	ASYPELLYAFGI	3	K	1-5	1	QQYNSFPWT	8	
	SA3-211	IgG1	3-30	4	ARDTWGSKWGSTLGY	29	K	1-27	4	QKYNSAPLT	12	
	SA3-213	IgG1	3-7	4	VGGGYNGY	17	L	7-46	3	LLLYSGPWV	15	
	SA3-214	IgM	1-18	5	ARDPSNTSGWREWFDP	13	K	3-20	4	QQYGSSPFT	6	
	SA3-218	IgM	3-9	4	VKGFSSGIGQIPGAY	16	K	3-15	1	QQYNNWPWT	8	
	SA3-219[16]	IgM	1-3	4	ARPKRTIAAAGIGNYFEY	11	K	1-39	2	QQSYITPGT	11	
	SA3-221[16]	IgM	1-3	4	ARPKRSIAAAGIGNYFEY	10	K	1-39	2	QQSYSSPGT	8	
	SA3-222[50]	IgM	4-39	4	ARLARRSSSRTYYFDY	16	L	1-40	3	QSYDSSLSTSV	7	
	SA3-223	IgG1	3-7	4	ARDRYSGAWYGIPFDY	5	L	1-44	1	AAWDDSLNGFLC	1	
	SA3-224[12]	IgM	4-59	4	TRNLGRTGGSYFFDY	11	L	1-47	3	AVWDDSLSGWV	4	
	SA3-228	IgM	3-73	4	ARHGSGIDY	6	L	2-14	2	SSYTSSSTLV	7	
	SA3-236	IgA1	3-7	6	ANTYSNIRPFYYWFGLDV	24	L	2-8	1	SSHAGSDTPFV	15	
	SA3-237[16]	IgM	1-3	4	ARPKRSIAAAGIGNYFEY	11	K	1-39	2	QQSYITPGT	7	
	SA3-238	IgM	3-23	4	ATRRYSGGVWYPFEY	8	K	1-27	4	QKVDSAPLT	12	
	SA3-239	IgG1	1-46	5	ARDAIAVAGRGWFDP	7	K	3-11	1	QQRSNWWT	3	
	SA3-240	IgM	3-23	4	AILRYTVTTPVSQ	3	L	1-47	3	AAWDDSLTGWV	2	
	SA3-242	IgA1	3-33	3	AKDLRQWDLLGTFDI	8	K	3-15	4	QQYNNWPWSPLT	24	
	SA3-244[34]	IgM	1-18	6	ARRPSTGTTGPGYGMDV	19	K	3-20	1	QLYGGSPPWT	8	
	SA3-253	IgG1	4-38-2	1	AKTRQQFIWD	15	L	1-40	3	QSYDRSLNWV	6	
	SA3-254	IgA1	1-18	1	GRDSYQRFSAPHH	19	K	3-15	2	QQYNNWPPTYT	4	
	SA3-255	IgM	3-74	4	ARGPWGG	15	L	2-11	2	RSYAGNFTFVV	13	
	SA3-256	IgM	3-33	4	AIGPKAYIVATMGEYYFEY	8	L	1-51	1	GTWDSSLSAYV	5	
	SA3-257	IgM	3-74	4	VRGGTIGVTGTDY	16	K	3-11	1	QQRSNWPQT	2	
	SA3-258	IgG3	4-4	4	ARALRLRGTYPYYFNL	43	K	1-39	2	TELQHPSD	25	
	SA3-259[34]	IgM	1-18	6	ARRPSTGTTGPGYGMDV	19	K	3-20	1	QLYGGSPPWT	7	
	SA3-260[3]	IgM	5-51	6	ARTATGTNHYYYYYYMDV	0	L	1-44	3	AAWDDSLNGPV	0	
	SA3-262	IgM	3-74	4	ARGGGSYFDY	4	L	2-8	1	SSYAGSNTPSV	4	
	SA3-265	IgM	1-3	4	AREAWGAAGSYHFDF	18	K	3-20	2	LQCGSSPRPGYT	10	
	SA3-266[16]	IgM	1-3	4	ARPKRSIAAAGIGNYFEY	10	K	1-39	2	QQSYSSPGT	9	
	SA3-267[17]	IgA2	3-33	4	AKRGDSCTGGVCSYFDY	10	L	8-61	3	VLYMGSGIWV	8	
	SA3-269	IgM	3-48	6	ARAWRGDGGGRPWRGLDV	5	L	6-57	3	QSYDSSIHWV	2	
	SA3-270	IgG1	3-33	3	AKDRPDPITMIVVGAFDI	0	L	4-69	2	QTWGTGIKR	3	

mAb expression ID	mAb clone ID	Ig class isotype	VH	JH	CDR H3	SHM VH	light chain	VK/VL	JK/JL	CDR K3/L3	SHM VK/VL	criteria for expression
	SA3-274[14]	IgM	3-74	4	VRGHSERYGKFED	8	L	2-14	3	SSYTRSSSWV	7	
	SA3-278	IgM	3-23	4	ANRIVGAPTGY	18	K	2-30	2	MQGTHWPYT	7	
	SA3-279	IgG1	3-13	2	VRAEYDSSGYYWYFDL	4	K	1-39	2	QQSYITPPEDT	2	
	SA3-280	IgM	3-7	4	ARQGNPNS	8	K	2-29	2	MQGIQFPRT	16	
	SA3-281	IgG1	1-69	5	ARAVTIFGVVINWFDP	23	L	2-8	1	SSYAGSNHFYG	12	
	SA3-284	IgG1	3-53	6	ARWGPNDYDILTGYSPHYYYYGMDV	4	K	1-5	3	QQYNSYSL	8	
	SA3-292	IgM	4-59	5	ARMPGGFDP	2	K	4-1	3	QQYYSTPFT	1	
	SA3-293	IgM	3-13	4	ARANYDSSGYYSLFDY	1	K	1-39	2	QQSYSTLSYT	1	
	SA3-297	IgG1	4-34	4	ARGLDHAKSGT	31	K	2-28	2	ASSTNSVH	6	
	SA3-302	IgG1	3-9	6	AKGHSPLHQYYYGMDV	4	L	2-8	3	SSYAGTNNVA	13	
	SA3-303K	IgM	1-69	5	ARDTTVTTMGWFDP	1	K	1-5	5	QQYNSYST	1	
	SA3-303L	IgM	1-69	5	ARDTTVTTMGWFDP	1	L	4-69	3	QTWGTGIPDWV	3	
	SA3-306	IgG1	5-51	4	ARLALPRVISYCFDS	15	K	1-33	4	QHHDNLPLT	11	
	SA3-308	IgA2	1-18	4	ARWRGSYCDKTGCQPFDY	21	K	3-20	2	QQYGSSSYT	11	
	SA3-314	IgM	4-59	6	ATYYYDSSGYNYGMDV	4	K	1-39	1	QQSYSIPLT	1	
	SA3-316K[22]	IgM	3-13	2	ARDISSSWYFDL	2	K	1-39	3	QQSYSTPPIT	3	
	SA3-316L	IgM	3-13	2	ARDISSSWYFDL	2	L	2-23	3	CSYAGSSTWV	2	
	SA3-318	IgG2	1-46	5	ARDWGRFMGQIDP	14	K	3-15	1	QQYKNWPRT	4	
	SA3-324	IgA2	3-23	6	AKGGVGTLSKTGMDV	17	K	1-39	1	EQSHSAPVT	16	
	SA3-325	IgG2	3-9	6	AKATLFHGYGLGYYYAMDV	9	K	2-28	2	MQALQTPPST	12	
	SA4-102	IgM	3-11	6	THLGRRDGYNYYYYGMDV	0	L	1-44	3	AAWDDSLNGPV	0	
	SA4-105	IgG1	1-24	5	ATLIGSCSETTCPRTGGFDP	35	L	2-23	3	SSYAGGGLWV	26	
	SA4-106L	IgM	1-8	3	AREFVGSYWGGAAFDI	3	L	2-14	3	SSYTRSSSWV	7	
	SA4-107	IgM	3-7	4	ARGGSYWRY	6	K	1-33	2	QQFDNFPRT	12	
	SA4-111	IgG1	4-4	6	ARGPCCSSPHGMDV	14	L	2-23	2	AHMQVVALG	9	
	SA4-114	IgM	3-33	4	AKDSHYYGSGSYRYFDY	9	L	1-51	3	GTWDTSLSVVV	8	
	SA4-115	IgM	4-39	5	ARHLKPRPESDWFDP	12	L	1-44	3	AAWDGGLNGPV	4	
	SA4-116	IgM	5-51	3	GRQGPYYYDSRGSVVGPRDEAFDI	6	L	1-40	3	QSYDSSLSGWV	3	
	SA4-118	IgG1	3-21	5	ARGLKMTTVSSSGAFDP	17	L	2-8	3	SSYAGNNHLV	10	
	SA4-119	IgG2	3-11	4	AKLLTGSSPFDY	27	L	3-21	3	QVWDGNSDWV	11	
	SA4-121	IgA2	3-33	4	AKDRGLGGDTNDY	13	K	1-27	4	QKYNSAPLT	8	
	SA4-126[8]	IgG1	3-21	4	ARAEYYFDY	17	L	1-44	3	AAWDDSLIGLG	10	
	SA4-129	IgG1	4-39	4	AKAVEGPVFDF	22	K	2-30	5	ARYTLASDH	12	
	SA4-133K	IgG1	3-23	6	AKGPTSSGYYFGMDV	10	K	3D-15	3	QQYNNWGSFT	8	
	SA4-133L	IgG1	3-23	6	AKGPTSSGYYFGMDV	10	L	6-57	3	QSYDNINQSPWV	6	
	SA4-134	n/d	3-23	6	RKLLQCVAPLRIDV	41	L	2-14	1	SSYTSSSTLYV	7	
	SA4-135K	IgM	3-9	6	AKDIRPYYYDSRDYYGMDV	1	K	3-20	4	QQYGSSLT	3	
	SA4-135L	IgM	3-9	6	AKDIRPYYYDSRDYYGMDV	1	L	2-23	3	CSYAGSSTWV	2	
	SA4-136	IgG1	3-43	4	AKDGVVATMGDYFDY	6	L	3-21	3	QVWDSSSDHWV	6	
	SA4-139	IgA1	3-53	6	ARDRAYYGSGSPDDYYGLDV	18	K	2-28	1	MQGLQTPPT	11	
	SA4-140	IgM	3-30	4	ARGRGSSGSPFDY	14	K	1-27	1	QKYNNAPWT	2	
	SA4-145	IgM	3-23	6	AKHSYEFSYYGMDV	16	K	2-28	4	MQALQSRLT	3	
	SA4-146	IgG1	3-30	4	ARVGDIYALREYSYDY	10	K	1-9	2	QQFKSYPYS	11	
	SA4-148	IgG1	3-11	6	ARDERRVIRGRYGMDV	16	L	1-51	3	AIWDSRLSTGRWV	14	
	SA4-149	IgM	5-51	3	ARGPGVVAATIPIGAFDI	0	K	3-20	4	QQYGSALT	3	
	SA4-150	IgG1	1-18	3	ARVQHWNSYVDAFDI	28	L	1-51	1	GTWDDSLSAGL	13	
	SA4-151	IgG2	3-30	6	SRGAEGSGRYYGSVDYYYVLDV	15	L	1-40	3	QSYDRTLSGWV	15	
	SA4-152	IgG2	4-59	5	ARDWVSGNSHGYNWFDP	25	K	3-11	1	QQRYHWPT	12	

mAb expression ID	mAb clone ID	Ig class isotype	VH	JH	CDR H3	SHM VH	light chain	VK/VL	JK/JL	CDR K3/L3	SHM VK/VL	criteria for expression
	SA4-155	IgG3	3-33	4	AKDPSGYDSGKTYFDY	5	L	3-21	1	QVWDSGSDPLYV	7	
	SA4-158	IgM	3-7	4	ARDSPFLRWKDY	6	K	3-15	4	QQYNNWPLT	6	
	SA4-159	IgM	1-46	4	AKSGGFWSVDY	19	L	2-8	1	SSNAGSSNLV	9	
	SA4-165	IgM	4-59	4	ATHIVRPTTTFAS	12	L	3-21	3	QVWDSSSDHRV	2	
	SA4-172	IgM	3-11	4	ARAPRMSDY	8	K	2-30	3	MQGTHWPFT	3	
	SA4-175	IgM	1-58	6	AAARYGSGRLYYYGMDV	7	K	4-1	1	HQYYSTPWT	3	
	SA4-189	IgM	3-7	6	ARGGMVYALDYYGMDV	1	L	1-47	3	AAWDDSLSGWV	3	
	SA4-194	IgG1	3-33	6	RKIWRLWFGDLSLTATVWTS	11	K	1-39	2	NRVTVPRTL	5	
	SA4-196K	IgM	3-74	5	ARGYCSSPSCPRPKGWFAP	8	K	4-1	2	QQYYNIPYT	8	
	SA4-196L	IgM	3-74	5	ARGYCSSPSCPRPKGWFAP	8	L	2-8	2	SSYAGSNNLV	4	
	SA4-199	IgG1	3-23	4	AKITVTHFDC	3	L	6-57	3	QSYDSSNWV	0	
	SA4-203[10]	IgM	3-74	4	ARGGLSGEMSKWGY	5	L	7-43	3	LLYYGGPWV	5	
	SA4-204	IgM	1-3	4	ARAGGKWNYDY	20	L	2-14	2	TSCTSSSTVL	11	
	SA4-205	IgM	3-53	4	ARSGGYSFDY	0	L	2-23	3	LICKVVALG	7	
	SA4-207	IgM	3-48	3	ATGLNNYDSSADRYALHI	14	L	1-44	3	ATWDDSFNGWL	20	
	SA4-211	IgM	4-38-2	4	AGFCSGGDCSPFDY	4	K	4-1	1	QQYYSTPRT	5	
	SA4-213	IgA1	3-48	4	ARSGNYRIDY	21	L	1-44	3	AAWDDSPTGWV	10	
	SA4-214[14]	IgM	3-74	4	ASMWGTANDY	9	L	2-14	3	AHIQLAALG	17	
	SA4-215	IgM	4-38-2	4	ARARQGVFDY	7	K	3-15	2	RQYNNWPYT	10	
	SA4-218[14]	IgM	3-74	4	ARWAPEGD	15	L	2-14	3	TSYTKSSTWV	12	
	SA4-219[48]	IgM	3-53	6	ARGDKATDGMDV	1	L	3-25	3	QSADSSGTWV	4	
	SA4-221	IgG1	5-51	3	ARPPAYCGGDCPIGAFDI	5	K	1-39	1	QQSYSTRT	4	
	SA4-223[14]	IgM	3-74	4	ARGLQAGGGWGDN	9	L	2-14	3	ISYTTSSTWV	5	
	SA4-226	IgM	3-74	4	ARGNSGFDY	13	K	3-11	4	QQRSNWPLT	11	
	SA4-235	IgG1	3-30	4	ARDRGYYDRSGYYTTLYFDY	3	L	6-57	3	QSYDSSNPSWV	2	
	SA4-237	IgM	3-9	4	AKDMGYDFWSTYNYFDY	3	L	1-40	3	QSYDSSLSGSV	1	
	SA4-239	IgM	1-18	5	ARVNRYSRPHWFDP	7	L	2-14	1	SSYTSSSTYV	5	
	SA4-240	IgG1	1-18	5	ARDGELLAWFDP	5	L	2-23	3	CSYAGSSTWV	4	
	SA4-241	IgM	4-4	3	ARRDSSRYPI	4	K	1-39	2	QQIYSTPYT	12	
	SA4-242	IgA1	4-34	4	ARAFRAGLLSPLAY	44	L	1-44	3	ATWDDSFKWLA	17	
	SA4-245	IgM	5-51	4	ARHPPDCSGGSCPFDY	9	L	6-57	2	QSYDSSIVV	3	
	SA4-246	IgM	4-39	4	ARHNSGTYYRFDY	6	L	2-14	1	SSYTSSNTRV	6	
	SA4-247[10]	IgA1	3-74	4	ARGGISGGMSTWAY	21	L	7-43	3	LLFFGAAWV	15	
	SA4-248[35]	IgG1	4-39	4	ARLRGPSRPGEGYYFDY	5	L	2-23	3	CSYAGGSTWV	7	
	SA4-249	IgM	3-74	4	VRGTRDGVGAWV	12	K	4-1	4	HQHYSSSPT	11	
	SA4-252	IgM	3-48	3	ARGAARAFDI	14	L	8-61	3	VLYMGSGIWV	4	
	SA4-253	IgM	3-23	4	AKEGAYCGGDCLYYFDY	3	K	2-28	5	MQALQTPIT	1	
	SA4-254	IgG1	5-51	6	ARLRDYGDYYYYGMDV	7	K	1-9	5	NSLIVTPP	4	
	SA4-255	IgA2	3-7	4	AKGPLGSGY	5	L	2-8	1	SSFAGSNSFV	15	
	SA4-256	IgG2	3-30	4	ARGRDYFVYSAIEY	26	L	8-61	3	ALYIGGAVNWV	23	
	SA4-259	IgG1	4-4	5	ARDSGIRGYNYFGP	30	K	1-5	2	QQYKSSPYT	26	
	SA4-262	IgM	3-7	4	ARAGSPAARDY	4	L	2-8	3	SSYAGSNSLV	7	
	SA4-264	IgG1	3-11	4	AREHGTGYSSYFDY	7	L	1-40	3	QSYDSSLSGWV	1	
	SA4-265K	IgM	3-74	4	ARGGVSGEMSNWAY	18	K	2D-30	1	CKVHTGGR	10	
	SA4-265L[10]	IgM	3-74	4	ARGGVSGEMSNWAY	18	L	7-43	3	LLFFGDAWV	12	
	SA4-266K	IgM	4-59	6	ARDKGFDFWSRYSWDYYYALDV	14	K	4-1	2	QQYYTSPPMYT	13	
	SA4-266L	IgM	4-59	6	ARDKGFDFWSRYSWDYYYALDV	14	L	2-8	3	SSYAGTNNVA	13	
	SA4-276[14]	IgM	3-74	4	ARASSYSYGYFDY	0	L	2-14	3	SSYTSSSTWV	2	

mAb expression ID	mAb clone ID	Ig class isotype	VH	JH	CDR H3	SHM VH	light chain	VK/VL	JK/JL	CDR K3/L3	SHM VK/VL	criteria for expression
	SA4-278	IgM	1-3	4	ARRDFYGSGSFHLGYGY	5	K	2-28	4	MQALQTPLT	3	
	SA4-280	IgM	4-59	4	ARGSIAVAGFDY	1	L	1-44	3	N/A	8	
	SA4-283	IgM	3-7	4	ARGGGVTFDN	10	L	2-11	3	CSYAGSHTWV	11	
	SA4-287	IgG1	4-59	5	VGKVNGAFWFDP	25	L	2-14	3	SSYTRANTWV	19	
	SA4-289	IgM	7-4-1	4	ARRGYCSSISCLGH	6	L	2-8	2	SSHAGSNNVV	6	
	SA4-299	IgG1	4-59	4	ASYYYDSSGYHYGFDY	0	K	1-39	3	QQSYSTPFT	7	
	SA4-302[10]	IgM	3-74	4	ARGGVSGEMSNWAY	17	L	7-43	3	LLFFGDAWV	9	
	SA4-309	IgM	5-51	6	ARLHYDFQYGLDV	9	K	3-15	1	QQYKNWPRT	5	
	SA4-310K	IgM	4-31	6	AALAAAGTYSYYYGMDV	1	K	1-39	4	QQSYSTLT	1	
	SA4-310L	IgM	4-31	6	AALAAAGTYSYYYGMDV	1	L	1-51	3	GTWDSSLSAGV	5	
	SA4-312	IgM	3-11	4	ARGLLADYGDYVYFDY	0	L	1-47	1	AAWDDSLSGYV	1	
	SA4-313	IgG2	3-11	6	AREVYEFSGGAMDV	23	L	2-14	1	SSFTSSDTLV	14	
	SA4-315	IgM	3-23	6	AKGMGSGLDV	20	L	1-51	3	GTWDSSLSAGV	5	
	SA4-321	IgM	3-7	6	GRAMQV	11	L	1-44	3	AAWDDSLSRWV	10	
	SA4-323	IgG2	6-1	4	ARGWLRSQDFEY	18	L	2-8	2	SSYAGSSYLL	11	
	SA4-326[35]	IgG1	4-39	4	ARVVRYSRGGGLDY	5	L	2-23	3	CSYAGSSTLV	2	
	SA5-124	IgG1	1-8	4	ARAPGFGESHNDY	3	L	3-21	1	QVWEGSGDHYV	8	
	SA5-125[19]	IgM	3-13	2	ARVRPTMTKGFDWYFDL	2	K	1-39	1	QQSYNTLGT	6	
	SA5-128	IgG1	3-30	6	AKTSGSYYYYYYGMDV	4	L	2-14	1	SSYTSSSTSYV	3	
	SA5-130	IgG1	3-23	2	AKGSQGYYDRSGYYLHDWYFDL	5	L	1-40	2	QSYDSSLSGLNVV	4	
	SA5-131	IgG1	3-15	4	TTDELYSGYEDPGDY	1	K	1-5	3	QQYNSYIFT	0	
	SA5-132[15]	IgG1	3-13	6	ARGVVTMVRGLTTYYYYYMDV	4	K	1-39	1	QQSYSSEWT	1	
	SA5-137[5]	IgG1	4-39	5	VRLRGAVRPGVPANWFDP	8	K	1-9	3	QQLNSYPLT	2	
	SA5-139	IgG1	3-21	4	ARDPYLEPGIKVAVY	2	L	6-57	3	QSYDSSNHWV	0	
	SA5-140[19]	IgM	3-13	2	ARVRPTMTKGFDSYFDL	36	K	1-39	1	QQSYNTLGT	5	
	SA5-144[18]	IgG1	3-13	6	ARALYGSGSYSTQAGYYYGMDV	3	K	1-39	3	NRVTGPSL	1	
	SA5-146	IgM	4-59	4	ARGGSNTWQLIFDY	13	K	4-1	5	QQYYSTPLT	11	
	SA5-150	IgG1	4-39	4	ARHSAQYSYDYFDY	3	K	1-33	4	QQYDNLPPNT	0	
	SA5-152	IgM	3-23	4	AKDPAVTIFGESDY	0	L	5-52	3	GTWHSNSKTHEE	1	
	SA5-154	IgG1	3-21	3	ARGGIGYYDSSGYYWAAPDDAFDI	1	L	1-40	2	QSYDSSLSGHVV	1	
	SA5-158	IgG1	3-15	3	TTELEWLLLEDDAFDI	0	K	3-20	5	QQYGSSPSIT	1	
	SA5-167	IgG1	3-30	6	AKDPSGGGCYSSGCYYYYGLDV	4	L	2-18	1	ASYTSKITFV	25	
	SA5-171[20]	IgM	3-23	4	AKDFVVVVAARSHDDYYFDY	3	K	1-5	4	QQYKNFPLT	33	
	SA5-173[19]	IgM	3-13	2	ARVRPTMTKGFDWYFDL	0	K	1-39	1	QQSYNTLGT	5	
	SA5-174K	IgA1	3-23	6	AKCIQLYYYGMDV	3	K	2-28	2	MQALQTPPNT	3	
	SA5-174L	IgA1	3-23	6	AKCIQLYYYGMDV	3	L	2-8	3	SSYAGTNNVA	13	
	SA5-175[23]	IgG2	3-30	6	AKGDDYGDLFYYGMDV	1	K	2-28	4	MQALQRTLT	1	
	SA5-180	IgM	3-30	6	AKDRHTASPPHYYYGMDV	4	K	4-1	4	QQYYSTPLT	4	
	SA5-187[4]	IgM	4-39	5	ARHSSSSPTSNWFDP	4	L	1-51	3	GTWDSSLNAGV	3	
	SA5-190	IgG2	4-39	3	TRHQSSRPGLDALIS	n/d	K	3-15	1	QQYKNWPRT	2	
	SA5-194	IgA1	3-48	4	AREGYYSGFDY	19	L	2-14	3	SSYRTDYTWV	12	
	SA5-196[5]	IgG1	4-39	5	ARLRGAVRPGVPANWFDP	10	K	1-9	3	QQLNSYPLT	0	
	SA5-197	IgG1	1-3	4	AREEVYCSGGSCSYRELDY	2	K	1-33	2	QQYDNLP	0	
	SA5-198	IgG1	3-13	5	ARAEHYCSGGRCYSWFDP	2	K	1-39	2	QQSYITTLYT	7	
	SA5-202	IgG1	3-9	4	AKDRHYDSSGYLTSGIDY	4	K	1-39	1	QQNYITPPA	2	
	SA5-208	IgG1	3-23	6	AKDSSSWYYGMDV	0	K	1-12	4	QQANSFPLT	2	
	SA5-209[23]	IgG2	3-30	6	AKGDDYGDLFYYGMDV	1	K	2-28	4	MQALQRTLT	1	
	SA5-210	IgG1	5-51	1	ETEGDCSGSSCYLVQILPA	56	K	1-33	3	QQYDNLPIT	1	

mAb expression ID	mAb clone ID	Ig class isotype	VH	JH	CDR H3	SHM VH	light chain	VK/VL	JK/JL	CDR K3/L3	SHM VK/VL	criteria for expression
	SA5-215	IgM	3-30	6	AKDGGAGVRGVKDYYYYGMDV	1	L	1-47	1	AAWDDSLSGYV	0	
	SA5-220	IgG3	1-69	6	ARDNPGVRGVPSYYYYGMDV	2	K	1-33	3	QQYDNLLS	3	
	SA5-221[21]	IgG1	4-39	5	ARLTPQAPGVVWFDP	2	L	2-23	2	CSYAGSSTYVV	2	
	SA5-225	IgM	3-15	1	TTDRGTSWSNPPFQH	12	K	2-30	4	MQGTHCSL	1	
	SA5-239	IgG1	4-39	5	ARVRGGYCSGGSCYPGGDIDP	14	L	2-8	2	AHMQAALW	5	
	SA5-243	IgG1	4-61	5	AKVVAATPFSSWFDP	2	K	3-11	2	QQRSNWPEVYT	2	
	SA5-244[20]	IgM	3-23	4	AKDFVVVVAARSHDDYYFDY	5	K	1-5	4	QQYNRFPLT	2	
	SA5-247[15]	IgG1	3-13	6	ARGVAVREDLYYYYYMDV	2	K	1-39	1	QESYSNPSWT	7	
	SA5-249	IgM	3-23	1	AKDGEQQILWGYFQQ	23	K	2-30	2	IQGTHWRGL	17	
	SA5-254	IgM	4-34	6	ARVTGYYYYYMDV	4	K	1-39	5	QQSYTTLIT	6	
	SA5-255	IgM	4-39	4	AREAGPLGPYYYDSSGYSD	3	K	3-15	2	QQFNNWPRT	3	
	SA5-257	IgM	4-39	4	ARTGMGSIVWSY	11	K	3-20	4	QQYDSSPLT	9	
	SA5-261	IgG1	3-48	4	ARGPSEMATIFFDY	5	K	3-11	5	QQRSNWPIT	4	
	SA6-102	IgG1	3-43D	4	AKDTTPYGSGSGVDY	4	K	1-33	4	QQYDNLPPGLT	29	
	SA6-103	IgG1	3-49	4	TRDLVGGYCSGGSCYETYYFDY	0	K	3-20	2	QQYGSSPGT	5	
	SA6-104	IgM	4-34	4	ALRNVVVAAKDY	3	K	1-39	2	QQSYSTPRT	1	
	SA6-107	IgM	1-3	5	ARDGSVGYYDSSGYYFNGDNWFDP	4	L	1-40	2	QSYDSSLSGSVV	1	
	SA6-111	IgG1	1-18	4	ALSYSRGWYYFDY	2	L	6-57	3	QSYDSSIT	3	
	SA6-112[36]	IgM	4-39	5	ARGGDILTGYDWFDP	4	L	1-40	2	QSYDSSLSGSYVV	1	
	SA6-115	IgG1	3-7	4	AREPTYYHGSGADY	1	K	3-11	1	QQRSNWPPWT	4	
	SA6-117	IgG1	1-46	4	ARGYSSSSQLIWNFGY	1	L	1-47	1	AAWDDSLSGPVLC	2	
	SA6-119[36]	IgG1	4-39	5	ARGGDILTGYDWFDP	5	L	1-40	2	QSYDSSLSASYVV	5	
	SA7-155	IgG1	3-30	6	AKDLAPVPEYYYYGMDV	6	L	1-44	3	AAWDDSLNGV	2	
	SA7-156	IgG1	1-69	4	ARELYTYGPPHY	22	L	1-44	3	ATWDDTRNGWV	13	
	SA7-157[7]	IgM	3-30	6	AKDRSVGATTSQSHYYYGMDV	9	L	1-51	2	GTWESSLNTGV	12	
	SA7-159[38]	IgM	3-23	4	AKDSGIWGTEVAGTNDY	9	K	4-1	2	SNIILLRTL	7	
	SA7-162[37]	IgM	3-7	3	ARDRAREYYYDSSGYYYSDAFDM	4	L	3-1	2	QAWDSSPV	11	
	SA7-163	IgG1	1-18	3	ARGRTLGATDAFDV	13	K	2-28	5	MQALQTPLT	4	
	SA7-166[38]	IgM	3-23	4	AKDSGIWGTEVAGTNDY	12	K	4-1	2	QQYYTPPYT	9	
	SA7-167[38]	IgM	3-23	4	AKDSGIWGTEVAGTNDY	8	K	4-1	2	QQYYTPPYT	10	
	SA7-169[38]	IgM	3-23	4	AKDSGIWGTEVAGTNDY	12	K	4-1	2	SNITLPRTL	11	
	SA7-171[7]	IgM	3-30	6	AKDRSVGATTSQSHYYYGMDV	5	L	1-51	2	GTWDSSLSTGV	5	
	SA7-174	IgG3	3-30	4	ARDWGQLVTLFDY	5	K	1-39	1	TELQYPSVD	4	
	SA7-175K	n/d	5-51	4	QRLPSQKETSMEADLT	36	K	4-1	2	QQYYSTPPYT	3	
	SA7-175L	n/d	5-51	4	QRLPSQKETSMEADLT	36	L	2-14	3	SSYTSSSTLG	11	
	SA7-178[37]	IgM	3-7	3	ARDRAREYYYDSSGYYYSDAFDM	4	L	3-1	2	QAWDSSPV	11	
	SA7-179	IgM	1-18	6	ARGEGPYYYDRSGYYLADYYGMDV	6	K	1-27	1	QKYNSAPQT	2	
	SA7-180[38]	IgM	3-23	4	AKDSGIWGTEVAGTNDY	12	K	4-1	2	QQYYTPPYT	15	
	SA8-101[39]	IgG1	4-59	4	ARDLKGTTCYDF	23	K	1-33	5	N/A	13	
	SA8-103	IgG1	3-7	2	ARKESDFWSGYINWYFDL	0	K	3-11	4	QQRSNWPP	3	
	SA8-106	IgM	5-51	4	ARHRTESGQLELDY	0	L	1-47	2	AAWDDSLSGPV	0	
	SA8-108	IgM	5-51	4	ARHGIAVAGTVVPDY	0	L	1-44	2	AAWDDSLNGPV	0	
	SA8-114[40]	IgM	4-59	6	ARDPGTWMYYYDGMDV	16	K	1-33	4	RH	18	
	SA8-119	IgG1	7-4-1	6	ARAQADSSGWYLGYYYGMDV	2	K	1-17	3	LQHNSYPH	5	
	SA8-133	IgG1	4-39	5	ARHSVVPAGDWFDP	5	K	1-5	2	QQYNSYSCS	4	
	SA8-140[40]	IgM	4-59	6	ARDPGTWMYYYDGMDV	15	K	1-33	4	RH	17	
	SA8-142K	IgG1	1-24	6	ATDRKYYYYGMDV	4	K	1-16	1	QQYNSYPLT	5	
	SA8-142L	IgG1	1-24	6	ATDRKYYYYGMDV	4	L	3-21	3	QVWDRNDHWV	20	

mAb expression ID	mAb clone ID	Ig class isotype	VH	JH	CDR H3	SHM VH	light chain	VK/VL	JK/JL	CDR K3/L3	SHM VK/VL	criteria for expression
	SA8-143	IgM	3-23	3	AKDVGYCSSTSCPKAFDI	1	K	1-33	3	QQYDNLPRLDFT	0	
	SA8-145[39]	IgG1	4-59	4	ARDLKGTTCYDY	22	K	1-33	4	QQYGNLPAH	17	
	SA8-146[40]	IgM	4-59	6	ARDPGTWMYYYDGMDV	14	K	1-33	4	RH	18	
	SA8-147[40]	IgM	4-59	6	ARDPGTWMYYYDGMDV	16	K	1-33	4	RH	16	
	SA8-148[25]	IgM	3-66	6	ARDLAVYGVDV	3	L	3-21	2	QVWDSSSDHPVV	0	
	SA8-150	IgM	3-48	6	ARAITILWYGMDV	2	L	2-23	1	CSYAGSSTFYV	3	
	SA9-183	IgG1	1-2	6	ARVDTTGTTFWLYYYYGMDV	0	K	3-11	3	HQRSNWPFT	6	
	SA9-184	IgM	3-7	6	ARAWGALGYYDSSGYYYDYSYYGMDV	5	L	2-14	2	SSYTSSSGV	9	
	SA9-186	IgM	3-7	5	REGGAPGAT	18	K	3-20	4	QQYDRFSLT	11	
	SA9-187	IgG2	4-61	2	ARDSNTGWFQNWYFDL	17	L	2-14	2	SSFTSITTHVI	9	
	SA9-188	IgG1	1-69	5	ARGGLWFGELLWFDP	0	K	1-39	1	QQSYSTPWT	6	
	SA9-189	IgM	4-34	2	ARGKAIFGVVIIYWYFDL	4	K	1-39	2	QQSYSTPYT	3	
	SA9-191	IgM	4-34	6	ARVGYSGYPHGLGLYYYYGMDV	8	K	1-39	1	QQSYSTPWT	9	
	SA9-192	IgA1	4-31	4	ARLVVPAGFAYYFDY	1	L	1-51	2	GTWDSSLSAVV	2	
	SA9-195	IgG1	3-30	4	ASPPQGGYDWVVDY	3	L	2-11	3	CSYAGTNWV	3	
	SA9-197	IgG1	5-51	4	ARQAVGATGDFDY	0	L	6-57	2	QSYDSSNHVV	1	
	SA9-200	IgG1	3-48	6	ASNVVNGFRNYYGMDV	1	K	3-20	1	QQYGSSPWT	6	
	SA9-201	IgA1	3-49	4	TRAVFCTSTDCYVGTGGHFDY	19	K	1-27	3	QKCNSAPQT	18	
	SA9-202	IgM	3-30	4	ARGYTGSTEGC	12	K	3-20	2	QQYNSSPYT	17	
	SA9-203	IgG1	4-30-4	6	AGGVWGRLGPAWGVPETLLFSLWIHLHL HQGPIGLPPGTLLQGAPS	1	L	1-51	2	GTWDSSLSAGRVV	5	
	SA9-205	IgM	3-23	5	AKAGTSSSYGLSWFDL	19	L	2-14	1	SSYTSSNTLV	6	
	SA10-102	IgG1	5-51	4	ARGIAVAGAPYFDY	0	L	1-44	1	AAWDDSLNGYV	0	
	SA10-103	IgG1	3-15	4	TTSGSYYYDSSGPTDDFDY	0	K	4-1	1	SNIIVLRGR	3	
	SA10-104K	IgM	3-20	4	ARHDSSGYYHPPGDY	0	K	1-5	2	QQYDSYYT	8	
	SA10-104L	IgM	3-20	4	ARHDSSGYYHPPGDY	0	L	2-23	2	CSYAGSSTSHVV	2	
	SA10-106	IgM	4-59	5	ARDHPPYLKLVRP	1	L	2-8	1	SSYAGSNNFA	2	
	SA10-108	IgG1	4-39	1	ARHPDGDYHAEYFQH	1	K	3-15	1	QQHKNCPRT	9	
	SA10-112	IgG1	3-15	4	TTDITIFGVVIGGFDY	4	L	6-57	2	QSYDSSNGDVV	0	
	SA10-113	IgG1	1-69	3	ARAVEMATINDAFDI	1	L	2-8	1	SSHAGSDTPFV	16	
	SA10-114	IgM	1-58	4	AAEGGSYVLVTGTLTT	1	L	2-14	2	SSYTSSSVV	2	
	SA10-116	IgM	3-15	2	VKFYGDCPRYFDL	13	K	1-33	1	QQSDNPPRT	13	
	SA10-117	IgG1	3-21	6	ASGGYCSGGSCPPFVYYYYGMDV	0	K	1-27	1	KSITVPPGR	3	
	SA10-118	IgA1	3-7	4	VRALGSGSY	10	L	1-44	1	AAWDDSLSGFV	7	
	SA10-119	IgM	4-61	4	ARDRAARPGSDYFDY	0	L	1-51	2	GTWDSSLSAGV	4	
	SA10-123	IgG1	3-21	4	ARIPAGYSGYDYDYFDY	0	L	2-14	3	SSYTSSSTR	5	
	SA10-125[6]	IgG3	1-58	3	AAPNCSGGSCYDAFDI	0	K	3-20	1	QQYGSSPWT	2	
	SA10-127	IgG1	3-23	3	AKDLDGDYRSFGAFDI	0	L	2-8	1	SSYAGSFYV	2	
	SA10-128	IgM	1-2	4	ERSLWFGIRL	17	K	4-1	2	QQYYTTPNT	12	
	SA10-131	IgM	1-18	4	ARVPYYYDSSGYTVFEYYFDY	2	L	1-40	2	QSYDSSLSGDVV	1	
	SA10-135	IgM	5-51	4	ARAITFGGVIEFDY	0	L	1-47	2	AAWDDSLSGVV	0	
	SA10-144	IgG1	1-18	6	ARFFVTMVQGENYYYGMDV	1	L	9-49	2	GADHGSGSNFVVV	1	
	SA10-147	IgM	1-18	5	ARTAVTNWFDP	9	K	1-12	4	QQANSFPRT	7	
	SA13-136	IgM	3-9	6	AKDIGHIREGYGMDV	1	L	2-14	2	SSYTSSSTLV	2	
	SA13-137	IgG1	3-9	4	AKDITGSYGDYFDY	1	L	3-21	1	QVWDSSGDHYV	3	
	SA13-140[15]	IgG3	3-13	6	ARGSDSSGYYYVRSYYYYYMDV	0	K	1-39	1	NRVTVPPPGR	5	
	SA13-143[41]	IgG1	4-61	5	AREVAPTPGLIWFDP	1	L	2-14	2	SSYTSSSTDVV	4	
	SA13-149	IgA2	4-61	4	ARVPVGSGDYYFDY	3	K	3-15	1	QQYKNWPRT	4	

mAb expression ID	mAb clone ID	Ig class isotype	VH	JH	CDR H3	SHM VH	light chain	VK/VL	JK/JL	CDR K3/L3	SHM VK/VL	criteria for expression
	SA13-150	IgM	4-39	4	ARHGVGQQLVVGEYYFDY	3	L	2-23	3	CSYAGSSTWV	3	
	SA13-151[41]	IgG1	4-61	5	AREVAPTPGLIWFDP	1	L	2-14	2	SSYTSSSTDVV	4	
	SA13-154[41]	IgG1	4-61	5	AREVAPTPGLIWFDP	1	L	2-14	2	SSYTSSSTDVV	4	
	SA13-161[3]	IgM	5-51	6	ARSASGSYGGYYYYYMDV	0	L	1-44	3	AAWDDSLNGPV	0	
	SA14-168	IgM	1-69	2	ARDLYVGDVNNHGGYFDL	0	K	3-11	1	QQRSNWPRT	0	
	SA14-170[51]	IgM	4-31	5	ARRREYSSTSWFDP	16	L	1-51	3	GTWDNSLSAWV	7	
	SA14-172[24]	IgM	3-48	4	VRVGHPDTLFAVDY	13	K	3-15	2	QQYNNWPRYS	4	
	SA14-174	IgM	4-39	4	ARHRSGSYGRDYFDY	1	L	1-51	2	GTWDSSLTHVV	2	
	SA14-175[24]	IgG1	3-48	4	VRVGHPDTLFGVDY	11	K	3-15	2	QQYNNWPRYS	6	
	SA14-177[24]	IgG1	3-48	4	VRVGHPDTLFGVDY	15	K	3-15	2	QQYNNWPRYS	4	
	SA14-179[24]	IgM	3-48	4	ARVGHPDTLFAVDH	13	K	3-15	2	QQYNNWPRYS	3	
	SA14-180[46]	IgM	3-74	4	ARGSGNFGFDY	8	L	1-40	3	QSYDTSLSDYV	5	
	SA14-185[24]	IgA1	3-48	4	ESRTSRYPFWSGL	30	K	3-15	2	QQYNNWPRYS	8	
	SA14-188	IgG1	3-9	4	AKGIWSGESIAARPGFDY	2	K	3-15	2	QQYNNWYS	2	
	SA15-101[42]	IgG2	4-61	4	ARVVAASPGDFYFDY	5	L	1-47	1	AAWDDSLSGYV	0	
	SA15-102	IgM	1-3	4	ARPRREWLLYYFDY	2	K	3-11	1	QQRSNWPQT	2	
	SA15-104[43]	IgM	1-46	4	ARGGLGSGSGSSEDKY	25	K	1-27	1	QKYNSAPWT	6	
	SA15-105[43]	IgM	1-46	4	ARGGLGSGSGSSEDKY	25	K	1-27	1	KSITVPRGR	5	
	SA15-108[42]	IgM	4-61	4	ARVVAATPGDYYFDY	4	L	1-47	1	AAWDDSLSGYV	0	
	SA15-109[43]	IgM	1-46	4	ARGGLGSGSGSSEDKY	25	K	1-27	1	QKYNSAPWT	1	
	SA15-110	IgM	1-69	4	ARVGYYYDSSGYPSYEYYFDY	1	L	1-40	2	QSYDSSLSGHVV	1	
	SA15-113	IgG1	1-69	1	ARNGSPYYYDNSGYYGVDEDFQH	0	L	1-40	2	QSYDSSLSGSV	1	
	SA15-114[46]	IgM	3-74	4	VQGYGDYSGNY	0	L	1-40	3	QSYDSSLSGWV	1	
	SA15-115	IgM	5-51	6	ARHVFGRGGGYYYYGMDV	0	L	1-44	2	AAWDDSLNGVV	0	
	SA15-117[45]	IgA1	4-31	4	ARDRGYTYGPFPLFDY	18	L	2-14	3	SSYTSTTTV	20	
	SA15-118	IgG1	4-39	5	ARLRGPLSPREDYRVWFDP	3	L	3-21	2	QVWDSSSGVV	0	
	SA15-120[45]	IgA1	4-31	4	ARDRGYTYGPFPLLDY	20	L	2-14	3	SSYTSTSTV	15	
	SA15-122	IgM	3-9	4	AKDILAIPGLFDT	13	L	4-69	7	QTWGTLGV	13	
	SA15-124[44]	IgM	3-20	4	TRGHGTHPRHYFDY	17	K	3-20	3	QQYGTSPLI	11	
	SA15-125[44]	IgM	3-20	4	VRGHGIHPRHYFDY	19	K	3-20	3	QQYGSSPLT	13	
	SA15-183[45]	IgA1	4-31	4	ARDRGYTYGPFPLLDY	20	L	2-14	3	SSYTSTSTV	15	
	SA15-190	IgM	4-4	5	AYVAAAGLNWFDP	8	K	1-39	2	QQSYNTPRT	10	
	SA15-192	IgM	4-61	4	ARVVAATPGDYYFDY	6	K	3-15	1	QQYKNWPRT	5	
	SA15-193	IgM	1-18	4	ARDPSNSSGRLVYFDY	18	K	3-11	2	QQRSSRPCT	5	

[(1) - (51)] Identical superscript numbers indicate mAbs that belong to clonally expanded clones when isolated from the same donor, or mAbs that belong to a public clonotype when isolated from multiple donors of our cohort.

[a-f] Letters indicate criteria on which the respective mAb was selected for expression: a) clonally expanded mAbs with the donor, (b) mAbs of public clonotypes within our dataset, (c) mAbs of public clonotypes found both in our dataset and CoV-AbDab, (d) mAbs of VH3-53/3-66 genes, (e) mAbs of VH genes with strongest enrichment in our dataset (VH1-58, VH3-13, VH3-30, VH4-39) or (f) randomly selected mAbs of other VH genes and that appeared only once.

Table S3. Sequences of antibodies strongly reactive[a] to RBD Beta

mAb expression ID	heavy chain variable sequence	light chain variable sequence
CS1 (VH3-30)	QVQLVESGGGVVQPGRSLRLSCAASGFPFSTYGMHWVRQAPGKGLEW VAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CAKDFQYVAATHSPYYYYGMDVWGQGTTVTVSS	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLACYQQKP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYYCQQYGSSPGVTFGPGTKVDIK
CS4 (VH3-30)	QVQLVESGGGVVQPGRSLRLSCAASGFTFGSYGMHWVRQAPGKGLEW VAVISDDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CAKDFGSTGTTLGYYGMDVWGQGTTVTVSS	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLP GTAPKLLIYRNNQRPSGVPDRFSGSKSGTSASLAISGLRSE DEADYYCAAWDDSLSGWVFGGGTKLTVL
CS8 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLECI GSIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLTSVTAADTAVYYCAR HEGSTSPLMVKNYFDYWGQGTLVTVSS	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKP GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQANSFPITFGQGTRLEIK
CS12 (VH3-30)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEW VAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CAKSGAPAAMRGYYYYGMDVWGQGTTVTVSS	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGHYPYWFQQ KPGQAPRTLIYDTSNKHSWTPARFSGSLLGGKAALTLSGA QPEDEADYYCLLSYSGAREVFGGGTKLTVL
CS15 (VH3-30)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEW VAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CAKAPYAYCSSTSCYADYYYGMDVWGQGTTVTVSS	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQ HPGKAPKLMIYEVSNRPSGVSNRFSGSKSGNTASLTISGLQ AEDEADYYCSSYTSSSVVFGGGTKLTVL
CS23 (VH3-53)	EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNYMNWVRQAPGKGLEW VSVIYSGGSTYYADSVKGRFTISRHNSKNTLYLQMNSLRAEDTAVYYC ARGTAMAYGMDVWGQGTTVTVSS	SYELTQPPSVSVAPGQTARITCGGNNIGGQSVHWYQQKPG QAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGD EADYYCQVWDSSSDHVVFGGGTKLTVL
CS24 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWI GSIYYSGSTYYNPSLTSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARQ FWTRPPSVWFDPWGQGTLVTVSS	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNYYVSWYQQL PRTAPKLLIYDNNERPSGIPDRFSGSKSGTSATLAITGLQTG DEADYYCGTWDSSLSAGVFGGGTKLTVL
CS26 (VH3-15)	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEW VGRIQSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAV YYCTTDPNQQPPRGYYFYYGLDVWGQGTTVTVSS	QTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGHYPYWFQQ KPGQAPMTLICDTSNKHSWTPARFSGSLLGDKAALTLSGA QPEDEAEYYCLLSYSGAPVVFGGGTKLTVL
CS27 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWI GSIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR GIAARPGDWHFDLWGRGTLVTVSS	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQL PGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQT GDEADYYCGTWDSSLSRGVFGGGTKLTVL
CS29 (VH3-7)	EVQLVESGGGLVQPGGSLRLSCAASRFTFSNYWMSWVRQAPGKGLEW VANIKQDGSEKYCVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYY CARALSMVRGVIIPPYFDYWGQGTLVTVSS	NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQR PGSAPTTVIYEDNQRPSGVPDRFSGSIDIYSNSASLTISGLK TEDEADYYCQSYDSSNHWVFGGGTKLTVL
CS30 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGDSISSSSYYWGWIRQPPGKGLEWI GSFYYSGSTYYNPSLKSRVTISVDTSKNLFSLKLSSVTAADTAVYYCAR RGWLRGYFDLWGRGTLVTVSS	NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQR PGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLK TEDEADYYCQSYDSTNHVVFGGGTKLTVL
CS31 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWI GSFYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAT QLWLRSNFDSWGQGTLVTVSS	NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWHQQR PGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLK TEDEADYYCQSYDSGNVVFGGGTKLTVL
CS34 (VH3-7)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEW VANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNILRAEDTAVYY CARSQSTSWHDYWGQGTLVTVSS	NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQR PGSAPTTVIYEDNQRPSGVPDRFSGSIDTSSNSASLTISGLK TEDEADYYCQSYDNNNHVVFGGGTKLTVL
CS37 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGCIRQPPGKGLECIG SIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARH VGPYSGYDKNNWFDPWGQGTLVTVSS	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKP GQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPED FAVYYCQQRSNWPLTFGGGTKVEIK
CS38 (VH3-13)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEW VSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYC ARDLTQDWYFDLWGRGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTHFTLAISSLQPEDF ATYYCQQSYSTPPITFGQGTRLEIK
CS39 (VH3-15)	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEW VGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAV YYCTTDKARNYYDSSGYEHDAFDIWGQGTMVTVSS	DIQMTQSPSSLSASVGDRVTITCRASQSISSFLNWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQSYSTLITFGQGTRLEIK
CS40 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWI GSIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR HAAPRPGDSWFDPWGQGTLVTVSS	DIQMTQSPSSVSASVGDRVTITCRASQAFSSWLAWYQQKP GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQANSFPTFGQGTRLEIK
CS41 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLECI GSIHYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR HAGPYSSSWIANWFDPWGQGTLVTVSS	DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPG KAPKLLIYAASTLQSGVPSRFSGSGSGTELTLTISSLQPEDF ATYYCQQLNSYPLTFGGGTKVEIK
CS42 (VH3-15)	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMNWVRQAPGKGLEW VGRIRSKTDGGTPDYAAPLKGRFTISRDDSKNTLYLQMNSLKTEDTAVY YCTTDSLDVGGGSYVNFDYWGQGTLVTVSS	DIQMTQSPSSLSVSVGDRVTITCQASQDISNYLNWYQQKP GKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPED IATYYCQQYDNLPLTFGGGTKVEIK
CS43 (VH4-39)	QLQLQESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWI GTIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR RLGPRGPFDNHGNHFDYWGQGTLVTVSS	DIQLTQSPSFLSASVGDRVIITCRASQGISSYLAWYQQKPG KAPKLLIYAASTLQSGVPSRFSGSGSGTEFTLTVSSLQPED FATYYCQQLNSYPWTFGQGTKVEIK
CS44 (VH1-58)	QVQLVQSGPEVKKPGTSVKVSCKASGITFTSSAVQWVRQARGQRLEWI GWIVVGSGNTNYAQKFQERVTITRDMSTSTAYMELSSLRSEDTAVYYC AAPYCSGGTCHDGFDIWGQGTMVTVSS	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYYCQQYGSSPWTFGQGTKVEIK
CS45 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWI GSIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQL PGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLGITGLQT

mAb expression ID	heavy chain variable sequence	light chain variable sequence
	QSSPKLGDDAFDIWGQGTMVTVSS	GDEADYYCGTWDSSLSVVVFGGGTKLTVL
CS46 (VH3-30)	QVQLVESGGGVVQPGRSLRLSCAASGFPFSNYGMHWVRQAPGKGLEW VAVISYDGSSQYYADSVKGRFTISRDNSKNTLYLQMNSLRGDDTAVYY CAKDRSVGATTSQYNYYYGMDVWGQGTTVTVSS	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQF PGTAPKLLIYDNDKRPSGIPDRFSGSKSGTSATLGITGLQT GDEADYYCGTWETSLSAEVFGGGTRLTVL
CS49 (VH3-53)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSYYMNWVRQPPGKGLEWV SVIYNGGNAYYADSVKGRFTISRDNSRNTLYLQMNSLRAEDTAVYYCA RGKWLRGAFDIWGQGTMVTVSS	NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQR PGSAPITVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLKT EDEADYYCQSYDSSDLWVFGGGTKLTVL
CS52 (VH7-4-1)	QVQLVQSGSELKKPGASVKVSCKASGYSFTSHAMNWVRQAPGQGLEW MGWINTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQISSLKAEDTAVYYC ARTSGWSGPSYGMDVWGQGTTVTVSS	QAVVTQEPSLTVSPGGTVTLTCASSTGAVTSGYYPNWFQ QKPGQAPRALIYSISNKHSWTPARFSGSLLGGKAALTLSG VQPEDEAEYYCLLYFGGAQYVFGTGTKVTVL
CS54 (VH3-53)	EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNYMNWVRQAPGKGLEW VSVIYSGGSTFYADSVKGRFTISRHNSKNTLYLQMSSLRAEDTAVYYCA RDLAVYGMDVWGQGTTVTVSS	EIVLTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQIP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYYCQQYDSSLITFGQGTRLEIK
CS56 (VH4-4)	QVQLRESGPGLAKPSGTLSLTCAVSGGSITSIYWWSWVRQPPGKGLEWI GEIYHSGSTNYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYFCASA PGTPWFDYWGQGTLVTVSS	QSALTQPASVSGSPGQSITISCTGTSSDVGRYNYVSWYQQ HPGKAPKLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGL QAEDEADYYCSSYTSSSTLYVFGTGTKVTVL
CS59 (VH1-58)	QVQLVQSGPEVKKPGTSVKVSCKASGFTFTSSAVQWVRQARGQRLEWI GWIVVGSGNTNYAQKSQERVTITRDLSTRTAYMELSSLRSEDTAVYYC AAPYCSGGSCFDAFDMWGQGTMVTVSS	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYYCQQYGSSLFTFGPGTKVDIK
CS65 (VH3-30)	QVQLVESGGGVVQPGRSLRLSCAASGFTFGSYGMHWVRQAPGKGLEW VAVISYDGSKKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CAKDLDIVLMVYAIPRGYYGMDVWGQGTTVTVSS	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQ HPGKAPKLMIYEVSKRPSGVSNRFSGSKSGNTASLTISGLQ AEDEAAYYCSSYTSSSPPVVFGGGTKLTVL
CS74 (VH4-31)	QVQLQESGPGLVKPSQTLSLTCTVSGDSISSGGYYWSWIRQHPGKGLE WIGYIYYSGSTYYNPSLKSRVTISVDTSNNQFSLKLSSVTAADTAVYFCA RDYGGNQNYFGYWGQGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCQASQDITNSLNWYQQKP GKAPKLLIYDASNLETGVPSSFSGSGSGTDFTFTISSLQPED IATYYCQQYDNLPLTFGGGTKVEIK
CS82 (VH3-53)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSHYMSWVRQAPGKGLEWV SVLYSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA RDLHSSGPFDAFDIWGQGTMVTVSS	DIQMTQSPSSLSASVGDRVAITCQASQDISNYLNWYQQKP GKAPKLLIYDASNLETGVPSRFSGGSGTDFTFTISSLQPE DIATYYCQQYDIVGGGTKVEIK
CS84 (VH4-38-2)	QVQLQESGPGLVKPSETLSLTCTVSGYSISSAYYWGWIRQPPGKGLEWI GSFFHSGSTYYNPSLKSRVTITVDTSKKQFSLKLSSVTAADTAVYYCAR DDYGDYAVSYWGQGTLVTVSS	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQ LPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQ AEDEADYYCQSYDSSLSALYVFGTGTKVTVL
CS85 (VH3-11)	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWV SYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCA RELLLLGYCSGGSCYPVGPDYWGQGTLVTVSS	NFMLTQPHSVSESPGKTVTISCTGSSGSIASNYVQWYQQR PGSAPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGLK TEDEADYYCQSYDSSNHWVFGGGTKLTVL
CS87 (VH3-13)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMYWVRQATGKGLEW VSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYC ARALYGSGSYSTQAGYYYGMDVWGQGTTVTVSS	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQSYRAFTFGPGTKVDIK
CS88 (VH1-18)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEW MGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVY YCARDYDYVWGSYPSACCYWGQGTLVTVSS	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQ HPGKAPKLMIYEVSNRPSGLSNRFSGSKSGNTASLTISGLQ AEDEADYYCSSYTSSTNWVFGGGTKLTVL
CS89 (VH3-53)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWV SLIYSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR DLSVAGGMDVWGQGTTVTVSS	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTIGRLEPED FAVYYCQQYGSSPPITFGQGTRLEIK
CS90 (VH3-13)	EVQLVESGGGLVRPGGSLRLSCAASGFTFSSYDMHWVRQGTGKGLEW VSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYC ARVRPTMTKGFDWYFDLWGRGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCRASQSISSFLNWYQQKPG KAPNLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQSYNTLGTFGQGTKVEIK
CS91 (VH3-53)	EVQLVESGGGLIQPGGSLRLSCAASGLTVSSNYMNWVRQAPGKGLEW VSLIYSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARWAGADGMDVWGQGTTVTVSS	EIVLTQSPGTLSLSPGERATLSCRASQSVSSTYLAWYQQKP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTITRLEPED FAVYYCQQYGSSQYTFGQGTKLEIK
CS92 (VH3-23)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSVISGSDGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC AKDFVVVVAARSHDDYYFDYWGQGTLVTVSS	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKP GKAPKLLIYKASSLESGVPSRFSGSGSGTEFTLTISSLQPDD FATYYCQQYKNFPLTFGGGTKVEIK
CS99 (VH1-69)	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEW MGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCA TQGGRFYCSGGSCYRYYFDYWGQGTLVTVSS	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYYCQQYGSSPLTFGEGTKVEIK
CS102 (VH1-58)	QVQLVQSGPEVKKPGTSVKVSCKASGFTFPSSAVQWVRQARGQRLEWI GWIVVGSGNTNYAQKFQERVTITRDMSTSTAYMELSSLRSEDTAVYYC AAPHCGGGSCYDGFDIWGQGTMVTVSS	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYFCQQYGSSPWTFGQGTKVEIK
CS103 (VH3-13)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEW VSTIGTSGDTYYPGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYC ARGGGDGYNLGLWYFDLWGRGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQRKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQSYSNPPPTFGPGTKVDIK
CS111 (VH3-64D)	EVQLVESGGGLVQPGGSLRLSCSASGFTFSSYAMHWVRQAPGKGLEYV SSISSNGGSTYYADSVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYCV KDVTVDTAMVTIFDNWGQGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDF ATYYCQQSYSTPTFGGGTKVEIK
CS112 (VH3-15)	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMTWVRQAPGKGLEW VGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNMLYLQMNSLKTEDTAV YYCTTDPGYTYSPAYWGQGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCRAGQSISSYLNWYQHKP GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQSYSTLFTFGPGTKVDIK

mAb expression ID	heavy chain variable sequence	light chain variable sequence
CS114 (VH1-69)	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYGISWVRQAPGQGLEW MGGIIPIFGTAYYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCA SSSPLLRYFDWPHEAIFDYWGQGTLVTVSS	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKP GQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPED FAVYYCQQRSNWSGITFGQGTRLEIK
CS115 (VH1-69)	QVQLVQSGAEVKRPGSSVKVSCKASGGTFSNYGFSWVRQAPGQGLEW MGGTSPLFHTPNYVQKFQDRVTITADESTTSVYMELNSLTSDDTAVYY CACSSGRWGVLGNYFDYWGQGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCQASQDITDYLNWYQQKP GQAPKLLIYDASNLETGVPSRFSGSGSGTDFTLTISSLQPED IATYYCQQYANLLTFGGGTKVEIK
CS116 (VH3-30)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEW VAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CAKGDDYGDLFYYGMDVWGQGTTVTVSS	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWY LQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCMQALQRTLTFGGGTKVEIK
CS117 (VH3-9)	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEW VSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYC AKDAFGDPQGLYGMDVWGQGTTVTVSS	DIQMTQSPSSLSASVGDRVTITCRASQSITSYLNWYQQKP GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQSYSTPLTFAQGTRLEIK
CS120 (VH3-30)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEW VAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNGLRAEDTAVYY CAKVLGSYCSGGSCYGGSFDYWGQGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKP GKAPKVLIYDASSLEAGVPSRFSGSGSGTDFTFTISSLQPED IATYYCQQYDNLPSFGGGTKVEIK
CS123 (VH4-59)	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIA YIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARS RGYNYGLGLGWFDPWGQGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCQASQDITNYLNWYQQKP GKAPKLLIYDASNLERGVPSRFSGSGSGTDFTFTISSLQAE DIATYYCQQYDDVPFTFGPGTKVDIK
CS124 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWI GSIHYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSMTAADTAVYYCAR HTGYYDSSGYYRLEYFQHWGQGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLYWYQQKP GKAPKVLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPE DIATYYCQQYDNLPLTFGGGTKVEIK
CS125 (VH1-18)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEW MGWISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVY YCARDGTSHYYDSSGYYGADRNWFDPWGQGTLVTVSS	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQ LPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQ AEDGADYYCQSYDSSLSGWVFGGGTKLTVL
CS127 (VH1-58)	QVQLVQSGPEVKKPGTSVKVSCKASGFTFTSSAVQWVRQARGQRLEWI GWIVVGSGNTNYAQKFQERVTITRDMSTSTAYMELSSLRSEDTAVYYC AAPNCSGGSCYDAFDIWGQGTMVTVSS	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYYCQQYGSSPWTFGQGTKVEIK
CS129 (VH3-48)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEW VSYISSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYC ARQPREYYDFWSGYRRLFYFDYWGQGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKP GKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPED IATYYCQQYDNLPLTFGGGTKVEIK
CS131 (VH3-53)	EVQLVETGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWV SVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA RWAQQLVPSENLKPYYYYYGMDVWGQGTTVTVSS	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYYCQQYGSSPGYTFGQGTKLEIK
CS134 (VH3-23)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC AKGTQPIPDYGDFFDPWGQGTLVTVSS	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYYCQQYGSSPPCTFGQGTKLEIK
CS135 (VH3-30)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEW VAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CAKGGGWYDYKGYYFDYWGQGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKP GKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPED IATYYCQQYDNLPITFGQGTRLEIK
CS136 (VH3-48)	EVQLVESGGGLVQPGGSLRLSCAASGFIFNNYEMNWVRQAPGKGLEWI SYISSGGTTVYYADSVKGRFTISRDNAKNSLYLQMSSLRAEDTALYYCV RVGHPDTLFGVDYWGQGTLVTVSS	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKP GQAPSLLIYGASTRATGIPARFSGSGSGTEFTLTISSLQSED FAVYYCQQYNNWPRYSFGQGTKLEIK
CS139 (VH3-48)	EVQLVESGGGLVQPGGSLRLSCAASGFTFNNYEMNWVRQAPGKGLEW VSYISSGGTTMYYADSVKGRFTISRDNAKNSLYLEMNSLRAEDTALYY CARVGHPDTLFGVEYWGQGILVTVSS	EIVMTQSPATLSVSPGERATLSCGASQSISSTLAWYQHKPG QAPRLLIYGASARATGIPARFSGSGSGTEFTLTISSLQSEDF AVYYCQQYNNWPRYSFGQGTKLEIK
CS143 (VH1-58)	QVQLVQSGPEVKKPGTSVKVSCKASGFTFSSSAVQWVRQARGQRLEWI GWIVVGSHNTNYAQKFQERVTITRDMSTSTAYMELSSLTSEDTAVYYC AAAIIASAAPDYWGQGTLVTVSS	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKP GQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPED FAVYYCQQRSNWPPYTFGQGTKLEIK
CS145 (VH1-46)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLE WMGIINPSGGSTSYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVY YCARGGIVPAATLLFDPWGQGTLVTVSS	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKP GKAPKLLIYKASSLESGVPSRFSGSGSGTEFTLTISSLQPDD FATYYCQQYNSYSCSFGQGTKLEIK
CS153 (VH1-58)	QVQLVQSGPEVKKPGTSVKVSCKASGFTFTSSAVQWVRQARGQRLEWI GWIVVGSGDTNYTQKFQERVTITRDMSTSTAYMELSSLRSEDTAVYYC AAPYCSGSSCLDGFDIWGQGTMVTVSS	EIVLTQSPDTLSLSPGERATLSCRASQSVRSSYLAWYQQKP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLAISRLEPED FAVYYCQQYGSSPWTFGQGTKVEIK
CS155 (VH3-23)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEW VSAISGSGGNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CAKDTYYDIFPDVFDIWGQGTMVTVSS	QSALTQPASVSGSPGQSITISCAGTSSDLGGYYYVSWYQH HPGKAPKLMIYEVSNRPSGISNRFSGSKSGNTASLTISGLQ AEDEADYYCSSYTSSSTLPVFGTGTKVTVL
CS156 (VH3-13)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEW VSAIGNAGDTYYPASVKGRFTISRENARNSLYLQMNSLRAGDTAVYYC ARVRPTMTKGFDWYFDLWGRGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKP GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQSYNTLGTFGQGTKVEIK
CS157 (VH3-13)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQGTGKGLEW VSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQMSSLRAGDTAVYYC ARGHFYGLIGYMDVWGKGTTVTVSS	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKL GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQSYSTPPLTFGGGTKVEIK
CS158 (VH3-13)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEW VSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYC ARAAYDILTGYYRGMDVWGKGTTVTVSS	DIQMTQSPSSLSASVGDRVTITCRASQNISSYLNWYQQKP GKAPKLLIYAASSLQSGVPSRFSGSGSGIDFTLTISSLQPED FATYYCQQSYNIASTFGQGTKVEIK
CS161 (VH3-66)	EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEW VSVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARDLAVYGMDVWGQGTTVTVSS	SYELTQPPSVSVAPGQTARITCGGNNIGSNSVHWYQQKPG QAPVLVVYDDSDRPSGIPERFSGSKSGNTATLTISRVEAGD EADYYCQVWDSSSDHPVVFGGGTKLTVL

mAb expression ID	heavy chain variable sequence	light chain variable sequence
CS163 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSRYYWGWIRQPPGKGLEWI GSIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR QVAWLPRDDYFDYWGQGTLVTVSS	QSALTQPPSASGSPGQSVTISCTGTSSDVGFYNYVSWYQQ HPGKAPKLMIYEVSKRPSGVPDRFSGSKSGNTASLTVSGL QAEDEADYYCSSYAGSNNYVVFGGGTKLTVL
CS165 (VH5-51)	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEW MGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC ARHMSGTHSSGWYERWFDPWGQGTLVTVSS	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLP GTAPKLLIYSNNQRPSGVPDRFSGSKSGTSASLAISGLQSE DEADYYCAAWDDSLNGPVFGGGTKLTVL
CS167 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWI GSIYYSGSTYYTPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARF TRFAGLYYFDYWGQGTLVTVSS	QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQQ HPGKAPKLLIYEVSKRPSGVPDRFSGSKSGNTASLTVSGLR ADDEADYYCSSYAGTVLFGGGTKLTVL
CS169 (VH3-33)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEW VAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMKSLRAEDTAVY YCARDRFYDYSSSGYSLDAFDIWGQGTMVTVSS	QSVLTQPPSVSEAPRQRVTISCSGSSSNIGNNAVNWFQQLP GKAPKLLIYYDDLLPSGVSDRFSGSKSGTSASLAISGLQSE DEADYYCAAWDDSLNAWVFGGGTKLTVL
CS170 (VH4-39)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWI GSIYYSGGTYSNPSLKSRVTISVDTSKNQLSLKLSSVTAADTAVYYCAR EVAPIKQWLVSYFDYWGQGTLVTVSS	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVQWYQQ LPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQ AEDEADYYCQSYDSSLSGLVFGGGTKLTVL
CS171 (VH3-30)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLQW VAIISYDESSKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYC AKDPPQFAVAGTGYFDYWGQGTLVTVSS	SYELTQPPSVSVAPGQTARITCGGNNIGSKNVHWYHQKPG QAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGD EADYYCQVWDSSSDPWVFGGGTKLTVL
CS172 (VH3-30)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEW VAFISYDGDDKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYF CAKAVYSYAYAVLYFDYWGQGTLVTVSS	NFMLTQPHSVSESPGKTVTISCTGSSGSFASNSVQWYQQR PGSAPTTMIYEDNHRPSGVPDRFSGSIDSSSNSASLTISGLK TEDEADYYCQSYDYNNHVVFGGGTKLTVL
CS173 (VH3-13)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEW VSAIGTAGDTYYPGSVKGRFTISRENAKNSLYLQMNSLRAEDTAVYYC ARGGAVIPVWYFDLWGRGTLVTVSS	DIQMTQSPSSLSASVGDRVTITCRASQSIGSYLNWYQQKP GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPED FATYYCQQSYSHPGITFGPGTKVDIK
CS175 (VH1-69)	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRNAISWVRQAPGQGLEW MGGIIPIFGTAHYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCA RREYSSTDWFDPWGQGTRVTVS	SYELTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPG QAPVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGD EADYYCQVWDSTSDHPGYVFGTGTKVTVL
CS176 (VH3-66)	EVQLVESGGGLVQPGGSLRLSCAASGLIVSSNYMSWVRQAPGKGLEW VSVLYSGGTTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC ARWGRVGATGLAFDIWGQGTMVTVSS	SYELTQPPSVSVAPGQTARISCGGNNIGSKSVHWYQQKPG QAPVLVVYDDSDRPSGIPERFSDSNSGNTATLTISRVEAGD EADYYCQVWDSSSDHHYVFGTGTKVTVL
CS179 (VH4-31)	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGAHYWSWIRQHPGKGLE WIGYIYYSGGTYYNPSLKSLVTISVDTSKNHFSLKLSSVTAADTAVYYC ARTTAPRPGSSWFDPWGQGTLVTVSS	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQL PGTAPKLLIYDNNKRPSGIPDRFSGSKSGTSATLAITGLQT GDEADYYCGTWDNTLSPGRGVFGGGTKLTVL
CS180 (VH1-58)	QVQLVQSGPEVKKPGTSVKVSCKASGFTFSRSAVQWVRQARGQRLEWI GWIVVGSGNTNYAQKFQERVTITRDMSTSAAYMELSSLRSEDTAVYYC AAPACSSTRCYDGFDIWGQGTMVTVSS	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKP GQAPSLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED FAVYYCQQYGSSPWTFGQGTKVEIK
CS181 (VH1-18)	QVQLVQSGAEVKKPGASVKVSCRASGYTFTSYGITWVRQAPGQGLEW MGWISVDNGNTKYAEKLQGRVTMTTDTSTSTAYMELRSLGSDDTAVY YCARDGGWTGIMGAINFDYWGQGTLVTVSS	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWCQQLP GTAPKLLIYRNNQRPSGVPDRFSGSKSGTSASLAISGLRSE DEADYYCATWDDSLSGWVFGGGTKLTVL
CS182 (VH3-53)	EVQLVETGGGLIQPGGSLRISCAASGLTVSSNYMNWVRQAPGKGLEWV SVIYSGGSTFYADSVKGRFTISRDNSRNTLYLQMNSLRAEDTAVYYCAR DLITYGMDVWGQGTTVTVSS	DIQLTQSPSFLSASVGDRVTITCRASQGINSYLAWYQQKPG KAPNLLIYAASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDF ATYSCQHLLTFGGGTKVEIK

[a] Strong binding to RBD Beta was defined as detectable binding in an RBD Beta ELISA at 10 ng/ml.

Table S4. X-ray data collection and refinement statistics

Data collection			
	CS23 + Beta RBD	CS44 + Beta RBD + COVA1-16	CV07-287 + wildtype RBD + COVA1-16
Beamline	ALS 5.0.1	SSRL 12-1	SSRL 12-1
Wavelength (Å)	0.97741	0.97946	0.97946
Space group	P 4_1 2_1 2	P 2_1 2_1 2_1	P 2_1 2_1 2_1
Unit cell parameters			
a, b, c (Å)	145.9, 145.9, 112.0	89.6, 121.0, 138.0	89.6, 121.5, 136.9
α, β, γ (°)	90, 90, 90	90, 90, 90	90, 90, 90
Resolution (Å) [a]	50.0–2.86 (2.96–2.86)	50.0–2.89 (2.99–2.89)	50.0–2.45 (2.54–2.45)
Unique reflections [a]	28,468 (2,764)	34,085 (3,312)	55,558 (5,448)
Redundancy [a]	24.5 (14.8)	10.3 (7.5)	12.5 (6.6)
Completeness (%) [a]	100.0 (99.5)	98.9 (99.5)	99.9 (99.2)
$<I/\sigma_I>$ [a]	9.2 (1.0)	14.0 (1.8)	19.3 (1.1)
R_{sym}[b] (%) [a]	25.6 (>100)	16.9 (83.2)	11.5 (>100)
R_{pim}[b] (%) [a]	5.2 (35.2)	5.3 (31.0)	3.3 (48.0)
$CC_{1/2}$[c] (%) [a]	98.2 (56.6)	98.4 (78.6)	97.4 (49.6)
Refinement statistics			
Resolution (Å)	46.9–2.86	40.6–2.89	40.5–2.45
Reflections (work)	28,466	34,078	55,547
Reflections (test)	2,000	1,687	2,728
R_{cryst}[d] / R_{free}[e] (%)	20.8/24.7	21.6/25.7	20.7/23.8
No. of atoms	4,783	8,323	8,512
Macromolecules	4,667	8,196	8,191
Ligands	87	89	96
Solvent	29	38	225
Average *B*-value (Å^2)	53	61	60
Macromolecules	52	61	60
Ligands	80	63	64
Solvent	34	37	51
Wilson *B*-value (Å^2)	49	57	51
RMSD from ideal geometry			
Bond length (Å)	0.003	0.005	0.003
Bond angle (°)	0.54	0.90	0.66
Ramachandran statistics[f]			
Favored	97.5	97.0	96.6
Outliers	0.00	0.19	0.00
PDB code	7S5P	7S5Q	7S5R

[a] Numbers in parentheses refer to the highest resolution shell.
[b] $R_{sym} = \Sigma_{hkl} \Sigma_i | I_{hkl,i} - <I_{hkl}> | / \Sigma_{hkl} \Sigma_i I_{hkl,i}$ and $R_{pim} = \Sigma_{hkl} (1/(n-1))^{1/2} \Sigma_i | I_{hkl,i} - <I_{hkl}> | / \Sigma_{hkl} \Sigma_i I_{hkl,i}$, where $I_{hkl,i}$ is the scaled intensity of the ith measurement of reflection h, k, l, $<I_{hkl}>$ is the average intensity for that reflection, and *n* is the redundancy.
[c] $CC_{1/2}$ = Pearson correlation coefficient between two random half datasets.
[d] $R_{cryst} = \Sigma_{hkl} | F_o - F_c | / \Sigma_{hkl} | F_o |$ x 100, where F_o and F_c are the observed and calculated structure factors, respectively.
[e] R_{free} was calculated as for R_{cryst}, but on a test set comprising 5% of the data excluded from refinement.
[f] From MolProbity (*45*).

Table S5. Hydrogen bonds and salt bridges identified at the antibody-RBD interface using the PISA program.

CS23	Dist. [Å]	RBD
Hydrogen bonds		
H:THR28[N]	3.1	ALA475[O]
H:SER31[OG]	3.3	ALA475[O]
H:ASN32[ND2]	3.2	ALA475[O]
H:TYR33[OH]	2.7	LEU455[O]
H:SER53[N]	3.3	TYR421[OH]
H:SER53[OG]	2.8	ARG457[O]
H:SER53[OG]	3.3	LYS458[O]
H:SER53[OG]	2.9	TYR473[OH]
H:GLY54[N]	2.9	TYR421[OH]
H:SER56[OG]	2.6	ASP420[OD2]
H:TYR58[OH]	3.5	THR415[OG1]
H:ARG94[NH1]	2.9	ASN487[OD1]
H:TYR100[OH]	3.9	GLN493[OE1]
H:GLY26[O]	2.7	ASN487[ND2]
H:SER31[O]	2.8	TYR473[OH]
L:GLN31[NE2]	3.2	TYR505[OH]
L:SER93[N]	3.5	TYR505[OH]
L:SER93[OG]	3.1	ASP405[OD2]
L:ASP95A[OD1]	2.9	ARG408[NH2]
L:SER93[O]	2.4	ARG408[NH2]
L:TRP91[O]	3.2	TYR505[OH]
Salt bridges		
L:ASP95A[OD2]	3.9	ARG408[NE]
L:ASP95A[OD1]	2.9	ARG408[NH2]
L:ASP95A[OD2]	3.5	ARG408[NH2]

CS44	Dist. [Å]	RBD
Hydrogen bonds		
H:CYS100B[N]	2.7	ALA475[O]
H:GLY53[O]	3.9	GLN493[NE2]
H:SER54[O]	3.6	GLN493[NE2]
H:GLY100[O]	2.7	TYR473[OH]
H:HIS100C[O]	2.9	ASN487[ND2]
H:ASP100D[OD1]	3.0	SER477[N]
H:ASP100D[OD1]	3.4	THR478[N]
H:ASP100D[OD1]	3.3	THR478[OG1]
H:ASP100D[OD2]	2.5	SER477[OG]
H:CYS100B[N]	2.7	ALA475[O]
H:GLY53[O]	3.9	GLN493[NE2]
H:SER54[O]	3.6	GLN493[NE2]
H:GLY100[O]	2.7	TYR473[OH]
H:HIS100C[O]	2.9	ASN487[ND2]
H:ASP100D[OD1]	3.0	SER477[N]
H:ASP100D[OD1]	3.4	THR478[N]
H:ASP100D[OD1]	3.3	THR478[OG1]
H:ASP100D[OD2]	2.5	SER477[OG]
H:CYS100B[N]	2.7	ALA475[O]
L:TYR32[OH]	3.4	PHE486[O]

CV07-287	Dist. [Å]	RBD
Hydrogen bonds		
H:CYS100B[N]	3.0	ALA475[O]
H:THR100[O]	3.9	TYR473[OH]
H:ASN100A[OD1]	3.8	SER477[N]
H:ASP100D[OD1]	3.0	SER477[N]
H:ASP100D[OD2]	2.6	SER477[OG]
H:ASP100D[OD1]	3.5	THR478[N]
H:ASP100D[OD1]	3.3	THR478[OG1]
H:TYR100C[O]	2.9	ASN487[ND2]
H:SER54[O]	3.6	GLN493[NE2]
H:CYS100B[N]	3.0	ALA475[O]
H:THR100[O]	3.9	TYR473[OH]
H:ASN100A[OD1]	3.8	SER477[N]
H:ASP100D[OD1]	3.0	SER477[N]
H:ASP100D[OD2]	2.6	SER477[OG]
H:ASP100D[OD1]	3.5	THR478[N]
H:ASP100D[OD1]	3.3	THR478[OG1]
H:TYR100C[O]	2.9	ASN487[ND2]
H:SER54[O]	3.6	GLN493[NE2]
H:CYS100B[N]	3.0	ALA475[O]
H:THR100[O]	3.9	TYR473[OH]
H:ASN100A[OD1]	3.8	SER477[N]

Table S6. Comparison of sequence features of Beta-elicited VH1-58 mAbs[a].

mAb		Heavy Chain				Light Chain		
ID	**patient**	**VH**	**DH**	**JH**	**CDR H3**	**VK/VL**	**JK/JL**	**CDR K3/L3**
cross-reactive mAbs								
CS44	SA5	VH1-58	DH2-15	JH3	AAPYCSGGTCHDGFDI	VK3-20	JK1	QQYGSSPWT
CS59	SA4	VH1-58	DH2-15	JH3	||||||S|--F|A||M	VK3-20	JK3	||||||LF|
CS102	SA4	VH1-58	DH2-15	JH3	|||H|G||S|Y|||||	VK3-20	JK1	|||||||||
CS127	SA10	VH1-58	DH2-15	JH3	|||N||||S|Y|A|||	VK3-20	JK1	|||||||||
CS153	SA4	VH1-58	DH2-15	JH3	|||||||SS|L|||||	VK3-20	JK1	|||||||||
CS180	SA2	VH1-58	DH2-2	JH3	|||A||STR|Y|||||	VK3-20	JK1	|||||||||
501Y-dependent mAbs								
CS143	SA4	VH1-58	DH2-2	JH4	AAAIIASAAPY	VK3-11	JK2	QQRSNWPPYT

[a]All Beta-elicited VH1-58 mAbs expressed in this study are shown.

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