SUPPLEMENTARY MATERIALS

Title: SARS-CoV-2 neutralizing antibody protects from lung pathology in a COVID-19 hamster model

Jakob Kreye[†,*], S Momsen Reincke[†], Hans-Christian Kornau, Elisa Sánchez-Sendin, Victor Max Corman, Hejun Liu, Meng Yuan, Nicholas C. Wu, Xueyong Zhu, Chang-Chun D. Lee, Jakob Trimpert, Markus Höltje, Kristina Dietert, Laura Stöffler, Niels von Wardenburg, Scott van Hoof, Marie A Homeyer, Julius Hoffmann, Azza Abdelgawad, Achim D Gruber, Luca D Bertzbach, Daria Vladimirova, Lucie Y Li, Paula Charlotte Barthel, Karl Skriner, Andreas C Hocke, Stefan Hippenstiel, Martin Witzenrath, Norbert Suttorp, Florian Kurth, Christiana Franke, Matthias Endres, Dietmar Schmitz, Lara Maria Jeworowski, Anja Richter, Marie Luisa Schmidt, Tatjana Schwarz, Marcel Alexander Müller, Christian Drosten, Daniel Wendisch, Leif E Sander, Nikolaus Osterrieder, Ian A Wilson, Harald Prüss[*]

[†] These authors contributed equally.

[*] Correspondence to:
Jakob Kreye & Harald Prüss
German Center for Neurodegenerative Diseases (DZNE) Berlin
c/o Charité – Universitätsmedizin Berlin
CharitéCrossOver (CCO), Charitéplatz 1, 10117 Berlin, Germany
Email: jakob.kreye@dzne.de; harald.pruess@dzne.de.

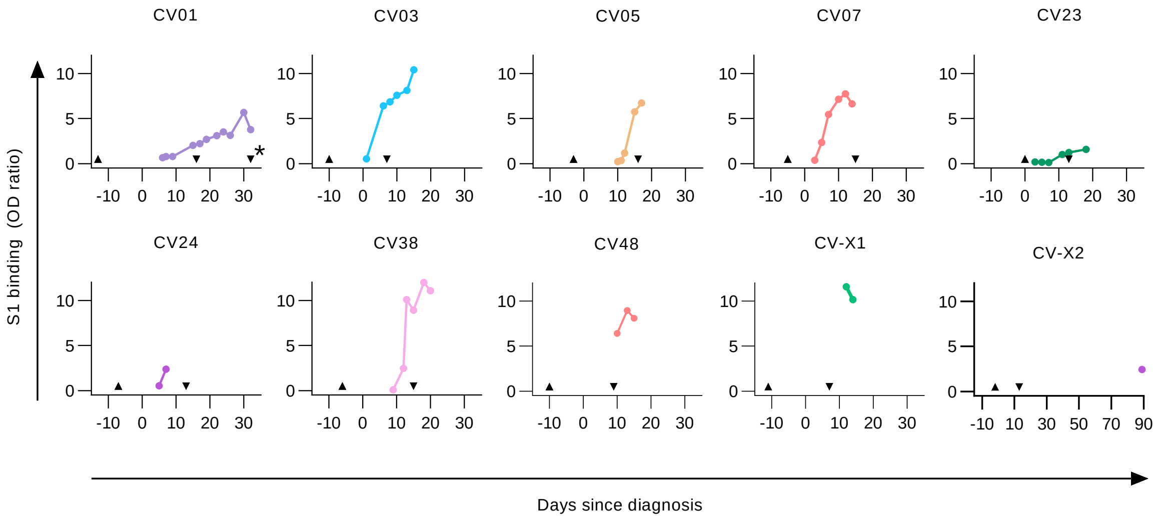


Fig. S1 | SARS-CoV-2-S1 serum IgG response from COVID-19 patients.

Serum IgG response determined as the normalized optical density (OD) in a SARS-CoV-2-S1 ELISA in relation to the time point of diagnosis defined by the first positive qPCR test. Upward arrowhead denotes the appearance of first symptoms. Downward arrowhead denotes the PBMC isolation. From patient CV01, PBMC samples were isolated at two time points as indicted by the second downward arrow with an asterisk (*).

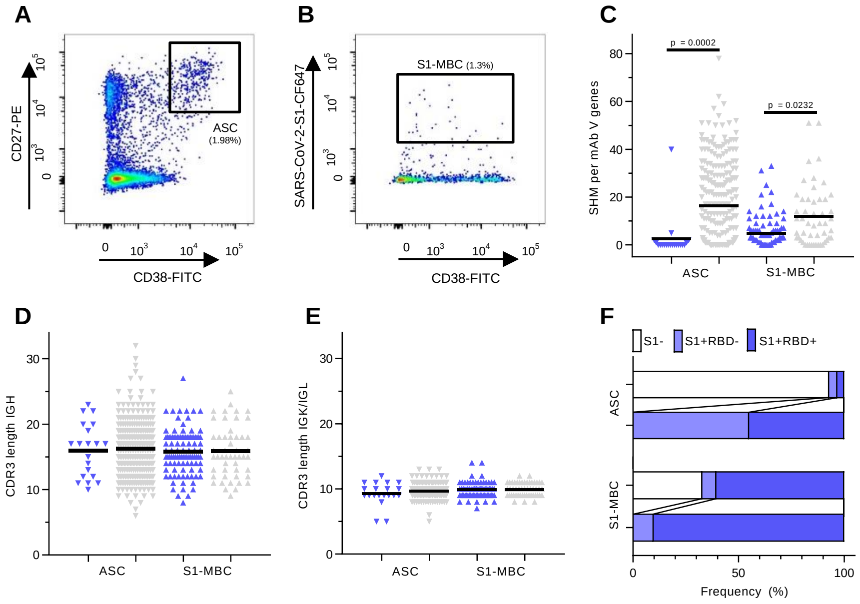


Fig. S2 | Flow cytometry gating and characteristics of immunoglobulin sequences.

(**A**-**B**) A representative flow cytometry plot from patient CV38 indicating gating on (**A**) CD19$^+$CD27$^+$antibody-secreting cells (ASC) and (**B**) SARS-CoV-2-S1-stained memory B cells (S1-MBC). Cells were pre-gated on live CD19$^+$ B cells. (**C**) Comparison of somatic hypermutation (SHM) count within immunoglobulin V genes combined from heavy and light chains of S1-reactive (S1+, blue) and non-S1-reactive (S1-, grey) mAbs. Statistical significance was determined using a one-way ANOVA (F = 19.22) with posthoc Tukey's multiple comparisons tests. (ASC: n = 20 S1+, n = 260 S1-; S1-MBC: n = 102 S1+, n = 50 S1-). All expressed mAbs are displayed. Each triangle represents a S1+ (blue) or S1- (grey) mAb, isolated from an ASC (pointing downwards) or a S1-MBC (pointing upwards). (**D**-**E**) Length comparison of complementarity-determining region (CDR) 3 amino acid sequences between S1+ and S1- mAbs within (**D**) heavy and (**E**) light chains. Symbols and colors have the same meaning as in (C). (**F**) Frequency of RBD-binder (S1+RBD+) and non-RBD-binder (S1+RBD-) relative to all expressed mAbs (upper lanes) and relative to S1+ mAbs (lower lanes).

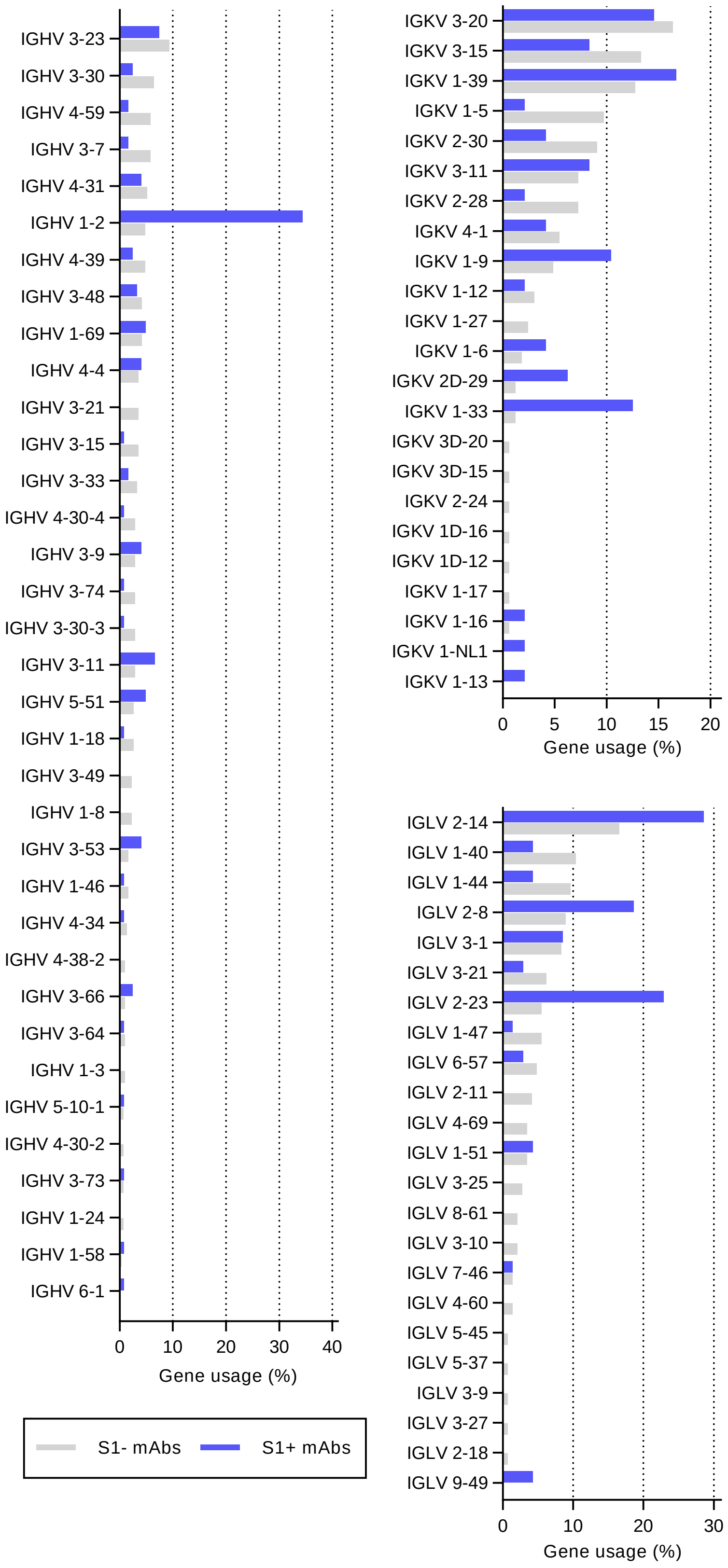
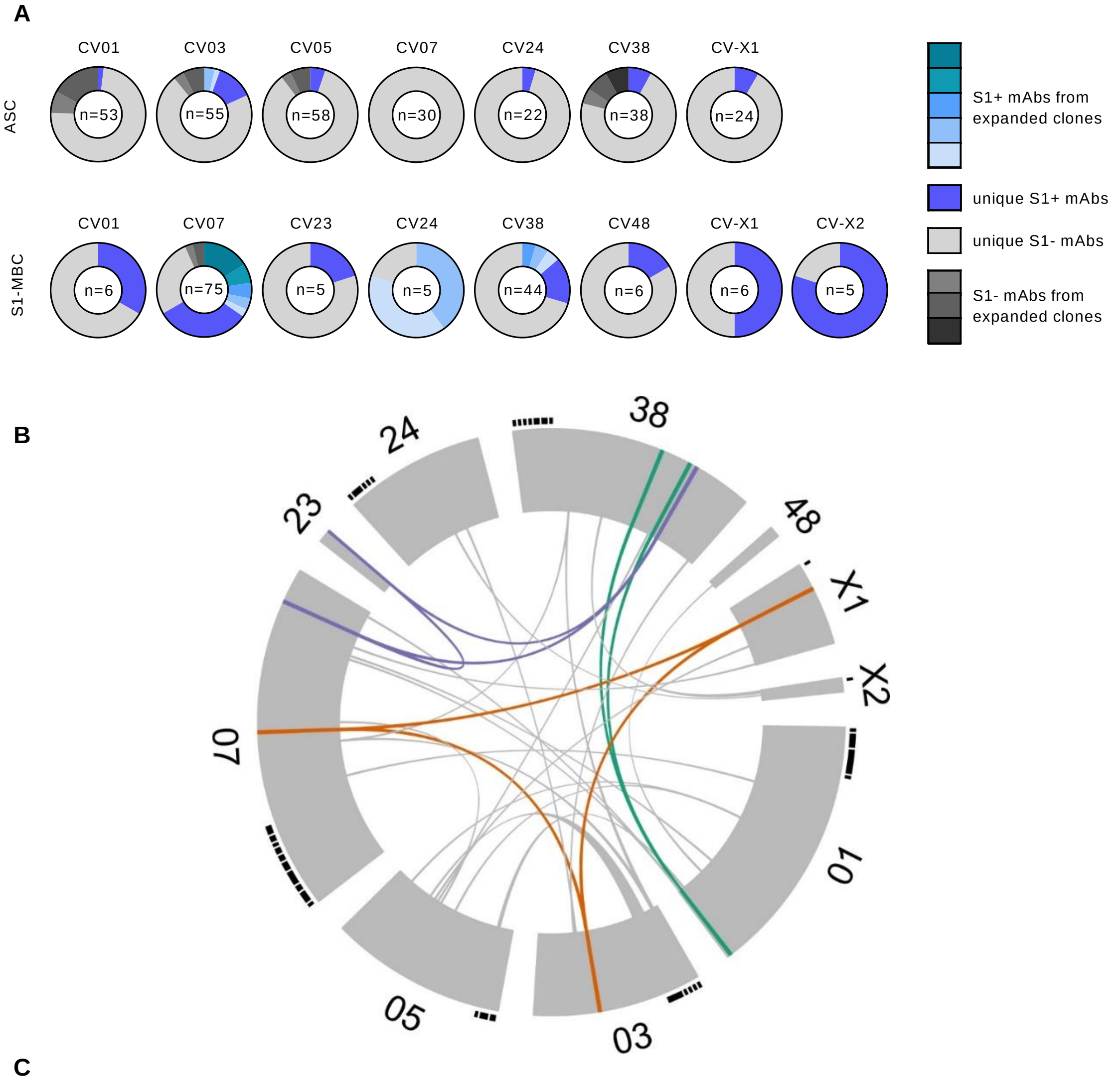

IGHV 3-23
IGHV 3-30
IGHV 4-59
IGHV 3-7
IGHV 4-31
IGHV 1-2
IGHV 4-39
IGHV 3-48
IGHV 1-69
IGHV 4-4
IGHV 3-21
IGHV 3-15
IGHV 3-33
IGHV 4-30-4
IGHV 3-9
IGHV 3-74
IGHV 3-30-3
IGHV 3-11
IGHV 5-51
IGHV 1-18
IGHV 3-49
IGHV 1-8
IGHV 3-53
IGHV 1-46
IGHV 4-34
IGHV 4-38-2
IGHV 3-66
IGHV 3-64
IGHV 1-3
IGHV 5-10-1
IGHV 4-30-2
IGHV 3-73
IGHV 1-24
IGHV 1-58
IGHV 6-1
0
10
20
30
40
Gene usage (%)
S1- mAbs
S1+ mAbs
IGKV 3-20
IGKV 3-15
IGKV 1-39
IGKV 1-5
IGKV 2-30
IGKV 3-11
IGKV 2-28
IGKV 4-1
IGKV 1-9
IGKV 1-12
IGKV 1-27
IGKV 1-6
IGKV 2D-29
IGKV 1-33
IGKV 3D-20
IGKV 3D-15
IGKV 2-24
IGKV 1D-16
IGKV 1D-12
IGKV 1-17
IGKV 1-16
IGKV 1-NL1
IGKV 1-13
0
5
10
15
20
Gene usage (%)
IGLV 2-14
IGLV 1-40
IGLV 1-44
IGLV 2-8
IGLV 3-1
IGLV 3-21
IGLV 2-23
IGLV 1-47
IGLV 6-57
IGLV 2-11
IGLV 4-69
IGLV 1-51
IGLV 3-25
IGLV 8-61
IGLV 3-10
IGLV 7-46
IGLV 4-60
IGLV 5-45
IGLV 5-37
IGLV 3-9
IGLV 3-27
IGLV 2-18
IGLV 9-49
0
10
20
30
Gene usage (%)

Fig. S3. | Comparison of variable gene usage.

Comparison of gene usage between SARS-CoV-2-S1-reactive (S1+) and non-reactive (S1-) mAbs is shown for immunoglobulin (**A**) variable heavy (IGHV), (**B**) variable kappa (IGKV) and (**C**) variable lambda (IGLV) genes. Bars depict percentage of gene usage of all expressed mAbs within each group.



C

	Patient	mAb	Reactivity	IGHV	IGHJ	CDR H3	IGKV/ IGLV	IGKJ/ IGLJ	CDR L3
🟪	CV07	HL CV07-255	RBD	1-2*02	4*02	ARDSRFSYVNGEFDY	2-23*02	3*02	CSYAGHSTWV
	CV23	HL CV23-121	S1-	1-2*02	4*02	ARELGSWDGRFDY	2-23*02	3*02	CSYAGSSTWV
	CV38	HL CV38-186	RBD	1-2*02	4*02	ARDQSPDILKSPFDY	2-23*03	3*02	CSYAGSSTFG
🟧	CV03	HK CV03-191	RBD	3-11*06	4*02	ARDLGYNRRFDY	1-33*01	4*01	QQYDNLPLT
	CV07	HK CV07-209	RBD	3-11*01	4*02	ARDGVIPPRFDY	1-33*01	4*01	QQYDNLPLT
	CV-X1	HK CV-X1-143	RBD	3-11*05	4*02	ARDLGYSTRFDY	1-33*01	4*01	QQYDNLPLT
🟩	CV01	HL CV01-273	RBD	4-4*02	4*02	ARGWGKGPPLGY	2-23*01	3*02	YSYAGSSTWV
	CV38	HL CV38-119	RBD	4-4*02	4*02	ARAWNFDY	2-23*01	3*02	CSYAGSSNWV
	CV38	HL CV38-180	n.exp.	4-4*02	4*02	ARRAAAGPRPYDY	2-23*01	3*02	CSYAGFSTWV

Fig. S4 | Clonal expansion and public clonotypes.

(**A**) Pie charts represent clonal relationship of all expressed mAbs from each donor separately for antibody secreting cells (ASC) and S1-stained memory B cells (S1-MBC). mAbs were considered S1-reactive (S1+) or non-S1-reactive (S1-) based on SARS-CoV-2-S1 ELISA measurements. Antibodies were considered to be clonally expanded when they were isolated from multiple cells. (**B**) Circos plot displays all isolated mAbs from ten donors. Interconnecting lines indicate relationship between mAbs that share the same V and J gene on both Ig heavy and light chain. Such public or shared clonotypes in which more than 50% of mAbs are S1-reactive are represented as colored lines. Small black angles at the outer circle border indicate expanded clones within the respective donor. (**C**) Properties of public clonotypes from

S1+ mAbs according to the colors used in (B) with sequence similarities between mAbs isolated from different donors, also within complementarity-determining region (CDR) three. IGHV, IGHJ IGKV, IGKJ, IGLV, IGLJ = V and J genes of immunoglobulin heavy, kappa, lambda chains; n.exp. = not expressed.

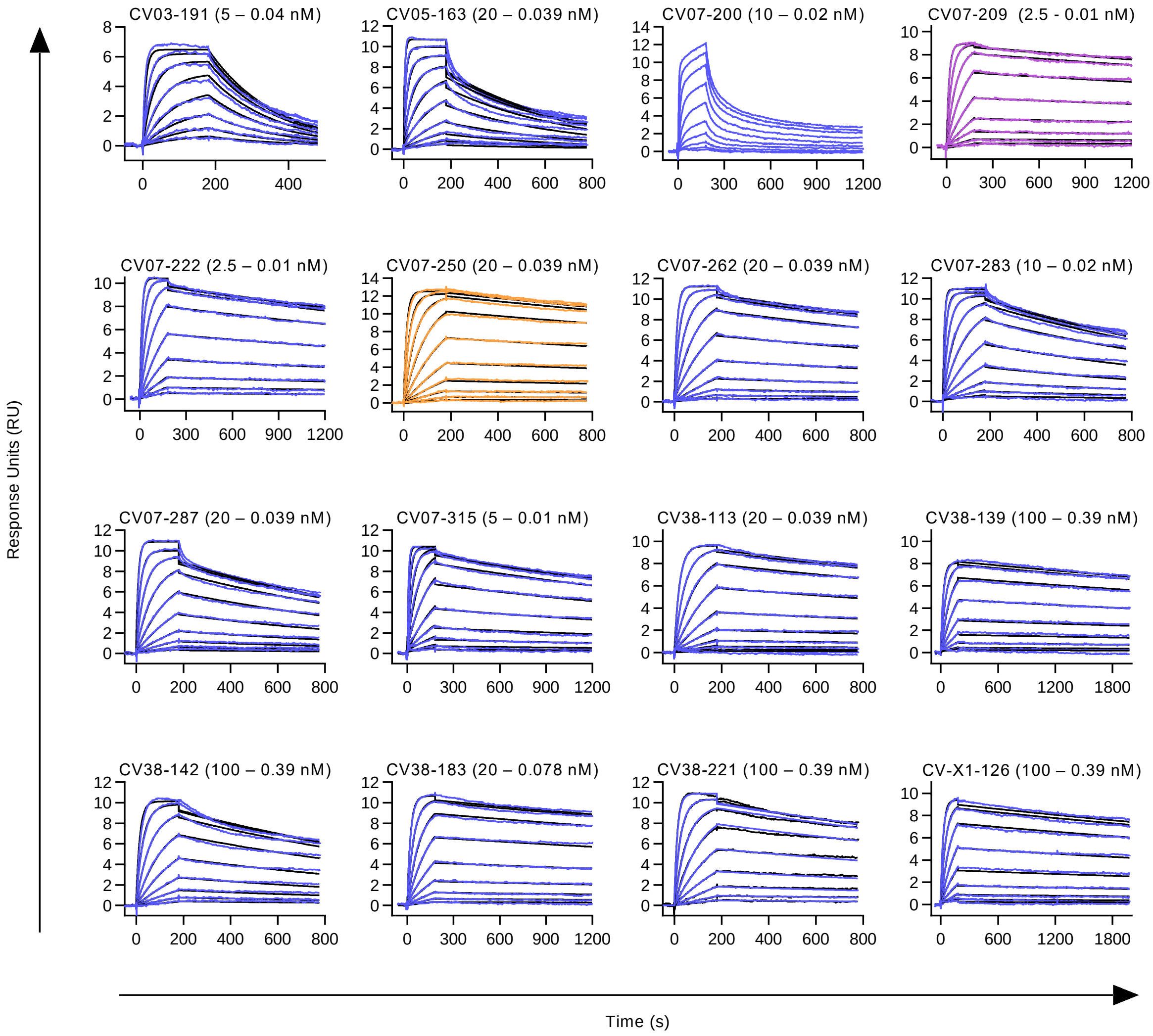


Fig. S5 | Binding kinetic measurements of mAbs to RBD.

Binding kinetics of mAbs to RBD were modeled (black) from multi-cycle surface plasmon resonance (SPR) measurements (blue, purple, orange). Fitted monovalent analyte model is shown. For CV07-200, neither a bivalent nor a monovalent analyte model described the data accurately (no model is shown). Three out of the 18 selected mAbs for detailed characterization (Top-18) were not analyzed using multi-cycle-kinetics: CV07-270 was excluded as it interacted with the anti-mouse IgG reference surface on initial qualitative measurements. CV07-255 and CV-X2-106 were not analyzed since they showed biphasic binding kinetics and relatively fast dissociation rates in initial qualitative measurements. Non-neutralizing CV03-191, a mAb not included in the Top-18 mAbs, was included in the multicycle experiments as it has the same clonotype as strongly neutralizing CV07-209 (Fig. S4C). All measurements are performed by using a serial 2-fold dilution of mAbs on reversibly immobilized SARS-CoV-2-S1 RBD-mFc.

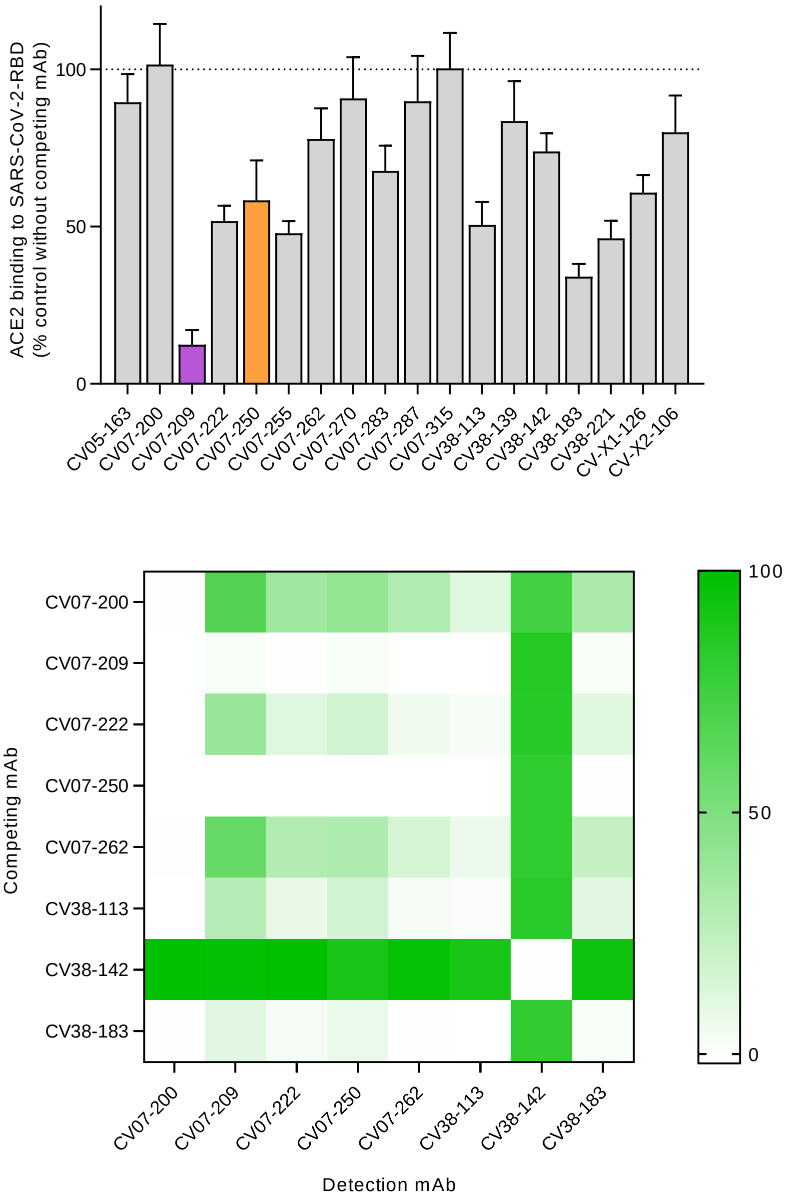


Fig. S6 | Competition of mAbs for RBD binding with ACE2 and between SARS-CoV-2 mAbs.

(**A**) ELISA-based measurements of human ACE2 binding to SARS-CoV-2 RBD after pre-incubation with the indicated neutralizing mAbs. Values are shown relative to antibody-free condition as mean+SD from three independent measurements. (**B**) Competition for RBD binding between combinations of potent neutralizing mAbs is illustrated as a heat map. Shades of green indicate the degree of competition for RBD binding of detection mAb in presence of 100-fold excess of competing mAb relative to non-competition conditions. Green squares indicate no competition. Values are shown as mean of two independent experiments.

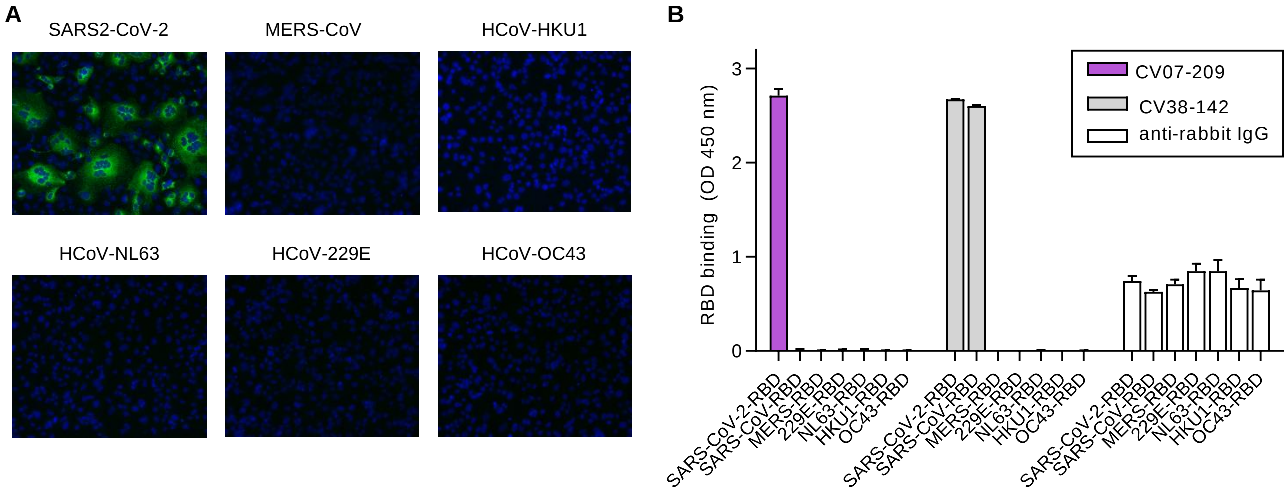


Fig. S7 | Binding specificity of mAbs within coronaviruses.

(**A**) Representative immunofluorescence staining on VeroB4 cells overexpressing spike protein of indicated coronavirus with SARS-CoV-2 mAb CV07-209 at 5 µg/ml. For all other 17 of the selected 18 mAbs (Top-18, Supplementary Table ST4), similar results were obtained. (**B**) Binding of indicated mAbs to fusion proteins containing the RBD of indicated coronaviruses and the constant region of rabbit IgG revealed by ELISA. For all other Top-18 mAbs, similar results were obtained as for CV07-209. Values indicate mean+SD from two wells of one experiment.

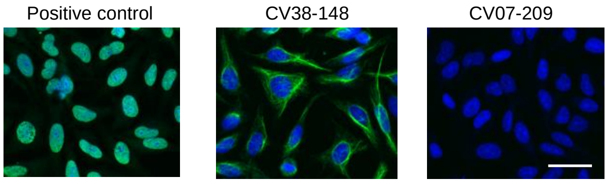


Fig. S8 | Representative staining on HEp-2 cells of selected S1-reactive antibodies.

Representative HEp-2 cell staining with a commercial anti-nuclear antibody as positive control revealed nuclear binding (left). S1-reactive non-neutralizing mAb CV38-148 exhibited cytoplasmatic binding (middle). Neutralizing mAb CV07-209 showed no binding (right). All mAbs selected for detailed characterization (Top-18, Supplementary Table ST4) revealed similar results like CV07-209 when used at 50 µg/ml.

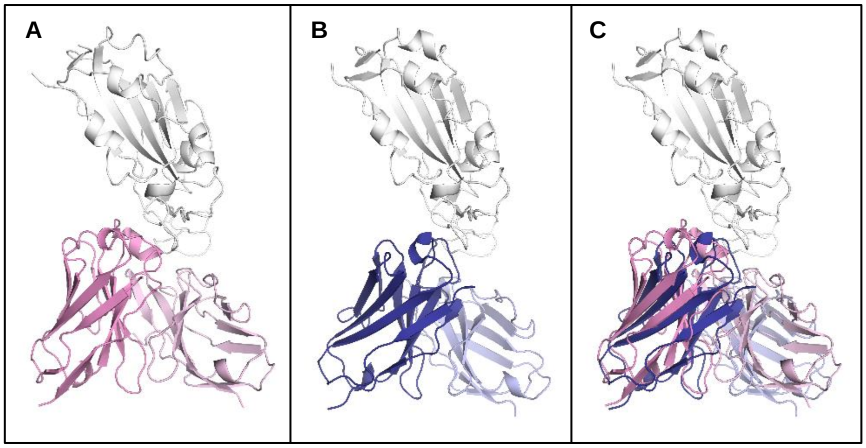


Fig. S9 | Structural comparison of CV07-270/RBD and P2B-2F6/RBD complexes.

(**A**) Structure of CV07-270 (pink) in complex with RBD (white). (**B**) Structure of P2B-2F6 (blue) in complex with RBD (white) (PDB 7BWJ) (Ju et al., 2020) (**C**) Structures of CV07-270/RBD and P2B-2F6/RBD were superimposed based on the RBD.

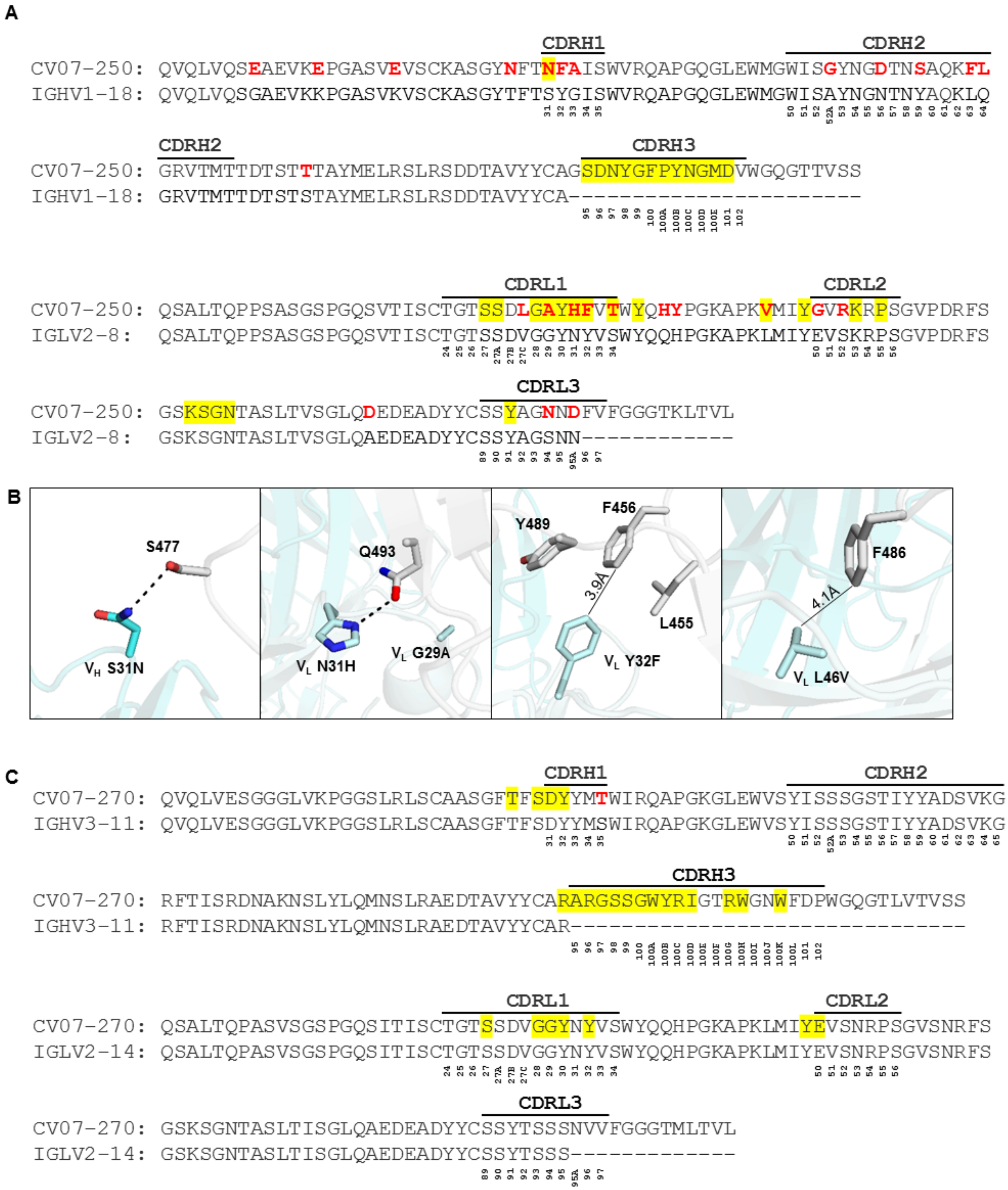


Fig. S10 | Comparison of sequences of CV07-250 and CV07-270 to their putative germline sequences.

(**A**) Alignment of CV07-250 with the germline IGHV1-18 sequence (nucleotide SHM rate 5.8%) and IGLV2-8 (nucleotide SHM rate 5.4%).

(**B**) Somatic mutations VH S31H, VL G29A, VL N31H, VL Y32F, VL S34T, and VL L46V are located in the CV07-250 paratope with other somatic mutations in all of the CDRs that may affect overall CDR conformation and interactions. Hydrogen bonds are represented by dashed lines. Distances between atoms are shown in solid lines. CV07-250 heavy chain is in dark cyan and light chain is in light cyan. SARS-CoV-2 RBD is in light grey. (**C**) Alignment of CV07-270 with the germline IGHV3-11 sequence (nucleotide SHM rate 0.7%) and IGLV2-14 (nucleotide SHM rate 0%). The regions that correspond to CDR H1, H2, H3, L1, L2, and L3 are indicated. Residues that differ from the germline are highlighted in red. Residues that interact with the RBD are highlighted in yellow. Residue positions in the CDRs are labeled according to the Kabat numbering scheme.

Supplementary Table ST1 | Description of patient cohort.

General	**Patient ID** (gender, age)	**CV01** (m, 21)	**CV03** (m, 46)	**CV05** (m, 61)	**CV07** (m, 32)	**CV23** (f, 44)	**CV24** (m, 64)	**CV38** (m, 70)	**CV48** (m, 48)	**CV-X1** (m, 46)	**CV-X2** (m, 57)
Patient history	Pre-existing conditions	N	CVD, Crohn's disease	N	N	atopic dermatitis, hypthyreosis	CVD	CVD	N	N	N
	Smoking	N	N	N	Y	N	N	Y (10 PY)	N	Y (7 PY)	N
Symptoms	Pulmonary and general symptoms	fever, cough, emesis	fever, cough, dyspnea, emesis	fever, cough, dyspnea, superinfection	fever, cough, dyspnea, respiratory failure	fever	fever, cough, dyspnea, emesis	fever, dyspnea, renal failure, atrial fibrillation	fever, cough, dyspnea, diarrhea	fever, cough, dyspnea, respiratory failure, diarrhea	fever, cough, epistaxis
	Neurological symptoms	loss of smell, muscle twitches	loss of smell, mood impairment, paresthesia	N	loss of smell	n/a	loss of smell	N	N	n/a	loss of smell
Disease course	Date symptom onset	17.02.2020	29.02.2020	27.02.2020	08.03.2020	20.03.2020	13.03.2020	12.03.2020	14.03.2020	15.03.2020	18.03.2020
	Days until diagnosis / hospitalization	13 / 13	10 / 11	3 / 13	5 / 6	0 / 0	7 / 8	6 / 14	10 / 9	11 / 12	2 / -
	SARS-CoV-2 serum IgG at PBMC isolation	2.0 / 3.8	6.4	5.7	6.6	1.2	n/a	8.9	6.4	n/a	n/a
	Days in hospital / on ICU	34 / 0	14 / 0	9 / 0	15 / 2	34 / 0	8 / 2	15 / 0	17 / 2	15 / 6	0 / 0
	Oxygen demand / days ventilation	N / 0	N / 0	N / 0	Y / 0	N / 0	Y / 0	Y / 0	Y / 0	Y / 3	N / 0
	Medication	N	N	AB, ACT	N	N	AB, ACT	AB, ACT, APT, Digitoxin	AB, ACT, APT, HCQ	AB, HCQ	N
Follow Up	Outcome	discharged	discharged	discharged	discharged	discharged	discharged	discharged	discharged	discharged	discharged

PBMCs from ten COVID-19 patients were included in immunoglobulin repertoire studies. General information, patients' history, symptoms of SARS-CoV-2 infection, disease course and outcome are listed for each donor. SARS-CoV-2 IgG is given as a ratio of optical density from time point of PBMC isolation (± one day).

Abbreviations: m = male, f = female, Y = yes, N = no, n/a = not available, CVD = cardiovascular disease, PY = pack years, AB = antibiotics, ACT = anticoagulation therapy, APT = antiplatelet therapy, HCQ = hydroxychloroquine.

Supplementary Table ST2 | Immunoglobulin sequence and functional screening data of all isolated mAbs.

mAb	Clonality	Source cell	Ig isotype	IGHV gene	IGHJ gene	CDR H3	SHM IGHV	IGKV/IGLV gene	IGKJ/IGLJ gene	CDR L3	SHM IGKV/ IGLV	S1 reactivity (OD ratio)	RBD reactivity	Estimated IC_{50} (ng/ml)
HL CV01-101		ASC	IgM	3-74	3	ARGSSNLFDI	7	1-44	3	AAWDDSLNGWV	4	0.1		
HL CV01-102		ASC	IgG1	3-21	4	ARSGGYSGYDYSHRIDY	25	2-14	3	SSYTLDSTVV	12	n.exp.		
HK CV01-103		ASC	IgA1	1-69	4	ASGWGMEYSSSSADY	0	3-11	2	QQRSNWPPYT	1	0.09		
HL CV01-104	1-2	ASC	IgM	1-18	4	ARADETMVQGVIPNFDY	4	2-8	2	SSYAGSNNVV	3	0.1		
HK CV01-107		ASC	IgA2	3-74	6	ARGRDCGGSSCYGYPYYGMDV	7	2-28	2	MQALHTPYT	4	n.exp.		
HK CV01-109	1-3	ASC	IgG2	3-7	4	ARAGSVGVVDY	12	2-30	1	MQGTHWPWT	8	0.1		
HK CV01-110		ASC	IgA1	3-7	4	VRDRGYCVGDVCYTVLDY	27	1-6	4	LHDYNYPPT	13	0.09		
HK CV01-111		ASC	IgM	3-15	1	TTWFYYDIRDH	24	3-11	2	QQRSNWPPFT	11	0.09		
HL CV01-112	1-2	ASC	IgM	1-18	4	ARADDTMVQGVIPNFDY	14	2-8	3	SSYAGSNNVV	2	0.03		
HK CV01-113		ASC	IgM	3-15	4	ASIYYDF	13	1-17	2	LHYNSVPYT	18	n.exp.		
HL CV01-114		ASC	IgM	1-2	4	ARGDAVARTLNLDY	8	1-44	2	AAWDDSLNGV	3	0.09		
HK CV01-116	1-3	ASC	IgM	3-7	4	ARAGNIGAVDY	14	2-30	1	MQGTHWPWT	1	0.02		
HL CV01-117		ASC	IgA1	3-49	4	GLSYYYDNGGYYSVPPIDV	20	2-8	3	SSYADSNNLV	9	n.exp.		
HK CV01-118	1-1	ASC	IgM	3-9	3	AKNSPSCADAVCYFDV	10	4-1	1	QQYYSAPRT	8	n.exp.		
HK CV01-120		ASC	IgA1	4-30-4	3	AREGVLITIFGVARDAFDI	1	3-20	2	QQYGSSPRT	1	0.09		
HK CV01-121		ASC	IgA1	4-38-2	4	SIWGGVQGVLQDY	22	3-15	2	QQYNDWPRT	7	0.09		
HK CV01-122	1-3	ASC	IgG2	3-7	4	ARAGSIASVDY	11	2-30	1	MQGTHWPWT	8	n.exp.		
HK CV01-123		ASC	IgM	3-7	4	AKGGWRYFDY	16	3-11	4	QQRSSWPLT	9	0.08		
HK CV01-124		ASC	IgM	3-23	4	AKYGSITIFGVVIIGYFYFDY	1	3-20	2	QQYGSSPAT	0	0.08		
HL CV01-125	1-2	ASC	IgA1	1-18	4	ARADYTMVQGVIPNFDY	7	2-8	2	SSYAGSNNVL	10	0.1		
HL CV01-126		ASC	IgA2	5-51	6	AGHVRYCISTNCYHYGMDV	5	5-45	3	MIWHTSAWV	6	0.10		
HK CV01-128	1-3	ASC	IgG2	3-7	4	ARAGDRGAVDY	13	2-30	1	MQGTHWPWT	8	0.11		
HL CV01-129	1-2	ASC	IgA1	1-18	4	ARADYTMVQGVIPNFDY	0	2-8	2	SSYAGSNNVV	4	n.exp.		
HK CV01-130		ASC	IgM	3-7	3	ARPGYSGNNWGEAFDI	0	4-1	1	QQYYDTLWT	13	0.09		
HK CV01-132		ASC	IgG1	4-59	6	ARDRGYNWNYYYYYGMDV	0	3-20	1	QQYGSSPST	2	0.1		
HK CV01-133	1-3	ASC	IgG2	3-7	4	ARAGSRGSVDY	21	2-30	1	MQGTHWPWT	13	0.1		
HK CV01-134		ASC	IgM	3-30	6	AKEKLDCSSTSCYFGFIYYYYYMDV	0	1-12	2	QQANSFPLT	1	0.09		
HL CV01-135		ASC	IgG1	3-11	4	ARESYEGSSFDY	10	6-57	3	QSYDSSNRRV	3	0.1		
HK CV01-137		ASC	IgG2	3-7	4	ARDYGRCGDY	18	3-11	2	QQGGNWPRT	9	0.11		
HK CV01-138		ASC	IgA1	4-39	5	ARHGYITIFGVVIIPGWFDP	0	3-15	1	QQYNNWPPWT	2	0.07		
HL CV01-139		ASC	IgM	4-39	4	ARHPDNELLPFDY	0	3-21	1	QVWDSSSDSYV	2	0.11		
HK CV01-140		ASC	IgM	3-30-3	2	ARDPRNYCHSNTCPVWYFDL	17	3-20	2	QQYGSSPRT	6	0.08		
HL CV01-141		ASC	IgG1	3-33	4	AREGNYGDYGGSFDY	0	3-10	3	YSTDSSGNHRV	0	n.exp.		
HL CV01-142		ASC	IgM	4-30-4	2	ARGPRITIFGVVIYWYFDL	0	1-40	2	QSYDSSLSGSGV	1	0.09		
HL CV01-144		ASC	IgG1	3-30	4	ARRDRIFEFGATREALDF	22	1-40	1	QSYDSSLSGYV	15	0.08		
HK CV01-145		ASC	IgM	3-23	5	AKVTWTTTGDS	19	1-5	1	QQYNSYPWT	7	0.10		
HK CV01-146	1-3	ASC	IgG1	3-7	4	ARAGDRGAVDY	17	2-30	1	MQGTQWPWT	10	0.09		
HK CV01-147		ASC	IgG1	3-30-3	5	ARERVNGRWLQLLTP	20	1-5	4	QQYDAYLS	16	0.09		
HK CV01-148	1-3	ASC	IgM	3-7	4	ARAGDRGAVDY	10	2-30	1	MQGTHWPWT	2	0.08		
HK CV01-149		ASC	IgM	1-18	4	AGYPRYNWNYDNRYYFDF	7	1-39	5	QQSYSAPIT	9	n.exp.		
HL CV01-151	1-2	ASC	IgM	1-18	4	ARADDTMVQGVIPNFDY	2	2-8	2	SSYAGSNNVV	4	0.07		
HK CV01-152		ASC	IgA1	1-3	6	ARGVGATIPYYYYYYMDV	2	1-5	1	QQYNSYSWT	1	0.1		
HK CV01-153		ASC	IgG1	4-4	6	AKVGGGNADHGPGYYYYYMDV	37	1-9	2	QELNRYPRT	17	0.07		
HK CV01-154	1-1	ASC	IgM	3-9	3	AKNSASCADDLCYFDI	15	4-1	1	QQYYSGPRT	7	0.08		
HK CV01-155		ASC	IgM	3-11	4	ARALPGGITIFGVVITEYYFDY	0	3-20	2	QQYGSSSYT	2	0.08		
HL CV01-158		ASC	IgG2	3-21	3	ARGDDYGEYTGAFDA	2	3-1	2	QAWDSSTVV	3	0.09		
HK CV01-159		ASC	IgA1	1-46	4	ARGGETQQRLVWDQKTDD	23	1-17	4	LQYNSYPLT	12	0.11		

mAb	Clonality	Source cell	Ig isotype	IGHV gene	IGHJ gene	CDR H3	SHM IGHV	IGKV/IGLV gene	IGKJ/IGLJ gene	CDR L3	SHM IGKV/ IGLV	S1 reactivity (OD ratio)	RBD reactivity	Estimated IC_{50} (ng/ml)
HK CV01-163	1-3	ASC	IgA1	3-7	4	ARAGSVGTVDY	22	2-30	1	MQGTHWPWT	16	0.08		
HK CV01-166		ASC	IgA1	3-15	4	TTEKGRYHLGGVFAN	11	4-1	4	QQYYSTPLT	8	n.exp.		
HL CV01-168		ASC	IgA1	5-51	4	VWTSRGYFDH	6	7-43	3	LFYYGGAWV	9	n.exp.		
HL CV01-169		ASC	IgM	3-30	4	ARDLSSGWSLDS	3	2-14	3	SSYTSSNTWV	4	0.07		
HL CV01-170		ASC	IgM	4-4	6	ARYCSSTSCYGYYYYGMDV	0	2-8	1	SSYAGSISYV	2	0.08		
HK CV01-171		ASC	IgG1	4-4	3	AKGGGSGWYYDAFDI	17	3-15	1	QQYNNWLRT	12	0.11		
HL CV01-174		ASC	IgM	1-18	4	ARDDWNYARGNFDY	3	2-14	2	SSYTSSSSVV	1	0.14		
HK CV01-175	1-3	ASC	IgM	3-7	4	ARAGGVGTVDY	11	2-30	1	MQGTLWPWT	2	0.1		
HL CV01-176	1-2	ASC	IgA1	1-18	4	ARADHTMVQGVIPNFDY	3	2-8	2	SSYTGRKNVV	6	0.1		
HK CV01-180	1-3	ASC	IgM	3-7	4	ARCDMAGTTDY	5	2-30	1	MQGTLWPWT	2	0.1		
HK CV01-181		ASC	IgG1	3-21	2	ARDLEGVETIFGVVIIPAYWYFDL	0	2-28	4	MQALQTRLT	3	0.08		
HL CV01-182		ASC	IgG1	3-23	4	AKDLKIGTLGWYYDFWSGYLPDPSNKIFDY	0	1-40	3	QSYDSSLSGWV	0	0.1		
HL CV01-183		ASC	IgM	3-73	3	TRVNPIQGAFYDALDI	6	1-51	2	GTWDSSLSVVV	7	0.11		
HK CV01-184		ASC	IgG2	4-59	4	ARFSSAAGVWALDH	11	4-1	2	QQYYTTPFT	7	n.exp.		
HL CV01-185		ASC	IgA1	1-69	6	ACDMVQGVAVLDV	13	2-14	2	SSYTSSSTVV	9	0.13		
HK CV01-186		ASC	IgG2	4-59	5	ARHGKSIPYSNYDWFDP	0	1-39	3	QQSYSTLPFT	0	0.09		
HK CV01-188		ASC	IgM	3-72	4	ARDLGANGDRFGN	4	4-1	1	QQYYSTPLT	2	0.08		
HK CV01-193		ASC	IgA1	3-15	4	ATDLGDYGDYMRS	13	1-12	2	QQANSFPYT	7	0.11		
HL CV01-194		ASC	IgM	4-59	4	AKKADPHSAFDY	6	2-11	1	CSYAGSYTYV	6	0.09		
HL CV01-195		ASC	IgM	3-7	1	VRELVVGRAEYFQD	0	1-44	2	AAWDDSLNGRV	1	3.37	++	>250
HK CV01-196		ASC	IgG1	3-30	3	AKDPGMLYPSAFDM	14	3-15	4	QQYNNWPPLT	13	n.exp.		
HL CV01-197		ASC	IgM	3-23	4	AKDQDGHYGGNPDMDH	10	2-8	3	SSYAGSNKMV	11	n.exp.		
HL CV01-198		ASC	IgG2	3-15	4	ATLTYGYSPY	11	2-14	1	SSYTSSTTYV	63	n.exp.		
HK CV01-199		ASC	IgA1	3-74	4	ASNFNRNDGY	14	2-30	4	IQSTHWPPN	13	n.exp.		
HK CV01-202		ASC	IgG1	4-30-4	4	ARMGNMFGYSVVDF	22	1-39	2	LQTYSAPYT	20	n.exp.		
HL CV01-203		ASC	IgA2	3-30	6	AKSEGKFYFYGVDV	9	1-47	1	AACDDSLSGHV	3	n.exp.		
HK CV01-205		ASC	IgG1	5-51	5	AREARWSFPSWFDP	6	3-15	2	QQYNNWPRF	7	n.exp.		
HK CV01-211		ASC	IgA1	5-51	4	ARLSSGWYGGFNFDY	0	3-20	2	QQYGSSPVYT	0	n.exp.		
HL CV01-212		ASC	IgM	3-30	4	AKCSYTSICKGWDGAH	14	2-14	2	SSFTTSYTLV	11	n.exp.		
HK CV01-213		ASC	IgG1	3-64	4	ARLQGTGYLDY	12	3-20	2	HQYGSSPRT	9	n.exp.		
HL CV01-215		ASC	IgM	3-48	5	ARQWAVNWFVP	7	2-14	2	SSHTSSSTVV	8	n.exp.		
HK CV01-220		ASC	IgA1	3-48	6	ARDVGTYESTSTGMDV	7	3-11	5	QQRGNWPPAT	11	n.exp.		
HL CV01-221		ASC	IgA1	3-30-3	4	ARGAPVDY	6	2-8	7	N/A	9	n.exp.		
HL CV01-222		ASC	IgA1	3-23	4	AKPGGEWYSSGWRFDY	2	1-47	2	AAWDDSLSGPV	0	n.exp.		
HL CV01-223		ASC	IgM	3-23	3	AKCGRTSCRVDAFDI	27	8-61	3	VLSMGGGVWV	13	n.exp.		
HL CV01-225		ASC	IgA1	3-53	3	ARDGGGSYPHRAFDI	1	2-14	2	SSYTSSSTSDVV	2	n.exp.		
HL CV01-226		ASC	IgG1	4-39	6	ARHATGTPPYYYYYMDV	2	3-1	1	QAWDSSTACV	3	n.exp.		
HL CV01-227		ASC	IgA1	3-30	4	AKGSPLLGFGGVDY	0	5-39	3	AIWYSSSLV	1	n.exp.		
HK CV01-228		ASC	IgA1	3-7	4	ARVGASDYDYVWGTRTLDS	11	4-1	1	QQCLTTPPWT	12	n.exp.		
HK CV01-229		ASC	IgG2	5-51	4	ARPYGAGTAHYFDY	9	4-1	4	QQYYGTPHT	8	n.exp.		
HL CV01-231	1-4	ASC	IgA1	4-39	6	ARHFHPGNYYYYYMDV	6	3-1	2	QAWDSSTYVV	3	n.exp.		
HL CV01-232		ASC	IgM	4-39	4	ARKYGDLHFDY	1	8-61	3	VLYMGSGISV	3	n.exp.		
HL CV01-233		ASC	IgM	4-39	3	ARSDARFLEWLFPDAFDI	3	2-23	2	CSYAGSTTFVV	3	n.exp.		
HL CV01-234		ASC	IgM	3-30	5	ARGSPFGGIRSGLGP	20	1-27	1	QKYNSAPWT	11	n.exp.		
HL CV01-238	1-4	ASC	IgG1	4-39	6	ARHPTGSGSYQYYYYYIDV	3	3-1	2	QAWDSSTVV	2	n.exp.		
HL CV01-241		ASC	IgA1	3-66	3	ARDRGYDSSGYTAADAFDI	2	1-5	1	QQYNSYST	6	n.exp.		
HL CV01-242		ASC	IgG1	4-31	5	ARGGYRNWFDP	3	2-11	3	CSYAGSYTWV	2	n.exp.		
HK CV01-244		S1-MBC	IgG1	5-10-1	6	ARLKGSVPPYYYNYMDV	18	2-28	4	MQGLQTPFI	7	n.exp.		
HK CV01-249		S1-MBC	IgA1	3-30-3	3	ARHNRAQGPSFDV	21	1-39	5	QQTYSVPTT	32	0.08		
HK CV01-254		S1-MBC	IgM	3-7	4	ASLLGGTVVNDY	4	4-1	2	QQYYSTQYT	2	0.09		

mAb	Clonality	Source cell	Ig isotype	IGHV gene	IGHJ gene	CDR H3	SHM IGHV	IGKV/IGLV gene	IGKJ/IGLJ gene	CDR L3	SHM IGKV/ IGLV	S1 reactivity (OD ratio)	RBD reactivity	Estimated IC_{50} (ng/ml)
HK CV01-257		S1-MBC	IgM	3-48	6	ARHPWDDYGDYYYYYMDV	5	3-20	2	QQYGSSLNT	2	10.92	++	>250
HL CV01-258		S1-MBC	IgG1	4-59	6	ARAVHGVDTGMVTYYYHYYMDV	7	3-21	2	QVWDNSIDHVV	5	0.08		
HL CV01-260		S1-MBC	IgA2	1-8	4	ARGREYYDFWSGYYN	3	2-14	3	SSYTRSNTVV	6	0.14		
HK CV01-266		S1-MBC	IgA1	3-15	3	TSERWLDAFDI	28	1-39	5	QQSYRSPPIT	24	n.exp.		
HL CV01-273		S1-MBC	IgA1	4-4	4	ARGWGKGPPLGY	2	2-23	3	YSYAGSSTWV	4	7.10	-	>250
HK CV01-274		S1-MBC	IgM	3-30	4	AKDNGDYACFDY	0	4-1	4	QQYYSTPLT	0	0.07		
HL CV01-276		S1-MBC	IgA1	1-2	6	ARDPFEYYDFWSGYYRGGMDV	2	2-14	3	SSYTSSSTRV	1	n.exp.		
HK CV03-101		ASC	IgG1	1-2	4	ARGLITWYYYYDSSAVDY	0	3-20	1	QQYGSSPWT	0	0.1		
HK CV03-103		ASC	IgM	3-21	5	ARDPDGHRSGWFDWFDP	3	1D-12	5	QQANSFPIT	4	n.exp.		
HL CV03-104		ASC	IgG1	1-18	6	ARDSHYYDSSGYYYLYYYYGTDV	1	3-25	1	QSADSSGTYV	0	0.09		
HK CV03-106	3-2	ASC	IgG1	4-31	3	ARGRTIFGVVSGAFDI	0	3-20	4	QQYGSSPLT	1	0.02		
HK CV03-107	3-2	ASC	IgG1	4-31	3	ARGRTIFGVVSGAFDI	0	3-20	4	QQYGSSPLT	2	0.10		
HL CV03-108		ASC	IgG1	3-15	6	TKTKNPPAYDFWSGYYRGRPPYYKYGMDV	20	1-40	1	QSYDNSLSEYDDV	10	0.1		
HL CV03-109		ASC	IgG1	5-10-1	4	ARHVGVGATHSPPFDY	0	1-40	2	QSYDSSLSGPTV	0	0.12		
HK CV03-110		ASC	IgG1	3-48	4	ARDLGSWYYLLDFDY	1	1-5	1	QQYNSYPRT	0	0.08		
HK CV03-112		ASC	IgG1	3-48	5	GRSSSWRYNWFDP	20	3-15	1	QQYNNWPPWT	13	0.03		
HL CV03-113		ASC	IgG1	3-15	4	TTDPYYEISSGYSPDY	44	2-11	2	N/A	34	0.09		
HL CV03-116		ASC	IgA1	4-59	6	ARVQGRGSGSYYSAYYYGMDV	0	1-40	1	QSYDSSLSGV	1	0.1		
HL CV03-117	3-3	ASC	IgG1	1-46	6	LRDGISTFGVVNHYYAMDV	16	2-14	1	SSYTSSSTVV	11	n.exp.		
HL CV03-118	3-3	ASC	IgG1	1-46	6	ARDGISTFGVVKHYYAMDV	26	2-14	1	SSYTTTTTLV	26	n.exp.		
HL CV03-120		ASC	IgG1	3-21	6	ARDSLITIFGVVIEAPDDYGMDV	0	2-14	2	SSYTSSSTVV	2	n.exp.		
HL CV03-121	3-1	ASC	IgG1	3-23	4	AKDYFVIPPAALYDY	0	1-51	2	GTWDSSLSAGV	3	n.exp.		
HL CV03-123		ASC	IgG1	3-23	5	VKELDDQLTLGGWFDP	36	2-23	3	CSYVGTATVV	26	0.11		
HL CV03-124		ASC	IgG1	5-51	4	ASSVRYFDWFDFDY	0	1-44	1	AAWDDSLNGYV	0	n.exp.		
HK CV03-129		ASC	IgG1	1-69	4	ARARRPTYSSSWGTFDY	0	1-39	1	QQSYSTPWT	0	0.09		
HK CV03-130		ASC	IgG1	4-59	4	ASGTYGGPYLFDY	19	1-5	1	QKYNTYPGT	12	n.exp.		
HK CV03-131		ASC	IgM	3-11	4	ARAGDMIVVAAFDY	0	3-20	4	QQYGSSPLT	0	0.08		
HK CV03-132		ASC	IgG1	3-7	6	ARGPQMVYALFPYYYYYGMDV	0	1-27	1	QKYNSAPWT	0	0.1		
HK CV03-135		ASC	IgG1	3-64	3	VMELYGSDVFDL	22	1-39	1	QQSYSTSWT	18	0.1		
HL CV03-138		ASC	IgM	3-74	4	ASYTWGRI	1	2-14	2	SSYTRSSTLVV	2	0.08		
HK CV03-139		ASC	IgM	4-39	6	ASQGPLPPILYDILTGYYLGDYYYGMDV	2	2-28	4	MQALQTPLT	1	0.09		
HK CV03-140		ASC	IgG1	3-49	4	TRDAYYYGSGSYSEGGH	0	3-11	3	QQRSNWPPLFT	0	0.09		
HK CV03-141		ASC	IgG1	4-38-2	6	ARDVTGYDNEDYYYYYGLDV	24	4-1	1	QQYYSSPRT	9	0.08		
HL CV03-142		ASC	IgM	3-53	4	AREGPDSGYLDY	7	4-69	3	QTWGTGIRV	6	0.11		
HK CV03-143		ASC	IgG1	3-48	4	ARDSGFWSGYYPGNFNY	0	1-33	4	QQYDNLPPLT	1	6.43	++	>250
HK CV03-144		ASC	IgG1	1-18	6	ARDPWIELRPPRNYYYNGMDV	11	2-28	1	MQALQTPRT	4	0.08		
HL CV03-145		ASC	IgG1	1-46	4	ARDSSDCSGGSCYRFDY	0	1-44	1	AAWDDSLNGYV	0	n.exp.		
HK CV03-146		ASC	IgM	3-23	4	AKDRTVTKTGLFYLDDC	10	1-39	5	QQSYSTPIT	6	0.08		
HL CV03-147	3-4	ASC	IgA1	3-23	4	ASQTGTGEVDY	0	3-1	1	QAWDSSTGV	0	4.2	-	n.t.
HL CV03-148	3-1	ASC	IgG1	3-23	4	AKGPRLLWFGELSPFDY	1	1-51	2	GTWDSSLSALV	1	4.58	-	n.t.
HL CV03-150	3-5	ASC	IgA1	3-23	6	VKGSGDIERMVSTLRYYFYGLEV	22	1-47	3	AVWDDSLSAWV	12	n.exp.		
HL CV03-151	3-5	ASC	IgA1	3-23	6	VKGSGDIERMVSTLRYYFYGLDV	17	1-47	3	AVWDDSLSAWV	10	n.exp.		
HL CV03-152		ASC	IgG1	3-30	4	AKSGEVFWFGRFRRDYLDY	11	1-44	2	AAWDDRLNGVV	12	0.1		
HK CV03-153		ASC	IgM	3-74	4	ARDSCTSTSCYESMK	7	1-5	1	QHYNSYPWM	5	0.12		
HK CV03-154		ASC	IgG1	1-24	6	ATSTVIAAAGTVHYYYYYGMDV	0	2-24	2	MQATQFPYT	0	0.11		
HK CV03-155		ASC	IgG1	3-33	6	ARDEKAYDFWSGYLSYYYYGMDV	1	2-30	2	MQGTHWPPYT	0	0.09		
HK CV03-156		ASC	IgG1	5-10-1	4	ARLLYYYDSSGYYLPSPIDY	0	1-33	4	QQYDNLLLT	0	0.54	++	>250
HL CV03-158	3-5	ASC	IgA1	3-23	6	VKGSGDIERMVSTLRYYFYGLDV	16	1-47	3	AVWDDSLSAWV	10	0.1		
HL CV03-160		ASC	IgM	5-10-1	4	ARLGADSSGYYLPSGGIGY	1	1-40	3	QSYDSSLSGSKV	0	0.09		
HL CV03-161		ASC	IgG1	4-39	2	ARQRKGWLQLRGNWYFDL	2	3-10	2	YSTDSSGNQVV	0	0.09		

mAb	Clonality	Source cell	Ig isotype	IGHV gene	IGHJ gene	CDR H3	SHM IGHV	IGKV/IGLV gene	IGKJ/IGLJ gene	CDR L3	SHM IGKV/ IGLV	S1 reactivity (OD ratio)	RBD reactivity	Estimated IC$_{50}$ (ng/ml)
HL CV03-162		ASC	IgM	3-74	4	ARGGGTVVTPGPDY	11	4-69	2	QTWGIGTHDVI	6	0.07		
HL CV03-163	3-5	ASC	IgG1	3-23	6	VKGSGDIERMVDALRYYFYGMDV	27	1-47	3	AAWDDSLSAWV	15	1.17	-	n.t.
HK CV03-166		ASC	IgA1	4-4	5	TRLYCSSGACYLGP	26	3-20	1	QQYGRSPT	12	0.08		
HL CV03-167		ASC	IgG1	1-46	5	ARGRDWFDP	1	2-23	3	CSYAGSSTWV	5	0.11		
HK CV03-168		ASC	IgG1	1-69	6	AREAFYDILTGYSSTPNHYYYGMDV	0	2-28	1	MQALQTPWT	0	0.1		
HK CV03-169		ASC	IgG1	3-74	4	ARDFYYDSSGFDY	0	1-39	1	QQSYSTPPWT	0	7.53	-	n.t.
HL CV03-170		ASC	IgG3	4-4	3	ARDTIGGHAFDI	0	3-21	3	QVWDSSSDHRV	2	0.09		
HL CV03-172		ASC	IgG1	1-24	5	ATSTLFSSVVPASWFDP	0	2-14	2	SSYTSSSTPVV	0	0.09		
HK CV03-173		ASC	IgM	1-2	3	ARILPSDYFWSGYYSIQETDAFDI	0	1-5	2	QQYNSYSSS	0	0.08		
HK CV03-174		ASC	IgG1	5-51	4	ARQVFIAVAGTGFDY	1	2-28	1	MQALQTPWT	0	2.68	-	> 250
HL CV03-175		ASC	IgG1	4-31	5	ARDFVSGPLMTENVPIYDSSGYYLTRYNWFDP	0	1-51	2	GTWDSSLSAVV	3	0.1		
HL CV03-177	3-4	ASC	IgG1	3-23	4	AKDSGSYLLN	0	3-1	1	QAWDSSTYV	1	3.3	-	n.t.
HL CV03-179		ASC	IgG1	1-2	6	AREDGSSPLGGGMDV	0	3-1	1	QAWDSSTYV	1	0.09		
HL CV03-180	3-5	ASC	IgA1	3-23	6	VKGSGDIERMVSSLRYYFYGLDV	15	1-47	3	AVWDDSLSAWV	12	0.09		
HK CV03-181		ASC	IgG1	1-69	4	ASTGHHQDASDY	0	3-11	3	QQRSNWPPRVT	0	0.07		
HL CV03-182		ASC	IgG1	1-2	4	ARERLAAAGTDFDY	1	1-40	1	QSYDSSLSDYV	2	0.09		
HL CV03-183	3-5	ASC	IgA1	3-23	6	VKGSGDIERMVSSLRYYFYGLDV	15	1-47	3	AVWDDSLSAWV	10	0.13		
HL CV03-185		ASC	IgG1	4-4	6	ARRGHTLLWYYYYGMDV	0	1-51	7	GTWDSSLSAGAV	2	1.82	-	> 250
HL CV03-186		ASC	IgG1	3-48	6	ARGQRGLPFYYYYGMDV	0	1-40	1	QSYDSSLSGSV	0	0.12		
HL CV03-188	3-5	ASC	IgA1	3-23	6	VKGSGDIERMVSTLRYYFYGLDV	16	1-47	3	AVWDDSLSAWV	14	0.08		
HK CV03-190		ASC	IgG1	4-4	6	ARGMGYDFWSGYSSYYGMDV	0	1-16	4	QQYNSYPLT	0	0.35	-	> 250
HK CV03-191		ASC	IgM	3-11	4	ARDLGYNRRFDY	0	1-33	4	QQYDNLPLT	1	6.16	++	> 250
HK CV03-192		ASC	IgG1	3-15	6	TTDPLRYYDSSGYLYYGMDV	1	2-28	4	MQALLTPST	1	0.12		
HL CV03-193		ASC	IgM	3-53	3	ARGGSWPNVFDI	11	8-61	3	VLYMGSGIWV	8	0.1		
HL CV03-195		ASC	IgG1	1-18	6	ARDRLRVRGVIKYYYYGMDV	0	3-25	3	QSADSSGTHWV	2	0.17		
HK CV05-101		ASC	IgA1	3-30	4	AKDRGYSSSWFSYLDS	13	3-20	4	QQYGSLRLT	9	n.exp.		
HK CV05-102	5-1	ASC	IgM	1-3	3	AREDTFSVFGVVTRGNAYDV	26	3-20	1	QQYGVSPRT	18	n.exp.		
HK CV05-104		ASC	IgA1	5-51	4	ARLGRSLQPNLGFDL	28	2-30	4	MQGSHWPLT	23	0.14		
HK CV05-107		ASC	IgG1	3-21	4	ARDSESAWNRIGNFYFDL	34	3-15	5	QQYNDWLIT	19	0.07		
HK CV05-108		ASC	IgG1	5-10-1	6	ARHHLKRGYATRYGMDV	0	1-39	1	QQSYSTPWT	0	0.12		
HK CV05-109		ASC	IgA1	4-31	4	ASLEGPYCSDTTCYEGGQGLDY	11	3-11	1	HQRGNWWT	6	0.09		
HK CV05-110	5-1	ASC	IgG1	1-3	3	AREDTFSVFGVVTRGNAYDV	26	3-20	1	QQYGVSPRT	18	0.08		
HL CV05-111		ASC	IgA1	3-33	6	ARDLDGDYVTYYYGMDV	1	2-14	2	SSYTSSSTPVV	1	8.39	++	> 250
HK CV05-113		ASC	IgG1	3-30	2	ASGDGYRNFWYFDI	31	2-28	4	MQALQTPT	13	0.09		
HL CV05-114		ASC	IgG1	3-30-3	4	ARTVGDYGDY	0	3-1	2	QAWDSSTVV	0	0.27		
HK CV05-115		ASC	IgG1	3-48	6	ARDRGGYSGYGPYYYGMDV	0	1-39	1	QQSYSTPWT	0	5.17	-	n.t.
HL CV05-116		ASC	IgA1	4-38-2	1	N/A	58	2-23	3	CSYAGAGSSNVV	18	n.exp.		
HK CV05-117		ASC	IgM	3-23	6	AKEKTSWLVAYYYGLDV	31	1-9	2	QQVNSHPHT	13	0.11		
HK CV05-118	5-2	ASC	IgA1	4-31	3	ARDYPFCGADCPWVDVFDI	23	3-15	1	QQYSNWPRT	30	0.09		
HK CV05-119		ASC	IgG1	3-30	4	AKPVGSSGYYEGGKPIDY	0	1-5	1	QQYNSYWT	3	0.12		
HL CV05-119		ASC	IgG1	3-30	4	AKPVGSSGYYEGGKPIDY	0	3-21	3	QVWDSSSDHWV	2	0.1		
HL CV05-120		ASC	IgG1	5-51	4	ARNRAGVIDY	0	6-57	3	QSYDSSNLWV	1	0.09		
HL CV05-121		ASC	IgA1	1-8	3	VRERIDYDHSGVSTSAFEF	27	1-44	1	GGWDDSLNGYV	17	0.09		
HL CV05-122		ASC	IgG1	3-23	6	AKGGYCSGGNCKMAHSYYGLDV	21	1-47	3	AAWDDSLSGHWV	7	0.07		
HK CV05-125		ASC	IgM	4-39	5	ASSNTASTMIVVVVQRNWFDP	0	3-15	5	QQYNNWPPIT	1	0.1		
HK CV05-126		ASC	IgG1	3-48	4	ARDRARAKWLAYSNYFDY	0	3-15	5	QQYNNWPL	0	0.11		
HL CV05-127		ASC	IgG1	3-33	4	ARDRVSSWEYYFDY	0	3-10	2	YSTDSSGNHRGV	1	0.12		
HL CV05-129	5-3	ASC	IgG1	4-59	6	ARDRVSGGMDV	0	3-21	2	QVWDSSSDHVV	2	n.exp.		
HL CV05-131		ASC	IgA2	3-23	4	ARGYIGYCSGSTCTTNGGGDY	23	1-51	2	VTWDSSLSAGV	8	n.exp.		
HL CV05-134		ASC	IgA1	3-23	3	AKAGIRGGISMVRAHFDI	6	2-8	1	SSYAGSNNFV	1	0.08		

mAb	Clonality	Source cell	Ig isotype	IGHV gene	IGHJ gene	CDR H3	SHM IGHV	IGKV/IGLV gene	IGKJ/IGLJ gene	CDR L3	SHM IGKV/ IGLV	S1 reactivity (OD ratio)	RBD reactivity	Estimated IC$_{50}$ (ng/ml)
HK CV05-135		ASC	IgG1	3-33	4	AREDTAMVQRFDY	0	1-39	2	QQSYSTHT	0	0.11		
HL CV05-135		ASC	IgG1	3-33	4	AREDTAMVQRFDY	0	3-1	2	QAWDSSNVV	2	0.1		
HK CV05-136		ASC	IgG1	1-69	6	ARGRDIVVESTDQDPMDV	14	4-1	5	QQYYSTSSIT	6	0.07		
HK CV05-138	5-2	ASC	IgA1	4-31	3	ARDYPFCGADCPWVDVFDI	15	3-15	1	QQYNNWPRT	12	0.06		
HL CV05-139		ASC	IgG3	3-23	6	AKDFSGANGDYYYYGMDV	0	3-25	3	QSADSSGTWV	2	0.09		
HK CV05-140		ASC	IgG1	4-59	4	AAGGGSGFYYF	30	1-5	2	QQYKSSSST	19	0.09		
HL CV05-143		ASC	IgG1	4-59	4	ARDRVAAGVDY	1	3-21	2	QVWDSSSDHVV	2	0.09		
HL CV05-144		ASC	IgG1	3-30-3	6	ARTPGDGMDV	0	3-10	2	N/A	1	0.1		
HL CV05-145		ASC	IgG1	5-10-1	4	ARHAIYCSGGSCYAYFDY	1	1-41	2	N/A	3	n.exp.		
HK CV05-146	5-2	ASC	IgA1	4-31	3	ARDYPFCGADCPWVDVFDI	22	3-15	1	QQYNNWPRT	24	0.09		
HK CV05-148		ASC	IgG1	4-39	4	ARQRTHTIFGVVVHFDY	1	4-1	1	QQYYSTPWT	1	0.1		
HK CV05-149		ASC	IgA1	4-59	6	ARGWGFPGSTNVHFYFYGLDV	29	1-9	1	QQLNSYRT	16	0.1		
HL CV05-151		ASC	IgM	4-59	6	AAGEVVTAISYYYYGMDV	0	3-1	2	QAWDSSSVV	2	0.4	-	>250
HK CV05-152		ASC	IgM	3-15	4	TTERIYDYVWGSYRYSDY	1	3-20	3	QQYGSSPVT	1	0.09		
HK CV05-153		ASC	IgA1	4-4	4	ARDLNV	28	3-15	3	QQYVNWPFT	26	0.07		
HK CV05-155		ASC	IgM	1-2	6	ARALRITMIVVVTHYGMDV	0	3-20	2	QQYGSSPYT	0	0.1		
HK CV05-157		ASC	IgG1	3-48	4	ARDKSDFWSGNFDY	15	1-33	2	QQYDNLLVT	7	0.1		
HL CV05-159		ASC	IgG1	4-38-2	4	ARDKVDYYPYYFDY	1	3-21	2	QVWDSSSDHRV	2	0.08		
HK CV05-162		ASC	IgG2	3-21	4	ARDQWSGTTVTSMGH	15	1-5	2	QQYDSNWYT	15	0.09		
HK CV05-163		ASC	IgG1	1-2	6	AREVMVRGALPPYGMDV	0	3-11	4	QQRSNWPPVT	0	10.44	++	25-250
HK CV05-164	5-2	ASC	IgA1	4-31	3	ARDYPFCGADCSWVDVFDI	21	3-15	1	QQYNNWPRT	13	0.1		
HK CV05-165		ASC	IgA1	3-74	4	AREGGDGFDY	13	1-5	4	QQYQSYPLA	14	0.1		
HK CV05-167		ASC	IgG1	1-69	3	ARGVEMATILPDDAFDI	0	3-15	4	QQYNNWPPVT	0	0.09		
HL CV05-169		ASC	IgA1	1-69	4	ARGSTHNNLFVMDY	22	7-46	2	FLSYSGVRGLFVV	17	0.06		
HL CV05-170		ASC	IgG1	1-2	6	ARVDTTGTTFWLYYYYGMDV	0	3-1	2	QAWDSSTALVV	1	0.11		
HK CV05-171		ASC	IgG1	4-30-4	4	ARLHGDYYYFDY	0	1-39	2	QQSYSTHT	5	n.exp.		
HL CV05-171		ASC	IgG1	4-30-4	4	ARLHGDYYYFDY	0	3-1	2	QAWDSSVV	0	0.09		
HK CV05-172		ASC	IgM	4-30-4	5	ARLSMTTVTRGNWFDP	0	1-39	2	QQSYSTHT	0	0.08		
HL CV05-174		ASC	IgG1	1-2	4	ARDLSNSGSSFDY	0	3-1	2	QAWDSSTADVV	0	0.11		
HK CV05-175		ASC	IgG1	1-46	3	VQDLGVRGGRRALDV	22	2-28	2	FQALQTPYT	7	0.11		
HK CV05-176		ASC	IgG1	3-53	5	ARGYPGGP	0	1-33	4	QQYDNLLT	0	0.18		
HK CV05-178		ASC	IgA2	3-23	3	AKDALGFCSGTSCYGEGAFDI	19	1-5	2	QQYNSYPYT	10	0.07		
HL CV05-178		ASC	IgA2	3-23	3	AKDALGFCSGTSCYGEGAFDI	19	2-23	3	CSYAGSSTWV	2	n.exp.		
HK CV05-181		ASC	IgG1	3-30-3	6	ARDLQYYDFWSGYLGTPGRYYYYGMDV	0	3-20	1	QQYGSSPPWT	0	0.07		
HL CV05-182	5-3	ASC	IgG1	4-59	6	ARDRVSGGMDV	0	3-21	2	QVWDSSSDHVV	1	n.exp.		
HK CV05-183		ASC	IgG1	3-30-3	6	ARDLRFLEWLFNVPYYYYYGMDV	0	1-9	2	QQLNSYPYT	0	0.11		
HL CV05-183		ASC	IgG1	3-30-3	6	ARDLRFLEWLFNVPYYYYYGMDV	0	2-23	3	CSFAGGITLV	14	n.exp.		
HK CV05-185		ASC	IgM	3-15	4	TTDRTYDYVWGSYRYRDY	0	1-39	4	QQSYSTLPRT	1	0.06		
HK CV05-187		ASC	IgG2	3-73	4	TTIGSGYGFGH	10	1-39	2	QQSYSTHT	1	n.exp.		
HL CV05-187		ASC	IgG2	3-73	4	TTIGSGYGFGH	10	2-11	2	CSYGGTYVL	11	0.1		
HL CV05-189		ASC	IgG1	3-9	6	AKAHSDPNYDFWSPDYYGMDV	1	2-14	2	SSYSTSSTKEV	5	0.10		
HL CV05-190		ASC	IgG1	3-30-3	4	ARGVYGDSGVDY	1	3-21	1	QVWDSSSDHLYV	1	0.08		
HK CV05-191		ASC	IgG2	3-11	6	ARDTSQSHMDV	15	2-30	2	MQGTHWPPYT	6	0.08		
HK CV05-192	5-1	ASC	IgG1	1-3	3	AREDTFSVFGVVTRGNAYDV	26	3-20	1	QQYGVSPRT	20	0.11		
HL CV05-194		ASC	IgG1	3-74	1	ARDRHTYSLEYFQH	0	6-57	3	QSYDSSNQV	1	0.08		
HL CV05-195		ASC	IgG1	3-30	4	AKEGSKGWLQSSCYFDY	0	3-25	2	QSADSSGTYQV	2	0.1		
HK CV07-102		ASC	IgG1	1-18	6	ARDLARVGWTWWYYYYGMDV	2	2-30	1	MQGTHWPRT	0	n.exp.		
HL CV07-103		ASC	IgM	3-23	4	AKVYGSNTHTPVDY	5	2-8	2	SSYAGSNNVV	4	0.09		
HK CV07-104		ASC	IgG1	3-7	6	ARDAARYYGMDV	24	1-39	2	QQSYSTPRT	10	0.09		
HK CV07-107		ASC	IgG3	3-23	6	AKDRRTMIVVVITNKYYYGMDV	0	1-5	4	QQYNSYPLT	0	0.11		

mAb	Clonality	Source cell	Ig isotype	IGHV gene	IGHJ gene	CDR H3	SHM IGHV	IGKV/IGLV gene	IGKJ/IGLJ gene	CDR L3	SHM IGKV/ IGLV	S1 reactivity (OD ratio)	RBD reactivity	Estimated IC_{50} (ng/ml)
HL CV07-108		ASC	IgM	3-15	4	TTDADTSPVV	4	4-69	3	QTWDTGIRV	7	0.08		
HK CV07-110		ASC	IgM	3-48	4	ARSLRMG	7	3-20	1	HQYGSIPRT	12	n.exp.		
HK CV07-113		ASC	IgA1	4-59	6	ARASFKMGTNYHYGMDV	13	1-27	3	QNYNSVPFT	12	0.08		
HK CV07-114		ASC	IgG1	1-2	4	TTLTAVVTPLGY	40	2-30	1	MQGTHWPRT	1	0.07		
HL CV07-118		ASC	IgM	3-15	3	TTDEQRNYCTSPNCRGGAFDI	7	4-69	3	QTWGTGIRV	7	n.exp.		
HK CV07-121		ASC	IgG1	4-39	5	MRQGDWNYSYYFDA	35	2-30	4	VQGTLWPLT	12	n.exp.		
HK CV07-127		ASC	IgA1	4-39	6	ARHPLALITIFGVSRQYGMDV	0	1-12	1	QQANSFPWT	1	0.1		
HL CV07-128		ASC	IgG2	3-30-3	4	ARELGTSGTLDS	23	2-14	3	LSHSTFTTPQWV	21	0.08		
HL CV07-129		ASC	IgG1	3-48	3	ASIASYDYVWGTNRPNDAFDI	17	2-23	1	CSYGGPRNLYV	15	0.09		
HL CV07-132		ASC	IgM	4-4	4	ARDRQYRGSDYNYYFDY	3	1-44	3	ATWDDSLNGRV	5	0.09		
HK CV07-133		ASC	IgG2	4-39	4	ARHQRPVTTFIDY	29	3-15	3	QHYKDWPPFFT	19	0.08		
HK CV07-134		ASC	IgG1	3-23	6	AKVMRDDFWSGYYNDYYYGMDV	6	3-20	2	QQYGRT	0	0.09		
HK CV07-136		ASC	IgG1	4-59	6	ARDNYSSRRYYYYYGMDV	0	3-20	1	QQYGSSPTWT	0	0.10		
HL CV07-137		ASC	IgM	4-30-4	5	ARLSMTTVTRGNWFDP	0	1-47	3	AAWDDSLSGWV	0	0.10		
HK CV07-138		ASC	IgA2	3-23	2	VKDFPFGGCTSTTTNCDLFFAL	21	2-24	1	MQATQFPRA	11	n.exp.		
HK CV07-139		ASC	IgG2	4-59	5	AGYLRNDNLDP	11	3-11	4	QQRSDWPLT	9	n.exp.		
HK CV07-140		ASC	IgA1	3-64	4	AREYYGLLTGYYLDL	19	1-39	1	QQSYSIPWT	24	0.08		
HK CV07-143	7-3	ASC	IgG1	3-23	4	AKEFSIGWGLFDS	17	3-11	5	QQRNNWPVT	13	n.exp.		
HK CV07-147		ASC	IgG1	1-2	6	ARDLYYDILTGYYMPMDV	4	3-11	5	QQRGNWPPIT	4	n.exp.		
HK CV07-151		ASC	IgG1	1-58	3	AADPGGVGYCSGGSCYRAFDI	1	3D-15	4	QQYNNWPPALT	0	0.09		
HL CV07-152		ASC	IgG1	1-69	3	ARLRVPLTAHDAFDI	0	1-40	3	QSYDSSVGV	3	0.09		
HL CV07-154		ASC	IgG1	1-69	6	ARAYCSGGSCYSYYYGMDV	2	3-1	2	QAWDSSTA	0	0.11		
HK CV07-155		ASC	IgM	4-59	6	ARVPREWLSPLYYG	2	1-5	1	QQYNSYQWT	0	0.09		
HL CV07-156		ASC	IgG1	3-9	4	VKDNARTRRGSFDY	15	2-23	1	CSYAGSNTYV	13	0.09		
HL CV07-159		ASC	IgG2	3-48	3	AREGELSNYDAFDI	18	2-11	1	CSYAGTHSYV	9	0.08		
HK CV07-161		ASC	IgG1	3-30	4	AKEGSKGWLQSSCYFDY	1	2-28	5	MQAFEPPAIT	40	0.12		
HK CV07-163		ASC	IgM	3-33	4	ARDWAVAGNFDY	14	3-20	5	QQYGASPPTT	7	0.09		
HL CV07-164		ASC	IgA1	1-46	4	ARDGSHWDFDY	22	2-14	3	SSYVSSDAWV	4	0.09		
HL CV07-165		ASC	IgM	3-53	4	ARRAASGWNFDY	9	2-23	3	CSYLGSATYV	19	n.exp.		
HK CV07-166		ASC	IgG1	1-18	6	ARDTWDIVIVPAASAYYGMDV	21	2-28	2	MQALQTHT	1	n.exp.		
HK CV07-172		ASC	IgM	3-15	4	TTDRTYDYVWGSYRYRDY	0	1-39	1	QQTFSSPPWT	27	0.07		
HK CV07-173		ASC	IgM	3-30	6	SKGFLEWLLRRYYYGMDV	3	1-9	3	QQLNSYPFT	0	0.07		
HK CV07-176		ASC	IgA1	5-51	6	ARHFGGSGSYYNGHWIPAYYYHGMDV	7	2-28	4	MQARQTPPLT	4	n.exp.		
HL CV07-176		ASC	IgA1	5-51	6	ARHFGGSGSYYNGHWIPAYYYHGMDV	7	2-8	2	SSYAGSTNLV	4	n.exp.		
HK CV07-178		ASC	IgG2	4-31	3	ARDRTMVVWNAFDI	17	1-39	1	QQSHSPSRT	13	0.18		
HL CV07-179		ASC	IgA1	3-7	5	ARESRLGIAIFDRRLRSWFGA	0	2-14	1	SSYTSSSTRV	0	n.exp.		
HK CV07-180		ASC	IgM	3-15	4	TTQHYDFWSGNYKPFAF	12	2-28	5	MQALQTLT	3	0.11		
HL CV07-181		ASC	IgA1	3-33	4	ARDEAAEYYFDY	1	3-25	3	QSADSSGTFWV	1	0.11		
HK CV07-183		ASC	IgG1	3-30	4	AKEGSKGWIQNSCYFDY	12	4-1	1	QQYYSTPPT	3	n.exp.		
HK CV07-185		ASC	IgA1	3-23	4	VKDPNWANGY	30	2-30	4	VQGTHWPLT	16	n.exp.		
HK CV07-186		ASC	IgA1	1-46	4	AKGRSTIFGVIVNQGDCYDY	9	1-27	4	QKYNSAPLT	4	0.10		
HK CV07-189		ASC	IgG1	3-23	4	AKDPHFDFWSGNYFDY	5	1D-12	4	QQANSFPLT	0	0.06		
HK CV07-190		ASC	IgM	4-31	3	ARDRGVTIFGVVIIDAFDI	1	3-20	4	QQYGSSPLT	0	0.05		
HK CV07-191		ASC	IgG1	1-18	6	SREGDLTIFGSVTNAYYYFGMDF	3	1-39	5	QQSYSTPIT	1	n.exp.		
HL CV07-196	7-1	S1-MBC	IgM	1-2	4	ARDLGIGVAGNLDH	4	2-8	3	SSYAGSNNWV	2	2.06	++	>250
HK CV07-199		S1-MBC	IgM	4-59	5	ARDRDSSGWYPNWFDP	2	1D-16	1	QQYNSYPRT	0	0.07		
HL CV07-200	7-2	S1-MBC	IgG1	1-2	6	ARGPFYYDNSGTLGGLDV	5	2-14	1	SSYTSSSTYV	1	8.57	++	25
HL CV07-201	7-4	S1-MBC	IgM	1-2	6	ATDRLVNTGVYTTGSMDV	8	2-23	1	CSYGGSSDYV	2	4.03	++	>250
HK CV07-202		S1-MBC	IgG1	3-53	6	ARDLYYYGMDV	4	1-9	4	QQLNNYSVT	2	8.87	++	25-250
HL CV07-203		S1-MBC	IgM	1-2	6	ARKQQPSSLSYYYYGMDV	1	1-40	3	QSYDSSLSGSWV	3	0.06		

mAb	Clonality	Source cell	Ig isotype	IGHV gene	IGHJ gene	CDR H3	SHM IGHV	IGKV/IGLV gene	IGKJ/IGLJ gene	CDR L3	SHM IGKV/ IGLV	S1 reactivity (OD ratio)	RBD reactivity	Estimated IC_{50} (ng/ml)
HL CV07-204		S1-MBC	IgM	4-39	6	ALCGYSYGSNYYYYGMDV	0	6-57	3	QSYDSSIWV	2	0.09		
HK CV07-205		S1-MBC	IgM	3-23	4	AKEYGYDSSGSGGDY	0	1-39	1	QQSYSTPNT	0	0.07		
HL CV07-205		S1-MBC	IgM	3-23	4	AKEYGYDSSGSGGDY	0	2-23	3	CSYAGSSTWV	2	n.exp.		
HK CV07-206		S1-MBC	IgM	1-2	6	AREGYYDFWSGYYTVYYYGMDV	0	1-5	1	QQYNSYWT	9	n.exp.		
HL CV07-206		S1-MBC	IgM	1-2	6	AREGYYDFWSGYYTVYYYGMDV	0	2-14	3	SSYTSSSTRV	1	3.98	++	250
HL CV07-208	7-2	S1-MBC	IgM	1-2	6	ARGPFYYDSSGTLGGMDV	3	2-14	1	SSYTSRNTYV	5	n.exp.		
HK CV07-209		S1-MBC	IgG1	3-11	4	ARDGVIPPRFDY	2	1-33	4	QQYDNLPLT	1	12.06	++	<25
HL CV07-210		S1-MBC	IgM	3-21	4	VSSGNYRFHY	8	2-14	1	SSYMSSSTPYV	4	0.18		
HL CV07-213	7-5	S1-MBC	IgM	1-8	4	ARGPSWNGYYYYFDY	6	1-44	2	ASWDDRLNGVV	7	0.1		
HK CV07-214		S1-MBC	IgG1	6-1	3	AREENAFDI	0	3-15	2	QQYSNWLLYT	4	7.69	++	>250
HK CV07-215		S1-MBC	IgM	3-48	3	AREGHAFDI	2	3-20	1	QQYGSSPSWT	1	0.08		
HK CV07-216		S1-MBC	IgM	3-7	4	VAWGTTPLGTSENN	16	2-30	2	MQHTHWPHT	11	0.08		
HL CV07-217	7-5	S1-MBC	IgM	1-8	4	ARGPSWNGYYYYFDY	6	1-44	2	ASWDDSLNGVV	8	0.12		
HL CV07-218		S1-MBC	IgM	3-23	4	AKRMGGNRFNPPVEY	12	1-40	3	HSYDSSLSASV	6	n.exp.		
HK CV07-219		S1-MBC	IgG2	3-11	6	ARDGIGQLWDDSYYYGLDV	15	2-30	2	MQGAHWPPYT	10	3.68	++	>250
HL CV07-221	7-4	S1-MBC	IgM	3-30	6	AKKAGYSSGWYTDYYYNGMDV	1	1-40	3	QSYDSSLRGV	4	0.15		
HL CV07-222		S1-MBC	IgG1	1-2	3	ARGPYYYDSSGSLGAFDI	5	2-23	1	CSYAGGSTSYV	2	12.03	++	<25
HL CV07-223	7-5	S1-MBC	IgM	1-8	4	VRGPSWNGYYYYFDY	6	1-44	2	ASWDDSLNGVV	3	0.08		
HL CV07-224		S1-MBC	IgM	5-51	6	ARLGPYYSSSSNGMDV	2	2-23	3	CSYAGSSTRV	3	0.08		
HK CV07-225		S1-MBC	IgG1	4-31	6	ARDTPPGYNWNYGPYGMDV	9	3-15	2	QQYNNWPPGYT	4	4.78	++	>250
HL CV07-226		S1-MBC	IgM	3-30	6	AKKAGYSSGWYTDYYYNGMDV	1	2-8	3	SSYTASNRG	41	n.exp.		
HL CV07-230		S1-MBC	IgM	3-9	4	AKEISGYYFDY	7	4-69	3	QTWGTGIHWV	14	0.08		
HL CV07-231	7-4	S1-MBC	IgM	3-30	6	AKKAGYSSGWYTDYYYNGMDV	1	1-40	3	QSYDSSLRGV	4	0.07		
HL CV07-235		S1-MBC	IgM	3-23	6	AKSTYGDYYYYYGMDV	7	2-14	3	NSYTSNSSLGV	8	6.16	++	>250
HK CV07-236		S1-MBC	IgM	3-53	4	AREYSSGWYDY	0	3-15	4	QQYNNWPLT	3	0.09		
HL CV07-237	7-2	S1-MBC	IgA1	1-2	6	ARGPFYYDSSGTLGGMDV	3	2-14	1	SSYTSSSTYV	0	5.58	+	n.t.
HL CV07-238		S1-MBC	IgM	1-8	6	ARTNWNYYYYYYGMDV	0	1-44	1	AAWDDSLNGYV	2	0.09		
HL CV07-239		S1-MBC	IgM	4-34	3	ARGRWYHDNNGYRSDAFDV	17	1-44	3	AAWDDSLNEV	9	0.07		
HL CV07-241		S1-MBC	IgM	3-74	4	ITSMFNNGFY	7	2-11	2	SSYAGSYTV	7	0.08		
HL CV07-242		S1-MBC	IgM	3-15	5	TTLWRLDP	46	7-46	3	LLTHTDSRV	11	n.exp.		
HL CV07-249	7-1	S1-MBC	IgM	1-2	4	ARDLGIGVAGNLDH	1	2-8	3	SSYAGSNNWV	3	2.87	+	n.t.
HL CV07-250		S1-MBC	IgG1	1-18	6	AGSDNYGFPYNGMDV	17	2-8	2	SSYAGNNDFV	16	8.27	++	25
HK CV07-251	7-3	S1-MBC	IgM	3-23	4	AKEFSIGWGLFDY	9	3-11	5	QQRNNWPVT	8	8.79	++	25-250
HK CV07-252		S1-MBC	IgG1	1-46	6	ARDKHWNNANYYYYGMDV	1	1-5	4	QQYNSYL	2	6.03	++	>250
HL CV07-254		S1-MBC	IgM	1-2	4	ARDQGGAALVGHSNY	10	2-23	2	CSYAGSSTWV	3	6.71	++	>250
HL CV07-255		S1-MBC	IgG1	1-2	4	ARDSRFSYVNGEFDY	3	2-23	3	CSYAGHSTWV	5	9.54	++	25
HL CV07-262		S1-MBC	IgG1	1-2	6	ARVGWYDFGTPGDYYYYYGMDV	6	2-23	1	CSYAGTSTFV	3	10.2	++	< 25
HK CV07-263		S1-MBC	IgG1	1-2	6	ADSGYWGSHYYYGMDV	3	2D-29	1	MQSIQLPLT	0	7.87	++	25-250
HL CV07-264	7-1	S1-MBC	IgA2	1-2	4	ARDLGIGVAGNLDH	1	2-8	3	SSYAGSNNWV	2	7.08	++	250
HK CV07-265		S1-MBC	IgG1	3-48	6	ARRRYSSSWYYYYGMDV	2	1-9	4	QQLNSYPLT	0	6.41	-	n.t.
HL CV07-266	7-4	S1-MBC	IgG1	1-2	6	ATDRLVNTGVYTTGSMDV	8	2-23	1	CSYGGSSDYV	2	4.62	++	>250
HL CV07-267	7-6	S1-MBC	IgA1	1-2	6	ARVFGPGLDCSSTSCYTYGMDV	2	2-23	3	CSYAGSSSWV	1	8.47	++	250
HL CV07-270		S1-MBC	IgG3	3-11	5	ARARGSSGWYRIGTRWGNWFDP	2	2-14	2	SSYTSSSNVV	0	8.53	++	25-250
HL CV07-271		S1-MBC	IgA1	1-2	6	ARVPFAYCSSTSCDRGTPYYYYYGMDV	0	2-14	2	SSYTSSSTLV	3	8.28	++	>250
HK CV07-272		S1-MBC	IgM	3-64	4	ARGLDNNGYYSGY	16	3-20	1	QQYGSSPRT	5	0.08		
HL CV07-274	7-7	S1-MBC	IgM	1-2	4	ARDQKNDILTGLGDY	4	2-8	3	SSYAGSNNWV	1	3.97	++	>250
HL CV07-275		S1-MBC	IgG1	3-66	4	ARDYYDSSGYYSSGGLGY	0	2-8	1	SSYAGSNNFV	0	4.51	++	>250
HL CV07-280	7-2	S1-MBC	IgA1	1-2	6	ARGPFYYDSSGTLGGMDV	2	2-14	1	SSYTSSSTYV	0	7.29	++	25-250
HL CV07-281	7-2	S1-MBC	IgM	1-2	6	ARGPFYYDSSGTLGGMDV	2	2-14	1	SSYTSSSTYV	0	5.07	+	n.t.
HL CV07-283	7-2	S1-MBC	IgA1	1-2	6	VRGPFYYDSSGPLGGMDV	7	2-14	1	SSYTSSSTYV	2	9.89	++	25

mAb	Clonality	Source cell	Ig isotype	IGHV gene	IGHJ gene	CDR H3	SHM IGHV	IGKV/IGLV gene	IGKJ/IGLJ gene	CDR L3	SHM IGKV/ IGLV	S1 reactivity (OD ratio)	RBD reactivity	Estimated IC_{50} (ng/ml)
HL CV07-284		S1-MBC	IgM	5-51	6	ASGGDYPYGMDV	5	1-44	3	AAWDDSLSAWV	1	0.87	++	>250
HL CV07-285	7-2	S1-MBC	IgA1	1-2	6	ARGPFYYDNSGTLGGLDV	5	2-14	1	SSYTSSSTYV	1	9.3	++	25
HL CV07-286		S1-MBC	IgG1	3-9	6	AKGGRYCSGTNCYEYYFFAMDV	8	2-8	2	SSYAGSNNNVV	3	0.09		
HK CV07-287		S1-MBC	IgG1	1-58	3	AAPYCSSTNCYDAFDI	0	3-20	1	QQYGSSPWT	0	9.25	++	25-250
HK CV07-289		S1-MBC	IgM	1-2	6	ARGAAMVTGYTYYYGLDV	3	3-20	5	QQYGSSPIT	2	0.07		
HL CV07-290	7-7	S1-MBC	IgM	1-2	4	ARDQKNDILTGLGDY	0	2-8	3	SSYAGSNNWV	0	3.02	++	>250
HL CV07-292	7-7	S1-MBC	IgM	1-2	4	ARDQKNDILTGLGDY	3	2-8	3	SSYAGSNNWV	0	7.92	++	250
HK CV07-293		S1-MBC	IgM	3-11	6	ARCNGGGACFYGMDV	10	4-1	5	QQYYSTLT	3	0.07		
HL CV07-293		S1-MBC	IgM	3-11	6	ARCNGGGACFYGMDV	10	2-14	3	SSYTISSTWV	4	0.07		
HL CV07-294	7-2	S1-MBC	IgM	1-2	6	ARGPFYYDSSGTLGGMDV	2	2-14	1	SSYTSSSTYV	0	5.69	++	>250
HL CV07-297		S1-MBC	IgM	3-53	4	ARRSASGWNFDY	13	2-8	3	SSYAGSNNLV	8	0.08		
HL CV07-299		S1-MBC	IgM	5-51	4	ATSHGYSGYELGY	9	2-14	3	SSYTSSSTVWV	29	n.exp.		
HK CV07-301		S1-MBC	IgG1	1-2	6	ARVDTTGTTFWLYYYYGMDV	2	2D-29	3	N/A	0	0.17		
HL CV07-301		S1-MBC	IgG1	1-2	6	ARVDTTGTTFWLYYYYGMDV	0	2-23	3	CSYAGSSTWV	2	n.exp.		
HK CV07-302		S1-MBC	IgA1	3-9	6	AKDKGPYYYYGMDV	0	2D-29	1	MQSIQLPQT	0	1.51	++	250
HL CV07-303	7-1	S1-MBC	IgM	1-2	4	ARDLGIGVAGNLDH	4	2-8	3	SSYAGSNNWV	3	4.71	++	250
HL CV07-304	7-6	S1-MBC	IgA1	1-2	6	ARVFGPGLDCSSTSCYTYGMDV	1	2-23	3	CSYAGSNSWV	2	8.08	++	>250
HL CV07-305	7-1	S1-MBC	IgM	1-2	4	ARDLGIGVAGNLDH	2	2-8	3	SSYAGSNNWV	2	0.93	++	>250
HK CV07-306		S1-MBC	IgA1	1-2	4	ARGTLYYDILTGSPNPPKLDY	0	1-39	1	QQSYSTPWT	0	8.25	++	250
HL CV07-307	7-2	S1-MBC	IgA2	1-2	6	ARGPFYYDNSGTLGGLDV	5	2-14	1	SSYTSSSTYV	1	9.27	++	25
HL CV07-309	7-2	S1-MBC	IgM	1-2	6	ARGPFYYDNSGTLGGLDV	5	2-14	1	SSYTSSSTYV	1	8.62	++	25-250
HL CV07-310	7-2	S1-MBC	IgA1	1-2	6	ARGPFYYDSSGTLGGMDV	3	2-14	1	SSYTSSSTYV	0	5.11	+	n.t
HL CV07-312		S1-MBC	IgM	1-2	6	ARIPIFGVVSTPGQYYYYGMDV	6	2-14	3	ISYTSSSTWV	1	0.18		
HL CV07-313	7-4	S1-MBC	IgA1	1-2	6	ATDRLVNTGVYTTGSMDV	9	2-23	1	CSYGGSSDYV	2	0.09		
HK CV07-315		S1-MBC	IgG1	3-9	6	AKDFLWDLHPPRYYGMDV	0	1-39	2	QQSYSTHA	1	0.16		
HL CV07-315		S1-MBC	IgG1	3-9	6	AKDFLWDLHPPRYYGMDV	0	1-51	3	GTWDSSLNGV	1	11.4	++	25
HL CV07-316	7-2	S1-MBC	IgA1	1-2	6	ARGPFYYDSSGTLGGMDV	2	2-14	1	SSYTSSSTYV	1	3.12	+	n.t
HL CV07-317	7-7	S1-MBC	IgM	1-2	4	ARDQKNDILTGLGHY	0	2-8	3	SSYAGSNNWV	0	2.53	++	>250
HK CV07-319		S1-MBC	IgM	1-2	5	ARGPFFFEVVVAEGFGWFDP	28	3-15	5	QQYNNWPPIT	1	n.exp.		
HL CV07-319		S1-MBC	IgM	1-2	5	ARGPFFFEVVVAEGFGWFDP	28	2-8	1	SSYAGSNVYV	0	n.exp.		
HL CV07-323	7-6	S1-MBC	IgA1	1-2	6	ARVFGPGLDCSSTSCYTYGMDV	0	2-23	3	CSYAGSSSWV	1	7.39	++	>250
HL CV07-324	7-2	S1-MBC	IgA1	1-2	6	ARGPFYYDSSSTLGGMDV	4	2-14	1	SSYTSSSTYV	3	11.02	++	25-250
HK CV23-101		S1-MBC	IgM	3-30	4	ARDWEYYGSGTKAFDY	9	1-13	4	QHFNSYPLT	9	4.33	++	>250
HL CV23-103		S1-MBC	IgA1	1-2	4	N/A	47	2-14	2	SSYTRSTAVV	19	n.exp.		
HL CV23-113		S1-MBC	IgM	5-51	4	ATTRGYSDYEFAY	11	2-8	3	SSYAGSNNFPWV	3	n.exp.		
HK CV23-114		S1-MBC	IgM	4-31	5	ARDLGPRSDFGSGSGVGVIDP	10	3-15	1	QQYHNWPPWT	5	n.exp.		
HL CV23-115		S1-MBC	IgM	1-2	3	ARGYYDILIGYATTHDAFDL	8	2-14	3	SSYTDSSTWV	6	n.exp.		
HK CV23-116		S1-MBC	IgM	3-21	6	ARASLVTMVRGAGNYMDV	0	3-11	5	QQRSNWPLT	0	0.11		
HL CV23-116		S1-MBC	IgM	3-21	6	ARASLVTMVRGAGNYMDV	0	2-23	3	CSYAGSRV	2	0.09		
HL CV23-121		S1-MBC	IgM	1-2	4	ARELGSWDGRFDY	0	2-23	3	CSYAGSSTWV	0	0.10		
HK CV23-126		S1-MBC	IgM	4-59	6	ARDTTSYCSGGSCYYNYGMDV	7	2-28	3	MQALQTPRT	3	0.07		
HL CV24-198	24-1	S1-MBC	IgA1	1-2	3	ARDLAYSMVRGISGI	7	2-23	3	CSYAGSNTWV	7	5.48	++	250
HL CV24-201	24-1	S1-MBC	IgA1	1-2	3	ARDLAYSMVRGISGI	7	2-23	3	CSYAGSNTWV	9	5.79	++	>250
HK CV24-220		S1-MBC	IgA2	3-48	4	ARDRGSGWSLDESYFDH	15	1-39	2	QQSKSIPYT	17	n.exp.		
HL CV24-223	24-5	S1-MBC	IgM	4-39	4	ARLRWLRGEFDY	0	6-57	3	QSYDSSTYWV	0	8.83	++	>250
HL CV24-226	24-5	S1-MBC	IgM	4-39	4	ARLRWLRGEFDY	0	6-57	3	QSYDSSTYWV	0	8.77	++	>250
HL CV24-236		S1-MBC	IgM	3-49	4	IRGGYGGNSGFDY	5	1-51	2	GTWDSSLSAVV	3	0.15		
HL CV24-243		ASC	IgM	3-7	4	ARLYSGNYFDY	6	4-69	3	QTWDTAIWV	14	n.exp.		
HK CV24-247		ASC	IgA1	3-48	5	ARGFYDILTGYYSFHFDL	16	1-5	1	QQYNTYWT	7	0.35		
HK CV24-248	24-2	ASC	IgG1	3-33	6	ARREGVADYYYYYGMDV	8	1-6	1	LQVYNYPWT	6	0.09		

mAb	Clonality	Source cell	Ig isotype	IGHV gene	IGHJ gene	CDR H3	SHM IGHV	IGKV/IGLV gene	IGKJ/IGLJ gene	CDR L3	SHM IGKV/ IGLV	S1 reactivity (OD ratio)	RBD reactivity	Estimated IC_{50} (ng/ml)
HL CV24-249		ASC	IgG1	1-18	6	AREYDYSNPNYYYYYGMDV	0	3-27	3	YSAADNMGV	1	0.08		
HK CV24-252		ASC	IgG1	3-74	6	VRVSGPFHDYFLYAMDV	19	3-20	1	QHYSAATWT	14	0.09		
HL CV24-253	24-3	ASC	IgA1	1-2	4	ARVFHGVITPFDY	12	5-37	2	MIWPSSAVV	7	0.07		
HK CV24-255		ASC	IgG1	4-34	4	ARGRLGFEELFRGVFFYYFDY	21	1-39	2	QQTFNSPRT	22	0.07		
HK CV24-256	24-4	ASC	IgM	3-49	5	TRAQEEKITMIRRIISWFDP	5	3-20	5	QQYGSSPIT	6	0.1		
HL CV24-260		ASC	IgG1	4-59	6	ARLLKSCTGGICQTYFYYAMDV	21	1-40	1	QSYDGSLSESAV	20	0.1		
HK CV24-262		ASC	IgA1	4-31	4	ARGTTYTIFGVVISPFDY	0	3-20	4	QQYGSSPLT	0	0.09		
HK CV24-265		ASC	IgG1	4-34	5	ARGAPGT	30	1-5	2	QHYSTFPYT	15	0.1		
HK CV24-268		ASC	IgG1	3-9	4	TTGYCRSNNCLTFYAF	20	1-39	2	QQSYRAPVT	13	0.08		
HL CV24-269		ASC	IgM	4-31	6	ARDYFGRSGSGSSLYYYYGMDV	0	3-1	2	QAWDSSTV	0	5.39	-	n.t.
HK CV24-271		ASC	IgG1	3-21	4	ARVAAAGQKYYFDY	0	1-9	4	QQLNS	0	0.12		
HL CV24-275		ASC	IgG1	3-30	6	AKVANVFMLYPRGSWGMDV	14	1-47	3	AAWDDSLSGWV	14	0.09		
HK CV24-280		ASC	IgG1	3-48	6	AAGSSTSPSPV	0	3-15	1	QQYNNWPRT	0	0.16		
HK CV24-282		ASC	IgG1	3-23	6	AKDRGRRLTHLGVAPDV	23	1-39	2	QQSYTTPYT	19	0.15		
HK CV24-283		ASC	IgM	3-66	4	CGGYGSSWYLDY	20	3-11	2	QQRSNWPYT	10	0.15		
HL CV24-284		ASC	IgG1	4-31	4	ARGGLSSRNGGNRSYSSSSFPLGRQDY	0	2-14	1	SSYTSSSTLYV	1	0.15		
HL CV24-285		ASC	IgM	5-51	4	ARFLSFVTSPTRYDY	6	2-14	1	SSYTSSSTLV	8	0.14		
HK CV24-286		ASC	IgG1	1-69	3	ARHLPLSGYYAFDV	22	3-20	2	QQYGSSPYT	13	0.19		
HK CV24-287		ASC	IgM	3-23	3	AKDRSGGILAGGSGGALDI	26	1-5	1	QQYSSYSRT	14	0.16		
HL CV24-290		ASC	IgG1	4-39	4	ARASEDISLERAYNYGLTIDF	10	3-9	2	QVWDSSTVV	6	0.16		
HL CV24-293		ASC	IgA1	3-7	6	ARENYDSSGYYYAYYYYGMDV	0	3-25	1	QSADSSGTYV	3	n.exp.		
HK CV24-294		ASC	IgM	3-9	4	ARGDLGIRYFDY	5	3-15	5	QQYNNWPPIT	1	n.exp.		
HL CV24-294		ASC	IgM	3-9	4	ARGDLGIRYFDY	5	2-23	3	CSYAGSSTWV	2	n.exp.		
HK CV24-296		ASC	IgG3	1-18	1	N/A	11	4-1	2	QQYHSTPPA	4	n.exp.		
HL CV24-296		ASC	IgG3	1-18	1	N/A	11	2-23	3	CSYAGSSTWV	2	n.exp.		
HK CV24-298		ASC	IgG1	3-33	3	ARGWGGDGYTVDAFDV	19	2-28	2	MQALQPPYI	9	n.exp.		
HK CV24-301		ASC	IgG1	1-46	5	ARSLYSGSYGAYNWFDP	19	3-11	4	LQRINWLT	13	n.exp.		
HK CV24-309		ASC	IgG1	4-61	6	AREQVLDPGLYYGIDV	29	1-39	2	QQSYSTHT	1	n.exp.		
HL CV24-309		ASC	IgG1	4-61	6	AREQVLDPGLYYGIDV	29	3-1	2	QAWDSDTVI	23	n.exp.		
HL CV24-310	24-3	ASC	IgG1	1-2	4	ARVFHGVITPFDF	19	5-37	2	MIWPSSDVV	4	n.exp.		
HL CV24-311		ASC	IgG1	1-2	4	ARGADIFITIFGVVIKENDY	0	2-18	2	SSYTSSSTLV	2	n.exp.		
HL CV24-314		ASC	IgM	3-30	4	ARGKNYGYSDDDLFQHFDY	3	7-43	3	LLHYGSSQLGV	12	n.exp.		
HK CV24-316		ASC	IgG1	1-69	6	ARALGLSGHGMDV	29	1-39	2	QHSYSTPHT	17	n.exp.		
HL CV24-317		ASC	IgG1	4-4	3	AKESWLELWLQGAGFDI	16	2-11	2	CSYGGSYTFVV	12	n.exp.		
HL CV24-319		ASC	IgG1	1-46	6	ARDLWMEYEYNDSGIQKTADQGMDV	16	3-1	3	QAWDINTVV	17	n.exp.		
HK CV24-321		ASC	IgM	3-33	3	ARDMVRGPNDASDI	10	1-12	4	QQANSFPLT	4	n.exp.		
HL CV24-322		ASC	IgG1	4-39	4	ARQRTHTIFGVVVHFDY	1	3-25	1	QSADSSGTYDV	3	n.exp.		
HK CV24-323	24-4	ASC	IgM	3-49	5	TRAQEEKITMIRRIISWFDP	5	3-20	5	QQYGSSPIT	6	n.exp.		
HK CV24-325	24-4	ASC	IgM	3-49	5	TRAQEEKITMIRRIISWFDP	5	3-20	5	QQYGSSPIT	8	n.exp.		
HK CV24-329		ASC	IgM	3-33	3	ARDMVRGPNDASDI	10	3-15	5	QQYNNWPPVT	3	n.exp.		
HK CV24-330	24-4	ASC	IgM	3-49	5	TRAQEEKITMIRRIISWFDP	5	3-20	5	QQYGSSPIT	11	n.exp.		
HL CV24-331		ASC	IgG1	3-23	6	AKEVPDIIVVAVAVGMDV	21	1-47	2	ASWDDSLSGVL	12	n.exp.		
HL CV24-332		ASC	IgG1	1-2	6	ARETRETYYDILTGYPFYYYFGMDV	9	1-51	2	GTWDGSLSAAV	11	n.exp.		
HL CV24-333		ASC	IgM	3-15	4	SSDLPKWGSGMADY	13	8-61	3	VLYMGSDIWA	12	n.exp.		
HK CV24-336	24-4	ASC	IgM	3-49	5	TRAQEEKITMIRRIISWFDP	5	3-20	5	QQYGSSPIT	8	n.exp.		
HK CV24-344	24-2	ASC	IgG1	3-33	6	ARREGVADYSYSCGMDV	10	1-6	1	LQVYNYPWT	11	n.exp.		
HK CV24-346		ASC	IgG1	1-69	3	ARSDDSSGYYYLKEENDAFDI	0	2-30	2	MQGTHWREYT	1	n.exp.		
HL CV24-347		ASC	IgG3	1-2	6	ARDRLYCSSTSCYTPYYYYYYGMDV	0	3-25	3	QSADSSGTYGV	3	n.exp.		
HL CV38-102		S1-MBC	IgG1	3-23	2	AKVETRGVGFDL	1	3-1	2	QAWDSSTVV	1	8.7	-	n.t.
HK CV38-103		S1-MBC	IgA1	3-11	4	ARDWNLSGYYGGGR	1	1-16	4	QQYNSYPLT	0	5.84	++	>250

mAb	Clonality	Source cell	Ig isotype	IGHV gene	IGHJ gene	CDR H3	SHM IGHV	IGKV/IGLV gene	IGKJ/IGLJ gene	CDR L3	SHM IGKV/ IGLV	S1 reactivity (OD ratio)	RBD reactivity	Estimated IC_{50} (ng/ml)
HK CV38-105		S1-MBC	IgG1	3-74	6	ARQRVARRRGFGESPFYYGLDV	22	1-6	1	LQNYNFPRT	7	0.26		
HL CV38-107	38-1	S1-MBC	IgA1	1-2	4	ARDGAQYILTGDFDY	0	2-8	1	SSYAGSNNYV	0	0.58	+	n.t.
HK CV38-113		S1-MBC	IgG1	3-53	4	ARGGRLADAAGDY	1	1-33	2	QQYDNLPSWT	1	11.47	++	25
HK CV38-114		S1-MBC	IgM	5-51	4	ARAGNDNSLDY	1	1-39	2	QQSYTTPYT	18	0.17		
HL CV38-114	38-4	S1-MBC	IgM	5-51	4	ARAGNDNSLDY	1	9-49	3	GADHGSGSNFVQKV	1	8.13	++	>250
HL CV38-115		S1-MBC	IgG1	3-7	5	ARDLYYYDSSGNGVNWFDP	3	1-40	1	QSYDSSLSGSYV	1	8.04	++	n.t.
HL CV38-117		S1-MBC	IgG1	4-30-4	4	ARVTRIYGSGSYCFDY	0	2-23	2	CSYVGSSTFVV	2	9.55	++	>250
HK CV38-118		S1-MBC	IgA1	4-59	4	ARAWSSSWYLDY	3	3-11	4	QQRSNWPPVT	0	0.51	+	n.t.
HL CV38-119		S1-MBC	IgA1	4-4	4	ARAWNFDY	0	2-23	3	CSYAGSSNWV	1	5.56	++	>250
HL CV38-122		S1-MBC	IgG1	3-23	3	AKVLDI	0	2-14	1	SSYTSSSTPYV	2	n.exp.		
HK CV38-124		S1-MBC	IgG1	4-59	6	ATYYYDSSGYPYGMDV	1	1-9	3	QQLNSYPG	3	6.07	++	>250
HL CV38-125	38-4	S1-MBC	IgG1	5-51	4	ARHQGYSSSSLGY	1	9-49	3	GADHGSGSNFVYMV	1	8.53	++	>250
HK CV38-127		S1-MBC	IgG1	3-33	4	ARDPEIVVGGVDY	0	2-30	2	MQGTHWPYT	0	3.45	++	>250
HK CV38-128		S1-MBC	IgA1	3-11	4	ARDWNLSGYYGGGR	0	1-39	2	QQSYTTPYT	18	0.15		
HK CV38-129		S1-MBC	IgG1	4-31	3	ARDQGASASWDAFDI	0	3-20	4	QQYGSSLT	0	2.24	++	>250
HK CV38-131		S1-MBC	IgA1	3-11	4	ARDHSVRFLEWLLPY	0	1-9	1	QQLNSYPWT	3	1.93	+	n.t.
HK CV38-132		S1-MBC	IgG1	4-31	4	ARAERSITIFGVVTSAFDY	1	4-1	2	QQYYSTPYT	0	1.24	+	n.t.
HK CV38-134		S1-MBC	IgG1	4-34	4	ASSGWYYPDY	3	3-20	4	QQYGSSPNT	0	7.98	++	>250
HL CV38-135		S1-MBC	IgG1	3-23	3	AKVTGLGNAFDI	3	3-1	2	QAWDSSTVV	0	7.19	-	n.t.
HL CV38-136		S1-MBC	IgG1	4-4	5	ARSSGRGRVVALGSFDP	1	2-23	3	CSYAGSSTWV	0	8.52	-	n.t.
HK CV38-139		S1-MBC	IgG1	3-53	4	ARGHYDLFDY	3	1-9	3	QQLNSYPPGT	0	8.33	++	25-250
HK CV38-140		S1-MBC	IgA1	4-31	4	ARAYDSSGYYPDY	0	1-39	4	QQSYSTLT	0	2.56	++	>250
HK CV38-142		S1-MBC	IgG1	5-51	4	ARIRGVYSSGWIGGDY	4	1-39	1	QQSYSTPRQWT	0	9.39	++	25
HL CV38-143	38-1	S1-MBC	IgM	1-2	4	ARDGAQYILTGDFDY	0	2-8	1	SSYAGSNNYV	0	2.30	+	n.t.
HK CV38-146		S1-MBC	IgG1	1-69	5	ARAATYYYDSSGYTPNWFDP	1	1-39	2	QQSYSTLYT	0	2.17	++	>250
HL CV38-147		S1-MBC	IgG1	3-9	4	AKDRRIAVAGTGEDYYFDY	4	3-21	2	QVWDSSSDQVV	1	11.7	++	250
HL CV38-148		S1-MBC	IgG1	3-66	4	ARSAPLVGAYSGIYFDY	2	9-49	2	GADHGSGSNFVV	1	7.26	++	>250
HK CV38-149	38-3	S1-MBC	IgM	3-9	4	AKNRVAGTIFGVGPFDY	0	1-6	4	LQDYNYPLT	1	0.73	-	n.t.
HK CV38-150		S1-MBC	IgG1	3-30	3	AKSQWLVLRHAFDI	0	2D-29	1	MQSIQLWT	0	11.04	-	n.t.
HL CV38-156		S1-MBC	IgG1	4-59	4	ARFSQYYYDSSGYDFDY	0	2-23	3	CSYAGSSSWV	3	0.42		
HK CV38-158		S1-MBC	IgM	3-15	6	TTDRWFGELFSAYYYYYGMDV	0	3-11	3	QQRSNWPPIFT	0	0.17		
HL CV38-159		S1-MBC	IgG1	1-2	4	ARGNTVFWSGPPLDY	0	2-14	1	SSYTSSSTYV	0	4.27	+	n.t.
HL CV38-160		S1-MBC	IgG1	3-23	3	AKVAGRGNAFDI	3	7-43	2	LLYYGGAL	3	n.exp.		
HK CV38-165		S1-MBC	IgG3	4-4	4	ARRSLGNYDSSGYDH	1	3-15	5	QQYNNWPPAIT	1	5.09	-	n.t.
HL CV38-165		S1-MBC	IgG3	4-4	4	ARRSLGNYDSSGYDH	1	1-44	1	AAWDDSLNGYV	0	0.15		
HL CV38-173		S1-MBC	IgG3	3-30-3	4	ARDYGGYNYN	4	3-1	2	QAWDSSTVV	0	9.92	-	n.t.
HK CV38-177	38-3	S1-MBC	IgG1	3-9	4	AKDMVVVAIFGVGPFDY	1	1-6	4	LQDYNYPLT	1	10.77	-	n.t.
HK CV38-179		S1-MBC	IgM	5-51	3	ARQRRPPGKRVLTMIVVVYNDAFDI	1	1-33	3	QQYDNLLFT	0	n.exp.		
HL CV38-179		S1-MBC	IgM	5-51	3	ARQRRPPGKRVLTMIVVVYNDAFDI	1	1-40	2	QSYDSSLSGSV	2	n.exp.		
HL CV38-180		S1-MBC	IgG1	4-4	4	ARRAAAGPRPYDY	2	2-23	3	CSYAGFSTWV	6	n.exp.		
HK CV38-181		S1-MBC	IgA1	1-2	3	ARDLGYSYLYGAFDI	1	3-11	4	QQRSNWPT	4	6.17	++	>250
HL CV38-182		S1-MBC	IgA1	1-69	2	AKELGYSGYGAHRYFDL	3	1-40	2	QSYDSSLSGVV	0	11.73	++	250
HL CV38-183		S1-MBC	IgG1	3-53	6	ARGDGWDNYYYGMDV	0	1-40	2	QSYDSSLSGSV	2	11.06	++	<25
HK CV38-184		S1-MBC	IgG1	4-39	5	ARGLGWFDP	0	1-NL1	2	QQYYSTPPRT	0	1.89	++	250
HL CV38-186		S1-MBC	IgG1	1-2	4	ARDQSPDILKSPFDY	1	2-23	3	CSYAGSSTFG	0	6.51	++	250
HL CV38-193		S1-MBC	IgA1	3-11	4	ARDISRNLHDFRPYYFDY	2	7-46	3	LLSYSGARV	1	1.53	+	n.t.
HL CV38-194		S1-MBC	IgG1	4-59	3	ARHDVYSSGWYGEGAFDI	2	1-40	3	QSYDSSLSGSWV	3	0.09		
HL CV38-199		ASC	IgG3	4-59	4	ARYYQDFDY	0	1-44	1	AAWDDSLNGPYV	1	0.07		
HK CV38-201		ASC	IgG1	3-30	4	AKDIVLVPAAIPVPIFDY	2	3-11	5	QQRSNWPPT	1	0.07		
HL CV38-202		ASC	IgG1	3-33	3	ARDSSQQQLAYAFDI	2	3-1	2	QAWDSSIVV	1	0.1		

mAb	Clonality	Source cell	Ig isotype	IGHV gene	IGHJ gene	CDR H3	SHM IGHV	IGKV/IGLV gene	IGKJ/IGLJ gene	CDR L3	SHM IGKV/ IGLV	S1 reactivity (OD ratio)	RBD reactivity	Estimated IC$_{50}$ (ng/ml)
HL CV38-205		ASC	IgG1	4-30-2	6	ARDHYPYYYYGMDV	0	6-57	2	QSYDSSTVV	1	0.09		
HK CV38-206		ASC	IgA2	3-7	6	ARKGNAIDV	3	1-5	2	LQYNSYSWYT	1	0.08		
HL CV38-207	38-5	ASC	IgA1	4-30-4	3	AKIRVRAGFRWAFDI	22	2-14	3	SSYTNTNTLV	20	0.09		
HL CV38-208		ASC	IgM	4-39	2	AHQSGNSGPWYFDL	0	8-61	2	VLYMGSGIVV	1	0.08		
HL CV38-210		ASC	IgG1	4-39	4	ARHVEPDYGGNSFDY	0	1-40	1	QSYDSSLSGYV	1	0.11		
HL CV38-211		ASC	IgG1	3-9	6	AKDISNKWLRLTQPYSYYGLDV	3	2-8	1	SSYAGSNIPYV	7	0.08		
HL CV38-213		ASC	IgG1	3-23	3	AKVLIRNGYDILTGYPYDAFDI	0	2-14	2	SSYTSSSTLV	0	3.15	+	n.t.
HL CV38-215		ASC	IgA1	3-30-3	4	ARDGYSAYDFGY	20	8-61	3	VLFMGSGTWV	18	n.exp.		
HK CV38-217		ASC	IgA1	4-30-2	4	ASGPAWELFDY	17	3-15	3	QSYHNWPL	15	0.10		
HK CV38-219		ASC	IgA1	4-39	4	ARQMRIGTIVVVPAALDY	2	3-20	1	QQYYSSPWT	5	0.07		
HK CV38-221		ASC	IgG1	3-66	4	ARGFGDYYFDY	4	3-20	2	QQLYT	1	10.74	++	25-250
HK CV38-222		ASC	IgG1	4-30-4	6	ARDPWQVTIFGVVIRYGMDV	0	1-9	2	QQLNSYPRT	3	0.09		
HL CV38-225		ASC	IgM	3-11	5	ARDLWFGRYWGNWLDP	10	1-51	3	GTWDNSLSAAV	7	0.09		
HL CV38-227		ASC	IgA1	3-66	6	ASEGRTTGTIVAYYYFAMDV	15	2-8	2	SSYAGRSNVV	15	0.09		
HK CV38-228	38-6	ASC	IgA1	4-31	4	AREKGTGDYYLDY	16	3-15	1	QQYNSWPRA	17	0.08		
HL CV38-229	38-5	ASC	IgA1	4-30-4	3	AKIRVRAGFRWAFDI	23	2-14	3	SSYTNTNTLV	20	0.09		
HL CV38-230		ASC	IgG1	3-53	4	ARDNSSNWYYFDS	8	3-25	1	QSADSSGTYV	10	n.exp.		
HL CV38-231		ASC	IgG1	3-33	6	ARDGLDDDYIWGSFKIRYYYMDV	1	2-8	3	SSYSGTTNFAQ	19	0.08		
HL CV38-232		ASC	IgA1	3-23	4	ASGTYRLGDY	26	1-44	3	AAWDDSLDGPV	15	n.exp.		
HL CV38-233		ASC	IgG1	4-4	5	VTGGRWRFDP	16	2-11	3	CSYAGTYTYWL	12	0.08		
HK CV38-235	38-2	ASC	IgA1	3-23	4	VRDLSSSDPWYFDF	15	3D-20	1	QQYGDSPRT	11	n.exp.		
HK CV38-236		ASC	IgG1	3-64	6	ARGGYEIVVVPDYYYYGMDV	0	3-20	4	QQYKD	0	5.74	-	n.t.
HK CV38-238	38-7	ASC	IgM	3-30	6	AKDPLNCSSTRCYTAWIYYYYGMDV	0	2D-29	4	MQSIQLPLT	0	0.09		
HK CV38-240	38-7	ASC	IgG1	3-30	6	AKDSVKGYSSGWYYYYYGMDV	0	2D-29	4	MQSIQLPLT	0	0.09		
HK CV38-242	38-2	ASC	IgA1	3-23	4	ARDLSSSDPWYFDF	14	3D-20	1	QQYGDSPRT	11	0.08		
HK CV38-243		ASC	IgM	3-21	4	ARDRSGWYRNLFDY	1	2-28	5	MQALQASIT	0	0.08		
HK CV38-245		ASC	IgG2	3-49	3	TRDFDHADSFDI	24	2-28	2	MQALHTPRYT	9	0.09		
HK CV38-248		ASC	IgG2	3-30	4	AKGFYDSGP	12	2-30	2	MQGTHWKT	3	0.10		
HL CV38-251		ASC	IgA2	3-23	6	AKDQTVSFFYYGMDV	5	1-47	1	ATWDDSLSGYV	10	0.07		
HK CV38-252		ASC	IgM	1-3	4	ARDNTNTWFGSIEY	36	4-1	3	QQNYATPLT	21	n.exp.		
HL CV38-255		ASC	IgG2	3-9	4	VREATRGAHFDC	32	2-8	1	SSYVGFNNLDNFV	19	0.07		
HK CV38-257		ASC	IgM	4-34	2	ARRIYYGDLGNWNFDL	24	1-16	4	QQYNSYPLT	20	n.exp.		
HL CV38-259		ASC	IgG1	1-69	4	ATLGYCSGGSCFPTGVFGY	0	7-46	3	LLSYSGARSWV	1	0.05		
HK CV38-263	38-6	ASC	IgA1	4-31	4	AREKGTGDYYLDS	21	3-15	1	QQYNSWPRA	21	0.09		
HK CV38-265		ASC	IgG1	3-23	6	AKDGHSMVRGVTMWGEFYYYYGMDV	0	3-15	2	QQYNNWPPYT	0	0.1		
HK CV38-270		ASC	IgG2	3-9	3	VRSRWQLTSSAFDM	33	1-9	4	QQLNKYPIT	25	n.exp.		
HK CV38-271	38-6	ASC	IgA1	4-31	5	AREKGTGDYYLDP	22	3-15	2	QQYNSWPRA	21	0.09		
HL CV38-273		ASC	IgG1	1-2	6	ARTYYYDSSGYRNYYYYGMDV	4	2-18	1	SLYTSSSTYV	0	0.18		
HK CV38-275		ASC	IgG1	3-15	4	TTDRGNSITIFGVVIIDRPY	0	3-20	2	QQYGSS	0	n.exp.		
HL CV38-276		ASC	IgA1	3-21	6	ARDEGSPGLDYYGMDV	1	2-14	2	SSYTSNTTLVV	4	0.08		
HL CV38-278	38-5	ASC	IgA1	4-30-4	3	AKIRVRAGFRWAFDI	21	2-14	3	SSYTNTNTLV	22	0.08		
HL CV38-281		ASC	IgG1	3-11	4	ARDMNYKYYYDSSGYPLLDY	0	1-44	3	AAWDDSLNGWV	0	0.15		
HK CV38-284		ASC	IgA1	3-49	4	IRARYYYDSSATFDY	18	1-39	4	QQCYSLPST	18	n.exp.		
HL CV38-286		ASC	IgA2	3-30	6	AKDASSPVYDFWSGYYNHLGMDV	0	3-21	3	QVWDSSSDQGV	2	0.11		
HK CV38-288		ASC	IgM	3-66	6	ARDYTVTTGGVDGMDV	0	3-11	1	QQRSNWPPWT	0	n.exp.		
HK CV38-289		ASC	IgA1	3-23	4	VSRAAVGQPEY	44)	1D-12	3	QQAYTLPRVT	35	n.exp.		
HK CV48-103		S1-MBC	IgG1	3-49	6	SRFYDYWNTFGLLLGSGLTFYHMDV	22	4-1	1	QQYCYTPWT	13	0.07		
HL CV48-104		S1-MBC	IgG1	1-69	5	ARDGQQLVRGWFDP	0	2-14	1	SSYTSSSTLYV	2	6.93	++	>250
HL CV48-107		S1-MBC	IgG1	4-39	4	ASENDYGEHDY	0	4-60	2	ETWDSNTRKVV	1	0.1		
HL CV48-109		S1-MBC	IgG1	3-30	4	VKGDTSAYWPSSLLIS	34	2-14	2	GSYATGSSPVV	17	0.10		

mAb	**Clonality**	**Source cell**	**Ig isotype**	**IGHV gene**	**IGHJ gene**	**CDR H3**	**SHM IGHV**	**IGKV/IGLV gene**	**IGKJ/IGLJ gene**	**CDR L3**	**SHM IGKV/ IGLV**	**S1 reactivity** (OD ratio)	**RBD reactivity**	**Estimated IC_{50}** (ng/ml)
HK CV48-110		S1-MBC	IgA1	3-33	4	ARDARYSAYELPDYFFDL	17	1-5	1	QQYKGSSWAT	10	n.exp.		
HL CV48-113		S1-MBC	IgG1	3-33	6	ARDGLDDDYIWGSFKIRYYYMDV	0	4-69	2	QTWGTGINVV	1	0.08		
HL CV48-119		S1-MBC	IgA2	3-23	4	AKTDRHWNHCD	18	2-14	2	SSYTGSSTLVA	18	0.08		
HL CV48-123		S1-MBC	IgM	1-3	4	ARNGGGLDQ	21	2-14	2	CSSTTSSTAV	12	n.exp.		
HK CV-X1-102		S1-MBC	IgG1	1-69	6	ARSPRPLIVVAEDGMDV	1	3-20	3	QQYGSSPFT	1	6.81	++	>250
HL CV-X1-109		S1-MBC	IgG1	1-2	4	ARGPLFWDTAMANFDY	0	2-14	3	N/A	4	0.12		
HK CV-X1-111		S1-MBC	IgM	3-49	4	NRELHNSVVVGVMGY	17	4-1	2	HHYYSPPYA	7	0.16		
HK CV-X1-112		S1-MBC	IgM	3-23	4	AKVGSGWYAFDY	16	3-15	1	QQYNKWPRT	5	0.09		
HL CV-X1-119		S1-MBC	IgG1	4-59	6	ARDRIMPLSYYYYYGMDV	0	1-44	3	AAWDDSLNGWV	0	0.17		
HK CV-X1-126		S1-MBC	IgG1	3-53	6	ARDLSEGGMDV	2	1-12	4	QQANGFPPL	2	11.78	++	25-250
HK CV-X1-128		S1-MBC	IgG1	5-51	6	ARTYDFWSGFDYYGMDV	3	3-11	3	QQRSNWPT	0	0.13		
HL CV-X1-131		S1-MBC	IgG1	3-30	4	ARMATTYPEHDPSLY	2	3-21	3	QVWDSSSDHWV	2	10.74	++	>250
HK CV-X1-136		ASC	IgM	4-31	5	AAWRGFAATGFDS	21	1-9	3	QQLKSYPLT	7	0.1		
HK CV-X1-137		ASC	IgA1	1-8	3	ATEGTILTTMTAGAFDL	26	1-12	2	QQTDNFPYT	18	0.17		
HK CV-X1-140		ASC	IgA1	1-69	4	ARFGGTSQSSGYYGFDN	23	2-28	2	MQPLQTPYT	11	0.08		
HL CV-X1-141		ASC	IgG1	3-23	6	VTHDFPDWPPGGGMDV	18	6-57	3	QSYDWSNQGV	10	0.16		
HK CV-X1-142		ASC	IgG2	1-18	4	STRGMAPHDY	28	1-39	1	HQTYDTWT	33	n.exp.		
HK CV-X1-143		ASC	IgG1	3-11	4	ARDLGYSTRFDY	0	1-33	4	QQYDNLPLT	0	6.76	++	>250
HK CV-X1-145		ASC	IgG1	5-51	4	AREDLTGPDY	8	2-30	2	MQGTHWPNT	1	0.16		
HL CV-X1-146		ASC	IgG1	3-23	4	ANNYYDNSGPDY	30	6-57	3	QSNDGSPSWV	20	0.15		
HL CV-X1-150		ASC	IgG1	5-51	4	ARHLVCGGSCYPFDY	0	3-21	3	QVWDSSSDHQV	1	0.33		
HL CV-X1-153		ASC	IgG3	3-33	4	ARDWFWRLGGVDY	0	8-61	2	VLYMGSGLVV	2	0.16		
HL CV-X1-157		ASC	IgA1	3-48	6	ATSYYDPSSAYSAHYAMDV	32	2-14	2	TSYTSLSPVV	20	0.09		
HK CV-X1-164		ASC	IgG1	1-2	6	ARSFGGFGGNYGMDV	3	1-39	5	QQSYSTPIT	0	0.13		
HL CV-X1-165		ASC	IgA2	3-48	4	ARDPIGTGSDY	13	1-51	2	GTWDSSLNAGV	9	0.13		
HK CV-X1-167		ASC	IgA2	3-74	5	ARAHSTTLYGWFDP	17	3-20	1	QHYVSSPLT	13	0.09		
HL CV-X1-171		ASC	IgA2	4-34	4	ARGFRKGSTFN	13	2-14	3	SSYTTSNTRE	15	0.09		
HK CV-X1-172		ASC	IgG1	3-48	6	ARDRLTIFGVAIDYYGMDV	0	1-12	4	QQANSFPALT	0	0.1		
HK CV-X1-173		ASC	IgG1	3-30	3	AKDYDSALCTGGTCTFDAFDF	27	1-27	1	QNYNSAPPWT	11	0.24		
HL CV-X1-174		ASC	IgG1	3-21	6	ATVQGDYVAGRAYYYGMDV	0	3-1	2	QAWDSSTAV	0	0.10		
HK CV-X1-175		ASC	IgG1	1-69	4	ARGLQGTHLDC	1	4-1	3	QQYYSTGFT	1	1.99	-	n.t.
HL CV-X1-177		ASC	IgG1	3-30	4	ARAETPASEIDY	0	3-1	2	QAWDSSHVV	1	0.08		
HK CV-X1-178		ASC	IgA1	3-49	6	TRDRPIDYGDLHIYYYGLDV	22	2-28	2	MQALQTPPT	8	0.1		
HK CV-X1-180		ASC	IgA1	4-39	5	LKDRTLQGNWFDP	26	3-11	5	QQRRDWPPVT	14	0.09		
HL CV-X1-183	X1-1	ASC	IgG1	3-30	4	ASKSPERGSFDY	26	2-14	1	SSYTNGSSLYV	7	n.exp.		
HL CV-X1-188		ASC	IgM	4-4	5	AKGGGPIVA	14	4-60	2	ETWDSNTRL	8	0.08		
HL CV-X1-189		ASC	IgG1	3-23	6	AKGRRYYDFWSGPMPYGMDV	1	2-14	3	SSYTSSSTLGV	10	0.09		
HL CV-X1-190	X1-1	ASC	IgG1	3-30	4	ANTSPGRGSFDY	9	2-14	1	SSYTNSSTLYV	13	0.08		
HK CV-X1-191		ASC	IgG1	4-31	4	ARQLRFLEWQYFDY	0	1-33	4	QQYDNLLT	0	n.exp.		
HK CV-X1-195		ASC	IgA1	3-64	4	VKGWGVKASSLGGDY	20	3-11	4	HQRSDWPRLT	11	n.exp.		
HK CV-X2-103		S1-MBC	IgA1	3-15	5	TTWRLGQDWFDP	17	1-39	4	QQSYSAPLT	14	0.81	++	>250
HL CV-X2-105		S1-MBC	IgA1	3-73	6	TRRFDPNQRNDYYYALDF	12	1-44	1	SAWDDSLNGYV	9	3.48	+	n.t.
HK CV-X2-106		S1-MBC	IgG1	1-69	6	ATRKETTVTTSLVYGMDV	1	1-39	2	QQSYSTPYT	2	9.14	++	250
HK CV-X2-107	X2-2	S1-MBC	IgA1	3-66	4	ARGKVGATGFEY	15	3-20	2	QQYGSSPPMYT	8	n.exp.		
HK CV-X2-108	X2-2	S1-MBC	IgA1	3-66	4	ARGKVGATGFED	10	3-20	2	QQYGSSPPMYT	8	n.exp.		
HK CV-X2-109		S1-MBC	IgM	5-51	3	ARLAHYYDRSGYSRADDAFDV	7	3-15	2	QQYNNWPPVYT	2	6.81	++	>250
HK CV-X2-117	X2-2	S1-MBC	IgA1	3-66	4	ARGKVGATGFED	10	3-20	2	QQYGSSPPMYT	9	0.08		
HK CV-X2-118		S1-MBC	IgG1	3-30	4	AKTGGPYCSGGSCYSALMDY	0	1-33	1	QQYDNLPPT	0	n.exp.		
HK CV-X2-123		S1-MBC	IgA1	4-4	6	ARDRTREGYHDTLTGEFYFYGTDV	33	3-20	2	QQYAMSPVT	27	n.exp.		

For clonality analysis mAbs from an identical donor were identified as clones when sharing the same V and J gene on both heavy and light chain and showing similarities within amino acid sequences of both CDR3. S1 reactivity was determined as a normalized optical density (OD) measured by SARS-CoV-2-S1 ELISA, with values above 0.5 considered as positive. From S1+ mAbs specificity to the RBD was determined using an RBD-ELISA and noted as negative (-), positive (+) or strongly positive (++), when detectable at 10 ng/ml. All strongly positive RBD+ mAbs were screened for neutralization of authentic SARS-CoV-2 (Fig. 1A), from which the IC_{50} was estimated.

Abbreviations: ASC = antibody-secreting cell, S1-MBC = S1-SARS-CoV2-enriched memory B cell, Ig = immunoglobulin, HC = heavy chain, KC = kappa chain, LC = chain, IGHV/IGHJ = immunoglobulin heavy chain variable/joining gene, IGKV/IGKJ = immunoglobulin kappa chain variable/joining gene, IGLV/IGLJ = immunoglobulin lambda chain variable/joining gene, CDR = complementarity-determining region, SHM = somatic hypermutations, n.exp. = not expressed, n. t. = not tested.

Supplementary Table ST3 | Public or common antibody response using VH3-53 and VH3-66 genes.

mAb	IGHV	IGHJ	CDR H3	IGKV/IGLV	IGKJ/IGLJ	CDR L3
RBD-494 (Cao et al.)	3-53	6	ARDLVVYGMDV	1-9	4	QQLNSYPFT
HK CV07-202	3-53*01	6*02	ARDLYYYGMDV	1-9*01	4*01	QQLNNYSVT
HL CV07-275	3-66*01	4*02	ARDYYDSSGYYSSGGLGY	2-8*01	1*01	SSYAGSNNFV
HL CV38-148	3-66*01	4*02	ARSAPLVGAYSGIYFDY	9-49*01	2*01	GADHGSGSNFVV
HK CV38-221	3-66*01	4*02	ARGFGDYYFDY	3-20*01	2*01	QQLYT
HK CV38-113	3-53*04	4*02	ARGGRLADAAGDY	1-33*01	2*02	QQYDNLPSWT
HK CV38-139	3-53*01	4*02	ARGHYDLFDY	1-9*01	3*01	QQLNSYPPGT
HL CV38-183	3-53*01	6*02	ARGDGWDNYYYGMDV	1-40*01	2*01	QSYDSSLSGSV
HK CV-X1-126	3-53*04	6*02	ARDLSEGGMDV	1-12*01	4*01	QQANGFSAL

Abbreviations: IGHV/IGHJ = immunoglobulin heavy chain variable/joining gene, IGKV/IGKJ = immunoglobulin kappa chain variable/joining gene. IGLV/IGLJ = immunoglobulin lambda chain variable/joining gene, CDR = complementarity-determining region.

Supplementary Table ST4 | Biophysical and functional characterization of the 18 most potent SARS-CoV-2 neutralizing mAbs.

mAb	**EC_{50}** (ng/ml)	**K_a** (s^{-1})	**K_d** ($M^{-1}s^{-1}$)	**K_D** (M)	**IC_{50}** (ng/ml)	**ACE2 binding reduction** (%)	**Tissue reactivity**
CV05-163	3.8	8.48 E+06	1.86 E-03	2.20 E-10	16.3	9.6	none
CV07-200	9.0	n/a	n/a	n/a	14.5	none	B / L*
CV07-209	4.1	2.40 E+07	1.44 E-04	6.00 E-12	3.1	73.9	none
CV07-222	5.5	2.98 E+07	2.07 E-04	6.97 E-12	7.8	36.9	B / L / C
CV07-250	8.7	4.05 E+06	2.28 E-04	5.64 E-11	3.5	59.9	none
CV07-255	4.8	n/a	n/a	n/a	14.5	51.6	L / H / C / K
CV07-262	12.1	4.27 E+06	3.37 E-04	7.90 E-11	7.1	25.5	none
CV07-270	14.2	n/a	n/a	n/a	82.3	7.5	L / H* / C
CV07-283	4.0	1.52 E+07	7.24 E-04	4.75 E-11	16.9	38.0	none
CV07-287	5.9	5.11 E+06	8.14 E-04	1.60 E-10	41.7	12.4	none
CV07-315	7.2	2.36 E+07	2.62 E-04	1.12 E-11	24.9	none	none
CV38-113	5.2	2.33 E+06	3.12 E-04	1.34 E-10	20.8	51.2	none
CV38-139	8.9	3.62 E+05	1.00 E-04	2.77 E-10	73.2	14.9	none
CV38-142	5.6	6.31 E+05	6.60 E-04	1.05 E-09	23.2	26.9	none
CV38-183	5.4	2.31 E+06	1.37 E-04	5.93 E-11	3.7	65.9	none
CV38-221	6.4	7.45 E+05	3.71 E-04	4.99 E-10	172.6	50.1	none
CV-X1-126	5.5	4.12 E+05	9.98 E-05	2.43 E-10	71.7	44.2	none
CV-X2-106	5.6	n/a	n/a	n/a	17.6	19.9	none

Abbreviations: EC_{50} = half-maximal effective concentration, K_a = association rate, K_d = dissociation rate, K_D = equilibrium dissociation constant, IC_{50} = half-maximal inhibitory concentration, B = brain, L = lung, H = heart, C = colon, K = kidney. An asterisk (*) indicates weak binding.

Supplementary Table ST5 | X-ray data collection and refinement statistics.

Data collection		
	CV07-250 + RBD	**CV07-270 + RBD**
Beamline	SSRL 12-1	SSRL 12-1
Wavelength (Å)	0.97946	0.97946
Space group	$P\ 2_1\ 2_1\ 2_1$	C 1 2 1
Unit cell parameters		
a, b, c (Å)	68.0, 80.1, 153.7	157.0, 151.8, 66.0
α, β, γ (°)	90, 90, 90	90, 95.4, 90
Resolution (Å) [a]	50.0–2.55 (2.59–2.55)	50.0–2.70 (2.75–2.70)
Unique reflections [a]	27,890 (2,659)	41,624 (2,089)
Redundancy [a]	8.8 (6.5)	4.7 (3.6)
Completeness (%) [a]	99.6 (98.9)	90.8 (90.8)
$\langle I/\sigma_I \rangle$ [a]	17.3 (1.1)	6.7 (1.1)
R_{sym}[b] (%) [a]	11.9 (94.6)	19.9 (80.6)
R_{pim}[b] (%) [a]	4.1 (38.9)	9.9 (50.5)
$CC_{1/2}$[c] (%) [a]	99.5 (71.0)	97.6 (67.6)
Refinement statistics		
Resolution (Å)	43.2–2.55	49.7–2.72
Reflections (work)	27,883	39,568
Reflections (test)	2,656	2,055
R_{cryst}[d] / R_{free}[e] (%)	20.7/25.9	22.6/26.7
No. of atoms	4,525	9,233
Macromolecules	4,420	9,165
Glycans	28	28
Solvent	77	40
Average *B*-value (Å^2)	52	44
Macromolecules	52	44
Fab	46	42
RBD	66	46
Glycans	100	77
Solvent	49	57
Wilson *B*-value (Å^2)	51	39
RMSD from ideal geometry		
Bond length (Å)	0.005	0.007
Bond angle (°)	0.74	1.27
Ramachandran statistics (%)		
Favored	96.1	96.8
Outliers	0.2	0.0
PDB code	6XKQ	6XKP

[a] Numbers in parentheses refer to the highest resolution shell.
[b] $R_{sym} = \Sigma_{hkl} \Sigma_i | I_{hkl,i} - \langle I_{hkl} \rangle | / \Sigma_{hkl} \Sigma_i I_{hkl,i}$ and $R_{pim} = \Sigma_{hkl} (1/(n-1))^{1/2} \Sigma_i | I_{hkl,i} - \langle I_{hkl} \rangle | / \Sigma_{hkl} \Sigma_i I_{hkl,i}$, where $I_{hkl,i}$ is the scaled intensity of the i^{th} measurement of reflection h, k, l, $\langle I_{hkl} \rangle$ 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] $R_{cryst} = \Sigma_{hkl} | F_o - F_c | / \Sigma_{hkl} | F_o | \times 100$, 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.

Supplementary Table ST6 | Hydrogen bonds and salt bridges identified at the antibody-RBD interface using the PISA program.

CV07-250	Distance (Å)	SARS-CoV-2 RBD
Hydrogen bonds		
H:TYR98[N]	3.0	A:ALA475[O]
H:ASN31[ND2]	3.4	A:SER477[OG]
H:ASN100C[ND2]	3.8	A:GLY485[O]
H:ASN100C[ND2]	2.9	A:PHE486[O]
H:ASN97[ND2]	2.8	A:ASN487[OD1]
H:ASN97[ND2]	2.7	A:TYR489[OH]
H:TYR100B[N]	3.5	A:TYR489[OH]
H:ASP96[OD1]	3.0	A:SER477[N]
H:ASP96[OD2]	2.7	A:SER477[OG]
H:ASP96[OD2]	3.5	A:THR478[N]
H:ASP96[OD2]	2.9	A:THR478[OG1]
H:SER95[OG]	2.9	A:ASN487[ND2]
H:PHE100[O]	3.4	A:TYR489[OH]
L:SER27A[OG]	3.2	A:TYR505[OH]
L:HIS31[N]	3.1	A:GLN493[OE1]
L:SER67[OG]	3.5	A:GLY446[O]
L:GLY68[N]	3.1	A:GLY446[O]
L:GLY68[N]	3.1	A:TYR449[OH]
L:ASN69[N]	3.8	A:GLN498[OE1]
L:ASN69[ND2]	3.7	A:GLN498[OE1]
L:TYR49[OH]	3.5	A:PHE486[N]

CV07-270	Distance (Å)	SARS-CoV-2 RBD
Hydrogen bonds		
H:TYR100B[OH]	2.8	A:SER349[OG]
H:SER98[N]	3.2	A:GLY447[O]
H:SER98[OG]	3.8	A:GLY447[O]
H:SER98[OG]	3.2	A:ASN448[OD1]
H:ARG100G[NH2]	2.9	A:GLU484[OE1]
H:ARG100G[NH1]	3.2	A:GLU484[OE2]
H:ARG100G[NH2]	3.0	A:GLU484[OE2]
H:THR28[OG1]	3.2	A:LYS444[NZ]
H:ASP31[OD1]	2.7	A:ARG346[NH1]
H:ASP31[OD2]	2.7	A:LYS444[NZ]
H:SER98[O]	2.7	A:TYR449[N]
H:SER98[O]	3.3	A:ASN450[N]
H:TYR100B[OH]	3.6	A:SER349[N]
Salt bridges		
H:ARG100G[NH2]	2.9	A:GLU484[OE1]
H:ARG100G[NH1]	3.2	A:GLU484[OE2]
H:ARG100G[NH2]	3.0	A:GLU484[OE2]
H:ASP31[OD1]	2.7	A:ARG346[NH1]
H:ASP31[OD1]	3.4	A:ARG346[NE]
H:ASP31[OD2]	2.7	A:LYS444[NZ]

Supplementary Table ST7 | Histopathological scoring of lung tissue from COVID-19 hamster model.

		|-------------- pneumonia ----------|																
Animal number	**Time point (dpi)**	**% Affected lung tissue**	**Degree of inflammation***	**Lymphocytes**	**Macrophages**	**Neutrophils**	**Epithelial cell necrosis of bronchi**[a]	**Bronchial inflammation**[a]	**Hyperplasia of bronchial epithelia cells**[b]	**Alveolar epithelial cell necrosis**	**Hyperplasia type II alveolar epithelial cells**[b]	**Alveolar edema**[c]	**Perivascular edema**[c]	**Perivascular lymphocytic cuffing**	**Endothelitis**	[a] **Bronchitis score**	[b] **Regeneration score**	[c] **Edema score**
P1	3	<5	1.0	0.0	1.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0
P2	3	<5	1.0	1.0	1.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0
P3	3	5	1.0	1.0	1.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
T1	3	10	1.5	1.0	1.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0
T2	3	25	3.0	2.5	2.0	3.5	3.5	4.0	0.0	3.0	2.0	1.5	0.0	2.0	2.0	3.8	1.0	0.8
T3	3	15	2.0	2.0	2.0	2.0	0.0	0.0	0.0	2.0	1.0	0.0	1.0	1.0	0.0	0.0	0.5	0.5
C1	3	15	2.5	2.0	2.0	3.0	2,5	3.0	0.0	3.0	1.0	2.0	1.0	1.0	2.0	3.0	0.5	1.5
C2	3	20	2.5	2.5	2.0	2.5	2,5	3.0	0.0	2.0	1.0	0.0	3.0	1.5	2.0	3.0	0.5	1.5
C3	3	20	2.5	2.0	2,5	2,5	2.0	2.0	0.0	3.0	2.0	0.0	2.0	1.0	2.0	2.0	1.0	1.0
P4	5	5-10	2.0	2.0	2.0	1.5	0.0	0.0	0.0	2.0	2.0	0.0	1.5	1.0	0.0	0.0	1.0	0.8
P5	5	<5	1.0	1.0	1.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0	1.0	1.0	0.0	0.0	0.0	0.5
P6	5	15	2.0	2.0	2.0	2.0	0.0	0.0	0.0	2.0	2.0	0.0	0.0	2.0	0.0	0.0	1.0	0.0
T4	5	5-10	2.0	2.0	1.5	1.0	0.0	0.0	0.0	1.0	2.0	0.0	0.0	2.0	0.0	0.0	1.0	0.0
T5	5	25	3.0	3.0	2.0	3.0	2.0	2.0	0.0	3.0	3.0	2.0	2.0	3.0	3.0	2.0	1.5	2.0
T6	5	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
C4	5	80	4.0	4.0	3.0	3.0	3.0	3.0	3.0	3.0	4.0	3.0	3.5	3.0	3.5	3.0	3.5	3.3
C5	5	15-20	2.5	3.0	2.5	2.0	2.0	2.0	1.5	2.0	2.0	2.5	0.0	3.0	2.0	2.0	1.8	1.3
C6	5	50	4.0	3.5	3.0	3.0	3.0	3.0	4.0	2.5	4.0	3.5	4.0	3.5	3.0	3.0	4.0	3.8
P7	13	20	2.0	2.0	2.0	1.0	0.0	0.0	0.0	1.5	0.0	1.5	0.0	1.5	0.0	0.0	0.8	0.8
P8	13	30	2.0	2.0	2.0	2.0	0.0	0.0	0.0	1.5	0.0	0.0	0.0	2.0	0.0	0.0	1.0	0.0
P9	13	30	2.0	2.0	2.0	2.0	0.0	1.0	1.0	1.5	0.0	0.0	0.0	2.0	0.0	0.5	1.5	0.0
T7	13	15	2.0	2.0	2.0	1.5	0.0	0.0	0.0	1.5	0.0	0.0	0.0	2.0	0.0	0.0	1.0	0.0
T8	13	5	1.0	1.5	1.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.5	0.0
T9	13	20	1.5	1.5	1.0	1.5	0.0	0.0	0.0	1.0	0.0	0.0	0.0	1.5	0.0	0.0	0.8	0.0
C7	13	5	1.0	1.0	1.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	0.8	0.0
C8	13	40	2.0	2.0	2.0	2.0	0.0	1.0	1.0	1.5	0.0	0.0	1.5	2.0	0.0	0.5	1.5	0.0
C9	13	10	1.0	1.0	1.0	1.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.5	0.8	0.0

Histopathological scoring of formalin-fixed paraffin-embedded lung tissue from hamsters of experimental groups as abbreviated (P = prophylactic, T = therapeutic, C = control) at indicated days post infection (dpi). Degree of inflammation (*) is scaled as (1) minimal, (2) mild,

(3) moderate or (4) severe. For all other parameters rating refers to occurrence rate from (1) sporadic, (2) mild, (3) moderate to (4) severe.

Scores were assessed as means from parameters with corresponding letters as indicated.