

1 **Human monoclonal antibodies block the binding of SARS-CoV-2 spike protein**
2 **to angiotensin converting enzyme 2 receptor**

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34 **Abstract**

35 The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has caused a
36 global pandemic of novel corona virus disease (COVID-19). To date, no prophylactic
37 vaccines or approved therapeutic agents are available for preventing and treating this
38 highly transmittable disease. Here we report two monoclonal antibodies (mAbs)
39 cloned from memory B cells of patients recently recovered from COVID-19, and both
40 mAbs specifically bind to the spike (S) protein of SARS-CoV-2, block the binding of
41 receptor binding domain (RBD) of SARS-CoV-2 to human angiotensin converting
42 enzyme 2 (hACE2), and effectively neutralize S protein-pseudotyped virus infection.
43 These human mAbs hold the promise for the prevention and treatment of the ongoing
44 pandemic of COVID-19.

45

46 **Main text**

47 According to World Health Organization (WHO) newly updated situation report on
48 March 18th, 2020, the corona virus disease 2019 (COVID-19) pandemic has
49 confirmed 191,127 cases and claimed 7,807 deaths worldwide¹. The etiological agent
50 of COVID-19 has been identified as a novel coronavirus, the severe acute respiratory
51 syndrome coronavirus 2 (SARS-CoV-2), belonging to *Sarbecovirus* subgenus (genus
52 *Betacoronavirus*, family *Coronaviridae*) and showing 79.6% and 96.2% sequence
53 identity in nucleotide to SARS-CoV and a bat coronavirus (BatCoV RaTG13),
54 respectively²⁻⁴. Like SARS-CoV infection, a substantial fraction of COVID-19 patients
55 exhibits severe respiratory symptoms and has to be hospitalized in intensive care unit
56 (ICU)⁵⁻⁸. Although the mortality rate of COVID-19 is significantly lower than that of
57 SARS-CoV infection, SARS-CoV-2 shows much higher human-to-human
58 transmission rate, rapidly leading to a global pandemic declared by WHO on March
59 11th, 2020⁹.

60 Currently, there are no approved prophylactic vaccines or therapeutic drugs that are
61 specific to COVID-19. Blocking monoclonal antibodies (mAbs), due to their
62 extraordinary antigen specificity, are one of the best candidates for neutralizing virus
63 infection^{10, 11}. Therefore, identifying and cloning blocking mAbs that can specifically
64 target surface viral proteins to block the viral entry to host cells is a very attractive
65 approach for preventing and treating COVID-19, in particular when effective vaccines
66 and therapeutics are unavailable in the outbreak of the COVID-19 pandemic. We then
67 sought to identify and clone blocking mAbs from the memory B cell repertoire of
68 recently recovered COVID-19 patients to prevent the entry of COVID-19 virus to the
69 host cells.

70 Similar to SARS-CoV, SARS-CoV-2 also utilizes highly glycosylated homotrimeric
71 spike (S) protein for receptor binding and virus entry^{3, 12-15}. The S protein of
72 SARS-CoV-2 consists of two subunits, S1 and S2. To engage host cell receptor

73 human angiotensin-converting enzyme 2 (hACE2), shared by both SARS-CoV and
74 SARS-CoV-2, S protein undergoes dramatic conformational changes to expose the
75 RBD and key residues for receptor binding. S protein is metastable, and binding of
76 RBD to hACE2 receptor likely leads to the shedding of S1 protein from S2 protein,
77 thus promoting S2-mediated virus-host membrane fusion and virus entry¹⁶⁻¹⁸. Given
78 the critical role of the RBD in initiating invasion of SARS-CoV-2 into host cells, it
79 becomes a vulnerable target for neutralizing antibodies. Thus far, the human mAbs
80 specifically target the SARS-CoV-2 RBD-hACE2 interaction have not been reported,
81 and a monoclonal antibody targeting S1 made from immunized transgenic mice
82 expressing human Ig variable heavy and light chains has been recently shown to
83 neutralize both SARS-CoV-2 and SARS-CoV infection, but by an unknown
84 mechanism that is independent of the blockade of RBD-hACE2 interaction¹⁹.

85 Prior to cloning SARS-CoV-2 RBD specific human mAbs, we first examined whether
86 patients recently recovered from COVID-19 had mounted anti-SARS-CoV-2 S1
87 protein IgG antibodies in sera. Among 26 recovered COVID-19 patients, we found
88 that the majority of these recruited patients were able to produce high titers of
89 SARS-CoV-2 S1-specific IgG antibodies and only 3 patients mounted relatively lower
90 anti-S1 IgG responses, by enzyme-linked immunosorbent assay (ELISA) (Fig. 1a).
91 Consistently, we also found that SARS-CoV-2 RBD specific IgG antibodies were
92 present in sera of all patients by ELISA (Fig. 1b). Next, we sought to investigate
93 whether RBD-specific antibodies in patient serum can block the binding of
94 SARS-CoV-2 RBD to hACE2. To this end, we set up an ELISA-based inhibition assay
95 to examine the blocking function of these antibodies. We noted that there were only 3
96 out of 26 patients showed effective blockade of SARS-CoV-2 RBD binding to hACE2
97 (Fig. 1c). Taken together, these results suggested that while all recovered COVID-19
98 patients can generate anti-S1 and anti-RBD antibodies, there were only a small
99 fraction of these antibodies can block the binding of RBD to hACE2 receptor. This
100 observation may be explained by transient and dynamic perfusion conformational

101 states of S protein that provide very limited window for the immunogenic epitopes of
102 RBD exposure to specific B cells²⁰.

103 Next, we set out to clone human monoclonal antibodies using the blood samples from
104 three COVID-19 recovered patients, of which their sera showed potent hACE2
105 receptor binding inhibition. To this end, we sorted each SARS-CoV-2 RBD specific,
106 IgG class-switched memory B cell into a single well of the 96-well microplates.
107 Subsequently, we used reverse transcription polymerase chain reaction (RT-PCR) to
108 amplify IgG variable heavy chain (VH) and light chain (VL) from each single memory B
109 cell. After cloning both VH and VL, we inserted both sequences into expression
110 plasmids that encoding constant regions of human IgG1 heavy chain and light chain
111 (Fig. 2a)²¹. We found that SARS-CoV-2 RBD specific, IgG-positive memory B cells
112 only enriched in COVID-19 recovered patients, but not in healthy controls (Fig. 2b),
113 suggesting the specificity of our sorting strategy. The representative RT-PCR and
114 cloning of IgG1 heavy chains and light chains to expression plasmids were shown in
115 Figure 2c and 2d. After antibody cloning, we acquired 3 pairs of IgG VHs and VLs
116 inserted expression plasmids and the CDR3 sequences of heavy chains were shown
117 in Figure 2e (analyzed with IMGT browser,
118 http://www.imgt.org/IMGT_vquest/analysis#sequence1_alj).

119 Finally, we expressed these paired plasmids encoding IgG VH and VL sequences and
120 named these three mAbs as 311mab-31B5, 311mab-32D4 and 311mab-31B9,
121 respectively. We first examined whether these human mAbs were able to bind to
122 SARS-CoV-2 RBD protein by ELISA. The results showed that all three mAbs strongly
123 and specifically bind to the RBD protein (Fig. 3a). Next, we tested whether these
124 mAbs can block the interaction between SARS-CoV-2 RBD and hACE2. We found
125 that both 311mab-31B5 and 311mab-32D4 could efficiently block SARS-CoV-2
126 RBD-hACE2 interaction (IC_{50} =0.0332, and 0.0450 μ g/ml, respectively), while
127 311mab-31B9 clone failed to inhibit such an interaction (Fig. 3b). The 31B5- and

128 32D4-mediated inhibition of RBD-hACE2 interaction was also evidenced by flow
129 cytometry analysis (Fig. 3c-e). Furthermore, we determined the neutralization of these
130 three mAbs using a SARS-CoV-2 S pseudotyped lentiviral particle²². In line with
131 ELISA- and flow cytometry-based blockade results, both 311mab-31B5 and
132 311mab-32D4 effectively neutralized pseudovirus entry to host cells ectopically
133 expressing hACE2 (IC₅₀=0.0338, and 0.0698 µg/ml, respectively). As expected,
134 311mab-31B9 clone failed to show any neutralization activities (Fig. 3f).

135 In conclusion, we have successfully cloned two human blocking mAbs using
136 SARS-CoV-2 RBD-specific memory B cells isolated from recovered COVID-19
137 patients. These two mAbs can specifically bind to SARS-CoV-2 RBD, block the
138 interaction between SARS-CoV-2 RBD and hACE2 receptor, and lead to efficient
139 neutralization of SARS-CoV-2 S protein pseudotyped virus infection. Such human
140 anti-SARS-CoV-2 RBD-hACE2 blocking mAbs hold great promise to be exploited as
141 specific prophylactic and therapeutic agents against ongoing SARS-CoV-2 pandemic.

142

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148 cstc2020jscx-fyzx0074 to Y.C.; cstc2020jscx-fyzx0135 to Y.C.).

149

150 **Author contributions**

151 X.C., R.L., Z.P., Q.C., Y.Y., R.Y., J.Z., L.G., Z.L, Q.H., L.X., J.T., Q.T., W.Y., L.H., and
152 X.Y. performed the experiments. L.Y. designed the study, analyzed the data and

153 wrote the paper with X.C., R.L., P.L., Y.C., Z.Q., X.Z., Y.W., K.D. and Z.Z.; and L.Y.,

154 Y.K. and Z.Q. supervised the study.

155

156 **Competing interests**

157 The authors declare no competing interests.

158

159 **Materials and methods**

160

161 **Human samples.** The 26 COVID-19 patients enrolled in the study were provided
162 written informed consent. Prior to blood collection, the patients were clinically
163 recovered and tested negative qPCR for SARS-CoV-2 virus RNA. Healthy control
164 subjects were 2 adult participants in the study. The study received IRB approval at
165 Chongqing Public Health Medical Center (2020-023-01-KY).

166

167 **PBMC and serum collection.** Blood samples were collected in cell preparation tubes
168 with or without sodium citrate (BD Bioscience). PBMCs were isolated from blood in
169 sodium citrate tubes using Ficoll (TBD Science), washed with PBS plus 2% FBS,
170 suspended in cell freezing medium (90% FBS plus 10% DMSO), frozen in freezing
171 chamber first at -80°C, and then transferred to liquid nitrogen. Sera were collected
172 from blood without sodium citrate treatment and stored in aliquots at -80°C.

173

174 **Single-cell sorting by flow cytometry.** For B cell enrichment, PBMCs were firstly
175 stained with FITC-conjugated anti-CD19 antibody (Biolegend) on ice for 30 min. Then,
176 FITC-CD19 stained PBMCs were enriched using anti-FITC MicroBeads (Miltenyi
177 Biotec) by following manufacturer's protocol. For surface staining, the enriched CD19⁺
178 B cells were stained with biotin-conjugated SARS-CoV-2 RBD protein (Sino Biological,
179 40592-V05H) at 4°C for 20 min, followed by PE-Cy7-conjugated streptavidin
180 (eBioscience), PE-conjugated anti-CD20 antibody (Biolegend), APC-conjugated
181 anti-human IgG (Fc) (Biolegend), APC-Cy7-conjugated anti-CD3 antibody (Biolegend),
182 APC-Cy7-conjugated anti-CD14 antibody (Biolegend), APC-Cy7-conjugated
183 anti-CD56 antibody (Biolegend) and APC-Cy7-conjugated LIVE/DEAD dye (Life
184 Technologies). Cell staining was performed in PBS containing 5% mouse serum
185 (wt/vol). For cell sorting, the stained SARS-CoV-2 RBD-specific IgG⁺ B cells were
186 single-cell sorted into 96-well plates loaded with 10 µl catch buffer and then stored at

187 -80°C. Catch buffer: to 1 ml of RNAase-free water (Tiangen Biotech), add 50 µl 1.5 M
188 Tris pH 8.8 (Beijing Dingguo Changsheng Biotech) and 40 µl Rnasin (NEB).

189

190 **RT-PCR and PCR cloning.** The heavy and light chain genes were PCR amplified as
191 previously described²¹. Briefly, single-cell sorted plates were thawed on ice and added
192 with 15 µl RT-PCR master mix following the one step RT-PCR kit protocol (Takara,
193 RR057A) with primers for IgG VH and IgG VL. RT-PCR program: 50°C for 30 min,
194 94°C for 2 min, 45 cycles of 94°C for 30 sec, 57°C for 30 sec and 72°C for 1 min. Then,
195 RT-PCR products were nested PCR-amplified with nested PCR master mix following
196 the HS DNA polymerase kit protocol (Takara, TAK R010) with primers for IgG VH or
197 IgG VL. Nested PCR program: 98°C for 4 min, 45 cycles of 98°C for 1 min, 57°C for 1
198 min and 72°C for 1 min. Next, heavy and light chain PCR products were purified and
199 nuclease digested with Age1-HF/Sal1-HF (NEB) and Age1-HF/BsiW1-HF (NEB),
200 respectively. The digested heavy and light chain genes were further cloned into
201 human IgG1 heavy chain and light chain expression vectors, respectively.

202

203 **Transfection.** Human embryonic kidney (HEK) 293T cells of 80-90% confluent in the
204 15 cm tissue culture plate were transfected with master mixture containing 9 µg heavy
205 chain plasmid, 9 µg light chain plasmid and 60 µl *TransIT*-293 Transfection reagent
206 (Mirus). The culture media was changed to basal media 24 hours-post transfection.
207 Then, the culture media was collected from the plate 2 days later.

208

209 **ELISA.** 50 ng of SARS-CoV-2 S1 protein (Sino Biological, 40591-V08H) or
210 SARS-Cov2 RBD protein (Sino Biological, 40592-V08B) in 100 µl PBS per well was
211 coated on ELISA plates overnight at 4°C. Then, the ELISA plates were blocked for 1
212 hour with blocking buffer (5% FBS plus 0.05% Tween 20). Next, mAbs or ten-fold
213 diluted patient sera were added to each well in 100 µl blocking buffer for 1 hour. After
214 washing with PBST, the bound antibodies were incubated with anti-human IgG HRP

215 detection antibody (Bioss Biotech) for 30 min, followed by washed with PBST, then
216 PBS and addition of TMB (Beyotime). The ELISA plates were allowed to react for 5
217 min and then stopped by 1 M HCl stop buffer. The optical density (OD) value was
218 determined at 450 nm.

219

220 **ELISA-based receptor-binding inhibition assay.** 200 ng of hACE2 protein (Sino
221 Biological, 10108-H08H) in 100 μ l PBS per well was coated on ELISA plates overnight
222 at 4°C. Then, the ELISA plates were blocked for 1 hour with blocking buffer (5% FBS
223 plus 0.05% Tween 20); meanwhile, three-fold serial dilutions of mAbs or ten-fold
224 diluted patient sera were incubated with optimal dose (based on EC₅₀) of SARS-Cov2
225 RBD protein (Sino Biological, 40592-V05H) for 1 hour. Then, the incubated mixtures
226 were added to ELISA plates and allowed to develop for 30 min, followed by PBST
227 washing and anti-mouse Fc HRP antibody (Thermo Fisher Scientific). Next, the ELISA
228 plates were washed with PBST, then PBS and added with TMB (Beyotime). After 5
229 min, the ELISA plates were stopped and determined at 450 nm. The half maximal
230 inhibitory concentration (IC₅₀) was determined by using 4-parameter logistic
231 regression.

232

233 **Flow cytometry-based receptor-binding inhibition assay.** 311mab mAbs or
234 isotype were incubated with optimal dose (based on EC₅₀) of SARS-Cov2 RBD
235 protein (Sino Biological, 40592-V05H) for 1 hour at RT. Then, the mixtures were
236 incubated with 10,000 hACE2-plasmid transiently transfected 293T cells for 40 min on
237 ice, followed by stained with Alexa Fluor 647-conjugated goat anti-mouse IgG
238 (Biolegend) and APC-Cy7-conjugated LIVE/DEAD dye (Life Technologies).

239

240 **Pseudovirus neutralization assay.** Spike protein of SARS-Cov-2 typed pseudovirus
241 was produced as previously described²². Concisely, HEK-293T cells were transfected
242 with psPAX2, pLenti-GFP and 2019-nCov S plasmids by using *TransIT*-293

243 Transfection reagent (Mirus). The culture media was changed to fresh media 12
244 hours-post transfection. And at 64 hours after transfection, supernatants were
245 harvested. For pseudovirus neutralization assay, three-fold serially diluted mAbs were
246 mixed with SARS-Cov-2 typed pseudovirus for 1 hour. Then, the mixture was
247 incubated with hACE2-expressing HEK-293T (hACE2/293T) cells overnight, followed
248 by change of fresh media. At 40 hours-post incubation, the luciferase activity of
249 infected hACE2/293T cells were detected by Dual-Luciferase Reporter Assay System
250 (Promega). The percent of infection was calculated as ratio of luciferase value with
251 mAbs to that without mAbs. The half maximal inhibitory concentration (IC_{50}) was
252 determined by using 4-parameter logistic regression.
253

254

255 **Figure legends**

256

257 **Figure 1 ELISA binding and blocking assays of COVID-19 patient sera. (a)** ELISA
258 binding assay of COVID-19 patient sera to ELISA plate coating of SARS-CoV-2 S1
259 protein. **(b)** ELISA binding assay of COVID-19 patient sera to ELISA plate coating of
260 SARS-CoV-2 RBD protein. **(c)** COVID-19 patient serum-mediated inhibition of the
261 SARS-CoV-2 S1 protein binding to hACE2 protein by ELISA. NC, negative control.
262 HD, healthy donor.

263

264 **Figure 2 Cloning human mAbs from single SARS-Cov2 RBD-specific IgG⁺**
265 **memory B cells of three recovered patients whose sera potentially blocked**
266 **RBD-hACE2 interaction. (a)** An overall strategy of anti-SARS-CoV-2 RBD mAbs. **(b)**
267 Flow cytometry analysis of SARS-CoV-2 RBD-specific IgG⁺ B cells in PBMCs of
268 healthy donor and patient XFQ. **(c)** Heavy and light Ig-chain encoding segments of
269 SARS-CoV-2 RBD-specific IgG⁺ B cells were amplified by single-cell RT-PCR. **(d)**
270 Endonuclease digestion of IgG VH and VL inserts in the plasmids. **(e)** CDR3
271 sequences of heavy chains.

272

273 **Figure 3 Characterization of mAbs against SARS-Cov2 RBD. (a)** Specificity of
274 mAbs (311mab-31B5, -32D4 and -31B9 clones) to SARS-CoV-2 RBD protein by
275 ELISA. **(b)** ELISA analysis of SARS-CoV-2 RBD-hACE2 interaction inhibited by
276 311mab-31B5, -32D4 and -31B9 mAbs. **(c)** Flow cytometry analysis of SARS-CoV-2
277 RBD-hACE2 interaction inhibited by 311mab-31B5, -32D4 and -31B9 mAbs. The
278 numbers adjacent to the outlined areas indicate the percentages of anti-mouse IgG⁺
279 hACE2-plasmid transiently transfected 293T cells, which are summarized in **(d)**. **(e)**
280 Mean fluorescence intensity of Alexa Fluor 647 anti-mouse IgG in anti-mouse IgG⁺
281 hACE2-plasmid transiently transfected 293T cells. **(f)** Antibody-mediated blocking of
282 luciferase-encoding SARS-Cov-2 typed pseudovirus into hACE2/293T cells. The data

283 are representative of two independent experiments with three replicates per group (a,
284 b, d-f; error bars in a, b, d-f indicate the SD).
285
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287 **References**

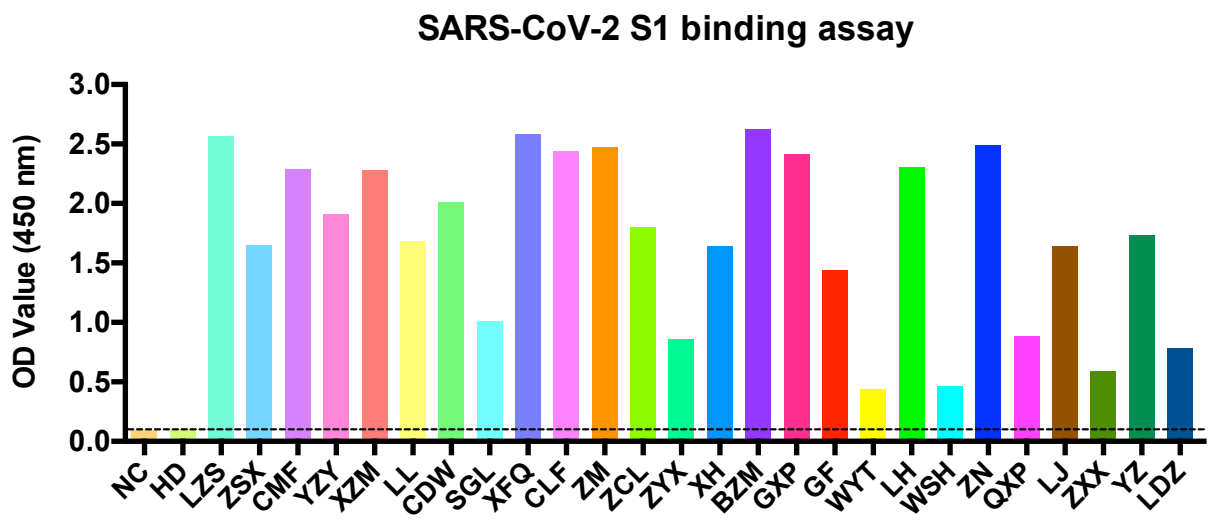
- 288 1. *World Health Organization.*
289 [https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200](https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200318-sitrep-58-covid-19.pdf?sfvrsn=20876712_2)
290 [318-sitrep-58-covid-19.pdf?sfvrsn=20876712_2](https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200318-sitrep-58-covid-19.pdf?sfvrsn=20876712_2). 2020.
- 291 2. Wu, F., et al., *A new coronavirus associated with human respiratory disease in*
292 *China*. *Nature*, 2020. **579**(7798): p. 265-269.
- 293 3. Zhou, P., et al., *A pneumonia outbreak associated with a new coronavirus of*
294 *probable bat origin*. *Nature*, 2020. **579**(7798): p. 270-273.
- 295 4. Zhu, N., et al., *A Novel Coronavirus from Patients with Pneumonia in China,*
296 *2019*. *N Engl J Med*, 2020. **382**(8): p. 727-733.
- 297 5. Huang, C., et al., *Clinical features of patients infected with 2019 novel*
298 *coronavirus in Wuhan, China*. *Lancet*, 2020. **395**(10223): p. 497-506.
- 299 6. Wang, D., et al., *Clinical Characteristics of 138 Hospitalized Patients With*
300 *2019 Novel Coronavirus-Infected Pneumonia in Wuhan, China*. *JAMA*, 2020.
- 301 7. Yang, X., et al., *Clinical course and outcomes of critically ill patients with*
302 *SARS-CoV-2 pneumonia in Wuhan, China: a single-centered, retrospective,*
303 *observational study*. *Lancet Respir Med*, 2020.
- 304 8. Chen, N., et al., *Epidemiological and clinical characteristics of 99 cases of*
305 *2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study*.
306 *Lancet*, 2020. **395**(10223): p. 507-513.
- 307 9. *World Health Organization.*
308 [https://www.who.int/dg/speeches/detail/who-director-general-s-opening-remar](https://www.who.int/dg/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19---11-march-2020)
309 [ks-at-the-media-briefing-on-covid-19---11-march-2020](https://www.who.int/dg/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19---11-march-2020). 2020.
- 310 10. Marston, H.D., C.I. Paules, and A.S. Fauci, *Monoclonal Antibodies for*
311 *Emerging Infectious Diseases - Borrowing from History*. *N Engl J Med*, 2018.
312 **378**(16): p. 1469-1472.
- 313 11. Saylor, C., E. Dadachova, and A. Casadevall, *Monoclonal antibody-based*
314 *therapies for microbial diseases*. *Vaccine*, 2009. **27 Suppl 6**: p. G38-46.

- 315 12. Jun Lan, J.G., Jinfang Yu, Sisi Shan, Huan Zhou, Shilong Fan, Qi Zhang,
316 Xuanling Shi, Qisheng Wang, Linqi Zhang, Xinquan Wang, *Crystal structure of*
317 *the 2019-nCoV spike receptor-binding domain bound with the ACE2 receptor.*
318 bioRxiv, 2020. **2020.02.19.956235**; doi:
319 <https://doi.org/10.1101/2020.02.19.956235>.
- 320 13. Li, F., *Structure, Function, and Evolution of Coronavirus Spike Proteins.* Annu
321 Rev Virol, 2016. **3**(1): p. 237-261.
- 322 14. Li, F., et al., *Structure of SARS coronavirus spike receptor-binding domain*
323 *complexed with receptor.* Science, 2005. **309**(5742): p. 1864-8.
- 324 15. Yan, R., et al., *Structural basis for the recognition of the SARS-CoV-2 by*
325 *full-length human ACE2.* Science, 2020.
- 326 16. Gui, M., et al., *Cryo-electron microscopy structures of the SARS-CoV spike*
327 *glycoprotein reveal a prerequisite conformational state for receptor binding.*
328 Cell Res, 2017. **27**(1): p. 119-129.
- 329 17. Kirchdoerfer, R.N., et al., *Pre-fusion structure of a human coronavirus spike*
330 *protein.* Nature, 2016. **531**(7592): p. 118-21.
- 331 18. Wrapp, D., et al., *Cryo-EM structure of the 2019-nCoV spike in the prefusion*
332 *conformation.* Science, 2020. **367**(6483): p. 1260-1263.
- 333 19. Chunyan Wang, W.L., Dubravka Drabek, Nisreen M.A. Okba, Rien van
334 Haperen, Albert D.M.E. Osterhaus, Frank J.M. van Kuppeveld, Bart L.
335 Haagmans, Frank Grosveld, Berend-Jan Bosch, *A human monoclonal*
336 *antibody blocking SARS-CoV-2 infection.* bioRxiv, 2020. **2020.03.11.987958**;
337 doi: <https://doi.org/10.1101/2020.03.11.987958>.
- 338 20. Pallesen, J., et al., *Immunogenicity and structures of a rationally designed*
339 *prefusion MERS-CoV spike antigen.* Proc Natl Acad Sci U S A, 2017. **114**(35):
340 p. E7348-E7357.
- 341 21. Smith, K., et al., *Rapid generation of fully human monoclonal antibodies*
342 *specific to a vaccinating antigen.* Nat Protoc, 2009. **4**(3): p. 372-84.

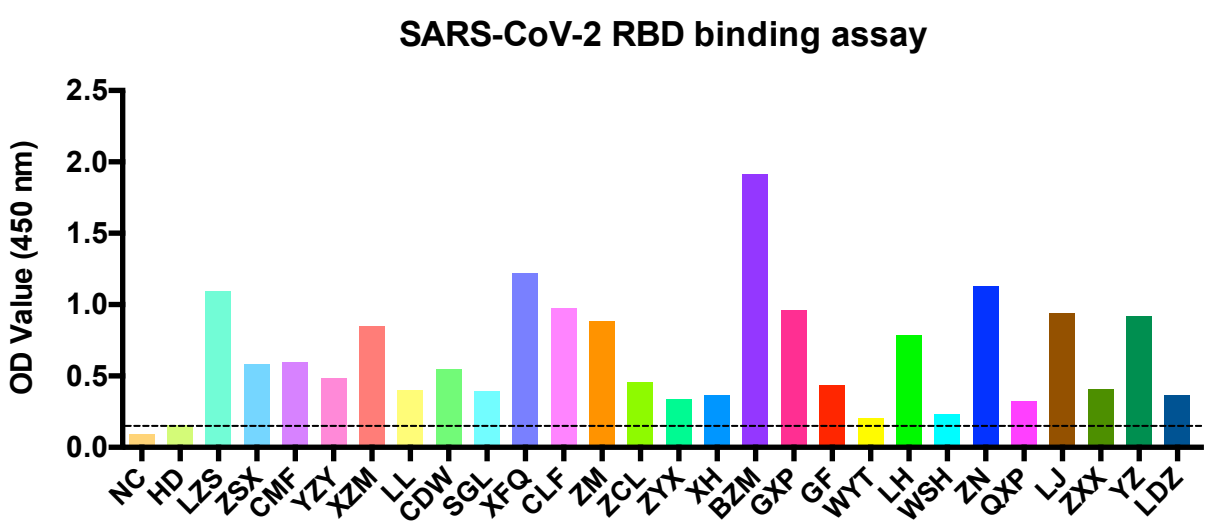
- 343 22. Xiuyuan Ou, Y.L., Xiaobo Lei, Pei Li, Dan Mi, Lili Ren, Li Guo, Ruixuan Guo,
344 Ting Chen, Jiaying Hu, Zichun Xiang, Zhixia Mu, Xing Chen, Jieyong Chen,
345 Keping Hu, Qi Jin, Jianwei Wang, Zhaohui Qian, *Characterization of spike*
346 *glycoprotein of 2019- nCoV on virus entry and its immune cross- reactivity with*
347 *spike glycoprotein of SARS-CoV*. Nature Communications, 2020.
348 **Doi:10.21203/rs.2.24016/v1**.
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Figure 1

a



b



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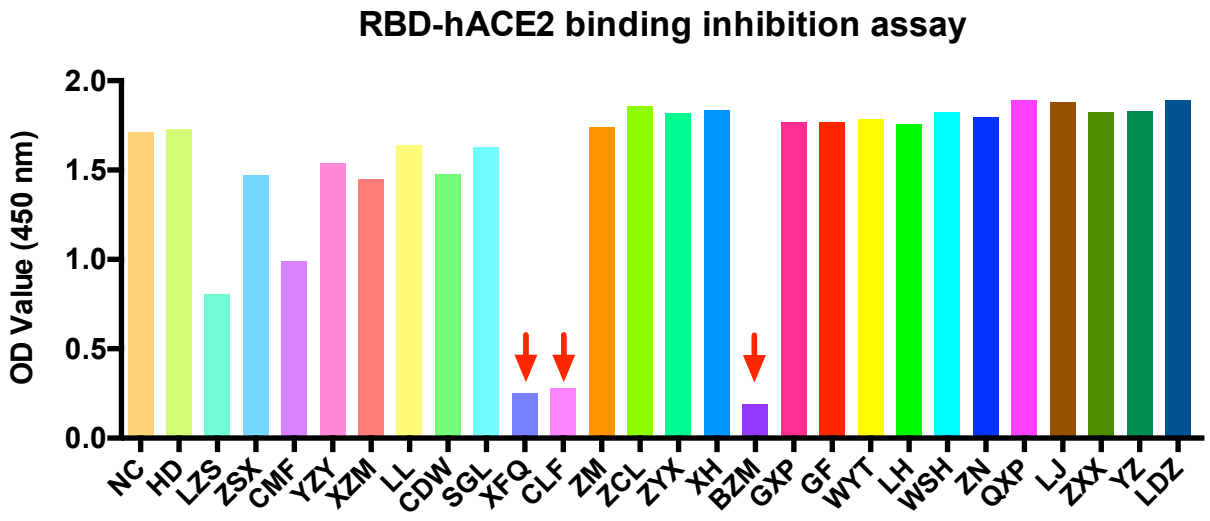
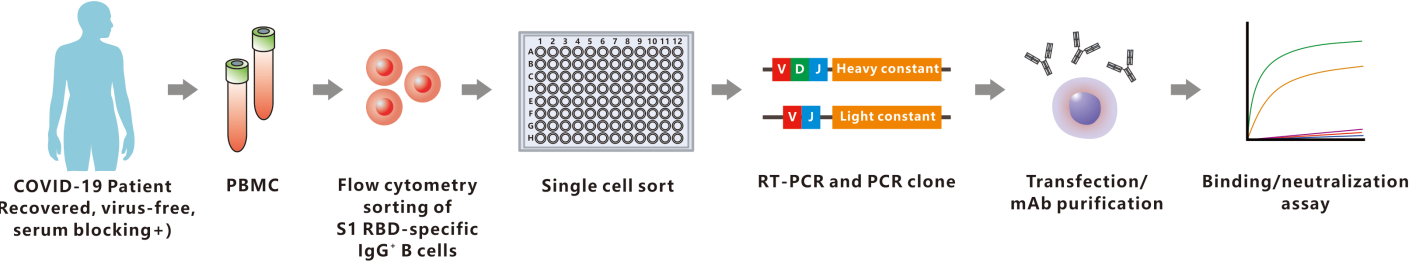
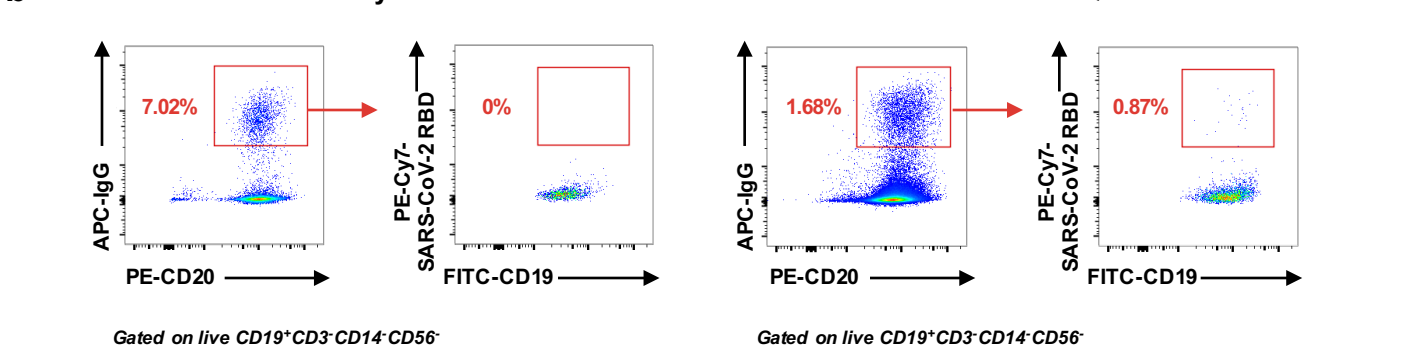


Figure 2

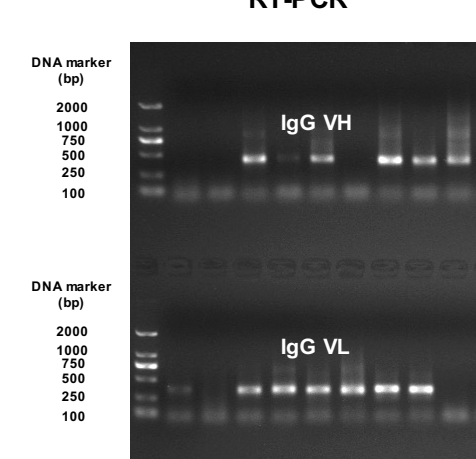
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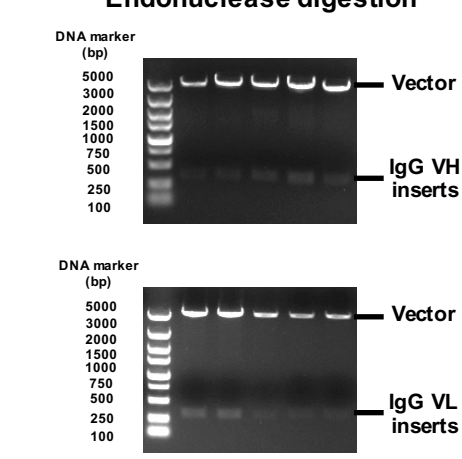
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d



e

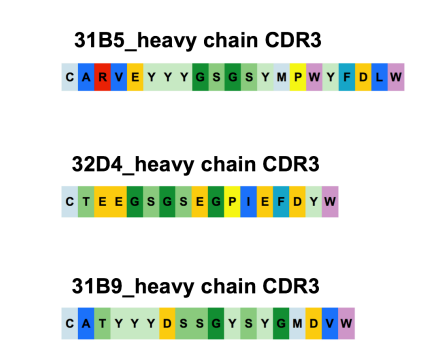
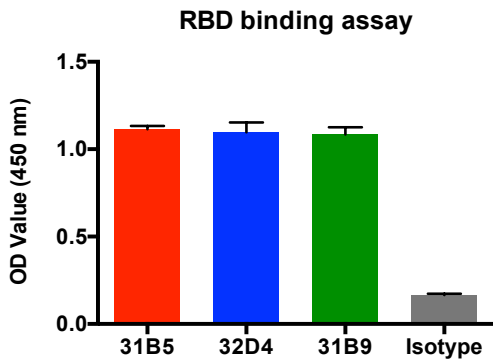
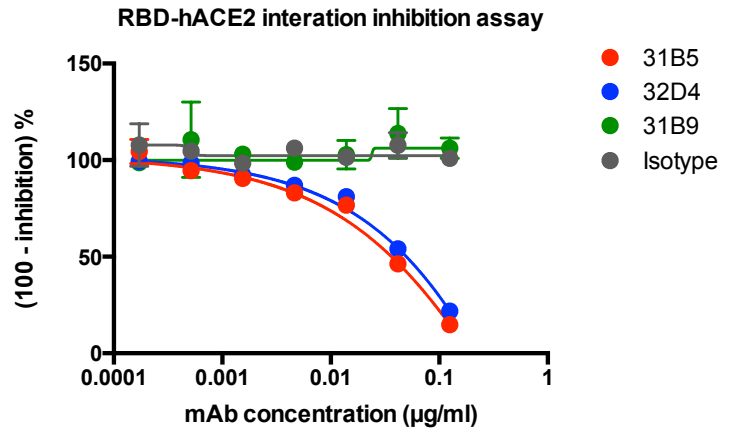
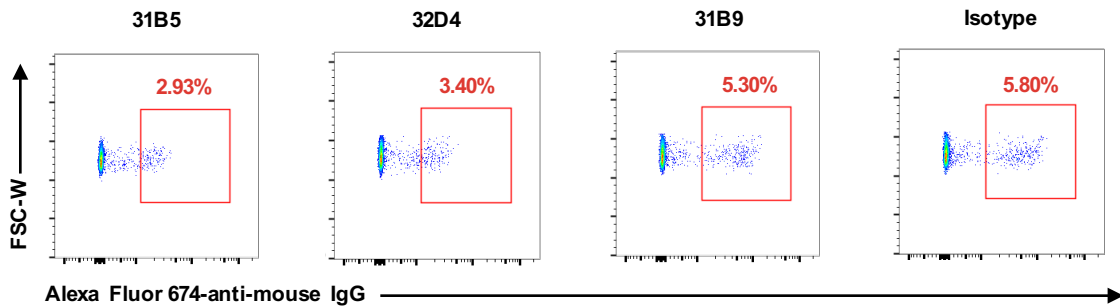
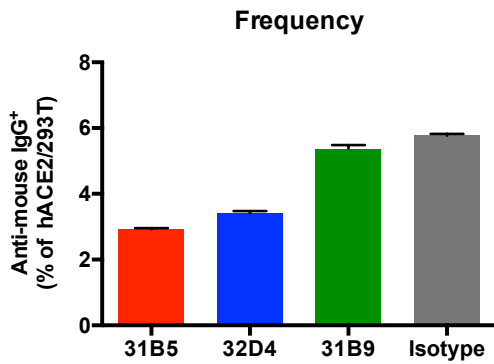
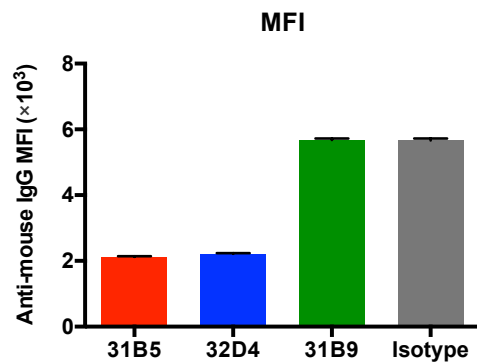


Figure 3**a****b****c****d****e****f**