

1 **TITLE:** An ultra-potent synthetic nanobody neutralizes SARS-CoV-2 by locking Spike into an
2 inactive conformation

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4 Michael Schoof^{1,2##}, Bryan Faust^{1,2,3,4#}, Reuben A. Saunders^{1,5#}, Smriti Sangwan^{1,2#}, Veronica
5 Rezelj^{6#}, Nick Hoppe^{3,4}, Morgane Boone^{1,2}, Christian B. Billesbølle^{3,4}, Cristina Puchades⁴,
6 Caleigh M. Azumaya⁴, Huong T. Kratochvil⁴, Marcell Zimanyi^{1,2}, Ishan Deshpande^{3,4}, Jiahao
7 Liang³, Sasha Dickinson⁴, Henry C. Nguyen⁴, Cynthia M. Chio⁴, Gregory E. Merz⁴, Michael C.
8 Thompson⁴, Devan Diwanji⁴, Kaitlin Schaefer⁴, Aditya A. Anand^{1,2}, Niv Dobzinski^{1,2}, Beth
9 Shoshana Zha⁷, Camille R. Simoneau^{10,11,12}, Kristoffer Leon^{10,11,12}, Kris M. White^{13,14}, Un Seng
10 Chio⁴, Meghna Gupta⁴, Mingliang Jin⁴, Fei Li⁴, Yanxin Liu⁴, Kaihua Zhang⁴, David Bulkley⁴, Ming
11 Sun⁴, Amber M. Smith⁴, Alexandria N. Rizo⁴, Frank Moss⁴, Axel F. Brilot⁴, Sergei Pourmal⁴,
12 Raphael Trenker⁴, Thomas Pospiech⁴, Sayan Gupta⁹, Benjamin Barsi-Rhynch³, Vladislav
13 Belyy^{1,2}, Andrew W. Barile-Hill⁸, Silke Nock^{1,2}, Yuwei Liu^{1,2}, Nevan J. Krogan^{4,5,10,11}, Corie Y.
14 Ralston⁹, Danielle L. Swaney^{4,5,10,11}, Adolfo García-Sastre^{13,14,15,16}, Melanie Ott^{10,11,12}, Marco
15 Vignuzzi⁶, QCRG Structural Biology Consortium^{4‡}, Peter Walter^{1,2*}, Aashish Manglik^{3,4,10,17*}

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17 **AFFILIATIONS:**

18 ¹Howard Hughes Medical Institute, University of California at San Francisco, San Francisco, CA,
19 USA.

20 ²Department of Biochemistry and Biophysics, University of California at San Francisco, San
21 Francisco, CA, USA.

22 ³Department of Pharmaceutical Chemistry, University of California at San Francisco, San
23 Francisco, CA, USA.

24 ⁴Quantitative Biosciences Institute (QBI) Coronavirus Research Group Structural Biology
25 Consortium, University of California, San Francisco, CA, USA.

26 ⁵Department of Cellular and Molecular Pharmacology, University of California at San Francisco,
27 San Francisco, CA, USA.

28 ⁶Viral Populations and Pathogenesis Unit, CNRS UMR 3569, Institut Pasteur, 75724, Paris,
29 Cedex 15, France

30 ⁷Department of Pulmonary, Critical Care, Allergy and Sleep Medicine, University of California
31 San Francisco, San Francisco, CA 94158, USA.

32 ⁸Cytiva Life Sciences, Marlborough, MA, USA.

33 ⁹Molecular Biophysics and Integrated Bioimaging and the Molecular Foundry, Lawrence
34 Berkeley National Laboratory, Berkeley, CA, USA.

35 ¹⁰Quantitative Biosciences Institute (QBI), University of California San Francisco, San
36 Francisco, CA, USA.

37 ¹¹J. David Gladstone Institutes, San Francisco, CA, USA.

38 ¹²Department of Medicine, University of California San Francisco, San Francisco, CA, USA.

39 ¹³Department of Microbiology, Icahn School of Medicine at Mount Sinai, New York, NY, USA.

40 ¹⁴Global Health and Emerging Pathogens Institute, Icahn School of Medicine at Mount Sinai,
41 New York, NY, USA.

42 ¹⁵Department of Medicine, Division of Infectious Diseases, Icahn School of Medicine at Mount
43 Sinai, New York, NY, USA

44 ¹⁶The Tisch Cancer Institute, Icahn School of Medicine at Mount Sinai, New York, NY, USA

45 ¹⁷Department of Anesthesia and Perioperative Care, University of California at San Francisco,
46 San Francisco, CA, USA.

47
48 # These authors contributed equally

49 ‡ Full listing in Supplementary Information

50 * To whom correspondence should be addressed; Email: michael@walterlab.ucsf.edu,
51 peter@walterlab.ucsf.edu, Aashish.Manglik@ucsf.edu

52 **ABSTRACT**

53 Without an effective prophylactic solution, infections from SARS-CoV-2 continue to rise
54 worldwide with devastating health and economic costs. SARS-CoV-2 gains entry into host cells
55 via an interaction between its Spike protein and the host cell receptor angiotensin converting
56 enzyme 2 (ACE2). Disruption of this interaction confers potent neutralization of viral entry,
57 providing an avenue for vaccine design and for therapeutic antibodies. Here, we develop single-
58 domain antibodies (nanobodies) that potently disrupt the interaction between the SARS-CoV-2
59 Spike and ACE2. By screening a yeast surface-displayed library of synthetic nanobody
60 sequences, we identified a panel of nanobodies that bind to multiple epitopes on Spike and
61 block ACE2 interaction via two distinct mechanisms. Cryogenic electron microscopy (cryo-EM)
62 revealed that one exceptionally stable nanobody, Nb6, binds Spike in a fully inactive
63 conformation with its receptor binding domains (RBDs) locked into their inaccessible down-
64 state, incapable of binding ACE2. Affinity maturation and structure-guided design of
65 multivalency yielded a trivalent nanobody, mNb6-tri, with femtomolar affinity for SARS-CoV-2
66 Spike and picomolar neutralization of SARS-CoV-2 infection. mNb6-tri retains stability and
67 function after aerosolization, lyophilization, and heat treatment. These properties may enable
68 aerosol-mediated delivery of this potent neutralizer directly to the airway epithelia, promising to
69 yield a widely deployable, patient-friendly prophylactic and/or early infection therapeutic agent to
70 stem the worst pandemic in a century.

71

72 **MAIN TEXT:**

73 Over the last two decades, three zoonotic β -coronaviruses have entered the human population,
74 causing severe respiratory symptoms with high mortality (1-3). The ongoing COVID-19
75 pandemic is caused by SARS-CoV-2, the most readily transmissible of these three
76 coronaviruses (4-7). SARS-CoV-2 has wrecked the world's economy and societies to an
77 unprecedented extent, to date (Aug. 14, 2020) causing 751,154
78 reported deaths around the globe (8). Although public health measures have slowed its spread
79 in many regions, infection hotspots keep reemerging. No successful vaccine or preventive
80 treatment has yet been manufactured for any coronavirus, and the time to develop an effective
81 and broadly available vaccine for SARS-CoV-2 remains uncertain. The development of novel
82 therapeutic and prophylactic approaches thus remains essential, both as temporary stopgaps
83 until an effective vaccine is generated and as permanent solutions for those segments of the
84 population for which vaccination proves ineffective or contraindicated.

85
86 Coronavirus virions are bounded by a membrane envelope that contains ~25 copies of the
87 homotrimeric transmembrane spike glycoprotein (Spike) responsible for virus entry into the host
88 cell (9). The surface-exposed portion of Spike is composed of two domains, S₁ and S₂ (10). The
89 S₁ domain mediates the interaction between virus and its host cell receptor, the angiotensin
90 converting enzyme 2 (ACE2), while the S₂ domain catalyzes fusion of the viral and host cell
91 membranes (3, 11-13). During its biogenesis, the Spike protein is proteolytically cleaved
92 between the S₁ and S₂ domains, which primes the virus for cellular entry (10). Contained within
93 S₁ is the receptor binding domain (RBD), which directly binds to ACE2. The RBD is attached to
94 the body of Spike by a flexible region and can exist in an inaccessible down-state or an
95 accessible up-state (14, 15). Binding to ACE2 requires the RBD in the up-state and enables
96 cleavage by host proteases TMPRSS2 or cathepsin, triggering a dramatic conformational
97 change in S₂ that enables viral entry (16). In SARS-CoV-2 virions, Spike oscillates between an
98 active, open conformation with at least one RBD in the up-state and an inactive, closed
99 conformation with all RBDs in the down-state (9, 11, 14, 15).

100
101 By screening a high-complexity yeast surface-displayed library of synthetic nanobodies, we
102 have uncovered a collection of nanobodies that block the Spike-ACE2 interaction. Biochemical
103 and structural studies revealed that two classes of these nanobodies act in distinct ways to
104 prevent ACE2 binding. Combining affinity maturation and structure-guided multimerization, we
105 optimized these agents and generated Spike binders that match or exceed the potency of most

106 monoclonal antibodies disclosed to date. Our lead neutralizing molecule, mNb6-tri, blocks
107 SARS-CoV-2 entry in human cells at picomolar efficacy and withstands aerosolization,
108 lyophilization, and elevated temperatures. mNb6-tri provides a promising approach to deliver a
109 potent SARS-CoV-2 neutralizing molecule directly to the airways for prophylaxis or therapy.

110

111 **RESULTS**

112 **Synthetic nanobodies that disrupt Spike-ACE2 interaction**

113 To isolate nanobodies that neutralize SARS-CoV-2, we screened a yeast surface-displayed
114 library of $>2 \times 10^9$ synthetic nanobody sequences. Our strategy was to screen for binders to the
115 full Spike protein ectodomain, in order to capture not only those nanobodies that would compete
116 by binding to the ACE2-binding site on the RBD directly but also those that might bind
117 elsewhere on Spike and block ACE2 interaction through indirect mechanisms. We used a
118 mutant form of SARS-CoV-2 Spike (Spike^{*},) as the antigen (15). Spike^{*} lacks one of the two
119 activating proteolytic cleavage sites between the S₁ and S₂ domains and introduces two
120 mutations to stabilize the pre-fusion conformation. Spike^{*} expressed in mammalian cells binds
121 ACE2 with a $K_D = 44$ nM (Supplementary Fig. 1), consistent with previous reports (17). Next, we
122 labeled Spike^{*} with biotin or with fluorescent dyes and selected nanobody-displaying yeast over
123 multiple rounds, first by magnetic bead binding and then by fluorescence-activated cell sorting
124 (Fig. 1A).

125

126 Three rounds of selection yielded 21 unique nanobodies that bound Spike^{*} and showed
127 decreased Spike^{*} binding in the presence of ACE2. Closer inspection of their binding properties
128 revealed that these nanobodies fall into two distinct classes. One group (Class I) binds the RBD
129 and competes with ACE2 (Fig. 1B). A prototypical example of this class is nanobody Nb6, which
130 binds to Spike^{*} and to RBD alone with a K_D of 210 nM and 41 nM, respectively (Fig. 1C; Table
131 1). Another group (Class II), exemplified by nanobody Nb3, binds to Spike^{*} ($K_D = 61$ nM), but
132 displays no binding to RBD alone (Fig. 1C, Table 1). In the presence of excess ACE2, binding of
133 Nb6 and other Class I nanobodies is blocked entirely, whereas binding of Nb3 and other Class II
134 nanobodies is decreased only moderately (Fig. 1B). These results suggest that Class I
135 nanobodies target the RBD to block ACE2 binding, whereas Class II nanobodies target other
136 epitopes and decrease ACE2 interaction with Spike allosterically or through steric interference.
137 Indeed, surface plasmon resonance (SPR) experiments demonstrate that Class I and Class II
138 nanobodies can bind Spike^{*} simultaneously (Fig. 1D).

139

140 Analysis of the kinetic rate constants for Class I nanobodies revealed a consistently greater
141 association rate constant (k_a) for nanobody binding to the isolated RBD than to full-length Spike*
142 (Table 1), which suggests that RBD accessibility influences the K_D . We next tested the efficacy
143 of our nanobodies, both Class I and Class II, to inhibit binding of fluorescently labeled Spike* to
144 ACE2-expressing HEK293 cells (Table 1, Fig. 1E). Class I nanobodies emerged with highly
145 variable activity in this assay with Nb6 and Nb11 as two of the most potent clones with IC_{50}
146 values of 370 and 540 nM, respectively (Table 1). For unexplained reasons, Class II nanobodies
147 showed little to no activity in this assay (Table 1, Fig. 1E).

148

149 Going forward, we prioritized two Class I nanobodies, Nb6 and Nb11, that combine potent
150 Spike* binding with relatively small differences in k_a between binding to Spike* or RBD. We
151 reasoned that the epitopes recognized by Nb6 and Nb11 would be more readily accessible in
152 the Spike protein on intact virions. For Class II nanobodies we prioritized Nb3 because of its
153 optimal stability and yield during purification.

154

155 **Nb6 and Nb11 target the RBD and directly compete with ACE2**

156 To define the binding sites of Nb6 and Nb11, we determined their cryogenic electron
157 microscopy (cryo-EM) structures bound to Spike* (Fig. 2A-B, Supplementary Fig. 2-4,
158 Supplementary Table 1). Both nanobodies recognize RBD epitopes that overlap the ACE2
159 binding site (Fig. 2E). For Nb6 and Nb11, we resolved nanobody binding to both the open and
160 closed conformations of Spike*. We obtained a 3.0 Å map of Nb6 bound to closed Spike*, which
161 enabled modeling of the Nb6-Spike* complex (Fig. 2A), including the complementarity
162 determining regions (CDRs). We also obtained lower resolution maps for Nb6 bound to open
163 Spike* (3.8 Å), Nb11 bound to open Spike* (4.2 Å), and Nb11 bound to closed Spike* (3.7 Å).
164 For these lower resolution maps, we could define the nanobody's binding orientation but not
165 accurately model the CDRs.

166

167 Nb6 bound to closed Spike* straddles the interface between two adjacent RBDs. The majority of
168 the contacting surfaces are contributed by CDR1 and CDR2 of Nb6 (Fig. 2C). CDR3 contacts
169 the adjacent RBD that is counterclockwise positioned when viewed from the top of Spike* (Fig.
170 2C). The binding of one Nb6 therefore stabilizes two adjacent RBDs in the down-state. We
171 surmise that this initial binding event pre-organizes the binding site for a second and third Nb6
172 molecule to stabilize the closed Spike* conformation. Indeed, binding of two Nb6 molecules
173 would lock all three RBDs into the down-state, thus highly favoring binding of a third Nb6

174 because binding would not entail any further entropic cost. By contrast, Nb11 bound to down-
175 state RBDs only contacts a single RBD (Fig. 2D).

176

177 **Nb3 interacts with the Spike S₁ domain external to the RBD**

178 Our attempts to determine the binding site of Nb3 by cryo-EM proved unsuccessful. We
179 therefore turned to radiolytic hydroxyl radical footprinting to determine potential binding sites for
180 Nb3. Spike*, either apo or bound to Nb3, was exposed to 5-50 milliseconds of synchrotron X-ray
181 radiation to label solvent-exposed amino acids with hydroxyl radicals. Radical-labeled amino
182 acids were subsequently identified and quantified by mass spectrometry of trypsin/Lys-C or Glu-
183 C protease digested Spike*(18). Two neighboring surface residues on the S₁ domain of Spike
184 (M177 and H207) emerged as highly protected sites in the presence of Nb3 (Supplementary
185 Fig. 5). The degree of protection is consistent with prior observations of antibody-antigen
186 interactions by hydroxyl radical footprinting (19). Both M177 and H207 are greater than 40 Å
187 distant from the ACE2 binding site on the RBD, suggesting that Nb3 may inhibit Spike-ACE2
188 interactions through allosteric means.

189

190 **Rationally engineered multivalency increases potency**

191 The structure of Nb6 bound to closed Spike* enabled us to engineer bivalent and trivalent
192 nanobodies predicted to lock all RBDs in the down-state. To this end, we inserted flexible Gly-
193 Ser linkers of either 15 or 20 amino acids to span the 52 Å distance between adjacent Nb6
194 monomers bound to down-state RBDs in closed Spike* (Supplementary Fig. 6). Both linker
195 lengths are too short to span the distance (72 Å) between Nb6 bound to a down-state RBD and
196 an up-state RBD that would co-exist in an open Spike. Moreover, binding of three RBDs in the
197 previously reported conformation of Nb6-bound open Spike* would be physically impossible
198 even with longer linker length because of steric clashes (Supplementary Fig. 6). By contrast, the
199 minimum distance between adjacent Nb11 monomers bound to either open or closed Spike* is
200 68 Å (Supplementary Fig. 6). We therefore predicted that multivalent binding by Nb6 constructs
201 would display significantly slowed dissociation rates due to the enhanced avidity afforded by
202 Spike's trimeric architecture.

203

204 We assessed multivalent Nb6 binding to Spike* by SPR. Both bivalent Nb6 with a 15 amino acid
205 linker (Nb6-bi) and trivalent Nb6 with two 20 amino acid linkers (Nb6-tri) dissociate from Spike*
206 in a biphasic manner. The dissociation phase can be fitted to two components: a fast phase with
207 kinetic rate constants k_{d1} of $2.7 \times 10^{-2} \text{ s}^{-1}$ for Nb6-bi and $2.9 \times 10^{-2} \text{ s}^{-1}$ for Nb6-tri, which are of the

208 same magnitude as that observed for monovalent Nb6 ($k_d = 5.6 \times 10^{-2} \text{ s}^{-1}$) and a slow phase that
209 is dependent on avidity ($k_{d2} = 3.1 \times 10^{-4}$ for Nb6-bi and $k_{d2} < 1.0 \times 10^{-6} \text{ s}^{-1}$ for Nb6-tri, respectively)
210 (Fig. 3A). The relatively similar k_d for the fast phase suggests that a fraction of the observed
211 binding for the multivalent constructs is nanobody binding to a single Spike* RBD. By contrast,
212 the slow dissociation phase of Nb6-bi and Nb6-tri indicates engagement of two or three RBDs.
213 We observed no dissociation for the slow phase of Nb6-tri over 10 minutes, indicating an upper
214 boundary for k_{d2} of $1 \times 10^{-6} \text{ s}^{-1}$ and subpicomolar affinity. This measurement remains an upper-
215 bound estimate rather than an accurate measurement because the technique is limited by the
216 intrinsic dissociation rate of Spike* from the chip imposed by the chemistry used to immobilize
217 Spike*.

218

219 We reasoned that the biphasic dissociation behavior could be explained by a slow
220 interconversion between up- and down-state RBDs, with conversion to the more stable down-
221 state required for full trivalent binding. According to this view, a single domain of Nb6-tri
222 engaged with an up-state RBD would dissociate rapidly. The system would then re-equilibrate
223 as the RBD flips into the down-state, eventually allowing Nb6-tri to trap all RBDs in closed
224 Spike*. To test this notion directly, we varied the time allowed for Nb6-tri binding to Spike*.
225 Indeed, we observed an exponential decrease in the percent fast-phase with a $t_{1/2}$ of 65 s (Fig.
226 3B), which, we surmise, reflects the timescale of conversion between the RBD up- and down-
227 states in Spike*. Taken together, dimerization and trimerization of Nb6 afforded 750-fold and
228 >200,000-fold gains in K_D , respectively.

229

230 **Class I and II nanobodies prevent SARS-CoV-2 infection**

231 We next tested the neutralization activity of trivalent versions of our top Class I (Nb6 and Nb11)
232 and Class II (Nb3) nanobodies against SARS-CoV-2 pseudotyped lentivirus. In this assay,
233 SARS-CoV-2 Spike is expressed as a surface protein on a lentiviral particle that contains a
234 ZsGreen reporter gene, which is integrated and expressed upon successful viral entry into cells
235 harboring the ACE2 receptor (20). Nb6 and Nb11 inhibited pseudovirus infection with IC_{50}
236 values of 2.0 μM and 2.4 μM , respectively, and Nb3 inhibited pseudovirus infection with an IC_{50}
237 of 3.9 μM (Fig. 3C, Table 1). Nb6-tri shows a 2000-fold enhancement of inhibitory activity, with
238 an IC_{50} of 1.2 nM, whereas trimerization of Nb11 and Nb3 resulted in more modest gains of 40-
239 and 10-fold (51 nM and 400 nM), respectively (Fig. 3C).

240

241 We next confirmed these neutralization activities with a viral plaque assay using live SARS-
242 CoV-2 virus infection of VeroE6 cells. Consistent with its activity against pseudotyped lentivirus,
243 Nb6-tri proved exceptionally potent, neutralizing SARS-CoV-2 with an average IC₅₀ of 160 pM
244 (Fig. 3D). Nb3-tri neutralized SARS-CoV-2 with an average IC₅₀ of 140 nM (Fig. 3D).

245

246 **Affinity maturation yields a femtomolar K_D Spike inhibitor**

247 We further optimized the potency of Nb6 by selecting high-affinity variants. To this end, we
248 prepared a new library, starting with the Nb6 coding sequence, in which we varied each amino
249 acid position of all three CDRs by saturation mutagenesis (Fig. 4A). After two rounds of
250 magnetic bead-based selection, we isolated a population of high-affinity clones. Sequencing
251 revealed two highly penetrant mutations: I27Y in CDR1 and P105Y in CDR3. We incorporated
252 these two mutations into Nb6 to generate matured Nb6 (mNb6), which binds with 500-fold
253 increased affinity to Spike* as measured by SPR (Fig. 4B). As a monomer, mNb6 inhibits both
254 pseudovirus and live SARS-CoV-2 infection with low nanomolar potency, a ~200-fold
255 improvement compared to Nb6 (Fig. 4I-J, Table 1).

256

257 A 2.9 Å cryo-EM structure of mNb6 bound to Spike* shows that, like the parent nanobody Nb6,
258 mNb6 binds to closed Spike (Fig. 4C, Supplementary Fig. 7). The higher resolution map allowed
259 us to build a model with high confidence and determine the effects of the I27Y and P105Y
260 substitutions. mNb6 induces a slight rearrangement of the down-state RBDs as compared to
261 both previously determined structures of apo-Spike* and Spike* bound to Nb6, inducing a 9°
262 rotation of the RBD away from the central three-fold symmetry axis (Fig. 4H) (14, 15). This
263 deviation likely arises from a different interaction between CDR3 and Spike*, which nudges the
264 RBDs into a new resting position. While the I27Y substitution optimizes local contacts between
265 CDR1 in its original binding site on the RBD, the P105Y substitution leads to a marked
266 rearrangement of CDR3 in mNb6 (Fig. 4F-G). This conformational change yields a different set
267 of contacts between mNb6 CDR3 and the adjacent RBD (Fig. 4D). Remarkably, an X-ray crystal
268 structure of mNb6 alone revealed dramatic conformational differences in CDR1 and CDR3
269 between free and Spike*-bound mNb6, suggestive of significant conformational heterogeneity
270 for the unbound nanobodies and induced-fit rearrangements upon binding to Spike* (Fig. 4E).

271

272 The binding orientation of mNb6 is similar to that of Nb6, supporting the notion that our
273 multivalent design would likewise enhance binding affinity. Unlike Nb6-tri, trivalent mNb6
274 (mNb6-tri) bound to Spike with no observable fast-phase dissociation and no measurable

275 dissociation over ten minutes, yielding an upper bound for the dissociation rate constant k_d of
276 $1.0 \times 10^{-6} \text{ s}^{-1}$ ($t_{1/2} > 8$ days) and a K_D of < 1 pM (Fig. 4B). As above, more precise measurements
277 of the dissociation rate are precluded by the surface chemistry used to immobilize Spike*.

278

279 mNb6-tri displays further gains in potency in both pseudovirus and live SARS-CoV-2 infection
280 assays with IC_{50} values of 120 pM (5.0 ng/mL) and 54 pM (2.3 ng/mL), respectively (Fig. 4H-I,
281 Table 1). Given the sub-picomolar affinity observed by SPR, it is likely that these viral
282 neutralization potencies reflect the lower limit of the assays. mNb6-tri is therefore an
283 exceptionally potent SARS-CoV-2 neutralizing antibody, among the most potent molecules
284 disclosed to date.

285

286 **Nb6, Nb6-tri, mNb6, and mNb6-tri are robust proteins**

287 One of the most attractive properties that distinguishes nanobodies from traditional monoclonal
288 antibodies is their extreme stability (21). We therefore tested Nb6, Nb6-tri, mNb6, and mNb6-tri
289 for stability regarding temperature, lyophilization, and aerosolization. Temperature denaturation
290 experiments using circular dichroism measurements to assess protein unfolding revealed
291 melting temperatures of 66.9, 62.0, 67.6, and 61.4 °C for Nb6, Nb6-tri, mNb6 and mNb6-tri,
292 respectively (Fig 5A). Aerosolization and prolonged heating of Nb6, mNb6, and mNb6-tri for 1
293 hour at 50°C induced no loss of activity (Fig 5B). Moreover, mNb6 and mNb6-tri were stable to
294 lyophilization and to aerosolization using a mesh nebulizer, showing no aggregation by size
295 exclusion chromatography and preserved high affinity binding to Spike* (Fig. 5C-D).

296

297 **DISCUSSION**

298 There is a pressing need for prophylactics and therapeutics against SARS-CoV-2 infection.
299 Most recent strategies to prevent SARS-CoV-2 entry into the host cell aim at blocking the
300 ACE2-RBD interaction. High-affinity monoclonal antibodies, many identified from convalescent
301 patients, are leading the way as potential therapeutics (22-29). While highly effective *in vitro*,
302 these agents are expensive to produce by mammalian cell expression and need to be
303 intravenously administered by healthcare professionals (30). Moreover, large doses are likely to
304 be required for prophylactic viral neutralization, as only a small fraction of systemically
305 circulating antibodies cross the epithelial cell layers that line the airways (31). By contrast, single
306 domain antibodies (nanobodies) provide significant advantages in terms of production and
307 deliverability. They can be inexpensively produced at scale in bacteria (*E. coli*) or yeast (*P.*

308 *pastoris*). Furthermore, their inherent stability enables aerosolized delivery directly to the nasal
309 and lung epithelia by self-administered inhalation (32).

310

311 Monomeric mNb6 is among the most potent single domain antibodies neutralizing SARS-CoV-2
312 discovered to date. Multimerization of single domain antibodies has been shown to improve
313 target affinity by avidity (32, 33). In the case of Nb6 and mNb6, however, our design strategy
314 enabled a multimeric construct that simultaneously engages all three RBDs, yielding profound
315 gains in potency. Furthermore, because RBDs must be in the up-state to engage with ACE2,
316 conformational control of RBD accessibility can serve as an added neutralization mechanism.
317 Indeed, our Nb6-tri and mNb6-tri molecules were designed with this functionality in mind. Thus,
318 when mNb6-tri engages with Spike, it prevents ACE2 binding by both directly occluding the
319 binding site and by locking the RBDs into an inactive conformation. Although a multitude of
320 other monoclonal and single-domain antibodies against SARS-CoV-2 Spike have been
321 discovered to date, there are few if any molecules as potent and stable as mNb6-tri (33-43).
322 Resistance to aerosolization, in particular, offers unprecedented opportunity for patient-friendly
323 nasal and pulmonary administration.

324

325 Our discovery of Class II neutralizing nanobodies demonstrates the presence of previously
326 unexplored mechanisms of blocking Spike binding to ACE2. For one Class II nanobody, Nb3,
327 we identified a likely binding site in the Spike S₁ domain external to the RBDs. Previously
328 discovered neutralizing antibodies from convalescent patients bind an epitope in a similar region
329 of Spike (24, 26, 27). Binding of Nb3 to this epitope may allosterically stabilize RBDs in the
330 down-state, thereby decreasing ACE2 binding. Pairing of Class I and Class II nanobodies in a
331 prophylactic or therapeutic cocktail could thus be a highly advantageous strategy for both potent
332 neutralization and prevention of escape variants. The combined stability, potency, and diverse
333 epitope engagement of our anti-Spike nanobodies therefore provide a unique potential
334 prophylactic and therapeutic strategy to limit the continued toll of the COVID-19 pandemic.

335

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- 483

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519

520 **Author Contributions**

521 M.Schoof purified Spike*, RBD, and ACE2 proteins, performed yeast display selections to
522 identify and affinity mature nanobodies, expressed and purified nanobodies, tested activity in
523 cell-based assays, cloned, expressed, and purified multivalent nanobody constructs, and
524 coordinated live virus experiments. B.Faust purified and characterized Spike* protein and
525 candidate nanobodies, developed, performed and analyzed SPR experiments for Spike* and
526 RBD-nanobody affinity determination, developed, performed and analyzed SPR binning,
527 experiments, determined optimal freezing conditions for cryo-EM experiments, processed,
528 refined and generated figures for Nb6, Nb11, and mNb6 EM datasets. R.A. Saunders expressed
529 and purified ACE2 and nanobodies, developed and performed cell-based assays for inhibition of
530 Spike* binding and pseudovirus assays for determining nanobody efficacy. S.Sangwan
531 expressed and purified Spike*, RBD, ACE2-Fc, and nanobodies, processed cryo-EM data,
532 optimized RBD-nanobody complexes for crystallography, grew crystals of mNb6, collected
533 diffraction data, and refined the X-ray crystal structure of mNb6. V.Rezelj tested efficacy of
534 nanobody constructs in live SARS-CoV-2 infection assays under the guidance of M.Vignuzzi.
535 N.Hoppe purified nanobodies, developed, performed and analyzed SPR binning experiments,
536 developed performed and analyzed variable Nb6-bi and Nb6-tri association experiments, and
537 performed thermal melting stability assays for nanobody constructs. M.Boone developed
538 approaches to express and purify nanobodies from *Pichia pastoris* and developed, performed,
539 and analyzed approaches to quantify nanobody efficacy in live virus assays. C.B.Billesbølle
540 expressed and purified Spike*, generated affinity maturation library for Nb6, performed yeast
541 display selections to identify mNb6, and built the synthetic yeast nanobody library with J.Liang.
542 I.Deshpande expressed and purified nanobody constructs. B.S.Zha performed live SARS-CoV-2
543 virus assays to test nanobody efficacy with guidance from O.Rosenberg. C.R.Simoneau and
544 K.Leon performed live SARS-CoV-2 virus assays to test nanobody efficacy with guidance from
545 M.Ott. K.M.White performed live SARS-CoV-2 virus assays to test nanobody efficacy with
546 guidance from A.Garcia-Sastre. A.W.Barile-Hill performed SPR experiments. A.A.Anand,
547 N.Dobzinski, B.Barsi-Rhyne, and Y.Liu. assisted in cloning, expression, and purification of
548 nanobody and pseudovirus constructs. V.Belyy performed single-molecule nanobody-Spike*
549 interaction studies. S.Nock prepared media and coordinated lab usage during UCSF's partial
550 shutdown. M.Zimanyi and S.Gupta performed radiolytic footprinting experiments with guidance

551 from C.Y.Ralston and analyzed mass spectrometry data generated by D.L.Swaney. Several
552 members of the QCRG Structural Biology Consortium played an exceptionally important role for
553 this project. C.Azumaya and C.Puchades determined optimal freezing conditions for cryo-EM
554 experiments, optimized data collection approaches, and collected cryo-EM datasets. A.F.Brilot,
555 A.Rizo, A.M.Smith, F.Moss, D.Bulkley, T.Popsiech collected cryo-EM data on Spike*-nanobody
556 complexes. S.Dickinson, H.C.Nguyen, C.M.Chio, U.S.Chio, M.Gupta, M.Jin, F.Li, Y.Liu,
557 G.E.Merz, K.Zhang, M.Sun analyzed cryo-EM data from 15 Spike*-nanobody complex datasets.
558 H.T.Kratochvil set up crystallization trials of various RBD-nanobody complexes, and crystallized,
559 collected diffraction data for, and refined the mNb6 structure. M.C.Thompson collected,
560 processed, and refined the mNb6 structure. R.Trenker, D.Diwanji, K.Schaefer expressed and
561 purified Spike*, and S.Pourmal purified RBD. A.Manglik expressed and purified Spike*, labeled
562 Spike* for biochemical studies, designed selection strategies for nanobody discovery, cloned
563 nanobodies for expression, designed affinity maturation libraries and performed selections,
564 analyzed SPR data, and performed nanobody stability studies. The overall project was
565 supervised by P.Walter and A.Manglik.

566

567 **Competing Interests**

568 M.Schoof, B.Faust, R.A.Saunders, N.Hoppe, P.Walter, and A.Manglik are inventors on a
569 provisional patent describing anti-Spike nanobodies described in this manuscript.

570

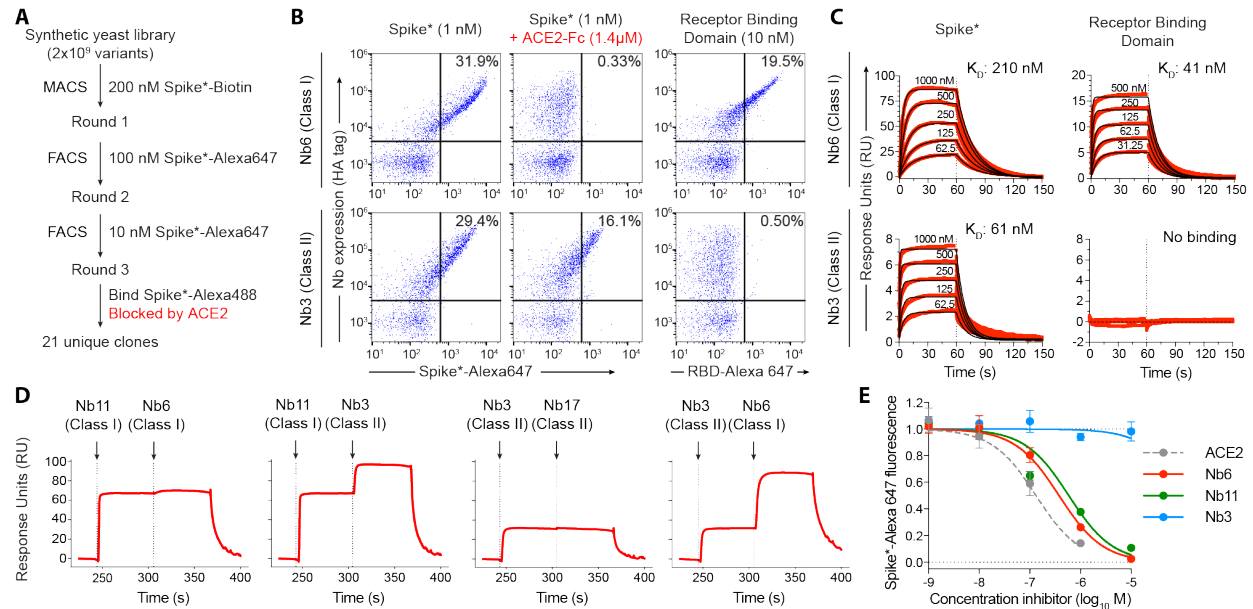
571 **Data and Materials Availability**

572 All data generated or analyzed during this study are included in this published article and its
573 Supplementary Information. Crystallographic coordinates and structure factors for mNb6 have
574 been deposited in the Protein Data Bank under accession code XXXX. Coordinates for
575 Spike*:Nb6 and Spike*:mNb6 complexes have been deposited in the Protein Data Bank under
576 accession codes XXXX and XXXX, respectively. Maps for Spike*:Nb6, Spike*:Nb11, and
577 Spike*:mNb6 have been deposited in the Electron Microscopy Data Bank under accession codes
578 XXXXX (Spike*-Nb6 Open), XXXXX (Spike*-Nb6 Closed), XXXXX (Spike*-Nb11 Open), XXXXX
579 (Spike*-Nb11 Closed), XXXXX (Spike*-mNb6 Closed). Plasmids for nanobody constructs used
580 in this study are available under a Material Transfer Agreement with the University of California,
581 San Francisco.

582

583 **MAIN TEXT FIGURES**

Figure 1



584

585

586 **Figure 1. Discovery of two distinct classes of anti-Spike nanobodies.** **A**, Selection strategy

587 for identification of anti-Spike nanobodies that disrupt Spike-ACE2 interactions using magnetic

588 bead selections (MACS) or fluorescence activated cell sorting (FACS). **B**, Flow cytometry of

589 yeast displaying Nb6 (a Class I nanobody) or Nb3 (a Class II nanobody). Nb6 binds Spike*-

590 Alexa 647 and receptor binding domain (RBD-Alexa 647). Nb6 binding to Spike* is completely

591 disrupted by an excess (1.4 μM) of ACE2-Fc. Nb3 binds Spike*, but not the RBD. Nb3 binding

592 to Spike* is partially decreased by ACE2-Fc. **C**, SPR of Nb6 and Nb3 binding to either Spike* or

593 RBD. Red traces are raw data and global kinetic fits are shown in black. Nb3 shows no binding

594 to RBD. **D**, SPR experiments with immobilized Spike* show that Class I and Class II nanobodies

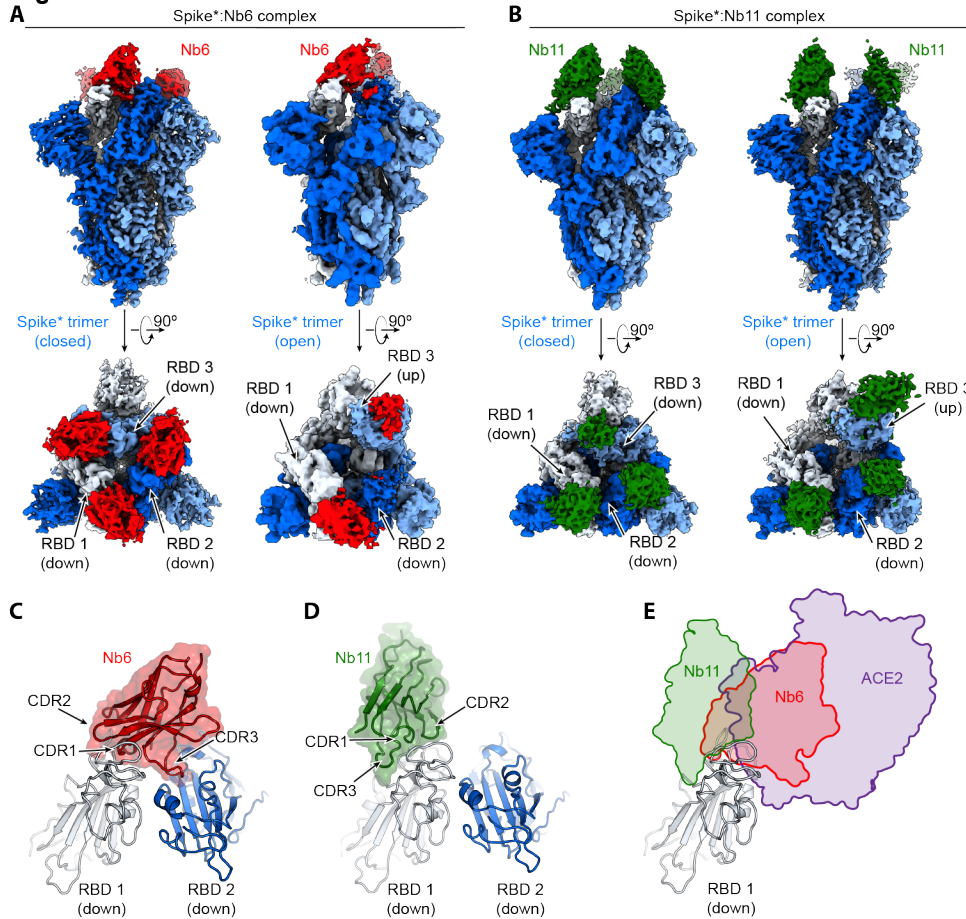
595 can bind Spike* simultaneously. By contrast, two Class I nanobodies or Class II nanobodies do

596 not bind simultaneously. **E**, Nanobody inhibition of 1 nM Spike*-Alexa 647 binding to ACE2

597 expressing HEK293T cells. n = 3 (ACE2, Nb3) or 5 (Nb6, Nb11) biological replicates. All error

598 bars represent s.e.m.

Figure 2

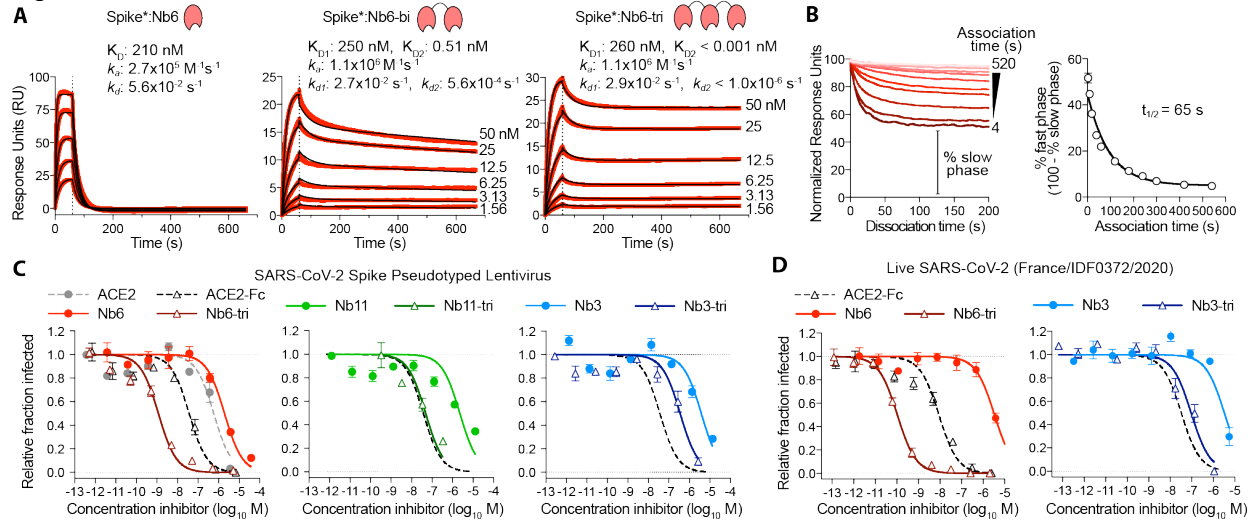


599

600

601 **Figure 2. Cryo-EM structures of Nb6 and Nb11 bound to Spike. A**, Cryo-EM maps of Spike*-
602 Nb6 complex in either closed (left) or open (right) Spike* conformation. **B**, Cryo-EM maps of
603 Spike*-Nb11 complex in either closed (left) or open (right) Spike* conformation. The top views
604 show receptor binding domain (RBD) up- or down-states. **C**, Nb6 straddles the interface of two
605 down-state RBDs, with CDR3 reaching over to an adjacent RBD. **D**, Nb11 binds a single RBD in
606 the down-state (displayed) or similarly in the up-state. No cross-RBD contacts are made by
607 Nb11 in either RBD up- or down-state. **E**, Comparison of RBD epitopes engaged by ACE2
608 (purple), Nb6 (red), or Nb11 (green). Both Nb11 and Nb6 directly compete with ACE2 binding.

Figure 3



609

610

611 **Figure 3. Multivalency improves nanobody affinity and inhibitory efficacy. A**, SPR of Nb6

612 and multivalent variants. Red traces show raw data and black lines show global kinetic fit for

613 Nb6 and independent fits for association and dissociation phases for Nb6-bi and Nb6-tri. **B**,

614 Dissociation phase SPR traces for Nb6-tri after variable association time ranging from 4 to 520

615 s. Curves were normalized to maximal signal at the beginning of the dissociation phase. Percent

616 fast phase is plotted as a function of association time (right) with a single exponential fit. $n = 3$

617 independent biological replicates. **C**, Inhibition of pseudotyped lentivirus infection of ACE2

618 expressing HEK293T cells. $n = 3$ biological replicates for all but Nb11-tri ($n = 2$) **D**, Inhibition of

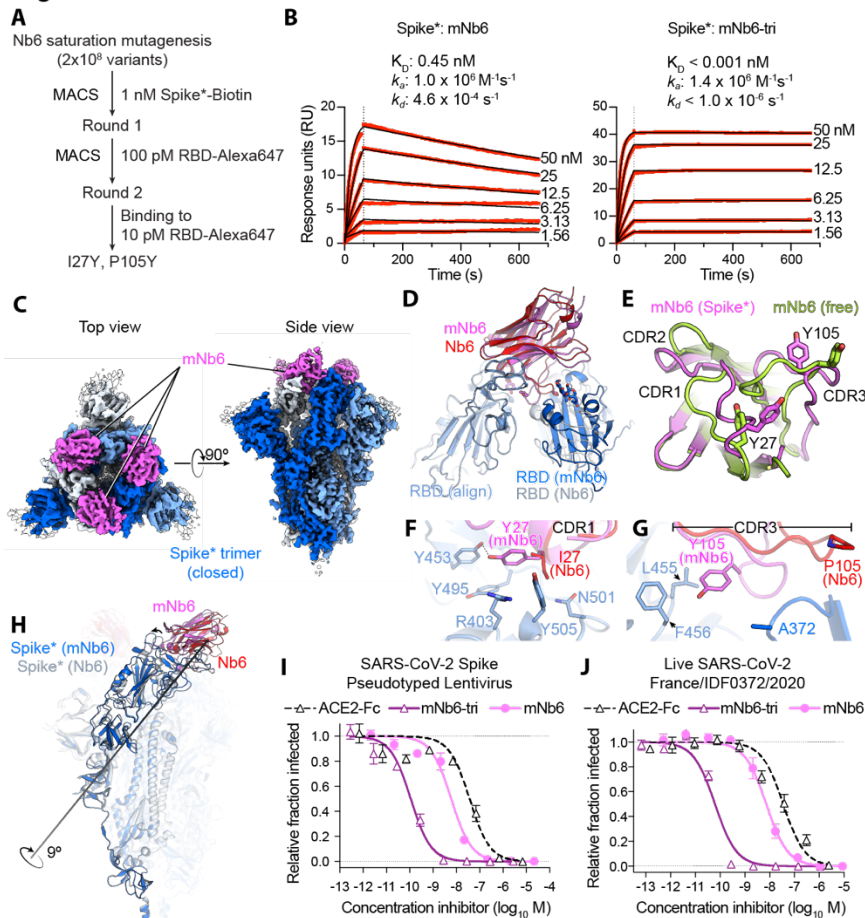
619 live SARS-CoV-2 virus. Representative biological replicate with $n = 3$ (right panel) or 4 (left

620 panel) technical replicates per concentration. $n = 3$ biological replicates for all but Nb3 and Nb3-

621 tri ($n = 2$). All error bars represent s.e.m.

622

Figure 4



623

624 **Figure 4. Affinity maturation of Nb6 yields a picomolar SARS-CoV-2 neutralizing**

625 **molecule. A,** A saturation mutagenesis library of Nb6 was subjected to two rounds of selection

626 to identify consensus mutations I27Y and P105Y. **B,** SPR of mNb6 and mNb6-tri binding to

627 immobilized Spike*. Red traces show raw data and black lines show global kinetic fit. No

628 dissociation was observed for mNb6-tri over 10 minutes. **C,** Cryo-EM structure of Spike*-mNb6

629 complex. **D,** Comparison of receptor binding domain (RBD) engagement by Nb6 and mNb6.

630 One RBD was used to align both structures (RBD align), demonstrating changes in Nb6 and

631 mNb6 position and the adjacent RBD. **E,** Comparison of mNb6 complementarity determining

632 regions in either the cryo-EM structure of the Spike*-mNb6 complex or an X-ray crystal structure

633 of mNb6 alone. **F,** CDR1 of Nb6 and mNb6 binding to the RBD. As compared to I27 in Nb6, Y27

634 of mNb6 hydrogen bonds to Y453 and optimizes pi-pi and pi-cation interactions with the RBD.

635 **G,** CDR3 of Nb6 and mNb6 binding to the RBD demonstrating a large conformational

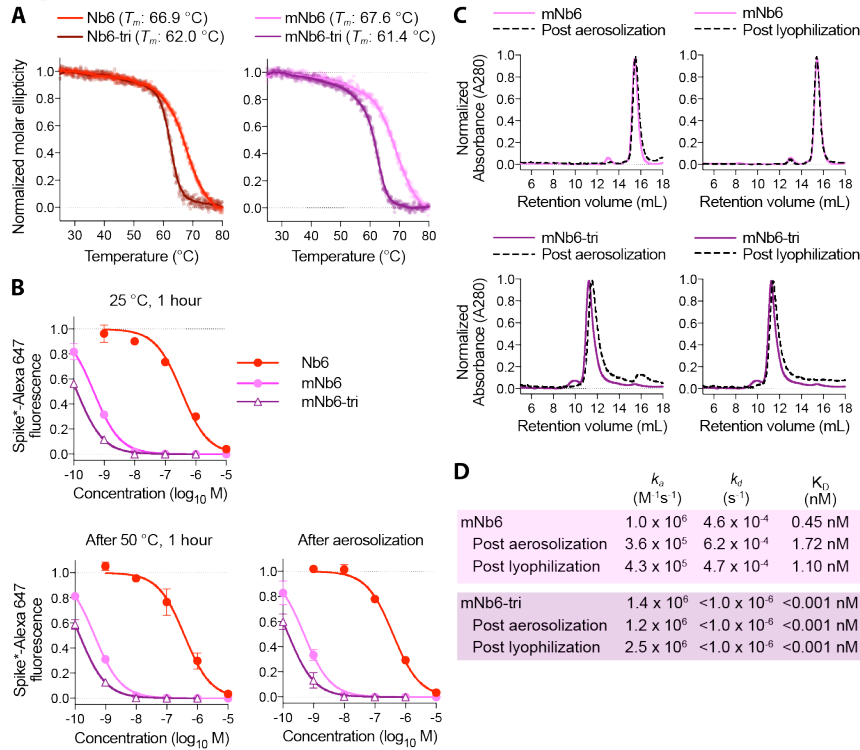
636 rearrangement of the entire loop in mNb6. **H,** Comparison of closed Spike* bound to mNb6 and

637 Nb6. Rotational axis for RBD movement is highlighted. **I,** Inhibition of pseudotyped lentivirus

638 infection of ACE2 expressing HEK293T cells by mNb6 and mNb6-tri. n = 3 biological replicates

639 **J**, mNb6 and mNb6-tri inhibit SARS-CoV-2 infection of VeroE6 cells in a plaque assay.
640 Representative biological replicate with n = 4 technical replicates per concentration. n = 3
641 biological replicates for all samples. All error bars represent s.e.m.
642

Figure 5



643

644

Figure 5. Nb6 and its derivates are robust proteins. A, Thermal denaturation of nanobodies

645

assessed by circular dichroism measurement of molar ellipticity at 204 nm. Apparent melting

646

temperatures (T_m) for each nanobody are indicated. **B,** Nanobody inhibition of 1 nM Spike*-

647

Alexa 647 binding to ACE2 expressing HEK293T cells after incubation at either 25 °C or 50 °C

648

for 1 hour or after aerosolization. **C,** Size exclusion chromatography of nanobodies after

649

lyophilization or aerosolization. **D,** Summary table of SPR kinetics data and affinities for

650

aerosolized or lyophilized mNb6 and mNb6-tri.

651

652 **Table 1. Anti-Spike nanobody affinity and neutralization potency**

Nanobody	Class	Spike* Binding			RBD Binding			Spike* Competition IC ₅₀ (s.e.m) (M) ^a	SARS-CoV-2 Pseudovirus IC ₅₀ (s.e.m.) (M) ^b	Live SARS-CoV-2 IC ₅₀ (s.e.m.) (M) ^c
		k _a (M ⁻¹ s ⁻¹)	k _d (s ⁻¹)	K _D (M)	k _a (M ⁻¹ s ⁻¹)	k _d (s ⁻¹)	K _D (M)			
Nb2	I	9.0x10 ⁵	5.3x10 ⁻¹	5.9x10 ⁻⁷	1.0x10 ⁶	9.9x10 ⁻¹	9.7x10 ⁻⁷	8.3x10 ⁻⁶ (1.7x10 ⁻⁶)	NP	NP
Nb3	II	1.8x10 ⁶	1.1x10 ⁻¹	6.1x10 ⁻⁸	NB			NC	3.9x10 ⁻⁶ (7.9x10 ⁻⁷)	3.0x10 ⁻⁶ (3.2x10 ⁻⁷)
Nb6	I	2.7x10 ⁵	5.6x10 ⁻²	2.1x10 ⁻⁷	2.1x10 ⁶	8.7x10 ⁻²	4.1x10 ⁻⁸	3.7x10 ⁻⁷ (4.9x10 ⁻⁸)	2.0x10 ⁻⁶ (3.5x10 ⁻⁷)	3.3x10 ⁻⁶ (7.2x10 ⁻⁷)
Nb8	I	1.4x10 ⁵	8.1x10 ⁻¹	5.8x10 ⁻⁶	6.6x10 ⁵	3.3x10 ⁻¹	5.1x10 ⁻⁷	4.8x10 ⁻⁶ (4.9x10 ⁻⁷)	NP	NP
Nb11	I	1.2x10 ⁶	1.6x10 ⁻¹	1.4x10 ⁻⁷	3.2x10 ⁶	2.4x10 ⁻¹	7.6x10 ⁻⁸	5.4x10 ⁻⁷ (1.2x10 ⁻⁷)	2.4x10 ⁻⁶ (5.4x10 ⁻⁷)	NP
Nb12	I	1.2x10 ²	2.0x10 ⁻⁴	1.6x10 ⁻⁶	Biphasic	Biphasic	Biphasic	2.5x10 ⁻⁷ (5.5x10 ⁻⁸)	1.2x10 ⁻⁶ (9.0x10 ⁻⁷)	NP
Nb15	I	1.7x10 ⁵	2.3x10 ⁻¹	1.3x10 ⁻⁶	6.0x10 ⁵	2.2x10 ⁻¹	3.6x10 ⁻⁷	2.2x10 ⁻⁶ (2.5x10 ⁻⁷)	6.7x10 ⁻⁶ (3.6x10 ⁻⁶)	NP
Nb16	I	1.1x10 ⁵	1.3x10 ⁻¹	1.3x10 ⁻⁶	NP			9.5x10 ⁻⁷ (1.1x10 ⁻⁷)	NP	NP
Nb17	II	7.3x10 ⁵	2.0x10 ⁻¹	2.7x10 ⁻⁷	NB			NC	7.6x10 ⁻⁶ (1.0x10 ⁻⁶)	NP
Nb18	II	1.4x10 ⁵	6.4x10 ⁻³	4.5x10 ⁻⁸	NB			5.2x10 ⁻⁵ (1.5x10 ⁻⁵)	NP	NP
Nb19	I	2.4x10 ⁴	1.1x10 ⁻¹	4.5x10 ⁻⁶	1.0x10 ⁵	8.9x10 ⁻²	8.8x10 ⁻⁷	4.1x10 ⁻⁶ (4.9x10 ⁻⁷)	2.4x10 ⁻⁵ (7.7x10 ⁻⁶)	NP
Nb24	I	9.3x10 ⁵	2.7x10 ⁻¹	2.9x10 ⁻⁷	2.4x10 ⁶	3.5x10 ⁻¹	1.5x10 ⁻⁷	7.5x10 ⁻⁷ (1.0x10 ⁻⁷)	NP	NP
ACE2	N/A	2.7x10 ⁵	1.2x10 ⁻²	4.4x10 ⁻⁸	NP	NP	NP	1.7x10 ⁻⁷ (6.6x10 ⁻⁸)	6.2x10 ⁻⁷ (1.7x10 ⁻⁷)	NP
mNb6	I	1.0x10 ⁶	4.5x10 ⁻⁴	4.5x10 ⁻¹⁰	1.1x10 ⁶	6.4x10 ⁻⁴	5.6x10 ⁻¹⁰	1.3x10 ⁻⁹ (4.1x10 ⁻¹⁰)	6.3x10 ⁻⁹ (1.6x10 ⁻⁹)	1.2x10 ⁻⁸ (2.5x10 ⁻⁹)
Nb3-bi	II	NP	NP	NP	NP	NP	NP	NP	3.6x10 ⁻⁷ (1.5x10 ⁻⁷)	1.8x10 ⁻⁷ (1.2x10 ⁻⁸)
Nb3-tri	II	Biphasic	Biphasic	Biphasic	NP	NP	NP	4.1x10 ⁻⁸ (1.6x10 ⁻⁸)	4.0x10 ⁻⁷ (1.6x10 ⁻⁷)	1.4x10 ⁻⁷ (4.9x10 ⁻⁸)
Nb6-bi	I	Biphasic	Biphasic	Biphasic	NP	NP	NP	NP	6.3x10 ⁻⁸ (1.5x10 ⁻⁸)	NP
Nb6-tri	I	Biphasic	Biphasic	Biphasic	NP	NP	NP	1.5x10 ⁻⁹ (5.2x10 ⁻¹⁰)	1.2x10 ⁻⁹ (2.5x10 ⁻¹⁰)	1.6x10 ⁻¹⁰ (2.6x10 ⁻¹¹)
Nb11-tri	I	Biphasic	Biphasic	Biphasic	NP	NP	NP	NP	5.1x10 ⁻⁸ (1.6x10 ⁻⁸)	NP
ACE2-Fc	N/A	NP	NP	NP	NP	NP	NP	5.3x10 ⁻⁹ (2.5x10 ⁻⁹)	4.0x10 ⁻⁸ (8.8x10 ⁻⁹)	2.6x10 ⁻⁸ (8.5x10 ⁻⁹)
mNb6-tri	I	1.4x10 ⁶	<1.0x10 ⁻⁶	<1.0x10 ⁻¹²	NP	NP	NP	4.0x10 ⁻¹⁰ (1.4x10 ⁻¹⁰)	1.2x10 ⁻¹⁰ (2.8x10 ⁻¹¹)	5.4x10 ⁻¹¹ (1.0x10 ⁻¹¹)

653

654 ^aAverage values from n = 5 biological replicates for Nb6, Nb11, Nb15, Nb19 are presented, all

655 others were tested with n = 3 biological replicates.

656 ^bAverage values from n = 2 biological replicates for Nb12, Nb17, and Nb11-tri are presented, all
657 others were tested with n = 3 biological replicates.

658 ^cAverage values from n = 2 biological replicates for Nb3, Nb3-bi, and Nb3-tri. n = 3 biological
659 replicates for all others.

660 NB – no binding

661 NC – no competition

662 NP – not performed