Nanobody Mediated Macromolecular Crowding Induces Membrane Fission and Remodeling in the African Trypanosome

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Abstract

The dense Variant Surface Glycoprotein (VSG) coat of African trypanosomes represents the primary host-pathogen interface. Antigenic variation prevents clearing of the pathogen by employing a large repertoire of antigenically distinct VSG genes, thus neutralizing the host's antibody response. To explore the epitope space of VSGs, we generated anti-VSG nanobodies and combined high-resolution structural analysis of VSG-nanobody complexes with binding assays on living cells, revealing that these camelid antibodies bind deeply inside the coat. One nanobody caused rapid loss of cellular motility, possibly due to blockage of VSG mobility on the coat, whose rapid endo- and exocytosis is mechanistically linked to *T. brucei* propulsion and whose density is required for survival. Electron microscopy studies demonstrated that this loss of motility was accompanied by rapid formation and shedding of nanovesicles and nanotubes, suggesting that increased protein crowding on the dense membrane can be a driving force for membrane fission in living cells.

Keywords

African Trypanosome, Host-Pathogen Interaction, Variant Surface Glycoproteins, Immune Epitope Mapping, Structural Biology, Nanovesicle Formation, Nanotube Formation, Protein Crowding, Membrane Fission

35 **Introduction**

36 *Trypanosoma brucei* and related parasites cause African sleeping sickness in humans and
37 Nagana in cattle. A distinguishing feature of these pathogens is a densely packed surface coat that
38 is populated almost entirely by the **V**ariant **S**urface **G**lycoprotein (**VSG**) in the mammalian-
39 infectious forms of the parasite. As *T. brucei* is an extracellular pathogen, the VSG coat is
40 extensively exposed to the immune system and is the primary surface of interaction within the
41 host. It is also highly antigenic, leading quickly to robust antibody mediated responses that are
42 neutralizing (Borst, 2002; Overath et al., 1994). However, parasites possess an extensive genetic
43 repertoire of antigenically distinct VSGs (2000+ genes and pseudogenes), allowing individual
44 parasites to switch the coat to another variant, thus creating a novel surface array to which the
45 immune system is naïve and must readapt. This process of antigenic variation repeats with
46 recurring cycles of parasite clearance, coat switching, and pathogen regrowth (Bangs, 2018).

47 In addition to antigenic variation, trypanosomes employ another immune evasion
48 mechanism, antibody clearance and subsequent recycling of VSG molecules. This process helps
49 evasion of complement-mediated immune destruction but is only effective at low antibody titer
50 (Engstler et al., 2007; Horn, 2014; Mugnier et al., 2016; Pal et al., 2003). Facilitated by the
51 remarkably high endocytosis rate at the flagellar pocket, anti-VSG antibodies are selectively
52 removed from VSG molecules within minutes (Engstler et al., 2004; Webster et al., 1990). This
53 requires high mobility of the VSG molecules and free lateral diffusion (Bülow et al., 1988; Hartel
54 et al., 2016, 2015).

55 The VSGs are glycosylated, homodimeric proteins of roughly 60 kDa comprised of two
56 subdomains: a long, rod-like N-terminal domain (NTD) spanning approximately 350 amino acids
57 followed by a C-terminal domain (CTD) of roughly 100 amino acids that attaches to the

58 glycophosphatidylinositol (GPI) anchor which links the protein to the membrane. The antigenic
59 region of the protein is considered to be the NTD and, in particular, the upper regions of the NTD
60 that would be exposed to the immune system in the dense packing of tens of millions of VSG
61 proteins on the surface (Schwede et al., 2015). The NTDs are composed of a tightly packed three-
62 helix-bundle decorated with extended insertions that produce top and bottom "lobes" at polar ends
63 of the rod-like, helical scaffolding.

64 Despite decades of research, very little is known about the interactions of immune proteins
65 with the VSG coat. Few studies have mapped any defined natural epitopes and at present no
66 antibody-VSG co-crystal structures exist. Reviewing multiple indirect studies (involving
67 monoclonal antibodies, nanobodies, polyclonal antisera, lectins, and proteases), Schwede et al.
68 propose that contrary to many discussions in published literature, a substantial portion of the N-
69 terminal domain (ending at the bottom lobe) of the VSGs could be accessible to the immune system
70 (Schwede et al., 2015).

71 In order to address this topic, we pursued structural studies of several camelid nanobodies
72 raised to the VSG coat. These provide both a biologically relevant context (as *T. brucei* related
73 species cause surra in camelids – (Radwanska et al., 2018)), as well as a system generally amenable
74 to crystallographic analysis (de Marco, 2011). While camels and llamas have a very similar
75 immune system to humans and rodents, there are variations. Nanobodies (Nbs) are single chain,
76 minimal variable region-containing antibody fragments consisting of one protein domain. They
77 tend to be highly stable and to crystallize very well and thus are useful alternatives to studying
78 pathogen-immune interactions if the larger mouse and human antibodies are challenging to
79 crystallize.

80 Previous studies have shown that high-affinity Nbs can be effectively raised to VSGs (Arbabi-
81 Ghahroudi, 2017). Addition of such Nbs to AnTat1.1 expressing *T. brucei* was shown to induce
82 trypanosome lysis even in the absence of the effector Fc domain (Stijlemans et al., 2017). This
83 effect was described to initiate quick immobilization of trypanosomes, enlargement of the flagellar
84 pocket and a major blockage of endocytosis. However, the mechanism mediating these phenomena
85 have remained obscure.

86 In this study, we used the camelid immune system (Figure S1) to generate a series of
87 nanobodies to *T. brucei* VSG2 (also known as VSG221 or VSG MITat1.2). X-ray crystallographic
88 studies reveal that these nanobodies bind not to the upper, exposed surface of the elongated VSG
89 molecules, but instead as much as 100 Å from the top. Indeed, we find that these nanobodies and
90 their corresponding camelid antibodies are also able to recognize the intact trypanosome coat on
91 living cells. These results demonstrate that VSG epitopes buried deeply in the dense surface coat
92 are in fact accessible to B-cells and secreted antibodies.

93 Similar to prior reports, this binding can be highly toxic to the parasite (Stijlemans et al., 2011,
94 2017) and we observed paralysis of the normally highly mobile trypanosomes within minutes of
95 nanobody addition. This paralysis was linked to a nanobody induced block on VSG diffusion in
96 the coat. Parasite movement and endo- and exocytosis of the coat are mechanistically linked and
97 essential for survival in the mammalian host. At the same time, VSG density on the coat is highly
98 regulated, and significant raising of the density adversely impacts VSG movement in the
99 membrane (Hartel et al., 2016), making the African trypanosome a unique model system for
100 studying the effects of protein crowding in living cells. Examination of the parasite by electron
101 microscopy after Nb binding demonstrated that loss of VSG mobility (and subsequent loss of
102 cellular motility) was accompanied by rapid formation and shedding of nanovesicles and

103 nanotubes, suggesting that increased protein crowding on this already dense membrane physically
104 drives membrane fission – the first example of this phenomenon in living cells.

105

106 **Results**

107 **Production and Crystal Structures of VSG2-Nanobody Complexes**

108 Nanobodies were generated from llamas immunized with the N-terminal domain of VSG2
109 (Methods). To ensure that the cloned genes were able to bind within surface coats and not only the
110 soluble form of the VSG, a filtering step of panning the library of B-cell clones against intact UV-
111 inactivated trypanosomes was added and all clones were scored by flow cytometry analysis as
112 binding to intact, live trypanosomes. From this we obtained a library of 69 distinct nanobodies
113 (belonging to 30 different CDR3 groups or B-cell lineages). We initially crystallized three different
114 clones complexed to VSG2 ($NB9_{VSG2}$, $NB11_{VSG2}$, and $NB14_{VSG2}$, Figure 1, Methods, Figure S2,
115 Table S1 and S2). Those structures revealed that all the nanobodies bound similarly to the same
116 epitope region and possessed a highly conserved consensus set of amino acids in the CDR1 and
117 CDR3 loops that characterized the majority of clones in the library, despite being derived from
118 independent B-cell lineages (discussed below). To identify other binding modalities, we searched
119 for clones in our library with the most divergent CDR regions. A few such were identified, and we
120 crystallized one of these ($NB19_{VSG2}$) which indeed bound in a distinct location on VSG2. However,
121 unexpectedly, this was not on the top, putative antigenic surface of the molecule, but nearly 100 Å
122 down from the upper surface at the bottom of the N-terminal domain and adjacent to the postulated
123 location of the CTD (Bartossek et al., 2017). The overall structure of VSG2 is not significantly
124 changed from that previously reported (Freymann et al., 1990), aligning with a root-mean-square-
125 deviation in 1440 atomic positions of 0.5 Å (single monomer).

126 **Nanobodies Bind Deep into the VSG Coat**

127 Three of the nanobodies ($NB9_{VSG2}$, $NB11_{VSG2}$, and $NB14_{VSG2}$) bind in an identical position.
128 The binding site is approximately 60 Å down from the upper lobe of VSG2 and formed by a
129 concave surface on the VSG 3-helix bundle about midway down the length of the rod-like NTD
130 (Figure 1A and B). This is consistent with a hypothesis that nanobodies are more likely to bind
131 concave or convex surfaces than flat ones (Stijlemans et al., 2004). Numerous side chains from the
132 second two helices of the helical bundle make contacts to the nanobodies (residues spanning 100-
133 115 and 280-302 of VSG2), with the primary contacts solvent-facing, predominantly hydrophilic
134 residues (e.g. Q111, T112, A285, E286, T301, and D313) as well as several minor side chain
135 contacts and backbone contacts (Figure 2A). These nanobodies interact with VSG2 through their
136 variable CDR1 and CDR3 loops (without any significant contacts from the CDR2 loop) with a
137 consensus set of side chains (CDR1 residues T28, S30, N31 and CDR3 residues L100, L101, S103,
138 Figure 2, A and C). In contrast, $NB19_{VSG2}$ binds underneath the bottom lobe of VSG2 purely
139 through CDR3 (Figure 2B). The contacts are a mixture of hydrophobic and polar interactions, but
140 with a preponderance of aromatic side chain stacking (π-stacking) interactions involving residues
141 W102, W112, and Y115 of $NB19_{VSG2}$ with the side chains Y375 and Y376 of VSG2.

142 **Nanobody Binding is Detectable on Living Parasites**

143 In order to examine the physiological relevance of these nanobodies and their unexpected
144 binding sites on VSG2, we performed a series of binding experiments to living trypanosomes.
145 Nanobodies harboring a C-terminal hexa-histidine (6xHis) tag were added to trypanosomes
146 expressing different VSGs and the cells analyzed with an anti-tag monoclonal antibody by
147 fluorescence-activated cell sorting (FACS, Methods, Figure 3). Nanobodies $NB9_{VSG2}$, $NB11_{VSG2}$,
148 and $NB14_{VSG2}$ were easily detected as binding to VSG2 expressing cells with several logs

149 difference in signal (Figure 3A), whereas nanobody $NB19_{VSG2}$ could not be detected. In contrast,
150 nanobodies did not bind other VSGs (Figure 3, B-D), thereby showing high specificity ($NB11_{VSG2}$
151 shown as an example). Verifying that the surface accessibility is not only limited to the relatively
152 small nanobodies, we created a sortaggable variant of the camelid heavy chain IgG2 antibody with
153 the corresponding $NB11_{VSG2}$ Ig domain and found it can, in fact, bind the live parasite coat (Figure
154 S3A).

155 The inability to detect $NB19_{VSG2}$ raised the possibility that the binding we observed in solution
156 and in the crystal structure was an artifact of using the soluble VSG2 as the antigen for
157 immunization. A second possibility was that the deep binding we observe in the crystal structure
158 buries $NB19_{VSG2}$ beyond the reach of IgG antibodies. To distinguish between these two models,
159 we directly labeled $NB19_{VSG2}$ and other nanobodies with fluorescent moieties. In one case we
160 chemically conjugated the fluorophore FITC to the proteins (to free amine groups, typically
161 exposed lysine residues), showing that the nanobodies generally could be detected and also how
162 they compare to a full anti-VSG2 IgG (Figure 3E). While a small shift in fluorescence intensity
163 can be observed for $NB19_{VSG2}$-FITC (compared to the non-stained sample, Supplementary Figure
164 3F), it showed significance in 2-tailed t-test ($p= 0.0109$, Supplementary Figure 3M). To further
165 probe binding, we sought to avoid whole-scale labeling of proteins chemically, and turned to a
166 single, site-specific covalent modification of the Nbs (Figure 3F, Methods). Here, we used the
167 transpeptidase enzyme sortase to attach peptide-linked 6-Carboxyfluorescein (FAM) to the C-
168 terminus of the nanobodies (Methods). In this case, all nanobodies showed binding to the living
169 trypanosomes, although $NB19_{VSG2}$ and $NB9_{VSG2}$ seem to have reduced relative fluorescence
170 intensity (yet with signal intensity over negative controls, Figure 3F). To buttress the positive
171 binding result for $NB19_{VSG2}$ by a third independent experiment, we also exposed living

172 trypanosomes to the nanobodies, thoroughly washed the cells, and then probed them by Western
173 blot (Figure 3G). All the nanobodies, including $NB19_{VSG2}$, were shown to have bound, whereas an
174 irrelevant nanobody raised to the *Helicobacter pylori* BabA antigen did not bind VSG2 expressing
175 trypanosomes.

176

177 **Probing Nb-VSG2 Interactions**

178 To further examine the interactions of the Nbs with VSG2, we created mutations in the
179 consensus site of CDR3 of $NB11_{VSG2}$ and two critical contacts to VSG2 from $NB19_{VSG2}$ (Figure
180 4). We focused on these two because $NB11_{VSG2}$ possess a highly similar consensus binding site to
181 $NB9_{VSG2}$ and $NB14_{VSG2}$, whereas $NB19_{VSG2}$ differs in the binding location and in sequence to the
182 others. The alteration of these important contacts led to a disruption of binding to VSG2 as assayed
183 by gel filtration chromatography. In particular, even single loss-of-contact mutations to the
184 $NB19_{VSG2}$ interface completely disrupted binding, whereas it required a triple mutant in $NB11_{VSG2}$
185 to abrogate complex formation, suggesting that the complex was more stable (Figure 4).

186

187 **Nanobodies to VSG2 Reduce Coat Mobility, Cause Stiffening of the Cell Body and Stall**
188 **Parasite Motion**

189 As previous reports had shown Nb-induced interference with trypanosome movement (Stijlemans
190 et al., 2011), VSG2 expressing wild type cells were treated with saturating amounts of the four
191 nanobodies. Only treatment with $NB11_{VSG2}$ resulted in reduced cell motility (Figure S4). While at
192 5 min post addition of $NB11_{VSG2}$ swimming behavior of the parasites remained largely normal
193 with individual cells actively swimming and changing direction, from 15 min onwards, cell

194 movement was clearly affected as trajectories became shorter and mostly unidirectional (Figure
195 5A and Figure S4C). A closer inspection of these trajectories suggested that the parasites were not
196 motionless, but that translocation was largely due to drift in the sample which is unavoidable in
197 recordings of this duration. Both swimming speed means and track displacement lengths were
198 extracted from the acquired data (Figures 5B, S5, and S6). Figure 5B (left panel) shows that the
199 mean velocity of $NB11_{VSG2}$ treated cells was reduced compared to that of untreated cells, while
200 $NB9_{VSG2}$, $NB14_{VSG2}$ and $NB19_{VSG2}$ treated cells behaved largely like the control. A comparison of
201 the track displacement length per second also showed smaller values with a narrower range of
202 distribution in $NB11_{VSG2}$ treated cells (Figure 5B, right panel).

203 As productive movement of trypanosomes was hampered under the influence of $NB11_{VSG2}$,
204 the viability of these cells was analyzed in hourly intervals for 8 hours via flow cytometry (Figures
205 5C and S7). One hour after $NB11_{VSG2}$ addition at least 80 % of treated cells were still alive, with
206 the proportion of dead cells increasing continuously up to 8 hours when about 25 % of cells were
207 still alive (Figure 5C and Table S3). The amount of nanobody used had a critical impact on cell
208 death (Figure S8, Table S3). A 1:1 molar ratio of $NB11_{VSG2}$ to VSG2 monomer was required and
209 sufficient to induce cell death with a sharp rise in the number of dead cells observed between
210 samples with a 0.9- and 1.1-fold excess, whilst higher Nb concentrations did not alter the kinetics
211 of the cellular response, suggesting that the VSG coat had been saturated with nanobody. Based
212 on these results all further experiments were carried out with a saturating 1.7-fold excess of
213 nanobody to VSG monomer.

214 We first explored whether nanobody binding might affect VSG diffusion in the cell surface
215 coat. Fluorescence recovery after photobleaching (FRAP) experiments were performed on
216 immobilized cells whose surface proteins had been fluorescently labeled. VSGs of untreated cells

217 exhibited a median mobile fraction of 83 % and diffusion coefficient of 0.020 $\mu m^2/s$. Addition of
218 the Nb resulted in a marked reduction of the median mobile fraction to 11 % with the diffusion
219 coefficient reduced to a median of 0.007 $\mu m^2/s$ (Figure 5D, left and right graph, respectively).
220 Hence, binding of $NB11_{VSG2}$ to VSG2 on the cell surface significantly affected the mobility of the
221 protein in the cell surface coat.

222 As depicted in Figure 5A, a severe restriction in motility was observed in ensemble
223 measurements between 5 and 15 min after addition of $NB11_{VSG2}$. This time period was therefore
224 chosen to acquire high-speed videos of treated and untreated individual cells (Figures 5E and F,
225 Videos S1 and S2). Nanobody-treated parasites were unable to swim productively. The flagellar
226 wave initiated at the tip of the flagellum, but did not progress through the whole cell body so that
227 the typical cellular waveform could not be observed (Bargul et al., 2016). The parasites were partly
228 paralyzed with increased stiffness and decreased ability to bend the cell body. This observation led
229 us to inspect the nanobody treated cells by electron microscopy.

230

231 **$NB11_{VSG2}$ Induces the Formation of Nanovesicles and Nanotubes on the Trypanosome**
232 **Surface**

233 Interestingly, scanning electron microscopy (SEM) of $NB11_{VSG2}$ treated VSG2-expressing
234 cells revealed the formation of nanovesicles and nanotube-like structures as early as 2 minutes
235 following addition of the nanobody (Figure 6, A and B). Initially, nanovesicles of around 200 nm
236 diameter originated mainly from the flagellum attachment zone (FAZ), the flagellar tip (FT) and
237 the posterior pole (PP) of the cell (Figure 6, A and B; Figure S9A, middle and lower inset). In
238 some parasites, the nanovesicles had formed vesicle chains (Figure 6B). In addition to these
239 nanovesicles and vesicle chains, nanotubes of slightly smaller diameter, that could be more than

240 1 µm in length appeared perpendicular to the FAZ (Figure S9A, upper inset). In the vast majority
241 of cells, nanovesicles and/or nanotubes had been formed after 2 min, while after 5 min all parasites
242 revealed this phenotype. Vesicles appeared on both sides of the FAZ and frequently at the origin
243 of the flagellum, the flagellar pocket (FP) (Figure S9, B and C). Likewise, nanotubes were present
244 in the vicinity of the FP (Figure S9C, left inset). Vesicles in close proximity to the FP tended to be
245 larger (275 nm) than those appearing at the FAZ (150 - 180 nm). In some trypanosomes, the
246 nanovesicles appearing alongside the FAZ seemed to fuse (Figure S9C, right inset), or to
247 redistribute towards the flagellar membrane. However, after 10 min of nanobody incubation,
248 nanovesicles and nanotubes were still present with roughly the same abundance, and, with very
249 little indication of a transition of nanovesicular chains to nanotubes suggesting that both structures
250 form independently (Figure 6C). After 15 min, the number of budding nanovesicles had decreased,
251 and the nanotubes were greatly elongated, thereby apparently forming bridges between parasites.
252 Some of the tubes seemed to be under tension (Figure S9D), while others formed catenated
253 structures.

254 Occasionally, smaller nanotubes or nanovesicles appeared to branch off the main tube (Figure
255 S9D, lower inset). The fact that most of the tens of micrometer long tubes were intact, without
256 showing breakpoints suggests that they are mechanically rather robust. This can be seen when
257 tubes bend around trypanosomes (Figure S9D, middle inset). These rigid membrane ropes may
258 well have additionally hampered trypanosome motility, as the parasites can be literally trapped in
259 a nanotubular network. A closer inspection of the apparent network built from nanotubes revealed
260 that most intersections in fact are crossings of two tubes without fusion (Figure S10A, upper inset),
261 while other intersections seemed to represent true membrane fusion (Figure S10A, lower inset).
262 The presence in nanotubes of nodes of similar size as nanovesicles is first seen after 20 minutes

263 (Figure S10A, middle inset). The endpoint of our observation window was 25 minutes, when the
264 nanotubes had formed concatenated or branched networks that are very difficult to trace by SEM
265 (Figure S10B). However, it seems noteworthy that at this time point nanovesicles also emanated
266 from the same trypanosome membrane areas as after 2 minutes of nanobody incubation, namely
267 along the FAZ, at the posterior pole and at the flagellar tip (Figure S10B). Interestingly, when we
268 looked at control parasites that had undergone the same experimental procedure, but without
269 exposure to the nanobody, we occasionally also observed nanovesicle formation at the FAZ, the
270 FT and the FP. Despite most trypanosomes displaying no or few nanovesicles (Figure S10C,
271 25 min), short nanovesicular chains could be observed in some parasites (Figure S10C, 10 min).
272 This suggests that the formation of nanovesicles at distinct cell surface subcompartments is a
273 biologically relevant process that can be triggered in a spectacular manner by anti-VSG nanobodies
274 (Figure S11).

275

276 **Nanovesicles and Nanotubes are Coated with VSGs and Bud from the Cell Surface**

277 To obtain more detailed information about the ultrastructure of the nanovesicles and
278 nanotubes, ultra-thin sections of trypanosomes, treated with nanobody for 15 min, were prepared
279 for transmission electron microscopy (TEM). The micrographs revealed an intracellular
280 architecture that was indistinguishable from that found in non-treated parasites. Figure S12A
281 shows perfect preservation of flagellar pocket structure, including the tight junction at the flagellar
282 pocket collar, the flagellar pocket matrix and the VSG coat. Frequently, clathrin coated pits were
283 visible, indicating that the endocytosis machinery was at least structurally not impaired. Circular
284 and flat endosomal cisternae were present, as well as class 2 clathrin coated vesicles (CCV II),
285 which are essential for cargo transport to late endosomes (Figure 6D) (Grünfelder et al., 2003).

286 Likewise, mitochondrion, nucleus, endoplasmic reticulum, acidocalcisomes, glycosomes, Golgi
287 and the subpellicular microtubule corset did not show any significant alterations (Figures 6E and
288 S12B). Hence, 15 min post-incubation with nanobodies, the parasite's intracellular architecture
289 was not impaired. Nevertheless, just as in SEM preparations, nanovesicles and nanotubes were
290 readily observable in these TEM samples. These vesicles were covered with an electron-dense
291 layer characteristic of the trypanosome's VSG surface coat, which was confirmed by
292 immunofluorescence analysis (Figure S13).

293 Interestingly, nanovesicles were found to be budding into the flagellar pocket. Figure 6D
294 shows a perfectly spherical budding vesicle, that is decorated with evenly spaced structures. The
295 inner diameter of this vesicle is 100 nm, and the outer structures have a size of about 20 nm, which
296 is similar to the size of membrane-embedded VSGs. Note that a clathrin-coated pit is being formed
297 at the same flagellar pocket. Interestingly, the same cell is shedding nanotubes at the flagellar
298 attachment zone. These are smaller in diameter than the FP-derived nanovesicles. From the
299 micrographs, it is not clear how the nanovesicles exit the FP, as the tight junction and flagellar
300 pocket collar are intact (Figure S12B). Figure 6E shows another example of concomitant formation
301 of large nanovesicles within the flagellar pocket and nanovesicles/nanotubes at the flagellar
302 attachment zone. These structures were probably the nanovesicular chains observed in SEM.
303 Interestingly, the TEM images show that the "vesicles" were not always fully separated by
304 membrane but had continuous content (Figure 6E, lower inset). In all these vesicles, electron-dense
305 particles were detected, which were identical with the cytoplasmic ribosomes in size and form
306 (Figure 6E, lower inset). As the flagellum is free of ribosomes, the segmented nanotubes and free
307 nanovesicles likely originate from the pellicular plasma membrane and not from the flagellum
308 (Figure S12D). In contrast, the smooth and long nanotubes observed with SEM after 15 minutes

309 of treatment, could well originate from the flagellar membrane, as shown in Figure S12C. In this
310 cell, multiple tubes bud from one flagellum. These are also covered by a VSG-coat, but do not
311 contain ribosome-like structures. The shedding of the smooth nanotubes must involve significant
312 mechanical forces, as is suggested by marked membrane deformations, both on the flagellar side
313 and on the nanotubes (Figure S12C, white arrows). In rare occasions, a nanotube branchpoint was
314 observed (Figure S12E), but it remains unclear how these branches can form. Figure S12F shows
315 that the tubes can be bent and deformed, which is in agreement with observations made in SEM
316 micrographs.

317 In conclusion, we have established that nanobodies can bind deep within the VSG-coat and
318 that binding can rapidly affect VSG mobility within the plasma membrane. Interestingly,
319 nanobody-binding leads to an almost instantaneous formation of nanovesicles and nanotubes on
320 the parasite cell surface, concomitant with stiffening of the cells and loss of parasite motility. Cell
321 death occurs significantly later and is probably a consequence of stalled motion, which inevitably
322 will affect cytokinesis.

323

324 **Discussion**

325

326 Using the camelid immune system to generate a collection of anti-VSG2 nanobodies, we have
327 been able to show through structural, biochemical, and cell biological experiments that nanobodies
328 can bind deeply into the trypanosome surface coat, even to the bottom of the NTD of the VSGs.
329 Using secondary IgG antibodies to detect the nanobodies, we also demonstrate that antibodies of
330 the mammalian immune system are able to reach into the densely packed coat of *T. brucei* to a
331 depth of ~50 Å, but have difficulty reaching further than ~80 Å below the coat surface (Figure
332 7A). Furthermore, using full camelid antibodies with the same nanobody domain, we show that

333 the camelid immune system can reach as far as the nanobodies themselves to bind to epitopes
334 buried as deep as 50 Å.

335 Our experimental results demonstrate that the antigenic surface of the VSGs extends well
336 beyond the upper surfaces of these molecules. Such conclusions are consistent with the
337 observations that the VSGs possess molecular surfaces with relatively high sequence divergence
338 as well as markedly distinguishing surface properties not only at the "top" of the NTD, but across
339 the entire molecule (Figure 7B). That the much more highly conserved CTD would be difficult for
340 antibodies to access (located more than 100 Å below the surface) as shown previously (Schwede
341 et al., 2011) and in our study, is also in harmony with this model.

342 We identified one Nb ($NB11_{VSG2}$) that was highly efficient in immobilizing and ultimately
343 killing cells, a marked motility phenotype which is in accordance with published work (Stijlemans
344 et al., 2011). In contrast, our work does not support the conclusion that this is due to impaired
345 endocytosis and hence impaired energy supply. The onset of the motility phenotype was within
346 minutes of nanobody addition and electron micrographs did not reveal any disruption in the
347 endomembrane system, including the endosomes. What we observed was a marked reduction in
348 cell body flexibility and increased stiffness of parts of the cell. This was not caused by paralysis
349 of the flagellum as it still initiated the beat which was however not propagated over the cell body.
350 Hence, the trypanosomes did not swim anymore. We hypothesize that the phenotype observed
351 could be related to the mobility and integrity of the surface coat. We have previously shown that
352 the VSG coat operates very close to a molecular crowding threshold, where a high lateral mobility
353 is balanced with the highest possible density of the protein (Hartel et al., 2016). When the VSG
354 density exceeds this threshold, translational diffusion in the surface coat is severely affected. This
355 is exactly what might occur in the experiments reported here. Binding of the nanobody increases

356 the hydrodynamic radius of the VSG dimers which results in a dramatic decrease in the mobile
357 fraction. Thus, rotational and translational diffusion of the VSGs is confined by steric hindrance.
358 Thermodynamics in confinement would cause tension within the VSG coat due to pressure forces.
359 If this were the case, there should be ultrastructural changes in surface topology of the
360 trypanosomes. Indeed, we observed dramatic changes of the trypanosome cell surface in electron
361 micrographs.

362 Membrane fission is essential for the life of all cells. Cytokinesis, the generation of organelles
363 such as the mitochondrion, ER and Golgi, as well as endomembrane trafficking are processes that
364 all depend on this type of membrane remodeling. Complex machineries involving many proteins
365 that can form helical scaffolds or constricting rings, as well as shallow membrane insertions, are
366 thought to control membrane fission (Snead et al., 2017; Campelo and Malhotra, 2012). Classic
367 examples are the clathrin or COP pathways and the ESCRT machinery. These pathways are well-
368 controlled in space and time, and they are highly energy-consuming. The total energy of membrane
369 vesiculation has been estimated to be in the range of several hundred k_BT, which means that
370 membrane fission requires significant mechanical forces, acting from outside onto the membrane.
371 This is exemplified by the massive clathrin assembly visible on a coated pit at the flagellar pocket
372 in Figure S12A.

373 The nanovesicles and nanotubes observed in this work on the trypanosome cell surface did
374 not show any structural features that differed from the plasma membrane. They were decorated
375 with an electron dense VSG layer but no additional coats that could be involved in vesicle
376 formation were detectable. This is not unexpected, as it is very unlikely that the parasites can sense
377 the nanobody addition, transduce this information and actively secrete a putative extracellular

378 fission-promoting machinery - all within seconds. Thus, it is most probably not an active cellular
379 process that drives nanovesicle and nanotube formation.

380 An attractive, alternative explanation for the phenotype would be protein-protein crowding.
381 The addition of nanobodies to the extremely dense VSG coat could - within seconds - raise the
382 protein density on the cell surface above the molecular crowding threshold. In fact, we have shown
383 that the lateral mobility of the VSG decreases rapidly after nanobody addition, which supports this
384 assumption. With the binding of nanobodies, mobility of the VSG becomes restricted and the coat
385 is therefore under tension. Collisions of nanobody-loaded VSGs will generate pressure (on one
386 side of the plasma membrane). This behavior of a crowded membrane protein has been likened to
387 that of compressed gas and it has been suggested to provide the pressure force required to initiate
388 and complete membrane vesiculation and tubulation (Snead et al., 2017). Thus, nanobody-
389 mediated protein crowding could provide the energy required for membrane fission. No cellular
390 machineries would be required to overcome the energy barrier. Membrane fission by protein-
391 protein crowding has been observed before, albeit only in artificial systems and is supported by
392 modeling approaches (Derganc and Čopič, 2016; Snead et al., 2017).

393 Our data suggest that this mechanism could also function in the cellular context. Due to its
394 uniformity, the trypanosome coat with its high density and essential mobility of the VSG is an
395 ideal model system to study this new mechanism of membrane fission in living cells. The fact that
396 we find nanotubes and nanovesicles also in untreated cells, albeit only occasionally, suggests that,
397 at least in trypanosomes, protein crowding-mediated extracellular vesiculation could be a
398 biologically relevant process. We surmise that by using this passive, density-controlled process,
399 the parasites can adjust the VSG-coat density, e.g. during cell division or VSG switching. Protein

400 crowding-mediated membrane shedding may well be effective on other cells with dense protein
401 coats.

402 Especially at early time points after addition of nanobodies, vesicle chains of increasing length
403 were observed. TEM images showed that the chains were not always composed of separated
404 vesicles but were often segmented, continuous volumes. There are few reports on vesicle chains
405 in biology. Outer membrane vesicle chains have been reported in *Myxococcus xanthus* (Remis et
406 al., 2014) and biopearling has been observed in a marine flavobacterium (Fischer et al., 2019).
407 However, the mechanisms underlying vesicle chain formation have not been studied. As
408 segmented membrane volumes are detectable already after 2 minutes in nanobody-treated
409 trypanosomes, we surmise that counteracting mechanical forces interrupt full fission of
410 nanovesicles. The segmented vesicle chains mainly appear at the FAZ and the flagellar pocket.
411 These regions continuously experience the forces exerted by the flagellar beat. It is tempting to
412 speculate that the flagellar force causes interruption of fission events. The protein crowding
413 pressure on the nascent vesicle could be strong enough to maintain the vesicle curvature. When a
414 new vesicle forms at the same position of the FAZ it would be connected to the previous one. In
415 this way, the continuous beat of the flagellum would produce segments of very similar size. After
416 about 15 minutes of nanobody treatment, the vesicle chains disappear. This is the time point when
417 the propagation of the flagellar beat is impaired, probably due to membrane tension caused by loss
418 of membrane through vesiculation. Thus, the force producing the segmented membrane volumes
419 decreases, resulting in a shift to tubulation. The resulting nanotubes can be tens of micrometers
420 long, and the wiggling cells entangle themselves in these rope-like structures. It is important to
421 note that fusion of nanotubes to neighboring parasites has not been observed, suggesting that cell-
422 cell communication via membrane bridges is not occurring.

423 In summary, the fast onset of membrane fission at "free" membrane compartments could be
424 explained by membrane tubulation through protein-protein crowding on the trypanosome cell
425 surface. Are the nanovesicles in fact exosomes or ectosomes (extracellular vesicles, EVs)?
426 Exosomes are produced by multivesicular bodies and secreted by exocytosis. This has previously
427 been observed in fly-stage *T. brucei* procyclic forms (Eliaz et al., 2017). Since we did not find any
428 changes in the endomembrane architecture, the vesicles formed after nanobody treatment are likely
429 not exosomes. The formation of extracellular vesicles in trypanosomes was first reported in 2016
430 (Szempruch et al., 2016). In contrast to our data, this work revealed that EVs were generated by
431 vesiculation of nanotubes that are highly fusogenic and originate from the flagellar membrane.
432 Thus, despite morphological similarities, the nanovesicles and nanotubes observed in the present
433 study are neither exosomes nor ectosomes, but rather the product of membrane fission through
434 protein-protein crowding. The trypanosome-nanobody system for the first time enables us to
435 systematically study a highly efficient mechanism by which the crowded protein environment on
436 the surface of cells causes changes in membrane shape.
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439 **REFERENCES**

440 Arbabi-Ghahroudi, M. (2017). Camelid Single-Domain Antibodies: Historical Perspective and
441 Future Outlook. Front Immunol *8*.

442 Bangs, J.D. (2018). Evolution of Antigenic Variation in African Trypanosomes: Variant Surface
443 Glycoprotein Expression, Structure, and Function. BioEssays *40*, 1800181.

444 Bargul, J.L., Jung, J., McOdimba, F.A., Omogo, C.O., Adung'a, V.O., Kruger, T., Masiga, D.K.,
445 and Engstler, M. (2016). Species-Specific Adaptations of Trypanosome Morphology and
446 Motility to the Mammalian Host. PLoS Pathog *12*, e1005448.

447 Bartossek, T., Jones, N.G., Schafer, C., Cvitkovic, M., Glogger, M., Mott, H.R., Kuper, J.,
448 Brennich, M., Carrington, M., Smith, A.S., et al. (2017). Structural basis for the shielding
449 function of the dynamic trypanosome variant surface glycoprotein coat. Nat Microbiol *2*, 1523–
450 1532.

451 de Beer, T.A.P., Berka, K., Thornton, J.M., and Laskowski, R.A. (2014). PDBsum additions.
452 Nucleic Acids Res *42*, D292–D296.

453 Borst, P. (2002). Antigenic variation and allelic exclusion. Cell *109*, 5–8.

454 Bülow, R., Overath, P., and Davoust, J. (1988). Rapid lateral diffusion of the variant surface
455 glycoprotein in the coat of Trypanosoma brucei. Biochemistry *27*, 2384–2388.

456 Campelo, F., and Malhotra, V. (2012). Membrane Fission: The Biogenesis of Transport Carriers.
457 Annu. Rev. Biochem. *81*, 407–427.

458 Derganc, J., and Čopič, A. (2016). Membrane bending by protein crowding is affected by protein
459 lateral confinement. Biochim. Biophys. Acta *1858*, 1152–1159.

460 Eliaz, D., Kannan, S., Shaked, H., Arvatz, G., Tkacz, I.D., Binder, L., Waldman Ben-Asher, H.,
461 Okalang, U., Chikne, V., Cohen-Chalamish, S., et al. (2017). Exosome secretion affects social
462 motility in Trypanosoma brucei. PLoS Pathog *13*, e1006245.

463 Engstler, M., Thilo, L., Weise, F., Grunfelder, C.G., Schwarz, H., Boshart, M., and Overath, P.
464 (2004). Kinetics of endocytosis and recycling of the GPI-anchored variant surface glycoprotein
465 in Trypanosoma brucei. J Cell Sci *117*, 1105–1115.

466 Engstler, M., Pfohl, T., Herminghaus, S., Boshart, M., Wiegertjes, G., Heddergott, N., and
467 Overath, P. (2007). Hydrodynamic flow-mediated protein sorting on the cell surface of
468 trypanosomes. Cell *131*, 505–515.

469 Fischer, T., Schorb, M., Reintjes, G., Kolovou, A., Santarella-Mellwig, R., Markert, S., Rhiel, E.,
470 Littmann, S., Becher, D., Schweder, T., et al. (2019). Biopearling of Interconnected Outer
471 Membrane Vesicle Chains by a Marine Flavobacterium. App. Environ. Microbiol. *85*.

472 Grünfelder, C.G., Engstler, M., Weise, F., Schwarz, H., Stierhof, Y.-D., Morgan, G.W., Field,
473 M.C., and Overath, P. (2003). Endocytosis of a glycosylphosphatidylinositol-anchored protein
474 via clathrin-coated vesicles, sorting by default in endosomes, and exocytosis via RAB11-positive
475 carriers. Mol. Biol. Cell *14*, 2029–2040.

476 Hartel, A.J., Glogger, M., Jones, N.G., Abuillan, W., Batram, C., Hermann, A., Fenz, S.F.,
477 Tanaka, M., and Engstler, M. (2016). N-glycosylation enables high lateral mobility of GPI-
478 anchored proteins at a molecular crowding threshold. Nat Commun *7*, 12870.

479 Hartel, A.J.W., Glogger, M., Guigas, G., Jones, N.G., Fenz, S.F., Weiss, M., and Engstler, M.
480 (2015). The molecular size of the extra-membrane domain influences the diffusion of the GPI-
481 anchored VSG on the trypanosome plasma membrane. Scientific Reports *5*, 10394.

482 Horn, D. (2014). Antigenic variation in African trypanosomes. Mol Biochem Parasitol *195*, 123–
483 129.

484 de Marco, A. (2011). Biotechnological applications of recombinant single-domain antibody
485 fragments. Microb Cell Fact *10*, 44.

486 McNicholas, S., Potterton, E., Wilson, K.S., and Noble, M.E.M. (2011). Presenting your
487 structures: the CCP4mg molecular-graphics software. Acta Crystallogr D Biol Crystallogr *67*,
488 386–394.

489 Mugnier, M.R., Stebbins, C.E., and Papavasiliou, F.N. (2016). Masters of Disguise: Antigenic
490 Variation and the VSG Coat in Trypanosoma brucei. PLoS Pathog *12*, e1005784.

491 Overath, P., Chaudhri, M., Steverding, D., and Ziegelbauer, K. (1994). Invariant surface proteins
492 in bloodstream forms of Trypanosoma brucei. Parasitology Today *10*, 53–58.

493 Pal, A., Hall, B.S., Jeffries, T.R., and Field, M.C. (2003). Rab5 and Rab11 mediate transferrin
494 and anti-variant surface glycoprotein antibody recycling in Trypanosoma brucei. Biochem J *374*,
495 443–451.

496 Pettersen, E.F., Goddard, T.D., Huang, C.C., Couch, G.S., Greenblatt, D.M., Meng, E.C., and
497 Ferrin, T.E. (2004). UCSF Chimera--a visualization system for exploratory research and
498 analysis. J Comput Chem *25*, 1605–1612.

499 Radwanska, M., Vereecke, N., Deleeuw, V., Pinto, J., and Magez, S. (2018). Salivarian
500 Trypanosomosis: A Review of Parasites Involved, Their Global Distribution and Their
501 Interaction With the Innate and Adaptive Mammalian Host Immune System. Front. Immunol. *9*,
502 2253.

503 Remis, J.P., Wei, D., Gorur, A., Zemla, M., Haraga, J., Allen, S., Witkowska, H.E., Costerton,
504 J.W., Berleman, J.E., and Auer, M. (2014). Bacterial social networks: structure and composition
505 of Myxococcus xanthus outer membrane vesicle chains. Environ. Microbiol. *16*.

506 Schwede, A., Jones, N., Engstler, M., and Carrington, M. (2011). The VSG C-terminal domain is
507 inaccessible to antibodies on live trypanosomes. Mol Biochem Parasitol *175*, 201–204.

508 Schwede, A., Macleod, O.J., MacGregor, P., and Carrington, M. (2015). How Does the VSG
509 Coat of Bloodstream Form African Trypanosomes Interact with External Proteins? PLoS Pathog
510 *11*, e1005259.

511 Snead, W.T., Hayden, C.C., Gadok, A.K., Zhao, C., Lafer, E.M., Rangamani, P., and
512 Stachowiak, J.C. (2017). Membrane fission by protein crowding. Proc. Natl. Acad. Sci. USA
513 *114*, E3258–E3267.

514 Stijlemans, B., Conrath, K., Cortez-Retamozo, V., Van Xong, H., Wyns, L., Senter, P., Revets,
515 H., De Baetselier, P., Muyldermans, S., and Magez, S. (2004). Efficient targeting of conserved
516 cryptic epitopes of infectious agents by single domain antibodies. African trypanosomes as
517 paradigm. J. Biol. Chem. *279*, 1256–1261.

518 Stijlemans, B., Caljon, G., Natesan, S.K.A., Saerens, D., Conrath, K., Pérez-Morga, D., Skepper,
519 J.N., Nikolaou, A., Brys, L., Pays, E., et al. (2011). High Affinity Nanobodies against the
520 Trypanosome brucei VSG Are Potent Trypanolytic Agents that Block Endocytosis. PLoS Pathog
521 *7*.

522 Stijlemans, B., De Baetselier, P., Caljon, G., Van Den Abbeele, J., Van Ginderachter, J.A., and
523 Magez, S. (2017). Nanobodies As Tools to Understand, Diagnose, and Treat African
524 Trypanosomiasis. Front Immunol *8*.

525 Szempruch, A.J., Sykes, S.E., Kieft, R., Dennison, L., Becker, A.C., Gartrell, A., Martin, W.J.,
526 Nakayasu, E.S., Almeida, I.C., Hajduk, S.L., et al. (2016). Extracellular Vesicles from
527 Trypanosoma brucei Mediate Virulence Factor Transfer and Cause Host Anemia. Cell *164*, 246–
528 257.

529 Webster, P., Russo, D.C., and Black, S.J. (1990). The interaction of Trypanosoma brucei with
530 antibodies to variant surface glycoproteins. J Cell Sci *96 (Pt 2)*, 249–255.

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533 **SUPPLEMENTARY FIGURES AND TABLES**

534 Figures 1-15, Table 1-3

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546

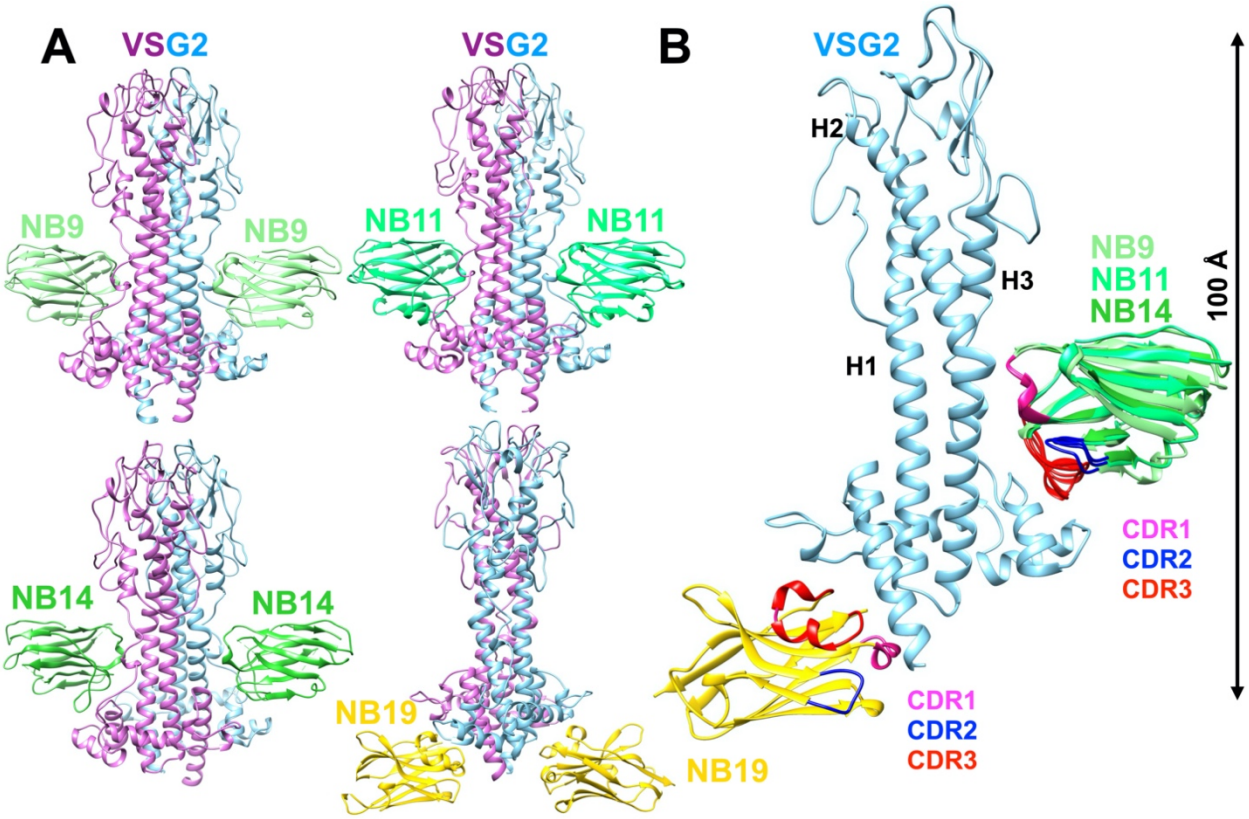
547 **AUTHOR CONTRIBUTIONS**

548 C.E.S., F.N.P., M.E. and N.G.J. conceived, initiated and coordinated the project, M.vS. produced
549 VSG2 for production of nanobodies. M.vS. and A.H. produced and crystallized $NB11_{VSG2}$ and
550 $NB14_{VSG2}$ complexes. A.H. produced and crystallized $NB9_{VSG2}$ and $NB19_{VSG2}$ complexes, all
551 complexes for membrane studies (with M.vS. also producing $NB11_{VSG2}$ and $NB14_{VSG2}$ for the
552 latter), collected the diffraction data and solved all structures. J.Z. aided in crystal preparation and
553 beamline data collection. H.H. and A.H. created sortaggable Nbs and the camelid heavy chain Ig2.
554 H.H., M.vS, and A.H performed anti-His FACs binding experiments. H.H and A.H produced the

555 FAM and FITC FACS data on live *T. brucei*, while A.H. executed FACS experiments on non-
556 VSG2 coats. L.H. performed all electron microscopy, parasite movement, coat diffusion, and
557 toxicity experiments. C.E.S., A.H., N.G.J. and M.E. wrote the manuscript. All authors discussed
558 the data and approved the final manuscript.

559 **DECLARATION OF INTERESTS**

560 The authors declare that they have no competing interests.



561

562 **Figure 1. Overall Structures of VSG2-NB Complexes**

563 **(A)** The four nanobody-VSG2 structures with $NB9_{VSG2}$ (NB9 in light green, top left), $NB11_{VSG2}$
564 (NB11 in lime green, top right), $NB14_{VSG2}$ (NB14 in green, bottom left) and $NB19_{VSG2}$ (NB19 in
565 gold, bottom right) and VSG2 (dimer shown in cyan/purple) are depicted as ribbon diagrams.
566 **(B)** Superposition of VSG2-NB complexes with similar coloring. The Complementarity-
567 Determining Regions (CDR or variable region) are shown in magenta (CDR1), blue (CDR2) and
568 red (CDR3). Structures illustrated with Chimera (Pettersen et al., 2004).

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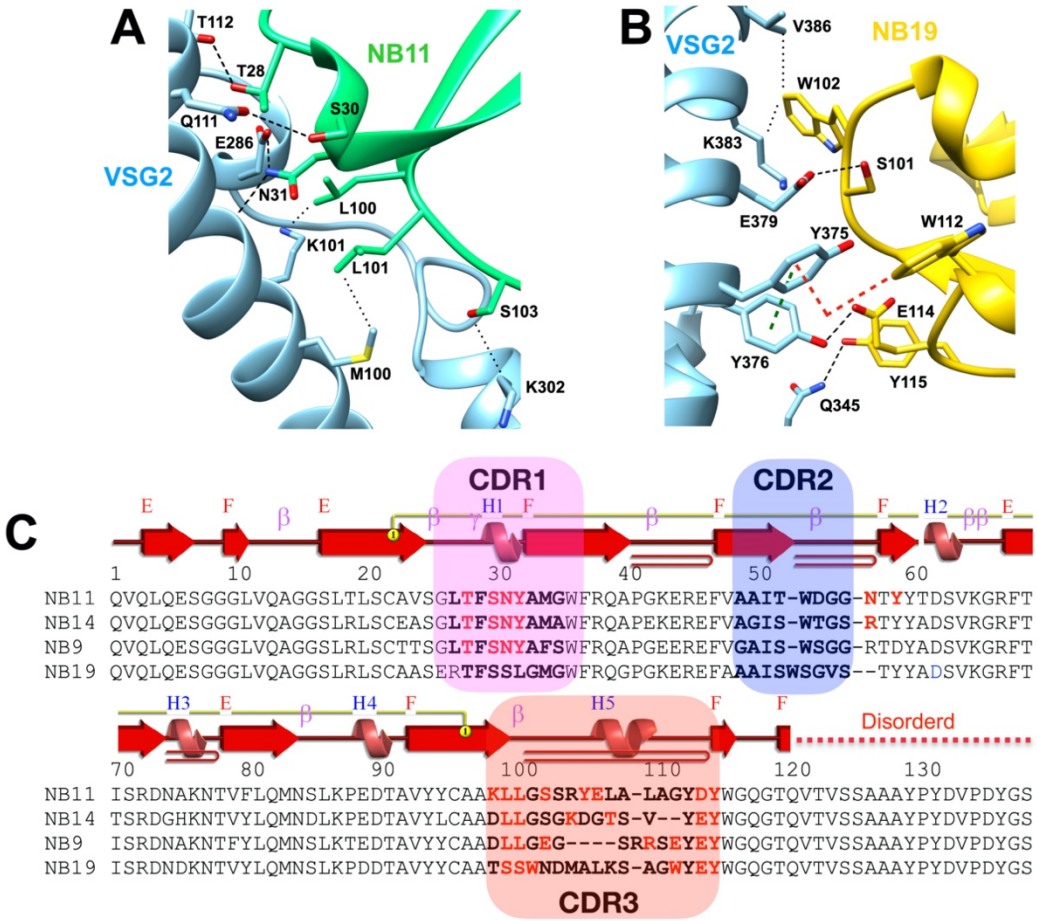

570

571 **Figure 2. Interactions of Nanobody CDR Variable Loops with VSG2**

572 **(A)** Close up of the interaction of the CDR3 loop from $NB11_{VSG2}$ (NB11) with VSG2. Side chains
573 from each protein have carbon atoms colored to match the ribbon diagram of the main chain, with
574 atoms of oxygen, nitrogen, and sulfur shown in red, blue, and yellow, respectively. Hydrogen
575 bonds (black bricks) are formed between T28, S30 and N31 (NBs) with T112, Q111 and E286
576 (VSG2), respectively. Residues L100, L101 and S103 of NB11 were found to form non-covalent
577 (black dots) bonds with K101, M100 and K302 of VSG2. **(B)** Close up of the interaction of the
578 CDR3 loop from NB19 with VSG2. Hydrogen bonds (black bricks) are formed between S101
579 (NB19) and E379 (VSG2), as well as between Y115 (NB19) and Q345 (VSG2). Residues W102

580 (NB19) and V386 and K383 were involved in non-covalent interactions. W112 of NB19 interacts
581 with Y375 of VSG2 in a parallel displaced π-stacking (red bricks) manner. This interaction is
582 further reinforced by a VSG2 intra-molecule T-shaped π-stacking (green bricks) between Y375
583 and Y376. **(C)** Sequence alignment and annotation of the four Nbs (numbering is for $NB11_{VSG2}$),
584 including secondary structural elements is shown together with highlighted regions of the CDR
585 variable loops (colored as in Figure 1b). Residues that make contacts with VSG2 are shown with
586 red letters. Structures illustrated with Chimera (Pettersen et al., 2004) and secondary structure with
587 PDBSum (de Beer et al., 2014).

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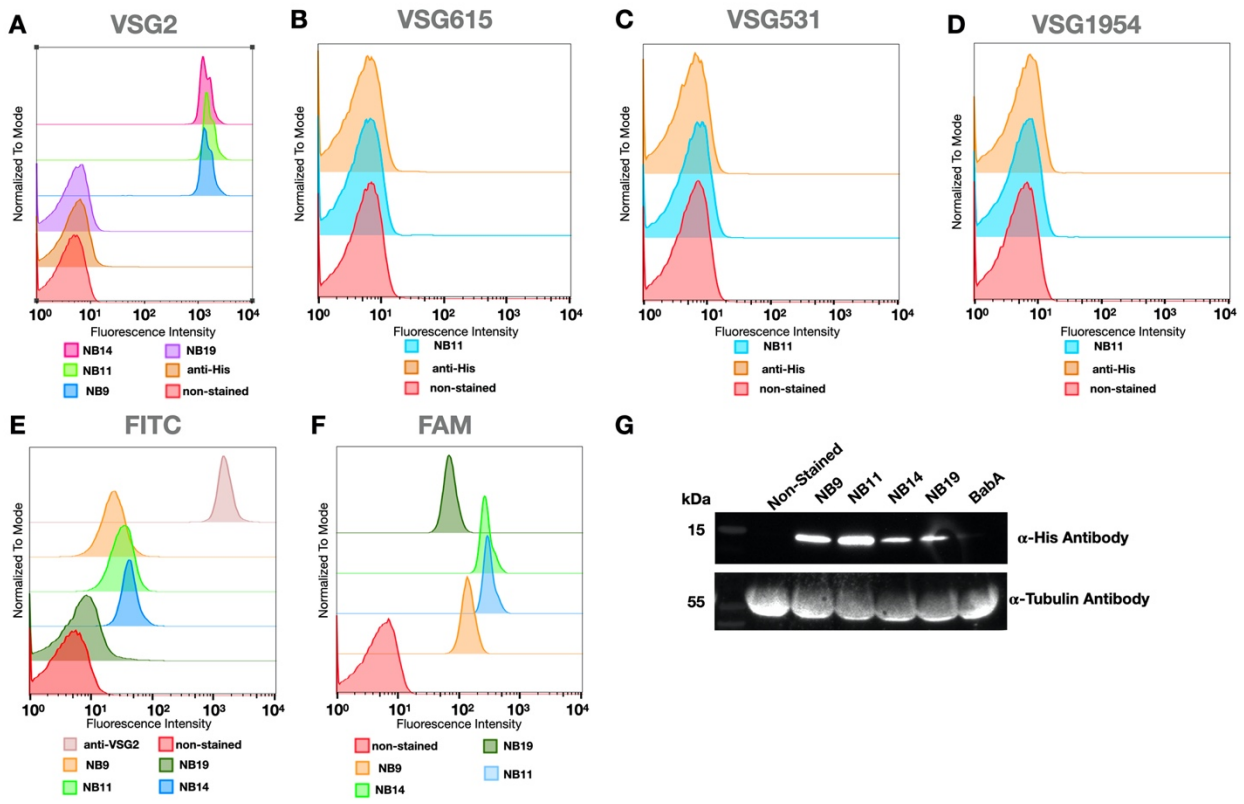

591

592 **Figure 3. Binding Assays of Nbs to Live Trypanosomes**

593 Different VSG-expressing *T. brucei* were incubated with various Nbs and visualized in different
594 ways by FACS. (A) VSG2-expressing bloodstream form (BSF) trypanosomes were incubated
595 with C-terminally His-tagged Nbs and visualized using an anti-His antibody, (B) VSG615-
596 expressing BSF trypanosomes (expressing a metacyclic VSG) were incubated with C-terminally
597 His-tagged Nbs and visualized using an anti-His antibody, (C) VSG531-expressing BSF
598 trypanosomes were incubated with C-terminally His-tagged Nbs and visualized using an anti-His
599 antibody, (D) VSG1954-expressing BSF trypanosomes (expressing a metacyclic VSG) were
600 incubated with C-terminally His-tagged Nbs and visualized using an anti-His antibody, (E)
601 VSG2-expressing bloodstream form (BSF) trypanosomes were incubated with FITC-labeled Nbs

602 and visualized through the fluorochrome's emission, (F) VSG2-expressing bloodstream form
603 (BSF) trypanosomes were incubated with Nbs sortagged with FAM and visualized through the
604 fluorochrome's emission (G) VSG2-expressing bloodstream form (BSF) trypanosomes were
605 incubated with C-terminally His-tagged Nbs, washed thoroughly, run on an SDS-PAGE gel, and
606 probed with an anti-His antibody. An irrelevant Nb (BabA, raised to a protein from *H. pylori*)
607 was used as a negative control. The same cells were probed with an anti-tubulin antibody to
608 provide a gel-loading standard.
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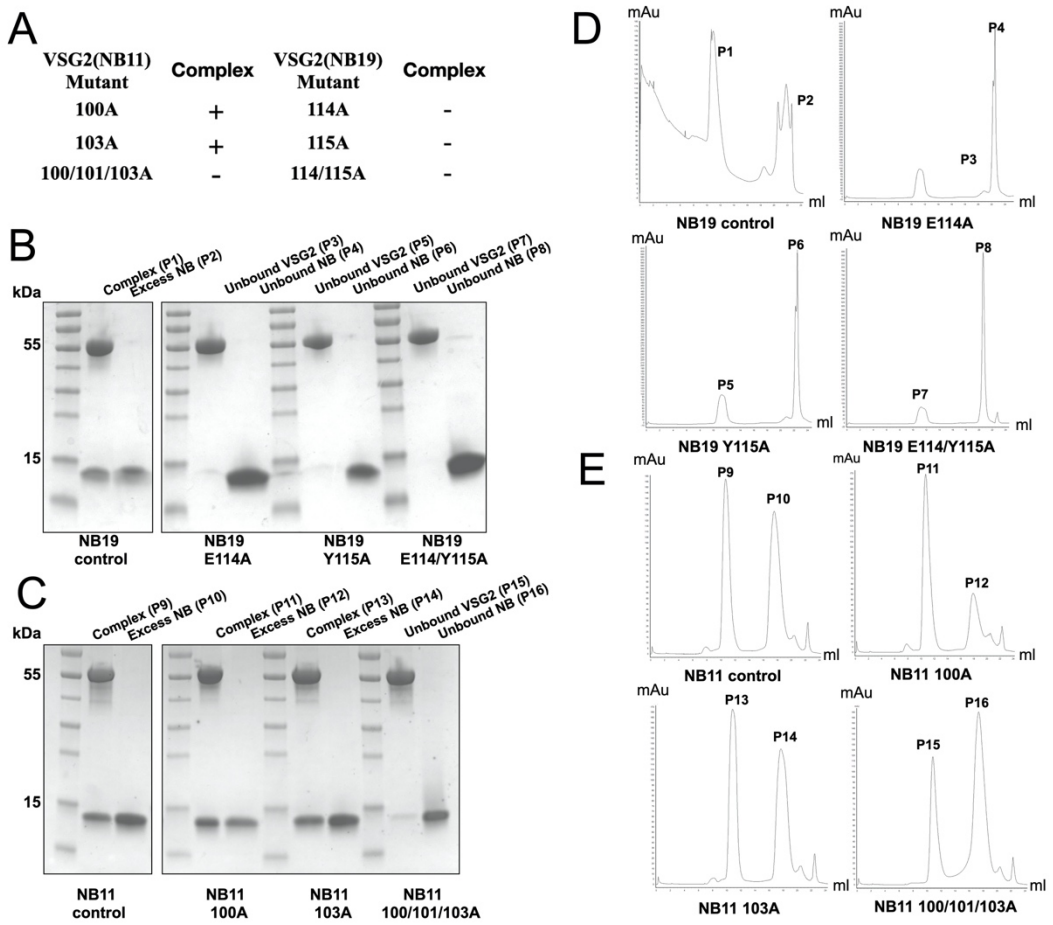

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611 **Figure 4. Mutations in the V-Loop Regions of Nanobodies Inhibit Complex Formation with**

612 **VSG2**

613 **(A)** Overview of $NB11_{VSG2}$ and $NB19_{VSG2}$ mutants in relation to their ability to bind VSG2.

614 $NB11_{VSG2}$ mutants L100A and L103A form a complex with VSG2 (+), while the triple mutant

615 L100/L101/S103 does not bind (-). For $NB19_{VSG2}$ all single and multiple mutants (E114A, Y115A,

616 E114/Y115A) fail to form a complex with VSG2 (-). **(B and C)** SDS-PAGE analysis of purified,

617 mixed VSG2 and nanobodies (wild type and mutant $NB11_{VSG2}$ and $NB19_{VSG2}$) analyzed by gel

618 filtration chromatography (see Methods). Peak elution fractions are shown and numbered. VSG2

619 corresponds to the 55 kDa band and nanobodies to the 15 kDa band. Gels were stained with

620 Coomassie blue. **(D and E)** FPLC chromatographs corresponding to the SDS-PAGE gels **(B and**

621 **C)** with corresponding peak numbers from the SDS-PAGE gels shown. The Y-axis displays the
622 UV_{280nm} absorbance (arbitrary units) and the X-axis the elution volume from the column (see
623 Methods).
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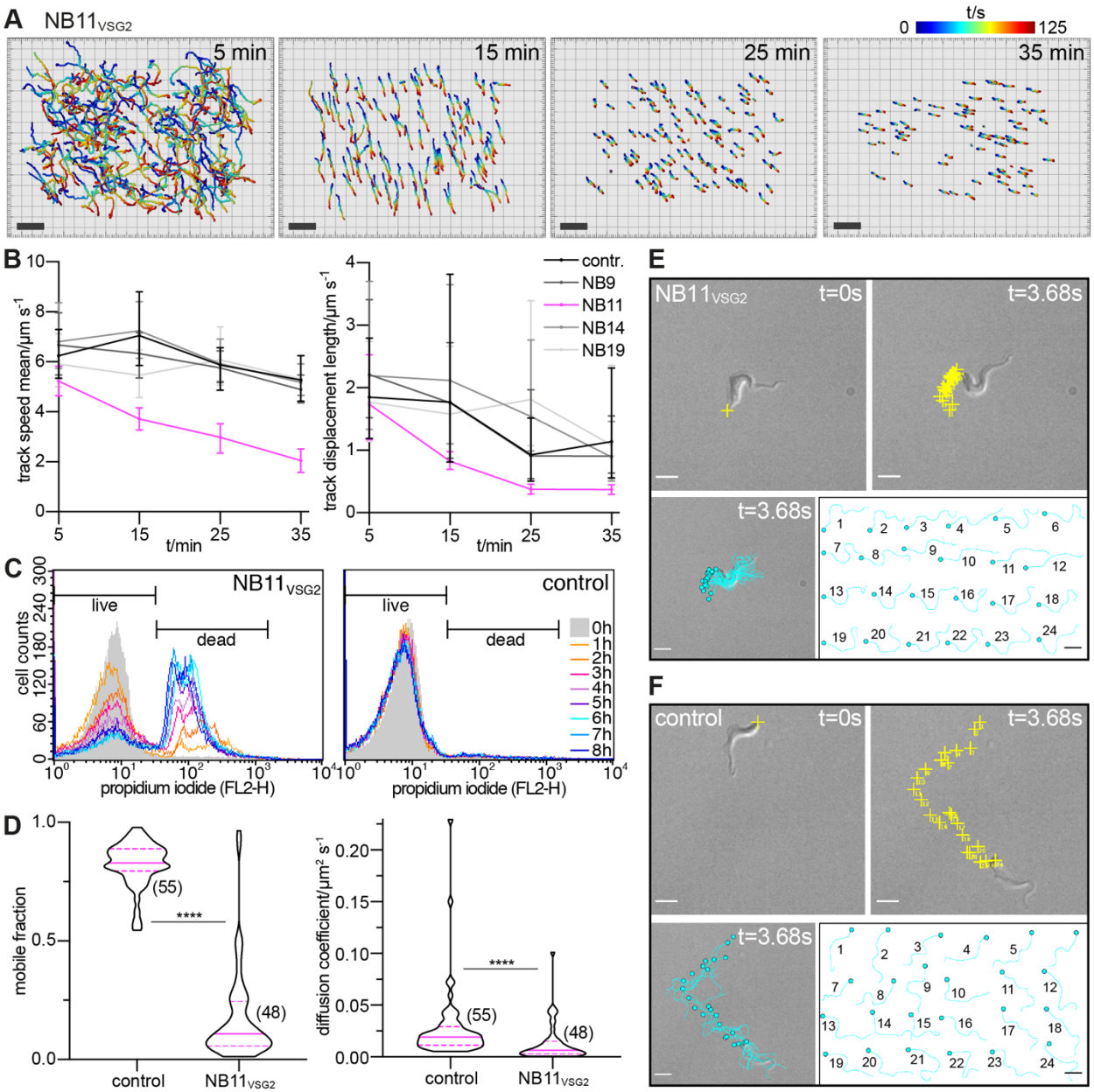

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628 **Figure 5. Nanobodies Reduce VSG Mobility, Paralyze, and Kill Trypanosomes**

629 **(A-E)** Cells were treated with a 1.7-fold molar excess of Nb to VSG monomer.

630 **(A)** $NB11_{VSG2}$ affects cell motility after 15 min of treatment. Individual cells in a population were

631 tracked for 125 s at 5, 15, 25 and 35 minutes post addition of $NB11_{VSG2}$ and analyzed using the

632 Imaris x64 software. Cells close to the border of the imaging region were removed by filtering to

633 simplify the images shown (s. Figure S4C for trajectories of complete data set). Trajectories are

634 color coded blue (t = 0 s) to red (t = 125 s). Scale bars, 100 µm. **(B)** Comparison of velocities
635 (track speed mean), left, and track displacement lengths per s, right, of untreated cells and cells
636 treated with four different nanobodies, $NB9_{VSG2}$, $NB11_{VSG2}$, $NB14_{VSG2}$ and $NB19_{VSG2}$. Data
637 extracted from trajectories shown in Figure S4 (median with bars representing the 25th and 75th
638 percentile of data points; see Figures S5 and S6 for scatter dot plots of the data). Both velocity and
639 track displacement are clearly most affected upon treatment with $NB11_{VSG2}$.
640 **(C)** Flow cytometry analysis to determine the extent of cell death over time following treatment
641 with $NB11_{VSG2}$. Left panel, treated cells, right panel, untreated control cells analyzed in hourly
642 intervals over a duration of 8 h. Propidium iodide was used as a dead cell marker. Each histogram
643 is based on 25.000 gated events (Figure S7 shows the gate settings for the Nb treated data set).
644 **(D)** The effect of nanobody binding on VSG diffusion was analyzed by fluorescence recovery after
645 photobleaching (FRAP) experiments on immobilized trypanosomes that were surface labeled with
646 ATTO 488. Untreated (control) and $NB11_{VSG2}$ treated cells were analyzed (n in brackets). Violin
647 plots showing the frequency distribution of the mobile fractions, left, and the diffusion coefficient,
648 right, of the VSG in control and $NB11_{VSG2}$ treated cells (median, solid magenta lines; 25th and
649 75th percentile, dashed magenta lines). There was a remarkable reduction in mobile fraction of
650 treated cells, median of 11 %, compared to that of untreated cells, median of 83 %. The median
651 diffusion coefficient of mobile VSGs following treatment with $NB11_{VSG2}$ was reduced to 0.007
652 $\mu m^2/s$ from 0.019 $\mu m^2/s$ for untreated cells. P values from an unpaired, two-tailed Mann-Whitney
653 test (**** = $P<0.001$) are shown in both graphs.

654 **(E, F)** Single cell analysis of an $NB11_{VSG2}$ treated **(E)** and an untreated **(F)** trypanosome. The
655 upper images show the first (left) and last (right) frame of a video (s. Videos S1 and S2) with the
656 posterior of the cell marked by a yellow cross in the first image and the posterior of every 40th
657 frame of the sequence marked in the second image. Whereas the flagellar beat generates a
658 propulsive force in wt cells the Nb treated cells initiate beats without the generation of a propulsive
659 force. Movement is visualized by tracing the cell shape (cyan lengthwise line through the center
660 of the cell with a circle marking the posterior) in every 40th frame, bottom row. Bottom left image,
661 traces at the position of the cell in the video sequence, bottom right images: the same traces
662 displayed individually to show differences in cell shape and orientation. Scale bars, 5 µm.

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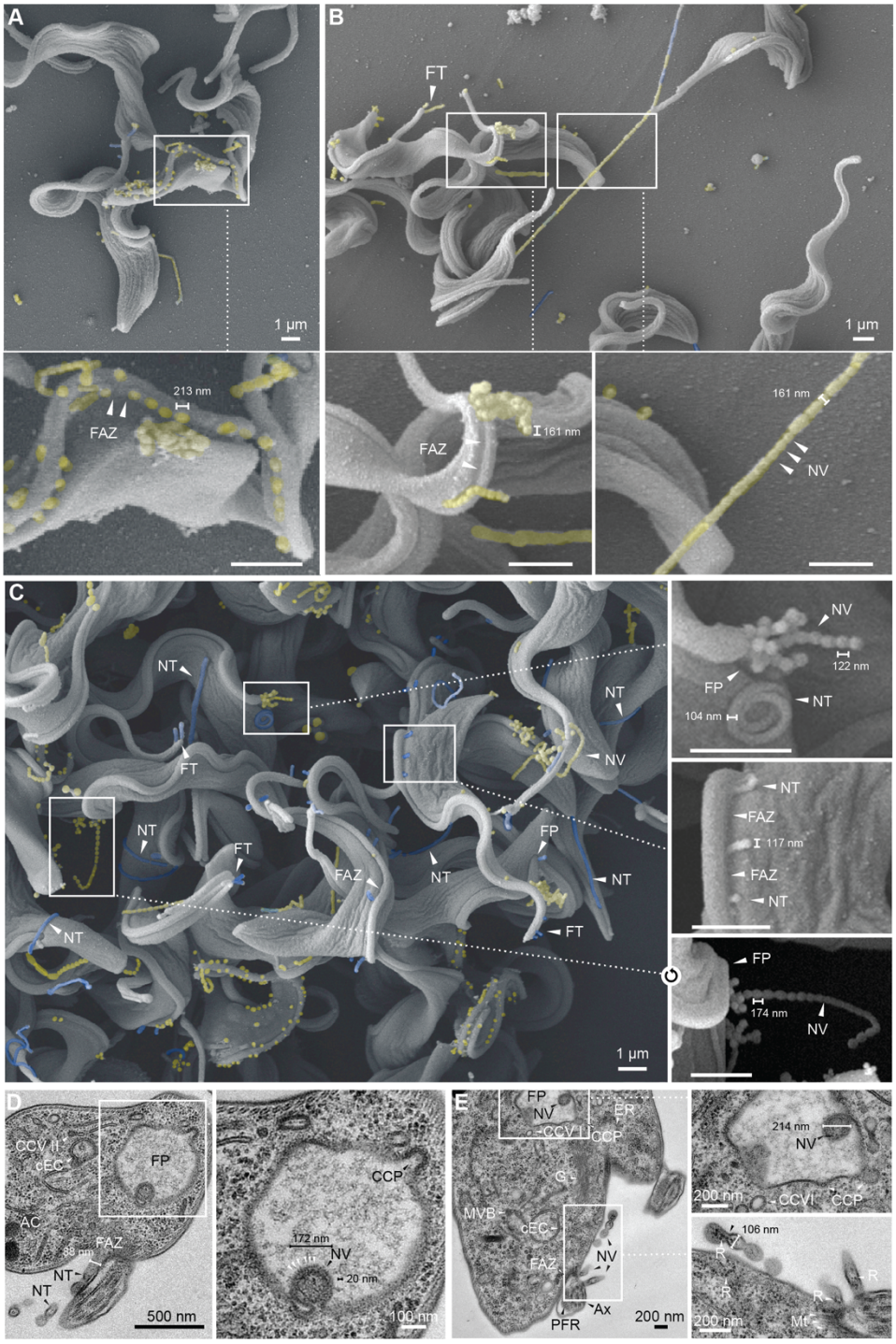

Figure 6. Nanobody Treatment Triggers Formation of Nanovesicles and Nanotubes

(A-C) Scanning electron micrographs of trypanosomes treated with a 1.7-fold molar excess of $NB11_{VSG2}$ compared to VSG monomer present. FT, flagellar tip; FAZ, flagellar attachment zone;

674 NV, nanovesicle; NT, nanotube; FP, flagellar pocket. Cells treated for only 2 min **(A,B)**
675 displayed nanovesicles (yellow) as well as some chains of nanovesicles (yellow) with diameters
676 of around 200 nm. Nanotube-like structures (blue) of slightly smaller diameter and lengths
677 exceeding 1 µm could also be observed. All structures emanated from around the FAZ, FT and
678 PP. Cells treated for 10 min **(C)** show an increased and roughly equal abundance of both
679 nanovesicles and nanotubes suggesting them to be independent structures. **(D,E)** TEM images of
680 chemically fixed VSG2 expressing cells treated with a 1.7-fold molar excess of $NB11_{VSG2}$
681 compared to VSG2 monomer present. CCVII, clathrin coated vesicle II; cEC, circular exocytic
682 carrier; FP, flagellar pocket; AC, acidocalcisome; FAZ, flagellar attachment zone; NT, nanotube;
683 NV, nanovesicle; CCP, clathrin coated pit; ER, endoplasmic reticulum; CCVI, clathrin coated
684 vesicle I; G, Golgi; MVB, multivesicular body; PFR, paraflagellar rod; Ax, axoneme; Mt,
685 mitochondrion; R, ribosome. **(D)** Concomitant formation of a nanovesicle in the flagellar pocket
686 and a nanotube from the proximity of the flagellar attachment zone (FAZ). Formation of a
687 clathrin coated pit in the FP is also apparent and suggests the endocytic pathway to be functional.
688 The budding NV has approx. 20 nm thick structures coating the outer membrane consistent with
689 the length of VSG molecules. **(E)** Concomitant formation of a nanovesicle in the flagellar pocket
690 and nanotubes from the proximity of the FAZ. Nanovesicles can form chains with continuous
691 content and contain electron-dense particles that resemble ribosomes found in the cytoplasm.

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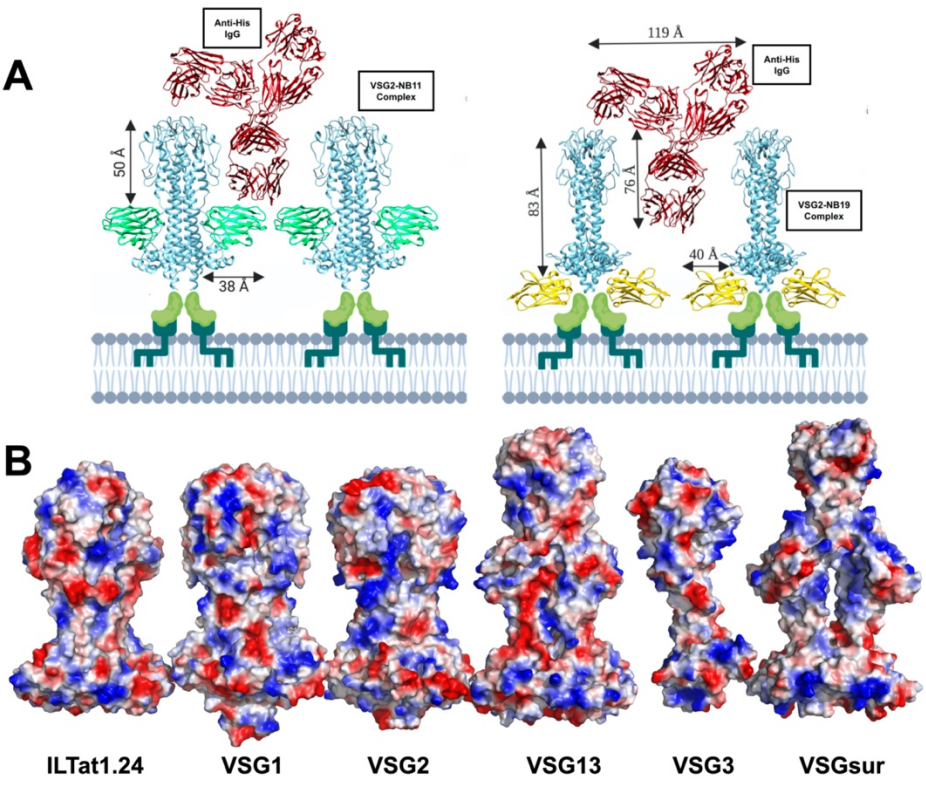

Figure 7. Nanobodies Provide a "Molecular Ruler" to Gauge VSG Accessibility

(A) Schematic of the interaction of an anti-His monoclonal IgG antibody with the VSG coat during FACS experiments. The trypanosome membrane is shown at the bottom with idealized lipids into which the (dark green) GPI anchor of the C-terminal domain (medium green) inserts. Above that is a ribbon diagram drawing of a VSG2 dimer (cyan) with a bound Nb ($NB9_{VSG2}$, $NB11_{VSG2}$, $NB14_{VSG2}$ superimposed in light green, left) or $NB19_{VSG2}$ (yellow, right). The IgG is shown as a ribbon diagram colored red (PDB ID 5DK3). **(B)** Panel of crystal structures of VSGs drawn as molecular surfaces colored by relative electrostatic potential (blue is positive/basic, red is negative/acidic, and white is neutral). RCSB PDB IDs for models used are ILTat1.24 (2VSG), VSG1 (5LY9), VSG2 (1VSG), VSG13 (6Z8H), VSG3 (6ELC), and VSGsur (6Z7A). Molecular graphics software used: Chimera (Pettersen et al., 2004), CCP4mg (McNicholas et al., 2011), and biorender.com Pro.