TMPRSS2 is a functional receptor for human coronavirus HKU1

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Abstract

Four endemic seasonal human coronaviruses causing common colds, HKU1, 229E, NL63 and OC43 circulate worldwide[1]. After binding to cellular receptors, coronavirus spike proteins are primed for fusion by transmembrane-serine protease 2 (TMPRSS2) or endosomal cathepsins[2-9]. NL63 uses angiotensin-converting enzyme 2 (ACE2) as a receptor[10], whereas 229E uses human aminopeptidase-N[11]. HKU1 and OC43 spikes bind cells through 9-O-acelytated sialic acid but their protein receptors remain unknown[12]. Here, we show that TMPRSS2 is a functional receptor for HKU1. TMPRSS2 triggers HKU1 spike-mediated cell-cell fusion and pseudovirus infection. Catalytically inactive TMPRSS2 mutants do not cleave HKU1 spike but allow pseudovirus infection. Furthermore, TMPRSS2 binds with high affinity to the HKU1 receptor binding domain (RBD) (K_d 334 and 137 nM for HKU1A and HKU1B genotypes) but not to SARS-CoV-2. Conserved amino acids within HKU1 RBD are essential for binding to TMPRSS2 and pseudovirus infection. Newly designed anti-TMPRSS2 nanobodies potently inhibit HKU1 spike attachment to TMPRSS2, fusion and pseudovirus infection. The nanobodies also reduce infection of primary human bronchial cells by an authentic HKU-1 virus. Our findings illustrate the various evolution strategies of coronaviruses, which use TMPRSS2 to either directly bind to target cells or to prime their spike for membrane fusion and entry.

Main

HKU1 was first identified from an elderly patient with severe pneumonia in Hong Kong in 2005[13]. HKU1 was later shown to cause common cold and benign respiratory symptoms, but complications include severe lower respiratory infections, particularly in young children, the elderly and immunocompromised individuals[14]. It is estimated that 70% of children seroconvert before the age of 6[15]. The global seroprevalence of HKU1 is similar to other seasonal human coronaviruses (hCoV) and is between 75 and 95%[15-17]. Three main viral genotypes have been identified, HKU1A, B and C. HKU1A and B spikes have 85% identity (Fig. 1a). HKU1C is a HKU1A/B recombinant and its spike shares 99% identity with HKU1B. Conserved regions in the HKU1A and B spikes include a putative RBD with a Receptor Binding Motif (RBM)[18,19], S1/S2 and S2/S2' cleavage sites[20] (Fig.1a).

Both HKU1 and OC43 spikes bind to 9-O-acetylated α2,8 linked disialosides on target cells[12,21,22]. Their protein receptors have not been identified. After receptor binding, the

65   coronavirus spike is cleaved at the S2' site by membrane bound proteases, such as TMPRSS2,

66   or by endosomal cathepsins, resulting in a conformational change of S2 that projects the fusion

67   peptide into the target membrane to drive fusion[23]. TMPRSS2 belongs to the type II

68   transmembrane serine protease (TTSP) family that comprises 19 cell-surface enzymes[24,25].

69   TTSPs are involved in many processes, including epithelial homeostasis, extracellular matrix

70   degradation, hormone and growth factor activation, and initiation of proteolytic cascades

71   through cleavage of membrane cellular proteins[24]. TMPRSS2 primes coronavirus spikes and

72   other viral envelope glycoproteins, such as influenza hemagglutinin, enabling fusion[26]. TTSPs

73   are synthesized as single-chain proenzymes that require proteolytic activation[24]. TMPRSS2

74   undergoes autocleavage into two subunits that remain attached by a disulfide bond[27]. In the

75   respiratory tract, TMPRSS2 is expressed in nasal, bronchial and small airways tissues, and more

76   particularly in ciliated cells that are the main target of HKU1[28,29]. Here, using cell-cell fusion

77   assays, infections with pseudovirus and live virus, as well as *in vitro* binding tests, we identify

78   TMPRSS2 as a high-affinity receptor for HKU1.

79

80   **Generation of anti-TMPRSS2 nanobodies**

81   To our knowledge, there are no currently available anti-TMPRSS2 antibodies that allow cell

82   surface staining, as most of the existing ones are directed towards cytosolic fragments of the

83   protein. We thus immunized an alpaca with the soluble ectodomain of a catalytically inactive

84   TMPRSS2 (S441A mutant) to produce VHH single-chain nanobodies. We isolated 5 VHHs

85   (A01, F05, A07, C11 and D01) that bind with an affinity in the nanomolar range to soluble

86   S441A TMPRSS2 (Extended Data Fig. 1a, Extended Data Table 1). We selected one VHH with

87   the highest affinity (A01) in order to generate a dimeric antibody with a human Fc domain that

88   efficiently stained TMPRSS2+ cells (Extended Data Fig. 1b).

89

90   **TMPRSS2 triggers spike-dependent fusion**

91   To investigate the effect of TMPRSS2 on HKU1 spike mediated fusion, we generated

92   plasmids encoding for the HKU1A (isolate N1 - NCBI: txid443239) and B (Isolate N5 - NCBI:

93   txid443241) spikes (Fig. 1a). In 293T cells that do not express TMPRSS2, transient transfection

94   led to surface expression of the two proteins, as assessed by flow cytometry using mAb10, a

95   pan S2 coronavirus antibody[30] (Extended Data Fig. 2a). To study cell-cell fusion, we used a

96   GFP-Split based model in which fused cells become GFP+ (Fig. 1b)[31]. HKU1A and B spikes

97   did not induce fusion alone but were highly fusogenic when co-expressed with TMPRSS2 in

98   293T cells (Fig. 1b, Extended Data Fig. 2b). In contrast, in experiments run in parallel, the

3

99 SARS-CoV-2 spike induced fusion when co-expressed with ACE2 and not with TMPRSS2

100 (Extended Data Fig. 2c). HKU1 also triggered syncytia when co-expressed with TMPRSS2 in

101 U2OS cells (Extended Data Fig. 2d).

102   As a control of specificity for HKU1 fusion, we tested a panel of 12 other surface proteases,

103 including the coronavirus receptors aminopeptidase-N (APN), dipeptidyl peptidase-4 (DPP4)

104 and ACE2, as well as TMPRSS4 and TMPRSS11D, that have been reported to cleave the

105 SARS-CoV-2 spikes[32-34]. The proteases were correctly expressed, as assessed by flow

106 cytometry (Extended Data Fig. 2e-i), but only TMPRSS2 triggered cell-cell fusion (Fig. 1c).

107   We next generated fluorescent TMPRSS2-mNeonGreen and HKU1A Spike-mScarlet-I to

108 follow fusion by video microscopy. When mixed 24 h after transfection, cells expressing spike

109 and cells expressing TMPRSS2 formed syncytia in less than 1 h, indicating that this process is

110 rapid (Extended Data Fig. 2j, Supp. videos 1-2). By expressing TMPRSS2 either on donor cells

111 (spike-transfected) or acceptor cells, we observed that the protease had to be on acceptor cells,

112 opposite of the spike to induce high levels of fusion (Fig. 1d).

113   We then investigated whether endogenous levels of TMPRSS2 were sufficient to induce

114 HKU1 spike-dependent fusion. We mixed HKU1A spike-expressing 293T donor cells with

115 Caco2 acceptor cells, that endogenously express low levels of TMRPSS2[35] (Extended Data Fig.

116 3). Spike expressing cells fused with parental Caco2 cells but not with Caco2 TMPRSS2-KO

117 cells, a Caco2 derivative in which the *tmprss2* gene was knocked down by CRISPR-Cas9 (Fig.

118 1e, Extended Data Fig. 3a-c). Silencing of TMPRSS2 using siRNA in Caco2 cells also

119 significantly reduced fusion with spike-expressing 293T cells (Extended Data Fig. 3d).

120   Altogether, these results indicate that TMPRSS2 expression enables HKU1A and B spike-

121 mediated cell-cell fusion.

122

123   **Inactive TMPRSS2 allows HKU1 infection**

124   To further analyze the role of TMPRSS2 in HKU1 spike fusion, we generated two well-

125 characterized TMPRSS2 mutants, R255Q and S441A[27] (Fig. 2a). R255 is in the auto-cleavage

126 site, and S441 is in the catalytic site; both mutations prevent TMPRSS2 autocleavage and

127 activity. As expected, R255Q and S441A were correctly expressed in 293T cells but lacked

128 catalytic activity, measured with a substrate generating a fluorescent signal upon cleavage[36]

129 (Extended Data Fig. 4a). We then studied the cleavage profile of TMPRSS2 and HKU1 spike

130 by western blot (Fig. 2b). We focused our analysis on HKU1A spike since none of the

131 polyclonal or monoclonal antibodies tested recognized the HKU1B spike by western blot.

132 When expressed alone, WT TMPRSS2 was cleaved while the mutants were not. When the

133 HKU1 spike was present, a similar profile of TMPRSS2 processing was observed. Without
134 TMPRSS2, the spike was partially cleaved into S1 and S2 subunits (Fig. 2b), most likely at the
135 polybasic furin cleavage S1/S2 site (Fig. 1a). WT TMPRSS2, but not the catalytically inactive
136 R255Q and S441A mutants, generated additional cleavage bands in the spike, including a 100
137 kDa band below the S2 band, which likely corresponds to the S2' fragment.

138   We then examined how the spike was cleaved by TMPRSS2 present on adjacent cells. To
139 this aim, we mixed spike expressing cells with TMPRSS2 expressing cells. We assessed by
140 western blot the processing of the spike 3 and 6 h after coculture (Extended Data Fig. 4b). The
141 spike cleavage by WT TMPRSS2 was slightly visible 3 h after coculture, and this process was
142 more marked at 6 h. Of note, syncytia were detected at 3 and 6 h post co-culture in the WT
143 TMPRSS2 condition.

144   The WT and mutant TMPRSS2 had slightly different levels of expression upon transfection
145 in 293T cells, when assessed by flow cytometry (Extended Data Fig. 4c, d). We thus adjusted
146 the amounts of plasmids to reach similar levels. The catalytically inactive TMPRSS2 mutants
147 barely induced cell-cell fusion with either HKU1A or B spikes (Fig. 2c), confirming the need
148 of spike cleavage for cell-cell fusion.

149   We next generated single-cycle HKU1 pseudoviruses − lentiviral particles pseudotyped with
150 HKU1 spikes − to further investigate the role of TMPRSS2 in HKU1 entry. The pseudovirus
151 strategy has been successfully used to study SARS-CoV-2 entry and to identify ACE2 as a
152 receptor for this virus[37]. HKU1A and B pseudoviruses did not infect parental 293T cells
153 efficiently, while transient expression of TMPRSS2 enabled high viral entry (Fig. 2d).

154   In striking contrast with their inability to trigger cell-cell fusion, the catalytically inactive
155 R255Q and S441A TMPRSS2 mutants readily allowed infection of 293T cells with HKU1A or
156 HKU1B pseudovirus (Fig. 2d). The TMPRSS2 mutants behave as expected regarding the
157 SARS-CoV-2 spike (D614G ancestral strain), which requires the enzymatic activity of the
158 protease for infectivity enhancement[37]. In 293T-ACE2 cells, WT TMPRSS2 increased SARS-
159 CoV-2 pseudotype entry by 8-fold, whereas this was not the case for the R255Q and S441A
160 mutants (Extended Data Fig. 4e). Together, our data show that catalytic activity of TMPRSS2
161 is not required for HKU1-mediated pseudovirus entry.

162   Coronavirus spike can either be processed by proteases at the surface of target cells, allowing
163 for membrane fusion, or by cathepsins in endosomes, allowing for entry after internalization[8].
164 As TMPRSS2 catalytic activity was not required for HKU1 entry, we examined the cytoplasmic
165 access route of pseudovirus in 293T cells expressing WT or S441A TMPRSS2. To this aim,
166 we performed infections in presence of SB412515, a cathepsin L inhibitor, or E64d, a pan-

167   cysteine protease inhibitor. The drugs were added 2 h before infection and maintained for 48 h.

168   SB412515 and E64d reduced the entry of HKU1A pseudovirus in S441A TMPRSS2 cells and

169   not in WT TMPRSS2 cells (Extended Data Fig. 4f). This strongly suggests that viral entry

170   occurs through endosomes with the catalytically inactive TMPRSS2 and at the surface with the

171   WT protease. With HKU1B, SB412515 and E64d had little or no effect on entry (Extended

172   Data Fig. 4g), suggesting that HKU1B might be cleaved by other proteases or requires less

173   cleavage to induce fusion, although it still uses TMPRSS2 as a receptor. Infection by both

174   HKU1A and HKU1B pseudoviruses was inhibited by hydroxychloroquine (HCQ) in S441A

175   TMPRSS2 cells, confirming an endocytic route with the mutant protease (Extended Data Fig.

176   4f, g).

177   We next asked whether TMPRSS2 could confer sensitivity to HKU1 pseudovirus in other

178   cell lines. We generated U2OS and A549 stably expressing WT or S441A TMPRSS2. We

179   reintroduced the two proteins in Caco2 TMPRSS2-KO cells. Flow cytometry demonstrated that

180   TMPRSS2 was expressed in this panel of cells (Extended Data Fig. 4h, i). The presence of WT

181   or S441A TMPRSS2 enabled infection to various extents of U2OS, A549 and Caco2 cells by

182   HKU1A and HKU1B pseudoviruses (Fig. 2e). Knock-out of TMPRSS2 significantly reduced

183   entry into Caco2 cells. Furthermore, in parental Caco2 cells, preincubation with Camostat, a

184   serine protease inhibitor known to inhibit TMPRSS2, did not affect HKU1 pseudovirus

185   infection, while, as expected, it diminished SARS-CoV-2 entry by two-fold (Extended Data Fig

186   4j), confirming the role of endogenous TMPRSS2 as a receptor.

187   The Vero E6-TMPRSS2 cell line[38] remained insensitive to HKU1 pseudovirus infection

188   (Extended Data Fig. 4k). Vero E6 cells are African green monkey kidney cells, it is thus

189   possible that other parameters (glycosylation, sialylation, adhesion molecules or other cellular

190   proteins, etc…) may regulate their sensitivity to HKU1.

191   We then analyzed the role of sialic acids during TMPRSS2-mediated HKU1 entry. We

192   treated U2OS TMPRSS2+ cells with Neuraminidase, an enzyme that removes (α2,3), (α2,6)

193   and (α2,8) linked sialic acids. Neuraminidase decreased binding of two sialic acid ligands,

194   Lectin SNA and Siglec E, without affecting surface levels of TMPRSS2 (Extended data Fig.

195   5). Neuraminidase reduced sensitivity of target cells to HKU1 pseudovirus infection in a dose-

196   dependent manner, suggesting that sialic acids are necessary to trigger efficient HKU1 entry in

197   TMPRSS2+ cells (Extended data Fig. 5).

198   Taken together, our results show that TMPRSS2 is required for HKU1 pseudovirus infection

199   but that its catalytic activity is dispensable, possibly because it can be rescued by other proteases

200   such as cathepsins.

6

201

HKU1 spike binds to TMPRSS2

We next generated recombinant ectodomains of HKU1A and B spikes to investigate their binding to TMPRSS2 expressing cells (Fig. 3a, b, Extended Data Fig. 6a). HKU1 spike bound weakly to WT TMPRSS2 and more strongly to TMPRSS2 S441A and R255Q, as assessed by flow cytometry. Addition of Camostat increased binding to WT TMPRSS2 (Fig. 3b, Extended Data Fig. 6a), indicating that the proteolytic activity of TMPRSS2 somehow interfered with our readout or decreased binding by degrading or shedding the bound spike. Alternatively, WT TMPRSS2's turnover might be faster than the mutants'. As expected, with a soluble SARS-CoV-2 spike, we detected binding to cells expressing ACE2 but not WT or mutant TMPRSS2 (Fig. 3b, Extended Data Fig. 6a, b), highlighting the different behaviors of HKU1 and SARS-CoV-2.

We then showed binding of the recombinant TMPRSS2 ectodomain to the HKU1A or B spikes by ELISA, but not to the SARS-CoV-2 spike (Fig. 3c). This indicates a direct interaction between TMPRSS2 and the HKU1 spike. Conversely, soluble ACE2 bound the SARS-CoV-2 but not the HKU1 spike by ELISA (Extended Data Fig. 6c). Due to the low yield of soluble WT TMPRSS2, we generated a soluble S441A mutant that could be obtained in amounts that allowed biophysical experiments. We expressed RBDs of the different viruses (residues 323-609 for HKU1A; 323-607 for HKU1B; 331-528 for SARS-CoV-2) to measure their affinity for S441A TMPRSS2 by biolayer interferometry (BLI). The RBDs from HKU1A and B interacted strongly with TMPRSS2, while the interaction of the SARS-CoV-2 RBD with TMPRSS2 was comparable to that of an irrelevant control protein (CD147) (Fig. 3d and Extended Data Fig. 6d-e). Using a range of S441A TMPRSS2 concentrations, affinity constants (K_d) of 334 nM and 137 nM were determined for HKU1A and B RBDs, respectively (Table 1, Extended Data Fig. 6d-e, SI 5, 6). The SARS-CoV-2 RBD bound to the ectodomain of ACE2 with a K_d of 92 nM (Extended Data Fig. 6f, Table 1).

HKU1 spike receptor binding motif

The residues W515 and R517 within the HKU1 RBD[19] have been reported to be critical for binding to an unknown cellular receptor[18]. We produced the recombinant HKU1B RBD with the W515A or R517A mutations. As assessed by BLI, the W515A mutation abrogated interaction with TMPRSS2, reaching response levels comparable to those obtained with a control protein, while the R517A mutation reduced binding by 2.8-fold (K_d=376 nM) (Fig. 3e, Extended Data Fig. 6g, h, Table 1, SI 5, 6). We also generated plasmids coding for the HKU1A

7

235 and HKU1B spikes with the W515A or R517A mutations. These mutants were correctly
236 expressed at the cell surface, as assessed by flow cytometry (Extended Data Fig. 6i) but they
237 lost their cell-cell fusion properties in the presence of TMPRSS2 (Fig. 3f). Their ability to
238 trigger pseudovirus entry was decreased by 2 to 3 logs, resulting in infection levels close to
239 background (Fig. 3g). Therefore, the conserved W515 and R517 residues within the HKU1A
240 and B RBDs are critical for binding to TMPRSS2, viral fusion and entry.

241

242 **Anti-TMPRSS2 VHHs block spike binding**
243 We then examined whether the anti-TMPRSS2 VHH inhibited the HKU1 receptor function
244 or the enzymatic activity of the protease. The 5 VHHs (A01, F05, A07, C11 and D01)
245 efficiently bound soluble S441A TMPRSS2 as assessed by BLI (Extended Data Fig. 1a and
246 Extended Data Table 1) and flow cytometry (Extended Data Fig. 7a). Three VHH (A07, C11
247 and D01) inhibited the HKU1B RBD–interaction with S441A TMPRSS2 measured by BLI
248 (Fig. 4a). The same three VHH reduced TMPRSS2 catalytic activity (Extended Data Fig. 7b).
249 Those nanobodies also inhibited HKU1A and B spike – TMPRSS2 mediated cell-cell fusion
250 (Fig. 4b, Extended Data Fig. 7c). We then examined their effect on viral entry independently
251 of their inhibition of the catalytic activity of TMPRSS2. They reduced pseudovirus infection of
252 293T cells expressing S441A TMPRSS2 in a dose-dependent manner (Fig. 4c, Extended Data
253 Fig. 7d). The two other nanobodies (A01 and F05), despite showing efficient binding to
254 TMPRSS2, did not interfere with its enzymatic activity and proviral roles (Fig. 4b, c and
255 Extended Data Fig. 7c-d), suggesting that they bind to regions different from those of three
256 active VHHs and that are not involved in HKU1 spike binding.

257

258 **Anti-TMPRSS2 VHH blocks HKU1 infection**
259 HKU1 does not grow in any cell line tested up to date but viral amplification in human
260 ciliated airway epithelial cell cultures has been reported[29,39,40]. We isolated an HKU1 virus from
261 a nasal swab of an individual suffering from a respiratory tract infection. To this end, we used
262 primary human bronchial epithelial cells (HBE cells) differentiated at the air/liquid interface
263 (ALI) for over 4 weeks. We first examined whether these cells were positive for TMPRSS2.
264 Immunofluorescence of HBE cells with the anti-TMPRSS2 VHH-A01-Fc revealed a
265 preferential staining of ciliated cells, with a positive signal accumulating at the cilia (Fig. 5a).
266 We then amplified the virus from the clinical sample by one passage on HBE cells. We observed
267 an increase of HKU1 viral RNA in apical culture supernatants, with concentrations peaking at
268 5×10^6 viral RNA copies/µL at 2-3 days post-infection (dpi) (Extended Data Fig. 8a).

8

269   Metagenomic sequencing of the viral supernatant identified a HKU1 genotype B (Extended

270   Data Fig. 8b), and no other virus was detected. For reasons that remain to be elucidated, our

271   attempts to further grow this HKU1B isolate in various cell lines, expressing WT or S441

272   TMPRSS2 were unsuccessful. However, the virus grew on a second passage on HBE cells,

273   indicating that it was infectious (Extended Data Fig. 8a).

274   We then asked whether the anti-TMPRSS2 nanobodies inhibited infection of HBE cells. We

275   preincubated target cells with the A07 VHH or a control nanobody and measured the spike

276   intensity by immunofluorescence 48 h post-infection (Fig. 5b). The A07 VHH strongly reduced

277   the appearance of infected cells, indicating that the spike binding and/or cleavage activities of

278   TMPRSS2 are necessary for a productive HKU1 infection.

279

280   **Discussion**

281   Here, we demonstrate that TMPRSS2 is a receptor for HKU1. TMPRSS2 triggers HKU1-

282   mediated cell-cell fusion, viral entry and binds with high affinity to both HKU1A and HKU1B

283   RBDs. The enzymatic activity of TMPRSS2 is required for HKU1-dependent cell-cell fusion

284   but not for entry of HKU1 pseudovirus. Two cathepsin inhibitors decrease HKU1A pseudovirus

285   infection mediated by the catalytically inactive TMPRSS2, but not by the wild-type protease.

286   This strongly suggests that after viral binding to TMPRSS2, viral particles expressing HKU1A

287   can either fuse at the plasma membrane if the protease is active or be internalized and processed

288   in the endosomal compartment when the protease is inactive. For HKU1B, other mechanisms

289   could be at play.

290   TMPRSS2 directly binds to HKU1 but not to SARS-CoV-2 spikes. The autocleavage of

291   TMPRSS2 is not required for binding. The affinity of HKU1A and HKU1B (K_d = 334 and 131

292   nM, respectively) is slightly below what we measured for the SARS-CoV-2 RBD interaction

293   with ACE2 (K_d = 92 nM). A conserved groove in a region of HKU1A and B spikes composed

294   of amino acid 505, 515, 517-521 and 528 has been proposed to be involved in binding to an

295   unknown receptor[18,19]. We show that the 515 and 517 residues of the spike are essential for

296   efficient binding to TMPRSS2, viral fusion and entry, thus adding evidence that this region

297   may be part of the RBM. Further structural studies are warranted to precisely map the amino-

298   acids and regions allowing the interactions between the spike and its receptor. Another protease,

299   Kalikrein 13 (KLK13) has been reported to cleave HKU1 spike[41]. Future work will help

300   addressing how KLK13 may modulate HKU1 interaction with TMPRSS2.

301   We further designed anti-TMPRSS2 VHH that inhibit TMPRSS2 binding to HKU1 spikes

302   and prevent cell-cell fusion and viral entry. The anti-TMPRSS2 nanobodies inhibit the

303 enzymatic activity of TMPRSS2 and hinder HKU1 pseudovirus entry using S441A TMPRSS2.
304 This strongly suggests that the spike binds close to the catalytic site of the enzyme. These
305 nanobodies confirmed the role of TMPRSS2 as a HKU1 receptor and provide useful tools to
306 interfere with TMPRSS2 function. TMPRSS2 also plays a role in the development of certain
307 cancers[42]. It will be worth studying how these nanobodies may target tumor cells or inhibit
308 infection of viruses relying on this enzyme, as an alternative to small molecule inhibitors[43].

309   Finally, we isolated an HKU1B live virus and report that TMPRSS2 is required for
310 productive infection of primary HBE cells, that are natural targets of the virus. It will be of
311 interest to further determine whether the HKU1 binding property, the enzymatic activity or
312 most likely both functions of TMPRSS2 are necessary to trigger HKU1 infection in these
313 primary cells. We were so far unable to amplify the virus in cell lines. Future work will be
314 necessary to understand which step of the viral life cycle is impaired in TMPRSS2+ cell lines,
315 or if another factor is required. It will be also worth examining whether soluble TMPRSS2,
316 known to be shed in the extracellular space, may interfere with HKU1 entry.

317   Human coronavirus receptors that have been identified so far and allow productive viral
318 entry are cell surface proteases. TMPRSS2 and other TTSP are known to prime human
319 coronaviruses for fusion by cleaving their spikes, generally after viral binding to target cells.
320 Of note, Omicron strains rely less on TMPRSS2 than previous SARS-CoV-2 lineages,
321 reflecting a constant adaptation of coronaviruses to their hosts[44]. Our study provides the first
322 evidence that TMPRSS2 also acts as a direct physical receptor for HKU1 entry, in addition to
323 its previously known role in cleaving the spike. ACE2 binding is an ancestral and evolvable
324 trait of sarbecoviruses[45,46] . TMPRSS2 binding may represent another parameter of coronavirus
325 evolution. Whether coronaviruses have lost affinity or sensitivity to TMPRSS2 during
326 evolution, or whether HKU1 has gained affinity for human or animal TMPRSS2 remains to be
327 determined. Our results highlight the critical role of TMPRSS2 and other proteases as
328 determinants of coronavirus tropism and pathogenesis[23].

329

Data availability

331   Raw sequence data (human reads removed) for the HKU1 virus were deposited in the
332 European Nucleotide Archive (ENA) portal (https://www.ebi.ac.uk/ena/) under bioproject
333 accession number PRJEB64017. The raw data of the main figures are available within the
334 supplementary information. The raw data of the extended data are available from the
335 corresponding author upon reasonable request.

336

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337   Supplementary Information is available for this paper.

338

339   Correspondence and requests for materials should be addressed to Olivier Schwartz.

340

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342

343   **Author contributions**

344   Experimental strategy design: NS, IF, CP, MMR, HM, FR, JB, OS

345   Data acquisition and analysis: NS, IF, CP, VM, MMR, EBS, FP, FGB, JP, CB, AMa, LG,

346   MOR, AMe, OA, HHW, MP, DD, ESL, JB

347   Vital materials and expertise: GCLF, MC, MD, VM, LVDH, PL

348   Manuscript writing: NS, JB, OS

349   Manuscript editing: NS, IF, CP, EBS, HM, FR, PL, JB, OS

350   All authors read and approved the final version of the manuscript.

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374

375 **Conflict of interest**

377

378

379 **References**

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514

Figure Legends

516
Figure 1. TMPRSS2 triggers HKU1 spike fusion. a. Alignment of HKU1A and B spikes.
NTD: N-terminal Domain. CTD: C-terminal domain. FP: Fusion-peptide. HR1/2: Heptad-
Repeat 1/2. TMD: Transmembrane Domain. Black: mismatch, white: deletion, boxed text
(Red): amino-acids of the putative RBM, S1/S2 and S2/S2' cleavage site. **b. TMPRSS2**
mediates HKU1 cell-cell fusion. 293T cells expressing either GFP1-10 or GFP11 (293T-GFP-
split cells) were transfected with HKU1 spike and TMPRSS2 or pQCXIP-empty control (Ctrl)
plasmids, fusion was quantified by measuring the GFP area after 20 h. Data are mean ± SD of
5 independent experiments. **c. Effect of a panel of proteases on cell-cell fusion.** 293T-GFP-
split cells were transfected with HKU1 spike and the indicated protease plasmids, fusion was
quantified by measuring the GFP area after 48 h. Data are mean ± SD of 3 independent
experiments. **d. TMPRSS2 has to be on the acceptor cell.** TMPRSS2 was transfected either
in donor cells and HKU1A spike or in acceptor cells. Fusion was quantified after 20 h. Left:
experimental design. Middle: representative images of GFP+ cells. Right: fusion quantification.
bar: 400 μm. Data are mean ± SD of 4 independent experiments. **e. Role of endogenous**
TMPRSS2. 293T donor cells expressing HKU1A spike were mixed with Caco2 acceptor cells
knocked-out or not for the *tmprss2* gene. Left: experimental design. Middle: representative
images of GFP+ cells. Right: fusion was quantified by measuring the GFP area after 20 h of
coculture. Data are mean ± SD of 3 independent experiments. **Statistical analysis:** b, d, e: Two-
sided unpaired t-test compared to control/parental condition. c: one Way ANOVA on non-
normalized data with Tukey's multiple comparisons.

537
Figure 2. Effect of wild-type and mutant TMPRSS2 on HKU1 cell-cell fusion and
pseudovirus infection. a. TMPRSS2 protein. TMPRSS2 is composed of a Transmembrane
Domain (TMD), a class A LDL receptor domain (LDLR), a Scavenger Receptor Cysteine-2
rich domain (SRCRD) and a serine peptidase. TMPRSS2 precursor autocleaves at R255-L256,
resulting in an active protease. **b. TMPRSS2 and spike cleavage.** WB of 293T transfected with
HKU1A spike and indicated TMPRSS2 mutants. One membrane was probed for S1, TMPRSS2
and actin, another for S2 and actin. For gel source data, see SI 1a, b. Representative blots of 3
independent experiments. Molecular weights: kDa. Arrows and # denote the uncleaved and
cleaved proteins, respectively. **c. Catalytically inactive TMPRSS2 mutants do not trigger**
HKU1 cell-cell fusion. Fusion of 293T-GFP split transfected with HKU1 spike and mutant
TMPRSS2 was quantified after 20 h and normalized to WT TMPRSS2. Ctrl: pQCXIP-Empty.
Left: HKU1A. Right: HKU1B. Data are mean ± SD of 3 independent experiments. **d.**
Catalytically inactive TMPRSS2 mutants mediate HKU1 pseudovirus infection. 293T
transfected with WT or mutant TMPRSS2 were infected by Luc-encoding HKU1 pseudovirus.
Luminescence was read 48 h post infection. Dotted line indicates background in non-infected
cells. Ctrl: pQCXIP-Empty. Data are mean ± SD of 6 (HKU1A) or 3 (HKU1B) independent
experiments. **e. HKU1 pseudovirus infection in cell lines stably expressing TMPRSS2.** Left:
U2OS cells. Middle: A549 cells. Right: Caco2 cells. The TMPRSS2 KO Caco2 cells were
stably transduced with indicated TMPRSS2. Data are mean ± SD of 3 (U2OS), 8 (A549), 4
(Caco2) independent experiments. **Statistical analysis:** c: one-way ANOVA on non-
normalized data with Dunnett's multi-comparison test compared to WT TMPRSS2 expressing
cells. d, e: one-way ANOVA on log-transformed data with Dunnett's multi-comparison test

560 compared to the untransfected (d), parental (e: U2OS and A549) or KO cells (e: Caco2),
561 ***p<0.0001.
562
563 **Figure 3. Analysis of HKU1 spike binding to TMPRSS2. a-b. Binding of soluble HKU1**
564 **spikes to 293T cells expressing TMPRSS2.** Cells were transfected with TMPRSS2 mutants
565 and incubated or not with 10 μM of Camostat. **a. TMPRSS2 levels** (assessed with a commercial
566 Ab) **b. Binding of soluble biotinylated trimeric spikes** measured by flow cytometry. One
567 representative experiment of 3 is shown. Ctrl: pQCXIP-Empty control plasmid. **c. Binding of**
568 **HKU and SARS-CoV-2 spikes on immobilized WT TMPRSS2 measured by ELISA.** Mean
569 of 2 independent experiments. **d. Binding of S441A TMPRSS2 to RBD coated receptors**
570 **quantified by Bio-layer interferometry (BLI).** One representative experiment of 4 is shown.
571 **e, f, g. Properties of W515A and R517A mutant HKU1 spikes.** Binding of TMPRSS2 to
572 wild type or mutant RBD coated receptors quantified by BLI. One representative experiment
573 of 4 is shown. **f.** 293T GFP-split cells were transfected with TMPRSS2 and the indicated HKU1
574 mutant spikes, fusion was quantified by measuring the GFP area after 24 h. **g.** 293T cells
575 expressing TMPRSS2 were infected by Luc-encoding mutant HKU1 pseudovirus.
576 Luminescence was read 48 h post infection. Dotted line indicates background. Data are mean
577 ± SD of 3 independent experiments. **Statistical analysis:** f: one-way ANOVA on non-
578 normalized data with Dunnett's multi-comparison test compared to WT TMPRSS2 expressing
579 cells. g: one-way ANOVA on log-transformed data with Dunnett's multi-comparison test
580 compared to WT Spike pseudotypes *p<0.05, **p<0.01, ***p<0.001.
581
582 **Figure 4. Anti-TMPRSS2 VHH nanobodies inhibit HKU1 binding to TMPRSS2, cell-cell**
583 **fusion and pseudovirus infection. a. Effect of VHHs on binding of HKU1B RBD to**
584 **TMPRSS2 measured by BLI**. One representative experiment of 2 is shown **b. Effect of VHHs**
585 **on HKU1-mediated cell-cell fusion.** 293T GFP-Split cells were transfected with TMPRSS2
586 and HKU1 spike in the presence of 1 μM of VHH, fusion was quantified 20 h later. Data were
587 normalized to the non-VHH treated condition (dotted line). Data are mean ± SD of 4
588 independent experiments. **c. Effect of VHHs on HKU pseudovirus infection**. 293T cells
589 transfected with S441A TMPRSS2 were treated with 1 μM VHH 2 h before infection.
590 Luminescence was read 48 h post infection. Data were normalized to the non-treated condition
591 for each virus (dotted line). Data are mean ± SD of 3 independent experiments. **Statistical**
592 **analysis**: b: one Way ANOVA data with Dunnett's multiple comparisons compared to non-
593 target VHH c: one Way ANOVA on log-transformed data with Dunnett's multiple comparisons
594 compared to non-target VHH *p<0.05, **p<0.01, ***p<0.001. p-values. Fusion, HKU1A: A07
595 0.0005, C11: 0.025, D01: 0.004, HKU1B: A07: 0.029, Infection: HKU1A: A01: 0.016, A07:
596 <0.0001, C11:0.0009, D01:<0.0001 HKU1B: A07/C11/D01: <0.0001
597
598
599 **Figure 5. Live HKU1 virus infection of human bronchial epithelial (HBE) cells. a.**
600 **TMPRSS2 staining of HBE cells.** Red: Phalloidin, Blue: DAPI, Green: TMPRSS2 stained
601 with VHH A01-Fc. Scale bars: top, 10 μm; bottom, 5 μm. Images are representative of 3
602 independent experiments. **b. Effect of the anti-TMPRSS2 VHH (A07) on HKU1 infection.**
603 The experimental design is represented. Infected cells were visualized with an anti-spike
604 antibody and scored. Representative images of spike staining 48 h post-infection are shown.
605 Spike pixel intensity in 5 random fields per experiment was measured and normalized to the
606 intensity in the infected but non-treated condition. Data are mean ± SD of 3 independent
607 experiments for infected conditions, and mean of 2 for uninfected condition. Scale bar: 20 μm.
608 **Statistical analysis:** Two-sided unpaired t-test compared to non-target VHH.

609

610 **Table 1:** Affinity (K_d) of the indicated RBD for TMPRSS2 or ACE2. ND (Non-Detectable)
611 denotes proteins for which interaction with the loaded sensor was similar or below the
612 interaction with an empty sensor.

613

614

615

616 **Methods**

617 **Plasmids**

618 Codon-optimized HKU1A (RefSeq: YP_173238.1) and B/C isolate N5P8, referred to
619 HKU1B (UniProtKB/Swiss-Prot: Q0ZME7.1) full spikes were ordered as synthetic genes
620 (GeneArt, Thermo Fisher Scientific) and cloned into a phCMV backbone (GeneBank:
621 AJ318514), by replacing the VSV-G gene. pQCXIP-Empty control plasmid was previously
622 described[31]. pQCXIP-BSR-GFP11 and pQCXIP-GFP1-10 were a kind gift from Yutaka Hata[47]
623 (Addgene plasmid #68716 and #68715). pCSDest-TMPRSS2 was a kind gift from Roger
624 Reeves[48] (Addgene plasmid # 53887). Mutations in the HKU1 spike and TMPRSS2 were
625 introduced using the NEB Q5 Side-Directed mutagenesis kit. Plasmids were sequenced before
626 usage. phCMV-HKU1-S-mNeonGreen and pCDEST-TMPRSS2-mScarlet-I were generated by
627 Gibson assembly. pCAGGS-based expression vectors N-terminal cMYC-epitope tagged
628 TMPRSS2, TMPRSS3, TMPRSS4, TMPRSS10, TMPRSS11A, TMPRSS11B, TMPRSS11D,
629 TMPRSS11E, TMPRSS11F and TMPRSS13 were a kind gift from Stefan Pöhlmann[34]. pLV-
630 EF1a-IRES-Hygro was a gift from Tobias Meyer (Addgene plasmid # 85134)[49]. pLV-EF1a-
631 DEST-IRES-Hygro was generated by Gibson assembly. pLV-TMPRSS2-Hygro was generated
632 by cloning TMPRSS2 from pCSDest-TMPRSS2 into pLV-EF1a-DEST-IRES-Hygro using
633 gateway cloning. pLV-TMPRSS2-S441A-Hygro and pLV-TMPRSS2-R255Q-Hygro were
634 generated by Q5 site directed mutagenesis (New England Biolabs).

635

636 **Cells**

637 HEK293T (293T), U2OS, VeroE6, A549 and Caco2/TC7 (Caco2) were from ATCC and
638 cultured in DMEM with 10% fetal bovine serum (FBS) and 1% penicillin/streptomycin (PS).
639 GFP-split cells were previously described[31] and cultured with 1 µg/mL of puromycin
640 (InvivoGen). Cells stably expressing TMPRSS2 were cultured with 100 µg/mL hygromycin.
641 Cells were routinely screened for mycoplasma. Cells were authenticated by genotyping
642 (Eurofins).

643

644 **Reagents**

645 SB412515 was purchased from Cayman Chemical, E64d and Camostat mesylate from

646 Sigma Aldrich, hydroxychloroquine from Merck, Neuraminidase (or Sialidase from

647 *Arthrobacter ureafaciens)* from Roche.

648

649 **Sequence alignments**

650 Alignments of HKU1 A and B spikes in Fig. 1a were performed using Protein Blast with

651 default settings (NCBI). Alignment figures were generated using the seqvisr package in R

652 (Github: 10.5281/zenodo.6583981).

653

654 **GFP-split fusion assay**

655 Cell–cell fusion assays were performed as previously described[31,50]. Briefly, 293T cells

656 stably expressing GFP1-10 and GFP11 were co-cultured at a 1:1 ratio (6×10^4 cells/well) and

657 transfected in suspension with Lipofectamine 2000 (Thermo) in a 96-well plate (uClear,

658 #655090) (10 ng of spike plasmid, indicated amounts of TMPRSS2 plasmids adjusted to 100 ng

659 DNA with pQCXIP-Empty). For Acceptor-Donor experiments, 293T GFP-split cells (GFP1-

660 10 and GFP11) were transfected separately in suspension with 500 ng of DNA (10% spike,

661 indicated amounts of TMPRSS2 plasmid adjusted to 500 ng with pQCXIP-Empty) for 30 min

662 at 37°C. Cells were washed twice and acceptor and donor cells were mixed and seeded at 6

663 $\times 10^4$ cells/well. For Caco2 KD experiments, Caco2 GFP11 cells were transfected with control

664 siRNA-directed against Luciferase: 5′-CGUACGCGGAAUACUUCGA-3′ or siGENOME

665 Human TMPRSS2 SMARTpool (#7113 - Horizon Discovery) at 50 nM using Lipofectamine™

666 RNAiMAX (Thermo Fisher Scientific) in a 6 well dish for 48 h. 293T GFP1-10 cells were

667 transfected with 10% of spike plasmid in a 6 well dish for 24 h. Caco2 KD or Caco2 KO cells

668 and 293T spike cells were mixed at a 1:1.5 ratio in a 96 well plate. The remaining Caco2 cells

669 were used for RNA extraction for qPCR. For all experiments, at 20 h post-transfection, images

670 covering 90% of the well surface, were acquired per well on an Opera Phenix High-Content

671 Screening System (PerkinElmer). The GFP area was quantified on Harmony High-Content

672 Imaging and Analysis Software.

673

674 **RNA Extraction, Reverse Transcription, and qPCR**

675 At 48 h post siRNA transfection, 5×10^5 Caco2 cells were lysed using RLT buffer

676 (QIAGEN) supplemented with 10 µL of β-mercaptoethanol. RNA extraction was performed

677 using the RNeasy plus mini kit (QIAGEN) according to the manufacturer's protocol. Reverse

678 transcription was performed using SuperScript II (Thermo Fisher Scientific) according to the

679 manufacturer's protocol. qPCR was performed using iTaq universal SYBR green supermix (Bio

680 Rad) on a QuantStudio 6 Real-Time PCR machine (Thermo Fisher Scientific). The following

681 primers were used: β-Tubulin forward: 5'-CTTCGGCCAGATCTTCAGAC-3', reverse: 5'-

682 AGAGAGTGGGTCAGCTGGAA-3'; TMPRSS2 forward: 5'-

683 GGGGATACAAGCTGGGGTTC-3', reverse: 5'-GATTAGCCGTCTGCCCTCAT-3'.

684

HKU1-spike-TMPRSS2 video microscopy

686 One million 293T cells were transfected either with 1 µg of pCDEST-TMPRSS2-scarlet-I or

687 phCMV-HKU1A S-NeonGreen plasmid in a 6-well plate using lipofectamine 2000 according

688 to the manufacturer's protocol. At 24 h post transfection, cells were harvested with PBS + 0.1%

689 EDTA and resuspended at 6 x 10^5 cells/mL in DMEM 10% FCS. The cells were mixed in

690 suspension at a 50/50 ratio and 100 µL were plated per well in a 96-well plate (uClear,

691 #655090). 30 min after plating, cells were imaged every 150 sec for 2.5 h at 37°C, 5% CO_2 on

692 an Opera Phenix High-Content Screening System (PerkinElmer).

693

Pseudovirus generation and infection

695 Pseudoviruses were produced by transfection of 293T cells as previously described[51].

696 Briefly, cells were cotransfected with plasmids encoding for lentiviral proteins, a luciferase

697 reporter, and the HKU1 spike plasmid. Pseudotyped virions were harvested 2 and 3 days after

698 transfection. Production efficacy was assessed by measuring infectivity or HIV Gag p24

699 concentration. For transfected cells (293T), infection was performed 24 h post-transfection, in

700 suspension using 10 ng of p24 and 2 x 10^4 cells in 100 µL. For the stable cell lines, infection

701 was performed on plated cells, with or without spinoculation (2 h at 2000 g), using 10-50 ng of

702 p24 per well and 2 x10^4 cells in 100 µL in a 96 well plate. The next day, 100 µL of media was

703 added. 48 h post-infection, 100 µL of media was carefully removed, and 100 µL of Bright-

704 Glo™ lysis buffer (ProMega) was added. After 10 min, luminescence was acquired using the

705 EnSpire in a white plate (PerkinElmer).

706

Isolation and characterization of a live HKU-1 virus

708 *Origin of the sample*

709 Respiratory material of sample MAL21 0303 was obtained in the winter of 2022-2023 at

710 Amsterdam UMC. Material was collected in Universal Transport Medium (Copan) and stored

711 at -80°C. Details on the disease of the patient are unknown as material were donated for research

712   anonymously. Presence of HCoV-HKU1 was determined via real time qPCR as described [52]
713   with primers: HKU1 forward: 5'-TCCTACTAYTCAAGAAGCTATCC-3'; HKU1 reverse 5'-
714   AATGAACGATTATTGGGTCCAC-3';   and   HKU1-probe   CY5   BHQ2
715   TYCGCCTGGTACGATTTTGCCTCA.

716

717   *HKU1 isolation and culture on Human nasal epithelium*
718   MucilAir™, reconstructed human nasal epithelium cultures that had been differentiated for
719   4 weeks were purchased from Epithelix (Saint-Julien-en-Genevois, France) and were cultured
720   in 700 µL MucilAir™ media on the basal side of the air/liquid interface (ALI) cultures and
721   monitored for healthy cilia movements. Cultures were kept at 34 °C under a 5% CO_2
722   atmosphere. One-hour prior to infection, mucus was removed from the apical side of the culture
723   by washing with HBSS (Gibco). For viral isolation, cells were infected with nasal swabs diluted
724   at a 1:4 ratio in universal transport medium (Copan) for 2 h at 34°C. Viral input was removed
725   and cells were washed three times with 200 µL of HBSS (Gibco). Apical side was harvested
726   twice every 24 h for 7 days by adding 200 µL HBSS for 10 min at 34°C and collecting the
727   liquid on the apical side and diluting it (1:1) in virus transport medium (Copan). The harvest
728   was centrifuged at 1000 g for 5 min to remove debris, 50 µL was used for qPCR and the
729   remaining samples were stored at -80°C. Passage 1 (P1) and P2 viral stocks were sequenced
730   with identical results.

731

732   *Sequencing of the HKU1 strain*
733   RNA was extracted from the cell supernatant using the QIAamp Viral RNA kit (Qiagen)
734   following the manufacturer instructions. Extracted RNA was treated with Turbo DNase
735   (Ambion) followed by ribosomal RNA[53]. RNA was reverse-transcribed into double stranded
736   cDNA using random hexamers, and libraries prepared using the Nextera XT kit (Illumina),
737   before sequencing on an Illumina NextSeq500 (2 × 75 cycles). Raw sequence data (human
738   reads removed) were deposited in the European Nucleotide Archive (ENA) portal
739   (https://www.ebi.ac.uk/ena/) under bioproject accession number PRJEB64017. To determine
740   the sequence of the acidic tandem repeat region of the genome, the region was amplified using
741   external   primers   (HKU1_ATR_L1   5'-ATGAAGCAATGGCCTCTCGT-3'   and
742   HKU1_ATR_R1 5'-CACAGAACGCAACCAACAGT-3'), before Sanger sequencing.

743   *Genome assembly*

744   Adapters and low-quality sequences of raw reads were removed using Trimmomatic v0.39[54].
745   We assembled the trimmed reads using megahit v1.2.9[55] with default parameters. The contigs
746   were queried against the NCBI non-redundant protein database using DIAMOND v2.0.4[56], to
747   look for potential contaminants in addition to the detected HKU1 genome. The Sanger data was
748   used with the assembled contigs to generate the final HKU1 scaffold, on which the trimmed
749   reads were mapped to generate the final consensus (Extended Data Fig. 8). The mapping data
750   was visually checked to confirm the accuracy of the obtained genome using Geneious Prime
751   2023. The sequence of the isolated virus was deposited in GenBank, ID: HCoV-
752   HKU1/NDL/IPP01/2022, accession number OR260091.

753   *Phylogenetic and recombination analysis*

754   All available complete HKU1 genome sequence data and metadata were retrieved from BV-
755   BRC (PMID: 36350631) (https://www.bv-brc.org/) in June 2023. Sequences were aligned
756   using MAFFT (v.7.467)[57] and the alignment was checked for accuracy using BioEdit v7.2.5.
757   We used a combination of six methods implemented in RDP4[58] (RDP, GENECONV, MaxChi,
758   Bootscan, SisScan, and 3SEQ) to detect potential recombination events in the newly reported
759   genome. The ModelFinder application[59], as implemented in IQ-TREE v2.0.6 (PMID:
760   25371430), was used to select the best-fitting nucleotide substitution model, and maximum-
761   likelihood phylogenies were inferred using complete genomes or the spike coding sequences.
762   Branch support was calculated using ultrafast bootstrap approximation with 1000 replicates[60].
763   The phylogenies were visualized using the auspice module from Nextstrain[61]. Interactive
764   phylogenies are available at: https://github.com/Simon-LoriereLab/HKU1

765

766   **Analysis of HKU-1 replication by RT qPCR**
767   Viral RNA was extracted from culture supernatants using the Quick-DNA/RNA Viral 96
768   Kit (Zymo) according to manufacturer's instructions. qPCR was run using the Luna Universal
769   Probe One-Step kit on a QuantStudio6 (Thermo) according to manufacturer's instructions using
770   the   following   primers   (HKUqPCR5:   5'-CTGGTACGATTTTGCCTCAA-3')   and
771   (HKUqPCR3: 5'-ATTATTGGGTCCACGTGATTG-3')[29] and TaqMan™ QSY probe (5'-
772   FAM-TTGAAGGCTCAGGAAGGTCTGCTTCTAA-QSY7-3'). A DNAString was used for
773   generating   a   standard   curve   (5'-
774   GGATCCTACTATTCAAGAAGCTATCCCTACTAGGTTTTCGCCTGGTACGATTTTGC
775   CTCAAGGCTATTATGTTGAAGGCTCAGGAAGGTCTGCTTCTAATAGCCGGCCAGG

776   TTCACGTTCTCAATCACGTGGACCCAATAATCGTTCATTAAGTAGAAGTAATTCT

777   AATTTTAGACATTCTGATTCTATAGTGAAACCTG-3')

778

779   **Human nasal epithelium VHH inhibition experiments**

780   One hour prior to infection, mucus was removed from the apical side of the culture by

781   washing with HBSS (Gibco). For viral infectivity assays, cells were incubated for 30 min with

782   50 μL of universal transport media (Yocon), containing monomeric non-target VHH93 (also

783   termed N-G9-3[62]) or anti-TMPRSS2 VHH A07 at 5 μM. Then $5x10^6$ viral copies were added

784   in 50 μL of universal transport medium for 2 h at 34°C (final VHH of concentration 2.5 μM).

785   Viral input was removed and cells were washed three times with 200 μL of HBSS (Gibco).

786   After 48 h, cells were fixed on the apical and basal sides with 4% PFA for 30 min. For imaging,

787   fixed cells were stained intracellularly with mAb10 at 1 μg/mL a pan anti-coronavirus spike

788   antibody[30], anti-TMPRSS2 VHH-A01-Fc at 6 μg/mL and phalloidin Atto-647 (Sigma-aldrich)

789   at 1:200 as described previously[63] and imaged using the LSM-700 confocal microscope (Zeiss).

790

791   **Image quantification**

792   To quantify the effect of the nanobodies on HKU1 infection of epithelia, the fluorescence

793   intensity of spike positive pixels of 5 fields (160 μm^2 each) spread over the surface of the sample

794   was measured using ImageJ-Fiji.

795

796   **CRISPR-Cas9 knock-out**

797   crRNAs TMPRSS2 (CGGATGCACCTCGTAGACAG) and pre-designed unspecific

798   crRNA used as control were ordered from Integrated DNA Technologies, IDT. crRNA and

799   tracrRNA were resuspended in IDT Duplex Buffer according to the manufacturer's instructions.

800   On the day of the nucleofection, duplexes were formed by mixing equimolar concentration of

801   crRNA and tracrRNA, followed by 5-min annealing at 95°C. 100 pmol of RNA duplexes were

802   then mixed (1:2) with 50 pmol TrueCut™ Cas9 Protein v2 (Thermo Fisher Scientific) for 10

803   min at RT to generate ribonucleoprotein (RNP) complexes. Caco2 were resuspended in SE cell

804   line buffer Solution (Lonza), mixed with RNP and Alt-R® Cas9 Electroporation Enhancer (90

805   pmol, IDT), and nucleofected in a 4D-Nucleofector™ System (Lonza) using the SE Cell line

806   4D-Nucleofector™ X Kit S (program DG-113). After nucleofection, cells were seeded in

807   DMEM 10% FBS. 48 h post transfection, cells were subcloned. Clones were screened for

808   TMPRSS2 knock-out by staining using VHH-A01-Fc and flow cytometry (immunostaining

809   section). Knock out was confirmed by PCR and sequencing the target region using the

810   following primers: forward (5'-AAGACGGAGGAGAAGGGTCA-3') and reverse (5'-

811   AGTTGTAGACACCTAGGGAGAA-3').

812

813   **Protein production**

814   *Construct design*

815   Spike, RBD, TMPRSS2 and ACE2 constructs were obtained from Genscript as codon-

816   optimized synthetic genes. Ectodomains from HKU1A (residues 14-1281) and B (residues 14-

817   1276) were cloned into pcDNA3.1(+), downstream of a murine Ig kappa signal peptide

818   (METDTLLLWVLLLWVPGSTG) and upstream of a thrombin cleavage site followed by a

819   His-tag. Spikes were stabilized by mutating the furin cleavage site (^{756}RRKRR^{760}>^{756}GGSGS^{760}

820   in HKU1A; ^{752}RRKRR^{756}>^{752}GGSGS^{756} in HKU1B;), two residues in the S2 subunit

821   (^{1071}AL^{1072}>^{1071}PP^{1072} in HKU1A; ^{1067}NL^{1068}>^{1067}PP^{1068} in HKU1B) and adding a Foldon

822   trimerization motif at the C-terminus. The ectodomain from the Wuhan SARS-CoV-2 Spike

823   (residues 1-1208) was cloned into pcDNA3.1(+) and was stabilized with 6 proline mutations

824   (F817P, A892P, A899P, A942P, K986P, V987P), as reported[64]. The furin site was also replaced

825   as above (^{682}RRAR^{685}>^{682}GSAS^{685}), a C-terminal Foldon motif was introduced, as well as

826   Hisx8, Strep, and Avi tags.

827   The RBDs (residues 323-609 for HKU1A; 323-607 for HKU1B; 331-528 for SARS-CoV-2

828   Wuhan) were cloned into pCAGGS (HKU1) or pcDNA3.1(+) (SARS-CoV-2), following a

829   murine immunoglobulin kappa signal peptide, and upstream of a thrombin cleavage site and *in-*

830   *tandem* Hisx8, Strep and Avi-tags. The WT TMPRSS2 ectodomain (residues 107-492)

831   followed by C-terminal tags (8xHis-tag and AviTag) was synthesized and cloned into

832   pcDNA3.1/Zeo(+) expression vector (Thermo Fisher Scientific). The TMPRSS2 ectodomain

833   with the S441A mutation was cloned into a modified pMT/BiP plasmid (Invitrogen; hereafter

834   termed pT350), which translates the protein in frame with an enterokinase cleavage site and a

835   double strep-tag at the C-terminal end. The ACE2 peptidase domain (residues 19-615) was

836   cloned in pcDNA3.1(+) with a murine immunoglobulin kappa signal peptide and a C-terminal

837   thrombin cleavage site followed by a Strep-tag. The coding sequences of the selected VHHs in

838   the vector pHEN6 were subcloned into a bacterial expression vector pET23 encoding a C

839   terminal His-tag using NcoI and NotI restriction sites.

840

841   *Protein expression and purification*

842   RBD, spike and ACE2-encoding plasmids were transiently transfected into Expi293F^{TM}

843   cells (Thermo-Fischer) using FectoPro DNA transfection reagent (PolyPlus) or

844   polyethylenimine (PEI) precipitation method, as previously described[65]. After 5 days at 37 °C,

845   cells were harvested by centrifugation and the supernatants were concentrated. The spike

846   proteins used for flow cytometry were purified from culture supernatants by high-performance

847   chromatography using the Ni Sepharose Excel Resin according to the manufacturer's

848   instructions (GE Healthcare) and dialyzed against PBS using Slide-A-Lyzer dialysis cassettes

849   (Thermo Fisher Scientific). The spike proteins used for ELISA were further purified by size-

850   exclusion chromatography (SEC) on a Superose6 10/300 column (Cytiva). Eluted fractions

851   were analyzed by SDS-PAGE and those containing bands of the expected molecular weight

852   were pooled, concentrated and further purified by SEC on a Superdex 200 10/300 column

853   (Cytiva). AviTagged SARS-CoV-2 tri-S used for flow cytometry was biotinylated using

854   Enzymatic Protein Biotinylation Kit (Sigma-Aldrich). HKU1A and HKU1B spike proteins

855   used for ELISA were biotinylated using EZ-Link™ Sulfo-NHS-biotinylation kit (Thermo

856   Fisher Scientific). The HKU1B RBD used for the BLI experiment with nanobodies was

857   biotinylated with the BirA biotin-protein ligase standard reaction kit (Avidity).

858   The pT350 plasmid encoding S441A TMPRSS2 was used to perform a stable transfection

859   on *Drosophila* S2 cells with the pCoPuro plasmid for puromycin selection. The cell line was

860   selected and maintained in serum-free insect cell medium (HyClone, GE Healthcare) containing

861   7 µg/mL puromycin and 1% penicillin/streptomycin. For protein production, the cells were

862   grown in spinner flasks until the density reached 10^7 cells/mL, at which point the protein

863   expression was induced with 4 µM CdCl2. After 6 days, the culture was centrifuged and the

864   supernatant was concentrated and used for affinity purification using a Streptactin column

865   (IBA). The eluate was concentrated and applied onto a Superdex 200 16/60 column (Cytiva)

866   equilibrated with 10 mM Tris-HCl (pH 8.0), 100 mM NaCl.

867   E. coli BL21pLysS cells were transformed with the plasmids encoding the different VHHs,

868   which were expressed in the cytoplasm after overnight induction with 0.5 mM IPTG at 16°C.

869   The cultures were centrifuged, the bacterial pellets were resuspended in 40 mL of lysis buffer

870   (20 mM Tris-HCl, 200 mM NaCl, 20 mM imidazole, pH 8.0) containing complete protease

871   inhibitor cocktail (Roche) and they were frozen at -80°C until used. On the purification day,

872   the resuspended pellets were thawed, sonicated (15 min, 9s on-pulse, 5s off-pulse), centrifuged

873   and loaded onto a HisTrap column. Bound proteins were eluted with a linear gradient of buffer

874   B (20 mM Tris-HCl, 200 mM NaCl, 500 mM imidazole, pH 8.0) and analyzed by SDS-PAGE.

875   Fractions with higher purity were pooled, concentrated and further purified by SEC on a

876 Superdex 75 16/60 column (Cytiva) pre-equilibrated in 10 mM Tris-HCl, 100 mM NaCl, pH
877 8.0.

878   The purity of the final protein samples was analyzed by SDS-PAGE followed by Coomasie
879 Blue staining or silver staining. For gels, see SI 2.

880

881 **Flow cytometry**

882   For Spike binding, 293T cells were transiently transfected with TMPRSS2 and maintained
883 in the presence or absence of Camostat (10 μM) for 24 h. The cells were incubated with soluble
884 biotinylated spike diluted in MACS buffer (PBS, 5 g/L BSA, 2 mM EDTA) at 2 μg/mL for
885 30 min at 4°C. The cells were then washed twice with PBS and then incubated with Alexa Fluor
886 647-conjugated streptavidin (Thermo Fisher Scientific, S21374, 1:400) for 30 min at 4°C. The
887 cells were washed once with PBS and fixed with 4% paraformaldehyde. The results were
888 acquired using an Attune Nxt Flow Cytometer (Life Technologies, software v3.2.1).
889 Transfection efficiency for TMPRSS2 was assessed by using either a commercial anti-
890 TMPRSS2 antibody (for the experiments performed at the initiation of the study), the anti-
891 TMPRSS2 monomeric VHH or the dimeric VHH A01-Fc (see below).

892   The staining with the commercial anti-TMPRSS2 antibody was performed on fixed cells by
893 staining intracellularly with rabbit anti-TMPRSS2 (Atlas HPA035787), for 30 min at RT in
894 PBS/BSA/Azide/0.05% Saponin followed by a Alexa Fluor 647 Goat anti-Rabbit antibody
895 (Thermo Fisher Scientific, A-21245, 1:500).

896   For the spike, transfection efficiency was measured at the surface of live cells using mAb10
897 diluted in MACS buffer for 30 min at 4°C, and a human secondary IgG. mAb10 is an antibody
898 generated from a SARS-CoV-2 infected patient which cross-reacts with HKU1[30].

899   Surface expression of TMPRSS2 was assessed on live cells by staining with anti-TMPRSS2
900 VHH-A01-Fc (described in the study) at 1 μg/mL, for 30 min at 4°C in MACS buffer, followed
901 by staining with Alexa Fluor 647-conjugated Goat anti-Human antibody (Thermo Fisher
902 Scientific, A-21445, 1:500). The control VHH Fc ctrl (R3VQFc) recognizes an unrelated
903 protein (phosphorylated Tau protein)[62].

904   The monomeric VHHs were used at 0.5 μg/mL in MACS buffer for 30 min at 4°C, staining
905 was revealed using a coupled anti-His antibody (R&D Systems, IC0501R, 1:1000).

906   Transfection efficiency for myc-tagged constructs was assessed on fixed cells by staining
907 intracellularly with mouse anti-c-myc antibody, clone 9E10 (Thermo - M4439), for 30 min at
908 RT in PBS/BSA/Azide/0.05% Saponin followed by an Alexa Fluor 647-conjugated Goat anti-
909 Mouse antibody (Thermo Fisher Scientific, A-21242, 1:500). Transfection efficiency of APN

910   (CD13) and DPP4 (CD26) was assessed on live cells by surface staining in MACS buffer with

911   CD13-PE (130-120-312, Miltenyi Biotec, 1:50) and CD26-PE (130-126-41, Miltenyi Biotec,

912   1:50) for 30 min at 4°C. The cells were washed twice with PBS and fixed with 4%

913   paraformaldehyde. The results were acquired using an Attune Nxt Flow Cytometer (Life

914   Technologies). Gating strategies are described in SI 3.

915

916   **Sialic acid staining**

917   Cells were harvested using PBS/0.1% EDTA for 5 min at 37°C, washed in PBS and stained

918   1 h at 4°C in PBS/1% SVF containing either 10 µg/mL Sambucus Nigra Lectin-FITC (Lectin

919   NSA) (L32479 – Thermo) or 2.5 µg/mL recombinant mouse Siglec E-Fc (551504 –

920   BioLegend). Cells were washed twice in PBS. Lectin-stained cells were fixed for 10 min in 4%

921   paraformaldehyde. Siglec-E-Fc stained cells were further incubated with Alexa Fluor 647-

922   conjugated Goat anti-Human antibody (Thermo Fisher Scientific, A-21445, 1:500) for 30 min

923   at 4°C before being fixed for 10 min in 4% paraformaldehyde.

924

925   **ELISA assay**

926   ELISAs were performed as previously described[66]. Briefly, high-binding 96-well ELISA

927   plates (Costar; Corning) were coated overnight with 250 ng/well of purified TMPRSS2 or

928   ACE2. After washing with 0.05% Tween 20-PBS (washing buffer), the plates were blocked for

929   2 h with 2% BSA, 1 mM EDTA, 0.05% Tween 20-PBS (Blocking buffer), washed, and

930   incubated with serially diluted soluble biotinylated spike proteins. Recombinant spike proteins

931   were tested at 100 µg/mL, and at 7 consecutive 1:2 dilutions in PBS. After washings, the plates

932   were revealed by incubation for 1 h with HRP-conjugated streptavidin (BD Biosciences) in

933   blocking buffer and by adding 100 µL of HRP chromogenic substrate (ABTS solution,

934   Euromedex) after washing steps. Optical densities were measured at 405 nm (OD_{405nm}) and

935   background values given by incubation of PBS alone in coated wells were subtracted.

936   Experiments were performed using HydroSpeed microplate washer and Sunrise microplate

937   absorbance reader (Tecan).

938

939   **BLI assay**

940   Affinity of recombinant RBDs towards the purified ectodomains of S441A TMPRSS2 or

941   ACE2 was assessed in real-time using a bio-layer interferometry Octet-Red384 device (Pall

942   ForteBio). Nickel-NTA capture sensors (Sartorius) were loaded for 10 min at 1000 rpm shaking

943   speed with the Wuhan RBD at 100 nM or the HKU1A/B RBDs at 200 nM in PBS. The sensors

26

944   were then blocked with PBS containing BSA at 0.2 mg/mL (assay buffer) and were incubated

945   at 1000 rpm with two-fold serially diluted concentrations (800 nM to 3.12 nM) of S441A

946   TMPRSS2 or ACE2 ectodomains in assay buffer. Association and dissociation were monitored

947   for 300 s and 240 s, respectively. Measurements for a reference sensor were recorded using a

948   sensor loaded with an unrelated protein (CD147) that was dipped at each analyte concentration.

949   A sample reference measurement was recorded from a sensor loaded with either RBD and

950   dipped in the assay buffer. Specific signals were calculated by double referencing, substracting

951   nonspecific signals obtained for the sensor and sample references from the signals recorded for

952   the RBD-loaded sensors dipped in S441A TMPRSS2 solutions. The steady-state signal was

953   plotted against the analyte concentration and the curve was fitted assuming a 1:1 binding model.

954   The affinity of the nanobodies for the S441A TMPRSS2 ectodomain was determined using

955   a similar procedure. Nickel-NTA capture sensors were loaded with each nanobody at 100 nM

956   in PBS, then blocked with assay buffer and incubated at 1000 rpm with two-fold serially diluted

957   concentrations (400 nM to 3.12 nM) of S441A TMPRSS2. Association and dissociation were

958   monitored for 240 s and 180 s, respectively. A sample reference measurement was recorded

959   from a sensor loaded with each nanobody and dipped in the assay buffer. Association and

960   dissociation profiles were fitted assuming a 1:1 binding model.

961   Experiments to identify anti-TMPRSS2 nanobodies that block binding to the HKU1 RBD

962   were performed by immobilizing the biotinylated HKU1B RBD on Streptavidin capture

963   sensors. They were blocked in assay buffer and dipped into solutions containing a pre-incubated

964   mixture of TMPRSS2 S441A (200 nM) and a nanobody (400 nM). The signal corresponding

965   to the association was recorded.

966

967   **TMPRSS2 enzymatic activity**

968   Enzymatic activity was measured using BOC-QAR-AMC (R&D Systems, ES014), a

969   substrate of TMPRSS2 that fluoresces when cleaved. For wild type and mutant TMPRSS2,

970   cells were transfected in a black bottom 96 well plate as described above. After 24 h, media

971   was replaced with 100 µL FCS free, phenol red free media, containing 100 µM of fluorogenic

972   substrate. Indicated concentration of inhibitors were added. When the assay was performed

973   with soluble TMPRSS2, 60 nM of soluble protein was added to the well and mixed with VHH

974   nanobodies for 15 min, before adding 100 µM of fluorogenic substrate.

975

976   **Western Blot**

977   Cells were lysed in TXNE buffer (1% Triton X-100, 50 mM Tris–HCl (pH 7.4), 150 mM

978   NaCl, 5 mM EDTA, 1X Roche cOmplete protease inhibitors) for 30 min on ice. Equal amounts

979   (10 μg) of cell lysates were analyzed by Western blot. The following antibodies were diluted

980   in WB buffer (PBS, 1% BSA, 0.05% Tween, 0.01% Na Azide): rabbit anti-human TMPRSS2

981   (Atlas antibodies cat# HPA035787, 1:1,000), mouse anti-beta actin (Abcam, 60008-1-Ig,

982   1:2,000), rabbit anti-HKU1 S1 polyclonal antibody (Thermofisher Scientific Cat #PA5-120768,

983   1:2,000) and rabbit anti-HKU1 S2 polyclonal antibody (Thermofischer Scientific #PA5-

984   120769, 1:1,000). Species-specific secondary DyLight-coupled antibodies were used

985   (1:10,000) and proteins were revealed using a Licor Imager. Images were processed using

986   Image Studio Lite software v5.2.5.

987

988   **Nanobody isolation and production**

989   **Alpaca immunization**

990   Animal procedures were performed according to the French legislation and in compliance

991   with the European Communities Council Directives (2010/63/UE, French Law 2013-118,

992   February 6, 2013). The Animal Experimentation Ethics Committee of Pasteur Institute

993   (CETEA 89) approved this study (2020-27412). One young adult male alpaca (Lama pacos)

994   was immunized at days 0, 17, and 24 with 150 μg of S4441A TMPRSS2. The immunogen was

995   mixed with Freund complete adjuvant for the first immunization and with Freund incomplete

996   adjuvant for the following immunizations. The immune response was monitored by titration of

997   serum samples by ELISA on coated TMPRSS2. The bound alpaca antibodies were detected

998   with polyclonal rabbit anti-alpaca IgGs[67].

999

1000   **Library construction and phage display**

1001   The blood of the immunized animal (about 300 mL) was collected and peripheral blood

1002   lymphocytes were isolated by centrifugation on a Ficoll (Cytiva, Velizy, France) discontinuous

1003   gradient and stored at −80°C until further use. Total RNA and cDNA were obtained as

1004   previously described[67]. The VHH repertoires were amplified from the cDNA by two successive

1005   PCR reactions and the VHH fragments were cloned into the SfiI/NotI restriction sites of pHEN6

1006   phagemid vector[62]. The selection of specific phage-VHHs was performed by phage display. A

1007   large number of phage-VHHs (10^{13}) was used to perform 3 rounds of panning. Briefly, Phage-

1008   VHHs were incubated for 1 h with TMPRSS2 that has been previously coated on an

1009   immunotube (Nunc). To remove non-specific binders, an extensive washing procedure was

1010   performed and specific phage-VHHs were eluted in 100 mM triethylamine (TEA). *E.coli* TG1

28

1011 at exponential growth phase were then infected with eluted phage-VHHs. Phage-VHHs were
1012 produced from individual colonies and binding of the phages to TMPRSS2 on plate was
1013 revealed with an anti-M13 monoclonal antibody conjugated to peroxidase (Abcam). The VHH
1014 nucleotide sequences were determined using M13-40 primer (Eurofins, Ebersberg, Germany).
1015

1016 **Production of VHHs**
1017 The coding sequences of the selected VHHs in the vector pHEN6 were subcloned into a
1018 bacterial expression vector pET23 encoding a C terminal His tag using NcoI and NotI
1019 restriction sites. Sequences of the VHH are available in SI 4. Transformed *E. coli* BL21pLysS
1020 cells expressed VHHs in the cytoplasm after overnight induction with 0.5 mM IPTG at 16°C.
1021 Purified VHHs were isolated on Co++ affinity columns from cytoplasmic extracts treated by
1022 10 U/mL Benzonase Nuclease (Merck) and Complete protease inhibitor (Roche), according to
1023 the manufacturer's instructions, followed by size exclusion chromatography (SEC) with a
1024 Superdex 75 column (Cytiva).
1025

1026 **Production of dimeric VHH-Fc**
1027 VHHs' engineered genes were cloned into a pFUSE-derived vector (InvivoGen); this vector
1028 harbors a human IgG1-Fc domain. Consequently, the VHH was expressed as a Fc-fusion
1029 bivalent antibody. The vector was used to transform Expi293F mammalian cells
1030 (ThermoFisher), and protein expression was carried out according to manufacturer's
1031 recommendations. Protein was purified from the expression medium by affinity
1032 chromatography on a 1 mL protein G column (Cytiva). After sample application, the column
1033 was washed with 20 column volumes of PBS and the protein was subsequently eluted with 10
1034 column volumes of PBS supplemented with 0.1 M Glycine (pH=2.3). Affinity-eluted VHH-Fc
1035 were finally polished on a HiLoad 16/600 Superdex 200pg Pre-packed column (Cytiva) using
1036 PBS buffer[68]
1037

1038 **Statistical analysis**
1039 Flow cytometry data were analyzed with FlowJo[TM] v10.8 software (BD Life Science).
1040 Calculations were all performed with Microsoft Excel 365. GraphPad Prism 9 for Mac was
1041 used to generate figures and for statistical analysis (GraphPad Software). Statistical significance
1042 between different conditions was calculated using the tests indicated in the corresponding figure
1043 legends.
1044

Illustrations

All illustrations were generated by using Inkscape. They can be re-used if cited properly.

Additional references

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1115
1116
1117
1118 **Extended Data**
1119
1120
1121 **Extended Data Figure 1. a. Binding of the 5 anti-TMPRSS2 VHH on recombinant**
1122 **TMPRSS2 measured by BLI. b, c. Comparison of one commercial TMPRSS2 antibody**
1123 **and of the dimeric anti-TMPRSS2 VHH A01-Fc.** 293T cells were transfected with WT
1124 TMPRSS2. 24 h later, cells were analysed by flow-cytometry. Staining with the commercial
1125 antibody was performed on fixed cells **(b)** while surface staining with the VHH was performed
1126 on live cells **(c)**.
1127
1128
1129 **Extended Data Figure 2. Effect of TMPRSS2 and other proteases on HKU1 cell-cell**
1130 **fusion. a, b. Surface expression and fusogenic activity of HKU1 spikes. a.** 293T cells were
1131 transfected with plasmids encoding for HKU1A or HKU1B spikes and stained 24 h later with
1132 mAb10, a pan anti-coronavirus spike antibody. Data are representative of 3 independent
1133 experiments**. b.** Cell-cell fusion mediated by HKU1A or HKU1B spikes. 293T GFP-Split cells
1134 were transfected with HKU1 spikes and TMPRSS2, fusion was visualized by the appearance
1135 of GFP+ cells. Data are representative of 6 independent experiments**.** Scale bar: 400 μm **c. Cell-**
1136 **cell fusion mediated by the SARS-CoV-2 spike.** 293T GFP-Split cells were transfected with
1137 SARS-CoV-2 spike, in the presence of ACE2 or TMPRSS2, fusion was visualized by the
1138 appearance of GFP+ cells. Data are mean ± SD of 3 independent experiments **d. U2OS cell-**
1139 **cell fusion mediated by HKU1A spike.** U2OS GFP-Split cells were transfected with HKU1A
1140 spike and TMPRSS2, fusion was visualized by the appearance of GFP+ cells 24 h later. Data

1141 are mean ± SD of 3 independent experiments. **e. Expression levels of myc-tagged proteases.**
1142 293T cells were transfected with a control plasmid or the indicated myc-tagged TMPRSS
1143 constructs and stained 24 h later with myc antibody 9E10. Left: Representative dot plots. Right:
1144 Percentage of positive cells. Data are mean ± SD of 3 independent experiments. **f. Surface**
1145 **expression of tagged and untagged TMPRSS2.** 293T cells were transfected with WT
1146 TMPRSS2 (TMPRSS2-Untagged) or a myc-tagged TMPRSS2 and surface stained for
1147 TMPRSS2 using VHH-A01-Fc. Left: Representative dot plots. Right: Percentage of positive
1148 cells. Data are mean ± SD of 3 independent experiments. **g, h, i . Surface expression of APN,**
1149 **DPP4 and ACE2.** 293T cells were transfected with APN, DPP4 or ACE2 plasmids, and surface
1150 stained with the respective antibodies 24 h later. Left: Representative dot plots. Right:
1151 Percentage of positive cells. Data are mean ± SD of 3 (TMPRSS2, APN, DPP4) or 4 (ACE2)
1152 independent experiments. **j. Images of time lapse microscopy of HKU1-mediated cell-cell**
1153 **fusion** (extracted from Supp. video 1). 293T cells were transfected either with TMPRSS2-
1154 scarlet-I or HKU1A S-NeonGreen. After 24 h, cells were mixed and imaged every 2.5 min for
1155 2 h at 37°C.
1156
1157 **Extended Data Figure 3. Knock-out and silencing of TMPRSS2 in Caco2 cells. a. Linear**
1158 **diagram of the organization of the TMPRSS2 gene**. The CRISPR-Cas9 targeting site is
1159 underlined and the proto-spacer recognition motif (PAM) is in bold. Rectangles represent
1160 exons, black for 5' and 3' untranslated regions, gray for coding regions. **b. Sequence analysis**
1161 **of the knock-out Caco2 clone.** Both alleles compared to the original wild-type sequence are
1162 shown. The knockout clone harbors an out-of-frame deletion and an insertion, resulting in a
1163 frameshift on both alleles. **c. Validation of TMPRSS2 knockout by TMPRSS2 surface**
1164 **staining.** Representative dot plots of VHH anti-TMPRSS2 (VHH-A01-Fc) surface staining of
1165 a WT and KO Caco2 obtained following CRISPR gene targeting. **d. Role of endogenous**
1166 **TMPRSS2 on cell-cell fusion assessed by siRNA.** 293T donor cells expressing HKU1A spike
1167 were mixed with Caco2 acceptor cells, silenced or not for TMPRSS2. Left: experimental
1168 design. Middle: relative expression of TMPRSS2 in Caco2 cells, assessed by RT-qPCR. Data
1169 were normalized to *β-Tubulin* levels. Relative mRNA expression normalized to siCtrl condition
1170 ($2^{-\Delta\Delta CT}$) was plotted. Right: fusion was quantified by measuring the GFP area after 20 h of
1171 coculture. Data are mean ± SD of 3 independent experiments. Statistical analysis: two-sided
1172 unpaired t-test compared to siCtrl cells. ***p<0.0001.
1173
1174 **Extended Data Figure 4. Effect of mutant TMPRSS2 on cell-cell fusion and pseudovirus**
1175 **infection a. Enzymatic activity of WT and mutant TMPRSS2.** 293T cells were transfected
1176 with WT and indicated TMPRSS2 mutants. 24 h post transfection, the catalytic activity was
1177 assessed using BoC-QAR-AMC fluorogenic substrate. Data are mean ± SD of 4 independent
1178 experiments. Statistical analysis: a: one-way ANOVA with Dunnett's multiple comparisons
1179 compared to Ctrl cells (transfected with pQCXIP-Empty). **p<0.01. **b. Effect of TMPRSS2**
1180 **on HKU1 spike expressed on adjacent cells.** 293T cells were transfected either with HKU1A
1181 spike or with the different TMPRSS2. 20 h post-transfection, cells were mixed at a 1:1 ratio,
1182 and let to settle. 3 or 6 h post-mixing, cells were harvested and lysed for WB. One membrane
1183 was probed for S1, TMPRSS2 and actin, another membrane was probed for S2 and actin. For
1184 gel source data, see SI 1c, d. Representative blots of 2. Molecular weights: kDa. The arrows
1185 and # denote the uncleaved and cleaved protein products, respectively. **c. Surface levels of WT**
1186 **and mutant TMPRSS2.** 293T cells were transfected with the indicated doses of TMPRSS2
1187 plasmid. 18 h post-transfection they were stained intracellularly for TMPRSS2 using the
1188 commercial antibody. Left: % of TMP positive cells. Right: Median fluorescent intensity
1189 (MFI). #: indicates the chosen plasmid ratios to achieve similar TMPRSS2 levels with WT and

1190   indicated mutants. Data are mean ± SD of 3 independent experiments. **d. Comparison of the**
1191   **anti-TMPRSS2 commercial antibody and VHH staining in 293T cells.** 293T cells were
1192   transfected with WT, R255Q and S441A TMPRSS2 plasmids. Cells were stained 24 h later
1193   with the indicated antibodies and analysed by flow cytometry. One experiment representative
1194   of 3 is shown. Light grey curves correspond to staining with control antibodies or VHH.
1195   Parental: untransfected cells. **e. Effect of WT and mutant TMPRSS2 on SARS-CoV-2**
1196   **pseudovirus infection.** 293T cells expressing ACE2 were transfected with WT and indicated
1197   TMPRSS2 mutants. 24 h later, cells were infected by Luc-encoding SARS-CoV-2 pseudovirus.
1198   Luminescence was measured after 48 h. Data are mean ± SD of 4 independent experiments.
1199   Statistical analysis: RM one-way ANOVA with Geisser-Greenouse correction on log-
1200   transformed data, with Dunnett's multiple comparisons compared to Ctrl cells (transfected with
1201   pQCXIP-Empty). **p<0.01. **f, g. Effect of SB412515, E64d or hydroxychloroquine (HCQ)**
1202   **on f. HKU1A or g. HKU1B pseudovirus infection**. 293T cells expressing WT or S441A
1203   TMPRSS2 were incubated for 2 h with the indicated drugs, before infection with HKU1A or
1204   HKU1B pseudoviruses. Luminescence was read 48 h post infection. Left: SB412515. Middle:
1205   E64d. Right: HCQ. Data are mean ± SD of 3 (E64d, HKU1B), 4 (E64d HKU1A, SB142515
1206   HKU1B), 5 (HCQ HKU1A) or 6 (HCQ HKU1B, SB412515 HKU1A) independent
1207   experiments. Statistical analysis: RM two-way ANOVA with Geisser-Greenouse correction on
1208   non-normalized log transformed data, with Dunnett's multiple comparisons compared to the
1209   non-treated conditions. **h, i. Surface levels of TMPRSS2 in different cell lines stably**
1210   **expressing WT or S441 TMPRSS2.** Cells were stained for TMPRSS2 using VHH-A01-Fc
1211   and analyzed by flow cytometry. Representative histograms are shown. **h.** Left: U2OS. Right:
1212   A549. Light grey: cells stained with a non-target control VHH-Fc. Dark grey: Unmodified
1213   parental cell lines. Dark and light blue: Cells transduced with either TMPRSS2 or TMPRSS2
1214   S441A mutant. **i.** Caco2. Light grey: cells stained with a non-target control VHH-Fc. Blue:
1215   Unmodified parental cell line. Dark Grey: TMPRSS2 KO Caco2. Dark and light blue:
1216   TMPRSS2 KO caco2 stably transduced with TMPRSS2 WT or S441A mutant expression
1217   vectors. **j. Effect of Camostat on endogenous TMPRSS2 in Caco2 cells.** Caco2 cells were
1218   incubated in the presence of 100 μM Camostat for 2 h, before infection with HKU1A, HKU1B,
1219   or SARS-CoV-2 (D614G or Delta) pseudovirus. Data are normalized to the infection in the
1220   absence of the drug. Data are mean ± SD of 3 (SARS-CoV-2) or 4 (HKU1) independent
1221   experiments. Statistical analysis: RM two-way ANOVA on non-normalized log transformed
1222   data, with Sidak's multiple comparisons compared to the non-treated conditions. **k.**
1223   **Susceptibility of Vero E6 and Vero E6-TMPRSS2 cells to HKU1 pseudovirus infection.**
1224   Left: pseudovirus infection. Right: TMPRSS2 surface levels. Dark grey: Parental cells. Dark
1225   blue: Cells transduced with TMPRSS2. Data are mean ± SD of 4 independent experiments.
1226
1227   **Extended Data Figure 5. Effect of neuraminidase on HKU1 pseudovirus infection.** U2OS-
1228   TMPRSS2 cells were treated with indicated concentration of neuraminidase from *Arthrobacter*
1229   *ureafaciens* for 24 h**. a. HKU1A and HKU1B pseudovirus infection in neuraminidase**
1230   **treated cells.** Cells were infected with HKU1 A or B pseudoviruses. Luminescence was read
1231   48 h post infection. Data were normalized to the non-treated condition. Data are mean ± SD of
1232   3 (4 mU/mL) or 4 (0, 20, 100 mU/mL) independent experiments. Statistical analysis: Mixed-
1233   effect analysis with Geisser-Greenhouse corrections (handles missing values) on non-
1234   normalized log transformed data, with Dunnett's multi-comparison test compared to non-
1235   treated cells. **b. Surface levels of TMPRSS2 in neuraminidase treated cells.** Left: % of TMP
1236   positive cells. Right: Median fluorescent intensity (MFI). Data are mean of 2 independent

1237 experiments. **c. Sambucus Nigra Lectin (SNA) binding on neuraminidase treated cells.**
1238 Treated cells were stained with fluorescent Lectin SNA which preferentially binds α-2,6- over
1239 α-2,3 linked sialic acids. Left: Representative histograms. Right: MFI. Data are mean of 2
1240 independent experiments. **d. Siglec-E binding on neuraminidase treated cells.** Treated cells
1241 were stained with recombinant Siglec-E-Fc protein which preferentially binds α2,8- over α2,3-
1242 and α2,6-linked sialic acids. Left: Representative histograms. Right: MFI. Data are mean ± SD
1243 of 3 independent experiments.
1244
1245 **Extended Data Figure 6. Binding of HKU and SARS-CoV-2 spikes to TMPRSS2 or ACE2.**
1246 **a. Binding of the indicated recombinant spikes to 293T cells expressing TMPRSS2.** Cells
1247 were transfected with WT or mutant TMPRSS2 and incubated or not overnight with 10 μM of
1248 Camostat. The spikes were then incubated for 0.5 h and their binding was revealed with
1249 streptavidin-647 and measured by flow cytometry. The % of cells binding to TMPRSS2 was
1250 quantified. Data are mean ± SD of 3 (HKU1A) or 4 (HKU1B, SARS-CoV-2) independent
1251 experiments. Two Way ANOVA with Dunnett's multiple comparisons compared to control
1252 cells with or without Camostat. Exact p-values: HKU1A: TMPRSS2 WT-: *0.029, TMPRSS2
1253 WT+:***<0.0001, TMPRSS2 R255Q-: **0.0010, TMPRSS2 R255Q+: **0,0013, TMPRSS2
1254 S441A-: ***0,0001, TMPRSS2 S441A+: ***<0.0001. HKU1B: ***<0.0001. **b. Binding of**
1255 **the indicated recombinant spikes to 293T cells expressing ACE2.** Cells were transfected
1256 with ACE2. The spikes were then incubated for 0.5 h and their binding was revealed with
1257 streptavidin-647 and measured by flow cytometry. The % of cells binding to ACE2 was
1258 quantified. Data are mean of 2 independent experiments. **c. Binding of the indicated soluble**
1259 **spikes on immobilized ACE2 measured by ELISA. d. Binding of S441A TMPRSS2 to**
1260 **HKU1A, HKU1B or SARS-CoV-2 RBD measured by BLI.** The response was measured at
1261 the indicated concentrations of spikes. Left: HKU1A. Middle: HKU1B. Right: SARS-CoV-2.
1262 One representative experiment of 4 is shown. **e. Determination of the affinity of HKU1A and**
1263 **B RBD for TMPRSS2 using the steady state method.** Circles: Experimental values. Black:
1264 Fitting of the experimental data **f. Binding of ACE2 to SARS-CoV-2 or HKU1B RBD**
1265 **quantified by BLI,** at different concentrations of spikes. **g. Binding of S441A TMPRSS2 to**
1266 **HKU1B mutants.** Response was measured by BLI at different concentrations of spikes. Left:
1267 HKU1B RBD mutant W515A. B: HKU1B RBD mutant R517A. **h. Determination of the**
1268 **affinity of HKU1B-R517A RBD for TMPRSS2 using the steady state method.** Circles:
1269 Experimental values. Black: Fitting of the experimental data. **i. Cell surface levels of WT and**
1270 **mutant HKU1 spikes.** 293T were transfected with the indicated WT or mutant HKU1A or B
1271 spikes, expression was measured by flow cytometry after 24 h, using the anti-spike mAb10.
1272
1273 **Extended Data figure 7. Characterization of anti-TMPRSS2 VHHs. a. Binding of VHHs**
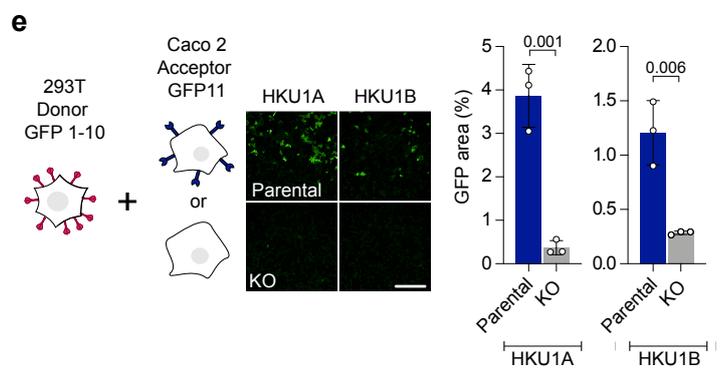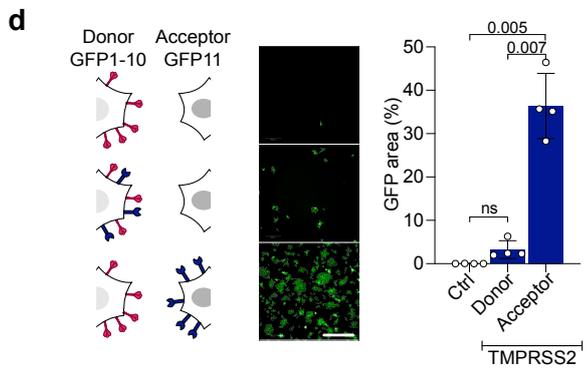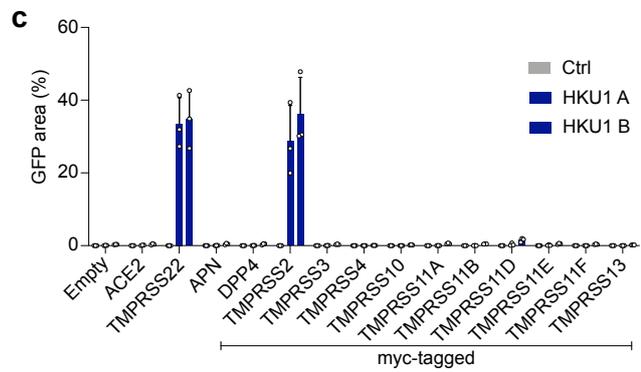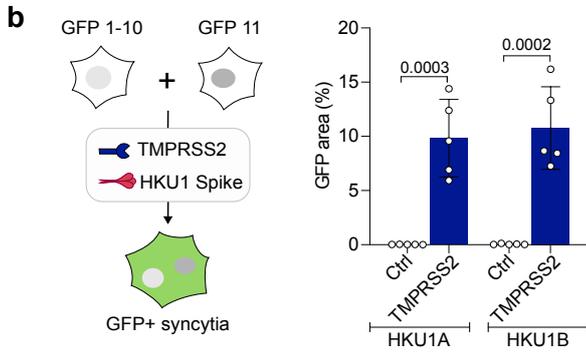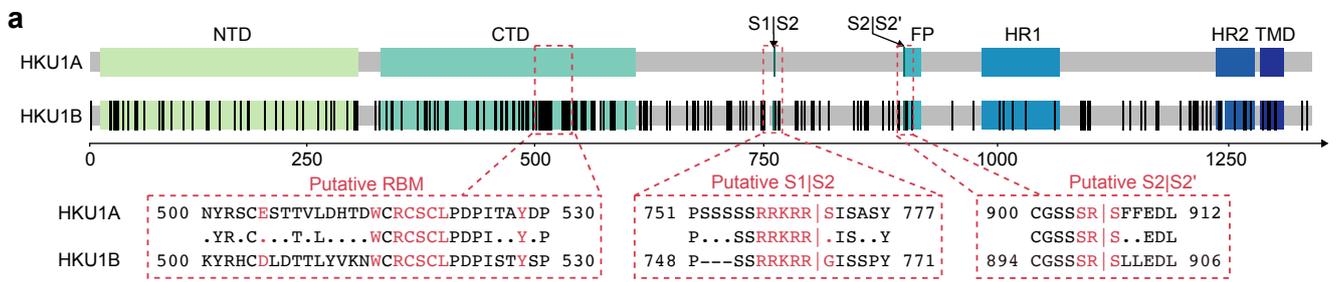1274 **on TMPRSS2-expressing cells.** 293T cells were transfected with TMPRSS2 S441A. Binding
1275 of the indicated VHHs (0.5 μM) was assessed by flow cytometry. Left: representative dot plots.
1276 Right: Quantification of the percentage of positive cells and MFI (Median Fluorescent Intensity
1277 of positive cells). Data are mean ± SD of three independent experiments **b. Effect of VHHs or**
1278 **Camostat on TMPRSS2 enzymatic activity.** Recombinant soluble TMPRSS2 was incubated
1279 with the indicated VHHs at different concentrations or with Camostat (1 μM). The initial rate
1280 of enzymatic activity, measured with a fluorescent substrate is plotted. One representative
1281 experiment of 3 is shown. **c. Effect of VHHs on HKU1A or HKU1B cell-cell fusion.** 293T
1282 GFP-Split cells were co-transfected with TMPRSS2 and HKU1 spike in the presence of
1283 indicated amounts of VHH. Fusion was quantified by measuring the GFP area after 20 h. Data
1284 were normalized to the non-treated condition for each spike. **d. Effect of VHHs on HKU1A**
1285 **or HKU1B pseudovirus infection**. 293T cells transfected with S441A TMPRSS2 were
1286 incubated with the indicated amounts of VHH for 2 h and infected by Luc-encoding
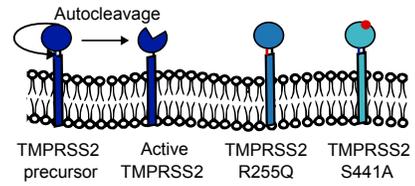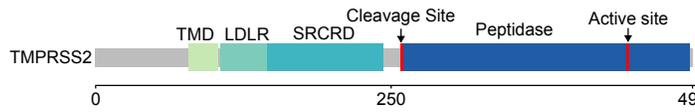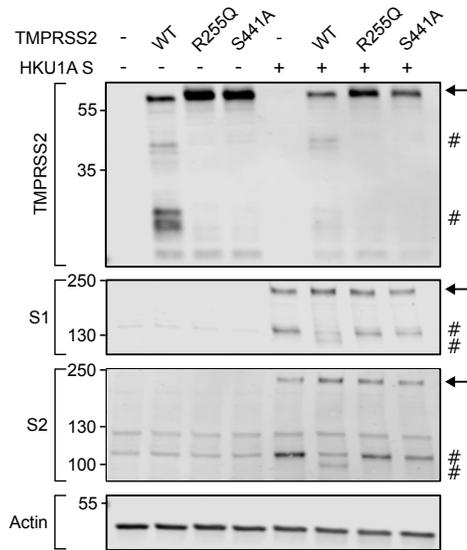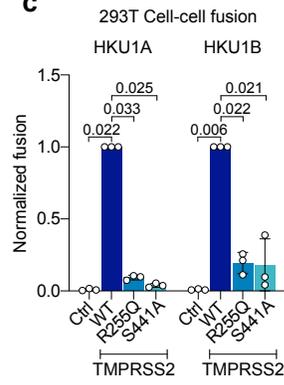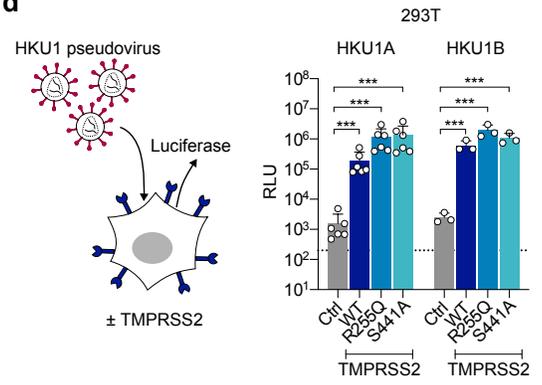
pseudovirus. Luminescence was read 48 h post infection. Data were normalized to the non-treated condition for each virus. Data are from one experiment representative of 3. **Statistical analysis**: c: One Way ANOVA with Dunnett's multiple comparisons compared to cells stained with a non-target antibody (VHH93). d: One Way ANOVA on log-transformed data with Dunnett's multiple comparisons compared to cells stained with a non-target antibody (VHH93).

Extended data Figure 8. Isolation and characterization of a live HKU1B virus. a. Viral RNA copies in the supernatant of HBE cells were quantified by RT-qPCR. The values at day 0 are the content of the input. Left: initial amplification (first passage). Right: Second amplification of the first passage virus (harvested at day 4) used at two dilutions (1/10 and 1/100) in duplicates. **b. Reads coverage and frequency of minor variants frequencies of the isolate sequencing data (first passage virus).** Intra-sample single-nucleotide variants frequencies were estimated using iVAR[69]. The genome organization of HKU1 is shown below the plot. **c, d. Phylogenetic analysis of HKU1**. Maximum likelihood phylogenies of human coronavirus HKU1 (n = 48) estimated using IQ-TREE v2 with 1000 replicates from **c**. the complete genome and **d.** spike coding sequences. The tree is midpoint rooted and ultrafast bootstraps values are shown on the main branches. A similar topology was obtained when rooting the tree using another embecovirus (OC43). The tip name corresponding to the newly isolated virus sequence is highlighted in bold and underlined. The tips names corresponding to the recombinant spikes used in this study are shown in bold.

Extended data Table 1. Affinity of the nanobodies for TMPRSS2 S441A and summary of their effect.

a

HKU1A

NTD CTD S1|S2 S2|S2' FP HR1 HR2 TMD

HKU1B

0   250   500   750   1000   1250

Putative RBM

HKU1A 500 NYRSCESTTVLDHTDWCRCSCLPDPITAYDP 530
.YR.C...T.L....WCRCSCLPDPI..Y.P
HKU1B 500 KYRHCDLDTTLYVKNWCRCSCLPDPISTYSP 530

Putative S1|S2

751 PSSSSSRRKRR|SISASY 777
P...SSRRKRR|.IS..Y
748 P---SSRRKRR|GISSPY 771

Putative S2|S2'

900 CGSSSR|SFFEDL 912
CGSSSR|S..EDL
894 CGSSSR|SLLEDL 906

b

GFP 1-10 + GFP 11

TMPRSS2
HKU1 Spike

GFP+ syncytia

GFP area (%)

0.0003   0.0002

Ctrl TMPRSS2   Ctrl TMPRSS2
HKU1A   HKU1B

c

GFP area (%)

Ctrl   HKU1 A   HKU1 B

Empty ACE2 TMPRSS22 APN DPP4 TMPRSS2 TMPRSS3 TMPRSS4 TMPRSS10 TMPRSS11A TMPRSS11B TMPRSS11D TMPRSS11E TMPRSS11F TMPRSS13

myc-tagged

d

Donor   Acceptor
GFP1-10   GFP11

GFP area (%)

0.005
0.007
ns

Ctrl Donor Acceptor
TMPRSS2

e

293T Donor GFP 1-10 + Caco 2 Acceptor GFP11 or

HKU1A HKU1B
Parental
KO

GFP area (%)

0.001

Parental KO
HKU1A

0.006

Parental KO
HKU1B

a

TMPRSS2

+Cam

S441A
R255Q
WT
Ctrl

TMPRSS2

b

TMPRSS2
± Camostat

Biotin-Spike

| HKU1A | HKU1B | SARS-CoV-2 |

S441A
R255Q
WT
Ctrl

+Cam

S441A
R255Q
WT
Ctrl

Biotin-Spike

c

ELISA - TMPRSS2

OD_{405nm}

Dose (µg/µL)

- S-HKU1A
- S-HKU1B
- S-SARS-CoV-2

d

BLI - TMPRSS2

Response (nm)

Time (s)

- RBD-HKU1A
- RBD-HKU1B
- RBD-SARS-CoV-2
- CD147

e

BLI

Time (s)

- RBD-HKU1B
- RBD-HKU1B-W515A
- RBD-HKU1B-R517A
- CD147

f

Cell-cell fusion

GFP area (%)

0.0003
0.0003
***
***

Ctrl WT W515A R517A WT W515A R517A
          HKU1A   HKU1B

g

HKU1 Pseudovirus

RLU

0.001
***
***
***

WT W515A R517A WT W515A R517A
    HKU1A   HKU1B

a HKU1B RBD-TMPRSS2 - BLI

Response (nm) vs Time (s)

Legend:
- Non-treated
- Non-target
- A01
- F05
- A07
- C11
- D01

b Cell-cell fusion

Fusion relative to mock

HKU1 A: Non-target, A01 (ns), F05 (ns), A07 (***), C11 (*), D01 (**)
HKU1 B: Non-target, A01 (ns), F05 (ns), A07 (*), C11 (ns), D01 (ns)

c Pseudotype infection

Entry relative to mock

HKU1 A: Non-target, A01 (*), F05 (ns), A07 (***), C11 (***), D01 (***)
HKU1 B: Non-target, A01 (ns), F05 (ns), A07 (***), C11 (***), D01 (***)

a

Phalloidin TMPRSS2 DAPI

b

Anti-TMPRSS2 Nanobodies   HKU1 virus

30min   2h

Spike intensity relative to non-treated (%)

0.0012

Non-Infected
Non-treated
Non-target
A07

Spike

Non-infected

Non-treated

Non-target

A07

Sensor	Ligand	K_d (nM)
RBD-HKU1A	TMPRSS2	334.3 ± 66.2
RBD-HKU1B	TMPRSS2	136.7 ± 20.8
RBD-HKU1B-W515A	TMPRSS2	ND
RBD-HKU1B-R517A	TMPRSS2	376.2 ± 96.4
RBD-SARS-CoV-2	TMPRSS2	ND
RBD-HKU1B	ACE2	ND
RBD-SARS-CoV-2	ACE2	92

Sensor	Ligand	K_d (nM)
RBD-HKU1A	TMPRSS2	334.3 ± 66.2
RBD-HKU1B	TMPRSS2	136.7 ± 20.8
RBD-HKU1B-W515A	TMPRSS2	ND
RBD-HKU1B-R517A	TMPRSS2	376.2 ± 96.4

a

VHH-A01 VHH-F05 VHH-A07 VHH-C11 VHH-D01

Response (nm) — Time (s)

400 nM
200 nM
100 nM
50 nM
25 nM
12.5 nM
6.25 nM
3.13 nM

b

293T + Ctrl   293T + TMPRSS2

TMPRSS2/Commercial Ab — FSC

5%   34%

Ctrl
TMPRSS2

TMPRSS2/Commercial Ab

c

293T + Ctrl   293T + TMPRSS2

TMPRSS2/VHH — FSC

2%   64%

Ctrl
TMPRSS2

TMPRSS2/VHH

a Surface expression

b Empty / TMPRSS2
HKU1A
HKU1B

c 293T + SARS-COV-2
GFP area (%)
Empty, TMPRSS2, ACE2

d U2OS + HKU1 A
GFP area (%)
Ctrl, TMPRSS2

e myc-tagged constructs

Secondary only 0% | Ctrl 0% | TMPRSS2-myc 37% | TMPRSS3-myc 15%
TMPRSS4-myc 27% | TMPRSS10-myc 16% | TMPRSS11A-myc 33% | TMPRSS11B-myc 19%
TMPRSS11D-myc 20% | TMPRSS11E-myc 24% | TMPRSS11F-myc 27% | TMPRSS13-myc 22%

% myc+ cells
Ctrl, TMPRSS2, TMPRSS3, TMPRSS4, TMPRSS10, TMPRSS11A, TMPRSS11B, TMPRSS11D, TMPRSS11E, TMPRSS11F, TMPRSS13

f VHH-A01-Fc α-TMPRSS2 staining
Ctrl 4%
TMPRSS2-Untagged 33%
TMPRSS2-myc 30%
% TMPRSS2+ cells
Ctrl, TMPRSS2-Untagged, TMPRSS2-myc

g α-APN-PE staining
Ctrl 0,3%
APN 12%
% APN+ cells
Ctrl, APN

h α-DPP4-PE staining
Ctrl 0,7%
DPP4 14%
% DPP4+ cells
Ctrl, DPP4

i α-ACE2 staining
Ctrl 1%
ACE2 26%
% ACE2+
Empty, ACE2

j HKU1-Spike TMPRSS2 Hoechst
45 min
60 min
75 min

a

TMPRSS2 genomic structure

CTGTGGTCCCCACTGTCTACGAGGTGCATCCGGCTCAGTACTACC
GACACCAGG**GGT****GACAGATGCTCCACGTAGGC**CGAGTCATGATGG

crRNA-TMPRSS2

b

TMPRSS2 knock-out clone sequence

```
WT        CGTAG-ACAGTGGGGACCACAGTGGGCT
Allele 1  CGTAGTACAGTGGGGACCACAGTGGGCT
                1 base insertion

WT        CGTAGACAGTGGGGACCACAGTGGGCTGT
Allele 2  CGTAGA----GGGGACCACAGTGGGCTGT
                4 base deletion
```

c

d

a

HKU1A

HKU1B

b

TMPRSS2 expression

c Lectin SNA binding

d Siglec-E-Fc binding

a

HKU1A

% of positive cells

TMPRSS2: -, -, WT, WT, R255Q, R255Q, S441A, S441A
Camostat: -, +, -, +, -, +, -, +

HKU1B

% of positive cells

TMPRSS2: -, -, WT, WT, R255Q, R255Q, S441A, S441A
Camostat: -, +, -, +, -, +, -, +

SARS-CoV-2

% of positive cells

TMPRSS2: -, -, WT, WT, R255Q, R255Q, S441A, S441A
Camostat: -, +, -, +, -, +, -, +

b

Binding to ACE2

% of positive cells

ACE2: -, +, -, +
Spike: HKU1B, SARS-Cov-2

c

ELISA -ACE2

OD 405nm

S-HKU1A
S-HKU1B
S-SARS-CoV-2

Dose (µg/µL)

d

RBD HKU1A

Response (nm)

Time (s)

RBD HKU1B

Response (nm)

Time (s)

RBD SARS-CoV-2

Response (nm)

Time (s)

800 nM
400 nM
200 nM
100 nM
50 nM
25 nM
12.5 nM
6.25 nM

e

Steady state

R

HKU1A
HKU1B

Concentration (nM)

f

Binding to ACE2

Response (nm)

Time (s)

200 nM
100 nM
50 nM
25 nM } SARS-CoV-2

200 nM
100 nM
50 nM
25 nM } HKU1B

g

RBD-HKU1B_W515A

Response (nm)

Time (s)

RBD-HKU1B_R517A

Response (nm)

Time (s)

800 nM
400 nM
200 nM
100 nM
50 nM
25 nM
12.5 nM
6.25 nM

h

Steady state

R

R517A

Concentration (nM)

i

HKU1A

R517A
W515A
WT

Spike

HKU1B

R517A
W515A
WT

Spike

a

b

TMPRSS2 enzymatic activity

Enzymatic activity

c

Inhibition of cell-cell fusion

HKU1 A

HKU1 B

d

Inhibition of pseudotype infection

HKU1 A

HKU1 B

a

Initial amplification

P1 infectivity

- 5x10^{6} RNA copies
- 5x10^{6} RNA copies
- 5x10^{5} RNA copies
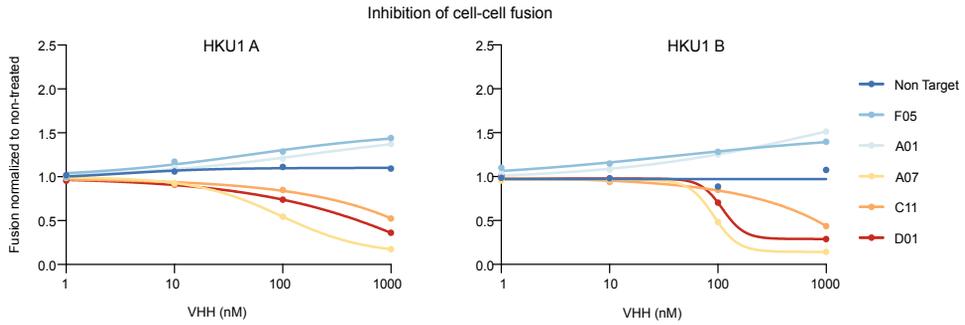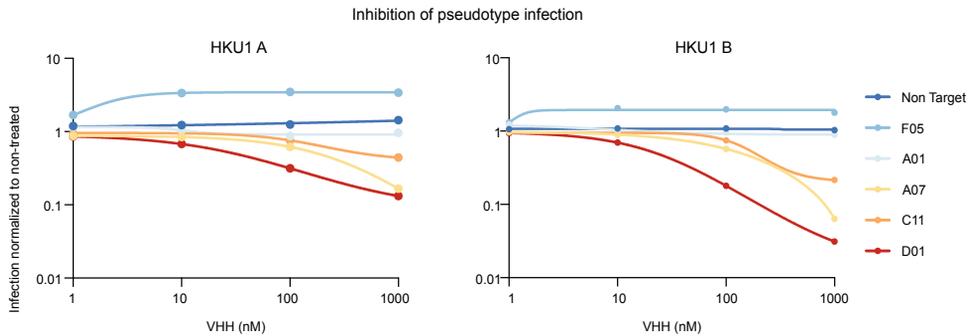- 5x10^{5} RNA copies

b

c

Genotype
- A
- B
- C

d

Nanobody	k_{on} (1/Ms)	k_{off} (1/s)	K_d (nM)	Enzymatic activity inhibition	Cell-cell fusion inhibition	Pseudotype infection inhibition
VHH-A01	$6.4.10^4$	$5.1.10^{-5}$	0.78	-	-	-
VHH-F05	$7.6.10^4$	$1.9.10^{-4}$	2.6	-	-	-
VHH-A07	$8.6.10^4$	$1.1.10^{-3}$	13.3	++	++	++
VHH-C11	$7.0.10^4$	$2.3.10^{-4}$	32.5	+	+	+
VHH-D01	$7.9.10^4$	$4.8.10^{-4}$	6.0	+	+	++