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Vectored Immunoprophylaxis and Treatment of SARS-

2 CoV-2 Infection

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18 variants

19 Summary

20 Vectored immunoprophylaxis was first developed as a means to establish engineered immunity 21 to HIV through the use of an adeno-associated viral vector expressing a broadly neutralizing 22 antibody. We have applied this concept to establish long-term prophylaxis against SARS-CoV-2 23 by adeno-associated and lentiviral vectors expressing a high affinity ACE2 decoy receptor. 24 Administration of decoy-expressing AAV vectors based on AAV2.retro and AAV6.2 by intranasal 25 instillation or intramuscular injection protected mice against high-titered SARS-CoV-2 infection. 26 AAV and lentiviral vectored immunoprophylaxis was durable and active against recent SARS-27 CoV-2 Omicron subvariants. The AAV vectors were also effective when administered up to 24 28 hours post-infection. Vectored immunoprophylaxis could be of value for immunocompromised 29 individuals for whom vaccination is not practical and as a means to rapidly establish protection 30 from infection. Unlike monoclonal antibody therapy, the approach is expected to remain active 31 despite continued evolution viral variants.

32 Introduction

The concept of vectored immunoprophylaxis was first proposed as an approach to establish protection against HIV infection by the vectored expression of a broadly neutralizing antibody¹, replacing the need to derive a vaccine immunogen capable of eliciting such antibodies. The approach has since been found to be effective as a therapeutic approach to suppressing virus replication the nonhuman primate SIV model using adeno-associated viruses (AAV) vectors expressing broadly neutralizing antibodies and is currently in clinical trials as a means to suppress HIV replication in infected individuals^{2,3}.

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41 Vectored immunoprophylaxis for SARS-CoV-2 through the expression of neutralizing monoclonal 42 antibodies is problematic because of the extraordinarily rapid evolution of the virus. Monoclonal 43 antibody therapy has been highly successful for the treatment of severe COVID-19, decreasing 44 hospitalization and deaths⁴ but has been largely sidelined by the extraordinarily rapid appearance 45 of viral variants that escape neutralization. The first Omicron variant, BA.1, contained 34 46 mutations in the spike protein, most of which were within or close to the spike protein receptor 47 binding domain and allowed for escape from most of the therapeutic monoclonal antibodies. The 48 Regeneron REGN-COV2 cocktail, a cocktail of REGN10933 and REGN10987 monoclonal 49 antibodies, and the Lilly LY-CoV555 potently neutralize the earlier variants of concern (Alpha, Beta, Gamma and Delta) but their IC₅₀s against the Omicron BA.1 variant was greatly increased⁵⁻ 50 51 ¹⁴. Vir/GSK VIR-7831 (Sotrovimab) was thought to maintain neutralizing activity against Omicrons 52 BA.1 and BA.2 but was later found to be 10.5- and 340-fold decreased in neutralizing activity against the variants^{8-10,12,14,15}. Lilly LY-CoV1404 maintained neutralizing titer against BA.1, BA.2 53 and BA.4/5¹⁶ but fails to neutralize the more recent, further mutated Omicron variants BQ1.1 and 54 55 XBB¹⁷. The extraordinarily rapid evolution of the virus is likely to continue over the next several years, imposing a challenge to the development of monoclonal antibodies from which the virus cannot escape. The rapidity of virus evolution is also a challenge for the design of effective vaccines.

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60 A strategy to inhibit virus entry that is less subject to escape by novel variants is that of receptor 61 decovs. The strategy is based on soluble forms of the protein, fused to the Fc domain of an immunoglobulin heavy chain to increase its half-life *in vivo*¹⁸. While viruses can mutate epitopes 62 63 in the spike protein driven by selective pressure to escape neutralization by antibodies elicited 64 from previous infection or vaccination, the spike protein needs to conserve high affinity binding to 65 its receptor, thereby preserving the neutralizing activity of the receptor decoy. Receptor decoys were first developed as a therapeutic for HIV infection^{19,20}. A recombinant protein consisting of 66 67 the ectodomain of CD4 fused to an immunoglobulin Fc domain was found to bind the viral 68 envelope glycoprotein gp120 with high affinity and potently neutralize the virus in vitro but in 69 clinical trials the protein showed no benefit. More recently, the concept was revived by Gardner 70 et al. who showed that an enhanced eCD4-lg protected rhesus macaques from multiple 71 challenges with SIV³.

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Receptor decoys for SARS-CoV-2 based on soluble forms of ACE2 have been developed by several groups²¹⁻²⁸. We previously reported the development of a receptor decoy protein termed an "ACE2 microbody" in which the ACE2 ectodomain is fused to the CH3 domain of a human immunoglobulin IgG1 heavy chain Fc region²¹. The decoy proteins, administered by intranasal (i.n.) instillation, have been shown in mouse and hamster models to protect from infection when given shortly prior to infection and to therapeutically suppress virus replication when given up to about 12 hours post-infection²⁹. The introduction of point mutations into the ACE2 spike protein binding region of the decoy to increased its affinity for the spike further increased the effectiveness
 of the proteins^{22,24,26}.

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83 Here, we applied vectored immunoprophylaxis to SARS-CoV-2 using AAV and lentiviral vector 84 vectors expressing a modified high affinity ACE2 microbody. AAV2.retro and AAV6.2 vectors, 85 administered either i.n. or by intramuscular (i.m.) injection, provided a high degree of protection 86 in ACE2 transgenic and Balb/c mouse models. The protection was long-lasting and was effective 87 against recent Omicron variants. The AAV vectors were also effective therapeutically when 88 administered shortly post-infection. The lentiviral vector-based decoy was also effective at 89 suppressing virus replication, providing protection that showed no sign of diminishing two months 90 after i.n. administration. Decoy vectored-immunoprophylaxis could be a highly useful means to 91 protect immunocompromised individuals for whom vaccination is less effective and could offer a 92 therapy that remains active against new variants as the emerge.

93 **Results**

94 Decoy-expressing AAV vectors inhibit SARS-CoV-2 infection.

95 To determine the feasibility of vectored prophylaxis for SARS-CoV-2, we constructed AAV vectors 96 expressing an ACE2 receptor decoy. The decoy, termed ACE2.1mb, is similar to the ACE2 97 microbody we previously reported²¹ that consists of the ACE2 ectodomain fused to a single CH3 98 domain of an IgG1 heavy chain Fc domain (Figure 1A). The protein has been modified by the 99 introduction of point mutations in the ACE2 spike protein binding region that were reported by 100 Chen et al. to increase affinity for the spike protein²² and by the introduction of an H345A point 101 mutation that inactivates its catalytic activity³⁰. The coding sequence was cloned into an AAV 102 vector containing a CAG promoter and virus stock was produced with AAV2.retro and AAV6.2 103 capsids. AAV2 and AAV6 are reported to have tropism for cells of the mouse and human lung and airway³¹⁻³³. AAV2.retro is a variant of AAV2 that was selected for increased tropism for the 104 central nervous system (CNS) and retrograde movement in axons^{34,35}. It has not been reported 105 106 to transduce lung cells but in pilot experiments, we found that it worked surprisingly well (not 107 shown). AAV6.2 is a variant of AAV6 that contains a single F129L mutation that was found to 108 increase the efficiency of mouse and human airway cell transduction³⁶. The ability of the vectors 109 to protect cells from SARS-CoV-2 infection was tested in the lung cell-line A549.ACE2 and the 110 microglial cell-line CHME3.ACE2. The cells were transduced with serial dilutions of the decov 111 vectors and then challenged 5 days later with D614G, BA.1, BA.2, BA.2.75, BA.4/5 and BQ.1 112 spike protein-pseudotyped lentiviruses carrying a luciferase reporter genome. At 2 days post-113 infection (dpi), luciferase activity in the cultures was measured. The results showed that both 114 decoy-expressing AAVs protected A549.ACE2 and CHME3.ACE2 cells from infection (Figure 115 **1B**). Virus with the D614G spike was the most potently neutralized by the decoy while BA.2 was 116 the most resistant, with a 20-33-fold higher ID₅₀ (defined as the multiplicity of infection (MOI) that resulted in a 50% decrease in luciferase activity). The low ID_{50} required to block infection indicates that the decoy was active on bystander cells and that it was not necessary to transduce all of the cells in order to protect the culture.

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121 The ability of the decoy-expressing vectors to inhibit SARS-CoV-2 live virus replication was tested 122 on A549, ACE2. CHME3, ACE2 and hSABCi-NS1.1 cells. The latter is a human small airway basal 123 cell-line grown in air-liquid interface culture conditions and differentiated into mature airway 124 epithelium cell-types the model the respiratory tract. The cells were transduced with decoy-125 expressing or control GFP.nLuc AAV2.retro and AAV6.2 vectors and challenged a day later with 126 SARS-CoV-2 WA1/2020. Virus replication was measured by RT-qPCR quantification of cell-127 associated viral RNA copies. The 3 cell-lines supported high levels of SARS-CoV-2 replication 128 (Figure 1C left). Transduction of the CHME3.ACE2 cells with either of the AAV vectors resulted 129 in a 4-5 log decrease in viral RNA, a level that was not significantly higher than uninfected cells. 130 Transduction of the cells by the control AAV had no effect on SARS-CoV-2 replication. The results 131 in the A549.ACE2 cells were similar (Figure 1C right). The vectors were also effective in the 132 hSABCi-NS1.1 human small airway basal cultures although the decrease was less pronounced 133 (50-100-fold) most likely because the cells did not support virus replication as high as in the other 134 cell-lines. The AAV6.2 vector was somewhat more effective than the AAV2.retro vector (Figure 135 **1D)**. Production of the decoy protein by the transduced CHME3.ACE2 and A549.ACE2 cells was 136 confirmed by pull-down of the protein from the culture supernatant on anti-His tag coated 137 magnetic beads and immunoblot analysis (Figure 1E). The CHME3.ACE2 cells were found to 138 produce about 2-fold more decoy than A549.ACE2 which may have contributed to the greater 139 extent of protection in these cells. The concentration of the decoy protein in the culture medium 140 was 0.2-0.6 μ g/ml, a concentration that was greater than the IC₅₀ 0.15 μ g/ml²¹.

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142 Vectored immunoprophylaxis *in vivo* by decoy-expressing AAV-vectors

143 The feasibility of vectored immunoprophylaxis for SARS-CoV-2 with the decoy-expressing AAV 144 vectors was tested in transgenic and non-transgenic mouse models. Decoy-expressing and 145 control GFP AAV2.retro and AAV6.2 vectors were administered to human ACE2 K18 transgenic 146 mice (hACE2 K18 Tg) i.n., i.v. or i.m. After 3 days, the mice were challenged with SARS-CoV-2 147 WA1/2020 and virus loads in the lung were measured 3-dpi (Figure 2A). The results showed that 148 vector administration i.n. strongly suppressed virus replication in the mice, decreasing the virus 149 load by 5-logs, a level that was indistinguishable from uninfected mice (Figure 2B). The control 150 vectors had no effect on virus loads. Histology showed that the lungs of infected untreated mice 151 had prominent signs of interstitial pneumonia with thickened alveolar septa and inflammatory cell 152 infiltration while the lungs of decoy-expressing AAV vectors-treated mice showed no signs of 153 pneumonia and were free of infiltrating inflammatory cells (Figure 2C). The lungs of mice treated 154 with the decoy AAV vectors alone in the absence of SARS-CoV-2 infection were clear, indicating 155 that the decoy vectors themselves did not cause pulmonary inflammation (Figure 2C). Treatment 156 with the decoy vectors prevented the characteristic loss of body mass associated with untreated 157 SARS-CoV-2 infection (Figure 2D). A concern regarding vectored immunoprophylaxis is that the 158 decoy protein or the vectors themselves might induce inflammatory responses in the lungs; 159 however, analysis of proinflammatory and anti-inflammatory cytokine levels (IFN α , IL-10, TNF α , 160 IL12-p70, IL-6 and MCP-1) showed no induction of these cytokines following administration of the 161 vectors (Figure S1).

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163 To test the effectiveness of the decoy vectors in protecting against the Omicron variants, Balb/c 164 mice, which support high level replication of SARS-CoV-2 Omicron variants through the

endogenous murine ACE2^{37,38}, were treated i.n. with decoy-expressing AAV or control AAV2.retro 165 166 or AAV6.2 vector and then challenged with Omicrons BA.1, BA.2 or BA.5. The results showed 167 that i.n. administration of decoy-expressing AAV vectors caused a dramatic decrease in virus 168 loads as compared to the control vectors (Figure 2E). The decoy-expressing vectors were most 169 effective against the BA.5 variant, decreasing the virus load 1,000-fold and least effective against 170 BA.2, decreasing virus load 100-fold (Figure 2E), a pattern that was similar to what was found 171 with the pseudotyped lentiviruses in vitro. Both AAV vectors were effective although the 172 AAV2.retro seemed to be slightly more suppressive against all three Omicrons. This conclusion 173 was confirmed in a dose-response analysis which showed that the decoy-expressing AAV2.retro 174 vector was about 10-fold more effective at virus load suppression. A 10,000-fold decrease in virus load required 1 x 10¹⁰ vector genomes (vg) for AAV2.retro. The same degree of suppression by 175 AAV6.2 required 1 x 10^{11} vg (**Figure S2**). 176

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178 Administration of the vectors i.n. delivered the vectors to the relevant organ but it was possible 179 that delivery by routes that targeted a different site in the body might also be effective given that 180 the decoy protein is stable *in vivo* and freely diffusible²⁹. In support of this approach, i.m. delivery 181 of AAV-vectored immunoprophylaxis was effective for the suppression of SIV replication in the macaque model³⁹. We therefore tested the effectiveness of i.v. and i.m. administration of the 182 183 decoy-expressing AAV vectors (Figure 2A). The results showed that i.m. administration was 184 highly effective, decreasing the virus load by 5-logs compared to control vector, a level that was 185 indistinguishable from uninfected mice (Figure 2F). I.v. administration was much less effective, 186 decreasing the virus load by only a 2-logs.

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188 Therapeutic use of vectored immunoprophylaxis for SARS-CoV-2.

189 The studies described above tested the prophylactic effect of the decoy-expressing AAVs 190 administered prior to SARS-CoV-2 infection. It was possible that the approach might also be 191 effective therapeutically by administration post-infection. The effectiveness of administration post-192 infection would depend on how soon post-infection they were administered and how fast the 193 vectors transduced lung cells and produced the encoded protein to establish an inhibitory 194 concentration in the respiratory tract. To determine this, we infected mice with SARS-CoV-2 and 195 then treated them at increasing times post-infection (Figure 2G). The results showed that the 196 decoy-expressing vectors were effective when administered concomitant with SARS-CoV-2 and 197 up to 12 hours post-infection (Figure 2G). The treatment was partially effective at 24-hours and 198 lost efficacy at 48-hours. The results demonstrate remarkably rapid transduction and biosynthesis 199 of the decoy protein by the AAV vectors. While this time course would appear to be too short to 200 be of therapeutic use, the kinetics closely mirror what is seen in monoclonal antibody therapy of SARS-CoV-2 in mouse models¹¹¹¹¹¹⁸ suggesting that in humans, where the time-course of 201 202 disease is slower, the AAV vectors might act with the kinetics similar to that of highly effective 203 monoclonal antibodies.

204

205 AAV decoy-expressing vectored immunoprophylaxis is highly durable.

Although AAV does not integrate at a significant frequency into the host cell genome, the genome remains stable in the host cell. In nonhuman primates and in clinical trials, AAV vectors have been shown to maintain long-term expression of an encoded gene *in vivo*⁴⁰. To test the durability of the decoy-expressing AAV vectors, we constructed AAV2.retro and AAV6.2 vectors that expressed a decoy-luciferase fusion protein. The vectors were administered i.n. to mice and the mice were live-imaged over the next 30 days. Expression by both vectors in the lungs was first detected 24 hours post-treatment and then increased to maximal by day 3 (Figure 3A). Expression levels

213 remained stable through day 14 after which they decreased slightly by day 30. Measurement of 214 luciferase activity in tissue homogenates further demonstrated durable expression by the vectors 215 (Figure 3B). The decoy proteins were readily detectable on day 1 and the following day, 216 expression increased 25-fold. To determine the durability of viral load suppression by the vectors, 217 mice were treated and then challenged with SARS-CoV-2 over a 30-day period. The results 218 showed that the decoy-expressing vectors strongly suppressed the virus loads of mice infected 219 that had been infected up to 30-days post-treatment (Figure 3C). Virus load suppression 220 appeared to begin to wane 30 days post-treatment but was still highly active, with the AAV2.retro 221 vector suppressing virus load nearly 1000-fold. The results were consistent with the slight 222 decrease in *in vivo* expression levels found for the decoy-luciferase fusion protein.

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Increased durability of vectored immunoprophylaxis with a decoy-expressing lentiviral
 vector.

226 The waning of protection established by the AAV vectors at 30 days led us to test whether a 227 different vector might be able to extend the durability protection. The use of an alternative vector 228 was also of interest in light of concerns about the possibly of pre-existing immunity to AAV in 229 some individuals noted in clinical trials⁴¹. Lentiviral vectors are generally not subject to pre-existing 230 immunity in humans. Moreover, because lentiviruses integrate into the host cell genome, the 231 vectors are maintained stably in the cell and in daughter cells that may be generated, allowing for 232 the possibility of long-term decoy expression and increased durability of protection. In addition, 233 pseudotyping of the vectors by VSV-G results in a broad target cell tropism. To test the feasibility 234 of lentiviral vectored immunoprophylaxis, we constructed a decoy-expressing lentiviral vector and 235 compared its effectiveness to the AAV vectors. Transduction of A549.ACE2 and CHME3.ACE2 236 cells with the vector showed that it expressed the decoy protein at a level similar to those of the

237 AAV vectors as measured in the supernatant pull-down assay (Figure S3). To determine the 238 potency of the protection, the cell-lines were transduced with a serial of the decoy-expressing 239 lentiviral vector and then challenged with the D614G and Omicron spike protein-pseudotyped 240 reporter viruses. The results showed that vector was highly protective against all of the variants 241 (Figure 4A). Overall, the potency of virus neutralization, calculated by the MOI required to 242 decrease infection by 50%, was very similar to that of the AAV vectors. As for the AAV vectors, 243 BA.2 was the most resistant to neutralization (8-fold in CHME3.ACE2 and 5.8-fold in A549.ACE2) 244 (Figure 4A, below). The ability of the vectors to neutralize the viruses at low MOIs confirmed that 245 only a small fraction of the cells needed to be transduced to protect the entire population.

246

247 To determine whether the decoy-expressing lentiviral vector could establish vectored 248 immunoprophylaxis, the vector was administered i.v. or i.n. and after 7 days, the mice were 249 challenged with WA1/2020 or Omicron BA.1. Virus loads in the lung were guantified 3-dpi (Figure 250 **4B**, **left**). In mice challenged with WA1/2020, i.v. injection resulted in a nearly 5-log decrease in 251 virus load while administration i.n. further decreased the virus load to undetectable levels (Figure 252 **4B**, middle). The analysis of proinflammatory and anti-inflammatory cytokine levels (IFN α , IL-10, 253 TNF α , IL12-p70, IL-6 and MCP-1) showed that administration of the lentiviral vector had no 254 significant effect on the levels of these cytokines (Figure S1). A dose-response analysis in which 255 mice were administered decreasing amounts of the vector i.v. or i.n. confirmed the great efficacy 256 of i.n. administration; at a dose of 1 X 10⁶ IU, virus loads were 100-fold lower in mice treated i.n. 257 compared to i.v. (Figure S4). Treatment with the vector also protected against Omicron BA.1 but 258 did not suppress virus replication to as great an extent, resulting in low level virus replication in 259 mice treated i.v. or i.n. To compare the protective effect of the vector with that of a therapeutic 260 monoclonal antibody, mice were administered the highly potent neutralizing monoclonal antibody

261 LY-CoV1404 by i.v. and i.n. routes and then infected with the Omicron BA.1 variant. The results 262 showed that the monoclonal antibody decreased the virus loads more effectively i.n. than i.v. but 263 was not as effective as the lentiviral vector (Figure 4B, right). To test the durability of lentiviral 264 vectored immunoprophylaxis, mice were treated i.v. or i.n. with decoy-expressing or control GFP-265 expressing lentiviral vector and challenged 7, 30 and 60 days later with SARS-CoV-2 WA1/2020. 266 The protection was found to persist over the 60-day time-course (Figure 4C). I.n. administration 267 of the vector caused a greater decrease in virus loads which interestingly, became even more 268 pronounced over time.

269

270 To understand the basis of the long-lasting protection provided by lentiviral vectored 271 immunoprophylaxis, we administered a GFP/luciferase-expressing lentiviral vector i.v. or i.n. and 272 determined the level of expression over the 60-day time-course by measuring luciferase activity 273 in cell lysates prepared from different tissues. The results showed that i.v administration resulted 274 in high level expression in the spleen at day-7 and moderate expression in the lungs and liver 275 (400-fold less in lung and 50-fold less in liver). The expression levels remained constant over the 276 time-course (Figure 4D). There was no detectable expression in nasal tissue and trachea. 277 Administration of the vector i.n. resulted in high level expression in the lung, moderate levels in 278 the trachea (about 30-fold less on day 7) and nasal tissue. Levels in the spleen and liver were 279 undetectable. Expression levels remained constant at 30-days. At 60-days, expression in the lung 280 increased about 8-fold, a finding that could explain the increase in virus load suppression at this 281 time-point in mice treated by i.n. administration of the vector (Figure 4C).

282

283 Comparison of lung cell-types transduced by the AAV and lentiviral vectors.

284 The effectiveness and longevity of the vectored immunoprophylaxis depends both upon the cell-285 types and half-lives of the cells transduced by the vectors. To understand the basis of durable 286 protection, we characterized the cell-types transduced in the lung by the AAV and lentiviral 287 vectors. Mice were administered GFP-expressing AAV and lentiviral vectors i.n. and the GFP+ 288 cells. The lungs were harvested 3 days later and the cells disaggregated. The cells were then 289 analyzed by flow cytometry using antibodies that distinguished various pulmonary cell-types. The 290 results showed that the majority of the cells transduced in the lungs by AAV2.retro and AAV6.2 291 were epithelial (79.5% and 94.2%, respectively) (Figure 5A). Of the cells transduced by 292 AAV2.retro, 20.5% were leukocytes while AAV6.2 transduced fewer leukocytes (5.8%). Analysis 293 of the transduced leukocytes showed that the majority of cells were interstitial macrophages and 294 neutrophils with smaller proportions of T cells, B cells, DCs, monocytes and alveolar 295 macrophages. The distribution of leukocytes transduced by AAV6.2 was roughly similar. The 296 lentiviral vector targeted a larger proportion of leukocytes (57%). Of the transduced leukocytes, 297 the greatest proportion were DCs (26.3%) with substantial contributions from B cells (20.7%) and 298 monocytes (18.5%) (Figure 5B). It is possible that the long-lasting expression by the lentiviral 299 vector resulted from the increased transduction of leukocytes, particularly of the DCs, as these 300 cells are thought to be long-lived residents in the lung⁴².

301 Discussion

302 Vectored prophylaxis was first developed as an approach to protect against HIV infection¹ in 303 which broadly neutralizing antibody was expressed in an AAV vector and was later expanded to 304 the use of an enhanced CD4-Ig fusion protein that established a high degree of resistance to SIV infection in treated macaques^{2,3}. We report here that that vectored expression of a high affinity 305 306 ACE2 microbody protein in which the ectodomain of ACE2 was mutated to increase its affinity for 307 the viral spike protein and inactivate catalytic activity fused to the CH3 domain of an IgG heavy 308 chain Fc²¹ established a high degree of protection from SARS-CoV-2 in mouse models. Decoy-309 expressing AAV2.retro and AAV6.2 vectors were both highly effective at establishing vectored 310 immunoprophylaxis in ACE2 K18 Tg and Balb/c mice. Mice treated with the decoy-expressing 311 AAV2.retro and AAV6.2 vectors were highly resistant to SARS-CoV-2 infection. Upon challenge 312 with high titered SARS-CoV-2 WA1/2020, viral RNA in the lungs 3-dpi was undetectable, 313 corresponding to a >10.000-fold decrease in virus loads; the lungs of the treated mice were free 314 of infiltrating leukocytes; there was no sign of pulmonary inflammation and the mice did not 315 experience the decrease in body weight that normally occurs in untreated or control vector-treated 316 mice. Delivery of the decoy by a lentiviral vector was as effective and appeared to be even more 317 durable. The vectors were well-tolerated; they did not disturb myeloid or lymphoid cell populations 318 and did not cause T cell activation or increased levels of proinflammatory cytokines in the sera. 319 The vectors established protection against a broad range of SARS-CoV-2 variants including the 320 recent Omicron subvariants BA.2.75, BA.4/5 and BQ.1. Protection was strongest against virus 321 with the parental D614G spike protein and somewhat less effective against the BA.2 variant, an 322 effect that was probably due to the relative decrease in spike protein affinity for ACE2¹⁶.

323

324 Administration of the decoy-expressing AAV2.retro and AAV6.2 vectors by i.n. instillation 325 suppressed virus replication in the mice for at least 30 days. The effectiveness of i.n. 326 administration of the AAV2.retro vector, which was somewhat greater than the AAV6.2 vector, 327 was surprising as its capsid was selected for high efficiency transduction of the CNS and 328 retrograde transport in neurons^{34,35}; its tropism for the respiratory tract has not, to our knowledge, 329 been previously described. The tropism of the AAV2 retro vector for lung and neuronal cells could 330 be clinically advantageous as a means to suppress SARS-CoV-2 replication in respiratory and 331 olfactory tissues. SARS-CoV-2 infection of ACE2 K18 Tg results in high virus loads in the brain 332 which was suppressed by administration of the decoy-expressing AAV2.retro vector (not shown). 333 Imaging of mice following administration of a luciferase-expressing AAV2.retro vector showed 334 transduction of the olfactory region of the brain (not shown).

335

336 In a previous report, Sims et al., used an AAV-expressed high affinity ACE2 decoy to protect mice 337 from SARS-CoV-2 infection⁵³. In that study, i.n. administration of a decoy-expressing AAVhu.68 338 vector caused at 30-fold decrease in Wuhan-Hu-1 SARS-CoV-2 virus load 7-dpi but at 4-dpi, 339 close to the time at which virus loads peak, had no significant effect on virus loads. In contrast, 340 we found that i.n. or i.m. administration of decoy-expressing AAV2.retro or AAV6.2 vectors 341 decreased virus loads 10,000-100,000-fold at the time of peak virus load. The increased 342 effectiveness of the therapy in our study does not appear to have resulted from differences in 343 increased neutralizing activity of the decoys which appeared to be similar in both studies (IC50s (37 ng/ml vs 20 ng/ml²⁹) or differences in vector dosage which also appeared to be similar. A 344 345 potential explanation is that of more efficient transduction of respiratory tract cells by the 346 AAV2.retro and AAV6.2 vectors.

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348 The effectiveness of i.m. injection with the AAV2.retro vector was encouraging because clinically this route of administration may be more practical than i.n. instillation⁴³. For reasons that are 349 350 unclear, i.m. injection of the AAV2.retro vector was 3-logs more effective than injection by that 351 route with the AAV6.2 vector. It is possible that the increased effectiveness of the vector was the 352 result of retrograde transport of the AAV2.retro capsid in myocytes or simply caused by more 353 efficient transduction of lung cells. The efficacy of i.m. injection of the vector suggests that decov 354 protein synthesized by transduced myocytes at the site of injection diffuses systemically, 355 establishing a concentration in the respiratory tract sufficient to inhibit virus replication. Similarly, 356 in the rhesus macaque SIV model, i.m. administration of AAV vectors expressing broadly 357 neutralizing antibodies suppressed virus loads of SIV, a virus that replicates in secondary 358 lymphoid organs^{3,39}. The long-lasting suppression of SIV replication by the vector suggests that 359 transduced terminally differentiated myocytes can produce AAV vector-encoded proteins for a 360 period of several years. Similarly, i.m. administration of a decoy-expressing AAV vector could 361 provide long-lived protection in humans. The protection could be more durable than that of the 362 extended half-life monoclonal antibodies currently in clinical use⁴⁴.

363

364 Unexpectedly, the decoy-expressing AAVs were also effective therapeutically. I.n. instillation of 365 the vectors as late as 24 hours post-SARS-CoV-2 infection suppressed virus replication, a time 366 course similar to what is found in the treatment of mice with highly potent neutralizing monoclonal 367 antibody⁸. The effectiveness of the decoy therapeutically demonstrates the rapid kinetics with 368 which the vectors transduce cells in the lung and program biosynthesis of the encoded protein. In 369 clinical practice, monoclonal antibody therapy is effective when given several days postinfection⁴⁵. The similarity in the timing with which the AAV vectors and monoclonal antibodies can 370 371 treat mice suggests that in humans, decoy-expressing AAV might be effective up to several days

post-infection, as is the case for the use of monoclonal antibodies. In mouse and hamster models, the administration of recombinant ACE2 decoy protein has previously been shown to be highly effective therapeutically^{28,46}. The proteins do not require viral transduction or biosynthesis in the lung and thus are expected to act faster; however, in clinical practice, their use will require large quantities of highly pure recombinant protein which is not the case for vectored immunoprophylaxis.

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379 Delivery of the decov protein with a lentiviral vector was also highly effective for the establishment 380 of vectored immunoprophylaxis. Like the AAV vectors, the lentiviral vector was most effective 381 administered by i.n. instillation, Unlike the AAV vectors, the lentiviral vector was also effective by 382 i.v. injection, a route that results mainly in the transduction of splenocytes, many of which are 383 DCs⁴⁷. Lentiviral vectored immunoprophylaxis appeared to be more durable than AAV vector, 384 remaining fully intact through the 60-day time course. Interestingly, the level of virus load 385 suppression intensified at the later time points, an effect that was probably the result of increased 386 expression levels of the decoy in the in lung as demonstrated using a luciferase-expressing 387 reporter vector. The parameters that affected the durability of protection by the two types of 388 vectors are unclear. The AAV vectors transduced a significantly higher proportion of lung 389 endothelial cells while the lentiviral vector high transduced a high proportion of leukocytes, many 390 of which were DCs. Endothelial cells are mitotically active, thus diluting the AAV genome copy 391 number over time. DCs are terminally differentiated and could remain resident in the lung for a 392 lona time.

393

AAV vectors are advantageous for clinical use because they are expressed long-term without integrating into the host cell genome and are replication-defective^{40,48-50}. The vectors are currently

396 in use in a large number of clinical trials for a broad range of diseases. There are over 20 AAV serotypes, each with unique tissue tropism⁵¹. AAV6.2 is a variant of AAV6 that contains a single 397 point mutation (F129L) introduced to increase lung cell tropism³⁶. AAV2.retro is an AAV2 variant 398 399 selected for retrograde transport in the CNS⁵². Both vectors administered i.n. protected mice from 400 infection. AAV2.retro, which has not been reported to transduce cells of the respiratory system 401 was, unexpectedly, somewhat more effective than AAV6.2. The majority of cells transduced by 402 both vectors were lung the epithelial cells although AAV2 retro transduced a large proportion of 403 neutrophils and monocytes.

404

405 The decoy-expressing lentiviral vector also strong protected mice from infection. Lentiviral vectors 406 are currently being developed for several clinical applications including CAR-T cells and SARS-CoV-2 vaccines^{54,55}. The vectors offer long-term expression and are not generally subject to pre-407 408 existing immunity⁵⁶. The protection established by i.n. administration of the decoy-expressing 409 vector remained intact over the 60-day time-course and was somewhat longer-lasting than that 410 of AAV vectored protection which started to wane after 30-days. The suppression of virus 411 replication by the lentiviral vector increased somewhat towards the end of the time-course, an 412 effect that was associated with a small increase in expression of the decoy-expressing lentiviral 413 vector in the lung. The increased durability of lentiviral-vectored immunoprophylaxis is 414 presumably the result of the transduction of a long-lived cell subpopulation in the lung although 415 the identity of this subpopulation is unclear. The lentiviral vector mainly transduced lung 416 leukocytes, many of which were DCs and monocytes that are thought to have short 2 day halflives^{57,58} and thus unlikely to account for the durable expression. The AAV vectors transduced a 417 418 higher proportion of lung epithelial cells, a cell-type which in mice, has a much longer 17 month 419 half-life⁵⁹. Possible explanations for the long-lasting protection provided by the lentiviral vector are

that a long-lived, subpopulation of tissue resident DC or myeloid cells had been transduced or that integration of the vector allows for persistence of its genome in dividing cell subpopulations of the lung. In most clinical applications, lentiviral vectors are used to transduce cells *ex vivo* that are later re-infused, a procedure that has been generally viewed as low-risk. The safety profile of integrating lentiviral vectors for direct injection has not been fully established⁶⁰⁻⁶².

425

426 A potential application of vectored immunoprophylaxis for SARS-CoV-2 is as a means of providing 427 protection to immunocompromised individuals for whom vaccination is less effective. Until 428 recently, the most effective protection available for such individuals was the AstraZeneca 429 Evusheld cocktail, a mixture of two monoclonal antibodies formulated for slow release by 430 intramuscular injection⁴⁴. However, the therapy may have become less effective as a result of 431 immunoevasion by new Omicron subvariants. Both of the monoclonal antibodies in the cocktail have decreased neutralizing titers against the Omicrons BA.1 and BA.2⁵⁻¹⁴ and recent findings 432 433 suggest that they may be inactive against the increasingly prevalent BQ.1 and BA.2.75 434 subvariants⁶³. This decrease in neutralizing activity contrasts with the decoy which maintains its 435 effectiveness against BQ.1 and BA.2.75.

436

AAV-based vectored immunoprophylaxis was effective therapeutically in the mouse models when delivered within a 24-hour window post-infection. The short window is at least partially a function of the rapid kinetics of virus replication and clearance in the mouse model as compared to in humans. While the decoy-expressing AAV lost efficacy at later time points in the infected mouse, the loss of effect was coincident with that found for treatment with a highly potent therapeutic monoclonal antibody. Monoclonal antibody therapy has been found to lessen disease symptoms when given to patients several days post-infection⁴⁵. If the comparison pertains in humans, the

window for which the AAV therapy remains effective in humans might be comparable to that formonoclonal antibody therapy.

446

447 Vectored immunoprophylaxis could be valuable in the case of a future pandemic spurred by the 448 zoonosis of a novel coronavirus. Species such as bats and pangolins harbor large numbers of coronaviruses with the ability to use hACE2^{64,65}. In the case of zoonosis of a coronavirus that used 449 450 ACE2 as its entry receptor, the decoy-expressing vectors reported here would be ready as an off-451 the-shelf agent available prior to the production of a vaccine. The protection established by the 452 vectors is more rapid than of vaccine as it does not require the induction of an immune response. 453 In the case of zoonosis of a virus that used a receptor other than ACE2 or if a novel SARS-CoV-454 2 variant were to emerge that switched its receptor usage, the decoy receptor approach could also be applicable. This would involve the identification of the entry receptor for the novel virus 455 456 and the construction of a soluble form of the protein to serve as a decoy. While a switch in receptor 457 usage is possible, it has not happened to date despite strong selective pressure on the viral spike 458 protein to alter its amino acid sequence.

459 **STAR Methods**

- 460 **Resource Availability**
- 461 **Lead Contact**
- 462 Further information and requests for resources and reagents should be directed to and will be
- 463 fulfilled by the Lead Contact, Nathaniel R. Landau (nathaniel.landau@med.nyu.edu).
- 464

465 **Materials Availability**

- 466 All unique DNA constructs, proteins and pseudotyped virus generated in this study are available
- 467 from the Lead Contact upon request.
- 468

469 Data and Code Availability

- The data used in this study are available upon request from the lead contact.
- This paper does not report original code.
- Any additional information required to reanalyze the data reported in this paper is
- 473 available from the lead contact upon request.
- 474
- 475 **Experimental Model and Subject Details**
- 476
- 477 Cells

478 293T cells were cultured in DMEM/10% FBS. Clonal cell-lines CHME3.ACE2 and A549.ACE2 479 were established by lipofection of CHME3 and A549 cells with plenti.ACE2⁶ using 480 lipofectamine2000 (Invitrogen). The cells were selected in 1 μg/ml puromycin and single cell 481 clones were evaluated by flow cytometry for high ACE2 expression. CHME3.ACE2, A549.ACE2 482 and ACE2.TMPRSS2.Vero E6 cells were maintained in medium with 1 μg/ml puromycin. hSABCi483 NS1.1 cells were differentiated in air-liquid interface cultures in transwell dishes at 1.5×10^5 484 cells/well. The cells were plated onto inserts coated with human type IV collagen (Sigma) in 485 PneumaCult Ex Plus medium (Stemcell Technologies). The cells were cultured at 37 °C under 486 5% CO₂. The medium in the upper and lower chambers was changed one day after plating and 487 the medium in the lower chamber was replaced every 2 days. The medium in the upper chamber 488 was removed the apical surface was washed with PBS weekly for 2 weeks.

489

490 Mice

491 C57BL/6 mice were from Taconic. Balb/c and hACE2 K18 Tg [B6.Cg-Tg(K18-ACE2)2Prlmn/J]
492 were from The Jackson Laboratory. Animal use and care was approved by the NYU Langone
493 Health Institutional Animal Care and Use Committee (#170304) according to the standards set by
494 the Animal Welfare Act.

495

496 Plasmids

497 The expression vectors used for the production of AAV vectors were AAV.retro Rep/Cap2 498 (Addgene 81070), Rep/Cap6 (Addgene 110770), pAdDeltaF6 (Addgene 112867) and pAAV-499 CAG-tdTomato. Rep/Cap6.2 expression plasmid was generated by overlap extension PCR using 500 Rep/Cap6 template to introduce the F129L mutation. The amplicon was cloned into the EcoR-I 501 and Nru-I sites of Rep/Cap6. To construct GFP/nanoluciferase-expressing AAV vectors pAAV-502 GFP.nLuc, pAAV-CAG-ACE2.1mb.nLuc and pAAV-CAG-ACE2.1mb, DNA fragments encoding 503 GFP.nLuc, ACE2.1mb.nLuc and ACE2.1mb were amplified by PCR and joined by overlap 504 extension PCR using primers containing Kpn-I and EcoR-I sites. The insert was removed from 505 pAAV-CAG-tdTomato by cleavage with Kpn-I and EcoR-I and replaced with similarly cleaved 506 amplicon. Decoy expression vector pcACE2.1mb has been previously described²¹. Expression

507	plasmids used to produce lentiviral pseudotypes were pMDL, pcVSV.G, pRSV.Rev, the lentiviral
508	transfer vector plenti.GFP.nLuc ⁶ . Expression vectors for the SARS-CoV-2 D614G, Omicron BA.1,
509	Omicron BA.2 spike proteins have been previously described ^{9,12,21} . Expression vectors for the
510	Omicron BA.4/5, BA.2.75 and BQ.1 spike proteins were constructed by overlap extension PCR
511	mutagenesis using the D614G 5 spike protein plasmid as template and cloned into pcDNA6.

512

513 Method Details

514

515 **AAV vector stocks**

AAV vector stocks were produced by cotransfection of 293T cells with pAAV-CAG-ACE2.1mb, pAdDeltaF6 and AAV.retro RepCap2 or Rep/Cap6.2 at a ratio of 25:25:30 by the calcium phosphate method. Virus-containing supernatant was harvested 2 days post-transfection. The virus was concentrated by ultracentrifugation on 40% sucrose cushion at 4°C for 16 hours at 30,000 x g, resuspended in PBS and concentrated on an Amicon Ultra Centrifugal Filter Unit (Millipore). Virus titers were measured by RT-qPCR with a primer pair and probe that hybridized to the AAV2 ITR sequences⁶⁶.

523

524 SARS-CoV-2 virus stocks

SARS-CoV-2 WA1/2020 (BEI Resources, NR-52281), Omicron BA.1 (BEI Resources, NR-526
56461), BA.2 (BEI Resources, NR-56781) and BA.5 virus (BEI Resources, NR-58616) stocks
were prepared by infection of ACE2.TMPRSS2.Vero E6 cells at an MOI=0.05 (BEI Resources, NR-56781). 2 hours post-infection, the input virus was removed and a day later, the viruscontaining supernatant was filtered through a 0.45 µm filter, concentrated on an Amicon Ultra
Centrifugal Filter Unit (Millipore) and frozen at -80°C in aliquots.

531

532 Decoy pull-down

533 CHME3.ACE2 or A549.ACE2 cells (1 x 10⁶) were infected with AAV2.retro, AAV6.2-ACE2.1mb 534 or plenti.ACE2.1mb at MOI=0.5. The virus was removed the following day and the supernatant 535 was harvested 3 days later. The decoy protein was pulled-down by a 1-hour incubation with 30 µl 536 nickel-nitrilotriacetic acid-agarose beads (QIAGEN) and eluted in Laemmle loading buffer. The 537 protein was then analyzed on an immunoblot probed with anti-His antibody and horseradish 538 peroxidase (HRP)-conjugated goat anti-mouse IgG secondary antibody (Sigma-Aldrich). The 539 signals were developed with Immobilon Crescendo Western HRP Substrate (Millipore) and 540 visualized on an iBright imaging system (Invitrogen).

541

542 **Pseudotype neutralization assay**

543 D614G, BA.1, BA.2, BA.2.75, BA.4/5 and BQ.1 spike protein-pseudotyped lentiviruses were 544 generated by co-transfection of 293T cells with pMDL, pRSV.Rev, plenti.GFP.nLuc and spike 545 protein expression vector and normalized for reverse transcriptase activity as previously 546 described⁵. CHME3.ACE2 and A549.ACE2 cells were transduced with serially diluted decoy-547 expressing AAV or lentiviral vector. The medium was removed the following day and the cells 548 were challenged with pseudotyped viruses (MOI=0.2). Luciferase activity in duplicate samples 549 was measured 2-dpi in an Envision 2103 microplate luminometer (PerkinElmer).

550

551 Flow cytometry

552 GFP-expressing AAV or lentiviral vectors were injected into hACE2 K18 Tg (AAV) or SAMHD1 553 Knockout mice (lentivirus) via i.n. injection. At 3-dpi, the lungs were homogenized in ACK buffer 554 and the cells were disaggregated by a 30-minute treatment with 1.5 mg/mL collagenase and 0.1 555 mg/mL DNase followed by passage through a 0.22 μm mesh. The cells were blocked with anti-556 CD16/CD32 and stained with Alexa 700-anti-CD45, PerCP-Cy5.5-anti-F4/80, APC-Cy7-SiglecF, 557 PE-Cy7-anti-CD11c, PE-Cy7-anti-CD19, APC-anti-CD3, Pacblue-anti-CD11b, PE-Cy5.5-anti-558 CD62L, APC-anti-CD14 and PE-Ly6C/Ly6G (Gr1) (BioLegend) and analyzed on a Beckman 559 CytoFLEX flow cytometer using with FlowJo software. Cell-types were classified as epithelial 560 (CD45-), alveolar macrophages (CD45+, F4/80+, SiglecF+), interstitial macrophages (CD45+, 561 F4/80+, SiglecF-), DCs (CD45+, F4/80-, CD11c+), T cells (CD45+, CD3+), B cells (CD45+, 562 CD19+), monocytes (CD45+, CD11b+, CD14+) and neutrophils (CD45+, CD62L+, Ly6C/Ly6G+). 563

564 Anti-inflammatory cytokine assay

hACE2 K18 Tg were administrated 1 x 10^{12} vg decoy-expressing AAV or 5 x 10^{6} IU decoyexpressing lentiviral vector. Mice treated with AAV or lentiviral vector were challenged 3- or 7days later, respectively, with 2 x 10^{4} PFU SARS-CoV-2 WA1/2020. Sera were harvested 3-dpi and IFN-γ, MCP-1, TNF-α, IL-10, IL-12 and IL-6 were measured by cytokine bead array using the BD Cytometric Bead Array Mouse Inflammation Kit (BD Biosciences).

570

571 *In vivo* and *in vitro* luciferase assays

572 Balb/c or SAMHD1 knockout mice were administered AAV2.retro or AAV6.2-ACE2.1mb.nLuc (1× 573 10^{12} vg) or plenti.GFP.nLuc (5 x 10^{6} IU) by i.n. instillation. The mice were imaged over 30 days by 574 the injection of 100 µl 1:40 diluted Nano-Glo substrate (Nanolight) and visualization on an IVIS 575 Lumina III XR (PerkinElmer). To measure luciferase activity in the tissues, organs were harvested 576 and homogenized in lysing matrix D tubes with a FastPrep-24 5G homogenizer (MP Biomedicals). 577 Nano-Glo Luciferase Assay Reagent (Nanolight) was added and luminescence was measured on 578 an Envision 2103 plate reader (PerkinElmer). 579

580 Live virus infection of cell-lines

581 CHME3.ACE2, A549.ACE2 and hSABCi-NS1.1 cells (2×10^5) were infected with AAV2.retro or 582 AAV6.2-ACE2.1mb at MOI=0.5. The medium was replaced 1-dpi and the following day, the cells 583 were infected with SARS-CoV-2 at MOI=0.01. The cultures were lysed 2-dpi after which RNA was 584 prepared and cell-associated viral RNA copies were quantified by reverse transcriptase RT-qPCR. 585 Absolute RNA copy numbers were calculated using a standard curve generated by the analysis 586 of a serially diluted *in vitro* transcribed synthetic subgenomic viral RNA using the 2– $\Delta\Delta$ CT method. 587

588 **Prophylactic and therapeutic administration of decoy-expressing vectors.**

589 For prophylaxis experiment, 6-8 weeks old hACE2 K18 Tg or Balb/c mice were anesthetized with isoflurane or ketamine-xylazine cocktail and injected with 80 μ l (i.n. or i.v. or i.m.) (1 x 10¹² vg) of 590 591 AAV2.retro or AAV6.2-decoy or 5 x 10⁶ IU of plenti.ACE2.1mb. After 1-30 days (AAV) and 1-60 592 days (lentivirus vector) of infection, the mice were infected i.n. with 2 x 10⁴ plaque-forming unit 593 (PFU) of SARS-CoV-2 WA1/2020 (hACE2 K18 Tg) or Omicron BA.1 or BA.2 or BA.5 (Balb/c). At 2-dpi (Omicron) or 3-dpi (SARS-CoV-2 WA1/2020), the mice were sacrificed and RNA was 594 595 prepared from 200 µl of lung lysate using the Quick-RNA MiniPrep kit (Zymo Research). For 596 therapeutic testing, hACE2 K18 Tg were infected i.n. with 2 x 10⁴ PFU SARS-CoV-2 WA1/2020. 597 The mice were infected 0-48 hours post-infection i.n. with 80 μ l (1 x 10¹² vg) of AAV2.retro or 598 AAV6.2-decoy. 3-dpi (SARS-CoV-2 WA1/2020), the mice were sacrificed and RNA was prepared 599 from 200 µl of the lung lysate using a Quick-RNA MiniPrep kit.

600

601 Virus loads

602 SARS-CoV-2 E gene subgenomic RNA levels were measured by reverse transcriptase RT-gPCR 603 with a TagMan probe. Lung RNA was mixed with TagMan Fast Virus 1-step Master Mix (Applied 604 Biosystems), 10 mM forward and reverse primers, and 2 mM probe. PCR cycles were 5 minutes 605 at 50°C, 20 seconds at 95°C, 40 cycles of 3 seconds at 95°C, 3 seconds at 60°C). E gene 606 subgenomic RNA copies were measured using forward primer subgenomic F (CGATCTCTTGTAGATCTGTTCTC), reverse primer E Sarbeco R and probe E Sarbeco P1)^{67,68}. 607 608 Tissue analyses were normalized to GAPDH mRNA copies measured using the mouse 609 GAPDH.forward (CAATGTGTCCGTCGTGGATCT) and mouse GAPDH.reverse 610 (GTCCTCAGTGTAGCCCAAGATG) GAPDH with mouse probe (FAM-611 CGTGCCGCCTGGAGAAACCTGCC-BHQ) human GAPDH.forward or 612 (GTCTCCTCTGACTTCAACAGCG) GAPDH.reverse and human 613 (ACCACCCTGTTGCTGTAGCCAA) with human GAPDH probe (FAM-TAGGAAGGACAGGCAAC-614 IBFQ). Absolute RNA copy numbers were calculated using a standard curve generated by the 615 analysis of a serially diluted in vitro transcribed synthetic subgenomic viral RNA containing the E 616 gene sequence (2019-nCoV E Positive Control, IDT: 10006896) using the 2- $\Delta\Delta$ CT method.

617

618 Histology

The lungs of SARS-CoV-2-infected mice were harvested 3-dpi. The tissue was fixed in 10% neutral buffered formalin for 72 hours at room temperature and then processed through graded ethanol, xylene and into paraffin in a Leica Peloris automated processor. 5 μm paraffin-embedded sections were deparaffinized and stained with hematoxylin (Leica, 3801575) and eosin (Leica, 3801619) on a Leica ST5020 automated histochemical strainer. Slides were scanned at 40× magnification on a Leica AT2 whole slide scanner and the images were transferred to the NYULH Omero web-accessible image database.

626

627 Statistical Analysis

628 Statistical significance was determined by Kruskal-Wallis test with post hoc Dunn's test.

- 629 Significance was calculated based on two-sided testing and is shown in the figures as the mean
- 630 ± SD with confidence intervals listed as *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

631

632 Study Approval

633 Animal procedures were performed with the written approval of the NYU Animal Research

634 Committee in accordance with all federal, state, and local guidelines.

635

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640

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- thank David J. Simon (Weill Cornell Medicine) for providing AAV plasmids.

645

646 **Author Contributions**

- T.T. and N.R.L. designed the experiments. T.T., B.M.D. and J.M. carried out the experiments. T.T.
- and N.R.L. wrote the manuscript. N.R.L. supervised the study and revised the manuscript.

649 **Figure legends**

650

Figure 1. AAV-ACE2.1mb prevents SARS-CoV-2 infection in cell culture.

(A) The domain structure of full-length ACE2 is shown above with the ectodomain, transmembrane (TM) and intracellular domain (IC). The structure of the decoy consisting of the ACE2 ectodomain, human lgG1-CH3 and carboxy-terminal His tag. The ACE2 domain contains three high affinity mutations as described by Chan et al. and a H345A mutation in the ACE2 peptidase catalytic site.

(B) A549.ACE2 and CHME3.ACE2 cells were transduced with a 5-fold serial dilution of
AAV2.retro and AAV6.2 decoy vectors and then challenged with ancestral D614G, Omicron BA.1,
BA.2, BA.2.75, BA.4/5 and BQ1 spike protein-pseudotyped lentiviral vectors. Luciferase activity
was measured 2-dpi. The curves shown above indicate the infectivity based on luciferase activity
normalized to mock vector-transduced cells. Each measurement is shown as the average of
duplicates. The table below shows that ID₅₀ calculated from the curves shown above.

(C) CHME3.ACE2 and A549.ACE2 cells were transduced with AAV2.retro-GFP.nLuc (GFP.Luc),
AAV6.2-GFP.nLuc, AAV2.retro-ACE2.1mb, AAV6.2-ACE2.1mb at MOI=0.5. 2 days post
transduction, the cells were infected with SARS-CoV-2 WA1/2020 (MOI=0.01). The cultures were
lysed 2-dpi and RNA was prepared. Viral RNA copy numbers were determined by RT-gPCR.

667 (D) hSABCi-NS1.1 cells were transduced with AAV2.retro-GFP.nLuc, AAV6.2-GFP.nLuc, 668 AAV2.retro-ACE2.1mb, AAV6.2-ACE2.1mb at MOI=0.5. 2 days post transduction, the cells were 669 infected with SARS-CoV-2 WA1/2020 (MOI=0.01). The cultures were lysed 2-dpi and RNA was 670 prepared. Viral RNA copy numbers were determined by RT-qPCR. Confidence intervals are 671 shown as the mean \pm SD. **P \leq 0.01. The experiment was done twice with similar results.

(E) CHME3.ACE2 and A549.ACE2 cells were transduced with AAV2.retro or AAV6.2-ACE2.1mb at MOI=0.5. 3-dpi, secreted decoy protein in the supernatant was pulled-down on NTA beads and bead-bound decoy was detected on an immunoblot probed with His-tag antibody. Pure recombinant decoy protein is shown at right as a standard and was used to determine the amount of protein pulled-down, which is shown below each lane as micrograms decoy pulled-down from 1 ml of culture supernatant. At right is shown decoy protein in the cell lysates is shown below with GAPDH as a loading control.

679

Figure 2. Vectored immunoprophylaxis by decoy-expressing AAV decoy vector and therapeutic use.

682 (A) The experimental scheme for testing decoy prophylaxis is diagrammed. hACE2 K18 Tg and 683 Balb/c mice were treated by i.v. injection or i.n. instillation with decoy-expressing AAV vector or control GFP.nLuc-expressing AAV vector (1 X 10¹² vg). 3 days post-treatment, the hACE2 K18 684 685 Tg mice were challenged with SARS-CoV-2 WA1/2020 and the Balb/c mice were challenged with 686 Omicron BA.1, BA.2 or BA.5 (2 x 10⁴ PFU). Viral RNA copies were quantified 2 days (Omicron) 687 or 3 days (SARS-CoV-2 WA1/2020) post-infection. 688 (B) Mice (n=3-4) were treated with decoy-expressing or control GFP-expressing AAV vectors and 689 challenged with SARS-CoV-2 WA1/2020. Viral RNA copies in the lungs were quantified 3-dpi. 690 (C) H&E stained lung sections from control and decoy-expressing AAV vectors and SARS-CoV-

- 691 2 infected mice are shown on the left (2 x, scale bars 500µm) and with the boxed area enlarged
 692 on the right (20 x, scale bars 50µm).
- 693 (D) Mice (n=3) were treated with decoy-expressing AAV vectors on day 0 and challenged with
- 694 SARS-CoV-2 WA1/2020 on day 3. Body weight was measured daily. As controls, the mice were

695 infected with SARS-CoV-2 WA1/2020 but not treated with AAV vector or treated with AAV vector
696 but not infected with SARS-CoV-2 WA1/2020.

(E) Balb/c mice (n=3-4) were treated with decoy-expressing or GFP-expressing control AAV
vectors and then infected 3 days later with Omicron BA.1, BA.2, or BA.5. Viral RNA copies in the
lungs were quantified 2-dpi.

700 (F) Mice (n=4) were administered decoy-expressing AAV vectors i.m. or i.v. and challenged 3-dpi

with SARS-CoV-2 WA1/2020. Infected but untreated and uninfected/untreated mice are includedas controls.

G. Therapeutic use of the decoy-expressing AAV vectors was tested as diagrammed (left). hACE2 K18 Tg (n=4) were infected with SARS-CoV-2 WA1/2020 (2 x 10^4 PFU) and then treated with decoy-expressing AAVs at time-points up to 48 hours post-infection. Viral RNA in the lung was quantified 3-dpi (right). As controls the mice were untreated (No AAV) or uninfected. Confidence intervals are shown as the mean ± SD. ***P≤0.001, ****P≤0.0001. The experiment was done twice with similar results.

709

710 Figure 3. Durable vectored immunoprophylaxis by decoy-expressing AAV vectors.

(A) Balb/c mice (n=3) were injected i.n. with decoy-luciferase fusion protein-expressing AAV
 vectors (1 X 10¹² vg). Luciferase activity was visualized by live imaging over 30 days at the
 indicated time points. Representative images of a mouse from each group are shown.

(B) Luciferase activity in lung tissue homogenates from mice treated with the decoy-luciferase
 expressing AAV vectors (n=2) was measured over the time course.

(C) The experimental scheme to test the durability of AAV vectored immunoprophylaxis is diagrammed (left). hACE2 K18 Tg (n=4) were injected with AAV decoy. At 1-, 2-, 3-dpi, the mice were challenged with SARS-CoV-2 (2 x 10^4 PFU) and viral RNA in the lungs was quantified. The results are shown as a histogram (right). SARS-CoV-2 infected/AAV untreated (No AAV) and AAV
 untreated/SARS-CoV-2 uninfected (Uninfected) controls are shown. Confidence intervals are

- shown as the mean \pm SD. ****P \leq 0.0001. The experiment was done twice with similar results.
- 722

723 Figure 4. Long-term vectored immunoprophylaxis by decoy-expressing lentiviral vector.

(A) A549.ACE2 and CHME3.ACE2 cells were transduced with a 5-fold serial dilution of decoyexpressing lentiviral vectors and then challenged with D614G, Omicron BA.1, BA.2, 2.75, BA.4/5
and BQ.1 spike protein-pseudotyped lentiviral vectors. Luciferase activity was measured 2-dpi
(above). The curves indicate infectivity based on luciferase activity normalized to mock vectortransduced cells. Measurements are the average of duplicates. ID₅₀s calculated from the curves
are shown in the table (below).

(B) Structure of lentiviral vector and experimental scheme are shown. hACE2 K18 Tg mice or Balb/c were injected with lentiviral vector (5 x 10^6 IU) i.p., i.v. or i.n. injection. One week later, the mice were challenged with 2 x 10^4 PFU of SARS-CoV-2 WA1/2020 (hACE2 K18 Tg) or Omicron (Omicron). Viral RNA in the lungs was quantified 3-dpi.

(C) Mice were administered luciferase-expressing lentiviral vector i.v. or i.n. (n=2). Tissues (nasal,
lung, trachea, spleen and liver) were harvested and luciferase activity was measured over 60
days at the indicated time-points.

(D) Decoy-expressing lentiviral vectors (5 x 10^6 IU) were administered i.v. or i.n. and after 7-, 30and 60-days challenged with SARS-CoV-2 (2 x 10^4 PFU). Viral RNA was quantified 3-dpi. Confidence intervals are shown as the mean ± SD. **P ≤ 0.01, ****P≤0.0001. The experiment was done twice with similar results.

741

742 Figure 5. Comparison of lung cell subpopulations transduced by AAV and lentiviral vectors.

743 (A) GFP-expressing AAV vectors were administrated i.n. After 3 days, the lungs were harvested 744 and the tissue were enzymatically disaggregated. The cells were analyzed by multi-color flow 745 cytometry with cell-type specific marker antibodies to distinguish subpopulations defined as 746 follows: Leukocytes (CD45+), epithelial (CD45-), alveolar macrophages (CD45+, F4/80+, 747 SiglecF+), interstitial macrophages (CD45+, F4/80+, SiglecF-), DCs (CD45+, F4/80-, CD11c+), T 748 cells (CD45+, CD3+), B cells (CD45+, CD19+), monocytes (CD45+, CD11b+, CD14+), 749 neutrophils (CD45+, CD62L+, Ly6C/Ly6G+). Representative flow cytometry plots of the GFP+ 750 cells and GFP+/CD45+ populations are shown on the left and the subpopulations within the 751 GFP+/CD45+ leukocytes are shown in the pie charts on the right. 752 (B) Mice were administered GFP-expressing lentiviral vector i.n. GFP+ cells in the lung were 753 analyzed by flow cytometry as in (A). Representative flow cytometry plots of the GFP+ cells and

754 GFP+/CD45+ populations are shown on the left and the subpopulations within the GFP+/CD45+

755 leukocytes are shown in the pie charts on the right.

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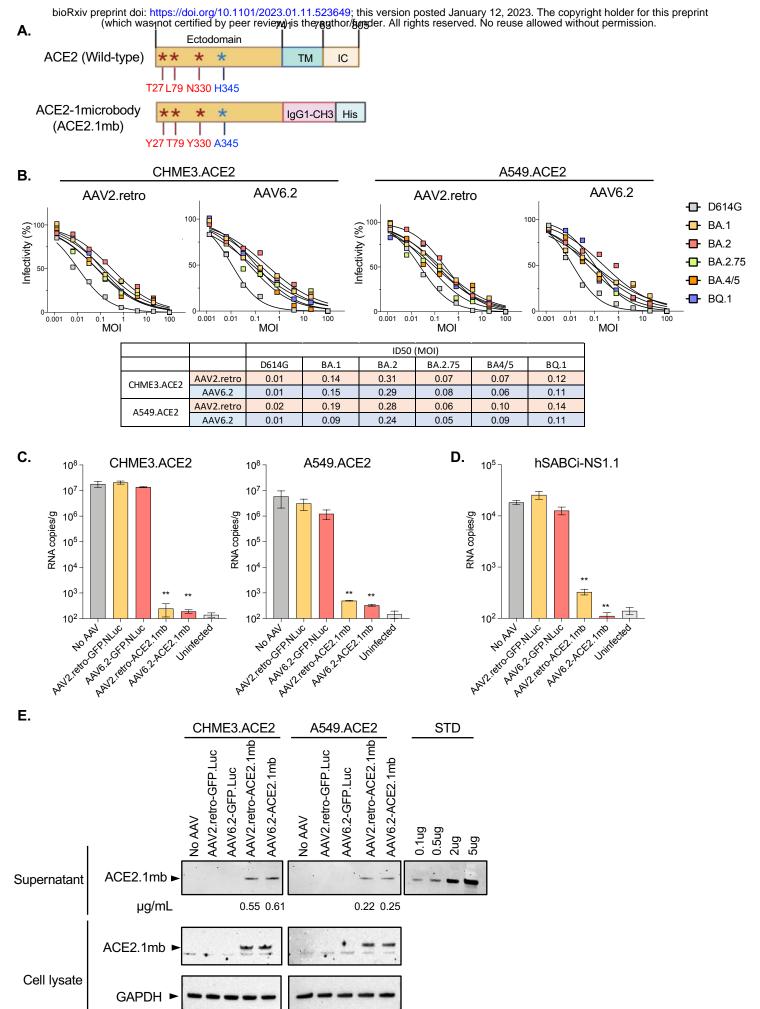
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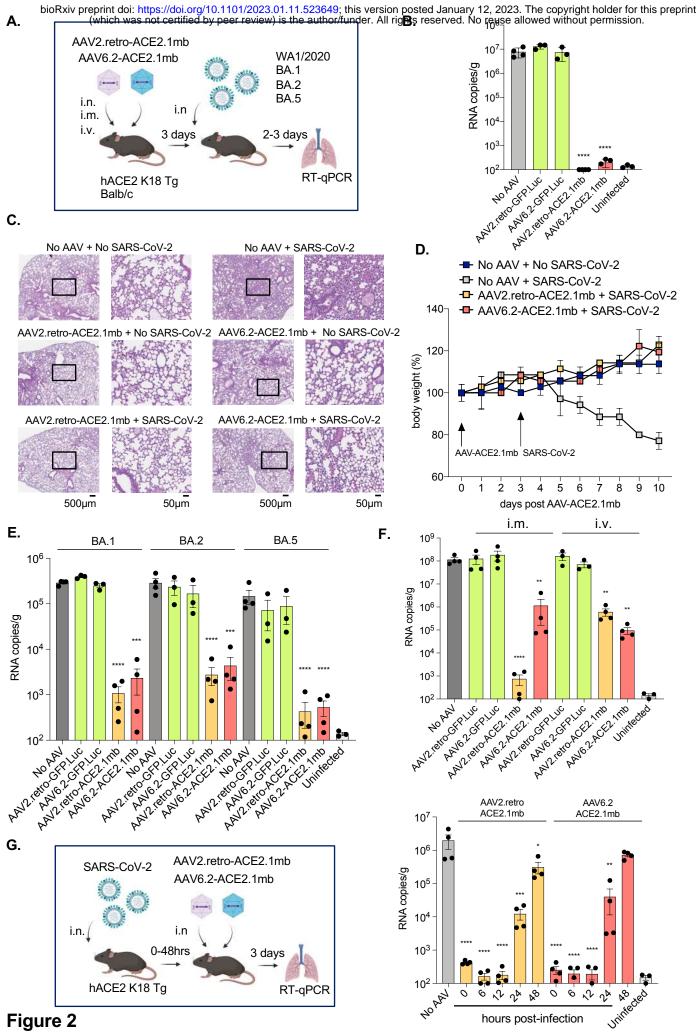
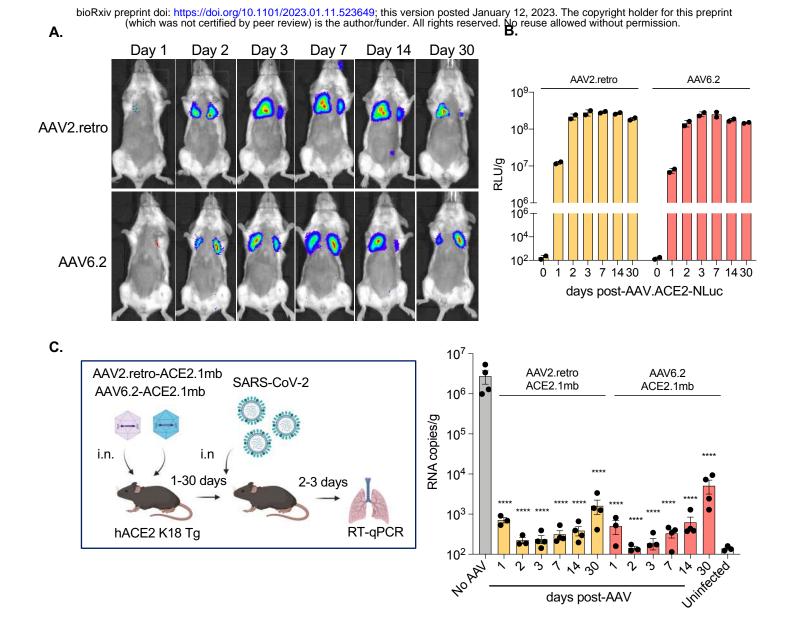
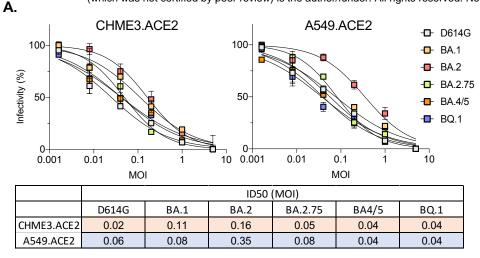


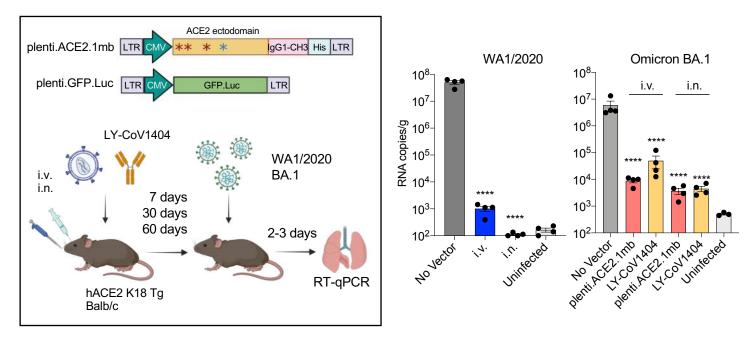
Figure 2

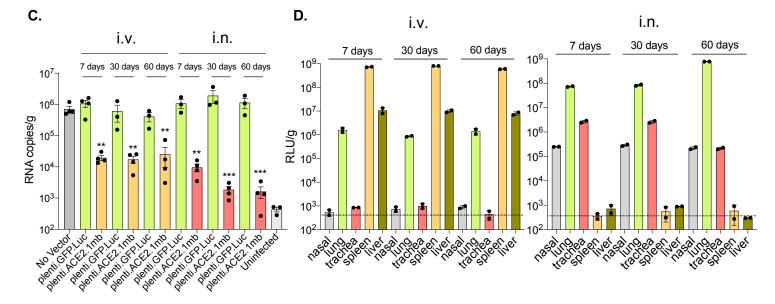


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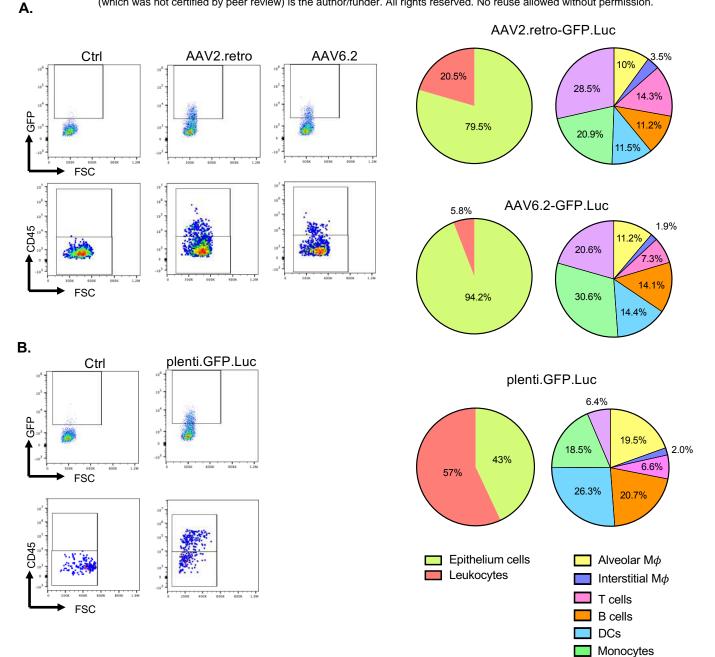


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Neutrophils

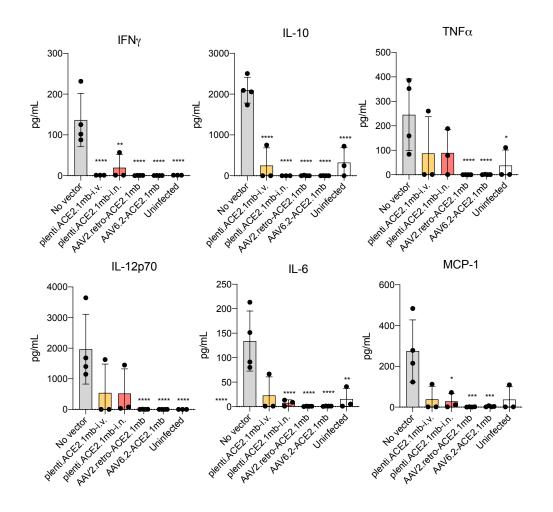


Figure S1. Intranasal injected AAV2.retro, AAV6.2-decoys and lentivirus-based ACE2.1mb didn't induce any inflammatory cytokine secretion.

Mice (n=4) were treated with the decoy-expressing AAV vectors (1 x 10^{12} IU) or decoy-expressing lentiviral vector (5 x 10^{6} IU). After 3 (AAV) or 7days (lentiviral vector), the mice were challenged with SARS-CoV-2 WA1/2020 and 3-dpi the levels of IFN γ , TNF α , IL-10, IL-6, MCP-1 and IL-12p70 in lung were measured by cytokine beads array. The Y-axis shows the concentration of each cytokine. The experiment was done twice with similar results. Confidence intervals are shown as the mean ± SD. *P ≤ 0.05, **P ≤ 0.01, ***P≤0.001, ****P≤0.0001.

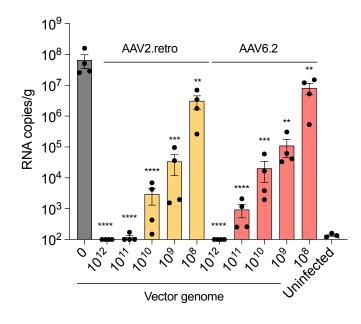


Figure S2. AAV-Decoy protected mice from SARS-CoV-2 infection.

Different doses of decoy-expressing AAV vectors (1 X 10^{12} , 1 X 10^{11} , 1 X 10^{10} , 1 X 10^{9} , 1 X 10^{8} vg) were administered to hACE2 K18 Tg (n=4) by i.n. instillation. 3 days post-AAV injection, mice were challenged with 1 X 10^{4} PFU of SARS-CoV-2 WA1/2020. At 3-dpi, subgenomic viral E gene RNA in the lung were quantified. Confidence intervals are shown as the mean ± SD. **P ≤ 0.01, ****P≤0.0001. The experiment was done twice with similar results.

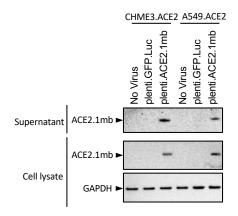


Figure S3. Lentivirus-based ACE2.1mb protected mice from SARS-CoV-2 infection.

CHME3.ACE2 and A549.ACE2 cells were transduced with decoy-expressing lentiviral vectors at an MOI of 0.5. 3-dpi, decoy protein secreted into the supernatant was pulled-down on NTA beads and bead-bound decoy protein was detected on an immunoblot probed with His-tag antibody. Decoy protein in the cell lysates is shown below with GAPDH as a loading control.

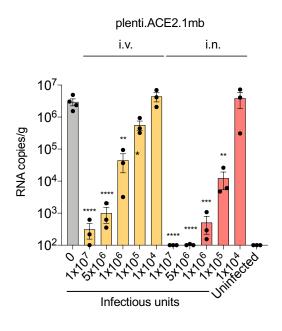


Figure S4. Lentivirus-based ACE2.1mb protect mice from SARS-CoV-2 infection.

hACE2 K18 Tg mice (n=3) were injected i.v. or i.n. with different amounts of decoy-expressing lentiviral vectors (1 X 10⁷, 1 X 10⁶, 1 X 10⁵, 1 X 10⁴ IU). One week later, the mice were challenged with 1 X 10⁴ PFU SARS-COV-2. At 3-dpi, lung subgenomic viral E RNA was quantified by RT-PCR. Confidence intervals are shown as the mean \pm SD. **P \leq 0.01, ***P \leq 0.001, ****P \leq 0.0001.