

## 1 **Supplementary Methods**

### 2 **Cell culture**

3 Vero E6 cells (Vero C1008, ATCC, Cat#CRL-1586, RRID: CVCL\_0574) were maintained in Dulbecco's  
4 Modified Eagle's Medium (DMEM) supplemented with 10% FBS, 1% Glutamine and 1%  
5 penicillin/streptomycin (Gibco). Virus infections were performed in DMEM with 2% FBS, 1% Glutamine  
6 and 1% penicillin/streptomycin.

7 Cultivation and differentiation of human blood-derived macrophages was performed at the Institute for  
8 Lung Research (Marburg, Germany) as described previously [79,80]. Briefly, macrophages were obtained  
9 from primary monocytes isolated by MACS CD14 positive selection from healthy donor buffy coats  
10 provided by the Centre for Transfusion Medicine and Haemotherapy, University Hospital Giessen and  
11 Marburg (Germany). All blood donors gave informed written consent for use of their blood samples for  
12 scientific purposes (Ethics approval number: 161/17). Freshly isolated monocytes were seeded in ultra-low  
13 attachment plates (Corning) and were left to adhere for 2 h in supplement-free RPMI medium (Gibco). After  
14 adhesion of cells, differentiation was initiated by addition of 1% human AB serum (Sigma) and monocytes  
15 were cultivated for seven days. Maturation to blood-derived macrophages was confirmed by microscopy.  
16 Cells were detached by incubation with pre-warmed PBS for 10 min and then seeded at a density of  $3 \times 10^5$   
17 cells/12well in 1 mL of fresh RPMI media. All cells were cultivated at 37°C and 5% CO<sub>2</sub>.

### 18 **Viruses**

19 All work with infectious SARS-CoV-2 was performed in the BSL-4 facility at the Institute of Virology,  
20 Philipps University Marburg (Marburg, Germany). BavPat1/2020 isolate (#026V-03883) was purchased from  
21 European Virus Archive Global (EVAg). The B.1.1.7 variant (BioProject no. PRJNA721582) was a clinical  
22 isolate and was isolated at the Institute of Virology, Philipps University Marburg (Marburg, Germany). The  
23 B.1.351 (GenBank Accession no. MW822592) variant was a clinical isolate and was isolated at the Institute  
24 for Medical Virology, University Hospital Frankfurt (Goethe University Frankfurt am Main, Germany). All

25 viruses were propagated on Vero76-TMPRSS2 cells using DMEM supplemented with 2% FBS, 1%  
26 Glutamine and 1% penicillin/streptomycin (Gibco). On day two (BavPat1/B.1.1.7/B.1351) after infection, cell  
27 culture supernatants were harvested, and titers were determined by immunoplaque and TCID<sub>50</sub> assay on  
28 VeroE6 cells.

### 29 **Surface Plasmon Resonance (SPR)**

30 The SPR assays were performed using a Biacore 8K system and a CM5 sensor chip (GE Healthcare). The  
31 running buffer for this experiment and all dilutions were done in 1 X HBS-EP+ (GE Healthcare Life Sciences  
32 BR100669). The CM5 sensor chip was activated with equal mixture of EDC/NHS for 420 sec at a flow rate  
33 of 10 ml/min and immobilized with Protein A/G (50 mg/ml in 10 mM acetate pH 4.5) for 420 sec at a flowrate  
34 of 10 ml/min resulting in  $\approx$  2400-2800 RU of Protein A/G on the surface. Subsequently, the sensor chip was  
35 deactivated with 1M ethanolamine HCl for 420 sec at a flowrate of 10 ml/min. DZIF-10c (1 mg/ml) was  
36 captured on the Protein A/G surface for 60 sec at a flowrate of 10 ml/min resulting in capture levels of  $\approx$  150  
37 RU. The analyte (SARS-COV2 RBD-His) was injected over the captured ligand for 120 sec at a flowrate of  
38 30 ml/min. The dissociation was done for 600 sec. The concentrations of the analyte were as follows: 0 nM,  
39 1.56 nM, 3.13 nM, 6.25 nM, 12.5 nM, and 25 nM. After each analyte injection was complete, the surface was  
40 regenerated by injecting 0.85% phosphoric acid for 30 sec at a flowrate of 30 ml/min. The analyte interaction  
41 with sensor surface (flow cell 1) and blank (HBS-EP+ or 0 nM analyte) were subtracted from the raw data.  
42 Sensorgrams were then fit globally to 1:1 Langmuir binding to provide on-rate ( $k_a$ ), off-rate ( $k_d$ ), and affinity  
43 ( $K_D$ ) values. The binding experiments for SARS-COV-2 RBD-His were performed three separate times using  
44 fresh dilutions.

### 45 **ELISA analysis**

46 ELISA plates were coated with 2 mg/ml of SARS-CoV-2 spike ectodomain, RBD, N-terminal truncated, or  
47 EBOV Makona glycoprotein (GP) ectodomain in PBS or monomeric SARS-CoV-2 spike ectodomain in 2 M  
48 Urea at 4°C overnight. Proteins were produced as previously described [25]. Next day, plates were blocked

49 with 5% BSA in PBS for 60 min at RT, incubated with primary antibody (starting concentration 10 µg/ml)  
50 in PBS for 120 min and secondary antibody (anti-human IgG-HRP; Southern Biotech 2040-05) diluted 1:2500  
51 in 1% BSA in PBS for 60 min at RT. ELISAs were developed with ABTS solution (Thermo Fisher 002024)  
52 and absorbance was measured at 415 nm and 695 nm.

### 53 **Pseudovirus neutralization assay**

54 SARS-CoV-2 pseudovirus particles were generated by co-transfection of individual plasmids encoding HIV  
55 Tat, HIV Gag/Pol, HIV Rev, luciferase followed by an IRES and ZsGreen, and the SARS-CoV-2 spike protein  
56 [33] into HEK 293T cells using the FuGENE 6 Transfection Reagent (Promega). Spike sequences from the  
57 following global strains REF were used: Wu01 spike (EPI\_ISL\_40671); BavP1 spike (EPI\_ISL\_406862);  
58 ARA36 spike (EPI\_ISL\_418432); DRC94 spike (EPI\_ISL\_417947); CA5 spike (EPI\_ISL\_408010) and NRW8  
59 spike (EPI\_ISL\_414508), B.1.1.7 variant [81] and B.1.351 variant [82]. Mutations were introduced by PCR  
60 into the Wu01 spike as backbone. Virus culture supernatant was harvested at 48 h and 72 h post transfection  
61 and stored at -80°C till use. The harvested virus was titrated by infecting 293T expressing ACE2 and after a  
62 48 h incubation at 37°C and 5% CO<sub>2</sub>, luciferase activity was determined after addition of luciferin/lysis  
63 buffer (10 mM MgCl<sub>2</sub>, 0.3 mM ATP, 0.5 mM Coenzyme A, 17 mM IGEPAL (all Sigma-Aldrich), and 1 mM  
64 D-Luciferin (GoldBio) in Tris-HCL) using a microplate reader (Berthold). For neutralization assays, a virus  
65 dilution with a relative luminescence units (RLU) of approximately 1000-fold in infected cells versus non-  
66 infected cells was selected. For testing neutralization potency of DZIF-10c, serial dilutions of DZIF-10c were  
67 co-incubated with pseudovirus supernatants for 1 h at 37°C, following which 293T-ACE-2 cells were added.  
68 After a 48-hour incubation at 37°C and 5% CO<sub>2</sub>, luciferase activity was determined using the luciferin/lysis  
69 buffer. After subtracting background RLU of non-infected cells, 50% inhibitory concentration (IC<sub>50</sub>) were  
70 calculated as the DZIF-10c concentration resulting in a 50% reduction in RLU compared to the untreated  
71 virus control wells. Each antibody dilution was tested in duplicates. IC<sub>50</sub> values were calculated by plotting  
72 a dose response curve in GraphPad Prism 7.0.

73 **SARS-CoV-2 Virus neutralization test (VNT100)**

74 SARS-CoV-2 neutralizing activity of human monoclonal antibodies was investigated based on a previously  
75 published protocol with slight modifications [25,83,84]. Briefly, monoclonal antibodies were serially diluted  
76 in DMEM supplemented with 2% FBS, 1% glutamine and 1% penicillin/streptomycin (Gibco) in 96-well  
77 plates before 100 PFU SARS-CoV-2 were added to each sample. Subsequently, Vero E6 cells (Vero C1008,  
78 ATCC, Cat#CRL-1586, RRID: CVCL\_0574) were washed with PBSdef, trypsinized and diluted in DMEM  
79 with 10% FBS, 1% glutamine and 1% penicillin/streptomycin. Cells were diluted in DMEM to a final  
80 concentration of 2% FBS, 1% glutamine and 1% pen/strep and 100 µl of the cell solutions was added to  
81 virus/antibody samples, corresponding to approximately 20.000 cells/well. Neutralization was defined as  
82 absence of cytopathic effect compared to virus controls (IC100). The following controls were included: back  
83 titration of virus dilution, positive control as an inter-assay neutralization standard (cells infected with  
84 SARS-CoV-2 and treated with an antibody with a known neutralizing titer), negative control (cells without  
85 infection and antibodies), cytotoxicity control (cells without infection, only treated with antibodies).

86 **Tissue culture infectious dose 50 (TCID50) Assay**

87 The amount of infectious SARS-CoV-2 particles from cell culture supernatants or lung homogenates was  
88 determined by TCID50 assay. Vero E6 cells were cultured in DMEM with 2% FBS, 1% glutamine, 1%  
89 penicillin/streptomycin in 96-well plates and were inoculated with 10-fold serial dilutions of supernatant  
90 samples or 5-fold serial dilutions of lung homogenates. At four days post infection, SARS-CoV-2 CPE was  
91 evaluated, and titers per ml or 25 mg lung tissue were calculated using the Spearman-Kaerber method [85].

92 **Detection of genomic RNA (gRNA) by quantitative real-time reverse transcription PCR (RT-qPCR)**

93 In order to quantify viral gRNA, nucleic acids were isolated from cell lysates or lung homogenates using  
94 the RNeasy Mini Kit (Qiagen) according to manufacturer's instructions. Total RNA amount was measured  
95 using a NanoDrop ND-100 spectrophotometer.

96 For analysis of SARS-CoV-2 genome copies, RNA was reverse transcribed and viral genome copies  
97 quantified by real-time PCR using the OneStep RT-PCR Kit (Qiagen) and the StepOne Real-Time PCR  
98 System (Applied Biosystems). Primers and probes targeting the E gene of SARS-CoV-2 (E Assay\_First Line  
99 Screening) as well as a positive control plasmid were purchased from idtdna (Berlin, Germany) [86]. Reverse  
100 transcription and amplification were performed using the following protocol: 55°C for 30 min, 95°C for 15  
101 min followed by 45 cycles of 95°C for 5 s, 60°C for 15 s and 72°C for 15 s. Quantification was carried out  
102 using a standard curve based on 10-fold serial dilutions of a plasmid DNA comprising the target region  
103 ranging from 103 to 106 copies.

104 E\_Sarbeco\_F1: ACAGGTACGTTAATAGTTAATAGCGT

105 E\_Sarbeco\_R2: ATATTGCAGCAGTACGCACACA

106 E\_Sarbeco\_P1: FAM-ACACTAGCCATCCTTACTGCGCTTCG-BBQ

107 MERS-CoV genome copies were determined using a previously published protocol [29,87]. Briefly, RNA  
108 was reverse transcribed and viral genome copies quantified by real-time PCR using the SuperScript III  
109 OneStep RT-PCR Kit (Invitrogen Life Technologies) and the StepOne Real-Time PCR System (Applied  
110 Biosystems). Primers and probes targeting the E gene of MERS-CoV were purchased from Tib-Molbiol  
111 (Germany). Reverse transcription and amplification were performed using the following protocol: 55°C for  
112 20 min, 95°C for 3 min followed by 45 cycles of 94°C for 15 s, 58°C for 30 s. Quantification was carried out  
113 using a standard curve based on 10-fold serial dilutions of appropriate cloned RNA ranging from 101 to 106  
114 copies.

115 upE\_Fwd: GCAACGCGCGATTTCAGTT

116 upE\_Rev: GCCTCTACACGGGACCCATA

117 upE\_PrB: FAM-CTCTTCACATAATCGCCCCGAGCTCG-TAMRA

118 **Detection of subgenomic RNA (sgRNA) by quantitative real-time reverse transcription PCR (RT-qPCR)**

119 Subgenomic RNA was determined according to a previously published protocol [17,62]. Nucleic acids were  
120 isolated as described before. SARS-CoV-2 subgenomic RNA of the E gene was reverse transcribed and copy  
121 numbers quantified by real-time PCR using the SuperScript III OneStep RT-PCR Kit (Invitrogen Life  
122 Technologies) and the StepOne Real-Time PCR System (Applied Biosystems). Primers and probes targeting  
123 the leader and the E gene of SARS-CoV-2, respectively, were purchased from Tib-Molbiol (Germany).  
124 Reverse transcription and amplification were performed using the following protocol: 55°C for 20 min, 95°C  
125 for 3 min followed by 45 cycles of 95°C for 10 s, 56°C for 15 s and 72°C for 15 s. Quantification was carried  
126 out using a standard curve based on 10-fold serial dilutions of a plasmid DNA comprising the target region  
127 ranging from 10<sup>1</sup> to 10<sup>7</sup> copies.

128 sgLead\_SARS2\_F: CGATCTCTTGTAGATCTGTTCTC

129 sgE\_SARS2\_R: ATATTGCAGCAGTACGCACACA

130 sgE\_SARS2\_P: FAM-ACACTAGCCATCCTTACTGCGCTTCG-BBQ

### 131 **Detection of mCherry mRNA by quantitative real-time reverse transcription PCR (RT-qPCR)**

132 To confirm transduction with AdV-hACE2, mRNA levels of the reporter mCherry was determined  
133 according to a previously published protocol [29]. Nucleic acids were isolated from lung homogenates as  
134 described before. mCherry mRNA was reverse transcribed and copy numbers quantified by real-time PCR  
135 using the SuperScript III OneStep RT-PCR Kit (Invitrogen Life Technologies) and the StepOne Real-Time  
136 PCR System (Applied Biosystems). Primers and probes targeting the mCherry gene were purchased from  
137 Tib-Molbiol (Germany). Reverse transcription and amplification were performed using the following  
138 protocol: 50°C for 30 min, 95°C for 15 min followed by 40 cycles of 95°C for 15 s, 48°C for 30 s and 72°C for  
139 20 s. Quantification was carried out using a standard curve based on 10-fold serial dilutions of appropriate  
140 cloned RNA ranging from 5x10<sup>2</sup> to 5x10<sup>5</sup> copies.

141 mcherry181for: CATGGTAACGATGAGTTAG

142 mcherry287rev: GTTGCCTTCCTAATAAGG

143 mcherry probe: FAM- TACCACCTTACTTCCACCAATCGG-BBQ

144 ***In vitro* ADE Assay**

145 For assessment of possible DZIF-10c-related enhancement of SARS-CoV-2 infection (ADE), human blood-  
146 derived macrophages were infected with SARS-CoV-2 in presence of different concentrations of DZIF-10c  
147 or IgG isotype control antibodies.  $2.5 \times 10^5$  macrophages were seeded in 12 well plates in 1 ml RPMI medium  
148 supplemented with 1% Glutamine, penicillin/streptomycin and non-essential amino acids. After adhesion,  
149 10% FBS was added and the cells were incubated for three to four days. Prior to infection with SARS-CoV-  
150 2 non-neutralizing IgG control antibodies or DZIF-10c in neutralizing and sub-neutralizing concentrations,  
151 respectively, were incubated for 1 h at 37°C together with 800 50% tissue culture infective doses (TCID<sub>50</sub>)  
152 SARS-CoV-2 (BavPat1/2020 isolate, European Virus Archive Global # 026V-03883). Directly before  
153 inoculation of macrophages with the antibody/virus mixture, 500 µl of the macrophage cell culture medium  
154 was transferred to a new 12 well plate and mixed with fresh supplemented 10% RPMI medium (storage  
155 medium). Subsequently, 800 µl of the antibody/virus mixture was added to the macrophages and cells were  
156 incubated for 4 h at 37°C. Afterwards, antibody/virus-containing medium was discarded and 1 ml storage  
157 medium was added to the cells. At four days post infection, CPE was evaluated and supernatants were  
158 collected and stored at -80°C. RNA isolation from cell lysates was performed using the RNeasy Mini Kit  
159 (Qiagen) according to manufacturer's instructions. In control settings, the experimental protocol was  
160 modified regarding virus and cells. MERS-CoV (EMC/2012) was used to show general susceptibility of  
161 macrophages to infection with coronaviruses. Vero E6 cells were used to demonstrate infectivity of the  
162 SARS-CoV-2 isolate as well as the neutralizing activity of DZIF-10c in this experimental setting.