

Direct and ultrasensitive bioluminescent detection of intact respiratory viruses

Alexander Gräwe¹, Harm van der Veer¹, Seino A.K. Jongkees², Jacky Flipse^{3,4}, Iebe Rossey⁵,
Robert P. de Vries⁶, Xavier Saelens⁵, Maarten Merkx^{1*}

1 Laboratory of Protein Engineering, Department of Biomedical Engineering and Institute for Complex
Molecular Systems, Eindhoven University of Technology, Eindhoven, The Netherlands. E-mail:
m.merkx@tue.nl

2 Department of Chemistry and Pharmaceutical Sciences, Amsterdam Institute of Molecular and Life
Sciences, Vrije Universiteit Amsterdam, Amsterdam, The Netherlands

3 Laboratory for Medical Microbiology and Immunology, Rijnstate Hospital, Arnhem, The Netherlands

4 Laboratory for Medical Microbiology and Immunology, Dicoon, Elst, the Netherlands

5 VIB Center for Medical Biotechnology, Department of Biochemistry and Microbiology, Ghent University,
Ghent, Belgium

6 Utrecht Institute for Pharmaceutical Sciences, Department of Chemical Biology and Drug Discovery,
Utrecht, The Netherlands

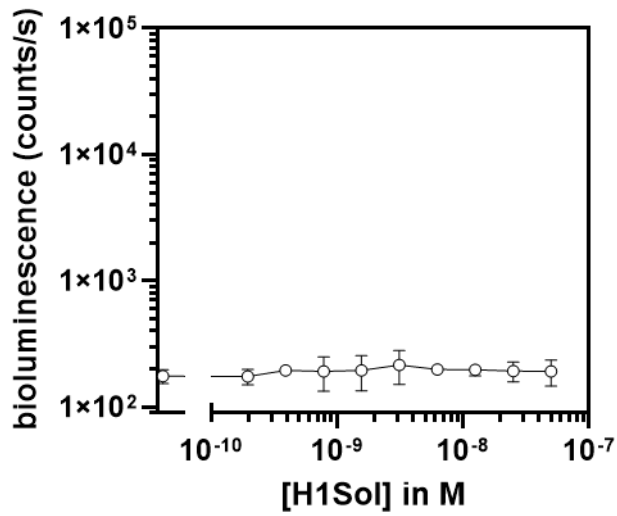
*Corresponding author: Maarten Merkx, m.merkx@tue.nl

Supporting Information

This PDF file includes:

- Figures S1 to S12
- Section S1 Supplementary Materials and Methods
- Section S2 Protein Sequences

28
29



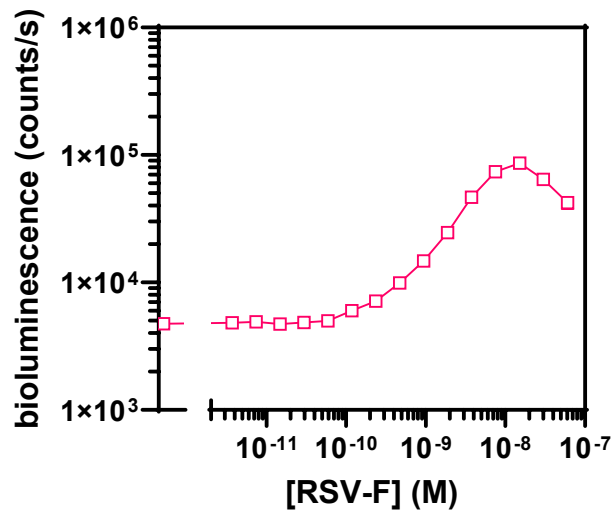
30

31 **Figure S1.**

32 **GLOVID without binders attached.**

33 LgBiT-Dog1 and SmBiT-Dog1 were mixed and used in titrations against soluble, trimeric viral
34 surface protein H1Sol (H1 from A/Solomon Islands/3/2006 (H1N1)). Experimental conditions:
35 5 nM LgBiT-Dog1, 5 nM SmBiT-Dog1, final NanoGlo dilution 1:1000, 1 h incubation 22 °C. Error
36 bars represent the standard deviation of n=3 replicates.

37
38



39

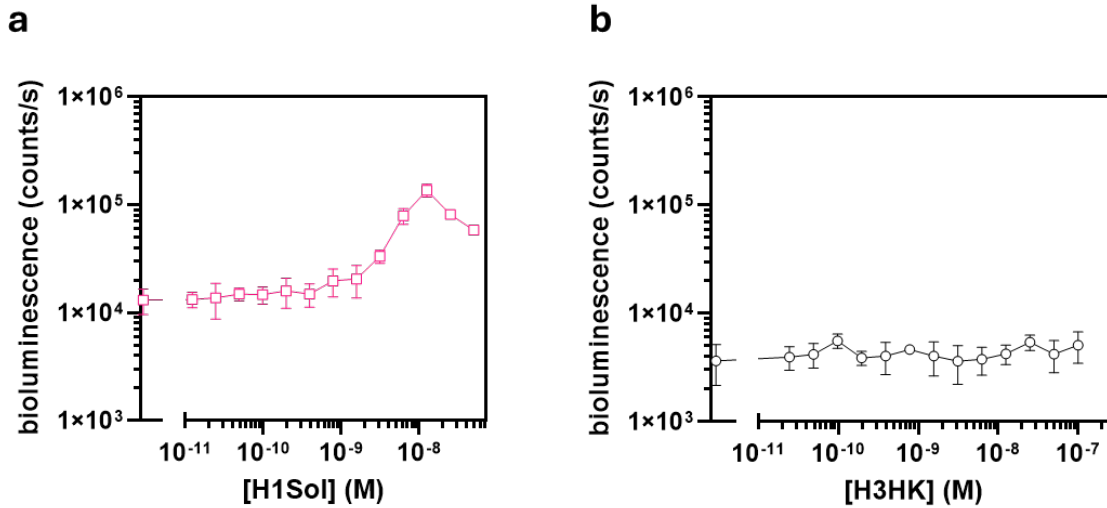
40 **Figure S2.**

41 **Trivalent GLOVID with F-VHH-4.**

42 GLOVID with anti-prefusion RSV-F nanobody F-VHH-4 conjugated to LgBiT-Dog3 and SmBiT-
43 Dog3 (trivalent system). Experimental conditions: 1 nM GLOVID components, 1xPBS + 1mg/ml
44 BSA, final NanoGlo dilution 1:2000, 1 h incubation 22 °C. The mean of n=3 replicates is shown,
45 with error bars too small to be depicted.

46

47



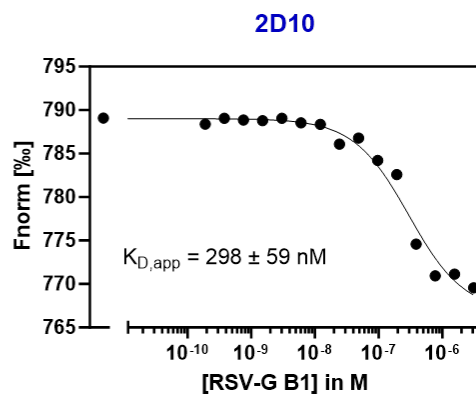
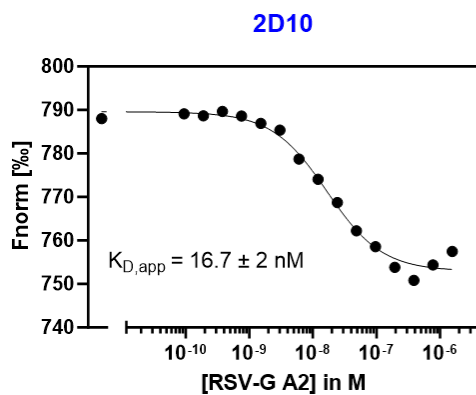
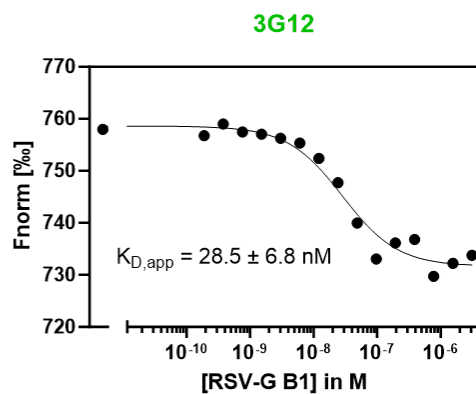
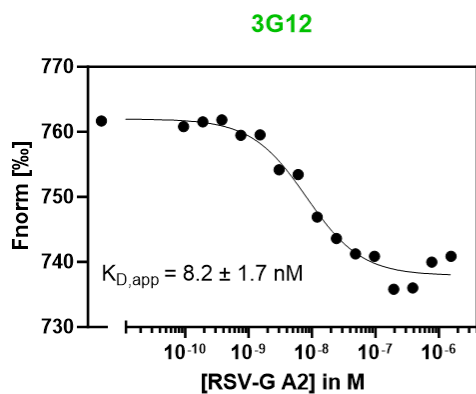
48

49 **Figure S3.**

50 **Trivalent GLOVID and control on H3HK with S5.**

51 a) Trivalent GLOVID where cyclic peptide S5 was conjugated to each LgBiT-Dog3 and SmBiT-
 52 Dog3 and used in titrations of H1Sol. b) Control GLOVID on H3HK with cyclic peptide S5
 53 conjugated to both sensor components. Experimental conditions: 2 nM LgBiT, 6 nM SmBiT,
 54 1xPBS, 1 h incubation at 22 °C, 1:1000 diluted NanoGlo. Error bars represent the standard
 55 deviation of n=3 replicates.

56



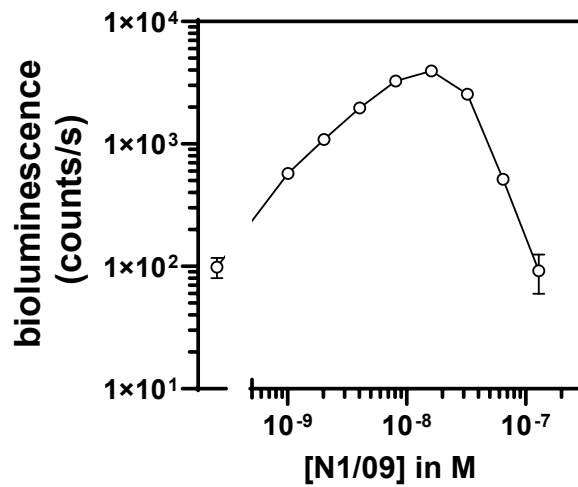
57

58 **Figure S4.**

59 **MST of scFv variants targeting RSV-G**

60 Microscale thermophoresis (MST) experiments for anti-RSV-G scFv versions of 3G12 and 2D10.
 61 A final concentration of Alexa647-labelled scFvs of 2 nM was used, with 60% excitation power
 62 and 40% MST power. MST on anti-N2 AS4C-HL-DogTag was previously described in (1). Shown
 63 are traces from single experiments.

64



65

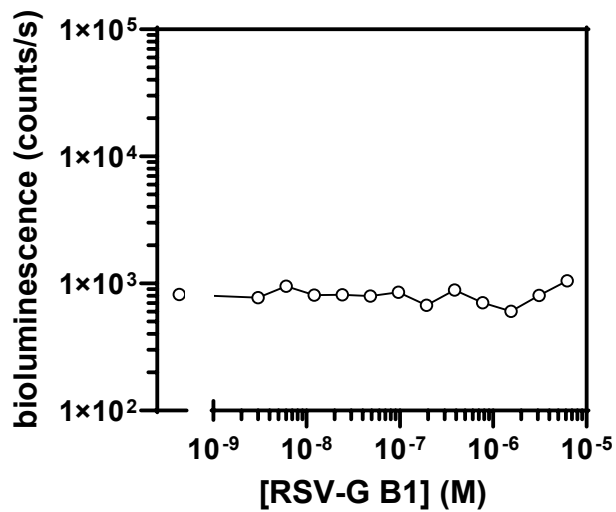
66 **Figure S5.**

67 **Monovalent GLOVID with 1GO1 scFv**

68 GLOVID assays with scFv binder 1GO1 conjugated to LgBiT-Dog1 and SmBiT-Dog1, targeting
 69 IAV N1/09. Experimental conditions: final GLOVID component concentration 2 nM, 1xPBS + 1
 70 mg/ml BSA, 16 h incubation at 4 °C, final NanoGlo dilution 1:2000. Error bars represent the
 71 standard deviation of n=3 replicates.

72

73



74

75 **Figure S6.**

76 **Controls of anti RSV-G GLOVID (1/2)**

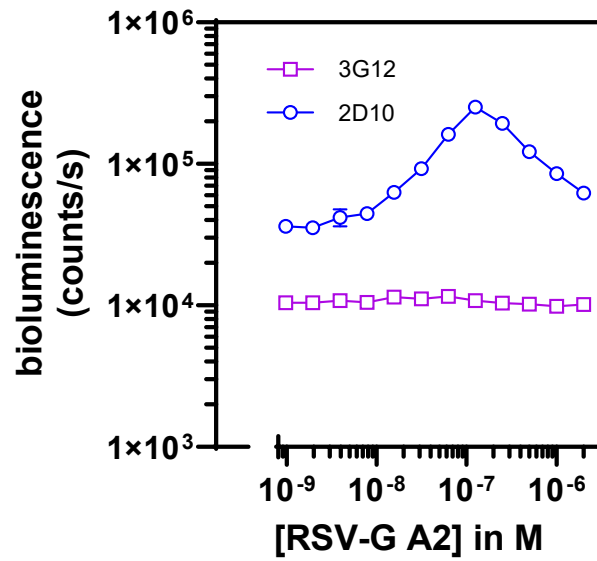
77 GLOVID on RSV-G B1 assay using a combination of 3G12-LgBiT and 2D10-SmBiT.

78 Experimental conditions: 1xPBS plus 1 mg/ml BSA, 2 nM each sensor component, 1 h incubation

79 at 22 °C, 1:2000 diluted NanoGlo substrate. The mean of n=3 replicates is shown, with error bars

80 too small to be depicted.

81



82

83 **Figure S7.**

84 **Controls of anti RSV-G GLOVID (2/2)**

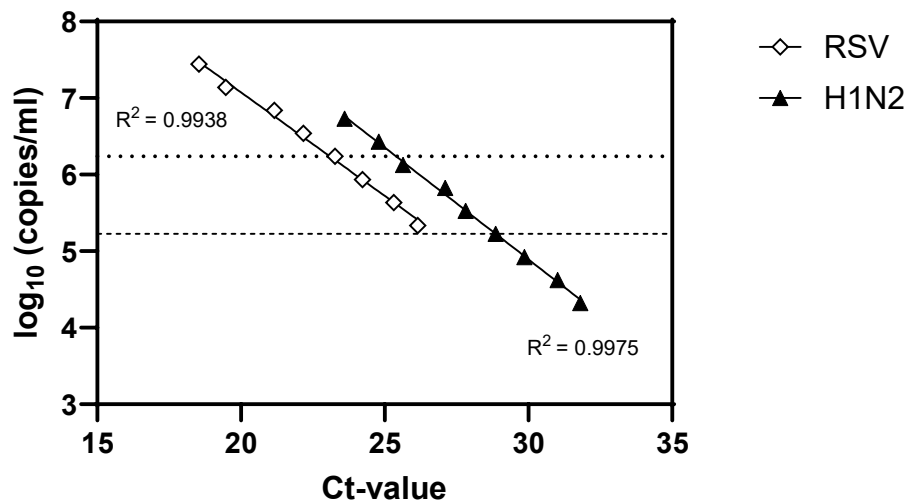
85 GLOVID on RSV-G A2 using the same scFv (3G12 or 2D10) on both sensor components.

86 Experimental conditions: 1xPBS plus 1 mg/ml BSA, 4 nM each sensor component, incubation 4

87 °C for 16 h to reach full binding equilibrium, 1:2000 diluted NanoGlo substrate. Error bars represent

88 the standard deviation of n=3 replicates.

89



90
91

92 **Figure S8.**

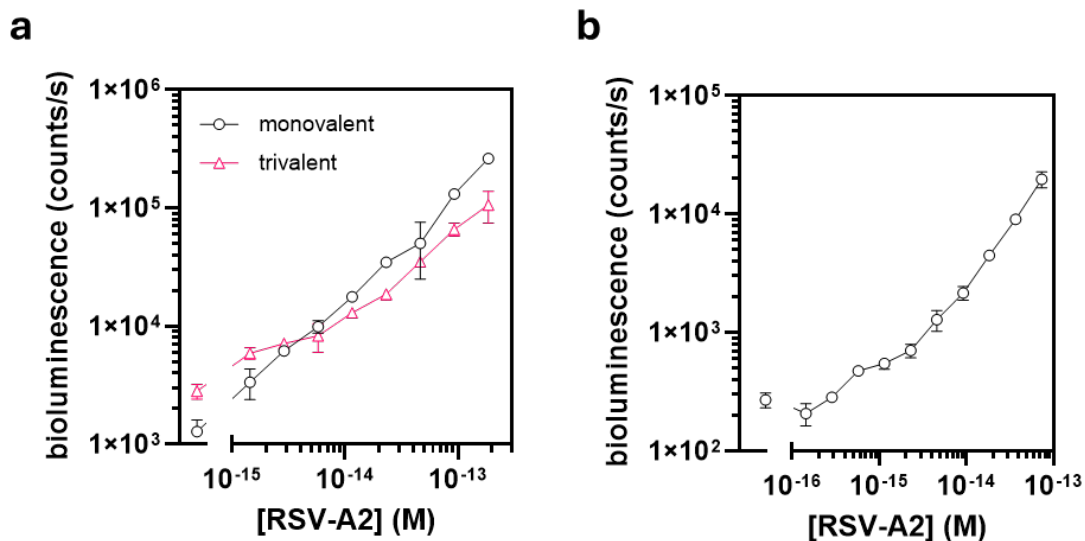
93 **RT-qPCR standard curves**

94 Standard curves of RT-qPCR on H1N2 (GeneXpert Flu/SARS/RSV triplex plus) and RSV-A2
 95 (Seegene RV essential). The dashed line corresponds to the LoD of the H1N2 GLOVID (Ct 28.86);
 96 the dotted line corresponds to the LoD of the RSV-A2 GLOVID (Ct 23.27). Data points represent
 97 single measurements from a dilution series of H1N2 or RSV-A2, respectively.

98
99
100

101
102

103
104

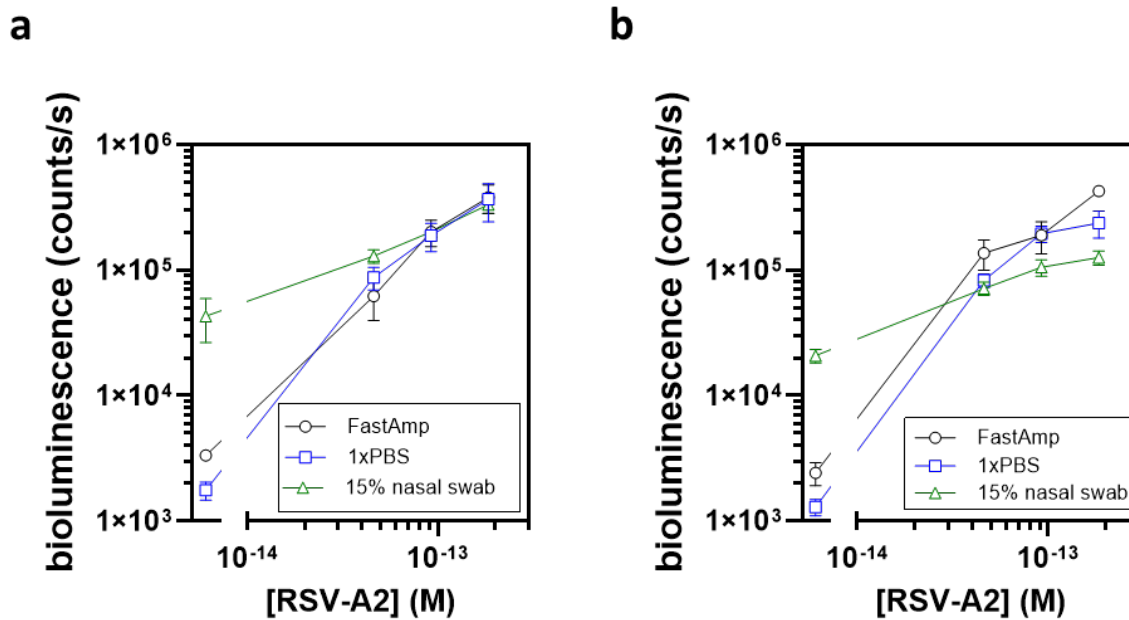


105
106

107 **Figure S9.**

108 **GLOVID assays targeting RSV-A2 via one surface protein.**

109 a) GLOVID assay that uses F-VHH-4 as binder, in monovalent fashion (F-VHH-4 fused to LgBiT-Dog1 and SmBiT-Dog1) and trivalent fashion (F-VHH-4 fused to LgBiT-Dog3 and SmBiT-Dog3);
 110 b) GLOVID assay that uses 3G12 (fused to LgBiT-Dog1) and 2D10 (fused to SmBiT-Dog1) as
 111 sensor parts. Experimental conditions: 4 nM final GLOVID component concentration, 1xPBS, final
 112 NanoGlo dilution 1:2000, 2 h incubation 22 °C. Error bars represent the standard deviation of n=3
 113 replicates.
 114
 115



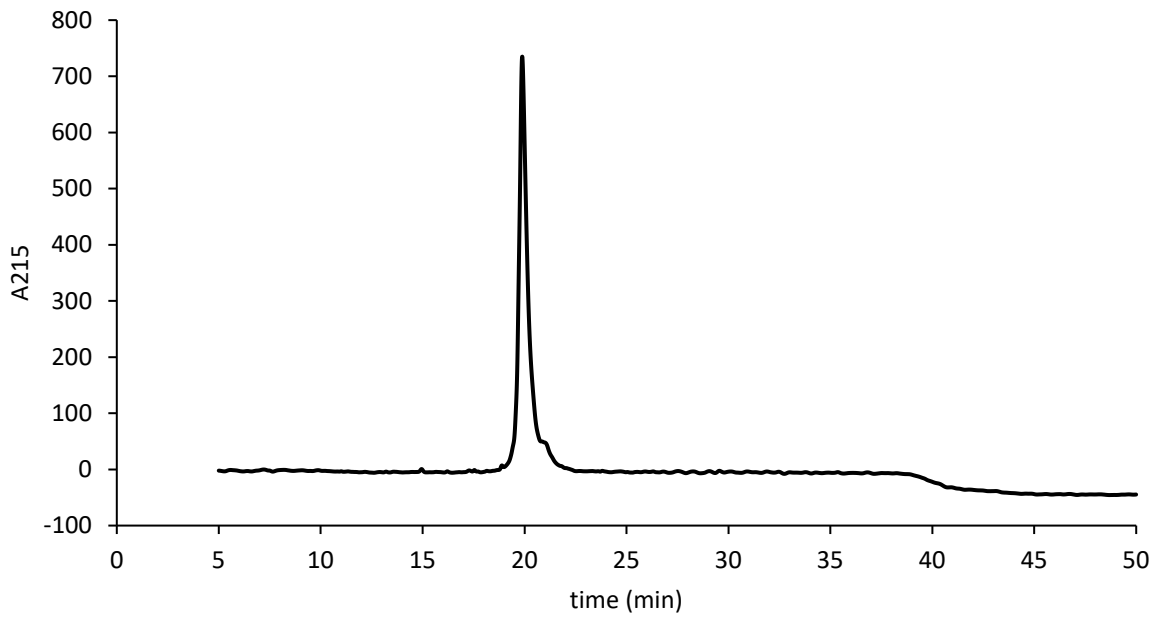
116
117

118 **Figure S10.**

119 **Spiking experiments in different matrices.**

120 Spiking experiment where virus (RSV-A2) was added to different matrices (FastAmp (Intact
121 Genomics), 1xPBS, 15% diluted nasal swab) and tested with GLOVID via F-VHH-4-LgBiT / F-
122 VHH-4-SmBiT (a) or 2D10-LgBiT / F-VHH-4-SmBiT (b). Experimental conditions: 3 nM LgBiT,
123 6 nM SmBiT, buffer as indicated in the legend, final NanoGlo dilution 1:1000, 1 h incubation at 22
124 °C. Error bars represent the standard deviation of n=3 replicates.

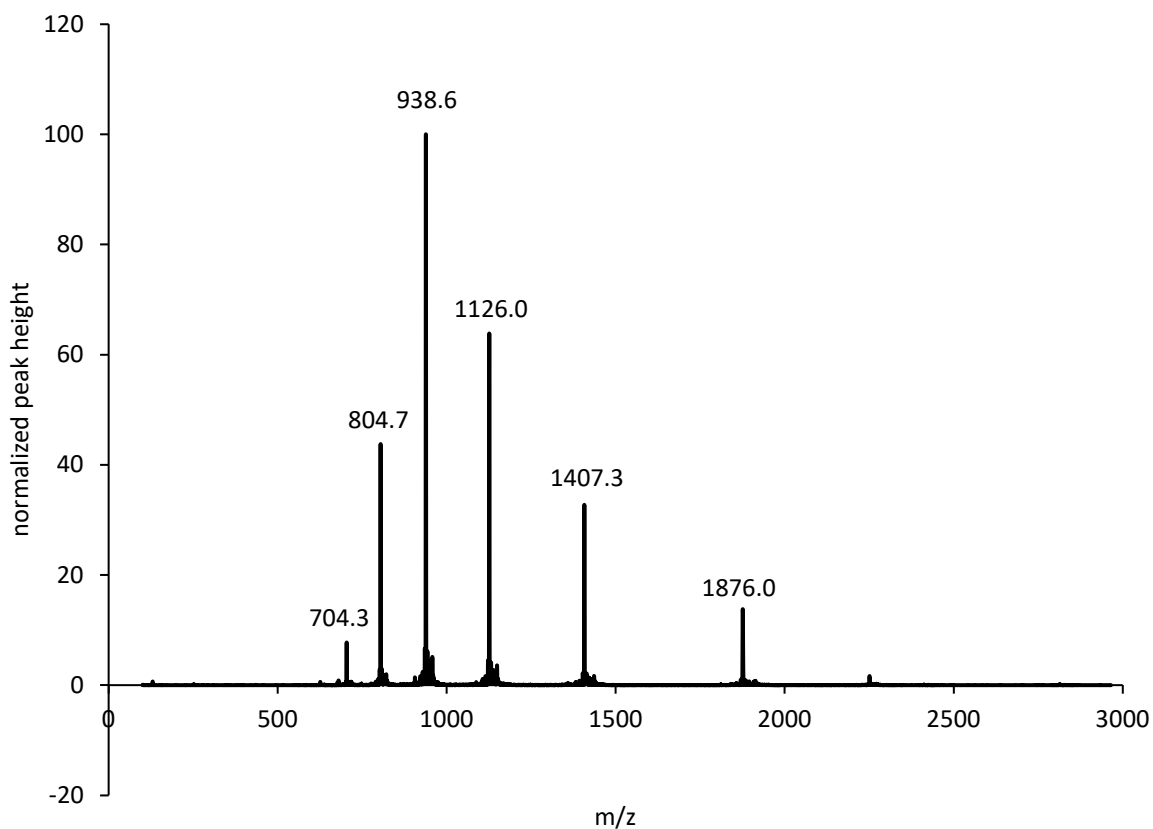
125



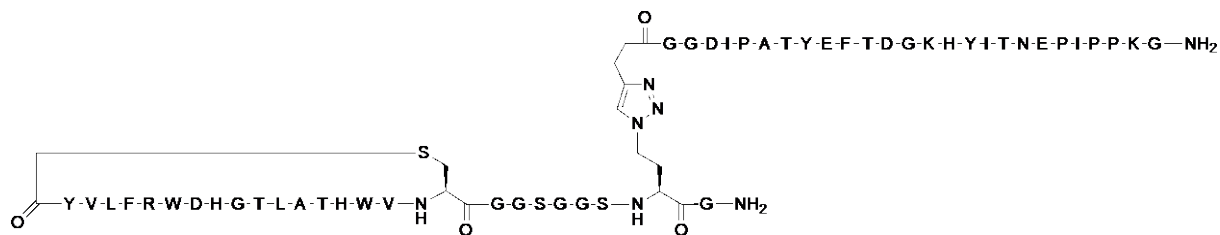
126
127 **Figure S11.**

128 **Analytical HPLC trace of purified final S5-dog tag product.**

129 The purification was performed on a C18 column, with an elution gradient 27.5-47.5% v/v
130 acetonitrile in water with 0.1% trifluoroacetic acid.
131



132



133

134

Figure S12.

135

Mass spectrum of HPLC peak at retention time 19.9 min (Figure S13).

136

Calculated for final product $C_{255}H_{364}N_{70}O_{74}S$: 5622.66, found 804.7 (calc. for $[M+7H]^{7+}$: 804.2),

137

938.6 (calc. for $[M+6H]^{6+}$: 938.1), 1126.0 (calc. for $[M+5H]^{5+}$: 1125.5), 1407.3 (calc. for

138

$[M+4H]^{4+}$: 1406.7), 1876.0 (calc. for $[M+3H]^{3+}$: 1875.2).

139

Section S1 – Supplementary Materials and Methods

Microscale Thermophoresis (MST) experiments

To estimate the K_D of the constructed 2D10-HL-DogTag and 3G12-HL-DogTag scFvs for binding to RSV-G variants, purified scFvs were labeled with Alexa647 and used in MST binding experiments. For labelling, the protein was concentrated using an Amicon filter (10 MWCO) and buffer exchanged to 0.2 M sodium bicarbonate pH 8.3 using PD SpinTrap G-25 columns (Cytiva) according to the manufacturer's protocol. 100 μ l of each protein at \sim 15 μ M was mixed with 10 μ l of Alexa-647 NHS Ester (Lumiprobe) freshly dissolved in DMSO (10 mg/ml) and incubated for 1 h at 22 °C with constant shaking. The reaction was purified from excess dyes by subsequently applying it to PD SpinTrap G-25 column twice. The concentration of the protein and the efficiency of labeling was calculated according to (2). Labelled scFvs were mixed with varying concentrations of target and incubated for 1 h at 22 °C in a volume of 40 μ l in 1xPBS & 0.02% Tween20 (final scFv concentration 2 nM). Capillaries were loaded and MST experiment was performed at 60% LED power and 40% MST power on a Monolith NT.115 (NanoTemper Technologies).

ddPCR

Viral RNA from virus samples was prepared for digital-droplet PCR (ddPCR) by adding an inactivation buffer (200 mM TCEP, 2 mM EDTA, 2 U/ μ l murine RNase inhibitor, 20 mM Tris-HCl, pH 8.0) to the sample in 1:1 ratio, followed by incubation at 95°C for 5 min. Subsequently, the 1-Step RT-ddPCR Advanced Kit for Probes (BioRad) was used in combination with the CFX96 thermocycler and the QX200 ddPCR system, using the following oligos and probes depending on the virus targeted. Data was analysed using BioRad QX One (v1.2). The oligos target the M gene of IAV and the M gene of RSV, respectively.

ddPCR oligo list

IAV targeting oligos	sequences (5' \rightarrow 3')
FLUAM-7-F	CTTCTAACCGAGGTCGAAACGTA
FLUAM-161-R	GGTGACAAGATTGGTCTTGTCTTTA
FLUAM-49-P	TCAGGCCCCCTCAAAGCCGAG
RSV targeting oligos	
RSVM-F	GGCAAATATGGAAACATACGTGAA
RSVM-R	TCTTTTCTAGGACATTGTATTGAACAG
RSVM-P	CTGTGTATGTGGAGCCTTCGTGAAG

Influenza A virus and RSV sample collection from residual clinical materials

Patients were swabbed with eSwab (Copan, Italy) flocked tips, containing 1 ml of liquid modified Amies fluid. Molecular diagnostics were performed using GeneXpert SARS-CoV-2/Flu/RSV rapid test (Cepheid, Sunnyvale, CA, USA), BioFire RP2.1plus rapid test (bioMérieux, France), and Allplex RV Essential assay RT-PCR (Seegene, Seoul, South Korea) combined with the FlowGO middle ware (LabHelp Labautomation, Bladel, the Netherlands) as previously described (3). Standard curves for correlating the ddRT-PCR experiments to GeneExpert and Seegene Ct-values were obtained from dilution series of the A/swine/Italy/114922/2014 (H1N2) and RSV-A2 stocks.

177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225

Section S2

Protein sequences

The used tags for protein purifications are hexa-His-tag (HHHHHH) and Strep-tag II (WSHPQFEK).

LgBiT-DogCatcher (LgBiT-Dog1):

Blue: LgBiT, Red: DogCatcher

MGTSVFTLEDFVGDWEQTAAYNLDQVLEQGGVSSLLQNLAVSVTPIQRIVRSGENALKI
DIHVIIPYEGLSADQMAQIEEVFKVVYPVDDHHFKVILPYGTLVIDGVTPNMLNYFGRPY
EGIAVFDGKKITVTGTLWNGNKIIDERLITPDGSMLEFRVTINSSGGGTKLGEIEFIKVDKTD
KKPLRGAVFSLQKQHPDYPDIYGAIDQNGTYQDVRTGEDGKLTFTNLSDGKYRLIENSEP
PGYKPVQNKPIVSFRIVDGEVRDVTIVPQGGGSWSHPQFEK*

DogCatcher-SmBiT (SmBiT-Dog1):

Red: DogCatcher, yellow: SmBiT101 (4)

MGTKLGEIEFIKVDKTDKKPLRGAVFSLQKQHPDYPDIYGAIDQNGTYQDVRTGEDGKLTFTNLSDGKYRLIENSEP
PPGYKPVQNKPIVSFRIVDGEVRDVTIVPQGKLGSGSGSGSGSG
GSGSGSGSGSGSGSGGENLYFQSGSGSGSGSGSGSGSGSGSGSGSGSGGTGSVTGYRLEFEK
SGSGSGSWSHPQFEK*

SD36-DogTag:

Blue: SD36, green: DogTag.

MGSVQLVESGGGLVQAGGSLKLSCAASGRTYAMGWFRQAPGKEREVAHINALGTRTY
YSDSVKGRFTISRDNANKNTEYLEMNNLKPEDTAVYYCTAQQQWRAAPVAVAAYEFW
QQGTQVTVSSGGSGSGTGDIPATYEFSTDGKHYITNEPIPPKGGSGGSWSHPQFEK*

HSB2.A-DogTag:

Blue: HSB2.A, green: DogTag.

MGSHHHHHHSSGGINVNPNCNTTKYQQLARTAVAIYNYHEQAHLTFVENLNCKEQGN
YYITLAATDDAGKKAIEYAKIGVVESAGWTGVVEEFKLVGSGSGSGSGSGSGSGSGS
SGTGDIPATYEFSTDGKHYITNEPIPPKGGSGGSWSHPQFEK*

SD38-DogTag:

Blue: SD38, green: DogTag.

MEVQLVESGGGLVQPGGSLRLSCAASISIFDIYAMDWYRQAPGKQRDLVATSRDGTN
YADSVKGRFTISRDNANKNTLYLQMNSLKPEDTAVYLCHVSLYRDPLGVAGGMGVYWG
K GALVTVSSKLGSGSGSGSGSGSGSGTGDIPATYEFSTDGKHYITNEPIPPKGGSGGSWSH
PQFEK*

F-VHH-4-DogTag:

Blue: F-VHH-4, green: DogTag

MGSQVQLQESGGGLVQPGGSLRLSCAASGFTLDYIYIGWFRQAPGKEREAVSCISGSSGS
TYYPDSVKGRFTISRDNANKNTVYLQMNSLKPEDTAVYYCATIRSSSWGGCVHYGMDYW
GKGTQVTVSSKLGSGSGSGSGSGSGSGTGDIPATYEFSTDGKHYITNEPIPPKGGSGGSWS
HPQFEK*

LgBiT-3xDogCatcher (LgBiT-Dog3)

Blue: LgBiT, red: DogCatcher (3 times)

226 MGTSVFTLEDFVGDWEQTAAYNLDQVLEQGGVSSLLQNLAVSVTPIQRIVRSGENALKI
 227 DIHVIIPYEGLSADQMAQIEEVFKVVYPVDDHFKVILPYGTLVIDGVTPNMLNYFGRPY
 228 EGIAVFDGKKITVTGTLWNGNKIIDERLITPDGSMLEFRVTINGGSGELTGGSGGSGGSGGS
 229 GSGSGSGEFAEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAFGGSGGSGGSGGSGG
 230 SGGSGGT**KLGEIEFIKVDKTDKKPLRGAVFSLQKQHPDY**PDYGAIDQNGTYQDVRTGED
 231 **GKLTFTNLSDGKYRLIENSEPPGYKPVQNKPIVSFRIVDGEVRDVTSIVPQ**TSTPTPTPTPTPT
 232 TPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT**AS**KLGEIEFIKVDKTDKKPLRGAVFSLQKQHP
 233 **DYPDIYGAIDQNGTYQDVRTGEDGKLTFTNLSDGKYRLIENSEPPGYKPVQNKPIVSFRIV**
 234 **DGEVRDVTSIVPQ**TGPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT**KLGEIEFIK**
 235 **VDKTDKKPLRGAVFSLQKQHPDY**PDYGAIDQNGTYQDVRTGEDGKLTFTNLSDGKYRL
 236 **IENSEPPGYKPVQNKPIVSFRIVDGEVRDVTSIVPQ**GGGSWSHPQFEK*

237
 238 3xDogCatcher-SmBiT (SmBiT-Dog3):
 239 Red: DogCatcher (3 times), yellow: SmBiT101

240 MGT**KLGEIEFIKVDKTDKKPLRGAVFSLQKQHPDY**PDYGAIDQNGTYQDVRTGEDGKL
 241 **TFTNLSDGKYRLIENSEPPGYKPVQNKPIVSFRIVDGEVRDVTSIVPQ**TSTPTPTPTPTPTPT
 242 PTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT**PAS**KLGEIEFIKVDKTDKKPLRGAVFSLQKQHPDY
 243 **PDYGAIDQNGTYQDVRTGEDGKLTFTNLSDGKYRLIENSEPPGYKPVQNKPIVSFRIVD**
 244 **EV**RDVTSIVPQ**TGPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT**KLGEIEFIK**VD**
 245 **KTDKKPLRGAVFSLQKQHPDY**PDYGAIDQNGTYQDVRTGEDGKLTFTNLSDGKYRLIE
 246 **NSEPPGYKPVQNKPIVSFRIVDGEVRDVTSIVPQ**GGSGELTGGSGGSGGSGGSGGSGGSGGS
 247 GEFAEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAFGGSGGSGGSGGSGGSGGSGG
 248 **T****VTGYRLFEKES**GGSHHHHHH*

249
 250 **scFvs:**

251 scFv sequences are listed in their secreted form, omitting the α -factor secretion signal present in
 252 pPICZalphaB.

253
 254 AS4C-HL-DogTag:

255 The original heavy and light chain sequences of the AS4C antibody were provided by Pramila Rijal
 256 and Alan Townsend. A heavy chain-light chain (HL) configuration scFv was designed based on
 257 these sequences.

258 Green: DogTag

259 EAEAAG(*AS4C_heavy_chain*)GGGGSGGGGSGGGGS(*AS4C_light_chain*)GTSGGGSGTGD**DIP**
 260 **ATYEFTDGKHYITNEPIPPKGGSGGSHHHHHH***

261
 262 1G01-HL-DogTag:

263 Underlined: 1G01-HL, green: DogTag

264 EAEAAGEVQLVESGGRALRPGGSLRLSCAASGFKFDDYAMSWVRQVPKGLEFVSGLN
 265 WNGDITAYTDSVKGRFTVSRDNAKNSLYLHINSPKPEDTALYYCARTSSWGDYTRGPEP
 266 KITWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSDIQLTQSPSFLSASVGDRITITCRAS
 267 QGIDGYLAWYQORPGKAPNLLIYAASLLQSGVPSRFSGSYGTEFTLTISSLOPEDFATYY
 268 CQHLDSYPLFTFGPGTKVDIKRTGTSGGGSGTGD**DIP****ATYEFTDGKHYITNEPIPPKGGSGG**
 269 SHHHHHH*

270
 271 2D10-HL-DogTag:

272 Underlined: 2D10-HL, green: DogTag

273 EAEAAGQVQLVQSGPEVKKPGASVRLSCKASGYVFTNYGVS^{WVRQAPGQGLEWMGWS}
 274 SPYNGNTYYAQKLKARVTMTTDTSTNTAYMELRSLRSDDTAVYYCGRDMLGVVQAVA
 275 GPFDSWGQGTLVTVSSASGGGGSGGGGSGGGGSGGGGDT**PMT**QSPSSVSASVGD**RVTISC**

276 RASQGISNSLAWYQQKLGKAPQLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFA
277 TYYCQQTNTFPFTFGPGTKVEVRRGTSGGGSGTGDIPATYEFTDGKHYITNEPIPPKGGSG
278 GSHHHHHH*

279 3G12-HL-DogTag

280 Underlined: 3G12-HL, green: DogTag

281 EAEAAGQLQLQESGPGLVKPSSETLSLTCTVSGGSISSSNYYWGWIRQPPGKGLEWIASIHD
282 SGSIYYNPSLRSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHLVWFGELRNNWFDP
283 WGQGLVTVASGGGGSGGGGSGGGGSGGGEIVMTQSPATLSVSPGERATLSCRASQSVN
284 SNLAWYQHKPGQAPRLLIYGASTRATGIPARFSGSGSGTDFTLTISSLQSEDFAVYYCQQY
285 NNWPLFGPGTKVDLKRRTGTSGGGSGTGDIPATYEFTDGKHYITNEPIPPKGGSGGSHHHH
286 HH*

287
288
289
290
291

292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307

References

1. A. Gräwe, C. M. Spruit, R. P. de Vries, M. Merkx, Bioluminescent detection of viral surface proteins using branched multivalent protein switches. *RSC Chem Biol* **5**, 148–157 (2024).
2. J. S. Nanda, J. R. Lorsch, “Labeling a Protein with Fluorophores Using NHS Ester Derivitization” in *Methods in Enzymology*, J. R. Lorsch, Ed. (2014) vol. 536, pp. 87–94.
3. J. Flipse, A. T. Tromp, D. Thijssen, N. van Xanten-Jans-Beken, R. Pauwelsen, H. J. van der Veer, J. M. Schlaghecke, C. M. A. Swanink, Optimization of the STARlet workflow for semi-automatic SARS-CoV-2 screening of swabs and deep respiratory materials using the RealAccurate Quadruplex SARS-CoV-2 PCR kit and Allplex SARS-CoV-2 PCR kit. *Microbiol Spectr* **12** (2024).
4. A. S. Dixon, M. K. Schwinn, M. P. Hall, K. Zimmerman, P. Otto, T. H. Lubben, B. L. Butler, B. F. Binkowski, T. MacHleidt, T. A. Kirkland, M. G. Wood, C. T. Eggers, L. P. Encell, K. V. Wood, NanoLuc Complementation Reporter Optimized for Accurate Measurement of Protein Interactions in Cells. *ACS Chem Biol* **11**, 400–408 (2016).