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Photochemical Identification of Auxiliary SARS-Cov-2 Host-Entry Factors using μ Map

Saori Suzuki^{1,‡}, Jacob B. Geri^{2,‡}, Steve D. Knutson^{2,‡}, Harris Bell-Temin³, Tomokazu Tamura¹, David F. Fernández², Gabby H. Lovett², Nicholas A. Till², Brigitte L. Heller¹, Jinchao Guo¹, David W. C. MacMillan^{2,4,**}, Alexander Ploss^{1,**}

¹Department of Molecular Biology, Princeton University, Princeton, NJ 08544, USA

²Department of Chemistry, Princeton University, Princeton, NJ 08544, USA

³Bristol Myers Squibb, Princeton, NJ 08540, USA

⁴Merck Center for Catalysis at Princeton University, Princeton, NJ 08544, USA

Abstract

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the infectious agent of the COVID-19 pandemic, remains a global medical problem. Angiotensin converting enzyme 2 (*ACE2*) was identified as the primary viral entry receptor, and transmembrane serine protease 2 (*TMPRSS2*) primes the spike protein for membrane fusion. However, *ACE2* expression is generally low and variable across tissues, suggesting auxiliary receptors facilitate viral entry. Identifying these factors is critical for understanding SARS-Cov-2 pathophysiology and

**Corresponding Authors Alexander Ploss – Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544, United States, aploss@princeton.edu David W. C. MacMillan – Merck Center for Catalysis at Princeton University, Princeton, New Jersey 08544, United States, dmacmill@princeton.edu.

‡S.S., J.B.G., and S.D.K. contributed equally.

Author Contributions

The manuscript was written through contributions of all authors. All authors have given approval to the final version of the manuscript.

Saori Suzuki‡ – Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544, United States

Jacob B. Geri‡ – Merck Center for Catalysis at Princeton University, Princeton, New Jersey 08544, United States; Department of Chemistry, Princeton University, Princeton, New Jersey 08544, United States

Steve D. Knutson‡ – Merck Center for Catalysis at Princeton University, Princeton, New Jersey 08544, United States; Department of Chemistry, Princeton University, Princeton, New Jersey 08544, United States

Harris Bell-Temin – Bristol Meyers Squibb, Princeton, New Jersey 08544, United States

Tomokazu Tamura – Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544, United States

David F. Fernández – Merck Center for Catalysis at Princeton University, Princeton, New Jersey 08544, United States; Department of Chemistry, Princeton University, Princeton, New Jersey 08544, United States

Gabby H. Lovett – Merck Center for Catalysis at Princeton University, Princeton, New Jersey 08544, United States; Department of Chemistry, Princeton University, Princeton, New Jersey 08544, United States

Nicholas A. Till – Merck Center for Catalysis at Princeton University, Princeton, New Jersey 08544, United States; Department of Chemistry, Princeton University, Princeton, New Jersey 08544, United States

Brigitte L. Heller – Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544, United States

Jinchao Guo – Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544, United States

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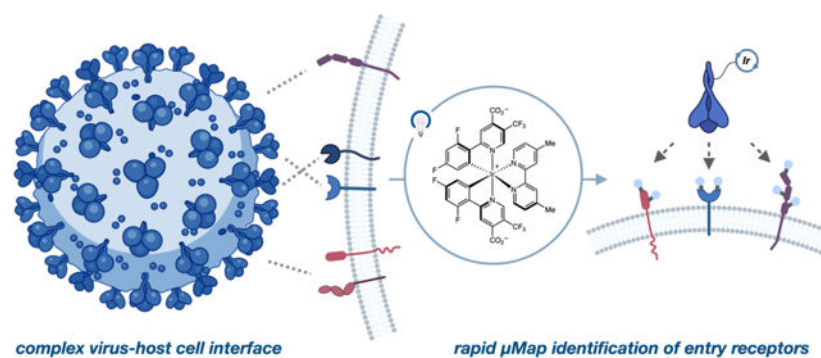
Proteomic datasets (XLSX)

Experimental procedures and supplementary figures (PDF)

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developing new countermeasures. However, profiling host-virus interactomes involves extensive genetic screening or complex computational predictions. Here, we leverage the photocatalytic proximity labeling platform μ Map to rapidly profile the spike interactome in human cells and identify 8 novel candidate receptors. We systemically validate their functionality in SARS-CoV-2 pseudoviral uptake assays with both Wuhan and Delta spike variants and show that dual expression of *ACE2* with either *NRP2*, *EPHA7*, *SLC6A15* or *MAL2* significantly enhances viral uptake. Collectively, our data show that SARS-CoV-2 synergistically engages several host factors for cell entry and establishes μ Map as a powerful tool for rapidly interrogating host-virus interactomes.

Graphical Abstract



INTRODUCTION

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the etiologic agent of the COVID-19 pandemic. Identifying viral entry and replication factors is key for understanding and resolving outbreaks, and angiotensin converting enzyme 2 (*ACE2*) has been identified as the obligate receptor for SARS-CoV and SARS-CoV-2.^{1,2} Cleavage of the viral spike protein by the transmembrane serine protease 2 (*TMPRSS2*) also facilitates SARS-CoV-2 membrane fusion.³⁻⁵ Although *ACE2* expression is higher in nasal epithelial cells, these levels decrease throughout the lower respiratory tract.^{1,2} While this implies nasal initiation of infection, transition mechanisms to deep lung pathogenesis in severe COVID are unknown.^{6,7} Similarly, COVID infections can rapidly progress throughout the body and cause multiple organ failure,⁸ yet *ACE2* expression is low or variable beyond gastrointestinal and respiratory tracts.⁹ Accordingly, it is likely that SARS-CoV-2 interacts with additional receptors, although viral entry outside of canonical pathways remains poorly characterized (Figure 1a).

Computational modeling of the receptor binding domain (RBD) has identified interactions with heparin sulfate for cell entry, and recent work validated functional associations with C-type lectin receptors¹⁰ and metabotropic glutamate receptor 2.¹¹ Additionally, results from two studies suggest that neuropilin-1 (*NRP1*) enhances *TMPRSS2*-mediated SARS-CoV-2 entry.^{12,13} While these studies elucidated additional viral entry routes, they also required extensive computational effort generated from crystal structures or validated hypotheses from *a priori* evidence of known receptors. Genetic knock-out screens can reduce bias and

allow identification of proviral proteins,¹⁴ yet these campaigns involve extensive library optimization and require suitable systems for transfection and engineering. In contrast, proximity labeling has emerged as a versatile methodology for unbiased interrogation of protein interactions via catalytic tagging of spatially connected biomolecules.¹⁵ APEX¹⁶ and BioID¹⁷ have found particular widespread application and have been recently utilized for investigating associations between SARS-Cov-2 viral components and intracellular host proteins. Although these studies demonstrated relevant interactions between the viral proteins and host signal peptidase complex¹⁸ as well as myosin heavy chain,¹⁹ these platforms require genetic engineering to introduce proximity labeling components and are limited in both spatial control and labeling resolution. To circumvent these challenges and investigate the native cell-surface interactome with greater precision, we hypothesized that our recently developed photocatalytic proximity labeling method, μ Map,²⁰ could directly profile the host-virus microenvironment and identify SARS-CoV-2 auxiliary receptors (Figure 1b,c). In contrast to peroxidase or biotin ligation strategies, μ Map uses iridium (Ir) photocatalysts to convert nearby diazirines into carbenes via Dexter energy transfer and biotinylate proteins within ~4 nm radius, offering high spatial and temporal control over labeling (Figure 1b).²⁰ This platform has been applied for small molecule target identification,²¹ mapping chromatin reorganization events,²² and rapidly profiling immunosynapse interactions.²⁰ Additionally, similar Ir-based photocatalytic proximity labeling strategies have also been recently developed for cataloging mitochondrial proteins in activated macrophages²³ and profiling surface proteins in breast cancer.²⁴ Rhodamine-based oxidation labeling has also provided new methodology for validating cell-surface microenvironments, underscoring the utility of light-mediated proximity labeling for interrogating cell-surface proteomes with high spatiotemporal precision.²⁵ Given this precedent, we sought to deploy μ Map to identify novel receptors of the SARS-CoV-2 spike protein.

RESULTS AND DISCUSSION

As an initial test, we first synthesized recombinant RBD and full-length spike-Ir conjugates and attempted photolabeling on HEK293T cells overexpressing *ACE2* (Figure S1). Cells were incubated with spike-Ir conjugates and then washed, and photolabeling was initiated in a 250 μ M biotin-diazirine solution under blue light irradiation. Compared with a free Ir control and parental 293T cells, we observed robust biotinylation of membrane proteins from trimer conjugates only in *ACE2*-expressing cells (Figure S2). Notably, RBD labeling produced few new bands beyond *ACE2* in these tests, yet the spike trimer displayed extensive biotinylation, revealing the possibility of novel interactions.

To perform μ Map analysis of the spike interactome in a native context, we identified Calu-3 human lung cells as they express both canonical entry factors *ACE2* and *TMPRSS2* (Figure S1) and have been previously utilized to study COVID pathophysiology.^{1,2} We were also particularly interested in utilizing the full-length spike protein (~180 kDa), as the N-terminal domain bears epitopes of neutralizing antibodies, yet its functional interactions are still unknown,^{26,27} suggesting it binds other host factors. We executed our photolabeling workflow followed by membrane lysate isolation, streptavidin enrichment, and quantitative proteomic analysis. Compared against a free Ir control, *ACE2* was strongly enriched (Figure

S3, Table S1), recapitulating our initial feasibility test. To delineate auxiliary interactions between the smaller RBD (~50 kDa) and full spike, we also performed μ Map with both conjugates and compared datasets. As expected, *ACE2* was not enriched as it binds both protein constructs, but we identified 8 enriched membrane proteins as candidate receptors for the full spike (Figure 1d, Table S2). *TMPRSS2* was not observed in any of our datasets, which is unexpected given its known role as a canonical SARS-CoV-2 entry factor along with *ACE2*.³⁻⁵ However, it is also known that the *TMPRSS2*-Spike interaction is transient after cleavage, and given that μ Map targeting of cell-surface proteins employs binding and several washing steps, we hypothesize that this contributed to lack of proteomic detection. Regardless, neuropilin-2 (*NRP2*) was highly enriched, and has high homology with *NRPI* which was reported to bind to the cleaved spike and facilitate SARS-CoV-2 entry.^{12,13} Cleft Lip And Palate Associated Transmembrane Protein 1 (*CLPTM1*) and Ephrin Receptor A7 (*EPHA7*) were also prioritized, the latter of which was reported as key for transmission of Kaposi's sarcoma-associated herpes virus and rhesus monkey rhadinovirus²⁸. We also identified Myelin and Lymphocyte Protein 2 (*MAL2*), recently reported as a herpes simplex virus 1 co-factor in oligodendrocytes.²⁹ Solute Carrier Family 6 Member 15 (*SLC6A15*), Myelin protein zero-like protein 1 (*MPZL1*), Laminin Subunit Gamma 2 (*LAMC2*), and Integrin Subunit Beta 5 (*ITGB5*) were also noted as candidate receptors (Figure 1d, Table S2). *LAMC2* was intriguingly identified in a microarray study as a possible SARS-CoV-2 transmission factor.³⁰ While these 8 annotated candidate proteins are not the sole transmembrane proteins enriched in our dataset (Figure 1d, Table S2), this group was selected due to their high enrichment and likelihood of interacting with the SARS-CoV-2 spike protein on the cell surface. Importantly, all candidates are known to be expressed in esophageal and respiratory tract tissues,³¹ and so we next sought to functionally test these receptors for viral infection.

We first generated SARS-CoV-2 pseudovirus particles (SARS-CoV-2pp) encoding Gaussia luciferase as a quantifiable proxy (Figure 2a). In line with previous observations, expression of *ACE2* or *TMPRSS2* in HEK293T and A549 cells resulted in significant entry enhancement (Figure S4). We next constructed a panel of A549 cell lines to display various combinations of cell-surface candidate factors. Importantly, we transduced cells with bicistronic lentiviral cassettes containing a zsGreen reporter to enable fluorescence-activated cell sorting and standardized expression of each markers, and *ACE2* levels were similarly gated using antibody staining (Figure S5). For additional rigor, we also measured expression of respective genes in sorted cell lines via quantitative PCR and verified similar mRNA levels (Figure S6). We next infected these lines with SARS-CoV-2pp, and while A549 cells expressing *ACE2* and/or *TMPRSS2* exhibited significant increases in viral uptake compared to parental cells, display of individual candidate factors provided no viral uptake enhancement (Figure 2b). However, cells stably expressing *ACE2* along with individual factors exhibited significantly enhanced viral entry (Figure 2c). In particular, dual expression of *ACE2* with *NRP2*, *CLPTM1*, *SLC6A15*, *EPHA7* or *MAL2* led to upwards of ~3-fold increases in viral uptake compared with cells only expressing *ACE2*, suggesting a synergistic cell entry mechanism. As expected, *TMPRSS2* conferred large uptake increases when expressed with *ACE2* (Figure 2b-e), yet no difference was observed in lines expressing *TMPRSS2* and each factor (Figure 2d) or in combination

with *ACE2* and *TMPRSS2* (Figure 2e). We hypothesized that these differences may be masked by enzymatic luciferase-based detection, so to observe uptake in greater detail, we infected *ACE2-TMPRSS2* triple expression lines displaying the highest enhancement (*NRP2*, *SLC6A15*, *EPHA7* and *MAL2*) with mScarlet reporter pseudoparticles (Figure 3). Quantifying individual populations via microscopy confirmed minimal entry in A549 cells as well as lines expressing only *ACE2*, but large enhancement was seen in *ACE2* lines simultaneously displaying *TMPRSS2* along with *NRP2*, *MAL2*, *EPHA7* or *SLC6A15*. Non-enveloped viral controls showed no uptake (Figure S7), reflecting spike-mediated entry (Figure 3a, b). Together, these results confirm the importance of *ACE2* and *TMPRSS2* for SARS-Cov-2 entry, and we excitingly demonstrate that *NRP2*, *SLC6A15*, *EPHA7* and *MAL2* significantly enhance viral uptake when expressed with *ACE2*.

Numerous SARS-CoV-2 variants have continued to emerge that are increasingly transmissible and/or less vulnerable to antibody neutralization. In particular, the Delta (B.1.617.2) variant that arose in India in late 2020 contains 8 amino acid mutations from the original Wuhan spike (Figure 4a).³² To test uptake with our identified receptors, we generated Delta SARS-CoV2-pp and repeated our luminescent entry assay and interestingly observed significant entry enhancement across all factors except for *ITGB5*, with upwards of ~5–7-fold increases in *ACE2-CLPTM1* and *ACE2-EPHA7* lines vs cells only expressing *ACE2* (Figure 4b). Conversely, the Wuhan strain only exhibited increased uptake in cell lines expressing both *ACE2* in combination with *NRP2*, *MAL2*, *EPHA7* or *SLC6A15* (Figure 2c), suggesting the higher transmissibility of the Delta variant is due in part to broader receptor tropism.

Lastly, we sought to probe whether candidate factors stably interact with SARS-Cov-2. Fluorophore-spike conjugates were generated, and each cell line was incubated with increasing amounts of the conjugate. After washing, fluorescence was measured to estimate bound protein remaining (Figure 5a). As expected, parental A549 cells displayed minimal interaction while cells expressing *ACE2* exhibited robust binding with low nM affinity (Figures S8, 5b). Intriguingly, the Delta spike variant exhibited significantly enhanced binding affinity in all *ACE2*-expressing lines, in agreement with working hypotheses regarding its higher transmissibility (Figure S9, 5b).³³ However, cell lines expressing each candidate displayed minimal binding, and dual expression with *ACE2* did not increase affinity compared with single expression of *ACE2* in either variant. Although we anticipated observing a binding enhancement, not all entry factors stably interact with the spike protein. In agreement with prior work, *TMPRSS2*-expressing cells did not stably bind (Figures S8, S9), despite the significant impact of the protease on viral uptake.¹ Similarly, *NRP1* was found to enhance cell entry, yet binding interactions with SARS-Cov-2 were undetectable in analogous assays.¹² While the candidate factors identified in this study functionally enhance uptake, our results suggest that interactions with the spike protein are transient, and synergistic associations between *ACE2* and a receptor ensemble likely contribute to spike binding and subsequent particle entry.

Understanding the molecular mechanisms of SARS-Cov-2 infection across human tissues is key to resolving the current pandemic and developing countermeasures for future outbreaks. Here we show that photocatalytic proximity labeling using μ Map is a rapid and powerful

tool for interrogating critical receptors at the host-virus interface. We profile the Wuhan spike interactome and identify at least four proteins, *NRP2*, *MAL2*, *EPHA7* and *SLC6A15*, as auxiliary SARS-Cov-2 entry receptors that significantly enhance uptake of both the original and Delta SARS-Cov-2 variant in human cells. The Omicron spike variant has now dominated global infections, and the molecular mechanisms of its high transmissibility and immune evasion remain poorly understood.^{34,35} Ongoing research in our group seeks to expand this work into emerging variants across human cell types to delineate these complex interactions. Additionally, we observed many intracellular proteins that were enriched in our datasets (Fig 1d, Tables S1, S2) that potentially interact with the SARS-CoV-2 spike protein. We hypothesize that these interactions are potentially resulting from internalized spike-Ir conjugates, and future efforts will validate and functionally investigate these potentially critical interactions. Moreover, we and the Rovis group have also recently reported red light-based strategies for photocatalytic proximity labeling,^{36, 37} and future efforts will deploy these platforms for studying host-virus interactions in complex *in vivo* environments. Together, this work demonstrates a powerful and generalizable methodology for rapidly elucidating entry mechanisms for a variety of pathogens in diverse cellular settings.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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REFERENCES

1. Hoffmann M, Kleine-Weber H, Schroeder S, Krüger N, Herrler T, Erichsen S, Schiergens TS, Herrler G, Wu NH, Nitsche A. et al. SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor. *Cell* 2020, 181 (2), 271–280.e278.
2. Li W, Moore MJ, Vasilieva N, Sui J, Wong SK, Berne MA, Somasundaran M, Sullivan JL, Luzuriaga K, Greenough TC et al. Angiotensin-converting enzyme 2 is a functional receptor for the SARS coronavirus. *Nature* 2003, 426 (6965), 450–454. [PubMed: 14647384]

3. Glowacka I, Bertram S, Müller MA, Allen P, Soilleux E, Pfefferle S, Steffen I, Tsegaye TS, He Y. & Gnirss K. Evidence that TMPRSS2 activates the severe acute respiratory syndrome coronavirus spike protein for membrane fusion and reduces viral control by the humoral immune response. *J. Virol.* 2011, 85 (9), 4122–4134. [PubMed: 21325420]
4. Matsuyama S, Nagata N, Shirato K, Kawase M, Takeda M. & Taguchi F. Efficient activation of the severe acute respiratory syndrome coronavirus spike protein by the transmembrane protease TMPRSS2. *J. Virol.* 2010, 84 (24), 12658–12664.
5. Shulla A, Heald-Sargent T, Subramanya G, Zhao J, Perlman S. & Gallagher T. A transmembrane serine protease is linked to the severe acute respiratory syndrome coronavirus receptor and activates virus entry. *J. Virol.* 2011, 85 (2), 873–882. [PubMed: 21068237]
6. Hou YJ, Okuda K, Edwards CE, Martinez DR, Asakura T, Dinno KH 3rd, Kato T, Lee RE, Yount BL, Mascenik TM et al. SARS-CoV-2 Reverse Genetics Reveals a Variable Infection Gradient in the Respiratory Tract. *Cell* 2020, 182 (2), 429–446.e414.
7. Ahn JH, Kim J, Hong SP, Choi SY, Yang MJ, Ju YS, Kim YT, Kim HM, Rahman MDT, Chung MK et al. Nasal ciliated cells are primary targets for SARS-CoV-2 replication in the early stage of COVID-19. *J. Clin. Invest.* 2021, 131 (13), e148517.
8. Delorey TM, Ziegler CG, Heimberg G, Normand R, Yang Y, Segerstolpe Å, Abbondanza D, Fleming SJ, Subramanian A. & Montoro DT COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. *Nature* 2021, 595 (7865), 107–113. [PubMed: 33915569]
9. Hikmet F, Méar L, Edvinsson Å, Micke P, Uhlén M. & Lindskog C. The protein expression profile of ACE2 in human tissues. *Mol Syst Biol* 2020, 16 (7), e9610.
10. Thépaut M, Luczkowiak J, Vivès C, Labiod N, Bally I, Lasala F, Grimoire Y, Fenel D, Sattin S. & Thielens N. DC/L-SIGN recognition of spike glycoprotein promotes SARS-CoV-2 trans-infection and can be inhibited by a glycomimetic antagonist. *PLoS Pathog.* 2021, 17 (5), e1009576.
11. Wang J, Yang G, Wang X, Wen Z, Shuai L, Luo J, Wang C, Sun Z, Liu R. & Ge J. SARS-CoV-2 uses metabotropic glutamate receptor subtype 2 as an internalization factor to infect cells. *Cell Discov.* 2021, 7 (1), 1–16. [PubMed: 33390590]
12. Daly JL, Simonetti B, Klein K, Chen KE, Williamson MK, Antón-Plágaro C, Shoemark DK, Simón-Gracia L, Bauer M, Hollandi R. et al. Neuropilin-1 is a host factor for SARS-CoV-2 infection. *Science* 2020, 370 (6518), 861–865. [PubMed: 33082294]
13. Cantuti-Castelvetri L, Ojha R, Pedro LD, Djannatian M, Franz J, Kuivanen S, van der Meer F, Kallio K, Kaya T, Anastasina M. et al. Neuropilin-1 facilitates SARS-CoV-2 cell entry and infectivity. *Science* 2020, 370 (6518), 856–860. [PubMed: 33082293]
14. Baggen J, Persoons L, Vanstreels E, Jansen S, Van Looveren D, Boeckx B, Geudens V, De Man J, Jochmans D. & Wauters J. Genome-wide CRISPR screening identifies TMEM106B as a proviral host factor for SARS-CoV-2. *Nat. Genet.* 2021, 53 (4), 435–444. [PubMed: 33686287]
15. Qin W, Cho KF, Cavanagh PE & Ting AY Deciphering molecular interactions by proximity labeling. *Nat. Methods* 2021, 18 (2), 133–143. [PubMed: 33432242]
16. Lam SS, Martell JD, Kamer KJ, Deerinck TJ, Ellisman MH, Mootha VK & Ting AY Directed evolution of APEX2 for electron microscopy and proximity labeling. *Nat. Methods* 2015, 12 (1), 51–54. [PubMed: 25419960]
17. Roux KJ, Kim DI, Raida M. & Burke B. A promiscuous biotin ligase fusion protein identifies proximal and interacting proteins in mammalian cells. *J. Cell Biol.* 2012, 196 (6), 801–810. [PubMed: 22412018]
18. Chen Z, Wang C, Feng X, Nie L, Tang M, Zhang H, Xiong Y, Swisher SK, Srivastava M. & Chen J. Interactomes of SARSCoV-2 and human coronaviruses reveal host factors potentially affecting pathogenesis. *EMBO J.* 2021, 40 (17), e107776.
19. Chen J, Fan J, Chen Z, Zhang M, Peng H, Liu J, Ding L, Liu M, Zhao C. & Zhao P. Nonmuscle myosin heavy chain IIA facilitates SARS-CoV-2 infection in human pulmonary cells. *Proc. Natl. Acad. Sci.* 2021, 118 (50), e2111011118.
20. Geri JB, Oakley JV, Reyes-Robles T, Wang T, McCarver SJ, White CH, Rodriguez-Rivera FP, Parker DL Jr, Hett EC & Fadeyi OO Microenvironment mapping via Dexter energy transfer on immune cells. *Science* 2020, 367 (6482), 1091–1097. [PubMed: 32139536]

21. Trowbridge AD, Seath CP, Rodriguez-Rivera FP, Li BX, Dul BE, Schwaib AG, Geri JB, Oakley JV, Fadeyi OO & Oslund RC Small molecule photocatalysis enables drug target identification via energy transfer. *bioRxiv* 2021. doi.10.1101/2021.08.02.454797, (accessed 08-01-2022).
22. Seath CP, Burton AJ, MacMillan DW & Muir TW Tracking chromatin state changes using μ Map photo-proximity labeling. *bioRxiv* 2021. doi.10.1101/2021.09.28.462236, (accessed 08-01-2022).
23. Huang Z, Liu Z, Xie X, Zeng R, Chen Z, Kong L, Fan X. & Chen PR Bioorthogonal photocatalytic Decaging-enabled mitochondrial proteomics. *J. Am. Chem. Soc.* 2021, 143 (44), 18714–18720.
24. Liu Z, Xie X, Huang Z, Lin F, Liu S, Chen Z, Qin S, Fan X. & Chen PR Spatially resolved cell tagging and surfaceome labeling via targeted photocatalytic decaging. *Chem* 2022, 8 (8), 2179–2191.
25. Müller M, Gräbnitz F, Barandun N, Shen Y, Wendt F, Steiner SN, Severin Y, Vetterli SU, Mondal M. & Prudent JR Light-mediated discovery of surfaceome nanoscale organization and intercellular receptor interaction networks. *Nat. Commun.* 2021, 12 (1), 1–17. [PubMed: 33397941]
26. Liu L, Wang P, Nair MS, Yu J, Rapp M, Wang Q, Luo Y, Chan JF, Sahi V, Figueroa A. et al. Potent neutralizing antibodies against multiple epitopes on SARS-CoV-2 spike. *Nature* 2020, 584 (7821), 450–456. [PubMed: 32698192]
27. Chi X, Yan R, Zhang J, Zhang G, Zhang Y, Hao M, Zhang Z, Fan P, Dong Y, Yang Y. et al. A neutralizing human antibody binds to the N-terminal domain of the Spike protein of SARS-CoV-2. *Science* 2020, 369 (6504), 650–655. [PubMed: 32571838]
28. Großkopf AK, Schlagowski S, Hörnich BF, Fricke T, Desrosiers RC & Hahn AS EphA7 Functions as Receptor on BJAB Cells for Cell-to-Cell Transmission of the Kaposi's Sarcoma-Associated Herpesvirus and for Cell-Free Infection by the Related Rhesus Monkey Rhadinovirus. *J. Virol.* 2019, 93 (15). e00064–19
29. López-Guerrero JA, de la Nuez C, Praena B, Sánchez-León E, Krummenacher C. & Bello-Morales R. Herpes Simplex Virus 1 Spread in Oligodendrocytic Cells Is Highly Dependent on MAL Proteolipid. *J Virol* 2020, 94 (4). e01739–19.
30. Basu A, Sarkar A. & Maulik U. Study of cell to cell transmission of SARS CoV2 virus particle using gene network from microarray data. *bioRxiv* 2020. doi.10.1101/2020.05.26.116780, (accessed 08-01-2022).
31. Consortium G. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. *Science* 2015, 348 (6235), 648–660. [PubMed: 25954001]
32. Liu Y, Liu J, Johnson BA, Xia H, Ku Z, Schindewolf C, Widen SG, An Z, Weaver SC & Menachery VD Delta spike P681R mutation enhances SARS-CoV-2 fitness over Alpha variant. *Cell Rep.* 2022, 39 (7), 110829.
33. Wu L, Zhou L, Mo M, Liu T, Wu C, Gong C, Lu K, Gong L, Zhu W. & Xu Z. SARS-CoV-2 Omicron RBD shows weaker binding affinity than the currently dominant Delta variant to human ACE2. *Signal Transduct. Target. Ther.* 2022, 7 (1), 1–3. [PubMed: 34980881]
34. Hui KP, Ho JC, Cheung M. c., Ng K. c., Ching RH, Lai K. l., Kam TT, Gu H, Sit K-Y & Hsin MK SARS-CoV-2 Omicron variant replication in human bronchus and lung ex vivo. *Nature* 2022, 603 (7902), 715–720. [PubMed: 35104836]
35. Liu L, Iketani S, Guo Y, Chan JF-W, Wang M, Liu L, Luo Y, Chu H, Huang Y. & Nair MS Striking antibody evasion manifested by the Omicron variant of SARS-CoV-2. *Nature* 2022, 602 (7898), 676–681. [PubMed: 35016198]
36. Buksh BF, Knutson SD, Oakley JV, Bissonnette NB, Oblinsky DG, Schwoerer MP, Seath CP, Geri JB, Rodriguez-Rivera FP & Parker DL μ Map-Red: Proximity Labeling by Red Light Photocatalysis. *Journal of the American Chemical Society* 2022, 144 (14), 6154–6162. [PubMed: 35363468]
37. Tay N; Ryu KA; Weber J; Olow A; Reichman D; Oslund R; Fadeyi O; Rovis T. Targeted Activation in Localized Protein Environments via Deep Red Photoredox Catalysis. *ChemRxiv* 2021. 10.26434/chemrxiv-2021-x9bjv, (accessed 08-01-2022).

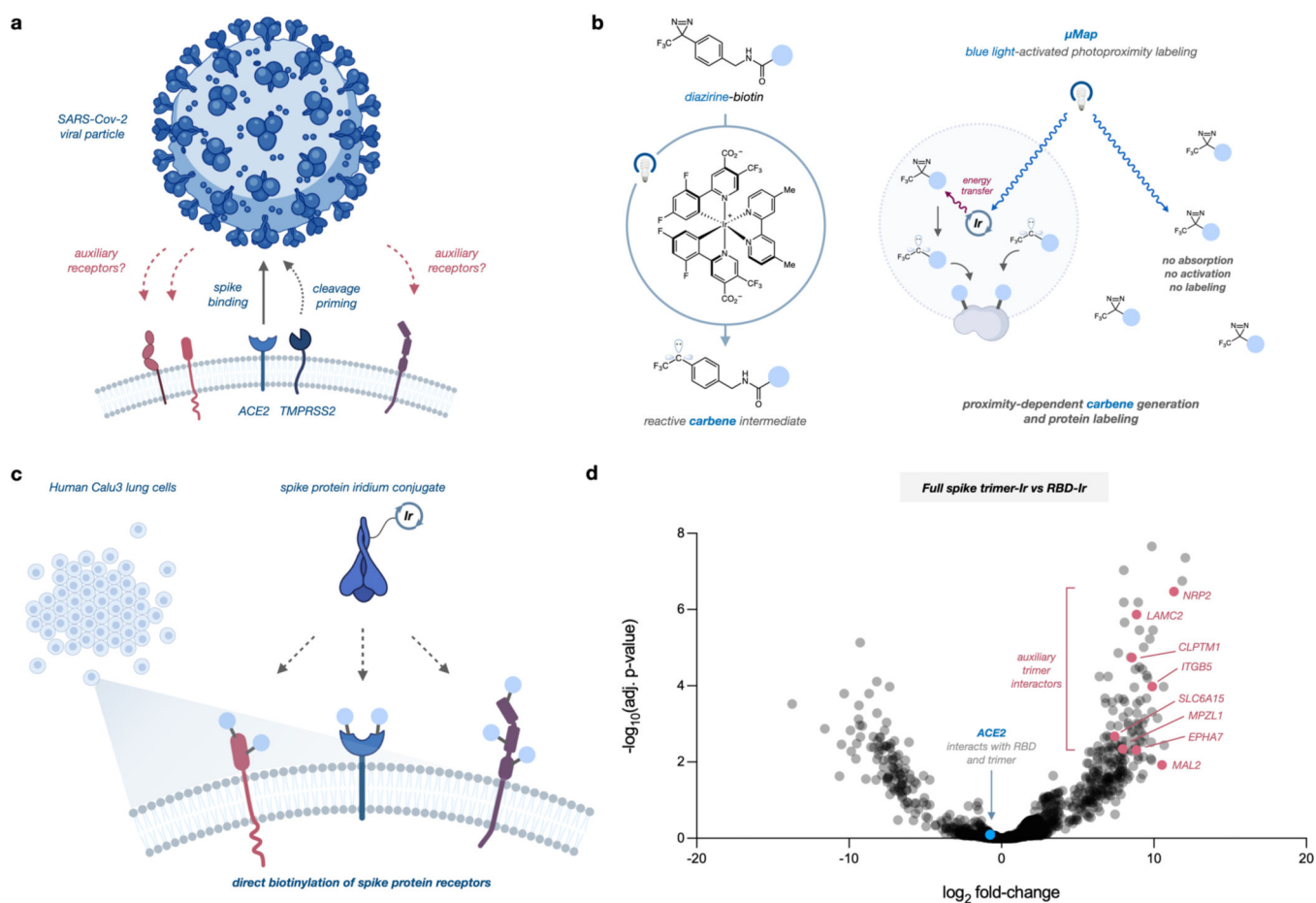


Figure 1.

a) SARS-Cov-2 utilizes *ACE2* and *TMPRSS2* for cell uptake, but additional entry factors are likely. b) μ Map photoproximity labeling via iridium photocatalysts that activate nearby diazirines into reactive carbenes. c) Iridium conjugation with SARS-Cov-2 spike protein enables rapid receptor identification. d) Quantitative proteomics volcano plot of candidate cell-surface proteins after incubation of Ir-spike proteins with Calu-3 cells and photolabeling. Dataset compares full-length spike protein against receptor-binding domain (RBD). *ACE2* interacts with both constructs and is thus near zero enrichment.

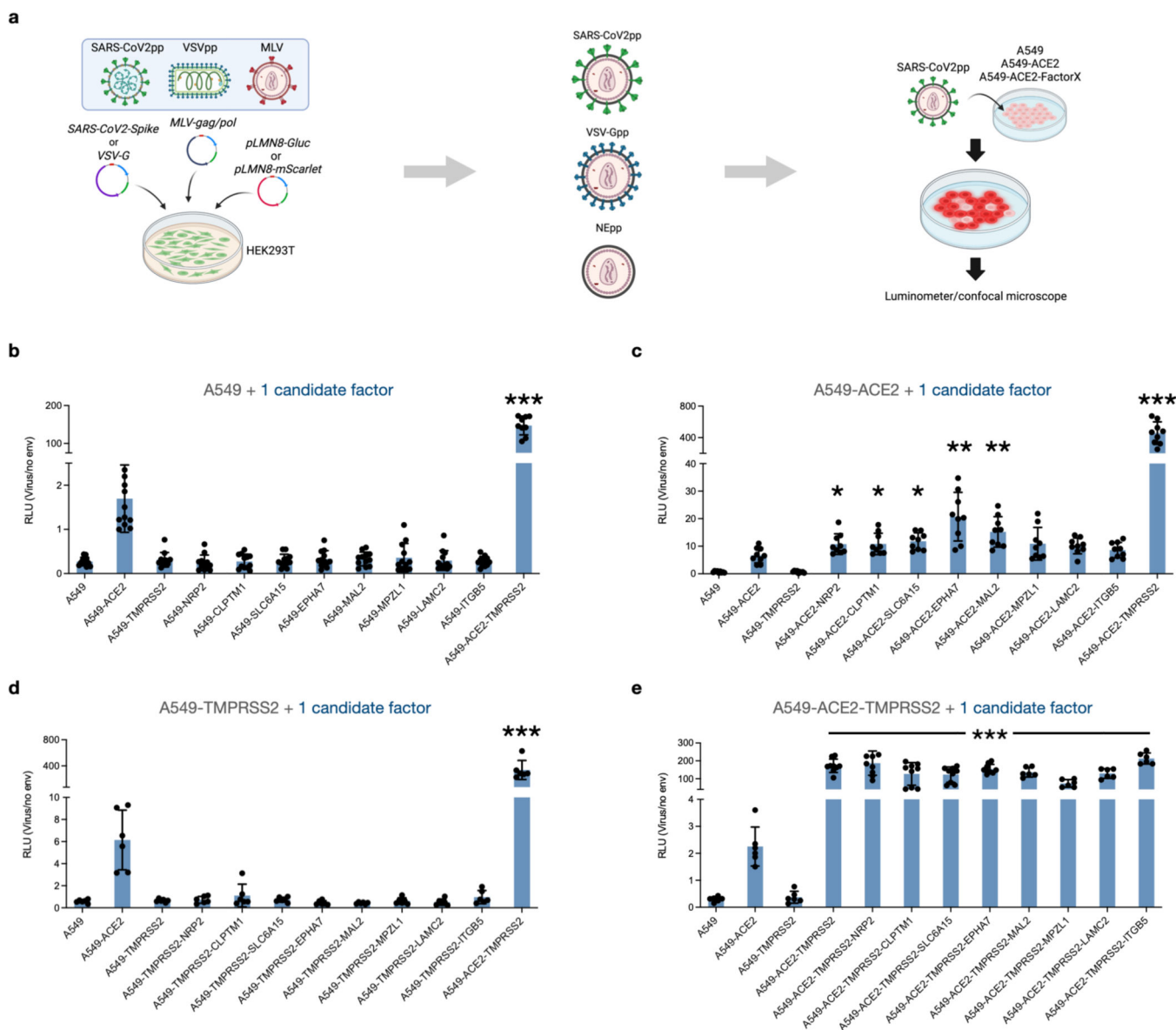


Figure 2. SARS-CoV-2 uptake is enhanced in cells expressing candidate receptors and ACE2.

a) Schematic for generating pseudoviral particles and infection. b-e) Virus uptake into A549 cells expressing *ACE2*, *TMPRSS2*, and/or entry factor candidates. Entry was measured as relative luminescent signal (RLU) normalized against non-enveloped particle control. Datapoints represent mean ($n = 6$) and error bars denote standard deviation. Independent t-tests between *ACE2* and expression lines are indicated * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

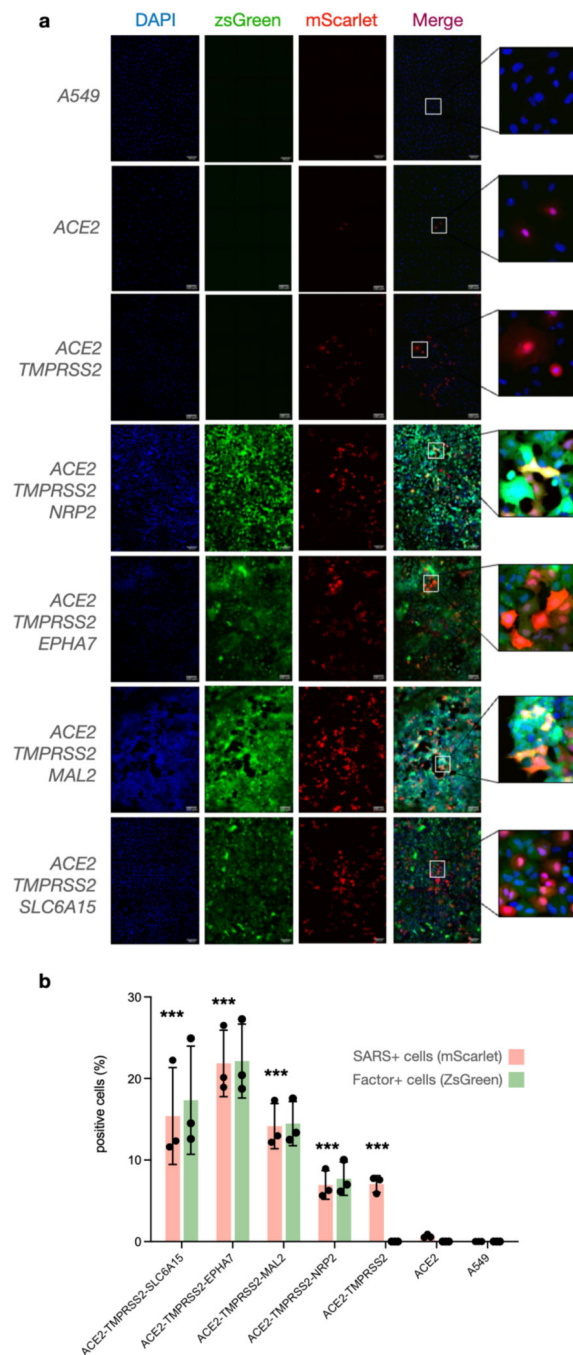


Figure 3. *NRP2*, *MAL2*, *EPHA7*, and *SLC6A15* significantly enhance SARS-Cov-2 entry.
 a) A549 cells expressing various factors were infected with SARS-CoV-2pp encoding mScarlet, stained with DAPI (blue), and visualized using fluorescence microscopy for factor expression (zsGreen) and viral uptake (red). Scale bar indicates 100 μ m, and insets display zoomed-in regions of each image. b) Entry quantification as percentage of red: (SARS positive)/(DAPI positive), green: percentage of (SARS positive)/(Factor positive). Datapoints represent mean from (n = 3), and error bars denote standard deviation.

Independent t-tests of SARS+ values between *ACE2* and *ACE2-TMPRSS2* triple expression lines are indicated as significant (***, $p < 0.001$)

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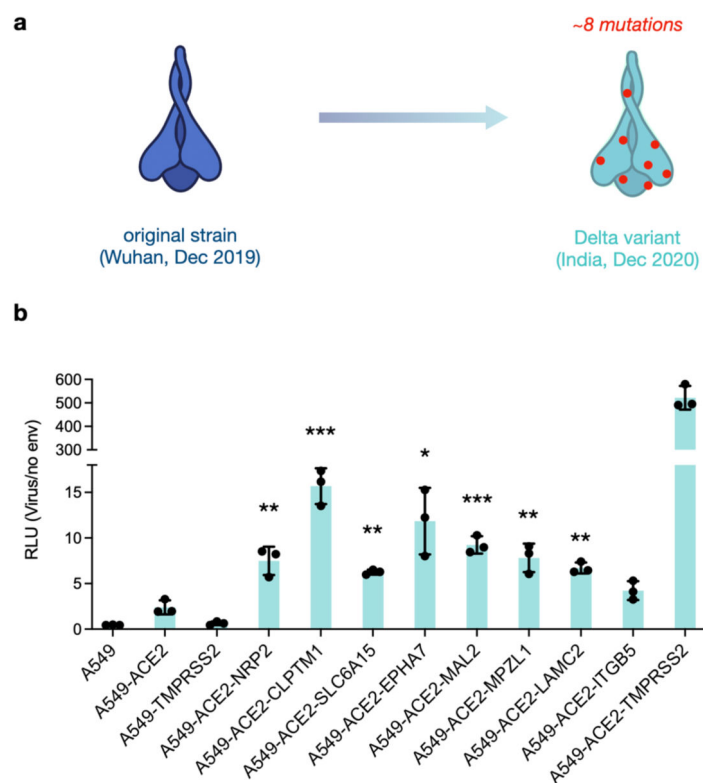


Figure 4. Candidate receptors enhance Delta variant spike-mediated uptake.

a) Delta variant spike harbors 8 mutations compared to Wuhan strain. b) Delta pseudovirus uptake in cells expressing *ACE2* and candidate factors. Entry was measured as relative luminescent signal (RLU) normalized against non-enveloped particle control. Datapoints represent mean ($n = 3$) and error bars denote standard deviation. Independent t-tests between *ACE2* and respective lines are indicated as significant * $p < 0.05$, ** $p < 0.01$, ***, $p < 0.001$.

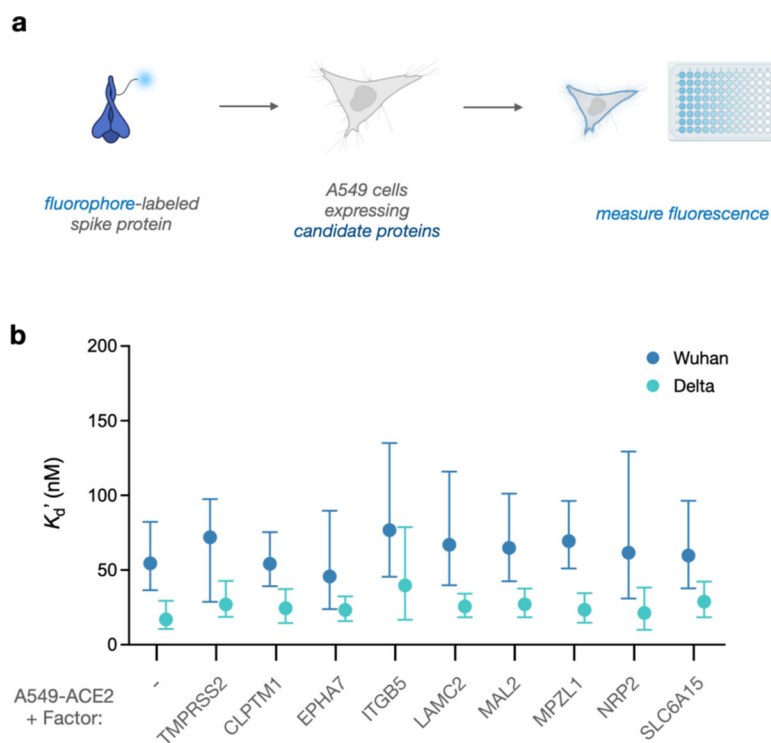


Figure 5. Candidate receptors do not enhance SARS-Cov-2 spike binding on human cells. a) Schematic for testing binding affinity of spike protein and candidate factors. b) Apparent dissociation constants (K_d) for SARS-Cov-2 spike from Wuhan (blue) and Delta (green) strains towards cells expressing *ACE2* and various cell-surface proteins. Datapoints represent mean ($n = 3$), and error bars denote 95% confidence intervals.