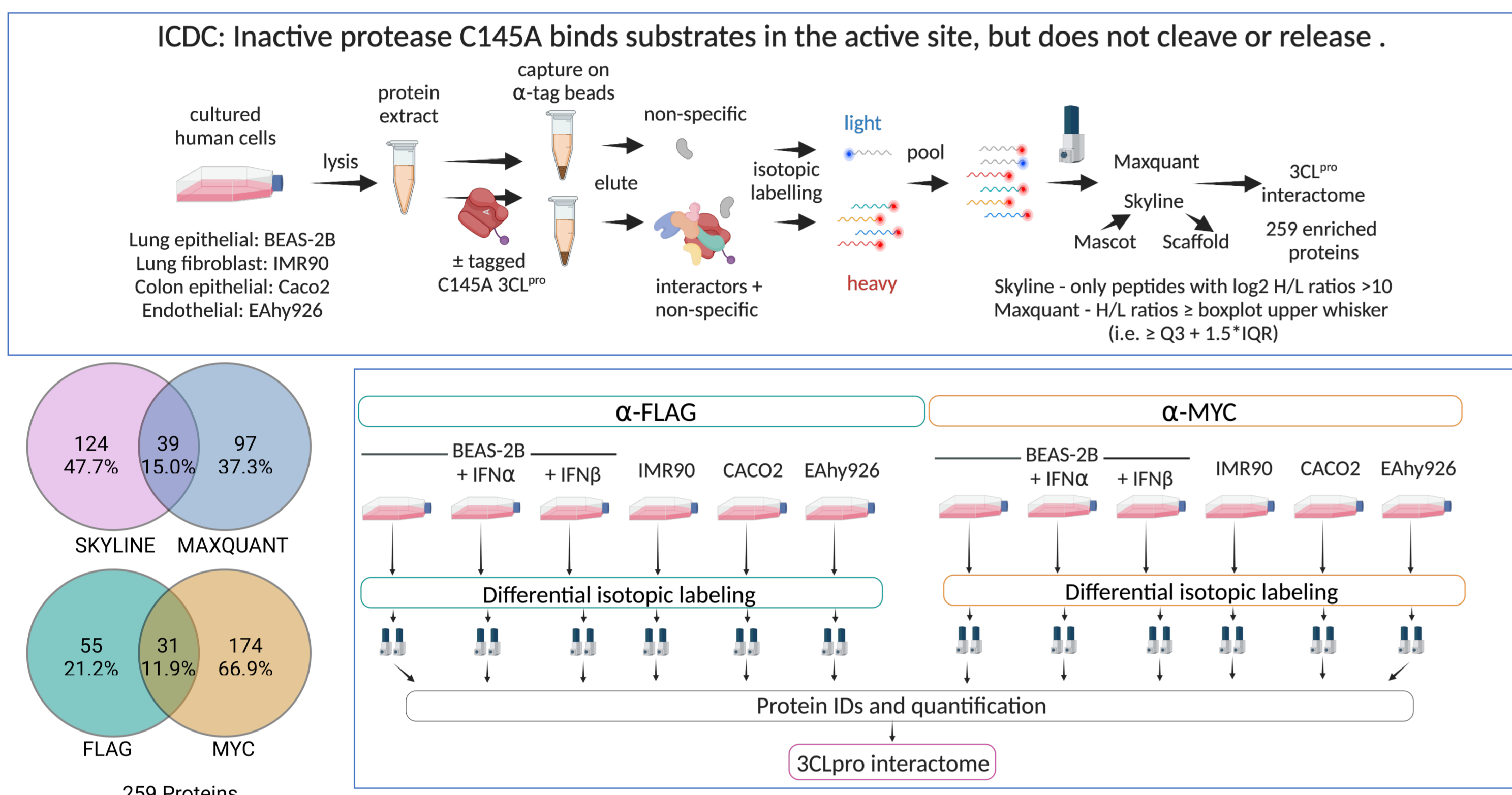


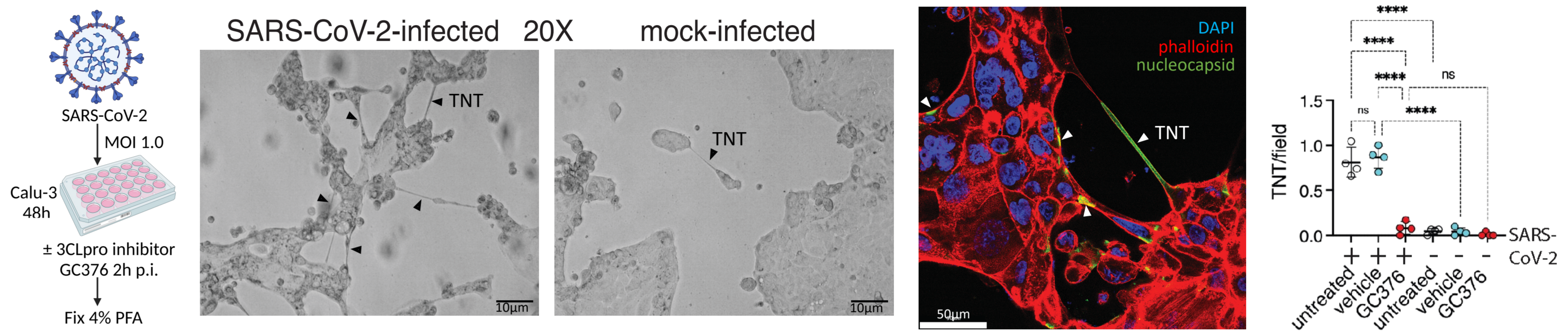
## 1. Background

The coronavirus SARS-CoV-2 and resulting disease COVID-19 continue to pose a significant threat, despite the availability of vaccines. The approval of the SARS-CoV-2 main protease (3CL<sup>pro</sup>, nsp5) inhibitor PAXLOVID<sup>TM</sup> to treat COVID-19 emphasizes the importance of this viral protease in SARS-CoV-2 pathology. To evaluate how 3CL<sup>pro</sup> modulates the human proteome to promote infection, we used ICDC (inactive catalytic domain capture) to identify interactors of 3CL<sup>pro</sup>, and further characterized cleavage of a subset of interactors that contain candidate 3CL<sup>pro</sup> cleavage sites.

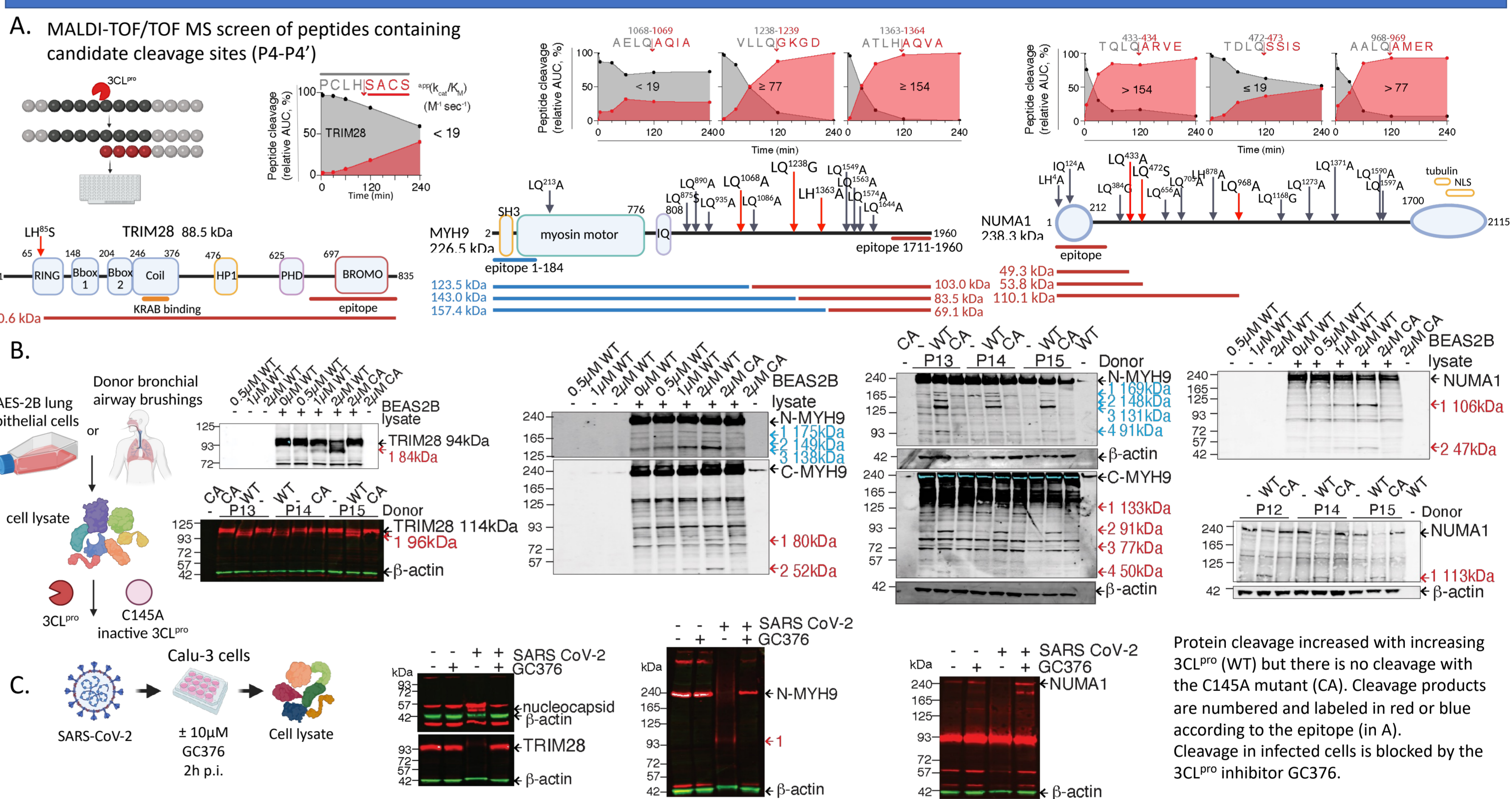
## 2. Inactive catalytic domain capture (ICDC) strategy



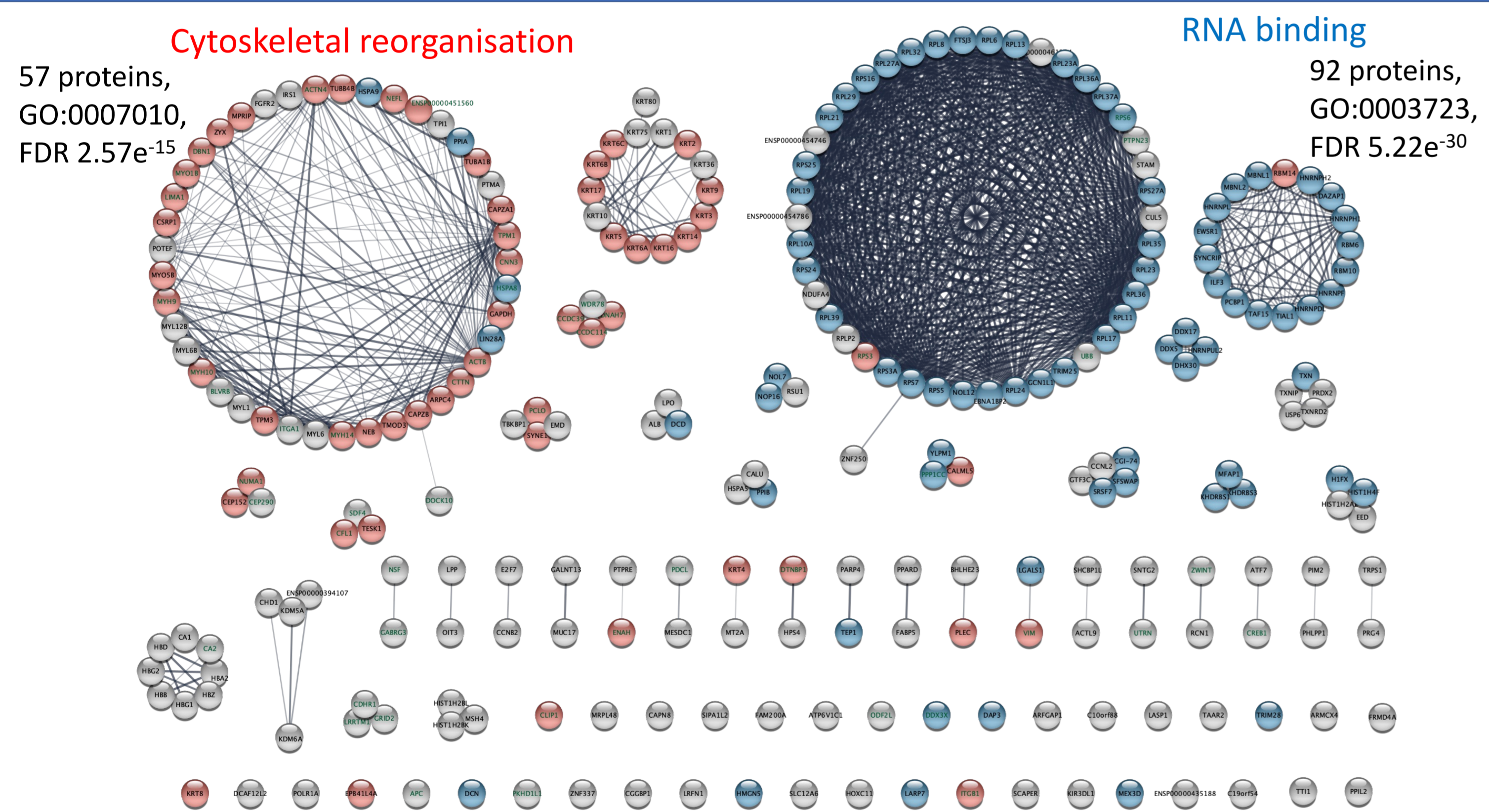
## 4. SARS-CoV-2 infection of human lung epithelial cells induces the formation of tunneling nanotubes (TNT) that contain virus



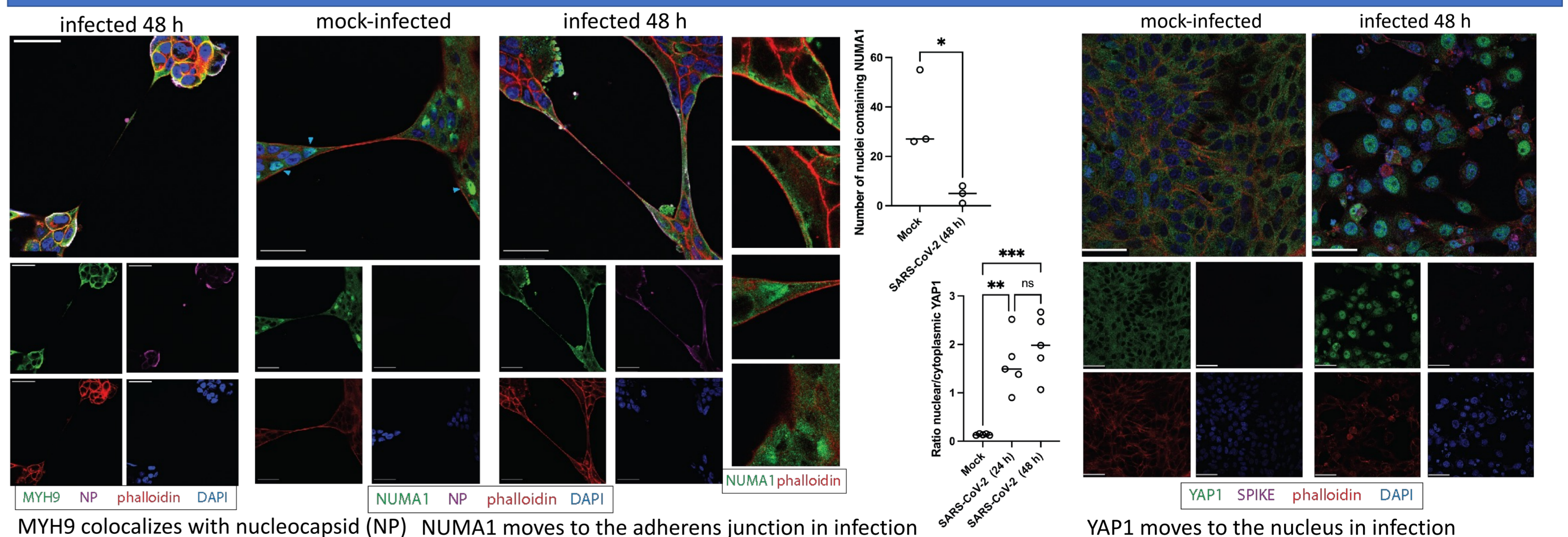
## 5. Proteins from the interactome are 3CL<sup>pro</sup> substrates



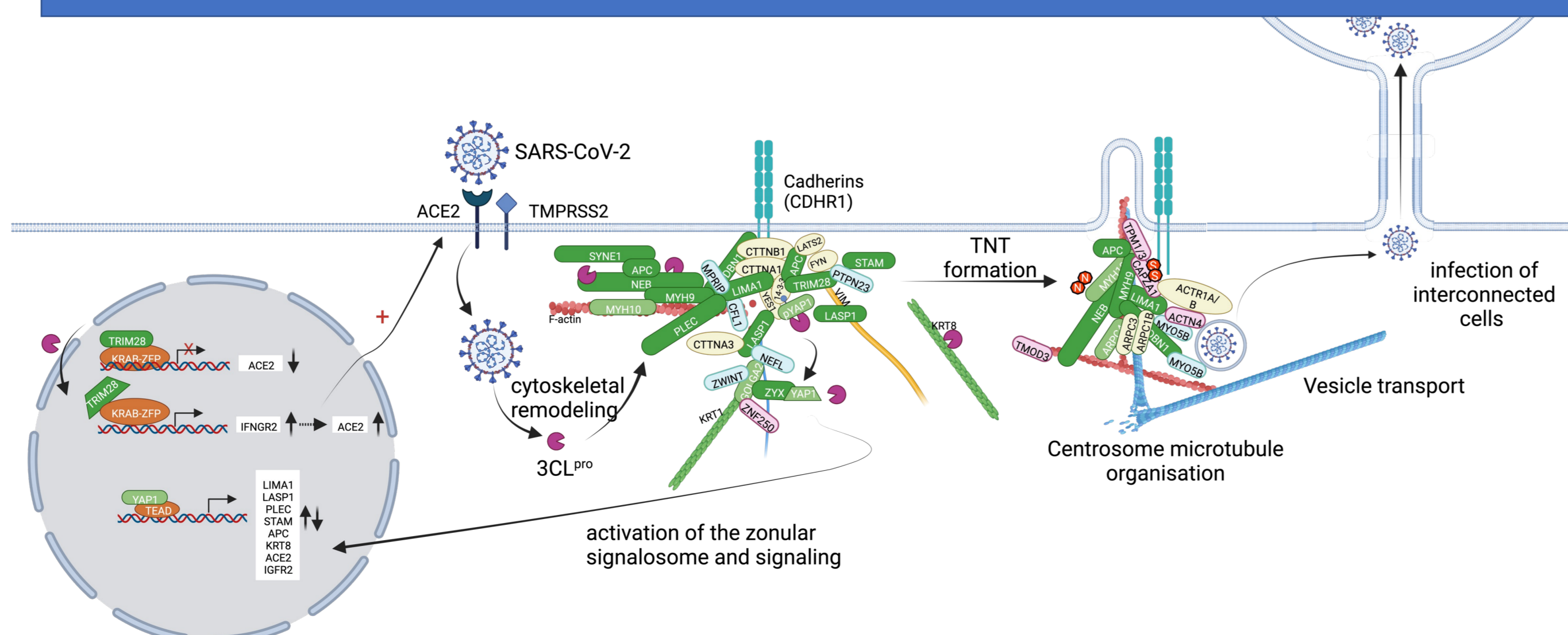
## 3. 3CL<sup>pro</sup> interactors are involved in RNA binding and cytoskeletal reorganisation



## 6. 3CL<sup>pro</sup> cleavage induces protein translocation and activation of the zonular signalsome



## Acknowledgements



## 7. Conclusions

1. ICDC significantly expanded the interactome of 3CL<sup>pro</sup> (nsp5).
2. Many interactors are involved in cytoskeletal organization.
3. Proteins with candidate 3CL<sup>pro</sup> cleavage sites were cleaved *in vitro* and in infected cells and cleavage was blocked by the 3CL<sup>pro</sup> inhibitor GC376.
4. Cleavage of proteins by 3CL<sup>pro</sup> in the adherens junction of lung epithelial cells stimulates protein translocation and disrupts cytoskeletal networks.
5. In infection of human lung epithelial cells, 3CL<sup>pro</sup> induces the formation of tunneling nanotubes that enable SARS-CoV-2 to infect distant cells.