



Fig. S10. Systemic modeling of SARS-CoV-2 interactions within human tissues.

a, S-binding receptor-like host factors were classified according to their functions in virus entry, immune regulation, the Wnt pathway, and protein trafficking. **b and c**, The mRNA expression level of each factor in different human tissues was derived from the Human Protein Atlas. The factor-mediated SARS-CoV-2 binding potentials in each tissue were calculated by dividing the factor expression level by its affinity for the S protein (K_d). **b**, Virus binding potentials of each tissue contributed by the S-binding host factors involved in virus entry, immune regulation, the Wnt pathway, and protein trafficking individually or in group combination. **c**, Virus infection rates (number of virus-positive samples) in the indicated tissues were derived from a recent biopsy study (Puelles *et al. N Engl J Med*, 2020), and these were clustered with ASK receptor-mediated virus binding potentials. In panel **b**, tissues or organs that were identified as positive for SARS-CoV-2 in the literature are labeled red.