

SARS-CoV-2 infection of sustentacular cells disrupts olfactory signaling pathways

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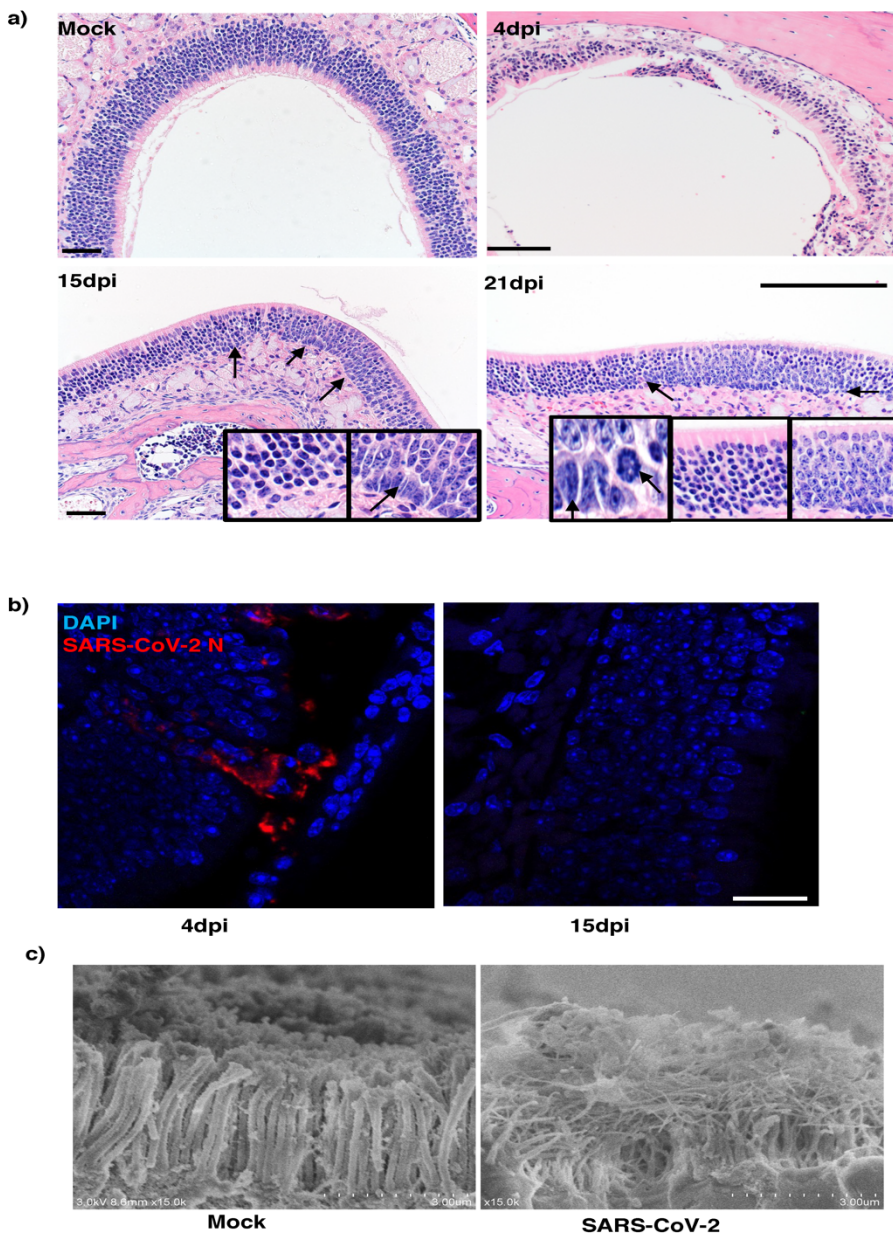


Fig S1

Supplementary Figure 1. Detection of viral RNA, and pathological changes in infected mice. (a) Histochemical analysis of OE from SARS2-N501Y_{MA30}-infected BALB/c mice shows disruption and recovery of OE. Uncommon sites of basal cell hyperplasia (arrow 15dpi) and hyperchromatic OSN nuclei were observed at 21 dpi (left inset, arrow; middle inset). Occasional fields of OE that were composed mostly of regenerative epithelia with larger nuclei (right inset,

arrows) were observed. Scale bar represents 83 μ m (b) Sections were prepared at the indicated times p.i. and analyzed by RNAScope for viral RNA (red). Scale bar 50 μ m. (c) SEM analysis shows uniform lawn of normal-appearing cilia in mock-infected OE but damaged cilia at 4dpi in K-18-hACE2 mice. Scale bar 3 μ m.

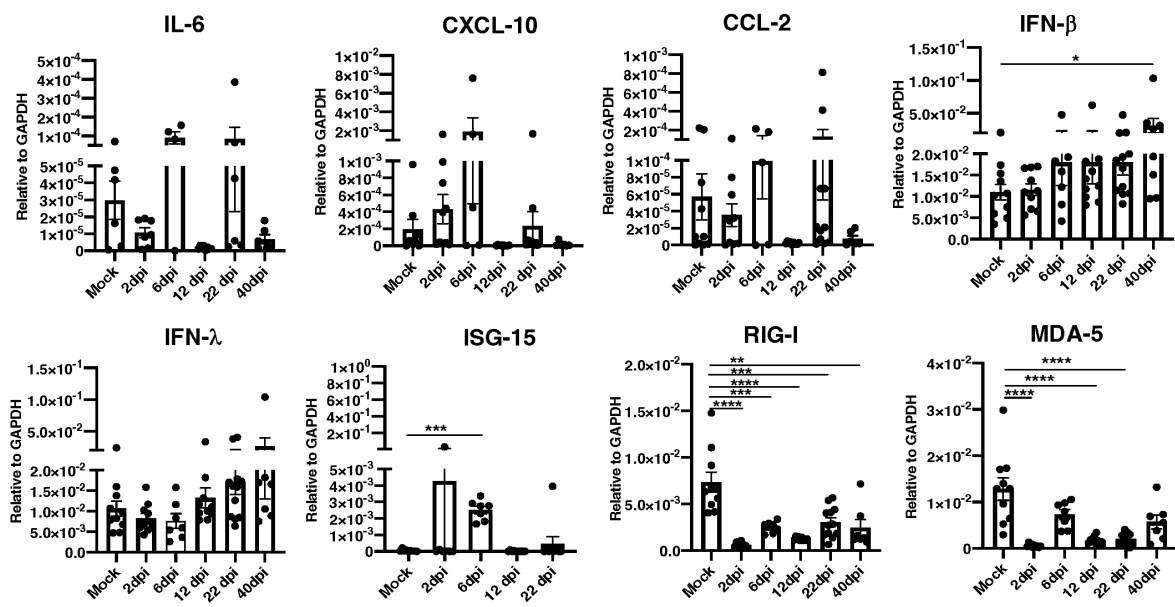
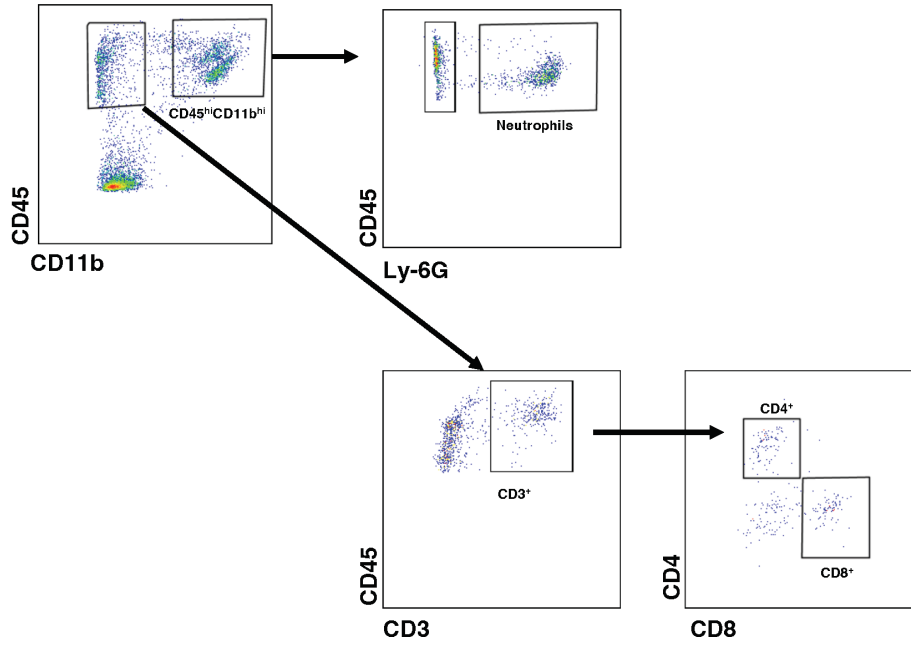


Fig S2

Supplementary Figure 2. Cytokine/chemokine expression profile in SARS-CoV-2 infected BALB/c mouse OE. (a) SARS2-N501Y_{MA30}-infected BALB/c mice OE were harvested at the indicated times p.i. Cytokine and chemokine mRNA expression was analyzed using qPCR. Data represent means \pm SEM of results pooled from two independent experiments with 7 mice per group. Data were analyzed using Mann-Whitney *U* tests. **P* < 0.05, ***P* < 0.01, ****P* < 0.001, *****P* < 0.0001.

a)



b)

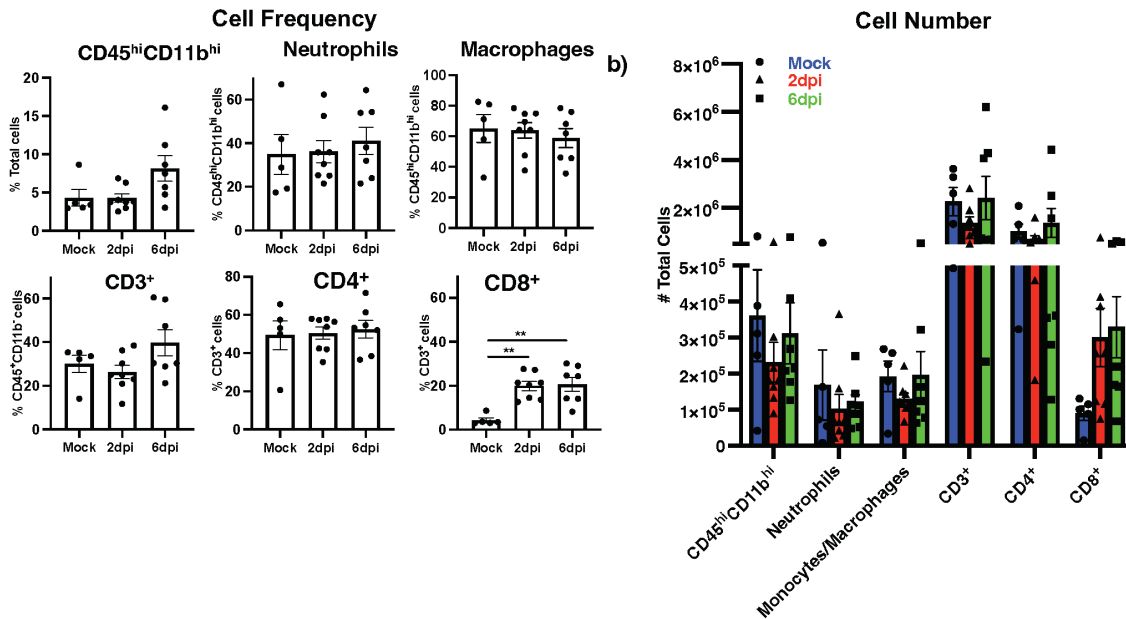


Fig S3

Supplementary Figure 3. Immune cell infiltration in olfactory epithelium after SARS-CoV-2 infection. BALB/c mice were infected with SARS-CoV-2. (a) Gating strategy for flow cytometric analysis of cells from OE. OE was harvested and analyzed for frequency (b) and numbers of infiltrating immune cells by flow cytometry (c). Data represent means \pm SEM of results pooled from two independent experiments with mock-5, 2 and 6 dpi-7 mice per group.