Supplemental Materials for:

Human nasal wash RNA-seq reveals distinct cell-specific innate immune responses between influenza and SARS-CoV-2

Kevin Gao^{1*}, Alan G. Derr^{2*}, Zhiru Guo^{1*}, Kerstin Nündel¹, Ann Marshak-Rothstein¹, Robert W.

Finberg^{1±}, and Jennifer P. Wang^{1±}

¹Department of Medicine, University of Massachusetts Chan Medical School, Worcester, MA,

USA

²Department of Bioinformatics and Integrative Biology, University of Massachusetts Chan

Medical School, Worcester, MA, USA

*, $^{\pm}$ These authors contributed equally to the work, respectively.

Corresponding author:

Jennifer P. Wang, M.D. Department of Medicine and Diabetes Center of Excellence 368 Plantation St. ASC 7-2047 Worcester, MA, 01605, USA Ph: 1-508-856-8414 email: Jennifer.Wang@umassmed.edu



Supplemental Figure 1. tSNE plots with specific transcriptional markers mapped.

Note: We identified a unique population of cells expressing high levels of caveolin-1 (*CAV1*) and modest amounts of *KRT7* in two COVID-19 donor samples, labeled "unk_COVID" in **Figure 1**. Expression of *CAV1* has been described in both nasal and bronchial cells and is involved in cell proliferation and inflammation. CAV1 expression on epithelial cells could be a response to pulmonary injury.



Supplemental Figure 2. tSNE plots showing cell type distribution in donor samples from influenza, COVID-19, or healthy controls.

Please see supplementary excel files included with the manuscript:

- Supplemental File 1. Donor status
- Supplemental File 2. Cell type distribution
- Supplemental File 3. DE analysis for cell subtypes, all samples
- Supplemental File 4. DE and GO analysis for major cell types, balanced samples
- Supplemental File 5. CellPhoneDB