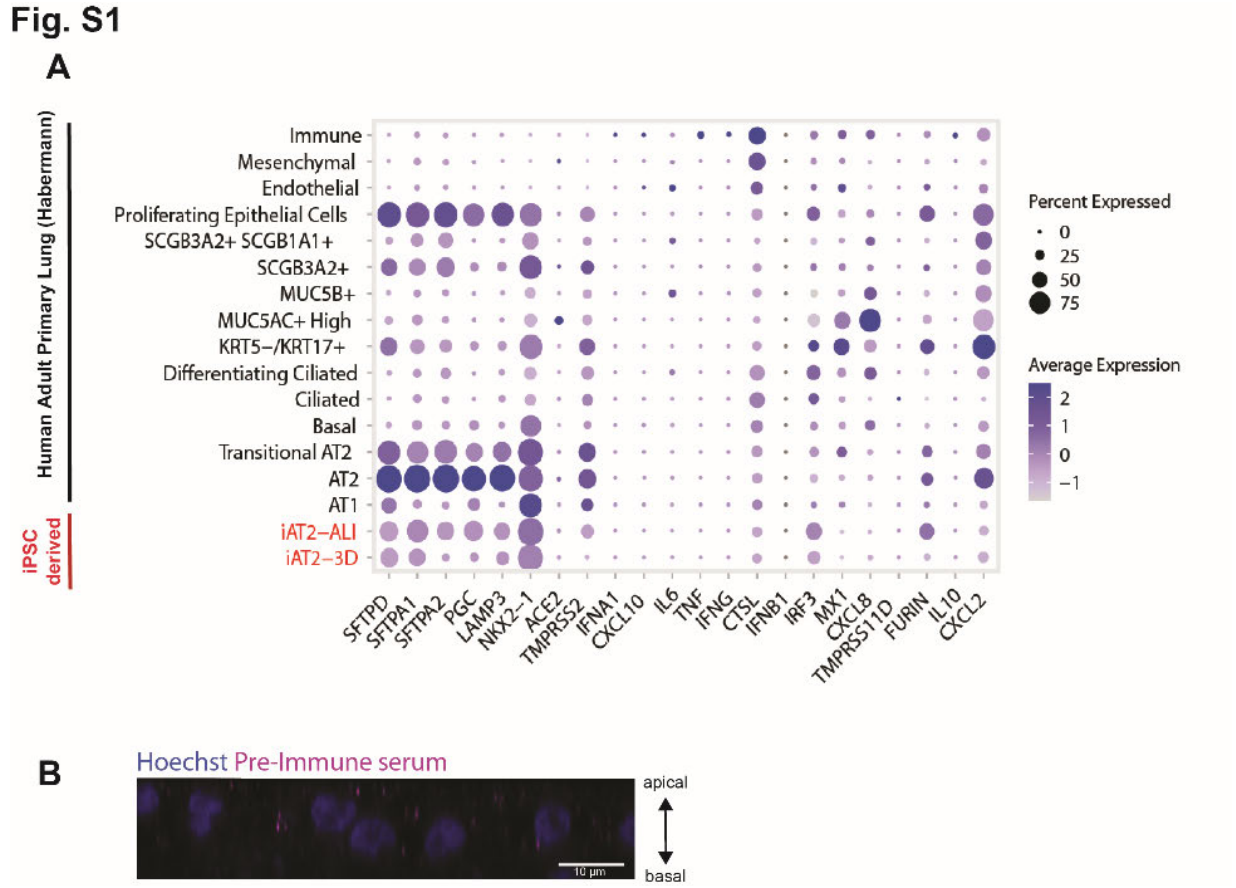

Fig. S1.

Single cell transcriptomic profiles of iPSC-derived vs primary lung cells. (A) Expression of selected genes profiled by scRNA-seq in iAT2s cultured head-to-head as either 3D spheres vs 2D air-liquid interface (ALI) cultures [6]. Comparison is made to a published adult primary lung epithelial dataset by Habermann [31]. Purple dot plots indicate expression frequencies and levels of transcripts associated with AT2 programs, cytokines, interferon signaling, or potential viral receptors. (B) Staining control of iAT2s in ALI culture (compare to ACE2 staining in main figure 1). Staining with preimmune serum rather than anti-ACE2 antibody shows no significant staining.

Fig. S2

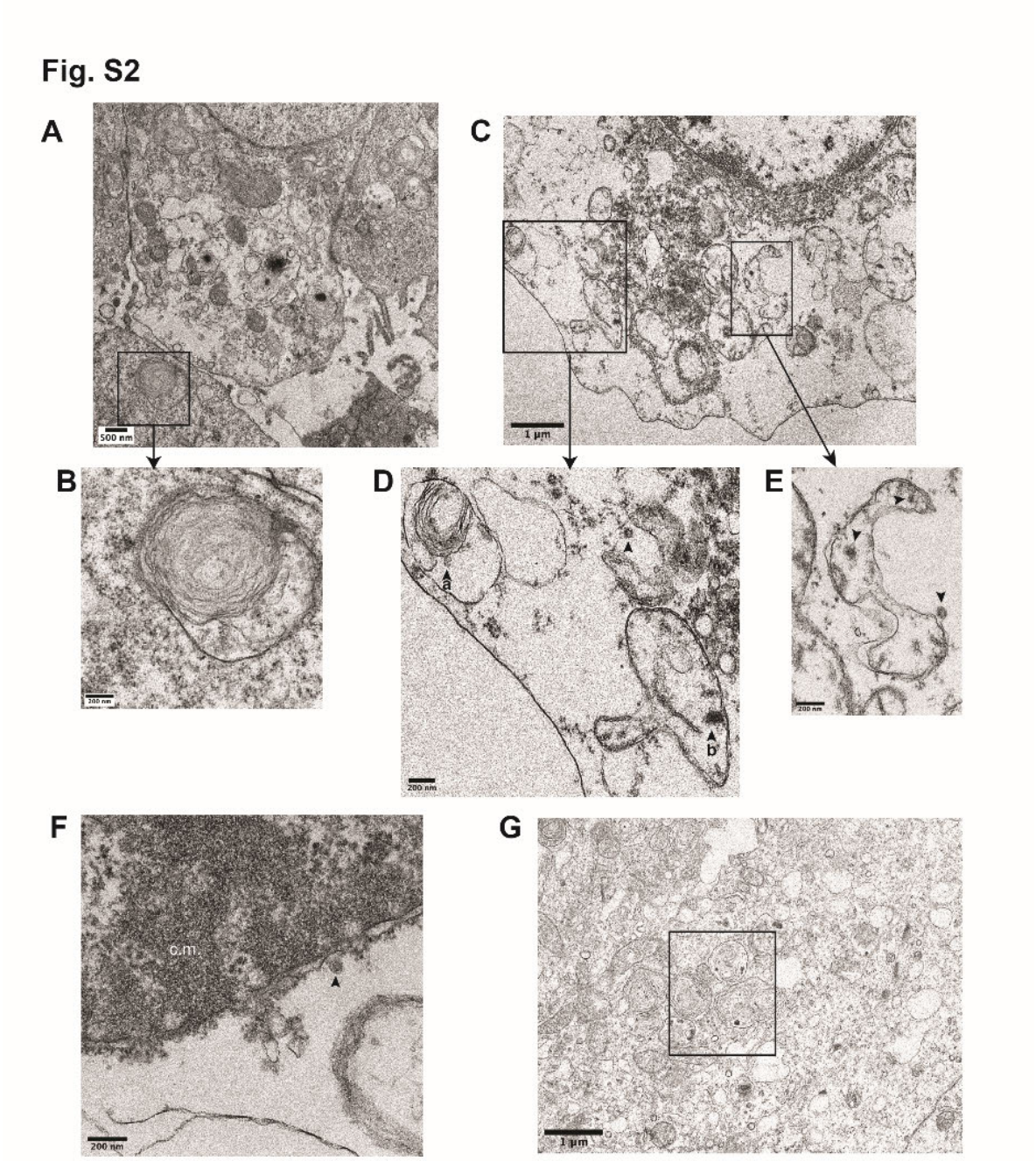

Fig. S2.

Ultrastructural analysis of iAT2s infected with SARS-CoV-2. (B) Transmission electron micrographs of mock-infected iAT2s at ALI (A-B) demonstrating lamellar body expression but no detectable virions**.** iAT2s at ALI infected with SARS-CoV-2 at an MOI of 140 and fixed 1 dpi (C-G) contain visible virions (C-E, G, arrowheads) in the cytoplasm (D,E), within lamellar bodies (D, arrowhead a) (G, see Fig. 2J for inset), and within double-membrane bound structures (D, arrowhead b) (E, arrowheads). Virions are also found extracellularly (F, arrowhead) and some iAT2s contain convoluted membranes (F, c.m.).

Fig. S3

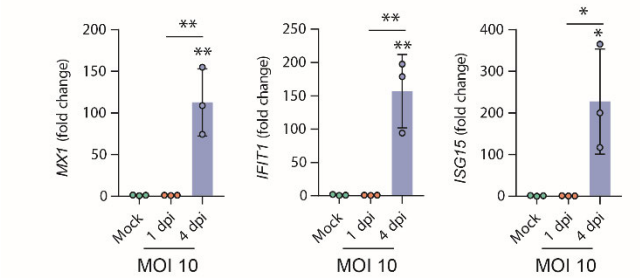

Fig. S3.

Interferon response in iATs infection at lower MOI. RT-qPCR of interferon stimulated genes (ISGs) in iAT2s infected with SARS-CoV-2 (MOI 10) at 1 and 4 dpi, (n=3). All bars represent mean +/- standard deviation. One-way ANOVA with multiple comparisons were performed.