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# SARS-CoV-2 entry factors are highly expressed in nasal epithelial cells together with innate immune genes

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## Supplementary Table 1

Genes	GO Accession Number: Class	PathCards
IDO1	GO:0002376: immune system process	NF-kappaB Signaling Viral mRNA translation
PI3	GO:0002376: immune system process	Defensins, Innate Immune System
CEACAM5	GO:0002376: immune system process	NF-kappaB Signaling
KYNU	GO:0002376: immune system process	Viral mRNA translation
TCN1	GO:0002376: immune system process	Innate Immune System NF-kappaB Signaling
S100P	GO:0002376: immune system process	Innate Immune System
IRAK3	GO:0002376: immune system process	Innate Immune System
TNFSF10	GO:0002376: immune system process	TNF signaling
NOS2	GO:0002376: immune system process	Innate Immune System
PTGES	GO:0002526: acute inflammatory response	Prostaglandin 2 biosynthesis and metabolism FM
MDK	GO:0002376: immune system process	NF-KappaB Family Pathway
RAB37	GO:0002376: immune system process	Innate Immune System
ASS1	GO:0002376: immune system process	Viral mRNA Translation
OAS1	GO:0002376: immune system process	Innate Immune System Immune response IFN alpha/beta signaling pathway
MX1	GO:0002376: immune system process	Innate Immune System Immune response IFN alpha/beta signaling pathway

**Supplementary Table 1** | Immune-associated genes in respiratory epithelial expression from the top 50 genes correlated with *ACE2* expression based on Spearman correlation analysis (with Benjamini-Hochberg-adjusted *p*-values) across all cells within the Vieira Braga, Kar *et al.* lung epithelial dataset. The characterization of genes was based on Gene Ontology classes from the Gene Ontology (GO) database and associated pathways in PathCards from the Pathway Unification Database.