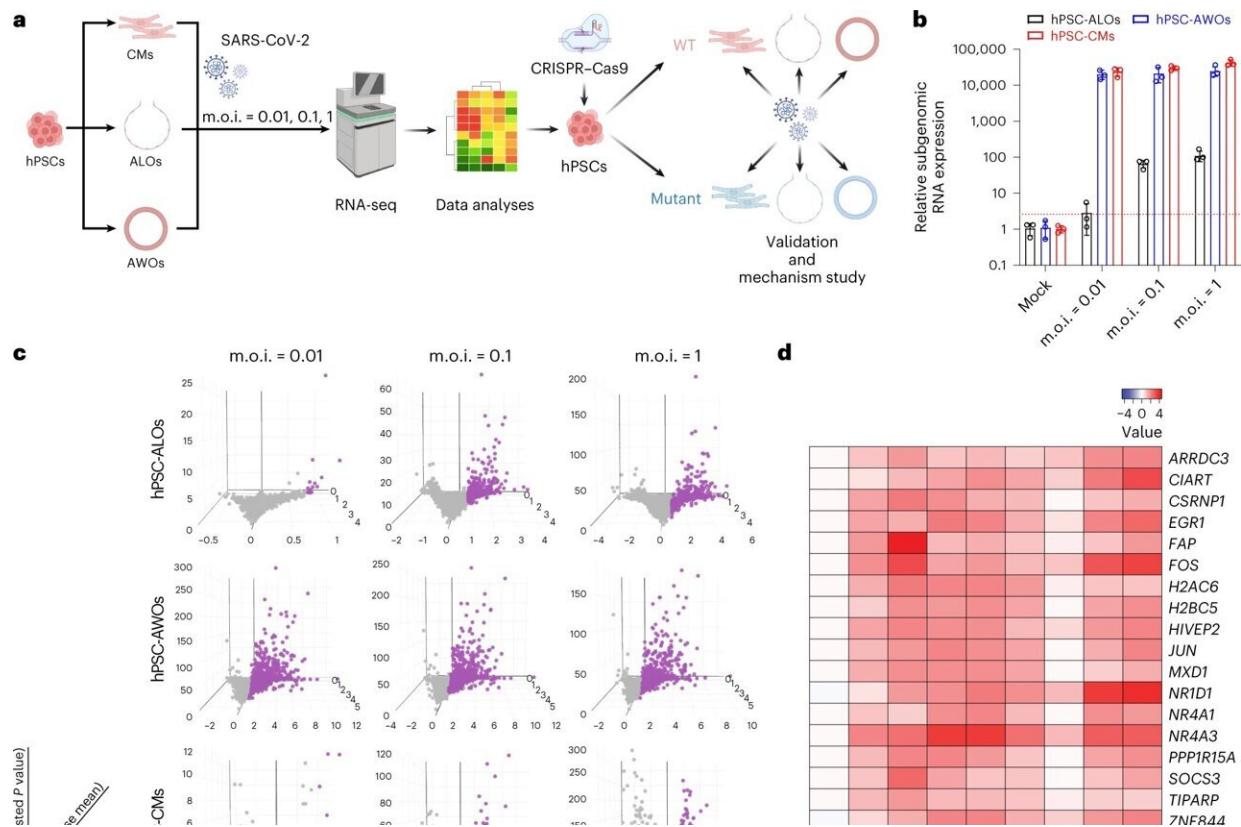


# Study identifies the human genes enabling SARS-CoV-2 infection

March 16 2023, by Jim Schnabel



A multi-organoid platform to identify genes involved in SARS-CoV-2 infection. **a**, Schematic of the experimental design. **b**, Levels of subgenomic viral transcripts, determined by qRT-PCR, in hPSC-derived AWOs, ALOs and CMs at 48 h.p.i. with SARS-CoV-2 at different m.o.i. (m.o.i. = 0.01, 0.10 and 1.00). The dashed red line indicates the detection limit. **c**, Three-dimensional analysis of transcriptional changes in hPSC-derived AWOs, ALOs and CMs infected at 48 h.p.i. (m.o.i. = 0.01, 0.10 and 1.00). The genes that were significantly changed ( $\log_2(\text{fold change}) > 0.75$ , base mean  $> 10$  and adjusted  $P$

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