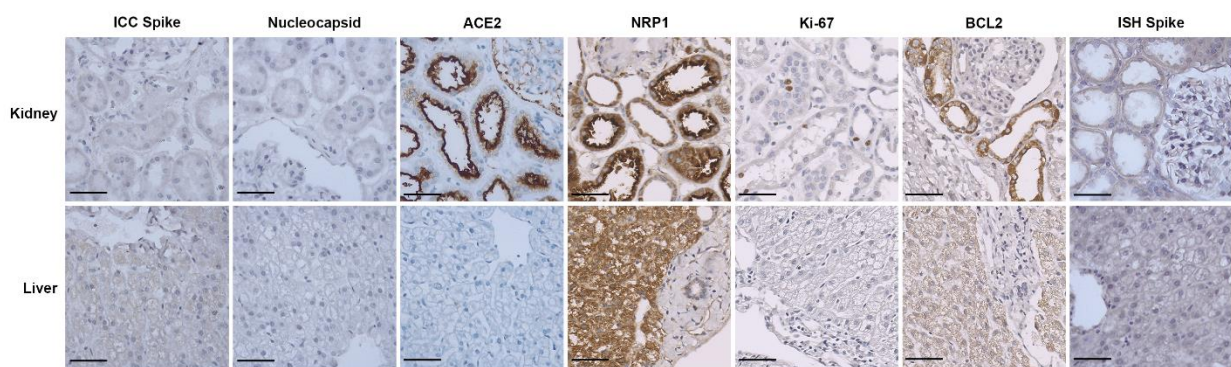**InfectionCMA: a Cell MicroArray Approach for Efficient Biomarker Screening in *in vitro* Infection Assays**

Ana C. Magalhães 1,2,3, Sara Ricardo 1,2,4, Ana C. Moreira 1,3,5, Mariana Nunes 1,2,3, Margarida Tavares 6,7,8, Ricardo J. Pinto 1,2,3, Maria Salomé Gomes 1,3,5 and Luisa Pereira 1,2,*
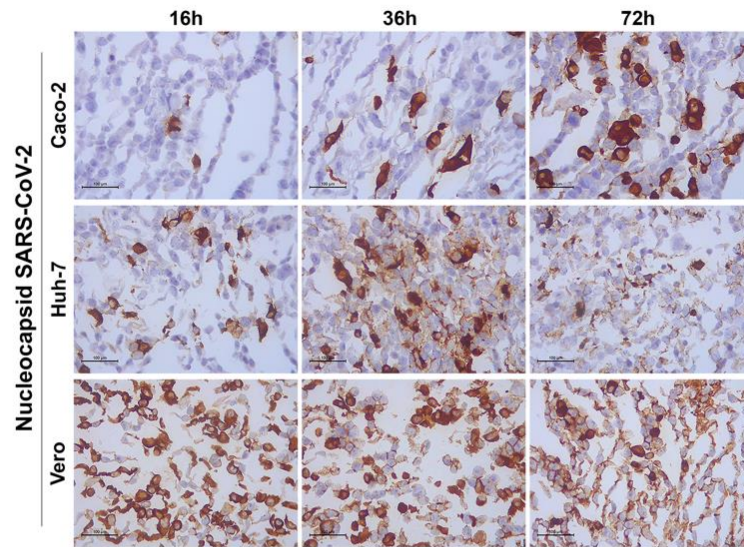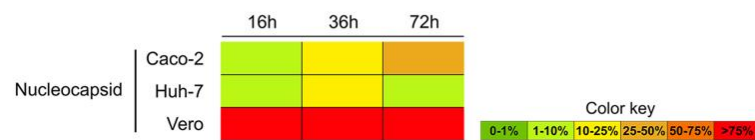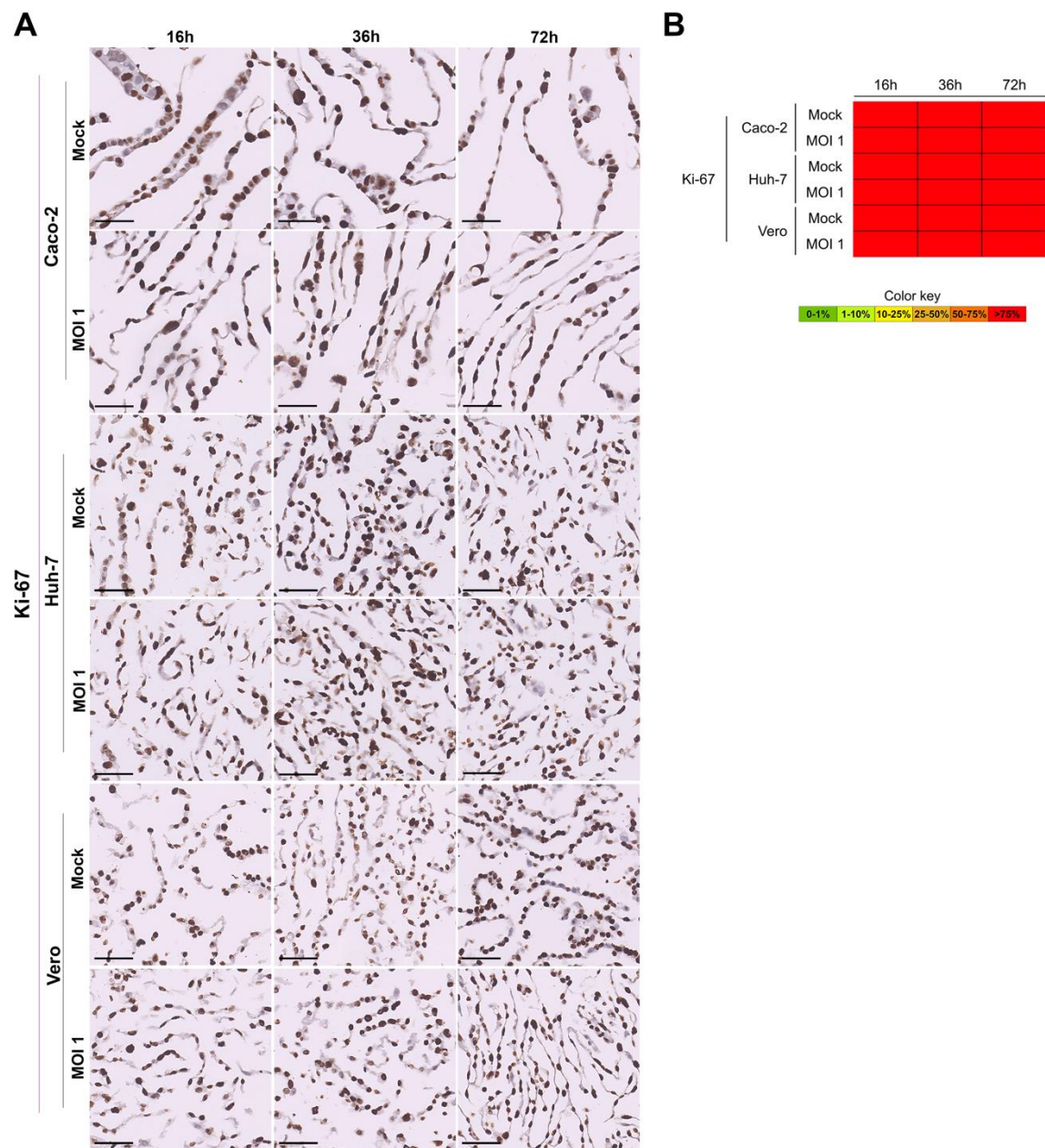
Supplementary Material:

Supplementary Figure S1- ICC for the spike, nucleocapsid, ACE2, NRP1, Ki-67 and BCL2, and ISH for the spike, in the tumour tissue cores of kidney and liver. Scale bar 50µm.
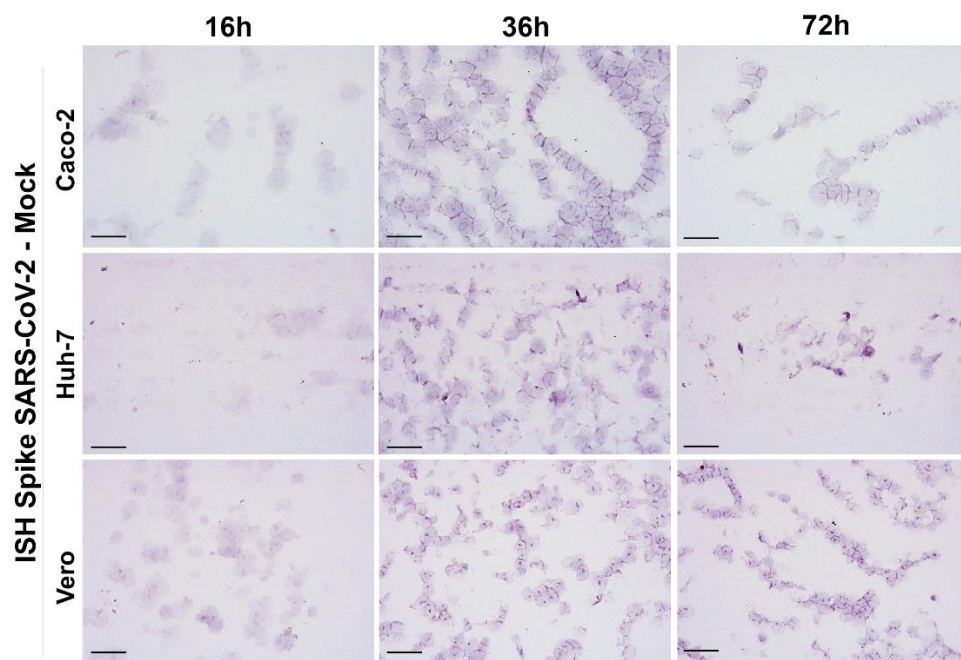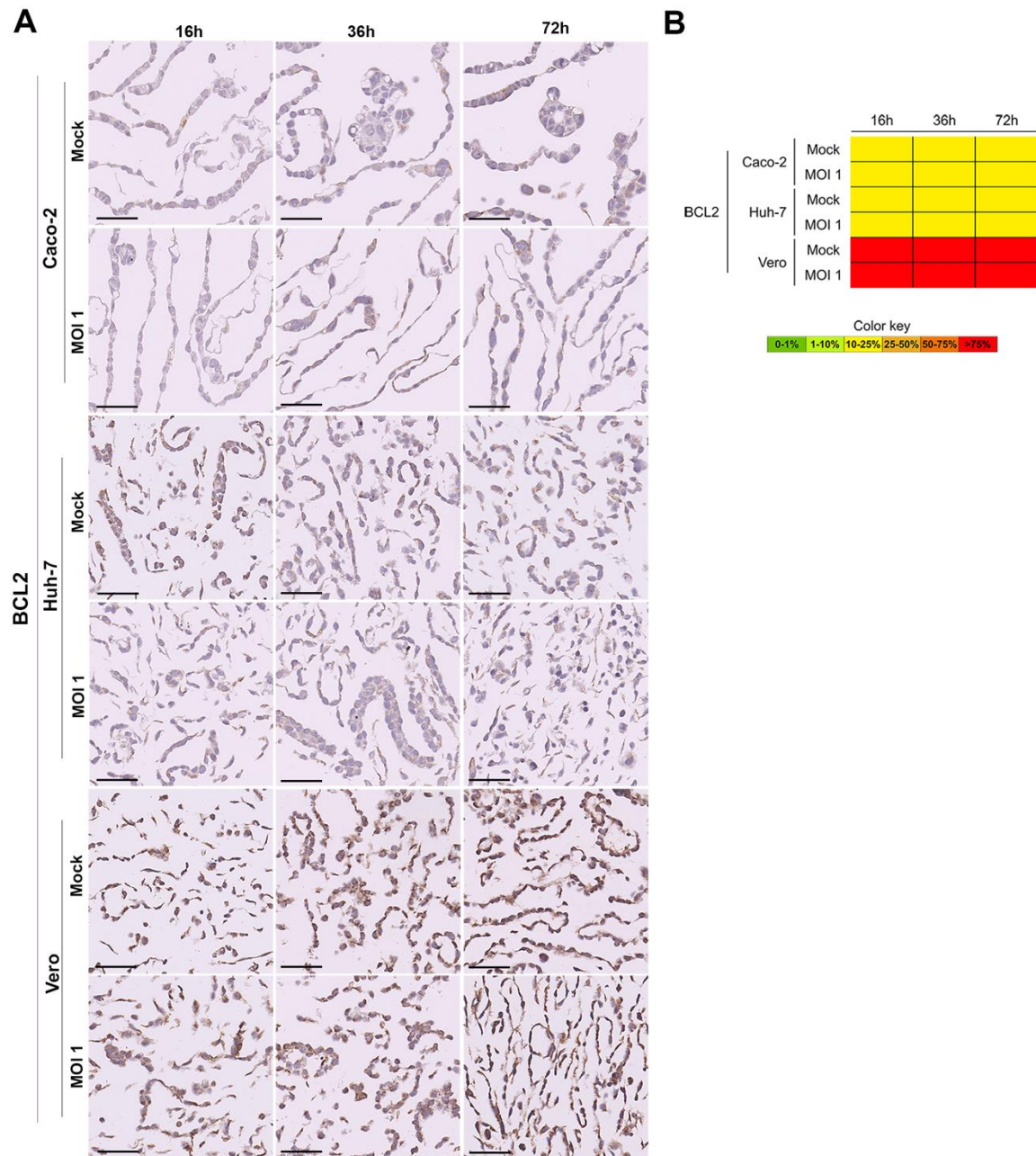
Supplementary Figure S2- Controls for the characterization of SARS-CoV-2 spike mRNA expression in the human (Caco-2 and Huh-7) and Vero cell lines, at different time-points, by ISH. Microscopic images with 100µm scale bar.

Supplementary Figure S3- Characterization of SARS-CoV-2 nucleocapsid expression in the human (Caco-2 and Huh-7) and Vero cell lines, at different time-points after infection with MOI 1, by ICC (A- light microscopic images with 100μm scale bar; B- heat map).

Supplementary Figure S4- Characterization of Ki-67 expression in the human (Caco-2 and Huh-7) and Vero cell lines, at different time-points after infection with MOI 1, by ICC (A- light microscopic images with 50μm scale bar; B- heat map).

Supplementary Figure S5- Characterization of BCL-2 expression in the human (Caco-2 and Huh-7) and Vero cell lines, at different time-points after infection with MOI 1, by ICC (A- light microscopic images with 50µm scale bar; B- heat map).