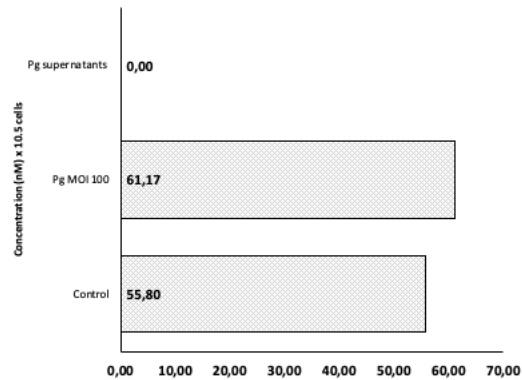
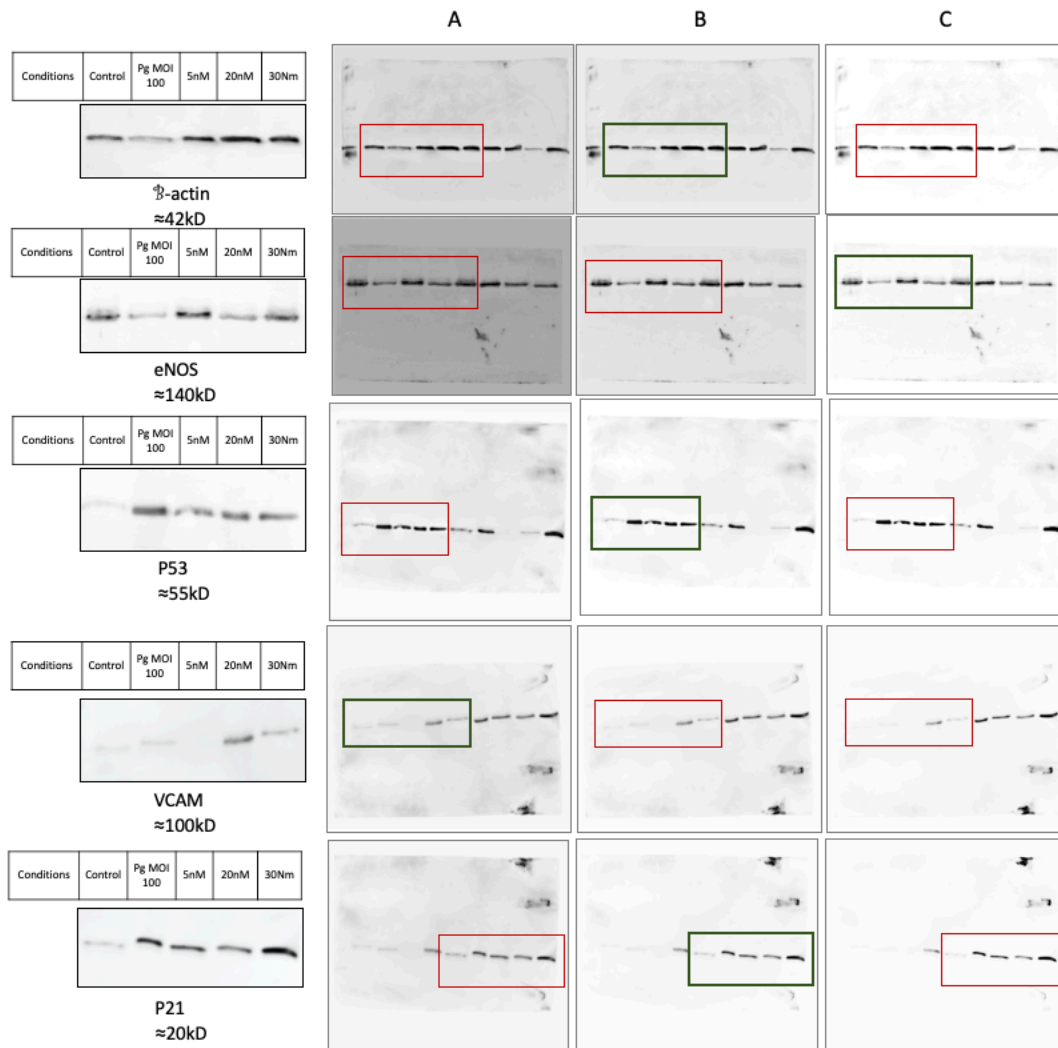


***Porphyromonas gingivalis* triggers the shedding of inflammatory endothelial microvesicles that act as autocrine effectors of endothelial dysfunction**

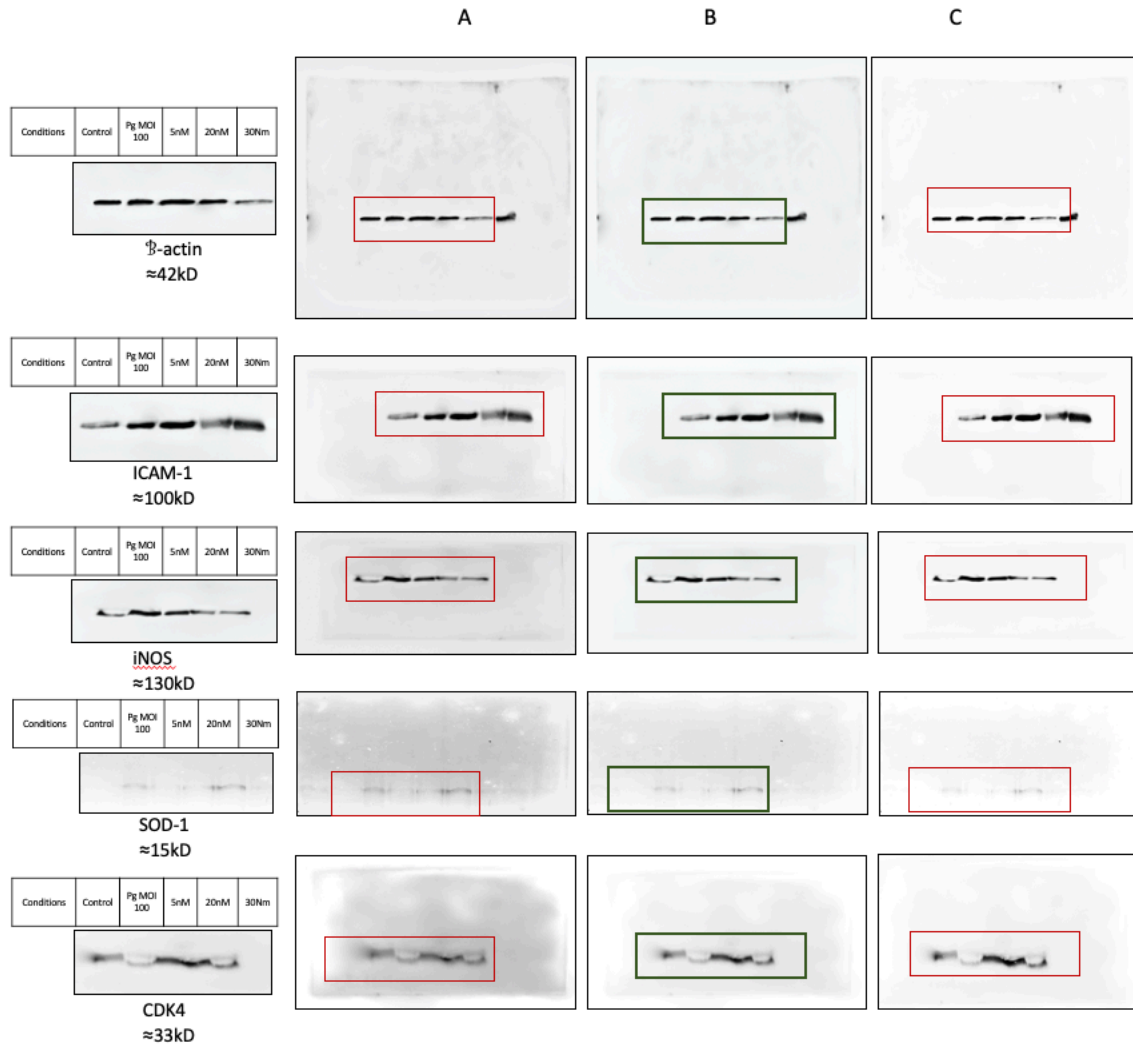
Isaac Maximiliano Bugueno, Fatiha Zobairi El-Ghazouani, Fareeha Batool, Hanine El Itawi, Eduardo Anglès-Cano, Nadia Benkirane-Jessel, Florence Toti and Olivier Huck



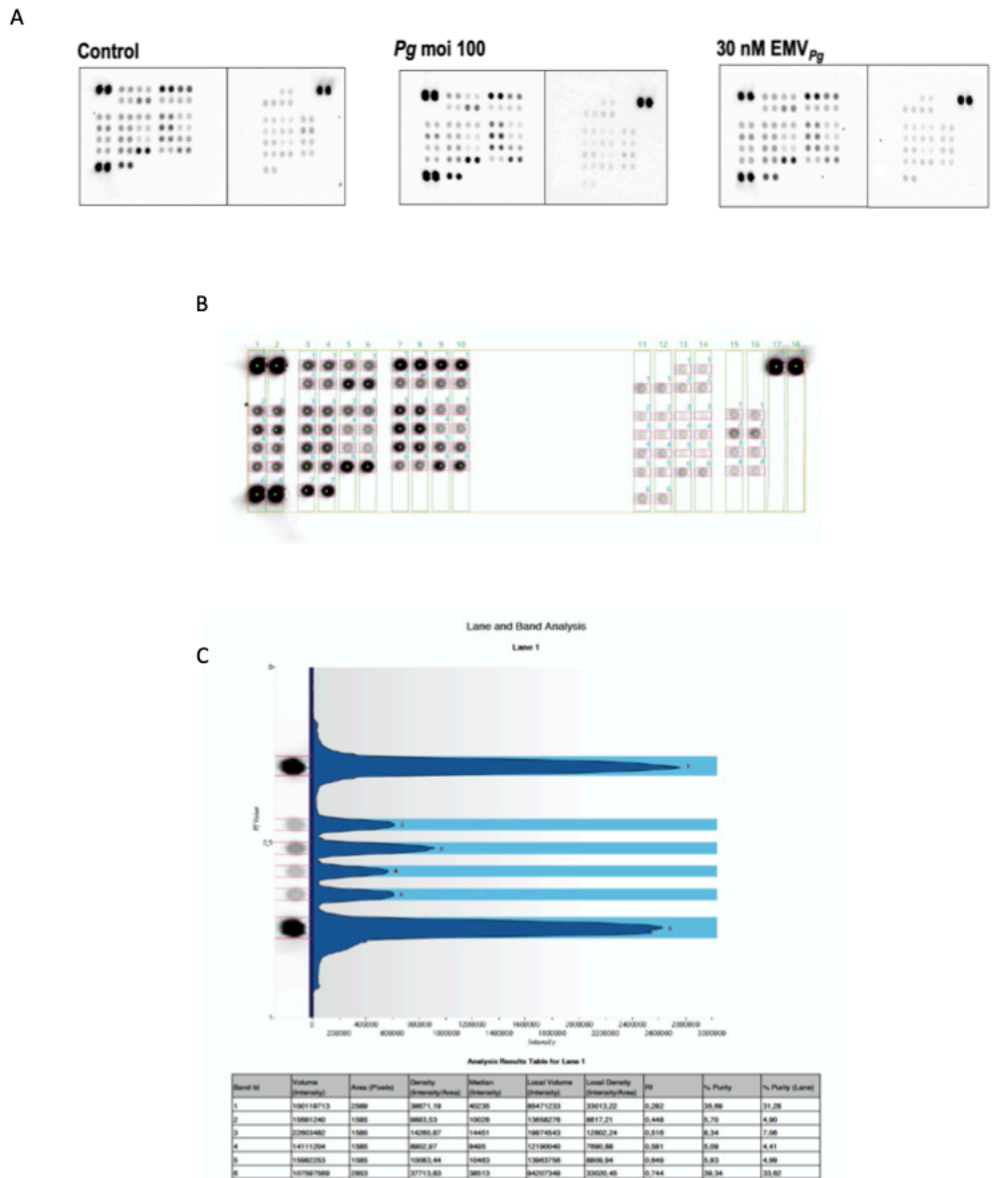
Supplemental Figure 1. EMV dosage. The generation of EMV from naïve EC (control), after 24h and of EC infected with *P.gingivalis* (*Pg*) (MOI=100) or *Pg* culture were measured in the supernatant by prothrombinase assay.



Supplemental Figure 2. Western Blots. The figure shows the original blots for β -actin, eNOS, P53, VCAM and P21, that were cut to indicate only the conditions that were chosen (Control, *Pg*, EMV_{*Pg*} 5nM, 20nM and 30 nM). Brightness and contrast modifications were performed as shown in panels A, B and C. The green boxes show the area that was presented in the left panel of the figure, the red boxes indicate the same area but with a different time exposure.



Supplemental Figure 3. Western blots. The figure shows the original blots for β -actin, ICAM-1, iNOS, SOD-1 and CDK-4, that were cut to indicate only the conditions that were chosen (Control, Pg, EMV_{Pg} 5nM, 20nM and 30 nM). Brightness and contrast modifications were performed as shown in panels A, B and C. The green boxes show the area that was presented in the left panel of the figure, the red boxes indicate the same area but with a different time exposure.



Supplemental Figure 4. Analysis of kinases activation induced by *P.gingivalis* infection (*Pg*) (MOI:100) and *EMV_{Pg}* (30 nM) for 24 h evaluated by phospho-kinase array. (A) The density of spots was measured by MyImage™ Analysis Software 2.0 (Thermofisher) for each molecule and each condition. (B-C) The figure shows how the analysis has been performed for each of the blots of the “Proteome Profiler Human Phospho-Kinase Array Assay” (R&D Systems, Lille, France). Each spot per column and per line was analyzed according to its intensity. This density of spots, corresponding to protein activation, was measured by MyImage™ Analysis Software 2.0 (Thermofisher) for each molecule and each condition.