

Supplemental Figure 1: Standardized gene expression level of control- and stretch-stimulated huECs

huECs from three different donors were exposed to biomechanical stretch for 6 hours or cultured under static conditions (control). Their transcriptome was analyzed by an Affymetrix microarray. The mean gene expression level of each gene and group was color-coded (log2-fold) identifying significant differences between both experimental conditions.



Supplemental Figure 2: Impact of PGE₂ on the proliferation of huECs

Human umbilical vein endothelial cells (huECs) were stimulated with 10 μ M PGE₂ or solvent for 24 h. Afterwards, cells were fixed with methanol and nuclear Ki67 (**A**, red fluorescence) was detected by immunofluorescence staining. Images were recorded using a fluorescence microscope IX83 (Olympus) and the number of Ki67-positive nuclei were automatically quantitated utilizing the TissueQuest Analysis software (TissueGnostics) version 4.0. Each dot in the scattergram (**B**) represents one Ki67-positive nucleus. Results from several experiments are summarized in **C** (*p<0.05 vs. control, n=3).



Supplemental Figure 3: Analysis of mouse RNA samples

Isolated branches of the mesenteric vein of male NMRI mice were exposed to a pressure level of 4 and 16 mm Hg. Afterwards, vessel segments were processed for RNA extraction. Expression of the genes encoding the cyclooxygenase 1 and 2 (Ptgs-1/2) was analyzed by qRT-PCR using S12 as a reference gene. Expression levels were calculated using the $\Delta\Delta$ Ct-method (n=4). N.s. not significant.



Supplemental Figure 4: Diclofenac treatment of pressure-exposed isolated mouse veins Isolated branches of the mesenteric vein of male NMRI mice were exposed to pressure levels of 16 mmHg in presence/absence of diclofenac. Protein samples generated from these blood vessels were pooled and analyzed by automated capillary electrophoresis/immunodetection (required, due to the low yield of protein; specified antigens were detected by antibodies and corresponding signals were automatically tracked by their size (kDa) and intensity (area under the curve). Signals specific for COX-1 (**A**) and COX-2 (**B**) were detected. β -actin served as loading reference (**C**).



Supplemental Figure 5: Analysis of the specificity of the MMP2-antibody Immunodetection of MMP2 in protein samples usually identifies MMP-2 proenzyme (~72 kDa) as well as activated MMP-2 (~62 kDa). The antibody applied in this study was capable to detect two antigens with appropriate size in protein samples from mouse arteries as evidenced by capillary electrophoresis/immunodetection.