

Supplementary figures

**Molecular background of toxic substances induced morphological alterations in the umbilical cord vessels and fetal red blood cells**

Szabolcs Zahorán<sup>1,†</sup>, Ágnes Márton<sup>1</sup>, Krisztina Dugmonits<sup>1</sup>, Payal Chakraborty<sup>1,‡</sup>, Ali Khamit<sup>1</sup>, Péter Hegyi<sup>2,3,4</sup>, Hajnalka Orvos<sup>5</sup> and Edit Hermeszt<sup>1,\*</sup>

<sup>1</sup> Department of Biochemistry and Molecular Biology, Faculty of Science and Informatics, University of Szeged, H-6701 Szeged, Hungary

<sup>2</sup> Institute for Translational Medicine, Medical School, University of Pécs, H-7601 Pécs, Hungary

<sup>3</sup> Centre for Translational Medicine, Semmelweis University, H-1085 Budapest, Hungary

<sup>4</sup> Division of Pancreatic Diseases, Heart and Vascular Center, Semmelweis University, H-1085 Budapest, Hungary

<sup>5</sup> Department of Obstetrics and Gynecology, Albert Szent-Györgyi Medical School, University of Szeged, H-6701 Szeged, Hungary

\* Correspondence: hermeszt@bio.u-szeged.hu; Tel.: +36-(62)-544-887

<sup>†</sup> Present address: Department of Microbiology and Molecular Medicine, Institute of Genetics and Genomics Geneva, Faculty of Medicine, University of Geneva, 1211 Geneva, Switzerland

<sup>‡</sup> Present address: Department of Pharmaceutical Technology, JIS University, 81, Nilgunj Road, Kolkata 700109, India.

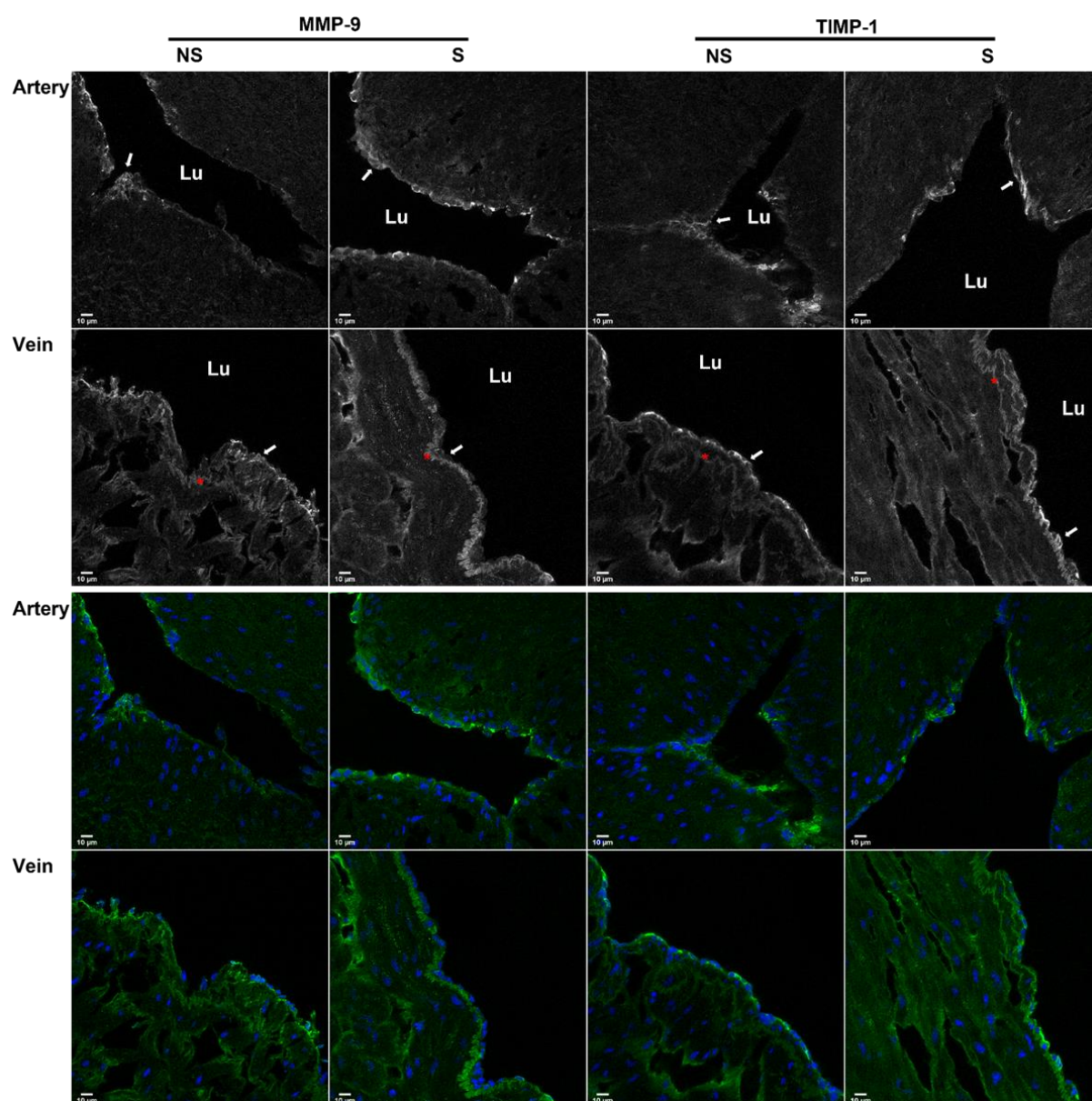
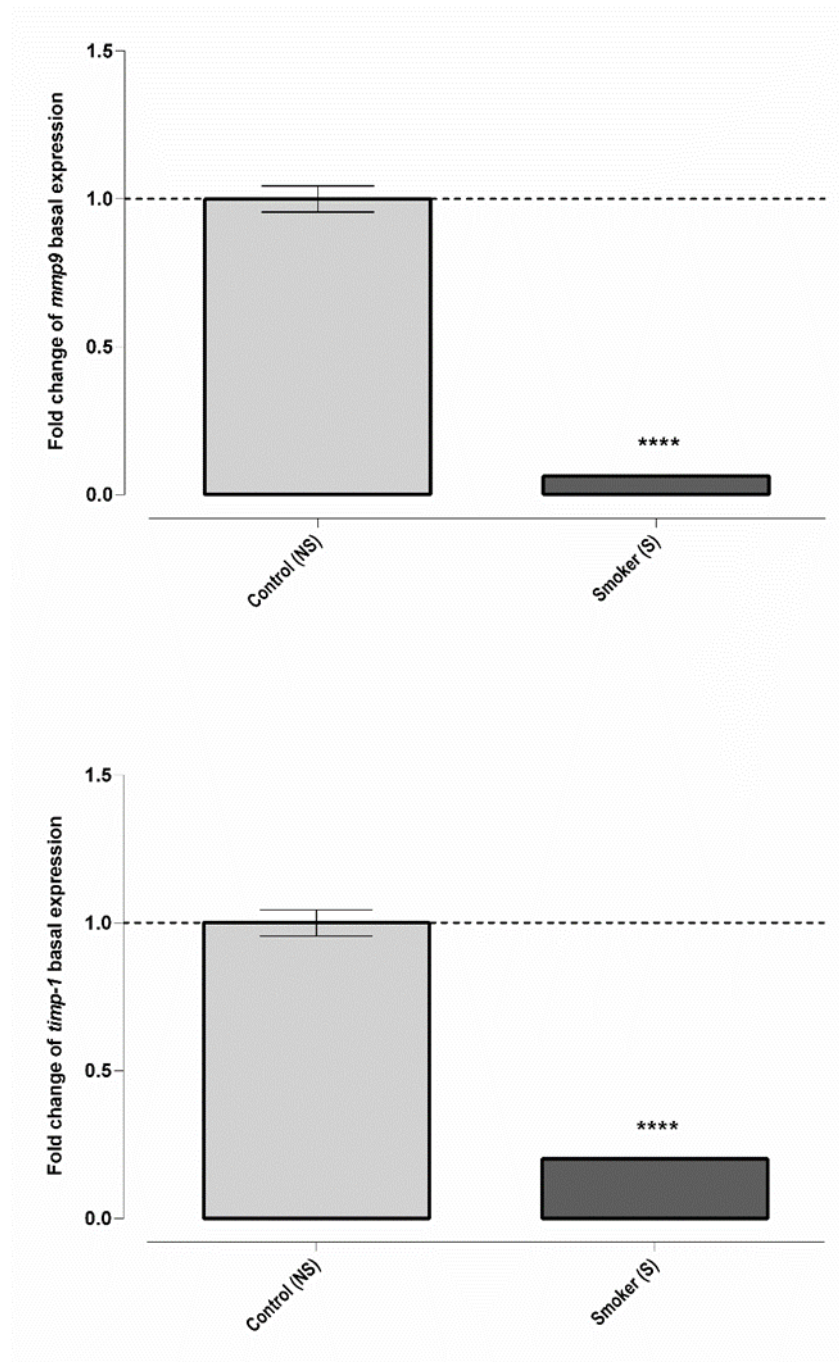


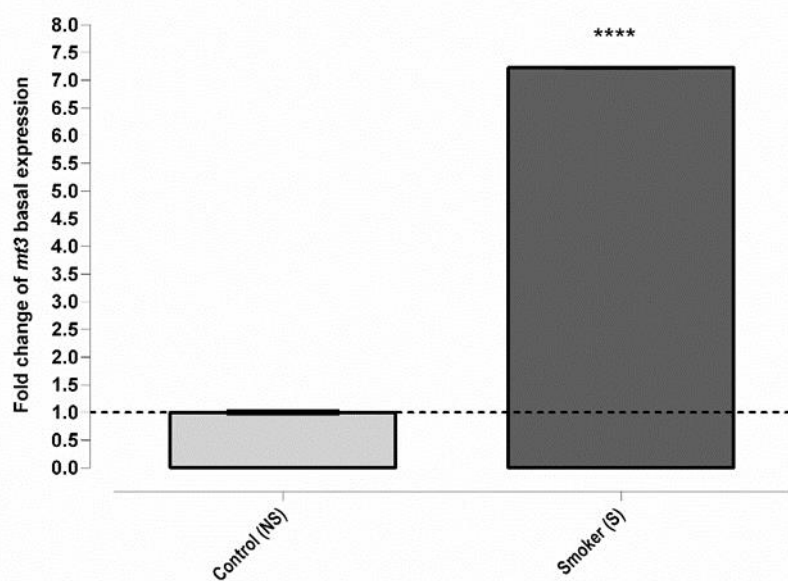
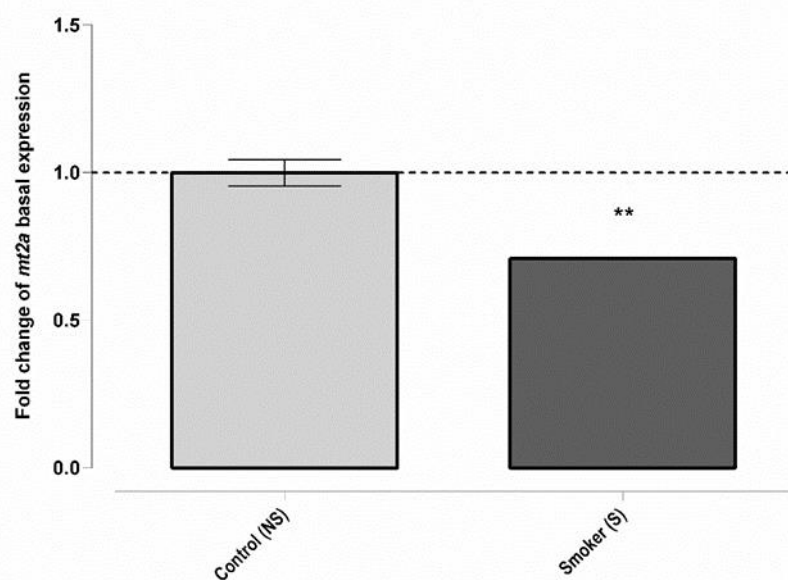
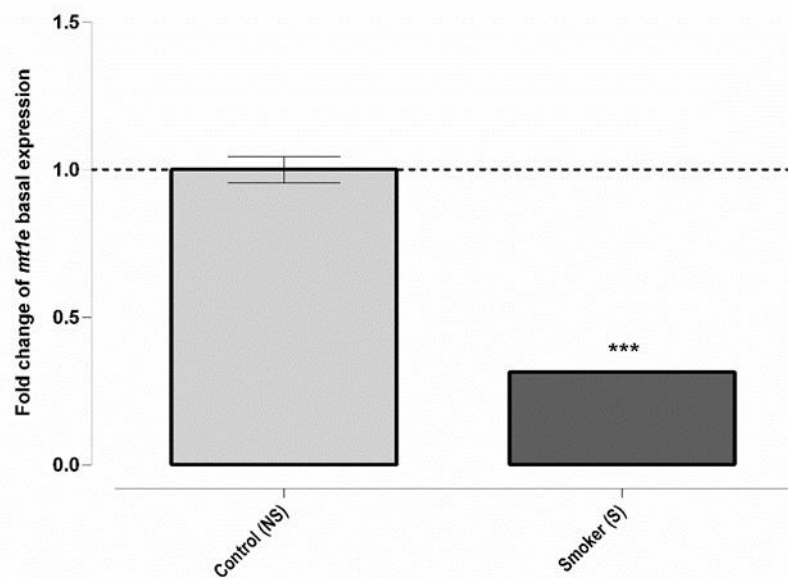
Figure S1. Representative confocal images of MMP-9 and TIMP-1 specific immunolabelling on the consecutive umbilical cord sections

Top two panels indicate the 8-bit images used for semi-quantification, corresponding to the TIMP-1 or MMP-9 channels, respectively. Bottom two panels are the merged DAPI, MMP-9/TIMP-1 images showing the exact localisation. White arrows – endothelial cells, Lu – vessel lumen, red asterisks – lamina basalis. Scale bar – 10 µm.



**Figure S2.** Differences in basal expression of *mmp-9* and *timp-1* genes in untreated Ns and S sample sets

Basal expression of *mmp-9* and *timp-1* genes in the samples with smoking origin relative to the untreated controls (dotted lines). Statistical analysis was done by using two-way (A) and one-way (B) ANOVA followed by Holm-Sidak's multiple comparisons test (\*\*\*\*  $P \leq 0.0001$ ).



**Figure S3.** Differences in basal expression of metallothionein genes in the untreated Ns and S sample sets

Basal expression of *mt-1e*, *mt2a* and *mt3* genes in sample sets with smoking origin relative to the untreated controls (dotted lines). Statistical analysis was done by using two-way (A) and one-way (B) ANOVA followed by Holm-Sidak's multiple comparisons test (\*\*  $P \leq 0.01$ ; \*\*\*  $P \leq 0.001$ ; \*\*\*\*  $P \leq 0.0001$ ).