

Supplementary Material

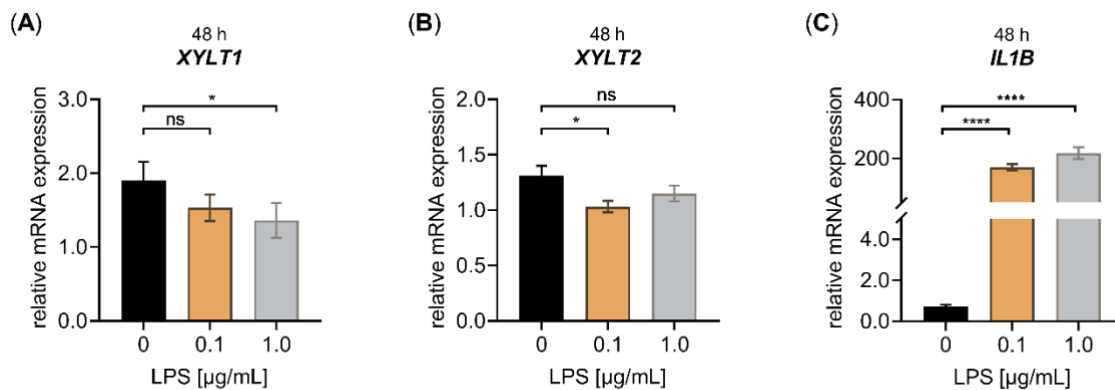


Figure S1. The effect of LPS on the relative *XYLT1*, *XYLT2* and *IL1B* mRNA expression of primary fibroblasts cultured in low-density culture conditions for 48 h. The NHDF ($n = 3$) were cultured at a cell density of 50 cells/mm² in growth medium supplemented with 10 % (*v/v*) FCS the day before the experiment. Treatment was performed with either 0 µg/mL LPS (black), 0.1 µg/mL LPS (orange) or 1.0 µg/mL LPS (grey) supplemented growth medium. The relative (A) *XYLT1*, (B) *XYLT2* and (C) *IL1B* mRNA-expression was analyzed after LPS treatment of NHDF for 48 h by qRT-PCR. All data are means \pm SEM of three biological and three technical replicates per donor-derived primary cell culture. Mann-Whitney *U* test: ns (not significant), * $p < 0.05$ and **** $p < 0.0001$.

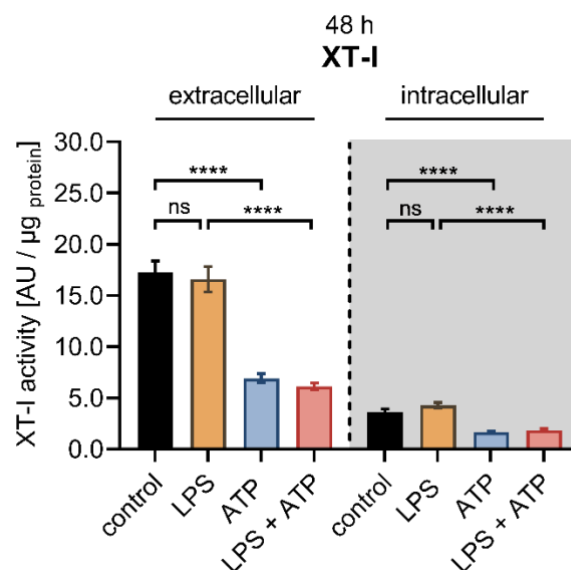


Figure S2. The cellular XT-I activity of primary fibroblasts after LPS and ATP treatment for 48 h. The NHDF ($n = 3$) were cultured at a cell density of 177 cells/mm² in growth medium supplemented with 10 % (*v/v*) FCS the day before the experiment. Cells were treated with either 0.1 µg/mL LPS (orange), 5 mM ATP (blue) or both 0.1 µg/mL LPS and 5 mM ATP (red) for 48 h. The cellular XT-I activity was determined in the cell culture supernatant (extracellular) and the corresponding cell lysates (intracellular, grey-shaded) by UPLC-ESI-MS/MS XT-I assay. The XT-I activity is expressed in AU per µg of protein. All data are means \pm SEM of three biological and three technical replicates per donor-derived primary cell culture. Mann-Whitney *U* test: ns (not significant) and **** $p < 0.0001$.

Table S1. The sequences, annealing temperatures (T_A) and expected product sizes of the oligonucleotides used for qRT-PCR analysis.

gene	5' to 3' primer sequences	T_A / °C	product size / bp
<i>CASP1</i>	CAGATGCCCACCACTGAAAGA GATCTCTTCACTTCCTGCCCAC	63	109
<i>CTSB</i>	CCACAGTGTCACCATCAA TAGCCACCATTACAGCCGTC	63	191
<i>IL1B</i>	ACAGATGAAGTGCTCCTTCCA GTCGGAGATTCGTAGCTGGAT	63	73
<i>IL8</i>	GAACTGAGAGTGATTGAGAGTGGA CTCTTCAAAAATTCTCCACAACC	63	134