

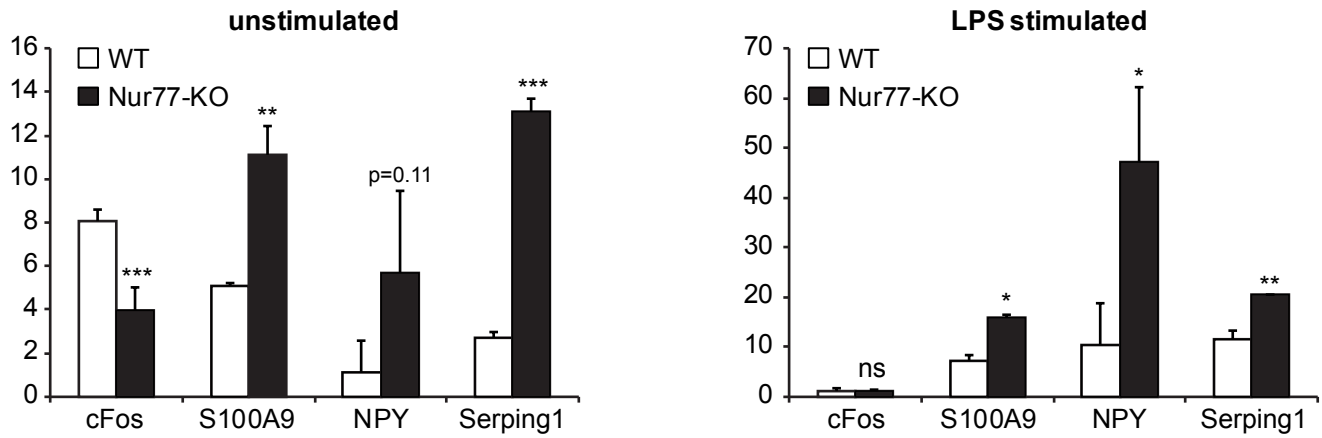


Figure S1. Verification of the microarray results by qRT-PCR.

mRNA expression of top differentially expressed genes, as determined by microarray analysis, cFos, S100A9, NPY and Serping1 in WT and Nur77-KO BMM was determined by qRT-PCR before (left panel) and after (right panel) treatment with 100 ng/ml LPS. Data are expressed as mean $\pm$ S.D. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, ns=not significant.