

Figure S1. Tat protein induces TNF- α and IL-10 in mouse peritoneal macrophages via its N-terminal domain (1-45).

(A-B) Primary mouse peritoneal macrophages isolated from Wt mouse were incubated with increasing amounts of recombinant GST-Tat proteins either full length (GST-Tat 1-101), its N-terminal fragment carrying the first 45 amino acid (GST-Tat 1-45), its central basic domain (GST-Tat 30-72) or an equal amount of GST protein alone (GST), LPS (TLR4 ligand) was used as positive controls. After 20 h of incubation, (A) mouse TNF- α and (B) mouse IL-10 were quantified in the supernatants of the cells by ELISA. The data represent means and standard deviation (SD) of three independent experiments. Statistical significance was analysed with One-way ANOVA follow with Bonferroni post tests and is marked as * for p < 0.05, ** p < 0.01, *** p < 0.001, ns non-significant. All bars are compared to "Untreated" cells otherwise specified (indicated with a black line above the compared bar).

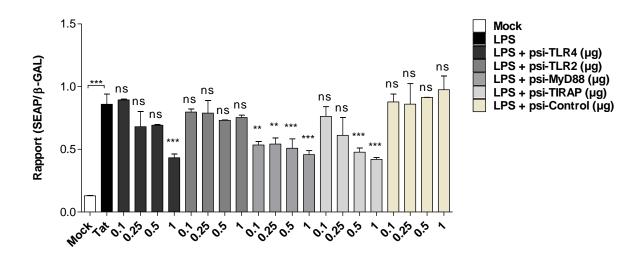


Figure S2. LPS-induced NF-κB activation in HEK TLR4/MD2-CD14 cell lines is inhibited in a dose-dependent manner by psi-TLR4, psi-MyD88, psi-TIRAP/MAL.

HEK cell lines expressing TLR4/MD2-CD14 were co-transfected with the NF-κB reporter plasmid (SEAP) together with same amounts of the pORF-LacZ. Cells were also co-transfected with the indicated amounts (in μg) of the plasmid encoding siRNA targeting TLR4, TLR2, MyD88, TIRAP/MAL, control siRNA or left without transfection with siRNA (white bars, Mock and black bar, LPS). After 24 h of transfection, cells were left untreated (white bars, Mock), or treated with LPS (100 ng/ml). 24 h after stimulation, NF-κB driven SEAP-reporter gene expression was measured in the culture supernatants. For normalization, cells were lysed and expression of β-galactosidase was quantified. The data represent means and standard deviation (SD) of three independent experiments. Statistical significance was analysed with One-way ANOVA follow with a Bonferroni post tests and are denoted with * for p < 0.05, ** p < 0.01, *** p < 0.001, ns non significant. All bars are compared to LPS-treated cells in the absence of co-transfection with any siRNA (Black bars) otherwise specified.