Suppl. Fig. 1. LPS induces TTP gene expression in BMMCs. WT BMMCs were left untreated (con) or stimulated with 3 µg/ml LPS for the indicated times. TTP mRNA expression was analyzed by RT-qPCR. Data obtained by analyzing cells from independent cultures are shown (the result obtained with BMMCs from culture #1 is already depicted in Fig. 2A). The relative expression ratios including primer efficiencies were calculated by the Pfaffl method [26].

Suppl. Fig. 2. LPS-induced production of TTP mRNA is dependent on p38. WT BMMCs were incubated with either DMSO or the indicated concentrations of BIRB0796 for 20 min and subsequently stimulated with 3 µg/ml LPS for 2 h. TTP mRNA was analyzed by RT-qPCR. Data obtained by analyzing cells from independent cultures are shown (the result obtained with BMMCs from culture #1 is already depicted in Fig. 2B). The relative expression ratios including primer efficiencies were calculated by the Pfaffl method [26].

Suppl. Fig. 3. TTP gene expression is detectable in WT BMMCs. WT (■) and TTP-deficient (KO) BMMCs (□) were left untreated (con) or stimulated with 3 µg/ml LPS for the indicated times. TTP mRNA was analyzed by RT-qPCR. Data obtained by analyzing cells from independent cultures are shown (the result obtained with BMMCs from culture #1 is already depicted in Fig. 5A). The relative expression ratios including primer efficiencies were calculated by the Pfaffl method [26].

Suppl. Fig. 4. Analysis of TTP mRNA stability in LPS-stimulated MCs. WT BMMCs were treated with 3 µg/ml LPS for 2 h. Subsequently, 5 µg/ml Actinomycin D (AcD) were added. After 0 min, 30 min, 1 h and 2 h cells were harvested and TTP mRNA was analyzed by RT-qPCR. All samples were normalized to the respective control. Each bar represents the mean ± SD of three independent BMMC

cultures.

Suppl. Fig. 5. Kinetics of MK2 activity in LPS-treated WT BMMCs. WT BMMCs were left untreated (con) or stimulated with either 3 μg/ml LPS or LPS and 100 ng/ml IGF-1 together for the indicated time points. IGF-1 was added as a strong activator of the PI3K pathway; see [28] for more details. Postnuclear supernatants (PS) were analyzed by immunoblotting with antibodies against phopsho-MK2 (top panel) and GAPDH (bottom panel).