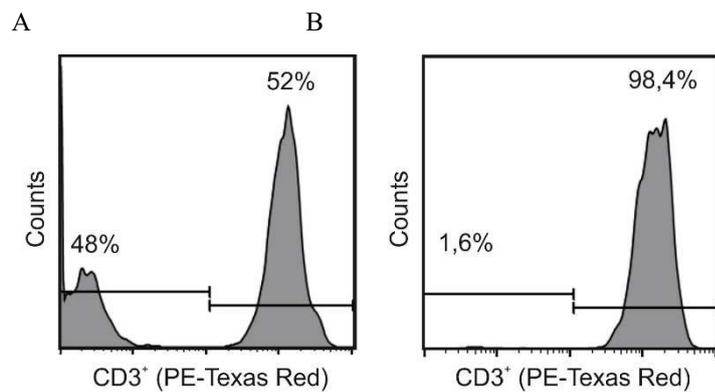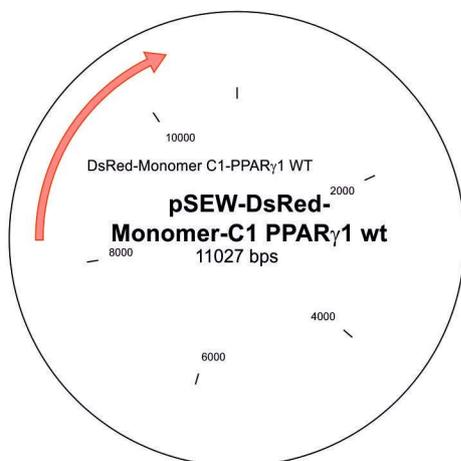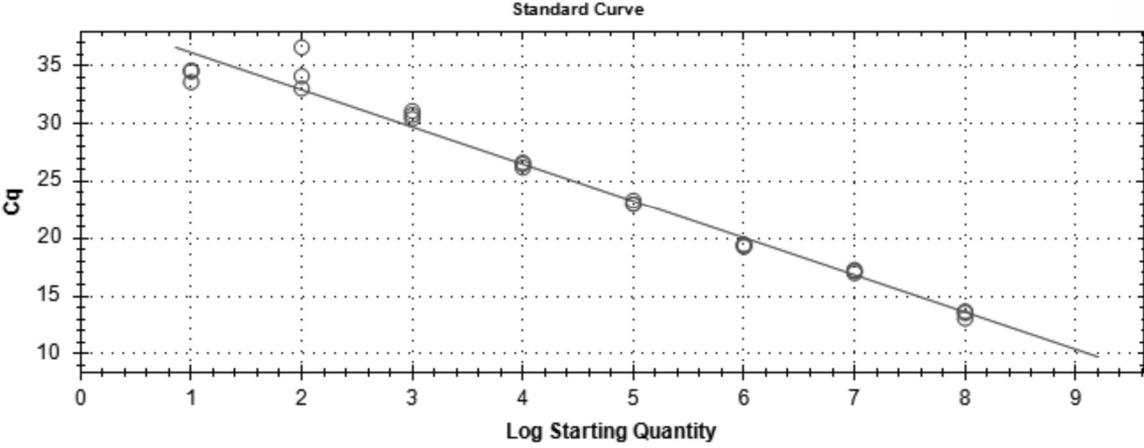**Legends to supplemental digital content**

Suppl. Fig. 1: Evaluation of autoMACS-dependent CD3$^+$ T cells enrichment by FACS analysis. Blood sample before (A) and after (B) MACS enrichment. Samples were stained with an anti-CD3-PE Texas Red antibody as described in Materials and Methods. CD3$^+$ enrichment was determined by FACS analysis. A representative result is shown.
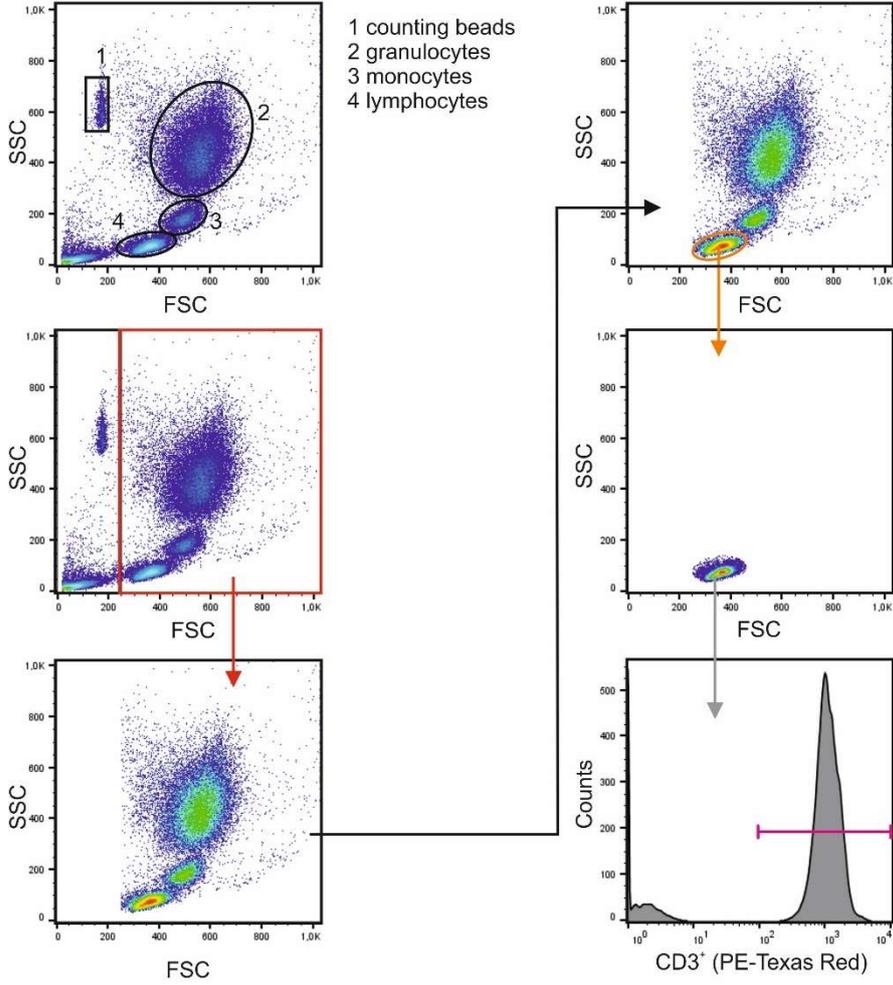

A   B

Suppl. Fig. 2: Map of PPARγ encoding vector, used to provide an absolute PPARγ quantification of the qPCR reaction.

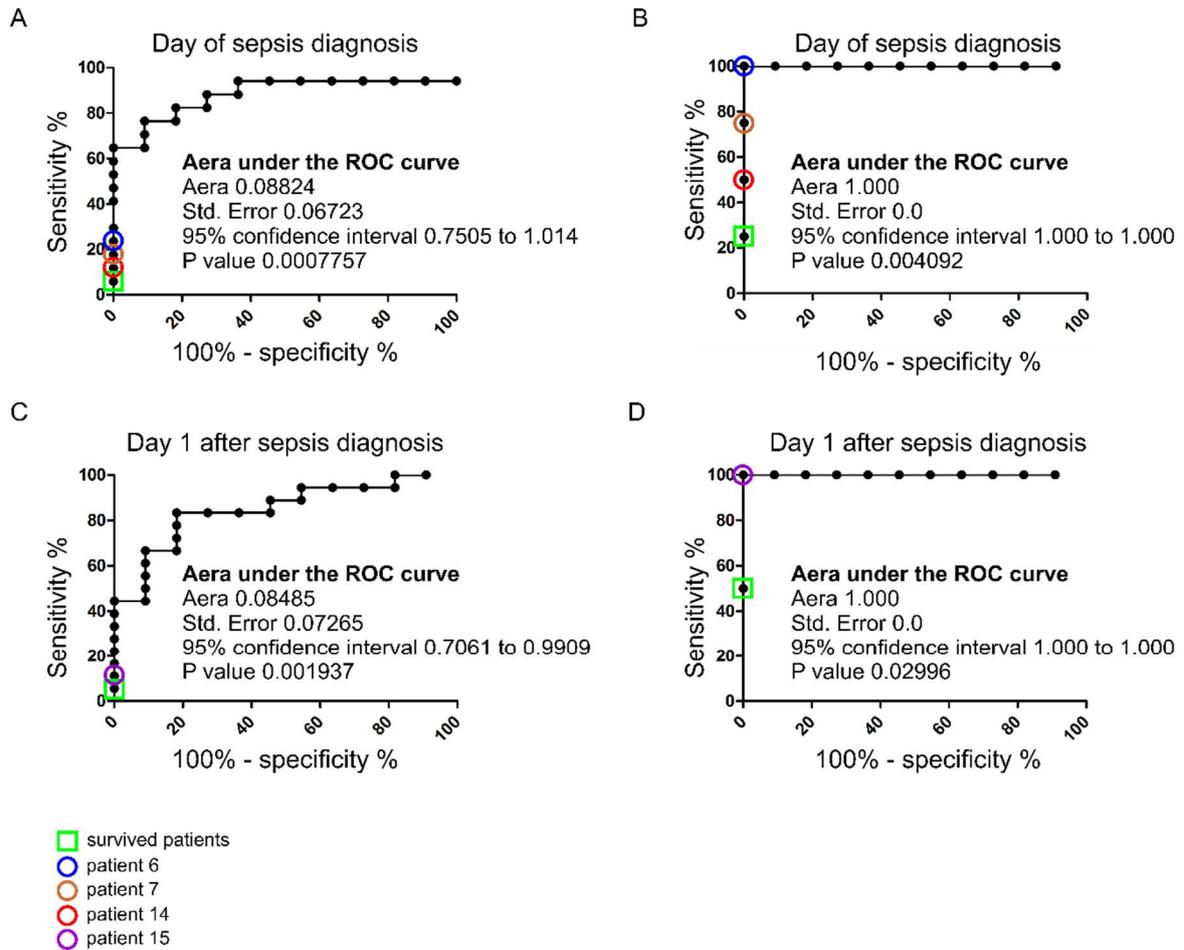DsRed-Monomer C1-PPARγ1 WT

pSEW-DsRed-Monomer-C1 PPARγ1 wt
11027 bps

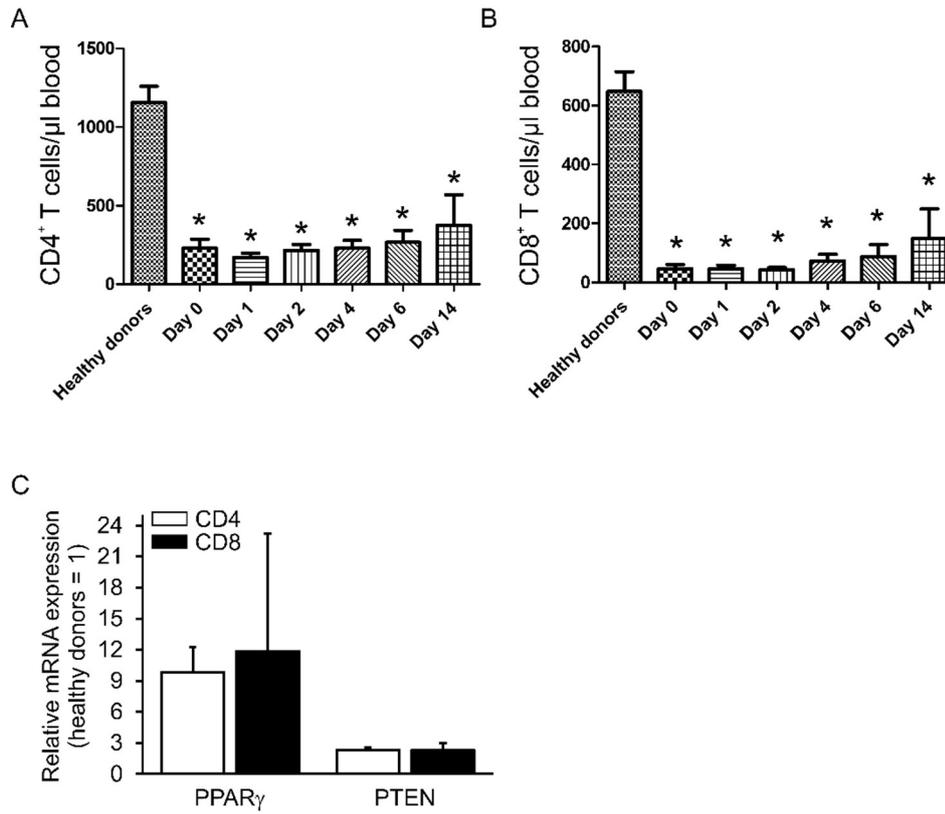**Suppl. Fig. 3:** PPARγ expression standard curve, using the vector depicted in Suppl. Fig. 2.

Suppl. Fig. 4: Gating strategy used to determine the number of CD3$^+$ T cells in blood. 200 µl of blood from septic patients or healthy donors were stained simultaneously with anti-CD3 PE-Texas Red antibody as described in Materials and Methods. Following erythrolysis, 50 µl of counting beads were added to the sample, directly before determining the T cell subpopulations by FACS analysis.

Suppl. Fig. 5: ROC curve analysis of PPARγ mRNA expression in healthy donors vs. sepsis patients. PPARγ mRNA expression in T cells derived from healthy donors was compared to PPARγ mRNA expression of (A) all sepsis patients on the day of sepsis diagnosis (A) and the next day (C). With a threshold of PPARγ mRNA expression of >7000 copies/25 ng mRNA of sepsis patients (see Fig. 3), PPARγ expression in all analysed samples is significantly different from PPARγ mRNA expression in healthy donors at the day of sepsis diagnosis (B) and the next day (D).

Suppl. Fig. 7: IL-6 protein expression in patients´ sera. IL-6 protein expression was routinely performed by the university laboratory with an IL-6 specific ELISA.