Supplementary figure 1. Gating strategy for GzmA and GzmK expression analysis. After 18 h of sepsis induction, WT, GzmA⁻/⁻ and GzmK⁻/⁻ mice were sacrificed. Spleens were collected aseptically, homogenized in 5 mL of RPMI medium and then erythrocytes were lysed. For analysis of GzmA and GzmK expression, 1x10⁶ splenocytes were stained with extracellular fluorescent labelled antibodies. Doublets (FSC-H vs FSC-A and SSC-H vs. SSC-A) were excluded. SSC-A vs. CD45⁺ gating was done to identify CD45⁺ cells population. For the first cocktail 3 subpopulations were identified: NK cell (NK1.1⁺CD3⁻), NKT cell (NK1.1⁺CD3⁺) and CD8 lymphocyte (CD8⁺CD3⁺) which were gated from NK1.1 negative cells. For the second cocktail CD4 T lymphocyte (CD4⁺CD3⁺) subpopulation was identified. Finally, for the third cocktail 4 subpopulations were identified: dendritic cell (CD11b⁺CD11c⁺), from CD11b⁺CD11c⁻ cells a Ly6G⁺ population was identified as neutrophils (CD11b⁺Ly6G⁺). Next, from Ly6G⁻ population a Ly6C⁺ population was identified as monocytes (CD11b⁺Ly6C⁺Ly6G⁻). Finally, from Ly6C⁻ population a CD11b++ population was identified as macrophages (CD11b++Ly6C⁻Ly6G⁻).