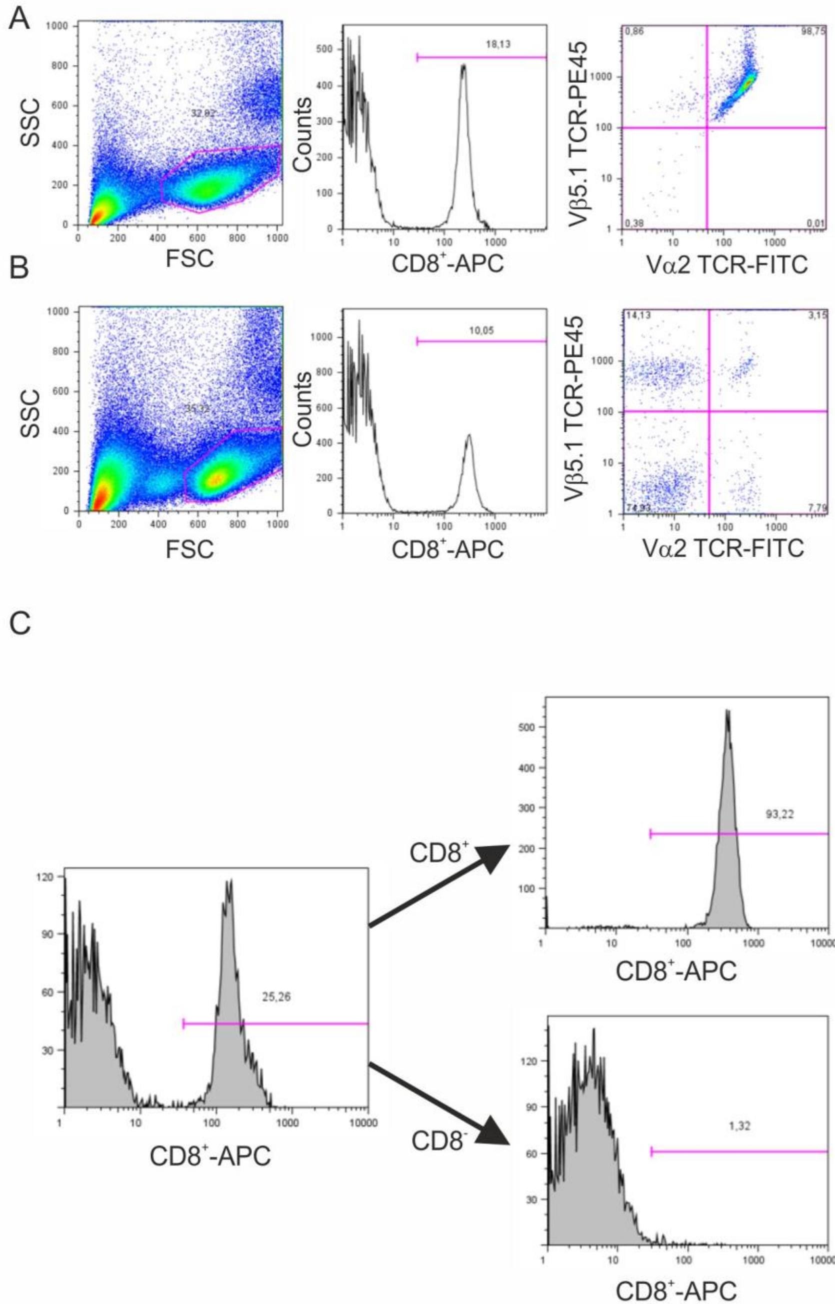
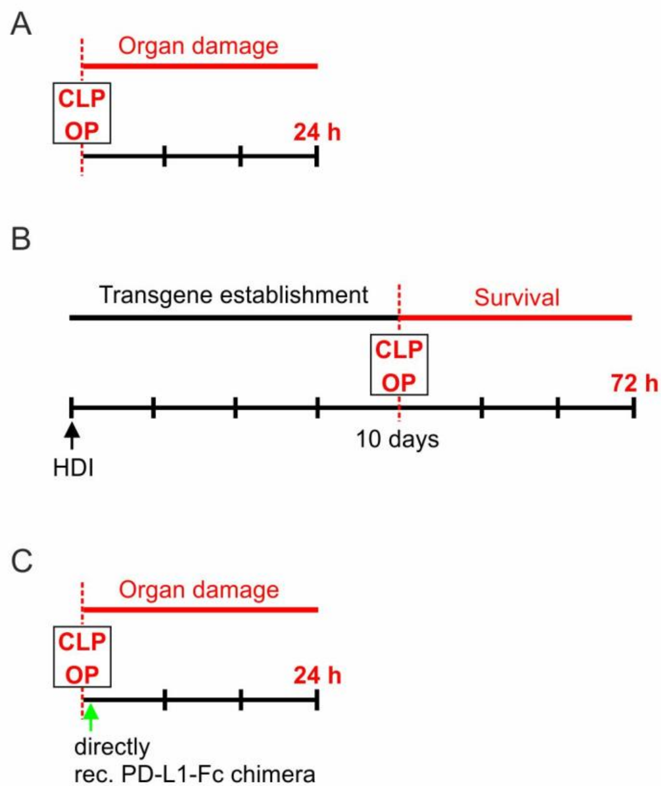
Supplementary Figures 1-3



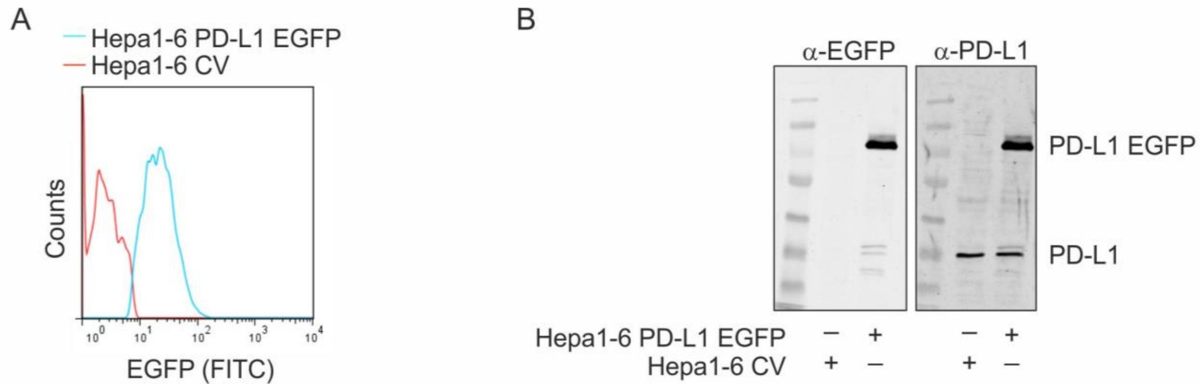
Supplementary Figure 1. Identification of OT-I mice and enrichment of CD8+ T cells from OT-I.

Blood was drawn intravenously from OT-I mice. Following direct blood staining with α-CD8+-APC, and α-Vß5.1-PE as well as α-Vα2 TCR-FITC to mark the OT-I specific transgenic α and β chain of cytotoxic T

cells, cell surface expression was determined by FACS analysis. Analysis was started with the FSC/SSC dot plot to set a marker-unspecific lymphocyte gate (left panel in **(A)** and **(B)**). Cells in this lymphocyte gate were used to identify cytotoxic T cells, known to express $CD8^+$ ($CD8^+$-APC) as shown in the middle panel of **(A)** and **(B)**. Finally, we utilized these $CD8^+$ cells to determine whether these cells express the transgenic TCR (Vß5.1/Vα2). The result is depicted in the right panel of **(A)** and **(B)**, showing that all $CD8^+$ T cells express Vß5.1/Vα2 in **(A)** and only less in **(B)**. Following single cell preparation and erythrolysis, $CD8^+$ T cells were enriched **(C)** as described in “Methods” by the Dynabeads FlowComp Mouse CD8 kit. Enrichment was from around 25% (as shown in the left panel) of splenocytes to approximately 93% following purification (upper right panel). Roughly 1% of $CD8^+$ T cells remain in the flow through (lower right panel). A representative isolation is shown.



Supplementary Figure 2. Schematic representation of the used experimental animal approaches. (A) Organ damage is determined following twenty-four hours h after CLP operation. **(B)** Survival of mice is analyzed for seventy-two hours following CLP-operation and, as indicated, ten days after hydrodynamic injection (HDI) of a transposon-based sleeping beauty system. **(C)** As a pharmacological setup the effect of recombinant PD-L1-Fc, directly applied following CLP operation, is determined twenty-four hours after CLP.



Supplementary Figure 3. Functional expression of PD-L1 in Hepa1-6 cells. (A) and **(B)** Hepa1-6 cells were lentivirally transduced as described in "Methods" with a control vector (CV) and a vector encoding for PD-L1 coupled to EGFP (PD-L1 EGFP). EGFP expression was determined by **(A)** FACS analyses and **(B)** Western blotting, which was stained for EGFP (left panel) and PD-L1 (right panel) expression