

**Figure S1, related to Figure 1**

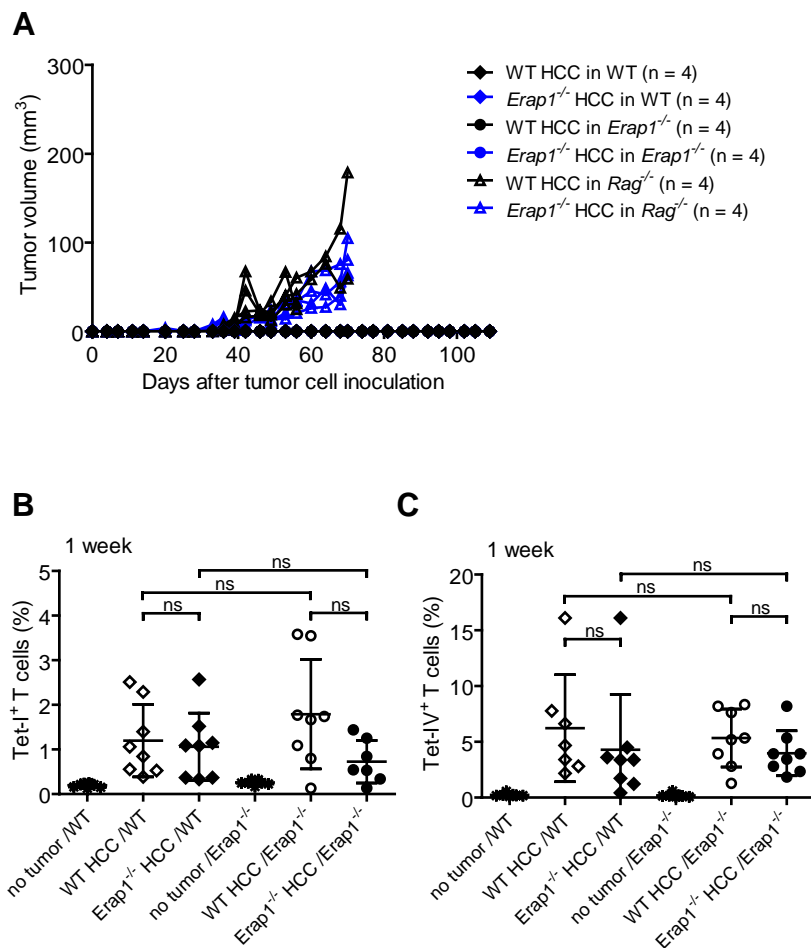
TAP-dependent peptide translocation in the presence of a high-affinity competitor peptide and activity measurements of recombinant mouse ERAP1 (rmERAP1).

(A) TAP transport was analyzed with 50  $\mu$ M of each peptide  $\pm$  50  $\mu$ M high-affinity competitor peptide (R9) and peptide translocation was calculated. C4: high-affinity peptide devoid of a N-core glycosylation site and labelled with fluorescein, E5: peptide not binding to TAP including a N-core glycosylation site and labelled with fluorescein, NST: reporter peptide including a N-core glycosylation site and labelled with fluorescein. The experimental threshold (red dotted line) was set for E5+ATP (no TAP-binding).

(B) Activity of rmERAP1 was measured by its ability to cleave the fluorogenic peptide substrate H-Leu-AMC. 6 ng rmERAP were incubated with 100  $\mu$ M H-Leu-AMC at 37°C. The released AMC was measured by a plate reader at excitation/emission wavelengths of 380/460 nm at the indicated time points.

(C) TAP transport was analyzed with 50  $\mu$ M of each peptide and  $\pm$  50  $\mu$ M high-affinity competitor peptide (R9) and peptide translocation was calculated. C4: high-affinity peptide devoid of a N-core glycosylation site and labelled with fluorescein, E5: peptide not binding to TAP including a N-core glycosylation site and labelled with fluorescein, NST: reporter peptide including a N-core glycosylation site and labelled with fluorescein. The experimental threshold (red dotted line) was set for E5+ATP (no TAP-binding).

(A-C) All data are represented as mean  $\pm$  SD, (A and C) two-way ANOVA.



**Figure S2**

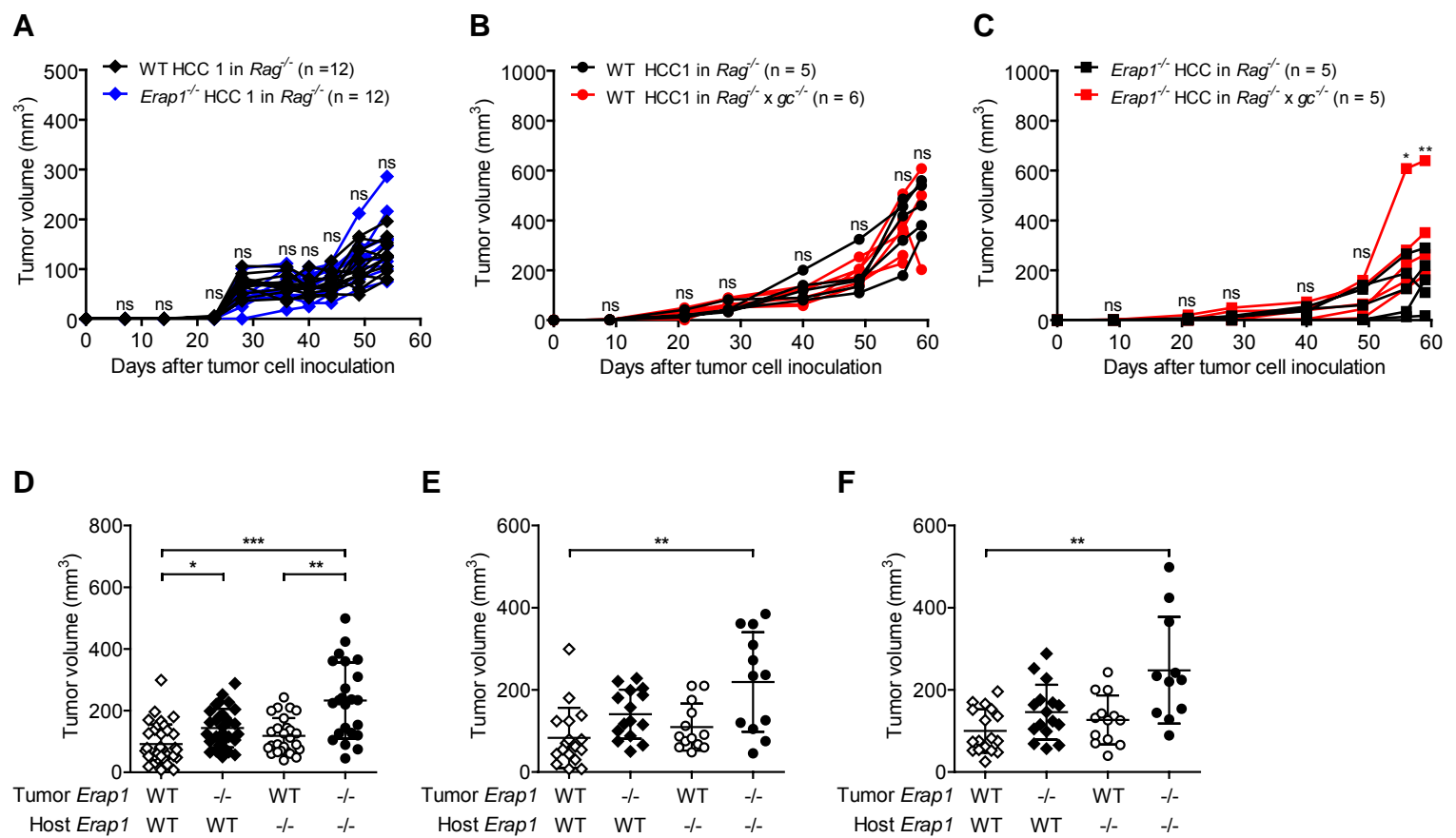
WT and *Erap1*<sup>-/-</sup> HCC are rejected in immune-competent WT and *Erap1*<sup>-/-</sup> recipients due to priming of TAg-I-specific (Tet-I<sup>+</sup>) and TAg-IV-specific (Tet-IV<sup>+</sup>) CD8<sup>+</sup> T cells.

(A) 1 × 10<sup>6</sup> WT or *Erap1*<sup>-/-</sup> HCC cells were injected s.c. into immune-competent WT (C57BL/6) and *Erap1*<sup>-/-</sup> recipients (control *Rag*<sup>-/-</sup> recipients) and the tumor volume was monitored. Shown is a single experiment .

(B) 1 × 10<sup>6</sup> WT or *Erap1*<sup>-/-</sup> HCC cells were injected s.c. into immune-competent WT (C57BL/6) and *Erap1*<sup>-/-</sup> recipients and the percentage of Tet-I<sup>+</sup> CD8<sup>+</sup> T cells among polyclonal CD8<sup>+</sup> T<sub>E</sub> cells in peripheral blood was determined one week post ATT.

(C) The experiment was conducted as in (B), and the percentage of Tet-IV<sup>+</sup> CD8<sup>+</sup> T cells was determined one week post ATT.

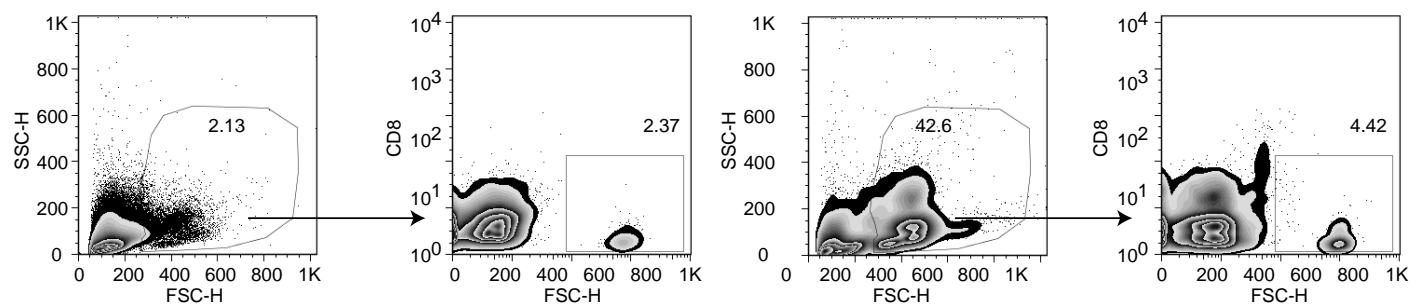
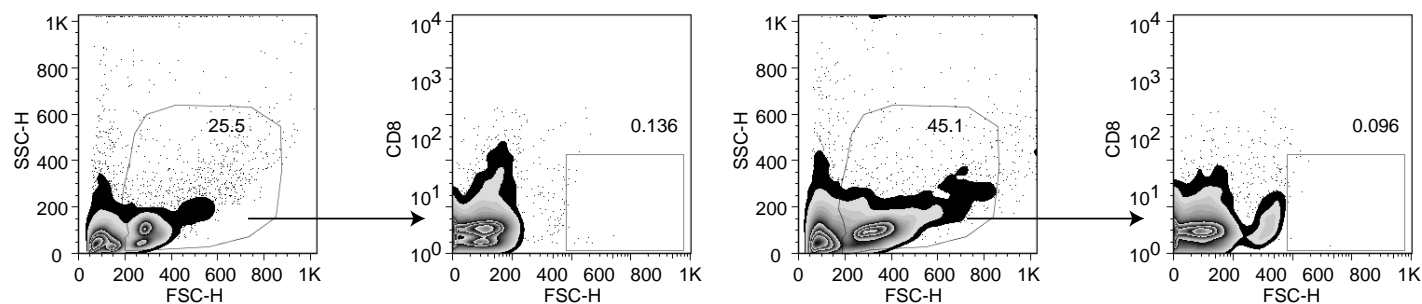
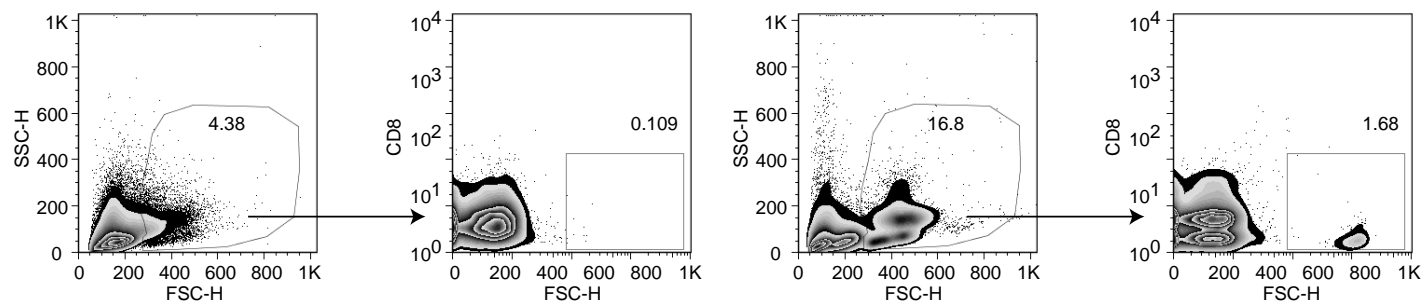
(B and C) Shown is a single experiment, all data are represented as mean ± SD, Kruskal-Wallis test.



**Figure S3, related to Figures 4 and 5**

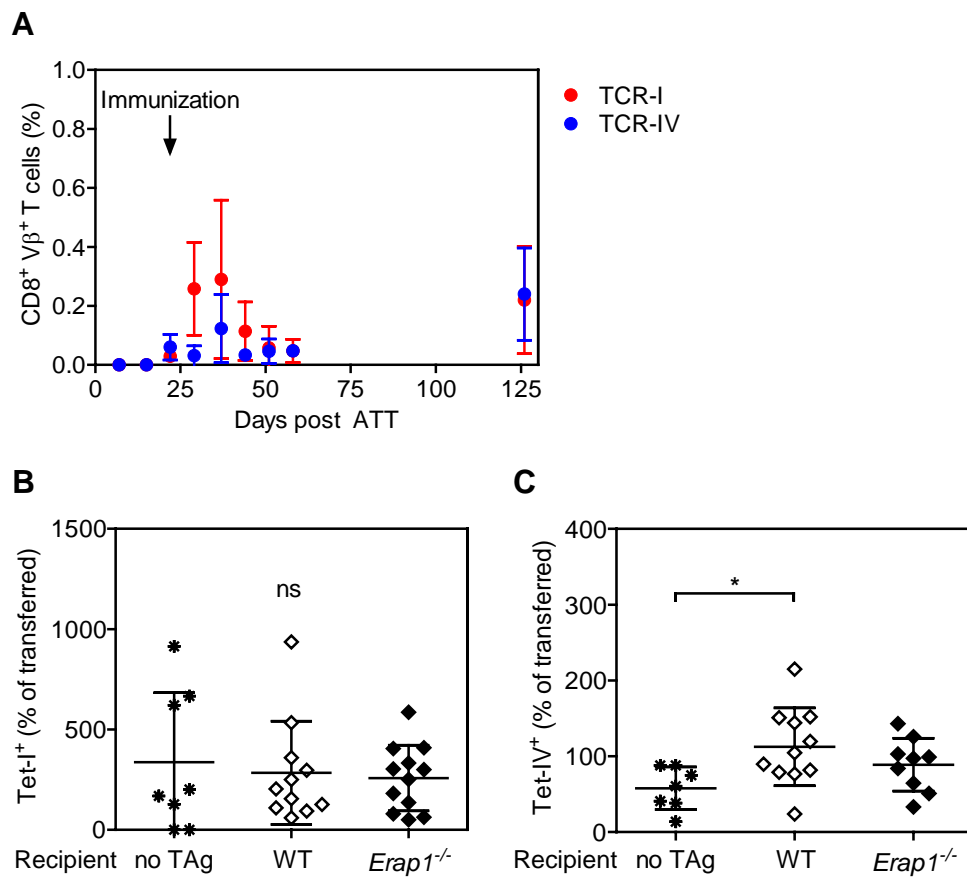
Role of NK cells in ERAP1-dependent tumor growth in H2<sup>b</sup> immune-deficient (*Rag*<sup>-/-</sup>) recipients.

- (A) WT and *Erap1*<sup>-/-</sup> HCC was grown in *Rag*<sup>-/-</sup> recipients and the tumor volume was monitored. Shown is one of four representative experiments with similar results, two-way ANOVA.
- (B) WT HCC was grown in NK cell-competent *Rag*<sup>-/-</sup> recipients and NK cell-deficient *Rag*<sup>-/-</sup> x *gc*<sup>-/-</sup> recipients and the tumor volume was monitored.
- (C) *Erap1*<sup>-/-</sup> HCC was grown in NK cell-competent *Rag*<sup>-/-</sup> recipients and NK cell-deficient *Rag*<sup>-/-</sup> x *gc*<sup>-/-</sup> recipients and the tumor volume was monitored.
- (B and C) Data of a single experiment are shown, two-way ANOVA.
- (D) Tumor size at the day of ATT shown for all *Rag*<sup>-/-</sup> H2<sup>b</sup> recipients (see Figure 4 and Table S3). WT→WT n = 34, *Erap1*<sup>-/-</sup>→WT n = 31, WT→*Erap1*<sup>-/-</sup> n = 26, *Erap1*<sup>-/-</sup>→*Erap1*<sup>-/-</sup> n = 23.
- (E) Tumor volume of TCR-I T cell-treated H2<sup>b</sup> *Rag*<sup>-/-</sup> recipients (see Figure 4C and Table S3B) at the day of ATT. WT→WT n = 17, *Erap1*<sup>-/-</sup>→WT n = 15, WT→*Erap1*<sup>-/-</sup> n = 13, *Erap1*<sup>-/-</sup>→*Erap1*<sup>-/-</sup> n = 12.
- (F) Tumor volume of TCR-IV T cell-treated H2<sup>b</sup> *Rag*<sup>-/-</sup> recipients (see Figure 4D and Table S3C) at the day of ATT. WT→WT n = 17, *Erap1*<sup>-/-</sup>→WT n = 16, WT→*Erap1*<sup>-/-</sup> n = 13, *Erap1*<sup>-/-</sup>→*Erap1*<sup>-/-</sup> n = 11.
- (D-F) Data of n = 4-5 experiments are represented as mean ± SD, Kruskal-Wallis test, \*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001.

**A**WT H2<sup>b</sup> / 1 weekWT H2<sup>b</sup> / 4 weeks**B**WT H2<sup>d</sup> / 1 weekWT H2<sup>d</sup> / 4 weeks**C***Erap1*<sup>-/-</sup> H2<sup>b</sup> / 1 week*Erap1*<sup>-/-</sup> H2<sup>b</sup> / 4 weeks**Figure S4, related to Figure 5**

Gating strategy.

White blood cells were gated on live cells and CD8<sup>+</sup> T cells, numbers are % gated cells exemplarily shown for (A) WT x *Rag*<sup>-/-</sup> recipients (WT H2<sup>b</sup>), (B) SCID recipients (WT H2<sup>d</sup>), and (C) *Erap1*<sup>-/-</sup> x *Rag*<sup>-/-</sup> recipients (*Erap1*<sup>-/-</sup> H2<sup>b</sup>) 1 week and 4 weeks after ATT.



**Figure S5, related to Figure 5**

Antigen-dependent expansion of TCR-I and TCR-IV T cells.

(A)  $1 \times 10^6$  TCR-I T cells and  $1 \times 10^6$  TCR-IV T cells were co-transferred into immune-deficient *Rag*<sup>-/-</sup> mice ( $n = 3$  mice per group). % CD8<sup>+</sup> Vβ7<sup>+</sup> TCR-I T cells and CD8<sup>+</sup> Vβ9<sup>+</sup> TCR-IV T cells were measured in at different time points after ATT in peripheral blood. Mice were immunized with irradiated TAg<sup>+</sup> 16.113 tumor cells on day 22 post ATT. Data are represented as mean  $\pm$  SD.

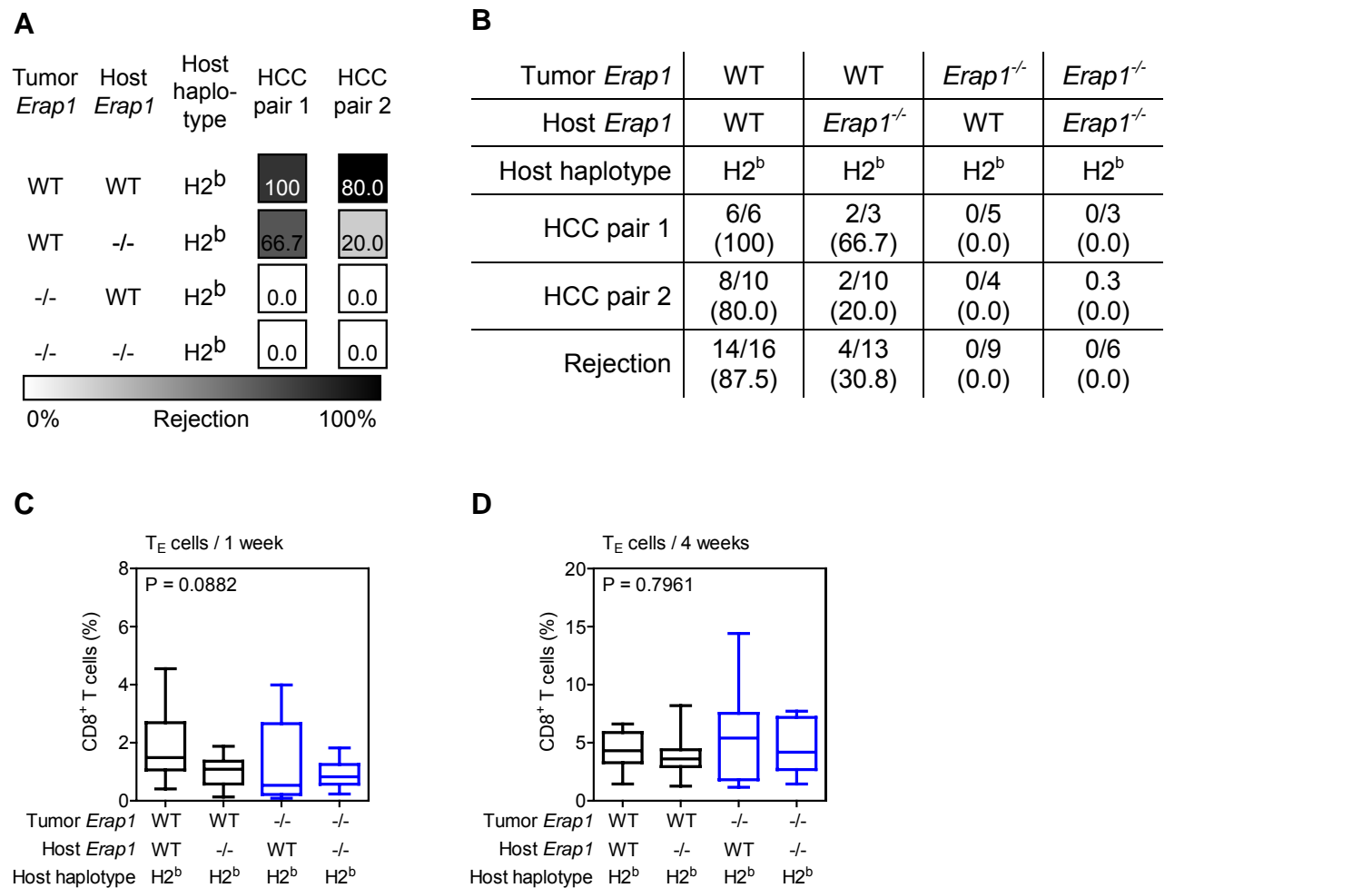
(B) TCR-I (Tet-I<sup>+</sup>) CD8<sup>+</sup> cells among polyclonal CD8<sup>+</sup> T<sub>E</sub> cells in peripheral blood on day 7 post ATT.

No Tag  $n = 8$ , WT  $n = 11$ , *Erap1*<sup>-/-</sup>  $n = 12$  mice.

(C) TCR-IV (Tet-IV<sup>+</sup>) CD8<sup>+</sup> cells among polyclonal CD8<sup>+</sup> T<sub>E</sub> cells in peripheral blood on day 7 post ATT.

No Tag  $n = 7$ , WT  $n = 11$ , *Erap1*<sup>-/-</sup>  $n = 9$  mice.

(B, C) Percentage was calculated according to % of Tet-I<sup>+</sup> (1.74) and Tet-IV<sup>+</sup> (17.5) CD8<sup>+</sup> T cells among  $1 \times 10^6$  polyclonal CD8<sup>+</sup> T<sub>E</sub> cells transferred on day 0. Data are represented as mean  $\pm$  SD, Kruskal-Wallis test, \* $p < 0.05$ .



**Figure S6, related to Figure 6**

TAg<sup>+</sup> HCC rejection through polyclonal CD8<sup>+</sup> T<sub>E</sub> cells and expansion of polyclonal CD8<sup>+</sup> T<sub>E</sub> cells after ATT.

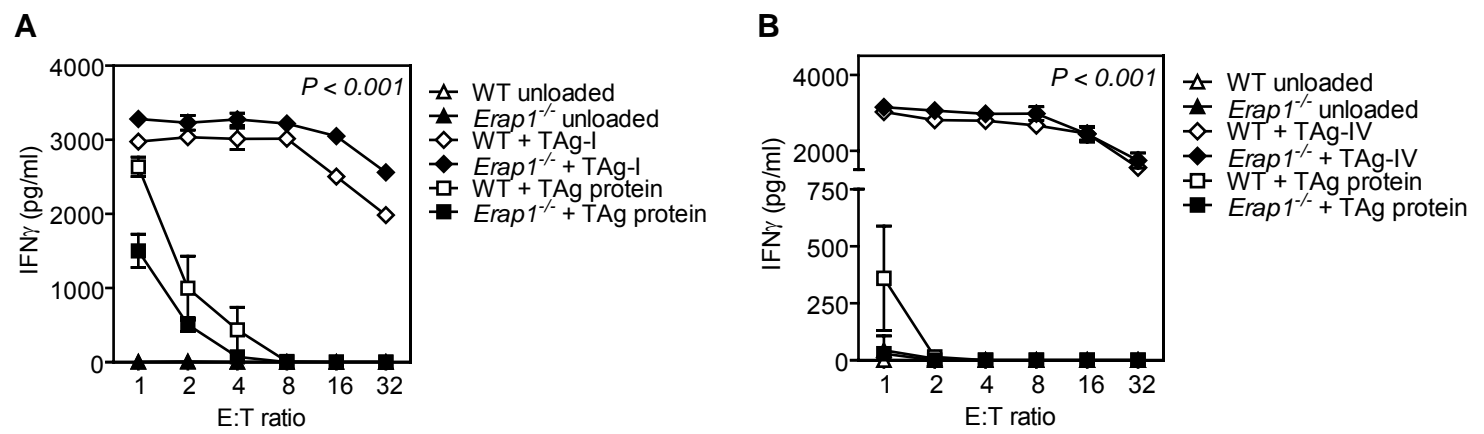
(A) Graphical representation of rejection of WT and *Erap1*<sup>-/-</sup> TAg<sup>+</sup> HCC by polyclonal CD8<sup>+</sup> T<sub>E</sub> cells in WT and *Erap1*<sup>-/-</sup> H2b<sup>+</sup> recipients.

(B) Numerical summary of the tumor rejection experiments using polyclonal CD8<sup>+</sup> T<sub>E</sub> cells. Data represent the number of analyzed mice of n = 2 - 6 experiments per HCC pair / group, % rejection are parenthesized.

(C) FACS analysis of CD8<sup>+</sup> T<sub>E</sub> cell expansion 1 week after ATT. WT→WT n = 10 mice, *Erap1*<sup>-/-</sup>→WT n = 14 mice, WT→*Erap1*<sup>-/-</sup> n = 8 mice, *Erap1*<sup>-/-</sup>→*Erap1*<sup>-/-</sup> n = 10 mice.

(D) FACS analysis of CD8<sup>+</sup> T<sub>E</sub> cell expansion 4 weeks after ATT. WT→WT n = 10 mice, *Erap1*<sup>-/-</sup>→WT n = 14 mice, WT→*Erap1*<sup>-/-</sup> n = 8 mice, *Erap1*<sup>-/-</sup>→*Erap1*<sup>-/-</sup> n = 10 mice.

(C and D) All data are represented as mean ± SD, Kruskal-Wallis test.



**Figure S7**

Analysis of ERAP1-dependent cross-presentation of TAg-I and TAg-IV by bone marrow-derived dendritic cells (BMDCs).

(A) Cross-presentation of TAg-I processed from full-length TAg protein was analyzed in CD11c<sup>+</sup> WT or *Erap1*<sup>-/-</sup> GM-CSF-differentiated BMDCs. After 7 days of co-culture with 20 ng/ml GM-CSF, BMDCs were loaded with 0.1  $\mu$ M TAg-I or 30 ng purified TAg protein for 2 hours at 37°C, and were co-cultured with TCR-I T cells for 18 hours. Release of IFN $\gamma$  was measured by ELISA.

(B) Cross-presentation of TAg-IV processed from full-length TAg protein was analyzed in CD11c<sup>+</sup> WT or *Erap1*<sup>-/-</sup> GM-CSF-differentiated BMDCs. The experiment was performed as described for (A), but BMDCs were co-cultured with TCR-IV T cells.

(A and B) Shown is one of two independent experiments with similar results. All data are represented as mean  $\pm$  SD, two-way ANOVA.