# Supplemental Figures

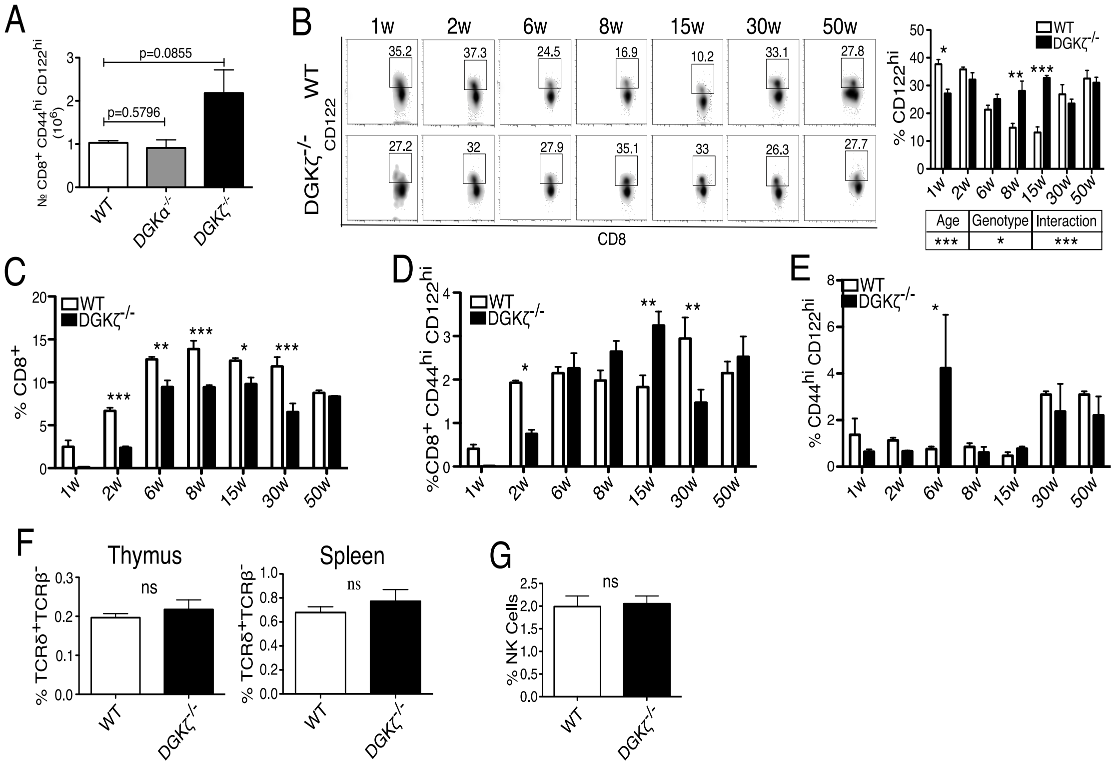

**Fig. S1. DGKζ-deficient mice have altered $CD8^+$ and $CD8^+CD122^+$ cell numbers**

**A.** Analysis of the total number of $CD44^{hi}CD122^{hi}$ $CD8^+$ T cells in WT (n=6), DGKα- (n=5) and DGKζ-deficient (n=6) mouse spleens. Mean ± SEM, unpaired Student's t-test with Welch's correction. **B.** Analysis of $CD122^{hi}$ $CD8^+$ T cells in spleens of WT and DGKζ-deficient mice at different ages. Left, flow cytometry of CD8 and CD122 markers (gated on $CD8^+$ cells). Right, $CD122^{hi}$ percentages gated on $CD8^+$. Mean ± SEM, two-way ANOVA and Bonferroni post-test ($n$ = 3/genotype and age, except $DGK\zeta^{-/-}$ 50 weeks, $n$ = 2). **C.** Analysis of $CD8^+$ population in spleens of WT and DGKζ-deficient mice at different ages. Mean ± SEM, two-way ANOVA and Bonferroni post-test ($n$ = 3/genotype and age, except $DGK^{-/-}$ 50 weeks, $n$ = 2). **D.** Analysis of $CD8^+CD44^{hi}CD122^{hi}$ population in spleens of WT and DGKζ-deficient mice at different ages. Mean ± SEM, statistical analyses and groups as above. **E.** Analysis of the $CD44^{hi}CD122^{hi}$ CD8 SP population in thymuses of WT and DGKζ-deficient mice at different ages. Percentages of $CD44^{hi}CD122^{hi}$ were analyzed in $CD8^+CD4^-$ cells. Mean ± SEM, Bonferroni post-test (n = 3/genotype and age, except DGKζ-/- 50 weeks, n = 2). **F.** Quantification of the γδ T cell population ($TCR\delta^+TCR\beta^-$) in thymus and spleen of WT and DGKζ-deficient mice. Data were acquired in two independent experiments. Mean ± SEM, $n$ = 6/genotype. Unpaired t test. **G.** Analysis of NK cells ($CD3^-NKP46^+$) in spleens of WT and DGKζ-deficient mice. Data were acquired in three independent experiments. Mean ± SEM, $n$ = 9 per genotype. Unpaired t test.

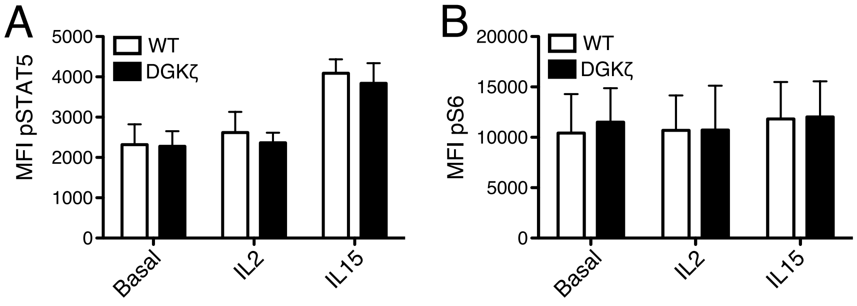

**Fig S2. DGKζ-deficient CD8$^+$ CD44$^{hi}$ cells show similar STAT5 and S6 phosphorylation intensity than WT cells**. The geometric mean of pSTAT5 (A) or pS6 (B) was quantified in the CD8$^+$ CD44$^{hi}$ pSTAT$^+$/pS6$^+$ population for the experiments described in figure 3. (Mean ± SEM; $n$ = 3/genotype, data were acquired in three independent experiments).

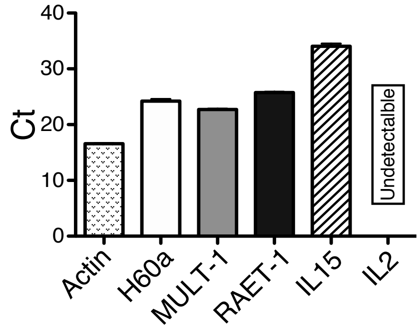

**Fig. S3. Analysis of mRNA levels for NKG2D ligands and cytokines in A20 cells**

mRNA levels of indicated molecules were analyzed by real-time qRT-PCR in A20 cells. Mean ± SEM.