

Figure S1 related to figure 1. IL-36 γ effect on CD8⁺ T cells. (A) Naïve CD4⁺ and CD8⁺ T (CD44⁻ CD62L⁺) cells were purified from spleen cells of C57BL/6 mice by FACS sorting. T cells were then stimulated in the Th1 condition for the time indicated. (96h +3h indicates that T cells were cultured for 96 h and subsequently re-stimulated with anti-CD3 for 3 h). Total RNA was subjected quantitative RT-PCR analysis (A) and RT-PCR (B) for IL-36R. RQ (relative quantification values) were calculated based on $\Delta\Delta$ CT method. (C and D) Naïve pmel-1 CD8⁺ T cells were stimulated with plate-bound 5 μ g/ml CD3 and 2.5 μ g/ml CD28 mAbs in the presence or absence of IL-36 γ at various concentrations as indicated. (C) Cell sizes (FSC) were determined by flow cytometry at 72 h.(D) The level of IL-2 and IFN- γ at 24 h after stimulation was measured by ELISA. (E to H) Naïve CD8⁺ T cells were stimulated with plate-bound 5 μ g/ml CD3 and 2.5 μ g/ml CD28 mAbs in the presence or absence of mouse IL-36 γ at various concentrations as indicated. CD25 mAbs (clone PC61, 20 μ g/ml) were added to cultures to block IL-2 signaling. (E) Cell sizes (FSC) were determined by flow cytometry at 72 h. IL-2 (F) or IFN- γ (G) secretion was determined by ELISA at 24 h. (H) Proliferation was determined by the CFSE-dilution assay at 72 h. Data are shown as mean \pm SEM. *** p < 0.001, ** p <0.01, * p<0.05. two-tailed unpaired Student's t-test. (I- L) Naïve CD8⁺ T cells were isolated from WT or Myd88^{-/-} B6 mice. They were subsequently stimulated with plate-bound 5 μ g/ml CD3 and 2.5 μ g/ml CD28 mAbs in the presence or absence of 100 ng/ml IL-36 γ for 72 h. (I) Cell sizes (FSC) were determined by flow cytometry. (J) IL-2 and (K) IFN- γ production was determined by ELISA. Data are shown as mean \pm SEM. ** p <0.01 two-tailed unpaired Student's t-test. (L) Proliferation was determined by the CFSE-dilution assay.

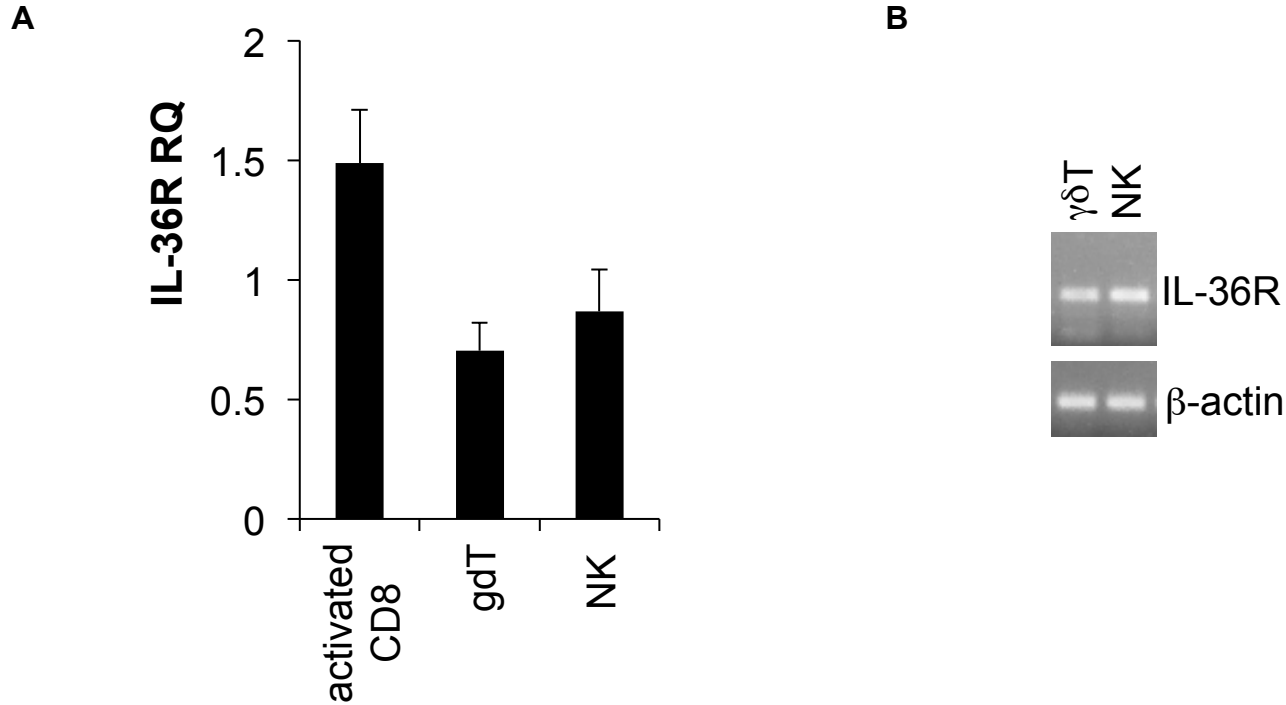


Figure S2 related to figure 2. IL-36R is expressed in NK and $\gamma\delta$ T cells. Naïve CD8⁺ T (CD44⁻ CD62L⁺), NK (DX5⁺) and $\gamma\delta$ T cells were purified from spleen cells of C57BL/6 mice by FACS sorting. T cells were then stimulated in the Th1 condition for 96 h. NK cells were cultured in the presence of IL-2 for 72 h and $\gamma\delta$ T cells were stimulated with CD3 mAbs and IL-2 for 72 h. Total RNA was purified and subjected to (A) quantitative RT-PCR analysis for IL-36R. RQ (relative quantification values) were calculated based on $\Delta\Delta$ CT method. Data are shown as mean \pm SEM. Data are shown as mean \pm SEM. (B) RT-PCR analysis.

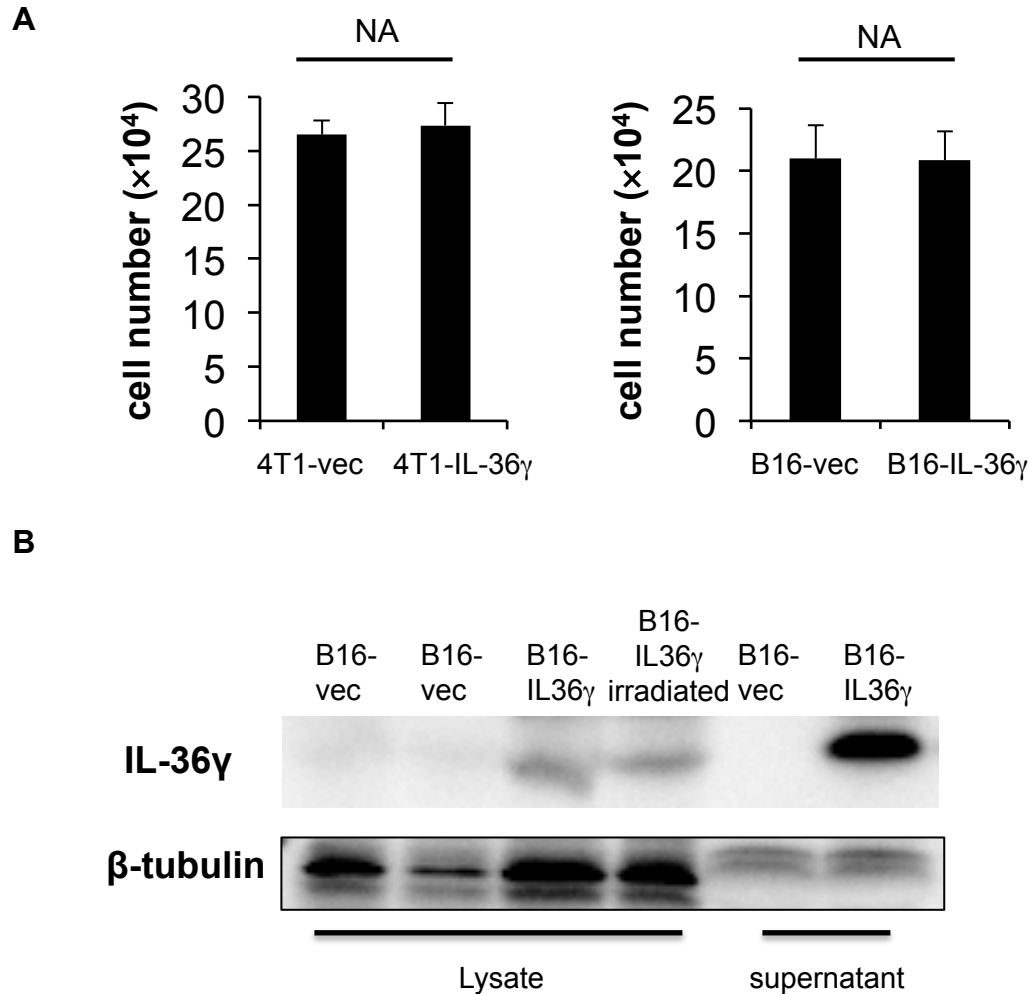


Figure S3 related to figure 3. Analysis of IL36 γ -expressing cell lines.

(A) The growth of IL-36 γ transfectants were comparable to the control cells. 4×10^4 4T1-vec, 4T1-IL-36 γ B16-vec or B16-IL-36 γ , cells were seeded into 24 wells with triplicates. The cells were cultured for 2 days, the number of live cells was determined by live cell counting after cells were stained with Trypan blue. Data (mean \pm SEM) are representative of three independent experiments. (B) Detection of IL-36 γ protein by Western blot. Supernatants were harvested from B16-vec or B16-IL-36 γ cell culture and concentrated 10 times. Cell lysates were made from B16-vec or B16-IL-36 γ cells. Western blot was performed using rabbit anti-IL1F9 antibody ((aa5-149) LS-C294790; LifeSpan Biosciences, Inc.)

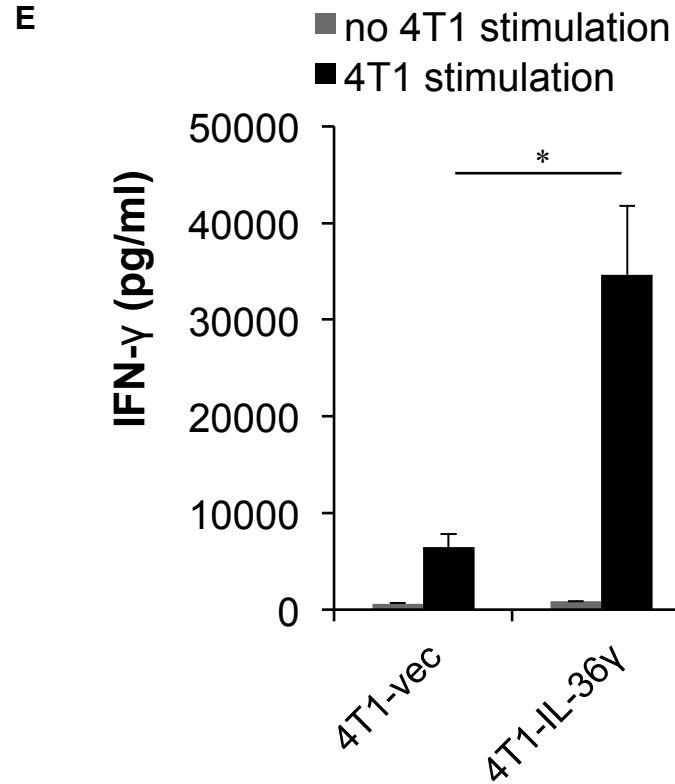
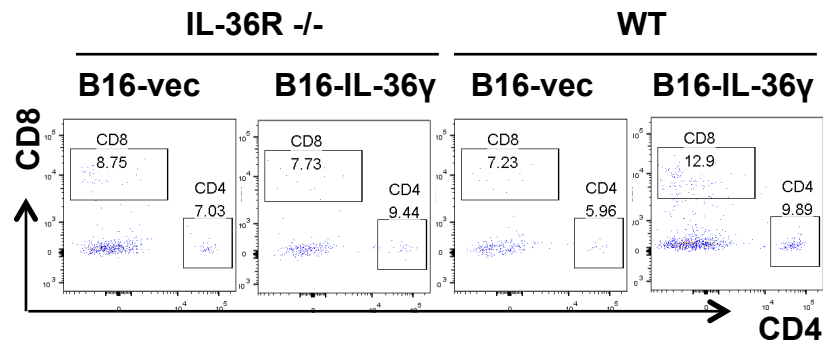
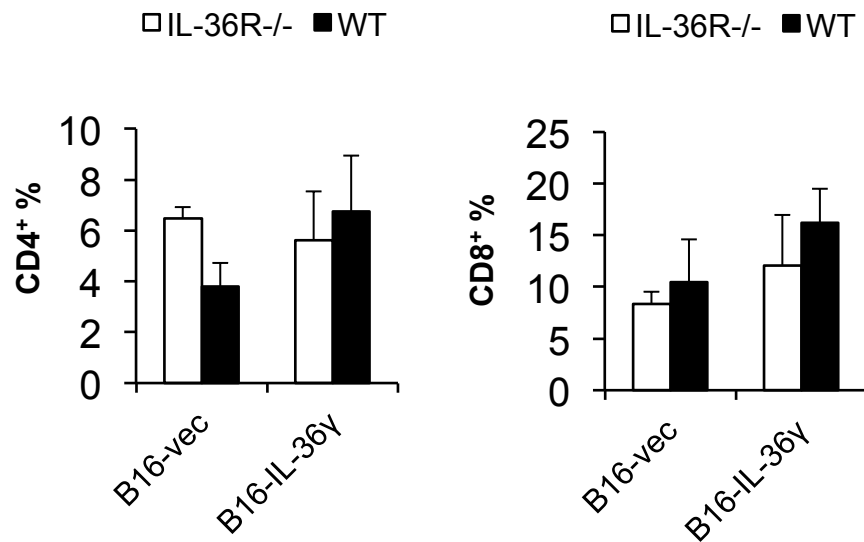


Figure S4 related to Figure 4. Tumoral expression of IL-36 γ influence antitumor immune responses. 1×10^5 B16-vector or B16-IL-36 γ cells were injected i.d. into B6 mice. On day 24, tumors were resected and processed to generate single cell suspensions. (A) Representative flow cytometric plots and percentages of CD8⁺ Ki67⁺ populations from the CD8⁺ in tumor microenvironment are shown. (B) Representative flow cytometric plots and percentages of CD4⁺ and Treg cells in the tumor microenvironment are shown. (C) Representative flow cytometric analysis of CD11b⁺ sub-populations and percentages of CD11b⁺ subpopulations of CD45⁺ immune cells and percentages of MHC class II expression on three CD11b⁺ sub-populations. (D) Tumors were resected and total RNA was extracted and subjected to RT-QPCR analysis. RQ (relative quantification values) were calculated based on $\Delta\Delta CT$ method. Results are shown as mean \pm SEM of four independent experiments. One tumor was used in each experiment. * $p < 0.05$ and ** $p < 0.01$, two-tailed unpaired Student's t-test. (E) Tumor antigen-specific CD8⁺ T cell responses were enhanced by IL-36 γ . 1×10^5 4T1-vector or 4T1-IL-36 γ cells were injected into the mammary fat pad of BALB/c mice. 30 days after inoculation, CD8⁺ T cells were purified from the spleens of these mice and re-stimulated with irradiated 4T1 cells for 72h in the presence of irradiated APC. The level of IFN- γ was then measured by ELISA. Results are shown as mean \pm SEM of three independent experiments. One pair of mice were used in each experiment. * $p < 0.05$, two-tailed unpaired Student's t-test.

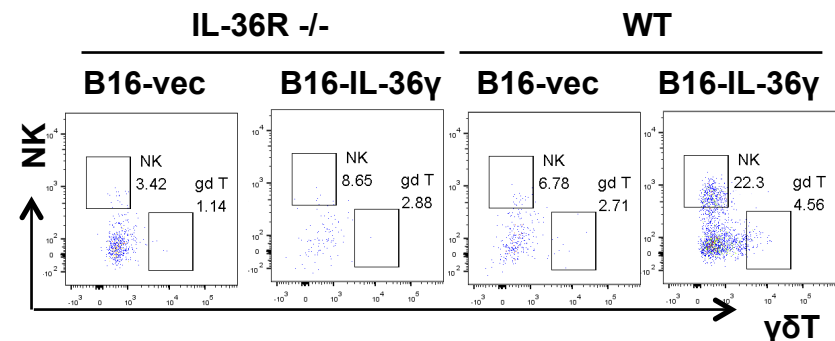
A



B



C



D

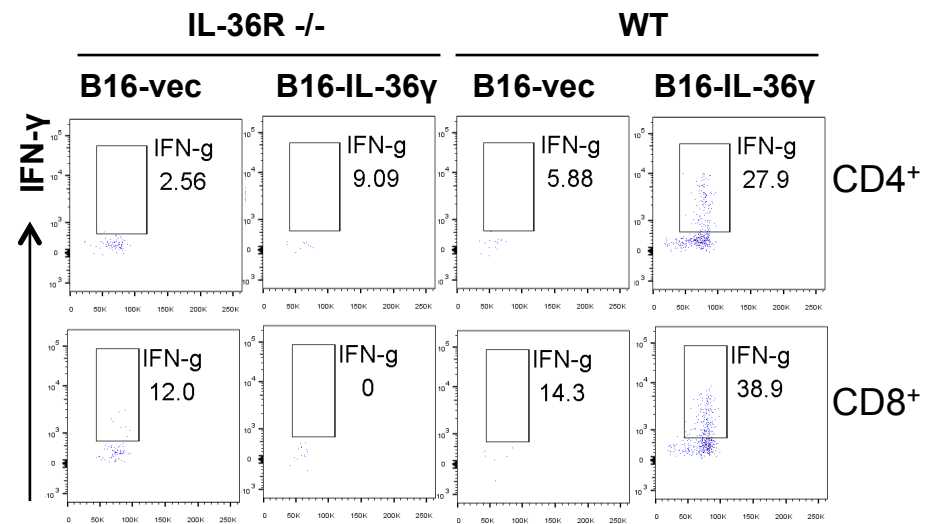
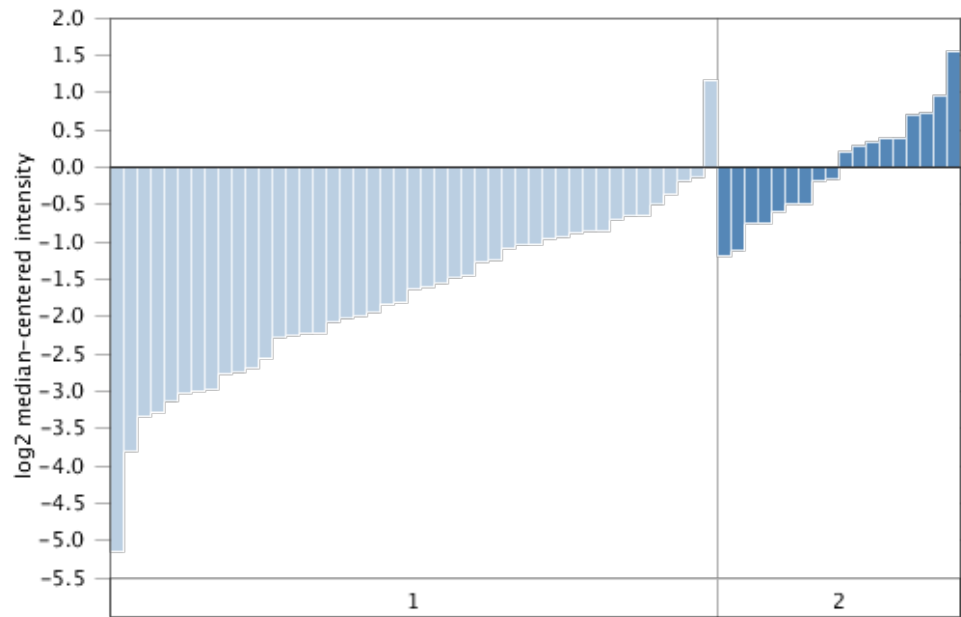


Figure S5 related to figure 5. Analysis of TIL in WT and IL-36R^{-/-} mice. 1×10^5 B16-vector (B16-vec) or B16-IL-36 γ cells were injected intradermally into WT and IL-36R^{-/-} mice. The tumors were resected on day 17 and TIL were subjected to the flow cytometric analysis. (A) Representative flow cytometric analysis of CD4, CD8 T cells among CD45⁺ TIL. (B) Percentages of the CD4⁺ and CD8⁺ T cells within the CD45⁺ TIL. (C) Representative flow cytometric analysis of NK and $\gamma\delta$ T cells among CD45⁺ TIL. (D) Representative flow cytometric analysis of IFN- γ ⁺ T cells among CD4⁺ and CD8⁺ TIL.



1. Cutaneous Melanoma (45)
2. Melanoma Precursor (18)

Figure S6 related to figure 8. IL-36 γ expression in melanoma and melanoma precursor. The data is generated after search oncomine database (www.oncomine.com) (Rhodes et al., 2004). The result is based on Talantov D et al's paper titled: Novel genes associated with malignant melanoma but not benign melanocytic lesions (Talantov et al., 2005).

Supplemental experimental procedures:

List of RT-QPCR primers

Genes	Forward	Reverse
IL-36R	AAACACCTAGCAAAAGCCCAG	AGACTGCCCGATTTTCCTATG
IFN- γ	CCTGCGGCCTAGCTCTGAG	GCCATGAGGAAGAGCTGCA
IL-12p35	CAATCACGCTACCTCCTCTTTT	CAGTGCAGGAATAATGTTTC
Granzyme B	CCACTCTCGACCCTACATGG	GGCCCCCAAAGTGACATTTATT
IL-17 α	CTCCAGAAGGCCCTCAGACTAC	GGGTCTTCATTGCGGTGG
IL-1 β	CTGAACTCAACTGTGAAATG	CGAGATTTGAAGCTGGATGC
IL-23p19	TGGCATCGAGAAACTGTGAGA	TCAGTTCGTATTGGTAGTCCTGTTA
TNF α	ATGAGCACAGAAAGCATGATC	TACAGGCTTGTCACCTCGAATT
IL-10	TGTCAAATTCATTCATGGCCT	ATCGATTTCTCCCCTGTGAA
β -actin	GAAATCGTGCGTGACATCAA	TGTAGTTTCATGGATGCCACAG

Supplemental reference

Rhodes, D. R., Yu, J., Shanker, K., Deshpande, N., Varambally, R., Ghosh, D., Barrette, T., Pandey, A., and Chinnaiyan, A. M. (2004). ONCOMINE: a cancer microarray database and integrated data-mining platform. *Neoplasia* (New York, NY) 6, 1-6.

Talantov, D., Mazumder, A., Yu, J. X., Briggs, T., Jiang, Y., Backus, J., Atkins, D., and Wang, Y. (2005). Novel genes associated with malignant melanoma but not benign melanocytic lesions. *Clinical cancer research : an official journal of the American Association for Cancer Research* 11, 7234-7242.