



## Supplementary Materials for

### **Progenitor and Terminal Subsets of CD8<sup>+</sup> T Cells Cooperate to Contain Chronic Viral Infection**

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References

## **Supplementary Materials:**

### **Materials and Methods:**

#### Human Subjects:

All human subjects were recruited at the Massachusetts General Hospital Gastrointestinal Unit and the Department of Surgery in accordance with the IRB approved study: "Cell mediated immunity in Hepatitis C virus infection"; Protocol # 1999-P-004983/54; MGH Legacy #: 90-7246. Liver specimens were obtained from explantation or resection of 8 patients with at least 5 years of chronic HCV infection, defined by positive anti-HCV antibody and detectable viral load. Three patients with treatment induced sustained virological response (SVR, undetectable viral load 6 months after end of treatment) were analyzed. SVR of all 3 patients was achieved at least 3 years prior to liver sampling. Intrahepatic lymphocytes (IHL) were extracted by mechanical disruption of liver tissue. The cell suspension was then washed twice in RPMI 1640 culture medium supplemented with 10% FBS, followed by centrifugation at 300 rpm each time to remove cell debris and hepatocytes. The final washing step was followed by centrifugation at 1500 rpm to obtain a pellet of IHL.

#### Mice and Infections:

All animals were housed at the University of Pennsylvania (Philadelphia, PA). Experiments were performed in accordance with protocols approved by the University of Pennsylvania Institutional Animal Care and Use Committee. Eomes<sup>flox/flox</sup>, Eomes<sup>gfp/+</sup>, and Tbx21<sup>-/-</sup> (T-bet KO) mice have been described previously (7, 20, 32). To examine CD8<sup>+</sup> T cell differentiation in the absence of Eomes, Eomes<sup>flox/flox</sup> mice were crossed to

CD4-Cre mice (Eomes cKO) (7). CD4-Cre<sup>+</sup> Eomes<sup>+/+</sup> or littermate CD4-Cre<sup>-</sup> Eomes<sup>ff</sup> mice were used as WT controls. Mice were infected with either 2 x 10<sup>5</sup> PFU of lymphocytic choriomeningitis virus (LCMV) Armstrong strain by i.p. injection to generate an acutely resolved infection or 4 x 10<sup>6</sup> PFU of LCMV clone 13 strain by i.v. injection to generate a chronic infection. The V35A variant of clone 13 has been previously described (19, 33).

*Flow cytometry and real-time PCR:*

All cells were stained with LIVE/DEAD® Fixable Dead Cell Stain (Invitrogen) to discriminate live from dead cells. Surface staining was performed as described previously (7, 34). Intracellular staining was performed using the Foxp3 / Transcription Factor Staining Buffer Set per manufacturer's instructions (eBioscience; San Diego, CA). Antibodies used for flow cytometry were purchased from BD Biosciences (CD4, CD8, CD19, CD44, 2B4, Ki-67; San Jose, CA), Biolegend (PD-1, Tim3, TNF- $\alpha$ , IFN- $\gamma$ , T-bet; San Diego, CA), R&D Systems (MIP-1 $\alpha$ ; Minneapolis, MN), or eBioscience (CD8, Lag3, CD160, 2B4, CD45.1, CD45.2, CD107a, Eomes). MHC class I peptide tetramers were made and used as described previously (30, 35). Data were collected on a BD LSRII (BD Biosciences) and analyzed with FlowJo software (Tree Star, Ashland, OR). Cell sorting was performed using a BD Aria II (BD Biosciences). qRT-PCR was carried out as previously described (7, 36). Gene expression was normalized to GAPDH. Target gene probes were purchased from Applied Biosystems (Foster City, CA).

### Total Body Estimation of Blood, Skin, and Bone Marrow:

Mice were weighed for total blood volume and surface area estimation. Total blood volume was estimated as 6% body weight (37). Total skin surface area (in cm<sup>2</sup>) was estimated as  $9.822 * (\text{mass in g})^{0.667}$  as described in (38). Total body bone marrow was estimated to be 7.9-fold of the yield from two femurs as previously described (35, 39, 40). Tissues were processed and hematopoietic cells isolated as described (35).

### Bone Marrow Chimeras

Bone marrow (BM) from WT (CD45.1<sup>+</sup>), T-bet KO (CD45.2<sup>+</sup>), and Eomes cKO (CD45.2<sup>+</sup>) donors was harvested. 5-10 x 10<sup>6</sup> donor cells were transferred i.v. into sublethally irradiated (450 rads) *Rag2*<sup>-/-</sup> recipients. 8 weeks after BM transfer, chimeras were infected with LCMV clone 13.

### BrdU Treatment and Detection

Animals were treated with 2mg of BrdU (Sigma-Aldrich; St. Louis, MO) i.p. daily for 7 days prior to tissue harvest and analysis. BrdU incorporation was assessed by the BrdU Flow Kit per manufacturer's instructions (BD Biosciences).

### CFSE labeling, temporal deletion and adoptive transfers:

At indicated days p.i., spleens were harvested from indicated CD45.2<sup>+</sup> donor mice. CD8<sup>+</sup> T cells were purified from splenocytes using magnetic beads according to manufacturer's protocol (CD8 negative selection; MACS beads; Miltenyi Biotec, Auburn, CA). Purified CD8<sup>+</sup> T cells were labeled with CFSE as described previously (30, 35),

and transferred i.v. into CD45.1<sup>+</sup> infection-matched controls. Temporal Eomes deletion with Tat-Cre was performed as described (36).

Statistical Analysis:

Student's t test (Paired and Unpaired), Mann-Whitney test, and 2-way ANOVA were performed using Prism software (Graphpad, La Jolla, CA).

**Figure Legends**

**Figure S1. Eomes expression is enhanced during chronic viral infection and segregates antiviral CD8<sup>+</sup> T cells with distinct functional properties.** (A) Flow cytometric analysis of GFP expression in D<sup>b</sup>gp33-specific CD8<sup>+</sup> T cells in WT (shaded) or *Eomes*<sup>gfp/+</sup> (open) mice at indicated days p.i. (B) Flow cytometric analysis of YFP (Blimp1) versus GFP (Eomes) expression in D<sup>b</sup>gp33-specific CD8<sup>+</sup> T cells on d8 post LCMV Armstrong infection of WT, single, or double reporter mice as indicated. (C) Flow cytometric analysis of IFN- $\gamma$  and TNF- $\alpha$  expression in *Eomes*<sup>hi</sup> and *Eomes*<sup>lo</sup> virus-specific CD8<sup>+</sup> T cells after stimulation with indicated LCMV peptides on d22 p.i. (2-way ANOVA). (D) Flow cytometric analysis of granzyme B expression in naïve (shaded) or *Eomes*<sup>+</sup> and *Eomes*<sup>-</sup> D<sup>b</sup>gp276-specific CD8<sup>+</sup> T cells (open) d22 post clone 13 infection. (A-D) Numbers denote frequency of gated population. (A-D) Data are representative of 2-5 independent experiments with at least three mice per experimental group. (E) Flow cytometric analysis of CD107a staining of naïve (shaded) or *Eomes*<sup>+</sup> and *Eomes*<sup>-</sup> MIP-1 $\alpha$ <sup>+</sup> CD8<sup>+</sup> T cells (open) after stimulation with gp276-286 peptide on d23 p.i. post clone 13 infection. Data is aggregated across three independent experiments. (F) PD-1

expression effectively separates cells with elevated T-bet (T-bet<sup>hi</sup>) versus elevated Eomes (Eomes<sup>hi</sup>). Flow cytometric analysis of T-bet, Eomes, and PD-1 expression in D<sup>b</sup>gp33-specific CD8<sup>+</sup> T cells d21 post clone 13 infection. (G) Eomes<sup>hi</sup> cells have enhanced cytotoxicity compared to T-bet<sup>hi</sup> cells. Cytotoxicity of sorted PD-1<sup>int</sup> (T-bet<sup>hi</sup>) and PD-1<sup>hi</sup> (Eomes<sup>hi</sup>) D<sup>b</sup>gp33-specific CD8<sup>+</sup> T cells on d22 p.i. (H) 2,000 *Eomes*<sup>gfp/+</sup> TCR-transgenic D<sup>b</sup>gp33-specific (P14) CD8<sup>+</sup> T cells were transferred into naïve recipients one day before infection with clone 13. Donor P14 cells from chronically infected mice were isolated on d22 p.i., sorted based on GFP expression, and added to target cells pulsed with LCMV-derived peptide gp33-41. % specific lysis was determined by the loss of target cells compared to control cells. Graphs display mean ± S.E.M. (D, E, H) (\*p<0.05, \*\*p<0.01; Paired t test). (F-H) Data are representative of 2-5 independent experiments.

**Figure S2. Genetic deletion of Eomes leads to loss of the T-bet<sup>lo</sup> PD-1<sup>hi</sup> population of exhausted CD8<sup>+</sup> T cells.** Rag KO hosts were sublethally irradiated and reconstituted with a 1:1 mixture of WT and EKO bone marrow, followed by infection with LCMV clone 13. (A) Flow cytometric analysis of T-bet and PD-1 expression in D<sup>b</sup>gp276-specific CD8<sup>+</sup> T cells d60 p.i. Numbers denote frequency of gated population. (B) MFI of T-bet and PD-1 expression from cells in (A). (\*p<0.05, \*\*p<0.01; Paired t test). All data are representative of 3 independent experiments with at least four mice.

**Figure S3. T-bet<sup>hi</sup> and Eomes<sup>hi</sup> exhausted CD8<sup>+</sup> T cell subsets have distinct population size and anatomical distribution.** (A) Eomes<sup>hi</sup> cells outnumber T-bet<sup>hi</sup>

cells. T-bet<sup>hi</sup> and Eomes<sup>hi</sup> populations of D<sup>b</sup>gp276-specific CD8<sup>+</sup> T cells were quantified for the total mouse (see Methods). Graph displays sum of all tissues in (B). (B) Individual organs contain distinct proportions of T-bet<sup>hi</sup> and Eomes<sup>hi</sup> populations. The frequency of T-bet<sup>hi</sup> and Eomes<sup>hi</sup> populations of D<sup>b</sup>gp276-specific CD8<sup>+</sup> T cells are displayed for each indicated organ. (C) Quantification of T-bet<sup>hi</sup> and Eomes<sup>hi</sup> populations of D<sup>b</sup>gp276-specific CD8<sup>+</sup> T cells are displayed for each indicated organ. (D) CD8<sup>+</sup> T cells from chronically infected CD45.2 mice were isolated d22 p.i. post clone 13 infection, sorted based on PD-1 expression and adoptively transferred into infection-matched CD45.1 recipient mice. (E) Two weeks post-transfer, virus-specific CD8<sup>+</sup> T cells were enumerated in indicated organs. All graphs display mean ± S.E.M. (\*p<0.05; Unpaired t test). All data are representative of 2-5 independent experiments with at least three mice per experimental group.

**Figure S4. T-bet and Eomes-dependent populations exhibit differential proliferation.** (A) Flow cytometric analysis of T-bet, Eomes, and PD-1 versus Ki-67 expression in D<sup>b</sup>gp33-specific CD8<sup>+</sup> T cells on d22 p.i. (B) Representative gating strategy for T-bet<sup>hi</sup> and T-bet<sup>lo</sup> populations for **Fig 2A, 2B**. (C) Flow cytometric analysis of Eomes expression versus BrdU incorporation for D<sup>b</sup>gp276-specific CD8<sup>+</sup> T cells in indicated tissues. (A-C) Data are representative of 3-4 independent experiments with at least three mice per experimental group. (D) CD8<sup>+</sup> T cells from CD45.2 LCMV clone 13 chronically infected mice were isolated d15 p.i., CFSE-labeled, and transferred into clone 13 infection-matched CD45.1 recipient mice. One week post-transfer, virus-specific CD8<sup>+</sup> T cells were analyzed for CFSE dilution. (E) CD8<sup>+</sup> T cells from CD45.2

LCMV Armstrong-immune (d30+) or clone 13 chronically infected (d30) mice were isolated, CFSE-labeled, and transferred into LCMV Armstrong-immune (d30+) or chronically infected (d30) CD45.1 recipient mice. One week post-transfer, virus-specific CD8<sup>+</sup> T cells were analyzed for CFSE dilution. (F) Flow cytometric analysis of CFSE dilution in D<sup>b</sup>gp33-specific donor CD8<sup>+</sup> T cells. Data are representative of 2 independent experiments. (G) Flow cytometric analysis of Ki-67 expression in D<sup>b</sup>gp33-specific CD8<sup>+</sup> T cells from WT, T-bet KO, and Eomes cKO mice at indicated days p.i. (\*\*p<0.01; \*\*\*p<0.001; Unpaired t test). Data are aggregated across 2 independent experiments.

**Figure S5. T-bet<sup>hi</sup> Eomes<sup>lo</sup> CD8<sup>+</sup> T cells convert to T-bet<sup>lo</sup> Eomes<sup>hi</sup> CD8<sup>+</sup> T cells.** (A) CD8<sup>+</sup> T cells from chronically infected CD45.2 mice were isolated d22 p.i. with LCMV clone 13, sorted based on PD-1 expression, CFSE-labeled, and transferred into infection-matched CD45.1 recipient mice. One week post-transfer, virus-specific CD8<sup>+</sup> T cells were analyzed for CFSE dilution. (B) Flow cytometric analysis of PD-1 expression versus CFSE dilution of sorted donor D<sup>b</sup>gp276<sup>+</sup>CD8<sup>+</sup> T cells in indicated organs. Populations in division 0-2, 3-6, and 7+ are indicated. Quantification of the indicated division is provided from the liver. Graph displays mean ± S.E.M. (\*p<0.05; Unpaired t test) (C) CD8<sup>+</sup> T cells from chronically infected *Eomes<sup>gfp/+</sup>* mice were isolated d15 p.i. with clone 13, sorted based on GFP expression, and adoptively transferred into infection-matched CD45.1 recipient mice. Two weeks post-transfer, virus-specific CD8<sup>+</sup> T cells were analyzed for GFP expression. (D) Flow cytometric analysis of GFP expression (open) of sorted D<sup>b</sup>gp276-specific *Eomes<sup>gfp/+</sup>* CD8<sup>+</sup> T cells 2 weeks post-transfer. (D) CD8<sup>+</sup> T cells from chronically infected *Eomes<sup>+/+</sup>* or *Eomes<sup>fff</sup>* mice were



isolated d15 p.i. with clone 13, treated with Tat-Cre *in vitro*, CFSE-labeled, and adoptively transferred into infection-matched CD45.1 recipient mice. Two weeks post-transfer, virus-specific CD8<sup>+</sup> T cells were analyzed for CFSE dilution. (E) CD8<sup>+</sup> T cells from chronically infected *T-bet*<sup>+/+</sup> or *T-bet*<sup>fl/fl</sup> mice were isolated d15 p.i. with clone 13, treated with Tat-Cre *in vitro*, CFSE-labeled, and adoptively transferred into infection-matched CD45.1 recipient mice. Two weeks post-transfer, virus-specific CD8<sup>+</sup> T cells were analyzed for CFSE dilution. (B, D) All data are representative of 3-4 independent experiments with 1-3 mice per experimental group.

**Figure S6. Loss of either T-bet or Eomes leads to reduced CD8<sup>+</sup> T cell responses during chronic infection.** Quantification of D<sup>b</sup>gp276-specific CD8<sup>+</sup> T cells from indicated organs of WT, T-bet KO (TKO), and EKO mice at d30 p.i. (\*p<0.05, \*\*p<0.01, \*\*\*p<0.001; Paired t test). Data are representative of 2 independent experiments with at least three mice per experimental group.

**Figure S7. Eomes acts cell-intrinsically to maintain CD8<sup>+</sup> T cell responses.** Mixed bone-marrow chimeras were generated as in Fig. S2. (A) Longitudinal frequency of D<sup>b</sup>gp33-specific CD8<sup>+</sup> T cells in the blood of infected mice. (B) Total D<sup>b</sup>gp33-specific and D<sup>b</sup>gp276-specific CD8<sup>+</sup> T cells in the spleens infected mice d60 p.i. (\*p<0.05; Paired t test). All data are representative of 3 independent experiments with at least four mice group.

**Figure S8. Deletion of Eomes leads to impaired viral control.** WT, TKO, and EKO mice were infected with LCMV clone 13 and assessed for viral control. Graphs display viral load in indicated tissues d90 p.i. Data are representative of 2 independent experiments with at least three mice per experimental group.

**Figure S9. Loss of Eomes<sup>hi</sup> progeny after removal of antigen is due to poor repopulation from T-bet<sup>hi</sup> progenitors.** (A) CD8<sup>+</sup> T cells from chronically infected CD45.2 mice were isolated d22 p.i., sorted based on PD-1 expression, and CFSE-labeled. Equal numbers of D<sup>b</sup>gp33-specific CD8<sup>+</sup> T cells were adoptively transferred into WT or V35A infection-matched CD45.1 recipient mice. Two weeks post-transfer, virus-specific CD8<sup>+</sup> T cells were analyzed for CFSE dilution. (B) 2,000 *Eomes*<sup>gfp/+</sup> TCR-transgenic D<sup>b</sup>gp33-specific (P14) CD8<sup>+</sup> T cells were adoptively transferred into naïve recipients one day before infection with clone 13. Donor P14 cells from chronically infected mice were isolated d22 p.i., sorted based on GFP expression, and adoptively transferred into WT or V35A infection-matched recipient mice. Two weeks post-transfer, donor P14 CD8<sup>+</sup> T cells were analyzed for GFP expression. (C) Flow cytometric analysis and quantification of GFP expression in sorted donor P14 CD8<sup>+</sup> T cells. Graph displays mean ± S.E.M. (\*p<0.05; Unpaired t test). Data are representative three mice per experimental group.

**Figure S10. Continued preferential BrdU incorporation in Eomes<sup>hi</sup> cells after months of sustained viremia.** Flow cytometric analysis of Eomes and PD-1 expression versus BrdU incorporation in D<sup>b</sup>gp276-specific CD8<sup>+</sup> T cells from CD4

depleted WT mice at d250 p.i. with clone 13. All data are representative of four mice across 2 independent experiments.

**Figure S11. T-bet and Eomes expression in systemic anti-HCV responses.**

Frequency of Eomes<sup>hi</sup> and T-bet<sup>hi</sup> HCV-specific CD8<sup>+</sup> T cells from the blood of subjects with resolved or chronic infection. ( $p > 0.05$ ; Unpaired t test).

Figure S1

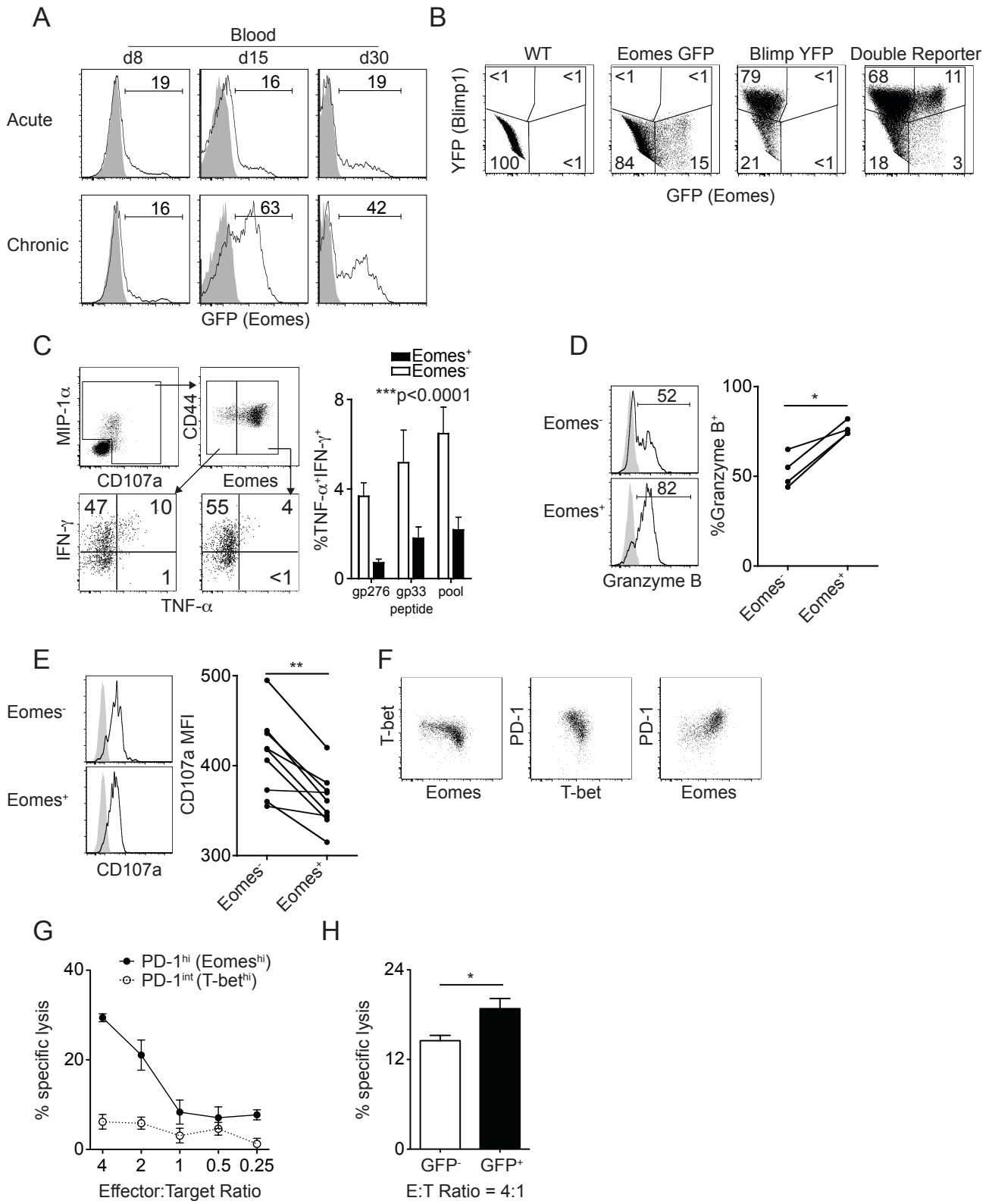


Figure S2

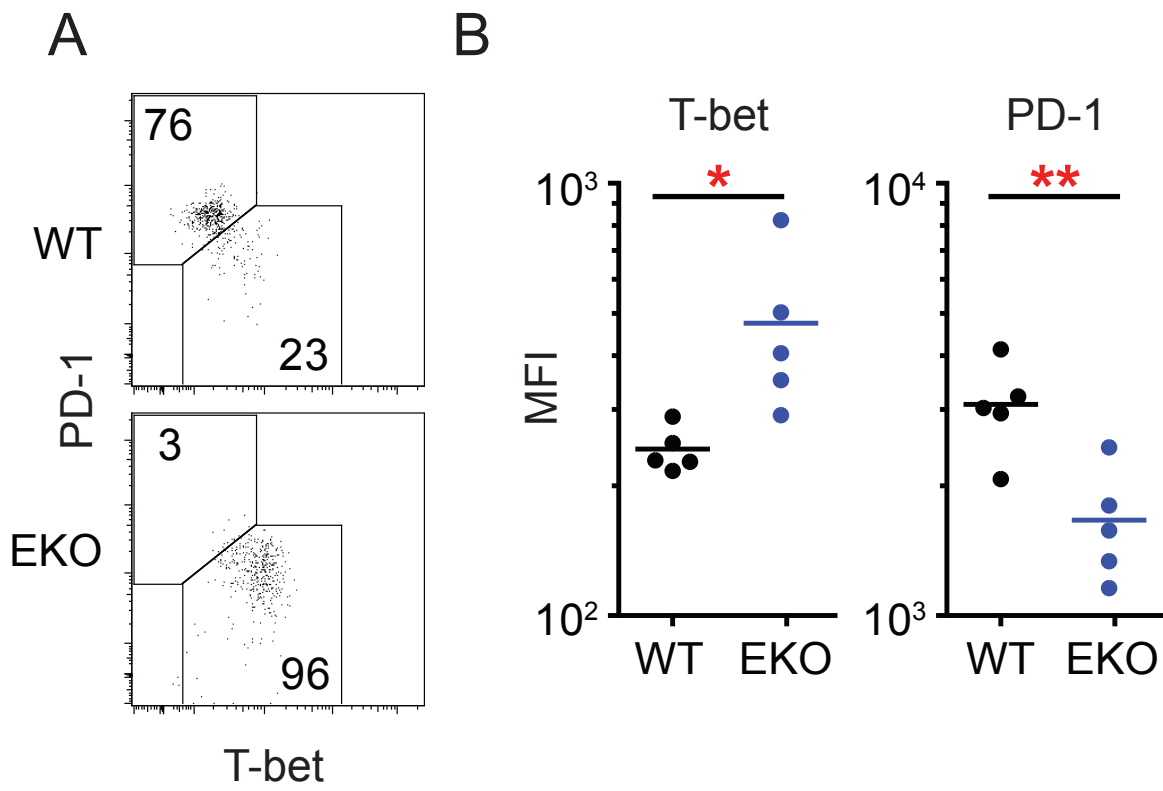


Figure S3

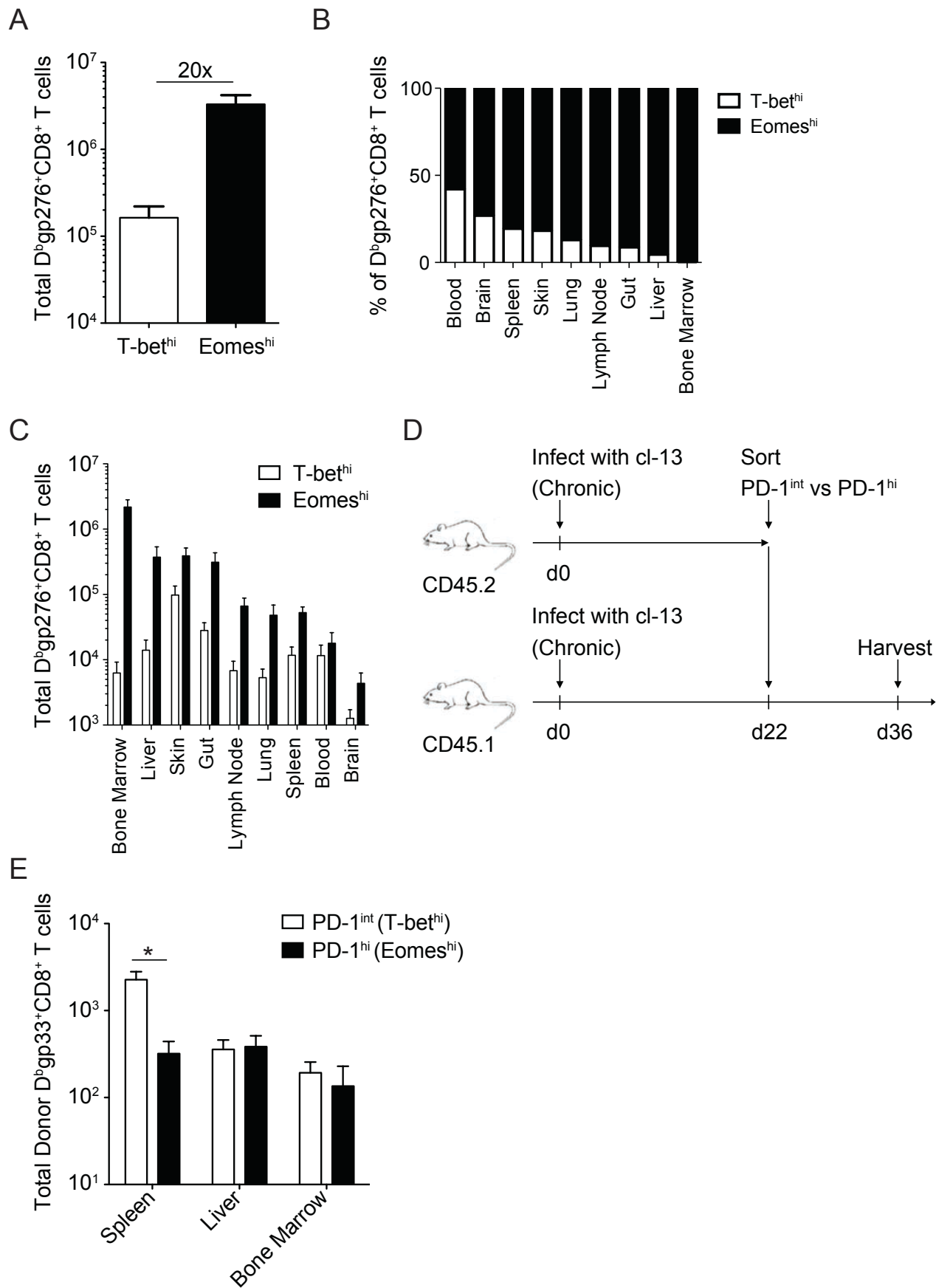


Figure S4

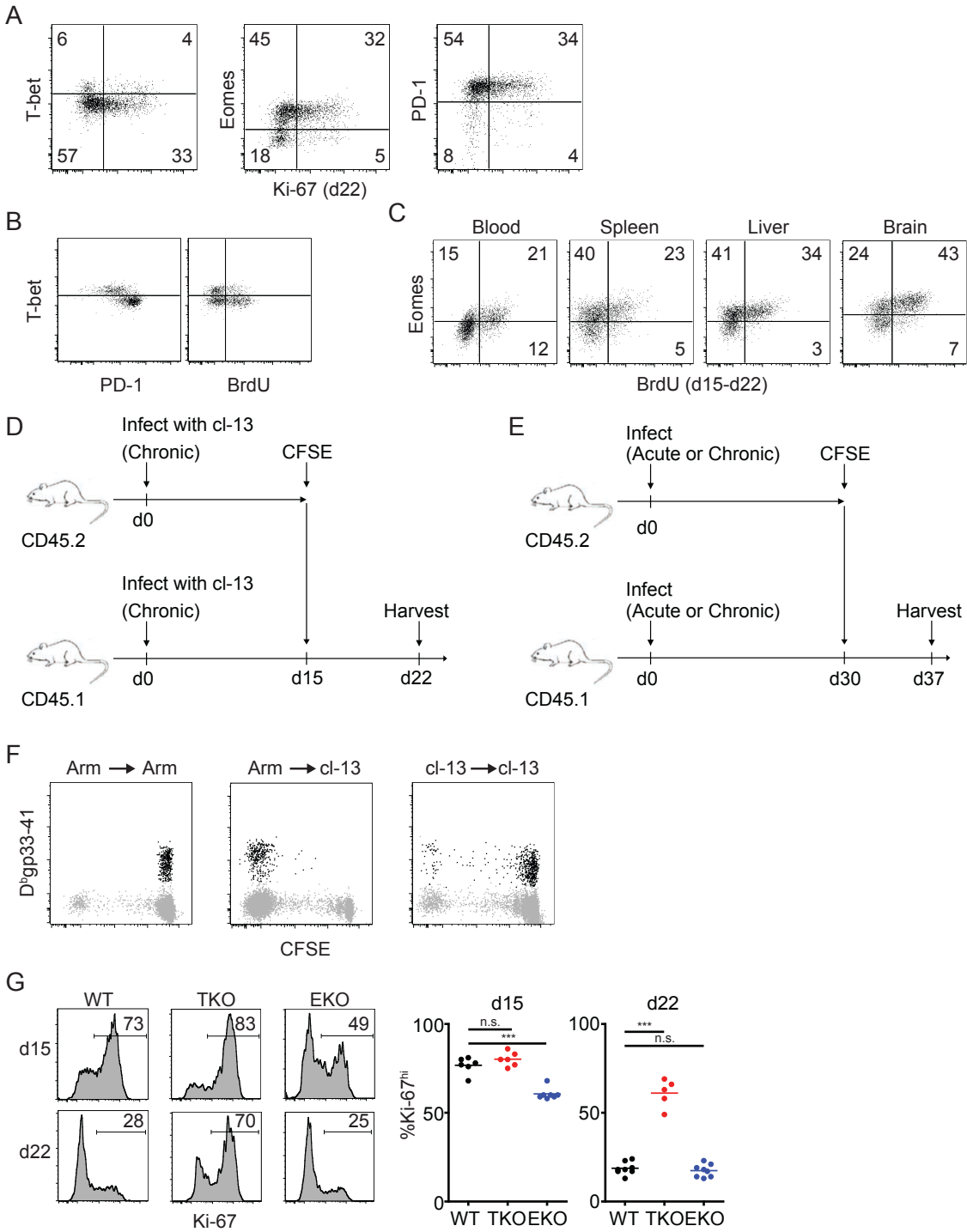


Figure S5

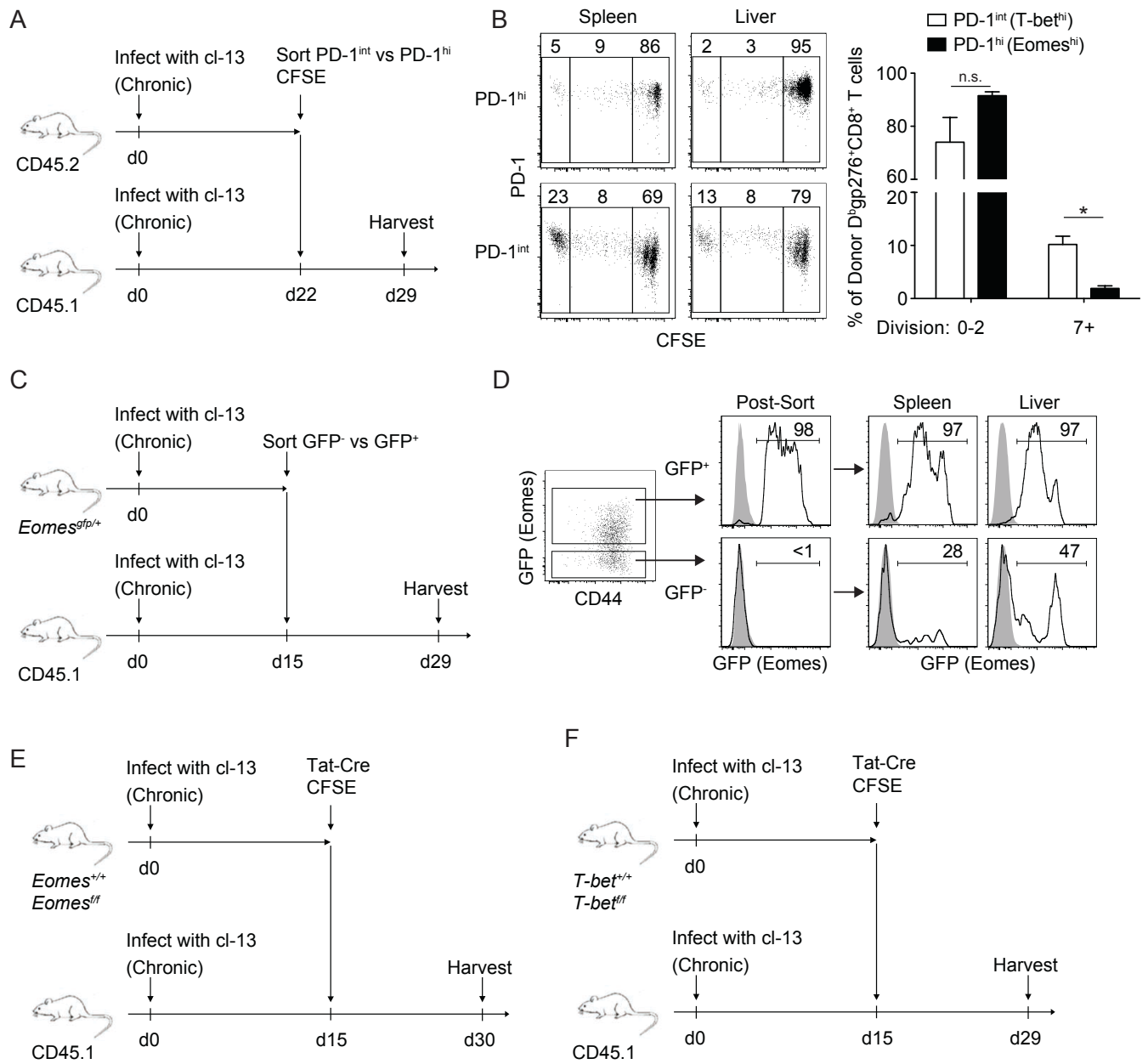




Figure S6

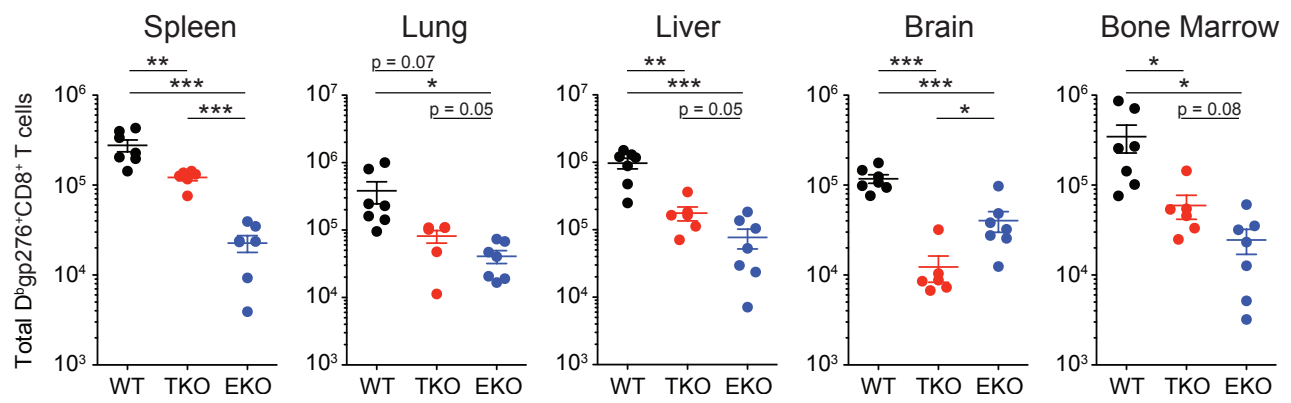


Figure S7

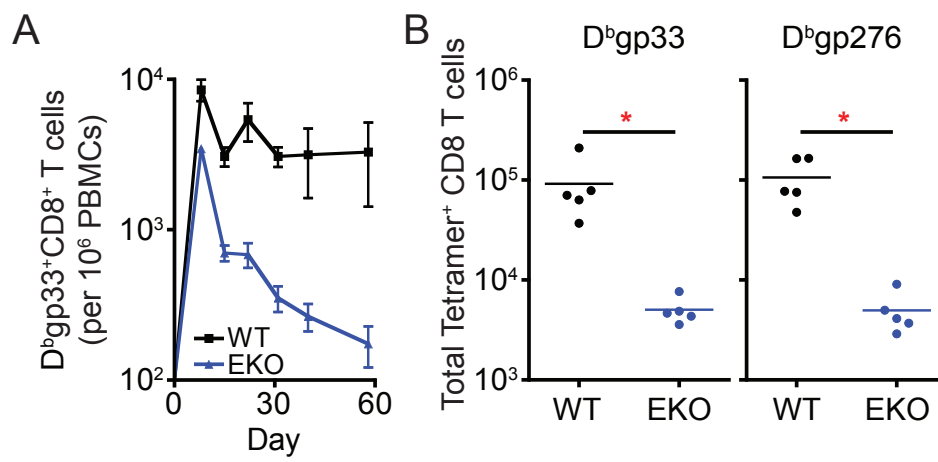


Figure S8

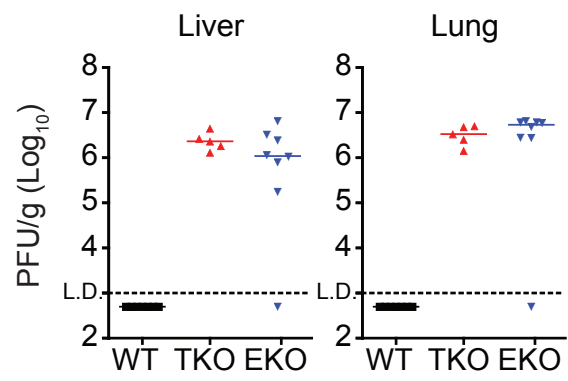


Figure S9

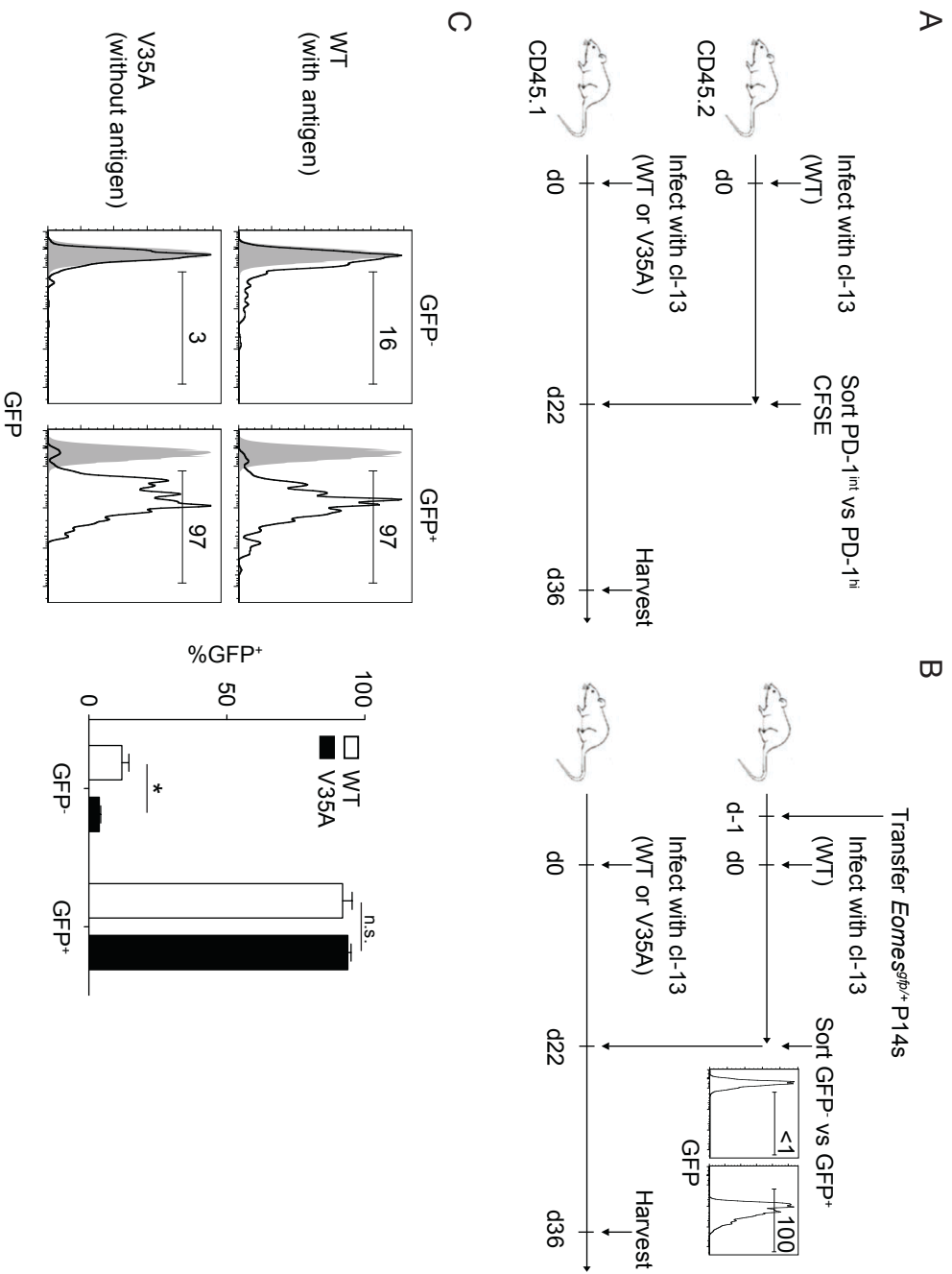


Figure S10

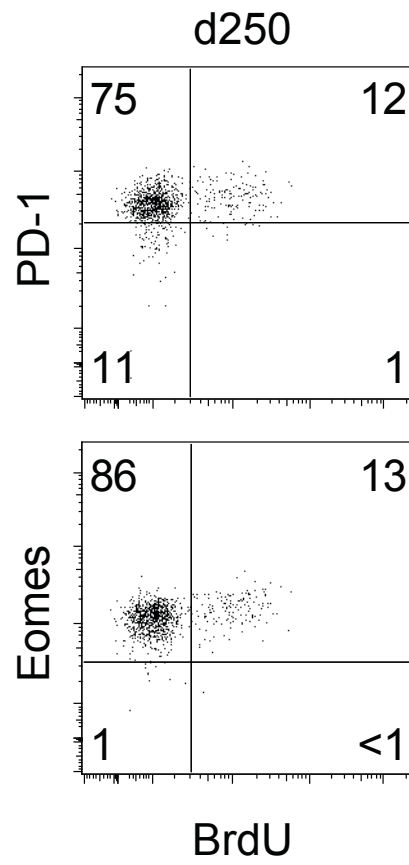
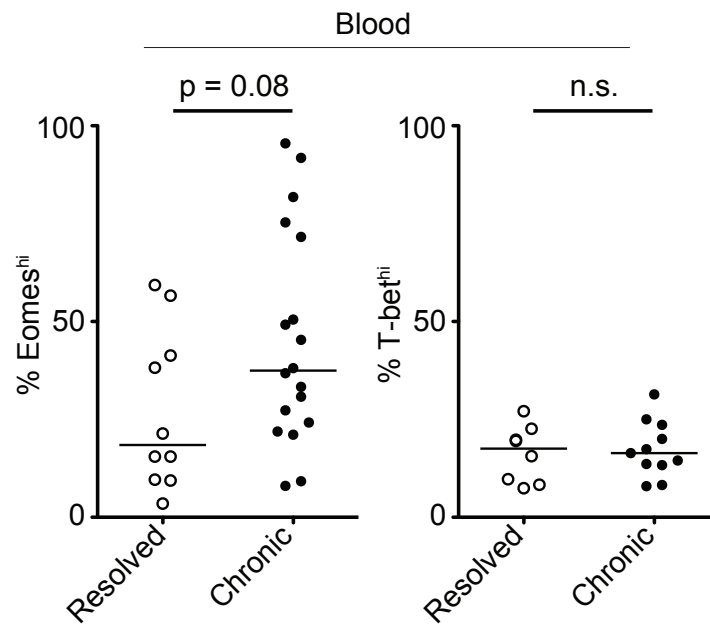


Figure S11



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