

# Supporting Information

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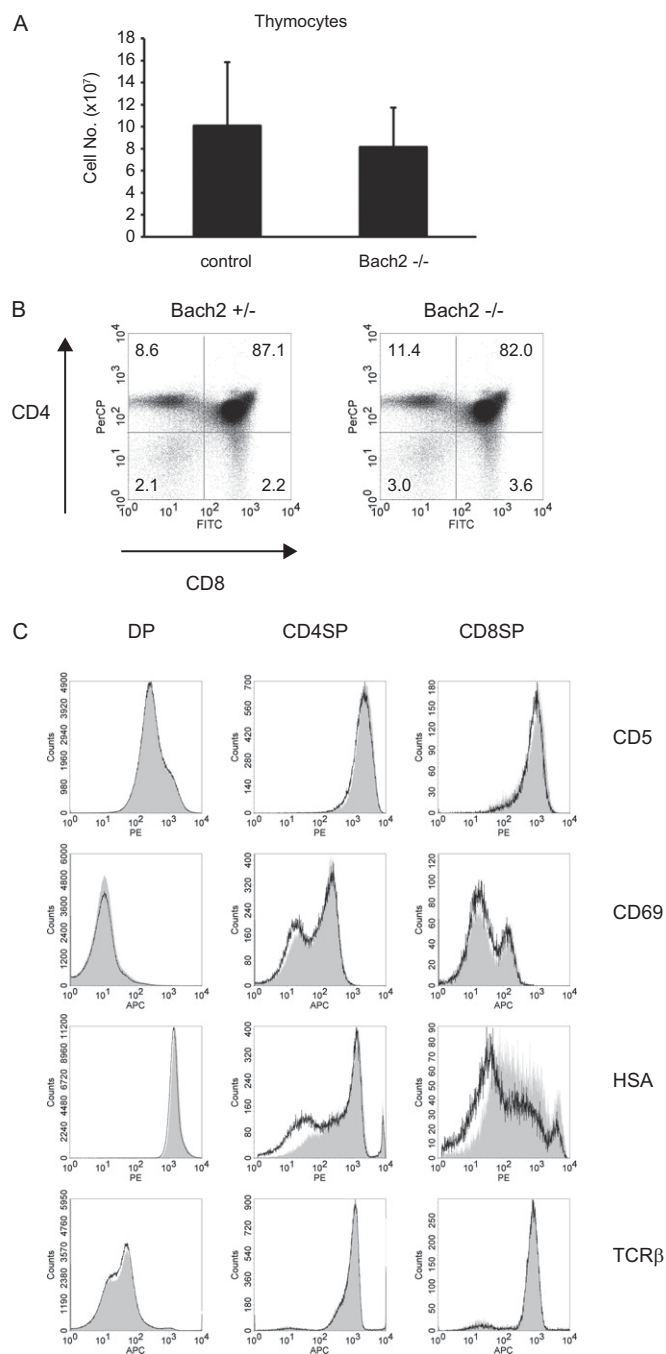
## SI Materials and Methods

**In Vitro Treg Assay.** CD4<sup>+</sup>CD45RB<sup>lo</sup>CD25<sup>+</sup> cells were sorted by FACS Aria and used as regulatory T cells (Treg). CD4<sup>+</sup>CD45RB<sup>hi</sup>CD25<sup>-</sup> cells were sorted and labeled with 5,6-carboxyfluorescein diacetate succinimidyl ester (CFSE) and used as conventional T cells (Tconv). Tconv cells ( $2.5 \times 10^4$  cells per well) were mixed with Treg cells at ratios indicated in Fig. S2F, and stimulated with  $6.3 \times 10^4$  per well of Dynabeads mouse T-Activator CD3/CD28 (Invitrogen) in a 96-well round bottom plate. After 3 d of culture, the cells were analyzed by

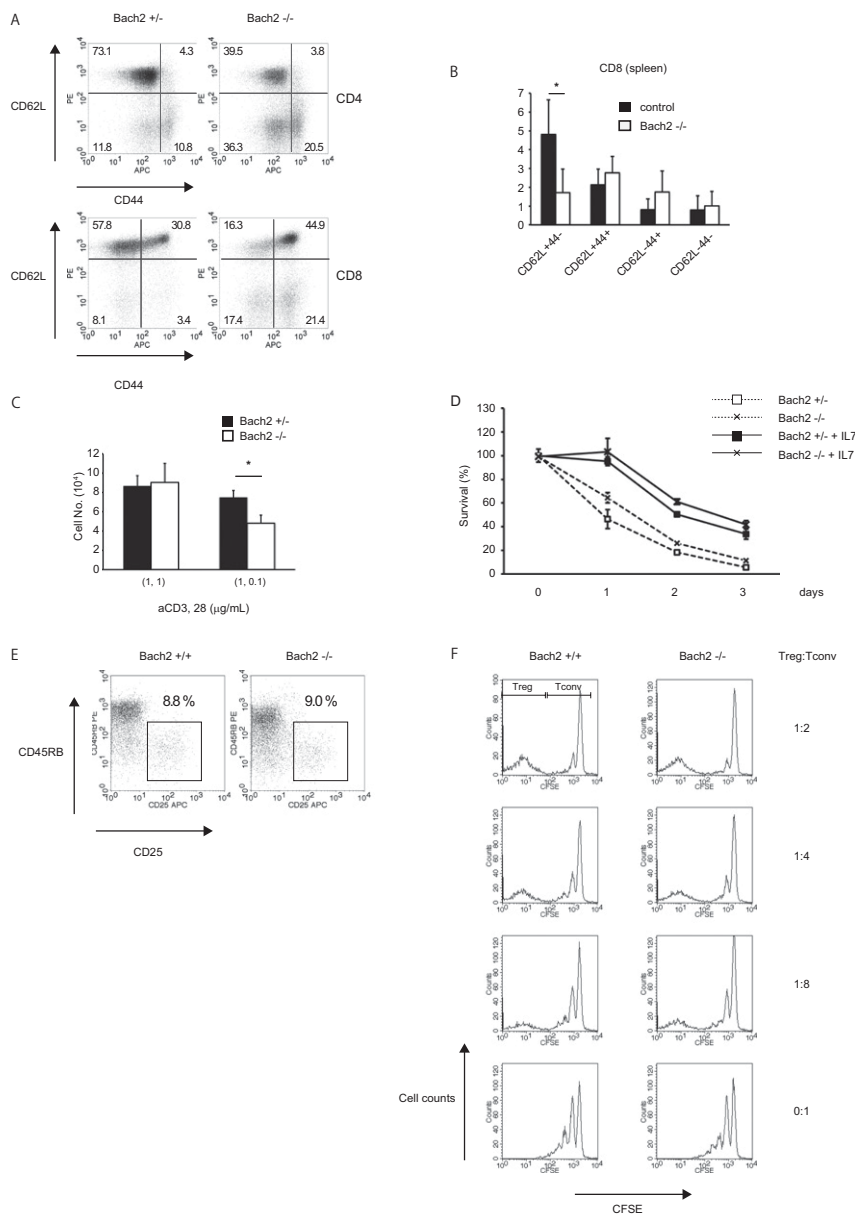
flow cytometer, and the proliferation was assessed by CFSE dilution.

**Colitis Model.** Colitis was induced in Rag1<sup>-/-</sup> mice by i.p. injection of  $5 \times 10^5$  of CD4<sup>+</sup>CD45RB<sup>hi</sup>CD25<sup>-</sup> T cells. Mice were monitored for weight loss and were killed after 9 wk. For histological analysis, frozen large intestine sections were stained with hematoxylin and eosin.

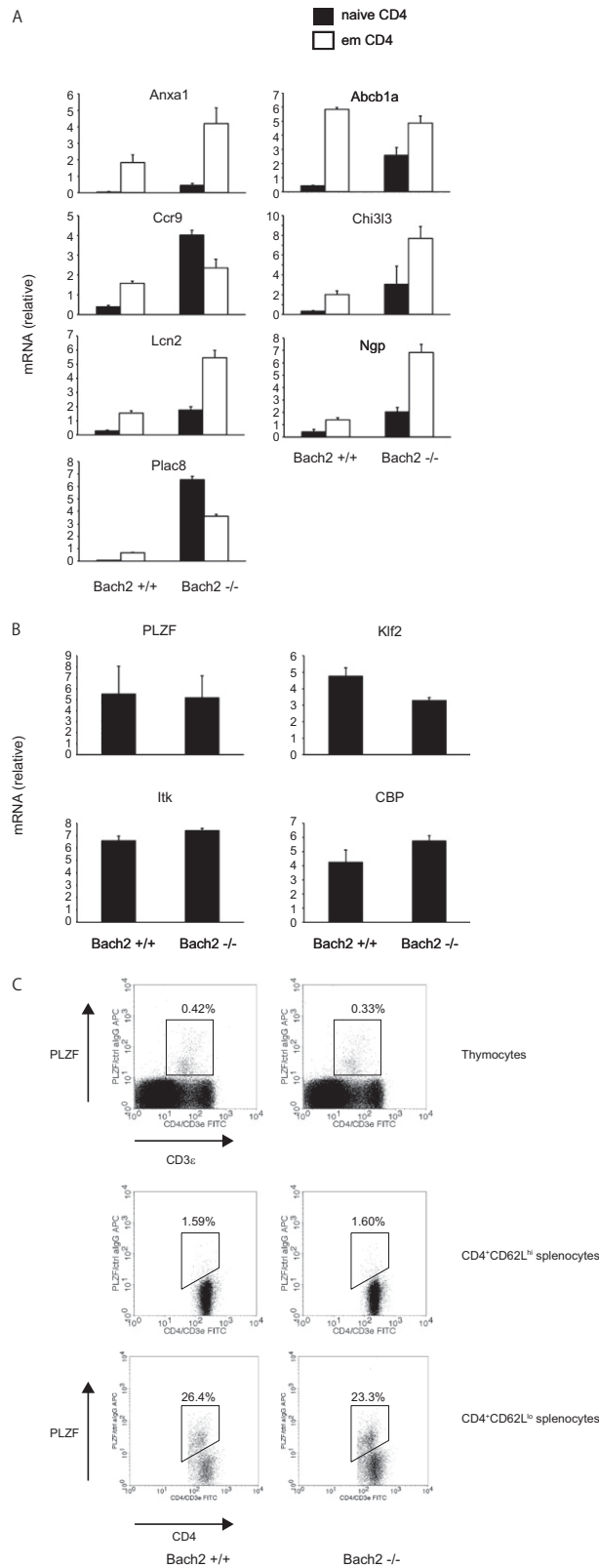
**Listeria monocytogenes Infection.** Control or Bach2 flox/flox  $\times$  lck-cre mice were infected with  $1.5 \times 10^4$  of *L. monocytogenes* (EGD strain) intraperitoneally. Mice were analyzed 7 d after infection.



**Fig. S1.** Thymocyte differentiation in *Bach2*<sup>-/-</sup> mice. (A) Cell numbers of thymocytes (mean  $\pm$  SD,  $n = 7$ ). (B) Thymocyte subpopulations by the CD4/CD8 expression in *Bach2*<sup>-/-</sup> mice. (C) Expression of differentiation markers in each thymocyte subpopulation. The open and filled gray histograms show *Bach2*<sup>-/-</sup> and <sup>+/-</sup> cells, respectively. APC, allophycocyanin; CD4SP, CD4 single positive; DP, double positive; HSA, heat stable antigen; PE, phycoerythrin; perCP, peridinin chlorophyll protein.

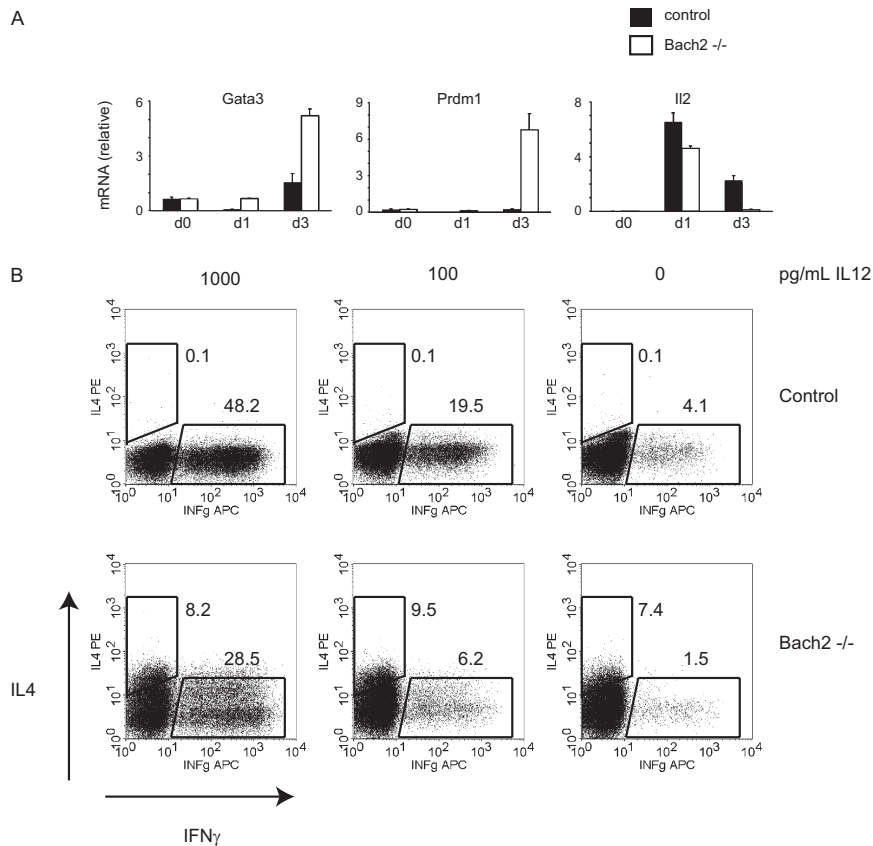


**Fig. S2.** Effects of Bach2 deficiency on mature peripheral T cells. (A and B) Naive and memory T cells in the spleen of Bach2<sup>+/+</sup> and <sup>-/-</sup> mice. FACS profiles (A) and the cellularity of each population (B) are shown. (C) Proliferation of peripheral T cells after TCR stimulation in vitro. Naive CD4 T cells were stimulated with the indicated amount of the plate-coated anti-CD3/CD28 Abs. (D) Survival capacities of Bach2<sup>+/+</sup> and Bach2<sup>-/-</sup> naive CD4 T cells. Cells were cultured in the presence or absence of IL7 without TCR stimulation. Cell numbers were shown as the percentages to those at day 0. (E) No difference was observed in the percentage of regulatory T cells (CD45RB<sup>lo</sup>CD25<sup>+</sup>, Treg) in CD4<sup>+</sup> splenocytes. Control or Bach2<sup>-/-</sup> splenocytes were stained with anti-CD4, CD45RB, and CD25 antibodies. The cells were analyzed by flow cytometer. The figure shows the expression of CD45RB and CD25 in CD4<sup>+</sup>-gated cells. The numbers in the panels indicate the percentages of Treg. (F) In vitro Treg assay did not show significant difference in suppressive activity of control and Bach2<sup>-/-</sup> Treg. Control or Bach2<sup>-/-</sup> Treg cells were sorted and mixed with CFSE-labeled wild-type conventional naive CD4<sup>+</sup> cells at the indicated ratios. The cells were stimulated with anti-CD3/28 beads for 3 d, and the proliferation of the cells was assessed by the dilution of CFSE. Data are expressed as mean  $\pm$  SD,  $n = 3$ , \* $P < 0.05$  in A–D.

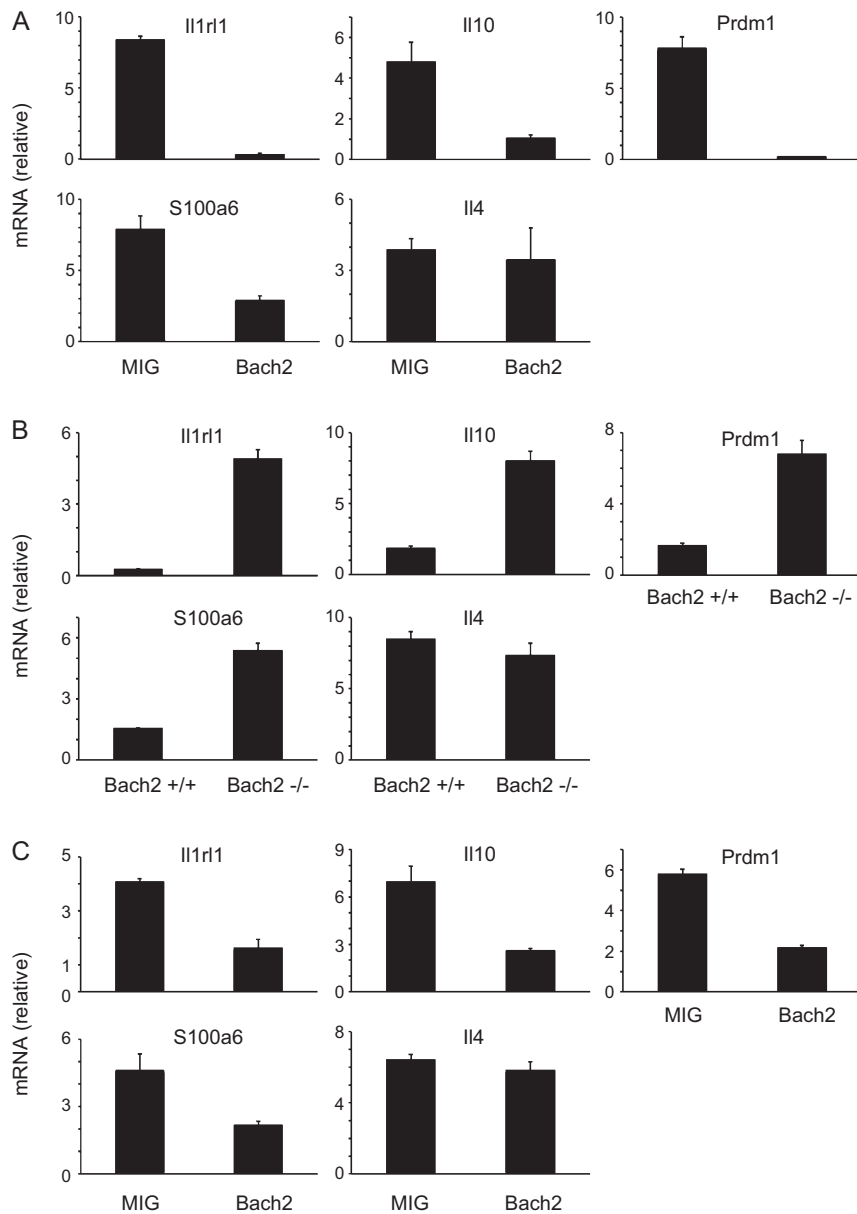


**Fig. S3.** Bach2 suppresses effector memory-related genes in naive T cells. (A) Altered gene expression profiles by Bach2 deficiency. mRNA expression of the genes other than the ones in Fig. 2 that are shown to be up-regulated in Bach2-deficient unstimulated and stimulated naive CD4 T cells in the microarray were examined by quantitative RT-PCR (qPCR) for naive and effector-memory CD4 T cells. (B) No alteration of the expressions of promyelocytic leukemia zinc finger protein (PLZF), IL2-inducible T-cell kinase (Itk), kruppel-like factor 2 (Klf2), and cAMP response element binding protein-binding protein (CBP) by Bach2 deficiency in T cells. The expressions of each gene in naive CD4 T cells were assessed by qPCR. (C) No significant difference was observed in PLZF protein expression of T-cell populations. Indicated T-cell populations were permeabilized and stained with anti-PLZF antibody and then analyzed by flow cytometer. The numbers in each panel are the percentages of PLZF<sup>+</sup> cells in each population. Data are expressed as mean  $\pm$  SD,  $n = 3$  in A and B. Abcb1a, ATP-binding cassette, sub-  
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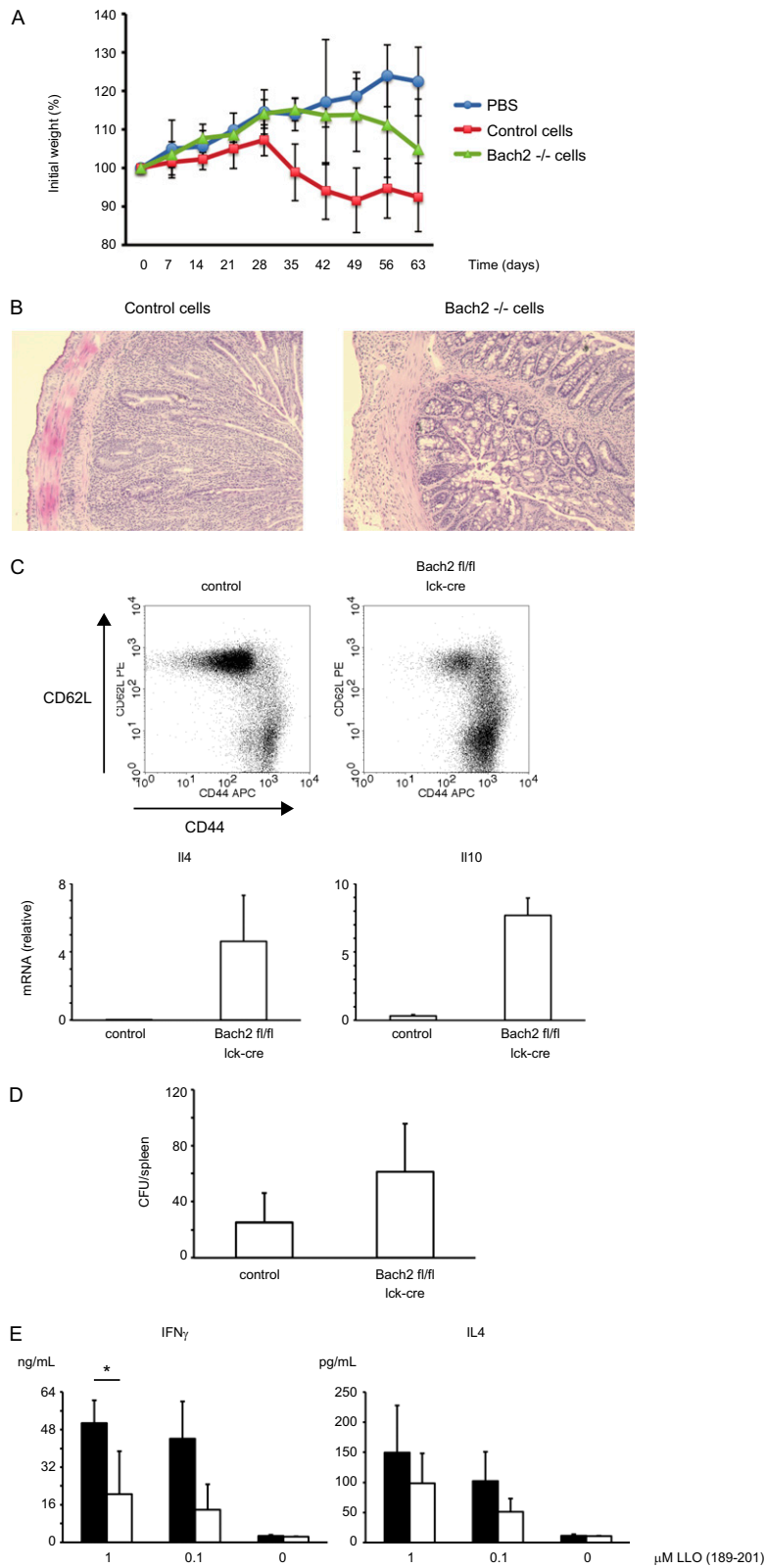
family B (MDR/TAP), member 1A; algG, anti-IgG Ab; Anxa1, annexin A1; Ccr9, CC chemokine receptor 9; Chi313, chitinase 3-like 3; em, effector-memory; Lcn2, lipocalin 2; Ngp, neutrophilic granule protein; Plac8, placenta-specific 8.



**Fig. 54.** Bach2-deficiency promotes Th2 differentiation. (A) Up-regulation of Th2-related genes GATA binding protein 3 (Gata3) and PR domain zinc finger protein 1 (Prdm1) in Bach2<sup>-/-</sup> CD4 T cells in addition to the ones in Fig. 6A whereas IL2 expression was decreased at day 3. mRNA expression of naive CD4 T cells was analyzed at day 0, 1, and 3 after stimulation with anti-CD3 and CD28 Abs. Data are expressed as mean  $\pm$  SD,  $n = 3$ . (B) Th differentiation of Bach2<sup>-/-</sup> CD4 T cells in the presence of IL-12. CD4 naive T cells were stimulated with anti-CD4 and CD28 Abs with or without graded amounts of IL-12. After 5 d, the cells were restimulated with phorbol-12-myristate-13-acetate (PMA) plus ionomycin in the presence of brefeldin A for 4 h. The intracellular IFN $\gamma$  and IL-4 were stained and analyzed by flow cytometer.

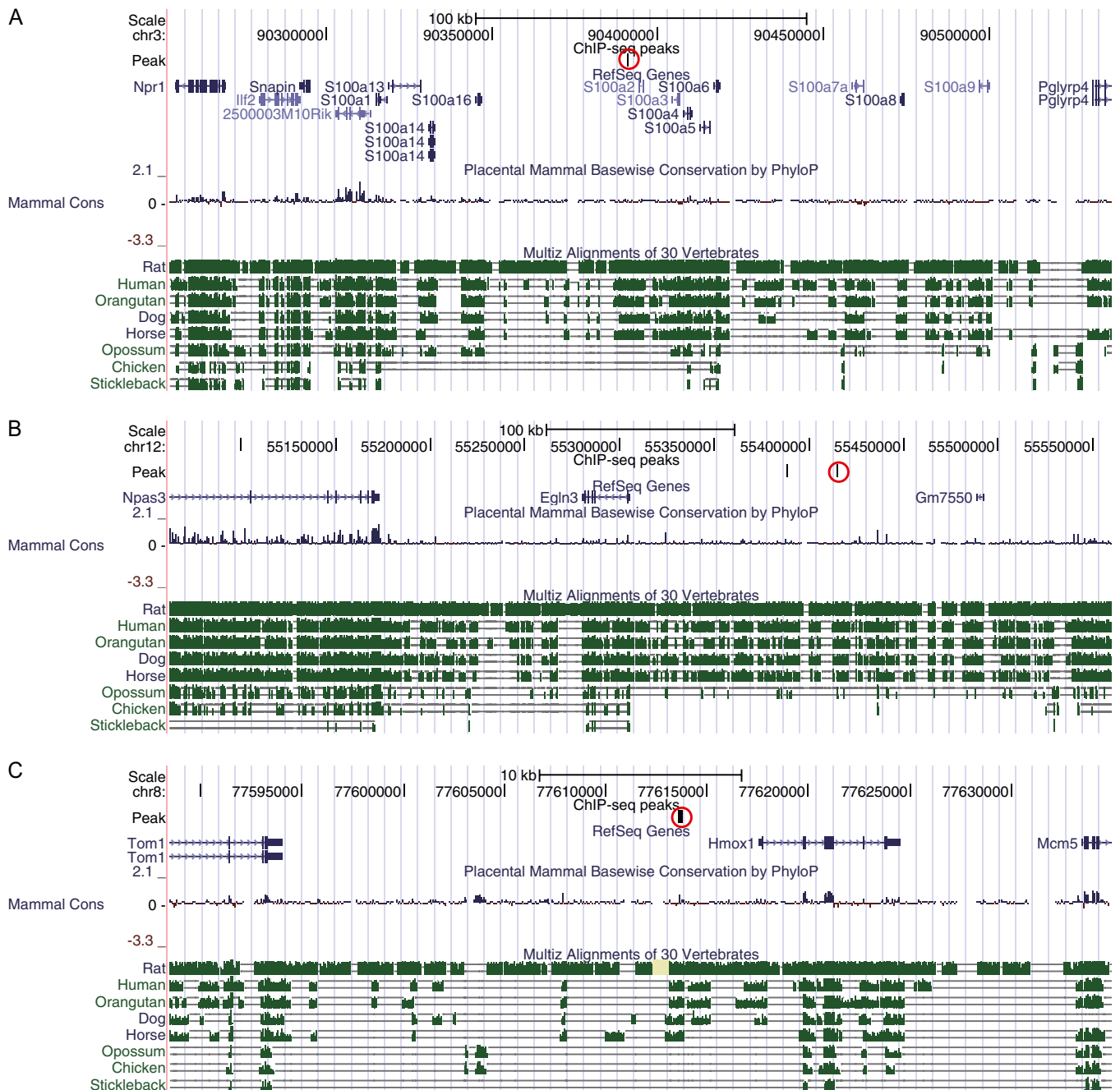


**Fig. S5.** Suppression of genes expression that are up-regulated in  $Bach2^{-/-}$  T cells by Bach2 overexpression. (A)  $Bach2^{-/-}$  naive CD4 T cells were stimulated and transduced by retrovirus-mediated transfection of Bach2 or control vector (MIG). On day 3 after transfection, mRNA was purified from and assessed by qPCR for each gene. (B) Control and  $Bach2^{-/-}$  naive CD4<sup>+</sup> T cells were stimulated at the same condition of A and B, and their mRNA expressions of the indicated genes were analyzed by qPCR. (C) WT effector-memory (CD62L<sup>lo</sup> CD44<sup>hi</sup>) CD4 T cells were stimulated and transduced with Bach2 or control vector (MIG), and mRNA expressions were assessed. Data are expressed as mean  $\pm$  SD,  $n = 3$ . *Il1r1*, interleukin-1 receptor-like 1; *S100a6*, S100 calcium binding protein a6.



**Fig. S6.** The effects of Bach2 deficiency on in vivo immune responses. (A and B) The effects on colitis induced by transfer of naive CD4 T cells. (A) Body weight of Rag1-deficient mice after the transfer of CD4<sup>+</sup>CD25<sup>-</sup>CD45RB<sup>hi</sup> naive T cells. Data are presented relative to initial body weight and as mean ± SD (*n* = 3–7). (B) Hematoxylin and eosin staining of colon sections from Rag1-deficient mice at 9 wk after the cell transfer as in A. (C–E) The effects on *L. monocytogenes* (LM) infection. Control or Bach2 conditional knockout (cKO) mice [Bach2 flox/flox (fl/fl) crossed with lck-cre] were infected with  $1.5 \times 10^4$  LM intraperitoneally. Mice were analyzed 7 d after infection. (C) Bach2 cKO shows similar phenotypes to Bach2<sup>-/-</sup> CD4 T cells. (Upper) CD62L and CD44 expression in CD4<sup>+</sup> cells of control or Bach2fl/fl x lck-cre mice. (Lower) mRNA expression of each gene in control or Bach2 fl/fl x lck-cre naive CD4 T cells at day 3 after TCR stimulation (anti-CD3 and CD28 mAbs). Data are expressed as mean ± SD, *n* = 3. (D) Numbers of viable LM in spleen are shown. CFU, colony forming unit. Data are expressed as mean ± SD. \* indicates statistical significance. Legend continued on following page

SD,  $n = 4-5$ . (E) IFN $\gamma$  and IL4 productions were measured by ELISA after 2 d ex vivo stimulation of total splenocytes with CD4-specific LM antigen (LLO 189–201). Data are expressed as mean  $\pm$  SD,  $n = 3-4$ .



**Fig. S7.** The genomic loci selected by Chromatin Immunoprecipitation (ChIP)-seq for FLAG-Bach2C. Screen shots from the UCSC Genome Browser (University of California, Santa Cruz) with ChIP-seq peaks (red circle) are shown. The scale is indicated in each graph. The peaks around the S100a gene cluster (A), egl nine homolog 3 [EglN3, encoding prolyl hydroxylase 3 (PHD3)] (B), and heme oxygenase 1 [Hmox1, encoding heme oxygenase 1 (HO-1)] (C) are shown. Npr1, natriuretic peptide receptor 1; Snapin, SNAP-associated protein; Pglyrp4, peptidoglycan recognition protein 4; chr, chromosome; Npas3, neuronal PAS domain protein 3; Tom1, target of myb1 homolog; Mcm5, minichromosome maintenance deficient 5.

## Other Supporting Information Files

[Dataset S1 \(XLSX\)](#)

[Dataset S2 \(XSLX\)](#)