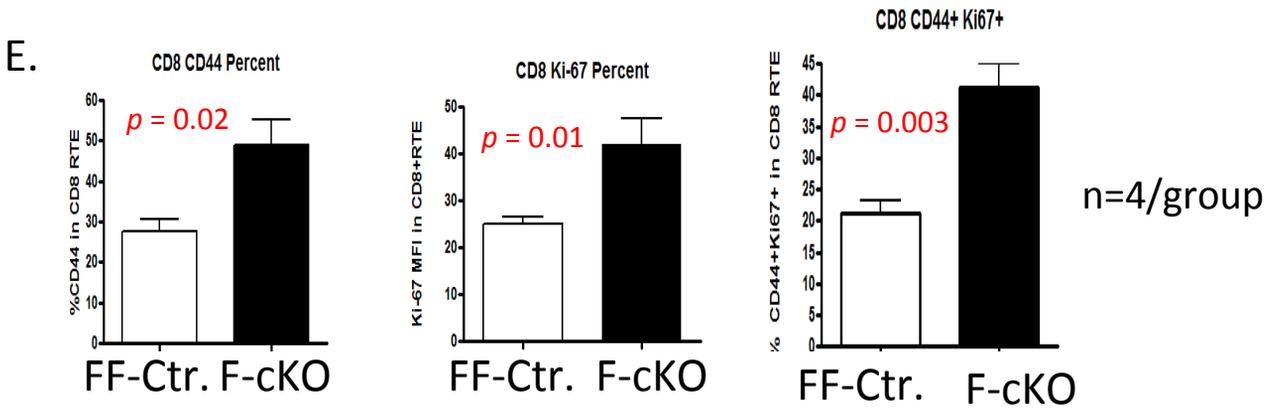
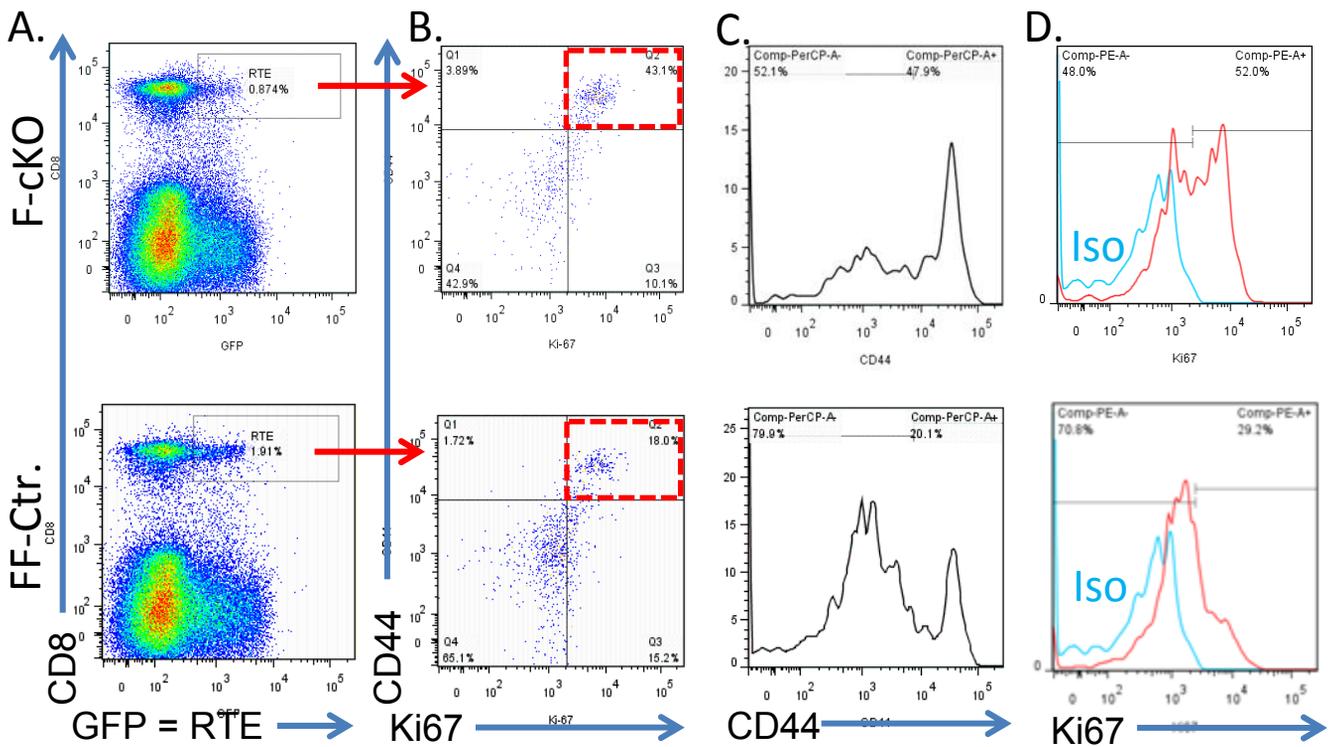


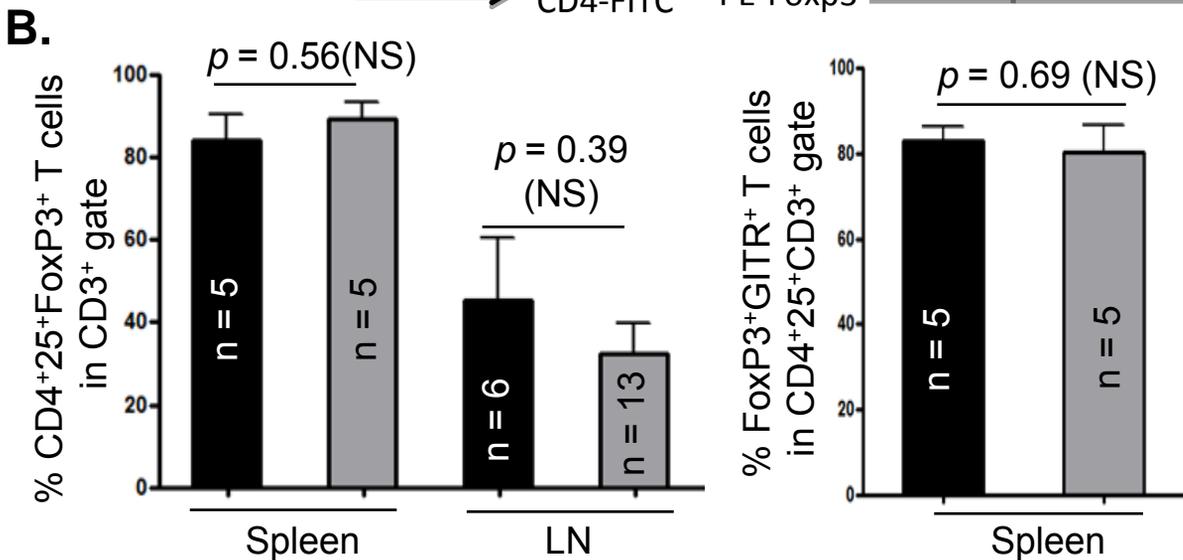
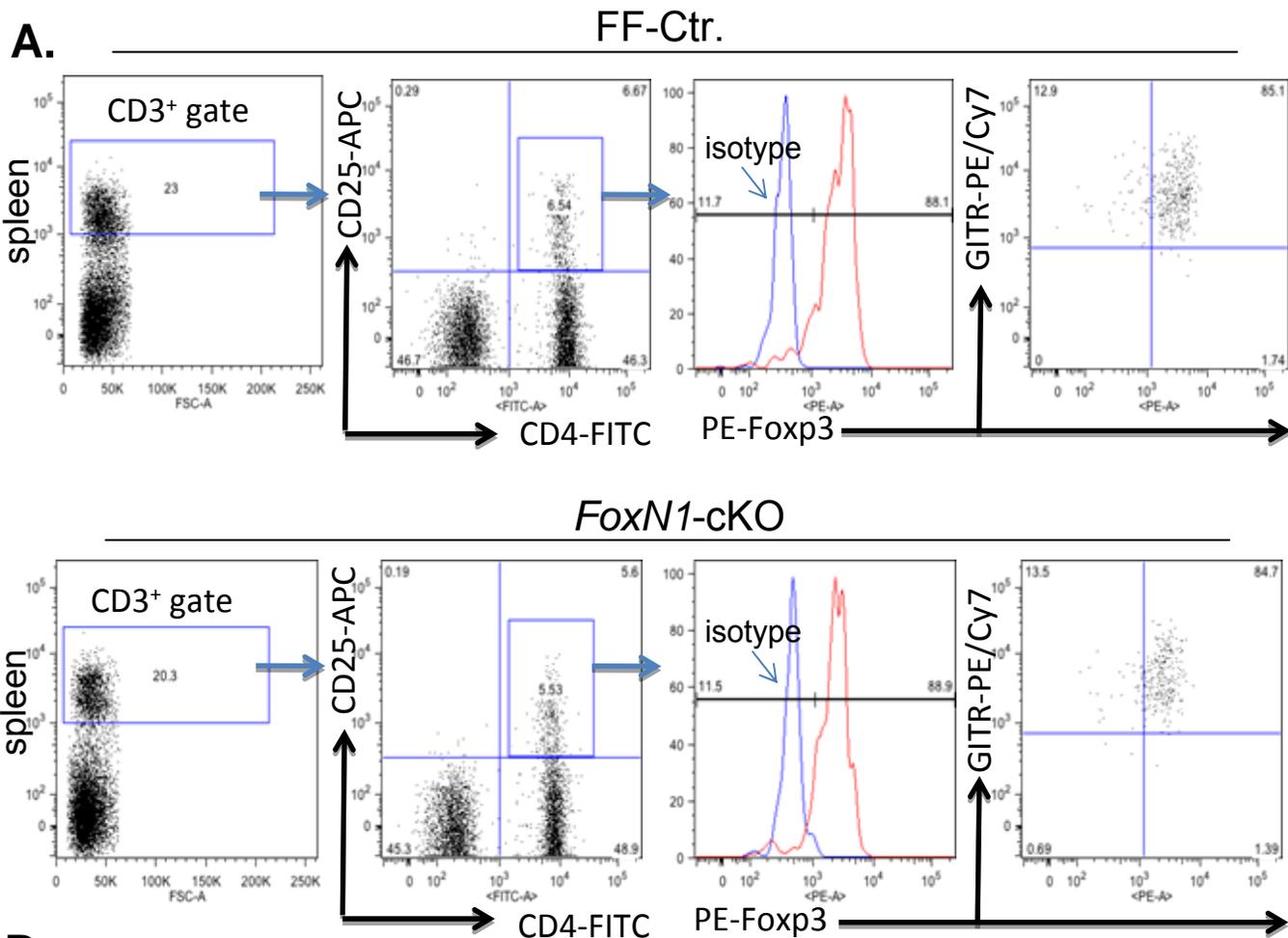
**Supplemental Table S1. List of mouse colonies used in this work**

<b>Colony</b>	<b>Targeted gene and generation</b>	<b>Significance</b>	<b>Jackson Lab #</b>
fx/fx-uCreER <sup>T</sup>	Two loxp tags were inserted into the <i>FoxNI</i> gene as described in previous publication (30) .	Accelerated Thymic involution in a young mouse	#012941 crossed to #004682
fx/fx-only	Same as above but no Cre gene	Use as littermate controls	#012941
RAG-GFP	Green fluorescent protein (GFP) <sup>+</sup> reporter gene is driven by <i>Rag</i> gene	Used to identify T and B cells that have recently undergone RAG recombination; used here as marker of recent thymic emigrants (RTE)	#005688
fx/fx-uCreER <sup>T</sup> or fx/fx-only carrying <i>Rag</i> -GFP	Crossbreeding fx/fx-uCreER <sup>T</sup> with <i>Rag</i> -GFP mice	Tracking of RTEs derived from an involuted thymus	(#012941 crossed to #004682) crossed to #005688
RAG <sup>-/-</sup>	<i>Rag1</i> gene knockout	Used as adoptive transplantation hosts due to without T and B lymphocytes	#002216
RIP-mOVA (Ovalbumi)	Chicken OVA driven by the RAT Insulin Promoter	Aire dependent mOVA expressed in mTEC as mock “self” antigen.	#005431
OT-II	Transgenic Tcr $\alpha$ Tcr $\beta$ recognizing chicken OVA in the context of I-A <sup>b</sup>	TCR transgenic producing CD4 SP thymocytes that binds OVA:MHC complex strongly	#004194
Aire <sup>-/-</sup>	<i>Aire</i> gene knockout	Used as positive controls of autoimmunity	#004743

(All mice have C57BL/6 genetic background)



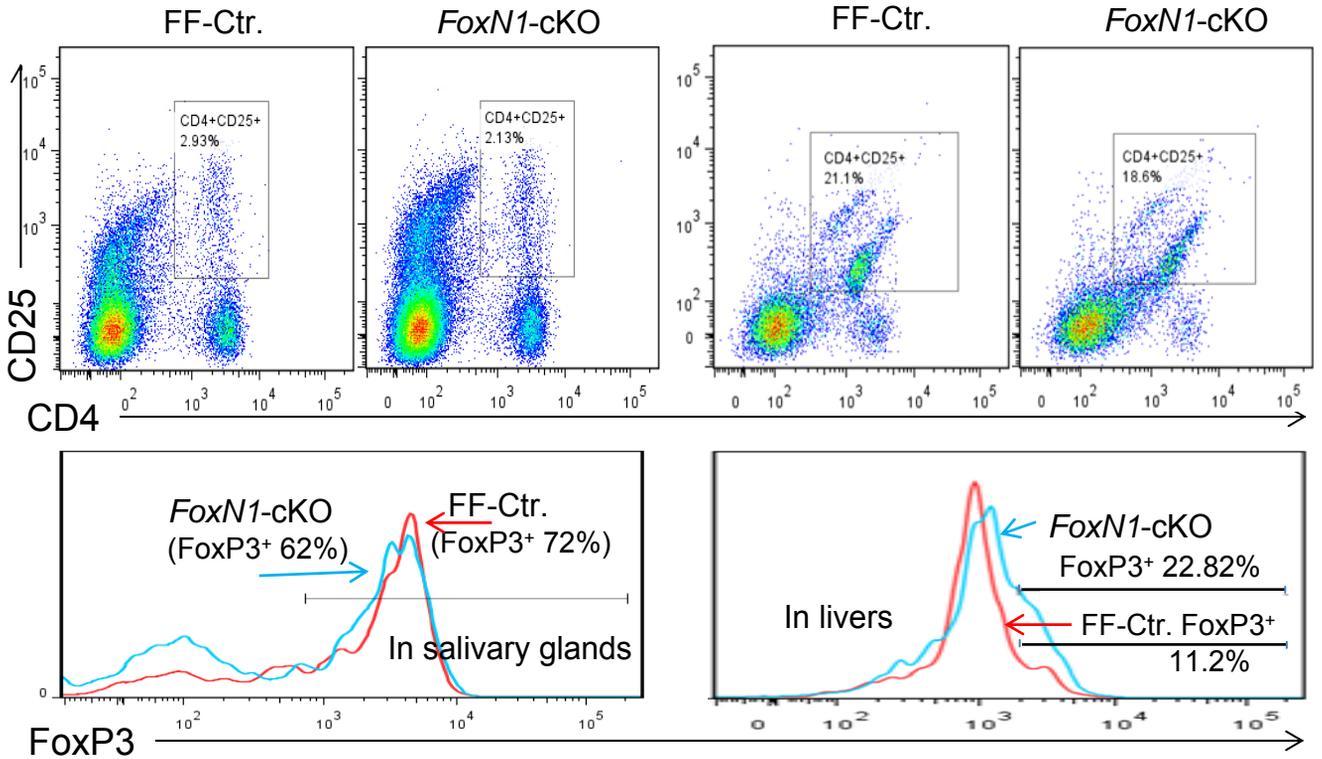
**Supplemental Fig. S1. CD8 Recent Thymic Emigrants from the atrophied thymus acquired an activated immune cell phenotype.** Peripheral spleen cells were freshly isolated from the F-cKO and FF-Ctr mice carrying RAG-GFP reporter. The cells were stained with CD8, CD44, and Ki67 antibodies, and CD8<sup>+</sup>GFP<sup>+</sup> cells were defined as CD8<sup>+</sup> RTEs. **(A)** Representative dot plots show CD8<sup>+</sup>GFP<sup>+</sup> gate; **(B)** CD44<sup>hi</sup>Ki67<sup>+</sup> cell gates (red boxes) in CD4<sup>+</sup> RTEs from *FoxN1* cKO (top panels) and control (bottom panels) mice. **(C)** Representative histograms of CD44<sup>hi</sup>; and **(D)** Ki67<sup>+</sup> in CD8<sup>+</sup> RTEs from *FoxN1* cKO (top panels) and control (bottom panels) mice. **(E)** Summarized results of % CD44<sup>hi</sup>, Ki67<sup>+</sup>, and CD44<sup>hi</sup>Ki67<sup>+</sup> double positive cells in CD8<sup>+</sup> RTEs (from left to right panels). A Student *t*-test was used to determine statistical significance between groups. All data are expressed as mean ± SEM.



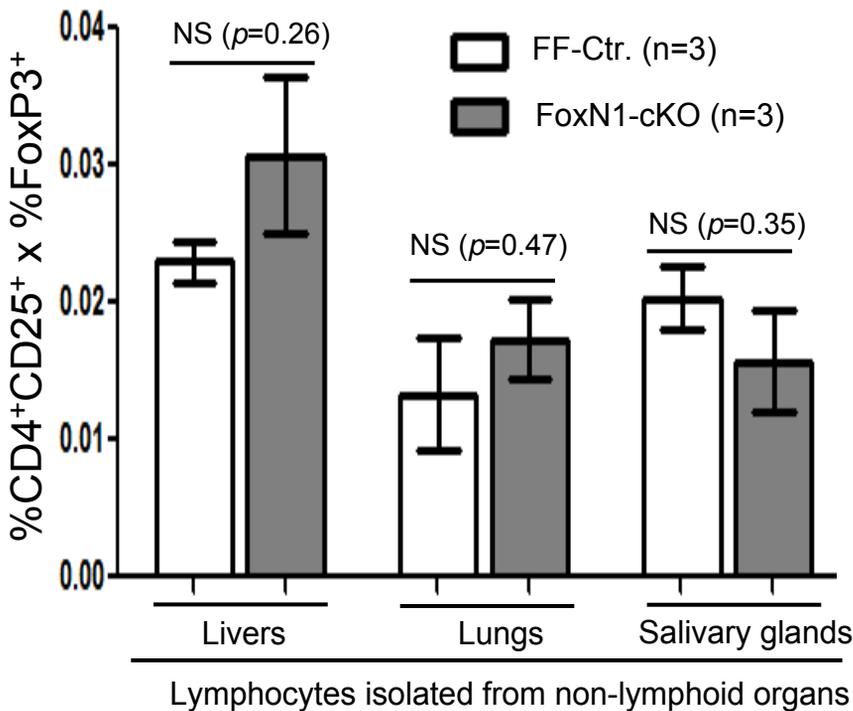
**Supplementary Figure S2. CD4<sup>+</sup> regulatory T cells in the periphery of F-cKO mice were not changed. (A)** Representative flow cytometry plots of spleen cells show gating strategy of Treg cells from spleen of *FoxN1-cKO* and FF-Ctr control mice. **(B)** Summarized results of the % CD4<sup>+</sup>CD25<sup>+</sup>FoxP3<sup>+</sup> (left panel), and % CD4<sup>+</sup>FoxP3<sup>+</sup>GITR<sup>+</sup> (right panel) functional Treg cells in the spleen and lymph nodes (LN) from *FoxN1-cKO* (grey bars) and age-matched FF-Ctr control mice (black bars) mice (n = animal numbers, NS = not significant). A Student *t*-test was used to determine statistical significance between groups. All data are expressed as mean ± SEM.

**A.** Lymphocytes enriched from salivary glands

Lymphocytes enriched from the livers



**B.**



**Supplementary Fig. S3. % of CD4<sup>+</sup> Treg cells in the liver, lung, and salivary glands were not significantly different between FoxN1-cKO and FF-Ctr mice.** (A) Representative flow cytometry results from salivary gland and liver lymphocytes enriched through two-layer density gradient centrifuge, showing CD4<sup>+</sup>CD25<sup>+</sup> and FoxP3<sup>+</sup> gates. (B) Summarized results of % T<sub>reg</sub> cells (CD4<sup>+</sup>CD25<sup>+</sup>FoxP3<sup>+</sup>) in the liver, lung, and salivary gland lymphocytes. (n = animal numbers, NS = not significant). A Student *t*-test was used to determine statistical significance between groups. All data are expressed as mean ± SEM.