

Expanded View Figures

Figure EV1. Loss of Tet1 and Tet3 does not impair stable programs in naturally occurring Tregs.

- A Representative flow plots and quantification of FoxP3 expression in cell proliferation dye-labeled Treg cells FACS sorted from *Tet1/2/3^{fl/fl}* and *Rorc(t)^{CreTg} Tet1/2/3^{fl/fl}* mice. Cells were sorted based on CD25 expression. Cells were activated *in vitro* for 72 h with anti-CD3/CD28 in the presence of 200 U/ml hIL-2 ($n = 3$ or 2 Figure Legends). Male mice were used in both experiments. Experiment was replicated two times.
- B Representative flow plots and quantification of CD25 expression in cell proliferation dye-labeled Treg cells FACS sorted from *Tet1/2/3^{fl/fl}*; and *Rorc(t)^{CreTg} Tet1/2/3^{fl/fl}* mice. Cells were activated as in (A). Experiment was replicated two times.
- C ICOS MFI quantification on *in vitro* activated Tregs at 48 h ($n = 3$ biological replicates). Data are mean $\pm$ SEM, unpaired two-tailed t-test. Experiment was replicated three times.
- D Representative flow plots depicting CFSE dilution upon proliferation of titrated CD4⁺ T effectors in the presence of 30 K control or *Rorc(t)^{CreTg} Tet1/3^{fl/fl}* Tregs, 3-day postactivation. Experiment was replicated three times.
- E Weight curve of control *Tet1/3^{fl/fl}* ($n = 14$ biological replicates) and *Rorc(t)^{CreTg} Tet1/3^{fl/fl}* ($n = 9$ biological replicates) female littermates treated with 1.5% DSS in drinking water for 7 days. Data are a summary of two independent experiments and are mean $\pm$ SEM, two-way ANOVA with Bonferroni's multiple comparison test.
- F Length of the small intestine at day 15 post-DSS treatment ($n = 5$ or 7 biological replicates). Data are mean $\pm$ SEM, unpaired Mann–Whitney t-test.
- G Length of the colon as in (F).
- H Weight curve of female Rag^{-/-} mice after T cell transfer colitis induced via transfer of naïve WT CD45.1 conventional CD4⁺ T cells alone ($n = 4$ recipient mice) or in combination with Tregs isolated from *Tet1/3^{fl/fl}* ($n = 5$ recipient mice) and *Rorc(t)^{CreTg} Tet1/3^{fl/fl}* littermates ($n = 4$ recipient mice). A ratio of 8:1 Teff: Treg cells was transferred. * $P < 0.05$, two-way ANOVA with Geisser–Greenhouse correction.
- I Cytokine analysis by flow cytometry of CD45.1 CD4⁺ effector cells isolated from the mLN of Rag^{-/-} mice 7-weeks post-T cell transfer-induced colitis. Cells were stimulated with PMA/Ionomycin for 5 h in the presence of Brefeldin + Monensin A and pre-gated on Live CD45.1⁺TCR β ⁺CD4⁺ cells for analysis. Data are mean $\pm$ SEM ($n = 7$ or 5 biological replicates), two-way ANOVA with Tukey's multiple comparison test. Experiment was replicated two times.
- J Quantification of CTLA4 and CD25 MFI among Control CD45.2 *Tet1/3^{fl/fl}* ($n = 5$ biological replicates) and CD45.2 *Rorc(t)^{CreTg} Tet1/3^{fl/fl}* ($n = 4$ biological replicates) Tregs in the mLN 7-week post-T cell transfer-induced colitis. Data are mean $\pm$ SEM, two-way ANOVA with Sidak's multiple comparison test.
- K Histopathological scoring of colon inflammation in Rag^{-/-} mice 7-week post-T cell transfer-induced colitis ($n = 4$ or 5 biological replicates). Data are mean $\pm$ SEM, Kruskal–Wallis test with Dunn's correction.
- L Representative H&E staining of the colon of Rag^{-/-} mice 7-week post-T cell transfer-induced colitis. Colon inflammation was evidenced by cellular infiltrates (arrows) in the lamina propria. Scale bar = 55 μ m.
- M MFI of intracellular Granzyme B and IL-10 in FACS-sorted CD25⁺ natural Tregs activated for 48 h in the presence of 50 U IL-2. Brefeldin + Monensin A were added 6 h prior to staining. Data are mean $\pm$ SEM ($n = 3$ biological replicates), two-way ANOVA with uncorrected Fisher's test. Experiment was replicated three times.

Data information: ns = not significant, $P > 0.05$, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Source data are available online for this figure.

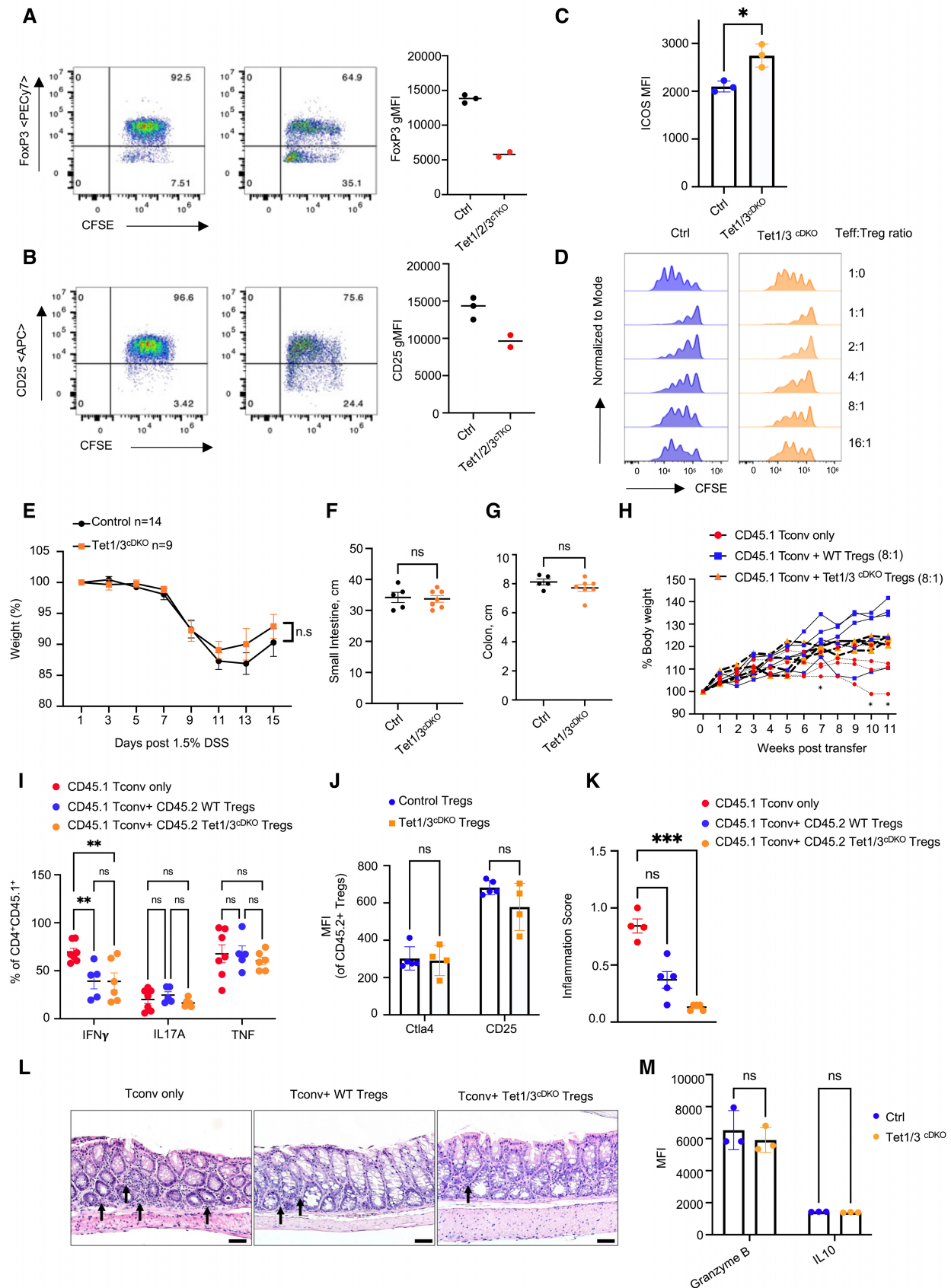


Figure EV1.

Figure EV2. Tet1 and 3 are required prior to lineage commitment of Treg cells from CD4⁺ T lymphocytes.

- A Quantification of CD24 MFI expression on DP, recently selected CD4⁺ TCRβ^{hi} CD24^{hi} CD69⁺ and mature CD4⁺ TCRβ^{hi} CD24^{lo} CD69⁺ thymocytes ($n = 12$ or 10 biological replicates). Data are shown as mean $\pm$ SEM, ANOVA test with Sidak's multiple comparison test and is a summary of two experimental replicates.
- B Representative flow plots and quantification of % dead cells among TCRβ^{hi} thymocytes measured by FLICA/Ghost dye or Annexin V/PI staining ($n = 3$ biological replicates/genotype). Data are shown as mean $\pm$ SEM, two-way ANOVA test with Sidak's multiple comparison test. Experiment was replicated two times.
- C Quantification of CD25⁺ FoxP3^{lo}, CD25⁺ FoxP3⁺, and CD25⁺ FoxP3⁺ cells among Live CD4⁺ T cells thymocytes of control *Tet1*^{fl/fl} ($n = 3$ biological replicates) and *Rorc*(t)^{CreTg} *Tet1*^{fl/fl} ($n = 6$ biological replicates) 6-day-old neonates. Data are shown as mean $\pm$ SEM, 2-way ANOVA with Sidak's multiple comparison test. Experiment was replicated two times.
- D Quantification of ICOS MFI expression on FoxP3⁺ T cells from the mesenteric lymph nodes of control *Tet1*^{fl/fl} ($n = 5$ biological replicates) and *Rorc*(t)^{CreTg} *Tet1*^{fl/fl} mice ($n = 5$ biological replicates). Data are mean $\pm$ SEM, unpaired two-tailed *t*-test. Experiment was replicated two times.
- E Quantification of ICOS MFI expression on FoxP3⁺ T cells from the mesenteric lymph nodes of control *Tet3*^{fl/fl} ($n = 5$ biological replicates) and *Rorc*(t)^{CreTg} *Tet3*^{fl/fl} mice ($n = 3$ biological replicates). Data are mean $\pm$ SEM, unpaired two-tailed *t*-test. Experiment was replicated two times.

Data information: ns = not significant, $P > 0.05$, *** $P < 0.001$, **** $P < 0.0001$.

Source data are available online for this figure.

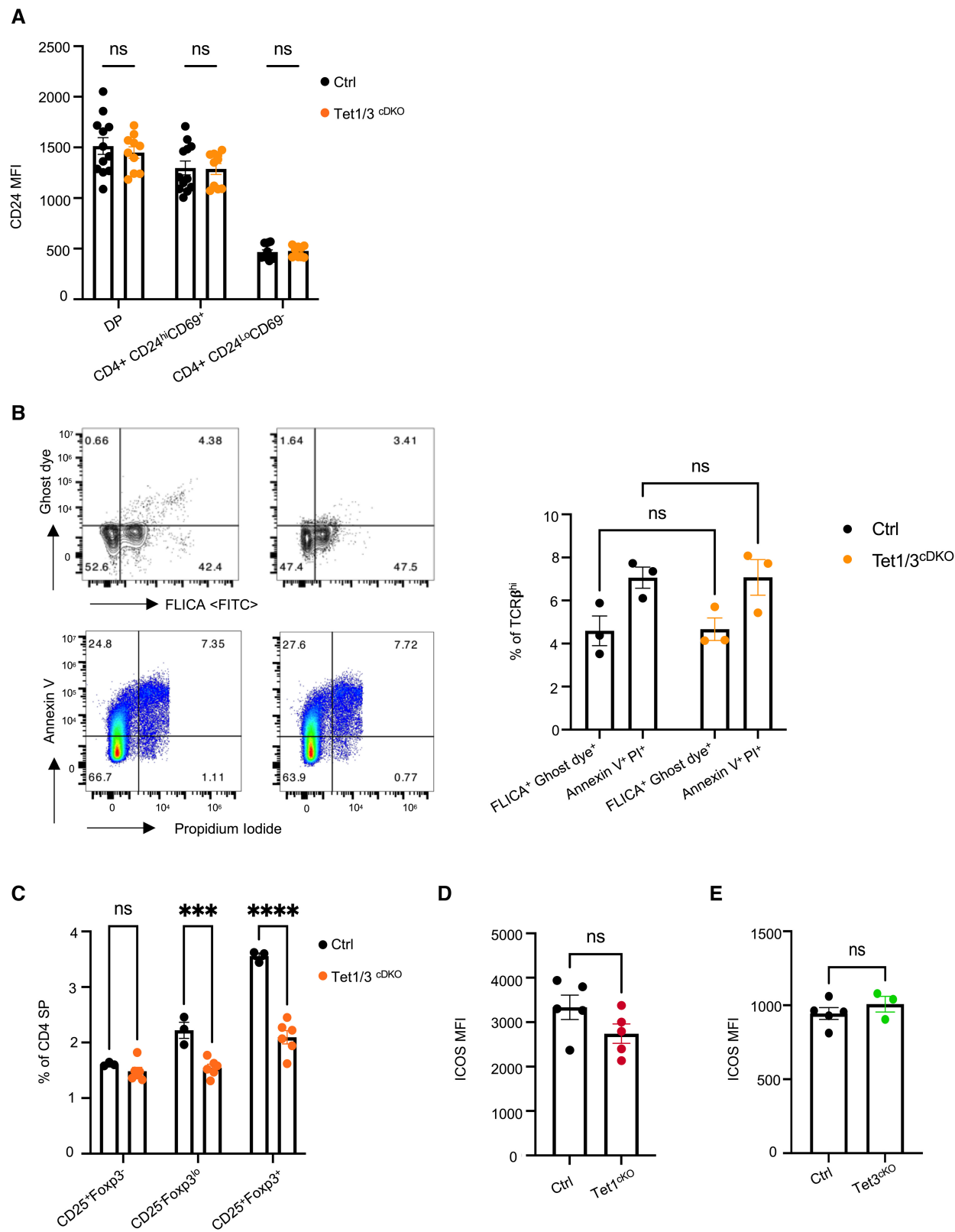


Figure EV2.

Figure EV3. Tet1 and 3 regulate Treg differentiation by modulating TCR signaling and IL-2 production.

- A Quantification of % FoxP3⁺ cells among CD4⁺ T cells, 72-h postactivation with anti-CD3/CD28 and 100 U/ml rhIL-2 and indicated doses of TGF- β ($n = 3$ biological replicates). Data are shown as mean $\pm$ SEM, two-way ANOVA with Bonferroni multiple comparison tests. Experiment was replicated three times.
- B Representative flow plots and quantification of FoxP3 MFI among CD4⁺ T cells described in Fig 4A.
- C FoxP3 MFI on CD4⁺ T cells activated as described in Fig 4A. Experiment was replicated three times.
- D Representative flow plot and quantification of YFP⁺FoxP3⁺ cells 72-h postactivation of sorted YFP⁻ naïve CD4⁺ T cells activated with anti-CD3/CD28 and 20 ng/ml TGF- β in the absence exogenous rhIL-2 ($n = 5$ biological replicates). Data are a summary of two independent experiments and shown as mean $\pm$ SEM, unpaired two-tailed t -test.
- E Quantification and representative flow plots of % Live cells across each division in CFSE-labeled CD4⁺ T cells 72-h postactivation with anti-CD3/CD28 in the absence of exogenous IL-2 and in the presence or absence of 20 ng/ml TGF- β ($n = 2$ or 3 biological replicates). Two-way ANOVA with Bonferroni multiple comparison test. Experiment was replicated at least three times.
- F Representative flow plot and quantification of FoxP3⁺ cells (bottom) 72-h postactivation with anti-CD3/CD28 (i) in the absence of TGF and IL-2 (ii) 20 ng/ml TGF- β and no exogenous IL-2 (iii) 20 ng/ml TGF- β and 10 μ g/ml of anti-mIL-2 blocking antibody and (iv) 20 ng/ml TGF- β , 10 μ g/ml of anti-mIL-2 blocking antibody and 100 U rhIL-2 ($n = 2$ or 3 biological replicates). Data are shown as means $\pm$ SEM, ANOVA test with Bonferroni multiple comparison tests. Experiment was replicated three times.

Data information: ns = not significant, ** $P < 0.01$, **** $P < 0.0001$.

Source data are available online for this figure.

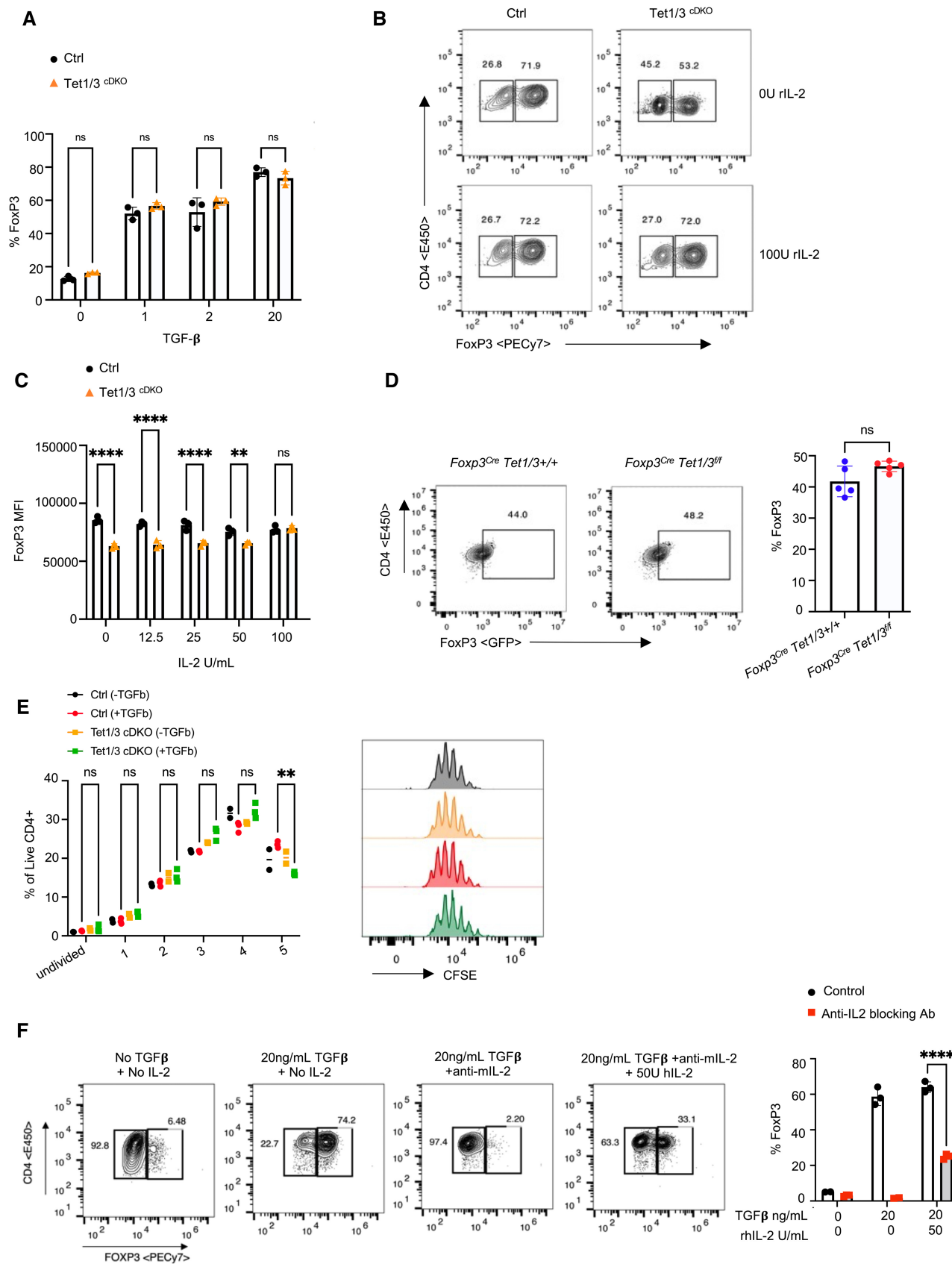


Figure EV3.

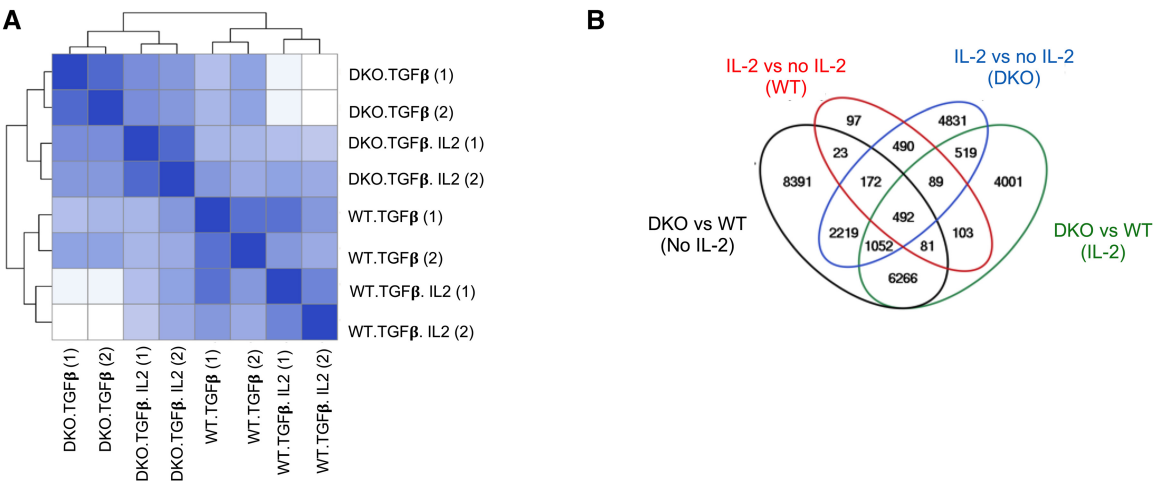


Figure EV4. Tet1 and 3-dependent IL-2 secretion shapes the early chromatin landscape of differentiating Tregs.

A Pearson correlations between accessibility profiles with a dendrogram showing the similarity between samples via hierarchical clustering. For each sample, the accessibility profile is the vector of log2-transformed normalized counts in peaks. DKO = *Rorc(t)^{CreTg} Tet1/3^{fl/fl}*.

B Venn diagram depicting common differentially accessible peaks among four comparisons: *Rorc(t)^{CreTg} Tet1/3^{fl/fl}* versus WT CD4⁺ T cells with no IL-2 treatment (DKO vs. WT (no IL-2)), IL-2-treated versus untreated WT CD4⁺ T cells (IL-2 vs. no IL-2 (WT)), IL-2-treated versus untreated *Rorc(t)^{CreTg} Tet1/3^{fl/fl}* CD4⁺ T cells (IL-2 vs. no IL-2 (DKO)), and *Rorc(t)^{CreTg} Tet1/3^{fl/fl}* versus WT CD4⁺ T cells with IL-2 treatment (DKO vs. WT (IL-2)).