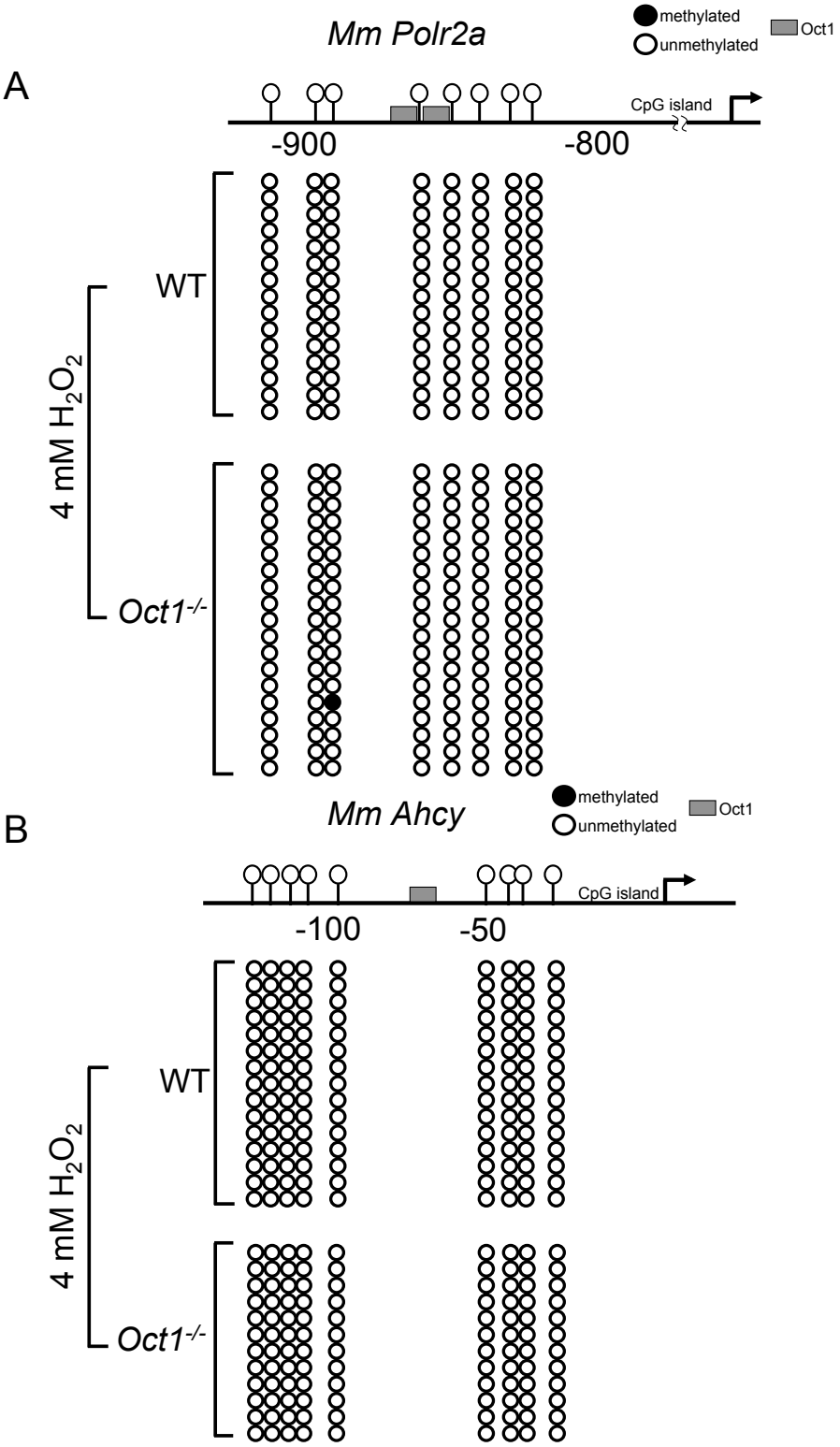
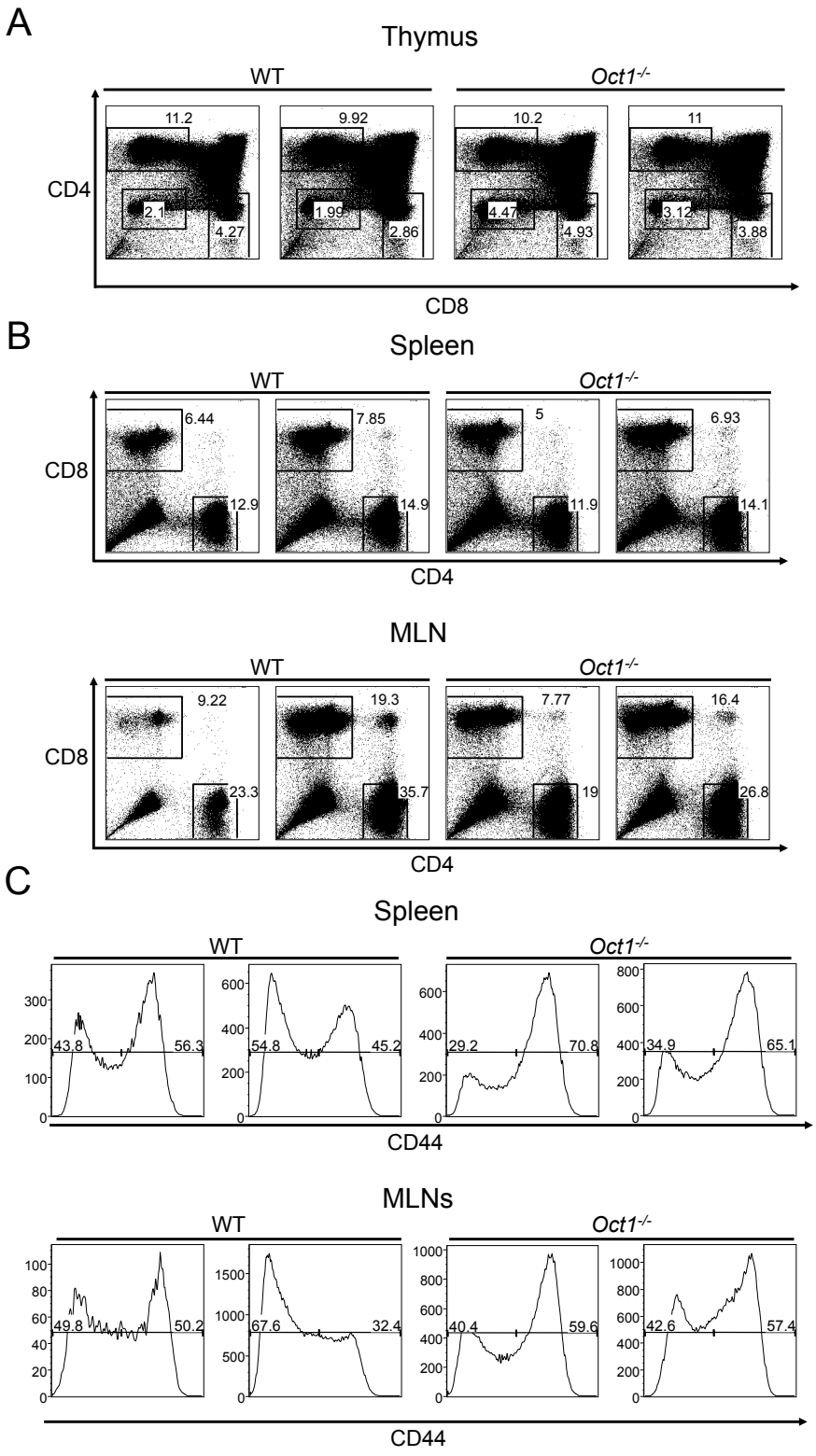


Fig. S1. (A) Bisulfite sequencing of the *Polr2a* regulatory region encompassing the Oct1 binding site in wild-type and Oct1 deficient MEFs exposed to 4 mM H_2O_2 for 1 hr , and then incubated without H_2O_2 for an additional 3 hr. METHODS: *Polr2a* forward primer: GGGAAAAGTTTGGGTTT GAATAT. *Polr2a* reverse primer: CAACTAAAATCTCTCATTAATATCCCC. (B) Similar experiment using murine *Ahcy*. Sequences *Ahcy* primers were: *Ahcy* forward, TGGTTTTTGGTGGTGTGTGGAT; *Ahcy* reverse, AAAACAAA AATCAACCTTACTC.


A
Thymus
WT
Oct1-/-
11.2
9.92
10.2
11
CD4
2.1
4.27
1.99
2.86
4.47
4.93
3.12
3.88
CD8
B
Spleen
WT
Oct1-/-
6.44
7.85
5
6.93
CD8
12.9
14.9
11.9
14.1
CD4
MLN
WT
Oct1-/-
9.22
19.3
7.77
16.4
CD8
23.3
35.7
19
26.8
CD4
C
Spleen
WT
Oct1-/-
43.8
56.3
54.8
45.2
29.2
70.8
34.9
65.1
CD44
MLNs
WT
Oct1-/-
49.8
50.2
67.6
32.4
40.4
59.6
42.6
57.4
CD44

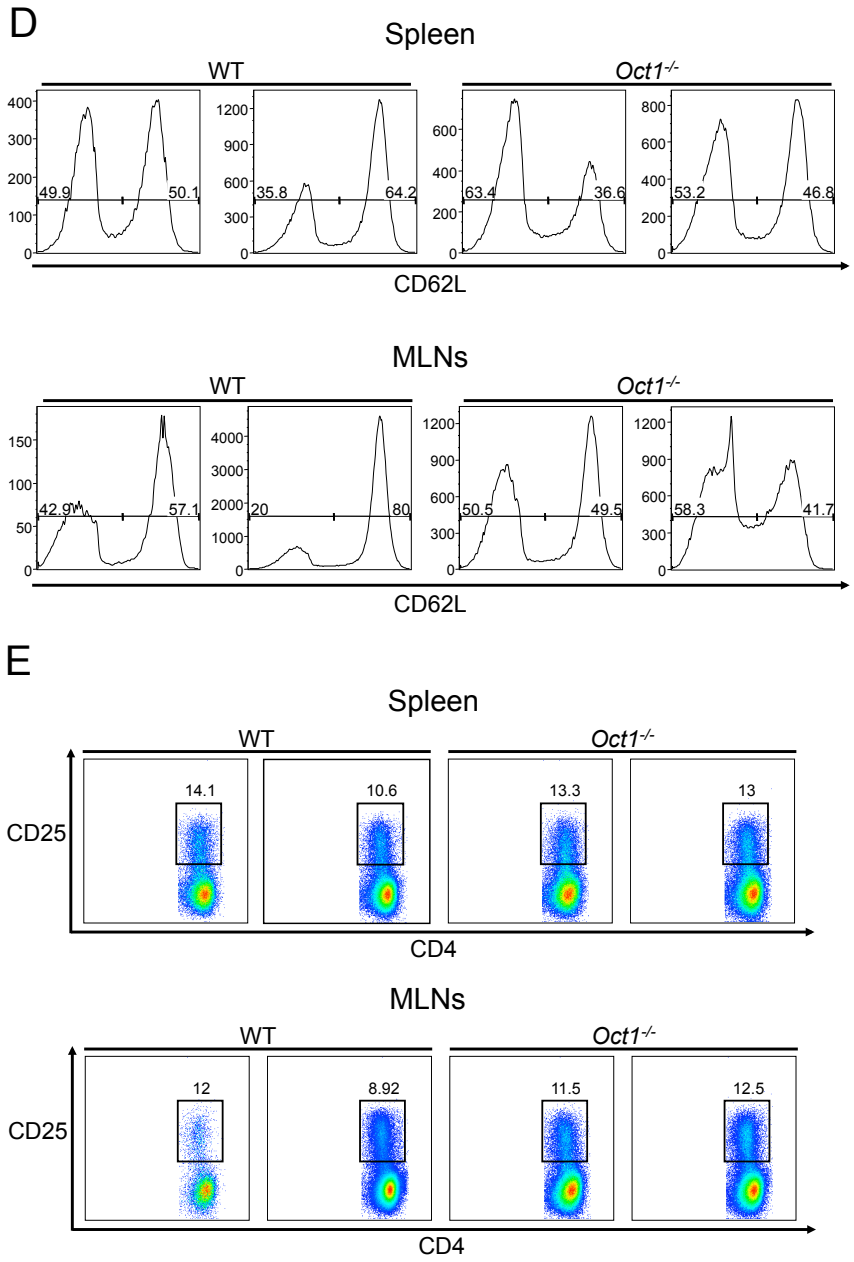


Fig. S2. T cell development and T cell subset distributions in Oct1 deficient transplant *Rag-1*$^{-/-}$ recipient animals. Four separate animals are shown, two transplanted with *Oct1*$^{-/-}$ fetal liver and two with wild-type littermate controls. (A) CD4/CD8 subsets in the thymus in transplant recipient mice are shown. (B) CD4/CD8 T cell populations in spleens and lymph nodes of recipient mice. MLN: mesenteric lymph nodes. (C) CD4+ T cell activation state. Cells were gated for CD4. (D) CD4+ T memory populations. Cells were gated for CD4. (E) Levels of CD4+ CD25+ subsets. Cells were gated for CD4. METHODS: Data were collected using a FACSCanto II (BD Biosciences) and analyzed with Flowjo software. T cells were stained with anti-CD4 (Alexaflour 700), anti-CD8 (PE-Cy7), anti-CD44 (PerCP), anti-CD62L (APC) and anti-CD25 (FITC) antibodies (eBioscience).

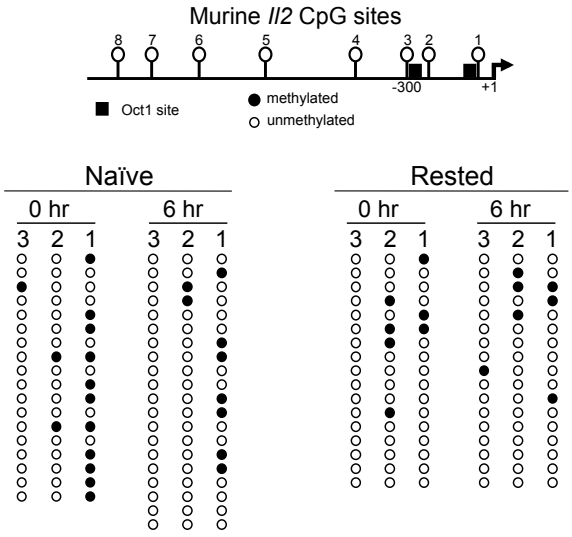


Fig. S3. *Il2* promoter bisulfite sequencing using purified naïve ($CD44^{low}$) helper T cells from spleens of wild-type C57BL/6 mice prior to CD3/CD28 stimulation, or 6 hr following stimulation. The right panel shows cells that were stimulated for two days, followed by an 8 day resting period in culture without stimulation. Cells were then restimulated for 6 hr.

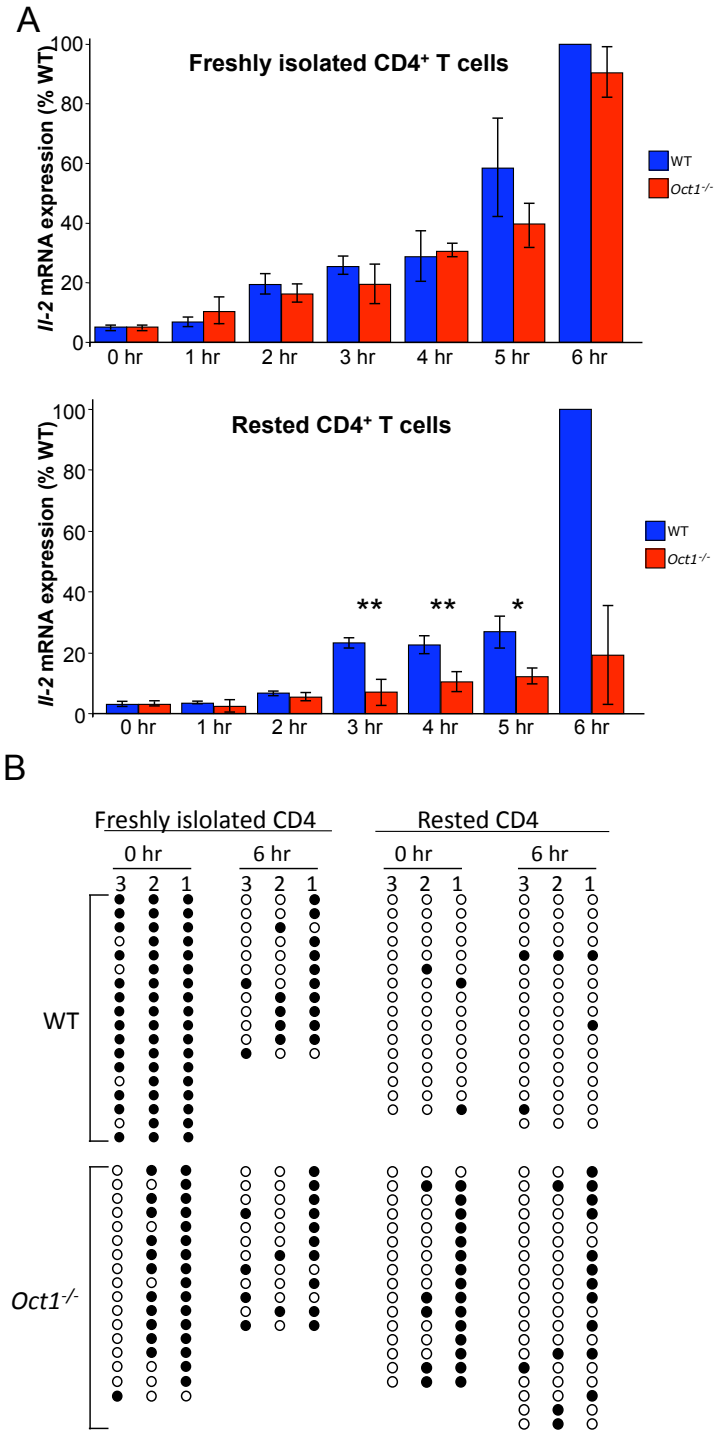


Fig. S4. (A) RT-PCR showing *Il2* mRNA expression in freshly isolated and rested, but previously stimulated, total CD4 splenic T cells following CD3/ CD28 ligation. METHODS: $CD4^+$ T cells were isolated using a MACS column and CD4 microbeads (Miltenyi). A time course is shown in which expression plotted as a percentage of the maximum signal (wild-type T cells, 6 hr). Values represent an average of three biological replicates. Error bars depict s.e.m. The unpaired Student's t test was used to generate *p* values for the data sets (*, $p<0.05$; **, $p<0.01$ and ***, $p<0.001$). (B) *Il2* promoter bisulfite sequencing using total CD4 splenic T cells.