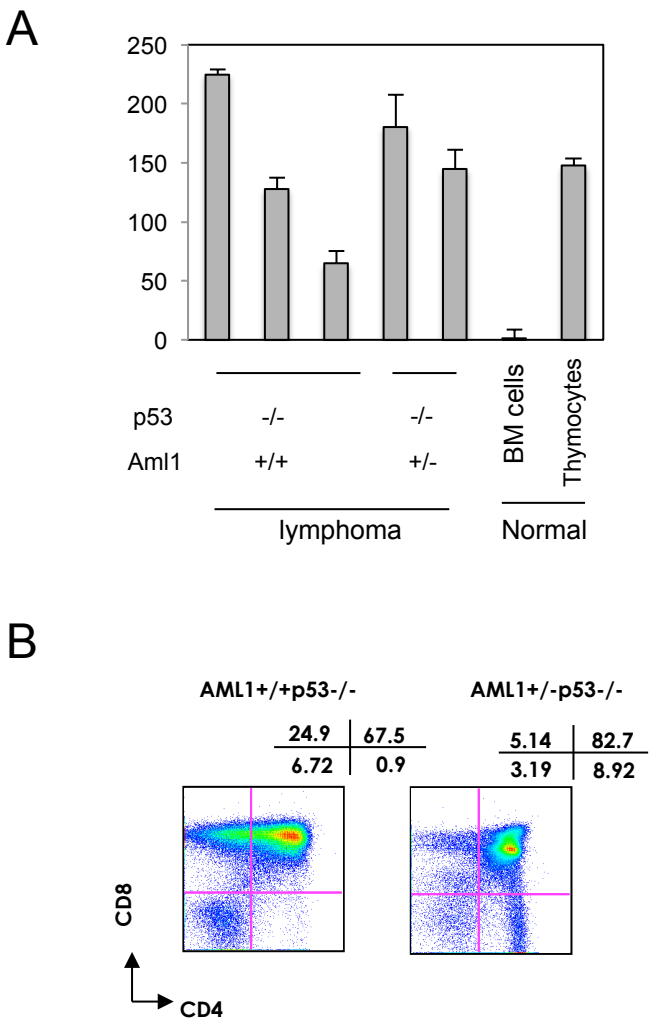
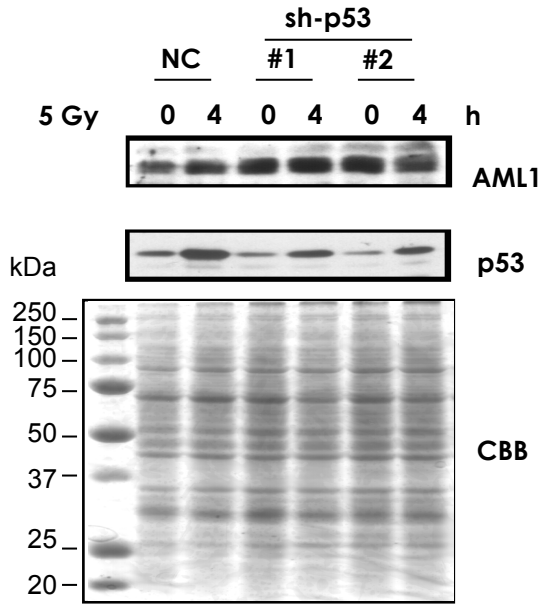
Supplemental Figure S1



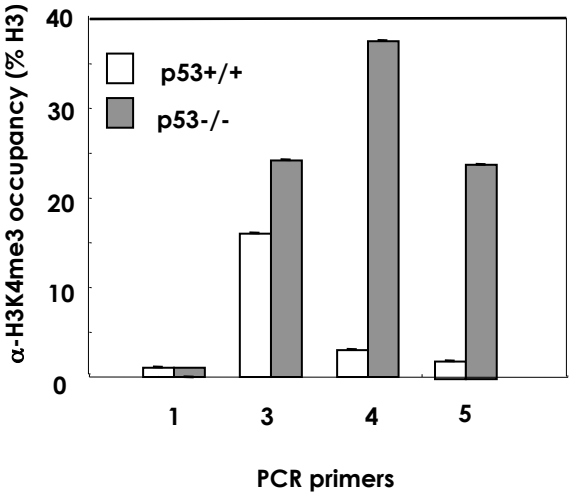
Supplemental Figure S1. Phenotypes of lymphomas. (A) The level of Pre T-cell antigen receptor alpha transcripts in T-cell lymphoma. Total RNA of thymus from mice with lymphoma and normal (wild type) was isolated and quantitative RT-PCR was performed as described in Experimental Procedures. The data shown are the means ± SEM. (B) Thymocytes, isolated from a T-cell lymphoma developed in an Aml1+/+ p53-/- mouse (left), or from the thymus of an Aml1+/- p53-/- mouse (right), were stained with anti-CD4, -CD8, -CD25, or -CD44 antibodies, and the relative frequency of the individual T-cell lineages was determined using flow cytometry.

Supplemental Figure S2



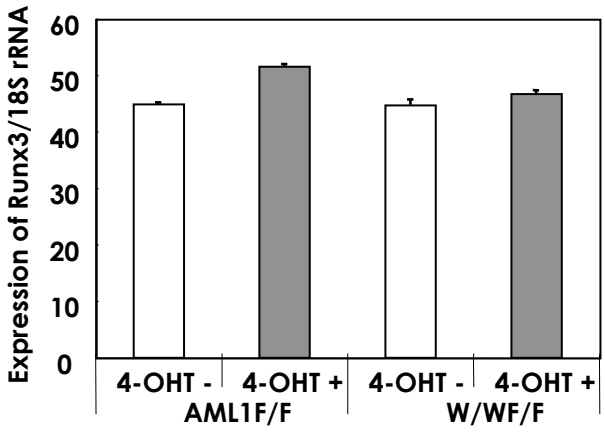
Supplemental Figure S2. Effects of p53 shRNA on AML1 expression. p53 shRNA treatment results in the induction of AML1 in the T-cell leukemia cell line MOLT4. Stable p53 shRNA (sh-p53) clones (#1 and #2) were isolated after selection by puromycin. Both these cells and untreated control cells (NC) were exposed to 5 Gy of IR and, after culture for the indicated periods, the cellular protein fraction was analyzed by western blotting with antibodies against p53 and AML1. Similar protein loading of each lane is indicated by CBB staining. Molecular weight markers are to the left.

Supplemental Figure S3



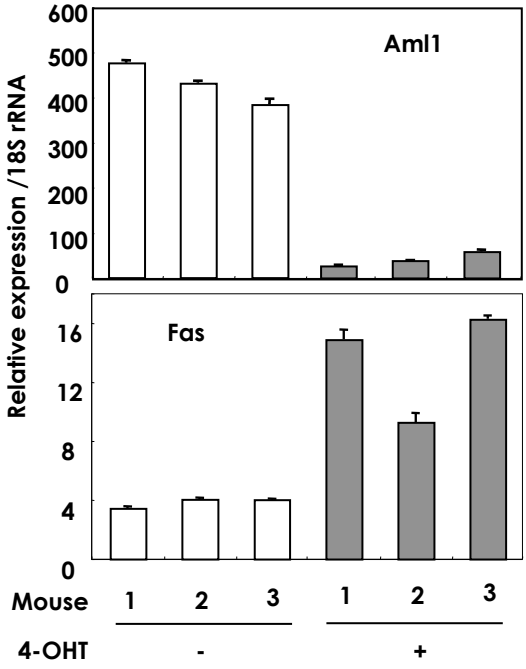
Supplemental Figure S3. Active chromatin modifications in the distal promoter regions of the mouse and human *AML1* genes.
ChIP assays for the detection of chromatin modification (Histone H3K4me3). The ChIP primers used corresponded to bases within the distal promoter region of the *Aml1* gene, as shown in Figure 4A. White bars: c-Kit^{+} bone marrow cells from *p53*$^{+/+}$ mice. Gray bars: c-Kit^{+} cells from *p53*$^{-/-}$ mice.

Supplemental Figure S4



Supplemental Figure S4. Effect of AML1 depletion on the Runx3 gene expression.
Splenic CD4-positive T-cells from *Aml1*$^{fl/fl}$ *ERT2-Cre* and *Aml1*$^{+/+}$*ERT2-Cre* mice were isolated using an antibody against CD4 and cultured for 5 days with (gray bars) or without (white bars) 4-OHT in the presence of IL-2. The expression of *Runx3* was measured by qRT-PCR. The data shown are means ± SEM.

Supplemental Figure S5



Supplementary Figure S5. Effect of AML1 depletion on *Fas* gene expression.
Depletion of AML1 induces expression of *Fas*. Bone-marrow cells from *Aml1$^{fl/fl}$ ERT2-Cre* mice were isolated and cultured in StemPro medium with cytokines (10 ng/ml): mouse 1, SCF and IL-3; mouse 2, SCF, IL-3 and G-CSF; mouse 3, SCF, IL-3 and GM-CSF. Cells were treated with or without 4-OHT for 5 days. Expression of *Aml1* and *Fas* was measured by qRT-PCR. The data shown are means ± SEM.