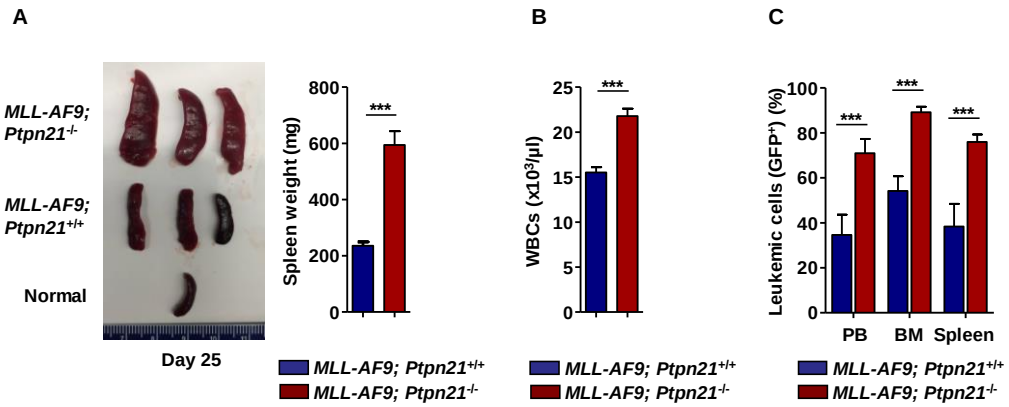
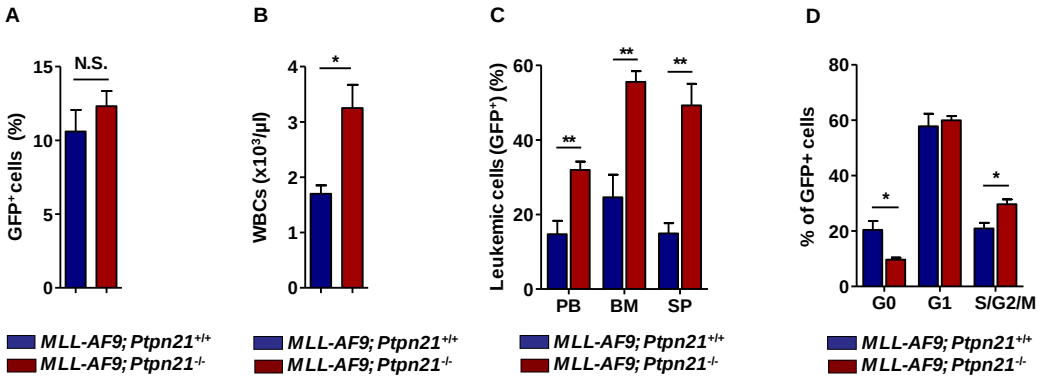
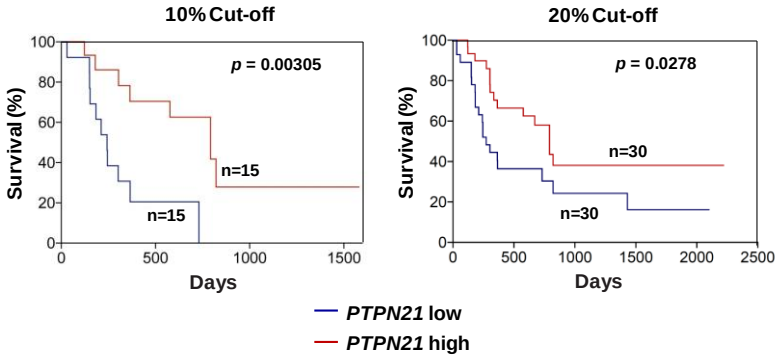


Supplementary Figure 1. Deletion of *Ptpn21* promotes development and progression of *MLL-AF9*-induced leukemia. Lin$^-$ cells isolated from *Ptpn21*$^{-/-}$ and *Ptpn21*$^{+/+}$ mice were infected with *MSCV-MLL-AF9-IRES-GFP* retrovirus. Entire cell populations (5x10^5 cells/mouse) were transplanted into sublethally irradiated (700 rad with a cesium irradiator) BoyJ mice for *in vivo* expansion of leukemic cells. GFP$^+$ leukemic cells sored from the recipient mice were transplanted into sublethally irradiated BoyJ mice. Twenty-five days after leukemic cell inoculation, recipient mice (n=5 mice per group) were sacrificed. Spleens were weighted (A), white blood cell counts in the peripheral blood were determined by a hematology analyzer (B), and leukemic cells (GFP$^+$) in the peripheral blood, BM, and spleen were assessed by FACS analyses (C). Data shown are mean ± standard deviation of all mice examined. *** $P < .001$.



Supplementary Figure 2. Enhanced growth of *MLL-AF9-Ptpn21*$^{-/-}$ leukemic cells *in vivo*. (A) Lin$^-$ cells isolated from *Ptpn21*$^{-/-}$ and *Ptpn21*$^{+/+}$ mice were infected with *MSCV-MLL-AF9-IRES-GFP* retrovirus. GFP$^+$ *MLL-AF9*-tranduced cells were sorted by FACS. 1x10^6 GFP$^+$ leukemia cells were transplanted into lethally irradiated (900 rad with an X-ray irradiator) BoyJ mice (n=6 mice per group). Seventeen hours after transplantation, BM cells were harvested and the frequency of homed GFP$^+$ leukemia cells were measured by FACS. (B-D) Lin$^-$ cells isolated from *Ptpn21*$^{-/-}$ and *Ptpn21*$^{+/+}$ mice were infected with *MSCV-MLL-AF9-IRES-GFP* retrovirus. GFP$^+$ *MLL-AF9*-tranduced cells were sorted by FACS. 6.6x10^4 GFP$^+$ leukemia cells were transplanted into lethally irradiated BoyJ mice (n=6 mice per group). Seventeen days after leukemic cell inoculation, recipient mice (n=3 to 4 mice per group) were sacrificed. White blood cell counts in the peripheral blood were determined by a hematology analyzer (B). GFP$^+$ leukemic cells in the peripheral blood, BM, and spleen (C) were assessed by FACS analyses. Cell cycle distribution of GFP$^+$ leukemic cells in the BM were determined by multi-color FACS analyses (n=3 mice per group) (D). Data shown are mean ± standard deviation of all mice examined. * $P < 0.05$; ** $P < 0.01$.



Supplementary Figure 3. Correlation of *PTPN21* expression levels with prognosis in AML patients. Data mining was performed to determine the correlation between the expression levels of *PTPN21* and the survival of AML patients in the TCGA database. Overall survival rates of AML patients with high and low *PTPN21* expression levels are shown (Left, 10% cut-off threshold; Right, 20% cut-off threshold). The Log-rank (Mantel-Cox) test was used to determine statistical significance.