Figure S1. Meta-analysis data. Meta-analysis revealed no significant difference in *IRX5* or *PRDM5* expression between patients with AML with or without *MLL*-t, oncogenic *KRAS*m or *PTPN11*m. Box plots are data of (A-C) *IRX5* reporter (ID. 210239) and (D-F) *PRDM5* reporter (ID. 220792) in patients with AML (A and D) with or without 11q23-r, (B and E) *KRAS*m, and (C and F) *PTPN11*m, based on cDNA microarray data deposited in Oncomine™. Numbers listed at the bottom are case numbers. Center line in box plot represents median value, box limits are 10th and 90th percentiles, and dots represent minimum and maximum values. *IRX5*, Iroquois-class homeodomain protein IRX-5; *PRDM5*, PR domain zinc finger protein 5; AML, acute myeloid leukemia; *MLL*, lysine methyltransferase 2A; *MLL*-t, *MLL* translocations; *PTPN11*, tyrosine-protein phosphatase non-receptor type 11; 11q23-r, *MLL* rearrangements; No 11q23-r, wild-type *MLL*; KRASm, oncogenic *KRAS* mutations; *KRAS*wt, wild-type *KRAS*; *PTPN11*m, oncogenic *PTPN11* mutations; *PTPN11*wt, wild-type *PTPN11*.

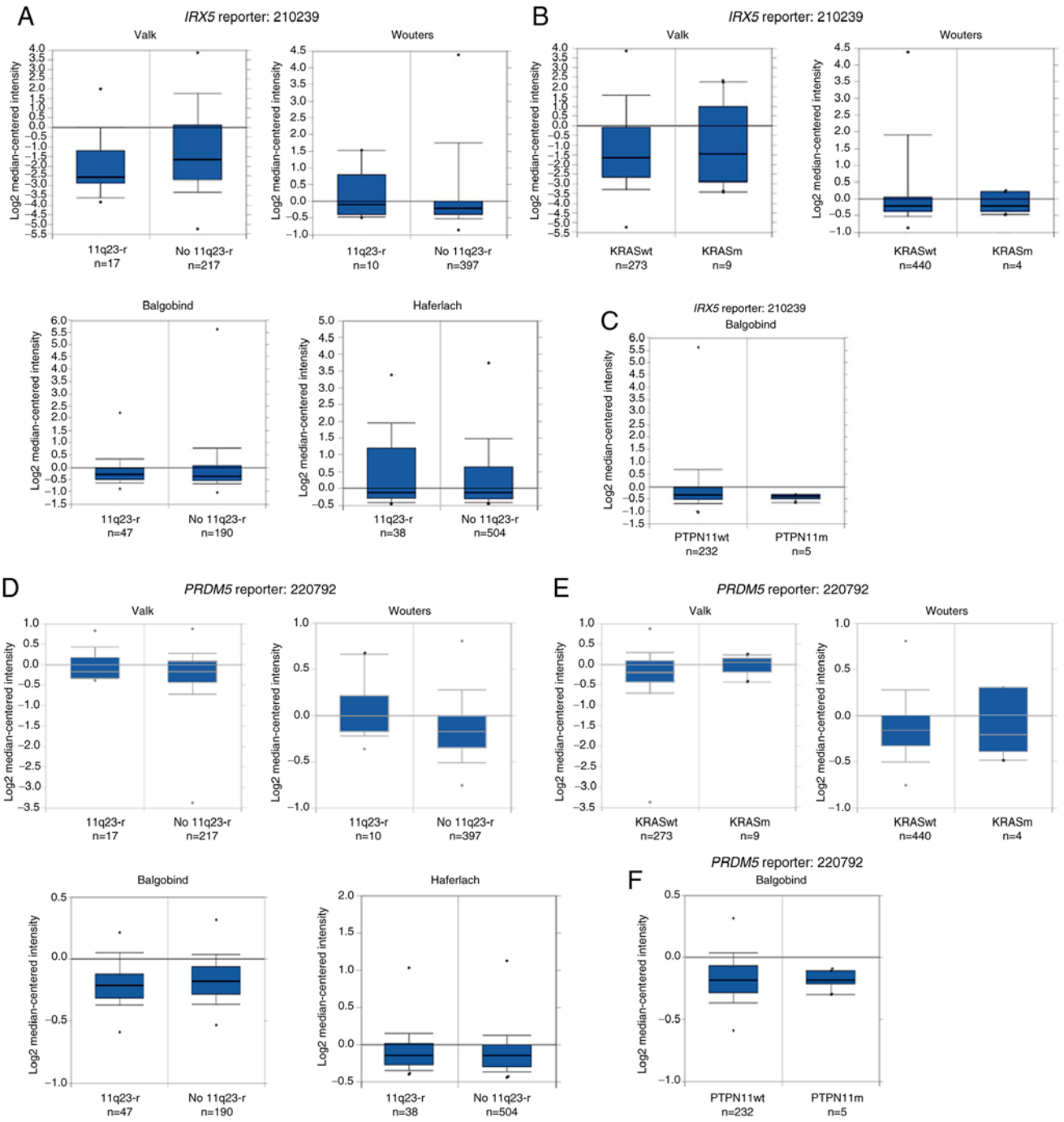

Figure S2. Characteristics of *Hoxa11*-knockdown and *MLL/AF10*-overexpression myeloid leukemia cells. (A and C) Cytologic (left) and immunophenotypic characteristics (right) and (B and D) cell growth curves of (A and B) APm-1-shV and APm-1-shH11-2 cells, or (C and D) 12G-V1 and 12G-H11-1 cells cultured in RPMI medium containing IL-3. Cell cytology was determined by Liu staining (oil immersion; magnification, x1,000). Immunophenotypic characteristics of cells were determined by flow cytometry (FACSCanto II). CD115, monocytic lineage marker. Cell growth curve was determined using a WST/Cell Counting Kit-8 assay. *MLL*, lysine methyltransferase 2A; APm-1, cells with *MLL/AF10(OM-LZ)* and oncogenic *PTPN11*^{G503A}; sh, short hairpin RNA; 12G, cells with *MLL/AF10(OM-LZ)* alone; *PTPN11*, tyrosine-protein phosphatase non-receptor type 11.

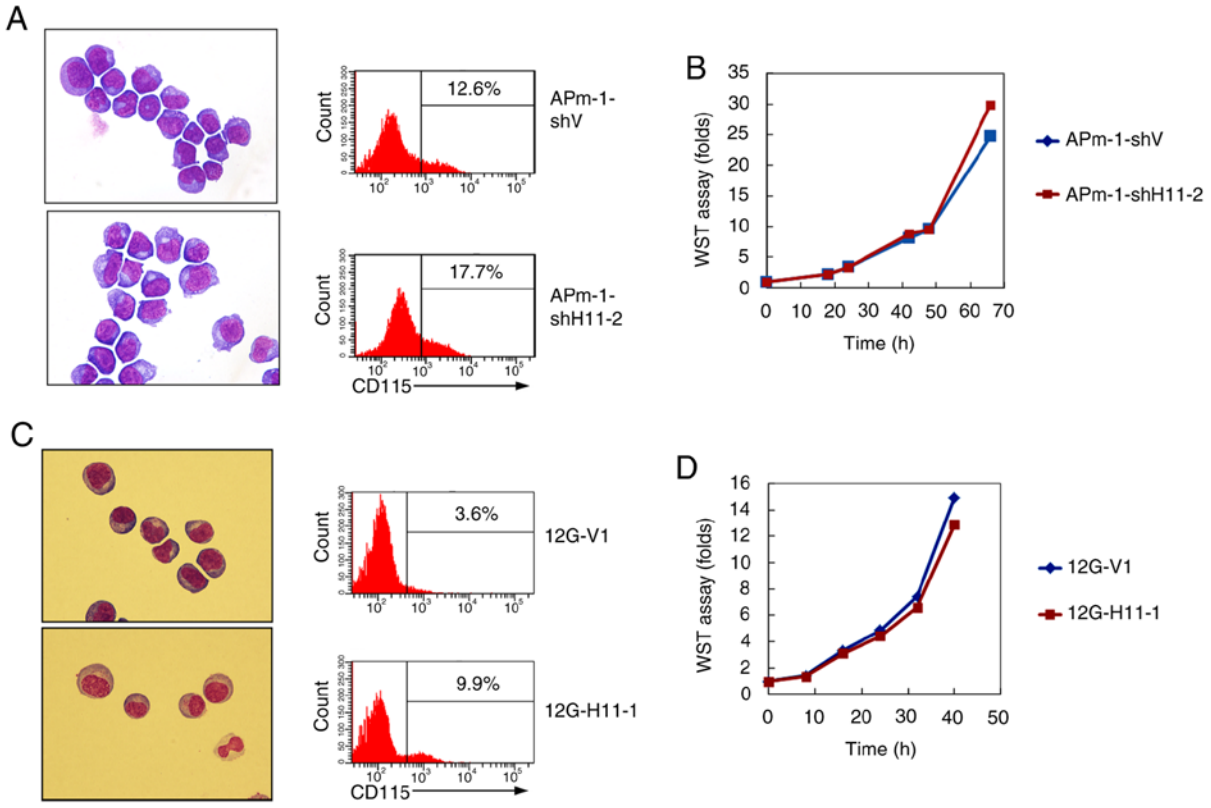

Figure S3. Competitive growth advantage of paired cell lines *in vivo* was determined by PCR-DNA sequencing. (A) DNA sequencing electropherogram of the 62th nucleotide (triangle, C for 12G-H11 and T for 12G-V) of PCR product. The PCR products were obtained by amplification of the 300-bp regions spanning the pMSCVpuro vector-*Hoxa11* junction (from 12G-H11) or vector multiple cloning sites (from 12G-V) using genomic DNA extracted from paired cell lines premixed at varying ratios. (B) A standard curve was generated using the peak height ratios of the 62th nucleotide [C/(C + T)] and cell ratios. Regression equation and R2 are shown on the right. (C) Representative DNA sequencing electropherogram of PCR product amplified from BM or spleen of the recipient mice intraperitoneally-injected with 1:1 premixed 12G-V and 12G-H11 cells (initial). The mice were sacrificed at 5 days, 6 weeks and 8 weeks post-transplantation (three mice for each time point). *MLL*, lysine methyltransferase 2A; 12G, cells with *MLL/AF10(OM-LZ)* alone; BM, bone marrow.

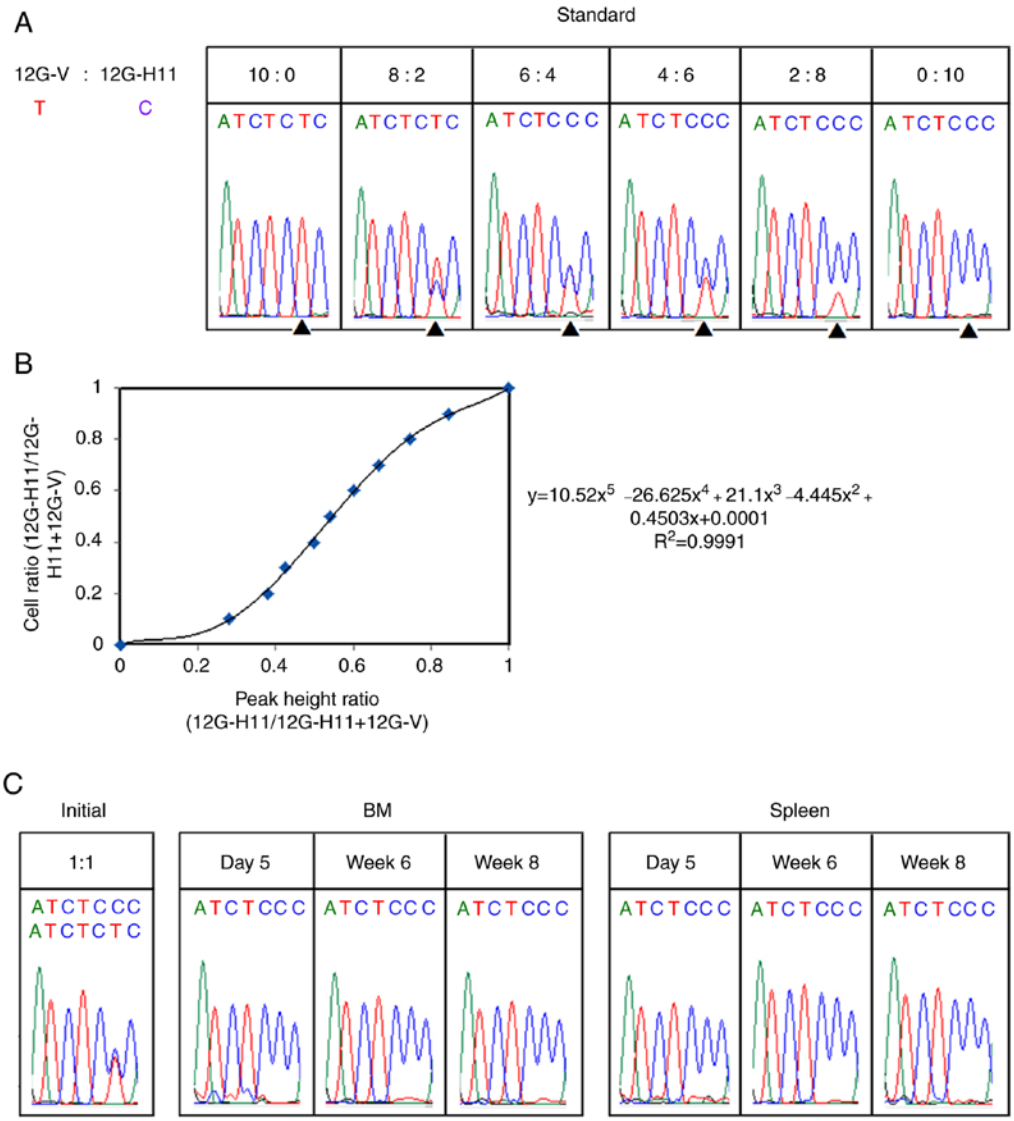

Figure S4. mRNA expression levels of *Hoxa11* in the *Hoxa11*-knockdown AK3G cell lines. Reverse transcription-quantitative PCR analysis was performed to determine *Hoxa11* expression levels in the *Hoxa11*-knockdown AK3G (AK3G-shH11-1, AK3G-shH11-2) and control (AK3G-shV) cell lines. *MLL*, lysine methyltransferase 2A; AK3G, cells with *MLL/AF10(OM-LZ)* and oncogenic *KRAS*^{G12C}; sh, short hairpin RNA.