

**Table S1**

Sequences of primer pairs for RT-qPCR are listed

**Fig. S7** Primer pairs for real-time qPCR

	Formward	Reverse
GAPDH	ATGGCCTTCCGTGTTCCCTAC	ATGCCTGCTTCACCACCTTC
Dmtf1	AGACTCCCCTGCTGCTTCTGT	GGAGTACCAGTGGGCTGTAAATG
Arf	CATGTTGTTGAGGCTAGAGAGGA	CTGCACCGTAGTTGAGCAGA
CDKN1a(p21)	GGCAGACCAGCATGACAGA	CTTCCTGTGGGCGGATTAG
CDKN2a(p16)	CCCGAACTCTTTCGGTCGT	TAGTGGGGTCCTCGCAGTTC
CDKN1b(p27)	CAGTGTCCAGGGATGAGGAAG	TTCGGGGAACCGTCTGAAA
CDKN1c(p57)	CAGGGTGTCCCTCTCCAAAC	AGATGCCCAGCAAGTTCTCTC
CDKN2c(p18)	AAACGTCAACGCTCAAATGG	CAAATTGGGATTAGCACCTCTG
CDK2	TGCACCAGGACCTCAAGAAA	GACACGGTGAGAATGGCAGA
CDK4	CAGTGGTGCCAGAGATGGAG	TCCACCAAGACTGGGAAAAGG
CDK6	TCACGGACGGACAGAGAAAC	CAGACCTCGGAGAAGCTGAA
CCND1	CCAGAGGCGGATGAGAACA	TGCGGTAGCAGGAGAGGAAG
CCND2	TCCCGACTCCTAAGACCCATC	TACCAGTTCCCACTCCAGCA
CCNB1	TGACGTAGACGCAGATGATGG	CACGACCCTGTAGGTATTTTGG
CCNE1	GATTGGCTGATGGAGGTGTG	TGGTGCAACTTTGGAGGGTA
CCNG1	GTGAAACCAGTGCAGATGGAG	CCTTTCCTCTTCAGTCGCTTTC
Jun-B	CGGATGGAGGGGAGAAGATTG	GATAGGAGGTCTGGGCGTTTG
C-Jun	TGCCCAAGAACGTGACCGA	CGCGGAGGTGACACTGGGAA
Bmi1	CAGGTTCAAAAACCAGACCAC	TGACGGGTGAGCTGCATAAA
human-GAPDH	QuantiTect Primer Assays (Qiagen; QT00079247)	
human-Dmtf1	GCATATCAGTTGTTGCACTTCC	TCACAGTCCCCTCAGTAACCTC
human-Arf	CATGTTGTTGAGGCTAGAGAGGA	CTGCACCGTAGTTGAGCAGA

### **Figure S1. Expression of mouse Dmtf1 in various hematopoietic cells**

Thymic cells along with spleen and BM MNCs were collected from WT (B6) mice. Spleen cells were subfractionated by cell sorting into CD4<sup>+</sup>, CD8<sup>+</sup>, B220<sup>+</sup>, and Gr1<sup>+</sup> cells (Left panel). BM MNCs were subjected to cell sorting to isolate KSL, c-Kit<sup>+</sup>, (Left panel) and all three subfractions of KSL cells shown in the Right panel. Expression of Dmtf1 was measured by RT-qPCR in each fraction as described in Methods.

### **Figure S2. Altered differentiation of T and B-cells after transplantation of Dmtf1<sup>-/-</sup> BM cells**

Distribution of T, B, and myeloid cells in the peripheral blood of recipient mice after transplantation was tracked by flow cytometric analysis as described in methods. (A) Representative dotplots from two mice defining lineage differentiation among donor and competitor cells in recipient mice transplanted with WT or KO MNCs. Percentages next to each gate reflects the absolute percentage of each phenotype of cells detected at 4 months post-transplantation. (B) Sequential measurement for frequencies of T, B, and myeloid cells in all recipient mice receiving after WT or KO MNCs. Data are mean  $\pm$  S.D (\*p<0.03, n=5).

### **Figure S3. BrdU incorporation in steady state SlamKSL cells**

The percentage of BrdU positive KSL or SlamKSL cells in steady state BM of WT and KO mice were determined as described in materials and method (n=3).

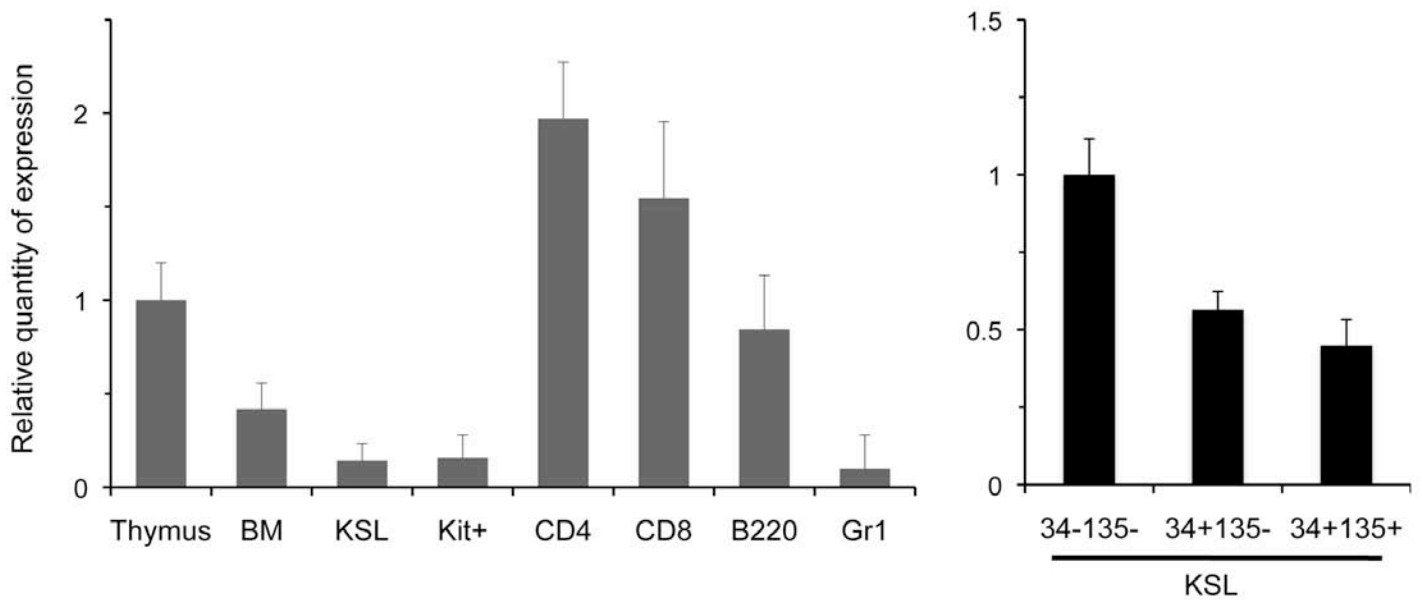
### **Figure S4. Self-renewal capacity of Dmtf1 KO HSC is sustained relative to that of WT HSC**

Competitive repopulation was performed and chimerism in recipient mice determined as described for Figure 5B. BM cells were collected and analyzed at 4 month after transplantation. Results shown are representative dotplots of the KSL frequencies in the marrow of recipients of fresh and cultured WT and KO cells. Chimerism in the BM of mice used for these analyses is shown below each dotplot.

### Figure S5. Expression of Dmtf1 and Arf

(A) Expression of human Dmtf1 and Arf were evaluated by RT-qPCR in different cells. Values are shown as relative levels compared to expression in 293T cells. (B) Vector constructs for human Dmtf1 and retroviral vectors used in this study.

**Fig S1**



**Fig. S2**

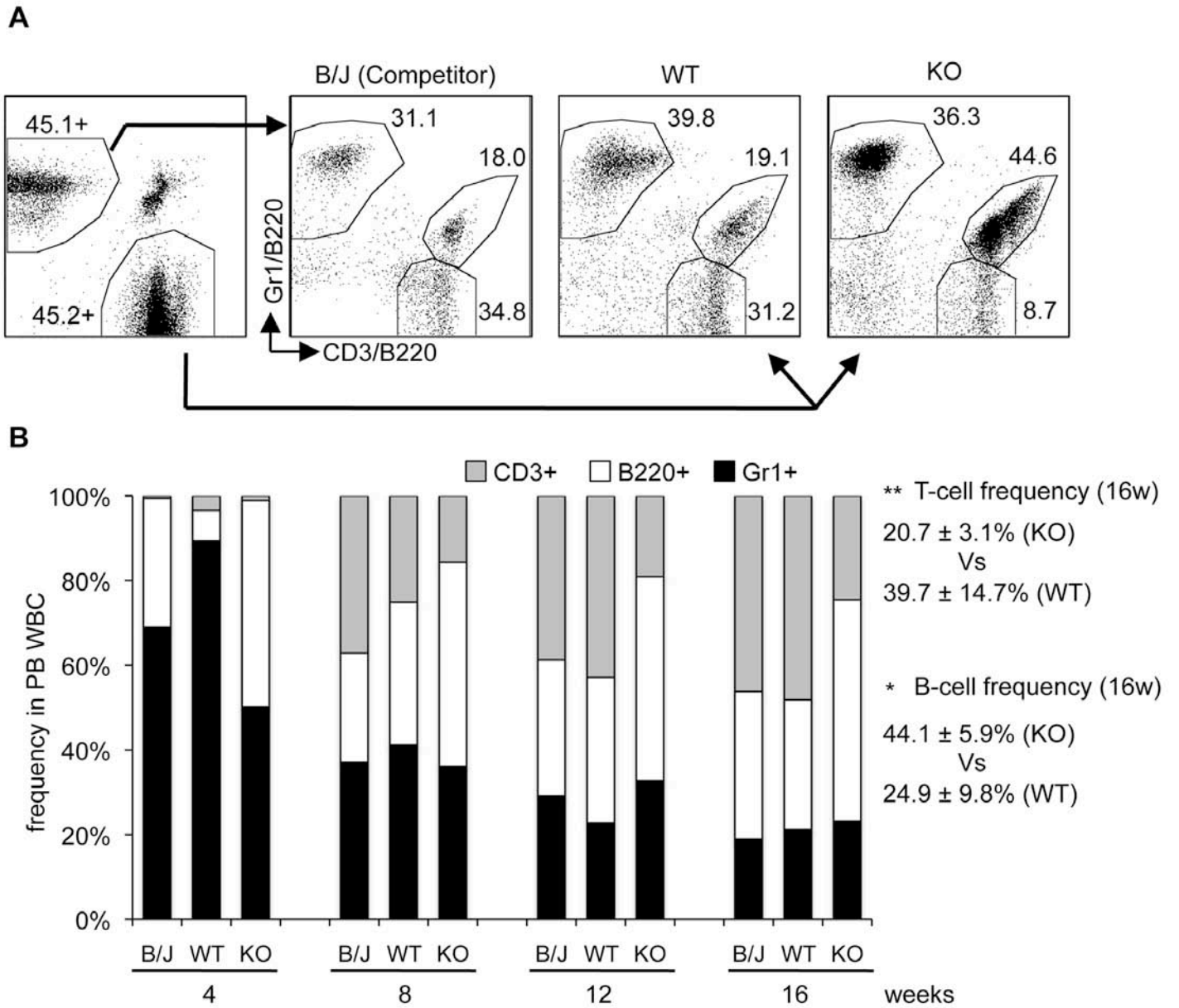
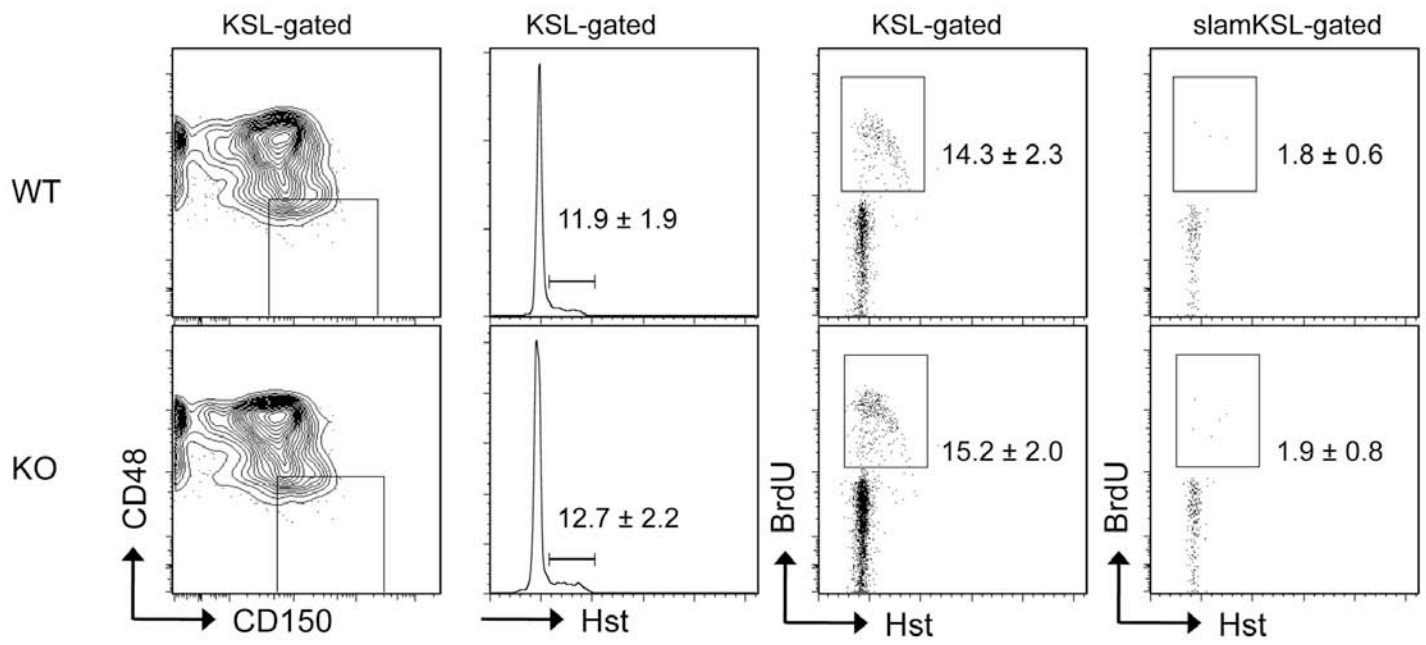
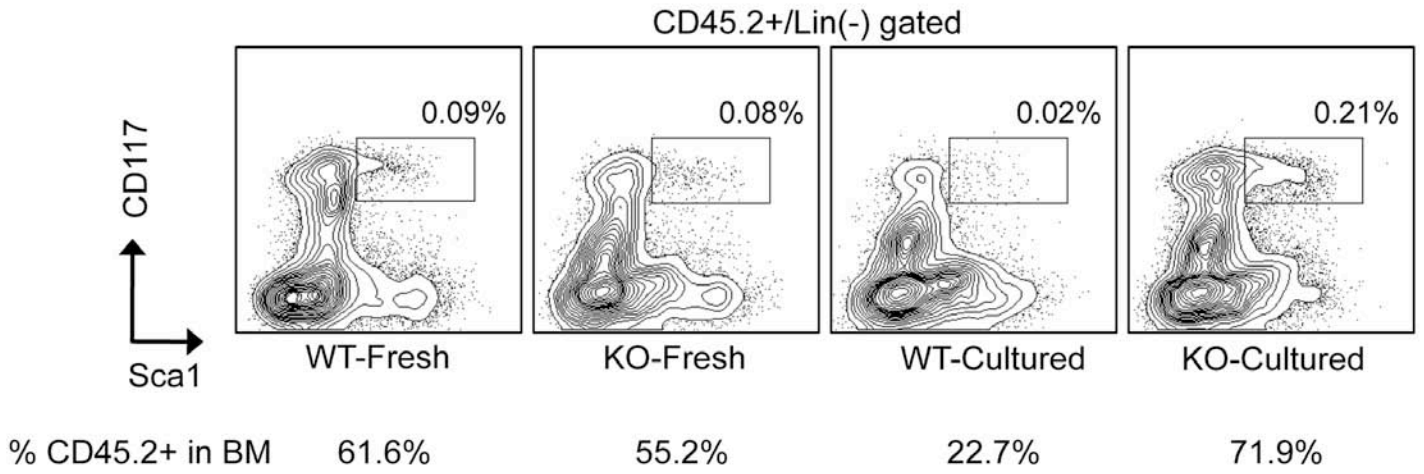


Fig. S3



**Fig. S4**



**Fig. S5**

