

## Supplemental data

### Supplemental Materials and Methods

Primers for real-time RT-PCR analyses of Gata1 and Scl nascent transcripts:

Gata1-a:

F: 5' AGCATCAGCACTGGCCTACT 3'

R: 5' GGCGGTACACCTATCCACAG 3'

Gata1-b:

F: 5' GTCCCCGAATCCTACCTCTC 3'

R: 5' TCCGCCAGAGTGTTGTAGTG 3'

Gata1-c:

F: 5' CCTAGCCCAGCTACATCAGC 3'

R: 5' TTCCTCGTCTGGATTCCATC 3'

Scl-a:

F: 5' GAGGTCCTAACCAGCCGAGT 3'

R: 5' CCCAGTTCACAACCCAGAAT 3'

Scl-b:

F: 5' TAGCAGGAGGGGACTGAAGA 3'

R: 5' CTCTTCACCCGGTTGTTGTT 3'

Scl-c:

F: 5' TTAGCTCCCTGGCTTCTCAG 3'

R: 5' CCGCACTACTTTGGTGTGAG 3'

### Supplemental Figure Legends

**Supplemental Fig. 1** (A) Mild increase of immature red cells (CD71<sup>+</sup> Ter119<sup>+</sup>) in the peripheral blood in *Mx-cre; tif1γ<sup>fl/fl</sup>* mice at 3-weeks post plpC injection (n=4, q=0.05) (B) PCR from bone marrow genomic DNA showing the complete excision of the floxed allele in KO mice. (C) MGG staining of c-kit<sup>hi</sup> CD71<sup>+</sup>Ter119<sup>-</sup> cells cytopspined from control and KO mice bone marrow. (D) FACS analysis showing no significant change of fetal liver erythropoiesis in *vav-cre; tif1γ<sup>fl/fl</sup>* mice. (E) PCR from fetal liver genomic DNA showing incomplete excision of the

floxed allele in KO mice.

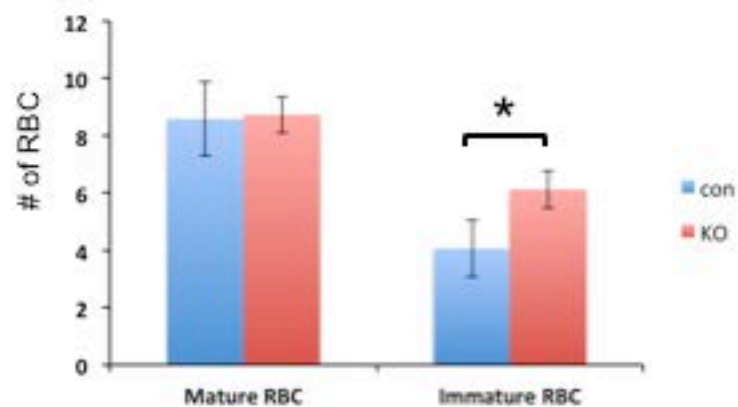
**Supplemental Fig.2** (A) Bone marrow FACS analyses showing similar B-cell and myeloid phenotypes in *vav-cre; tif1 $\gamma$ <sup>fl/fl</sup>* mice as in *Mx-cre; tif1 $\gamma$ <sup>fl/fl</sup>* mice (n=4, \*\*\*  $q \leq 0.001$ . \*\*  $q \leq 0.01$ ). (B & C) The levels of bone marrow progenitors and HSCs in *Mx-cre; tif1 $\gamma$ <sup>fl/fl</sup>* mice at 3-week post pl-pC injection (n=3, \* $q \leq 0.05$ ).

**Supplemental Fig. 3** Percentage of CD45.2+ cells in peripheral blood of recipients at (A) 3-week post transplantation, before pl-pC injection, and (B) 16-week post plpC injection, (n=9, \*\*\*  $q \leq 0.001$ ).

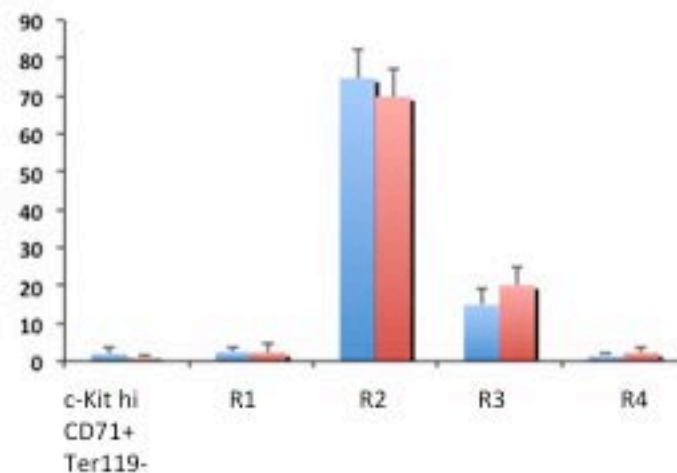
**Supplemental Fig. 4** Quantitative (real-time) RT-PCR measuring the levels of nascent transcripts of Gata1 and Scl. **Top:** A schematic diagram showing the amplified regions of PCR products (a, b, c) that encompass exon/intron boundaries. **Bottom:** real-time RT-PCR analyses to compare the levels of nascent transcripts showing in the top panels in R2 stage of erythroid cells between *vav-cre; tif1 $\gamma$ <sup>fl/fl</sup>* (KO) mice and *vav-cre; tif1 $\gamma$ <sup>fl/+</sup>* (con) mice. Results are shown as fold changes (KO vs. con), normalized to the transcript level of  $\beta$ -actin. Error bars represent mean  $\pm$  SD from three independent experiments.

Sup fig.1

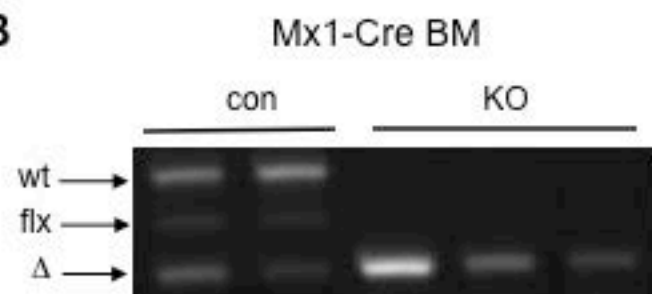
**A**



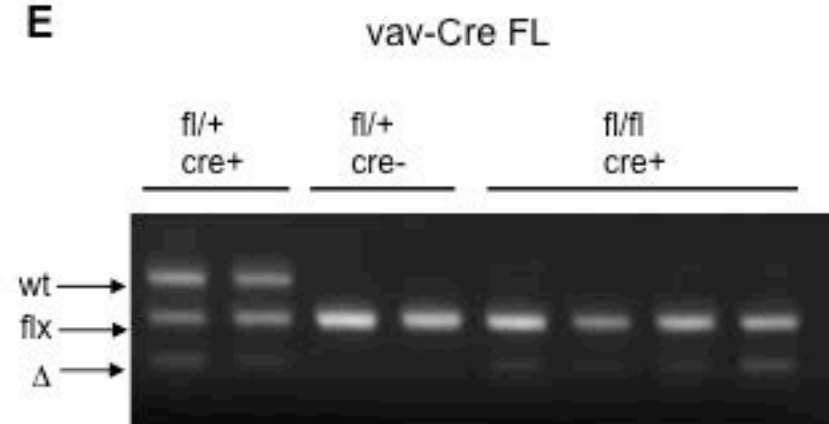
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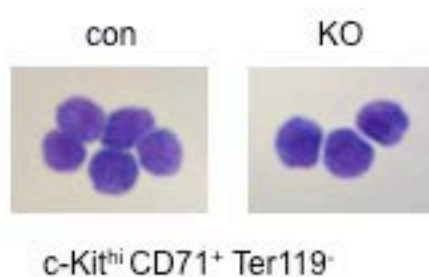
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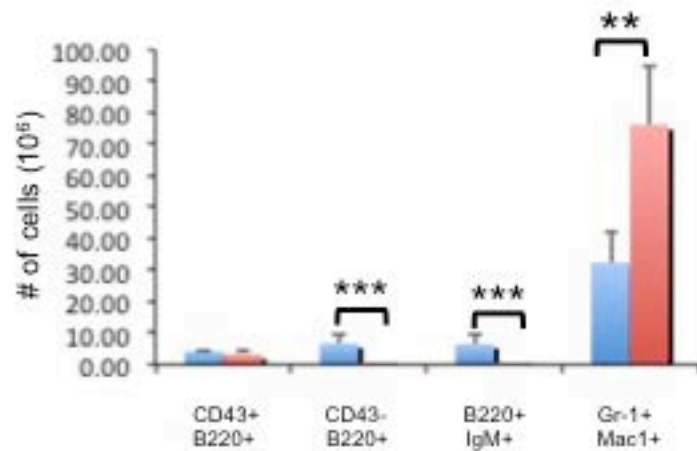
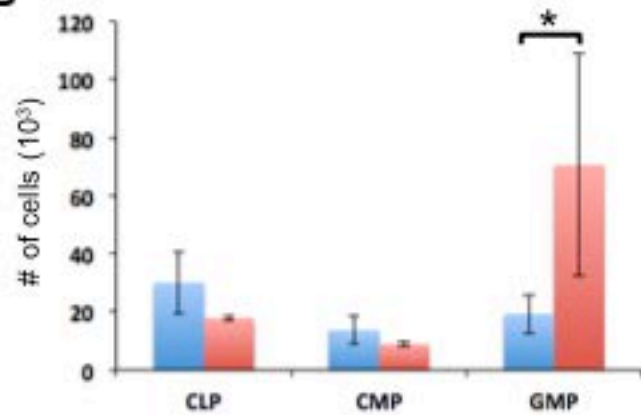
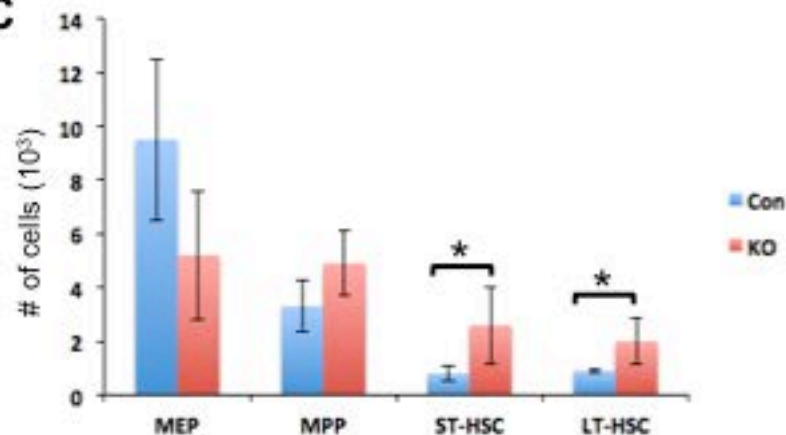


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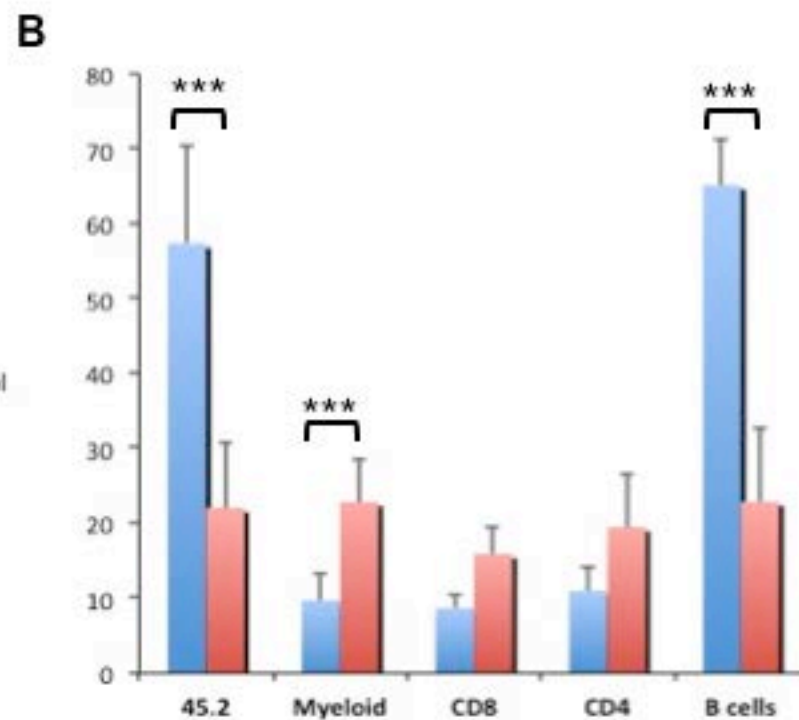
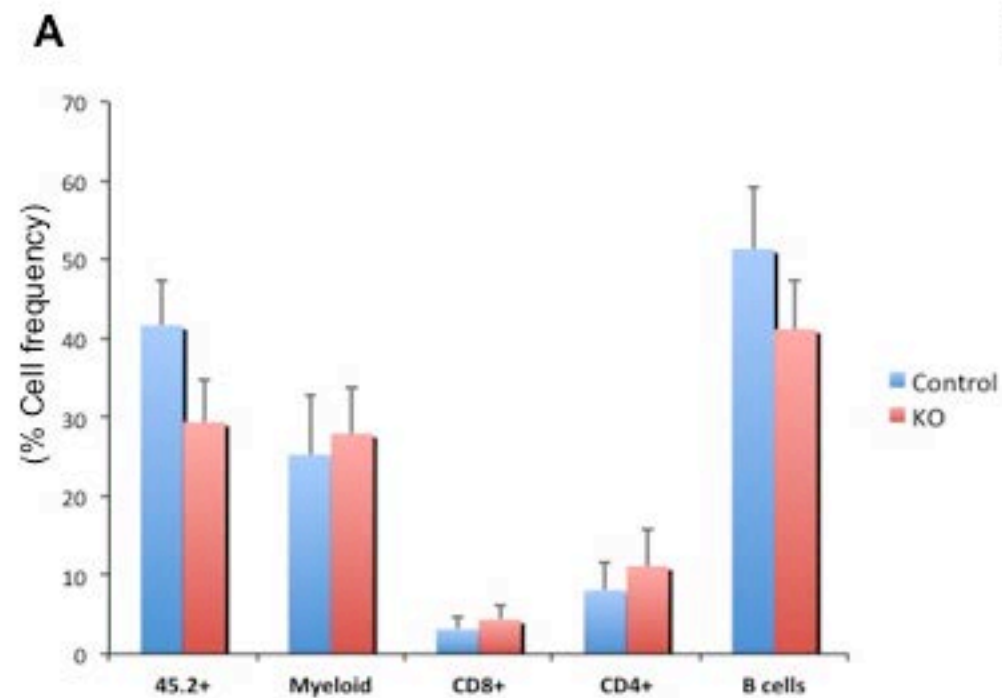


**C**



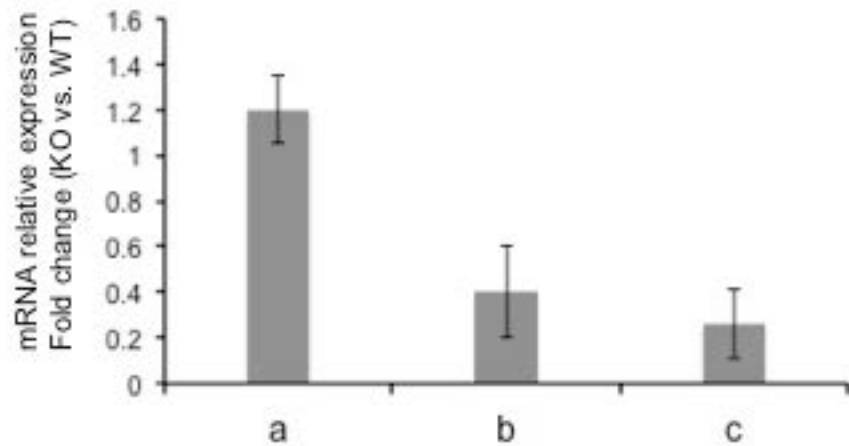
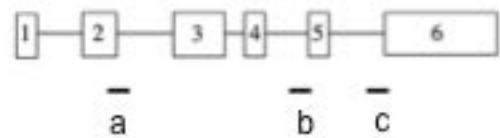
**A****B****C**

Sup fig.3



Sup fig.4

*Gata1*



*Scf*

