Supplemental data

Supplemental Table 1. Sequences of primers for RT-PCR on cultivated of EPCs

Transcript	Sequence
Ccr1	(F) 5’-TTTTAAGGCCCAGTGGGAGTTCACTCACC-3’
	(R) 5’-TGGTATAGCCACATGCCTTTGAAACAGCTG-3’
Ccr2	(F) 5’-CCTGCAAAGACCAGAAGAGG-3’
	(R) 5’-GATGGCCAAGTTGAGCAGAT-3’
Ccr5	(F) 5’-ACGGTGTTCAATTTTCCAGC-3’
	(R) 5’-GCAAGAAGCGACTTTATGGC-3’
Cxcr4	(F) 5’-TCCTGCCCACCATCTACTTC-3’
	(R) 5’-TTTCAGCCAGCAGTTTCCTT-3’
Flk1	(F) 5’-AGTGGCTCTGTCCTCCAAGA-3’
	(R) 5’-GCAAACCTTCCAAAACCAAA-3’
Vegf	(F) 5'-TCCAACATCACCATGCAGAT-3'
	(R) 5'-CATCTGCAAGTACGTTCGTT-3'
Tgfb1	(F) 5’-GGGCAAGACAGTCATCGAAT-3’
	(R) 5’-TTGGTTTTTGGTCACGTTCA-3’
Hgf	(F) 5’-GCTTGGCATCCACGATGTTC-3’
	(R) 5’-CCCTCACATGGTCCTGATCC-3’
β-*actin*	(F) 5'-TTCTACAATGAGCTGCGTGTGGC-3'
	(R) 5'-CTCATAGCTCTTCTCCAGGGAGGA-3'

(F): Forward primer, (R): Reverse primer

Legends to Supplemental Figures

Supplemental Figure 1. The protein levels of CCL3, CCL4, and CCL5 at the wound sites of WT mice were determined by ELISA. All values represent mean ± SEM (n=6). **, $P < 0.01$, vs. uninjured skin (time=0).

Supplemental Figure 2. Hydroxyproline content in wound site of WT and *Ccr5*$^{-/-}$ mice. All values represent mean ± SEM (n=6). *, $P < 0.05$, vs. WT mice.

Supplemental Figure 3. Neovascularization was immunohistochemically evaluated with anti-VE-cadherin mAb at 6 days after injury. (A) Representative results from four animals are shown here. Original magnification, x 200. (B) The vascular areas were identified as VE-cadherin-positive areas with Adobe PhotoShop. Values represent mean ± SEM (n=4). **, $P < 0.01$, vs. WT mice.

Supplemental Figure 4. Hydroxyproline content in wound site of BM chimera mice. All values represent mean ± SEM. *, $P < 0.05$, vs. WT recipients transferred WT donor BM cells; #, $P < 0.05$, vs. *Ccr5*$^{-/-}$ recipients transferred *Ccr5*$^{-/-}$ donor BM cells.

Supplemental Figure 5. Quantitative evaluation of Flk-1^{+}/CD34^{+} EPCs by flow cytometric analysis at the indicated time intervals after injury. Representative results from six independent experiments are shown here; (A) BM, (C) peripheral blood, and (E) wound sites. Changes in percentage of Flk-1^{+}/CD34^{+}cells in BM (B), peripheral blood (D), and wound sites (F) are shown. Values represent mean ± SEM (n=6). **, $P < 0.01$, vs. WT mice.

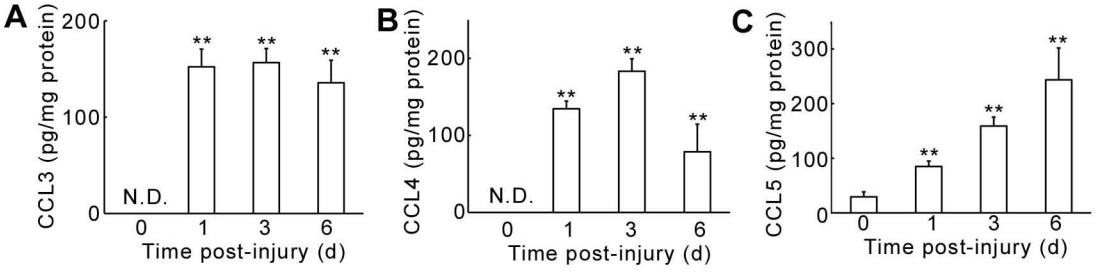
Supplemental Figure 6. Immunofluorescence analysis of c-Kit^{+}/Tie-2^{+} cells (left panel) and c-Kit^{+}/Tie-2^{+}/CCR5^{+} cells (right panel) in the wound of WT mice at 4 days after injury. Representative results from six independent experiments are shown. Original magnification, x 400.

Supplemental Figure 7. (A) BM mononuclear cells were cultured as described in Materials and Methods. After a 4-day culture, adhered and spindle-shaped cells were recognized as EPCs and the cells reached confluent monolayer at 14 days after the culture. Original magnification, x 100. (B) On day 4, cultured EPCs were characterized with both AcLDL uptake (Dil) and BS-1 lectin binding (FITC). Original magnification, x 100. (C) To identify the characteristics of the cells, 4-day cultured cells were subjected to immunofluorescent staining was with anti-Tie-2, together with AcLDL uptake and BS-1 lectin binding. Original magnification, x 200. (D) Double-color immunofluorescence analysis of the obtained EPCs using anti-Tie-2 and anti-CCR5, followed by DAPI. Some of cultivated Tie-2^{+} EPCs expressed CCR5.

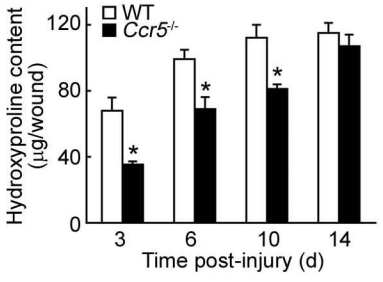
Supplemental Figure 8. The gene expression of *Vegf*, *Tgfb1* and *Hgf* in the resultant EPCs by RT-PCR analysis. Representative results from six independent experiments are shown here.

Supplemental Figure 9. The gene expression of *Ccr1*, *Ccr2*, *Ccr5*, *Cxcr4* and *Flk-1* in the resultant EPCs by RT-PCR analysis. Representative results from six independent experiments are shown here.

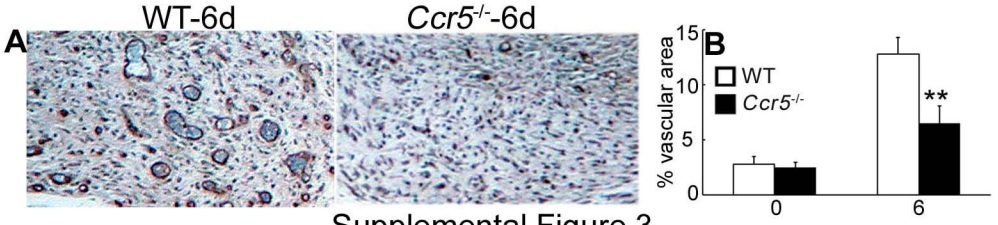
Supplemental Figure 10. (A) and (B) The mRNA expression of *Cxcl12* and *Ccl2* at the wound sites of WT and *Ccr5*$^{-/-}$ mice by quantitative RT-PCR analyses. (C) and (D) Protein levels of CXCL12 and CCL2 at the wound sites of WT and CCR5$^{-/-}$ mice by ELISA analyses. Values represent mean ± SEM (n=6).



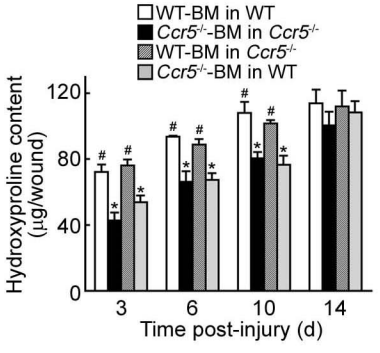
Supplemental Figure 1



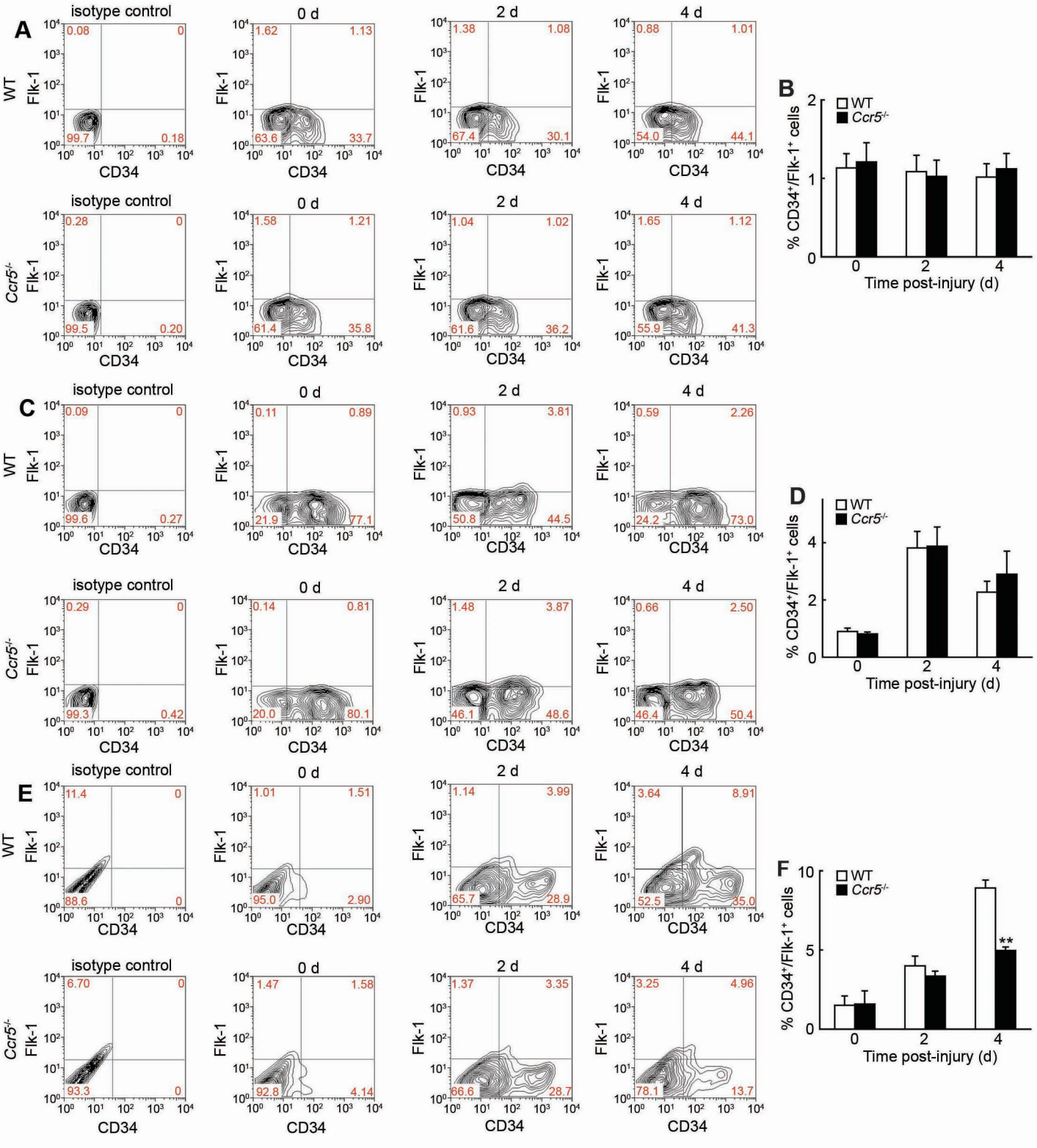
Supplemental Figure 2



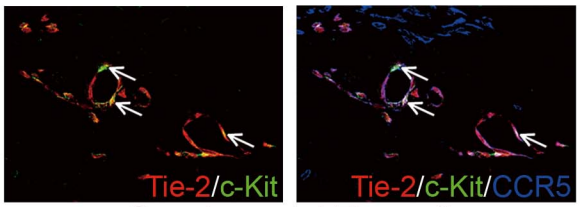
Supplemental Figure 3



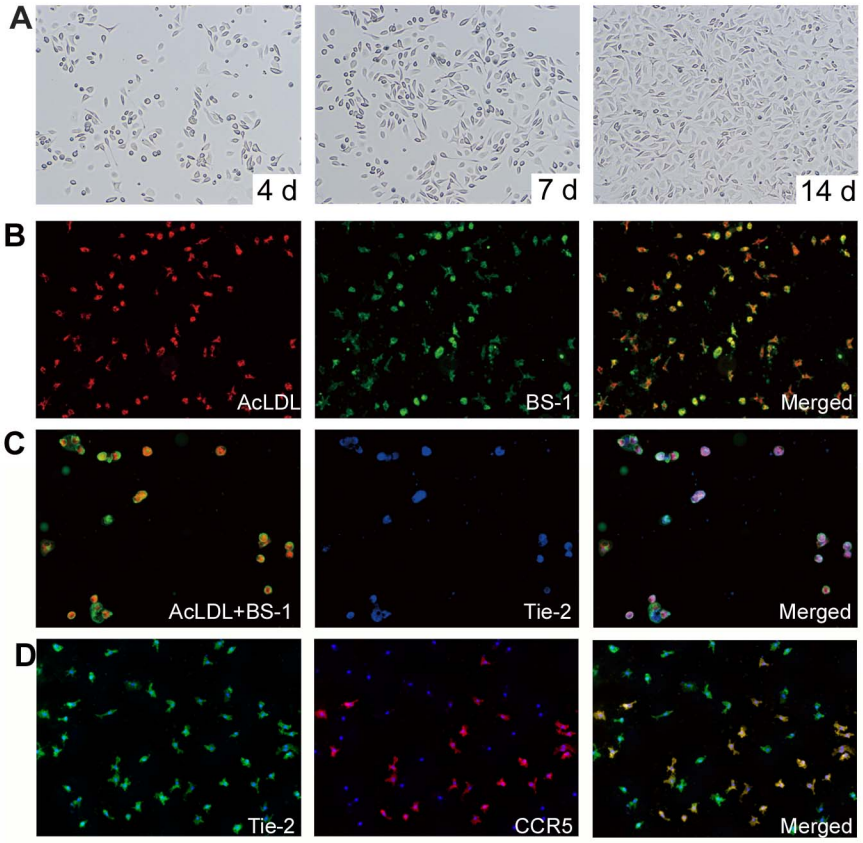
Supplemental Figure 4



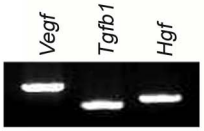
Supplemental Figure 5



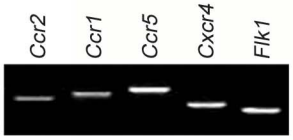
Supplemental Figure 6



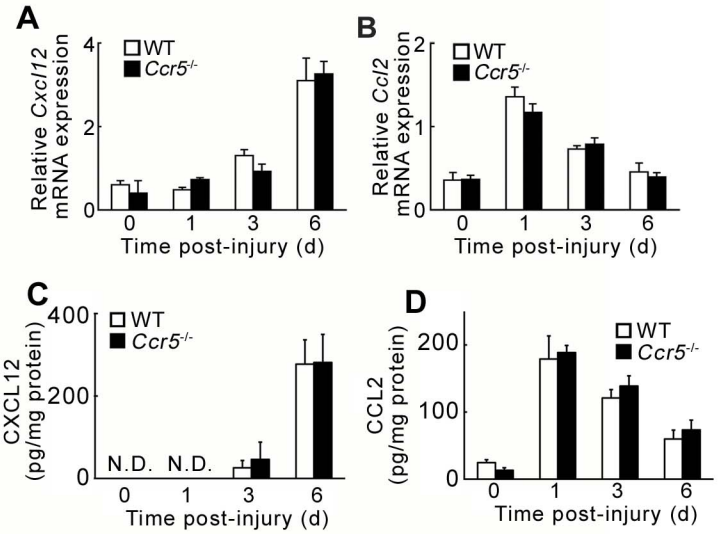
Supplemental Figure 7



Supplemental Figure 8



Supplemental Figure 9



Supplemental Figure 10