

## **SUPPLEMENTAL INFORMATION**

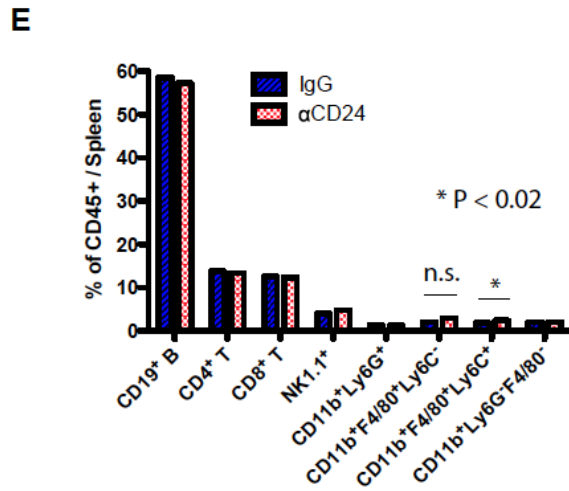
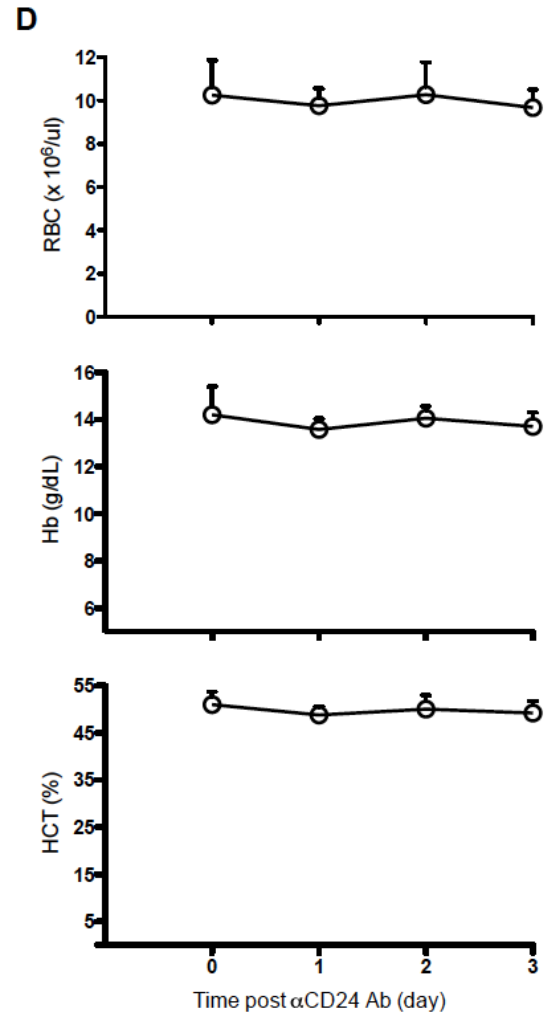
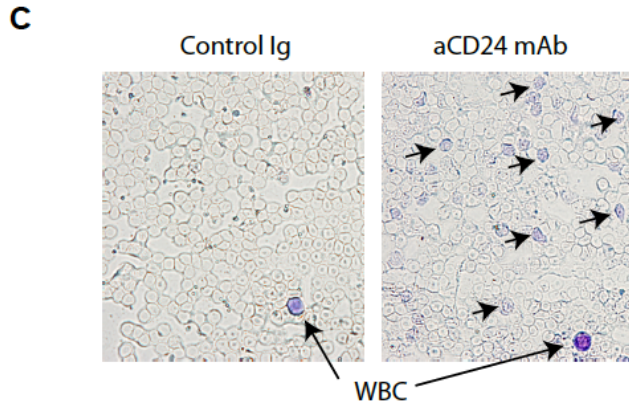
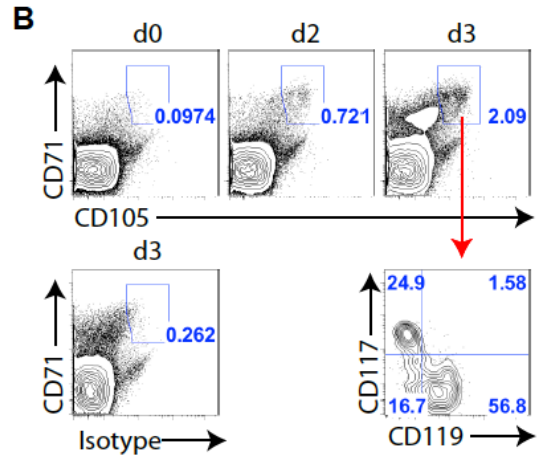
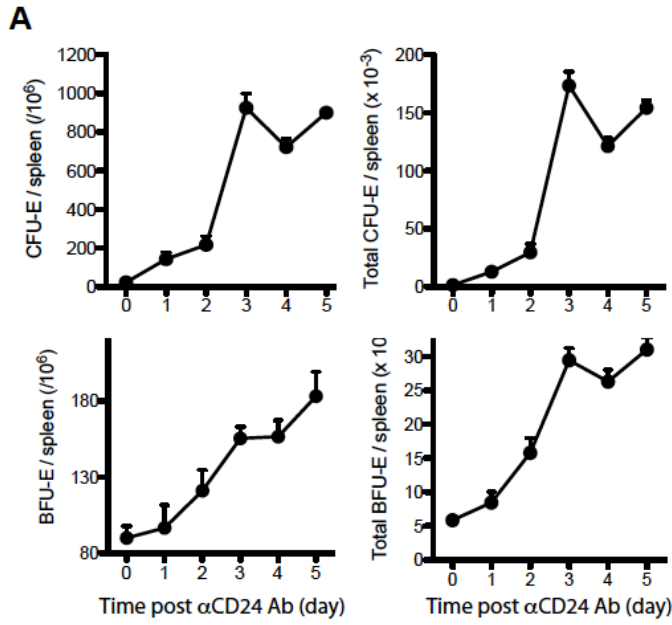
**Stress-associated erythropoiesis initiation is regulated by type 1 conventional dendritic cells**

T.S. Kim *et al.*

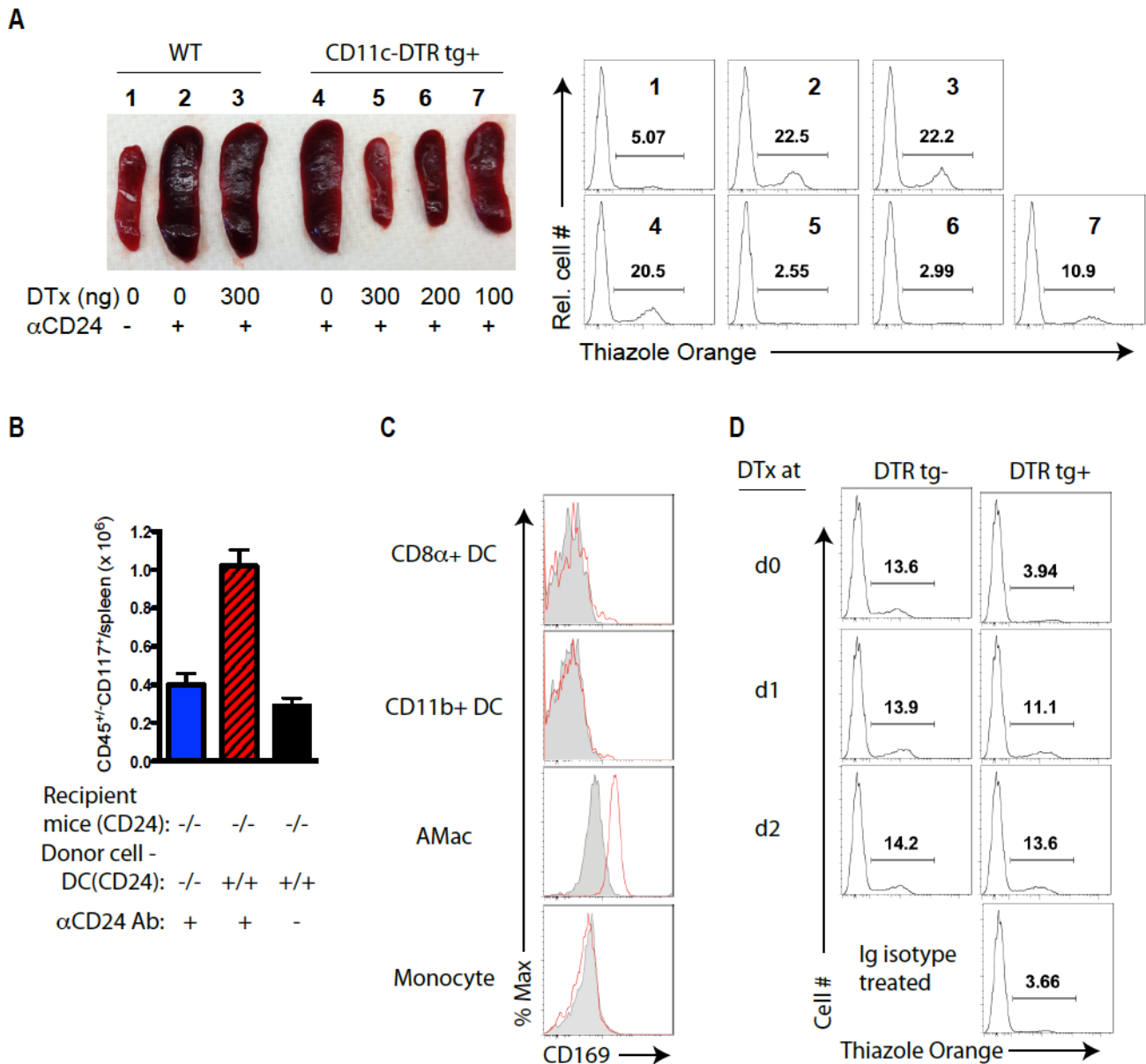
**Supplemental Figures 1-10**

**Supplemental Table 1**

**References for supplemental data**



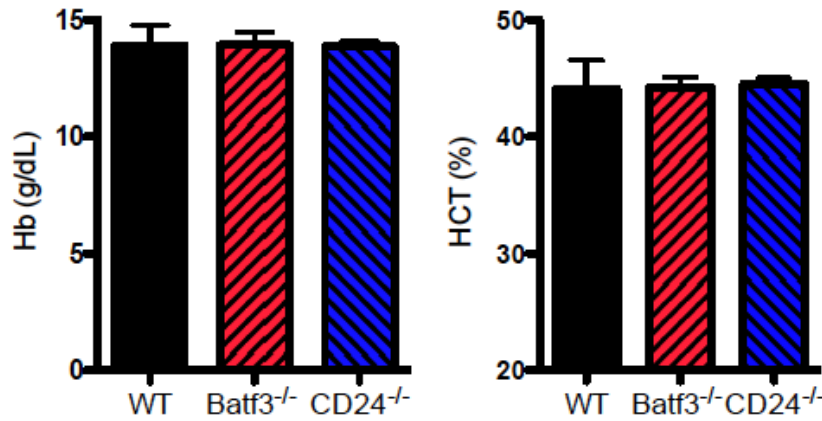
**Supplemental Figure 1. Analyses on erythroid progenitors, reticulocytes, hematologic values, and leukocyte subpopulations (Ter119<sup>+</sup>CD45<sup>+</sup> cells) in the spleen following administration of monoclonal  $\alpha$ CD24 antibody.** WT B6 mice were infused intraperitoneally (i.p.) with 100  $\mu$ g control rat IgG2b or  $\alpha$ CD24 mAb (clone M1/69). **(A and B)** Analyses on the erythroid progenitors in the spleens of Ab treated mice. Erythroid progenitors were identified by i) colony forming assays and ii) surface marker expression. **(A)** For colony forming assays, single cell suspensions were prepared from spleens at indicated days post Ab treatment. Selective CFU-E and BFU-E colony forming activities were measured using methylcellulose-based media (MethoCult<sup>TM</sup> SF M3436, Stem Cell Technologies). CFU-E and BFU-E colonies were identified at d2 and d7 (and d10 – data not shown), respectively, in culture by morphologic examination under light microscope (4x), and frequency (per 10<sup>6</sup>) (left panels) and total (right panels) CFU-E (top panels) and BFU-E (bottom panels) colonies were enumerated over time **(A)**. Data represent triplicates of 2 - 4 independent experiments at each time point. **(B)** Flow-cytometric analyses on the identification of erythroid progenitors. Splenocytes prepared from mice treated with  $\alpha$ CD24 Ab were examined for surface expression of Kit, CD105, and CD71 at indicated days post treatment. At 5 days post Ab treatment, **(C)** peripheral blood smear was prepared and subjected for Wright Giemsa staining for reticulocytosis (small arrows) under light microscope (10x). **(D)** Hematological values (RBC counts, Hb and HCT levels) were analyzed on the Hemavet 850 FS automated CBC analyzer (n = 5 - 10). **(E)** Single cell suspensions prepared from spleens were analyzed for cellular types by flow cytometric-based phenotyping (n  $\geq$  5).



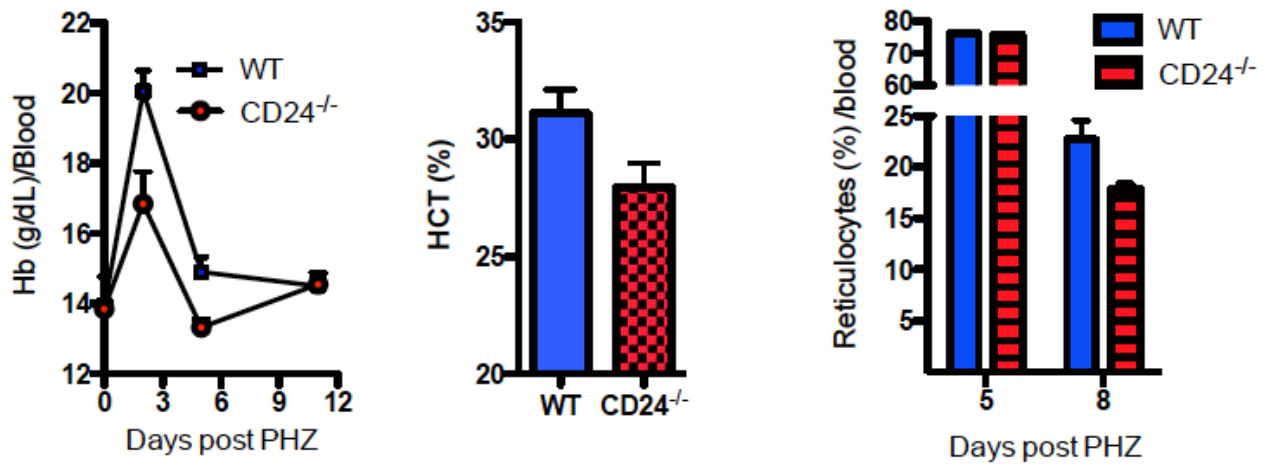
**Supplemental Figure 2. Dendritic cells are critical during the inductive phase of stress erythropoiesis after CD24 engagement.** (A) CD11c-DTR mice were administrated i.p. graded doses of diphtheria toxin (DTx). At 4 hrs post DTx administration, DC-ablated mice were infused i.p. with Ig or M1/69, and were necropsied at d5 for gross appearance of the spleens (left panels), circulating reticulocytes (right) and CD45<sup>+</sup>Ter119<sup>+</sup> erythroid progenitors in the spleen (data not shown). Data represent at least two independent experiments. (B) CD24<sup>-/-</sup> mice were received intravenously (i.v.) bone marrow-derived DC (BMDC) prepared from either wt or CD24<sup>-/-</sup> mice prior to  $\alpha$ CD24 mAb (M1/69) treatment. At d5 post treatment, erythroid progenitors (CD45<sup>+</sup>CD117<sup>+</sup>) in the spleens were enumerated (n = 4-5/group). (C) Surface expression of CD169 in naïve mice. CD8 $\alpha$ <sup>+</sup> DC, CD11b<sup>+</sup> DC and F4/80<sup>+</sup>Ly6C<sup>+</sup> monocytes

were isolated from spleens and stained with anti-CD169 mAb. Alveolar macrophages were used as a positive control for CD169 staining. **(D)** CD11c-DTR mice were administrated i.p. with 100  $\mu$ g of DTx at the indicated days post M1/69 treatment. DC-ablated Ab-treated mice were necropsied at d5 for measuring circulating reticulocytes. A representative of circulating reticulocytes in the blood (%) is shown. Data represent at least three independent experiments.

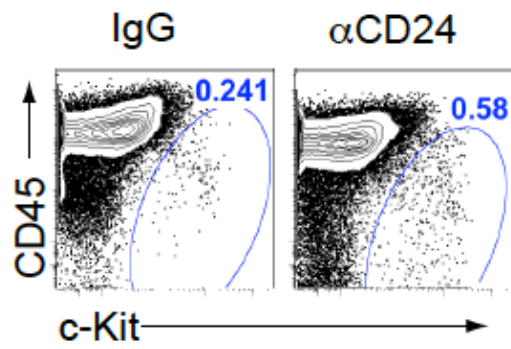
**A**



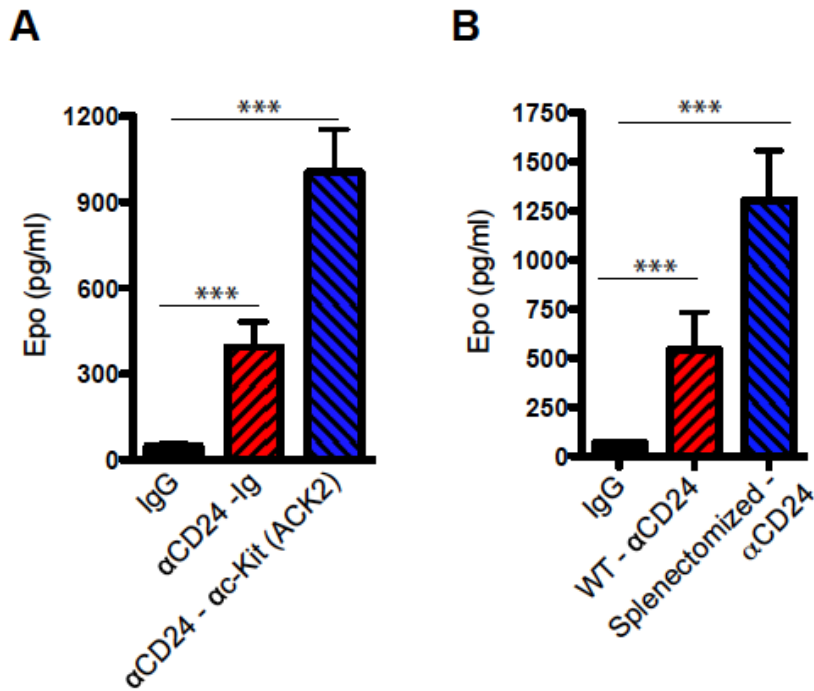
**B**



**Supplemental Figure 3. Levels of Hb and HCT in mice deficient in *Batf3* or *CD24* under normoxic condition and after phenylhydrazine-induced hemolytic anemia.** Phenylhydrazine (PHZ; Sigma-Aldrich) diluted in saline-buffered solution (40 mg/kg body weight, daily) was injected intraperitoneally on three consecutive days. Control mice were similarly injected with an equivalent volume of sterile saline solution (0.15 M NaCl). Mice were sacrificed the indicated days. HCT was measured at d5. Data represent mean  $\pm$  SEM ( $n > 5$  in **A** and  $n = 4-5$  in **B**).

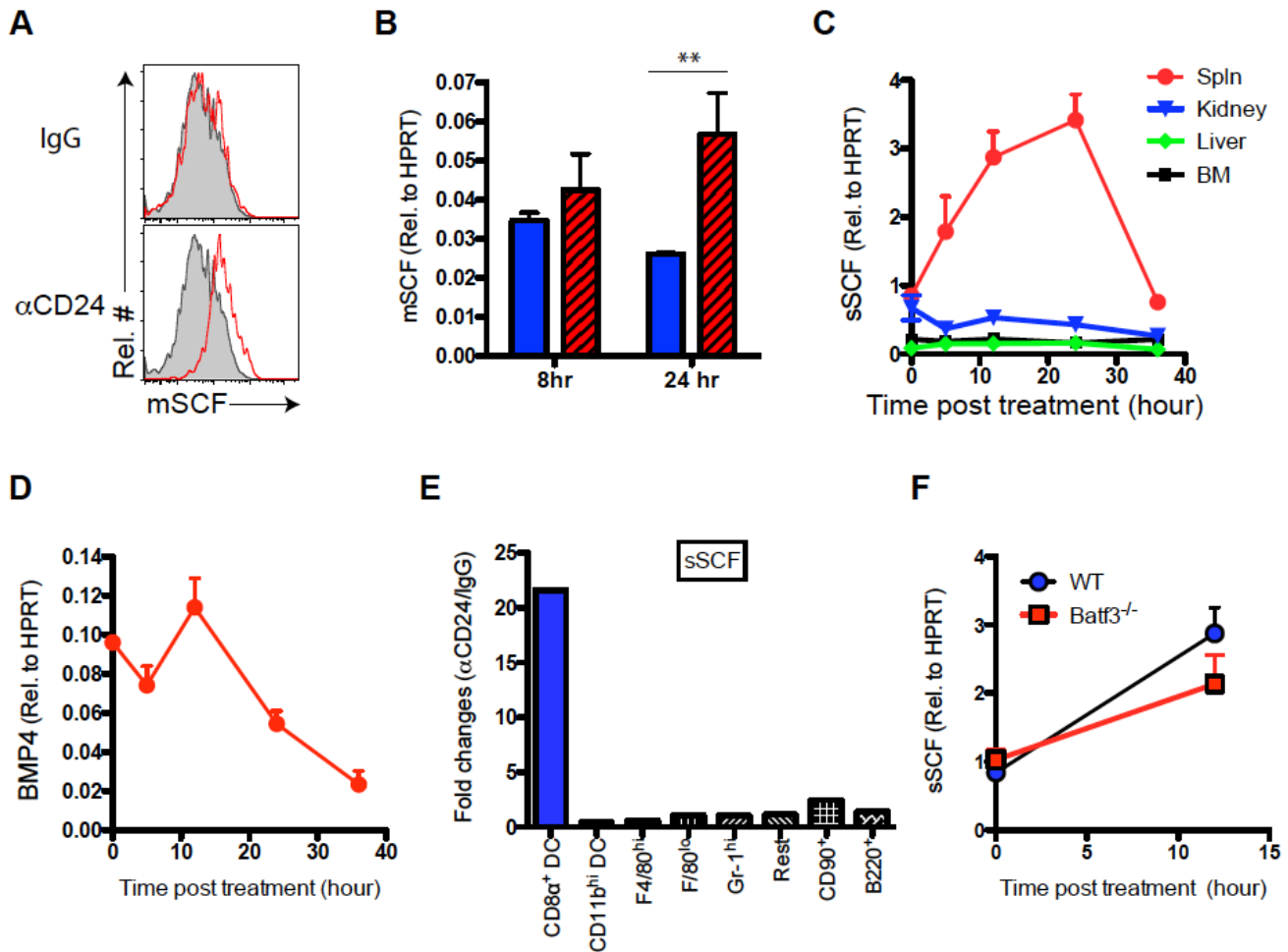


**Supplemental Figure 4.** Representative flow cytometric analyses of CD45<sup>+</sup>Kit<sup>+</sup> proerythroblastic cells in the spleen of M1/69-treated WT B6 mice at 24 hrs post treatment (> 20).

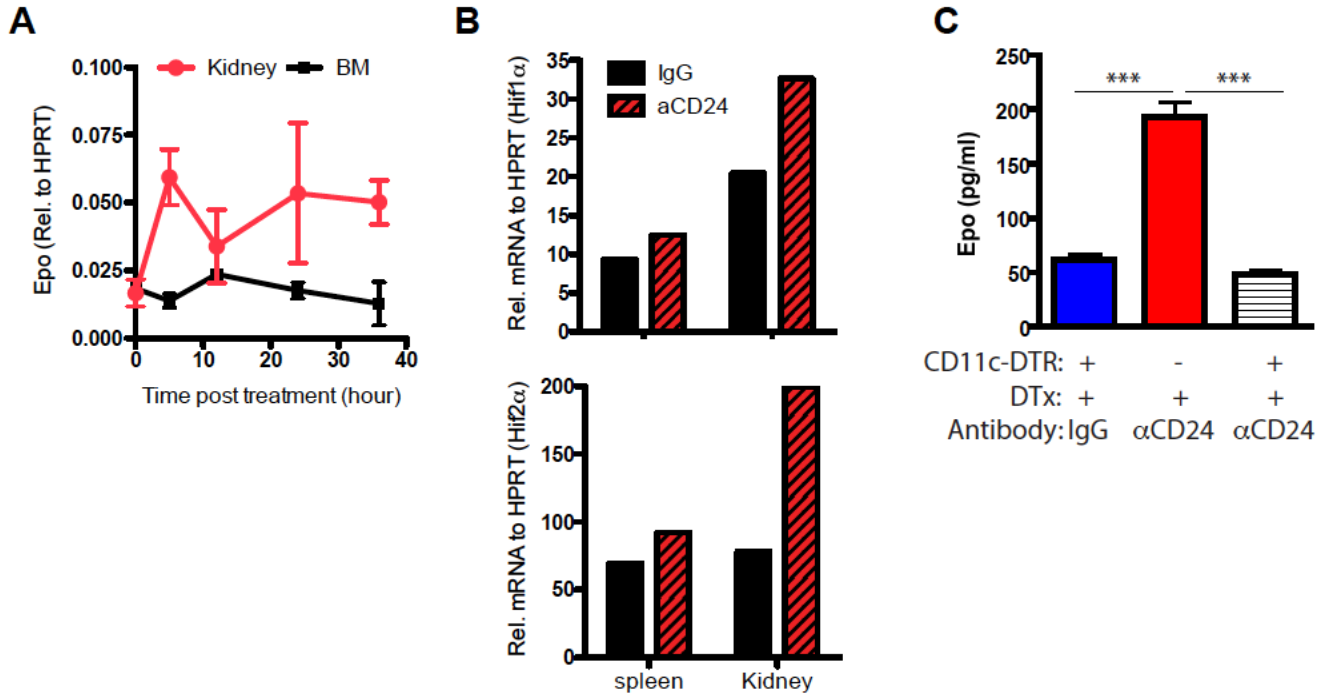


**Supplemental Figure 5. Serum Epo production in the presence of anti-Kit blocking mAb (ACK2) and splenectomized mice after αCD24 engagement.** (A) WT B6 mice were treated i.p. with Kit signaling blocking antibody (clone ACK2) at days 0 and 1 (200 μg/each injection) post M1/69 treatment. (B) Splenectomized mice were treated i.p. with 100 μg of M1/69. Sera were collected on day 3 post Ab treatment and subject to ELISA for EPO detection. Data represent mean ± SEM (n= 3 - 7); \*\*\*P < 0.001.

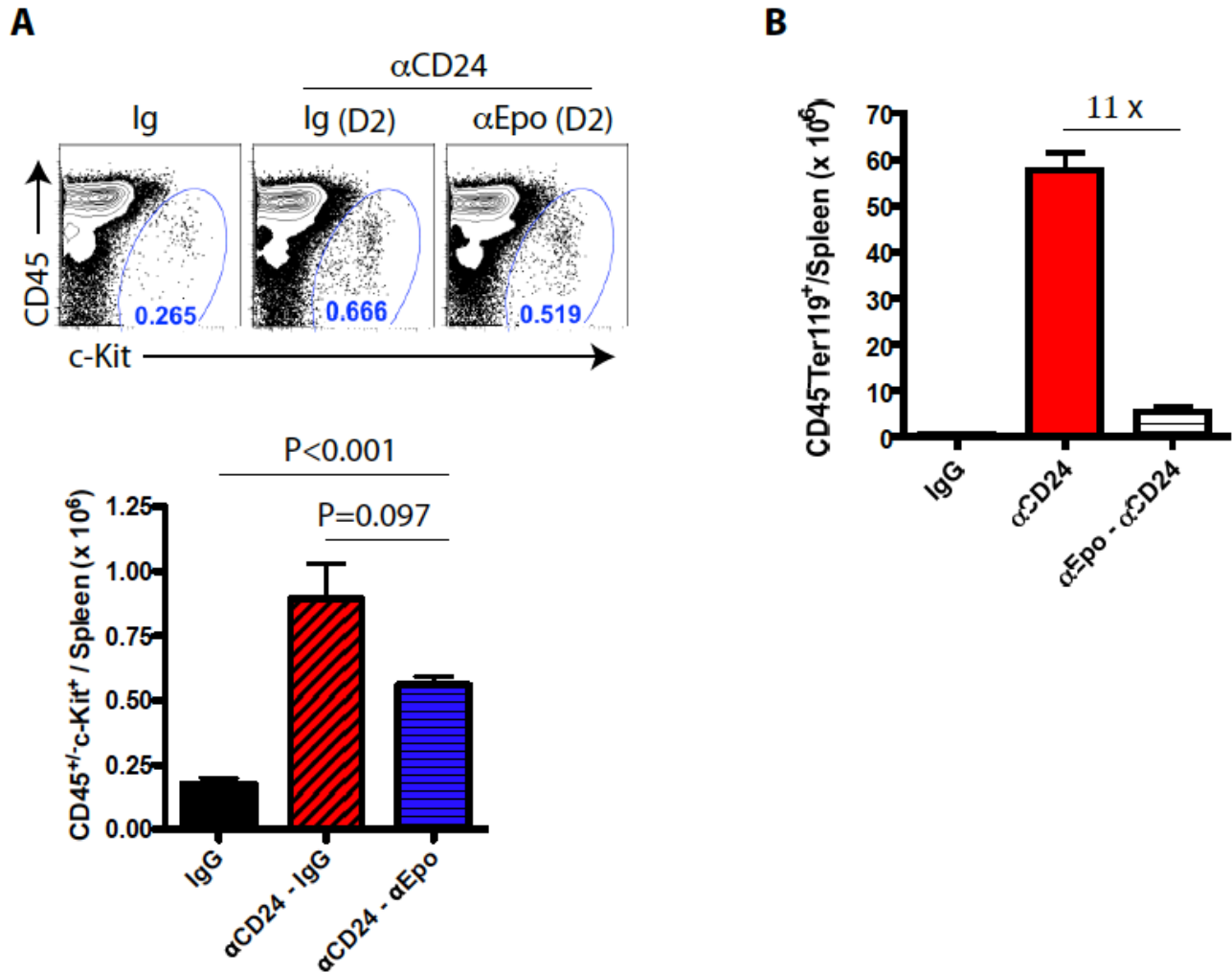




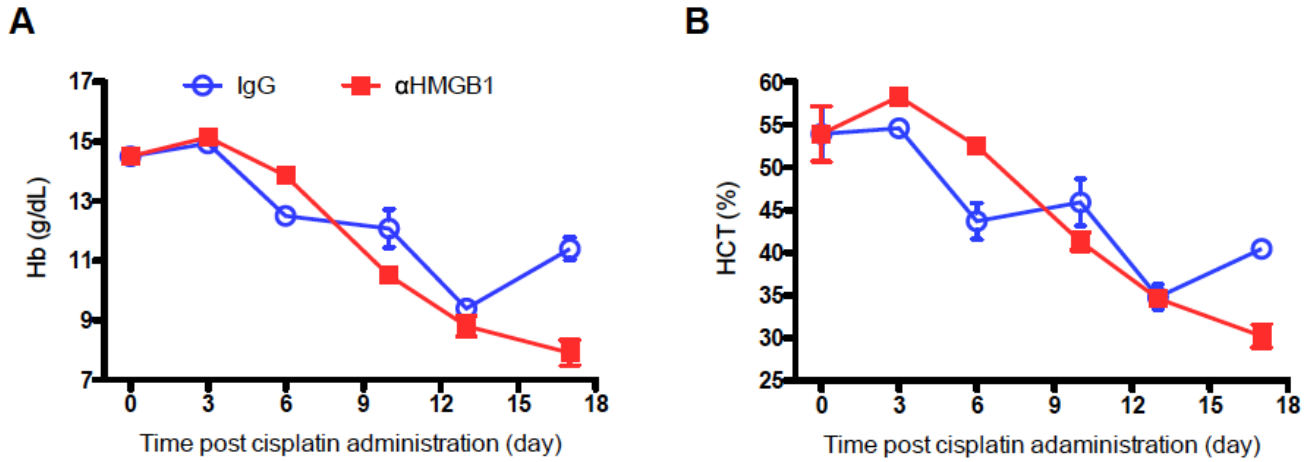
**Supplemental Figure 6. DC production of SCF upon CD24 ligation.** (a and b) Murine BMDCs were stimulated *in vitro* with M1/69 for 18 hrs and stained for surface (membrane) SCF expression for analysis by flow cytometry (A) or mRNA by qRT-PCR at 8 and 24 hrs post M1/69 incubation (B). Data in B represent mean  $\pm$  SEM of triplicates of two independent experiments; \*\*P < 0.01. (C) Kinetic analyses of soluble SCF mRNA in various organs after M1/69 treatment. (D) BMP4 mRNA expression in the spleens of the M1/69-treated mice at the indicated times. (E) Analyses of soluble SCF mRNA expression among cell types sorted from spleens of M1/69-treated mice at 15 hrs (n = 4 mice pooled/sorting). Data represent two independent experiments. (F) Examination of sSCF mRNA expression in the spleens of M1/69-treated WT or Batf3 $^{-/-}$  mice at the indicated time points. Data in C, D, and F represent mean  $\pm$  SEM (= 3 – 5).



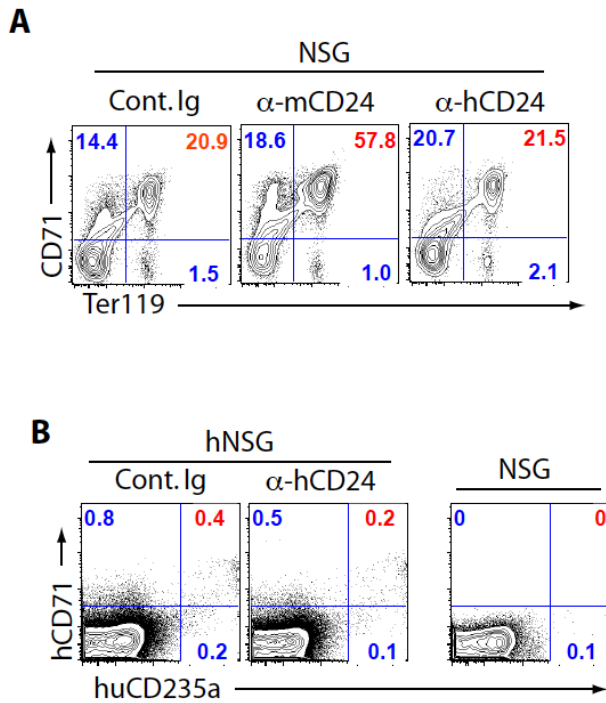
**Supplemental Figure 7. cDCs are required for renal EPO production upon CD24 engagement.** (A) Kinetic analyses of EPO mRNA expression in the Kidney and BM of M1/69-treated mice over time. (B) Analyses of Hif-1/2 $\alpha$  mRNA expression in the Kidney and spleen of M1/69-treated mice at 1 day post Ab treatment. (C) DC requirement for serum EPO production after CD24 engagement. CD11c-DTR mice were administrated i.p. with DTx (100 ng) at 4 hr prior to M1/69 treatment. Sera were collected and measured at day 3 post Ab treatment by ELISA. Data represent mean  $\pm$  SEM (= 3 – 5); \*\*\*P < 0.001.



**Supplemental Figure 8. Impact of Epo signaling blockade on the activation and expansion of early and late erythroid progenitors.** WT B6 mice were treated i.p. with anti-Epo antibody (MAB959, R&D systems) at days 0 and 1 (200  $\mu$ g/each injection) post M1/69 treatment. **(A)** Spleens were collected on day 3 post Ab treatment and evaluated for early erythroid progenitors (CD45<sup>+</sup>-CD117<sup>+</sup>) by flow cytometry. Data represent mean  $\pm$  SEM (n = 4 - 6). **(B)** Late erythroid progenitors (CD45<sup>+</sup>Ter119<sup>+</sup>) in the spleen were examined at d5 post M1/69 treatment. Data shown represent mean  $\pm$  SEM of pooled mice of at least two independent experiments (n = 4 - 6).



**Supplemental Figure 9. HMGB1/CD24 sensor system is required for efficient stress erythropoiesis.** Mice were treated i.v. with cisplatin daily at days 0, 1, and 2. The cisplatin-treated mice also received  $\alpha$ HMGB1 mAb (clone 3E8, 200  $\mu$ g) i.p. at days 1, 2 and 3 post cisplatin treatment. Retro-orbital blood samples (30 – 50  $\mu$ l) were collected at the indicated days and immediately analyzed on the Hemavet 850 FS automated CBC analyzer for Hb (**A**) and HCT (**B**). Data shown represent mean  $\pm$  SEM of pooled mice of at least two independent experiments (n = 3 – 5).



**Supplemental Figure 10. Detection of murine, but not human, erythroid progenitors in the spleens of humanized mice after CD24 engagement.** NOD/SCID/IL-2R $\gamma$ -null (NSG) mice and humanized mice (hNSG) were treated i.p. with control Igs, or Abs against mouse (M1/69) or human (eBioSN3 or ML5) CD24, respectively. Ab-treated mice were necropsied at d5 for the measurement of erythroid progenitors in the spleens after staining with erythroid-lineage markers specific for mouse (CD71<sup>+</sup>Ter119<sup>+</sup>) (**A**) or human (hCD71<sup>+</sup>CD235a<sup>+</sup>) (**B**). Data represent at least two independent experiments.

## Supplemental Table 1. Primer sequences used for qRT-PCR

<u>Gene Name</u>	<u>Sequence</u>	<u>Reference</u>
<b><u>Mouse</u></b>		
EPO	Forward: 5'-GGGTGCCCCGAACGTCCCAC-3' Reverse; 5'-AGATGAGGCGTGGGGGAGCA-3'	Sakoda <i>et al.</i>
Hif1a	Forward: 5'-TCTGGATGCCGGTGGTCTAG-3' Reverse; 5'-TGCAGTGAAGCACCTTCCAC-3'	Sakoda <i>et al.</i>
Hif2a	Forward: 5'-TCAGTGCGAACATGGCCCCCGA-3' Reverse; 5'-AGCACTGTGGCGGGAACCCA-3'	Sakoda <i>et al.</i>
BMP4	Forward: 5'-TGCTGGCGAGCCCGCTTCTG-3' Reverse; 5'-TGCGTCGCTCCGAATGGCACTAC-3'	Millot <i>et al.</i>
mSCF	Forward: 5'-TCCCGAGAAAGGGAAAGC-3' Reverse; 5'-CTGCCCTTGTAAGACTTGACTG-3'	Gu <i>et al.</i>
sSCF	Forward: 5'-TTATGTTACCCCCTGTTGCAG-3' Reverse; 5'-CTGCCCTTGTAAGACTTGACTG-3'	Gu <i>et al.</i>
<b><u>Human</u></b>		
mSCF	Forward: 5'-GATGTTTTGCCAAGTCATTGTTGG-3' Reverse; 5'-ACTGACTCTGGAATCTTTCTCAGG-3'	Hachiya <i>et al.</i>
sSCF	Forward: 5'-GGACTTTGTAGTGGCATCTGAA-3' Reverse; 5'-CTAAGGGAGCTGGCTGCAA-3'	Wygrecka <i>et al.</i>
b-actin	Forward: 5'-ATTGCCGACAGGATGCAGGAA-3' Reverse; 5'-GCTGATCCACATCTGCTGGAA-3'	Wygrecka <i>et al.</i>

**Reference:**

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Wygrecka M. *et al.* Mast cells and fibroblasts work in concert to aggravate pulmonary fibrosis: role of transmembrane SCF and the PAR-2/PKC-alpha/Raf-1/p44/42 signaling pathway. *Am J Pathol* 182: 2094–2108 (2013).

Millot S. *et al.* Erythropoietin stimulates spleen BMP4-dependent stress erythropoiesis and partially corrects anemia in a mouse model of generalized inflammation. *Blood* 2010;116(26):6072-6081.

Gu Y. *et al.* (2009) Steel factor controls primordial germ cell survival and motility from the time of their specification in the allantois, and provides a continuous niche throughout their migration. *Development* 136: 1295–1303.