

# A requirement for Lim domain binding protein 1 in erythropoiesis

LiQi Li,<sup>1</sup> Jan Y. Lee,<sup>1</sup> Jennifer Gross,<sup>1</sup> Sang-Hyun Song,<sup>2</sup> Ann Dean,<sup>2</sup> and Paul E. Love<sup>1</sup>

<sup>1</sup>Section on Cellular and Developmental Biology, Eunice Kennedy Shriver National Institute of Child Health and Human Development, and <sup>2</sup>Laboratory of Cellular and Developmental Biology, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Bethesda, MD 20892

**During erythrocyte development, the nuclear cofactor Lim domain binding protein 1 (Ldb1) functions as a core subunit of multiprotein DNA binding complexes that include the transcription factors Scl and Gata-1 and the Lim-only adapter Lmo2. Scl, Gata-1, and Lmo2 are each required for erythropoiesis, suggesting that Ldb1-nucleated transcription complexes regulate key steps during erythropoiesis. We documented a requirement for Ldb1 in erythropoiesis in mice. Analysis of *ldb1*<sup>-/-</sup> embryos revealed a critical requirement for Ldb1 during primitive erythropoiesis, and conditional inactivation of *ldb1* at later stages of gestation and in adult mice demonstrated that Ldb1 is continuously required for both definitive erythropoiesis and megakaryopoiesis. Down-regulation of Ldb1 in erythroblasts inhibited the expression of multiple erythroid-specific and prosurvival genes. These results represent the first unequivocal demonstration of a role for Ldb1 in erythropoiesis *in vivo* and establish a critical function for Ldb1-nucleated complexes in regulating the erythroid/megakaryocyte transcriptional program.**

CORRESPONDENCE  
Paul E. Love:  
lovep@mail.nih.gov

Abbreviations used: BFU-E, burst forming unit-erythroid; CFC, colony forming cell; CMP, common myeloid progenitor; EryP, primitive erythrocyte; ESC, embryonic stem cell; GMP, granulocyte-macrophage progenitor; HSC, hematopoietic stem cell; Ldb1, Lim domain binding protein 1; LK, Lin<sup>-</sup>Sca1<sup>-</sup>c-kit<sup>+</sup>; LSK, lineage<sup>lo/-</sup>Sca-1<sup>+</sup>c-kit<sup>+</sup>; MEL, mouse erythroleukemia; MEP, megakaryocyte-erythroid progenitor; pI:pC, polyinosinic-polycytidyllic acid.

Erythropoiesis follows a stepwise differentiation process that involves the commitment of hematopoietic stem cells (HSCs) to lineage-restricted progenitors and to terminally differentiated red blood cells. The first wave of erythropoiesis, designated primitive erythropoiesis, is transient and begins around embryonic day (E) 7.5 in the mouse extraembryonic yolk sac and/or aorta-gonad-mesonephros (Palis et al., 1999; Baumann and Dragon, 2005). Primitive erythrocytes (EryPs) represent the predominant blood cells in circulation until E12, when a second wave of erythroblasts generated in the fetal liver gives rise to definitive adult-type erythrocytes.

Erythropoiesis is critically dependent on the activity of the zinc finger transcription factor Gata-1 which is required for the expression of erythroid-specific genes (Welch et al., 2004). Gata-1 binds to several different cofactors, including Fog, Runx1, PU.1, EKLF, Lmo2, and SP1, and can function as both a transcriptional activator and a transcriptional repressor (Wadman et al., 1997; Johnson et al., 2007; Kim and Bresnick, 2007; Tripic et al., 2009). Multi-subunit complexes containing Gata-1 in addition to the basic helix-loop-helix transcription factors Scl/Tal1 and E2A and the nuclear adapters

Lmo2 and Lim domain binding protein 1 (Ldb1) have also been described in erythroid cell lines (Wadman et al., 1997). These multimeric complexes bind to important regulatory sites at erythroid genes, and at the  $\beta$ -globin locus, Ldb1 facilitates long-range promoter-enhancer interactions that are necessary for transcription (Xu et al., 2003; Song et al., 2007). Together, these results suggest that Ldb1 complexes may represent an important instrument for activating erythroid-specific gene transcription during development. Supporting this idea, Lmo2, Gata-1, and Scl are each essential for erythropoiesis suggesting that these proteins function cooperatively (Pevny et al., 1991; Warren et al., 1994; Robb et al., 1995, 1996; Shviddasani et al., 1995; Porcher et al., 1996; Schlaeger et al., 2005).

In this study, we examined the role of Ldb1 in erythroid development by evaluating the impact of *ldb1* deletion on erythropoiesis using both conventional and conditional *ldb1*-deficient mice. Our results reveal an essential and continuous

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role for Ldb1 in both primitive and definitive erythropoiesis as well as in adult megakaryopoiesis. Short hairpin (sh) RNA-mediated knockdown of Ldb1 resulted in the down-regulation of multiple erythroid/megakaryocyte-specific genes as well as genes important for erythrocyte survival. These findings represent the first comprehensive demonstration of an *in vivo* role for Ldb1 in erythropoiesis and provide strong support for the idea that an Ldb1-nucleated multiprotein complex serves as a primary mechanism through which Gata-1 exerts its positive regulatory function in erythroid gene transcription.

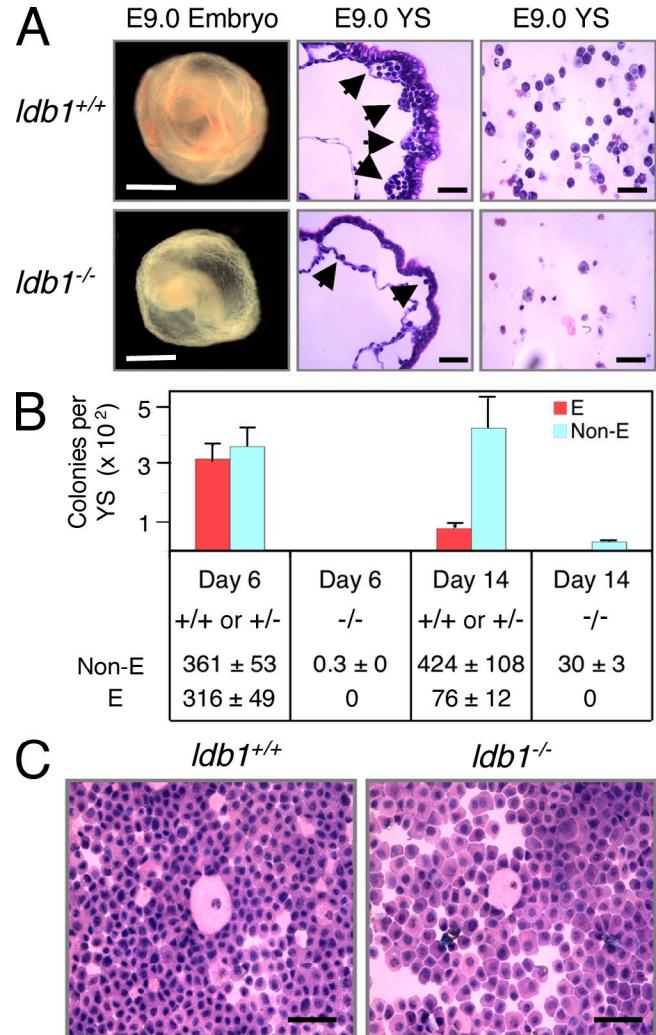
## RESULTS AND DISCUSSION

### Ldb1 expression in the hematopoietic lineage

To examine Ldb1 expression in the hematopoietic lineage, adult bone marrow and fetal liver cells were stained intracellularly with affinity-purified polyclonal Ldb1 antisera. FACS analysis revealed that Ldb1 levels are highest in lineage<sup>lo/-</sup>Sca-1<sup>+</sup>c-kit<sup>+</sup> (LSK) cells (Fig. S1 A), which are known to contain hematopoietic progenitors including HSCs (Ikuta and Weissman, 1992; Morrison et al., 1995). Indeed, in a separate study we found that Ldb1 is critical and continuously required for HSC maintenance (unpublished data). Slightly lower levels of Ldb1 were detected in lineage-committed progenitor populations (common myeloid progenitors [CMPs], megakaryocyte-erythroid progenitors [MEPs], and granulocyte-macrophage progenitors [GMPs]; Fig. S1 A). Interestingly, Ldb1 was also expressed at all stages of erythroid development but was strongly down-regulated in mature myeloid (Gr1<sup>+</sup>) and lymphoid (B and T) cells (Fig. S1, B and C), suggesting that Ldb1 may also have an important and specific function in erythropoiesis (Fig. S1 C).

### Defective primitive erythropoiesis in the absence of Ldb1

It was reported previously that benzidine-positive cells are undetectable in *ldb1*<sup>-/-</sup> yolk sacs, suggesting absent or defective primitive erythropoiesis (Mukhopadhyay et al., 2003). In agreement with this observation, *in vitro*-cultured embryoid bodies derived from *ldb1*<sup>-/-</sup> ES cells did not generate erythroid lineage cells, although myeloid lineage cells could be generated in the absence of Ldb1 (Fig. S2 A). Mesoderm/hemangioblast marker genes and genes involved in Ldb1 complex formation (*lmo2*, *scl*, *gata2*, and *gata1*) were expressed in day 5 *ldb1*<sup>-/-</sup> embryoid bodies, but no expression of erythroid-specific genes was detectable at any time point analyzed (Fig. S2, B and C; and not depicted). Consistent with these data, there was no evidence of blood formation in E9 *ldb1*<sup>-/-</sup> embryos (Fig. 1 A, left). E9 *ldb1*<sup>-/-</sup> yolk sac blood islands contained extremely low numbers of cells (Fig. 1 A, middle) that included rare myeloid blasts but no erythroblasts (Fig. 1 A, right). To evaluate the differentiation potential of progenitor cells in *ldb1*<sup>-/-</sup> yolk sacs, single cell suspensions from E9 yolk sacs were cultured *in vitro* in hematopoietic differentiation medium. Cells from E9 *ldb1*<sup>-/-</sup> yolk sacs generated  $\sim$ 10-fold fewer total colonies than cells from control yolk sacs (Fig. 1 B and not depicted). In addition, although control yolk sac cells gave rise to both erythroid and



**Figure 1.** *Ldb1* is required for primitive erythropoiesis. (A) E9.0 embryos were photographed, paraffin embedded, and sectioned for H&E staining. Left, E9.0 *ldb1*<sup>+/+</sup> and *ldb1*<sup>-/-</sup> embryos from an *ldb1*<sup>-/-</sup>  $\times$  *ldb1*<sup>+/+</sup>-mating showing yolk sacs and blood vessels. Bars, 500  $\mu$ m. Center, H&E staining of E9.0 embryos showing yolk sac blood islands. Arrows designate hematopoietic cells in yolk sac blood islands. Bars, 50  $\mu$ m. Original magnification, 400x. Right, Giemsa staining of cytopsins prepared from E9.0 yolk sac. Bars, 50  $\mu$ m. Original magnification, 400x. Data are representative of 3 *ldb1*<sup>-/-</sup> embryos and 11 littermate controls. Controls consisted of *ldb1*<sup>+/+</sup> and *ldb1*<sup>+/+</sup> embryos, which were phenotypically indistinguishable (not depicted). (B) Single cell suspensions from yolk sacs were prepared for *in vitro* methylcellulose culture. Erythroid (E) and non-erythroid (non-E) CFCs in E9.0 *ldb1*<sup>-/-</sup>, *ldb1*<sup>+/+</sup>, and *ldb1*<sup>+/+</sup> yolk sacs. Colonies were counted on days 6 and 14 after the initiation of the *in vitro* culture. One representative of two experiments is shown. Values are expressed as means  $\pm$  SD. (C) Giemsa staining of cytopsins prepared from day 14 methylcellulose cultures derived from E9.0 *ldb1*<sup>+/+</sup> or *ldb1*<sup>-/-</sup> YS. Bars, 50  $\mu$ m. Original magnification 400x. Images are representative of two experiments.

nonerythroid colonies that were apparent by day 6 of culture, *ldb1*<sup>-/-</sup> yolk sac cells generated only nonerythroid colonies consisting of myeloid blasts or mature macrophages that were

apparent only after 10–14 d of culture (Fig. 1, B and C and not depicted). Together, these results demonstrate that hematopoietic specification is impaired and primitive erythropoiesis is abrogated in the absence of *ldb1*.

### **Ldb1 is required for definitive fetal erythropoiesis**

To examine the role of Ldb1 in definitive erythropoiesis, we used a conditional deletion allele of *ldb1* (*ldb1<sup>fl/fl</sup>*) generated in ES cells by homologous recombination (Suleiman et al., 2007). Although *ldb1<sup>-/-</sup>* mice die between E9 and E10, *Ldb1<sup>fl/fl</sup>* mice were viable and fertile and exhibited no hematopoietic defects (unpublished data). Cre-recombinase-mediated deletion of the *ldb1<sup>fl</sup>* alleles in oocytes recapitulated the early embryonic lethality observed in *ldb1<sup>-/-</sup>* mice (unpublished data). Because our results indicated that Ldb1 was required for normal hematopoietic specification and primitive erythropoiesis, we generated mice in which conditional deletion of *ldb1* was mediated by the tyrosine kinase with immunoglobulin and epidermal growth factor homology domains 2 (Tie2) Cre transgene (Kisanuki et al., 2001). In a previous study, it was shown that HSCs are generated in normal numbers and primitive erythropoiesis is partially rescued in Tie2Cre *scl<sup>fl/fl</sup>* embryos but that Tie2Cre-mediated gene deletion occurs in fetal liver hematopoietic progenitor cells that give rise to definitive erythrocytes (Schlaeger et al., 2005).

To increase the probability that *ldb1* would be completely deleted after Cre expression, one *Ldb1* allele was deleted in the germline to generate *ldb1<sup>+/Δ</sup>* mice. Tie2Cre *ldb1<sup>+/Δ</sup>* mice were then crossed with *ldb1<sup>fl/fl</sup>* mice to generate Tie2Cre *ldb1<sup>fl/Δ</sup>* embryos. Tie2Cre-mediated deletion of the *ldb1<sup>fl</sup>* allele in fetal liver cells was confirmed by PCR of genomic DNA (Fig. S3 C). Tie2Cre *ldb1<sup>fl/Δ</sup>* embryos developed normally through E12. However, by E12.5, all Tie2Cre *ldb1<sup>fl/Δ</sup>* embryos exhibited widespread hemorrhage and edema (Fig. S3 A). Fetal liver size and cellularity were markedly decreased in E11.5–14.5 Tie2Cre *ldb1<sup>fl/Δ</sup>* mice (Fig. S3, A and B) and no embryos survived beyond E14.5.

EryPs were detected in the blood of all E12.5 Tie2Cre *ldb1<sup>fl/Δ</sup>* embryos; however, a maturation defect was apparent from the high percentage of mitotic and basophilic cells and the high frequency of immature erythroid blasts (Fig. 2 A). This phenotype was strikingly similar to that observed in E12.5 Tie2Cre *scl<sup>fl/fl</sup>* mice (Schlaeger et al., 2005). The reduced cellularity in Tie2Cre *ldb1<sup>fl/Δ</sup>* fetal livers was due primarily to low numbers of erythroid (Ter119<sup>+</sup>) cells (Fig. 2 B) and was most obvious on E13.0 and thereafter, when the definitive erythroid pool was rapidly expanding in control embryos but not in Tie2Cre *ldb1<sup>fl/Δ</sup>* embryos (Fig. 2 C and Fig. S3 B). Importantly, although the total number of fetal liver cells was decreased in E12.5 Tie2Cre *ldb1<sup>fl/Δ</sup>* mice, the number of LSKs was normal at this time point indicating that the erythropoietic defects were not secondary to HSC depletion (Fig. 2 B). Analysis of downstream populations revealed a reduction in Lin<sup>-</sup>Sca1<sup>-</sup>c-kit<sup>+</sup> (LK) fetal liver cells in Tie2Cre *ldb1<sup>fl/Δ</sup>* mice, reflecting a marked decrease in the number of MEP (Fig. 2, B and C). In contrast, the number of CMP and

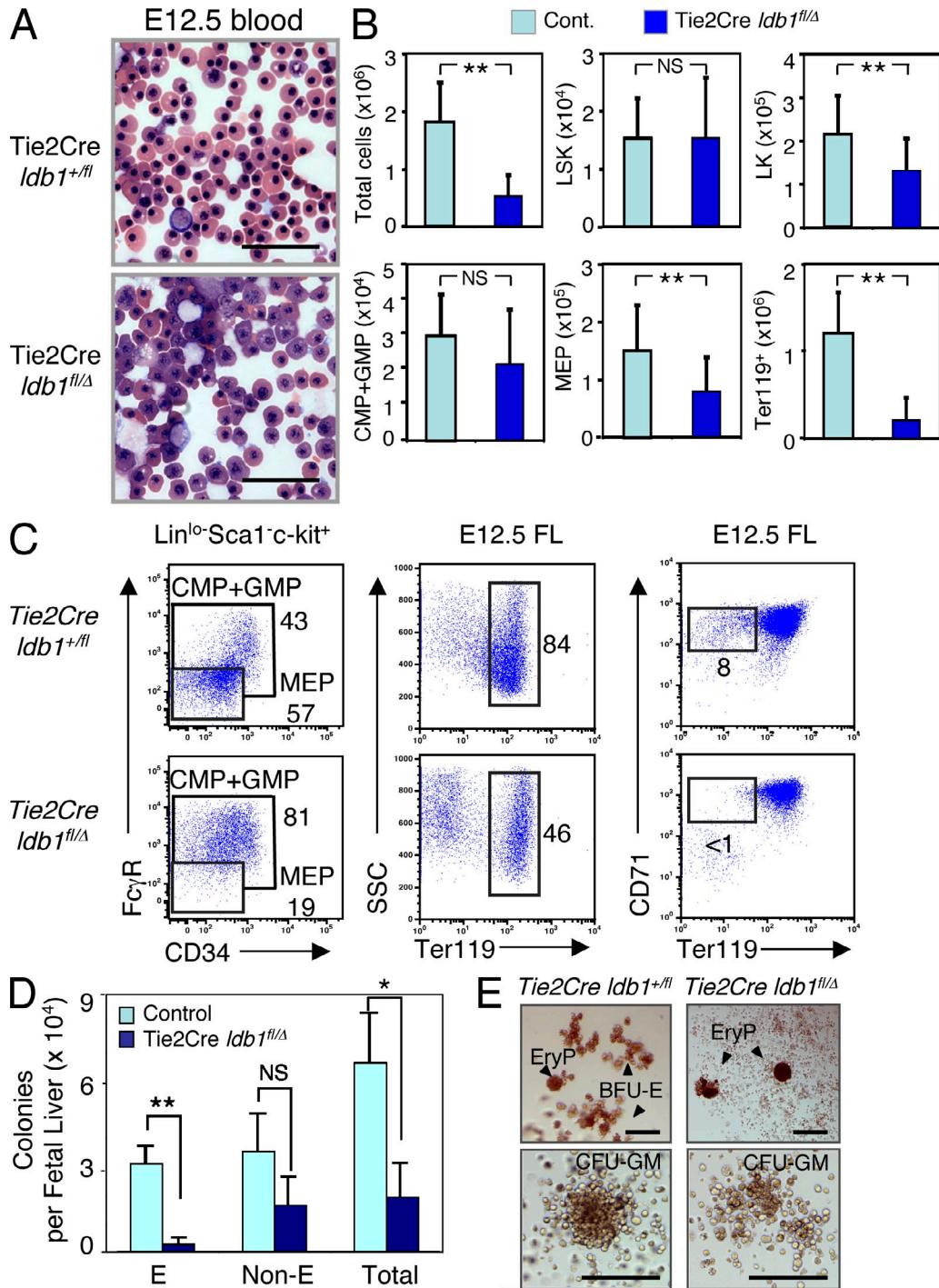
GMP fetal liver LK cells was only slightly reduced in E12.5 Tie2Cre *ldb1<sup>fl/Δ</sup>* mice, pointing to an early erythroid-specific defect (Fig. 2, B and C). Immature CD71<sup>hi</sup>Ter119<sup>low-med</sup> pro-erythroblasts and total Ter119<sup>+</sup> cells were also strongly reduced in Tie2Cre *ldb1<sup>fl/Δ</sup>* embryos (Fig. 2, B and C).

To evaluate the developmental potential of E12.5 Tie2Cre *ldb1<sup>fl/Δ</sup>* fetal liver cells, we next performed in vitro methylcellulose progenitor assays. After 8 d of culture, colonies were identified by visual inspection and enumerated. The number of erythroid colonies originating from Tie2Cre *ldb1<sup>fl/Δ</sup>* fetal liver cells was strongly reduced relative to controls (Fig. 2, D and E). In addition, erythroid colonies from Tie2Cre *ldb1<sup>fl/Δ</sup>* mice were derived almost exclusively from EryP–colony forming cells (CFCs; Fig. 2 E). In contrast, most erythroid colonies from control fetal livers were derived from definitive burst forming unit–erythroid (BFU-E) progenitors (Fig. 2, D and E; and not depicted). The near absence of definitive BFU-E colonies in Tie2Cre *ldb1<sup>fl/Δ</sup>* fetal liver cultures is consistent with the reduced number of fetal liver erythroid progenitors (MEPs; Fig. 2, B and C). In contrast, the number of nonerythroid CFU-macrophage (M) and CFU-GM progenitors were not significantly reduced in Tie2Cre *ldb1<sup>fl/Δ</sup>* fetal livers, identifying a selective requirement for *ldb1* in erythroid development (Fig. 2, D and E).

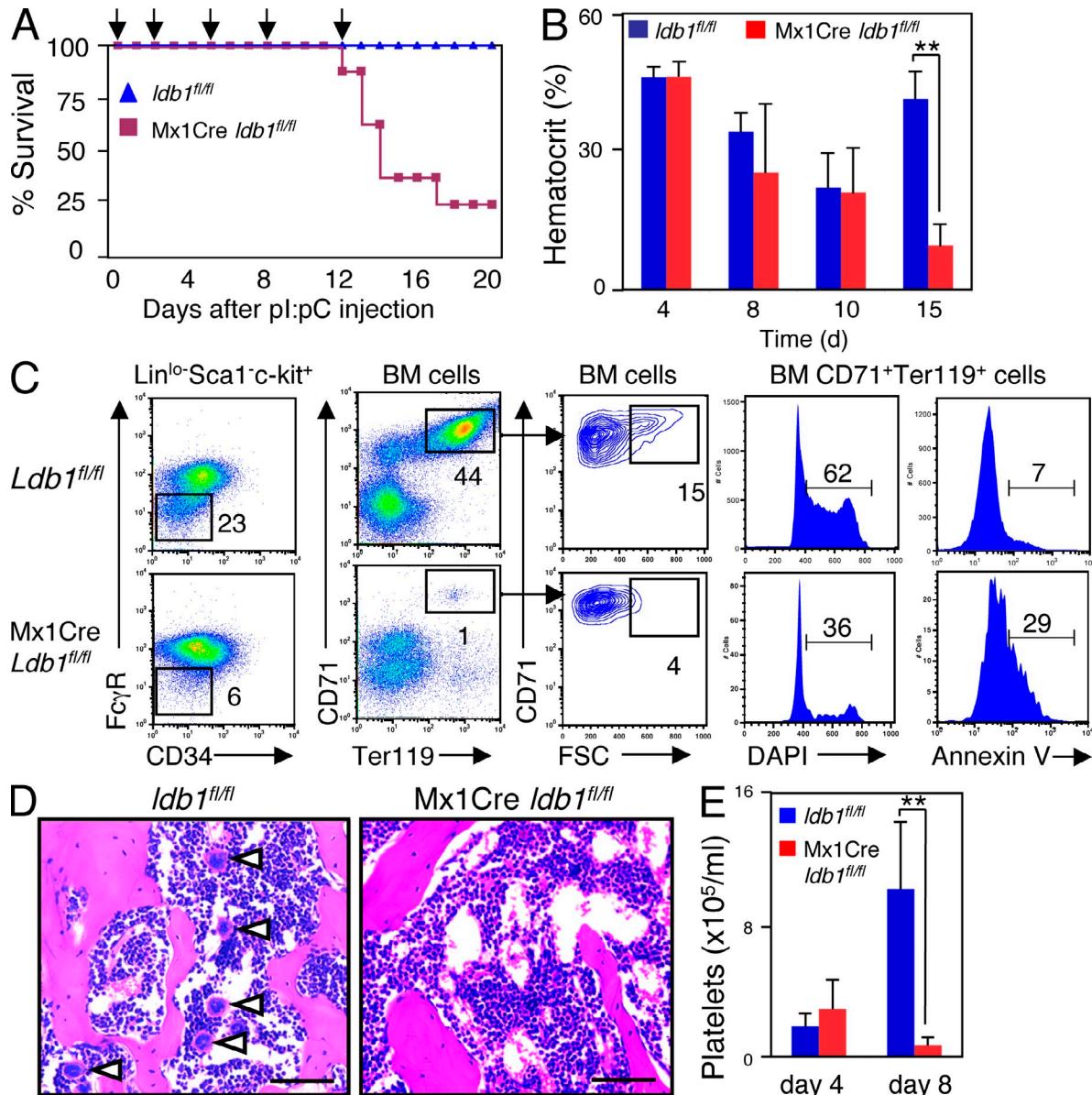
### **Ldb1 is continuously required for adult erythropoiesis and megakaryopoiesis**

To determine if Ldb1 is also required for adult erythropoiesis, we generated Mx1Cre *ldb1<sup>fl/fl</sup>* mice so that *ldb1* deletion could be induced by injection of polyinosinic-polycytidyl acid (pI:pC; Kühn et al., 1995). As shown in Fig. 3 A, most Mx1Cre *ldb1<sup>fl/fl</sup>* mice, but not control *ldb1<sup>fl/fl</sup>* mice, died within 20 d of pI:pC injection. As reported previously, injection of pI:pC causes a transient anemia (Hall et al., 2003), and this was observed in both control and Mx1Cre *ldb1<sup>fl/fl</sup>* mice (Fig. 3 B). However, although the hematocrit normalized 14 d after pI:pC injection in control mice, the hematocrit continued to decline in Mx1Cre *ldb1<sup>fl/fl</sup>* mice (Fig. 3 B). The total number of bone marrow cells was also dramatically decreased in Mx1Cre *ldb1<sup>fl/fl</sup>* mice after pI:pC-mediated Ldb1 deletion (unpublished data). Similar to Tie2Cre *ldb1<sup>fl/Δ</sup>* mice, Lin<sup>lo/-</sup>Sca1<sup>-</sup>c-kit<sup>hi</sup>CD34<sup>lo</sup>FcγR<sup>lo</sup> MEP populations, as well as CD71<sup>+</sup>Ter119<sup>+</sup>erythroblasts, were significantly reduced in pI:pC-treated Mx1Cre *ldb1<sup>fl/fl</sup>* mice (Fig. 3 C and Fig. S4 A). BFU-E and mixed (erythroid/myeloid) colonies were virtually absent in day 8 methylcellulose cultures of bone marrow cells from pI:pC-treated Mx1Cre *ldb1<sup>fl/fl</sup>* mice (Fig. S4, B and C). Similar to the results obtained with Tie2Cre *ldb1<sup>fl/Δ</sup>* fetal liver cells, granulocyte/macrophage colony formation was much less affected by inactivation of *ldb1* in adult bone marrow cells (Fig. S4 C).

FACS analysis of the few CD71<sup>+</sup>Ter119<sup>+</sup>erythroblasts present in Mx1Cre *ldb1<sup>fl/fl</sup>* mice after pI:pC-induced deletion of *ldb1* revealed an increase in the percentage of apoptotic (annexin V<sup>+</sup>) cells as well as a reduced percentage of cycling cells, indicating a requirement for Ldb1 in cell survival (Fig. 3 C and



**Figure 2.** *ldb1* is required for definitive fetal erythropoiesis. (A) Giemsa-stained peripheral blood from E12.5 Tie2Cre  $ldb1^{+/fl}$  and Tie2Cre  $ldb1^{fl/fl}$  embryos. Bars, 50  $\mu$ m. Original magnification, 400x. One representative of three experiments is shown. (B) Number of total fetal liver cells, LSK cells, LK cells, CMPs + GMPs, MEPs, and Ter119<sup>+</sup> cells in E12.5  $ldb1^{fl/fl}$  Tie2Cre and control embryos (controls consisted of littermate  $ldb1^{+/fl}$   $\pm$  Tie2Cre and  $ldb1^{fl/fl}$  embryos). NS, not significant; \*\*, P < 0.01. MEP, CMP, and GMP populations were designated as shown in C. Ter119<sup>+</sup> cell counts were obtained from 39 control embryos and 9 Tie2Cre  $ldb1^{fl/fl}$  embryos. LSK, LK, CMP+GMP, and MEP cell counts were obtained from 32 control embryos and 12 Tie2Cre  $ldb1^{fl/fl}$  embryos. Values are expressed as means  $\pm$  SD. (C) Lin<sup>lo</sup>-Sca1<sup>-</sup>c-kit<sup>+</sup> cells, CD34<sup>+</sup>, Fc $\gamma$ R<sup>lo</sup>–CD34<sup>lo</sup>– MEPs (left), total (Ter119<sup>+</sup>) erythroid cells (center), and CD71<sup>hi</sup>Ter119<sup>lo</sup> proerythroblasts (right) in E12.5 Tie2Cre  $ldb1^{fl/fl}$  and Tie2Cre  $ldb1^{+/fl}$  mice. Numbers are the percentage of cells in the indicated gate. (D) Numbers of erythroid (E), non-erythroid (non-E), and total colonies in day 8 methylcellulose cultures from E12.5 control and Tie2Cre  $ldb1^{fl/fl}$  fetal livers. NS, not significant; \*, P < 0.05; \*\*, P < 0.01. One representative of three experiments is shown. Values are expressed as means  $\pm$  SD. (E) Representative primitive erythroid (EryP), definitive erythroid (BFU-E), and myeloid (CFU-GM) colonies from Tie2Cre  $ldb1^{+/fl}$  and Tie2Cre  $ldb1^{fl/fl}$  fetal livers at day 8 of culture. Bars, 200  $\mu$ m. Original magnification, 50x. Images are representative of duplicate cultures from three litters.



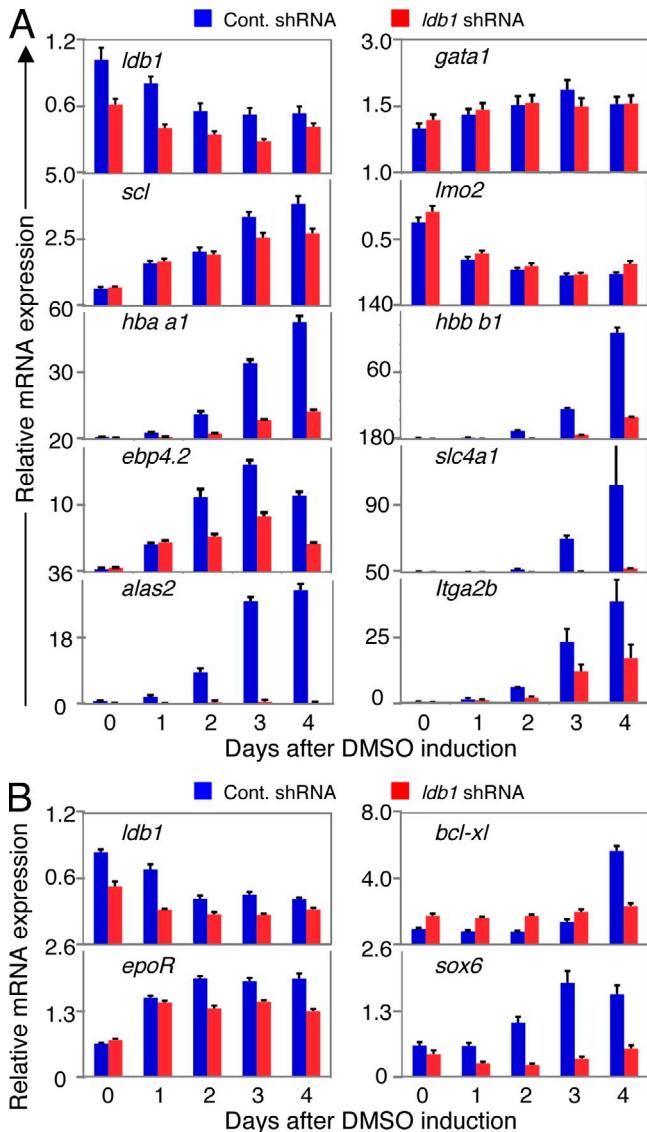
**Figure 3. *Ldb1* is continuously required for erythropoiesis and megakaryopoiesis in adults.** (A) Survival plot of adult MxCre *ldb1*<sup>fl/fl</sup> mice ( $n = 8$ ) and control *ldb1*<sup>fl/fl</sup> mice ( $n = 6$ ) after repeated pl:pC injection (arrows). (B) Hematocrits of MxCre *ldb1*<sup>fl/fl</sup> and control *ldb1*<sup>fl/fl</sup> mice after injection of pl:pC on days 1, 3, and 5. \*\*,  $P < 0.01$ . Values are expressed as means  $\pm$  SD. (C) Lin<sup>lo</sup>-Sca1+c-kit+Fc $\gamma$ R<sup>lo</sup>-CD34<sup>lo</sup> (MEP), CD71<sup>hi</sup>Ter119<sup>lo</sup> proerythroblasts, and Ter119+CD71+ erythroblasts in BM of indicated mice after pl:pC injection. Numbers are the percentage of cells in the indicated gate. Histograms show the percentage of cycling (DAPI<sup>int-hi</sup>) and apoptotic (annexin V<sup>+</sup>) Ter119+CD71+ erythroblasts. (D) H&E-stained sternal sections from pl:pC-injected MxCre *ldb1*<sup>fl/fl</sup> and *ldb1*<sup>fl/fl</sup> mice. Arrows indicate megakaryocytes. Bars, 50  $\mu$ m. (E) Peripheral blood platelet counts on days 4 and 8 after initial pl:pC injection. \*\*,  $P < 0.01$ . Values are expressed as means  $\pm$  SD. In C and D, mice were injected with pl:pC on days 1, 3, and 5 and sacrificed on day 8. In B-E, data shown are from four MxCre *ldb1*<sup>fl/fl</sup> mice and six littermate controls. Controls included *ldb1*<sup>fl/fl</sup> mice and *ldb1*<sup>fl/fl</sup> mice  $\pm$  MxCre.

Fig. S4 A). To determine if *Ldb1* is also important for megakaryocyte survival, sternal sections were obtained from pl:pC-treated MxCre *ldb1*<sup>fl/fl</sup> and control *ldb1*<sup>fl/fl</sup> mice and stained with hematoxylin and eosin (H&E). Strikingly, as early as 8 d after pl:pC injection, no megakaryocytes were detectable in sternal sections from pl:pC-treated MxCre *ldb1*<sup>fl/fl</sup> mice, pointing to a critical role for *Ldb1* in megakaryocyte survival (Fig. 3 D). In agreement with this finding, platelet counts in

the peripheral blood of MxCre *ldb1*<sup>fl/fl</sup> mice were markedly reduced relative to control *ldb1*<sup>fl/fl</sup> mice 8 d after pl:pC injection (Fig. 4 B).

#### ***Ldb1* is required for the expression of erythroid, megakaryocyte, and prosurvival genes**

To evaluate the impact of *Ldb1* down-regulation on the expression of erythroid- and megakaryocytic-specific genes,



**Figure 4. Ldb1 complexes regulate expression of erythroid, megakaryocytic, and prosurvival genes.** Stable clones of MEL cells expressing *ldb1* shRNA or control shRNA were treated with 1.5% DMSO to induce erythroid differentiation. Total RNA was isolated at the indicated times and gene expression was quantified by real-time RT-PCR with  $\beta$ -actin as control. (A) Expression of genes encoding Ldb1 complex subunits and erythroid/megakaryocytic lineage proteins are shown. (B) Expression of prosurvival genes (*bcl-xl*, *epoR*, and *sox6*) in MEL cells expressing *ldb1* shRNA or control shRNA after induction with DMSO. Results shown are representative of two independent induction experiments. Values are expressed as means  $\pm$  SD.

we analyzed gene expression in a Friend mouse erythroleukemia (MEL) cell line expressing a stable construct encoding *ldb1* shRNA (Song et al., 2007). Differentiation of the MEL cell line was stimulated by DMSO, which has been shown to induce the expression of erythroid- and megakaryocyte-specific transcripts (Friend et al., 1973). As shown in Fig. 4 A, *ldb1* transcripts were reduced by 20–50% in both uninduced and DMSO-induced *ldb1* shRNA MEL cells. Interestingly,

knockdown of *ldb1* strongly inhibited the induced expression of several erythroid genes including  $\alpha$ - and  $\beta$ -globin, *ebp4.2*, *slc4a1*, and *alas2* (Fig. 4 A). In addition, expression of the megakaryocyte-specific transcript *itga2b* was also markedly decreased (Fig. 4 A). These results confirm and extend previous studies supporting a critical requirement for Ldb1 in erythroid gene expression (Xu et al., 2003; Anguita et al., 2004; Lahil et al., 2004; Song et al., 2007). The dramatic increase in apoptotic erythroblasts after in vivo deletion of *ldb1* (Fig. 3 C) also prompted us to examine the effect of *ldb1* knockdown on the expression of erythroid prosurvival factors. As shown in Fig. 4 B, expression of three prosurvival genes, *epor*, *bcl-xl*, and *sox6*, was also significantly decreased in *ldb1* shRNA MEL cells, especially at later time points in cell culture when these genes were highly induced in control cells (Fig. 4 B). These results indicate that Ldb1 protein complexes regulate the expression of prosurvival as well as erythroid- and megakaryocyte-specific genes.

In the present study, we relate data demonstrating a critical, continuous, and specific role for Ldb1 in both erythropoiesis and megakaryopoiesis. These results are consistent with the high expression of Ldb1 in erythroid progenitors (Fig. S1) and with the observation that deletion of *ldb1* leads to a severe developmental block at the common megakaryocyte/erythroid progenitor stage (Fig. 2 C and Fig. 3 C). Deletion of *ldb1* severely impacted the erythroid/megakaryocyte lineages but had little effect on the development of myeloid cells. Using B cell– or T cell–specific Cre transgenes, we also found no evidence of a requirement for *ldb1* in lymphocyte development (unpublished data). A similar nonmandatory role for *lmo2* in T cell development was also demonstrated (McCormack et al., 2003).

Our results indicate that an important function of Ldb1 during erythropoiesis is to induce the expression of lineage-specific and prosurvival genes, presumably via its documented role as a key subunit of Ldb1/Lmo2/Scl/E2A/Gata-1 multimeric complexes (Fig. 4). Ldb1 nucleated complexes have been shown to regulate the expression of several erythroid genes including  $\alpha$ - and  $\beta$ -globin, *ebp4.2*, and *gypA* (Xu et al., 2003; Anguita et al., 2004; Lahil et al., 2004; Song et al., 2007). In addition, genome-wide profiling studies have detected Ldb1 at most Gata-1–bound DNA elements in erythroid cell lines, suggesting that Ldb1 complexes represent a major instrument for Gata-1–mediated gene activation (Tripic et al., 2009; Soler et al., 2010). In this paper, we provide evidence that down-regulation of Ldb1 severely impairs the induced expression of multiple erythroid- and/or megakaryocyte-specific genes in erythroleukemia cells. Interestingly, the expression of genes encoding other Ldb1 complex subunits, including *lmo2*, *gata-1*, and *scl*, was not as severely affected by down-regulation of *ldb1*, indicating that failure to assemble functional Ldb1 complexes, rather than reduced expression of Ldb1 complex subunits, is responsible for the reduction in erythroid gene expression (Fig. 4). In summary, these results establish an essential function for Ldb1 during erythrocyte and megakaryocyte development and survival

and suggest that Ldb1-nucleated complexes represent an important mechanism by which Gata-1 activates gene transcription in these lineages.

## MATERIALS AND METHODS

**Mice.** Tie2Cre and Mx1Cre transgenic mice were purchased from The Jackson Laboratory. All mice were bred and maintained in a National Institutes of Health (NIH) Research Animal Facility in accordance with the specifications of the Association for Assessment and Accreditation of Laboratory Animal Care. Mouse protocols were approved by the NIH Animal Care and Use Committee.

**Ldb1 antibody and Ldb1 intracellular staining.** Polyclonal rabbit anti-sera were raised against Ldb1 peptide MLDRDVGPTPMYPPTYLEPCamide, affinity purified, and conjugated with Alexa Fluor 647 (A20186; Invitrogen). Purified rabbit IgG (AB-105-C; R&D Systems) conjugated in the same way served as background control. Freshly isolated single cell suspensions were surface stained, fixed with 2% formaldehyde, permeabilized with 0.5% Triton X-100 (Bio-Rad Laboratories) in PBS, stained with Alexa Fluor 647-conjugated rabbit anti-Ldb1 or rabbit IgG, and analyzed by flow cytometry.

**Embryonic stem cell (ESC) lines.** The generation of *ldb1<sup>+/−</sup>* ESCs (Mukhopadhyay et al., 2003), *ldb1<sup>−/−</sup>* ESCs (Hwang et al., 2008), and *ldb1<sup>fl/fl</sup>* ESCs (Suleiman et al., 2007) has been described previously.

**ESC culture and embryoid body formation.** Undifferentiated ESCs were cultured in modified DME (Invitrogen) containing 15% FCS and LIF on mitomycin-treated embryonic fibroblast feeders. To generate embryoid bodies, ESC cultures were trypsinized until 5–10 cell clusters were formed. Trypsinization was stopped by addition of 10 ml IMDM medium containing 10% fetal calf serum and cells were incubated for 45 min at 37°C to allow reattachment of embryonic fibroblasts. ESCs were transferred to 10-cm bacterial Petri dishes and incubated in IMDM plus 15% FCS for 3–6 d in the presence of 40 ng/ml SCF and observed for the formation of embryoid bodies. Embryoid bodies generated in the primary culture were harvested by gravity sedimentation and plated in secondary methylcellulose cultures containing 50 ng/ml of recombinant mouse (rm) SCF, 10 ng/ml rm IL-3, and 10 ng/ml rh IL-6 or 50 ng/ml rm SCF and 3 U/ml rh Epo (STEMCELL Technologies Inc.).

**CFC assays.** Assays for hematopoietic progenitors in fetal liver or adult bone marrow were performed by culturing enumerated cells in methylcellulose-based IMDM medium containing 3 U/ml of recombinant human (rh) Epo, 50 ng/ml rm SCF, 10 ng/ml rm IL-3, and 10 ng/ml rh IL-6 (STEMCELL Technologies Inc.). For cultures of fetal liver cells and bone marrow cells,  $2.5 \times 10^4$ – $10^5$  cells were plated in duplicate and scored for colony formation at day 8. For yolk sac cultures, single cell suspensions of E9 yolk sacs were made, divided in half, and plated in duplicate.

**Flow cytometry and cell cycle analysis.** Conjugated antibodies, including mouse and hamster IgG isotype controls, were purchased from BD or eBioscience. The lineage marker (Lin) mixture for fetal liver cells included the following biotinylated antibodies: CD3-ε (145-2C11), CD4 (GK1.5), CD8-α (53-6), CD8-β (53-5.8), TCR-β (H57-597), TCR-γδ (GL3), CD19 (1D3), B220 (RA3-6B2), Gr1 (RB6-8C5), Ter119, CD49b (Dx5), and NK1.1 (PK136). Lin mixture for adult bone marrow cells included all of these plus Mac-1 (M1/70). Other conjugated antibodies used for surface staining included: CD34 (RAM34), CD43 (S7), CD71 (C2), c-kit (2B8), Sca1 (D7), and FcγIII/IIR (2.4G2). Biotinylated primary antibodies were detected by incubation of antibody-coated cells with streptavidin-PerCP-Cy5.5 or APC-Cy7 in a two step staining procedure. Percentage of apoptotic cells was determined by annexin V (BD) staining according to the manufacturer's instructions. For cell cycle analysis, cells were surface stained, fixed in 2% formaldehyde, permeabilized in 0.1% NP-40, and then stained with DAPI (Invitrogen). Data were acquired with a FACSCalibur or LSR II flow cytometer and analyzed with FlowJo software (Tree Star, Inc.).

**RT-PCR and quantitative RT-PCR.** The MEL cell line expressing *ldb1* shRNA has been described previously (Song et al., 2007). For gene expression studies, total cell RNA was isolated using PicoPure RNA isolation kit (Arcturus), and 100 ng of each RNA sample was reverse transcribed using SuperScript first-strand synthesis system (Invitrogen) and assayed by RT-PCR. Transcript quantification was performed with a LightCycler 480 (Roche). Duplicates were run for each sample in a 96-well plate. β-Actin was used as the endogenous reference gene. All quantitative RT-PCR reactions were run in three independent experiments. The relative quantification method was used, with the ratio of the mRNA level for the gene of interest normalized to the level of β-actin and the mean of control bone marrow samples as the calibrator value. The specificity of the products was confirmed based on melting curves and electrophoresis.

**Genotyping and deletion analysis of Tie2Cre *ldb1<sup>fl/fl</sup>* mice and Mx1Cre *ldb1<sup>fl/fl</sup>* mice.** PCR genotyping of Tie2Cre *ldb1<sup>fl/fl</sup>* mice and Mx1Cre *ldb1<sup>fl/fl</sup>* mice was performed on tail DNA. Primers used for detection of the Cre transgene were 5'-CGATGCAACGAGTGTGAGG-3' and 5'-GACTT-GCTGTCAGTTGGTCGT-3'. For Tie2Cre *ldb1<sup>fl/fl</sup>* mice, a combination of the following three oligonucleotide primers were used to detect the wild-type *Ldb1*, the *Ldb1<sup>fl</sup>*, and the Cre-mediated deleted (*Ldb1<sup>d</sup>*) alleles: *Ldb1S* 5'-CAGCAAACGGAGGAAACGGAAGATGTCAG-3', *Ldb1AS* 5'-CTTATGTCGACCACAGCCATGCATGTCAGTG-3', and *Ldb1A* 5'-TCAGGC-TGGCCTTAAACCTAA-3'. *Ldb1S*-*Ldb1AS* amplified a 320-bps wild-type allele fragment and 445-bps floxed allele fragment. *Ldb1A*-*Ldb1AS* amplified a 390-bps *Ldb1* Cre-mediated recombination allele fragment. For Mx1Cre *ldb1<sup>fl/fl</sup>* mice, a combination of the following three oligonucleotide primers were used to detect the wild-type *Ldb1*, the *Ldb1<sup>fl</sup>*, and the Cre-mediated deleted (*Ldb1<sup>d</sup>*) alleles: *Ldb1A* 5'-TCAGGCTGGCCTTAAACCTAA-3', *Ldb1B* 5'-TGGGACTACAAGGCTGAGAACAA-3', and *Ldb1C* 5'-TGGCT-GAGCTTATGTCACCA-3'. *Ldb1B*-*Ldb1C* amplified a 458-bp wild-type allele fragment and a 534-bp floxed allele fragment. *Ldb1A*-*Ldb1C* amplified a 342-bp *Ldb1* deleted allele fragment.

**Conditional inactivation of *Ldb1* in adult mice.** To inactivate *ldb1* in adult hematopoietic cells, 250 μl pI:pC (1 mg/ml; GE Healthcare) was injected intraperitoneally into each mouse on days 1, 3, and 5 (the day of the first injection was designated day 1). Mice were sacrificed on day 8 unless otherwise noted. Cells obtained from bone marrow or spleen were either analyzed directly or cultured in methylcellulose to analyze their colony forming potential.

**Online supplemental material.** Fig. S1 shows *Ldb1* expression in hematopoietic cells. Fig. S2 shows impaired erythroid developmental potential of *ldb1<sup>−/−</sup>* ESCs. Fig. S3 shows defective erythropoiesis in Tie2Cre *ldb1<sup>fl/fl</sup>* embryos. Fig. S4 shows that *Ldb1* is continuously required for survival and expansion of erythroblasts in adults. Online supplemental material is available at <http://www.jem.org/cgi/content/full/jem.20100504/DC1>.

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