Gata2 as a Crucial Regulator of Stem Cells in Adult Hematopoiesis and Acute Myeloid Leukemia

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SUMMARY

Subversion of transcription factor (TF) activity in hematopoietic stem/progenitor cells (HSPCs) leads to the development of therapy-resistant leukemic stem cells (LSCs) that drive fulminant acute myeloid leukemia (AML). Using a conditional mouse model where zinc-finger TF Gata2 was deleted specifically in hematopoietic cells, we show that knockout of Gata2 leads to rapid and complete cell-autonomous loss of adult hematopoietic stem cells. By using short hairpin RNAi to target GATA2, we also identify a requirement for GATA2 in human HSPCs. In Meis1a/Hoxa9-driven AML, deletion of Gata2 impedes maintenance and self-renewal of LSCs. Ablation of Gata2 enforces an LSC-specific program of enhanced apoptosis, exemplified by attenuation of anti-apoptotic factor BCL2, and re-instigation of myeloid differentiation—which is characteristically blocked in AML. Thus, GATA2 acts as a critical regulator of normal and leukemic stem cells and mediates transcriptional networks that may be exploited therapeutically to target key facets of LSC behavior in AML.

INTRODUCTION

Hematopoiesis is contingent on a rare pool of self-renewing hematopoietic stem cells (HSCs) and progenitors that are regulated by a combination of a cell-extrinsic program, imparted by the bone marrow (BM) niche in which they reside, and a cell-autonomous program driven by transcription factors (TFs), which regulate gene expression (Beck et al., 2013). Through loss-of-function genetic mouse models, the differentiation-stage requirement for specific TFs in myeloid and lymphoid committed progenitors has been characterized comprehensively (Orkin, 2000); yet, with few exceptions (Hock et al., 2004; Kranc et al., 2009; Pajerowski et al., 2010), the transcriptional program critical to adult HSC survival remains unclear.

Perturbed TF activity in the form of TF chromosomal translocations and loss- or gain-of-function genetic and epigenetic mutations in TFs has been implicated in the pathogenesis of hematologic malignancies, including acute myeloid leukemia (AML). AML is driven by a subset of leukemia cells—namely leukemic stem cells (LSCs) (Bonnet and Dick, 1997)—which are acknowledged to underpin leukemic growth and maintenance and, notably, are refractory to standard AML chemotherapeutics (Cradock et al., 2013; Ishikawa et al., 2007; Saito et al., 2010). Like their normal HSC counterparts, however, the requirement for TFs in LSC function is poorly defined; thus a deeper understanding of transcriptional regulation in this setting will afford insights toward specific targeting of LSCs, which will be necessary for improving the clinical armamentarium in AML.

Gata2, part of the zinc finger family of GATA family of TFs (Nagai et al., 1994), has been identified as a critical regulator of HSCs during ontogenesis of the hematopoietic system (Tsai et al., 1994). Constitutive lack of Gata2 (Gata2−/−) leads to embryonic fatality at embryonic day 10.5 (E10.5) due to anemia (Tsai et al., 1994). Chimera experiments demonstrated that Gata2−/− embryonic stem cells were unable to contribute to the formation of myeloid and lymphoid cells at the fetal liver (FL) developmental stage and in adult mice, suggesting that Gata2 acts as a crucial regulator of HSCs (Tsai et al., 1994). To formally assess the requirement for Gata2 in HSCs during embryonic development, using conditional knockout (KO) genetic models, Gata2 has been deleted in hemogenic endothelium cells, before the generation of HSCs using Vec-Cre (de Pater et al., 2013; Lim et al., 2012), and immediately following HSC formation using Vav-Cre (de Pater et al., 2013). Through functional analysis of Gata2-deficient cells from temporally restricted hematopoietic organs...
(aorta-gonad-mesonephros, FL) in these embryonic settings, Gata2 has been revealed as a pivotal regulator of cell-autonomous HSC generation and, thereafter, for HSC survival in the embryo. By analysis of haploinsufficient Gata2\textsuperscript{+/-} mice that express reduced Gata2, we and other laboratories have examined the impact of Gata2 gene dosage in adult hematopoiesis (Guo et al., 2013; Ling et al., 2004; Rodrigues et al., 2005). BM from Gata2\textsuperscript{+/-} mice displayed a reduction in abundance of immunophenotypically defined HSCs and in functionality during transplantation assays (Guo et al., 2013; Rodrigues et al., 2005). This was associated with decreased HSC proliferation, enhanced HSC quiescence and apoptosis, and attendant downregulation of anti-apoptotic BCL-XL in Gata2\textsuperscript{+/-} mice (Ling et al., 2004; Rodrigues et al., 2005). Gata2 haploinsufficiency also reduces granulocyte-macrophage progenitor (GMP) cell function while leaving other myeloid committed progenitors intact (Rodrigues et al., 2008). Conversely, forced expression of GATA2 in adult HSCs has similarly implicated Gata2 as a critical level-dependent regulator of adult HSC proliferation and differentiation (Persons and Allay, 1999).

Emphasizing the biological and clinical imperative to maintain normal GATA2 expression in adult hematopoiesis, deregulated GATA2 expression has been linked to the pathogenesis of pre-leukemic myelodysplastic syndrome (MDS) and AML. In its capacity as a tumor suppressor gene, loss of GATA2 expression in the context of sporadic or hereditary GATA2 haploinsufficiency mutations in coding or enhancer regions leads to immunodeficiency syndromes that predispose to MDS/AML when secondary mutations are attained (Hahn et al., 2011; Hsu et al., 2013; Soukup et al., 2019). Far more frequently, however, GATA2 overexpression has been implicated as a harbinger of poor prognosis in adult and pediatric AML, suggesting an oncogenic role for GATA2 in AML (Luesink et al., 2012; Vicente et al., 2012). Yet the requirement for GATA2 in AML cell fate decisions, including in the AML-propagating LSC compartment, remains poorly defined.

Using a genetic mouse model harboring conditional alleles of Gata2 and an inducible Mx1-Cre (Gata2\textsuperscript{fl/fl};Mx1-Cre\textsuperscript{+}), in which Gata2 expression can be deleted acutely in hematopoietic cells on administration of the interferon-\(\alpha\) mimic, polyinosinic-polycytidylic acid (pIpC), we investigated the hitherto unknown requirement for Gata2 in adult HSCs and LSCs. We identify Gata2 as an essential TF for adult HSC survival in BM and a unique hematopoietic TF required throughout HSC ontogeny. Using a gene knockdown (KD) approach, we independently demonstrate a conserved regulatory role for GATA2 in human cord blood (CB) hematopoietic stem/progenitor cells (HSPCs). Finally, we show that Gata2 regulates LSC capacity to propagate AML through modulation of self-renewal, apoptosis and myeloid differentiation rates.

**RESULTS**

**Gata2 Is Essential for Cell-Autonomous Adult HSC Maintenance**

We first assessed Gata2 expression in prospectively isolated HSPCs from adult BM. Gata2 expression was highest in HSCs, multipotent progenitors and hematopoietic progenitor cells-1/2, reduced in committed myeloid progenitor cells, and nearly extinguished in terminally differentiated blood cell populations (Figure 1A).

Next, to assess the requirement for Gata2 in adult HSC maintenance, we bred Gata2 harboring conditional alleles of Gata2 (Gata2\textsuperscript{fl/fl} mice) with Mx1-Cre to obtain a cohort of Gata2\textsuperscript{fl/fl};Mx1-Cre\textsuperscript{+} or control mice (Gata2\textsuperscript{fl/fl};Mx1-Cre\textsuperscript{-}) and administered pIpC on alternate days for 10 days to achieve acute deletion of Gata2 (Gata2 KO). The impact of Gata2 on hematopoiesis was assessed 14 days after the last injection of pIpC (Figure 1B). Near complete loss of GATA2 protein and Gata2 transcript was confirmed in BM by western blot and qPCR analysis, respectively (Figures 1B and S1A). BM cellularity was significantly attenuated in Gata2 KO mice in comparison with control mice (Figure S1B). Immunophenotypic analysis revealed that, while lymphoid lineages remained intact, a striking reduction of myeloid and erythroid cells was observed in the BM and/or peripheral blood (PB) of Gata2 KO mice (Figures 1C, S1C, and S1D). To identify the origin of myeloid and erythroid cell loss in the context of Gata2 deficiency, we assessed HSPCs from BM of Gata2 KO mice and found a near complete loss of cells in the LSK compartment (which contain HSCs and primitive progenitor cells) and LK compartment (comprising committed myeloid and erythroid progenitors) (Figure 1D). To investigate the kinetics of HSC loss after Gata2 deletion, we assessed the BM of Gata2 KO mice 5 days after the last pIpC dose (Figure 1B). Remarkably, we observed a near complete depletion of myeloid cells and LSK and LK cells by day 5 (Figures 1E and 1F), indicating a rapid loss of HSCs immediately following Gata2 deletion, consistent with a profound HSC survival defect.

Mx1-Cre mediates gene deletion in hematopoietic cells, extramedullary tissues, and in the BM niche (Kühn et al., 1995). To stringently evaluate whether Gata2 functions to regulate HSC maintenance cell autonomously, we transplanted CD45.2\(^{+}\) BM cells from Gata2\textsuperscript{fl/fl};Mx1-Cre\textsuperscript{+} or control mice, which have not received pIpC, together with unfractonated CD45.1\(^{+}\) BM cells in a competitive transplant (Figure 1G). Similar engraftment was observed in the PB of recipients transplanted with Gata2\textsuperscript{fl/fl};Mx1-Cre\textsuperscript{+}...
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and control cells before Gata2 deletion (Figure 1H). Six weeks after transplantation, Gata2 deletion was induced by plpC administration, and efficient Gata2 deletion in CD45.2+ BM cells of recipients transplanted with Gata2fl/fl;Mx1-Cre cells was confirmed 14 days after the last plpC dose (Figure 1I). We observed a decrease in the frequency of CD45.2+ Gata2 KO cells in BM, and to a lesser extent in PB (Figure 1J). Further immunophenotypic analysis revealed a complete loss of myeloid cells in BM and PB and a significant reduction of erythroid cells in BM (Figures S1E and S1F). Strikingly, only CD45.1+ BM support cells were able to contribute to HSPC maintenance; no CD45.2+ Gata2 KO cells were detectable within the LSK and LK compartments (Figures 1K and 1L). To test that HSPC loss was not merely due to an attenuation of cell surface markers that define HSCs, such as Sca-1 and c-kit, we isolated vestigial Gata2 KO CD45.2+ BM cells from primary recipients and transplanted them together with unfractonated CD45.1+ competitor cells into secondary recipients (Figure 1G). Four weeks after transplantation we found no Gata2 KO cells in the BM or PB of the mice transplanted with Gata2 KO BM cells (Figure 1M).

Having shown entire loss of the myeloid lineage while lymphoid cells were preserved at 14 days after the last injection of plpC in the BM of Gata2 KO mice, we next investigated whether the lack of multi-lineage failure after Gata2 deletion was due to the relatively longer lifespan of lymphoid cells compared with myeloid cells. To test this directly, we performed a long-term transplantation assay to abolish Gata2 expression in a cell-autonomous manner and monitored mice for 16 weeks to study the impact of Gata2 deletion on long-term hematopoiesis (Figure 1N). Analysis of PB revealed a continual decline in contribution of Gata2 KO cells to blood lineages of recipient mice, with less than 5% engraftment of Gata2 KO cells detectable at 16 weeks after Gata2 deletion, indicating a multi-lineage defect in Gata2 KO cells (Figure 1O). In addition, BM analysis showed an absence of CD45.2+ Gata2 KO cells in the LSK compartment at 16 weeks (Figure 1P). Full deletion of the Gata2 gene was achieved in residual PB and BM Gata2 KO cells at 16 weeks (Figure 1Q).

To eliminate the possibility of Gata2-dependent extrinsic HSC regulation through the BM niche, we transplanted un-fractonated CD45.1+ BM cells into lethally irradiated CD45.2+ Gata2fl/fl;Mx1-Cre+ or control mice. Six weeks after transplantation, we administered plpC to obtain Gata2-deficient (Gata2 KO) or control BM niche recipient mice and monitored the engraftment for up to 12 weeks (Figure 1Q). The frequency of CD45.1+ cells in the PB of Gata2 KO recipients remained comparable with those transplanted in control mice (Figures S1H and S1I). In concert, these data demonstrate that Gata2 is critically required for cell-autonomous maintenance of HSCs and multi-lineage hematopoiesis.

Figure 1. Gata2 Is Essential for Cell-Autonomous HSC Maintenance

(A) Gata2 expression in hematopoietic cells compared with Gata2 expression in HSCs (n = 3 independent experiments). Statistical analyses: one-way ANOVA.

(B) Top: control and Gata2fl/fl;Mx1-Cre mice received six injections of plpC on alternate days and were analyzed 15 or 24 days after the first injection. Bottom: Gata2 protein level in BM cells from control and Gata2 KO at day 24 after plpC administration against GAPDH.

(C and D) Fluorescence-activated cell sorting (FACS) plots of (C) myeloid (Gr1+Mac1+) and (D) hematopoietic stem and progenitor cells (HSPCs) from control and Gata2 KO mice at day 24 (n = 4).

(E and F) FACS plots showing (E) myeloid cells and (F) HSCs from control and Gata2 KO mice at day 15 (n = 3).

(G) CD45.2+ BM cells from untreated control or Gata2fl/fl;Mx1-Cre mice were transplanted with CD45.1+ WT BM cells into irradiated recipients. Six weeks later, mice received six doses of plpC. Fourteen days after last plpC dose (day 24) mice were analyzed and CD45.2+ BM cells transplanted into secondary irradiated recipients.

(H) Frequency of CD45.2+ cells in PB at week 6, before plpC injection (n = 4).

(I) Representative gel showing genotyping of donor-derived CD45.2+ fraction BM from plpC-treated recipient mice. Δ, excised allele; fl, undeleted conditional allele.

(J) Frequency of CD45.2+ cells in BM and PB at day 24 (n = 4).

(K) FACS plots of CD45.1+ versus CD45.2+ chimera in LSKs from transplanted mice at day 24 (n = 4).

(L) Frequency of CD45.2+ cells in LSK and LK cells at day 24 (n = 4).

(M) Frequency of CD45.2+ cells in BM and PB 4 weeks after secondary transplantation (n = 4).

(N) CD45.2+ BM cells from untreated control and Gata2fl/fl;Mx1-Cre mice were transplanted with CD45.1+ WT BM cells into irradiated recipients. Six weeks later, mice received six doses of plpC and were analyzed for reconstitution for up to 16 weeks after last plpC dose.

(O) Frequency of CD45.2+ cells in PB after plpC injection (n = 4). Error bars depict SD. Statistical analyses: one-way ANOVA.

(P) FACS plots of CD45.1+ versus CD45.2+ chimera in LSK cells at week 16 (n = 3).

(Q) Representative gel showing genotyping of donor CD45.2+ fraction of the BM and PB of plpC-treated recipients at week 16. Δ, excised allele; fl, undeleted conditional allele.

Data are mean ± SEM and n denotes number of mice per genotype unless otherwise stated. Statistical analyses: Mann-Whitney U test unless otherwise indicated. *p < 0.05, **p < 0.01.
GATA2 Regulates Human CB HSPC Function

Having shown the requirement for Gata2 in mouse adult HSC function, we next sought to assess whether this role was conserved in human HSPCs. Using a bicistronic lentiviral vector system carrying a GFP reporter and short hairpin (shRNA) targeted to GATA2 expression in CB CD34+ HSPCs, we conducted functional analysis in colony-forming cells (CFCs) and long-term culture-initiating cell (LTC-IC) assays following GATA2 KD (Figure 2A). Reduction in GATA2 expression was confirmed in CB CD34+ cells transduced with two independent KD constructs (Figure 2B). Overall CFC growth capacity and lineage-specific CFCs (e.g., BFU-E) were markedly reduced using either GATA2 KD constructs (Figure 2C). Limiting dilution LTC-IC analysis revealed a marked reduction in HSPC frequency using both KD constructs, in keeping with the lack of multipotent progenitors (CFC-GEMM) observed in CFC assays following GATA2 KD (Figures 2C and 2D). Together these data demonstrate that GATA2 functions as a critical regulator of human HSPC function.

Figure 2. GATA2 is a Crucial Regulator of Human CB HSPC Function

(A) CB CD34+ cells were transduced with lentiviruses encoding a short hairpin against human GATA2 (or scramble control) and a GFP reporter. GFP+ cells were FACS sorted and plated into CFC or LTC-IC.

(B) Relative GATA2 mRNA expression in CB CD34+ cells compared with GAPDH (n = 3 independent experiments).

(C) Colony-forming units (CFU) per 500 CD34+ GFP+ cells plated (n = 3 independent experiments). Statistical analyses: one-way ANOVA. Data are mean ± SEM.

(D) Top: plot showing representative log-fraction of the limiting dilution model for the LTC-IC assay. The dotted lines give the 95% confidence interval. Bottom: LTC-IC frequency calculated using ELDA software (n = 2 independent experiments).

* p < 0.05, **** p < 0.0001.

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Acute Deletion of Gata2 Impairs LSC Maintenance and Self-Renewal in Meis1a/Hoxa9-Driven AML

To investigate the requirement of Gata2 in LSCs, we employed a tractable retroviral leukemogenic assay in which leukemic transformation of murine C-KIT+ HSPCs is driven by overexpression of Meis1a/Hoxa9, which is observed in 40% of AML patients (Dorsam et al., 2004; Lawrence et al., 1993). Meis1a/Hoxa9-transduced cells were serially replated for three rounds in a CFC assay to generate pre-LSCs, which, when injected into primary lethally irradiated mice, become LSCs and cause AML (Figure 3A). Given that Gata2KO;Mx1-Cre+ mice lack HSPCs by day 15 after plpC administration (Figure 1F), we instead co-transduced HSPCs from non-induced Gata2fl/fl;Mx1-Cre+ or control mice with retroviruses expressing Meis1a and Hoxa9, and after three rounds of CFC we harvested Meis1a/Hoxa9 pre-LSC and transplanted them into primary recipients together with unfractionated BM support cells (Figure 3A). We monitored leukemia development by episodic bleedings (Figure 3B) and induced Gata2 deletion with plpC once the percentage of leukemic cells in the PB reached 20%–25%, a threshold for the diagnosis of AML. Leukemia cells in the PB of recipients transplanted with Gata2KO;Mx1-Cre+ pre-LSCs were dramatically reduced at weeks 4 and 6 after plpC treatment (Figure 3C). Consistent with this, recipients of Gata2 KO LSCs succumbed to AML with a significantly delayed latency compared with recipients of control LSCs, indicating that Gata2 deletion impairs LSC maintenance (Figure 3D). Notably, these results were obtained with 33% recipients harboring Gata2 KO leukemic cells with complete Gata2 deletion.

To investigate whether Gata2 deletion also compromises LSC self-renewal, we prospectively isolated LSCs from BM of mice exhibiting complete deletion of Gata2 or controls by fluorescence-activated cell sorting and transplanted them into secondary recipients together with unfractionated BM support cells (Figure 3A). Recipients transplanted with Gata2 KO LSCs developed AML more slowly than recipients transplanted with control LSCs (Figure 3E). Taken together, these data demonstrate that Gata2 is required for LSC maintenance, self-renewal, and leukemia propagation in a Meis1a/Hoxa9-driven AML mouse model.

That recipients of Gata2 KO LSCs eventually succumb to AML demonstrates that, in striking contrast to their normal HSC counterparts (Figure 1), LSCs survive Gata2 loss, suggesting differential requirements for Gata2 in subsets of C-KIT+ HSPCs during transformation. The cell of origin for Meis1a/Hoxa9-driven AML in C-KIT+ HSPCs is either LSK or common myeloid progenitor (CMP) but not GMP (Wang et al., 2010). We investigated which of these HSPC subsets was dependent on Gata2 during transformation in Meis1a/Hoxa9-driven AML. Meis1a/Hoxa9 LSK and CMP-derived pre-LSCs from Gata2fl/fl or Gata2+/- mice were transduced with lentiviruses encoding Cre and iVenus reporter. Transduced iVenus+ cells were serially plated in CFC assays for three rounds, and were immunophenotypically assessed at each stage for expression of C-KIT+, as a marker of LSCs, and GR1 and MAC1 myeloid differentiation markers, which are blocked in AML development. While LSC and MAC1 expression was similar between genotypes in LSK and CMP compartments throughout replating (Figures S2A–S2D), LSK cells from Gata2 KO
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A

![Diagram showing gene expression levels with -log10(p-value) scale.](image)

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had enhanced GR1 expression in CFC3 (Figure S2E). In contrast, a relative blockade in GR1 expression was observed from Gata2 KO in Meis1a/Hoxa9-transformed CMP at CFC3 (Figure S2F). These data suggest that HSC-enriched LSKs mediate GATA2 regulation of transformation in Meis1a/Hoxa9 AML, whereas CMPs regulate transformation in this setting independently of GATA2.

Acute Deletion of Gata2 Promotes an LSC-Specific Program of Apoptosis and Myeloid Differentiation in Meis1a/Hoxa9-Driven AML

To examine the molecular signature governing LSC maintenance and self-renewal driven by GATA2, we performed global gene expression analysis by RNA sequencing (RNA-seq) of Meis1a/Hoxa9 expressing pre-LSCs (CD45.2+seq) of Gata2 KO and control LSCs. We observed a decrease in bulk AML cells and a 3-fold reduction in the abundance of LSC (CD45.2+c-kit+) in recipients together with unfractionated CD45.1+ BM support cells (Figure 3F). When the levels of AML in PB reached 25%, we administered plpC to delete Gata2 in LSCs and analyzed mice 7 days after the last dose of plpC (Figure 3F). The frequency of AML cells in PB was comparable between both genotypes before plpC administration (Figure 3G), yet in mice harboring Gata2 KO LSCs there was a 3.5-fold reduction in the PB at 7 days after administration of the last dose of plpC (Figure 3G). Splenomegaly, a hallmark of AML, was markedly reduced in recipients with Gata2 KO LSCs 7 days after the last plpC injection (Figures 3H and 3I). This corresponded to a reduced population of engrafting AML cells in the spleen of Gata2 KO LSC recipients (Figure 3J). Immunophenotypic analysis was also conducted on BM, which revealed a decrease in bulk AML cells and a 3-fold reduction in the abundance of LSC (CD45.2+c-kit+) in recipients harboring Gata2 KO LSCs (Figures 3K–3M). Full deletion of Gata2 was achieved in Gata2 KO/LSCs (Figures 3N). Using pathway analysis of RNA-seq using the Gene Ontology Consortium and gene set enrichment analysis, we observed differential upregulation of pathways modulating metabolic processes and pathways that curtail cell proliferation and downregulation of G-coupled receptor signaling, oxidative phosphorylation, and C-MYC target genes in Gata2 KO LSCs (Figures 4A and S3A). Furthermore, Gata2 KO LSCs exhibited dampening of lysosome signaling, which targets AML LSCs (Sukhai et al., 2013), and the nuclear factor-κB signaling pathway, the activation of which is associated with a pro-inflammatory environment permissive for the development and maintenance of AML (Figures S3A and S3B) (Wang et al., 2014; Zambetti et al., 2016).

To identify GATA2 target genes specific to LSCs rather than HSCs, we compared RNA-seq data from Gata2 KO LSCs with GATA2 target genes identified from HSCs. As genetic deletion of Gata2 entirely abolishes immunophenotypically defined HSCs (Figure 1), we instead conducted RNA-seq on HSCs from Gata2 haploinsufficient mice bearing a single floxed allele deleted by Vav-iCre (Gata2f/f;Vav-iCre+) in vivo, where adult HSCs remain isolatable but are reduced in abundance (de Pater et al., 2013) (our unpublished observations). Using Ingenuity Pathway Analysis of differentially expressed genes in HSCs and LSCs, we found that several GATA2-mediated biological pathways, including ERK/MAPK and interleukin-4 signaling, were shared between HSCs and LSCs (Figure S3C). Seventy genes were differentially expressed in Gata2f/f;Vav-iCre+ HSCs and 689 differentially expressed in Gata2 KO LSCs, yet a mere 4 GATA2 target genes (Lphn2, Mllt3, Gimap4, and Zhx2) were common to both HSCs and LSCs. Thus, the vast majority of GATA2 target genes identified here were exclusive to LSCs. In agreement with the notion that lack of Gata2 engenders an anti-leukemic effect in LSCs, established AML tumor suppressors or oncogenes were up- or downregulated, respectively, in Gata2 KO LSCs (Figure 4B).

As expected, previously identified GATA2 target genes were deregulated in Gata2 KO LSCs (Figure 4C). We observed gene signatures in Gata2 KO LSCs consistent with re-activation of both lymphoid and erythroid differentiation potential (e.g., Epo-R) (Figure 4C). Most notably, Gata2 KO LSCs registered a robust pro-apoptotic and myeloid cell differentiation gene signature (Figures 4A–4D). These data suggest that ablation of Gata2 could alleviate the myeloid differentiation and apoptotic block in AML LSCs—cell fates that are characteristic and indispensable for facilitating AML maintenance and propagation (Ishikawa et al., 2007; Sykes et al., 2015).

Next, to directly assess whether apoptosis was augmented in Gata2 KO LSCs, we conducted an annexin V assay on Gata2 KO LSCs at 7 days after the last plpC injection (Figure 3F), which indeed confirmed an increase
in apoptosis (Figure 5A). Using intracellular flow cytometry, we measured protein levels of crucial apoptotic regulators in Gata2 KO LSCs or control LSCs. Between Gata2 KO LSCs and their LSC control counterparts, no changes were discernible with respect to the mean fluorescence intensity (MFI) of PS3, or the activation of the survival-promoting

**Figure 5. Deletion of Gata2 in LSCs Leads to an Increase in Apoptosis and Enhanced Myeloid Differentiation**

Analyses were performed in control or Gata2 KO LSCs using the experimental design in Figure 3F.

(A) Frequency of annexin V+ cells in LSCs (n = 6–7).

(B) Representative histogram plot showing the levels of BCL2 protein in control and Gata2 KO LSCs.

(C) MFI of BCL2 in LSCs in relation to the MFI of isotype control (n = 6–7).

(D) Representative histogram plot showing the levels of Mac1 and Gr1 protein in leukemic cells. Red dotted line indicates the highest expression of each marker.

(E) Gating strategy to distinguish AML blast cells with differentially expressed Gr1 and Mac1 levels: Gr1 hiMac1 hi, Gr1 loMac1 hi, Gr1 hiMac1 lo, and Gr1 loMac1 lo. Representative FACS plots showing an increase in Gr1 hiMac1 hi population after deletion of Gata2 in LSCs.

(F) Frequency of the indicated populations in BM of leukemic mice (n = 6–7). Statistical analyses: one-way ANOVA.

Data are mean ± SEM and n denotes number of mice used per genotype. Statistical analyses: Mann-Whitney U test unless otherwise indicated. *p < 0.05, **p < 0.01.
phosphatidylinositol 3-kinase-AKT (Figures S3D and S3E). Given that BCL-XL regulates cell survival in the context of GATA factor-dependent erythroid cell differentiation (Gregory et al., 1999), we assessed BCL-XL expression in Gata2 KO LSCs and Gata2 haploinsufficient HSCs from both Mx1-Cre or Vav-Cre systems, but found that expression was unperturbed in all settings (Figures S3F, S3H, and S3I). In stark contrast, a significant reduction in the MFI of anti-apoptotic protein BCL2 was found only in Gata2 KO LSCs (Figures S3B, S3C, S3G, and S3I). Thus, acute deletion of Gata2 produces a rapid loss of LSCs, consistent with perturbed cell survival and mediated partly by attenuation of BCL2 expression. Furthermore, GATA2-mediated regulation of Bcl2 in LSCs represents a novel GATA-dependent cell survival mechanism specific to LSCs rather than HSCs.

Having identified an enhanced myeloid differentiation gene signature in Gata2 KO LSCs, we next asked whether this reflected GATA2-mediated alterations in myeloid differentiation of AML blasts in vivo. Using immunophenotyping, we analyzed the differentiation status of total BM from mice harboring Gata2 KO LSCs at 7 days after the last pIpC injection (Figure 3F). A trend toward increased GR1 or MAC1 expression was observed in bulk AML cells derived from Gata2 KO LSCs (Figure SD), which mapped specifically to a significant increase in the abundance of GR1highMAC1high myeloid cells (Figures SE–SF). Together with gene expression profiling data of Gata2 KO LSCs, these data support the contention that ablation of Gata2 in LSCs increases their differentiation capacity in vivo, raising the possibility that targeting the GATA2 differentiation affiliated transcriptional network in LSCs could pave the way toward novel therapeutics in AML.

DISCUSSION

In this report, to explore the genetic requirement for Gata2 in adult hematopoiesis, we employed a conditional gene-targeting approach using the Mx1-Cre system to specifically delete Gata2 in hematopoietic cells from adult mice. Consistent with data using ER-Cre-mediated deletion of the Gata2 C-terminal zinc-finger domain (Li et al., 2016), we demonstrate that acute genetic ablation of Gata2 leads to a rapid and complete cell-autonomous loss of adult HSCs and multi-lineage potential. Therefore, Gata2 joins a select list of TFs that are indispensable for adult HSC maintenance and survival (Hock et al., 2004; Kranc et al., 2009; Pajerowski et al., 2010). Loss-of-function studies in mice have identified various TFs required for distinct temporal and developmental stages of hematopoiesis, as typified by Runx1, which is required for HSC generation from hemogenic endothelium, but expendable for HSC maintenance for the remainder of gestation and in adult HSCs in the BM (Chen et al., 2009). Cited2, a reported upstream regulator of Gata2 in hematopoiesis (Saito et al., 2015), is a pivotal functional regulator of embryonic and adult HSCs, yet genetic KO models also highlight key stage-specific requirements during HSC development. For example, conditional genetic KO of Cited2 in adult hematopoiesis using Mx1-Cre demonstrated the requirement for Cited2 in adult HSC survival via Ink4a/Arf and p53 (Krac et al., 2009). In contrast, conventional germline deletion of Cited2 produced isolatable HSCs at the FL stage, although Cited2−/− HSCs were impaired both in abundance and functionality (Chen et al., 2007). Here, in concert with data from de Pater et al. (2013), we importantly define Gata2 as a unique TF that is necessary throughout HSC ontogenesis—from cell-autonomous HSC generation (using the Vec-Cre system) and HSC survival (using the Vav-Cre model) in the nascent blood system of the embryo to adult HSC maintenance in BM. Evi1, another upstream regulator of Gata2 in hematopoiesis, mirrors the requirement of Gata2 for HSC survival during development and in the adult (Goyama et al., 2008; Sato et al., 2008; Yuasa et al., 2005), although the explicit requirement for Evi1 in HSC generation from hemogenic endothelium in the embryo remains untested and merits further investigation.

Using a lentiviral-based shRNA KD approach, we extended this study to examine the currently ill-defined requirement for Gata2 in human HSPCs. Mirroring data from the Mx1-Cre genetic mouse model, we observed that reducing GATA2 expression in human CB CD34+ cells profoundly altered HSPC function, as assessed by CFC and LTC-IC assays. Together, these data identify GATA2 as a regulator of human HSPCs, which may bear relevance for understanding clinical GATA2 haploinsufficiency syndromes (Dickinson et al., 2011; Hahn et al., 2011; Katsumura et al., 2018; Soukup et al., 2019), in which the impact of GATA2 mutations in HSPCs remains unclear. Identifying and characterizing the genetic and epigenetic dependencies of specific HSPC population(s) transformed by loss-of-function GATA2 mutations and associated secondary mutations, such as ASXL1, may offer mechanistic insights into the wide range of complex pathologies and lineage-specific hematopoietic effects eventually leading to MDS/AML in GATA2 haploinsufficiency syndromes.

Considering that accumulating evidence also suggests an oncogenic function for GATA2 when it is overexpressed in pediatric and adult AML (Luesink et al., 2012; Vicente et al., 2012), we elected to interrogate the requirement for Gata2 in LSCs by using an in vivo model of AML driven by Meis1/Hoxa9. Genetic deletion of Gata2 delayed in vivo AML development by impairing the maintenance and self-renewal of LSCs. Of note, gene expression patterns in...
**Gata2 KO** LSCs diametrically opposed those observed in the setting of either Gata2 overexpression- or in Gata2 haploinsufficiency-related models (Katayama et al., 2017; Nandakumar et al., 2015; Tipping et al., 2009). For example, lymphoid differentiation blockade and c-Myc expression activation has been observed in the context of Gata2 overexpression studies (Nandakumar et al., 2015; Tipping et al., 2009), whereas Gata2 KO LSCs display a gene signature consistent with reactivation of lymphoid differentiation and downregulation of MYC target genes. Similarly, in leukemic cells from Gata2 haploinsufficiency-related models (Katayama et al., 2017), in which Gata2 acts as a tumor suppressor rather than an oncogene, enrichment for oxidative phosphorylation and MYC target genes was observed, yet Gata2 KO LSCs from Meis1a/Hoxa9 AML demonstrate reduction in oxidative phosphorylation pathways. Thus, ablation of Gata2 in LSCs pares down pro-oncogenic stimuli indicating the potential for therapeutic intervention in AML.

To this end, deletion of Gata2 enhanced LSC apoptosis, enriched for a pro-apoptotic and myeloid differentiation signature in LSCs, and caused AML blast cell differentiation, suggesting that characteristic biological traits of AML—enhanced leukemic cell survival and a myeloid differentiation block—can be ameliorated through inhibition of Gata2 or targeting the GATA2 transcriptional network in LSCs. Whether direct, transient inhibition of Gata2 in LSCs is a possibility remains to be tested and is questionable given the pivotal role identified here for Gata2 in adult hematopoiesis and the known tumor-promoting role of GATA2 in the context of haploinsufficiency. However, in favor of this proposition, the proteasome inhibitor K7174, which inhibits GATA2, has been found to be beneficial in the treatment of multiple myeloma (Imagawa et al., 2003; Kikuchi et al., 2013; Majik et al., 2012). We speculate that, alternatively, it may be feasible to selectively target the GATA2 transcriptional network in LSCs as GATA2 LSC target genes identified here were specific to LSCs and not HSCs (Iwasaki et al., 2015; Kikushige et al., 2010), which likely reflects differential transcriptional dependencies for Gata2 in different cellular contexts (Rodrigues et al., 2005, 2008).

Our study suggests that the GATA2 pro-apoptotic transcriptional network in LSCs, exemplified by Bcl2, may be particularly susceptible to therapeutic targeting in AML, while sparing normal HSPCs (Lagadinou et al., 2013; Pollyea et al., 2018). Auspiciously, responses of BCL2 pharmacological inhibitor, venetoclax, in combination with standard AML chemotherapy agents, cytarabine, or hypomethylating agents, azacytidine and decitabine, are favorable compared with conventional induction therapy (Konopleva and Letai, 2018). Furthermore, venetoclax resistance in AML may be circumvented by using an inhibitor toward another BCL2 family member, MCL1 (Ramsey et al., 2018).

The characteristic myeloid differentiation block observed in AML has been overcome successfully in a subtype of AML, acute promyelocytic leukemia (APL), where a combination of all-trans retinoic acid (ATRA) and arsenic trioxide (ATO) has now become the mainstay of treatment for APL patients (Lallemand-Breitenbach and De Thé, 2013). Evidence suggests that the combination of ATRA and ATO cures APL by invoking myeloid differentiation in LSCs and their progeny, AML blasts, thereby precipitating LSC exhaustion (Werner et al., 2014; Zheng et al., 2007). However, attempts to replicate induction of myeloid differentiation in a similar manner across the genetic and clinically diverse AML subtypes have met with limited success (Sykes et al., 2016). We show here that ablation of Gata2 in a non-APL AML model of LSCs overrides the myeloid differentiation block coupled to a depletion of LSC survival and self-renewal ability, presumably by promoting myeloid differentiation and apoptosis at the expense of self-renewing LSCs. Because LSCs are central to therapy resistance and relapse in AML (Craddock et al., 2013; Ishikawa et al., 2007; Saito et al., 2010), further investigation into how these LSC cell fates are coordinated and transcriptionally regulated by GATA2 should lead to an understanding of whether combinatorial therapies are needed to effectively exhaust the functionality of LSCs in AML.

Finally, the data presented here should also have direct relevance to cancer stem cell (CSC) biology beyond AML. Bearing in mind that LSCs serve as a paradigm for CSCs in other tissues, this study may hold significant importance for understanding GATA2-mediated transcriptional programming and developing clinical therapies against CSCs in prostate and lung cancer, in which GATA2 is overexpressed and linked to aggressiveness (Kumar et al., 2012; Vidal et al., 2015).

**EXPERIMENTAL PROCEDURES**

**Mice**

Gene targeting of Gata2flfl mice has been described previously (Charles et al., 2006), and mice were provided by Prof. Julian Downward. Gata2flfl mice were bred with Mx1-Cre and Vav-cre mice (Vukovic et al., 2016). Gata2 conditional gene deletion in the Mx1-Cre model was achieved by administration of six to eight intraperitoneal injections of pIpC every other day (0.25 mg per dose; GE Healthcare). All animals used for experiments were 8- to 12 weeks old in a C57Bl/6 genetic background in accordance with UK Home Office regulations.

**Meis1a/Hoxa9 Leukemic Transformation Assay**

Meis1a-puro and Hoxa9-neo MSCV plasmids were used as described previously (Vukovic et al., 2015). Further information provided in Supplemental Experimental Procedures.
Transplantation Assays
CS7BL/6 SJL (CD45.1), or CS7BL/6 (CD45.2) for niche experiment, adult recipient mice were irradiated with a split dose of 1,000 cGy ($^{137}$Cs source) 24 h before transplantation. Further information provided in Supplemental Experimental Procedures.

Flow Cytometry
Samples were analyzed with a BD LSRFortessa and sorting experiments were performed with a FACSAria Fusion (BD Biosciences). Antibodies used are listed in Table S1. Further information provided in Supplemental Experimental Procedures.

CB CD34+ HSPCIs Isolation and Culture
Umbilical CB was obtained from full-term healthy pregnancies at the Maternity Unit of the University Hospital of Wales, Cardiff, following informed consent and approval from the South East Wales Research Ethics Committee in accordance with the 1964 Declaration of Helsinki. Further detailed information provided in Supplemental Experimental Procedures.

qRT-PCR and Western Blot
Further information provided in Supplemental Experimental Procedures.

RNA-Seq and Bioinformatics
RNA-seq was performed on CD45.2+ c-kit+ LSCs. Further information provided in Supplemental Experimental Procedures.

Statistical Analyses
Further information provided in Supplemental Experimental Procedures.

ACCESSION NUMBERS
The accession number for the Gata2 LSC RNA-seq reported in this paper is GEO: GSE133245. The accession number for the Gata2 HSC RNA-seq reported in this paper is GEO: GSE133248.

SUPPLEMENTAL INFORMATION
Supplemental Information can be found online at https://doi.org/10.1016/j.stemcr.2019.07.005.

AUTHOR CONTRIBUTIONS
J.B.M.-G. designed and performed the experiments, analyzed/interpreted the data, prepared figures, and contributed to the manuscript preparation. M.V. designed the experiments, analyzed/interpreted the data, and wrote the manuscript.

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Supplemental Information

Gata2 as a Crucial Regulator of Stem Cells in Adult Hematopoiesis and Acute Myeloid Leukemia

Supplemental Experimental Procedures

Meis1a/Hoxa9 leukemic transformation assay

The day before transduction, 1 million c-Kit+ cells were pre-stimulated with IMDM 10% FBS containing 40 ng/mL SCF, 20 ng/mL IL-3, and 20 ng/mL IL-6. Cells were transduced with retroviruses encoding Meis1a/Hoxa9 using retronectin-coated plates. 6 hours after the first transduction, cells were transduced for a second time in a new retronectin-coated plate containing retroviruses. Next day, medium containing antibiotics geneticin 418 (G418) (1 mg/ml) and puromycin (1.5 µg/ml) was added to select transduced Meis1a/Hoxa9 cells. 72 hours later, 5,000 live cells were plated in CFC1 in M3231 (STEMCELL Technologies) and replated every 6 days for up to 3 rounds of CFC. Pre-LSCs were harvested and enriched for c-kit from CFC3 plates and transplanted into lethally-irradiated primary recipients. LSCs from moribund mice showing symptoms of AML were sorted and transplanted into lethally-irradiated secondary recipients.

Transplantation assays

For cell-autonomous transplantation, 500,000 CD45.2+ unfractionated BM cells from Gata2 mice, together with 500,000 unfractionated CD45.1+ BM support cells, were injected in the tail vein of lethally-irradiated CD45.1+ mice. For secondary transplantation, 500,000 CD45.2+ BM cells were transplanted alongside 500,000 unfractionated CD45.1+ BM support cells into lethally-irradiated CD45.1+ mice. For niche studies, 500,000 unfractionated BM cells from CD45.1+ mice were transplanted into the tail vein of lethally-irradiated Gata2fl/fl;Mx1-Cre mice. For leukemia assays, 250,000 pre-LSCs were injected into lethally-irradiated CD45.1+ mice alongside 200,000 unfractionated CD45.1+ BM support cells. For secondary transplants of LSCs, 10,000 c-kit+ CD45.2+ BM cells from leukemic mice were injected into lethally-irradiated CD45.1+ mice together with 200,000 unfractionated CD45.1+ BM support cells.

Flow cytometry

Extracellular staining was carried out in PBS 2% FBS with an incubation time of 25' in the dark at 4°C. To exclude dead cells from the analysis, 1:10,000 µL
of DAPI (20 µg/mL) was added prior to acquisition. For the annexin V assay, cells were incubated in annexin binding buffer (BioLegend) containing annexin V (BioLegend) for 25’ in the dark at RT. Annexin binding buffer was added to stop the reaction, and 2 µL of diamidino-2-phenylindole (DAPI, 20 µg/ml) (Molecular probes) was added prior to acquisition. For intracellular flow cytometry, cells were fixed with 1% methanol-free PFA (ThermoFisher) for 15’ on ice and then permeabilized in PBS 0.1% Saponin (Sigma) 2% BSA (ThermoFisher) for 15’ on ice and stained for 1 hour on ice with a fluorescence-labelled antibody diluted in the permeabilisation buffer.

**Generation of lentiviruses**
Lentiviral vectors were diluted in water, and then mixed with calcium chloride (Sigma). This mixture was added dropwise to 2x HEPES buffered saline (HBS; Sigma) and after 15’ incubation, added to the media of HEK293T cells at 70% confluency in a 10-cm dish. Supernatant containing lentiviruses was collected at 24 hours after transfection of HEK293T cells and filtered in a 0.45 µm filter (Sigma) prior to use or storage at -80C.

**Cord blood CD34⁺ HSCPs isolation and culture**
Highly enriched human CD34⁺ cells (>90%) were derived from CB mononuclear cells using MiniMACS (Miltenyi Biotech, UK) using manufacturer’s instructions. CB derived CD34⁺ HSPC purity was confirmed by two-color flow cytometric analysis using anti-CD45 PerCP (Biolegend, UK) and CD34-PE (BD Biosciences, UK). CD34⁺ cells were pre-stimulated overnight in StemSpan (STEMCELL Technologies) supplemented with 100 ng/mL of SCF, 100 ng/mL of FLT3L, 10 ng/mL IL6, 10 ng/mL IL3, and 25ng/mL G-CSF, 1% Pen/Strep, 10 uM HEPES. Lentiviruses containing shRNA against human GATA2 and scrambled vector (Genecopoeia) were bound to retronectin-coated plates by centrifugation at 2,100 xG, at RT, for 2:30h. CD34⁺ cells were then added to viruses-retronectin-coated plates and incubated for 4 days. GFP⁺ cells were sorted and plated into CFC assays in H4434 for 14 days. For LTC-IC assays, GFP⁺ cells were plated onto irradiated MS5-stromal cells for 5 weeks, with half-media changes every 7 days. Media was then replaced with enriched H4435 and colonies from LTC-IC were
enumerated at day 14 and LTC-IC frequency was calculated using ELDA software.

**Lentiviral-Cre mediated deletion**

Meis1a/Hoxa9 LSK and CMP derived pre-LSCs from Gata2\(^{\text{fl/fl}}\) or Gata2\(^{+/+}\) mice were transduced with lentiviruses encoding Cre and iVenus reporter marker using the retronectin-coated system as explained above. Transduced iVenus+ cells were plated in colony assays for up to three rounds, and were immunophenotypically assessed using Mac1, Gr1, and c-kit.

**RNA-sequencing and Bioinformatics**

RNA from CD45.2\(^{+}\)c-kit\(^{+}\) LSCs was extracted with the RNAeasy micro kit (Qiagen). Total RNA quality and quantity was assessed using Agilent 2100 Bioanalyzer and a RNA Nano 6000 kit (Agilent Technologies). 30-260ng of Total RNA with a RIN value >8 was depleted of ribosomal RNA using the NEBNext® rRNA Depletion Kit (Human/Mouse/Rat), (New England BioLabs, NEB) and the sequencing libraries were prepared using the NEB® Ultra™ II Directional RNA Library Prep Kit for Illumina® (NEB). The steps included RNA fragmentation and priming, 1st strand cDNA synthesis, 2nd strand cDNA synthesis, adenylation of 3’ ends, adapter ligation, PCR amplification (11-cycles) and validation. The manufacturer’s instructions were followed. The libraries were validated using the Agilent 2100 Bioanalyzer and a high-sensitivity kit (Agilent Technologies) to ascertain the insert size, and the Qubit® (Life Technologies) was used to perform the fluorometric quantitation. Following validation, the libraries were normalized to 10nM, pooled together and clustered on the cBot™2 following the manufacturer’s recommendations. The pool was then sequenced using a 75-base paired-end (2x75bp PE) dual index read format on the Illumina® HiSeq4000 according to the manufacturer’s instructions.

To remove adapter sequencer and poor quality ends of reads, trimming was performed using Trim Galore, a wrapper tool which uses cutadapt and FastQC to trim and perform QC on the trimmed. Trimming was performed in paired-end mode. Trimmed reads were mapped against the GRCm38.p6
mouse genome using STAR. STAR was run with the MultimapNMax=1 flag, meaning reads mapping to more than 1 location were considered unmapped. Expression counts for both exons and transcripts were calculated, using Subread feature Counts Version 1.6.2 (Liao et al., 2014), a program for assigning sequence reads to genomic features. To define the exon and transcript locations (raw reads calculation), the GENCODE M18 gene model was used. Read summarization (counting) was generated for paired end read fragments - it was summarized at exon level and then grouped at transcript level. To provide stringent and robust data, reads overlapping more than one feature were excluded from the count summary (according to authors recommendations (Liao et al., 2014).

Differentially expressed genes were identified using a DEseq2 Bioconductor package (Love et al., 2014) analysis within the R environment for statistical computing software on normalised count data. For multiple testing and false discovery issues, the generated p-values were corrected using the FDR method (Benjamini and Hochberg, 1995).

The Gene ontology over-representation analyses (GO ORA) for biological processes (BP) were undertaken using the AmiGO website service. Gene Set Enrichment Analysis (Subramanian et al., 2005) was applied against categories and mouse gene mappings obtained from the Gene Ontology Consortium using data ranked by a scoring metric generated by multiplying the sign of fold change by its inverse p-value”. Heat maps of differentially significant genes were generated using the Morpheus online software tool (Broad Institute).

For Ingenuity Pathway Analysis, RNA-seq datasets with FDR <0.05 were investigated for the common canonical pathways between HSCs and LSCs using the Ingenuity Pathway Analysis software (Qiagen-Bioinformatics). Enriched pathways were selected by Fischer’s Exact Test.

**RT–quantitative PCR**
Gene expression analyses were performed using Taqman probes for mouse
Gata2 [Mm00492301_m1] or human GATA2 [Hs00231119_m1]. Differences in input cDNA were normalized with mouse Hprt [Mm03024075_m1] or human GAPDH (Hs02758991_g1) mRNA expression levels were determined by the $2^{\Delta\Delta CT}$ method of relative quantification (Schmittgen and Livak, 2008).

**Western Blot**

BM cells were washed with cold PBS and re-suspended in lysis buffer containing 10x RIPA buffer (CST), protease inhibitor cocktail (Merck), phosphatase inhibitor cocktail 2 (Merck), phosphatase inhibitor cocktail 3 (Merck) and 1.5 mM Phenyl methane sulfonl fluoride (PMSF; Merck) in ddH$_2$O. Samples were separated in 4-15% Mini-protean pre-cast gel (Bio-rad) and transferred to a 0.2 µm PVDF membrane with trans-blot turbo (Bio-rad). Membrane was blocked in 5% milk and immunobloted with Rb anti-GATA2 ab (Abcam ab109241) and mouse anti-GAPDH (Merck CB1001) overnight at 4 degrees. Membranes were incubated with HRP-conjugated anti-rabbit (abcam ab97051) or anti-mouse IgG (Sigma A4416) and detected with enhanced chemiluminescent (ECL) reagents (WBLUF0100, Merck Millipore).

**Statistical analyses**

FACS data were analyzed using FlowJo 10.0.8 (Tree Star, Inc) software and all results graphed using GraphPad Prism 7 (GraphPad Software Inc, CA). Data are presented as mean ± standard error of mean (SEM). Significant differences were calculated using Mann–Whitney U test or one-way ANOVA (*p<0.05, **p<0.01, ***p<0.001, **** p<0.0001). Kaplan-Meier survival curve statistics were determined using the log-rank (Mantel-Cox) test.
**Supplementary references**


### Table S1. List of antibodies used in study.

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Supplementary Figure 1 – linked to figure 1

Figure S1 (linked to Figure 1). *Gata2* is essential for cell autonomous adult HSC maintenance. (A) *Gata2* mRNA levels in BM cells from control and *Gata2* KO at day 24 after plpC administration. Hprt was used as endogenous control for mRNA quantification (n = 4). (B) WBC count from 2 femurs and 2 tibias at day 24 after plpC administration (n = 4). (C) Number of myeloid (Gr1⁺Mac1⁺), erythroid (Ter119⁺), B lymphoid (B220⁺), and T lymphoid (CD3⁺) cells in BM at day 24 (n = 4). Statistical analyses: one-way ANOVA. (D) Frequency of myeloid, B lymphoid, and T lymphoid cells in PB at day 24 (n = 4). Statistical analyses: one-way ANOVA. (E) Frequency of CD45.2⁺ cells of the indicated populations in BM at day 24 in cell-autonomous setting (n = 4). Statistical analyses: one-way ANOVA. (D) Frequency of CD45.2⁺ cells of the indicated populations in PB at day 24 in cell-autonomous setting (n = 4). Statistical analyses: one-way ANOVA. (G) BM cells from CD45.1⁺ WT mice were transplanted into lethally-irradiated untreated *Gata2fl/fl;Mx1-Cre* and control recipient mice. Six weeks later, the mice received six doses of plpC. The mice were monitored for up to twelve weeks after last plpC dose to analyze the impact of the BM microenvironment. (H) Frequency of CD45.1⁺ cells in PB at week 6, before plpC (n = 2-5). (I) Frequency of CD45.1⁺ cells in PB at the indicated time points after plpC administration (n = 2 control and n = 5 *Gata2* KO recipients). Statistical analyses: one-way ANOVA. Data are mean ± SEM. Statistical analyses: Mann–Whitney U test unless otherwise indicated.
Figure S2 – linked to Figure 3

Figure S2 (linked to Figure 3). Cell of origin for GATA2 mediated transformation of Meis1a/Hoxa9 AML (A-B) MFI of c-kit at CFC1-to-CFC3 from (A) LSK and (B) CMP derived Meis1a/Hoxa9 Gata2^{fl/fl} and Gata2^{+/+} transduced with lentiviral-Cre (n = 3). (C-D) MFI of Mac1 at CFC1-to-CFC3 from (C) LSK and (D) CMP derived Meis1a/Hoxa9 Gata2^{fl/fl} and Gata2^{+/+} transduced with lentiviral-Cre (n = 3). (E-F) MFI of Gr1 at CFC1-to-CFC3 from (E) LSK and (F) CMP derived Meis1a/Hoxa9 Gata2^{fl/fl} and Gata2^{+/+} transduced with lentiviral-Cre (n = 3). White bar in graph depicts Gata2^{+/+} and Cre and blue bar depicts Gata2^{fl/fl} and Cre. Statistical analyses: two-way ANOVA.
Figure S3 – linked to Figure 4 and Figure 5

Transcriptional signature of *Gata2 KO* LSCs shows deregulated apoptotic and myeloid differentiation pathways. (A) GSEA plots showing lysosome, oxidative phosphorylation signature and c-Myc targets gene sets in control LSCs compared to *Gata2 KO* LSCs. (B) Heat map reflecting expression levels of NF-κB pathway genes that are significantly differentially expressed between control and *Gata2 KO* LSCs. (C) Biological processes commonly shared between *Gata2 KO* HSC and LSC target genes. Analyses was performed using the Ingenuity Pathway Analysis software. Data is shown as –log10 (p-value). (D-F) MFI of (D) p53, (E) pSer473-Akt, and (F) Bcl-xL in LSCs in relation to the MFI of isotype control (n = 6–7; E n = 4). (G and H) MFI of (G) BCL2 and (H) BCL-XL in HSCs from control and *Gata2*+/fl; *Mx1-Cre*+ mice 24 days after the first pIpC injection (n = 3). (I and J) MFI of (I) BCL2 and (J) BCL-XL in HSCs from 8-week old control and *Gata2*+/fl; *Vav-iCre*+ mice (n = 4). Data are mean ± SEM. Statistical analyses: Mann–Whitney U test.