

**From stem cell to red cell:**

**regulation of erythropoiesis at multiple levels by multiple proteins, RNAs and chromatin modifications**

Shilpa M. Hattangadi<sup>1,2</sup> \* Piu Wong<sup>1\*</sup>, Lingbo Zhang<sup>1,3,4</sup>, Johan Flygare<sup>1,5</sup>, and Harvey F. Lodish<sup>1, 6,7,8</sup>

<sup>1</sup> Whitehead Institute for Biomedical Research, 9 Cambridge Center, Cambridge, MA 02142, USA

<sup>2</sup> Division of Hematology/Oncology, Children's Hospital Boston, Boston, MA 02115, USA

<sup>3</sup> Computation and Systems Biology, Singapore-MIT Alliance, Singapore 117576

<sup>4</sup> Stem Cell and Developmental Biology, Genome Institute of Singapore, A\*STAR, Singapore 138627

<sup>5</sup> Present Address: Department of Molecular Medicine and Gene Therapy, Lund Stem Cell Center, BMC A12, 221 84 Lund, Sweden

<sup>6</sup> Department of Biology and

<sup>7</sup> Department of Biological Engineering, Massachusetts Institute of Technology, Cambridge, Massachusetts 02142, USA

\* Equal contribution

<sup>8</sup> Corresponding author: Whitehead Institute for Biomedical Research, 9 Cambridge Center, Cambridge, MA 02142; e-mail [lodish@wi.mit.edu](mailto:lodish@wi.mit.edu); phone 617-258-5216; fax 617-258-6768.

## **Abstract**

This article reviews the regulation of production of red blood cells at several levels. We focus on the regulated expansion of BFU-E erythroid progenitors by glucocorticoids and other factors that occurs during chronic anemia, inflammation, and other conditions of stress. We also highlight the rapid production of red cells by the coordinated regulation of terminal proliferation and differentiation of committed erythroid CFU-E progenitors by external signals such as erythropoietin and adhesion to a fibronectin matrix. We discuss the complex intracellular networks of coordinated gene regulation by transcription factors, chromatin modifiers, and miRNAs that regulate the different stages of erythropoiesis.

## Introduction

In mammals, definitive erythropoiesis first occurs in the fetal liver with progenitor cells from the yolk sac<sup>1</sup>. Within the fetal liver and the adult bone marrow, hematopoietic cells are formed continuously from a small population of pluripotent stem cells that generate progenitors committed to one or a few hematopoietic lineages (**Figure 1**). In the erythroid lineage, the earliest committed progenitors identified *ex vivo* are the slowly proliferating burst-forming unit–erythroids (BFU-E). Early BFU-E cells divide and further differentiate through the mature BFU-E stage into rapidly dividing colony-forming unit–erythroids (CFU-E)<sup>2</sup>. CFU-E progenitors divide three to five times over 2–3 days as they differentiate and undergo many substantial changes, including a decrease in cell size, chromatin condensation, and hemoglobinization, leading up to their enucleation and expulsion of other organelles<sup>3</sup>.

In humans the lifespan of red blood cells is 120 days. Under normal conditions ~1% of red cells are synthesized each day but red cell production can increase substantially during times of acute or chronic stress, such as acute trauma or hemolysis. Exquisite short-term control of erythropoiesis is regulated by the kidney-derived cytokine erythropoietin (Epo), which is induced under hypoxic conditions and stimulates the terminal proliferation and differentiation of CFU-E progenitors<sup>4</sup>. BFU-E cells respond to many hormones in addition to Epo, including stem cell factor (SCF), insulin like growth factor 1 (IGF-1), glucocorticoids (GCs), and interleukins 3 and 6 (IL-3, and IL-6). In cases of chronic erythroid stress, such as hemolysis, the number of CFU-E progenitors is insufficient to produce the needed red cells even under high Epo levels, and the body responds by producing more of these progenitors from BFU-Es<sup>5</sup>. It is not entirely known which cells in the fetal liver or adult bone marrow produce these and other regulatory cytokines, or how they interact to regulate the division of BFU-E cells and control their self-renewal and their ability to differentiate into more mature CFU-E progenitors.

At each stage of red blood cell production, intracellular signal transduction proteins and transcription factors activated downstream of these hormones interact with a group of DNA-binding and other transcription factors and chromatin modifiers as well as with multiple non-coding regulatory RNAs, such as microRNAs; many of these transcription factors and non-coding RNAs are essential for the function and/or identity of these progenitor cells. Here we summarize the ways in which red cell production is regulated at each differentiation stage: through cytokines, transcription factors and cofactors, post-translational modifications of histones, and miRNAs. We start with the terminal proliferation and differentiation of CFU-E erythroid progenitors, as this step is very well understood, and then work backwards toward the less understood processes of formation and function of BFU-E progenitors.

## Extracellular signals regulating proliferation and differentiation of CFU-E progenitors

Erythropoietin has long been understood to be the major factor governing erythropoiesis and its role in regulating the expansion, differentiation, apoptosis, and activation of erythroid specific genes is well characterized<sup>4</sup>. The first phase of CFU-E erythroid differentiation is highly Epo dependent, whereas later stages are no longer dependent on Epo<sup>6-8</sup>. Consistent with this, Epo receptors are lost as erythroid progenitors undergo terminal proliferation and differentiation<sup>9</sup>.

The extracellular matrix protein fibronectin is also important for erythropoiesis<sup>10</sup>; fibronectin and Epo regulate erythroid proliferation in temporally distinct steps. During the first day in culture CFU-E erythroid progenitor cells undergo two divisions, upregulate the transferrin receptor, and begin expression of Ter119 and several hundred other erythroid- important genes. This stage requires Epo but is independent of fibronectin. During the second day there are 2-3 rapid cell divisions with short or absent G1 and G2 stages; most cells are in S or M. There is then complete repression of all gene transcription, chromatin condensation, nuclear condensation, and enucleation. Adhesion to fibronectin, but not the presence of Epo, is essential for the last 1-2 terminal cell divisions and promotes enucleation.  $\alpha_4$ ,  $\alpha_5$ , and  $\beta_1$  are the principal integrins expressed on erythroid progenitors, and fibronectin fragments that engage  $\alpha_4\beta_1$  (but not  $\alpha_5\beta_1$ ) integrin support normal terminal proliferation. In the absence of fibronectin a fraction of cultured erythroblasts enucleate but these generate larger-than-normal "reticulocytes." We do not know whether this is related to macrocytic anemias where large poorly hemoglobinized red cells are produced. Taken together, these data suggest a two-phase model for growth factor and extracellular matrix regulation of erythropoiesis, with an early Epo-dependent, integrin-independent phase followed by an Epo-independent,  $\alpha_4\beta_1$  integrin-dependent phase.

Binding of Epo to Epo receptors (EpoRs) on the surface of erythroid progenitors triggers activation of multiple intracellular signal transduction pathways, including the Stat5 (Signal transducer and activator of transcription 5), Phosphoinositide -3 kinase/Akt, and Shc/Ras/Mitogen-Activated Kinase (MAPK) pathways. Elimination of either of the first two pathways leads to significant apoptosis of early progenitors and reduced output of erythrocytes<sup>11,12</sup>. In contrast, blocking the Ras/ MAPK pathway has only subtle effects on terminal erythropoiesis<sup>13</sup>.

Disruption of the Stat5 pathway, in contrast, revealed not only the cellular role of this factor in erythropoiesis, but also the regulation of red cell production by expansion of earlier progenitor and stem cell populations. While many (albeit hypomorphic) adult Stat5a<sup>-/-</sup>5b<sup>-/-</sup> mice have a normal or near-normal steady-state hematocrit, they are deficient in generating high erythropoietic rates in response to stress and have very high endogenous levels of Epo in the blood<sup>14</sup>. Stat5 is essential for the high erythropoietic rate during fetal development: the double-knockout embryos are severely anemic: erythroid progenitors are present in low numbers, show higher levels of apoptosis, and are less responsive to Epo<sup>15</sup>.

Jak2 stimulates proliferation of erythroid precursors in part through activation of Id1 by binding of Stat5 to a downstream enhancer of Id1<sup>16</sup>. Id1 expression levels also correlate with the levels of the constitutively-active mutant Jak2V617F in both transgenic cell lines as well as patients with polycythemia-vera (PV). Stat5's role in iron metabolism has also been established by evaluation of HSC-targeted knockdown of Stat5; these mice displayed microcytic, hypochromic anemia indicative

of iron deficiency, and showed 50% decreased levels of the transferrin receptor (Tfr1) on their erythroblasts and 80% decreased Tfr1 mRNA levels. Tfr1 was shown to be a direct transcriptional target of Stat5A by chromatin immunoprecipitation studies<sup>17</sup>.

Stat5 is activated by other homodimeric cytokine receptors – the thrombopoietin receptor in megakaryocytes and the prolactin receptor in mammary glands – but activates very different sets of genes in these cells compared to erythroid progenitors. Clearly Stat5 interacts with different resident transcription factors and chromatin modifying enzymes in different cell types. In addition, using reintroduction of minimal Epo receptor chimeras that lack many of the intracellular tyrosines required for known downstream signaling via Jak2 docking into EpoR-knockout tissue, it was found that Epo might actually signal through other pathways. Direct Epo-EpoR targets include tyrosine phosphatase Prl1 and Rank (receptor activator of NFkB) as well as three regulators of protein synthesis (EF1 $\alpha$ , eIF3-p66 and Nat1)<sup>18</sup>.

### **Transcriptional regulators of erythroid proliferation and function.**

In erythroid cells Stat5 and other Epo- regulated transcriptional regulators interact with a relatively small number of lineage-restricted transcriptional regulators, including GATA-1, SCL/Tal1, LMO2, LDB1, Klf1, and Gfi-1b, to produce mRNAs essential for erythropoiesis (**Figures 1 and 2**). These crucial regulators are found in numerous combinations of multiprotein complexes; their functions have been established by gene-targeting knockout mouse models as well as by studies of rare diseases of ineffective erythropoiesis (reviewed in<sup>19,20</sup>) Other transcriptional regulators, such as Bcl-11a, have been identified that mainly affect the transition between fetal  $\gamma$  and adult  $\beta$  globins<sup>21</sup>. Dysregulation of signaling pathways downstream of many of these regulators leads to the development of specific leukemias and myeloproliferative disorders<sup>22,23</sup>. However, how distinct complexes interact to repress or activate specific gene expression programs is still poorly understood. Recent techniques such as Chromatin Immunoprecipitation (ChIP) coupled with massive parallel sequencing (ChIP-seq), combined with gene expression profiling and bioinformatic analysis, have begun to uncover additional interactions between known regulators as well as some understanding of the interplay between these complexes and the local nucleosome environment<sup>24</sup>.

GATA1, discovered as the first member of the family of factors to bind the DNA consensus sequence (A/T)GATA(A/G) through two zinc fingers characteristic of the family<sup>25</sup>, has been extensively studied. Yet, it turns out that the annotation of GATA consensus sites is a poor predictor of in vivo GATA1 binding to erythroid-specific genes<sup>26</sup>. In fact, the bulk of GATA1 binding occurs at distal regulatory elements, with very few (only about 10-15%) in the proximal promoter regions<sup>27,28</sup>. These GATA1-bound sites were all enriched for monomethylated H3K4 (H3K4me1), a marker found predominately at distal enhancer elements<sup>29,30</sup>, providing further evidence that GATA1 acts primarily through distal enhancers<sup>31</sup>. Motif analysis of the activated genes revealed highly enriched consensus sequences for SCL/Tal1 at GATA1-bound sites<sup>27,28,31-33</sup>, suggesting that GATA1 activation occurs in concert with the SCL/Tal1 coregulator. In erythroid cells, SCL/Tal1 forms a complex with the ubiquitous bHLH protein E2A, and also the LIM domain containing factors LMO2 and Ldb1<sup>19</sup>. This activating complex, along with GATA1, binds to composite GATA1/E-box domains spaced approximately 9-11nt apart (reviewed in<sup>20</sup>). The components of the GATA1 repressor complexes are much less clear, and probably include FOG1, the repressor Gfi-1b, and/or the chromatin modifiers EZH2 and core PRC2 component EED (reviewed in<sup>20</sup>) (Figure 2).

Similar to GATA1, other components of the activation complex are also necessary for red blood cell development; Lmo2, GATA1, and SCL/Tal1 knockout mice are all anemic and die of lack of primitive erythropoiesis during fetal development<sup>19</sup>. Embryos lacking Ldb1 show defective primitive erythropoiesis and targeted-deletion of Ldb1 via Mx-Cre expression in adult mice results in severe anemia and ultimate death, confirming that Ldb1 is also required for adult definitive erythropoiesis. Genome-wide location analysis of SCL/Tal1 binding of components of this complex confirmed the reciprocal findings of GATA1 binding described above: that the majority of SCL/Tal1 sites are also outside the proximal promoter region<sup>32</sup>. After combining Ldb1 ChIP-seq with chromosome conformation capture sequencing (3C), one group discovered that Ldb1 binds directly to the HS2, HS3, and HS4 DNA hypersensitive sites of the globin locus control region (LCR), despite the fact that there are no direct Ldb1 binding sites there<sup>34</sup>.

Klf1 (formerly called EKLF) is a zinc finger transcription factor that recognizes a subset of extended CACC box motifs and is remarkably erythroid-restricted<sup>35</sup>; its essential role in erythropoiesis has been established for quite some time<sup>19</sup>. Similar to the GATA1 activation complex, genome-wide location analysis of Klf1 binding has revealed that the majority of Klf1-bound sites are more than 10kb away from any known gene<sup>36</sup>. Comparing the Klf and GATA1 binding site maps, one group<sup>36</sup> discovered that almost half (48%) of the Klf1 sites were within 1kb of GATA1 sites and few contained the SCL/Tal1 consensus sequence or overlapped with SCL/Tal1-GATA1 co-occupied sites. This suggested that GATA1 and Klf1 may activate genes in a complex distinct from that which contains Tal1 (reviewed in<sup>20</sup>).

Even more interesting, Klf1 may actually be responsible for recruiting regions of chromatin with active transcription into transcription factories rather than the machinery moving to the chromatin. Several studies in the past decade have shown that nascent transcription actually occurs within a limited number of nuclear foci containing high concentrations of active RNA Pol II and transcriptional machinery<sup>37</sup> and that even distant actively-transcribed chromatin colocalizes to these active areas rather than moving the machinery itself. In erythroid tissue, Klf1 is found to colocalize to these areas of active transcription, and through looping experiments using the 4C technique, it was confirmed that Klf can recruit active chromatin to these transcription factories

<sup>38</sup>

Other transcription factors have emerged as critical determinants of erythropoiesis. Similar to SCL/TAL1, LYL-1 is a transcription factor containing a basic helix-loop-helix motif. The defect in erythropoiesis in Lyl-1 knockout hematopoietic cells can be partially explained by their higher rate of apoptosis associated with a decreased level of Bcl-x<sub>L</sub><sup>39</sup>. Loss of the related POZ-Kruppel family transcription factor, LRF (or Zbtb7a/Pokemon), leads to lethal embryonic anemia and causes an Epo-unresponsive macrocytic anemia in adult mice<sup>40</sup>. Apoptosis of erythroid cells due to deficiency of LRF can be rescued by loss of the proapoptotic factor, Bim. Although Lrf knock-out mice share a similar phenotype with Stat5a/5b knock-out mice<sup>15</sup>, Epo-STAT5 signaling remains intact in the absence of LRF, given the observation that Bcl-x<sub>L</sub> is induced upon Epo stimulation and also the MAPK and PI3K pathways are activated normally in Lrf-null erythroblasts<sup>40</sup>. Lrf is a direct target of GATA1 and also GATA-1 physically interacts with LRF in activating direct target genes<sup>28</sup>. A positive feedback loop by which GATA-1 mediates LRF activation could be critical for erythropoiesis.

## **Regulated pausing of RNA Polymerase II (Pol II) during erythroid differentiation**

Genome-wide studies in several cell types showed that Pol II is frequently stalled at promoters shortly after transcription initiation. In some cells the percentage of pausing may be as high as 90% of expressed genes, supporting the concept that regulation Pol II elongation is a critical step in gene expression<sup>41-43</sup>. Recruitment of P-TEFb (Positive transcription elongation factor b) kinase promotes elongation by phosphorylating Spt5 and Pol II. Studies on the murine globin gene cluster illustrate the regulation of transcriptional elongation through release of paused Pol II; globin gene transcription is dramatically increased only following significant binding of NF-E2, TFIIIB, and Pol II to the promoter. Deletion of the locus control region reduces phosphorylation of Pol II and subsequent Pol II elongation, resulting in a 90% decrease of globin transcription<sup>44</sup>. Zebrafish bearing a loss- of-function mutation in transcriptional intermediary factor 1 gamma (TIF-1 $\gamma$ ) are extremely anemic. TIF-1 modulates the outcome of erythroid or myeloid decision from HSCs by controlling the balance of gata-1 and pu.1 level<sup>45</sup>. In the absence of TIF-1 $\gamma$  recruitment of p-TEFb and FACT is impaired, which in turn reduces the phosphorylation level of Pol II and Pol II elongation<sup>46</sup>.

### Epigenetic changes in chromatin during erythroid differentiation

In many developmental systems posttranslational modifications of histones are crucial in regulating gene expression (**Figure 2**;<sup>47,48</sup>.) While some modifications tend to be associated with gene activation or repression states, the actual situation is generally more complex. For example, the level of the epigenetic histone mark H3K79me2, added by the H3K79 methyltransferase Dot1, is correlated with transcriptional activation and elongation in *Drosophila* cells<sup>49</sup> as well as in higher eukaryotes such as human ES cells<sup>41</sup>. However, location analysis on human T-cells revealed that the H3K79me2 mark showed no preferential association with either gene activation or repression<sup>50</sup>, raising the possibility that there is tissue specificity of the regulation of gene expression by H3K79me2 levels. H3K79 methylation occurs within the globin locus, suggesting a role in erythropoiesis. Indeed, loss of Dot1 greatly impairs both primitive and definitive yolk sac erythropoiesis, and BFU-E colonies number and size are significantly reduced in Dot1 knockout mice<sup>51</sup>. Importantly, the relative levels of two crucial regulators, GATA2 and Pu.1 (Sfp1), are critical in determining the cell fate of hematopoietic progenitors: high Pu.1 and low GATA2 result in myeloid differentiation, low Pu.1 and high GATA2 lead to erythroid differentiation. The ratio of Pu.1 to GATA2 was reversed by Dot1L knockdown, resulting in high Pu.1 and low GATA2 levels in Dot1L-deficient yolk-sac erythroid progenitors. The effect of H3K79me2 on the level of Pu.1 is probably indirect because loss of H3K79me2 leads to high levels of Pu.1.

As a second example, the H3K4me3 modification at transcriptional start sites is commonly associated with gene activation and transcription initiation by RNA polymerase II. However, the H3K4 modification often colocalizes with H3K27me3 modifications, which are associated with repressed genes. Such chromatin regions marked both by H3K27me3 and H3K4me3 are termed "bivalent domains". Many are found in embryonic stem cells on genes encoding key developmental transcription factors<sup>52</sup>. Similar bivalent domains occur in human primary hematopoietic stem/progenitor cells (CD133<sup>+</sup>) that can differentiate into CD36-expressing erythrocyte precursors<sup>30</sup>. In CD133<sup>+</sup> cells promoter regions of 2910 genes bear this bivalent domain mark, including numerous genes involved in development and differentiation. Of these genes 19% lost the H3K27me3 mark during erythroid differentiation; in the CD133<sup>+</sup> cells a substantial fraction of these genes were enriched with H3K4me1 and H3K9me1 marks as well as bound Pol II, suggesting that these genes

are “poised” for activation during erythroid differentiation concomitant with the loss of the repressive H3K27me3 mark.

In addition to trimethylated H3K4me3 and H3K27me3, other histone modifications often mark transcriptionally “poised” genes in erythroid progenitors. Although H3K4me3 and the dimethylated H3K4me2 are concordant at most genes, multipotential hematopoietic cells contain a subset of genes that are marked by H3K4me2 but not H3K4me3. These genes are transcriptionally silent in progenitors and are highly enriched in lineage-specific hematopoietic genes. The H3K4me2 mark is rapidly lost on nonerythroid genes during erythroid differentiation, accompanied by repression of these genes. On the other hand, gain of the H3K4me3 mark correlated with transcriptional activation upon erythroid differentiation. Thus the H3K4me2<sup>+</sup>-H3K4me3<sup>-</sup> on nonerythroid genes may regulate their repression during erythroid development<sup>53</sup>.

Several epigenetic regulatory mechanisms control gene induction and repression during erythroid development. Changes in gene expression are not accompanied by significant changes in histone modifications such as H3K4me3 and H3K27me3 after GATA-1 is reintroduced into a GATA1-null erythroblast cell line to induce differentiation<sup>54</sup>. Changes in H4K16ac and H3K79me2 levels, rather than H3K4me3 and H3K27me3, are most predictive of the direction in changes in gene expression during terminal fetal liver erythroid differentiation<sup>55</sup>. Since H3K4me3 is usually associated with transcriptional initiation, while H3K79me2 is tightly correlated with transcription elongation, control of Pol II elongation could be a mechanism for regulating erythroid gene expression. This may be mediated by GATA1 or TAL1 or their associated complexes, especially since nearby regions of genes induced during terminal erythroid development are cooccupied by these factors<sup>54</sup>.

The precise timing of chromatin switch(es) associated with erythroid differentiation is unclear. Several modifications at the  $\beta$  globin locus—DNA demethylation, formation of DNase I hypersensitive sites, and onset of activation-associated histone modifications—occur during the S phase of an early erythroid cell cycle following stimulation of CFU-E proliferation<sup>56</sup>. This raises the possibility that one window of time during DNA replication allows structural changes in chromatin associated with newly synthesized DNA.

### **Interplay of cell cycle and terminal erythroid differentiation**

In many developmental systems, terminal differentiation is tightly coupled with irreversible exit from the cell cycle. Erythroid cells usually undergo 3-5 cell divisions during terminal differentiation, preceded by an irreversible exit from the cell cycle. Work on Rb<sup>57</sup>, E2F4<sup>58</sup>, and cyclin D<sup>59</sup> have established that cell division is highly coupled to erythroid differentiation, as defects in those genes result in fetal anemia. Moreover, a crucial step in activating erythroid gene expression occurs during the S phase of an early erythroid cell cycle following CFU-E activation<sup>56</sup>. This transition involves repression of a cyclin-dependent kinase (cdk) inhibitor, p57(kip2), which in turn causes the downregulation of Pu.1, an antagonist of GATA-1 function<sup>56</sup>. Much remains to be learned about the interplay of cell cycle regulation and erythroid gene expression, especially since several agents that slow the cell cycle have been shown to induce gamma globin gene expression in adult erythroid cells<sup>60</sup>.

## Histone deacetylation and erythroblast enucleation

Although in all vertebrates the erythroid precursor nucleus becomes highly condensed and the chromatin transcriptionally inactive as erythropoiesis progresses, the process of enucleation—the budding off and ultimate extrusion of this condensed, inactive erythroid nucleus—is unique to mammals. Our understanding of this elaborate process of mammalian enucleation has advanced significantly since the earliest morphological documentation of the phenomenon decades ago<sup>61</sup>. This intricate developmental process involves multiple molecular and cellular pathways including histone deacetylation, actin polymerization, vesicle trafficking and cytokinesis, cell-matrix interactions, and even specific miRNAs (reviewed in<sup>62</sup>). Importantly, enucleation is not restricted to definitive erythroid cells; primitive yolk-sac derived erythropoiesis also exhibits chromatin condensation and enucleation<sup>63</sup>. While nuclear condensation is thought to be critical for mammalian enucleation, chromatin condensation also occurs in many other tissue types, including rather ubiquitous cellular processes such as cell division and apoptosis. Apoptotic mechanisms such as caspase activation are known to be responsible for enucleation of lens epithelia and keratinocytes, although the process is not similar to enucleation of erythroid precursors (reviewed in<sup>62</sup>).

Certain histone modifications affect not only binding of regulatory proteins but also the stability of chromatin itself. Global levels of several acetylation marks on histones, including H3K9Ac, H4K5Ac, H4K8Ac, and H4K12Ac are significantly reduced during the terminal stages of erythroid differentiation, concomitant with a decrease in the levels of the histone acetyltransferase (HAT) GCN5<sup>64</sup>. Administration of histone deacetylase (HDAC) inhibitors to human erythroid precursors cultured from CD34+ cells inhibited terminal differentiation<sup>65</sup>. Similarly, treatment of Friend-virus infected murine spleen erythroblasts with HDAC inhibitors blocked enucleation<sup>66</sup>. The HDAC most important for erythropoiesis is likely HDAC2, since either specific pharmacological inhibition or shRNA knockdown of HDAC2 blocked chromatin condensation and enucleation of mouse fetal liver erythroblasts in vitro<sup>67</sup>. Deacetylation of histones generates a positive charge on the corresponding lysine residue; one plausible hypothesis is that these new positive charges interact with the negative charges on the phosphodiester bonds of DNA to facilitate DNA and chromatin condensation.

## Regulation of erythropoiesis by microRNAs

MicroRNAs are a class of recently identified small regulatory RNAs that downregulate expression of their target genes by either mRNA degradation or translational inhibition or both<sup>68,69</sup>. Specific microRNAs are important regulators of several aspects of erythropoiesis, including erythroid lineage determination, erythroid progenitor proliferation, terminal erythroid differentiation and enucleation (**Table 1**). For example, miR-150 is enriched in human umbilical cord blood megakaryocyte-erythrocyte and megakaryocyte progenitors, relative to erythroid progenitors. Overexpression and knockdown assays in MEP cells showed that miR-150 induces differentiation towards the megakaryocytic lineage and inhibits erythroid lineage differentiation through downregulation of one principal target gene, MYB<sup>70</sup>.

Several other microRNAs regulate terminal proliferation and differentiation of erythroid progenitor cells. miR-221 and miR-222 are downregulated during erythroid differentiation of cultured cord blood CD34+ progenitors. Overexpression of miR-221 and miR-222 in CD34+ progenitor cells impaired proliferation and accelerated differentiation of erythroid precursors. This effect is mediated by

downregulation of one principal target gene, KIT, which encodes the receptor for stem cell factor and which is required for proliferation of erythroid progenitors<sup>71</sup>. miR-24 functions as a negative regulator of activin signaling by downregulating the mRNA encoding the activin type I receptor ALK4. In cultured CD34+ cells, miR-24 is downregulated during erythroid differentiation, which is inversely correlated with the upregulation of its target gene ALK4. In both CD34+ and K562 erythroleukemia cells, gain- and loss-of-function studies demonstrated that the downregulation of miR-24 is required for normal erythroid differentiation<sup>72</sup>. miR-223 is also downregulated during erythroid differentiation of cord blood CD34+ progenitor cells. Overexpression of miR-223 impaired erythroid differentiation by downregulating LMO2, a critical transcription factor that is upregulated during erythroid differentiation of CD34+ progenitor cells and is required for erythroid differentiation<sup>73</sup>. Thus downregulation of several microRNAs is essential during terminal erythroid differentiation.

In contrast, two co-transcribed microRNAs, miR-144 and miR-451, are highly induced during terminal erythroid differentiation and regulate expression of key erythroid- important genes. miR-144 and miR-451 are highly induced in the erythroid cell line G1E-ER4 when GATA-1 expression is restored by the treatment with estradiol, and chromatin immunoprecipitation experiments demonstrated that miR-144/451 is a direct transcriptional target of GATA-1<sup>74</sup>. Knockdown of miR-451 in Zebrafish embryos by injection of antisense morpholinos impaired erythropoiesis<sup>74,75</sup>, establishing its importance in erythropoiesis. In Zebrafish *gata2* is one important direct target gene of miR-451<sup>75</sup>. Upregulation of miR-144 is required for Zebrafish embryonic  $\alpha$ -globin gene expression through the downmodulation of its direct target gene *Klfd*<sup>76</sup>.

Knockout mice deficient for the miR-144/451 cluster display a cell autonomous impairment of late erythroblast maturation, resulting in erythroid hyperplasia, splenomegaly, and a mild anemia<sup>77-79</sup>. Importantly, these mice exhibit ineffective erythropoiesis in response to oxidative stress. One important direct target gene downmodulated by miR-451 is 14-3-3 $\zeta$ , a phospho-serine/threonine-binding protein that inhibits nuclear accumulation of the transcription factor FoxO3, a positive regulator of erythroid anti-oxidant genes. In miR-144/451<sup>-/-</sup> erythroblasts, the excess 14-3-3 $\zeta$  causes a partial relocalization of FoxO3 from nucleus to cytoplasm with dampening of its transcriptional program, including reduced expression of genes that encode the important anti-oxidant proteins catalase and glutathione peroxidase 1. Importantly, shRNA suppression of 14-3-3 $\zeta$  protects miR-144/451<sup>-/-</sup> erythrocytes against peroxide-induced destruction, and restores catalase activity<sup>77-79</sup>. These studies thus define an important role for miR-144/451 in regulating a subset of erythroid- important genes.

In human trisomy 13, there is delayed switching and persistence of fetal hemoglobin (HbF). By analyzing partial trisomy cases, miR-15a and miR-16-1 were identified as potential candidates causing elevated fetal hemoglobin expression. Indeed, increased expression of these microRNAs in primary human erythroid progenitor cells resulted in elevated fetal hemoglobin gene expression. One important direct target of these microRNAs, Myb, plays an important role as a negative regulator of  $\gamma$ -globin gene expression<sup>80</sup>.

Regulated expression of several other microRNAs is important for erythroblast chromatin condensation and enucleation. The majority of microRNAs present in CFU-E erythroid progenitors are downregulated during terminal erythroid differentiation. Of the predominant developmentally down-regulated miRNAs, ectopic overexpression of miR-191 in mouse fetal liver erythroid progenitors blocked erythroid enucleation but had minor effects on proliferation or erythroid differentiation. Two

developmentally upregulated genes, *Riok3* and *Mxi1*, that are required for chromatin condensation and enucleation, are direct miR-191 targets. Both overexpression of miR-191 and knockdown of *Riok3* or *Mxi1* impaired the normal downregulation of histone acetyltransferase Gcn5 (whose downregulation is required for histone deacetylation and chromatin condensation<sup>60</sup>). Thus normal down-regulation of miR-191 is essential for erythroid chromatin condensation and enucleation by allowing up-regulation of *Riok3* and *Mxi1* and downregulation of Gcn5<sup>81</sup>.

In addition to the microRNAs listed above, many other microRNAs are also abundant and developmentally regulated during erythroid differentiation<sup>81</sup>. However, ectopic expression of the majority of microRNAs in cultured CFU-E stage progenitors, effectively preventing their normal downmodulation during terminal differentiation, had subtle or no effects on erythropoiesis<sup>81</sup>. This may indicate that these microRNAs are relatively weak regulators of gene expression, or indicate that these miRNAs affect differentiation under conditions different than those in culture. This is well illustrated by a recent report showing that miR-144/451<sup>-/-</sup> mice is only mildly anemic. However, when exposed to phenylhydrazine-induced hemolysis, more than half of miR-144/451<sup>-/-</sup> mice died while all wild type mice fully recovered<sup>78</sup>.

In addition to microRNAs, another class of non-coding RNA, lncRNAs (long non-coding RNA) has recently been shown to be crucial for important biological processes, such as the p53 response<sup>82</sup> and stem cell reprogramming<sup>83</sup>. It will be interesting to explore the potential function that lncRNAs may play in red blood cell production.

### **Stress erythropoiesis and enhanced self-renewal of early committed red cell BFU-E progenitors**

Red blood cell levels are normally tightly regulated by Epo, which stimulates erythropoiesis by promoting survival, proliferation, and terminal differentiation of CFU-E cells and more mature erythroblasts. Since normal Epo levels are very low, red cell output from CFU-E cells can be increased more than one order of magnitude by increased Epo production or by injection of recombinant Epo. However because each Epo-responsive CFU-E cell in the bone marrow can undergo only 3-5 terminal cell divisions under maximum Epo stimulation, the number of CFU-E cells limits the maximum Epo-dependent erythrocyte output. Steady-state erythropoiesis alone is therefore not able to correct the red blood cell deficiency during extreme conditions such as recovery from bone marrow irradiation or chronic anemia. During such conditions of stress erythropoiesis new CFU-Es are produced from the most immature committed definitive erythroid progenitor cells, the Burst Forming Unit-Erythroid (BFU-E) cells. Formation of BFU-E and CFU-E progenitors does not require Epo receptor activation<sup>6</sup>. One BFU-E progenitor cell can form hundreds of thousands of erythroblasts *in vitro*; its name is derived from the large burst of red colonies formed in methylcellulose after 7 days culture. The ability of BFU-E progenitors to undergo limited self-renewal during stress erythropoiesis allows rescue of lethally irradiated mice from anemia, and re-transplantation also protects secondary and tertiary recipients<sup>84</sup>. In this regard stress erythropoiesis is similar to definitive fetal liver erythropoiesis and Friend Virus-induced erythroleukemia, two other situations where similar mechanisms induce erythroid progenitors to undergo self-renewal rather than to differentiate.

**Stress erythropoiesis is regulated by Stem cell factor, glucocorticoids, Bone morphogenic protein 4 and Hedgehog signaling in addition to tissue hypoxia.**

### *Microenvironment*

Early observations showed that erythropoiesis moves from the bone marrow to the spleen during stress erythropoiesis (Figure 3)<sup>85,86</sup>. The importance of factors in the microenvironment for sustaining BFU-E self-renewal was further suggested by the fact that splenectomized mice are resistant to Friend erythroid leukemia virus induced erythroid leukemia<sup>87</sup>. Furthermore, fetal liver and spleen-derived stromal cell lines are superior to cells derived from bone marrow for supporting fetal BFU-E proliferation,<sup>88-90</sup>. In order to identify factors that promote BFU-E self-renewal, researchers have therefore studied the spleen and fetal liver milieu, in addition to determining the effect of physiological responses to stress such as increased levels of stress hormones.

### *Glucocorticoids*

Release of cortisol from the adrenal glands is increased during conditions of stress erythropoiesis, such as sepsis or severe trauma. The therapeutic effect of the glucocorticoid analog prednisone in patients with the red cell progenitor disorder Diamond-Blackfan Anemia (DBA) is well documented, though severe side effects limit its use<sup>91,92</sup>.

Mice that lack the glucocorticoid receptor or express only a glucocorticoid receptor defective in DNA binding and transactivation have normal steady state erythropoiesis, while stress erythropoiesis is severely impaired<sup>93,94</sup>. In particular, mice with defective or missing glucocorticoid receptors fail to respond to phenylhydrazine-induced hemolysis by increasing CFU-E numbers in the spleen. For unknown reasons the glucocorticoid effect on stress erythropoiesis is antagonized by p53 activation, and p53<sup>-/-</sup> mice respond to hypoxic stress faster than normal, as shown by the rapid increase of CFU-E and c-Kit<sup>+</sup>/CD34<sup>+</sup> cells in the spleen<sup>95</sup>. Glucocorticoids support stress erythropoiesis by inducing expression of Myb, Kit, and Lmo2 and inhibiting Gata1 expression<sup>95,96</sup>. Of those changes in gene expression only upregulation of Kit mRNA is detected 4 hours after glucocorticoid stimulation of BFU-E cells<sup>97</sup>.

The role of glucocorticoids in stress erythropoiesis can be studied *in vitro* by culturing early erythroid progenitors in medium containing SCF, glucocorticoids, and Epo<sup>93,97-99</sup>. As during *in vivo* stress erythropoiesis, *in vitro* proliferation of fetal liver erythroblasts is severely decreased by a mutation in the glucocorticoid receptor that disrupts dimerization<sup>93,94</sup>. The stimulatory effects of glucocorticoids on red cell production therefore likely requires glucocorticoid receptor dimerization, which is required for efficient transactivation of promoters with glucocorticoid receptor element (GRE) full-sites but which may also be necessary for gene repression<sup>93,94</sup>. These results suggest that the mechanisms regulating stress erythropoiesis are evolutionarily conserved, and possibly part of an ancient cortisol-mediated stress response to trauma, which also leads to increased blood pressure and glucose levels<sup>100</sup>.

Using BFU-E and CFU-E cells purified from mouse fetal liver by a new flow cytometric techniques (both BFU-Es and CFU-Es are kit-positive and negative for Ter119, B220, Mac-1, CD3, Gr-1, CD32/16, Sca-1, CD41 and CD34, while BFU-Es express low levels of CD71 and CD24a compared to CFU-Es) and cultured in a serum-free medium containing only SCF and IGF-1, it was shown that that glucocorticoids induce limited self-renewal of BFU-E cells, and not of CFU-E cells or erythroblasts. Glucocorticoids thereby protect BFU-E cells from exhaustion, and in parallel, over time increase the number of CFU-E cells formed from each BFU-E greater than 10-fold<sup>97</sup>. We proposed a physiological model of stress erythropoiesis where increased levels of glucocorticoids help maintain the earliest erythroid progenitors, increase CFU-E output, and at the same time stimulate terminal differentiation, thus promoting both a rapid and long-lasting increase in red blood cell production.

Identification of BFU-Es as the target cell of GCs in SE, together with our novel method to isolate BFU-Es, will allow studies towards development of novel erythropoiesis stimulating agents that act by promoting SE by the same mechanisms employed by GCs.

### *Stem cell factor*

SCF (Kit ligand) exists both in a soluble and a membrane-bound form. Kit signaling is not only important for erythroid progenitor proliferation, but also for HSC growth, mast cell function, melanogenesis, and spermatogenesis. Fetal liver hepatic progenitors that express very high levels of SCF and support expansion of hematopoietic stem cells likely also support BFU-E self-renewal during fetal liver erythropoiesis<sup>101</sup>. The stress response of enhanced CFU-E formation in murine spleen upon phenylhydrazine treatment is drastically reduced by infusion of anti-kit antibodies, reiterating the importance of SCF in stress erythropoiesis<sup>102</sup>. SCF binding to Kit induces activation of PI3K, and inhibition of PI3K results in decreased numbers of BFU-E and CFU-E cells in vivo and reduced erythroblast proliferation in vitro<sup>103,104</sup>. SCF counteracts BFU-E differentiation in part by inducing expression of Myc, which prevents terminal erythroid maturation<sup>64,105</sup>.

### *Bone morphogenic protein 4*

Bone morphogenic protein 4 (BMP4) is also essential for stress erythropoiesis. The flexed-tail mouse strain, which expresses a dominant-negative Smad5 mutant that inhibits BMP4 signaling, exhibits a neonatal anemia that resolves 2 weeks after birth<sup>106-108</sup>. This demonstrates that while BMP4 signaling through Smad5 is not required to maintain adult or fetal liver hematopoiesis, it is essential for stress erythropoiesis<sup>109,110</sup>. Indeed, during stress erythropoiesis, BMP4 expression is induced by hypoxia in spleen stromal cells<sup>111,112</sup>. In order for BFU-E cells to be responsive to BMP4 they need to be "primed" with Sonic Hedgehog (SHH), a morphogen that is also synthesized and secreted by cells in the spleen microenvironment<sup>113</sup>. BMP4, in turn, activates the transcription factor Smad5 as well as Scl and Gata2, which enhances the probability of BFU-E self-renewal over differentiation (Figure 3)<sup>84,114,115</sup>.

### *Hypoxia*

Interestingly, glucocorticoids induce expression of genes in BFU-E cells that contain promoter regions highly enriched for hypoxia-induced factor 1alpha (HIF1 $\alpha$ ) binding sites, suggesting that activation of HIF1 $\alpha$  may enhance or replace the effect of glucocorticoids on BFU-E self-renewal. Indeed, HIF1 $\alpha$  activation by a prolyl hydroxylase inhibitor (PHI) synergized with glucocorticoids and enhanced production of CFU-Es and then erythroblasts ~170-fold<sup>97</sup>. While earlier observations showed that hypoxia supports BFU-E self-renewal through effects on spleen stroma<sup>116</sup>, these findings demonstrate an additional effect intrinsic to BFU-E cells.

## **Prospectus**

These studies have provided profound insights into the multiple complex mechanisms by which the body regulates the number of red blood cells within a narrow normal range. Equally importantly, they

provide novel insights into possible treatments for anemias and other red cell disorders. For example, recent advances in the understanding the regulation of beta-hemoglobin switching could lead to better therapies for disorders such as beta thalassemia and sickle cell disease<sup>117</sup>. Increased understanding of how genetic and epigenetic programs regulate different stages of red cell development may enable large- scale production of functional red blood cells from hematopoietic or other tissues for clinical blood transfusions. Furthermore, deeper understanding of mechanisms regulating BFU-E self-renewal and thus the output of CFU-E progenitors and mature erythroid cells could result in development of drugs that stimulate the physiological mechanisms of stress erythropoiesis. These drugs could be useful in treating relatively erythropoietin-resistant anemias, including patients with bone marrow failure disorders such as Diamond Blackfan anemia, trauma, sepsis, and possibly anemia of malaria as well as the ~18% of kidney dialysis patients who fail to respond to Epo. One such example is pharmacologically induced HIF1 $\alpha$  activation, which leads to increased erythroblast production at physiological concentrations of glucocorticoids<sup>97</sup>.

## **Acknowledgments**

This work was supported in part by NIH grants P01 HL 32262, DK068348, and DK067356, grant C-382-641-001-091 from the Singapore - Massachusetts Institute of Technology Alliance (SMA), and by a research grant from Amgen, Inc. JF was supported by a fellowship from the Swedish Research Council and stipends from the Diamond-Blackfan Anemia Foundation, Maja och Hjalmar Leanders Stiftelse and The Sweden-America Foundation. PW received a Croucher Foundation Postdoctoral Research Grant; SH was supported by K08 DK076848 from NIDDK; and LZ was supported by a graduate fellowship from the Singapore - Massachusetts Institute of Technology Alliance (SMA). We are grateful for useful discussions with Vijay Sankaran and Leif Si-Hun Ludwig and appreciate the graphics rendered by Tom DiCesare.

## **Author Contributions**

S.M.H. and P.W. had equal contributions; S.M.H., P.W., L.Z., J.F., and H.F.L. wrote the paper. The authors have no conflicts of interest.

## Literature Cited

1. Palis J, Robertson S, Kennedy M, Wall C, Keller G. Development of erythroid and myeloid progenitors in the yolk sac and embryo proper of the mouse. *Development*. 1999;126(22):5073-5084.
2. Elliott S, Pham E, Macdougall IC. Erythropoietins: a common mechanism of action. *Exp Hematol*. 2008;36(12):1573-1584.
3. Fawcett DWaRPJ. Bloom & Fawcett: Concise Histology (ed 1st): Arnold Publishers; 1997.
4. Molineux G, Foote M, Elliott S. Erythropoiesis and Erythropoietins (Second Edition) Birkhauser; 2009.
5. Dolznig H, Grebien F, Deiner EM, et al. Erythroid progenitor renewal versus differentiation: genetic evidence for cell autonomous, essential functions of EpoR, Stat5 and the GR. *Oncogene*. 2006;25(20):2890-2900.
6. Wu H, Liu X, Jaenisch R, Lodish HF. Generation of committed erythroid BFU-E and CFU-E progenitors does not require erythropoietin or the erythropoietin receptor. *Cell*. 1995;83(1):59-67.
7. Kieran MW, Perkins AC, Orkin SH, Zon LI. Thrombopoietin rescues in vitro erythroid colony formation from mouse embryos lacking the erythropoietin receptor. *Proc Natl Acad Sci U S A*. 1996;93(17):9126-9131.
8. Lin CS, Lim SK, D'Agati V, Costantini F. Differential effects of an erythropoietin receptor gene disruption on primitive and definitive erythropoiesis. *Genes Dev*. 1996;10(2):154-164.
9. Zhang J, Socolovsky M, Gross AW, Lodish HF. Role of Ras signaling in erythroid differentiation of mouse fetal liver cells: functional analysis by a flow cytometry-based novel culture system. *Blood*. 2003;102(12):3938-3946.
10. Eshghi S, Vogelesang MG, Hynes RO, Griffith LG, Lodish HF. Alpha4beta1 integrin and erythropoietin mediate temporally distinct steps in erythropoiesis: integrins in red cell development. *J Cell Biol*. 2007;177(5):871-880.
11. Lodish HF, Ghaffari S, Socolovsky M, Tong W, Zhang J. Signaling by the Erythropoietin Receptor In: Molineux G, Foote M, Elliott S, eds. Erythropoiesis and Erythropoietins (Second Edition) Birkhauser; 2009:155-174.
12. Ghaffari S, Kitidis C, Zhao W, et al. AKT induces erythroid-cell maturation of JAK2-deficient fetal liver progenitor cells and is required for Epo regulation of erythroid-cell differentiation. *Blood*. 2006;107(5):1888-1891.
13. Zhang J, Lodish HF. Endogenous K-ras signaling in erythroid differentiation. *Cell Cycle*. 2007;6(16):1970-1973.
14. Socolovsky M, Nam H, Fleming MD, Haase VH, Brugnara C, Lodish HF. Ineffective erythropoiesis in Stat5a(-/-)5b(-/-) mice due to decreased survival of early erythroblasts. *Blood*. 2001;98(12):3261-3273.
15. Socolovsky M, Fallon AE, Wang S, Brugnara C, Lodish HF. Fetal anemia and apoptosis of red cell progenitors in Stat5a(-/-)5b(-/-) mice: a direct role for Stat5 in Bcl-X(L) induction. *Cell*. 1999;98(2):181-191.
16. Wood AD, Chen E, Donaldson IJ, et al. ID1 promotes expansion and survival of primary erythroid cells and is a target of JAK2V617F-STAT5 signaling. *Blood*. 2009;114(9):1820-1830.
17. Zhu BM, McLaughlin SK, Na R, et al. Hematopoietic-specific Stat5-null mice display microcytic hypochromic anemia associated with reduced transferrin receptor gene expression. *Blood*. 2008;112(5):2071-2080.
18. Sathyanarayana P, Dev A, Fang J, et al. EPO receptor circuits for primary erythroblast survival. *Blood*. 2008;111(11):5390-5399.
19. Cantor AB, Orkin SH. Transcriptional regulation of erythropoiesis: an affair involving multiple partners. *Oncogene*. 2002;21(21):3368-3376. 10.1038/sj.onc.1205326.
20. Kerenyi MA, Orkin SH. Networking erythropoiesis. *J Exp Med*. 2010;207(12):2537-2541.

21. Bauer DE, Orkin SH. Update on fetal hemoglobin gene regulation in hemoglobinopathies. *Curr Opin Pediatr.* 2011;23(1):1-8.
22. Gilliland DG, Jordan CT, Felix CA. The molecular basis of leukemia. *Hematology Am Soc Hematol Educ Program.* 2004:80-97.
23. Rosenbauer F, Tenen DG. Transcription factors in myeloid development: balancing differentiation with transformation. *Nat Rev Immunol.* 2007;7(2):105-117.
24. Tijssen MR, Cvejic A, Joshi A, et al. Genome-wide Analysis of Simultaneous GATA1/2, RUNX1, FLI1, and SCL Binding in Megakaryocytes Identifies Hematopoietic Regulators. *Dev Cell.* 2011;20(5):597-609.
25. Wall L, deBoer E, Grosveld F. The human beta-globin gene 3' enhancer contains multiple binding sites for an erythroid-specific protein. *Genes Dev.* 1988;2(9):1089-1100.
26. Bresnick EH, Martowicz ML, Pal S, Johnson KD. Developmental control via GATA factor interplay at chromatin domains. *J Cell Physiol.* 2005;205(1):1-9.
27. Fujiwara T, O'Geen H, Keles S, et al. Discovering hematopoietic mechanisms through genome-wide analysis of GATA factor chromatin occupancy. *Mol Cell.* 2009;36(4):667-681.
28. Yu M, Riva L, Xie H, et al. Insights into GATA-1-mediated gene activation versus repression via genome-wide chromatin occupancy analysis. *Mol Cell.* 2009;36(4):682-695.
29. Heintzman ND, Ren B. The gateway to transcription: identifying, characterizing and understanding promoters in the eukaryotic genome. *Cell Mol Life Sci.* 2007;64(4):386-400.
30. Cui K, Zang C, Roh TY, et al. Chromatin signatures in multipotent human hematopoietic stem cells indicate the fate of bivalent genes during differentiation. *Cell Stem Cell.* 2009;4(1):80-93.
31. Cheng Y, Wu W, Kumar SA, et al. Erythroid GATA1 function revealed by genome-wide analysis of transcription factor occupancy, histone modifications, and mRNA expression. *Genome Res.* 2009;19(12):2172-2184.
32. Kassouf MT, Hughes JR, Taylor S, et al. Genome-wide identification of TAL1's functional targets: insights into its mechanisms of action in primary erythroid cells. *Genome Res.* 2010;20(8):1064-1083.
33. Tripic T, Deng W, Cheng Y, et al. SCL and associated proteins distinguish active from repressive GATA transcription factor complexes. *Blood.* 2009;113(10):2191-2201.
34. Soler E, Andrieu-Soler C, de Boer E, et al. The genome-wide dynamics of the binding of Ldb1 complexes during erythroid differentiation. *Genes Dev.* 2010;24(3):277-289.
35. Miller II, Bieker JJ. A novel, erythroid cell-specific murine transcription factor that binds to the CACCC element and is related to the Kruppel family of nuclear proteins. *Mol Cell Biol.* 1993;13(5):2776-2786.
36. Tallack MR, Whittington T, Yuen WS, et al. A global role for KLF1 in erythropoiesis revealed by ChIP-seq in primary erythroid cells. *Genome Res.* 2010;20(8):1052-1063.
37. Jackson DA, Hassan AB, Errington RJ, Cook PR. Visualization of focal sites of transcription within human nuclei. *EMBO J.* 1993;12(3):1059-1065.
38. Schoenfelder S, Sexton T, Chakalova L, et al. Preferential associations between co-regulated genes reveal a transcriptional interactome in erythroid cells. *Nat Genet.* 2010;42(1):53-61.
39. Capron C, Lacout C, Lecluse Y, et al. LYL-1 deficiency induces a stress erythropoiesis. *Exp Hematol.* 2011;39(6):629-642.
40. Maeda T, Ito K, Merghoub T, et al. LRF is an essential downstream target of GATA1 in erythroid development and regulates BIM-dependent apoptosis. *Dev Cell.* 2009;17(4):527-540.
41. Guenther MG, Levine SS, Boyer LA, Jaenisch R, Young RA. A chromatin landmark and transcription initiation at most promoters in human cells. *Cell.* 2007;130(1):77-88.
42. Muse GW, Gilchrist DA, Nechaev S, et al. RNA polymerase is poised for activation across the genome. *Nat Genet.* 2007;39(12):1507-1511.

43. Zeitlinger J, Stark A, Kellis M, et al. RNA polymerase stalling at developmental control genes in the *Drosophila melanogaster* embryo. *Nat Genet.* 2007;39(12):1512-1516.
44. Sawado T, Halow J, Bender MA, Groudine M. The beta -globin locus control region (LCR) functions primarily by enhancing the transition from transcription initiation to elongation. *Genes Dev.* 2003;17(8):1009-1018.
45. Monteiro R, Pouget C, Patient R. The gata1/pu.1 lineage fate paradigm varies between blood populations and is modulated by tif1gamma. *EMBO J.* 2011;30(6):1093-1103.
46. Bai X, Kim J, Yang Z, et al. TIF1gamma controls erythroid cell fate by regulating transcription elongation. *Cell.* 2010;142(1):133-143.
47. Suganuma T, Workman JL. Signals and combinatorial functions of histone modifications. *Annu Rev Biochem.* 2011;80:473-499.
48. Talbert PB, Henikoff S. Histone variants--ancient wrap artists of the epigenome. *Nat Rev Mol Cell Biol.* 2010;11(4):264-275.
49. Schubeler D, MacAlpine DM, Scalzo D, et al. The histone modification pattern of active genes revealed through genome-wide chromatin analysis of a higher eukaryote. *Genes Dev.* 2004;18(11):1263-1271.
50. Barski A, Cuddapah S, Cui K, et al. High-resolution profiling of histone methylations in the human genome. *Cell.* 2007;129(4):823-837.
51. Feng Y, Yang Y, Ortega MM, et al. Early mammalian erythropoiesis requires the Dot1L methyltransferase. *Blood.* 2010;116(22):4483-4491.
52. Bernstein BE, Mikkelsen TS, Xie X, et al. A bivalent chromatin structure marks key developmental genes in embryonic stem cells. *Cell.* 2006;125(2):315-326.
53. Orford K, Kharchenko P, Lai W, et al. Differential H3K4 methylation identifies developmentally poised hematopoietic genes. *Dev Cell.* 2008;14(5):798-809.
54. Wu W, Cheng Y, Keller CA, et al. Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. *Genome Res.* 2011;21(10):1659-1671.
55. Wong P, Hattangadi SM, Cheng AW, Frampton GM, Young RA, Lodish HF. Gene induction and repression during terminal erythropoiesis are mediated by distinct epigenetic changes. *Blood.* 2011 Aug 22. [Epub ahead of print]
56. Pop R, Shearstone JR, Shen Q, et al. A key commitment step in erythropoiesis is synchronized with the cell cycle clock through mutual inhibition between PU.1 and S-phase progression. *PLoS Biol.* 2010;8(9).
57. Sankaran VG, Orkin SH, Walkley CR. Rb intrinsically promotes erythropoiesis by coupling cell cycle exit with mitochondrial biogenesis. *Genes Dev.* 2008;22(4):463-475.
58. Kinross KM, Clark AJ, Iazzolino RM, Humbert PO. E2f4 regulates fetal erythropoiesis through the promotion of cellular proliferation. *Blood.* 2006;108(3):886-895.
59. Kozar K, Ciemerych MA, Rebel VI, et al. Mouse development and cell proliferation in the absence of D-cyclins. *Cell.* 2004;118(4):477-491.
60. Sankaran VG, Xu J, Orkin SH. Advances in the understanding of haemoglobin switching. *Br J Haematol.* 2010;149(2):181-194.
61. Muir AR, Kerr DN. Erythropoiesis: an electron microscopical study. *Q J Exp Physiol Cogn Med Sci.* 1958;43(1):106-114.
62. Ji P, Murata-Hori M, Lodish HF. Formation of mammalian erythrocytes: chromatin condensation and enucleation. *Trends Cell Biol.* 2011;21(7):409-415.
63. Palis J, Malik J, McGrath KE, Kingsley PD. Primitive erythropoiesis in the mammalian embryo. *Int J Dev Biol.* 2010;54(6-7):1011-1018.
64. Jayapal SR, Lee KL, Ji P, Kaldis P, Lim B, Lodish HF. Down-regulation of Myc is essential for terminal erythroid maturation. *J Biol Chem.* 2010;285(51):40252-40265.

65. Fujieda A, Katayama N, Ohishi K, et al. A putative role for histone deacetylase in the differentiation of human erythroid cells. *Int J Oncol.* 2005;27(3):743-748.
66. Popova EY, Krauss SW, Short SA, et al. Chromatin condensation in terminally differentiating mouse erythroblasts does not involve special architectural proteins but depends on histone deacetylation. *Chromosome Res.* 2009;17(1):47-64.
67. Ji P, Yeh V, Ramirez T, Murata-Hori M, Lodish HF. Histone deacetylase 2 is required for chromatin condensation and subsequent enucleation of cultured mouse fetal erythroblasts. *Haematologica.* 2010;95(12):2013-2021.
68. Bartel DP. MicroRNAs: target recognition and regulatory functions. *Cell.* 2009;136(2):215-233.
69. Guo H, Ingolia NT, Weissman JS, Bartel DP. Mammalian microRNAs predominantly act to decrease target mRNA levels. *Nature.* 2010;466(7308):835-840.
70. Lu J, Guo S, Ebert BL, et al. MicroRNA-mediated control of cell fate in megakaryocyte-erythrocyte progenitors. *Dev Cell.* 2008;14(6):843-853.
71. Felli N, Fontana L, Pelosi E, et al. MicroRNAs 221 and 222 inhibit normal erythropoiesis and erythroleukemic cell growth via kit receptor down-modulation. *Proc Natl Acad Sci U S A.* 2005;102(50):18081-18086.
72. Wang Q, Huang Z, Xue H, et al. MicroRNA miR-24 inhibits erythropoiesis by targeting activin type I receptor ALK4. *Blood.* 2008;111(2):588-595.
73. Felli N, Pedini F, Romania P, et al. MicroRNA 223-dependent expression of LMO2 regulates normal erythropoiesis. *Haematologica.* 2009;94(4):479-486.
74. Dore L, Amigo J, Dos Santos C, et al. A GATA-1-regulated microRNA locus essential for erythropoiesis. *Proc Natl Acad Sci U S A.* 2008;105(9):3333-3338.
75. Pase L, Layton J, Kloosterman W, Carradice D, Waterhouse P, Lieschke G. miR-451 regulates zebrafish erythroid maturation in vivo via its target gata2. *Blood.* 2009;113(8):1794-1804.
76. Fu Y, Du T, Dong M, et al. Mir-144 selectively regulates embryonic alpha-hemoglobin synthesis during primitive erythropoiesis. *Blood.* 2009;113(6):1340-1349.
77. Patrick D, Zhang C, Tao Y, et al. Defective erythroid differentiation in miR-451 mutant mice mediated by 14-3-3zeta. *Genes Dev.* 2010;24(15):1614-1619.
78. Rasmussen K, Simmini S, Abreu-Goodger C, et al. The miR-144/451 locus is required for erythroid homeostasis. *J Exp Med.* 2010;207(7):1351-1358.
79. Yu D, dos Santos C, Zhao G, et al. miR-451 protects against erythroid oxidant stress by repressing 14-3-3zeta. *Genes Dev.* 2010;24(15):1620-1633.
80. Sankaran VG, Menne TF, Scepanovic D, et al. MicroRNA-15a and -16-1 act via MYB to elevate fetal hemoglobin expression in human trisomy 13. *Proc Natl Acad Sci U S A.* 2011;108(4):1519-1524.
81. Zhang L, Flygare J, Wong P, Lim B, Lodish HF. miR-191 regulates mouse erythroblast enucleation by down-regulating Riok3 and Mxi1. *Genes Dev.* 2011;25(2):119-124.
82. Huarte M, Guttman M, Feldser D, et al. A large intergenic noncoding RNA induced by p53 mediates global gene repression in the p53 response. *Cell.* 2010;142(3):409-419.
83. Loewer S, Cabili MN, Guttman M, et al. Large intergenic non-coding RNA-RoR modulates reprogramming of human induced pluripotent stem cells. *Nat Genet.* 2010;42(12):1113-1117.
84. Harandi OF, Hedge S, Wu DC, McKeone D, Paulson RF. Murine erythroid short-term radioprotection requires a BMP4-dependent, self-renewing population of stress erythroid progenitors. *J Clin Invest.* 2010;120(12):4507-4519.
85. McCulloch EA, Siminovitch L, Till JE. Spleen-Colony Formation in Anemic Mice of Genotype Ww. *Science.* 1964;144:844-846.

86. Hara H, Ogawa M. Erythropoietic precursors in mice with phenylhydrazine-induced anemia. *Am J Hematol.* 1976;1(4):453-458.
87. Kreja L, Seidel HJ. On the role of the spleen in Friend virus (F-MuLV-P) erythroleukemia. *Exp Hematol.* 1985;13(7):623-628.
88. Slaper-Cortenbach I, Ploemacher R, Lowenberg B. Different stimulative effects of human bone marrow and fetal liver stromal cells on erythropoiesis in long-term culture. *Blood.* 1987;69(1):135-139.
89. Yanai N, Matsuya Y, Obinata M. Spleen stromal cell lines selectively support erythroid colony formation. *Blood.* 1989;74(7):2391-2397.
90. Ohneda O, Yanai N, Obinata M. Microenvironment created by stromal cells is essential for a rapid expansion of erythroid cells in mouse fetal liver. *Development.* 1990;110(2):379-384.
91. Flygare J, Karlsson S. Diamond-Blackfan anemia: erythropoiesis lost in translation. *Blood.* 2007;109(8):3152-3154.
92. Vlachos A, Ball S, Dahl N, et al. Diagnosing and treating Diamond Blackfan anaemia: results of an international clinical consensus conference. *Br J Haematol.* 2008;142(6):859-876.
93. Bauer A, Tronche F, Wessely O, et al. The glucocorticoid receptor is required for stress erythropoiesis. *Genes Dev.* 1999;13(22):2996-3002.
94. Reichardt HM, Kaestner KH, Tuckermann J, et al. DNA binding of the glucocorticoid receptor is not essential for survival. *Cell.* 1998;93(4):531-541.
95. Ganguli G, Back J, Sengupta S, Wasylyk B. The p53 tumour suppressor inhibits glucocorticoid-induced proliferation of erythroid progenitors. *EMBO Rep.* 2002;3(6):569-574.
96. von Lindern M, Zauner W, Mellitzer G, et al. The glucocorticoid receptor cooperates with the erythropoietin receptor and c-Kit to enhance and sustain proliferation of erythroid progenitors in vitro. *Blood.* 1999;94(2):550-559.
97. Flygare J, Rayon Estrada V, Shin C, Gupta S, Lodish HF. HIF1alpha synergizes with glucocorticoids to promote BFU-E progenitor self-renewal. *Blood.* 2011;117(12):3435-3444.
98. Kolbus A, Blazquez-Domingo M, Carotta S, et al. Cooperative signaling between cytokine receptors and the glucocorticoid receptor in the expansion of erythroid progenitors: molecular analysis by expression profiling. *Blood.* 2003;102(9):3136-3146.
99. Wessely O, Deiner EM, Beug H, von Lindern M. The glucocorticoid receptor is a key regulator of the decision between self-renewal and differentiation in erythroid progenitors. *EMBO J.* 1997;16(2):267-280.
100. Sapolsky RM, Romero LM, Munck AU. How do glucocorticoids influence stress responses? Integrating permissive, suppressive, stimulatory, and preparative actions. *Endocr Rev.* 2000;21(1):55-89.
101. Chou S, Lodish HF. Fetal liver hepatic progenitors are supportive stromal cells for hematopoietic stem cells. *Proc Natl Acad Sci U S A.* 2010;107(17):7799-7804.
102. Broudy VC, Lin NL, Priestley GV, Nocka K, Wolf NS. Interaction of stem cell factor and its receptor c-kit mediates lodgment and acute expansion of hematopoietic cells in the murine spleen. *Blood.* 1996;88(1):75-81.
103. Huddleston H, Tan B, Yang FC, et al. Functional p85alpha gene is required for normal murine fetal erythropoiesis. *Blood.* 2003;102(1):142-145.
104. Bakker WJ, van Dijk TB, Parren-van Amelsvoort M, et al. Differential regulation of Foxo3a target genes in erythropoiesis. *Mol Cell Biol.* 2007;27(10):3839-3854.
105. Munugalavadla V, Dore LC, Tan BL, et al. Repression of c-kit and its downstream substrates by GATA-1 inhibits cell proliferation during erythroid maturation. *Mol Cell Biol.* 2005;25(15):6747-6759.
106. Hegde S, Lenox LE, Lariviere A, et al. An intronic sequence mutated in flexed-tail mice regulates splicing of Smad5. *Mamm Genome.* 2007;18(12):852-860.

107. Lenox LE, Perry JM, Paulson RF. BMP4 and Madh5 regulate the erythroid response to acute anemia. *Blood*. 2005;105(7):2741-2748.
108. Subramanian A, Hegde S, Porayette P, Yon M, Hankey P, Paulson RF. Friend virus utilizes the BMP4-dependent stress erythropoiesis pathway to induce erythroleukemia. *J Virol*. 2008;82(1):382-393.
109. Singbrant S, Karlsson G, Ehinger M, et al. Canonical BMP signaling is dispensable for hematopoietic stem cell function in both adult and fetal liver hematopoiesis, but essential to preserve colon architecture. *Blood*. 2010;115(23):4689-4698.
110. Singbrant S, Moody JL, Blank U, et al. Smad5 is dispensable for adult murine hematopoiesis. *Blood*. 2006;108(12):3707-3712.
111. Wu DC, Paulson RF. Hypoxia regulates BMP4 expression in the murine spleen during the recovery from acute anemia. *PLoS ONE*. 2010;5(6):e11303.
112. Millot S, Andrieu V, Letteron P, 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.
113. Perry JM, Harandi OF, Porayette P, Hegde S, Kannan AK, Paulson RF. Maintenance of the BMP4-dependent stress erythropoiesis pathway in the murine spleen requires hedgehog signaling. *Blood*. 2009;113(4):911-918.
114. Lugas JJ, Chung YS, Mills JC, et al. GATA2 functions at multiple steps in hemangioblast development and differentiation. *Development*. 2007;134(2):393-405.
115. Fuchs O, Simakova O, Klener P, et al. Inhibition of Smad5 in human hematopoietic progenitors blocks erythroid differentiation induced by BMP4. *Blood Cells Mol Dis*. 2002;28(2):221-233.
116. Perry JM, Harandi OF, Paulson RF. BMP4, SCF, and hypoxia cooperatively regulate the expansion of murine stress erythroid progenitors. *Blood*. 2007;109(10):4494-4502.
117. Sankaran VG, Nathan DG. Reversing the hemoglobin switch. *N Engl J Med*. 2011;363(23):2258-2260.

**Table1 microRNAs are important regulators for erythropoiesis**

MicroRNA	Organism and experimental system	Function	Target	Reference
miR-150	Human cord blood megakaryocyte-erythrocyte and megakaryocyte progenitor (MEP)	miR-150 induces differentiation towards the megakaryocytic lineage at the expense of erythroid lineage.	<i>MYB</i>	70
miR-221 and miR-222	Human cord blood CD34+ cells	Downregulation of miR-221 and miR-222 is required for terminal erythroid progenitor proliferation.	<i>KIT</i>	71
miR-24	Human cord blood CD34+ cells and K562 cell line	Downregulation of miR-24 is required for terminal erythroid differentiation.	<i>ALK4</i>	72
miR-223	Human cord blood CD34+ cells	Downregulation of miR-223 is required for terminal differentiation.	<i>LMO2</i>	73
miR-144	Zebrafish embryo	miR-144 is required for Zebrafish embryonic $\alpha$ -globin gene expression.	<i>Klfd</i>	76
miR-451	Zebrafish embryo	miR-451 is required for Zebrafish erythropoiesis.	<i>Gata2</i>	75
	Knockout mice	miR-451 is required for steady state erythropoiesis and resistance to oxidation during stress erythropoiesis.	<i>14-3-3zeta</i>	78
miR-15a and miR-16-1	Human cord blood CD34+ cells	miR-15a and miR-16-1 were identified as potential candidates causing elevated fetal hemoglobin expression. Increased expression in elevated fetal hemoglobin gene expression.	<i>MYB</i>	80
miR-191	Mouse primary erythroid progenitors	The downregulation of miR-191 is required for erythroblast chromatin condensation and enucleation.	<i>Riok3</i> and <i>Mxi1</i>	81

## Figure Legends

### **Figure 1: An overview of erythropoiesis: regulation at multiple levels by multiple proteins and miRNAs**

Formation of red blood cells from hematopoietic stem cells is regulated by signaling through both external factors (blue) such as cytokines and fibronectin as well as intracellular factors such as transcription factors (black) and miRNAs (red). Below the differentiation network, a timeline and images are shown for *in vitro* methylcellulose colony formation of murine BFU-Es, and CFU-Es.

### **Figure 2. Transcription factors, Pol II status and histone modifications associated with actively transcribed and repressed genes in erythroid cells.**

For genes activated during differentiation (lower panel), the GATA-1 activation associated proteins exist in different complexes (as indicated by the double arrows) through binding to both distal regulatory regions and promoter regions near the TSS. H3K4me2 and H3K4me3 are enriched in some of these bound regions. TIF-1 and the SCL complex recruit pTEF-b to promote Pol II elongation by phosphorylating DSIF, NELF and Pol II. SCF could be the link between the GATA-1 complex and Pol II elongation machinery. H3K79me2 and H3K36me3 are often enriched in the transcribed portion of the gene.

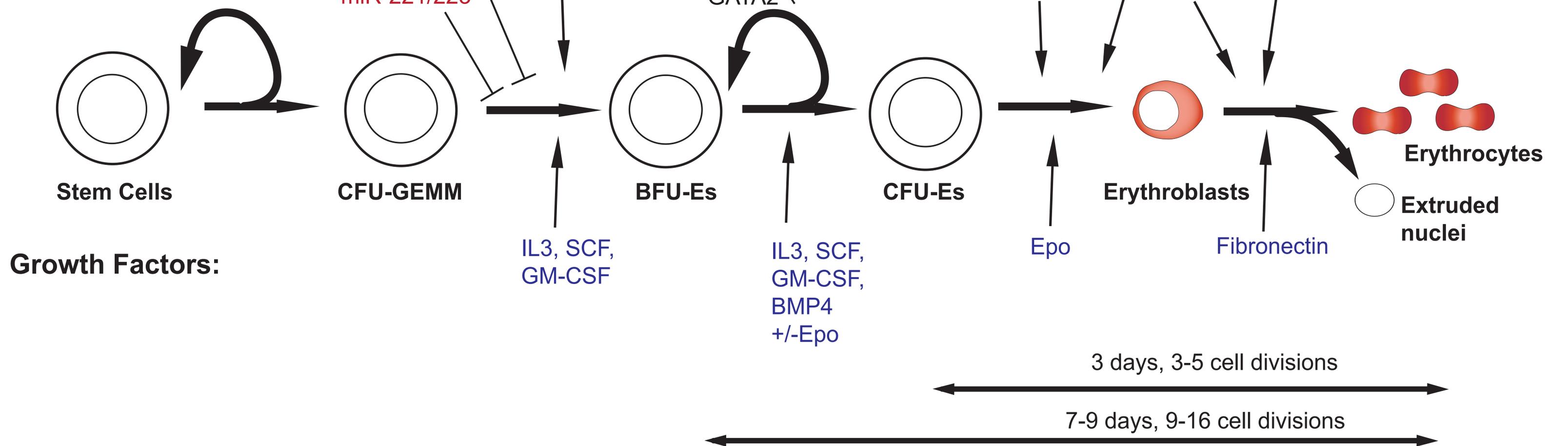
Among repressed genes (upper panel), the GATA-1 repressor complexes are less clear and could exist in different forms as indicated by the double arrows. H3K27me3 is enriched near the TSS. Pol II is either not bound or is paused around the TSS. In the absence of TIF-1, recruitment of p-TEFb is impaired, and DSIF and NELF inhibit the phosphorylation of Pol II and Pol II elongation.

### **Figure 3: BFU-E self renewal: The probability of erythroid progenitor self-renewal versus differentiation depends on extrinsic and intrinsic factors.**

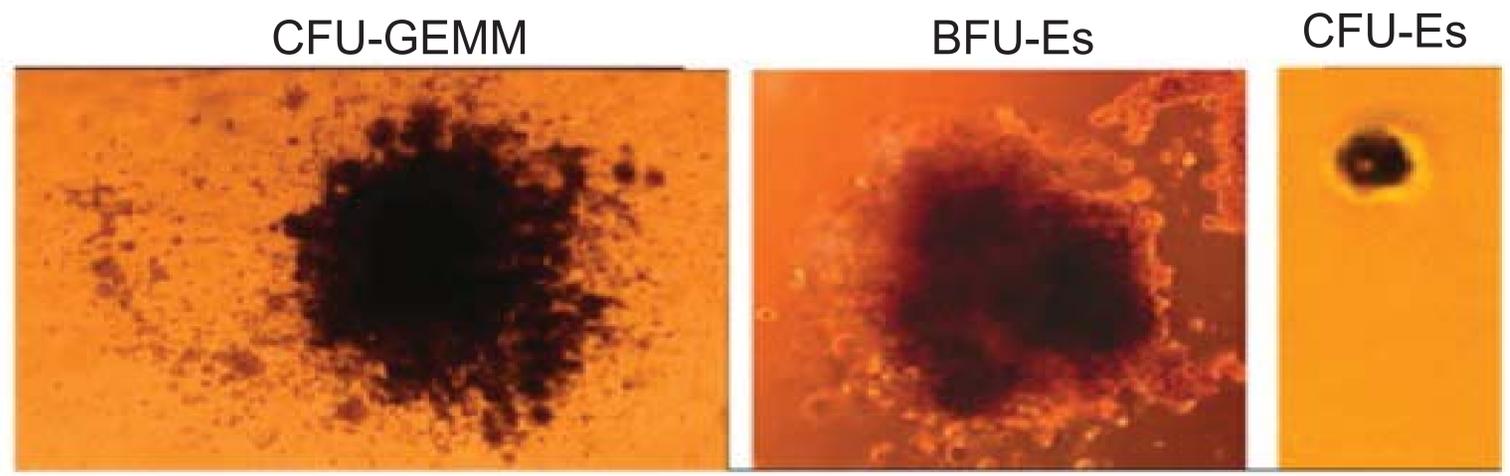
BFU-E progenitors either self-renew or differentiate depending on the body's need for generation of CFU-E's and Epo-dependent erythroblasts. While BFU-E self-renewal is very limited during steady-state erythropoiesis in the bone marrow, it is virtually limitless in the spleen during conditions of stress erythropoiesis. The cytokines Scf, Bmp4, and Shh promote self-renewal in addition, as does stimulation by glucocorticoids (GCs) and hypoxia. These signals activate transcription factors Myc, Smad5, Scl, Gata2, Myb and Hif1a.

**Figure 1.**

**Transcription factors,  
small RNAs, and  
DNA-binding factors:**



**Colonies:**

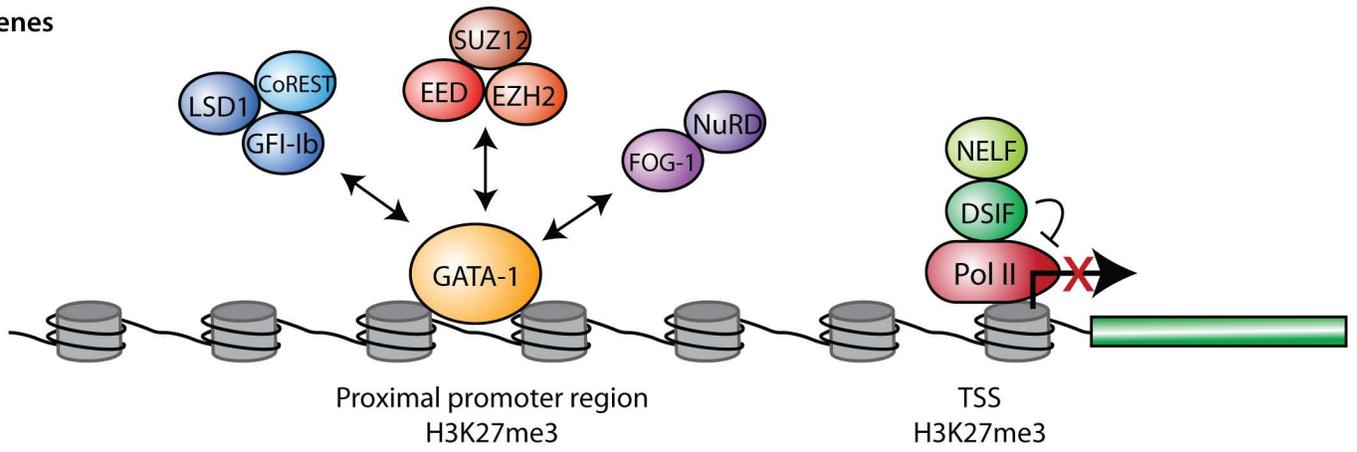


From [bloodjournal.hematologylibrary.org](http://bloodjournal.hematologylibrary.org) at UNIV OF KANSAS MEDICAL CENTER on November 4, 2011. For personal use only.

# Figure 2

From [bloodjournal.hematologylibrary.org](http://bloodjournal.hematologylibrary.org) at UNIV OF KANSAS MEDICAL CENTER on November 4, 2011. For personal use only.

## Repressed genes



## Induced genes

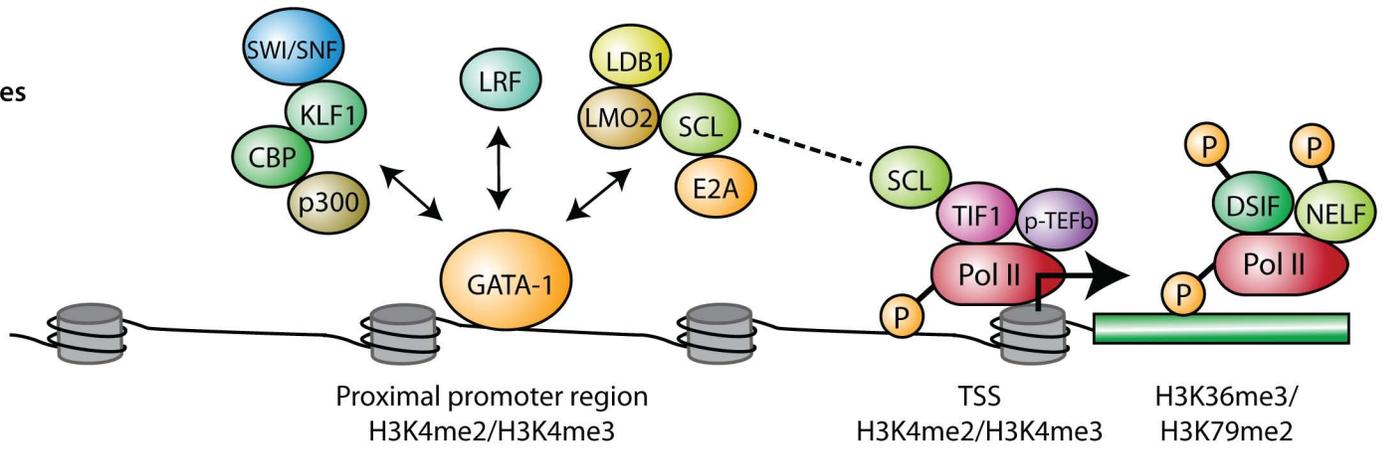


Figure 3

