Figure S1. Emetine dissolves spontaneous and arsenite-induced SGs.

Differentiating CD34+ cells were collected at different days of *in vitro* differentiation (Day 6 is shown here) and cultured in the absence (UN, upper panel) or presence (EM, upper panel) of emetine (20 μ M) for 120 minutes before processing for immunofluorescence microscopy using antibodies specific for SGs (eIF3b, green), PBs (S6K1-hedls, red) or SGs/PBs (eIF4E, blue). Alternatively, cells were cultured in the absence (SA, lower panel) or presence (EM, lower panel) of emetine for 60 minutes before adding sodium arsenite (500 μ M) for 45 minutes and processing for immunofluorescence microscopy. Enlarged views (3.2 fold) of boxed areas depict separate channels and merged views of SGs/PS with or without different drug treatments.

Figure S2. CD34+ bone marrow cells lineage differentiation in *in vitro* culture. (A)

CD34+ cells, collected at different days of *in vitro* differentiation in media supporting erythroid, myeloid and megakaryocytic differentiation were stained with MGG to identify the morphology of the cells. Representative erythroid cells are shown (magnification 50x). **(B)** Differentiating CD34+ cells, cultured in the same conditions described in panel A, were also stained for cell surface markers specific for mature erythrocytes (GlyA-FITC), megakaryocytes (CD41-FITC) or myeloid cells (CD11b-PECy5) to assess lineage differentiation. **(C)** Percentage of hemoglobin-positive CD34+ cells, assed by DAF staining, is also shown. Data are the means ± SEM from three independent experiments. **(D)** Percentage of immature (CD71+/GlyA-) and mature (CD71+/GlyA+) erythroid cells containing SGs on the 6th day of *in vitro* differentiation. Values are the means of three independent experiments in which at least 100 cells were counted. **(E)** HRI knockdown efficiency in CD34+ hematopoietic cells was investigated using RT-qPCR and reported as

mRNA level of the target gene normalized against β -actin housekeeping gene expression

level. Results represent the means of three independent experiments performed in triplicate ± SEM. P value shows t-test probability compared to FLuc treated samples.

Figure S3. Mice blood parameters and SGs positive erythroid cells in whole murine and human bone marrow samples. (A) Mice normal physiological parameters recorded at the time of sacrifice for bone marrow staining shown in Figure 2. Averages with standard deviation are shown for 7 mice. (B) The percentage of immature (CD71+/Ter119-) and mature (CD71+/Ter119+) murine erythroid cells containing SGs was calculated by immunofluorescence microscopy. Values are the means of three independent fields in which at least 100 cells were counted. (C) Percentage of immature (CD71+/GlyA-) and mature (CD71+/GlyA+) erythroid cells containing SGs, from a healthy human donor's whole bone marrow. Values are the means of three independent fields in which at least 100 cells were counted.

Figure S4. HRI, G3BP and α -globin mRNA levels and absolute numbers of cell

viability. (A) Efficiency of G3BP knockdown in CD34+ hematopoietic cells. G3BP efficiency was investigated using RT-qPCR and reported as mRNA level of the target gene normalized against β -actin housekeeping gene expression level. Results represent the means of three independent experiments performed in triplicate ± SEM. P value shows t-test probability compared to FLuc treated samples. (B) Real-time PCR was used to quantify α -globin mRNA level. mRNA expression levels are normalized against β -actin housekeeping transcripts. Results represent the means of three independent experiments performed in triplicate ± 300 mRNA level. mRNA expression levels are normalized against β -actin housekeeping transcripts. Results represent the means of three independent experiments performed in triplicate ± SEM. P values are derived from student's t-test compared to FLuc infected samples. (C) Absolute numbers of live and dead cells after 7 days (A) of G3BP knock down treatment.

May-Grünwald-Giemsa staining and DAF

At least 10X10⁵ CD 34+ cells were collected at different days of the *in vitro* differentiation and were cytospun on the slides and air dried. Slides were then placed in methanol for 5 minutes, air dried and placed in MGG (Sigma-Aldrich) stain for 10 min. Slides were then rinsed with water and allowed to air dry before examination with immersion oil and 50X objective.

Hemoglobinization of *in vitro* differentiating human CD34+ was assayed by DAF (2,7diaminofluorene; Sigma-Aldrich) staining at different days of culture. Assay was performed as previously described [24], with minor modifications. At least 300 cells per sample were scored and blue cells were counted positive.

Quantitative real-time PCR

RT-qPCR on CD34+ cells was performed as follows: 200 ng of total RNA from CD34+ cells infected with Lentiviruses containing shRNA against Firefly luciferase or HRI or G3BP was used to generate first strand cDNA using oligo dT primers from the Superscript III reverse transcription kit (Invitrogen). RT–qPCR was performed using Taqman supermix (Applied Biosystems) for HRI and SYBRgreen supermix (Applied Biosystems) for G3BP in a 7900HT Sequence Detection System (Applied Biosystems). Beta actin was used as an internal control. Relative changes of mRNA amounts were calculated based on the $\Delta\Delta$ Ct method. HRI Taqman Expression System (Hs 00205264_m1) and Taqman β -actin probe (401846) were purchased from Applied Biosystems. Primers for G3BP (Forward, CTTATGTCCATGGGGGATTG; Reverse, TCACCTGGACTACCACACCA), and α -globin (Forward, ACTGAACCTGACCGTACAACGCTGGCGAGT; Reverse, AGCAGGCAGTGGCTTAGAG) were purchased from IDT, Integrated DNA Technologies Inc., Coralville, IA, USA.

FIG S1

elF3/S6K1-hedls/elF4E

UN







SA 500μ**M 45'**

elF3 S6K1 elF4E MERGE

EM 20μM 60' + SA 45'





elF3 S6K1 elF4E MERGE



elF3 S6K1 elF4E MERGE

FIG S2



FIG S3

Α

Normal Hematological Paramete	al Hematological Parameters		
Number of Mice	7		
White blood counts (k/ul)	5.4971 +/- 1.9600		
НСТ (%)	54.3286 +/- 2.2199		
Platelet counts (k/ul)	583.0000 +/- 350.0100		





Treatments (DAY 7)	Absolute number of live cells (x10E4)	Absolute number of dead cells (x10E4)
shFLuc	172 +/- 2.08	12 +/- 2.89
shG3BP-G3	113 +/- 1.53	37 +/- 1.15
shG3BP-F11	164 +/- 0.58	32 +/- 2.08
shG3BP-F12	145 +/- 2.64	35 +/- 4.58

Supplementary Information Table S1. List of antibodies and siRNA/shRNA target sequences used in this study.

Antibody	Source
Goat anti-elF3b	Santa Cruz Biotechnology
Goat anti-TIA-1	Santa Cruz Biotechnology
Mouse anti-S6K1	Santa Cruz Biotechnology
Rabbit anti-eIF4E	Santa Cruz Biotechnology
Rabbit anti-eIF4G	Santa Cruz Biotechnology
Rabbit anti-RCK	Bethyl Laboratories
Mouse anti-G3BP	BD Biosciences
Rabbit anti-G3BP	Bethyl Laboratories
Rabbit anti-elF2 α	Santa Cruz Biotechnology
Rabbit anti-Phospho S51-eIF2 α	StressGen
Rabbit anti- α globin 898	Dr Weiss, Philadelphia
Rabbit anti-GAPDH	Santa Cruz Biotechnology
Anti-human CD71-PECy5-conjugated antibody	BD Biosciences
Anti-human GLYA-FITC-conjugated antibody	BD Biosciences
Anti-human CD11b-PECy5-conjugated antibody	BD Biosciences
Anti-human CD41a-FITC-conjugated antibody	BD Biosciences
Anti-mouse CD71-FITC-conjugated antibody	BD Pharmigen
Anti-mouse TER119-APC-conjugated antibody	BD Pharmigen
Anti-mouse CD41-FITC-conjugated antibody	BD Pharmigen
Anti-mouse CD11b-ALEXA FLUOR 488-	BD Pharmigen
conjugated antibody	
Cy2-HRP-conjugated secondary antibodies	Jackson Immunoresearch Labs
Cy3-HRP-conjugated secondary antibodies	Jackson Immunoresearch Labs
Cy5-HRP-conjugated secondary antibodies	Jackson Immunoresearch Labs

shRNA Target sequence	Source
Firefly Luciferase	The RNAi Consortium, Broad Institute
G3BP-G3 CCAGGCTTTGAGGAGATTCAT	The RNAi Consortium, Broad Institute
G3BP-F11 GCCTGTAAGAAATACAGGATT	The RNAi Consortium, Broad Institute
G3BP-F12 CGGGAATTTGTGAGACAGTAT	The RNAi Consortium, Broad Institute

shRNA Target sequence	Source
Firefly Luciferase	The RNAi Consortium, Broad Institute
HRI-29 GGATTGGATAGTCGAGAGAAA	The RNAi Consortium, Broad Institute
HRI-30 GAATTGGTAGAAGGTGTGTTT	The RNAi Consortium, Broad Institute
HRI-65 CAGAGCTATTACTCACTTAAT	The RNAi Consortium, Broad Institute