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## Journal Article

**Author(s):**

Bernitz, Jeffrey M.; Rapp, Katrina; Daniel, Michael G.; Shcherbinin, Dmitrii; Yuan, Ye; Gomes, Andreia; Waghray, Avinash; Brosh, Ran; Lachmann, Alexander; Ma'ayan, Avi; Papatsenko, Dmitri; Moore, Kateri A.

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# Memory of Divisional History Directs the Continuous Process of Primitive Hematopoietic Lineage Commitment

Jeffrey M. Bernitz,<sup>1,2,3,8</sup> Katrina Rapp,<sup>1,2</sup> Michael G. Daniel,<sup>1,2,3</sup> Dmitrii Shcherbinin,<sup>4,5</sup> Ye Yuan,<sup>1,2,3</sup> Andreia Gomes,<sup>1,2,6</sup> Avinash Waghay,<sup>1,2,3</sup> Ran Brosh,<sup>1,2</sup> Alexander Lachmann,<sup>7</sup> Avi Ma'ayan,<sup>7</sup> Dmitri Papatsenko,<sup>4</sup> and Kateri A. Moore<sup>1,2,\*</sup>

<sup>1</sup>Department of Cell, Developmental and Regenerative Biology, Icahn School of Medicine at Mount Sinai, One Gustave L. Levy Place, Box 1496, New York, NY 10029, USA

<sup>2</sup>Black Family Stem Cell Institute, Icahn School of Medicine at Mount Sinai, One Gustave L. Levy Place, Box 1496, New York, NY 10029, USA

<sup>3</sup>The Graduate School of Biomedical Sciences, Icahn School of Medicine at Mount Sinai, One Gustave L. Levy Place, Box 1496, New York, NY 10029, USA

<sup>4</sup>Skoltech Center of Life Sciences, Skolkovo Institute of Science and Technology, Moscow 121205, Russia

<sup>5</sup>Institute of Biomedical Chemistry (IBMC), Moscow 119121, Russia

<sup>6</sup>Doctoral Programme in Experimental Biology and Biomedicine, University of Coimbra, 3004-517 Coimbra, Portugal

<sup>7</sup>Department of Pharmacological Sciences, Mount Sinai Center for Bioinformatics, Icahn School of Medicine at Mount Sinai, New York, NY 10029, USA

<sup>8</sup>Present address: Department of Biosystems Science and Engineering, Eidgenössische Technische Hochschule (ETH) Zurich, Basel, Switzerland

\*Correspondence: kateri.moore@mssm.edu

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## SUMMARY

Hematopoietic stem cells (HSCs) exist in a dormant state and progressively lose regenerative potency as they undergo successive divisions. Why this functional decline occurs and how this information is encoded is unclear. To better understand how this information is stored, we performed RNA sequencing on HSC populations differing only in their divisional history. Comparative analysis revealed that genes upregulated with divisions are enriched for lineage genes and regulated by cell-cycle-associated transcription factors, suggesting that proliferation itself drives lineage priming. Downregulated genes are, however, associated with an HSC signature and targeted by the Polycomb Repressive Complex 2 (PRC2). The PRC2 catalytic subunits *Ezh1* and *Ezh2* promote and suppress the HSC state, respectively, and successive divisions cause a switch from *Ezh1* to *Ezh2* dominance. We propose that cell divisions drive lineage priming and *Ezh2* accumulation, which represses HSC signature genes to consolidate information on divisional history into memory.

## INTRODUCTION

Hematopoietic stem cells (HSCs) represent a critical source of regenerative cells for curative therapies for a vast array of immunohematological disorders. As such, understanding the mechanisms that regulate their regeneration and lineage commitment are important for the *ex vivo* production and expansion of cells for therapy. *In vivo*, adult HSCs reside in a quiescent state and proliferate infrequently in the absence of stress (Bernitz et al., 2016; Qiu et al., 2014; Wilson et al., 2008). When HSCs proliferate *in vivo* their regenerative potential progressively declines (Qiu et al., 2014). This phenomenon was previously proposed by the Generation-Age Hypothesis (Rosendaal et al., 1976, 1979), which states that HSC regenerative potential is determined by the number of its past divisions. While not explicitly stated, this hypothesis also implies that HSCs must store information about their divisional history as a form of memory, without which past divisions could not exert an effect on HSC function. Presently there is no explanation for how past cell divisions result in HSC functional decline or how memory of these divisions is stored.

The polycomb repressive complex 2 (PRC2) is canonically involved in the silencing of gene expression. It accomplishes this through the addition of di- and trimethylation

of the tails of histone 3 at lysine 27 (H3K27me2 and H3K27me3), enabling chromatin compaction and gene silencing (Cao et al., 2002; Czermin et al., 2002; Kuzmichev et al., 2002; Margueron et al., 2008; Muller et al., 2002). Although PRC2 is composed of several proteins, the four major components are EED, SUZ12, EZH1, and EZH2. EZH1, and EZH2 are the catalytic subunits, and while both are capable of methylating H3K27, EZH1 performs this function weakly and mostly in the context of EZH2 loss (Margueron et al., 2008; Shen et al., 2008; Xu et al., 2015). Both require occupation within the PRC2 complex for functional activity, but they rarely interact with each other (Margueron et al., 2008; Shen et al., 2008; Xu et al., 2015), suggesting mutual exclusivity in PRC2 complex occupancy and competition with each other for interaction with other PRC2 complex members. Indeed, *Ezh1* and *Ezh2* tend to have opposite expression patterns. *Ezh2* is frequently associated with a proliferative state (Attwooll et al., 2005; Bracken et al., 2003), whereas *Ezh1* is found in post-mitotic or quiescent populations including myotubes, aging kidney, and HSCs (Hidalgo et al., 2012; Margueron et al., 2008; Mousavi et al., 2012; Stojic et al., 2011). While EZH1/2 are primarily associated with gene repression, an increasing body of evidence shows that they both play non-canonical roles in gene activation, indicating complex and context-specific functional behavior



(Henriquez et al., 2013; Mousavi et al., 2012; Stojic et al., 2011; Xu et al., 2012, 2015; Yan et al., 2016).

The role of PRC2 in HSC biology is complex, with different studies reporting seemingly conflicting results. EZH1 has been reported to both maintain (Hidalgo et al., 2012; Mochizuki-Kashio et al., 2015) and repress HSC functional potential (Vo et al., 2018). Likewise, EZH2 has been reported to be dispensable for HSC function in the adult (Mochizuki-Kashio et al., 2011, 2015; Xie et al., 2014), while being essential for HSCs during development (Majewski et al., 2008; Mochizuki-Kashio et al., 2011; Xie et al., 2014). The latter are likely due to the tight associations between *Ezh2*, the proliferative state, and the rapidly dividing HSC population in the embryo. *Ezh2* also prevents HSC exhaustion when overexpressed (Kamminga et al., 2006), but restricts HSC activity upon genetic ablation (Majewski et al., 2008) and predisposes cells to malignant transformation when deleted (Mochizuki-Kashio et al., 2015) while preventing disease progression in MLL-AF9 leukemia (Neff et al., 2012). Finally, *Ezh2* is one of the most commonly reported mutated genes in diverse forms of leukemia, lymphoma, and myeloproliferative neoplasms (Bejar et al., 2011; Danis et al., 2016; Ernst et al., 2010; McCabe et al., 2012; Nikoloski et al., 2010). While it is clear that the PRC2 components have diverse and clinically important roles in HSC biology, current understanding of their functional dynamics is incomplete.

Here we report on RNA sequencing (RNA-seq) data from HSCs that differ only in their divisional history. We find progressive changes in the transcriptome of these cells associated with a switch from dormancy and multipotency to cellular activation and lineage priming as cells increase their divisional history. Underlying this process is a switch from *Ezh1* to *Ezh2* expression. As *Ezh2* accumulates due to progressive division, it suppresses HSC signature genes. We propose that the *Ezh1*-to-*Ezh2* switch restricts stem cell potential and suggests a mechanism for how HSCs store information into the memory of their divisional history.

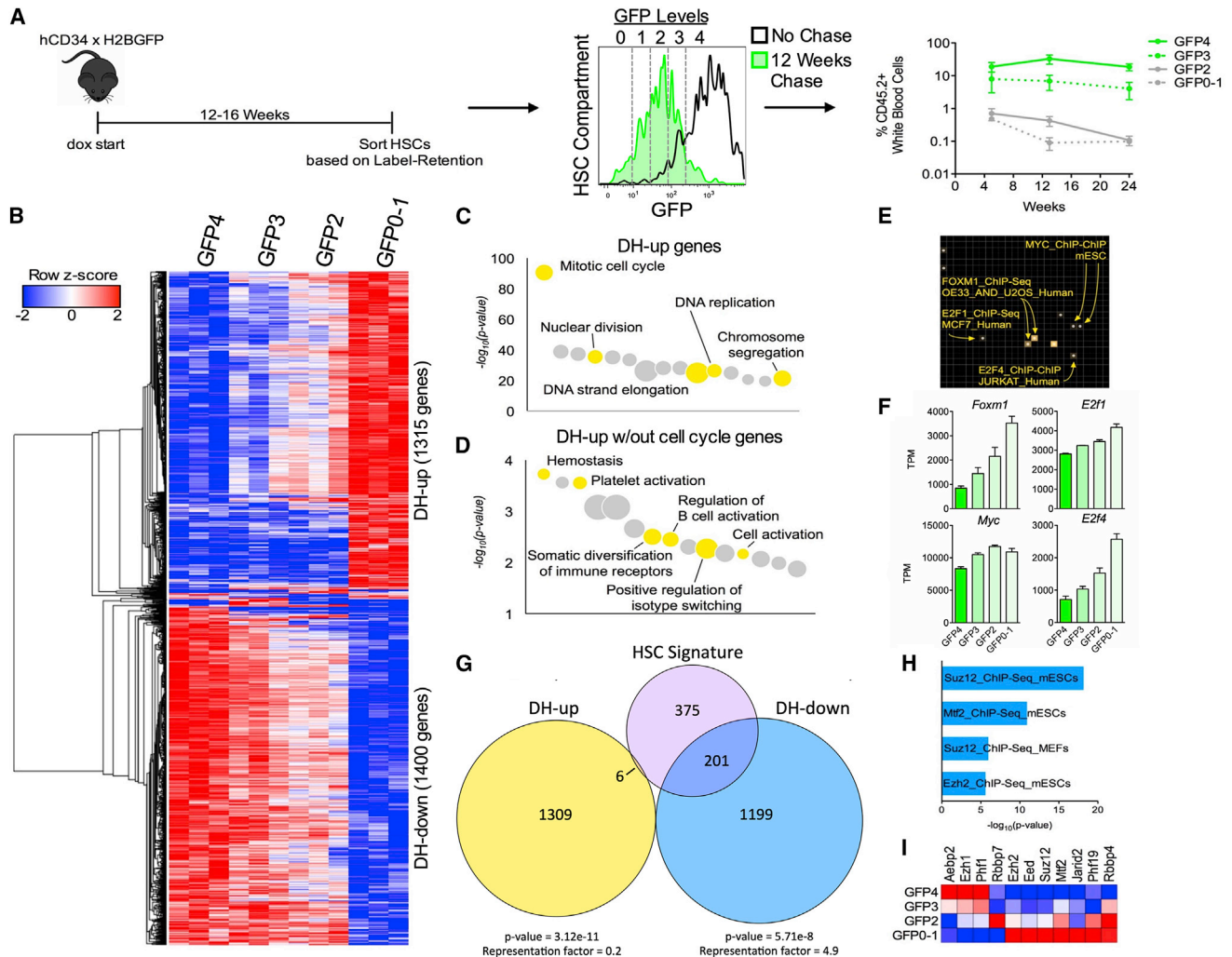
## RESULTS

### Gene Expression Changes with Divisional History Are Progressive

To gain molecular insight into how memories of divisional history are stored, we examined gene expression changes that occur as HSCs divide within a young HSC population. For RNA-seq analysis, we used an H2BGFP Tet-off hematopoietic stem and progenitor (HSPC)-specific label-retaining system (Bernitz et al., 2016; Qiu et al., 2014) to sort the HSC compartment (Lin<sup>−</sup>SCA-1<sup>+</sup>C-KIT<sup>+</sup>CD48<sup>−</sup>FLK2<sup>−</sup>CD150<sup>+</sup>) into four subpopulations based on GFP-label retention, which represent incremental increases with respect to divisional history (Figures 1A and

S1). In this experimental setup, cells labeled GFP4 are considered dormant and retain the greatest regenerative potential, whereas the GFP0–GFP1 population has the greatest divisional history and the smallest regenerative potential. Our analysis identified 2,715 differentially expressed genes (DEGs) across the four populations (false discovery rate <0.05 with fold change >1.5, Table S1). Hierarchical clustering revealed that nearly all DEGs grouped into two categories that either increase or decrease in expression as HSCs divide (hereafter referred to as divisional history upregulated/downregulated [DH-up and DH-down] genes, Figure 1B and Table S2). These changes are progressive and indicate a continuum of gene expression changes that occur with divisions, rather than discrete stages of differentiation. We compared these two gene sets with our previously published microarray expression data from Lin<sup>−</sup>SCA-1<sup>+</sup>C-KIT<sup>+</sup> (LSK) cells also differing in divisional history (Qiu et al., 2014), and found that the DH-up and DH-down genes were largely consistent with the previous analysis (Figures S2A and S2B).

Next, we computed enriched gene ontology (GO) terms for the genes that change with divisional history. As anticipated, DH-up genes are enriched for terms associated with the cell cycle (Figure 1C). To better understand changes in processes other than the cell cycle, we excluded genes associated with the GO terms “mitotic cell cycle,” “nuclear division,” “DNA replication,” and “cell cycle phase transition” (GO:0000278, GO:0000280, GO:0006260, and GO:0044770, respectively) from the list of DH-up genes to generate a cell-cycle-depleted gene list. This list included terms associated with mRNA processing, protein translation, metabolic, and biosynthetic processes (data not shown), consistent with published literature on HSC exit from dormancy (Cabezas-Wallscheid et al., 2017). However, we also found enrichment in GO terms associated with cell activation and diverse mature lineage fates (Figure 1D). We then examined the expression of genes associated with lineage development and maturation. Many of these genes increase their expression with cell divisions, albeit at low levels (Figures 2A and 2B). Transcription factor (TF) chromatin immunoprecipitation (ChIP)-x enrichment analysis (ChEA) identifies E2F1, E2F4, FOXM1, and MYC as significantly enriched near the promoters of the genes from the cell-cycle-depleted gene list (Figure 1E). E2Fs, FOXM1, and MYC are proliferation-associated TFs critical for cell-cycle progression (Bretones et al., 2015; Trimarchi and Lees, 2002; Wierstra and Alves, 2007; Wu et al., 2001), and *cMyc* is known to be essential for HSC differentiation (Wilson et al., 2004). Importantly, all of these TFs increase their expression progressively with divisional history (Figure 1F). Cumulatively, these data indicate that proliferation-associated TFs drive HSC activation and lineage priming, suggesting that early lineage priming of HSCs is a function of cell divisions.



**Figure 1. Homeostatic HSC Divisional History Is a Progressive Process**

(A) Schematic of experimental setup (left) with representation of the HSC compartment divided on the basis of divisional history (middle), and regenerative potential of each fraction after transplantation (right). Transplantation data are a re-analysis of data from [Qiu et al. \(2014\)](#). dox, doxycycline.

(B) Heatmap of genes differentially expressed along HSC divisional history. Hierarchical clustering reveals two clusters that are progressively upregulated (DH-up) or downregulated (DH-down) with divisional history.

(C and D) GO analysis of all DH-up genes (C) and DH-up genes after the removal of genes associated with the cell cycle (D). Circle size corresponds to the number of genes related to each functional category. Notable terms are colored.

(E) ChIP-x enrichment analysis (ChEA) of factors associated with the promoters of cell-cycle-depleted DH-up genes from (D).

(F) Expression changes of enriched transcription factors identified in (E). Data represent mean  $\pm$  SEM with  $n = 3$  from three independent experiments.

(G) Venn diagram depicting overlap of published HSC signature gene list ([Cabezas-Wallscheid et al., 2014](#)) to DH-up and DH-down genes. Statistically significant overlap calculated using Fisher's exact test; representation factors greater and less than 1 indicate more and less overlap, respectively, than expected by two independent groups.

(H) ChEA of DH-down genes.

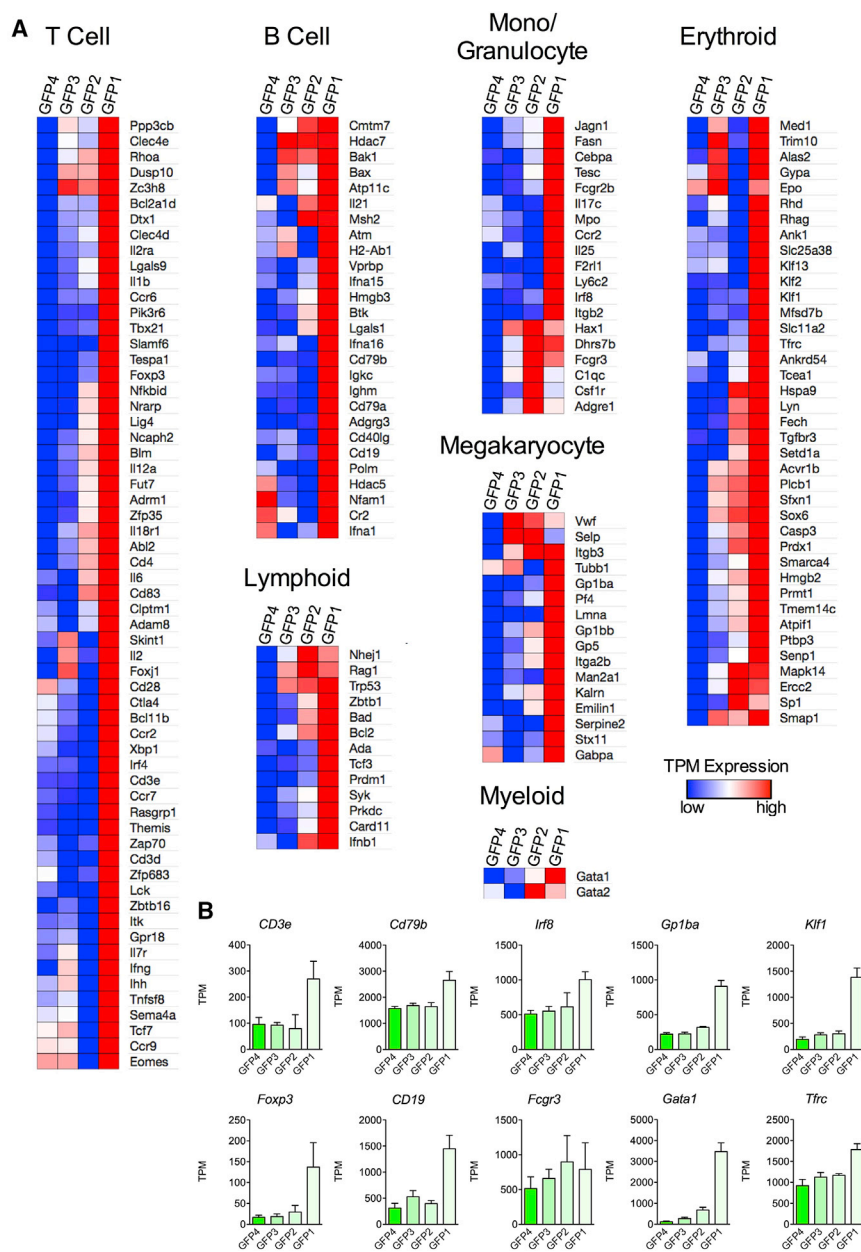
(I) Heatmap displaying the expression changes of PRC2 components with HSC divisional history.

See also [Figures S1 and S2](#).

Next, we examined the expression of DH-down genes. As DH-up genes were associated with cell activation and lineage priming, we hypothesized that DH-down genes were

associated with an HSC "state." We compared both gene sets with a published gene signature for HSCs ([Cabezas-Wallscheid et al., 2014](#)) and found a significant overlap between





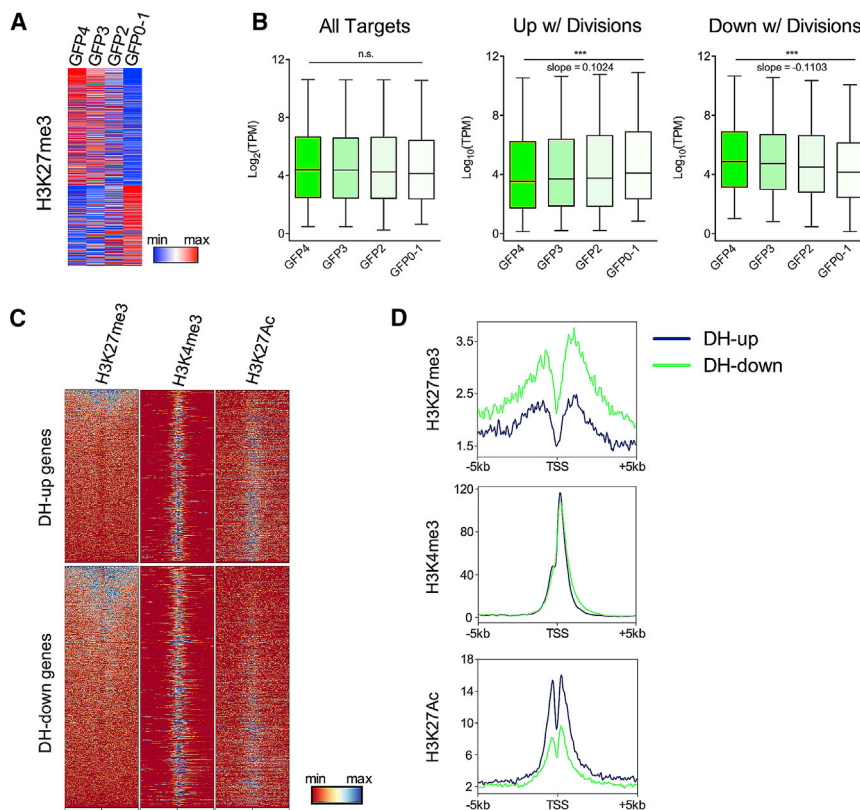
**Figure 2. Lineage Priming Occurs as a Function of Divisional History**

(A) Expression of genes associated with the maturation and development of five major lineages within the hematopoietic hierarchy.

(B) Selected genes from each lineage displaying low-level expression that increases with divisional history. Data represent mean  $\pm$  SEM from three independent experiments.

DH-down genes and HSC signature genes (Figure 1G). Gene set enrichment analysis (GSEA) of the molecular overlap stem cell signature (Wilson et al., 2015) also shows a significant enrichment toward genes highly expressed in the GFP4 population that decrease with divisions (Figure S2C). Additionally, both cell surface markers used to enrich for stem cell identity and HSC-specific reporters (Acar et al., 2015; Cabezas-Wallscheid et al., 2017; Chen et al., 2016; Gazit et al., 2014; Sawai et al., 2016) are highly expressed in the dormant GFP4 population, and progressively decrease with divisions (Figure S2D) with the exception of *Cttnl1*, which has no

clear expression pattern across HSC divisions (Figure S2D). Finally, comparison of gene signatures associated with HSC and multipotent progenitor (MPP) populations shows that MPP signatures are associated with high divisional histories, further indicating that differentiation is associated with progressive cell divisions (Figure S2E). Interestingly, MPP4s, reported as lymphoid-primed MPPs, are enriched for genes high in dormant cells. This suggests that fewer divisions are needed to generate MPP4 from HSCs, consistent with studies showing limited lineage priming in this population (Rodríguez-Fraticelli et al., 2018).



**Figure 3. Dynamics of H3K27me3 Target Gene Expression with HSC Divisions**

(A) Global HSC H3K27me3 target gene expression across HSCs of various divisional histories. Data are k-means clustered into two groups to reveal expression changes with divisional history. H3K27me3 targets identified by Sun et al. (2014).

(B) Quantification of gene expression changes with divisional history of all H3K27me3 targets (left), targets that increase in expression with divisions (center), and targets that decrease in expression with divisions (right). The box plots represent the first and third quartiles, with whiskers extending to the 5<sup>th</sup> and 95<sup>th</sup> percentile. \*\*\* $p < 0.001$  by one-way ANOVA followed by test for linear trend.

(C) Heatmaps of H3K27me3 (Sun et al., 2014), H3K4me3 (Sun et al., 2014), and H3K27Ac levels (Lara-Astiaso et al., 2014) within DH-up and DH-down gene sets.

(D) Density plots depicting the data in (C). See also Figure S3.

We next performed ChEA to identify factors regulating DH-down genes. Interestingly, many DH-down genes are targets of PRC2 members (Figure 1H). PRC2 is classically known to repress target gene expression, and the expression of several PRC2 components is enhanced during cell proliferation due to binding of their promoter regions by E2F proteins (Bracken et al., 2003). We also found that many PRC2 complex members increase their expression with divisional history (Figure 1I). These data suggest that cell divisions result in the progressive activation of PRC2 complex gene expression, which may play a role in silencing HSC signature genes that decrease in expression with each division.

### Chromatin Marks Are Dynamic with Divisional History

To better understand the role of PRC2 in the regulation of HSC signature genes, we examined gene expression changes of PRC2 target genes with progressive HSC divisions. We extracted information from HSCs on the genome-wide distribution of the repressive mark H3K27me3, a mark specifically deposited by PRC2 (Figure 3A) (Sun et al., 2014). An examination of all H3K27me3 target genes, on average, showed no significant changes in their expression with divisional history (Figure 3B). However, clustering the H3K27me3 targets by

expression patterns identified two groups that either increase or decrease in expression with progressive divisions (Figures 3A and 3B). Interestingly, this type of analysis based on divisional history reveals increasing expression of genes that are targets of PRC2-mediated repression in HSCs (Table S3). This trend is also observable with the active marks H3K4me3 and H3K27Ac (Figure S3 and Table S3). It is unlikely that these H3K27me3 targets are continuously methylated throughout divisional history while simultaneously changing their expression. Rather, it is more likely that different genes are targets for repression at specific divisional history stages. Collectively, this analysis suggests that chromatin mark deposition and removal may exhibit dynamic patterns with cell divisions.

We then took the reverse approach and looked for enrichment of activating and repressive chromatin marks on DH-up and DH-down genes. We found that DH-up genes are largely depleted of the repressive H3K27me3 mark but are enriched for the activating mark H3K27Ac (Figures 3C and 3D). In contrast, DH-down genes are enriched for H3K27me3 and depleted of H3K27Ac. These data corroborate the ChEA analysis identifying PRC2 complex members as potential regulators of DH-down genes (Figure 1H). H3K4me3 was not differentially regulated between DH-up and DH-down genes (Figures 3C and 3D),



consistent with the notion that H3K4me3 is an indicator rather than an instructor of transcription (Howe et al., 2017). Together, these data show that DH-down genes are enriched for targets of PRC2 H3K27me3 in HSCs.

### The PRC2 Catalytic Subunit *Ezh1* Activates while *Ezh2* Represses HSC Signature Genes

Analysis of H3K27me3 in HSCs showed that this histone mark is dynamic with divisional history and that DH-down genes are enriched for targets of PRC2 repression. To better understand the dynamics of this process, we began by examining expression of the PRC2 catalytic subunits *Ezh1* and *Ezh2*. *Ezh1* and *Ezh2* exhibit opposite expression patterns, with *Ezh1* highest in dormant fractions and *Ezh2* expression increasing with progressive cell divisions (Figure 1I). This is consistent with data indicating *Ezh1* and *Ezh2* correlate with quiescent and proliferative states, respectively (Margueron et al., 2008). To gain insight into how these different catalytic subunits regulate H3K27me3 deposition during different divisional history stages, we examined *Ezh1*<sup>-/-</sup> HSC microarray gene expression data (Hidalgo et al., 2012). Genes that increased in expression with *Ezh1* knockout (hereafter referred to as “*Ezh1* Repressed”) are associated with the GFP0–1 HSC fraction (Figures 4A and S4A) and are enriched for cell-cycle genes (Figure S4B). ChEA also revealed these genes to be targets of cell-cycle TFs FOXM1, E2F4, and P53, as well as of PRC1 and PRC2 members (Figure S4C). In contrast, genes with dampened expression in *Ezh1*<sup>-/-</sup> HSCs (hereafter referred to as “*Ezh1* Activated”) were enriched in dormant HSCs (Figure 4A). Indeed, we found a significant overlap of *Ezh1*-Activated and DH-down genes (Figure 4B), many of which are important for HSC function (Cabezas-Wallscheid et al., 2014, 2017; Frelin et al., 2013; Ku et al., 2012; Miyamoto et al., 2007; Riddell et al., 2014; Wilson et al., 2015; Yalcin et al., 2008). The transcript of *SCA-1*, *Ly6a*, which highly correlates with stem cell function (Wilson et al., 2015), is included among *Ezh1* Activated genes, and also shows stepwise decreases with progressive HSC divisions at the protein level (Figure S5).

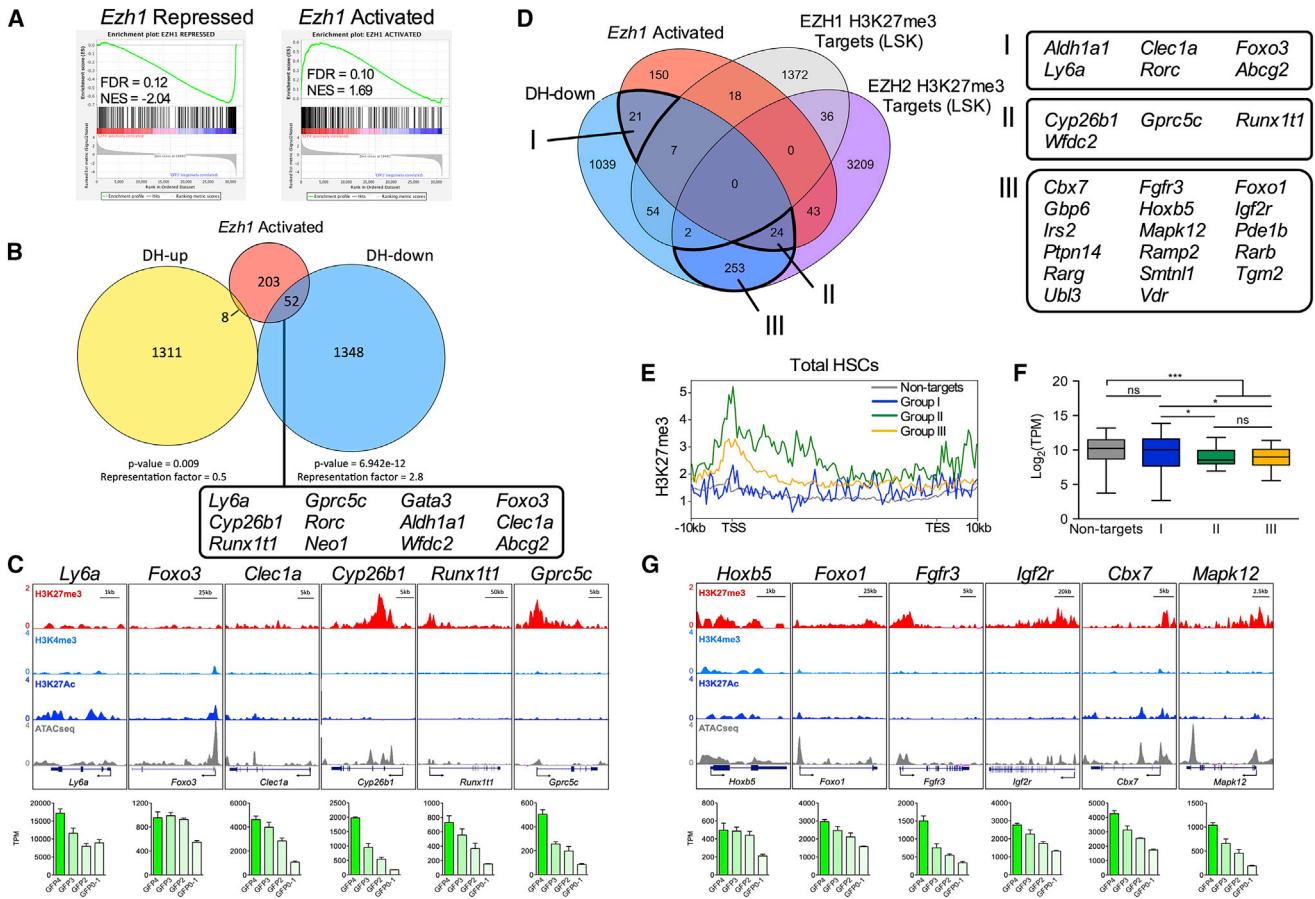
We then examined the chromatin landscape of genes within this overlap. By simultaneously comparing *Ezh1* Activated and DH-down genes with identified targets of EZH1- and EZH2-mediated H3K27me3 in HSPCs (Mochizuki-Kashio et al., 2015), we were able to dissect the specific roles of EZH1 and EZH2 in activating and repressing HSC signature genes. This comparison identified several overlapping groups, including three of particular interest: DH-down genes activated by EZH1 that are not targets for H3K27me3 repression (group I), DH-down genes activated by EZH1 that are targets for EZH2-mediated H3K27me3 repression (group II), and DH-down genes that are EZH2 H3K27me3 targets not regulated by EZH1 (group III).

Roughly half of the overlap between *Ezh1* Activated and DH-down genes are targets of EZH2-specific H3K27me3 repression (group II, Figures 4C and 4D), suggesting that the switch from *Ezh1* to *Ezh2* with progressive divisions causes these genes to switch from an activated to repressed state (Figures 4C and 4D). Furthermore, EZH2-specific H3K27me3 targets include 19.8% of DH-down genes (groups II and III), many of which are important for HSC identity and function (Figure 4D; Cabezas-Wallscheid et al., 2014; Chen et al., 2016; Klauke et al., 2013; Qiu et al., 2014; Wilson et al., 2015). Analysis of the chromatin profiles of these three groups in total HSCs (HSCs not subdivided by divisional history) revealed that group II and group III genes have H3K27me3 peaks centered at their transcriptional start site, indicative of transcriptional repression (Figure 4E). In contrast, group I genes show no H3K27me3 enrichment above background levels (Figures 4E and 4G). Consistent with these data, genes in groups II and III have lower average expression levels in total HSCs than those in group I (Figure 4F). Cumulatively, these data suggest that EZH1 promotes the expression of genes important for the stem cell state, and EZH2 targets HSC signature genes for repression, a subset of which are activated by EZH1. Thus, a divisional history-dependent *Ezh1*-to-*Ezh2* switch could be involved in the suppression of HSC function as cells divide.

### Inhibiting *Ezh2* Prevents the Loss of Self-Renewal Potential with Progressive Divisions

Our data predict a genetic switch whereby EZH1 represses cell divisions and activates key genes associated with HSC identity, while EZH2 accumulates with progressive divisions to repress these HSC genes. To test these predictions, we inhibited EZH2 activity during HSC growth in culture to find out whether regenerative loss with divisions could be prevented. We sorted either HSCs, gating on the highest 30% of *SCA-1* expression to enrich for dormant cells (Figure S5A), or GFP4 HSCs from the 34/H2BGFP mice, and plated them in long-term culture (LTC) on AFT024 stroma with or without media containing the EZH2 inhibitor (Figure 5A). AFT024 cells maintain HSCs in culture and enable their proliferation (Kokkaliaris et al., 2016; Moore et al., 1997), allowing us to test the effect of EZH2 inhibition on regenerative potential after several rounds of division in LTC. The EZH2 inhibitor GSK126 is over 150-fold more specific to EZH2 than EZH1 (McCabe et al., 2012), limiting the probability that an effect would be due to EZH1 inhibition. After 4 weeks of primary culture, hematopoietic cells were harvested and replated on fresh stroma at limiting dilution without inhibitor, and the presence of cobblestone area-forming cells (CAFCs) was scored a week later. Similarly cells were also plated into a colony-forming unit (CFU) assay to determine LTC-initiating cell numbers.





**Figure 4. EZH1 Activates and EZH2 Represses HSC Signature Genes**

(A) GSEA of *Ezh1*-Activated and *Ezh1*-Repressed genes (Hidalgo et al., 2012).

(B) Venn diagram of the overlap between *Ezh1*-Activated, DH-up, and DH-down genes. Genes displayed from the overlap are implicated or involved in HSC identity. p values by Fisher's exact test.

(C) Representations of the chromatin state of genes identified within the *Ezh1*-Activated and DH-down overlap from (B), as well as each gene's expression change over divisional history (below). Gene expression data represent mean  $\pm$  SEM with  $n = 3$  from three independent experiments.

(D) Venn diagram depicting the overlap between DH-down, *Ezh1*-Activated, and EZH1- or EZH2-mediated H3K27me3 target genes (Mochizuki-Kashio et al., 2015). Genes implicated or involved in HSC identity from three distinct groups (I, II, III) are displayed.

(E and F) Mean H3K27me3 levels (E) and expression (F) of genes from groups I–III in the total HSC population. Non-targets are DH-down genes not targeted by EZH1 activation or H3K27me3. \* $p < 0.05$ , \*\*\* $p < 0.001$  by Kruskal-Wallis test followed by Dunn's test for multiple comparisons.

(G) Representation of the chromatin state of genes identified in group III, with corresponding changes in expression with divisional history. Gene expression data represent mean  $\pm$  SEM with  $n = 3$  from three independent experiments.

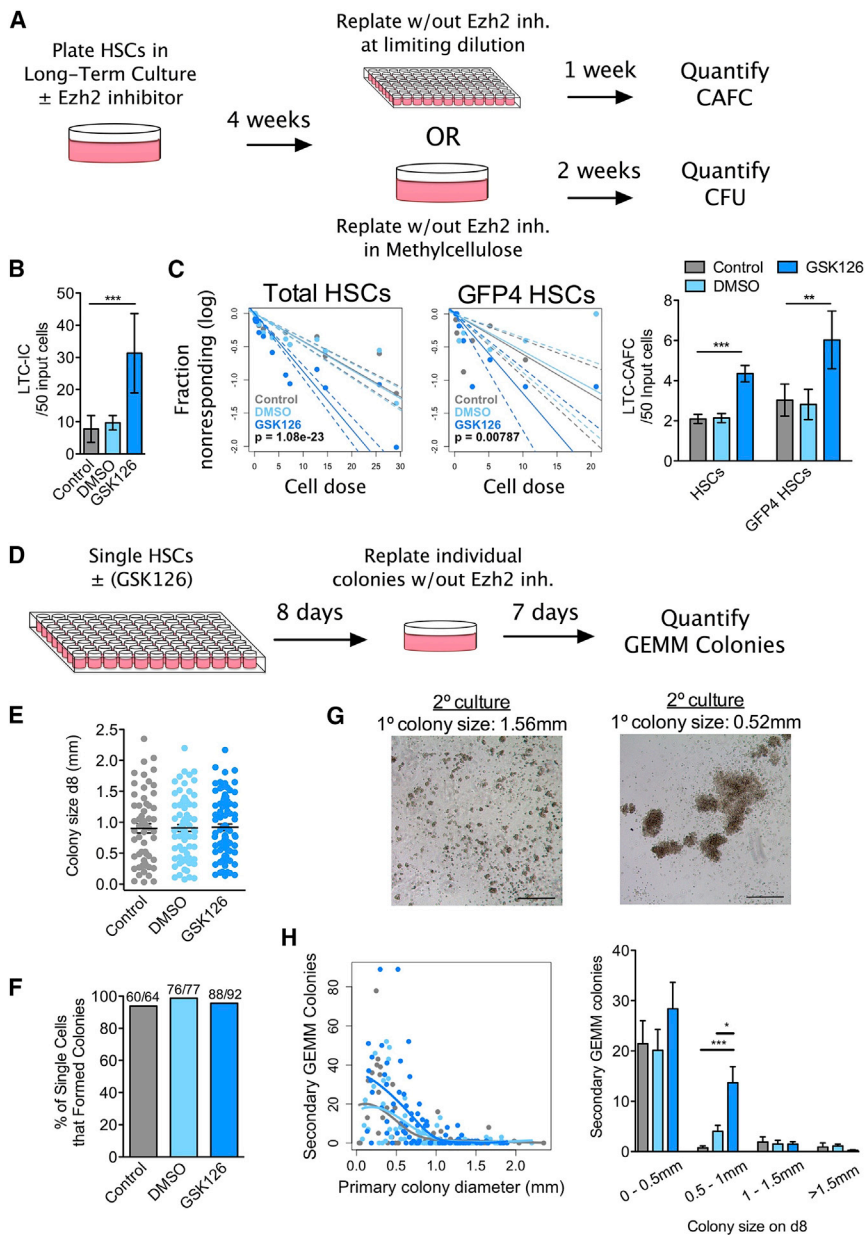
Data displayed in (C) and (G): H3K27me3 and H3K4me3 (Zheng et al., 2015), H3K27Ac (Lara-Astiaso et al., 2014), and ATAC-seq (Shih et al., 2016). See also Figures S4 and S5.

Adding GSK126 increased the frequency of regenerative, clonogenic cells that were present after 4 weeks in LTCs (Figures 5B and 5C), suggesting EZH2 inhibition prevents regenerative decline with progressive divisions.

To further test our predictions, we established a single-cell divisional history CFU assay. This assay tests the self-renewal capacity of single HSCs by examining the CFU potential of its progeny as a function of previous division in culture (Figure 5D). After sorting single HSCs and culturing for 8 days,

colony diameter was measured as a surrogate for divisional history. Colonies of roughly 0.45 mm diameter contained approximately 600–700 cells, indicating that the initially sorted HSC divided at least nine times to produce colonies of this size. The entire colony was then harvested and transferred to methylcellulose medium and allowed to grow for another 7 days. At the end of the second round of culture, granulocyte, erythroid, macrophage, megakaryocyte (GEMM) colonies were quantified and compared with





**Figure 5. EZH2 Inhibition Delays Loss of Self-Renewal with Cell Divisions**

(A) Experimental setup testing EZH2 inhibition in LTC.

(B) Number of CFUs after 4 weeks of LTC derived from 50 cells initiating the culture (LTC-IC). Data represent mean  $\pm$  SEM;  $n = 7$  cultures from three independent experiments, statistical significance by multiple linear regression.

(C) Limiting dilution analysis of CAFC after 4 weeks in LTC. Data represent mean  $\pm$  95% confidence interval from  $n = 10$  (Total HSCs) and  $n = 3$  (GFP4 HSCs) cultures; statistical significance by chi-squared likelihood ratio.

(D) Schematic of experimental setup. (E and F) Colony number (E) and clonogenicity (F) of colonies after 8 days in primary cultures. Line and error bars in (E) represent mean  $\pm$  SEM from three independent experiments.

(G) Images of secondary cultures produced from larger (1.56 mm, left) and smaller (0.52 mm, right) primary colonies. Only secondary colonies like those in the right panel were counted as secondary GEMM colonies. Scale bars, 300  $\mu$ m.

(H) Comparison of colony size in primary culture with the number of GEMM colonies in secondary culture with and without EZH2 inhibitor. Plots of raw data with local polynomial fit (left) and binned data (right).  $n = 60, 76$ , and  $88$  for control, DMSO-treated, and GSK126-treated cells, respectively, from three independent experiments. Data represent mean  $\pm$  SEM; statistical significance by Kruskal-Wallis test with Dunn's test for multiple comparisons. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ .

the size of the primary colony, giving a measure of regenerative potential as a consequence of proliferation in primary culture. We found that GSK126 did not alter clonogenicity or average colony size (Figures 5E and 5F) of colonies in primary culture. As expected, in secondary cultures colony-forming potential declined after a threshold of primary colony size of 0.5 mm (Figures 5G and 5H). Importantly, inhibiting EZH2 catalytic activity delayed the loss of secondary CFU potential with increased primary colony size (Figures 5G and 5H). Cumulatively, data from both the long-term cultures and single-cell colony assays indicate that EZH2 inhibition delays the loss of regenerative potential with successive divisions.

## DISCUSSION

Understanding how to preserve stem cell function has been at the heart of HSC research for decades. Despite the wealth of information on individual genes, niches, or processes that act to preserve HSC function, little progress has been made in implementing this understanding to maintain and expand HSCs without causing regenerative decline. Studies focusing on the relationship between divisional history and function have revealed that increasing divisional history correlates with and causes decreased HSC regeneration (Beerman et al., 2013; Bernitz et al., 2016; Qiu et al., 2014; Walter et al., 2015), cumulatively



indicating that HSCs must store information about their past divisions. Thus, robust HSC expansion is difficult to achieve because enforcing HSC divisions results in the loss of their stem cell properties. However, to date no mechanistic link has been provided to explain how cell divisions negatively influence HSC regeneration. Here, we performed RNA-seq on HSC populations that differ only in their divisional history to help elucidate this link.

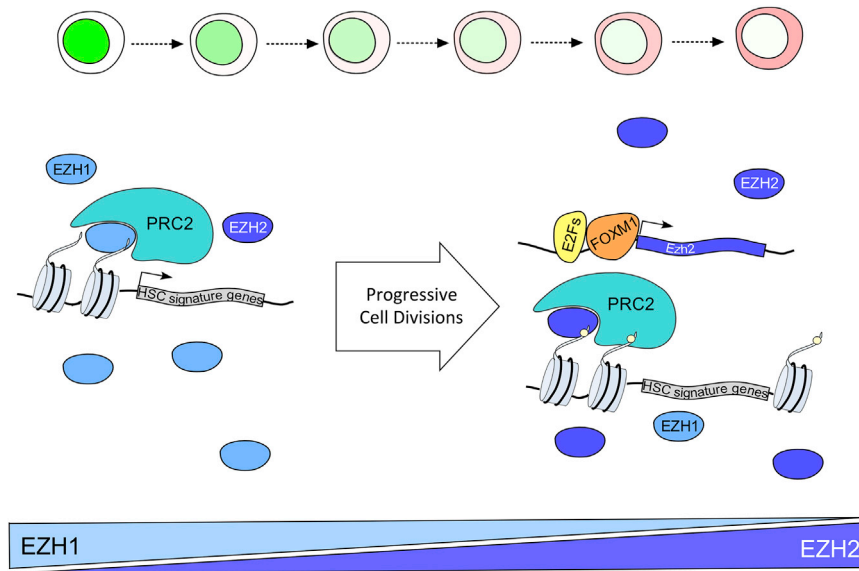
Our analyses indicate that increasing divisional history results in the progressive loss of HSC signature genes and progressive activation of genes broadly associated with proliferation and cellular activation. A model of progressive change over divisions is consistent with emerging notions of a differentiation continuum that occurs within the stem and progenitor compartment as cells make commitment decisions (Cabezas-Wallscheid et al., 2017; Velten et al., 2017), and contrasts with models in which cells transit through discrete states. Our data also support the body of work on HSC exit from dormancy that highlights the requirement of metabolic activation and cMyc expression to begin differentiation out of the stem cell compartment, indicating the importance of cell divisions in this process (Cabezas-Wallscheid et al., 2017; Signer et al., 2014; Wilson et al., 2004). Surprisingly, we find that even within the highly purified HSC compartment, genes associated with mature lineage identity increase in expression with progressive divisions. Indeed, recent work using single-cell RNA-seq indicates that lineage commitment is a progressive process whereby HSCs steadily acquire lineage fates along the continuum of low-primed undifferentiated states (Laurenti and Gottgens, 2018; Rodriguez-Fraticelli et al., 2018; Velten et al., 2017). Taken together, this suggests that cell divisions themselves begin the process of lineage priming at the level of the HSC and that divisional history is a major factor contributing to transcriptional heterogeneity.

Our analyses also implicate components of PRC2 as key molecular factors in the loss of HSC function with divisions. Different PRC2 components play both enhancing and repressive roles at different times during development and at different gene doses (Hidalgo et al., 2012; Kamminga et al., 2006; Lee et al., 2015; Lessard et al., 1999; Mochizuki-Kashio et al., 2011, 2015; Vo et al., 2018; Xie et al., 2014; Xu et al., 2015). Through compartmentalizing HSCs by divisional history, however, we are able to help clarify these complex phenomena. The expressions of many PRC2 components are activated by cell divisions (Bracken et al., 2003) and are classically associated with the repression of target gene expression. Consistent with these canonical patterns, we find increased expression of core PRC2 components *Ezh2*, *Suz12*, and *Eed* with HSC divisions. This is then correlated with a decline in expression of HSC signature genes, many of which are targets of EZH2-mediated H3K27me3

deposition. These results support work showing that *Ezh2*, *Suz12*, and *Eed* function to restrict HSC self-renewal and promote differentiation (Mochizuki-Kashio et al., 2011, 2015; Xie et al., 2014), whereby these genes would accumulate with divisions and suppress HSC signature genes. Indeed, by inhibiting the histone methyltransferase property of EZH2, we found we could delay the loss of secondary colony formation in a cell-division-dependent manner (Figure 5).

In contrast to these PRC2 members, *Ezh1* expression exhibits the opposite pattern of expression and declines with divisions. This is consistent with findings indicating preferential *Ezh1* expression in quiescent cell populations (Hidalgo et al., 2012; Margueron et al., 2008; Mousavi et al., 2012). Additionally, through cross-comparison of our data with gene expression data from *Ezh1* knockout HSCs, our work implicates EZH1 as an important driver of genes promoting a primitive HSC state (Hidalgo et al., 2012). While gene activation is a less commonly described feature of PRC2 components, it is consistent with an increasing body of work indicating non-canonical roles of EZH1 in gene activation (Mousavi et al., 2012; Vo et al., 2018; Xu et al., 2015). In particular, we found that several genes important in retinoic acid signaling, recently shown to be critical to HSC maintenance (Cabezas-Wallscheid et al., 2017), are putative targets of EZH1 activation. This notion that EZH1 may activate HSC signature genes while EZH2 accumulates to suppress them also partially explains complex results with EZH2 loss in cancer. EZH2 loss of function is frequently associated with hematological transformation and clonal hematopoiesis (Bejar et al., 2011; Ernst et al., 2010; Mochizuki-Kashio et al., 2015; Nikoloski et al., 2010). This suggests that EZH2 loss prevents the silencing of many potent HSC genes upon progressive divisions, many of which are associated with cancer progression and leukemia. This is consistent with data showing that leukemic transformation in *Ezh2*<sup>-/-</sup> cells is dependent on EZH1 functional activity (Mochizuki-Kashio et al., 2015), and with reports in early T cell precursor acute lymphoblastic leukemia showing that EZH2 is important for suppressing stem cell-associated genes (Danis et al., 2016). In light of our results, the data suggest that EZH2 accumulation with progressive divisions functions as a fail-safe to restrict the potential of stem cell-associated genes.

Recent work in both mouse and human HSCs found *Ezh1*-Repressed multilineage potential during the emergence of HSC during development via direct occupancy and H3K27me3-associated repression of multipotency and lymphoid genes (Vo et al., 2018). While this appears to contradict our findings, it is known that embryonic and adult HSCs switch from a fetal to an adult program at 4 weeks after birth. This switch corresponds to a shift from proliferation to quiescence (Bowie et al., 2006),



**Figure 6. HSCs Remember Their Cell Divisions via a Divisional History-Dependent EZH1-to-EZH2 Switch**

HSCs with the lowest divisional history express high levels of *Ezh1*. EZH1 associates with the promoters of HSC signature genes to ensure their expression. With each cell division, E2Fs and Foxm1—typical cell-cycle-associated transcription factors—bind to and activate *Ezh2*'s promoter to induce *Ezh2* expression. With progressive divisions, the expression of *Ezh2* increases, allowing it to outcompete EZH1 for PRC2 occupancy and mark the promoters of HSC signature genes with H3K27me3. This progressively restricts HSC regenerative potential and initiates lineage commitment. Progressive divisions are visualized by dilution of the H2BGFP from the nucleus, and lineage commitment is indicated by the accumulation of red in the cytoplasm.

SOX17 dependence to SOX17 independence (Kim et al., 2007), and *Ezh2* dominance to *Ezh1* dominance (Vo et al., 2018). EZH2 can be phosphorylated to both modify its histone methyltransferase activity and switch its role as a transcriptional repressor to a transcriptional activator in a context-specific manner (Xu et al., 2012; Yan et al., 2016). It is conceivable that EZH1 could undergo similar changes in activity as HSCs transition from an active to a quiescent state during postnatal life, given the largely conserved amino acid sequence between the two proteins, with a known canonical to non-canonical EZH2 phosphorylation site S21 being preserved in EZH1 (Xu et al., 2012).

In summary, our data suggest a model in which HSCs record their divisional history in part through an *Ezh1*-to-*Ezh2* switch (Figure 6). *Ezh1* is highly expressed in dormant HSCs and plays a role in activating HSC signature genes and suppressing cell divisions. As HSCs divide, cell-cycle-associated TFs are activated. These TFs appear to drive the expression of lineage-commitment genes and *Ezh2*, increasing their expression with divisions over time. With progressive divisions, EZH1 and EZH2 compete for occupation within the PRC2 complex. As EZH2 outcompetes EZH1, EZH2 targets genes associated with an HSC signature for H3K27me3 suppression. This results in a feedforward loop. Every division contributes to *Ezh2* activation, which increases the probability of HSC signature gene suppression. This reduces the ability of HSCs to maintain quiescence, increasing the probability of more divisions (Figure 6). Thus, information about divisional history is stored as H3K27me3 on HSC signature genes. These marks are propagated and maintained across time by persistent *Ezh2* expression, consolidating divisional history into memory.

Recent work in the field has found the presence of lineage-restricted self-renewing progenitor populations within the HSC compartment (Carrelha et al., 2018; Yamamoto et al., 2013). Given the hierarchical loss of lineage potential described in these populations, it would be of interest to test whether this loss is associated with cells of greater divisional history. In the homeostatic contexts we describe here, the consequences of divisional history appear irreversible, permanently restricting HSC regeneration. How this record changes during stress and regeneration that occur in a transplantation setting or in culture reported to expand HSCs (Wilkinson et al., 2019) will play a crucial role in further unlocking the mechanistic differences between homeostasis and stress as well as mechanisms of HSC self-renewal.

## EXPERIMENTAL PROCEDURES

### Contact for Reagent and Resource Sharing

Information and requests for reagents may be directed to the corresponding author, K.A.M. (kateri.moore@mssm.edu).

### Experimental Model and Subject Details

TetO-H2BGFP and hCD34-tTA were maintained as previously described (Qiu et al., 2014). C57BL/6-Tg(UBC-GFP)30Scha/J (UBC-GFP) were acquired and maintained as previously described (Bernitz et al., 2017). Mice were maintained on doxycycline for 12–16 weeks prior to analysis to reveal various divisional histories. Both male and female mice were used. Animal experiments were approved by the Institutional Animal Care and Use Committee and conducted in accordance with the Animal Welfare Act.



## Method Details

### Sample Preparation and Flow Cytometry

BM cells were harvested from tibias, femurs, and pelvic bones and prepared for sorting as previously described (Bernitz et al., 2016). Cells were analyzed on an LSRII (Becton Dickinson) flow cytometer and sorted on an Influx (Becton Dickinson). HSCs were sorted using the Lin<sup>-</sup>SCA-1<sup>+</sup>C-KIT<sup>+</sup>CD48<sup>-</sup>FLK2<sup>-</sup>CD150<sup>+</sup> phenotype. Label retention was defined by gating above the background GFP levels found in heterozygous single transgenic TetO-H2BGFP HSCs.

### RNA Sequencing

Total RNA was isolated from sorted HSC populations using TRIzol Reagent (Life Technologies) with the addition of 15 µg (15 µg/mL) Glycobule (Life Technologies) prior to RNA precipitation. Isolated RNA integrity was assessed via RNA 6000 pico chip on an Agilent 2100 Bioanalyzer (Agilent Technologies). Up to 1 ng of total RNA from each sample was taken for library preparation using a SMART-Seq v4 Ultra Low Input RNA Kit for sequencing (Clontech) following the manufacturer's instructions. The resulting cDNA was quantified using the Quant-iT PicoGreen dsDNA Assay Kit (Invitrogen), the cDNA size and integrity was assessed by Bioanalyzer, and 100–300 pg of cDNA was used to prepare libraries for mRNA sequencing using a Nextera XT DNA Sample Preparation Kit (Illumina). Barcoded library concentration and quality were quantified by Qbit (Invitrogen) and Bioanalyzer (Agilent), and the libraries were pooled together and sequenced on the Illumina HiSeq 2000 sequencer platform using a 75-nt single-read setting.

### RNA-Seq, ChIP-Seq, and ATAC-Seq Data Analysis

Details are described in Supplemental Experimental Procedures.

### In Vitro Cultures

Details are described in Supplemental Experimental Procedures.

## ACCESSION NUMBERS

RNA-seq datasets have been deposited to the Gene Expression Omnibus database. The accession number for the RNA-seq data reported in this paper is GEO: GSE145772.

## SUPPLEMENTAL INFORMATION

Supplemental Information can be found online at <https://doi.org/10.1016/j.stemcr.2020.03.005>.

## AUTHOR CONTRIBUTIONS

Conceptualization, J.M.B. and K.A.M.; Methodology, J.M.B. and K.A.M.; Software, J.M.B., D.S., Y.Y., A.G., R.B., and A.L.; Validation, M.G.D. and K.R.; Formal Analysis, J.M.B., D.S., Y.Y., A.G., R.B., and A.L.; Investigation, J.M.B., M.G.D., A.G., A.W., and K.R.; Resources, A.M., D.P., and K.M.; Data Curation, J.M.B., D.S., and A.L.; Writing—Original Draft, J.M.B. and K.A.M.; Writing—Review & Editing, J.M.B., M.D., K.R., and K.A.M.; Visualization, J.M.B.; Supervision, A.M., D.P., and K.A.M.; Funding Acquisition, K.A.M.

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