



HAL
open science

An IDH1-vitamin C crosstalk drives human erythroid development by inhibiting pro-oxidant mitochondrial metabolism

Pedro Gonzalez-Menendez, Manuela Romano, Hongxia Yan, Ruhi Deshmukh, Julien Papoin, Leal Oburoglu, Marie Daumur, Anne-Sophie Dumé, Ira Phadke, Cédric Mongellaz, et al.

► **To cite this version:**

Pedro Gonzalez-Menendez, Manuela Romano, Hongxia Yan, Ruhi Deshmukh, Julien Papoin, et al.. An IDH1-vitamin C crosstalk drives human erythroid development by inhibiting pro-oxidant mitochondrial metabolism. *Cell Reports*, 2021, 34 (5), pp.108723. 10.1016/j.celrep.2021.108723 . hal-03161590

HAL Id: hal-03161590

<https://hal.science/hal-03161590>

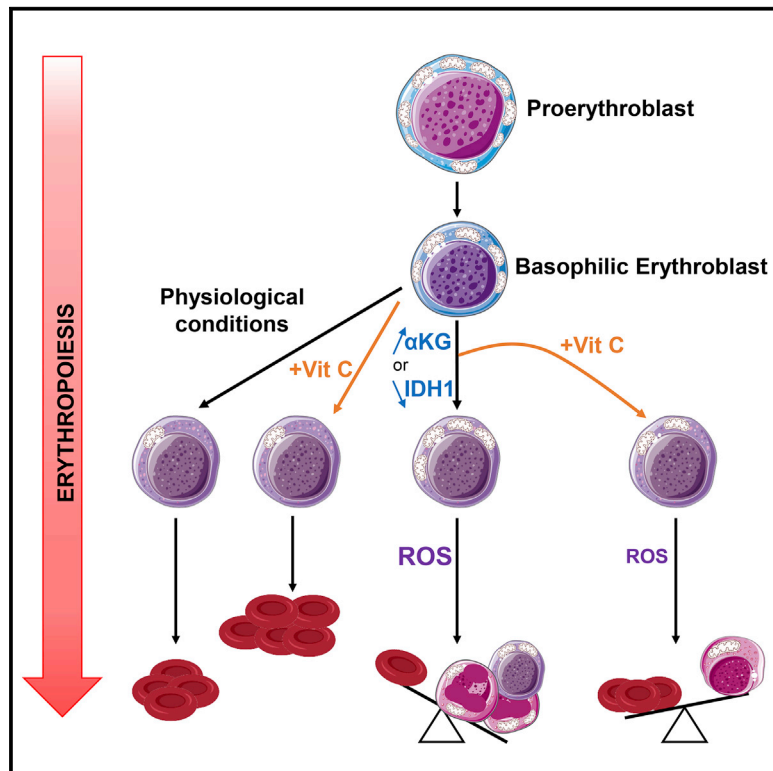
Submitted on 7 Mar 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

An IDH1-vitamin C crosstalk drives human erythroid development by inhibiting pro-oxidant mitochondrial metabolism

Graphical Abstract



Authors

Pedro Gonzalez-Menendez, Manuela Romano, Hongxia Yan, ..., Narla Mohandas, Naomi Taylor, Sandrina Kinet

Correspondence

pedro.gonzalez-menendez@igmm.cnrs.fr (P.G.-M.),
taylor4@mail.nih.gov (N.T.),
kinet@igmm.cnrs.fr (S.K.)

In Brief

Gonzalez-Menendez et al. show that terminal erythroid differentiation is dependent on the suppression of mitochondrial metabolism. Disturbances in levels of the α -ketoglutarate and IDH1 TCA-cycle regulators result in ineffective erythropoiesis, with generation of morphologically abnormal erythroblasts. Vitamin C restores redox homeostasis and rescues late-stage erythropoiesis by scavenging reactive oxygen species.

Highlights

- Glutamine-dependent OXPHOS drives early erythroid differentiation
- OXPHOS-induced ROS inhibit erythroblast enucleation
- IDH1 downregulation augments ROS, leading to pathological erythroid differentiation
- Vitamin C rescues erythroid differentiation under conditions of oxidative stress



Article

An IDH1-vitamin C crosstalk drives human erythroid development by inhibiting pro-oxidant mitochondrial metabolism

Pedro Gonzalez-Menendez,^{1,2,10,*} Manuela Romano,^{1,2,10} Hongxia Yan,^{1,3} Ruhi Deshmukh,⁴ Julien Papoin,⁵ Leal Oburoglu,^{1,2} Marie Daumur,^{1,2} Anne-Sophie Dumé,^{1,2} Ira Phadke,^{1,2,6} Cédric Mongellaz,^{1,2} Xiaoli Qu,³ Phuong-Nhi Bories,⁷ Michaela Fontenay,^{2,7} Xiuli An,³ Valérie Dardalhon,^{1,2} Marc Sitbon,^{1,2} Valérie S. Zimmermann,^{1,2} Patrick G. Gallagher,⁸ Saverio Tardito,^{4,9} Lionel Blanc,⁶ Narla Mohandas,³ Naomi Taylor,^{1,2,7,11,*} and Sandrina Kinet^{1,2,*}

¹Institut de Génétique Moléculaire de Montpellier, Univ. Montpellier, CNRS, Montpellier, France

²Laboratory of Excellence GR-Ex, Paris 75015, France

³New York Blood Center, New York, NY, USA

⁴Cancer Research UK Beatson Institute, Glasgow G61 1BD, UK

⁵The Feinstein Institute for Medical Research, Manhasset, NY, USA

⁶Pediatric Oncology Branch, NCI, CCR, NIH, Bethesda, MD, USA

⁷Service d'Hématologie Biologique, Assistance Publique-Hôpitaux de Paris, Institut Cochin, Paris, France

⁸Departments of Pediatrics and Genetics, Yale University School of Medicine, New Haven, CT, USA

⁹Institute of Cancer Sciences, University of Glasgow, Glasgow G61 1QH, UK

¹⁰These authors contributed equally

¹¹Lead contact

*Correspondence: pedro.gonzalez-menendez@igmm.cnrs.fr (P.G.-M.), taylor4@mail.nih.gov (N.T.), kinet@igmm.cnrs.fr (S.K.)
<https://doi.org/10.1016/j.celrep.2021.108723>

SUMMARY

The metabolic changes controlling the stepwise differentiation of hematopoietic stem and progenitor cells (HSPCs) to mature erythrocytes are poorly understood. Here, we show that HSPC development to an erythroid-committed proerythroblast results in augmented glutaminolysis, generating alpha-ketoglutarate (α KG) and driving mitochondrial oxidative phosphorylation (OXPHOS). However, sequential late-stage erythropoiesis is dependent on decreasing α KG-driven OXPHOS, and we find that isocitrate dehydrogenase 1 (IDH1) plays a central role in this process. IDH1 downregulation augments mitochondrial oxidation of α KG and inhibits reticulocyte generation. Furthermore, IDH1 knockdown results in the generation of multinucleated erythroblasts, a morphological abnormality characteristic of myelodysplastic syndrome and congenital dyserythropoietic anemia. We identify vitamin C homeostasis as a critical regulator of ineffective erythropoiesis; oxidized ascorbate increases mitochondrial superoxide and significantly exacerbates the abnormal erythroblast phenotype of IDH1-downregulated progenitors, whereas vitamin C, scavenging reactive oxygen species (ROS) and reprogramming mitochondrial metabolism, rescues erythropoiesis. Thus, an IDH1-vitamin C crosstalk controls terminal steps of human erythroid differentiation.

INTRODUCTION

Hematopoietic stem cell (HSC) numbers as well as their differentiation state are tightly regulated throughout the lifetime of an individual, allowing the sustained production of all mature blood lineages under physiological conditions. Circulating mature erythrocytes are a terminally differentiated product of HSCs that have undergone a series of lineage-fate engagements that gradually restrict their potential, resulting in a commitment to the erythroid lineage. Commitment defines the beginning of erythropoiesis; a three-stage process characterized by early erythropoiesis, terminal erythroid differentiation, and reticulocyte maturation. Early erythropoiesis is characterized by commitment of multilineage progenitor cells into erythroid progenitor cells, with proliferation and development into erythroid

burst-forming unit cells, followed by erythroid colony-forming unit cells and proerythroblasts. Terminal erythroid differentiation begins with proerythroblasts differentiating in a stepwise manner to early then late basophilic erythroblasts, polychromatic erythroblasts, and orthochromatic erythroblasts that enucleate to become reticulocytes.

Erythropoiesis is a metabolically daunting process when evaluated at the level of cell numbers. In healthy adults, committed erythroid progenitors support the production of 2.4 million erythrocytes per second via a synchronized regulation of iron, glucose, fatty acid, and amino acid metabolism. Iron is indispensable for heme biosynthesis in erythroblasts (Oburoglu et al., 2016). The utilization of both glutamine and glucose in *de novo* nucleotide biosynthesis is a *sine qua non* for erythroid differentiation (Oburoglu et al., 2014), and glutamine-derived



production of succinyl-coenzyme A (succinyl-CoA) is also required for the production of heme (Burch et al., 2018). Furthermore, amino acids regulate mTOR signaling (Chung et al., 2015) as well as lipid metabolism (Huang et al., 2018) during erythropoiesis. The critical nature of metabolism in erythroid differentiation is further highlighted by the recent identification of “metabolic regulators” as an erythropoietin (EPO)-induced phosphorylation target set (Held et al., 2020).

It is important though to note that terminal erythroid differentiation is a distinctive process; each mitosis results in the production of daughter cells that differ, morphologically and functionally, from their parent cells. This sequential maturation is tightly regulated at each stage of erythroid differentiation, associated with decreased cell size, enhanced chromatin condensation, progressive hemoglobinization, and changes in membrane organization and transcriptome specificities (An et al., 2014; Hu et al., 2013; Li et al., 2014; Ludwig et al., 2019; Schulz et al., 2019). Moreover, during the late stages of mammalian terminal erythroid differentiation, erythroblasts expel their nuclei and lose all organelles, including mitochondria (Moras et al., 2017). Thus, the constraints of a late-stage terminally differentiating erythroblast differ significantly from that of an erythroid-committed progenitor early in erythroid development. Indeed, in mice, early-stage erythroid progenitors have been found to require mTORC1-mediated mitochondrial biogenesis and reactive oxygen species (ROS) production (Liu et al., 2017; Luo et al., 2017; Zhao et al., 2016), while terminal erythropoiesis requires that cells be protected from oxidative stress (Case et al., 2013; Filippi and Ghaffari, 2019; Hyde et al., 2012; Xu et al., 2019; Zhao et al., 2016).

Significant differences in murine versus human erythroid development have been documented, especially as relates to the diversity of erythroid progenitor subpopulations in human bone marrow (BM) (Gautier et al., 2020; Schulz et al., 2019; Yan et al., 2018). Furthermore, regarding oxidative stress, it is important to note that murine and human erythropoiesis differ dramatically as a function of vitamin C/ascorbate plasma concentrations and expression of the SLC2A1/GLUT1 transporter, shuttling dehydroascorbic acid (DHA) across the membrane and rapidly reducing it to ascorbate (reviewed by May et al., 2001). Indeed, humans exhibit a deficiency in vitamin C production, due to inactivation of L-gulonolactone oxidase (GLO), the enzyme that catalyzes the terminal step of L-ascorbic acid (AA) biosynthesis (Burns, 1957). While human erythrocytes express the highest level of the GLUT1 transporter, harboring greater than 200,000 molecules per cell (Helgerson and Caruthers, 1987; Mueckler, 1994), we found that erythroid GLUT1 expression is a specific feature of mammals that have lost the ability to synthesize AA from glucose (Montel-Hagen et al., 2008a, 2008b). This potential evolutionary compensation, and subsequent alterations in the ability of plasma vitamin C to scavenge ROS/reactive nitrogen species (RNS), make it critical to evaluate the stepwise changes that regulate the progression of human erythropoiesis.

Here, we demonstrate that during the early stages of human red blood cell development, erythroid progenitors exhibit increased oxidative phosphorylation (OXPHOS) activity. This correlated with the increased generation of the alpha-ketogluta-

rate (α KG) TCA-cycle intermediate, generated by the anaplerotic utilization of glutamine, and a directly augmented OXPHOS. However, upon terminal differentiation of erythroblasts, mitochondrial biomass, OXPHOS, mitochondrial ROS, and superoxide production were all markedly decreased. Supraphysiological levels of α KG markedly attenuated terminal erythroid differentiation and enucleation. The impact of α KG was directly coupled to its role in mitochondrial metabolism, as enucleation was similarly inhibited by mitochondrial ROS and superoxide, induced by MitoParaquat (MitoPQ) or DHA. Moreover, enucleation was rescued by ROS scavengers, including vitamin C, glutathione (GSH), N-acetylcysteine (NAC), and vitamin E.

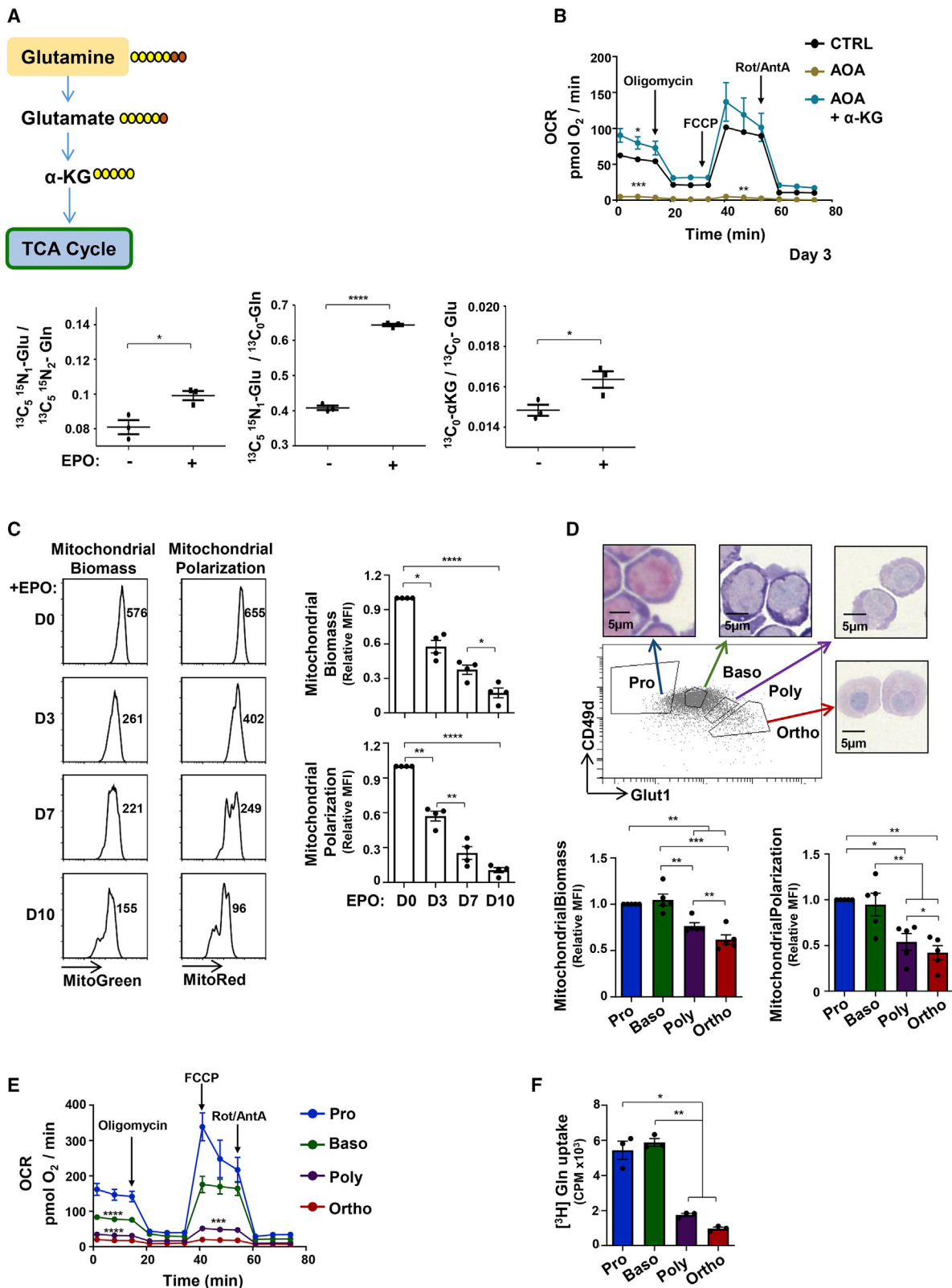
We identified the cytoplasmic isocitrate dehydrogenase 1 (IDH1) enzyme, catalyzing the interconversion between α KG and isocitrate, as a critical enzyme in this process. Lentiviral-mediated downregulation of IDH1, by significantly increasing mitochondrial metabolism and mitochondrial superoxide production, dramatically inhibited enucleation and resulted in the generation of abnormal multinucleated erythroblasts. Notably, both α KG and DHA markedly exacerbated the negative impact of IDH1 downregulation, while the vitamin C antioxidant rescued erythroid differentiation. Indeed, the vitamin-C-mediated quenching of ROS in erythroblasts accelerated human erythroid differentiation. This effect was specific to an IDH1-vitamin C axis; inhibition of TET2 in late-stage erythroblasts did not attenuate enucleation. Thus, our data identify IDH1 as a critical regulator of redox homeostasis, promoting late-stage erythropoiesis. Furthermore, these results highlight the therapeutic potential of vitamin C in human erythropoiesis, especially under pathological conditions where ROS are increased and vitamin C levels are not sufficient to combat oxidative damage.

RESULTS

Early erythropoiesis is associated with augmented glutamine utilization and OXPHOS

As glutaminolysis is required for erythroid lineage specification (Oburoglu et al., 2014), we evaluated the utilization of glutamine during early stages of human erythropoiesis at day 4 following recombinant erythropoietin (rEPO) stimulation, a time point at which the erythroid markers CD36, CD71 (transferrin receptor), and glycophorin A (GlyA) are upregulated (Figure S1A). The anaplerotic contribution of glutamine can be evaluated by tracing glutamine labeled with heavy stable carbons and nitrogens ($^{13}\text{C}_5\text{ }^{15}\text{N}_2$). As shown in Figure 1A, the portion of glutamate derived from $^{13}\text{C}_5\text{ }^{15}\text{N}_2$ glutamine, a measure of glutaminase activity, increased significantly following erythropoietin-induced erythroid differentiation of human CD34⁺ progenitors ($p < 0.05$; Figure 1A). Additionally, the contribution of labeled glutamine to the pool of glutamate ($^{13}\text{C}_5\text{ }^{15}\text{N}_1$ glutamate/ $^{13}\text{C}_0$ glutamate) as well as the portion of $^{13}\text{C}_5$ labeled α KG increased significantly upon erythroid differentiation. This glutamate-derived generation of α KG was critical for OXPHOS in erythroid progenitors, as the oxygen consumption rate (OCR) was abrogated by the aminoxyacetic acid (AOA) transaminase inhibitor, blocking conversion of glutamate to α KG, and was completely restored by α KG supplementation (Figure 1B).

These data show that glutamine supports the tricarboxylic acid (TCA) cycle and downstream OXPHOS via the cataplerotic



(legend on next page)

utilization of α KG. As each stage of terminal erythroid differentiation is defined by a decreased cell size with the final stage of erythropoiesis resulting in enucleation and reticulocyte maturation, we assessed whether mitochondrial biomass and transmembrane polarization decrease following commitment of progenitors to an erythroid lineage fate. Indeed, both mitochondrial biomass and polarization, evaluated by MitoGreen and MitoRed staining, respectively, decreased massively upon erythroid differentiation, monitored as a function of day of differentiation (days 0–10) as well as on erythroblast subsets fluorescence-activated cell sorting (FACS) sorted on the basis of their CD49d/GLUT1 staining profiles ($p < 0.05$ to $p < 0.0001$; Figures 1C, 1D, and S1B).

These changes in mitochondrial biomass and polarization had functional consequences on terminal erythroid differentiation (Figure 1D). Erythroblasts at distinct stages of differentiation exhibited significant differences in their levels of OXPHOS, as estimated by their OCRs; basal OCR decreased from 146.9 ± 15.5 to 17.5 ± 0.6 pmol O_2 /min between the proerythroblast and orthochromatic erythroblast stages of differentiation ($p < 0.0001$; Figure 1E). Notably, the respiratory capacities of both polychromatic and orthochromatic subsets were minimal; neither of these terminal subsets exhibited a spare respiratory capacity, as measured by the ability of the cell to increase its respiration in response to an Carbonyl cyanide-4-(trifluoromethoxy)phenylhydrazone (FCCP)-mediated disruption of mitochondrial membrane potential (Figure 1E). Similarly, these differences were also detected with increasing time after EPO induction (Figure S1C). Consistent with a critical role for glutamine in the oxidative potential of the erythroblast, glutamine uptake was significantly higher in proerythroblasts and basophilic erythroblasts than in polychromatic/orthochromatic erythroblasts ($p < 0.01$; Figure 1F). Thus, in marked contrast with the high-energy state of early erythroid progenitors, terminal maturation results in a significant attenuation of glutamine uptake and an associated decrease in OXPHOS.

α KG increases mitochondrial function while negatively regulating terminal erythroid differentiation and enucleation

As decreased mitochondrial function of terminally differentiated erythroblasts was associated with decreased glutamine uptake,

we evaluated whether α KG, the anaplerotic product of glutamine that enters into the TCA cycle, directly contributed to the erythroblast's respiratory capacity. Importantly, we found that α KG directly regulates the metabolic state of progenitors, as the injection of a cell-permeable α KG immediately augmented the maximal respiratory capacity of erythroblasts at both day 3 and day 7 of EPO induction ($p < 0.001$ and $p < 0.0001$; Figure 2A). This increase in OXPHOS did not alter the generation of CD34⁻CD36⁺ committed erythroid colony-forming unit (CFU-E) progenitors or GlyA⁺ erythroblasts or the upregulation of CD36 or CD71 erythroid markers (Figures 2B and S2A). While α KG did not alter mitochondrial biomass or polarization at early stages of development (day 3; Figure S2B), it substantially affected these parameters when it was added only at later stages (from days 7 to 10). Mitochondrial biomass and polarization were significantly higher in α KG-supplemented late-stage erythroblasts than in control erythroblasts ($p < 0.01$ and $p < 0.001$; Figure 2C). Furthermore, progression from the CD49d⁺GLUT1⁺ basophilic erythroblast to the CD49d⁻Glut1⁺ orthochromatic stage was significantly inhibited by α KG ($p < 0.05$ and $p < 0.01$; Figure 2D). This phenomenon was also associated with a significantly attenuated level of enucleation, decreasing by $32\% \pm 7\%$ and $52\% \pm 7\%$ in the presence of α KG at days 10 and 14 of erythroid differentiation, respectively ($p < 0.001$ and $p < 0.01$; Figure 2D). Notably, this effect was specific to α KG and was not recapitulated by other TCA-cycle intermediates such as succinate or citrate (Figure S2C).

Augmented mitochondrial superoxide generation at the basophilic erythroblast stage abrogates terminal erythroid differentiation and enucleation

Generation of ROS within mitochondria is associated with the oxidative function of these organelles (Adam-Vizi and Tretter, 2013; Murphy, 2009), and α KG can directly contribute to ROS generation through the catalytic activity of α KG dehydrogenase (α KGDH) (Starkov et al., 2004; Tretter and Adam-Vizi, 2004). NADH produced by α KGDH also stimulates superoxide production by complex I of the electron transport chain (ETC; Figure 3A) (Adam-Vizi and Tretter, 2013; Murphy, 2009). We therefore evaluated whether addition of α KG, the substrate of α KGDH, alters

Figure 1. Early erythropoiesis results in increased metabolism followed by decreased mitochondrial activity during terminal erythroid differentiation

(A) Schematic representation of glutamine conversion to α -ketoglutarate (α KG), showing the metabolism of [¹³C₅¹⁵N₂] heavy-labeled glutamine (Gln) carbons (yellow) and nitrogens (orange; top). Peak area ratios of heavy atoms from [¹³C₅¹⁵N₂]Gln into glutamate ([¹³C₅¹⁵N₁]Glu), the relative level of [¹³C₅¹⁵N₁]Glu, and the portion of [¹³C₅] α KG at day 4 of differentiation in the absence or presence of rEPO are shown (\pm SEM). Horizontal lines represent mean levels. Each dot represents an individual technical replicate, representative of one of two independent experiments.

(B) Oxygen consumption rates (OCRs), a measure of OXPHOS, were monitored by sequential injection of oligomycin, FCCP, and rotenone/antimycin A (Rot/AntA) as indicated. Mean basal oxygen consumption, maximal consumption following FCCP, and minimal levels following inhibition of the electron transport chain (ETC) Rot/AntA (bottom panel) are presented at day 3 of erythroid differentiation in control conditions (CTRL), in the presence of the AOA transaminase inhibitor (1 mM) or AOA + α KG (3.5 mM). Means \pm SEM are presented ($n = 3$).

(C) Mitochondrial biomass and polarization were evaluated by MitoTracker Green and MitoTracker Red staining, respectively, at days 0, 3, 7, and 10 of differentiation ($n = 4$).

(D) Pro-erythroblasts (Pro) and basophilic (Baso), polychromatic (Poly), and orthochromatic (Ortho) erythroblasts were sorted as a function of their GLUT1/CD49d profile (top panel). H&E staining of sorted erythroblasts is shown. Mitochondrial biomass and polarization were evaluated as in (C), and means \pm SEM are presented ($n = 5$).

(E) OCR was monitored 15 h post-sorting and means \pm SEM are presented ($n = 6$).

(F) Glutamine uptake was monitored 18 h following sorting using L-[3,4-³H (N)]glutamine (0.5 μ Ci) for 10 min at room temperature (RT). Uptake is expressed as mean counts per minute (CPM) for triplicate samples \pm SEM.

Statistical significance was determined by a one-way ANOVA with Tukey's post hoc test (* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$).

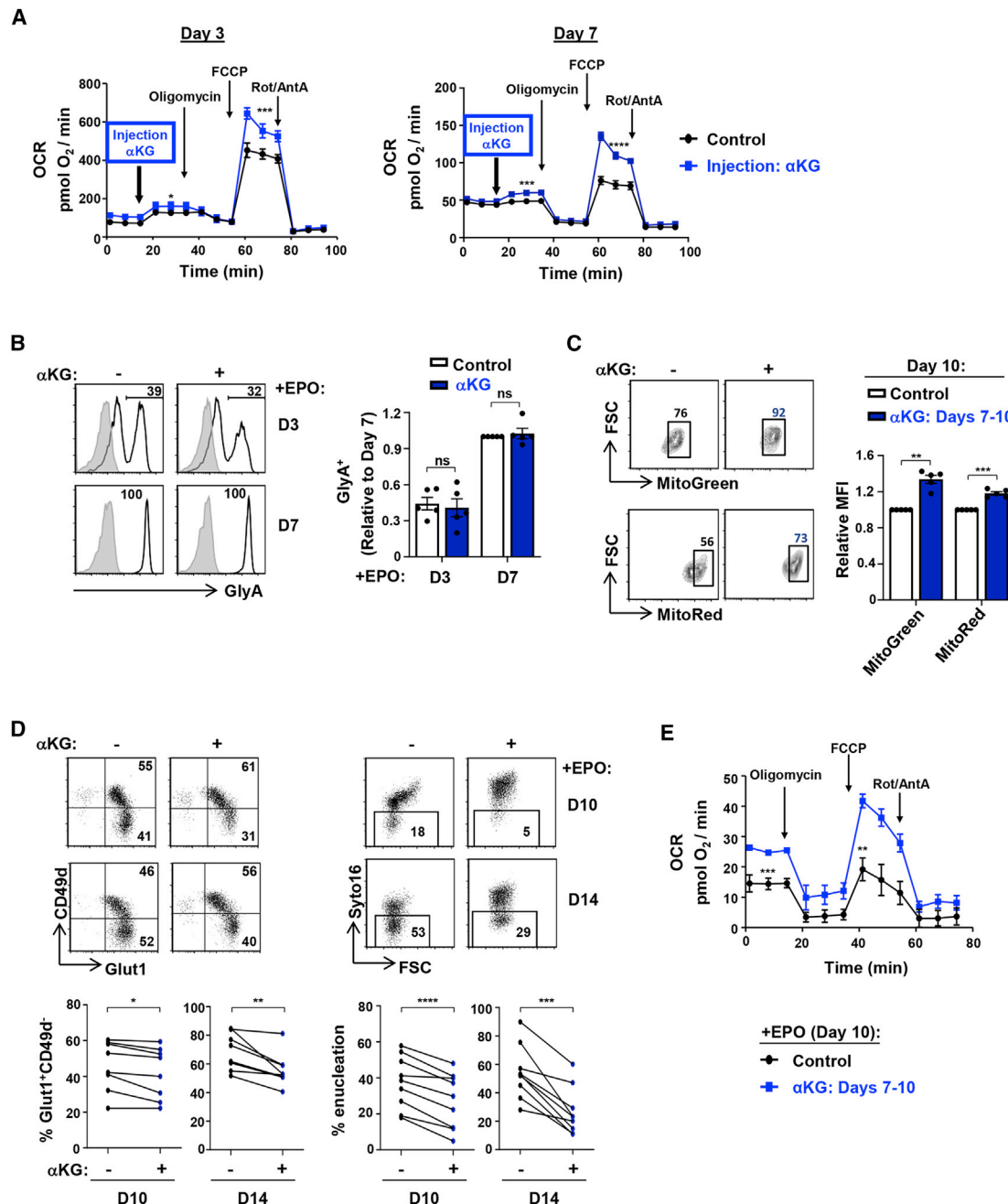


Figure 2. αKG increases mitochondrial function while significantly inhibiting terminal erythroid differentiation and enucleation

(A) CD34⁺ HSPCs were differentiated with EPO, and OXPHOS was evaluated at days 3 (left) and 7 (right) directly following injection of cell-permeable αKG (3.5 mM, blue line) into the Seahorse analyzer. Mean OCR ± SEM are presented for the indicated conditions (n = 5–6 per time point).

(B) Progenitors were stimulated with rEPO in the absence (–) or presence (+) of αKG. Expression of GlyA was monitored at days 3 and 7, and representative histograms (left) are shown (gray histograms, isotype controls; black lines, specific staining). Mean levels of GlyA⁺ cells were quantified in the different conditions (right), with levels at day 7 arbitrarily set at 1 (means ± SEM of five independent experiments; ns, nonsignificant).

(C) Mitochondrial biomass and mitochondrial membrane potential (MMP) were monitored following erythroid differentiation in the absence (–) or presence (+) of αKG (between days 7 and 10). Representative dot plots showing the percentages of cells with high mitochondrial biomass and MMP at day 10 are presented (left). Mean biomass and MMP (±SEM) are presented (right; n = 5).

(D) CD49d/Glut1 profiles of GlyA⁺ erythroblasts differentiated in the absence or presence of αKG (starting at day 7) were monitored at days 10 and 14 of differentiation, and representative dot plots are shown (top left). Percentages of Glut1⁺CD49d⁻ orthochromatic erythroblasts are shown for eight individual donors (bottom left). Erythroblast enucleation was evaluated as a function of Syto16 nucleic acid staining, and representative dot plots indicating the percentages of Syto16⁻ enucleated cells are presented (top right). Percentage enucleation in nine individual donors is presented (bottom right).

(legend continued on next page)

the redox state of the cell. Direct measurement of mitochondrial superoxide with the fluorescent MitoSOX indicator showed that α KG induced a 1.3-fold increase in superoxide ($p < 0.01$) as well as an overall increase of 1.3-fold in all mitochondrial ROS ($p < 0.001$), monitored as a function of DHR123 fluorescence (MitoROS) (Figure 3B).

These data suggested that the negative impact of α KG on erythroid maturation was linked to its role in altering the erythroblast redox state. We therefore assessed whether directly increasing mitochondrial superoxide would inhibit erythroid maturation. Erythroblasts were treated with MitoPQ, a newly synthesized paraquat compound that is targeted to the mitochondria by conjugation to the lipophilic tri-phenylphosphonium cation (Robb et al., 2015). This compound selectively increases superoxide production within mitochondria at 1,000-fold higher efficiency than untargeted paraquat (PQ) (Robb et al., 2015); within the mitochondria, mitoPQ²⁺ is reduced to the radical monocation at the flavin site of complex I and the monocation then reacts with O₂ to generate superoxide (O₂⁻) (Figure 3C). MitoPQ dramatically increased mitochondrial superoxide (MitoSOX), MitoROS, and mitochondrial biomass (MitoGreen) in differentiating erythroblasts ($p < 0.01$ and $p < 0.05$; Figure 3D). The impact of both MitoPQ and α KG was specific to mitochondrial ROS, as total intracellular ROS levels were not significantly changed (Figures S3A and S3B). Notably, short-term MitoPQ treatment significantly altered late erythropoiesis, with a 25% \pm 5% decrease in erythroblast enucleation ($p < 0.01$; Figure 3E).

To assess whether mitochondrial superoxide production has similar effects on erythroblasts at different stages of differentiation, we FACS-sorted early basophilic and late orthochromatic erythroblasts on the basis of their GLUT1/CD49d profiles. Representative cytopins are shown in Figure 3F. Notably, MitoPQ dramatically decreased the ability of basophilic erythroblasts to differentiate to reticulocytes, attenuating enucleation by 94% \pm 3% ($p < 0.001$; Figure 3F). In contrast, the maturation of orthochromatic erythroblasts was not affected by MitoPQ treatment (Figure 3F). These data show that a cell type that exhibits only very minimal OXPHOS potential, such as an orthochromatic erythroblast (Figure 1E), is not sensitive to a drug whose impact is dependent on mitochondrial function. In contrast, selectively increasing superoxide production in the mitochondrial matrix of an early erythroblast significantly inhibits erythroid maturation, revealing the critical role of this pathway in the proper progression of erythroid differentiation.

DHA and vitamin C have opposing effects on erythroid maturation

As we found that oxidative stress, monitored as a function of mitochondrial superoxide production and OXPHOS, was associated with attenuated late-stage erythroid differentiation and enucleation, it was of interest to determine whether these parameters were directly responsible for these observed effects. Vitamin C has the potential to promote a redox environment,

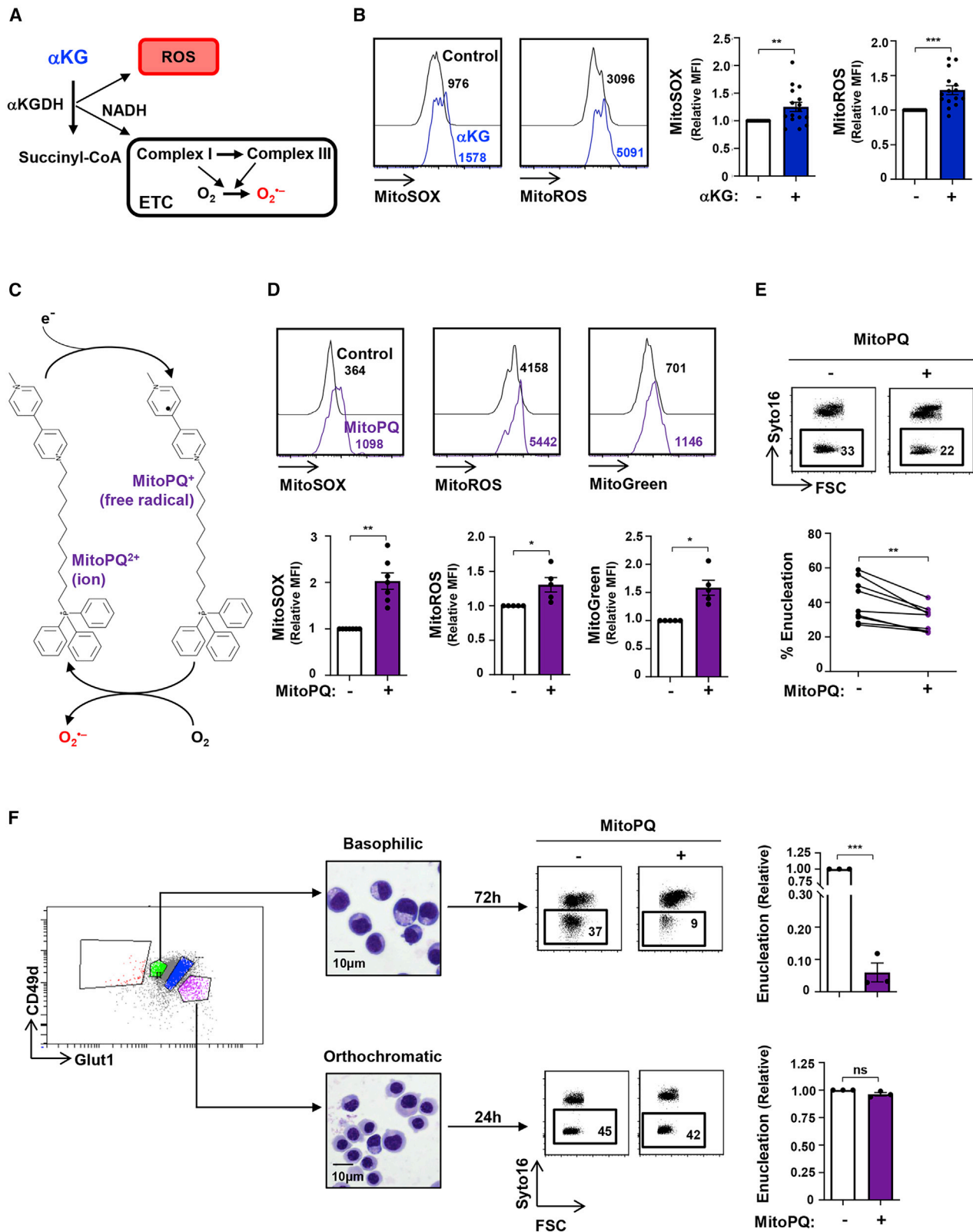
but its activity is countered by the oxidized form of vitamin C, DHA. The rapid reduction of intracellular DHA to vitamin C (Figure 4A) results in concomitant increases in endogenous ROS in tumor cell lines (Kc et al., 2005; Yun et al., 2015), but its role in erythroid cells is not known. Of note, DHA is transported via the GLUT1 glucose transporter, the most highly expressed transporter on human erythrocytes (Bianchi and Rose, 1986; Helgersson and Carruthers, 1987; May, 1998; Montel-Hagen et al., 2008b, 2009). We found that the addition of DHA significantly increased mitochondrial biomass and superoxide production in differentiating erythroblasts (Figure 4B). The DHA-induced increase in superoxide production was associated with a significant decrease in the enucleation of late-stage erythroblasts (from a mean of 40% \pm 3% to 24% \pm 3%; $p < 0.0001$; Figure 4C). Thus, under all tested conditions of superoxide production, enucleation of late-stage erythroblasts was severely attenuated.

Based on these data, it was important to evaluate whether vitamin C would have opposing effects on the redox state of erythroblasts and, subsequently, on erythroid maturation. As vitamin C is extremely labile, undergoing oxidation to DHA in culture media with a half-life of \sim 70 min (Yun et al., 2015), we evaluated the effect of AA-2-phosphate, which is resistant to spontaneous oxidation (Frikke-Schmidt and Lykkesfeldt, 2010; Hata and Senoo, 1989; Manning et al., 2013). This phosphorylated vitamin C molecule significantly enhanced the antioxidant capacity of the developing erythroblast, with a 23% \pm 3% decrease in mitochondrial superoxide production ($p < 0.0001$; Figures 4D and S3C). To evaluate whether vitamin C can alter an imbalanced high oxidative state in erythroblasts, we tested its impact on α KG-induced metabolic changes in differentiating erythroblasts. Vitamin C significantly diminished mitochondrial superoxide production as well as mitochondrial biomass and polarization ($p < 0.0001$, $p < 0.01$, and $p < 0.05$; Figures 4E and S3D). Moreover, we found that while both α KG and MitoPQ significantly increased the percentages of erythroblasts in the S-G2/M phases of the cell cycle (with cell death remaining $<15\%$), vitamin C decreased cell-cycle progression to control levels ($p < 0.05$ and $p < 0.01$; Figures 4F, S3E, and S3F).

Most importantly, vitamin C rescued the enucleation defect observed in these erythroblasts ($p < 0.0001$; Figure 4G). This effect was due to the reduced form of vitamin C; as only the long-acting derivative and not the labile form of vitamin C promoted enucleation (Figure S3G). Moreover, other ROS scavengers, including NAC (a thiol-containing antioxidant), GSH (the most abundant antioxidant), and Trolox (a water-soluble analog of vitamin E lacking the phytyl chain), recapitulated the actions of vitamin C, significantly augmenting terminal enucleation in the presence of α KG (Figure S4A). Similarly to the data shown above, highlighting the regulation of erythroid differentiation by mitochondrial metabolism at early erythroblast stages (Figure 3F), vitamin C significantly increased enucleation of sorted basophilic erythroblasts, but not orthochromatic erythroblasts (Figure S4B).

(E) OCR was evaluated on day 10 erythroid progenitors in control conditions (black line) and following addition of α KG at day 7 (blue line). Mean levels \pm SEM are presented ($n = 5-6$).

ns, nonsignificant; * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.



(legend on next page)

The ensemble of these data strongly suggests that the impact of vitamin C is due to its alteration of the redox state of the erythroblast. However, as autophagy is also a critical regulator of enucleation (Keerthivasan et al., 2011), we evaluated the impact of vitamin C following Spautin1-mediated inhibition of autophagy (Liu et al., 2011). As expected, Spautin significantly inhibited enucleation ($p < 0.01$), but vitamin C did not rescue this defect (Figure S5A), highlighting an autophagy-independent role of vitamin C in erythroid differentiation. Iron and its uptake as diferric transferrin by the transferrin receptor CD71 are also critical for erythroid differentiation (Kautz and Nemeth, 2014), and we therefore evaluated a potential crosstalk between iron and vitamin C. Interestingly, in the absence of transferrin, vitamin C did not increase enucleation in α KG-treated erythroblasts, but its presence (50 or 200 μ g/mL) positively affected enucleation (Figure S5B). Thus, vitamin C and other ROS scavengers decrease the redox state of erythroblasts, promoting enucleation under conditions of α KG-induced oxidative stress in a transferrin-dependent manner.

Vitamin C accelerates the erythroid differentiation of cord blood, peripheral blood, and BM progenitor cells

The ability of vitamin C to rescue erythroid differentiation under conditions of augmented oxidative stress led us to evaluate its potential to directly modulate erythroid differentiation of CD34⁺ hematopoietic stem and progenitor cells (HSPCs) from different sources. CD34⁺ progenitors from cord blood (CB), adult peripheral blood (PB), and BM were directly differentiated with rEPO. While BM-derived progenitors differentiated much more rapidly than CB- and PB-derived progenitors to an erythroid-committed CFU-E (CD34⁺CD36⁺), vitamin C did not alter the erythroid progenitor continuum (Figure S5C). In agreement with previous data (Yan et al., 2018), CB progenitors exhibited a delayed generation of GlyA⁺ erythroblasts compared to PB and BM progenitors (Figure 5A). Notably, vitamin C significantly increased the percentages of GlyA⁺ cells ($p < 0.05$) and increased maturation to a GlyA⁺CD105⁻ state by 2.1- \pm 0.5-fold ($p < 0.01$, Figure 5A), without altering cell growth (Figure S5D). Furthermore, vitamin C resulted in an enhanced enucleation of erythroid progenitors generated from these three sources (Figure 5B). Thus, vitamin C significantly accelerates erythroid differentiation and enucleation of human CD34⁺ progenitors, irrespective of their source of origin.

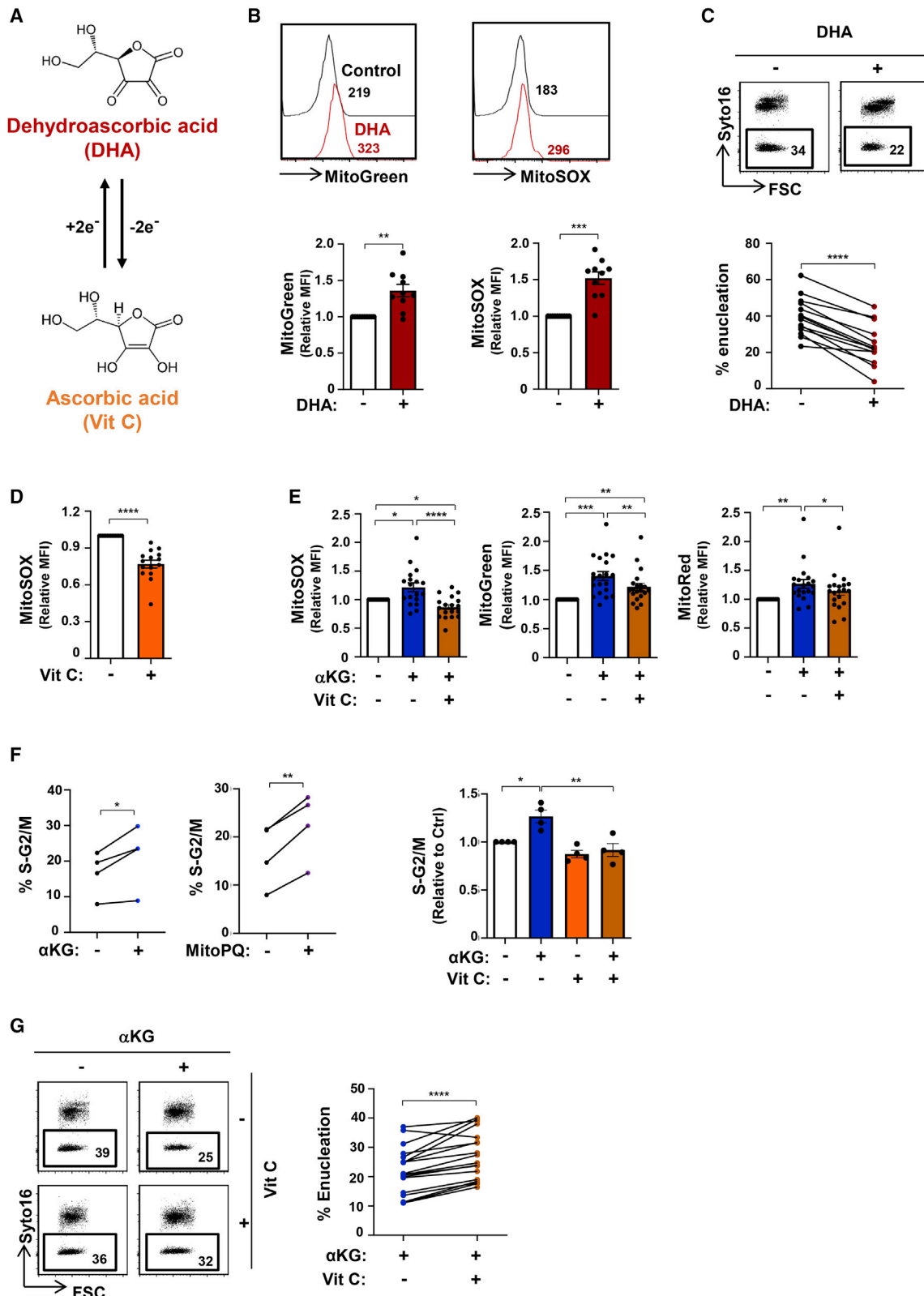
IDH1 activity regulates mitochondrial activity in differentiating erythroblasts

The data presented above demonstrated that conditions that increase mitochondrial activity in human erythroblasts, including ectopic α KG and MitoPQ, inhibit terminal erythroid differentiation. Under physiological conditions, α KG is mobilized in the mitochondria, where it can be converted to succinyl-CoA by α KGDH, producing ROS and the NADH that provides electrons for the ETC (Figure 6A). α KG can be generated from isocitrate in the mitochondria by IDH2/IDH3 and interconverted in the cytoplasm by IDH1. Interestingly, transcripts of all three enzymes are significantly reduced during erythroid differentiation, potentially suggesting a negative role for these pathways in late-stage erythroblasts (Figure S6A). As mitochondrial biomass is markedly decreased during erythroid differentiation, we evaluated the role of the cytoplasmic IDH enzyme, IDH1, in erythroid differentiation by an shIDH1-mediated approach. Using two independent short hairpin RNAs (shRNAs), shIDH1-1 and shIDH1-2, we detected a 36% \pm 7% and 54% \pm 5% reduction, respectively, and as such used shIDH1-2 in the differentiation experiments (Figure S6B).

Importantly, *IDH1* knockdown did not inhibit erythroid differentiation, as monitored by the generation of CFU-E, GlyA⁺ erythroblasts or upregulation of the CD36 or CD71 erythroid markers (Figures 6B, S6C, and S6D). However, downregulating IDH1 resulted in a decreased expansion (Figure S6E) and significantly increased mitochondrial superoxide production, mitochondrial biomass, and polarization ($p < 0.01$; Figures 6C and S6F). In accord with these data, *IDH1* knockdown augmented the OXPHOS capacity of the cells, with a 3.0- and 3.7-fold increase in basal and maximal OCR levels, respectively (shIDH1-2 construct) (Figure 6D). Notably, the function of IDH1 appears to be substantially more critical for the differentiation of erythroid as compared to non-erythroid progenitors. The percentages of progenitors transduced with a scramble shRNA (shControl) or shIDH1 lentiviral vector harboring the GFP reporter gene remained approximately stable over a 6-day period, with 47%–57% GFP⁺ cells, in the absence of rEPO. These cells had a myeloid phenotype as shown by a CD11b⁺, CD33⁺, CD13⁺ phenotype (Figure S6G). However, following rEPO-mediated erythroid induction, the percentages of shControl cells decreased by 24%, while the percentages of shIDH1-transduced cells decreased by 56% (Figure 6E).

Figure 3. Mitochondrial superoxide production impedes erythroid enucleation

(A) Schematic of the generation of mitochondrial reactive oxygen species (ROS) via the conversion of α KG to succinate, of which superoxide is a major source. (B) The impact of α KG (3.5 mM) on mitochondrial superoxide and mitochondrial ROS production in erythroblasts was evaluated at day 10 of erythroid differentiation as a function of MitoSOX and MitoROS, respectively. Representative histograms and MFIs are shown (left). Staining in the presence of α KG was normalized to control conditions, and relative median fluorescence intensities (MFIs) are presented ($n = 15$ –16, right). (C) Schematic of MitoParaquat (MitoPQ) cycling within the mitochondria; mitoPQ²⁺ is reduced to the radical monocation at the flavin site of complex I, and the monocation then reacts with O₂ to generate superoxide (O₂⁻) (Robb et al., 2015). (D) Differentiating erythroblasts were treated with MitoPQ (50 μ M) at day 7 of differentiation, and representative histograms of mitochondrial superoxide, ROS, and biomass at day 10 are presented (top). MFIs are presented relative to control conditions ($n = 5$ –6, bottom). (E) The impact of MitoPQ on enucleation was evaluated at day 10 by Syto16 staining, and representative dot plots are presented (top). Percent enucleation in nine independent experiments is shown (bottom). (F) The impact of MitoPQ on early basophilic erythroblasts as compared to late orthochromatic erythroblasts was determined by FACS sorting erythroblast populations as a function of their GLUT1/CD49d profiles (left), and representative cytopspins of the sorted subsets are shown (middle). Early basophilic and late orthochromatic subsets were then cultured for 72 h or 24 h, respectively, in the absence (–) or presence (+) of MitoPQ, and enucleation was evaluated (right). Enucleation was quantified relative to control conditions ($n = 3$). ns, nonsignificant; * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$.



(legend on next page)

To better understand the negative selection of erythroid progenitors with downregulated IDH1, we performed metabolomic and flux experiments following IDH1 knockdown. First, we found that at day 4 of IDH1 downregulation (~50%; Figure S6B), there was a mean decrease of α KG and citrate of 43% and 21%, respectively (Figure 6F). These data highlight the importance of the IDH1 enzyme in the generation of α KG and its interconversion to citrate. Furthermore, they demonstrate the role of glutamine metabolism in the generation of these intermediates in early erythroid progenitors (day 4); a mean of 75.1% and 69.0% of α KG and citrate harbored ^{13}C carbons from glutamine, respectively (Figure 6G). Several groups have also found that the relative ratio of α KG to citrate regulates differentiation, either by inhibiting (Carey et al., 2015; Vardhana et al., 2019) or priming (TeSlaa et al., 2016; Tischler et al., 2019) stem cell differentiation. In this regard, it is interesting to note that erythroid differentiation resulted in the loss of both α KG and citrate between days 4 and 7 of differentiation, with a mean loss of 87% and 68%, respectively ($n = 2$ biological experiments performed in triplicate; Figure 6G). These data point to a greater loss of α KG than citrate, consistent with a negative role of high α KG levels in late erythroid differentiation (Figure 2). Furthermore, following IDH1 downregulation, TCA intermediates were maintained at a higher level, with decreases in α KG and citrate of only 31% and 36%, respectively (Figure 6G). Thus, the premature inhibition of IDH1 alters the physiological loss of TCA-cycle intermediates upon erythroid differentiation.

Vitamin C rescues terminal erythroid differentiation in the absence of IDH1

Under conditions of IDH1 downregulation, mitochondrial metabolism was augmented, as shown by increased superoxide production and OXPHOS (Figures 6C and 6D). On the basis of these data, we hypothesized that *IDH1* knockdown would attenuate late-stage erythroid differentiation and enucleation, and this was indeed the case. Following transduction of CD34⁺ HSPCs with a vector harboring an shIDH1 RNA, the emergence of Glut1⁺CD49⁻ orthochromatic erythroblasts was significantly decreased (shIDH1-2 construct, $p < 0.01$; Figure 7A). Furthermore, enucleation was decreased by $59\% \pm 2\%$ (shIDH1-2 construct, $p < 0.0001$; Figure 7B), and this effect was detected even when

IDH1 was downregulated at day 4 post-rEPO-induced differentiation (Figure S7A). Consistent with an impact of IDH1 on the redox state of the cell, both α KG and DHA exacerbated the effect of *IDH1* knockdown on erythroblast enucleation, from $47\% \pm 8\%$ to $27\% \pm 8\%$ and $24\% \pm 4\%$, respectively ($p < 0.01$ and $p < 0.05$; Figure 7C). Most importantly, vitamin C significantly increased enucleation under these conditions by $35\% \pm 13\%$ ($p < 0.05$, Figure 7D). Intriguingly, other ROS scavengers, including NAC, GSH, and Trolox, did not increase enucleation, even though they were present throughout the differentiation period (Figure S7B). Importantly, vitamin C, but not NAC, GSH, or Trolox, decreased mitochondrial superoxide generation ($p < 0.05$; Figure S7C). Thus, collectively, these data show that IDH1-induced decreases in mitochondrial OXPHOS are required for the later stages of terminal erythroid differentiation and enucleation. However, under conditions of decreased IDH1 expression, this negative effect can be counteracted by a vitamin-C-mediated modulation of the intracellular redox balance.

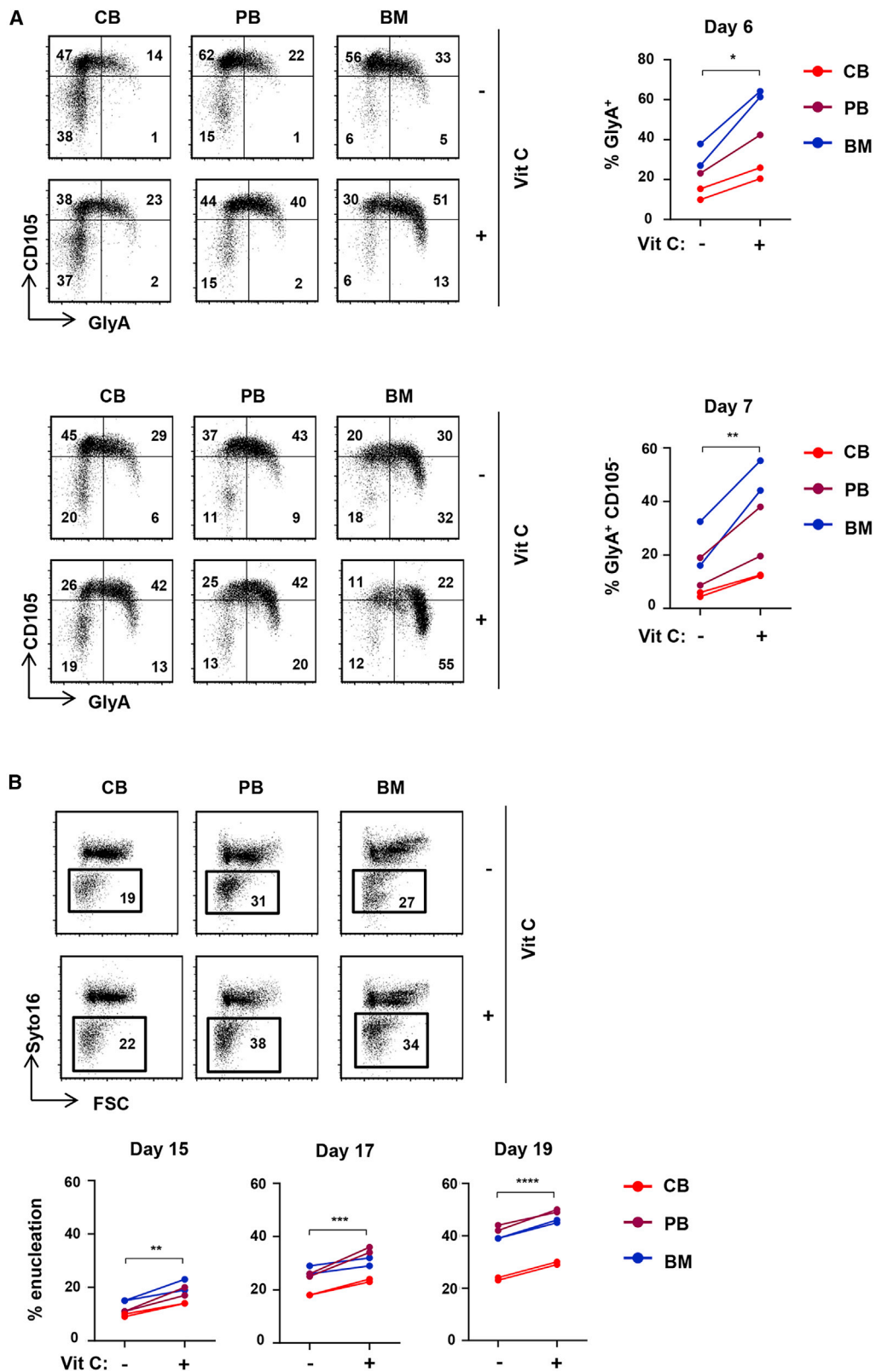
As α KG and vitamin C act as cofactors in supporting the dioxygenase activity of TET2, it was important to assess whether the effects that we detected here were coupled to their impact on TET2 activation (Inoue et al., 2016). However, if α KG served only to support the dioxygenase activity of TET2, then its presence would be expected to augment erythroid differentiation, while our data showed the opposite effect (Figure 2). To directly address this point and evaluate the role of an α KG/TET2 as compared to an α KG/IDH1 axis, we downregulated TET2 by an shRNA approach (Yan et al., 2017). TET2 levels decrease with differentiation ($p < 0.0001$; Figure S7D), but mRNA levels were further diminished by a mean of 55% by shRNA-mediated knockdown (Figure S7E). While this downregulation resulted in a significant delay in the generation of GlyA⁺ terminal erythroblasts ($p < 0.0001$; Figure S7F), it did not delay enucleation when the shRNA-mediated knockdown of TET2 was performed at day 4 of differentiation (Figure 7E). Moreover, enucleation in shTET2-treated erythroid progenitors was not augmented by vitamin C (Figure 7E). These data strongly imply distinct roles for IDH1 and TET2 in regulating enucleation of late-stage erythroid progenitors.

Mutations in IDH1/IDH2 are strongly associated with myelodysplastic syndromes (MDSs) that are characterized by

Figure 4. Antagonistic roles of dehydroascorbic acid and vitamin C on mitochondrial oxidative stress and erythroblast enucleation

- (A) Schematic of the interconversion between dehydroascorbic acid (DHA) and ascorbic acid (vitamin C) via a two-electron reduction/oxidation process, respectively.
- (B) The impact of DHA (1 mM) on mitochondrial superoxide production and biomass in late erythroblasts was evaluated between days 7 and 10 after EPO induction, and representative histograms of MitoGreen and MitoSOX staining, respectively, are shown (top). Quantification relative to control conditions is shown ($n = 10$, bottom).
- (C) Enucleation was evaluated at day 10 after EPO induction in the absence (–) or presence (+) of DHA (days 7–10), and representative dot plots are shown (top). Percent enucleation in 14 independent experiments is presented (bottom).
- (D) The impact of the stable L-ascorbic acid (AA) 2-phosphate derivative of vitamin C (100 μM) was evaluated on mitochondrial superoxide generation (days 7–10), and MFIs were quantified relative to control conditions ($n = 15$, bottom).
- (E) The impact of vitamin C on α KG-mediated increases in MitoSOX, MitoGreen, and MitoRed staining was evaluated by flow cytometry, and relative MFIs are presented ($n = 18$ –20).
- (F) The percentages of cells in S-G2/M of the cell cycle were evaluated in the indicated conditions by phosphatidylinositol (PI) staining ($n = 4$, left). The percentages of erythroid progenitors in S-G2/M were evaluated relative to control conditions, and means \pm SEM are presented (right).
- (G) Enucleation was evaluated in the presence or absence of vitamin C and α KG. Representative histograms (left) as well as changes in percent enucleation are presented ($n = 18$, right).

* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.



(legend on next page)

ineffective erythropoiesis (reviewed by [Bejar and Steensma, 2014](#); [Fenaux et al., 2014](#)). The anemia that dominates the early course of MDS is associated with an aberrant erythroid differentiation marked by the generation of multinucleated erythroblasts ([Abdel-Wahab and Levine, 2013](#)). Notably, we found that *IDH1* knockdown increased the percentages of erythroblasts with abnormal multinucleated erythroblasts from $10\% \pm 1\%$ to $23\% \pm 2\%$ ($p < 0.05$; [Figure 7F](#)). Moreover, vitamin C markedly decreased the generation of these abnormal erythroblasts, not only in *IDH1*-knockdown erythroblasts but also in normal erythroblasts, to $4\% \pm 0.4\%$ and $4\% \pm 0.2\%$, respectively ($p < 0.05$ and $p < 0.01$; [Figure 7F](#)). These data suggest that the multinucleated erythroblasts detected in MDS patients may be associated with an increased mitochondrial metabolism. Vitamin C, a redox scavenger, significantly attenuated the generation of these abnormal cells.

DISCUSSION

The generation of ROS and its intricate relationship with cellular redox homeostasis is a critical regulator of stem cell homeostasis. Notably, low ROS levels, associated with low mitochondrial biogenesis and activity, are necessary for HSC quiescence and self-renewal ([Filippi and Ghaffari, 2019](#); [Jang and Sharkis, 2007](#); [Qian et al., 2016](#); [Suda et al., 2011](#); [Takubo et al., 2013](#); [Tan and Suda, 2018](#); [Vannini et al., 2016](#); [Yu et al., 2013](#)). Conversely, HSC division and differentiation occur under conditions that promote mitochondrial biogenesis and OXPHOS ([Chen et al., 2008](#); [Mantel et al., 2010](#); [Maryanovich et al., 2015](#); [Yu et al., 2013](#)). In the context of erythropoiesis, it has been shown that early erythroid development requires induction of mitochondrial ROS, a consequence of OXPHOS ([Liu et al., 2017](#); [Zhao et al., 2016](#)). Here, we show that glutamine metabolism, via the anaplerotic contribution of α KG into the TCA cycle, directly increases OXPHOS in human erythroid precursors. This increased OXPHOS promoted erythroid commitment and early erythropoiesis, but terminal erythroid differentiation was dependent on the suppression of TCA-cycle-linked mitochondrial networks. Elevated intracellular α KG levels, with associated increased OXPHOS and ROS, inhibited late-stage erythroid maturation and enucleation.

Mechanistically, we identify the catalysis of α KG by the cytoplasmic *IDH1* enzyme as a critical step in erythropoiesis; the negative repercussions of *IDH1* downregulation in terminal erythroid differentiation was further exacerbated by elevated α KG levels. Furthermore, the impact of a mitochondria-targeted redox cyler, MitoPQ ([Robb et al., 2015](#)), highlights the importance of mitochondrial superoxide as a specific inhibitor of erythroblast maturation and enucleation. Interestingly, all tested ROS

scavengers, including NAC, GSH, vitamin E, and vitamin C, rescued the α KG-mediated decrease in enucleation, but only vitamin C rescued enucleation following *IDH1* downregulation. This is critical in the context of human erythroid differentiation, where the absence of ascorbate synthesis, resulting in 1 mg/kg recommended exogenous supplements for humans ([Pauling, 1970](#)), is significantly lower than the hepatic production rate of 200 mg/kg/day in vitamin-C-synthesizing animals ([Chatterjee, 1973](#); [Stone, 1979](#)). Thus, scavenging by vitamin C is likely to be suboptimal. Indeed, we found that a stable vitamin C analog rescued human terminal erythroid differentiation and enucleation in all tested conditions of oxidative stress.

Ascorbate, transported by the SVCT1/SLC23A1 and SVCT2/SLC23A2 solute carriers, regulates whole-body homeostasis of vitamin C and protection to oxidative stress, respectively ([Savini et al., 2008](#); [Tsukaguchi et al., 1999](#); [Wilson, 2005](#)). While vitamin C has been shown to enhance erythropoiesis in hemodialysis patients with refractory anemia ([Attallah et al., 2006](#); [Gastaldello et al., 1995](#); [Seibert et al., 2017](#); [Sirover et al., 2008](#)), other studies have found that ascorbate induces hemolysis of mature erythrocytes ([Zhang et al., 2016](#)). These apparent discrepancies are likely due to the oxidation state of vitamin C. The loss of a single electron from ascorbate results in the generation of an unstable ascorbate radical, which can then lose a second electron to generate DHA ([Padayatty and Levine, 2016](#)). Unlike vitamin C, the two-electron oxidized DHA intermediate is transported by the GLUT1 glucose transporter ([Bianchi and Rose, 1986](#); [McNulty et al., 2005](#); [Rumsey et al., 1997, 2000](#); [Vera et al., 1993](#)). Thus, cellular uptake of the reduced and oxidized forms of vitamin C is regulated, at least in part, by the expression of their specific transporters. SVCT2 is expressed at very high levels on HSCs, with levels decreasing as a function of erythroid development and differentiation ([Agathocleous et al., 2017](#)). Conversely, GLUT1 is upregulated during human terminal erythroid differentiation ([Montel-Hagen et al., 2008b](#); [Mueckler, 1994](#)), promoting DHA transport ([May, 1998](#); [Montel-Hagen et al., 2008b, 2009](#)). Thus, during intermediate steps of HSPC development, both ascorbate and DHA can potentially be transported into the cell.

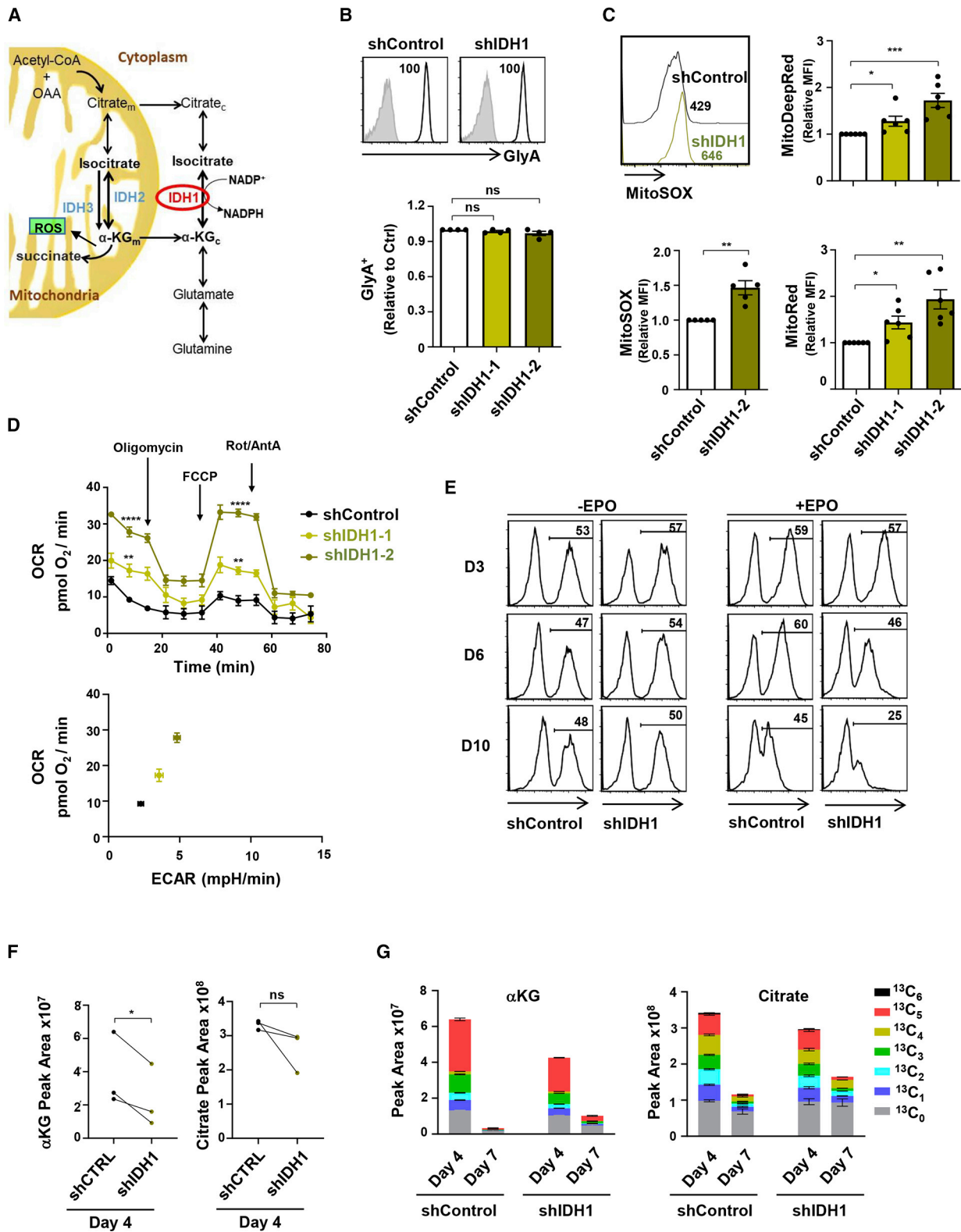
One of the difficulties in studying ascorbate function is its stability. Previous research showed that freshly prepared minimum essential medium α (α MEM) culture media, but not liquid α MEM, supported T cell differentiation from hematopoietic progenitors; the difference between these formulations was due to the lability of vitamin C in the latter ([Manning et al., 2013](#)). Furthermore, several groups found that the negative impact of vitamin C on the growth of cancer cells was actually due to the GLUT1-mediated uptake of DHA, resulting in the accumulation of ROS and subsequent cell death ([Yun et al., 2015](#); [Zhang et al., 2016](#)).

Figure 5. Vitamin C promotes erythroid commitment of EPO-stimulated progenitors from CB, BM, and PB and significantly accelerates erythroid maturation

(A) CD34⁺ HSPCs were isolated from CB, PB, and BM. Progenitors were differentiated with EPO in the absence or presence of vitamin C (100 μ M) and erythropoiesis monitored as a function of CD105/GlyA profiles. Representative profiles at days 6 (top left) and 7 (bottom left) of differentiation are presented. Quantification of GlyA⁺ cells at day 6 (n = 5, top right) and GlyA⁺CD105⁻ cells at day 7 (n = 5, bottom right) is presented.

(B) The impact of vitamin C on enucleation was evaluated in CB, PB, and BM HSPCs, and representative plots at day 17 are presented (top). Quantification of enucleation at days 15, 17, and 19 is presented (n = 6, bottom).

*p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001.



(legend on next page)

Indeed, we similarly found that the standard labile form of L-ascorbate markedly decreased erythroblast maturation and enucleation, even in the absence of ascorbate oxidase. However, under conditions where erythroid differentiation was performed in the presence of the stable ascorbate 2-phosphate analog (Hata and Senoo, 1989; Frikke-Schmidt and Lykkesfeldt, 2010; Takamizawa et al., 2004), erythroid differentiation was enhanced. Thus, care must be taken in evaluating studies using the conventional labile ascorbate, as it may not be maintained in a reduced state.

Ascorbic acid has also gained prominence as an anti-cancer therapeutic modality because of its ability to alter the activity of the Tet2 demethylase (Shenoy et al., 2018). Loss of function mutations in *TET2* are one of the most frequent events in myeloid dysplasia and leukemias (Bejar et al., 2011; Busque et al., 2012; Delhommeau et al., 2009; Kosmider et al., 2011). The initiation of demethylation by the TET family of dioxygenases occurs via the introduction of the intermediate mark 5-hydroxymethylcytosine (5hmC), and this function is dependent on several cofactors, including ascorbate, α KG, ferrous iron, and oxygen (Chen et al., 2013; Dang et al., 2009). Indeed, recent studies have shown that ascorbate is able to compensate for TET2 deficiency and suppress leukemogenesis, albeit via both TET2-dependent and TET2-independent mechanisms (Agathocleous et al., 2017; Cimmino et al., 2017). A crosstalk between ascorbate and TET2 in the metabolic status of a hematopoietic progenitor is suggested by the finding that wild-type TET2 protects murine erythroblasts from oxidative stress (Guo et al., 2017). Moreover, downregulation of TET2 in human erythroid progenitors negatively regulated human erythropoiesis in a manner that was independent of any detectable alterations in 5-methylcytosine (5mC) levels (Qu et al., 2018; Yan et al., 2017). These data are in agreement with independent studies showing that terminal erythroid differentiation requires that erythroblasts be protected from oxidative stress (Case et al., 2013; Filippi and Ghaffari, 2019; Hyde et al., 2012; Xu et al., 2019; Zhao et al., 2016).

Our study highlights the importance of ascorbate in regulating the redox state of human erythroid progenitors, especially under

conditions of altered oxidative metabolism. Increases in intracellular α KG and decreases in cytoplasmic IDH1 both augmented oxidative stress and diminished erythroid maturation. IDH1, like Tet2, is mutated in a high percentage of MDS patients (Kosmider et al., 2010; Wang et al., 2017), with anemia dominating the early course of disease. Moreover, recent studies have highlighted the potential for vitamin C to promote the differentiation of IDH1-mutated AML progenitors (Mingay et al., 2018). Our data show that even in the absence of mutation, low levels of wild-type IDH1 suppress late erythroid differentiation. While the specific role of IDH1 in OXPPOS has not yet been fully delineated, it is interesting to note that IDH1 downregulation in neuronal cells resulted in an increase in ROS (Calvert et al., 2017). Furthermore, mutation of IDH1, but not IDH2, has been found to increase OXPPOS in transformed cells (Grassian et al., 2014), and wild-type IDH1 regulates the reductive carboxylation of α KG for *de novo* lipogenesis (Calvert et al., 2017; Metallo et al., 2011).

IDH-regulated α KG production has also been shown to regulate cell fate and differentiation by modulating epigenetic marks via Tet2-induced changes in global histone and DNA demethylation (Carey et al., 2015; TeSlaa et al., 2016; Tischler et al., 2019; Xiao et al., 2012). Notably, under the conditions of erythroid differentiation studied here, α KG levels attenuated terminal erythroid differentiation and late-stage erythropoiesis, while a second TET2 cofactor, ascorbate, exhibited an opposing effect, enhancing and accelerating terminal differentiation. Other agents, such as oxidized ascorbate and MitoPQ, attenuated erythroid differentiation by inducing oxidative stress. Furthermore, while TET2 downregulation delayed early erythroblast differentiation, it did not negatively impact terminal differentiation and enucleation. Together, these data strongly suggest complementary roles for TET2 and IDH1, with the latter playing a critical role in late-stage human erythropoiesis via its impact on redox homeostasis.

These data may promote mechanistic insights into inherited hematologic disease. Like MDS patients, a feature that characterizes patients with congenital dyserythropoietic anemia is the presence of multinucleated or multi-lobulated erythroblasts

Figure 6. IDH activity regulates mitochondrial superoxide production and OXPPOS in differentiation erythroblasts

(A) Schematic representation of the catalytic reactions regulating glutamine catabolism. Glutamine is interconverted to glutamate and cytosolic α KG (α KG_c). Isocitrate dehydrogenase 1 (IDH1), a cytosolic enzyme, catalyzes the production of isocitrate from α KG, promoting both forward and reverse reactions. Conversion of mitochondrial α KG (α KG_m) to succinate results in the generation of ROS.

(B) The expression of GlyA was monitored in shControl- and shIDH1-transduced cells at day 7 day of differentiation, and representative histograms (gray, isotype control; black, specific staining) are shown (top). GlyA expression in cells transduced with one of two different shIDH1 clones (shIDH1-1 and shIDH1-2) was evaluated, and relative levels are presented (n = 4, bottom).

(C) The impact of IDH1 downregulation on MitoSOX was evaluated at day 10. Representative histograms (top left) and quantification of relative MFIs (n = 5) are presented (bottom left). MitoTracker Deep Red (top right) and MitoTracker Red (bottom right) staining in shIDH1-transduced erythroblasts relative to control conditions, are presented (n = 6).

(D) OCR was determined in FACS-sorted shControl- as well as shIDH1-transduced erythroblasts at day 10 of differentiation as indicated (n = 6, top). An OCR/extracellular acidification rate (ECAR) energy map is presented (bottom).

(E) The evolution of shControl- and sh-IDH1-transduced progenitors was monitored as a function of GFP expression at days 3, 6, and 10 of differentiation in the absence (–) or presence (+) of EPO (n = 3).

(F) Total levels of α KG and citrate were evaluated by high-performance liquid chromatography-mass spectrometry (HPLC-MS) at day 4 of erythroid differentiation in shControl- and shIDH1-transduced progenitors, and mean levels are shown (n = 3 independent experiments, with statistical difference evaluated by a one-tailed t test).

(G) The isotopologues of α KG and citrate derived from [¹³C₅-¹⁵N₂]Gln are presented from one experiment with three replicates for day 4 and two replicates for day 7.

ns, not significant; *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001.

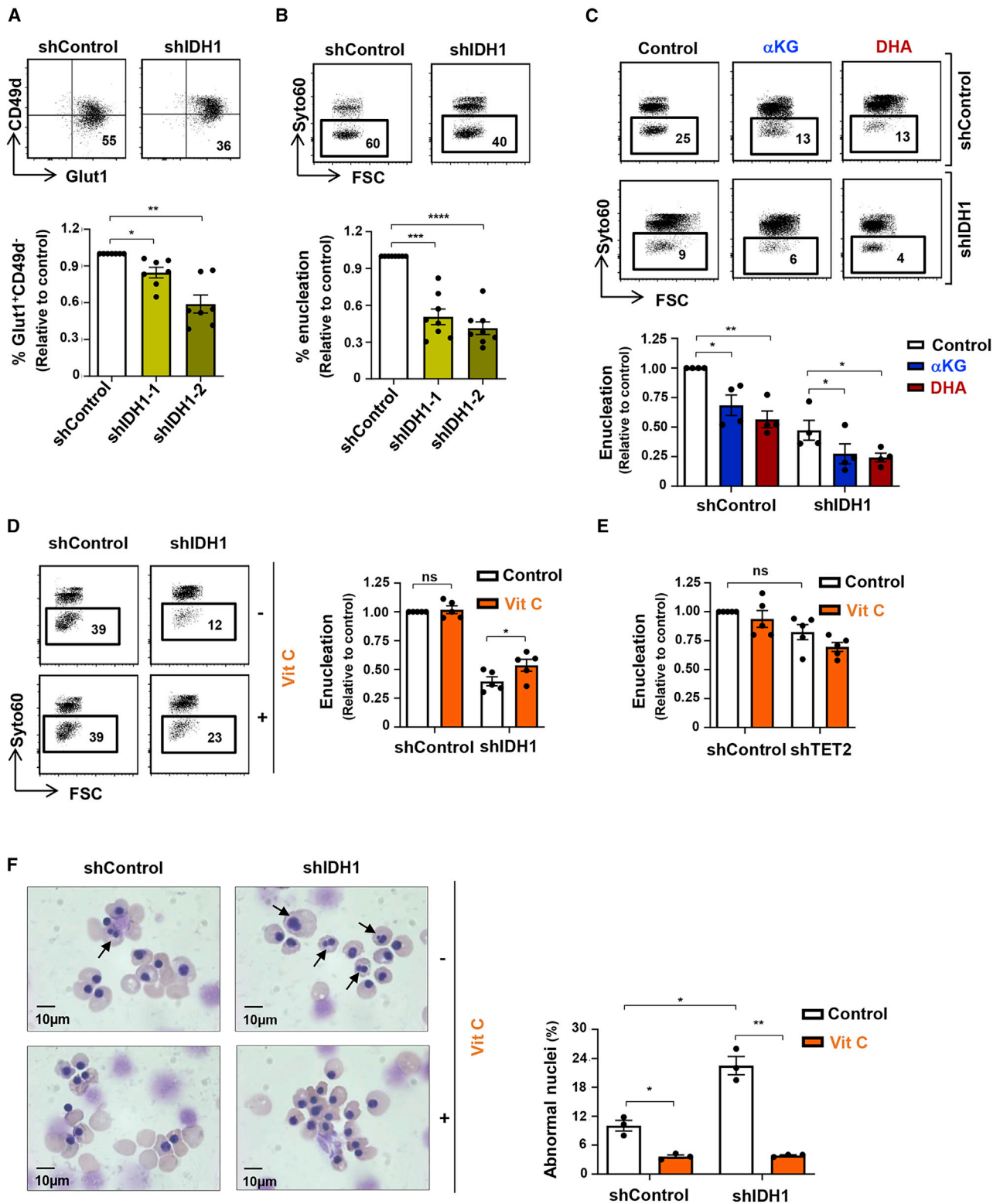


Figure 7. Vitamin C rescues dyserythropoiesis due to IDH1 downregulation

(A) Late-stage erythroblast differentiation was monitored as a GLUT1⁺CD49d⁻ phenotype, and representative dot plots are presented (top). The percentages of GLUT1⁺CD49d⁻ erythroblasts were evaluated following transduction with shIDH1-1 or shIDH1-2 vectors, and mean levels ± SEM relative to control cells are presented (n = 7, bottom).

(legend continued on next page)

(Crocketon et al., 1969; Goasguen et al., 2018; Iolascon et al., 1996). IDH1 knockdown resulted in a significant augmentation in the percentage of abnormal multinucleated orthochromatic erythroblasts, and even more importantly, ascorbate reduced these levels back to baseline. Thus, these data provide the first evidence that the abnormal erythroblast morphology observed in diverse dyserythropoietic diseases may be coupled to oxidative stress. Furthermore, our data suggest that antioxidant treatment of these disorders in humans, a species with suboptimal redox capacity (Johnson et al., 2008), with stable ascorbate analogs could potentially restore redox homeostasis, quenching ROS and subsequently rescuing defective late-stage erythropoiesis.

STAR★METHODS

Detailed methods are provided in the online version of this paper and include the following:

- KEY RESOURCES TABLE
- RESOURCE AVAILABILITY
 - Lead contact
 - Materials availability
 - Data and code availability
- EXPERIMENTAL MODELS AND SUBJECT DETAILS
 - CD34⁺ cell isolation and *ex vivo* differentiation assays.
- METHODS DETAIL
 - Cytospin preparation
 - Flow cytometry
 - Virus production and transduction of CD34⁺ progenitor cells
 - Quantitative real time PCR
 - Mass spectrometry (LC-MS)
 - Seahorse analysis
 - Glutamine uptake assays
- QUANTIFICATION AND STATISTICAL ANALYSIS

SUPPLEMENTAL INFORMATION

Supplemental Information can be found online at <https://doi.org/10.1016/j.celrep.2021.108723>.

ACKNOWLEDGMENTS

We thank all members of our laboratories for discussions and scientific critique. We are grateful to Myriam Boyer of Montpellier Rio Imaging for support in cytometry experiments. We are indebted to the Tissue Donation Pro-

gram at Northwell Health for providing access to BM samples. We thank the Unité de Thérapie Cellulaire and the hospital clinics of Clémentville and Saint-Roch (Montpellier, France) for their generous efforts in providing access to CB samples. We also thank Catherine Winchester for critical reading of the manuscript. P.G.-M. was supported by a fellowship from the Clarin-COFUND EU Program (Principado de Asturias, Spain), M.R. was supported by a fellowship from GR-Ex, and L.O. was supported by Ligue and ARC fellowships. S.T. is supported by funding from Cancer Research UK (C596/A17196 and A23982). This work was supported by generous funding from the NIH (grant DK32094 to P.G.G., N.M., S.K., and N.T. and grants HL144436 and HL152099 to L.B.); FRM, ARC, and French national (ANR) research grants (NutriDiff); and the French laboratory consortiums (Labex) EpiGenMed and GR-Ex. N.T. is presently supported by the NCI Intramural Program.

AUTHOR CONTRIBUTIONS

P.G.-M., M.R., S.K., and N.T. conceived the study; P.G.-M., M.R., H.Y., R.D., J.P., L.O., S.T., V.D., C.M., M.S., V.S.Z., L.B., N.M., S.K., and N.T. were involved in study design; and P.G.-M., M.R., H.Y., R.D., J.P., L.O., S.T., C.M., M.D., A.-S.D., I.P., X.Q., P.-N.B., and S.K. performed experiments. All authors participated in data analysis. P.-G.M., S.K., and N.T. wrote the manuscript with important critical input from M.R., H.Y., L.O., S.T., X.A., V.D., M.S., V.S.Z., P.G.G., L.B., and N.M.

DECLARATION OF INTERESTS

M.S. and S.K. are inventors on a patent describing the use of a ligand for evaluation of GLUT1 expression (N.T. gave up her rights). M.S. is a co-founder of METAFORA Biosystems, focusing on metabolite transporters under physiological and pathological conditions, and is head of the scientific board.

Received: June 10, 2020

Revised: November 26, 2020

Accepted: January 12, 2021

Published: February 2, 2021

REFERENCES

- Abdel-Wahab, O., and Levine, R.L. (2013). Mutations in epigenetic modifiers in the pathogenesis and therapy of acute myeloid leukemia. *Blood* 121, 3563–3572.
- Adam-Vizi, V., and Tretter, L. (2013). The role of mitochondrial dehydrogenases in the generation of oxidative stress. *Neurochem. Int.* 62, 757–763.
- Agathocleous, M., Meacham, C.E., Burgess, R.J., Piskounova, E., Zhao, Z., Crane, G.M., Cowin, B.L., Bruner, E., Murphy, M.M., Chen, W., et al. (2017). Ascorbate regulates haematopoietic stem cell function and leukaemogenesis. *Nature* 549, 476–481.
- An, X., Schulz, V.P., Li, J., Wu, K., Liu, J., Xue, F., Hu, J., Mohandas, N., and Gallagher, P.G. (2014). Global transcriptome analyses of human and murine terminal erythroid differentiation. *Blood* 123, 3466–3477.
- Ashley, R.J., Yan, H., Wang, N., Hale, J., Dulmovits, B.M., Papoin, J., Olive, M.E., Udeshi, N.D., Carr, S.A., Vlachos, A., et al. (2020). Steroid resistance in

(B) Enucleation of shControl- and shIDH1-transduced erythroblasts was assessed on GFP⁺ cells at day 14, and representative histograms are presented (top). Enucleation levels, relative to control cells, were quantified (n = 8, bottom).

(C) The impact of αKG and DHA on erythroblast enucleation following IDH1 knockdown was evaluated between days 7 and 10, and representative histograms are presented (top). Enucleation relative to control conditions was quantified (n = 4, bottom).

(D) The impact of vitamin C on enucleation of control and IDH1-downregulated erythroblasts was evaluated between days 7 and 10. Representative histograms (top) and quantifications (bottom) are presented (n = 5). Changes in mitochondrial superoxide were evaluated by MitoSOX staining, and MFIs are presented (n = 4).

(E) TET2 was downregulated in erythroid progenitors by shTET2 lentivirus (day 4), and enucleation was monitored at day 10 in the presence or absence of vitamin C. Means ± SEM are presented (n = 5, one-way ANOVA with Tukey's post hoc test).

(F) Nuclear morphology of orthochromatic erythroblasts differentiated from shControl- and shIDH1-transduced progenitors in the absence or presence of vitamin C was monitored. Representative cytopins are shown (left), and the quantification of orthochromatic erythroblasts with abnormal nuclei was determined by counting 500–1,000 cells (n = 3, right).

ns, not significant; *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001.

- Diamond Blackfan anemia associates with p57Kip2 dysregulation in erythroid progenitors. *J. Clin. Invest.* **130**, 2097–2110.
- Attallah, N., Osman-Malik, Y., Frinak, S., and Besarab, A. (2006). Effect of intravenous ascorbic acid in hemodialysis patients with EPO-hyporesponsive anemia and hyperferritinemia. *Am. J. Kidney Dis.* **47**, 644–654.
- Bejar, R., and Steensma, D.P. (2014). Recent developments in myelodysplastic syndromes. *Blood* **124**, 2793–2803.
- Bejar, R., Stevenson, K., Abdel-Wahab, O., Galili, N., Nilsson, B., Garcia-Manero, G., Kantarjian, H., Raza, A., Levine, R.L., Neuberg, D., and Ebert, B.L. (2011). Clinical effect of point mutations in myelodysplastic syndromes. *N. Engl. J. Med.* **364**, 2496–2506.
- Bianchi, J., and Rose, R.C. (1986). Glucose-independent transport of dehydroascorbic acid in human erythrocytes. *Proc. Soc. Exp. Biol. Med.* **181**, 333–337.
- Burch, J.S., Marcero, J.R., Maschek, J.A., Cox, J.E., Jackson, L.K., Medlock, A.E., Phillips, J.D., and Dailey, H.A., Jr. (2018). Glutamine via α -ketoglutarate dehydrogenase provides succinyl-CoA for heme synthesis during erythropoiesis. *Blood* **132**, 987–998.
- Burns, J.J. (1957). Missing step in man, monkey and guinea pig required for the biosynthesis of L-ascorbic acid. *Nature* **180**, 553.
- Busque, L., Patel, J.P., Figueroa, M.E., Vasanthakumar, A., Provost, S., Hamilou, Z., Mollica, L., Li, J., Viale, A., Heguy, A., et al. (2012). Recurrent somatic TET2 mutations in normal elderly individuals with clonal hematopoiesis. *Nat. Genet.* **44**, 1179–1181.
- Calvert, A.E., Chalastanis, A., Wu, Y., Hurley, L.A., Kouri, F.M., Bi, Y., Kachman, M., May, J.L., Bartom, E., Hua, Y., et al. (2017). Cancer-associated IDH1 promotes growth and resistance to targeted therapies in the absence of mutation. *Cell Rep.* **19**, 1858–1873.
- Carey, B.W., Finley, L.W., Cross, J.R., Allis, C.D., and Thompson, C.B. (2015). Intracellular alpha-ketoglutarate maintains the pluripotency of embryonic stem cells. *Nature* **518**, 413–416.
- Case, A.J., Madsen, J.M., Motto, D.G., Meyerholz, D.K., and Domann, F.E. (2013). Manganese superoxide dismutase depletion in murine hematopoietic stem cells perturbs iron homeostasis, globin switching, and epigenetic control in erythrocyte precursor cells. *Free Radic. Biol. Med.* **56**, 17–27.
- Chatterjee, I.B. (1973). Evolution and the biosynthesis of ascorbic acid. *Science* **182**, 1271–1272.
- Chen, C., Liu, Y., Liu, R., Ikenoue, T., Guan, K.L., Liu, Y., and Zheng, P. (2008). TSC-mTOR maintains quiescence and function of hematopoietic stem cells by repressing mitochondrial biogenesis and reactive oxygen species. *J. Exp. Med.* **205**, 2397–2408.
- Chen, Q., Chen, Y., Bian, C., Fujiki, R., and Yu, X. (2013). TET2 promotes histone O-GlcNAcylation during gene transcription. *Nature* **493**, 561–564.
- Chung, J., Bauer, D.E., Ghamari, A., Nizzi, C.P., Deck, K.M., Kingsley, P.D., Yen, Y.Y., Huston, N.C., Chen, C., Schultz, I.J., et al. (2015). The mTORC1/4E-BP pathway coordinates hemoglobin production with L-leucine availability. *Sci. Signal.* **8**, ra34.
- Cimmino, L., Dolgalev, I., Wang, Y., Yoshimi, A., Martin, G.H., Wang, J., Ng, V., Xia, B., Witkowski, M.T., Mitchell-Flack, M., et al. (2017). Restoration of TET2 function blocks aberrant self-renewal and leukemia progression. *Cell* **170**, 1079–1095.e20.
- Crookston, J.H., Crookston, M.C., Burnie, K.L., Francombe, W.H., Dacie, J.V., Davis, J.A., and Lewis, S.M. (1969). Hereditary erythroblastic multinuclearity associated with a positive acidified-serum test: a type of congenital dyserythropoietic anaemia. *Br. J. Haematol.* **17**, 11–26.
- Dang, L., White, D.W., Gross, S., Bennett, B.D., Bittinger, M.A., Driggers, E.M., Fantin, V.R., Jang, H.G., Jin, S., Keenan, M.C., et al. (2009). Cancer-associated IDH1 mutations produce 2-hydroxyglutarate. *Nature* **462**, 739–744.
- Delhommeau, F., Dupont, S., Della Valle, V., James, C., Trannoy, S., Massé, A., Kosmider, O., Le Couedic, J.P., Robert, F., Alberdi, A., et al. (2009). Mutation in TET2 in myeloid cancers. *N. Engl. J. Med.* **360**, 2289–2301.
- Fenaux, P., Haase, D., Sanz, G.F., Santini, V., Buske, C., and Group, E.G.W. (2014). Myelodysplastic syndromes: ESMO Clinical Practice Guidelines for diagnosis, treatment and follow-up. *Ann. Oncol.* **25**, 57–69.
- Filippi, M.D., and Ghaffari, S. (2019). Mitochondria in the maintenance of hematopoietic stem cells: new perspectives and opportunities. *Blood* **133**, 1943–1952.
- Frikke-Schmidt, H., and Lykkesfeldt, J. (2010). Keeping the intracellular vitamin C at a physiologically relevant level in endothelial cell culture. *Anal. Biochem.* **397**, 135–137.
- Gastaldello, K., Vereerstraeten, A., Nzame-Nze, T., Vanherweghem, J.L., and Tielemans, C. (1995). Resistance to erythropoietin in iron-overloaded haemodialysis patients can be overcome by ascorbic acid administration. *Nephrol. Dial. Transplant.* **10** (Suppl 6), 44–47.
- Gautier, E.F., Leduc, M., Ladli, M., Schulz, V.P., Lefèvre, C., Boussaid, I., Fontenay, M., Lacombe, C., Verdier, F., Guillonnet, F., et al. (2020). Comprehensive proteomic analysis of murine terminal erythroid differentiation. *Blood Adv.* **4**, 1464–1477.
- Goasguen, J.E., Bennett, J.M., Bain, B.J., Brunning, R., Vallespi, M.T., Tomonaga, M., Zini, G., and Renault, A.; The International Working Group on Morphology of MDS (2018). Dyserythropoiesis in the diagnosis of the myelodysplastic syndromes and other myeloid neoplasms: problem areas. *Br. J. Haematol.* **182**, 526–533.
- Grassian, A.R., Parker, S.J., Davidson, S.M., Divakaruni, A.S., Green, C.R., Zhang, X., Slocum, K.L., Pu, M., Lin, F., Vickers, C., et al. (2014). IDH1 mutations alter citric acid cycle metabolism and increase dependence on oxidative mitochondrial metabolism. *Cancer Res.* **74**, 3317–3331.
- Guo, S., Jiang, X., Wang, Y., Chen, L., Li, H., Li, X., and Jia, Y. (2017). The protective role of TET2 in erythroid iron homeostasis against oxidative stress and erythropoiesis. *Cell. Signal.* **38**, 106–115.
- Hata, R., and Senoo, H. (1989). L-ascorbic acid 2-phosphate stimulates collagen accumulation, cell proliferation, and formation of a three-dimensional tissuelike substance by skin fibroblasts. *J. Cell. Physiol.* **138**, 8–16.
- Held, M.A., Greenfest-Allen, E., Jachimowicz, E., Stoeckert, C.J., Stokes, M.P., Wood, A.W., and Wojchowski, D.M. (2020). Phospho-proteomic discovery of novel EPO signal transducers including thioredoxin-interacting protein as a mediator of EPO-dependent human erythropoiesis. *Exp. Hematol.* **84**, 29–44.
- Helgerson, A.L., and Carruthers, A. (1987). Equilibrium ligand binding to the human erythrocyte sugar transporter. Evidence for two sugar-binding sites per carrier. *J. Biol. Chem.* **262**, 5464–5475.
- Hu, J., Liu, J., Xue, F., Halverson, G., Reid, M., Guo, A., Chen, L., Raza, A., Galili, N., Jaffray, J., et al. (2013). Isolation and functional characterization of human erythroblasts at distinct stages: implications for understanding of normal and disordered erythropoiesis in vivo. *Blood* **121**, 3246–3253.
- Huang, N.J., Lin, Y.C., Lin, C.Y., Pishesha, N., Lewis, C.A., Freinkman, E., Farquharson, C., Millán, J.L., and Lodish, H. (2018). Enhanced phosphocholine metabolism is essential for terminal erythropoiesis. *Blood* **131**, 2955–2966.
- Hyde, B.B., Liesa, M., Elorza, A.A., Qiu, W., Haigh, S.E., Richey, L., Mikkola, H.K., Schlaeger, T.M., and Shirihai, O.S. (2012). The mitochondrial transporter ABC-me (ABCB10), a downstream target of GATA-1, is essential for erythropoiesis in vivo. *Cell Death Differ.* **19**, 1117–1126.
- Inoue, S., Lemonnier, F., and Mak, T.W. (2016). Roles of IDH1/2 and TET2 mutations in myeloid disorders. *Int. J. Hematol.* **103**, 627–633.
- Iolascon, A., D'Agostaro, G., Perrotta, S., Izzo, P., Tavano, R., and Miraglia del Giudice, B. (1996). Congenital dyserythropoietic anemia type II: molecular basis and clinical aspects. *Haematologica* **81**, 543–559.
- Jang, Y.Y., and Sharkis, S.J. (2007). A low level of reactive oxygen species selects for primitive hematopoietic stem cells that may reside in the low-oxygenic niche. *Blood* **110**, 3056–3063.
- Johnson, R.J., Gaucher, E.A., Sautin, Y.Y., Henderson, G.N., Angerhofer, A.J., and Benner, S.A. (2008). The planetary biology of ascorbate and uric acid and their relationship with the epidemic of obesity and cardiovascular disease. *Med. Hypotheses* **71**, 22–31.

- Kautz, L., and Nemeth, E. (2014). Molecular liaisons between erythropoiesis and iron metabolism. *Blood* *124*, 479–482.
- Kc, S., Cárcamo, J.M., and Golde, D.W. (2005). Vitamin C enters mitochondria via facilitative glucose transporter 1 (Glut1) and confers mitochondrial protection against oxidative injury. *FASEB J.* *19*, 1657–1667.
- Keerthivasan, G., Wickrema, A., and Crispino, J.D. (2011). Erythroblast enucleation. *Stem Cells Int.* *2011*, 139851.
- Kim, F.J., Manel, N., Garrido, E.N., Valle, C., Sitbon, M., and Battini, J.L. (2004). HTLV-1 and -2 envelope SU subdomains and critical determinants in receptor binding. *Retrovirology* *7*, 41.
- Kinet, S., Swainson, L., Lavanya, M., Mongellaz, C., Montel-Hagen, A., Craveiro, M., Manel, N., Battini, J.L., Sitbon, M., and Taylor, N. (2007). Isolated receptor binding domains of HTLV-1 and HTLV-2 envelopes bind Glut-1 on activated CD4+ and CD8+ T cells. *Retrovirology* *4*, 31.
- Kosmider, O., Gelsi-Boyer, V., Slama, L., Dreyfus, F., Beyne-Rauzy, O., Quesnel, B., Hunault-Berger, M., Slama, B., Vey, N., Lacombe, C., et al. (2010). Mutations of IDH1 and IDH2 genes in early and accelerated phases of myelodysplastic syndromes and MDS/myeloproliferative neoplasms. *Leukemia* *24*, 1094–1096.
- Kosmider, O., Delabesse, E., de Mas, V.M., Cornillet-Lefebvre, P., Blanchet, O., Delmer, A., Recher, C., Raynaud, S., Bouscary, D., Viguié, F., et al.; GOELAMS Investigators (2011). TET2 mutations in secondary acute myeloid leukemias: a French retrospective study. *Haematologica* *96*, 1059–1063.
- Li, J., Hale, J., Bhagia, P., Xue, F., Chen, L., Jaffray, J., Yan, H., Lane, J., Gallagher, P.G., Mohandas, N., et al. (2014). Isolation and transcriptome analyses of human erythroid progenitors: BFU-E and CFU-E. *Blood* *124*, 3636–3645.
- Liu, J., Xia, H., Kim, M., Xu, L., Li, Y., Zhang, L., Cai, Y., Norberg, H.V., Zhang, T., Furuya, T., et al. (2011). Beclin1 controls the levels of p53 by regulating the deubiquitination activity of USP10 and USP13. *Cell* *147*, 223–234.
- Liu, X., Zhang, Y., Ni, M., Cao, H., Signer, R.A.J., Li, D., Li, M., Gu, Z., Hu, Z., Dickerson, K.E., et al. (2017). Regulation of mitochondrial biogenesis in erythropoiesis by mTORC1-mediated protein translation. *Nat. Cell Biol.* *19*, 626–638.
- Loisel-Meyer, S., Swainson, L., Craveiro, M., Oburoglu, L., Mongellaz, C., Costa, C., Martinez, M., Cosset, F.L., Battini, J.L., Herzenberg, L.A., et al. (2012). Glut1-mediated glucose transport regulates HIV infection. *Proc. Natl. Acad. Sci. USA* *109*, 2549–2554.
- Ludwig, L.S., Lareau, C.A., Bao, E.L., Nandakumar, S.K., Muus, C., Ulirsch, J.C., Chowdhary, K., Buenostro, J.D., Mohandas, N., An, X., et al. (2019). Transcriptional states and chromatin accessibility underlying human erythropoiesis. *Cell Rep.* *27*, 3228–3240.e7.
- Luo, S.T., Zhang, D.M., Qin, Q., Lu, L., Luo, M., Guo, F.C., Shi, H.S., Jiang, L., Shao, B., Li, M., et al. (2017). The promotion of erythropoiesis via the regulation of reactive oxygen species by lactic acid. *Sci. Rep.* *7*, 38105.
- Manel, N., Kim, F.J., Kinet, S., Taylor, N., Sitbon, M., and Battini, J.L. (2003). The ubiquitous glucose transporter GLUT-1 is a receptor for HTLV. *Cell* *115*, 449–459.
- Manning, J., Mitchell, B., Appadurai, D.A., Shakya, A., Pierce, L.J., Wang, H., Nganga, V., Swanson, P.C., May, J.M., Tantin, D., and Spangrude, G.J. (2013). Vitamin C promotes maturation of T-cells. *Antioxid. Redox Signal.* *19*, 2054–2067.
- Mantel, C., Messina-Graham, S., and Broxmeyer, H.E. (2010). Upregulation of nascent mitochondrial biogenesis in mouse hematopoietic stem cells parallels upregulation of CD34 and loss of pluripotency: a potential strategy for reducing oxidative risk in stem cells. *Cell Cycle* *9*, 2008–2017.
- Maryanovich, M., Zaltsman, Y., Ruggiero, A., Goldman, A., Shachnai, L., Zaidman, S.L., Porat, Z., Golan, K., Lapidot, T., and Gross, A. (2015). An MTCH2 pathway repressing mitochondria metabolism regulates haematopoietic stem cell fate. *Nat. Commun.* *6*, 7901.
- May, J.M. (1998). Ascorbate function and metabolism in the human erythrocyte. *Front. Biosci.* *3*, d1–d10.
- May, J.M., Qu, Z., and Morrow, J.D. (2001). Mechanisms of ascorbic acid recycling in human erythrocytes. *Biochim. Biophys. Acta* *1528*, 159–166.
- McNulty, A.L., Stabler, T.V., Vail, T.P., McDaniel, G.E., and Kraus, V.B. (2005). Dehydroascorbate transport in human chondrocytes is regulated by hypoxia and is a physiologically relevant source of ascorbic acid in the joint. *Arthritis Rheum.* *52*, 2676–2685.
- Metallo, C.M., Gameiro, P.A., Bell, E.L., Mattaini, K.R., Yang, J., Hiller, K., Jewell, C.M., Johnson, Z.R., Irvine, D.J., Guarente, L., et al. (2011). Reductive glutamine metabolism by IDH1 mediates lipogenesis under hypoxia. *Nature* *481*, 380–384.
- Mingay, M., Chaturvedi, A., Bilenky, M., Cao, Q., Jackson, L., Hui, T., Moksa, M., Heravi-Moussavi, A., Humphries, R.K., Heuser, M., and Hirst, M. (2018). Vitamin C-induced epigenomic remodelling in IDH1 mutant acute myeloid leukaemia. *Leukemia* *32*, 11–20.
- Montel-Hagen, A., Blanc, L., Boyer-Clavel, M., Jacquet, C., Vidal, M., Sitbon, M., and Taylor, N. (2008a). The Glut1 and Glut4 glucose transporters are differentially expressed during perinatal and postnatal erythropoiesis. *Blood* *112*, 4729–4738.
- Montel-Hagen, A., Kinet, S., Manel, N., Mongellaz, C., Prohaska, R., Battini, J.L., Delaunay, J., Sitbon, M., and Taylor, N. (2008b). Erythrocyte Glut1 triggers dehydroascorbic acid uptake in mammals unable to synthesize vitamin C. *Cell* *132*, 1039–1048.
- Montel-Hagen, A., Sitbon, M., and Taylor, N. (2009). Erythroid glucose transporters. *Curr. Opin. Hematol.* *16*, 165–172.
- Moras, M., Lefevre, S.D., and Ostuni, M.A. (2017). From erythroblasts to mature red blood cells: organelle clearance in mammals. *Front. Physiol.* *8*, 1076.
- Mueckler, M. (1994). Facilitative glucose transporters. *Eur. J. Biochem.* *219*, 713–725.
- Murphy, M.P. (2009). How mitochondria produce reactive oxygen species. *Biochem. J.* *417*, 1–13.
- Oburoglu, L., Tardito, S., Fritz, V., de Barros, S.C., Merida, P., Craveiro, M., Mamede, J., Cretenet, G., Mongellaz, C., An, X., et al. (2014). Glucose and glutamine metabolism regulate human hematopoietic stem cell lineage specification. *Cell Stem Cell* *15*, 169–184.
- Oburoglu, L., Romano, M., Taylor, N., and Kinet, S. (2016). Metabolic regulation of hematopoietic stem cell commitment and erythroid differentiation. *Curr. Opin. Hematol.* *23*, 198–205.
- Padayatty, S.J., and Levine, M. (2016). Vitamin C: the known and the unknown and Goldilocks. *Oral Dis.* *22*, 463–493.
- Pauling, L. (1970). Evolution and the need for ascorbic acid. *Proc. Natl. Acad. Sci. USA* *67*, 1643–1648.
- Qian, P., He, X.C., Paulson, A., Li, Z., Tao, F., Perry, J.M., Guo, F., Zhao, M., Zhi, L., Venkatraman, A., et al. (2016). The Dlk1-Gtl2 locus preserves LT-HSC function by inhibiting the PI3K-mTOR pathway to restrict mitochondrial metabolism. *Cell Stem Cell* *18*, 214–228.
- Qu, X., Zhang, S., Wang, S., Wang, Y., Li, W., Huang, Y., Zhao, H., Wu, X., An, C., Guo, X., et al. (2018). TET2 deficiency leads to stem cell factor-dependent clonal expansion of dysfunctional erythroid progenitors. *Blood* *132*, 2406–2417.
- Robb, E.L., Gawel, J.M., Aksentijević, D., Cochemé, H.M., Stewart, T.S., Shchepinova, M.M., Qiang, H., Prime, T.A., Bright, T.P., James, A.M., et al. (2015). Selective superoxide generation within mitochondria by the targeted redox cyclor MitoParaquat. *Free Radic. Biol. Med.* *89*, 883–894.
- Rumsey, S.C., Kwon, O., Xu, G.W., Burant, C.F., Simpson, I., and Levine, M. (1997). Glucose transporter isoforms GLUT1 and GLUT3 transport dehydroascorbic acid. *J. Biol. Chem.* *272*, 18982–18989.
- Rumsey, S.C., Daruwala, R., Al-Hasani, H., Zarnowski, M.J., Simpson, I.A., and Levine, M. (2000). Dehydroascorbic acid transport by GLUT4 in *Xenopus* oocytes and isolated rat adipocytes. *J. Biol. Chem.* *275*, 28246–28253.
- Savini, I., Rossi, A., Pierro, C., Avigliano, L., and Catani, M.V. (2008). SVCT1 and SVCT2: key proteins for vitamin C uptake. *Amino Acids* *34*, 347–355.
- Schulz, V.P., Yan, H., Lezon-Geyda, K., An, X., Hale, J., Hillyer, C.D., Mohandas, N., and Gallagher, P.G. (2019). A unique epigenomic landscape defines human erythropoiesis. *Cell Rep.* *28*, 2996–3009.e7.

- Seibert, E., Richter, A., Kuhlmann, M.K., Wang, S., Levin, N.W., Kotanko, P., and Handelman, G.J. (2017). Plasma vitamin C levels in ESRD patients and occurrence of hypochromic erythrocytes. *Hemodial. Int.* *21*, 250–255.
- Shenoy, N., Creagan, E., Witzig, T., and Levine, M. (2018). Ascorbic acid in cancer treatment: let the phoenix fly. *Cancer Cell* *34*, 700–706.
- Sirover, W.D., Siddiqui, A.A., and Benz, R.L. (2008). Beneficial hematologic effects of daily oral ascorbic acid therapy in ESRD patients with anemia and abnormal iron homeostasis: a preliminary study. *Ren. Fail.* *30*, 884–889.
- Starkov, A.A., Fiskum, G., Chinopoulos, C., Lorenzo, B.J., Browne, S.E., Patel, M.S., and Beal, M.F. (2004). Mitochondrial alpha-ketoglutarate dehydrogenase complex generates reactive oxygen species. *J. Neurosci.* *24*, 7779–7788.
- Stone, I. (1979). Eight decades of scurvy. *Australas. Nurses J.* *8*, 28–30.
- Suda, T., Takubo, K., and Semenza, G.L. (2011). Metabolic regulation of hematopoietic stem cells in the hypoxic niche. *Cell Stem Cell* *9*, 298–310.
- Swainson, L., Kinet, S., Manel, N., Battini, J.L., Sitbon, M., and Taylor, N. (2005). Glucose transporter 1 expression identifies a population of cycling CD4+ CD8+ human thymocytes with high CXCR4-induced chemotaxis. *Proc. Natl. Acad. Sci. USA* *102*, 12867–12872.
- Takamizawa, S., Maehata, Y., Imai, K., Senoo, H., Sato, S., and Hata, R. (2004). Effects of ascorbic acid and ascorbic acid 2-phosphate, a long-acting vitamin C derivative, on the proliferation and differentiation of human osteoblast-like cells. *Cell Biol. Int.* *28*, 255–265.
- Takubo, K., Nagamatsu, G., Kobayashi, C.I., Nakamura-Ishizu, A., Kobayashi, H., Ikeda, E., Goda, N., Rahimi, Y., Johnson, R.S., Soga, T., et al. (2013). Regulation of glycolysis by Pdk functions as a metabolic checkpoint for cell cycle quiescence in hematopoietic stem cells. *Cell Stem Cell* *12*, 49–61.
- Tan, D.Q., and Suda, T. (2018). Reactive oxygen species and mitochondrial homeostasis as regulators of stem cell fate and function. *Antioxid. Redox Signal.* *29*, 149–168.
- TeSlaa, T., Chaikovsky, A.C., Lipchina, I., Escobar, S.L., Hochedlinger, K., Huang, J., Graeber, T.G., Braas, D., and Teitell, M.A. (2016). α -Ketoglutarate accelerates the initial differentiation of primed human pluripotent stem cells. *Cell Metab.* *24*, 485–493.
- Tischler, J., Gruhn, W.H., Reid, J., Allgeyer, E., Buettner, F., Marr, C., Theis, F., Simons, B.D., Wernisch, L., and Surani, M.A. (2019). Metabolic regulation of pluripotency and germ cell fate through α -ketoglutarate. *EMBO J.* *38*, 38.
- Tretter, L., and Adam-Vizi, V. (2004). Generation of reactive oxygen species in the reaction catalyzed by alpha-ketoglutarate dehydrogenase. *J. Neurosci.* *24*, 7771–7778.
- Tsukaguchi, H., Tokui, T., Mackenzie, B., Berger, U.V., Chen, X.Z., Wang, Y., Brubaker, R.F., and Hediger, M.A. (1999). A family of mammalian Na⁺-dependent L-ascorbic acid transporters. *Nature* *399*, 70–75.
- Vande Voorde, J., Ackermann, T., Pfetzer, N., Sumpton, D., Mackay, G., Kalna, G., Nixon, C., Blyth, K., Gottlieb, E., and Tardito, S. (2019). Improving the metabolic fidelity of cancer models with a physiological cell culture medium. *Sci. Adv.* *5*, eaau7314.
- Vannini, N., Girotra, M., Naveiras, O., Nikitin, G., Campos, V., Giger, S., Roch, A., Auwerx, J., and Lutolf, M.P. (2016). Specification of haematopoietic stem cell fate via modulation of mitochondrial activity. *Nat. Commun.* *7*, 13125.
- Vardhana, S.A., Arnold, P.K., Rosen, B.P., Chen, Y., Carey, B.W., Huangfu, D., Carmona Fontaine, C., Thompson, C.B., and Finley, L.W.S. (2019). Glutamine independence is a selectable feature of pluripotent stem cells. *Nat. Metab.* *1*, 676–687.
- Vera, J.C., Rivas, C.I., Fischbarg, J., and Golde, D.W. (1993). Mammalian facilitative hexose transporters mediate the transport of dehydroascorbic acid. *Nature* *364*, 79–82.
- Wang, N., Wang, F., Shan, N., Sui, X., and Xu, H. (2017). IDH1 mutation is an independent inferior prognostic indicator for patients with myelodysplastic syndromes. *Acta Haematol.* *138*, 143–151.
- Wilson, J.X. (2005). Regulation of vitamin C transport. *Annu. Rev. Nutr.* *25*, 105–125.
- Xiao, M., Yang, H., Xu, W., Ma, S., Lin, H., Zhu, H., Liu, L., Liu, Y., Yang, C., Xu, Y., et al. (2012). Inhibition of α -KG-dependent histone and DNA demethylases by fumarate and succinate that are accumulated in mutations of FH and SDH tumor suppressors. *Genes Dev.* *26*, 1326–1338.
- Xu, P., Palmer, L.E., Lechauve, C., Zhao, G., Yao, Y., Luan, J., Vourekas, A., Tan, H., Peng, J., Schuetz, J.D., et al. (2019). Regulation of gene expression by miR-144/451 during mouse erythropoiesis. *Blood* *133*, 2518–2528.
- Yan, H., Wang, Y., Qu, X., Li, J., Hale, J., Huang, Y., An, C., Papoin, J., Guo, X., Chen, L., et al. (2017). Distinct roles for TET family proteins in regulating human erythropoiesis. *Blood* *129*, 2002–2012.
- Yan, H., Hale, J., Jaffray, J., Li, J., Wang, Y., Huang, Y., An, X., Hillyer, C., Wang, N., Kinet, S., et al. (2018). Developmental differences between neonatal and adult human erythropoiesis. *Am. J. Hematol.* *93*, 494–503.
- Yu, W.M., Liu, X., Shen, J., Jovanovic, O., Pohl, E.E., Gerson, S.L., Finkel, T., Broxmeyer, H.E., and Qu, C.K. (2013). Metabolic regulation by the mitochondrial phosphatase PTPMT1 is required for hematopoietic stem cell differentiation. *Cell Stem Cell* *12*, 62–74.
- Yun, J., Mullarky, E., Lu, C., Bosch, K.N., Kavalier, A., Rivera, K., Roper, J., Chio, I.I., Giannopoulou, E.G., Rago, C., et al. (2015). Vitamin C selectively kills KRAS and BRAF mutant colorectal cancer cells by targeting GAPDH. *Science* *350*, 1391–1396.
- Zhang, Z.Z., Lee, E.E., Sudderth, J., Yue, Y., Zia, A., Glass, D., Deberardinis, R.J., and Wang, R.C. (2016). Glutathione depletion, pentose phosphate pathway activation, and hemolysis in erythrocytes protecting cancer cells from vitamin C-induced oxidative stress. *J. Biol. Chem.* *291*, 22861–22867.
- Zhao, B., Mei, Y., Yang, J., and Ji, P. (2016). Erythropoietin-regulated oxidative stress negatively affects enucleation during terminal erythropoiesis. *Exp. Hematol.* *44*, 975–981.

STAR★METHODS

KEY RESOURCES TABLE

| REAGENT or RESOURCE | SOURCE | IDENTIFIER |
|--|---|---------------------------------|
| Antibodies | | |
| Anti-hCD11b-PE (clone Bear1) | Beckman Coulter | Cat#IM2581U; RRID: AB_131334 |
| Anti-hCD13-PC7 (clone Immuno103.44) | Beckman Coulter | Cat#A46528 |
| Anti-hCD33 (clone D3HL60.251) | Beckman Coulter | Cat#A07775 |
| Anti-hCD34-FITC (clone 581) | Becton Dickinson | Cat#55582; RRID:AB_396150 |
| Anti-hCD34-APC (clone 581) | Becton Dickinson | Cat#555824; RRID:AB_398614 |
| Anti-hCD34-PE (clone 81) | Beckman Coulter | Cat#A07776 |
| Anti-hCD36-APC (clone FA6.152) | Beckman Coulter | Cat#A87786 |
| Anti-hCD36-FITC (clone FA6.152) | Beckman Coulter | Cat#B49201; RRID:AB_2848117 |
| Anti-hCD36-PB (clone FA6.152) | Beckman Coulter | Cat#B43302 |
| Anti-hCD49d-APC (clone HP2/1) | Beckman Coulter | Cat#B01682 |
| Anti-hCD71-APC (clone MA-A712) | Becton Dickinson | Cat#551374; RRID:AB_398500 |
| Anti-hCD71-APC-AF750 (clone MA-A712) | Beckman Coulter | Cat#A89313; RRID:AB_2800452 |
| Anti-hCD105- PECE594 (clone 266) | Becton Dickinson | Cat#562380; RRID:AB_11154054 |
| Anti-hGlyA-PC7 (clone 11E4B-7-6) | Beckman Coulter | Cat#A71564; RRID:AB_2800449 |
| Anti-hGlyA-APC (clone GA-R2 (HIR2)) | eBioscience/ThermoFisher | Cat#17-9987-42; RRID:AB_2043823 |
| Anti-hGlyA- BV421 (clone GA-R2 (HIR2)) | Becton Dickinson | Cat#562938 |
| Anti-hIL3R-PC7 (clone 6H6) | eBioscience/ThermoFisher | Cat#25-1239-42; RRID:AB_1257136 |
| Goat anti-Rabbit IgG Alexa Fluor 405 | Molecular Probes/ThermoFisher | Cat#A-31556; RRID:AB_221605 |
| GLUT1 RBD-GFP | Metafora Biosystems | Cat#GLUT1_G100 |
| GLUT1 RBD-rFc | Metafora Biosystems | Cat#GLUT1_R100 |
| Bacterial and virus strains | | |
| Top 10 Competent cells | ThermoFisher | Cat#C404010 |
| Biological samples | | |
| Human umbilical cord blood | Unité De Thérapie Cellulaire de Montpellier | N/A |
| Human peripheral blood | New York Blood Center | N/A |
| Human bone marrow | Northwell Health | N/A |
| Chemicals, peptides, and recombinant proteins | | |
| 2-Phospho-L-ascorbic acid | Sigma-Aldrich | Cat#A8960 |
| tetramethylchromane-2-carboxylic acid (TROLOX) | Sigma-Aldrich | Cat#238813 |
| N-Acetylcysteine | Sigma-Aldrich | Cat#A9165 |
| Ascorbate Oxidase from Cucurbita sp. | Sigma-Aldrich | Cat#A0157 |
| L-Ascorbic acid | Sigma-Aldrich | Cat#A92902 |
| O-(Carboxymethyl)hydroxylamine hemihydrochloride (AOA) | Sigma-Aldrich | Cat#C13408 |
| Diethylsuccinate | Sigma-Aldrich | Cat#112402 |
| Dimethyl α -ketoglutarate | Sigma-Aldrich | Cat#349631 |
| L-Glutathione reduced | Sigma-Aldrich | Cat#G4251 |
| MitoParaquat | Abcam | Cat#ab146819 |
| Spautin-1 | Sigma-Aldrich | Cat#SML0440 |
| Tri-sodium Citrate dihydrate | Sigma-Aldrich | Cat#S4641 |
| C13-GlutamineL-Glutamine (13C5,15N2) | Cambridge Isotope Laboratories | Cat#CNLM-1275-H-PK |

(Continued on next page)

| <i>Continued</i> | | |
|---|--------------------------------|----------------------------------|
| REAGENT or RESOURCE | SOURCE | IDENTIFIER |
| L-[3,4- ³ H(N)]-Glutamine | Perkin Elmer | Cat#NET551250UC |
| Oligomycin | Sigma-Aldrich | Cat#O4876 |
| FCCP | Sigma-Aldrich | Cat#C2920 |
| Rotenone | Sigma-Aldrich | Cat#R8875 |
| Antimycin A | Sigma-Aldrich | Cat#A8674 |
| DMSO | Sigma-Aldrich | Cat#D2650 |
| Human recombinant IL-3 | R&D Systems | Cat#203-IL-010 |
| Human recombinant IL-6 | R&D Systems | Cat#206-IL-010 |
| rhuSCF | Amgen | N/A |
| Stem Spam CC100 | Stem Cell | Cat#02690 |
| EPREX | Janssen | Cat#3400936992368 |
| Human holo-transferrin | Sigma-Aldrich | Cat#T0665 |
| Human insulin solution | Sigma-Aldrich | Cat#9278 |
| Heparin | Sanofi | Cat#3400930484500 |
| Bovine serum albumin | Sigma-Aldrich | Cat#A8806 |
| IMDM | Life Technologies/ThermoFisher | Cat#21980032 |
| StemSpam SFEM | Stem Cell | Cat#09650 |
| StemSpam H3000 | Stem Cell | Cat#09850 |
| RPMI w/o glutamine and glucose | Pan Biotech | Cat#P04-17550 |
| Seahorse XF Assay Medium | Agilent Technologies | 102365-100 |
| Seahorse XF Calibrant Solution | Agilent Technologies | 100840-000 |
| Ultima Gold liquid scintillation cocktail | Perkin Elmer | Cat#6013329 |
| <i>Critical commercial assays</i> | | |
| Anti-hCD34 MicroBead kit | Miltenyi Biotec | Cat#130-046-702; RRID:AB_2848167 |
| RNeasy Mini kit | QIAGEN | Cat# 74104 |
| QuantiTect™ Reverse Transcription Kit | QIAGEN | Cat# 205311 |
| <i>Experimental models: cell lines</i> | | |
| Jurkat E6-1 | ATCC | TIB-152 |
| 293 T cells | ATCC | CRL-3216 |
| <i>Oligonucleotides</i> | | |
| IDH1 forward: 5'-GGGTTGGCCTTTGTATCTGA-3' | IDT | Custom order |
| IDH1 reverse: 5'-TTTACAGGCCAGATGAAGC-3' | IDT | Custom order |
| IDH2 forward: 5'-TGGCTCAGGTCCTCAAGTCT-3' | IDT | Custom order |
| IDH2 reverse: 5'-CTCAGCCTCAATCGTCTTCC-3' | IDT | Custom order |
| IDH3a forward: 5'-GCGCAAACATTTGACCTTT-3' | IDT | Custom order |
| IDH3a reverse: 5'-TGCACGACTCCATCAACAAT-3' | IDT | Custom order |
| TET2 forward: 5'-AGCAGCAGCCAATAGGACAT-3' | IDT | Custom order |
| TET2 reverse: 5'-AGGTTCTGTCTGGCAAATGG-3' | IDT | Custom order |
| βactin forward: 5'-GTCTCCCTCCATCGTG-3' | IDT | Custom order |
| βactin reverse: 5'-TTCTCCATGTCGTCAG-3' | IDT | Custom order |

(Continued on next page)

Continued

| REAGENT or RESOURCE | SOURCE | IDENTIFIER |
|-----------------------------------|-------------------------------|---|
| Recombinant DNA | | |
| TRC2pLKO sh Tet2 | Sigma Aldrich | Cat# TRCN0000418976 |
| TRC2pLKO sh IDH1 | Sigma Aldrich | Cat# TRCN0000312463 |
| TRC1pLKO sh IDH1 | Sigma Aldrich | Cat# TRCN0000027284 |
| TRC1pLKO sh non-mammalian control | Sigma Aldrich | Cat# SHC002 |
| Software and algorithms | | |
| FlowJo (version 10) | BD Biosciences | https://www.flowjo.com/ |
| Prism (version 8) | GraphPad Software | https://www.graphpad.com/scientific-software/prism/ |
| Wave (version 2) | Agilent Technologies | https://www.agilent.com/en/product/cell-analysis/real-time-cell-metabolic-analysis/xf-software/seahorse-wave-desktop-software-740897 |
| Xcalibur 2.2 | ThermoFisher | http://www.casco-documentation.com/content/dam/tfs/ATG/CMD/cmd-documents/oper/oper/ms/lc-ms/soft/Man-XCALI-97209-Xcalibur-22-Acquisition-ManXCALI97209-D-EN.pdf |
| LCquan 2.7 | ThermoFisher | https://assets.thermofisher.com/TFS-Assets/CMD/manuals/LCquan-Admin-2-7.pdf |
| TraceFinder 4.1 | ThermoFisher | https://www.thermofisher.com/us/en/home/industrial/mass-spectrometry/liquid-chromatography-mass-spectrometry-lc-ms/lc-ms-software/lc-ms-data-acquisition-software/tracefinder-software.html |
| Other | | |
| CM-H2DCFDA | Molecular Probes/Thermofisher | Cat#C6827 |
| Dihydrorhodamine 123 | Molecular Probes/Thermofisher | Cat#D23806 |
| Mitotracker Deep Red FM | Molecular Probes/Thermofisher | Cat#M22426 |
| MitoTracker Green FM | Molecular Probes/Thermofisher | Cat#M7514 |
| MitoTracker Red CMXRos | Molecular Probes/Thermofisher | Cat#M7512 |
| MitoSox Red | Molecular Probes/Thermofisher | Cat#M36008 |
| Propidium Iodide | Sigma-Aldrich | Cat#P4170 |
| Syto16 | Molecular Probes/Thermofisher | Cat#S7578 |
| Syto60 | Molecular Probes/Thermofisher | Cat#S11342 |

RESOURCE AVAILABILITY

Lead contact

Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Naomi Taylor (taylor4@mail.nih.gov).

Materials availability

This study did not generate new unique reagents. All lentiviral vectors generated in this study are available on request.

Data and code availability

This study did not generate datasets or code.

EXPERIMENTAL MODELS AND SUBJECT DETAILS

CD34⁺ cell isolation and *ex vivo* differentiation assays.

All studies involving human samples were conducted in accordance with the declaration of Helsinki. CD34⁺ cells were isolated from umbilical cord blood within 24h of vaginal delivery of full-term infants after informed consent and approval by the “Committee for the Protection of Persons” (IRB) of the University Hospital of Montpellier. Peripheral blood from leukoreduction filters and bone marrow were obtained from deidentified donors at the New York Blood Center and the North Shore-LIJ Health System, respectively, after informed consent and approval from the respective IRBs. Approximately 60 UCB, 10 PB and 6 BM samples were used in this study. Samples did not contain any identifiers including sex, race, or ethnic origin. All samples were split such that they were used in all experimental groups. As such, there was no need to use any specific criteria to allocate biological samples to experimental groups. For the vast majority of experiments, at least 3 biological samples were used. For experiments presented in [Figures 1A, 6F, and 6G](#), 2 biological samples were employed and technical triplicates were evaluated for both samples.

CD34⁺ cells (1×10^5 cells/ml) were expanded in StemSpan H3000 media (StemCell Technologies Inc) supplemented with StemSpan CC100 (StemCell Technologies Inc) at 37°C with a humidified 5% CO₂ atmosphere. Cells were plated in 24-well *Nunc* Delta surface plates (*Nunc, Thermo Fisher Scientific*). After 4 days of expansion, cells were differentiated in IMDM medium (Invitrogen) supplemented with human holo-transferrin (200 mg/L, Sigma-Aldrich), human insulin (10 mg/L, Sigma-Aldrich), rhuSCF (10 ng/ml, Amgen), rhulL-3 (1 ng/ml, R&D Systems). Erythropoiesis was induced by addition of 3 U/ml recombinant human erythropoietin (rEPO; Eprex, Janssen-Cilag). In some experiments, CD34⁺ cells were not expanded and erythropoiesis was directly induced after selection (data in [Figure 5](#)). Cytokines were supplemented every 3-4 days at the same time that media was renewed. Cells were centrifuged at 300 g for 10min at RT and then resuspended in fresh media to maintain cell concentrations between 0.1 and 1.5×10^6 cells/ml. In some experiments, progenitors were differentiated in the presence of 3.5 mM cell permeable dimethyl α -ketoglutarate (DMK, Sigma-Aldrich), 5 mM diethylsuccinate (Sigma Aldrich), 8 mM citrate (Sigma-Aldrich), 1 mM aminooxyacetate (AOA, Sigma-Aldrich), 50 μ M MitoParaquat (MitoPQ, Abcam), 1 mM L-ascorbic acid (AA, Sigma-Aldrich), 100 μ M 2-phospho-L-ascorbic acid (Vit C, Sigma-Aldrich), 100 μ M N-acetylcysteine (NAC, Sigma-Aldrich), 100 μ M reduced glutathione (GSH, Sigma-Aldrich), 100 μ M of the water-soluble analog of vitamin E (TROLOX, Sigma Aldrich), or 10 μ M of specific and potent autophagy inhibitor-1 (Spautin-1, Sigma-Aldrich). Ascorbate oxidase (1 U/mL, Sigma-Aldrich) was used to completely oxidize L-ascorbic acid to DHA in culture medium before treating the cells. Drugs were freshly added after every media change. In experiments where cells were co-cultured with α -KG (DMK, 3.5 mM) in the presence of antioxidants, α -KG was administered 2 hours after the addition of the corresponding antioxidant. As MitoPQ and TROLOX were dissolved in DMSO, control conditions included cultures using the same concentration of DMSO (0.05 and 0.1%, respectively).

METHODS DETAIL

Cytospin preparation

Cytospins were prepared on glass slides (5×10^4 cells in 200 μ L of PBS), using the Thermo Scientific Shandon 4 Cytospin (300 g for 5 min). Slides were stained with May-Grünwald solution (Sigma-Aldrich) for 5 min, rinsed in 40 mM Tris buffer for 90 s, and subsequently stained with Giemsa solution (Sigma-Aldrich) for 15 minutes. Cells were imaged using a Leica DM2000 inverted microscope under 100 \times objective magnification.

Flow cytometry

Expression of the CD34, CD36, CD49d, CD71, CD105 ([Ashley et al., 2020](#)), Glycophorin A, IL3R, CD11b, CD13, and CD33 surface markers was monitored on $1\text{--}2 \times 10^5$ cells using the appropriate fluorochrome-conjugated monoclonal antibodies at a 1:100 dilution (mAb), except for CD36-APC and CD71-AF750 mAbs that were used at a 1:200 and 1:500 dilution, respectively (Beckman Coulter, Becton Dickinson, eBiosciences), in a total volume of 100 μ l as previously described ([Hu et al., 2013](#); [Schulz et al., 2019](#)). Cells were incubated in the dark for 20 minutes in PBS containing 2% FBS at 4°C and then washed once in the same medium at 300 g for 10 min prior to evaluation. GLUT1 expression was monitored by binding to its retroviral envelope ligand (RBD) fused to eGFP (1:25 dilution in 50 μ l; Metafora biosystems) or to the RBD-rFc fusion protein (1:25 dilution in 50 μ l) for 30 minutes in PBS containing 2% FBS at 37°C followed by staining with an Alexa Fluor 405-coupled anti-rabbit IgG antibody (1:100 dilution in 100 μ l) at 4°C as previously reported ([Kim et al., 2004](#); [Kinet et al., 2007](#); [Manel et al., 2003](#); [Swainson et al., 2005](#)). Mitochondrial biomass was assessed in a total volume of 50 μ l by MitoTrackerGreen or MitoTrackerDeepRed staining (20 nM; Invitrogen, Molecular Probes), while mitochondrial transmembrane potential levels were monitored by staining with MitoTrackerRed (50 nM; Invitrogen, Molecular Probes). Mitochondrial superoxide production, mitochondrial ROS levels and total ROS levels were assessed by staining with MitoSOX, Dihydro-odamine 123 and CM-H2DCFDA, respectively (5 μ M; Invitrogen, Molecular Probes). Incubations were performed in the dark for 20 minutes in PBS + 2% FBS at RT. Enucleation was evaluated by staining with the SYTO16 or SYTO60 nucleic acid stain (1 μ M and 0.5 μ M, Invitrogen, Molecular Probes) for 15 minutes in PBS + 2% FBS at RT. Cell cycle analysis was performed by staining for DNA using 50 μ g/mL propidium iodide (PI; Sigma-Aldrich) following permeabilization in 100 μ l of 0.1% Triton X-100. To assess cell death, cells were incubated with PI (10 μ g/ml). Cell sorting was performed on a FACSAria high-speed cell sorter (BD

Biosciences) and analyses were performed on a FACS-Canto II (BD Biosciences) cytometers. A minimum of 10,000 events were recorded for each staining. Data analyses were performed using FlowJo software (Tree Star, Ashland, OR).

Virus production and transduction of CD34⁺ progenitor cells

Lentiviral pLKO.1 plasmids harboring shRNAs directed against *IDH1* (shRNA IDH1-1: Clone ID: TRCN0000027284 and shRNA IDH1-2: ID: TRCN0000312463) and lentiviral TRC2-pLKO plasmid harboring shRNA against TET2 (ID: TRCN0000418976) (Yan et al., 2017) were obtained from Sigma-Aldrich. Cells were transduced with the shRNA IDH1-1 lentiviral plasmid, the shRNA IDH1-2 plasmid or the shRNA TET2 plasmid where the 714bp sequence encoding for EGFP was inserted in place of the puromycin gene at the unique BamHI and KpnI restriction sites. Virions were generated by transient transfection of 293T cells (2–3 × 10⁶ cells/100mm plate in 7 mL DMEM) with these vectors (10 mg) together with the Gag-Pol packaging construct PsPax2 (5 mg) and a plasmid encoding the VSV-G envelope, pCMV-VSV-G (2.5 mg), as described previously (Loisel-Meyer et al., 2012). Cells were transfected for at least 18 hours, and transfection efficiency was verified by monitoring GFP fluorescence by microscopy. Viral supernatant was harvested 24 hours post-transfection and virions were concentrated by overnight centrifugation at 4°C at 1,500 g (with no break). Virions were resuspended in approximately 20 μL of RPMI with 10% FBS (per plate of cells), aliquoted and stored at –80°C. Titers were determined by serial dilutions of virus preparations on Jurkat cells and are expressed as Jurkat transducing units (TU/ml).

Prior to transduction of CD34⁺ hematopoietic stem and progenitor cells (HSPCs), cells were expanded for 3 days in StemSpan medium (Stem cell Technologies Inc) supplemented with 5% fetal bovine serum (FBS), 25 ng/ml rhuSCF (Amgen), 10 ng/ml rhull-3 and 10 ng/ml rhull-6 (R&D) at 37°C with a humidified 5% CO₂ atmosphere. 5 × 10⁵ cells were then exposed to viral supernatants containing 4.8 × 10⁵ TU to 9.9 × 10⁵ TU (representing a multiplicity of infection of 1–2). After 72h of transduction, CD34⁺ cells (1 × 10⁵ cells/ml) were cultured in presence of rEPO (3 U/ml) to induce erythropoiesis. Transduction efficiency was monitored as a function of GFP expression or after puromycin selection at 72h post-transduction, as per the lentiviral vector. In some experiments, cells were transduced at day 4 of erythroid differentiation (i.e., at day 4 following addition of EPO) under the same conditions as described above, and transduction efficiency was monitored at day 7 of differentiation.

Quantitative real time PCR

Total RNA was isolated at the indicated time points and cDNA was synthesized using the RNeasy Mini kit and the QuantiTect™ Reverse Transcription Kit (QIAGEN) as per the manufacturer's instructions. Quantitative PCR of cDNAs was performed using the Quantitect SYBR green PCR Master mix (Roche) with 10 ng of cDNA (by NanoDrop) and 0.5 μM primers in a final volume of 10 μL. Primer sequences are as follows: *IDH1*: 5'-GGGTTGGCCTTTGTATCTGA-3' (forward) / 5'-TTTACAGGCCAGATGAAGC –3' (reverse); *IDH2*: 5'-TGGCTCAGGTCCTCAAGTCT-3' (forward) / 5'-CTCAGCCTCAATCGTCTTCC-3' (reverse); *IDH3a*: 5'-GCGCAAAA CATTGACCTTT-3' (forward) / 5'-TGCACGACTCCATCAACAAT-3' (reverse); *TET2*: 5'-AGCAGCAGCCAATAGGACAT-3' (forward) / 5'-AGGTTCTGTCTGGCAAATGG-3' (reverse); and β -actin: 5'-GTCTTCCCCTCCATCGTG-3' (forward) / 5'-TTCTCCATGTCGTCCC AG-3' (reverse). Amplification of cDNAs was performed using the LightCycler 480 (Roche). Cycling conditions included a denaturation step for 5 min at 95°C, followed by 40 cycles of denaturation (95°C for 10 s), annealing (63°C for 10 s) and extension (72°C for 10 s). After amplification, melting curve analysis was performed with denaturation at 95°C for 5 s and continuous fluorescence measurement from 65°C to 97°C at 0.1°C/s. Each sample was amplified in triplicate. Data were analyzed by LightCycler® 480 Software (Version 1.5) and Microsoft Excel. Relative expression was calculated by normalization to β -actin as indicated (delta-Ct). Real-time PCR CT values were analyzed using the 2(-Delta Delta C(T)) method to calculate fold expression (ddCt).

Mass spectrometry (LC-MS)

For profiling of intracellular metabolites, 10⁶ cells were incubated in IMDM medium without glutamine and were supplemented with 2mM uniformly labeled ¹³C₅-¹⁵N₂ glutamine (Cambridge Isotope Laboratories) for 6 hours (Figure 1A) or 18 hours (Figures 6F and 6G). Cells were rapidly washed in ice-cold PBS, centrifuged twice (400 g for 4 min), and metabolites were extracted in a solution of 50% methanol, 30% acetonitrile, 20% water after shaking for 20 min at 4°C. The solutions were then recentrifuged for 10 min at 16,000 g at 4°C. The volume of the extraction solution was adjusted to achieve a constant ratio of 2 × 10⁶ cells/ml. Alternatively, the peak areas resulting from the intracellular samples were normalized to the number of cells obtained at the end of the incubation period in parallel wells. Supernatants were stored at –20°C until analysis. Samples were analyzed by HPLC-MS as described previously (Vande Voorde et al., 2019). Data were analyzed with Xcalibur 2.2, LCQuan 2.7 and TraceFinder 4.1 software (Thermo scientific). Samples were performed in triplicate, and at least 2 different biological samples were evaluated for each condition.

Seahorse analysis

Oxygen consumption rates (OCR) and extracellular acidification rates (ECAR) were measured using the XFe-96 Extracellular Flux Analyzer (Seahorse Bioscience, Agilent). The calibration plate was filled with 200 μL Milli-Q water per well and kept at 37°C overnight. At least 2 hours prior to the assay, water was replaced by 200 μL XF calibrant (Agilent)/ well. Culture plates were treated with 20 μL/well of 0.1mg/mL of Poly-D-Lysine for at least 1 hour at RT. Poly-D-Lysine (Sigma-Aldrich) solution was then removed and plates was washed twice with 200 μL Milli-Q water/well, dried, and kept at 4°C until the assay was performed. Cells (2.5 × 10⁵) were placed in 50 μL XF medium (non-buffered DMEM containing 10 mM glucose and 2 mM GlutaMax, pH 7.3–7.4, Agilent), centrifuged in a carrier tray (300 g for 3min with no break), and incubated for 30 min at 37°C. An additional 130 μL XF medium was added during the

calibration time (20–30 min at 37°C). Cells were monitored in basal conditions and in response to oligomycin (1 μM; Sigma-Aldrich), FCCP (1 μM; Sigma-Aldrich), rotenone (100 nM, Sigma-Aldrich) and antimycin A (1 μM; Sigma-Aldrich). In some experiments, αKG (DMK, final concentration of 3.5 mM) was injected directly into the well before the sequential addition of oligomycin, FCCP, rotenone and antimycin A during the Mito Stress Test. Wave software (Agilent) was employed for running the Seahorse assay and analysis. Samples were performed at least in triplicate and generally 5–6 points per experiment and at least 3 independent experiments.

Glutamine uptake assays

Cells (5×10^5) were washed twice in 1.5 mL of PBS containing 2% FBS at 400 g for 4 min at RT, and starved for glutamine by incubation at 37°C in 30 μl glutamine-free RPMI for 30 min. Radiolabeled glutamine-L-[3,4-³H(N)] (Perkin Elmer) was added to a final concentration of 0.5 μM (0.5 μCi/mL in a total volume of 50 μL). Cells were incubated for 10 min at room temperature, washed twice in cold PBS containing 2% FBS (1000 g, 3 min), and solubilized in 500 μL of a 0.1% SDS solution. Radioactivity was measured in 4.5 mL liquid scintillation (Perkin Elmer) using a Hidex 300 SL counter. Each independent experiment was performed in triplicate.

QUANTIFICATION AND STATISTICAL ANALYSIS

Data are represented as individual values or means. Error bars represent the standard error of the mean (SEM). Data were analyzed with GraphPad Software (GraphPad Prism), and *P*-values were determined by one-way ANOVA (Tukey's post hoc test) or *t* tests, as indicated in the corresponding text and figure legends. Two-tailed *t* tests were used in all figures except for Figure 6F where a one-tailed *t* test was used. Tests were paired or unpaired as indicated and a normal distribution was used in all experiments. All statistical details of experiments can be found in the figure legends. Significance is indicated as * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ and **** $p < 0.0001$ as evaluated by GraphPad. The graphical abstract was created using BioRender and Servier Medical Art.

Supplemental Information

An IDH1-vitamin C crosstalk drives human erythroid development by inhibiting pro-oxidant mitochondrial metabolism

Pedro Gonzalez-Menendez, Manuela Romano, Hongxia Yan, Ruhi Deshmukh, Julien Papoin, Leal Oburoglu, Marie Daumur, Anne-Sophie Dumé, Ira Phadke, Cédric Mongellaz, Xiaoli Qu, Phuong-Nhi Bories, Michaela Fontenay, Xiuli An, Valérie Dardalhon, Marc Sitbon, Valérie S. Zimmermann, Patrick G. Gallagher, Saverio Tardito, Lionel Blanc, Narla Mohandas, Naomi Taylor, and Sandrina Kinet

Supplemental Information

An IDH1-vitamin C crosstalk drives human erythroid development by inhibiting pro-oxidant mitochondrial metabolism

Pedro Gonzalez-Menendez, Manuela Romano, Hongxia Yan, Ruhi Deshmukh, Julien Papoin, Leal Oburoglu, Marie Daumur, Anne-Sophie Dumé, Ira Phadke, Cédric Mongellaz, Xiaoli Qu, Phuong-Nhi Bories, Michaela Fontenay, Xiuli An, Valérie Dardalhon, Marc Sitbon, Valérie S. Zimmermann, Patrick G. Gallagher, Saverio Tardito, Lionel Blanc, Narla Mohandas, Naomi Taylor and Sandrina Kinet

Supplemental Information Titles

Supplemental Figure 1. **Ex vivo erythroid differentiation of human CD34⁺ progenitors is associated with a loss in oxidative phosphorylation.** Related to Figure 1.

Supplemental Figure 2. **α KG does not alter mitochondrial function during early stages of erythropoiesis and other TCA cycle metabolites do not inhibit enucleation.** Related to Figure 2.

Supplemental Figure 3. **Impact of vitamin C on α KG- and MitoPQ-induced oxidative stress in erythroid progenitors.** Related to Figures 3 and 4.

Supplemental Figure 4. **Ascorbic acid as well as other ROS scavengers rescue erythroid progenitors from oxidative stress.** Related to Figure 4.

Supplemental Figure 5. **The impact of Vitamin C on enucleation is independent of autophagy but is dependent on transferrin uptake.** Related to Figures 4 and 5.

Supplemental Figure 6. **Downregulation of IDH1 does not alter erythroid commitment or early erythroblast generation.** Related to Figure 6.

Supplemental Figure 7. **Vitamin C but no other ROS scavengers rescues enucleation and decreases mitochondrial stress in IDH1-downregulated progenitors.** Related to Figure 7.

Supplemental Information

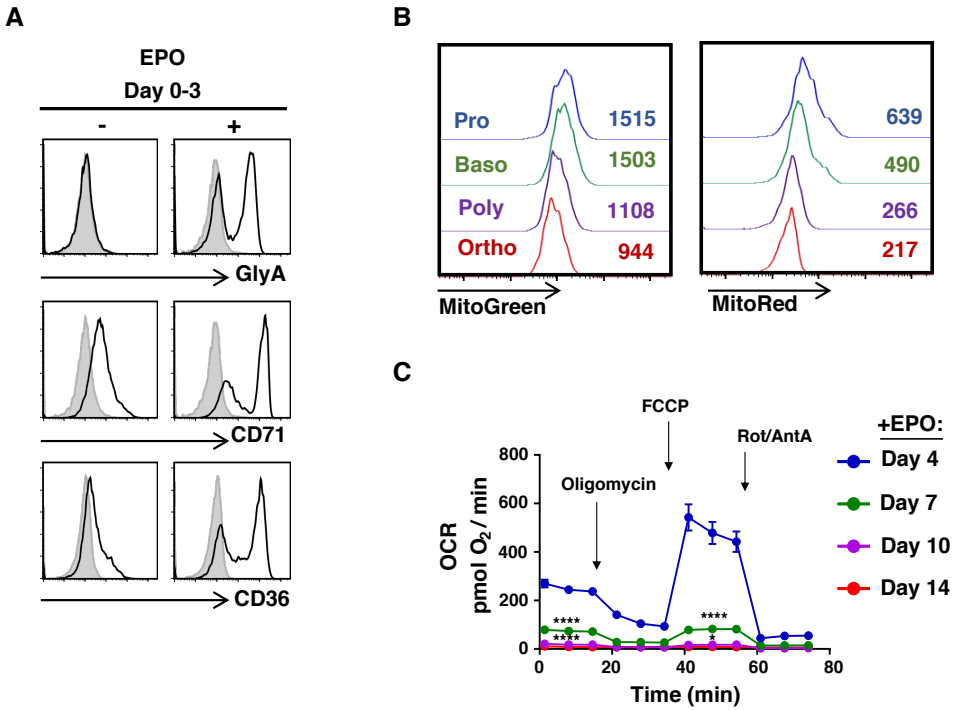


Figure S1. *Ex vivo* erythroid differentiation of human CD34⁺ progenitors is associated with a loss in oxidative phosphorylation. Related to Figure 1. (A) The phenotype of CD34⁺ progenitors differentiated in the absence (-) or presence (+) of recombinant erythropoietin (EPO). Representative histograms showing expression of GlyA, CD71, and CD36 are presented (data are representative of 1 of 10 independent experiments). **(B)** Representative histograms of mitochondrial biomass and polarization are shown for pro, basophilic, polychromatic, and orthochromatic erythroblasts, and mean levels are presented in Figure 1D. **(C)** CD34⁺ progenitors were differentiated in the presence of recombinant erythropoietin (EPO) and OCR, a measure of oxidative phosphorylation, was monitored at the indicated days of erythroid differentiation. Basal oxygen consumption, maximal consumption following FCCP, and minimal levels following inhibition of the electron transport chain with rotenone/antimycin A (Rot/AntA) are presented as means \pm SEM (n=6). ****p<0.0001

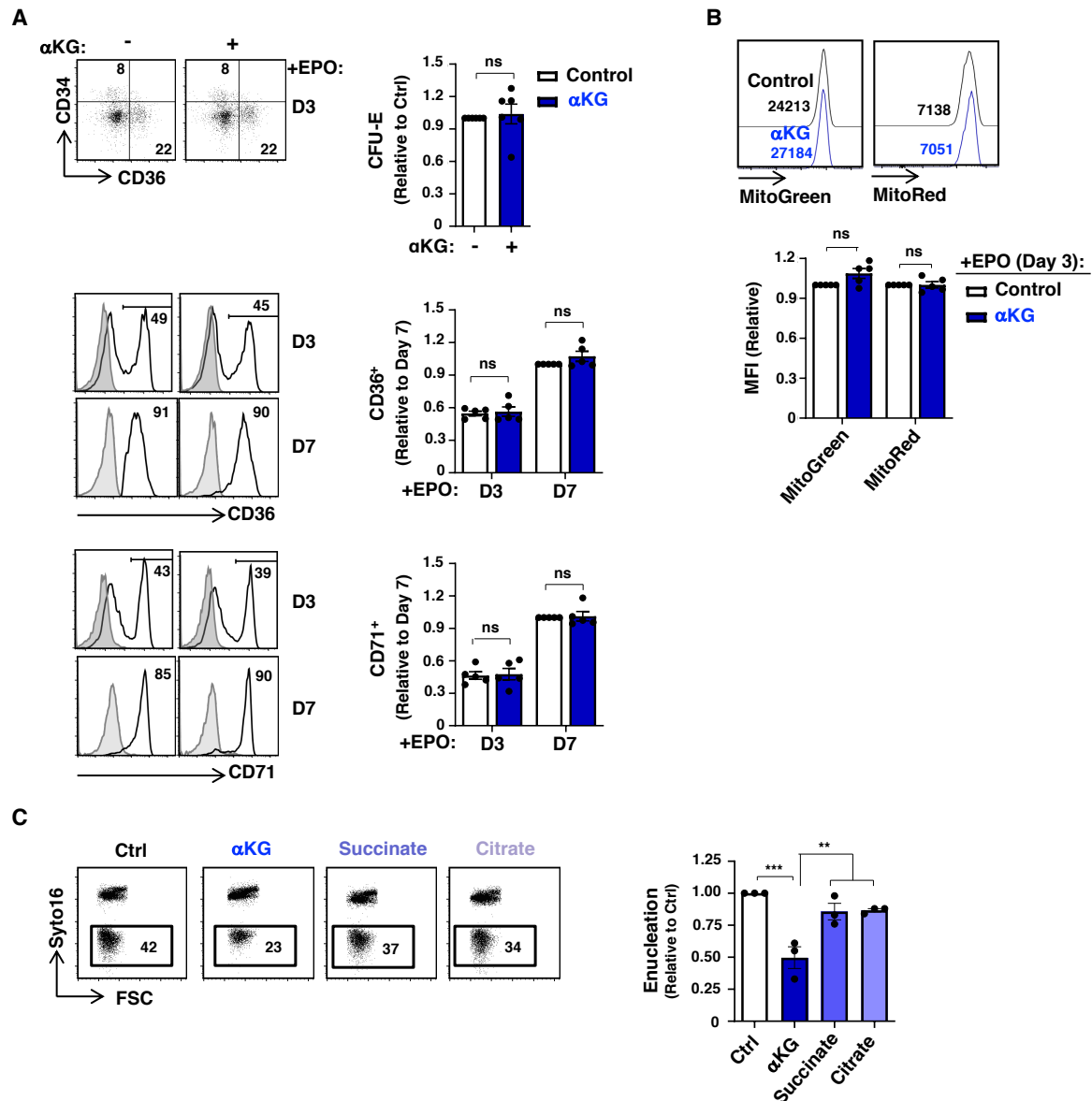


Figure S2. α KG does not alter mitochondrial function during early stages of erythropoiesis and other TCA cycle metabolites do not inhibit enucleation. Related to Figure 2. (A) The impact of α KG (3.5 mM) on early stages of erythropoiesis was evaluated at days 3 and 7 of EPO-induced differentiation. The induction of $CD36^+CD34^-$ CFU-E was monitored at day 3 and representative $CD34/CD36$ profiles as well as a quantification of the percentages of CFU-E relative to control are shown (top; $n=6$, non-significant, ns). Induction of $CD36$ (middle) and $CD71$ (bottom) during erythroid differentiation were monitored and representative histograms and quantifications ($n=4-5$) are presented (right). (B) Mitochondrial biomass and polarization were evaluated by flow cytometry and representative histograms as well as a quantification of MFI relative to control conditions are presented ($n=5$, bottom). (C) Differentiated erythroblasts were treated with α KG, succinate (5 mM) or citrate (8 mM) at day 7 and enucleation was evaluated at day 10 by Syto16 staining. Representative histograms (left) as well as means \pm SEM ($n=3$ independent experiments) are shown. ** $p<0.01$, *** $p<0.001$, ns, non-significant

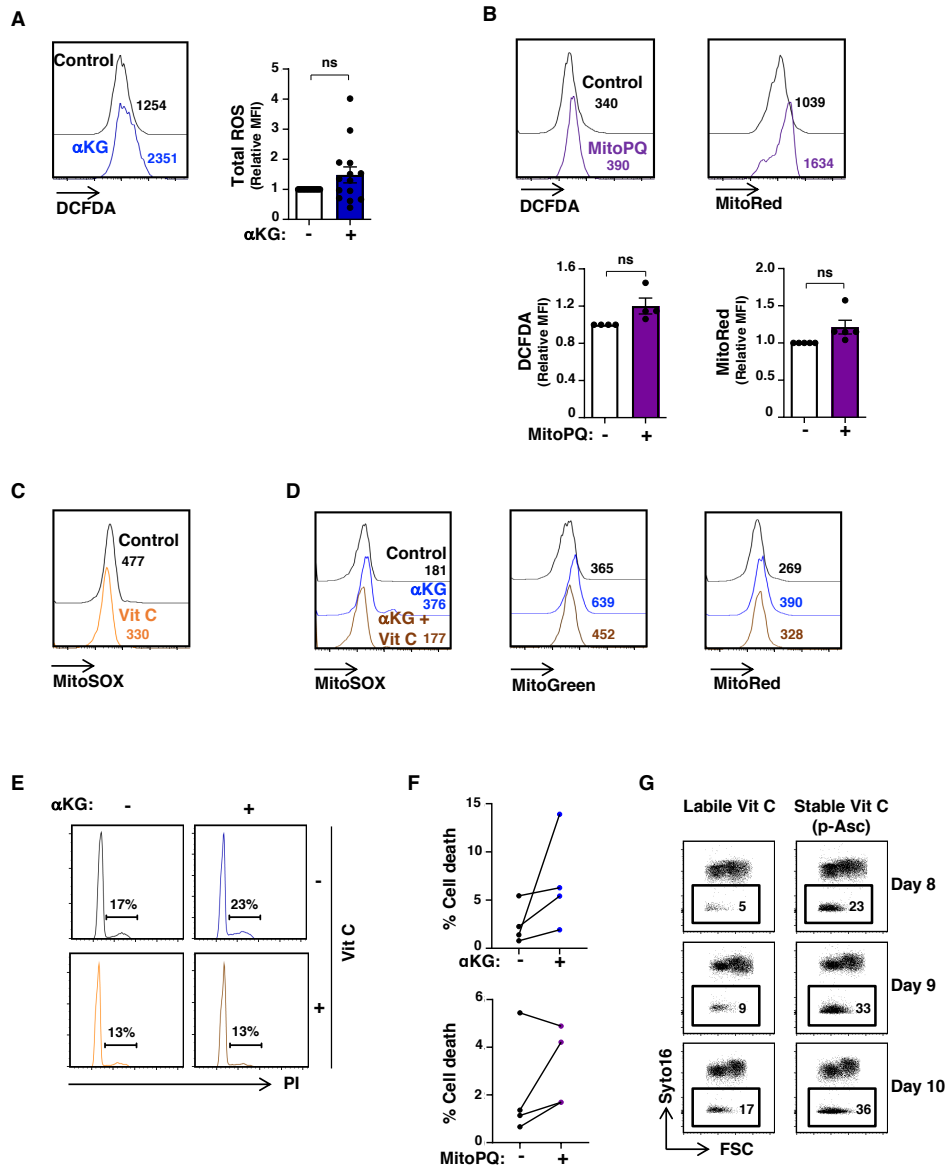


Figure S3. Impact of vitamin C on α KG- and MitoPQ-induced oxidative stress in erythroid progenitors. Related to Figures 3 and 4. (A) Total intracellular ROS levels were evaluated on erythroblasts differentiated from day 7-10 in the absence (control) or presence of α KG, as a function of CM-H2DCFDA staining. Representative histograms (left) and quantifications in 12 independent experiments (right) are shown. (B) Total ROS levels and mitochondrial polarization were evaluated in the absence or presence of MitoPQ and representative histograms (top) and MFI quantifications (bottom) are presented ($n=4$). (C) The impact of L-ascorbic acid 2-phosphate ($100\mu\text{M}$) was evaluated on the generation of mitochondrial superoxide between days 7 and 10 after EPO induction and representative histograms are shown with quantification provided in panel 4E. (D) The ability of Vit C to alter α KG-mediated increases in mitochondrial superoxide, biomass and membrane potential was evaluated by flow cytometry and representative histograms are shown. (E) Representative histograms of PI staining show the percentages of cells in S-G2/M of the cell cycle with quantifications provided in panel 4F. (F) Cell death was evaluated in the absence or presence of α KG (3.5mM , top) and MitoPQ ($50\mu\text{M}$, bottom) and data from 4 independent experiments are presented. (G) $\text{CD}34^+$ HSPCs were differentiated to the erythroid lineage by treatment with rEPO for 7 days. At day 7, erythroid cells were cultured in the presence of L-ascorbate and ascorbate 2-phosphate ($100\mu\text{M}$), presenting labile and stable vitamin C, respectively (Hata and Senoo, 1989). Enucleation was evaluated 24, 48 and 72h later; at days 8, 9, and 10 of differentiation, respectively. Representative dot plots of Syto16 staining are shown and the percentages of enucleated cells are indicated.

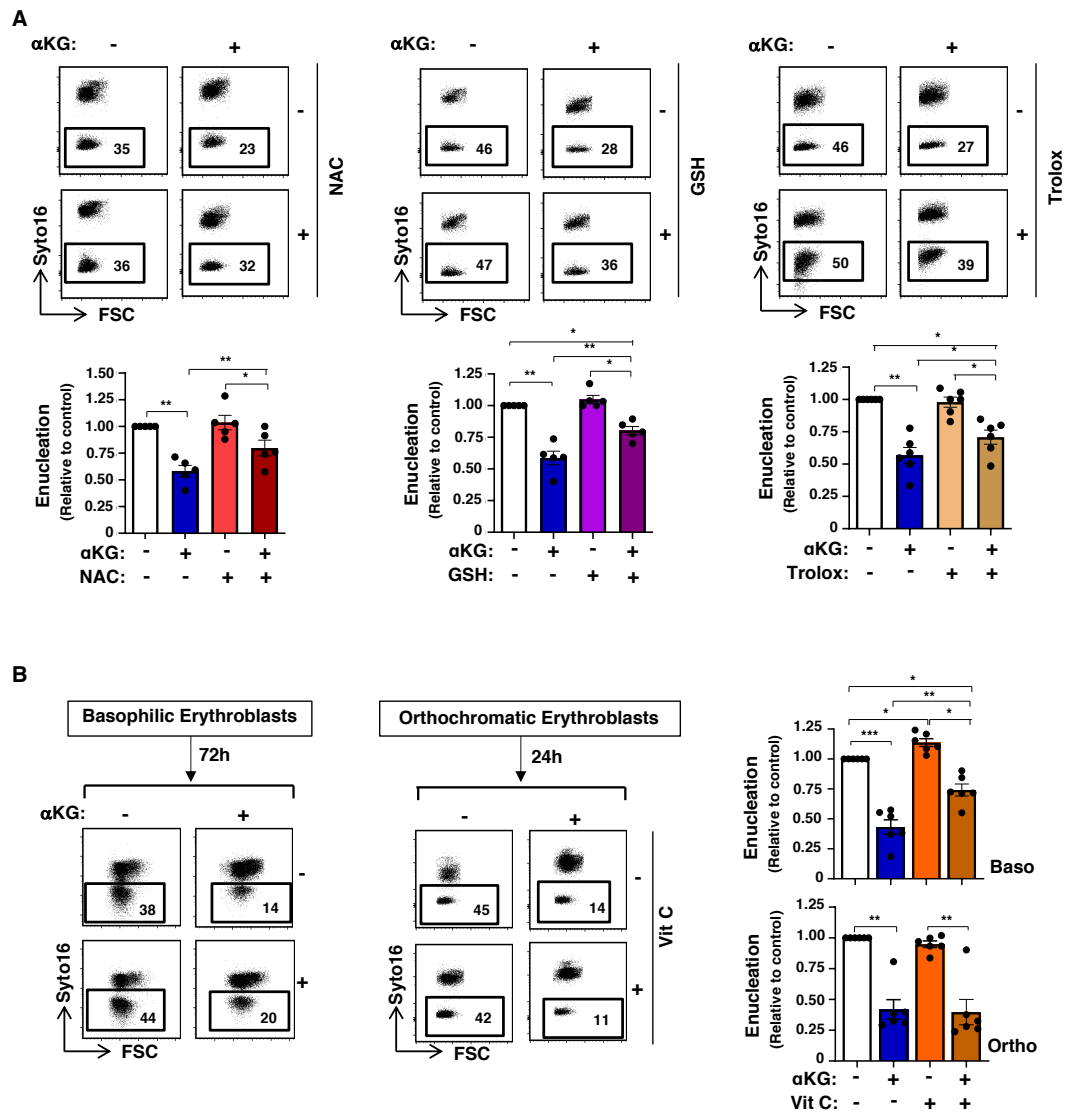


Figure S4. Ascorbic acid as well as other ROS scavengers rescue erythroid progenitors from oxidative stress. Related to Figure 4. (A) The impact of ROS scavengers on the α KG-mediated decrease in enucleation was evaluated for NAC (100 μ M, left), GSH (100 μ M, middle) and Trolox (100 μ M, right). Representative plots (top) and means \pm SEM of 5-6 independent experiments (bottom) are presented. (B) Early basophilic (left) and late orthochromatic (right) subsets were FACS-sorted and then differentiated for 72h or 24h, respectively, in the absence (-) or presence (+) of α KG and/or Vit C as indicated. Enucleation was evaluated by Syto16 staining and representative plots are presented (left). Enucleation in experimental groups was calculated relative to control conditions and mean levels are presented (right, n=6). ns, not significant; *p<0.05, ** p<0.01, ***p<0.001

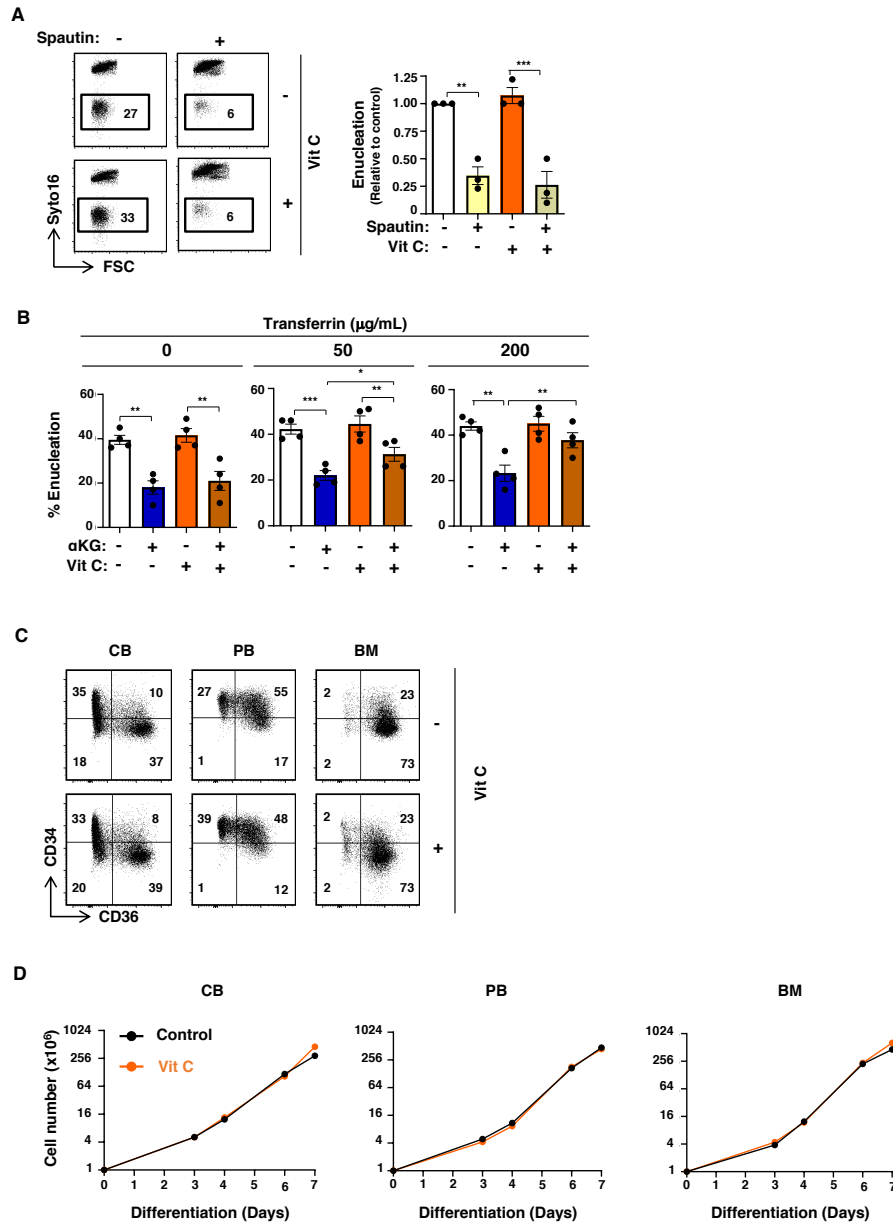


Figure S5. The impact of Vitamin C on enucleation is independent of autophagy but is dependent on transferrin uptake. Related to Figures 4 and 5. (A) The impact of Vit C on erythroid enucleation under conditions of a Spautin (10 µM)-mediated inhibition of autophagy was evaluated at day 10 of erythroid differentiation. Representative plots (left) and means ± SEM of 3 independent experiments (right) are shown. (B) Erythroblasts were differentiated in the absence or presence of transferrin (50 or 200 µg/ml), αKG (3.5mM) and Vit C (100µM) between days 7 and 10 of differentiation and enucleation was monitored by Syto16 staining. Means ± SEM of 4 independent experiments are presented. (C) CD34 HSPCs isolated from CB, PB, and BM were differentiated with EPO (+) in the absence (-) or presence of vitamin C (Vit C) for 4 days. The differentiation of CFU-E (CD34⁺CD36⁺) was monitored as a function of CD34/CD36 staining and representative plots are shown. (D) Growth of EPO-differentiated CB-, PB- and BM-derived progenitors was evaluated in the absence (-) or presence of vitamin C. Fold-increase at days 3, 4, 6 and 7 differentiation is shown for one representative experiment (n=2). *p<0.05, **p<0.01, ***p<0.001

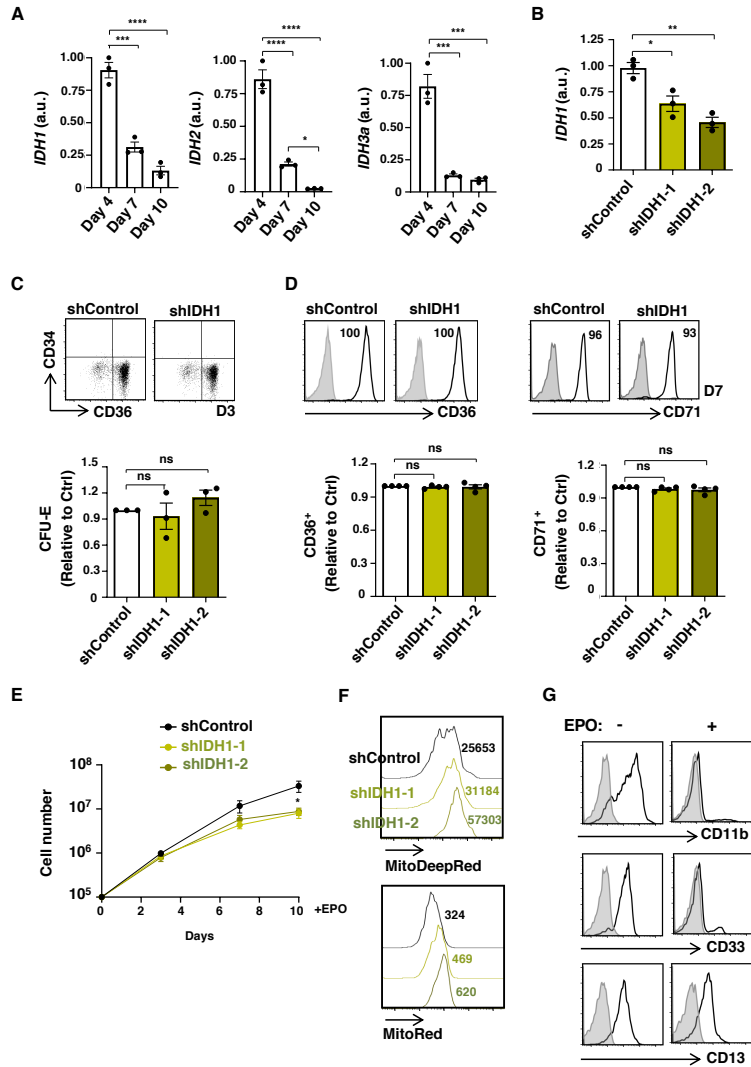


Figure S6. Downregulation of IDH1 does not alter erythroid commitment or early erythroblast generation. Related to Figure 6. (A) mRNA levels of IDH1, IDH2 and IDH3 were evaluated by qRT-PCR and means \pm SEM relative to β -actin are shown (technical triplicates, representative of 1 of 2 independent experiments). (B) The efficacy of the two shIDH1 vectors was evaluated by monitoring IDH1 mRNA levels by qRT-PCR. Mean levels \pm SEM relative to β -actin following transduction with shIDH1-1 and shIDH1-2 are presented. (C) Generation of CFU-E, defined as CD34⁺CD36⁺, were evaluated in shControl- and shIDH1-transduced progenitors at day 3 of differentiation. Representative dot plots (top) and quantification of the relative induction of CFU-E (bottom) are shown (n=3). (D) Differentiation of erythroblasts was evaluated by induction of the CD36 and CD71 markers and representative histograms (top) and quantifications (bottom) are shown (n=4). (E) The expansion of control and IDH1-downregulated progenitors was evaluated at the indicated day and means \pm SEM of 5 independent experiments are shown. (F) Representative histograms of MitoDeepRed (top) and MitoRed (bottom) staining in shControl- and shIDH1-transduced progenitors at day 10 of differentiation. (G) The phenotype of CD34⁺ progenitors expanded in the absence (-) or presence (+) of EPO is shown at day 7 of differentiation as a function of CD11b, CD33 and CD13 staining. Solid line and shaded histograms represent specific and non-specific staining, respectively. ns, non-significant; * p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

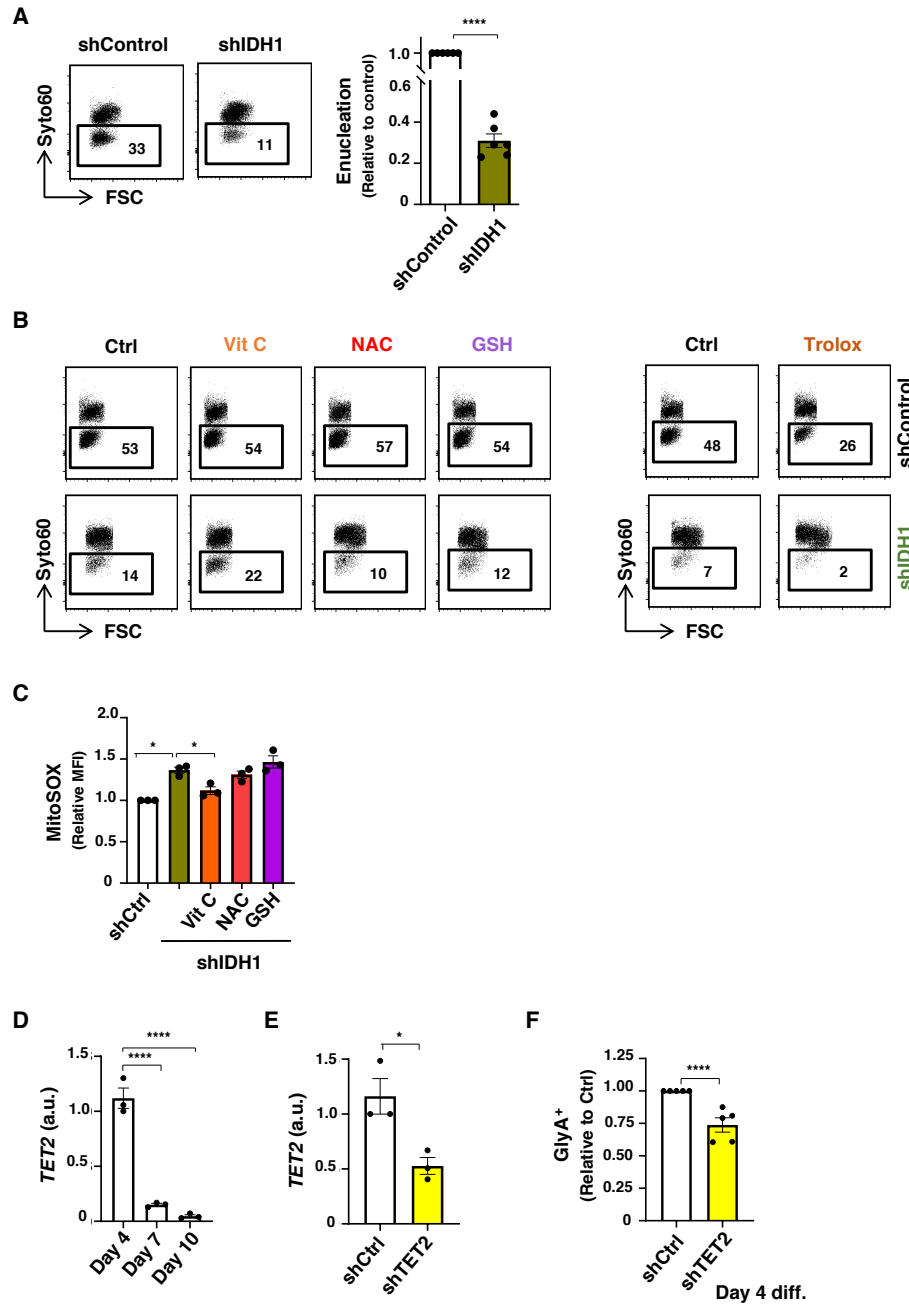


Figure S7. Vitamin C but no other ROS scavengers rescues enucleation and decreases mitochondrial stress in IDH1-downregulated progenitors. Related to Figure 7. (A) IDH1 was downregulated in erythroid progenitors (day 4) by transduction with shIDH1-encoding lentiviral particles and enucleation was monitored at day 10 of differentiation. Representative plots (left) and means \pm SEM (right) are presented ($n=6$, 1-way ANOVA with Tukey's post-hoc test). **(B)** The impact of ROS scavengers (Vit C, NAC, GSH and Trolox; 100 μ M) on the shIDH1-mediated decrease in enucleation was evaluated at day 10 of differentiation. Representative plots are presented ($n=2$). **(C)** The impact of Vit C, NAC, GSH and Trolox (with DMSO as a control) was evaluated on the shIDH1-mediated increase in MitoSOX at day 10. Means \pm SEM of 3 independent experiments are shown. **(D)** TET2 mRNA levels were evaluated at days 4, 7 and 10 of differentiation and means \pm SEM of 3 independent experiments are shown. **(E)** The shTET2-mediated downregulation of TET2 was evaluated by qRT-PCR and means \pm SEM relative to β -actin are shown. **(F)** The impact of shTET2 on erythroid development was evaluated at day 4 of differentiation as a function of GlyA staining. The relative levels of GlyA in 5 independent experiments were normalized to control progenitors. ns, not significant; * $p<0.05$, **** $p<0.0001$