Renal erythropoietin-producing cells (REPCs) remain in the kidneys of patients with chronic kidney disease, but these cells do not produce sufficient erythropoietin in response to hypoxic stimuli. Treatment with HIF stabilizers rescues erythropoietin production in these cells, but the mechanisms underlying the decreased response of REPCs in fibrotic kidneys to anemic stimulation remain elusive. Here, we show that fibroblast-like FOXD1+ progenitor-derived kidney pericytes, which are characterized by the expression of α1 type I collagen and PDGFRβ, produce erythropoietin through HIF2α regulation but that production is repressed when these cells differentiate into myofibroblasts. DNA methyltransferases and erythropoietin hypermethylation are upregulated in myofibroblasts. Exposure of myofibroblasts to nanomolar concentrations of the demethylating agent 5-azacytidine increased basal expression and hypoxic induction of erythropoietin. Mechanistically, the profibrotic factor TGF-β1 induced hypermethylation and repression of erythropoietin in pericytes; these effects were prevented by 5-azacytidine treatment. These findings shed light on the molecular mechanisms underlying erythropoietin repression in kidney myofibroblasts and demonstrate that clinically relevant, nontoxic doses of 5-azacytidine can restore erythropoietin production and ameliorate anemia in the setting of kidney fibrosis in mice.
DNA methyltransferase inhibition restores erythropoietin production in fibrotic murine kidneys

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Renal erythropoietin-producing cells (REPCs) remain in the kidneys of patients with chronic kidney disease, but these cells do not produce sufficient erythropoietin in response to hypoxic stimuli. Treatment with HIF stabilizers rescues erythropoietin production in these cells, but the mechanisms underlying the decreased response of REPCs in fibrotic kidneys to anemic stimulation remain elusive. Here, we show that fibroblast-like FOXD1+ progenitor-derived kidney pericytes, which are characterized by the expression of α1 type I collagen and PDGFRβ, produce erythropoietin through HIF2α regulation but that production is repressed when these cells differentiate into myofibroblasts. DNA methyltransferases and erythropoietin hypermethylation are upregulated in myofibroblasts. Exposure of myofibroblasts to nanomolar concentrations of the demethylating agent 5-azacytidine increased basal expression and hypoxic induction of erythropoietin. Mechanistically, the profibrotic factor TGF-β1 induced hypermethylation and repression of erythropoietin in pericytes; these effects were prevented by 5-azacytidine treatment. These findings shed light on the molecular mechanisms underlying erythropoietin repression in kidney myofibroblasts and demonstrate that clinically relevant, nontoxic doses of 5-azacytidine can restore erythropoietin production and ameliorate anemia in the setting of kidney fibrosis in mice.

Introduction
Low levels of plasma erythropoietin (EPO) that are disproportional to the degree of anemia are often observed in patients with chronic kidney disease (CKD) (1, 2). However, the oxygen-EPO-hemoglobin feedback loop is still operating, even if at a lower set point (3). Indeed, plasma EPO concentrations in patients with CKD decline after blood transfusion and measurably increase after hemorrhage, even while levels remain low to the point of anemia (4, 5). Although hepatocytes can produce EPO in patients with CKD after hemorrhage, it is possible that renal EPO-producing cells (REPCs) continue functioning in fibrotic kidneys, but their response to anemic stimulation decreases (6). A recent clinical trial studied an inhibitor of prolyl-hydroxylase domain (PHD) enzyme, FG-2216, which stabilizes HIFs independent of oxygen availability in hemodialysis (HD) patients and healthy volunteers (7). FG-2216 increases plasma EPO levels 30.8-fold in HD patients with fibrotic kidneys, 14.5-fold in anephric HD patients, and 12.7-fold in healthy volunteers, demonstrating that enhancement of HIFs can stimulate endogenous EPO production and retain REPC function in fibrotic kidneys (7).

REPCs, which have long projections between tubules and blood vessels, are detected in the interstitium (8–13). Lineage-tracing studies have revealed that the majority of REPCs in the healthy kidney are derived from myelin protein 0–expressing (PO-expressing) cells, which are positive for CD73 (also known as ecto-5′-nucleotidase), PDGFRβ, and p75 nerve growth factor receptor and negative for PECAM-1 (also known as CD31) (11). In kidney fibrosis induced by unilateral ureteral obstruction (UUO), PO-derived cells differentiate into α smooth muscle actin (αSMA)+ myofibroblasts, whose Epo expression decreases (11, 14). Even though various treatments can increase EPO in patients or animals with CKD (7, 11, 14), the mechanisms underlying the decreased response of myofibroblasts to the anemic stimulation remain elusive.

The regulation of Epo transcription is tissue specific (15, 16). While the hypoxia response element–positive (HRE+) 3′-enhancer of the Epo gene has been confirmed to be liver specific in mice beyond embryonic day 14.5, the HRE+ kidney-specific element has remained unexplored until recently (15, 16). Storti and colleagues reported that a functional HIF2α-dependent HRE in the distal 5′-enhancer is REPC specific (16). In vitro analyses have shown that methylation of the CpG islands in the promoter and 5′-untranslated region (5′-UTR) can inhibit Epo expression through recruiting methyl-CpG binding proteins to the promoter and hindering the binding of nuclear proteins in Hep3B human hepatoma cell line (17, 18). Moreover, methylation-free regulatory elements are a prerequisite for Epo expression in many human cancer cell lines (19, 20).

FOXD1+ progenitors arise in the area of the neural crest and appear earlier in the same locations as PO+ progenitors. FOXD1+ progenitors give rise to essentially the same cells in the mature kidney as PO+ progenitors (11, 21). FOXD1+ progenitor-derived,
**Results**

*Kidney pericytes produce EPO.* Renal Epo mRNA and plasma EPO concentrations were increased in mice after phlebotomy (Figure 1A). Renal expression of the other HIF-regulated genes, including prolyl-hydroxylase 2 (Phd2), Phd3, and Vegfa, was not changed (Figure 1A). We generated Epo<sup>RES-<i>IRES-RFP</i></sup> reporter mice by knocking IRES-RFP into Epo 3′-UTR (Supplemental Figure 1A; supplemental material available online with this article; doi:10.1172/JCI82819DS1). Renal expression of RFP and Epo increased in parallel after phlebotomy (Supplemental Figure 1B). EPO-RFP<sup>+</sup> cells were detected and increased in the peritubular interstitium (Supplemental Figure 1C). Kidney pericytes were FOXD1<sup>+</sup> progenitor-derived, Col1a1-GFP<sup>+</sup>, PDGFR<sup>β</sup>, CD73<sup>+</sup>, and p75<sup>+</sup> cells (Supplemental Figure 2). We crossed Epo<sup>RES-<i>IRES-RFP</i></sup> reporter mice to Col1a1-GFP<sup>+</sup> mice to study the Epo expression in Col1a1-GFP<sup>+</sup> pericytes. EPO-RFP was detectable in less than 10% of Col1a1-GFP<sup>+</sup> pericytes in control Epo<sup>RES-<i>IRES-RFP</i></sup>-Col1a1-GFP<sup>+</sup> mice; however, the percentage increased to more than 80% after phlebotomy (Figure 1B and Supplemental Figure 3, A and B). The increase of Epo expression was confirmed in Col1a1-GFP<sup>+</sup> PDGFR<sup>β</sup> pericytes isolated from kidneys of Col1a1-GFP<sup>+</sup> mice after phlebotomy (Figure 1C). We then cultured the isolated kidney pericytes in chambers containing 21% or 0.5% O<sub>2</sub> and confirmed the change of oxygenation and hemoglobin concentration (21–27). During fibrogenic injury, the pericytes proliferate and differentiate into myofibroblasts that produce pathogenic extracellular collagenous matrix, which leads to kidney fibrosis and function failure (22–31). In accordance with previous studies that refer to REPCs as fibroblast-like cells that might transit to myofibroblasts and contribute to kidney fibrosis (10, 11, 14), FOXD1<sup>+</sup> progenitor-derived, Col1a1-GFP-PDGFR<sup>β</sup> pericytes might provide a good model for studying the molecular mechanisms underlying the regulation of EPO expression in healthy and fibrotic kidneys. Moreover, TGF-β1, a well-recognized cytokine inducing pericyte-myofibroblast transition (29, 30), can induce Rasal1 methylation through DNA methyltransferase 1 (DNMT1), thereby leading to perpetuation of fibroblast activation and kidney fibrosis (32). We propose that TGF-β1-induced methylation of Epo 5′-regulatory elements may provide a molecular basis for a decreased Epo response of REPCs to anemic stimulation in CKD.
the induction of EPO by hypoxia in pericytes (Figure 1, D and E). Cobalt chloride (CoCl₂), an inducer of hypoxia-like responses, increased Epo expression in cultured kidney pericytes (Figure 1, F and G). IOX2, a specific PHD2 inhibitor, increased EPO expression in pericytes as well (Figure 1H). IOX2, a specific PHD2 inhibitor, increased EPO expression in pericytes as well (Figure 1H).

Kidney pericytes produce EPO through HIF2α regulation. To verify whether FOXD1 progenitor-derived pericytes produced EPO through HIF2α regulation that has been demonstrated in REPCs (33–35), we crossed Foxd1Cre/+ mice with mice with a homozygous conditional Hif2a allele (Hif2afl/fl mice) to knockout Hif2α in pericytes specifically. The recombination of the conditional Hif2α allele in Foxd1Cre/+ Hif2afl/fl mice was confirmed by PCR using kidney genomic DNA as the template (Figure 2A). Plasma levels of blood urea nitrogen (BUN) and creatinine were not different between Foxd1Cre/+ Hif2afl/fl mice and control mice (Figure 2B). The knockout band was confirmed in Foxd1Cre/+ Hif2afl/fl mice. Foxd1Cre/+ Hif2αfl/fl control mice only show the Hif2αfl/fl band. Analyses of hematocrit in Foxd1Cre/+ Hif2αfl/fl and Foxd1Cre/+ Hif2αfl/fl mice. n = 10 per group per time point. (C and D) Expression of renal Hif2α, Hif1α, and Epo plasma levels in 8-week-old adult mice. (E–G) Hematocrit, renal Epo expression, and plasma EPO levels in 8-week-old adult mice with and without phlebotomy. Student’s t test and 1-way ANOVA were used for analyses of data in B–D and E–G, respectively. *P < 0.05, †P < 0.01, ‡P < 0.001.

Transition to myofibroblasts decreases EPO expression. We then performed UUO surgery in a mouse model used to study the contralateral (CL) control and UUO fibrotic kidneys simultaneously. Phlebotomy induced robust Epo expression in CL kidneys but failed to do so in UUO kidneys (Figure 3, A and B). Phlebotomy did not affect Phd3, which had increased expression in UUO kidneys (Figure 3B). Renal Phd2 expression was not changed by UUO injury or phlebotomy (Supplemental Figure 6). Pericytes differentiated to αSMA⁺ myofibroblasts that retained PDGFRβ after UUO injury (Supplemental Figure 7). Analysis of pericytes and myofibroblasts isolated from CL and UUO kidneys, respectively, showed that phlebotomy-induced Epo expression was only noted in pericytes (Figure 3C). The expression of Vegfa and Phd3, but not Phd2, was higher in myofibroblasts, and expression was not changed by phlebotomy (Figure 3C). IOX2 increased Epo expression in cultured myofibroblasts to a much lesser degree than in pericytes (Figure 3D).

We induced the second model of kidney fibrosis by feeding mice with chow containing 0.25% adenine for 21 days (Supplemental Figure 8, A–D, and Figure 3E). Compared with that in mice fed with regular chow, renal Epo expression failed to increase significantly after phlebotomy in mice fed with adenine chow, although their plasma level increased to a lesser level (Figure 3, F–H). Renal expression of Vegfa and Phd3 was not changed by adenine feeding and phlebotomy (Supplemental Figure 8E). Analysis of kidney pericytes and myofibroblasts isolated from mice fed with regular and adenine chow, respectively, reconfirmed that myofibroblasts failed to have a significant increase in Epo expression after phlebotomy (Figure 3I).
Because most mice fed with adenine chow daily did not survive after 3 weeks, we used a protocol of alternate feeding to establish a chronic model with anemia (Supplemental Figure 9A). With the elevated levels of plasma BUN and creatinine, hematocrit decreased progressively, without an increase of plasma EPO concentration in mice fed with regular and adenine chows in alternate weeks (Supplemental Figure 9, B–D). Epo expression decreased in kidneys but increased in livers (Supplemental Figure 9E).

Hypermethylation of Epo 5’-regulatory elements in kidney myofibroblasts. To study the mechanisms underlying the repression of Epo in kidney myofibroblasts, genomic DNA obtained from normal kidney pericytes and UUO kidney myofibroblasts isolated from Col1a1-GFP Tg mice were subjected to methylation assay. Combined bisulfite restriction analysis (COBRA) showed that Epo promoter and 5’-UTR amplified from sodium bisulfite–converted genomic DNA of myofibroblasts was digested by restriction enzyme BstUI, suggesting the presence of hypermethylation (Figure 4, A and B). We confirmed the hypermethylation of Epo promoter and 5’-UTR in myofibroblasts again by bisulfite genomic sequencing (BGS) and methylation-specific PCR (MSP) (Figure 4, C–F). Hypermethylation of the distal HRE 5’-enhancer in myofibroblasts was confirmed by BGS as well (Figure 4G).

5-Azacytidine restores Epo expression in myofibroblasts and TGF-β1-exposed pericytes. To gain insights into the role of hypermethylation in Epo expression of myofibroblasts, we isolated and cultured kidney myofibroblasts 14 days after UUO surgery and treated these cells with 500 nM 5-azacytidine (Aza) (Figure 5A). We found that transient 3-day exposure of myofibroblasts to Aza led to evident inhibition on expression of pericytes and myofibroblasts cultured in the presence of TGF-β1 (Figure 5H). Moreover the expression of Dnmt1 was decreased by Aza treatment (Figure 5G), suggesting the potential of demethylation to redifferentiate myofibroblasts back to pericytes. However, Aza did not affect the expression of Phd3 and Vegfa expression but did not affect Phd3 (Figure 5K).
Aza restores EPO expression and ameliorates anemia in mouse models of kidney fibrosis. We then confirmed the expression of Dnmt isoforms by quantitative PCR in mouse models of kidney fibrosis induced by UUO and adenine (Figure 6A and Supplemental Figure 8F). Confocal microscopy detected DNMT1 in kidney myofibroblasts of Col1a1-GFP<sup>tg</sup> mice (Figure 6B). DNMT3a, not DNMT3b, was expressed in both pericytes and myofibroblasts (Figure 6B). Because the UUO mouse model, which showed normal hematocrit and plasma levels of BUN and creatinine, could be used to study the CL control and UUO fibrotic kidneys simultaneously, we first...
treated mice with Aza or PBS vehicle (Veh) after UUO surgery to study whether DNA demethylation restored Epo expression in fibrotic kidneys (Figure 6C). The demethylating effect of Aza on Epo 5′-regulatory elements of kidney myofibroblasts was confirmed (Supplemental Figure 10). Phlebotomy induced Epo expression in CL kidneys but failed to do so in UUO kidneys of mice treated with Veh (Figure 6, D and E). In UUO kidneys, Aza treatment increased not only the basal expression of Epo but also phlebotomy-induced expression (Figure 6, D and E). However, the expression of Hif1α and Hif2α was not changed by Aza treatment (Supplemental Figure 11). Epo expression in CL kidneys and plasma EPO concentration were not changed by Aza treatment, suggesting normally functioning CL kidneys as the major source of plasma EPO in the UUO kidney fibrosis model (Figure 6, D–F).

We next studied the effect of Aza treatment on anemia and EPO expression in the adenine-induced kidney fibrosis model (Figure 7A). Indeed, Aza treatment attenuated the decrease of hematocrit and increased renal Epo expression and plasma EPO concentration in adenine-induced CKD mice, without adverse effects on white cell and platelet counts in peripheral blood (Figure 7, B and C, and Supplemental Figure 12). Further analyses revealed that Aza treatment led to a greater EPO response than phlebotomy (Figure 7, B and C). In addition, Aza treatment attenuated kidney fibrosis and the elevation of plasma BUN and creatinine levels (Figure 7, D and E).

Discussion

These studies report that FOXD1+ progenitor-derived, Col1a1-GFP-PDGFRβ− kidney pericytes provide a good model for studying the molecular mechanisms underlying EPO regulation in healthy and fibrotic kidneys. Our data indicate that pericytes produce EPO through HIF2α regulation, but their EPO production capability is repressed by methylation of Epo 5′-regulatory elements when they differentiate into myofibroblasts during kidney fibrosis. We show compelling evidence that Aza at low nontoxic doses can restore EPO production and ameliorate anemia in mouse CKD models by targeting DNA methylation.

Our data support previous studies that demonstrated REPCs in fibrotic kidneys and their EPO production capability activated by HIF stabilizers (7, 11, 14). Although many in vitro studies have shown the association between methylation of Epo 5′-regulatory elements and inhibition of Epo expression in human cancer cell lines (17–20), our data provide the first evidence to our knowledge that methylation of Epo 5′-regulatory elements inhibited the baseline expression and anemic induction of Epo in fibrotic kidneys and myofibroblasts. Demethylation of in vitro cultured myofibroblasts and TGF-β1–exposed pericytes by Aza at a clinically relevant and nontoxic concentration increased baseline expression and hypoxic induction of Epo. Moreover, low-dose Aza treatment in mouse CKD models restored baseline expression and enhanced anemic induction of Epo in fibrotic kidneys, possibly through demeth-
ylating Epo 5′-regulatory elements in myofibroblasts, thereby increasing the plasma EPO concentration and ameliorating renal anemia. The potential effect of Aza on the redifferentiation of myofibroblasts into pericytes could also contribute to the restoration of Epo expression. In addition, our data showed that low-dose Aza treatment could prevent kidney fibrosis in mouse CKD models. The antifibrotic property of Aza could be ascribed to not only the potential effect of Aza on redifferentiating myofibroblasts back into pericytes, but also to the effect of Rasal1 demethylation in myofibroblasts that was reported previously (32). Although Rasal1 demethylation was shown to deactivate myofibroblasts, we are not sure whether the dose of 10 mg/kg Aza every other day in mice with folic acid nephropathy attenuated fibrosis through cytotoxic effect (32). Our own pilot experiments have shown adverse effects, including myelosuppression and body weight loss in mice after UUO surgery and in adenine-induced CKD mice treated with daily injection of Aza for 5 days per week at doses higher than or equal to 2 mg/kg and 0.5 mg/kg, respectively. Although it is not

Figure 6. Aza restores EPO expression in fibrotic kidneys induced by UUO. (A) Expression of Dnmt isoforms in CL and UUO kidneys after surgery. n = 10 per group. (B) Confocal images of DNMT1, DNMT3a, DNMT3b, and nidogen staining on kidney sections of Col1a1-GFP mice. Arrowheads highlight Col1a1-GFP*DNMT1 or Col1a1-GFP*DNMT3a* cells. Original magnification, ×400. Scale bar: 20 μm. (C) Schema illustrating Aza or Veh treatment in mice after UUO surgery. Phlebotomy was or was not performed 1 day before analyses at day 14 after UUO surgery. n = 10 per group. (D–F) Hematocrit, renal Epo expression, and plasma EPO levels in mice after UUO surgery and treatment with Veh or Aza according to the schema in C. One-way ANOVA was used for data analyses. *P < 0.05, †P < 0.01, ‡P < 0.001.
clear whether the high doses of Aza used in folic acid nephropathy attenuate fibrosis through cytotoxic effect (32), the low and nontoxic doses used in this study will be clinically applicable and safer for the treatment of renal fibrosis and anemia. In cancer treatment, toxic doses used in this study will be clinically applicable and safer.

Attenuate fibrosis through cytotoxic effect (32), the low and non-toxic doses of Aza used in folic acid nephropathy might inhibit the anemic induction of EPO production. At low nontoxic doses, the demethylating agent Aza has produced a reversal of the possible downside of long-term HIF overactivation induced by PHD inhibitor (44).

In summary, kidney pericytes produce EPO through HIF2α regulation, but this function is repressed by demethylation of Epistatin in kidney pericytes. Although the PHD inhibitor can stabilize HIFs and increase plasma EPO levels in some of HD patients with atrophic kidneys (7), absolute insufficiency of HIFs should not be the reason for renal anemia, because hypoxia in the renal interstitium has been considered a hallmark of injury and mediator of CKD progression (42, 43). Our data support that methylation of Epo expression in CKD by hindering the association of HIFs and the other transacting proteins with the regulatory elements (17, 18). Apparently the PHD inhibitor might attenuate the demethylation-induced inhibition of Epo expression in kidney myofibroblasts through robust increase of HIFs for transcription initiation. However, one of the mechanisms underlying the absence of response to the PHD inhibitor in some of the patients might be hypermethylation that is too extensive to be overcome by enhanced HIFs (7). The other possible mechanism would be renal fibrosis so extensive that no viable myofibroblasts existed to produce EPO. Moreover, we should be concerned about the possible downside of long-term HIF overactivation induced by PHD inhibitor (44).

Methods
Animals. Collal-GFP<sup>+</sup> mice, with Collal-expressing cells that expressed GFP, were generated and validated as previously described (22). B6;129S4-Foxd1<sup>tm1(GFP/cre)</sup>/J (referred to herein as Foxd1<sup>tm1(GFP/cre)</sup>), B6.Cg-Gt(Rosa)26Sortm2(Acta2<sup>tdTomato</sup>)Hze/J, and STOCK Epas1<sup>tm1Msx1</sup> (referred to herein as Hif2α<sup>−/−</sup>) mice were obtained from The Jackson Laboratory (23, 34, 45). Epo<sup>−/−</sup>/RFP<sup>−/−</sup> mice on the C57BL/6 back-
green, and red colocalization, respectively. αSMA+ cells were identi-
cified by the presence of greater than 75% of the cell area immediately
surrounding nuclei (detected by DAPI) staining positive with Cy3 fluo-
rescence, which is indicative of antigen expression. Specific cells were
marked by the presence of greater than 75% of the cell area immediately
surrounding nuclei (detected by DAPI) staining positive with Cy3 fluo-
rescence, which is indicative of antigen expression.

Administration of Aza to mouse models of kidney fibrosis. Mice
received subcutaneous daily injections of PBS Veh or Aza (0.5 mg/kg,
Sigma-Aldrich) for 5 days per week after UUO surgery, as outlined in
Figure 6C. Mice fed with regular or adenine chow received subcuta-
nous daily injections of Veh or Aza (0.125 mg/kg, reduced dose for
decreased kidney function) for 5 days per week starting at week 3, as
outlined in Figure 7A.

Tissue preparation and histology. Mouse tissues were prepared and
stained as previously described (29). Primary antibodies against the
following proteins were used for immunolabeling: αSMA-Cy3 (C6198,
clone IA4, Sigma-Aldrich), DNMT1 (5032, Cell Signaling Technol-
ogy), DNMT3b (70-205, Cosmo Bio Co. LTD.), DNMT3a (sc-20703),
nidogen (sc-33706, Santa Cruz Biotechnology), p75 NGF receptor
(ab8875, Abcam), CD73 (550738, BD Biosciences), and PDGFRβ (a
gift from William Stallcup, Burnham Institute, La Jolla, California,
USA). Fluorescence-conjugated secondary antibody labeling (111-
MSP1–405) was used for immunolabeling.

Isolation and culture of kidney pericytes and myofibroblasts. Peri-
cytes and myofibroblasts were isolated from normal and day 14 UUO
kidneys, respectively, as described previously (29). In brief, kidney
was diced and incubated at 37°C for 45 minutes with Liberase (0.5
mg/ml, Roche Applied Science) and DNase (100 U/ml, Roche Applied
Science) in HBSS. After centrifugation, cells were resuspended in 5
ml PBS/1% BSA and filtered (40 μm). Pericytes and myofibroblasts
were isolated by sorting GFP+PDGFRβ+CD31+ E-cadherin+ cells using a
FACSARia cell sorter (BD Biosciences) and cultured in DMEM with
10% FBS. The percentages of pericytes and myofibroblasts of the
total kidney cells gated in FACS plots isolated from normal and day
14 UUO kidneys were 0.7% ± 0.3% and 12.9% ± 0.8%, respectively.
Passage 0 cells were used for experiments. In hypoxia experiments,
cells were washed with 1× PBS (pH 7.4) and renewed culture medium
and then placed in an incubator with 21% O₂ or in a hypoxia chamber
(INVIVO200, Ruskinn Technology Ltd.) with 0.5% O₂ for 48 hours.
Cellular RNA was harvested by adding the RLT buffer provided in the
RNeasy Mini Kit (Qiagen) immediately after cells were taken out of
the incubator and the supernatant was removed for storage. In CoCl₂
(Sigma-Aldrich) or IOX2 (Tocris Bioscience) experiments, cells were
washed with 1× PBS and renewed culture medium and with or without
CoCl₂ or IOX2. Cellular RNA was harvested at indicated time points.
In TGF-β1 stimulation experiments, cells were washed with 1× PBS
and renewed culture medium and with or without 5 ng/ml TGF-β1
(R&D Systems) in the presence of 500 ng/ml Aza (Sigma-Aldrich)
or Veh. Cellular RNA and genomic DNA were harvested at indicated
time points. In myofibroblast culture, cells were treated with 500
ng/ml Aza for 3 days and then harvested for Western blot analysis of
dNMT1 or treated with CoCl₂ or Veh after a 2-day Aza-free period.
Cellular RNA was then harvested after CoCl₂ or Veh treatment.

PCR. Total RNA was extracted using the RNeasy Mini Kit
(Qiagen). The purity of each sample was determined based on the ratio
of A260 to A280. cDNA was synthesized using the iScript cDNA Syn-
thesis Kit (Bio-Rad). Genomic DNA was extracted using the DNase
Blood & Tissue Kit (Qiagen). Conventional and quantitative PCR were
performed using methods described previously (28). Expression levels
were normalized by ubiquitin C (Ubc) or Gapdh. The specific primer
pairs used for PCR are listed in Supplemental Tables 1 and 2.

COBRA. Genomic DNA was prepared from Colla1-GFP+PDG-
FRβ+CD31+E-cadherin+ cells and myofibroblasts isolated from
normal kidneys and kidneys 14 days after UUO surgery of Colla1-GFP+
mice, respectively. Sodium bisulfite conversion of genomic DNA was
performed using the EZ DNA Methylation Kit according to the manu-
facturer’s protocol (ZYMO Research). PCR using bisulfite-converted
genomic DNA as the template and the primers shown in Supplemental
Table 2 would amplify the genomic DNA fragments containing pro-
moter and 5′-UTR of Epo. Unmethylated and methylated controls were
from mouse sperm genomic DNA and Methylated Mouse Genomic
DNA Standard, respectively (ZYMO Research). Equal amount of the
PCR products were incubated in buffer with or without restriction
enzyme BstUI at 60°C for 3 hours (New England Biolabs), and then
electrophoresis was performed in a 1% agarose gel.

BGS. Genomic DNA was prepared and sodium bisulfite con-
version of genomic DNA was performed as described for those in
COBRA. PCR products of the genomic DNA fragment containing pro-
moter and 5′-UTR or distal 5′-enhancer amplified from bisulfite-con-
verted genomic DNA using the primers shown in Supplemental Table
2 were gel purified with the QIAquick Gel Extraction Kit (QIAGEN).
The eluted DNA fragments were ligated into pGEM-T Easy Vector
(Promega Corporation) for sequencing. Four colonies for each mouse
were randomly chosen for sequencing.

MSP. Genomic DNA was prepared and sodium bisulfite con-
version of genomic DNA was performed as described for those in
COBRA. Bisulfite-converted genomic DNA was amplified with
methylation-specific or unmethylation-specific primer pairs shown in
Supplemental Table 3. Unmethylated and methylated controls were
from mouse sperm genomic DNA and Methylated Mouse Genomic
DNA Standard, respectively (ZYMO Research). The PCR
products were analyzed by electrophoresis. The electrophoresis
result was shown as a virtual gel. The percentage of methylation of
**Western blot analysis.** Total cellular protein extracted using RIPA buffer was subjected to Western blot analysis using methods described previously (28). The following primary antibodies were used to detect protein: DNMT1 (5032, Cell Signaling Technology) and β-actin (4967, Cell Signaling Technology).

**Detection of EPO in plasma and culture media.** Mouse heparin plasma and pericyte culture supernatant stored in a –80°C freezer after collection were transferred into a –20°C Freezer 12 to 16 hours prior to analysis and thawed on ice before analysis. The analysis was performed according to the protocol of provided in the Mouse Erythropoietin Quantikine ELISA Kit (R&D Systems).

**Statistics.** Data are expressed as mean ± SEM. Statistical analyses were carried out using GraphPad Prism (GraphPad Software). Statistical significance was evaluated by Student’s t tests or 1-way ANOVA. P values of less than 0.05 were considered significant.

**Study approval.** All animal studies were carried out under a protocol approved by the Institutional Animal Care and Use Committee of the National Taiwan University College of Medicine. Address correspondence to: Shuei-Liong Lin, Graduate Institute of Physiology, No. 1, Jen-Ai Road Section 1, Taipei, Taiwan 100. Phone: 886.2.23123456, ext. 88235; E-mail: slin@ntu.edu.tw. Or to: Yung-Ming Chen, Department of Internal Medicine, No. 7, Chung-Shan South Road, Taipei, Taiwan 100. Phone: 886.2.23123456, ext. 65993; E-mail: cheny@ntuh.gov.tw.

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**Author contributions**

YTC, CCY, SYP, YHC, FCC, CFL, MHT, and HLH carried out experiments and analyzed data. CHL, WCC, MSW, TSC, and YMC participated in experiment design and data analysis. YMC and SLL designed and directed the project, carried out experiments, analyzed data, and wrote the manuscript.

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YTC, CCY, SYP, YHC, FCC, CFL, MHT, and HLH carried out experiments and analyzed data. CHL, WCC, MSW, TSC, and YMC participated in experiment design and data analysis. YMC and SLL designed and directed the project, carried out experiments, analyzed data, and wrote the manuscript.

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