Duchenne muscular dystrophy (DMD) is a severe and progressive muscle-wasting disease caused by mutations in the dystrophin gene. Although dystrophin deficiency in myofiber triggers the disease’s pathological changes, the degree of satellite cell (SC) dysfunction defines disease progression. Here, we have identified chicken ovalbumin upstream promoter–transcription factor II (COUP-TFII) hyperactivity as a contributing factor underlying muscular dystrophy in a dystrophin-deficient murine model of DMD. Ectopic expression of COUP-TFII in murine SCs led to Duchenne-like dystrophy in the muscles of control animals and exacerbated degenerative myopathies in dystrophin-deficient mice. COUP-TFII–overexpressing mice exhibited regenerative failure that was attributed to deficient SC proliferation and myoblast fusion. Mechanistically, we determined that COUP-TFII coordinated a regenerative program through combined regulation of multiple promyogenic factors. Furthermore, inhibition of COUP-TFII preserved SC function and counteracted the muscle weakness associated with Duchenne-like dystrophy in the murine model, suggesting that targeting COUP-TFII is a potential treatment for DMD. Together, our findings reveal a regulatory role of COUP-TFII in the development of muscular dystrophy and open up a potential therapeutic opportunity for managing disease progression in patients with DMD.
COUP-TFII regulates satellite cell function and muscular dystrophy

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Duchenne muscular dystrophy (DMD) is a severe and progressive muscle-wasting disease caused by mutations in the dystrophin gene. Although dystrophin deficiency in myofiber triggers the disease’s pathological changes, the degree of satellite cell (SC) dysfunction defines disease progression. Here, we have identified chicken ovalbumin upstream promoter–transcription factor II (COUP-TFII) hyperactivity as a contributing factor underlying muscular dystrophy in a dystrophin-deficient murine model of DMD. Ectopic expression of COUP-TFII in murine SCs led to Duchenne-like dystrophy in the muscles of control animals and exacerbated degenerative myopathies in dystrophin-deficient mice. COUP-TFII-overexpressing mice exhibited regenerative failure that was attributed to deficient SC proliferation and myoblast fusion. Mechanistically, we determined that COUP-TFII coordinated a regenerative program through combined regulation of multiple promyogenic factors. Furthermore, inhibition of COUP-TFII preserved SC function and counteracted the muscle weakness associated with Duchenne-like dystrophy in the murine model, suggesting that targeting COUP-TFII is a potential treatment for DMD. Together, our findings reveal a regulatory role of COUP-TFII in the development of muscular dystrophy and open up a potential therapeutic opportunity for managing disease progression in patients with DMD.

Introduction

Skeletal muscle is the most abundant tissue in the body and is important for critical functions such as movement, posture maintenance, and whole-body metabolism. It has been known for more than a century that skeletal muscle possesses an extraordinary capacity for self-repair, a process that is absolutely dependent on a small population of stem/progenitor cells, termed satellite cells (SCs) (1–3). In resting muscles, SCs remain quiescent. Upon exposure to environmental insults, SCs exit their dormant state, quickly expand. Most of these SCs differentiate and either fuse with existing fibers or give rise to new myofibers, thereby fully restoring damaged tissue (2, 3). Any abnormalities in SC specification, proliferation, differentiation, or self-renewal will lead to muscle atrophy and can aggravate chronic muscle diseases such as Duchenne muscular dystrophy (DMD).

DMD, the most common lethal genetic disorder in children, affects approximately 1 in 3,500 live-born males worldwide (4). Loss of dystrophin in patients causes muscle membrane fragility, which results in repetitive myofiber degeneration and regeneration and the replacement of muscles by fibrofatty tissues and ultimately leads to progressive paralysis and premature death (4). The mdx mouse, which bears the same genetic defect as that found in patients with DMD, reproduces the degenerative changes and is the most frequently used mouse model in DMD research (5, 6). Despite recent advances in DMD treatment, current therapies do not cure the disease (4), highlighting the need for a new strategy and a better understanding of the molecular events underlying DMD etiology.

Chicken ovalbumin upstream promoter–transcription factor II (COUP-TFII), also known as NR2F2, is a member of the nuclear orphan receptor superfamily. COUP-TFII is broadly detected in stem/progenitor cells in multiple tissues and has a profound impact on adult stem cell biology (7–9). Initial evidence of a role for COUP-TFII in myogenesis emerged from in vitro cell–based studies (11–13); however, little is known about its in vivo function in muscle development and diseases. In an effort to search for new players that contribute to muscular dystrophy, we queried multiple microarray data sets and found that COUP-TFII transcripts were enriched in patients with DMD compared with those in healthy individuals (14, 15). Considering that COUP-TFII protein is primarily detected in SCs in resting muscles (Figure 1, A and B), we generated mouse models expressing COUP-TFII protein specifically in the stem cell compartment. Early activation of COUP-TFII induces dystrophy-like defects in normal muscles that progressively worsen with aging. Consistently, SC-specific COUP-TFII activation exacerbates muscle wasting in the mdx mutant and hinders regenerative responses in WT mice suffering transient injury. The inefficient tissue repair arises from deficient myoblast expansion and fusion and correlates with the dysregulation of cyclin D1 (Cnd1), myogenic factor 5 (Myl5), caveolin 3 (Cav3), and chemokine (C-X-C motif) receptor 4 (Cxcr4) genes. Furthermore, mice with concurrent loss of COUP-TFII and dystrophin show improved muscleaturality and are protected from progressive myopathies. Together, our findings demonstrate the previously unrecognized effects of COUP-TFII on modulating SC behavior and highlight it as a potential candidate for therapeutic intervention of degenerative muscle diseases.
upregulated in patients with DMD (Supplemental Figure 1A; supplemental material available online with this article; doi:10.1172/JCI87414DS1) (14, 15). Similarly, an elevated level of COUP-TFII was found in the diaphragm muscle of mdx mice (Supplemental Figure 1B). Interestingly, while muscles from dystrophic patients have higher levels of COUP-TFII, treatments that ameliorate clinical phenotypes reduce COUP-TFII transcription (16). The potential link between COUP-TFII and muscular dystrophy is further substantiated by the fact that many genes affiliated with genetic or acquired myopathies are differentially expressed in

Results

COUP-TFII-overexpressing mice develop Duchenne-like dystrophy upon aging. In patients with DMD, dystrophin is lost in muscles in the fetal stage, while the deterioration of muscle function is progressive, suggesting that there are critical secondary factors that compound the dystrophin deficit. To identify novel molecules acting downstream of dystrophin loss, we interrogated public databases for differentially regulated genes between patients with muscular disorders and age-matched healthy individuals. Among the variably expressed genes, COUP-TFII mRNA was

Figure 1. Transgenic expression of COUP-TFII induces dystrophic symptoms upon aging. (A and B) WT TA muscles were stained for COUP-TFII, PAX7, and laminin to illustrate the expression of COUP-TFII. (C) Myc staining indicates COUP-TFII–expressing SCs in TA muscles 1 week after tamoxifen injection. Image is representative of 5 independent experiments. (D) Lean body mass in control (CTRL, n = 5) and COUP-TFII OE (CII OE, n = 8) mice. (E) Representative images highlight spinal curvature in COUP-TFII–transgenic animals. (F) Time and distance to fatigue with forced treadmill running in the control (n = 7) and COUP-TFII OE (n = 6) animals. (G) Representative images of H&E-stained soleus muscles and (H) quantification of muscle fiber caliber in control (n = 6) and COUP-TFII OE (n = 5) mice. Arrowheads in G indicate the central-nucleated fibers. (I) eMHC- and trichrome-stained soleus muscles. Fibrosis was analyzed by trichrome staining (right). Scale bars: 20 μm (A and B), 10 μm (C), 50 μm (G and H). *P < 0.05, **P < 0.01, and ***P < 0.001, by Student’s t test. Data represent the mean ± SEM.
COUP-TFII function in muscle development and disease. To test this, we used an inducible Pax7 CreERT2/+ mouse strain to achieve ectopic expression of COUP-TFII protein in SCs (COUP-TFII OE) (22). One week after tamoxifen-stimulated recombination, the Myc-tagged COUP-TFII transgene (23) was exclusively found in the SC position in muscle fibers (Figure 1C). More important, the extent of COUP-TFII overexpression in our transgenic animal was comparable to the levels observed in DMD patients and mdx mice (Supplemental Figure 1, A and B). Further analyses using freshly isolated SCs revealed an approximately 6-fold induction of COUP-TFII within the stem cell population (Supplemental Figure 1D). Unexpectedly, at 20 months of age, mice harboring the COUP-TFII transgene developed many features resembling pathological hallmarks of human DMD (24, 25). For instance, aberrant COUP-TFII activity has been connected to human diseases including congenital diaphragmatic hernia, prostate cancer, and heart failure (18–20). Together, these observations support a hypothesis that COUP-TFII may play a role in muscular dystrophy.

In uninjured muscles, COUP-TFII protein was primarily identified in the characteristic SC position, as COUP-TFII+ cells resided underneath the surrounding basal lamina and coexpressed the SC marker paired box 7 (PAX7) (Figure 1, A and B). Using COUP-TFII-LacZ–knockin mice (21), we verified the SC-specific location of COUP-TFII, because β-gal signals were recognized in small, de novo fibers with centrally positioned myonuclei on days 8 and 12 after injury (Supplemental Figure 1C). Therefore, we reasoned that the SC compartment may represent the central site of COUP-TFII activity in muscle development and disease. To test this, we used an inducible Pax7CreERT2/+ mouse strain to achieve ectopic expression of COUP-TFII protein in SCs (COUP-TFII OE) (22). One week after tamoxifen-stimulated recombination, the Myc-tagged COUP-TFII transgene (23) was exclusively found in the SC position in muscle fibers (Figure 1C). More important, the extent of COUP-TFII overexpression in our transgenic animal was comparable to the levels observed in DMD patients and mdx mice (Supplemental Figure 1, A and B). Further analyses using freshly isolated SCs revealed an approximately 6-fold induction of COUP-TFII within the stem cell population (Supplemental Figure 1D). Unexpectedly, at 20 months of age, mice harboring the COUP-TFII transgene developed many features resembling pathological hallmarks of human DMD (24, 25). For instance,
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COUP-TFII–transgenic mice had prominent weight loss and a lean body mass that was approximately 25% lighter than that of their WT littermates (Figure 1D and Supplemental Figure 1E). Similar to patients with DMD, COUP-TFII OE mice had apparent spinal curvature (kyphosis), indicative of paraspinal muscle weakness (Figure 1E). To further assess whole-body muscle strength and endurance, mice underwent treadmill tests, and the running time and distance to exhaustion were recorded. COUP-TFII–expressing mice ran for a significantly shorter time and distance than did their control counterparts, underscoring a progressive myopathy in the mutants (Figure 1F).

Histologically, muscles in the COUP-TFII OE mice were enriched with small myocytes, and their fiber size distribution showed the typical leftward shift toward smaller fibers (Figure 1, G and H, and Supplemental Figure 1F), implying that the decreased mean cross-sectional area (CSA) may partially account for the muscle atrophy in our transgenic animals. Moreover, fibers from COUP-TFII OE mice harbor additional histopathological signatures of muscular dystrophy such as the appearance of centralized myonuclei, the increment of embryonic myosin heavy chain (eMHC+), immature fibers, and intramuscular fibrosis (Figure 1, G and I, and Supplemental Figure 1G). During postnatal muscle development, the first 3–4 weeks are the most dynamic period in which PAX7+ cells actively proliferate and continuously incorporate into growing muscles (26, 27). Given that ectopic COUP-TFII protein was induced in juvenile SCs on post-

Figure 3. Impaired muscle recovery in COUP-TFII–transgenic mice suffering acute injury. (A) Representative H&E–stained TA muscles showed the course of regeneration in control and COUP-TFII OE mice at different time points after injury. Images are representative of 4 animals for each genotype at different time points. (B) Histograms represent the frequency distribution across TA muscles according to the cross-sectional area at post-damage day 12 (n = 6). (C and D) Two days after injury, TA muscle were pulsed with BrDU for 2 hours prior to tissue harvesting and were stained with BrDU Ab. Percentage of BrDU+ cells over total nuclei in control (n = 5) and COUP-TFII OE (n = 6) mice. (E and F) Representative images of PAX7 immunostaining and quantitative measurement of PAX7+ cells 5 days after muscle damage (n = 6). (G) Immunostaining for MHC, eMHC, and Myc 12 days after chemical injection. (H) TA muscles were examined 2 months after CTX-induced injury. Data are representative of 3 independent experiments. Scale bars: 50 μm. **P < 0.01 and ***P < 0.001, by 2-tailed Student’s t test. Data represent the mean ± SEM.
compartment and was colocalized with PAX7 in COUP-TFII OE and COUP-TFII OE mdx mice (Supplemental Figure 2, A–D). By 4 months of age, muscle hypertrophy and fiber regeneration were evident in the dystrophic diaphragms, whereas forced expression of COUP-TFII impaired tissue recovery, as indicated by obvious muscle atrophy with a few centrally nucleated newborn fibers in the COUP-TFII OE mdx mice (Figure 2, A and B, and Supplemental Figure 3A). Adult myogenesis recapitulates fetal muscle development by transiently expressing eMHC (3). In line with the de novo fiber synthesis defects, COUP-TFII OE mdx mice had a significantly lower number of differentiating eMHC + cells relative to those detected in control animals (Figure 2, C and D). In mdx mice, SCs actively replicate to provide myonuclear input for newly formed fibers, whereas a decline in progenitor cell proliferation was disclosed in the dystrophic COUP-TFII OE strain through p-histone H3 staining and BrdU labeling (Supplemental Figure 3, natal day 10, it is not surprising that a large portion of differentiated myotubes were marked with the Myc-tagged transgene over time (Supplemental Figure 1H), raising an interesting possibility that sustained expression of COUP-TFII beyond the stem/progenitor cell stage may also contribute to the DMD-like symptoms observed in our transgenic animals.

**Accelerated dystrophic phenotypes in COUP-TFII OE mdx mice.** To produce a mouse model that more closely resembled more the conditions seen in patients in whom COUP-TFII was upregulated in conjunction with dystrophin mutation, we bred the COUP-TFII transgene into the murine mdx background. Previous studies have documented that the mdx mouse diaphragm reproduced the pathological changes typical of DMD in humans (6), therefore, we focused on the diaphragm muscles in our analyses. One week after the initial injection of tamoxifen into 4-week-old animals, the Myc-tagged COUP-TFII transgene was mostly found in the SC compartment and was colocalized with PAX7 in COUP-TFII OE and COUP-TFII OE mdx mice (Supplemental Figure 2, A–D). By 4 months of age, muscle hypertrophy and fiber regeneration were evident in the dystrophic diaphragms, whereas forced expression of COUP-TFII impaired tissue recovery, as indicated by obvious muscle atrophy with a few centrally nucleated newborn fibers in the COUP-TFII OE mdx mice (Figure 2, A and B, and Supplemental Figure 3A). Adult myogenesis recapitulates fetal muscle development by transiently expressing eMHC (3). In line with the de novo fiber synthesis defects, COUP-TFII OE mdx mice had a significantly lower number of differentiating eMHC + cells relative to those detected in control animals (Figure 2, C and D). In mdx mice, SCs actively replicate to provide myonuclear input for newly formed fibers, whereas a decline in progenitor cell proliferation was disclosed in the dystrophic COUP-TFII OE strain through p-histone H3 staining and BrdU labeling (Supplemental Figure 3,
Accordingly, SC homeostasis, enumerated by PAX7 immunoreactivity, dropped by 60% in COUP-TFII OE mdx animals (Figure 2, E and F). Muscle regenerative function declines with aging, in which aged SCs fail to activate and proliferate in response to damage signals, thus impeding the reparative process (28). Elevated levels of p16INK4a and p19ARF proteins are found in almost all murine tissues with advanced age and are commonly used as biomarkers of in vivo senescence (29). We then assayed p16INK4a and p19ARF signals in diaphragm muscles, and comparison of mdx with COUP-TFII OE mdx mice showed no appreciable difference in cellular senescence (Supplemental Figure 4, A–C). SA-β-gal is another well-accepted aging-associated marker (30). Consistently, we found that β-gal density was not altered in mdx animals with or without the COUP-TFII transgene (Supplemental Figure 4D). Similarly, we found no difference in the incidence of apoptosis, as COUP-TFII OE mdx and mdx strains had similar cleaved caspase 3 immunoreactivity (Supplemental Figure 4E). Taken together, we conclude that defective cell expansion probably underlies COUP-TFII action in the setting of muscular dystrophy.

The inefficient tissue repair in the compound mutants rendered the tissue unable to keep up with ongoing necrosis, so that muscle wasting occurred. Consistently, lean body mass was reduced by 1.5 fold in mdx mice carrying the COUP-TFII minigen (Figure 2G and Supplemental Figure 4F). Because of muscle hypotrophy, COUP-TFII OE mdx mice had worse dystrophic signs and showed severe kyphosis (Figure 2H). Likewise, treadmill and grip tests further demonstrated a profound loss of muscle strength and performance in the compound mutants (Figure 2, I and J). Collectively, we observed exaggerated DMD pathology when COUP-TFII overexpression cooperated with dystrophin mutation, whereby elevated COUP-TFII activity largely abolished the SC-mediated reparative response, leading to severe muscle wasting and acceleration of DMD progression.

**COUP-TFII negatively regulates regenerative myogenesis.** Next, we investigated how the continuous presence of COUP-TFII affects the outcome of transient muscle damage. To do this, 6-week-old control and COUP-TFII OE mice were treated with tamoxifen for 5 consecutive days, and the tibialis anterior (TA)
muscles were damaged via cardiotoxin (CTX) injection 1 week later. Eight days after injury, necrotic muscles in the control animals were efficiently replaced by newly synthesized fibers (Figure 3A). In striking contrast, TA muscles in COUP-TFII OE mice were filled with small, regenerating myoblasts and abundant mononucleated cells (Figure 3A). By day 12, developing WT myocytes were evenly spaced and uniformly sized, a sign of their maturation (Figure 3A). Conversely, COUP-TFII OE muscles had small fiber diameters and immature development (Figure 3, A and B, and Supplemental Figure 5A). Likewise, muscle repair triggered by barium chloride (BaCl2) injury was also compromised with upregulation of COUP-TFII (Supplemental Figure 5B).

Muscle reconstitution demands SC activation, proliferation, differentiation, and fusion in an orderly fashion (2). Dysfunction of one or more of these processes could lead to the regenerative failure seen in COUP-TFII–transgenic animals. To explore the mechanistic action of COUP-TFII, we first examined the expression pattern of COUP-TFII after the regenerative insult. As shown in Supplemental Figure 5C, COUP-TFII mRNA levels were high in uninjured muscles but rapidly diminished in the cell-expansion phase, suggesting that COUP-TFII reduction may facilitate myoblast proliferation. In support of this view, COUP-TFII OE mice displayed a slower rate of cell propagation compared with that seen in WT muscles, as evidenced by BrdU incorporation (Figure 3, C and D), quantitative PCR (qPCR) of cell-cycle–related genes, and p-histone H3 immunostaining (Supplemental Figure 5, D and E). Acute injury provokes a relatively synchronous regenerative program, in which the changes in cell proliferation in tissues largely reflect the difference within the SC population (2). Correspondingly, COUP-TFII–transgenic mice had a dramatic reduction (60%) in the number of PAX7+ cells on day 5 after injury (Figure 3, E and F).

During tissue recovery, mononucleated myoblasts have to fuse with each other or with preexisting fibers to form multinucleated myotubes (2, 3). Twelve days after injury, eMHC expression declined in mature MHC+ fibers in the control muscles, while fibers in COUP-TFII OE mice maintained strong eMHC signals, reflecting inefficient myoblast fusion and delayed maturation (Figure 3G). In addition to SCs, other non-PAX7+ progenitors may also give rise to mature myotubes during fiber reconstitution (31, 32). Lineage-tracing experiments using a Myc tag clearly indicated that almost all the centrally nucleated fibers in COUP-TFII OE mice were originated from Myc+ precursors (SCs) in which COUP-TFII was continuously expressed (Figure 3G), providing evidence...
that sustained COUP-TFIJ activation indeed impedes lineage progression at the fusion stage. Most strikingly, 2 months after the initial chemical injury, TA muscles in COUP-TFIJ OE mice were predominantly composed of small, immature eMHC+ fibers and widespread fibrotic tissues (Figure 3H), emphasizing a permanent destruction of muscle maturation and remodeling under the conditions in which COUP-TFIJ signaling was high.

**COUP-TFIJ represses the proliferative capacity of muscle stem cells.** SCs purified through FACS can proliferate, differentiate, and form multinucleated myotubes. To minimize the potential variations in cell stage and genetic background, we isolated primary SCs from mice carrying a COUP-TFIJ over- or underexpression allele, which mostly expressed PAX7 protein and readily differentiated into myotubes upon induction (Supplemental Figure 6, A and B). Next, we asked whether we could reproduce the in vivo proliferation deficits using in vitro cultures. To this end, we infected SCs derived from CAG-S-COUP-TFIJ mice (23) with adenovirus expressing either GFP (Ad-GFP) or Cre recombinase (Ad-Cre) to induce COUP-TFIJ protein expression. Eleven days after viral delivery, control myoblasts underwent a 9-fold amplification compared with a 2-fold increase in Ad-Cre–infected COUP-TFIJ OE cells (Figure 4A). This growth arrest was mainly due to low cell proliferation rates, as the percentage of BrdU+ cells was decreased by 2.3 fold after COUP-TFIJ induction (Figure 4, B and C). Consistently, cell-cycle–associated genes such as cyclins, cyclin-dependent kinases, and their downstream effectors were coordinately downregulated in COUP-TFIJ–overexpressing cells 3 days after virus infection (Supplemental Figure 6C).

Among those suppressed cell-cycle regulators, Ccnd1, a key player of cell-cycle progression (33), and Myf5 were upregulated in the COUP-TFIJ–silencing cells (Figure 4D and Supplemental Figure 6D). Myf5 encodes a key myogenic factor that not only delimits the onset of postnatal myogenesis but also supports myoblast expansion during regeneration (34). Similar to the in vitro data, cycling SCs in COUP-TFIJ–transgenic mice had lower Ccnd1 and Myf5 expression levels than did their control mice (Supplemental Figure 5D). It has been documented that COUP-TFIJ represses downstream targets via direct binding to the consensus AGGTCA motif with variable spacing (7). Through a ChIP assay, we identified and validated the putative COUP-TFIJ response elements in the evolutionarily conserved region on the Ccnd1 and Myf5 genes, supporting a direct control of these molecules by COUP-TFIJ (Figure 4E). As is the case in an acute injury paradigm (Supplemental Figure 5D), CCND1- and MYF5-immunoreactive cells were more frequently detected in muscles from mdx strains than in muscles from COUP-TFIJ OE mdx strains (Figure 4, F and G, and Supplemental Figure 6, E and F).

Insulin-like growth factor 1 (IGF-1) has been shown in muscle stem cells to exert pleiotropic functions including cell migration, proliferation, and differentiation (3). As previously reported (35, 36), IGF-1 signals were specifically but transiently detected in activated SCs and small, regenerating myocytes in dystrophic diaphragm muscles (Supplemental Figure 7A). As noted above, COUP-TFIJ derepression largely blocked dystrophin loss–induced muscle repair (Figure 2 and Supplemental Figure 3), so it was expected that COUP-TFIJ OE mdx mice would have reduced numbers of IGF-1+ cells in comparison with numbers in mdx controls (Supplemental Figure 7A). However, IGF-1 was not directly controlled by COUP-TFIJ, because IGF-1 mRNA did not change in COUP-TFIJ–dysregulated SCs (Supplemental Figure 7, C and D). This conclusion is further supported by the fact that IGF-1 expression was similar on a per-cell basis between control and COUP-TFIJ OE mdx mice (Supplemental Figure 7A). Another secreted growth factor, granulocyte-CSF (G-CSF), has been shown to promote SC expansion and to maintain a long-term regenerative response in dystrophic animals (37, 38). Analysis of G-CSF expression via IHC showed no difference between COUP-TFIJ OE mdx mice and their control counterparts (Supplemental Figure 7B). Likewise, G-CSF transcript levels did not alter in the COUP-TFIJ–over- or underexpressing cells (Supplemental Figure 7, C and D).

Deficient myoblast fusion in COUP-TFIJ–expressing cells. During muscle reconstitution, fusion of singly nucleated myoblasts into multinucleated myocytes is indispensable for restoring normal musculature and contractile strength (39, 40). A recurrent defect occurring in COUP-TFIJ–transgenic mice is the loss of myofiber size and strength, implicating an obligate cell-intrinsic function for COUP-TFIJ in muscle maturation. In accordance with the histological characterizations (Figure 3), qPCR results also indicated a shift in gene expression from mature myotubes (Ckm and Myh2) to immature myoblasts (Myh3 and myogenin) in COUP-TFIJ OE muscles (Supplemental Figure 8A), supporting the notion of a potential link between defects in myoblast fusion and high levels of COUP-TFIJ.

To directly assess whether COUP-TFIJ is a potent factor disrupting myotube formation, we used an SC differentiation assay, in which the fusion process can be recapitulated in vitro. As presented in Figure 5A, myoblasts harboring the COUP-TFIJ transgene displayed a marked decline in their fusion capacity. In particular, 73% of cells in the control preparation developed into myotubes containing 2 or more myonuclei, but only 43% of the COUP-TFIJ–expressing myoblasts fused to myotubes (Figure 5B). Concordantly, fusion-incompetent COUP-TFIJ OE cells lacked the induction of the terminal differentiation marker creatine kinase (Ckm) with persistent expression of the early myogenic genes Myh3 and myogenin (Figure 5C).

To define the molecular targets mediating COUP-TFIJ action, we screened genes critical for myoblast fusion (39, 40) and found that the expression of Cav3 and Cxcr4 was dysregulated in COUP-TFIJ–mutant cells (Figure 5D and Supplemental Figure 8B). Caveolin 3 (Cav3) is a muscle-specific form of the caveolin gene family, and Cav3-deficient cells cannot undergo appropriate myoblast fusion (41, 42). Cxcr4 encodes a chemokine receptor that is required for myotube formation and muscle regeneration (43). Thus, the transcriptional repression of Cav3 and Cxcr4 by COUP-TFIJ will hamper muscle cell maturation. Significantly, Cxcr4 and Cav3 were clearly downregulated in regenerating COUP-TFIJ OE muscles (Supplemental Figure 8A). In WT mice, caveolin 3 was detected at the sarcolemma of newborn fibers, while its sarcolemma-specific expression was either missing or dramatically reduced in our transgenic mice (Figure 5E). To determine whether Cav3 and Cxcr4 are direct downstream targets of COUP-TFIJ, we performed ChIP-qPCR analyses and demonstrated the binding of COUP-TFIJ to the Cav3 and Cxcr4 gene enhancers/promoters (Figure 5F). In luciferase assays, ablation of COUP-TFIJ pro-
moted the Cxcr4 enhancer-driven reporter activity, while mutations in the putative COUP-TFII-binding motif partially abolished the induction (Supplemental Figure 8C), corroborating the link between COUP-TFII occupancy and gene regulation. Altogether, our experiments provide compelling evidence that COUP-TFII exerts a critical regenerative impact over the control of Ccnd1, Myf5, Cav3, and Cxcr4 genes.

Reduction of COUP-TFII activity attenuates the degenerative myopathies in mdx mice. Motivated by the idea that loss of COUP-TFII might confer a protective effect in muscular dystrophy, we generated mouse models having a mutation on the COUP-TFII allele (COUP-TFII–/– (COUP-TFII-KO) background, in which COUP-TFII mRNA levels were reduced more than 90% within the SC population (Supplemental Figure 9A). In general, SC-specific COUP-TFII–KO mice did not display overt abnormalities at baseline and had normal muscle size and architecture (Supplemental Figure 9B). Next, we assayed COUP-TFII deletion efficiency in the diaphragm muscle in COUP-TFII–KO mdx mutants and found that COUP-TFII protein was largely absent in PAX7+ cells 7 days after tamoxifen administration (Supplemental Figure 9C).

Three months after tamoxifen-mediated recombination, histology of the mdx diaphragm revealed extensive mineralization and muscular fibrosis, while COUP-TFII ablation in dystrophic animals ameliorated DMD pathology including reduced calcium deposits and matrix accumulation (Figure 6, A and B, and Supplemental Figure 10A). As a quantitative measure of collagen density, the mean hydroxyproline content was 25% lower in COUP-TFII–KO mdx diaphragms than that in control mdx mouse diaphragms (Figure 6C). Excessive matrix accumulation (fibrosis) is a particular hallmark of DMD patients that becomes more severe over time. By 11 months of age, a similar but more prominent reduction in collagen was seen in both diaphragm (Supplemental Figure 10B) and TA (Supplemental Figure 10, C and D) muscles in double-KO animals.

Contrary to the decreased SC density in COUP-TFII OE mdx mutants (Figure 2, E and F), immunostaining for PAX7 uncovered a 40% increase in PAX7-expressing cells in COUP-TFII-null dystrophic mice (Figure 6, D and E), implying a hastened and long-lasting regenerative response in the absence of COUP-TFII. Of note, BW and lean body mass did not differ in 4-month-old dystrophic animals with or without COUP-TFII (Supplemental Figure 11A). Intriguingly, whole-body muscle breakdown, as determined by serum creatine kinase (CK) activity, was significantly lower in COUP-TFII–KO mdx mice as compared with their mdx counterparts (Figure 6F). Sarcolemma integrity, examined by Evans blue dye (EBD) infiltration, confirmed the reduction of muscle damage by COUP-TFII depletion (Supplemental Figure 11, B and C). Histological examination consistently showed overall structural improvements in TA muscles in mdx mice lacking COUP-TFII (Supplemental Figure 12A). Moreover, the number of infiltrating neutrophils (myeloperoxidase [MPO] and Ly-6G) and macrophages (F4/80) was substantially reduced in COUP-TFII–deficient mdx animals (Supplemental Figure 12B), underscoring an attenuation of inflammation, a typical feature of DMD muscles. Those histopathological improvements truly reflected the motor function augmentation, as COUP-TFII-null dystrophic mice were stronger and had better physical activity than did their counterparts (Figure 6, G and H). Together, these parameters support a beneficial effect with COUP-TFII loss, as depletion of COUP-TFII protein mitigates the dystrophic responses and delays the critical hallmarks of DMD, an observation that is consistent with the improved muscularity seen in double-KO animals.

Discussion
SCs are self-renewing muscle stem cells that assure postnatal muscle growth and repair throughout life (27). During neonatal muscle development, PAX7+ stem/progenitor cells extensively proliferate, differentiate, and fuse with existing fibers, leading to a 4-fold increase in total muscle mass (26, 44). Considering its critical function in myoblast fusion, activation of COUP-TFII in juvenile SCs and its derived myoblasts hampers muscle maturation, with a mean fiber CSA that is decreased by 40% in advanced age (Figure 1H and Supplemental Figure 1F). A failure of muscle growth may arise from deficient expansion of individual muscle fibers and/or a decrease in total fiber numbers (27). Given that high levels of COUP-TFII impair SC expansion (Figure 4), the possible decline of myonuclear accretion during the perinatal growth period probably contributes to the muscle wasting in COUP-TFII OE mice (Figure 1D). Muscle loss is a serious consequence of muscular dystrophy, and COUP-TFII-transgenic animals display additional DMD indices such as central nucleation, fiber size variability, eMHC+ cells, muscular fibrosis, spinal deformity, and exacerbation of muscle dysfunction (Figure 1). As such, we conclude that COUP-TFII hyperactivity is indeed a secondary causative factor affecting muscular dystrophy. Reinforcing this notion, forced expression of COUP-TFII further sensitizes the mdx mutants to myopathic changes (Figure 2), emphasizing a synergistic effect when combining COUP-TFII upregulation with dystrophin loss. Together, our findings highlight the contribution of SCs to the pathogenesis of muscular dystrophy and support the perception that, in addition to muscle membrane instability, DMD is also a disease of SC dysfunction, as recently suggested (45, 46).

Differentiation of SCs into multinucleated myotubes is a multistep process orchestrated by various myogenic factors and signaling molecules. Myf5 is a muscle-specific transcription factor that directs the myogenic progression of SCs. Previous studies have reported that adult MYF5 depletion leads to progressive myopathy, mild defects in regeneration, and worsened dystrophic pathology in mdx mutants (47), phenotypes that were fully recapitulated by our COUP-TFII-expressing mice (Figure 1–3). However, the dysregulated MYF5 expression can only contribute to, but cannot fully explain, the action of COUP-TFII, as the phenotypes in COUP-TFII OE and COUP-TFII OE mdx mutants are far more severe than those of MYF5–null and Myf5–/– mdx mice. Therefore, we identified additional targets such as Cav3, Ccnd1, and Cxcr4. Caveolin 3 is the genetic basis of autosomal dominant limb-girdle muscular dystrophy (41), and a reduction of CAV3 protein provokes modest fiber degeneration, muscular atrophy, spinal kyphosis, variation in fiber caliber, and slightly increased fibrotic tissue (48–50), symptoms that were phenocopied by COUP-TFII-transgenic animals (Figure 1). Intriguingly, Cav3 is mainly expressed during the differentiation of myogenic cells, and COUP-TFII inhibits Cav3 expression in developing muscles (Figure 5E and Supplemental Figure 8A), pointing to a relevance
of COUP-TFII derepression in myofiber and muscle dysfunction. Additionally, CXCR4-null mice also display the same limb myogenic defects seen in COUP-TFII OE mice (51). Collectively, the phenotypes seen in Myf5, Cav3, and Cxcr4 mutants correspond nicely with those of COUP-TFII-transgenic animals, supporting the existence of a regulatory network in which COUP-TFII lies upstream of Myf5, Cond1, Cav3, and Cxcr4 to control SC differentiation and muscle regeneration.

The proliferation of SCs not only produces myogenic progenitors for muscle repair but also maintains the stem cell reservoir. The altered SC homeostasis in COUP-TFII–mutant mice (Figure 2, E and F; Figure 3, E and F; Figure 6, D and E) strongly suggests a requirement of COUP-TFII for replenishing the reserve cell lineage. Consistently, COUP-TFII directly controls the transcripts of Wnt- and Notch-signaling molecules (9, 11), key factors dictating the fate of SC progeny (3). Furthermore, Myf5 is a well-known determining factor controlling muscle cell fate specification (2, 3). COUP-TFII suppresses Myf5 expression, hence limiting the degree of myogenic commitment. In agreement with this, COUP-TFII–expressing SCs are less prone to entering myogenic paths, as we barely detected MYF5+ progenitors, eMHC+ developing myoblasts, or centralized myonuclei in COUP-TFII OE mdx mice (Figure 2, B–D, Figure 4G, and Supplemental Figure 6F). Thus, it would be interesting to clarify in future studies how COUP-TFII balances stem cell self-renewal and lineage specification.

Although our data favor the interpretation that an autonomous defect within the stem cell compartment leads to muscle dysfunction, several lines of evidence suggest that aberrant COUP-TFII expression on myofibers and myocytes may also contribute to the dystrophy pathology. First, augmented COUP-TFII activity on developing fibers explicitly blocks cell-cell fusion, resulting in muscle atrophy in aged mice as well as regenerative failure in transient injury (Figure 1 and 3). Second, COUP-TFII represses Cav3 expression on myocytes (Figure 5), which in turn elicits mild degenerative responses in COUP-TFII OE animals (Figure 1). A third aspect, the decreased muscle degeneration in COUP-TFII–KO mdx mice, agrees with our observation of an effect of COUP-TFII loss in protecting dystrophin-deficient muscles under conditions of stress (Figure 6F and Supplemental Figure 11, B and C). One plausible explanation might invoke the fiber-type switch initiated by COUP-TFII deficit, as dystrophic muscles with a higher degree of slow-twitch fibers are generally more resistant to contractile injury (52). COUP-TFII has been consistently reported to regulate muscle cell metabolism, mitochondrial function, and PGC-1α expression, key factors controlling muscle fiber types (19, 53). Together, these observations reveal a potential function of COUP-TFII beyond SCs that needs further exploration.

A prerequisite for developing efficacious DMD therapy is the generation of an animal model that faithfully mimics the disease progression in humans. Although they carry the same mutation in the DMD gene, mdx mice have only mild symptoms of the disease (5, 6). In the present study, by coupling COUP-TFII hyperactivity with dystrophin loss, we simultaneously targeted 2 major cell types participating in DMD pathology, creating a unique mouse model with exacerbated muscle wasting that more closely approximates that seen in humans. As such, our COUP-TFII OE mdx mice will be a valuable tool in DMD research and preclinical studies.

However, sustained COUP-TFII expression permanently disrupts the fusion of regenerating myoblasts (Figure 3H), which, to our knowledge, has never been reported in other animal models. In this regard, we believe our COUP-TFII-transgenic mice will serve as excellent tools for the investigation of cell-cell fusion in vivo.

In patients with DMD, SC-mediated regeneration initially restores muscle function deterioration. However, such repair is eventually depleted, owing to SC dysfunction. Thus, sustaining the stem cell reservoir and long-term regenerative potential could be an important direction for combating DMD. Here, we show that blunting of COUP-TFII activity stimulates SC lineage, attenuates the dystrophic response, and slows down muscle weakness in mdx mice. COUP-TFII is a member of the nuclear receptor superfamily and contains a ligand-binding pocket that is therapeutically accessible by small, drug-like molecules (54). Hence, it is tempting to speculate that pharmacological blockade of COUP-TFII action using its inhibitors/antagonists might curb muscle wasting and extend patient survival. In summary, we believe our studies provide compelling evidence of novel functions of COUP-TFII in directing SC development and highlight the therapeutic potential of targeting COUP-TFII in DMD or other degenerative muscle disorders.

Methods

Animals. Mice were bred and housed in a pathogen-free facility. The COUP-TFIIfl/fl, CAG-S-COUP-TFII, and COUP-TFIIfl/fl mice were generated in our laboratory as described previously (21, 23). Pax7CreERT2/+ strains harboring a tamoxifen-inducible CntfERT2 fusion under the control of a Pax7 promoter (22) were provided by Charles Keller (Oregon Health & Science University, Portland, Oregon, USA). The Pax7CreERT2/+ strains were then crossed with mice carrying the CAG-S-COUP-TFII or COUP-TFIIfl/fl allele to generate SC-specific COUP-TFII overexpressing (COUP-TFII OE) and underexpressing (COUP-TFII–KO) mice, respectively. mdx mice and their control counterpart C57BL/10ScSnJ mice were acquired from The Jackson Laboratory. COUP-TFII OE and COUP-TFII–KO mice were then bred with mdx mutants to produce COUP-TFII OE mdx and COUP-TFII–KO mdx strains. The mice used were at different ages for different experiments, as indicated in the text and figure legends. Mice randomized according to sex were randomly assigned to both the control and test groups, and we ensured that experimental groups were balanced in terms of animal age and sex. In particular, we used both male and female mice in the acute injury paradigm, such as that shown in Supplemental Figure 5C, Supplemental Figure 5D, and Supplemental Figure 8A. Sample size was determined empirically according to previous studies in the assessment of experimental variability. Premature death of animals was the criterion for exclusion. Mice used in the study were on a mixed background; in particular, COUP-TFII OE mice were on a 129Sv/Ev X C57BL/6 background, while COUP-TFII OE mdx and COUP-TFII–KO mdx mice were on a mixed 129Sv/Ev X C57BL/6 X C57BL/10 genetic background. Animals were genotyped by the appropriate PCR-based strategies and were caged together and treated in the same manner. Neither the technician nor the investigator could distinguish between the mice during the experiment or when assessing outcomes. Tamoxifen (Sigma-Aldrich) was dissolved in sunflower seed oil and was injected i.p. into mice at 1 mg per 50 g of BW for 5 consecutive days.

Histology and IHC. Muscle tissues were dissected, fixed, and processed as paraffin or frozen sections (11, 55). For paraffin sec-
tions, muscles were fixed in 4% paraformaldehyde overnight and
processed for routine paraffin histology. For frozen sections, dis-
sected muscles were briefly fixed in freshly prepared 4% para-
formaldehyde and snap-frozen in liquid nitrogen–cooled isopene-
tane. Tissues were embedded in OCT compound and cut into
10-μm-thick cross sections. Immunostaining was performed with
an M.O.M. Kit (Vector Laboratories) following the manufacturer’s
protocol. Immunofluorescence was conducted using a TSA Kit
(Molecular Probes) as described previously (11). β-Gal staining of
the cryostat sections was performed as reported previously (11).
H&E, trichrome, and von Kossa staining were carried out using
standard procedures. For fiber size distribution analyses, H&E-
stained images were manually delineated and analyzed using
ImageJ software (NIH) to measure the cross-sectional area of
individual muscle fibers (>400 fibers/animal).

The following primary Abs were used: COUP-TFII (1:2,000;
PP-H7147; R&D Systems); PAX7 (1:25; PAX7; DSHB); laminin (1:500;
L9393; Sigma-Aldrich); MHC (1:50; MF20; DSHB); eMHC (1:20;
F1.652; Developmental Studies Hybridoma Bank [DSHB]); desmin
(1:100; M0760; Dako); c-Myc (1:1,000; sc-40; Santa Cruz Biotech-
nology Inc.); MPO (1:200; MA516630; Biotechnology Inc.); Myc tag
(1:100; 2278; Cell Signaling Technology); IGF-1 (1:500; sc-302;
Santa Cruz Biotechnology Inc.); Bax (1:100; M0760; Dako); caspase
3 (1:100; 9661; Cell Signaling Technology); cleaved caspase 3
(1:100; 9661; Cell Signaling Technology); GGF (1:100; 9661; Cell
Signaling Technology); p16INK4a (undiluted; Rb-9041-P0; NeoMarker);
CCND1 (1:1,000; 2278; Cell Signaling Technology); MYF5 (1:100;
M0760; Dako); c-Myc (1:1,000; sc-40; Santa Cruz Biotech-
nology Inc.); p19 ARF (1:200; NB200-106; Novus Biologicals);
Inubron (1:100; 2278; Cell Signaling Technology); F4/80 antigen
(1:200; MA516630; Biotechnology Inc.); MPO (1:100; MAB3147;
R&D Systems); PAX7 (1:25; PAX7; DSHB); laminin (1:500;
P5147; Roche); CAV3 (1:2,000; 610420, BD Biosciences); p16INK4a
(undiluted; 7054713; Roche); Alexa Fluor 594 donkey anti-mouse IgG
(1:500; 550291; BD Pharmingen); F4/80 antigen (1:200; MA516630;
Biotechnology Inc.); MPO (1:100; MAB3147; R&D Systems); IGF-1
(1:500; 550291; BD Pharmingen); F4/80 antigen (1:200); MAS16630;
Thermo Fisher Scientific); Alexa Fluor 594 donkey anti-mouse IgG
(1:500; A-21203; Invitrogen, Thermo Fisher Scientific); and Alexa
Fluor 488 goat anti-rabbit IgG (1:500; A-11034; Invitrogen, Thermo
Fisher Scientific).

For in vivo BrdU labeling, mice were anesthetized and weighed.
A single dose of BrdU (GE Healthcare) reagent was i.p. injected at
1 ml/100 g of BW into control and COUP-TFII OE mice 2 days after
damage, and TA muscles were collected 2 hours later. For chronic
injury models, diaphragm muscles were collected 20 hours after BrdU
administration. Immunostaining for BrdU Ab was performed following
the protocol provided by the manufacturer (550803; BD Biosciences).

Senescence-associated β-gal activity was detected in frozen sections
using the Senescence β-Galactosidase Staining Kit (Cell Signaling
Technology). Hydroxyproline content was determined following a protocol
provided on the TREAT-NMD website (http://www.treat-nmd.eu/).

**SC isolation, culture, differentiation, and staining.** SC isolation
was performed as previously reported (55), and Thomas Rando
of Stanford University (Stanford, California, USA) provided the
detailed protocol. Briefly, after sacrifice, hind-limb skeletal muscles
were removed, mechanically disaggregated, and dissociated using
gentleMACS Dissocator (Miltenyi Biotec). The muscle suspension
was then digested with collagenase and dispase. Digested muscles
were filtered through a 40-μm cell strainer and washed to yield
a mononuclear cell suspension. The cells were stained with Vcam-
biontin (1:75; 553331; BD Biosciences); CD31-FITC (1:75; 553372;
BD Biosciences); CD45-FITC (1:75; 553080; BD Biosciences); and Sca-
1-FITC (1:75; 553335; BD Biosciences). Streptavidin-PE-cy7 (1:75;
557598; BD Biosciences) was used to amplify the Vcam signal. Cells
were sorted using a FACSaria II cell sorter (BD Biosciences) at the
Cytometry and Cell Sorting Core of Baylor College of Medicine.
Isolated SCs were either directly used for RNA extraction or cultured
for proliferation and differentiation assays.

SCs isolated from CAG-S-COUP-TFII and COUP-TFIIi/fl mice were
cultured in growth medium containing Ham’s F10, 20% FBS, bFGF (5
ng/ml) (R&D Systems), and 1% penicillin-streptomycin as previously
described (55). Primary SCs were treated with adenovirus expressing
GFP or Cre recombinase to activate or ablate the COUP-TFII gene.
The virus-infected cells were then transferred to differentiation media
(DMEM supplemented with 2% horse serum and 1% penicillin-strep-
tomycin) to induce myogenic development. Differentiated SCs were
stained with MHC Ab to visualize multinucleated myotubes. The fusion
index was calculated as the percentage of nuclei within myotubes
containing at least 2 nuclei as a ratio of total nuclei in the field.

For immunostaining of myotubes, cells were grown on culture
slides (BD Biosciences) in induction medium for 5 days. Cells were
then fixed with 4% paraformaldehyde, washed, and permeabilized
with 0.3% Triton X-100 for 10 minutes. Cells were blocked with 10%
serum for 30 minutes, followed by incubation with MHC Ab (1:50;
MF20; DSHB) for 2 hours. Cells were washed in PBS and incubated
with the secondary Ab Alexa Fluor 594 donkey anti-mouse IgG for 1
hour. After washing, culture slides were mounted with Vector Labo-
ratories Mounting Medium. BrdU staining was conducted using the
BrdU In-Situ Detection Kit (BD Biosciences). BrdU incorporation was
determined as the percentage of BrdU− cells to total nuclei in the field.

**Muscle damage, serum CK, and EBD measurements.** CTX from Naja
mossambica and BaCl2 (Sigma-Aldrich) was dissolved in sterile saline to a
final concentration of 10 μM and 1.2%, respectively. CTX and BaCl2 were
aliquoted and stored at –20°C. Before injury, mice were anesthetized
by isoflurane inhalation or i.p. injection of 2.5% Avertin (Sigma Aldrich).
Mouse legs were shaved and cleaned with alcohol. TA muscle was inject-
ed with 100 µl CTX or BaCl2 using an insulin syringe. After injection,
animals were kept on a heating pad until recovery. The damaged TA mus-
cles were collected at the indicated times (Figure 3A and Supplemental
Figure 5B) and stained with H&E using routine procedures.

Serum CK activity was analyzed as an overall measure of whole-
body muscle breakdown. Four-month-old animals were anesthetized,
and blood was obtained from the periorbital vascular plexus. Serum
CK levels were measured by the Comparative Pathology Laboratory at
Baylor College Medicine.

To evaluate muscle fiber integrity, 1% EBD dissolved in sterile
saline was administrated by i.p. injection at a dose of 1% of BW. Twenty
hours later, muscle was dissected, processed, and cut for histological
analyses. Muscle sections were stained with laminin to visualize mus-
cle fiber, and EBD was detected as red autofluorescence.

**RNA extraction and quantitative real time PCR (RT-qPCR).** Total RNA
was isolated from SCs and TA muscles using TRIzol reagent (Invitro-
gen, Thermo Fisher Scientific). RNA was then digested with DNase and
reverse transcribed with random primers using SuperScript II reverse
transcriptase (Invitrogen, Thermo Fisher Scientific). Expression of genes
of interest was assessed using standard qPCR approaches with either
inventoried TaqMan primer/probe mix or SYBR Green-based real-
time PCR. Reactions were run in triplicate, and automatically detected
threshold cycle (Ct) values were compared among samples. Levels of
gene expression were normalized to the level of 18s rRNA, Gapdh, or
cyclophilin A housekeeping genes. TaqMan probes were all from Invitro-

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gen (Thermo Fisher Scientific): COUP-TFI (Mm00772789_m1); Ccnd1 (Mm00432359_m1); Myf5 (Mm00435125_m1); Ckm (Mm01314877_m1); myogenin (Mm00446194_m1); Myh3 (Mm01332643_m1); Cav3 (Mm00725536_s1); Cxcr4 (Mm01996749_s1); Mki67 (Mm01278617_m1); Cona1 (Mm01266311_m1); E2f1 (Mm00432999_m1); Pax7 (Mm01354484_m1); 18s rRNA (4319413E); Igf1 (Mm00439560_m1); GCSF (Mm00438334_m1); Ccnd2 (Mm1612362_m1); Cdk4 (Mm00726334_s1); Cdk6 (Mm01313422_m1); Csnal (Mm00432337_m1); Cnca2 (Mm00430863_m1); Cdk2 (Mm00443947_m1); Ccnb1 (Mm03053893_g); Cdc25a (Mm00483616_m1); Cdc25b (Mm00499136_m1); Cdc25c (Mm00486872_m1); Cdc6 (Mm03048221_m1); Myh2 (Mm01332564_m1). The following SYBR Green primers were used: cyclophilin A (forward) 5′-TGGCACCATTCCGGACCCAAA-3′, (reverse) 5′-ATGGCCTGTTGGCAGACTCC-3′; Gapdh (forward) 5′-GGCAAAATGAGGGATGTTGTC-3′, (reverse) 5′-AATTTGGCCGT-GAGTTCTGAC-3′; Lmb1 (forward) 5′-CTTCGAGATGACTAGGCGG-GGC-3′, (reverse) 5′-TAACTGCTTTTTGGCGGCAG-3′; and Cav3 (forward) 5′-ACAAAGGCTCTAGTACCTGCT-3′, (reverse) 5′-TCCGTT-GTGCCTCTTGGCTCA-3′.

ChIP. ChIP assays were performed in cultured SCs following the protocol provided by EMD Millipore with specific anti-COUP-TFI (R&D Systems) and anti-mouse IgG Ab (EMD Millipore). Bound fraction and input DNA were subjected to qPCR using the following primers: Ccnd1 control primer (forward) 5′-CGGCACTGAGCTCCACT-3′, (reverse) 5′-CGAGAGAAGTTGGGAGAC-3′; Myf5 control primer (forward) 5′-TGGAGAAGTTGGGAGAC-3′, (reverse) 5′-CGGCACTGAGCTCCACT-3′; Ccnd2 ChIP primer (forward) 5′-GGTGCCTAAAAACGACCTGA-3′, (reverse) 5′-TAACTGCTTTTTGGCGGCAG-3′; and Cdc2 ChIP primer (forward) 5′-ACAAAGGCTCTAGTACCTGCT-3′, (reverse) 5′-TCCGTT-GTGCCTCTTGGCTCA-3′.

EcR primers. EcR primers (forward) 5′-ATGGAAGTTGGGAGAC-3′, (reverse) 5′-CGGCACTGAGCTCCACT-3′; and Cav3 EcR primers (forward) 5′-ACAAAGGCTCTAGTACCTGCT-3′, (reverse) 5′-TCCGTT-GTGCCTCTTGGCTCA-3′. ChIP primer (forward) 5′-ACAAAGGCTCTAGTACCTGCT-3′, (reverse) 5′-TCCGTT-GTGCCTCTTGGCTCA-3′.

Transfection and luciferase assays. CXCR4 WT enhancer and the mutant form were synthesized by Integrated DNA Technologies and cloned into a pLuc-MCS vector (Agilent Technologies). The predicted COUP-TFI-binding motif was mutated from TAACCTCAAGCT to GTCCCTCAATTAG. Myoblasts carrying the COUP-TFI WT allele were first infected with Ad-GFP and Ad-Cre viruses to ablate COUP-TFI protein. WT and mutant CXCR4 luciferase reporters were then transfected into virus-treated SCs using Lipofectamine 2000 (Invitrogen, Thermo Fisher Scientific). Luciferase activity was measured 48 hours later according to the manufacturer’s instructions (Promega).

Statistics. All data are shown as the mean ± SEM of at least 3 biological replicates. Statistical significance was calculated using a 2-tailed Student’s t test, assuming normal distribution and equal variance among different samples. Statistical significance is signified in the figure legends as *P < 0.05, **P < 0.01, and ***P < 0.001.

Study approval. All animal experimental procedures were reviewed and approved by the IACUC of Baylor College of Medicine, and all experiments were performed in compliance with the institutional guidelines of Baylor College of Medicine.

Author contributions. XX, SYT, and MJT conceptualized and designed the study. XX performed and analyzed the experiments. XX, SYT, and MJT wrote, discussed, and edited the manuscript.

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