this approach to confer body-wide therapeutic benefits. The accompanying articles from Wagers and colleagues (*41*) and Olson and colleagues (*42*) adopt a similar approach to CRISPR-Cas9–based correction of dystrophic mice using delivery with AAV9, demonstrating generality across muscle-tropic AAV serotypes. Moreover, the Wagers group's demonstration of efficient editing of Pax7-positive muscle satellite cells (*41*) suggests that gene correction may improve as the mature muscle fibers are populated with the progeny of these progenitor cells, as was observed in mosaic mice generated by CRISPR-Cas9 delivery to single-cell zygotes (*27*). Indeed, we have observed that dystrophin restoration by genome editing is maintained for at least 6 months after treatment (fig. S14).

Continued optimization of vector design will be important for potential clinical translation of this approach, including evaluation of various AAV capsids and tissue-specific promoters. Additionally, although dual-vector administration has been effective in body-wide correction of animal models of DMD (*43*), optimization to engineer a single-vector approach may increase efficacy and translatability. These three studies (*41*, *42*) establish a strategy for gene correction by a single-gene editing treatment that has the potential to achieve effects similar to those seen with weekly administration of exon-skipping therapies (*8*, *9*, *30*, *31*). More broadly, this work establishes CRISPR-Cas9–mediated genome editing as an effective tool for gene modification in skeletal and cardiac muscle and as a therapeutic approach to correct protein deficiencies in neuromuscular disorders and potentially many other diseases. The continued development of this technology to characterize and enhance the safety and efficacy of gene editing will help to realize its promise for treating genetic disease.

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SUPPLEMENTARY MATERIALS

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Materials and Methods
Figs. S1 to S22
Tables S1 to S4
References (*44*–*48*)

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GENE EDITING

In vivo gene editing in dystrophic mouse muscle and muscle stem cells

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Frame-disrupting mutations in the *DMD* gene, encoding dystrophin, compromise myofiber integrity and drive muscle deterioration in Duchenne muscular dystrophy (DMD). Removing one or more exons from the mutated transcript can produce an in-frame mRNA and a truncated, but still functional, protein. In this study, we developed and tested a direct gene-editing approach to induce exon deletion and recover dystrophin expression in the *mdx* mouse model of DMD. Delivery by adeno-associated virus (AAV) of clustered regularly interspaced short palindromic repeats (CRISPR)–Cas9 endonucleases coupled with paired guide RNAs flanking the mutated *Dmd* exon23 resulted in excision of intervening DNA and restored the *Dmd* reading frame in myofibers, cardiomyocytes, and muscle stem cells after local or systemic delivery. AAV-*Dmd* CRISPR treatment partially recovered muscle functional deficiencies and generated a pool of endogenously corrected myogenic precursors in *mdx* mouse muscle.

Duchenne muscular dystrophy (DMD) is a progressive muscle degenerative disease caused by point mutations, deletions, or duplications in the *DMD* gene that cause genetic frame-shift or loss of protein expression (*1*). Efforts under development to reverse the pathological consequences of DYSTROPHIN deficiency in DMD aim to restore its biological function through viral-mediated delivery of genes encoding shortened forms of the protein, up-regulation of compensatory proteins, or interference with the splicing machinery to "skip" mutation-carrying or mutation-adjacent exons in the mRNA and produce a truncated, but still functional, protein [reviewed in (*2*)].

The potential efficacy of exon-skipping strategies is supported by the relatively mild disease course of Becker muscular dystrophy (BMD) patients with in-frame deletions in *DMD* (*3*, *4*), and by the capacity of antisense oligonucleotides (AONs), which mask splice donor or acceptor sequences surrounding mutated exons in *DMD*

mRNA, to restore biologically active DYSTROPHIN protein in mice (*5*, *6*) and humans (*7*, *8*). Yet limitations remain for the use of AONs, including variable efficiencies of tissue uptake, depending on antisense oligonucleotide (AON) chemistry, a requirement for repeated AON injection to maintain effective skipping, and the potential for AON-associated toxicities [(*9*, *10*) and supplementary text].

Here, we sought to address these limitations by developing a one-time, multisystemic approach based on the genome-editing capabilities of the clustered regularly interspaced short palindromic repeats (CRISPR)–Cas9 system. This system, originally coopted from *Streptococcus pyogenes* (Sp), couples a DNA double-strand endonuclease with short "guide" RNAs (gRNAs) that provide target specificity to any site in the genome that also contains an adjacent "NGG" protospacer-adjacent motif (PAM) (*11*–*14*), which enables targeted gene disruption, replacement, and modification.

To apply CRISPR/Cas9 for exon deletion in DMD, we first established a reporter system for CRISPR activity by "repurposing" the existing Ai9 mouse reporter allele, which encodes the fluorescent tdTomato protein downstream of a ubiquitous CAGGS promoter and "floxed" STOP cassette (*15*, *16*) (fig. S1A). Exposure to SpCas9, together with paired gRNAs targeting near the Ai9 loxP sites (hereafter, Ai9 gRNAs), resulted in excision of intervening DNA and expression of tdTomato (fig. S1, A, B, and E). We next designed and tested paired gRNAs (hereafter, *Dmd*23 gRNAs) (fig. S1C) that were directed 5′ and 3′ of mouse *Dmd* exon 23, which in *mdx* mice carries a nonsense mutation that destabilizes *Dmd* mRNA and disrupts DYSTROPHIN expression (*17*). Finally, we coupled the paired *Dmd*23 and Ai9 gRNAs using a two-plasmid system that links expression of the CRISPR activity reporter (tdTomato) to genome editing events at the *Dmd* locus (fig. S1D). In vitro transfection of primary satellite cells from *mdx* mice carrying the Ai9 allele (hereafter, *mdx;Ai9* mice) with SpCas9 + Ai9-*Dmd*23 coupled gRNAs induced gene editing at both the Ai9 locus, demonstrated by tdTomato expression (fig. S1E), and *Dmd* locus, detected by genomic polymerase chain reaction (PCR) (Fig. 1A) and confirmed by amplicon sequencing (fig. S1F). *Dmd* editing was not detected in *mdx;Ai9* cells receiving Ai9 gRNAs alone (Fig. 1A), although tdTomato expression was equivalently induced (fig. S1E).

In order to confirm that CRISPR-mediated *Dmd* editing results in irreversible genomic modification and production of exon-deleted mRNA and protein, primary satellite cells from *mdx;Ai9* mice were cotransfected with SpCas9 + Ai9 or Ai9-*Dmd*23 gRNAs, isolated by fluorescence-activated cell sorting (FACS) on the basis of tdTomato expression, expanded in vitro (*18*), and differentiated to myotubes. Reverse transcription–PCR (RT-PCR) (Fig. 1B) and amplicon sequencing (fig. S1G) from these myotubes detected exon 23–deleted *Dmd* mRNA in cells receiving Ai9-*Dmd*23–coupled gRNAs but not in cells receiving only Ai9 gRNAs. TaqMan analysis (*9*) further indicated that exon 23–deleted transcripts represented 24 to 47% of total *Dmd* mRNA in cells receiving Ai9-*Dmd*23–coupled gRNAs, whereas exon 23 deletion was undetectable with Ai9 gRNAs alone (fig. S1H). DYSTROPHIN protein expression was also restored in CRISPR-modified *mdx;Ai9* cells, as detected by Western blot of in vitro differentiated myotubes (Fig. 1C) and immunostaining of muscle sections from *mdx* mice transplanted with gene-edited *mdx;Ai9* satellite cells (Fig. 1D and fig. S1I). These data demonstrate that CRISPR/Cas9 can direct sequence-specific modification of disease alleles in primary muscle stem cells that retain muscle engraftment capacity.

We next adapted CRISPR for delivery by means of AAV, using the smaller Cas9 ortholog from *Staphylococcus aureus* (SaCas9), which can be packaged in AAV and programmed to target any locus in the genome containing an "NNGRR" PAM sequence (*19*). We generated Sa gRNAs targeting Ai9 and introduced several base modifications into the gRNA scaffold to enhance gene targeting by SaCas9 (fig. S2, A to C). Using this modified scaffold, we tested *Dmd*23 Sa gRNAs (fig. S2D) and produced AAVs encoding SaCas9 and Ai9 Sa gRNAs or *Dmd*23 Sa gRNAs in a dual (fig. S3A) or single (fig. S3B) vector system. Comparison of exon 23 excision efficiencies in transduced *mdx* myotubes demonstrated more efficient excision by dual AAV-CRISPR (fig. S3, C and D), as compared with single vector AAVs. Therefore, to test the potential for in vivo *Dmd* targeting by CRISPR/Cas9, we pseudotyped dual AAVs (AAV-SaCas9 + AAV-Ai9 gRNAs; hereafter, AAV-Ai9 CRISPR) to serotype 9, which exhibits robust transduction of mouse skeletal and cardiac muscle (*20*), and injected these AAVs into the tibialis anterior (TA) muscles of *mdx;Ai9* mice (7.5E+11 vg each). Four weeks later, muscles were harvested to assess genome-editing events. TdTomato fluorescence was detected in muscles injected with AAV-Ai9 CRISPR but not in muscles injected with vehicle alone (fig. S4A). Codelivery of AAV9-SaCas9 + AAV9-*Dmd*23 gRNAs (hereafter,

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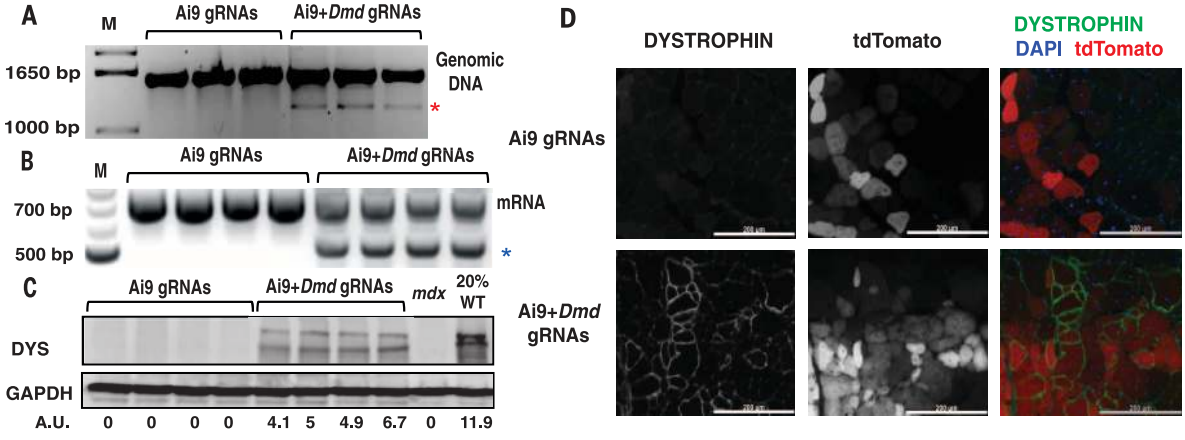

Fig. 1. DYSTROPHIN expression in CRISPR-modified dystrophic satellite cells. (**A**) Detection of exon 23 excision by genomic PCR in myotubes derived from satellite cells transfected with SpCas9 and Ai9 gRNAs (left lanes) or coupled Ai9-*Dmd*23 gRNAs (right lanes). Unedited genomic product, 1572 base pair (bp); gene-edited product (red asterisk), 1189 bp. M, molecular size marker. (**B**) RT-PCR detection of exon 23–deleted mRNA. Unedited RT-PCR product, 738 bp; exon 23–deleted product (blue asterisk), 525 bp. (**C**) Western blot detecting DYSTROPHIN in myotubes derived from gene-edited satellite cells. A.U., arbitrary unit, normalized to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (loading control). DYS, DYSTROPHIN; WT, wild type. (**D**) DYSTROPHIN immunofluorescence in *mdx* muscles transplanted with satellite cells transfected in vitro with SpCas9 + Ai9 gRNAs (top) or SpCas9 + Ai9-*Dmd*23–coupled gRNAs (bottom). For merge: green, DYSTROPHIN; red, tdTomato; blue, 4′,6′-diamidino-2-phenylindole (DAPI) (nuclei). Scale bar, 200 μm. See also fig. S1.

AAV-*Dmd* CRISPR) likewise yielded robust and specific modification of the *Dmd* locus in TA muscles in vivo. Genomic PCR (Fig. 2A) and Sanger sequencing (fig. S4B) demonstrated exon 23 excision in muscles injected with AAV-*Dmd* CRISPR but not AAV-Ai9 CRISPR. Next-generation sequencing indicated minimal activity at the predicted highest-ranking genomic off-target sites (fig. S12). RT-PCR (Fig. 2B) and sequencing (fig. S4C) further confirmed the presence of exon 23–deleted *Dmd* mRNA in muscles receiving AAV-*Dmd* CRISPR, with an average exon 23 excision rate of 39% ±1.8% (fig. S3E). In vivo CRISPR-mediated targeting of *Dmd* exon 23–restored DYSTROPHIN expression in skeletal muscle, as detected by Western blot (Fig. 2C), immunofluorescence (Fig. 2D), and capillary immunoassay (fig. S5A). Other pathological hallmarks of dystrophy were also restored in AAV-*Dmd* CRISPR–injected muscles, including sarcolemmal localization of the multimeric dystrophin-glycoprotein complex and neuronal nitric-oxide synthase (figs. S6 and S7). In contrast, DYSTROPHIN expression was undetectable by Western blot (Fig. 2C) and present only on rare revertant fibers in *mdx;Ai9* mice receiving control AAV-Ai9 CRISPR (Fig. 2D) (*21*). Finally, to evaluate the functional consequences of CRISPR-mediated induction of exon 23–deleted DYSTROPHIN, we subjected a subset of *mdx;Ai9* mice injected intramuscularly with AAV-*Dmd* CRISPR to in situ muscle force assessment. Muscles receiving AAV-*Dmd* CRISPR showed significantly increased specific force (Fig. 2E) and attenuated force drop after eccentric damage (Fig. 2F), as compared with contralateral, vehicle-injected muscles and also AAV-Ai9 CRISPR injected muscles. In contrast, differences in specific force (Fig. 2E) and force drop (Fig. 2F) for AAV-Ai9 CRISPR injected mice did not vary significantly between the virus-injected and vehicle-injected muscles.

We next evaluated the potential for multisystemic gene editing in vivo using AAV-CRISPR. Dual AAV-Ai9 CRISPR vectors (1.5E+12 vg each) were coinjected intraperitoneally into *mdx;Ai9* mice at postnatal day 3 (P3). Three weeks later, widespread tdTomato expression was detected in all cardiac and skeletal muscles analyzed (fig. S8A). Parallel injections of *mdx;Ai9* mice with AAV-*Dmd* CRISPR revealed exon 23–deleted transcripts in multiple skeletal muscles and cardiac muscle, with targeting levels varying from 3 to 18% in different muscle groups (Fig. 3A and fig. S3F). Exon 23 was not excised in animals receiving AAV-Ai9 CRISPR instead (Fig. 3A, and figs. S3F and S8B). Finally, Western blot (Fig. 3B and fig. S8C), immunofluorescence (Fig. 3C), and capillary immunoassay (fig. S5B) confirmed that DYSTROPHIN protein was largely absent in muscles of control *mdx;Ai9* mice receiving AAV-Ai9 CRISPR and was restored in mice receiving AAV-*Dmd* CRISPR. Similar systemic dissemination of AAV and excision of exon 23 in multiple organs were seen in two adult mice injected intravenously with AAV-*Dmd* CRISPR at 6 weeks of age (fig. S9).

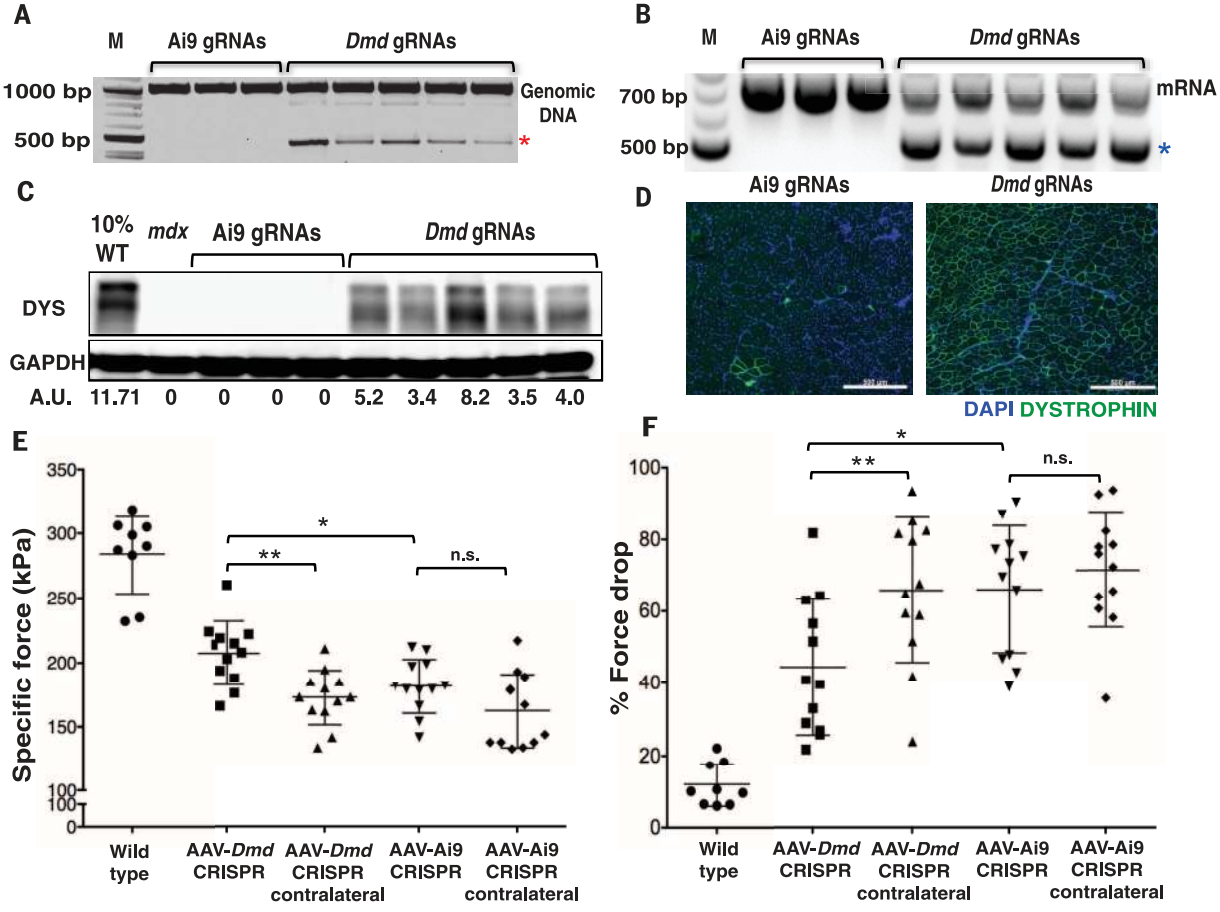

Fig. 2. AAV-CRISPR enables in vivo excision of *Dmd* exon 23 and restores DYSTROPHIN expression in adult dystrophic muscle. (**A** and **B**) Detection of exon 23 excision in TA muscles from *mdx;Ai9* mice injected intramuscularly with AAV-Ai9 CRISPR (left lanes) or AAV-*Dmd* CRISPR (right lanes) by genomic PCR (A). Unedited product, 1012 bp; exon-excised product, 470 bp; and RT-PCR (B). Asterisks mark gene-edited bands. M, molecular size marker. (**C**) Western blot detecting DYSTROPHIN in muscles injected with AAV-Ai9 CRISPR (left) or AAV-*Dmd* CRISPR (right), with relative signal intensity determined by densitometry at bottom. A.U., arbitrary unit, normalized to GAPDH. (**D**) Representative immunofluorescence images for DYSTROPHIN (green) and DAPI (blue) in *mdx;Ai9* muscles injected with AAV-Ai9 (left) or AAV-*Dmd* (right) CRISPR. Scale bar, 500 μm. (**E** and **F**) Muscle-specific force (E) and decrease in force after eccentric damage (F) for wild-type mice injected with vehicle (n = 9), *mdx;Ai9* mice injected with AAV-*Dmd* CRISPR in the right TA and vehicle in the left TA (n = 12), or *mdx;Ai9* mice injected with AAV-Ai9 CRISPR in the right TA and vehicle in the left TA (n = 12). *P < 0.05, **P < 0.01, n.s., not significant, one-way analysis of variance (ANOVA) with Newman-Keuls multiple comparisons test.

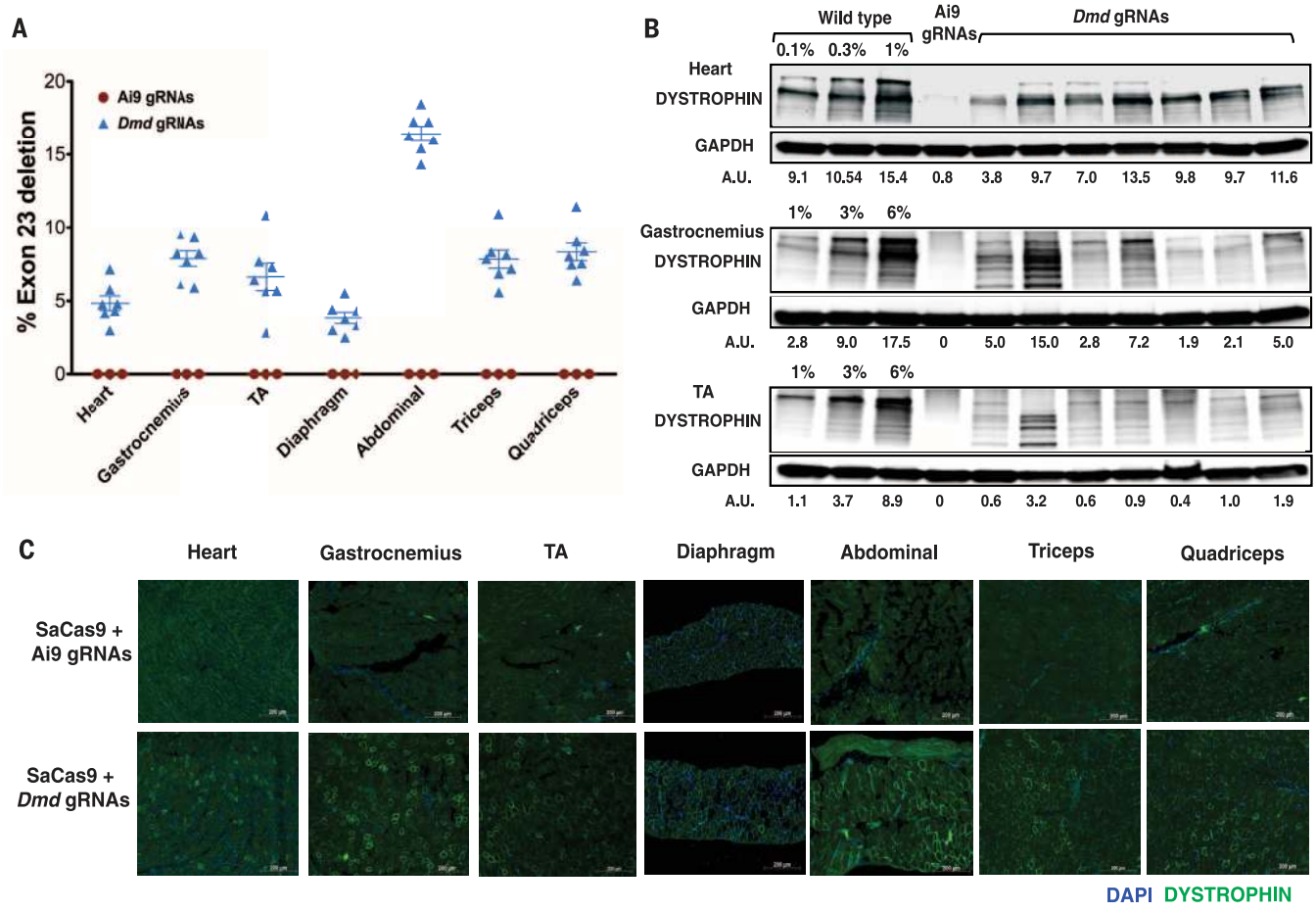

Fig. 3. Systemic dissemination of AAV-CRISPR targets *Dmd* exon 23 and restores DYSTROPHIN in dystrophic cardiac and skeletal muscles. (**A**) Exon 23–deleted transcripts in muscles quantified by TaqMan quantitative RT-PCR. Data plotted for individual mice [$n = 7$ receiving AAV-*Dmd* CRISPR (blue) and $n = 3$ receiving AAV-Ai9 CRISPR (red)] and overlaid with mean ± SEM. (**B**) Western blots detecting DYSTROPHIN in the indicated muscles of *mdx;Ai9* mice receiving systemic AAV-CRISPR. Right lanes correspond to muscles from seven different mice injected intraperitoneally with AAV-*Dmd* CRISPR. Relative signal intensity, determined by densitometry, presented as A.U., arbitrary unit normalized to GAPDH. (**C**) Representative immunofluorescence staining for DYSTROPHIN (green) in *mdx;Ai9* mice injected with AAV-Ai9 (top) or AAV-*Dmd* (bottom) CRISPR. Blue, DAPI (nuclei). Scale bar, 200 μm.

Dystrophic pathology and other muscle injuries activate muscle stem cells (also known as satellite cells), which leads to regenerative responses that add new nuclei to damaged fibers [(*2*) and supplementary text]. To evaluate AAV-CRISPR gene editing in satellite cells in vivo, we crossed *mdx;Ai9* mice with Pax7-ZsGreen animals, in which satellite cells are specifically marked by green fluorescence (*22*), and we injected these animals intramuscularly or systemically with AAV9 encoding Cre (hereafter, AAV-Cre) or Ai9-CRISPR components. Muscles were harvested 2 weeks later (Fig. 4A) and analyzed by FACS. TdTomato expression was apparent in Pax7-ZsGreen+ satellite cells after local or systemic delivery of AAV-Cre or AAV-Ai9 CRISPR (Fig. 4B and fig. S10, A to C), although excision rates were lower for AAV-Ai9 CRISPR than for AAV-Cre. In vitro differentiation of ZsGreen+ satellite cells from mice receiving intramuscular or systemic AAV-Cre or AAV-Ai9 CRISPR produced tdTomato+ myotubes, demonstrating preservation of myogenic potential in AAV-transduced and gene-edited satellite cells (Fig. 4C and fig. S10D). TdTomato+ gene–edited satellite cells also engrafted recipient *mdx* muscle and contributed to in vivo muscle regeneration after transplantation (fig. S10E).

We next analyzed *Dmd* editing in Pax7-ZsGreen+ satellite cells after intramuscular or systemic delivery of AAV-*Dmd* CRISPR or AAV-Ai9 CRISPR. Satellite cells were isolated by FACS, expanded, and differentiated in vitro (Fig. 4A). RT-PCR revealed a truncated *Dmd* transcript of the expected size and sequence for gene-edited *Dmd* in satellite cell–derived myotubes from many of the AAV-*Dmd* CRISPR-injected muscles but none of the AAV-Ai9 CRISPR-injected muscles (Fig. 4D and fig. S10, F, H, and I). Quantification of exon 23 excision revealed variable efficiencies (fig. S10, G and J), which likely reflected targeting of only a subset of endogenous satellite cells that may be variably represented among the isolated and cultured cells. Finally, genomic PCR and amplicon sequencing confirmed targeted excision at the *Dmd* locus in satellite cell–derived myotubes (fig. S10K), and capillary immunoassay analysis revealed restored DYSTROPHIN expression (fig. S10L). As expected, injection of AAV-*Dmd* CRISPR did not induce tdTomato expression in satellite cells or myofibers of *mdx;Ai9* mice (fig. S11).

In summary, this study provides proof-of-concept evidence supporting the efficacy of in vivo genome editing to correct disruptive mutations in DMD in a relevant dystrophic mouse model. We show that programmable CRISPR complexes can be delivered locally and systemically to terminally differentiated skeletal muscle fibers and cardiomyocytes, as well as muscle satellite cells, in neonatal and adult mice, where they mediate targeted gene modification, restore DYSTROPHIN expression, and partially recover functional deficiencies of dystrophic muscle. As prior studies in mice and humans indicate that DYSTROPHIN levels as low as 3 to 15% of wild type are sufficient to ameliorate pathologic symptoms in the heart and skeletal muscle (*23*–*26*) and that levels as low as 30% can suppress the dystrophic phenotype altogether (*27*), the restoration of DYSTROPHIN achieved here by one-time administration of AAV-*Dmd* CRISPR clearly encourages further evaluation and optimization of this system as a new candidate modality for the treatment of DMD (see supplementary text).

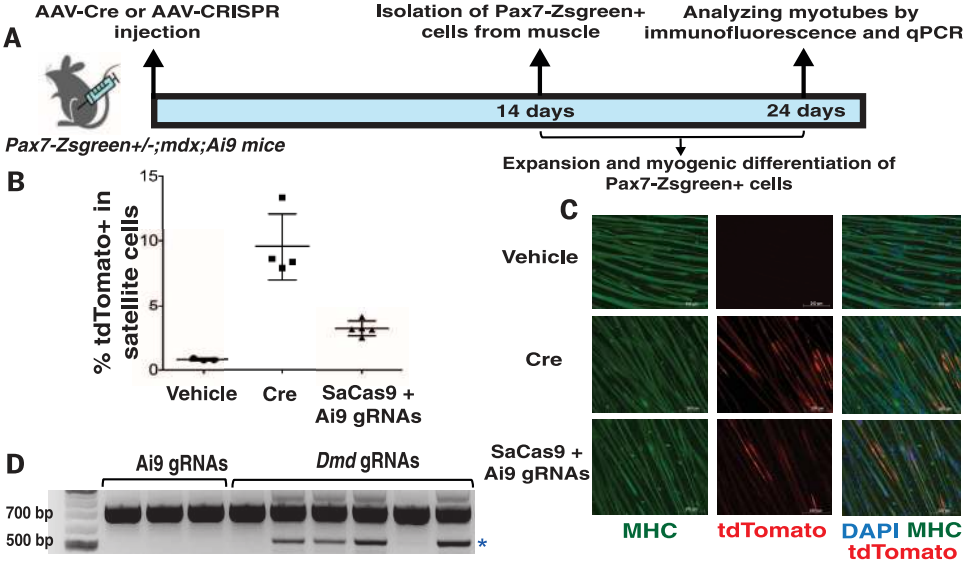

Fig. 4. Satellite cells in dystrophic muscles are transduced and targeted with systemically disseminated AAV-CRISPR. (**A**) Experimental design. (**B**) Percentage of ZsGreen+ satellite cells expressing tdTomato after intraperitoneal injection of *Pax7-ZsGreen*$^{+/-}$*;mdx;Ai9* mice. Individual data points overlaid with mean ± SD; vehicle (n = 3), AAV-Cre (n = 4), AAV-Ai9 CRISPR (n = 5). (**C**) Representative immunofluorescence of myotubes differentiated from FACS sorted satellite cells from mice injected intraperitoneally with vehicle, AAV-Cre, or AAV-Ai9 CRISPR. Green, myosin heavy chain (MHC); red, tdTomato; blue, DAPI (nuclei). Scale bar, 200 μm. (**D**) Exon 23–deleted *Dmd* mRNA in satellite cell–derived myotubes from mice previously injected intraperitoneally with AAV-*Dmd* CRISPR (right lanes), compared with control AAV-Ai9 CRISPR (left lanes).

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SUPPLEMENTARY MATERIALS

www.sciencemag.org/content/351/6271/407/suppl/DC1
Materials and Methods
Supplementary Text
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