

1136 Supplementary materials for
1137 **Mini-dCas13X-mediated RNA editing restores dystrophin expression in a**
1138 **humanized mouse model of Duchenne muscular dystrophy**
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1167 dystrophin expression.

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1169 analysis *in vivo*.

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1171 analysis *in vivo*.

1172 Figure S13. Gene editing 3 weeks after systemic delivery of mxABEs in
1173 *DMD*^{E30mut} mice.

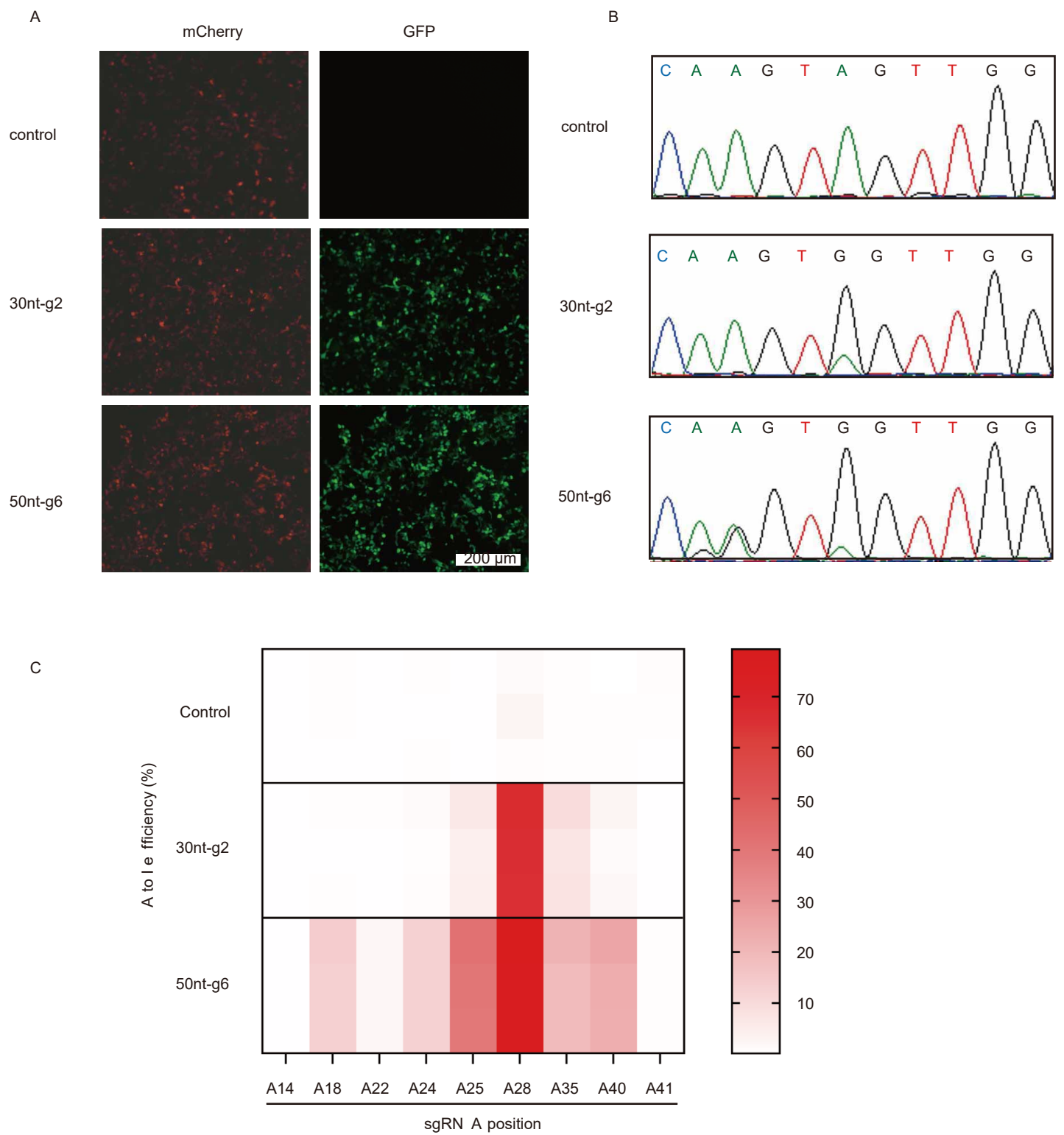
1174 Figure S14. AAV9-mxABE expression and dystrophin protein level after
1175 systemic delivery in *DMD*^{E30mut} mice.

1176 Figure S15. Histological analysis of dystrophin expression 3 weeks after
1177 systemic delivery of AAV9-mxABE in *DMD*^{E30mut} mice.

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1179 AAV9-mxABE.

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1187 systemic administration of AAV-mxABE.
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1189 untreated DMD^{E30mut} mice 6 months after systemic administration of
1190 AAV-mxABE.
1191 Figure S22. Host immune response to AAV-mxABE treatment indicates no
1192 overt toxicity after 6 months.
1193 Figure S23. Systemic delivery of AAV-mxABE rescues dystrophin deficiency in
1194 adult DMD^{E30mut} mice.
1195 Figure S24. Immunostaining of dystrophin in adult DMD^{E30mut} mice 6 weeks
1196 after systemic injection of AAV-mxABE.
1197 Tables S1. Target sgRNA and primer sequences.
1198 Supplemental Sequences
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Figure S1



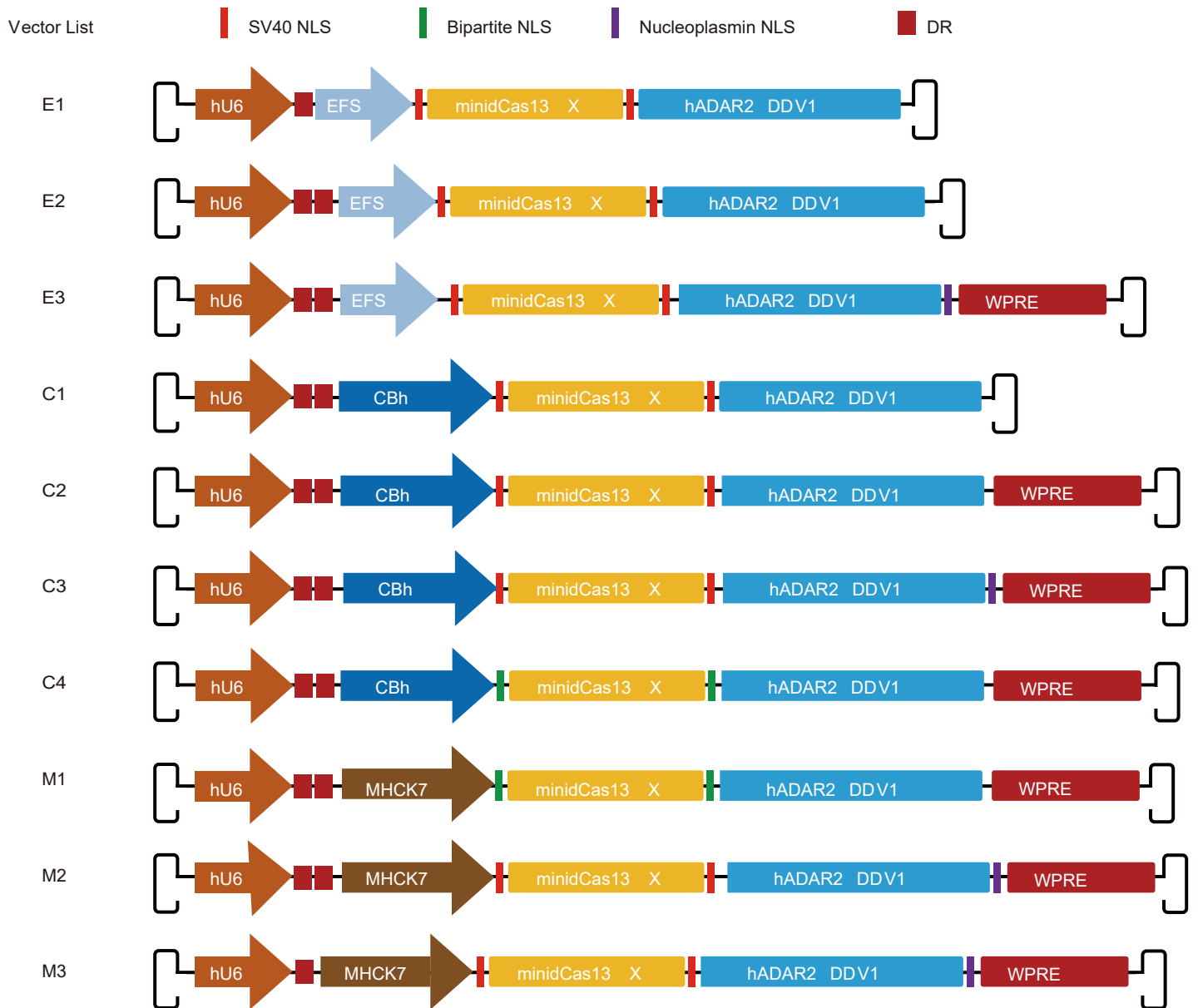
1224 **SUPPLEMENTAL FIGURES**

1225
1226 **Figure S1. *In vitro* studies of c.4174C>T mutation correction using**
1227 **mxABE constructs.**

1228 A. Fluorescence microscopy images of HEK293T cells transfected with
1229 reporter alone, or reporter and mxABE constructs. Scale bar, 200 μ m. B.
1230 Representative Sanger sequencing trace of reporter transcripts. C.
1231 Measurements of the representative gRNA (30 nt-g2 and 50 nt-g6) effect on
1232 bystander A to I editing efficiency (n=3).

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Figure S2



1268 **Figure S2. Construction of 10 mxABE expression cassettes.**

1269 The mxABE expression cassettes contained different promoters (EFS, CBh,
1270 MHCK7), direct repeat (DR) numbers (single, dual DR), nuclear localization
1271 signals (NLS), and were constructed with or without a translational regulatory
1272 element (WPRE).

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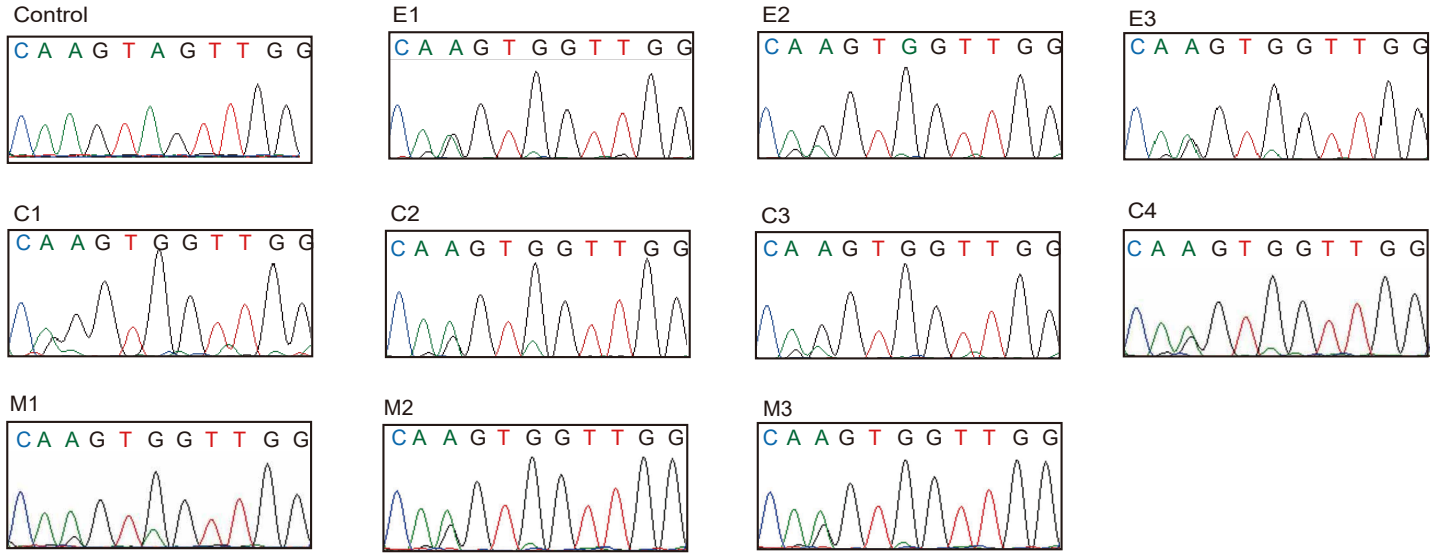
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Figure S3

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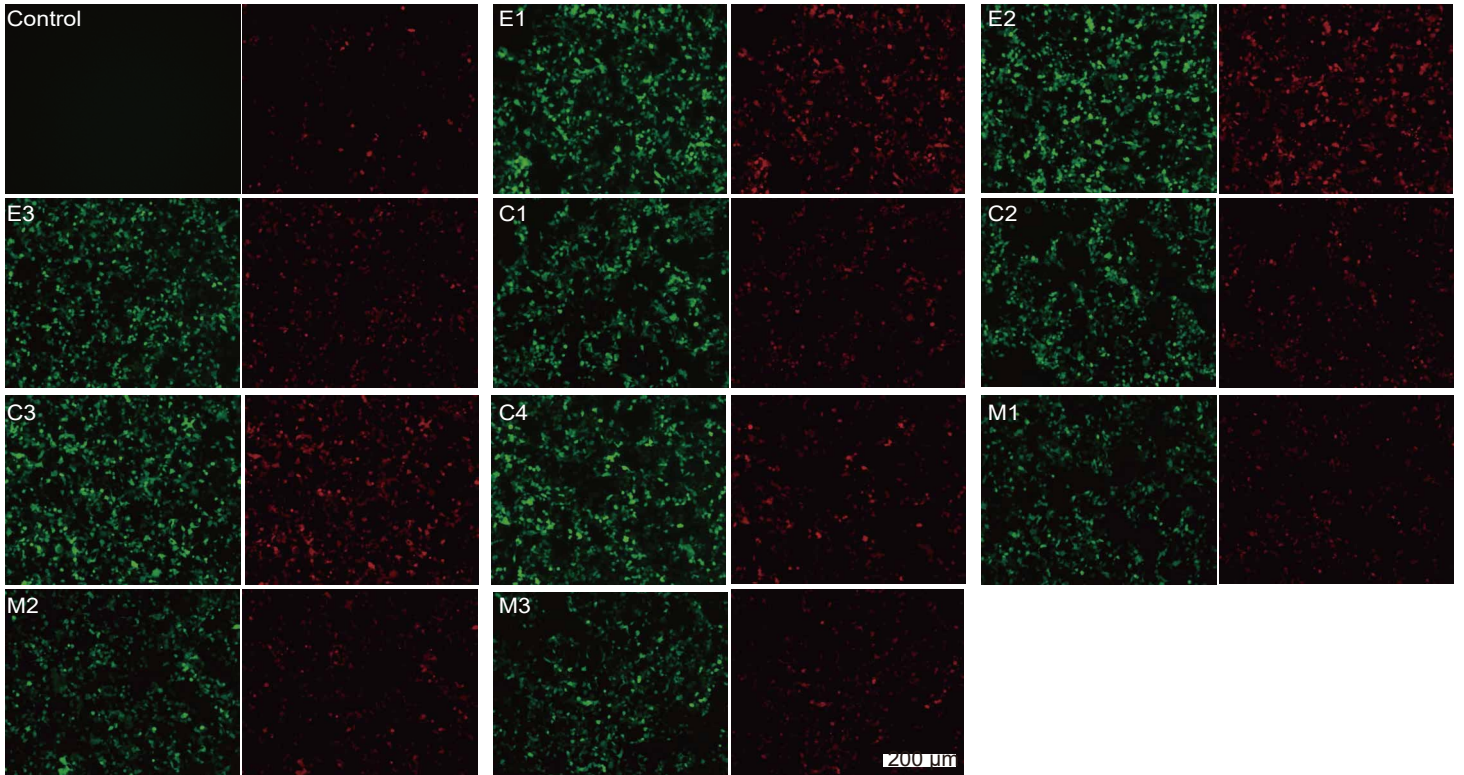
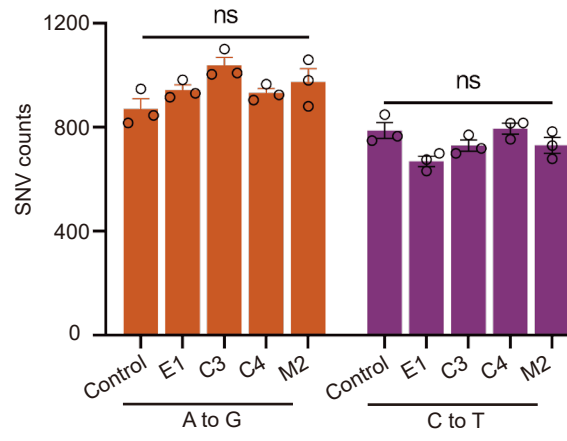


Figure S3. Representative Sanger sequencing trace of reporter transcripts.

A. Sanger sequencing results showing representative A to I conversion on reporter transcripts by different mxABE editors. B. Fluorescence microscopy images of HEK293T cells transfected with reporter alone or with reporter and mxABE construct. Scale bar, 200 μ m. Figure S3B and S1A showed similar results but from different experiments investigating the effect of gRNA length and construct expression elements on mutation correction efficiency respectively.

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Figure S4



1356 **Figure S4. Evaluation of SNV counts *in vitro* using transcriptome-wide**
1357 **off-target analysis.**

1358 The transcriptome-wide off-target effect of different mxABE constructs
1359 targeting the DMD c.4174C>T mutation were performed *in vitro*. The E1
1360 mxABE construct was driven by an EFS promoter; C3 and C4 were driven by
1361 an CBh promoter; and M2 was driven by an MHCK7 promoter. Non-targeting
1362 mxABE construct was analyzed as a control. Values are shown as mean \pm
1363 SEM (n=3). NS, not statistically significant in multiple comparison test using
1364 ANOVA (P< 0.01).

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Figure S5

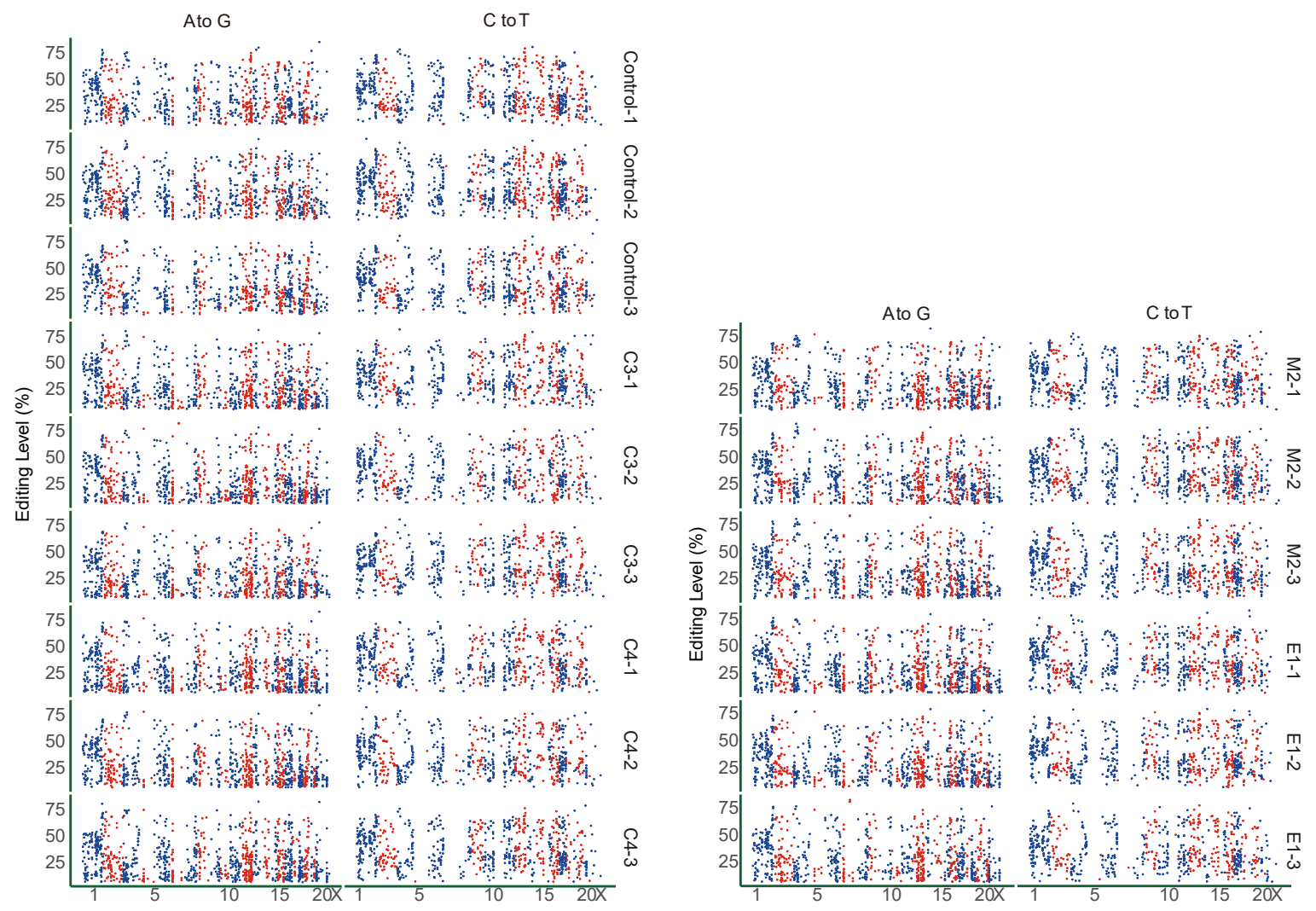
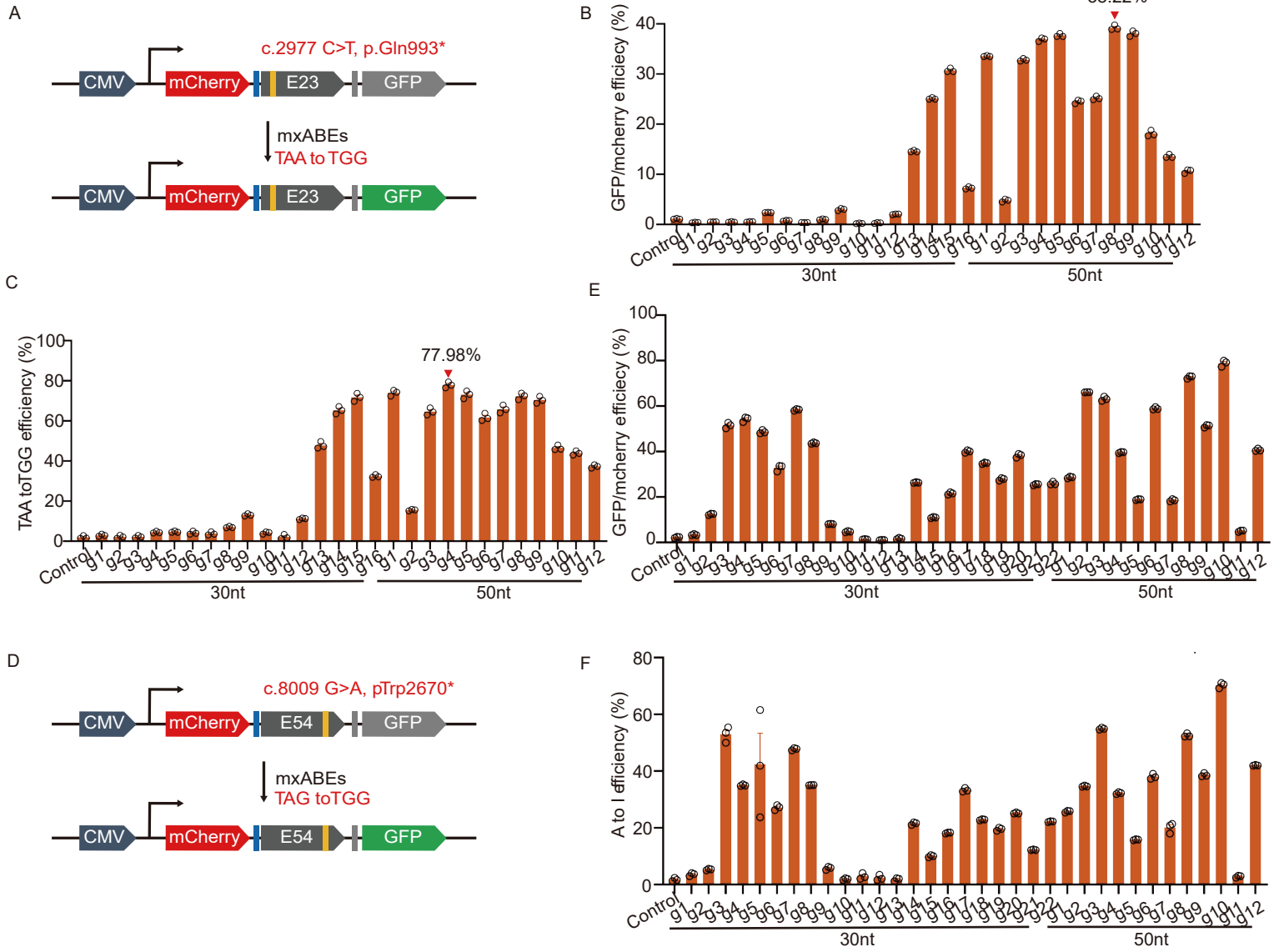


Figure S5. Manhattan plots of transcriptome-wide off-target RNA editing analysis for different mxABE constructs.

Non-targeting mxABE construct (control) and E1, C3, C4, and M2 constructs were transfected into HEK293T cells. mCherry-positive cells were sorted and endogenous transcripts were analyzed by deep sequencing. The x and y axes are proportionally enlarged with each Manhattan plot to make the axis legend clear (n=3).

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Figure S6



1444 **Figure S6. mxABE-mediated A to I correction of other mutations in the**
1445 ***DMD* gene.**

1446 Schematic diagram of reporter cassettes containing an mCherry sequence
1447 fused with 2A peptide, mutant human *DMD* exon 23 (A) or exon 54 (D) and
1448 ATG-removed GFP. Correction of the stop codon within the target sequence
1449 would allow EGFP expression. Flow cytometry analysis of GFP expression in
1450 HEK293T cells transfected with 28 gRNAs targeting exon 23 (B) and exon 54
1451 (E). Deep sequencing of the reporter RNA after GFP rescue experiment in
1452 exon 23 (C) and exon 54 (F). Data are represented as mean \pm SEM (n=3).

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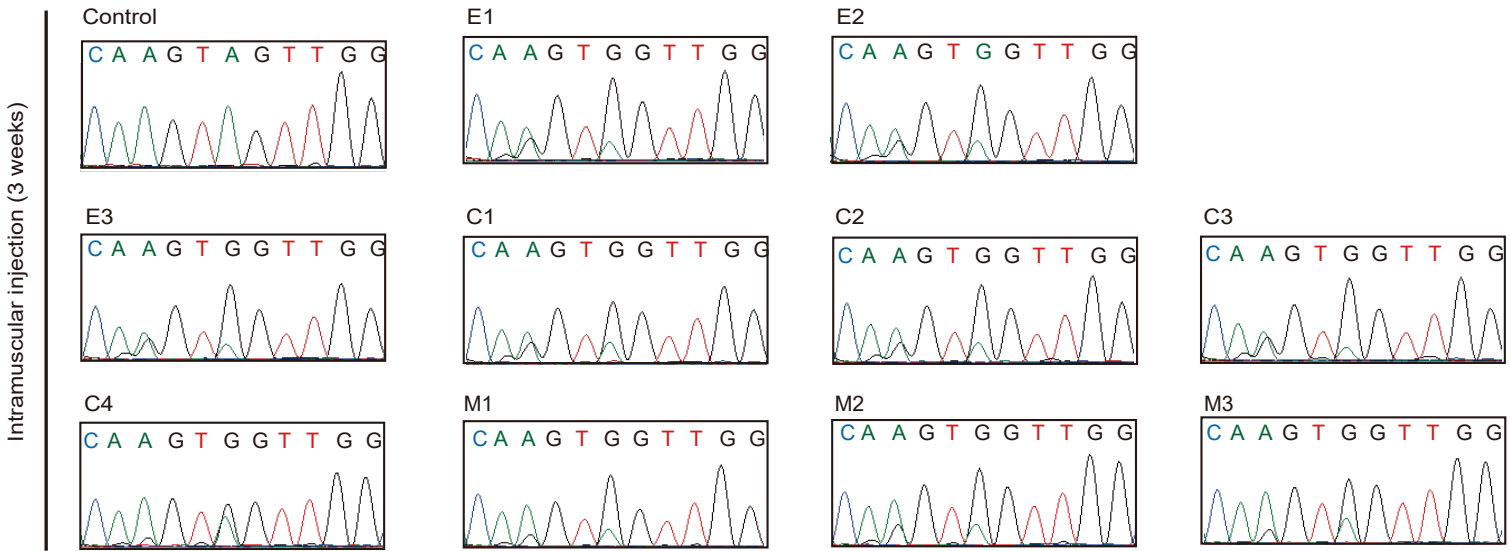
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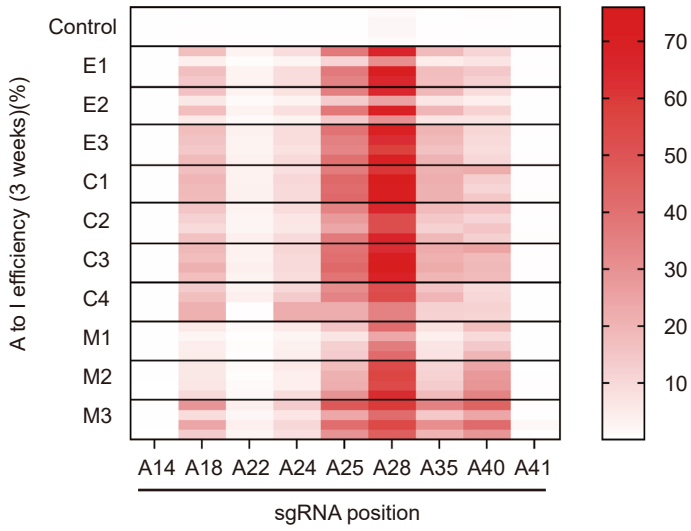
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Figure S7

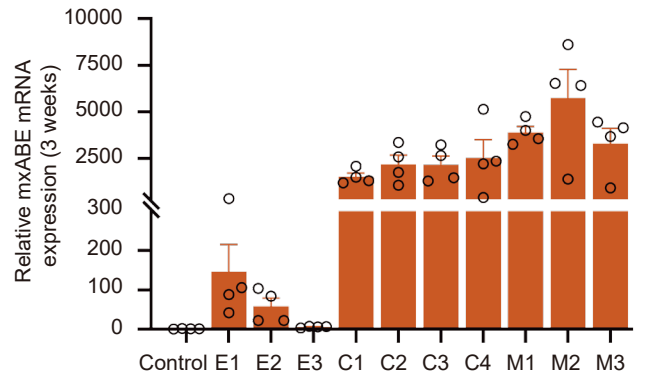
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1488 **Figure S7. *In vivo* DMD gene editing by IM injection with mxABEs at 3**
1489 **weeks.**

1490 A. Representative Sanger sequencing trace of *DMD* transcripts 3 weeks after
1491 IM injection with ten AAV9-mxABE particles. B. Heat map indicates the A>G
1492 edits in the vicinity of the target. C. qPCR analysis of mxABE expression in TA
1493 muscles 3 weeks after intramuscular injection. Values are shown as mean \pm
1494 SEM (n=4).

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Figure S8

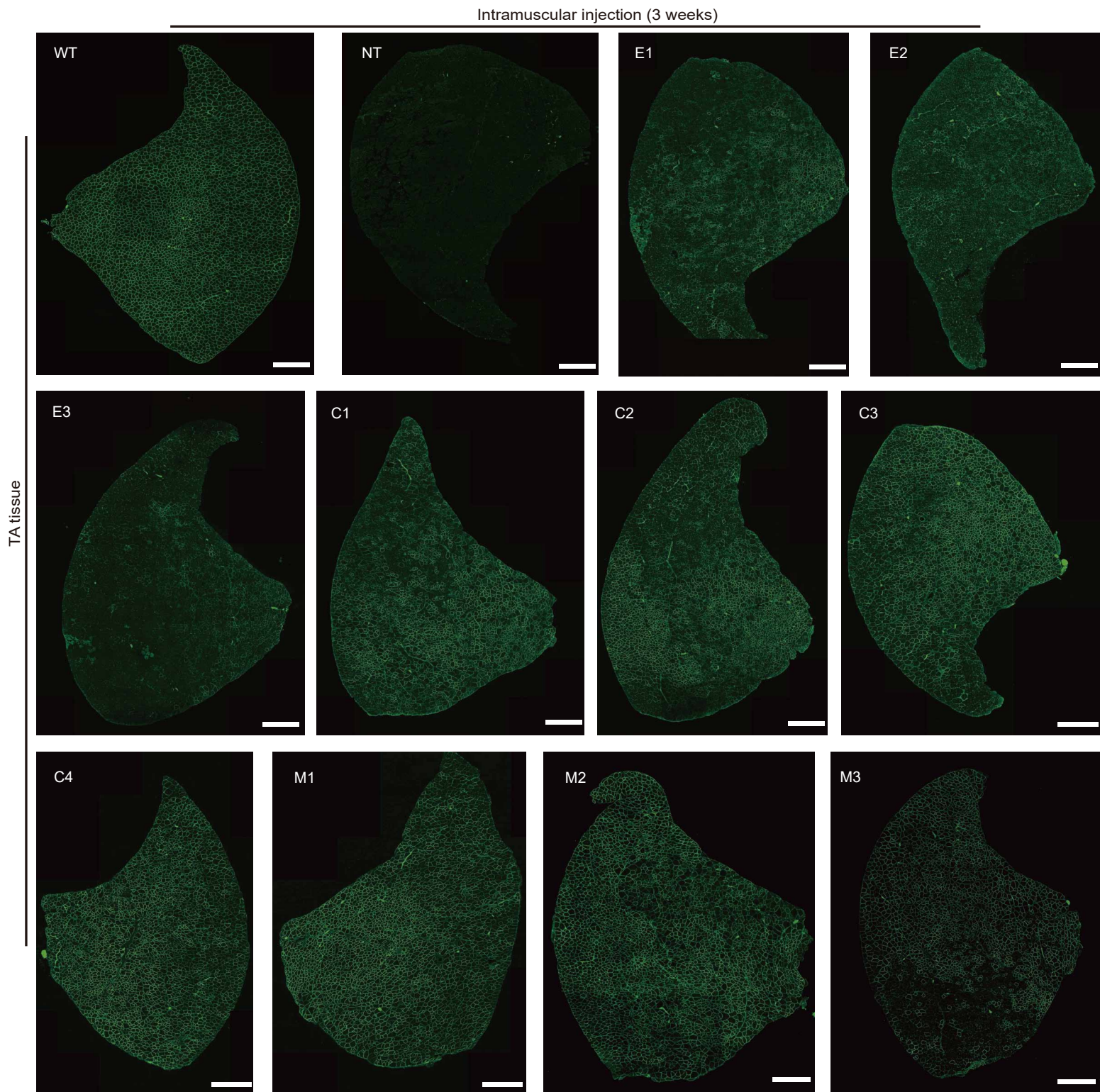
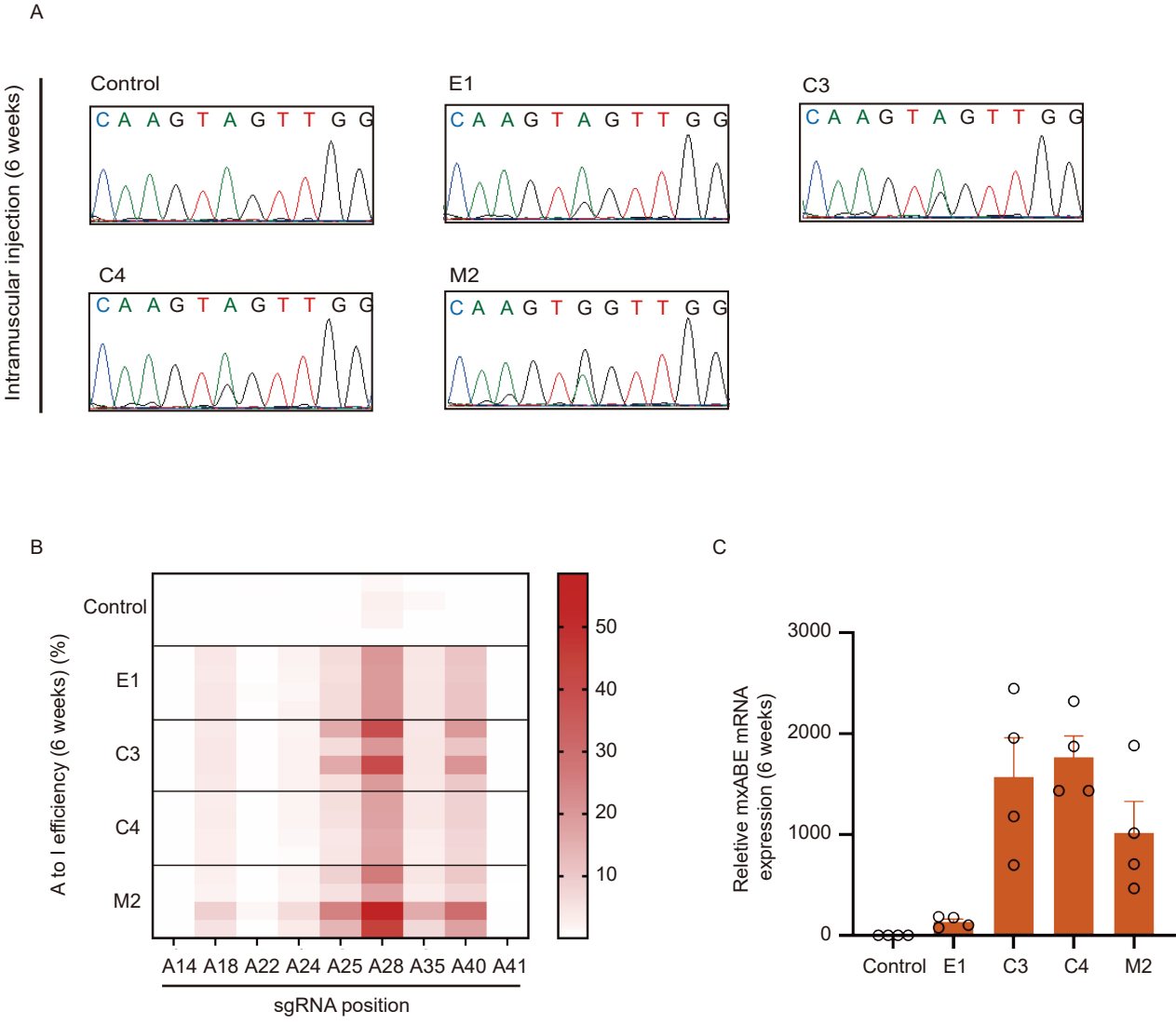


Figure S8. Rescue of dystrophin expression following IM injection of mxABEs in DMD^{E30mut} mice.

Dystrophin immunohistochemistry of entire TA muscle. Control mice were injected with saline. Dystrophin (Abcam, ab15277) is shown in green. Scale bar, 500 μ m.

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Figure S9



1576 **Figure S9. In vivo *DMD* gene editing by IM injection with mxABEs after 6**
1577 **weeks.**

1578 A. Representative Sanger sequencing trace of *DMD* transcripts 6 weeks after
1579 IM injection with four AAV9-mxABE particles. B. Heat map indicates the A>G
1580 edits in the vicinity of the target. C. qPCR analysis of mxABE expression in TA
1581 muscles 6 weeks after intramuscular injection. Values are shown as mean \pm
1582 SEM (n=4).

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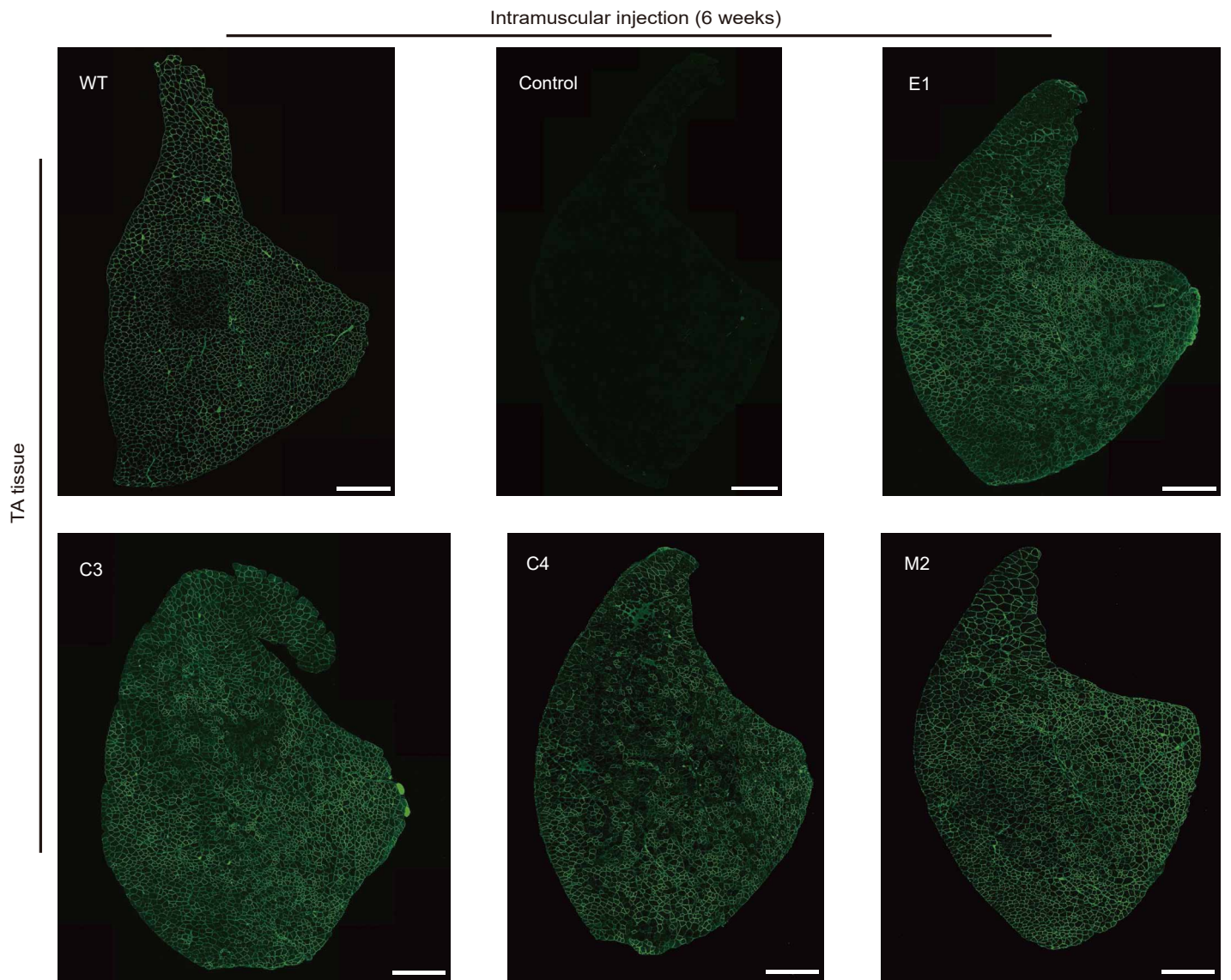
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1620 **Figure S10. Intramuscular AAV9 delivery of gene editing components**
1621 **rescues dystrophin expression.**

1622 Immunohistochemistry of dystrophin in entire TA muscle 6 weeks after
1623 intramuscular AAV9 delivery. Control mice were injected with saline.
1624 Dystrophin (Abcam, ab15277) is showed in green. Scale bar, 500 μ m.

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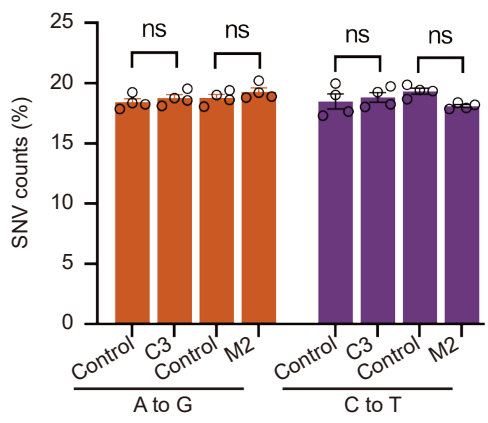
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Figure S11



1664 **Figure S11. Calculation of SNV counts by transcriptome-wide off-target**
1665 **analysis *in vivo*.**

1666 The transcriptome-wide off-target effect of two AAV9-mxABEs (C3 and M2)
1667 were analyzed *in vivo*. Control mice were injected with saline. Values are
1668 shown as mean \pm SEM (n=4). NS, not statistically significant using unpaired
1669 two-tailed Student's t tests (P<0.01).

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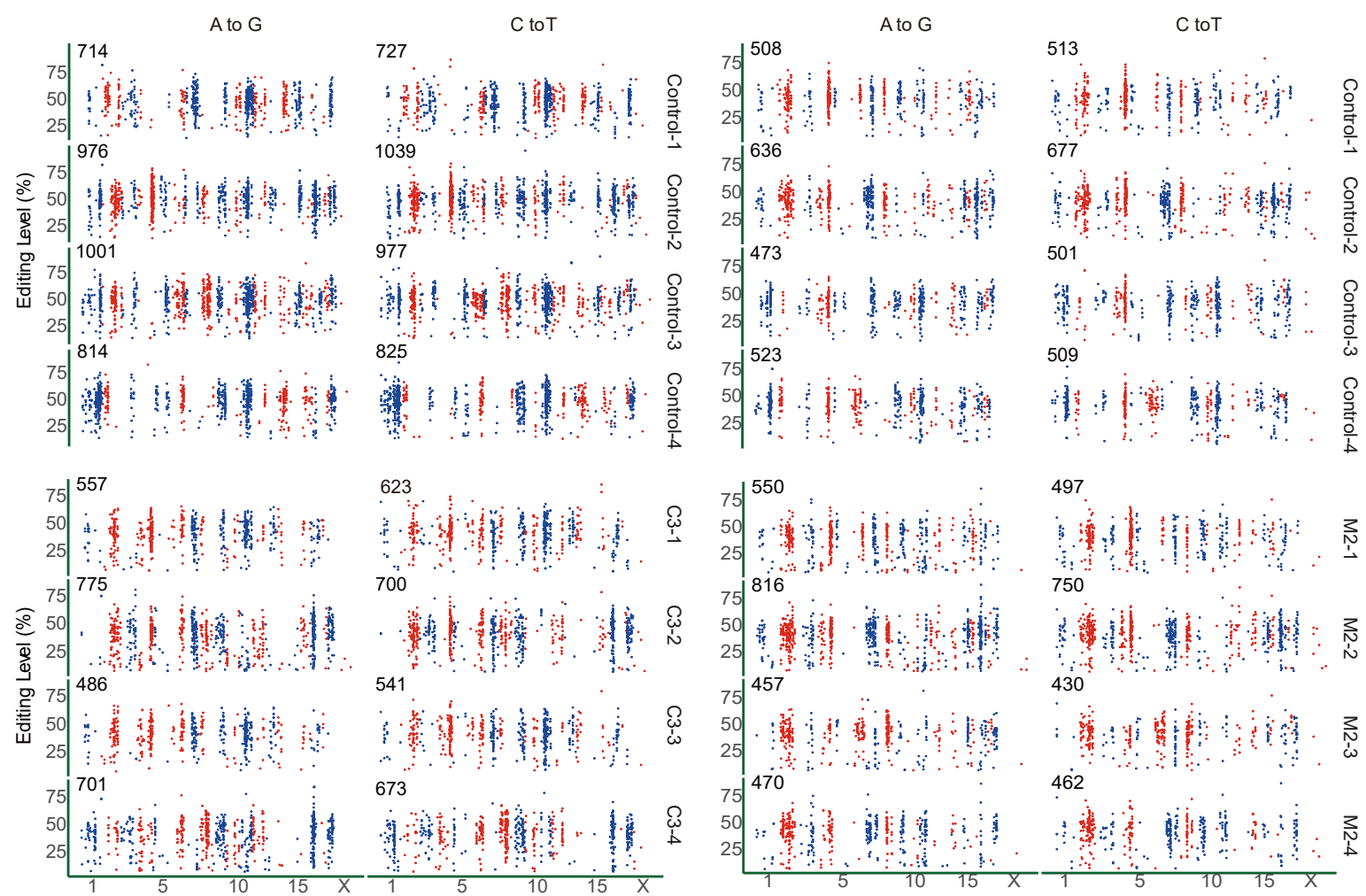
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Figure S12



1708 **Figure S12. Manhattan plots of transcriptome-wide off-target RNA editing**
1709 **analysis *in vivo*.**

1710 Control mice were injected with saline. The x and y axes are proportionally
1711 enlarged with each Manhattan plot to make the axis legend clear. n=4.

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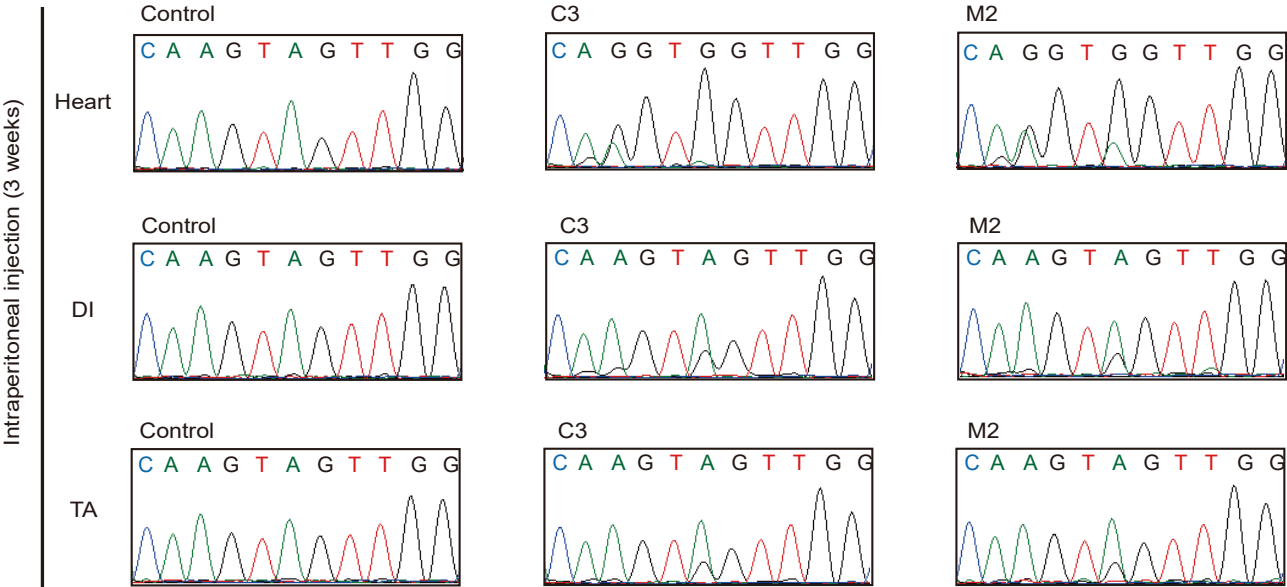
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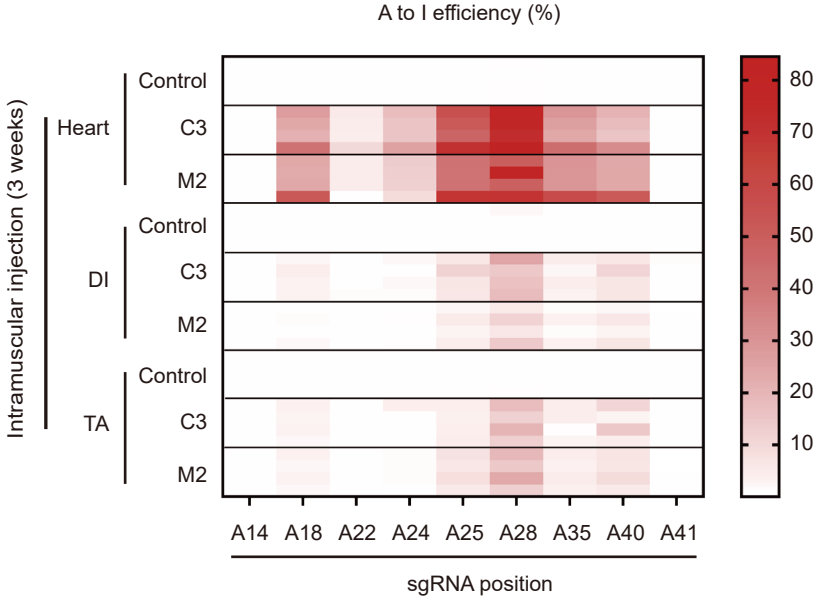
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Figure S13

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1752 **Figure S13. Gene editing 3 weeks after systemic delivery of mxABEs in**
1753 **DMD^{E30mut} mice.**

1754 A. Representative Sanger sequencing trace of *DMD* transcripts in TA, DI, and
1755 cardiac muscle 3 weeks after intraperitoneal (IP) injection with C3 and M2
1756 particles. B. Heat map indicates the A>G edits in the vicinity of the target in
1757 indicated tissues. n=4.

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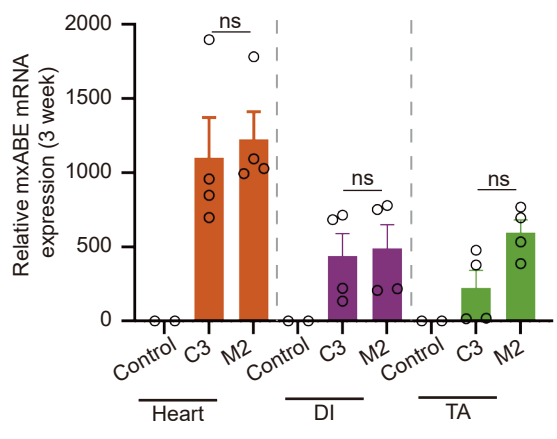
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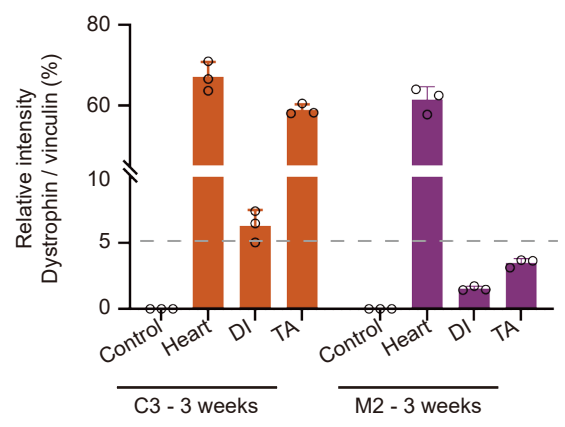
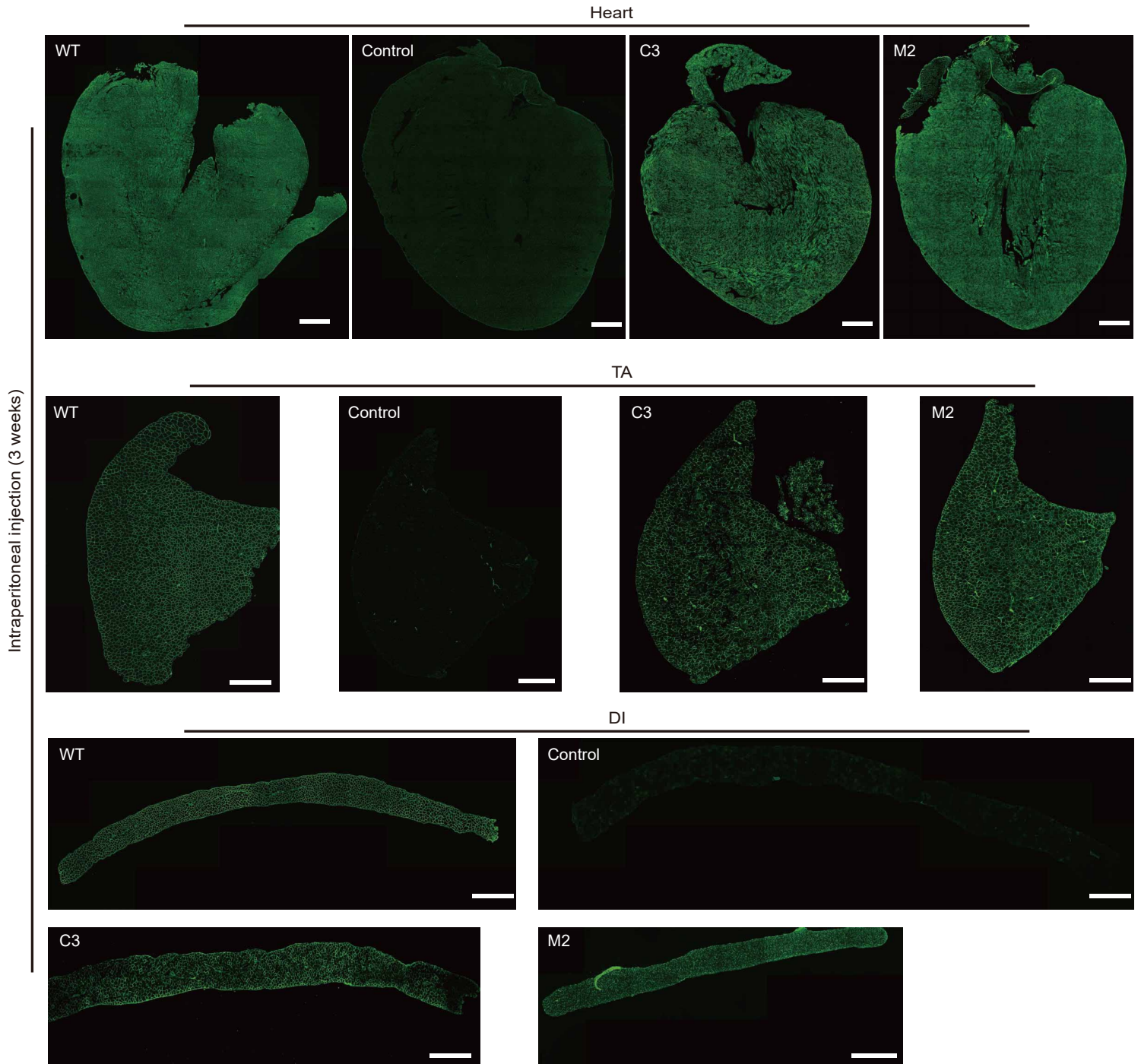


Figure S14. AAV9-mxABE expression and dystrophin protein levels after systemic delivery in DMD^{E30mut} mice.

A. qPCR analysis of mxABE expression in TA, DI, and heart muscles 3 weeks after systemic delivery (n=4). B. Relative dystrophin (Sigma, D8168) intensity was calibrated against a vinculin (CST, 13901S) internal control before normalizing to the WT control. The results showed restoration of dystrophin in TA, DI, and heart muscles of DMD^{E30mut} mice 3 weeks after systemic delivery of AAV9-packaged C3 and M2 (n=3). Values are shown as mean ± SEM. NS, not statistically significant using unpaired two-tailed Student's t tests (P<0.01).

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Figure S15



1840 **Figure S15. Histological analysis of dystrophin expression 3 weeks after**
1841 **systemic delivery of AAV9-mxABE in DMD^{E30mut} mice.**

1842 Whole-muscle scanning of TA, DI, and heart of DMD^{E30mut} mice 3 weeks after
1843 systemic delivery AAV9-C3 and M2 particles. Control mice were injected with
1844 saline. Dystrophin (Abcam, ab15277) is showed in green. Scale bar, 500 μ m.

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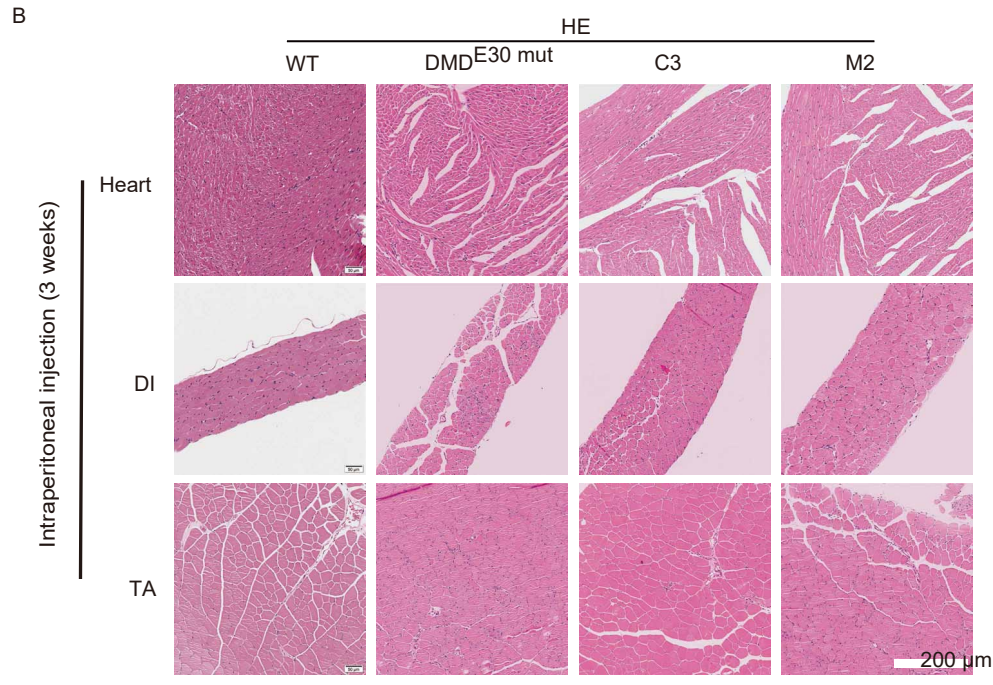
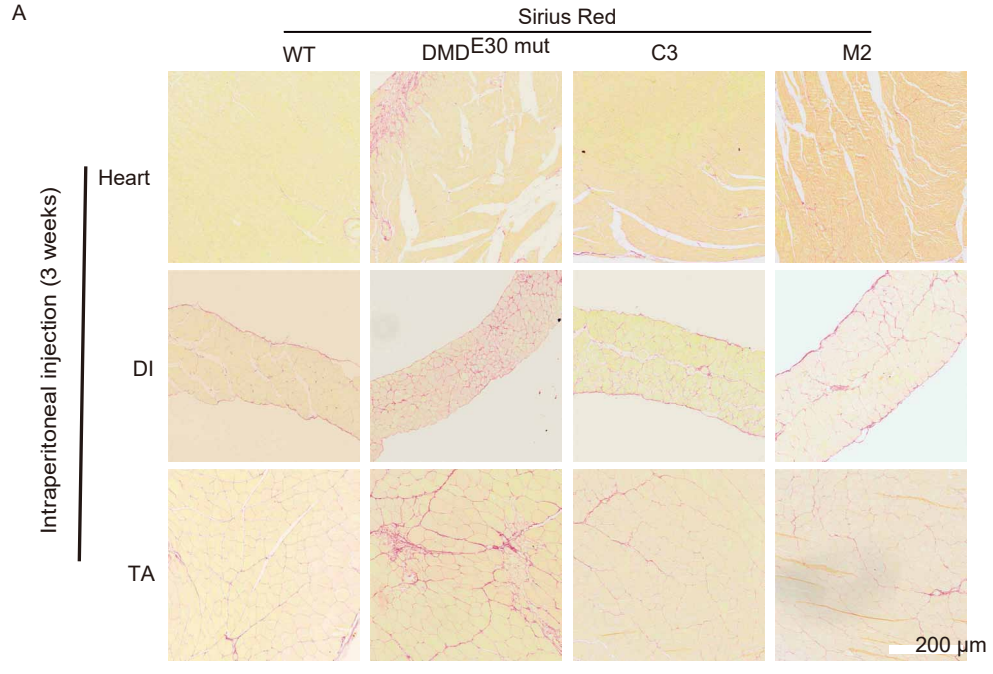
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Figure S16

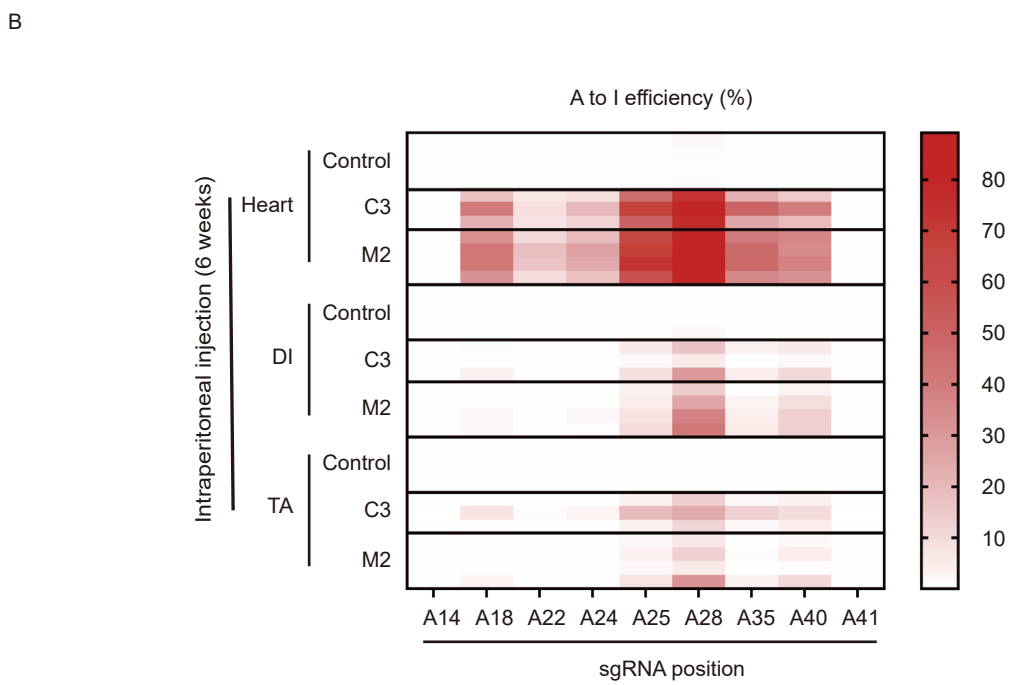
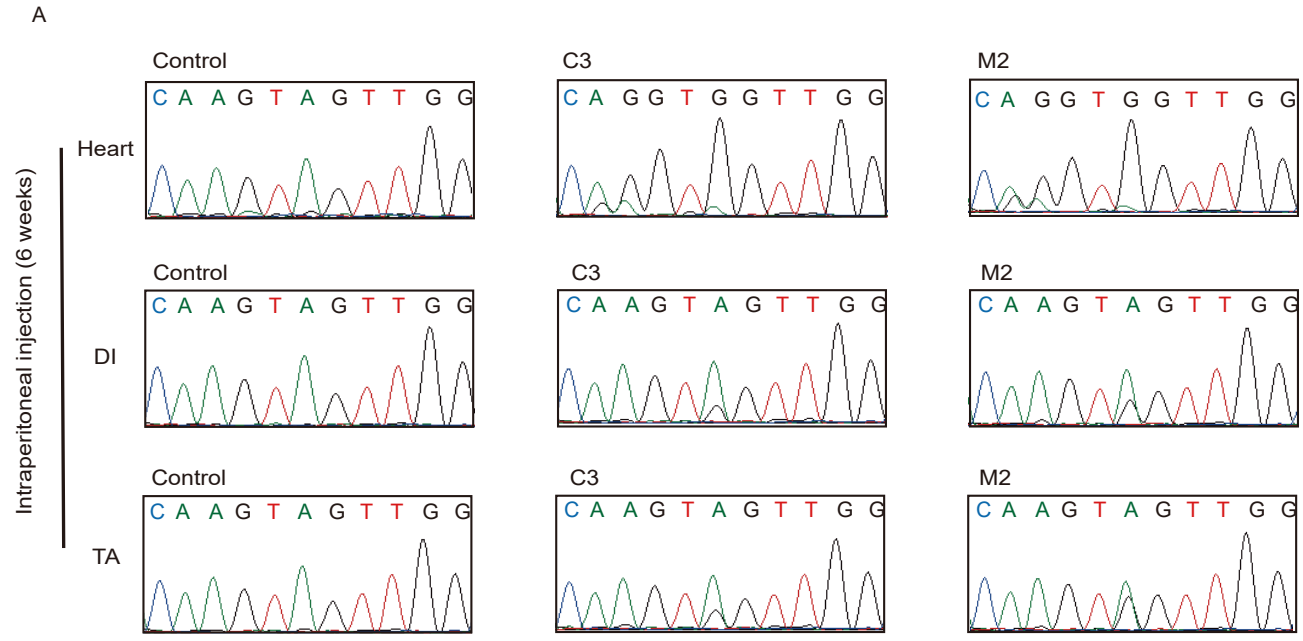


1884 **Figure S16. Histological analysis 3 weeks after systemic delivery of**
1885 **AAV9-mxABE.**

1886 Sirius red staining (A) and HE staining (A) of TA, DI, and heart of WT,
1887 untreated DMD^{E30mut} mice and DMD^{E30mut} mice treated with AAV9-mxABE 3
1888 weeks after systemic injection. n=4 for each group. Scale bars, 200 μ m.

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Figure S17



1928 **Figure S17. Base editing efficiency achieved by systemic delivery of**
1929 **mxABE after 6 weeks.**

1930 A. Representative Sanger sequencing trace of *DMD* transcripts in TA, DI, and
1931 heart tissues 6 weeks after intraperitoneal (IP) injection with C3 and M2
1932 particles. B. Heat map shows base editing rates in tissues indicated after IP
1933 injection with C3 (n=3) and M2 (n=4).

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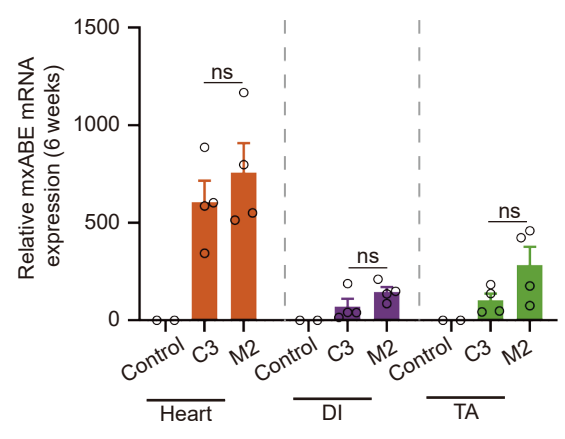
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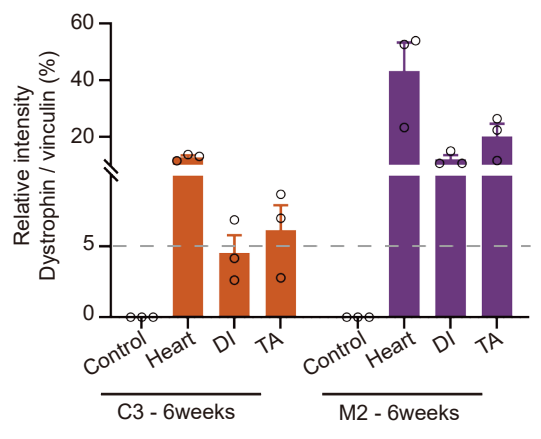
1971

Figure S18

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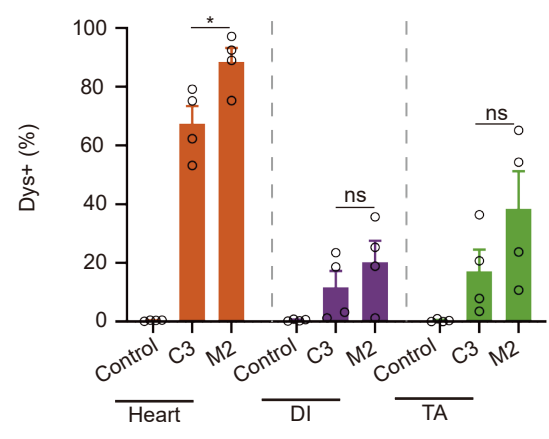


Figure S18. mxABE expression and dystrophin restoration level after 6-week administration of AAV-mxABE systemically.

A. qPCR analysis of mxABE expression in TA, DI, and heart muscles 6 weeks after systemic delivery (n=4). B. Relative dystrophin (Sigma, D8168) intensity was calibrated against a vinculin (CST, 13901S) internal control before normalizing to the WT control. The results showed restoration of dystrophin in TA, DI, and cardiac muscles of DMD^{E30mut} mice 6 weeks after systemic delivery of C3 and M2 AAV-mxABE (n=3). C. Percentage of Dys+ tissue area in TA, DI, and heart from treated and untreated DMD^{E30mut} mice (n=4). Values are shown as mean ± SEM. NS, not statistically significant using unpaired two-tailed Student's t test (P<0.01).

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Figure S19

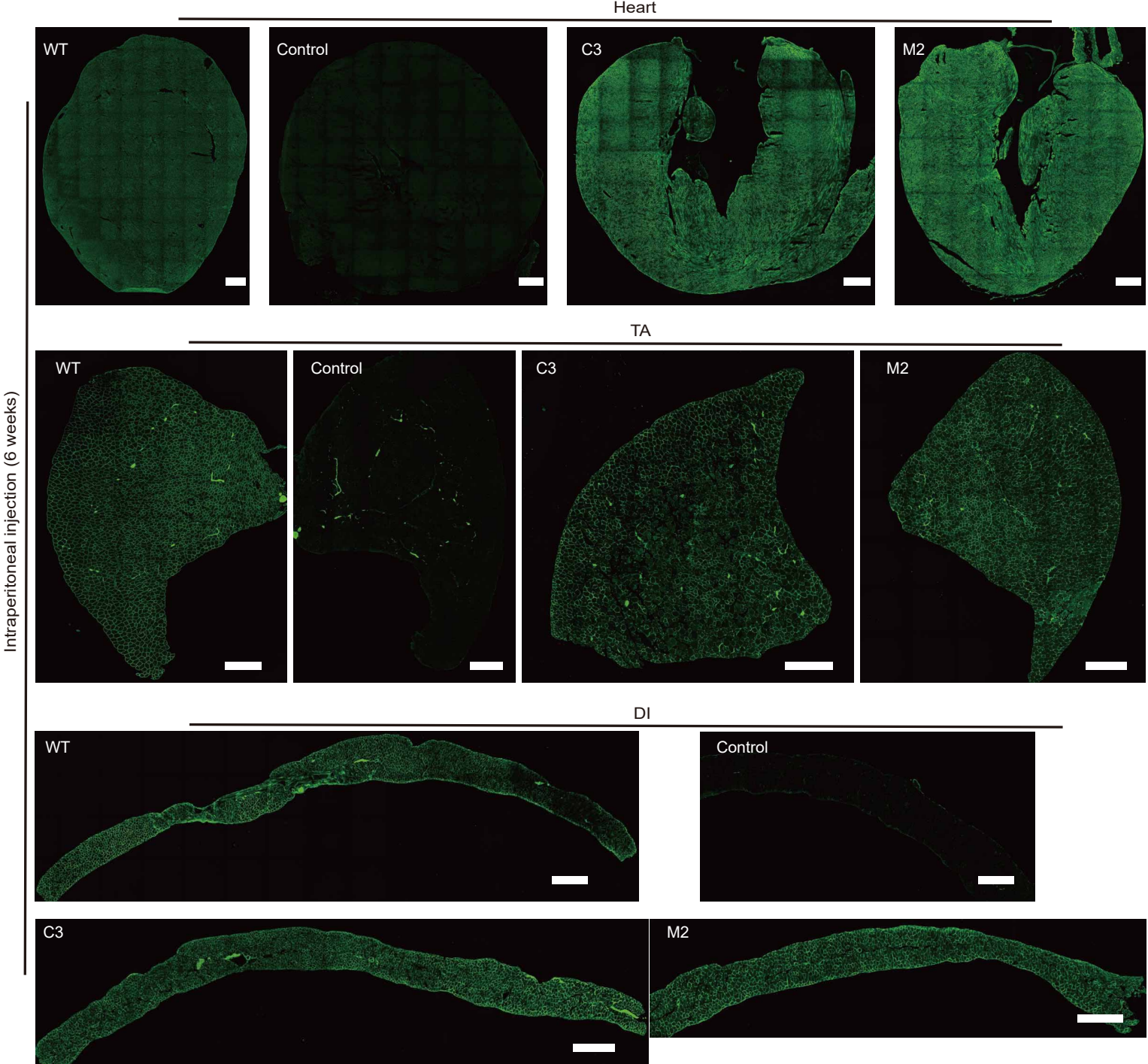


Figure S19. Immunostaining of dystrophin in heart, TA, and DI tissues 6 weeks after systemic administration of AAV-mxABE.

Whole-muscle scanning of TA, DI, and heart muscle of DMD^{E30mut} mice 6 weeks after systemic delivery of AAV9-C3 and M2 particles. Control mice were injected with saline. Dystrophin (Abcam, ab15277) is shown in green. Scale bar, 500 μ m. Images shown in both Figure 6C and Figure S19 were obtained from the same tissue at 20x magnification. Figure 6C showed the local region staining image rather than the reconstituted whole-tissue scanning image in Figure S19.

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Figure S20

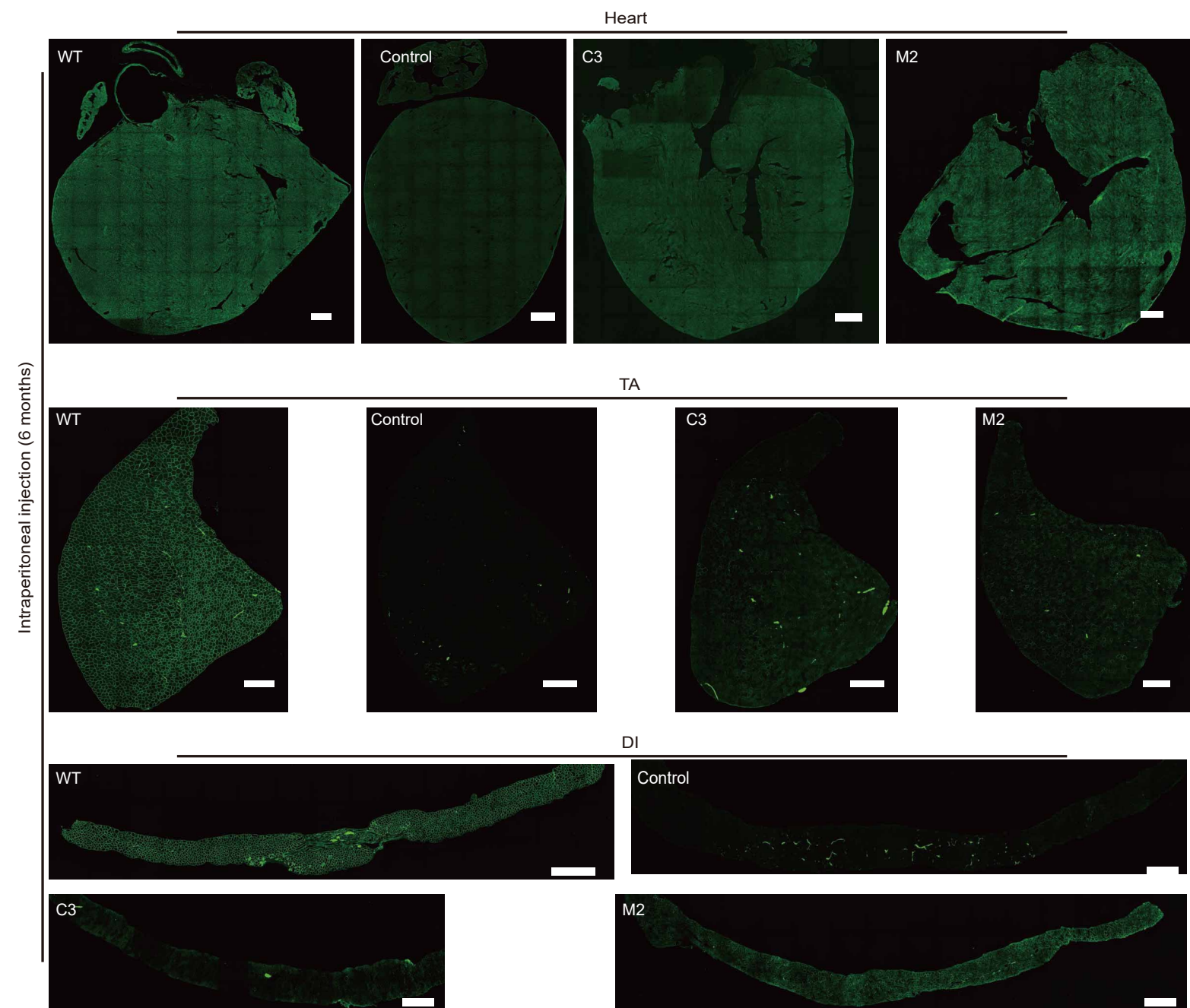
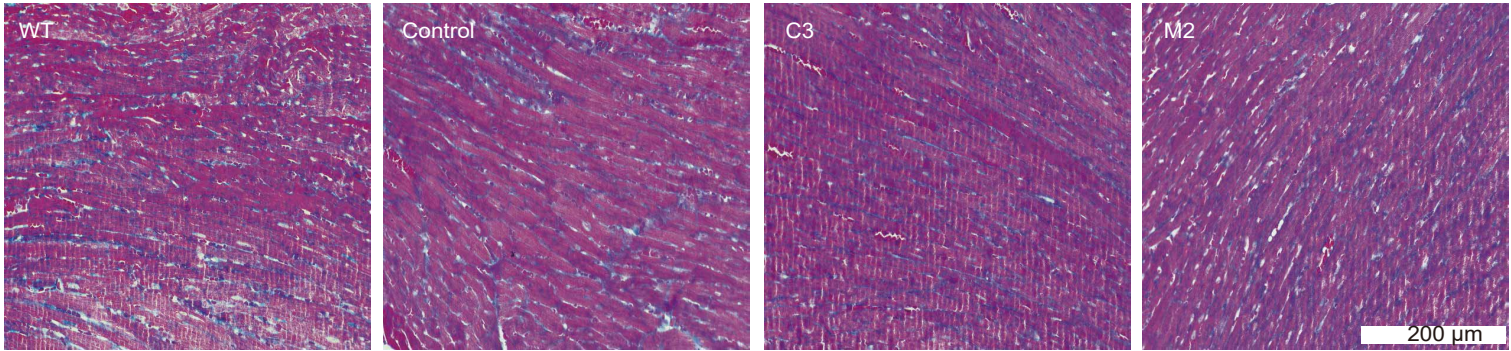


Figure S20. Immunostaining of dystrophin in heart, TA, and DI 6 months after systemic administration of AAV-mxABE.

Whole-muscle scanning of TA, DI, and heart muscle of DMD^{E30mut} mice 6 months after systemic delivery of AAV9-C3 and M2 particles. Control mice were injected with saline. Dystrophin (Abcam, ab15277) is shown in green. Scale bar, 500 μ m.

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Figure S21



2104 **Figure S21. Collagen staining shows no obvious fibrosis in treated and**
2105 **untreated hearts 6 months after systemic administration of AAV-mxABE.**
2106 Scale bar, 200 μm .

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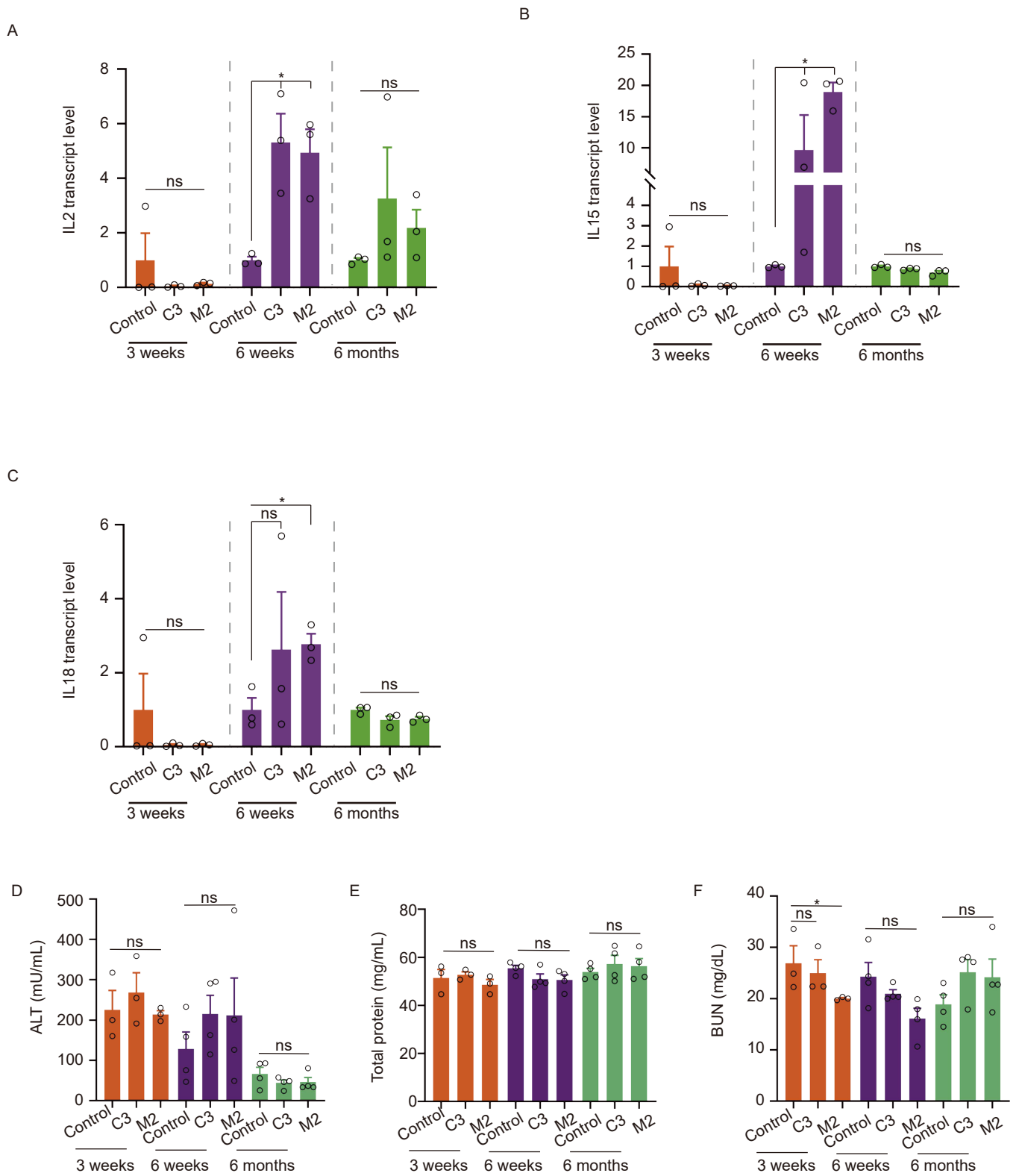
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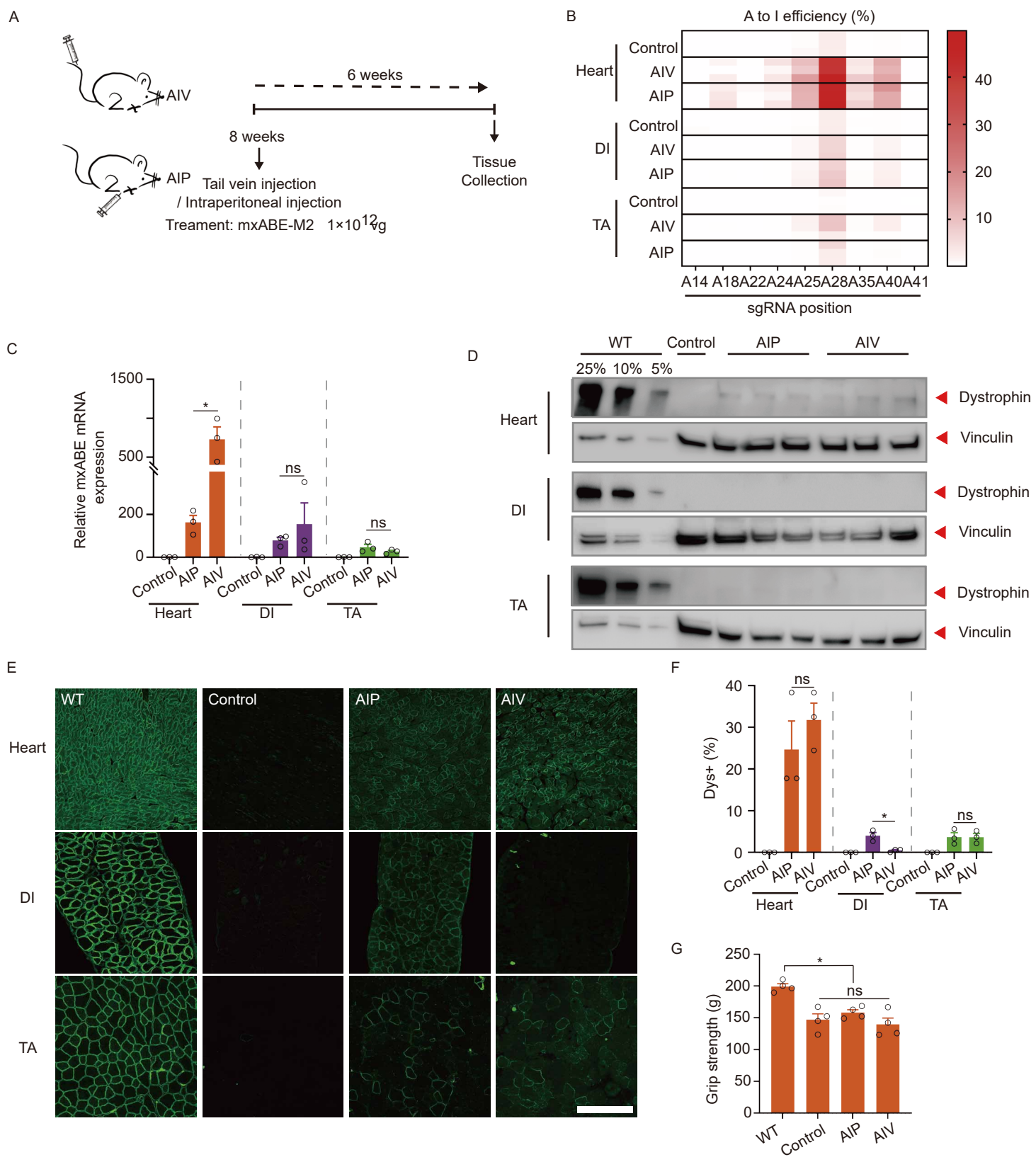


2148 **Figure S22. Host immune response to AAV-mxABE treatment indicates**
2149 **no overt toxicity after 6 months.**

2150 (A-C) IL2, IL15, and IL18 transcript levels at baseline for untreated mice, 3
2151 weeks, 6 weeks, and 6 months for treated mice (n=3). (D-F) No obvious
2152 change in ALT, total protein and BUN level after AAV-mxABE treatment (n=3).
2153 Significance is indicated by asterisk ($P < 0.05$). NS represents not statistically
2154 significant using unpaired two-tailed Student's t test.

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Figure S23

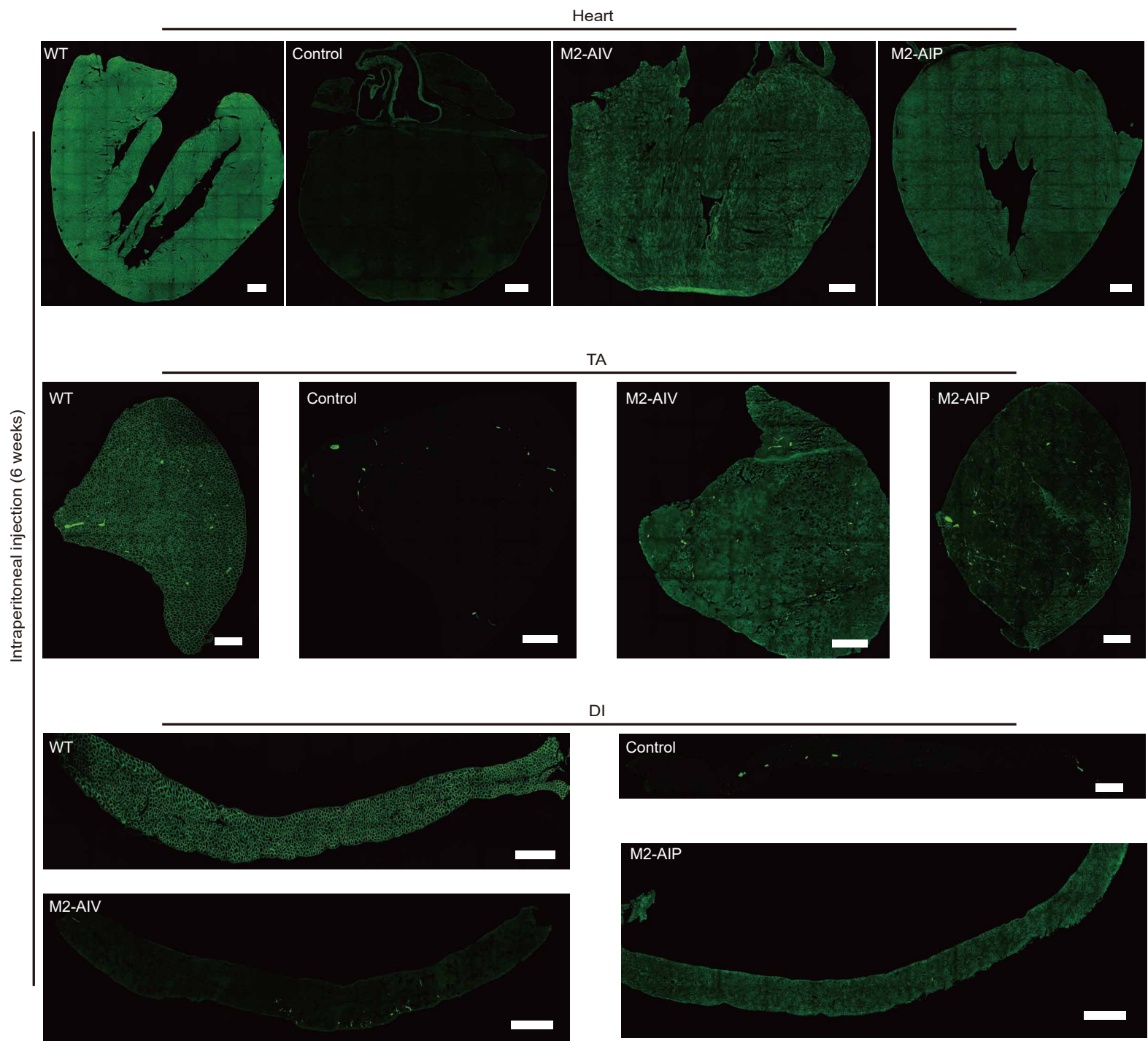


2192 **Figure S23. Systemic delivery of AAV-mxABE rescued dystrophin**
2193 **deficiency in adult DMD^{E30mut} mice.**

2194 A. Experimental design for mxABE administration and therapeutic analysis in
2195 adult DMD^{E30mut} mice. Both intravenous (AIV group) and intraperitoneal (AIP
2196 group) injection of AAV-mxABE were evaluated. B. Heatmap shows base
2197 editing rate in heart, DI, and TA muscles (n=3). C. mxABE expression level in
2198 heart, DI, and TA muscles. D. Dystrophin restoration level analyzed by western
2199 blot in heart, DI, and TA muscles of treated and untreated mice. E. Tissue
2200 section immunostaining for dystrophin in heart, DI, and TA muscles of treated
2201 and untreated mice. Scale bar, 200 μ m. F. Quantification of Dys+
2202 immunostaining in (E) (n=3). G. Forelimb grip strength was measured in WT,
2203 DMD^{E30mut} mice, and DMD^{E30mut} mice treated with AAV9-M2 (n=4).
2204 Significance is indicated by asterisk ($P < 0.05$). NS represents not statistically
2205 significant using unpaired two-tailed Student's t test.

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Figure S24



2236 **Figure S24. Immunostaining of dystrophin in adult DMD^{E30mut} mice 6**
2237 **weeks after systemic injection of AAV-mxABE.**

2238 Scale bar, 500 μ m.

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Supplementary Table S1: Target sgRNA and primer sequence.

Experiment	Primer name	Primer sequence (5'-3')
sgRNA for generation DMD ^{E30mut} model	DMD-T7sgRNA1	CTTCTTCTATTTAGGCTGTG
	DMD-T7sgRNA2	AGCTTATATCACTGACAAGG
Genotyping of DMD ^{E30mut} mice	DMD ^{E30mut} -2333F	ATTCATATAGGGCTTCAGTTCC
	DMD ^{E30mut} -2333R	CATCTGTTTTAATAGTGTGCAT
RT-PCR primer flanking exon 30	RT-DMD-358F	AATCAGATTCGTCTATTGGCACA
	RT-DMD-358R	CCCTTTGGTTGGCATCCTT
RNA base editing sgRNA for exon 30	30nt-g1	GCTGCCAACCACCTTGCAATGAATGTGAGG
	30nt-g2	AGCTGCCAACCACCTTGCAATGAATGTGAG
	30nt-g3	TGCAATATAAGCTGCCAACCACCTTGCAAT
	30nt-g4	CTGCAATATAAGCTGCCAACCACCTTGCAA
	30nt-g5	AAGCTGCCAACCACCTTGCAATGAATGTGA
	30nt-g6	TAAGCTGCCAACCACCTTGCAATGAATGTG
	30nt-g7	ATAAGCTGCCAACCACCTTGCAATGAATGT
	30nt-g8	TATAAGCTGCCAACCACCTTGCAATGAATG
	30nt-g9	ATATAAGCTGCCAACCACCTTGCAATGAAT
	30nt-g10	AATATAAGCTGCCAACCACCTTGCAATGAA
	30nt-g11	CAATATAAGCTGCCAACCACCTTGCAATGA
	30nt-g12	GCAATATAAGCTGCCAACCACCTTGCAATG
	50nt-g1	TGCAATATAAGCTGCCAACCACCTTGCAATGAATGTGAGGGACTCCTGGA
	50nt-g2	CTGCAATATAAGCTGCCAACCACCTTGCAATGAATGTGAGGGACTCCTGG
	50nt-g3	CCACCTTGCTGCAATATAAGCTGCCAACCACCTTGCAATGAATGTGAGG
	50nt-g4	TCCACCTTGCTGCAATATAAGCTGCCAACCACCTTGCAATGAATGTGAG
	50nt-g5	TCTGCAATATAAGCTGCCAACCACCTTGCAATGAATGTGAGGGACTCCTG
	50nt-g6	GTCTGCAATATAAGCTGCCAACCACCTTGCAATGAATGTGAGGGACTCCT
	50nt-g7	TGTCTGCAATATAAGCTGCCAACCACCTTGCAATGAATGTGAGGGACTCC

	50nt-g8	TTGTCTGCAATATAAGCTGCCAACCCTTGTCAATGAATGTGAGGGACTC
	50nt-g9	CTTGTCTGCAATATAAGCTGCCAACCCTTGTCAATGAATGTGAGGGACT
	50nt-g10	CCTTGTCTGCAATATAAGCTGCCAACCCTTGTCAATGAATGTGAGGGAC
	50nt-g11	ACCTTGTCTGCAATATAAGCTGCCAACCCTTGTCAATGAATGTGAGGGA
	50nt-g12	CACCTTGTCTGCAATATAAGCTGCCAACCCTTGTCAATGAATGTGAGGG
RT-PCR primer for	RT-rep765F	CCACAACGAGGACTACACCA
Reporter	RT-rep765R	TCCTTGAAGTCGATGCCCTT
qPCR primer	GAPDH-119F	TCAACGACCCCTTCATTGACC
	GAPDH-119R	CTTCCCGTTGATGACAAGCTTC
	Cas13X-140F	GCCATGCAGAAATAATATCTCGG
	Cas13X-140R	CATTCTCCTTCAGCCTAAACCC
RNA base editing sgRNA for exon 23	50nt-g1	CTGAGATAGTATAGGCCACTccATTGCTCTTGCAGAGAACTTTGTAAAGC
	50nt-g2	GCTGAGATAGTATAGGCCACTCCATTGCTCTTGCAGAGAACTTTGTAAAG
	50nt-g3	TGCTGAGATAGTATAGGCCACTCCATTGCTCTTGCAGAGAACTTTGTAAA
	50nt-g4	GTGCTGAGATAGTATAGGCCACTCCATTGCTCTTGCAGAGAACTTTGTAA
	50nt-g5	GGTGCTGAGATAGTATAGGCCACTCCATTGCTCTTGCAGAGAACTTTGTA
	50nt-g6	TGGTGCTGAGATAGTATAGGCCACTCCATTGCTCTTGCAGAGAACTTTGT
	50nt-g7	GTGGTGCTGAGATAGTATAGGCCACTCCATTGCTCTTGCAGAGAACTTTG
	50nt-g8	CACAGTGGTGCTGAGATAGTATAGGCCACTCCATTGCTCTTGCAGAGAAC
	50nt-g9	TCACAGTGGTGCTGAGATAGTATAGGCCACTCCATTGCTCTTGCAGAGAA
	50nt-g10	AGTGGTGCTGAGATAGTATAGGCCACTCCATTGCTCTTGCAGAGAACTTT
	50nt-g11	CAGTGGTGCTGAGATAGTATAGGCCACTCCATTGCTCTTGCAGAGAACTT
	50nt-g12	ACAGTGGTGCTGAGATAGTATAGGCCACTCCATTGCTCTTGCAGAGAACT
	30nt-g1	TAGTATAGGCCACTCCATTGCTCTTGCAGA
	30nt-g2	ATAGTATAGGCCACTCCATTGCTCTTGCAG
	30nt-g3	GATAGTATAGGCCACTCCATTGCTCTTGCAG
	30nt-g4	AGATAGTATAGGCCACTCCATTGCTCTTGC
	30nt-g5	GAGATAGTATAGGCCACTCCATTGCTCTTGC
	30nt-g6	TGAGATAGTATAGGCCACTCCATTGCTCTTGC

	30nt-g7	CTGAGATAGTATAGGCCACTCCATTGCTCT
	30nt-g8	GCTGAGATAGTATAGGCCACTCCATTGCTC
	30nt-g9	TGCTGAGATAGTATAGGCCACTCCATTGCT
	30nt-g10	GTGCTGAGATAGTATAGGCCACTCCATTGC
	30nt-g11	GGTGCTGAGATAGTATAGGCCACTCCATTG
	30nt-g12	AGTATAGGCCACTCCATTGCTCTTGCAGAG
	30nt-g13	TAGGCCACTCCATTGCTCTTGCAGAGAACT
	30nt-g14	ATAGGCCACTCCATTGCTCTTGCAGAGAAC
	30nt-g15	TATAGGCCACTCCATTGCTCTTGCAGAGAA
	30nt-g16	GTATAGGCCACTCCATTGCTCTTGCAGAGA
RNA base editing sgRNA for exon 54	50nt-g1	TGTAATTCATACCTTTTATGAATGCTTCTCCAAGAGGCATTGATATTCTC
	50nt-g2	GTAATTCATACCTTTTATGAATGCTTCTCCAAGAGGCATTGATATTCTCT
	50nt-g3	CATACCTTTTATGAATGCTTCTCCAAGAGGCATTGATATTCTCTGTTATC
	50nt-g4	TCATACCTTTTATGAATGCTTCTCCAAGAGGCATTGATATTCTCTGTTAT
	50nt-g5	TTCATACCTTTTATGAATGCTTCTCCAAGAGGCATTGATATTCTCTGTTA
	50nt-g6	ATTCATACCTTTTATGAATGCTTCTCCAAGAGGCATTGATATTCTCTGTT
	50nt-g7	AATTCATACCTTTTATGAATGCTTCTCCAAGAGGCATTGATATTCTCTGT
	50nt-g8	TAATTCATACCTTTTATGAATGCTTCTCCAAGAGGCATTGATATTCTCTG
	50nt-g9	ATACCTTTTATGAATGCTTCTCCAAGAGGCATTGATATTCTCTGTTATCA
	50nt-g10	TACCTTTTATGAATGCTTCTCCAAGAGGCATTGATATTCTCTGTTATCAT
	50nt-g11	ACCTTTTATGAATGCTTCTCCAAGAGGCATTGATATTCTCTGTTATCATG
	50nt-g12	CCTTTTATGAATGCTTCTCCAAGAGGCATTGATATTCTCTGTTATCATGT
	30nt-g1	CATACCTTTTATGAATGCTTCTCCAAGAGG
	30nt-g2	TCATACCTTTTATGAATGCTTCTCCAAGAG
	30nt-g3	TTCATACCTTTTATGAATGCTTCTCCAAGA
	30nt-g4	ATACCTTTTATGAATGCTTCTCCAAGAGGC
	30nt-g5	TACCTTTTATGAATGCTTCTCCAAGAGGCA
	30nt-g6	ACCTTTTATGAATGCTTCTCCAAGAGGCAT
	30nt-g7	TCTCCAAGAGGCATTGATATTCTCTGTTAT

30nt-g8	TTCTCCAAGAGGCATTGATATTCTCTGTTA
30nt-g9	TATGAATGCTTCTCCAAGAGGCATTGATAT
30nt-g10	TTATGAATGCTTCTCCAAGAGGCATTGATA
30nt-g11	TTTATGAATGCTTCTCCAAGAGGCATTGAT
30nt-g12	TTTTATGAATGCTTCTCCAAGAGGCATTGA
30nt-g13	CTTTTATGAATGCTTCTCCAAGAGGCATTG
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30nt-g15	CTTCTCCAAGAGGCATTGATATTCTCTGTT
30nt-g16	GCTTCTCCAAGAGGCATTGATATTCTCTGT
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30nt-g18	AATGCTTCTCCAAGAGGCATTGATATTCTC
30nt-g19	GAATGCTTCTCCAAGAGGCATTGATATTCT
30nt-g20	TGAATGCTTCTCCAAGAGGCATTGATATTC
30nt-g21	ATGAATGCTTCTCCAAGAGGCATTGATATT
30nt-g22	ATGCTTCTCCAAGAGGCATTGATATTCTCT

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2302 **Supplemental sequences AAV constructs' sequences of C1 to C4, E1 to**
2303 **E4 and M1 to M3**

2304 C1 to C4 AAV constructs are CBh-driven mxABE. CBh promoter sequence is
2305 highlighted in red

2306 E1 to E4 AAV constructs are EFS-driven mxABE. EFS promoter sequence is
2307 highlighted in green

2308 M1 to M3 AAV constructs are MHCK7-driven mxABE. MHCK7 promoter
2309 sequence is highlighted in blue

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2313 CCTGCAGGCAGCTGCGCGCTCGCTCGCTCACTGAGGCCGCCCGGGCG
2314 TCGGGCGACCTTTGGTCGCCCCGGCCTCAGTGAGCGAGCGAGCGCGCA
2315 GAGAGGGAGTGGCCAACCTCCATCACTAGGGGTTCTGCGGCCTCTAGAg
2316 gagggcctattcccatgattcctcatattgcatatacgatacaaggctgtagagagataattggaattaatt
2317 tgactgtaaacacaaagatattagtaaaaaaacgtgacgtagaaagtaataatttcttgggtagttgacgttt
2318 taaaattatgttttaaaatggactatcatatgcttaccgtaactgaaagtatttcgatttcttggctttatatacttG
2319 TGGAAAGGACGAAACACCGGCTGGAGCAGCCCCCGATTTGTGGGGTGA
2320 TTACAGCgTCTGCAATATAAGCTGCCAACCACTTGTCAATGAATGTGAGGG
2321 ACTCctGCTGGAGCAGCCCCCGATTTGTGGGGTGATTACAGCTTTTTTTTc**cg**
2322 **ttacataacttacggtaaatggcccgctggctgaccgccaacgacccccgccattgacgtcaatagta**
2323 **acgccaatagggactttccattgacgtcaatgggtggagtatttacggtaaaactgccactggcagtacac**
2324 **aagtgtatcatatgccaaagtagccccctattgacgtcaatgacggtaaatggcccgctggcattGtccc**
2325 **agtacatgaccttatgggactttcctacttggcagtacatctacgtattagtcacgctattaccatggcaggt**
2326 **gagccccacgttctgcttactctccccatctccccccccctccccaccccccaatttgtattatttttaattat**
2327 **ttgtgcagcgtatggggcgggggggggggggggggcgcgccaggcgggcgggcgggcgag**
2328 **ggcgggggcgggcgaggcgagaggtgcgggcgagccaatcagagcggcgcgctccgaaagttt**
2329 **cctttatggcgaggcgggcgggcgggcgggcctataaaaagcgaagcgcgggcgggcgggagtcgc**
2330 **tgcgacgctgccttcgccccgtccccgctccgcccgcctcgcgcccggccccggctctgactgacc**
2331 **gcgttactcccacaggtgagcggggcgggacggcccttctcctccgggctgtaattagctgagcaagaggtta**
2332 **agggttaagggatggttgggtgggttattaatgttaattacctggagcacctgctgaaatcacttttttc**
2333 **aggttGGaccggtGCCACCATGGCCCCAAGAAGAAGaGGAAGGTGCTGAGC**
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2335 TGCTGCTGTTTCAGAGACATCCTGGCCCAGCTGGGAAGAATCCCCGCCGA
2336 GGCCTACGAGTACTACCACGGCGAGCAGGGTGATAAGAAGAGAGCTAAC
2337 GACAATGAGGGCACAAATCCCAAGCGGCACAAGGACAAGTTCATCGAAT
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2339 ACGCCACATCGTGCGGGAAGAGGCCGGCGCCGGCGATGAGCACAAGAA
2340 GCACCGGACCAAGGGAAAGGTGGTGGTGGACTTCAGCAAGAAGGACGA
2341 GGACCAGAGCTACTATATCTCCAAGAACAACGTGATCGTGCGGATCGACA
2342 AGAACGCCGGCCCTAGAAGCTACCGGATGGGCCTGAACGAGCTGAAGTA
2343 CCTCGTGCTGCTGAGCCTGCAGGGGAAGGGCGACGATGCCATCGCCAA
2344 GCTGTACAGATACAGACAGCACGTGGAGAACATCCTGGATGTGGTGAAG
2345 GTGACCGATAAGGATAACCACGTGTTCTGCCCCGCTTCGTGCTGGAGC

2346 AGCACGGCATCGGCAGAAAGGCCTTCAAGCAGCGGATCGATGGACGGG
2347 TGAAGCACGTGCGGGGCGTGTGGGAGAAGAAGAAGGCCGCCACCAATG
2348 AAATGACCCTGCACGAGAAGGCCAGAGACATCCTGCAGTACGTGAACGA
2349 AACTGCACCCGGTCCTTCAACCCTGGCGAATACAACAGACTGCTGGTG
2350 TGCCTGGTGGGCAAGGACGTGGAGAACTTTCAGGCCGGCCTGAAGCGG
2351 CTGCAGCTGGCCGAAAGGATCGATGGCCGGGTGTACTCCATCTTCGCC
2352 AGACCAGCACCATCAATGAGATGCACCAGGTGGTGTGCGACCAGATCCT
2353 GAACCGGCTGTGCAGAATCGGCGACCAGAAGCTGTACGATTACGTGGGA
2354 CTGGGCAAGAAGGACGAAATCGACTACAAGCAGAAGGTGGCCTGGTTCA
2355 AGGAGCACATCAGCATCCGGAGAGGATTCCTGAGAAAGAAGTTCTGGTA
2356 CGATAGCAAGAAGGGATTCGCAAAGCTGGTGGAGGAACACCTGGAGTCC
2357 GGCGGCGGCCAGCGCGACGTGGGCCTGGACAAGAAGTACTACCACATC
2358 GACGCCATCGGCAGATTTCGAGGGCGCCAACCCCGCCCTGTACGAGACC
2359 CTGGCCAGAGATCGGCTGTGCCTCATGATGGCCCAGTACTTCCTGGGCA
2360 GCGTGAGAAAGGAACTGGGCAACAAGATTGTGTGGAGCAACGACAGCAT
2361 CGAACTGCCTCCAAGAAGAAGCGGAAGGTGGGTGGAGGCGGAGGTTT
2362 TGGGGGAGGAGGTAGTGGCGGTGGTGGTTCAGGAGGCGGCGGAAGCca
2363 gctgcattaccgcaggttttagctgacgctgtctcacgcctggtcctgggtaagtttggtagctgaccgaca
2364 acttctcctcccctcacgctcgcagaaaagtgtggtgagctcgtcatgacaacaggcacagatgtaaa
2365 gatgccaaggtgataagtgtttctacaggaACcaaatgtattaatggtgaatacatgagtgatcgtggccttg
2366 cattaatgactgccatgcagaaataatatctcgagatccttgctcagatttctttatacacaacttgagcttta
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2369 aatcctggaagaaccagcagatagacacccaaatcgtaaagcaagaggacagctacggaccaaaata
2370 gagtctggtcaggggacgattccagtgcgctccaatgcgagcatccaaacgtgggacggggtgctgcaa
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2372 cactgctcagcatttctgtagccatttacttctcagcatcatcctgggagcctttaccacggggaccac
2373 cttccagggccatgtaccagcggatctccaacatagaggacctgccacctctctacacctcaacaagcct
2374 ttgctcagtggcatcagcaatgcagaagcacggcagccagggaaggcccccaacttcagtgtcaactgg
2375 acggtaggacgactccgctattgaggtcatcaacgccacgactgggaaggatgagctgggcccgcgctcc
2376 cgctgtgtaagcACGCGTTGTACTGTGCTGGATGCGTGTGCACGGCAAGGT
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2378 AGTCCAAGCTGGCGGCAAAGGAGTACCAGGCCGCCAAGGCCGCGTCTGT
2379 TCACAGCCTTCATCAAGGCGGGGCTGGGGGCCTGGGTGGAGAAGCCCA
2380 CCGAGCAGGACCAGTTCTCACTCACGtaccatacgatgtccagattacgcttatcccta
2381 cgacgtgcctgattatgcatacccatatgatgtccccgactatgccGCGGCCGCTGATTACAAA
2382 GACGATGACGATAAGtaaATCGAATTCGCTCGAGATAATCAACCTCTGGA
2383 TTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTT
2384 ACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCC
2385 GTATGGCTTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTAGTTCTTGCCAC
2386 GGCGGAACTCATCGCCGCTGCCTTGCCCGCTGCTGGACAGGGGCTCG
2387 GCTGTTGGGCACTGACAATTCCGTGGTGTGTTTATTTGTGAAATTTGTGATGC
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