

Supplementary information

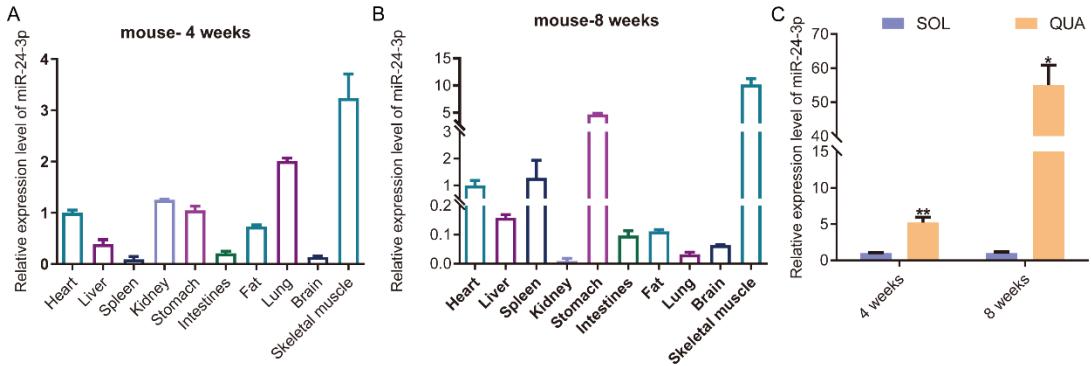


Figure S1 miR-24-3p expression pattern in skeletal muscle

(A-B) miR-24-3p expression in different tissues at weeks 4 and 8 of mouse development. (C) miR-24-3p expression in fast and slow muscles at weeks 4 and 8 of mouse development. Data are presented as mean \pm S.E.M and analyzed for statistical differences between groups using unpaired two-tailed t-tests. * $p < 0.05$, ** $p < 0.01$.

Table S1 Primer sequences for reverse transcription and qPCR

Name	Sequence(5'-3')
miR-24-3p	RT: GTCGTATCCAGTGCAGGGTCCGAGGTATTG CACTGGATACGACCTGTT F: GCGTGGCTCAGTTCAGCAG R: GCCCTGCATCTTGAAATCTGA
Pig-U6	F: CTCGCTTCGGCAGCACA R: AACGCTTCACGAATTGCGT
Pig- β -ACTIN	F: GCGGCATCCACGAAACTAC R: TGATCTCCTCTGCATCCTGTC
Pig-GAPDH	F: AGGTCGGTGTGAACGGATTG R: TGTAGACCATGTAGTTGAGGTCA
Pig-NEAT	F: GTCGATGCCCTAACATG R: GGTTAGCACGGAACCTACA
Pig-KI67	F: AGCCCGTATCTGGTGCAAAA R: CCTGCATCTGTGTAAGGGCA
Pig-PCNA	F: AAGTCAAATCTGGTCTTAGCC R: CACTGCTGGGATGCTTGAA
Pig-CDK4	F: TGGTTACAAGTGGTGGGACA R: CTGGAGCACGGTACCAAGAGT

Pig-CYCLIN A	F: GCAGCAGCCTTCATTTAGC R: GGTGAAGGTCCAGGAGACAA
Pig-CYCLIN D2	F: GTGCTGGCAAGTTGAAGTG R: GCGAACTTGAAGTCAGTGGC
Pig-MyoD	F: ATGAGACATCCCCCTACTTCTACCA R: GTCCCCAGCCCCTATCTTCC
Pig-MyoG	F: CCTGCTCAGCTCCCTCAAC R: CACAGCCACATCCTCCACT
Pig-MyHC	F: GTTCAGAGAAAGGCATCCAAA R: GAGAGTGACCGACACCACAAGTG
Pig-MYH7	F: AAGGGCTTGAACGAGGAGTAGA R: TTATTCTGCTTCCTCCAAAGGG
Pig-MYH4	F: ATGAAGAGGAACCACATTA R: TTATTGCCCTCAGTAGCTTG
Pig-MYH1	F: AGAAGATCAACTGAGTGAAC R: AGAGCTGAGAAACTAACGTG
Pig-MAPK14	F: CTACAGAGAACTGCGGTTACT R: GTAAGCTTCTGACATTTACAA
Pig-NLK	F: TGGATATTGAGCCGGATAGA R: GCAAGAGACCAGATTCTGGAA
Pig-NEK4	F: CAATTAGATGCCTCTAATGAGCT R: CTCTAGTAATATTGTAGAGG
Pig-PIM1	F: GCAAGACCTCTCGACTTTATC R: CGATGAGGATGTTCTCGTCCTT
Pig-PSKH1	F: CATCATGCCAAGGGTTCTTCA R: TGCCTGGATGGTAGTAGAGCA
Mouse-U6	F: CTCGCTTCGGCAGCACA R: AACGCTTCACGAATTGCGT
Mouse-Gapdh	F: CCTGTTGCTGTAGCCGTATT R: CATCAAGAAGGTGGTGAAGC
Mouse-Pax7	F: CCTGGAACAGACAGAGAGGGAGCAGGAGAG R: GTGAGTTCTTCACTCTGCGCTCGTGC
Mouse-Ki67	F: TGCCCGACCCTACAAAATG R: GAGCCTGTATCACTCATCTGC
Mouse-Pcna	F: GGGTGAAGTTTCTGCAAGTG R: GTACCTCAGAGCAAACGTTAGG
Mouse-Cdk4	F: ACAAGTAATGGGACCGTCAAG R: GGGTGTGCGTATGTAGACTG

Mouse-Cyclin D1	F: GCCCTCCGTATCTTACTTCAAG R: GCGGTCCAGGTAGTCATG
Mouse-Cyclin E1	F: GCGAGGATGAGAGCAGTTC R: AAGTCCTGTGCCAAGTAGAAC
Mouse-MyOD	F: CCAGCACTACATTGGCGACTAAT R: GCTCCAATATGCTGGACAGGCAGT
Mouse-MyOG	F: GCCCAGTGAATGCAACTCCCACA R: CAGCCGCGAGCAAATGATCTCCT
Mouse-MyHC	F: ACAAGCTGCAGCTGAAGGTG R: TCATTCAAGGCCCTTGGCAC
Mouse-Myh7	F: ACAAGCTGCAGCTGAAGGTG R: TCATTCAAGGCCCTTGGCAC
Mouse-Myh1	F: TGCAACAGTTCTCAACCAC R: GCCAGGTCCATCCAAAGT
Mouse-Myh2	F: CCAGCTGCACCTCTCGTTGCCAG R: CATGGGAAAGATCTGGTCTTCTT
Mouse-Myh4	F: CCTGGAACAGACAGAGAGGAGCAGGAGAG R: GTGAGTCCCTCACTCTGCGCTCGTGC
Mouse-Mapk14	F: GTTTCTCATCTACCAAGATCCT R: TAGCCTGTCACTCATCATCA
Mouse-Nlk	F: GAGTCTTCCGGAAATTGAAGAT R: AGATCACTCTGCATCAATTCT
Mouse-Nek4	F: ATTACATGAGCCCTGAGCTGTT R: GTGCTGTAAACTTTGGCATT
Mouse-Pim1	F: TTCGGCTCGGTCTACTCTGGCAT R: ACCTTCTCAACAGGACCA
Mouse-Pskh1	F: TATCAAGATGATAGAGACCA R: AGCTCCATCACCATATACAC

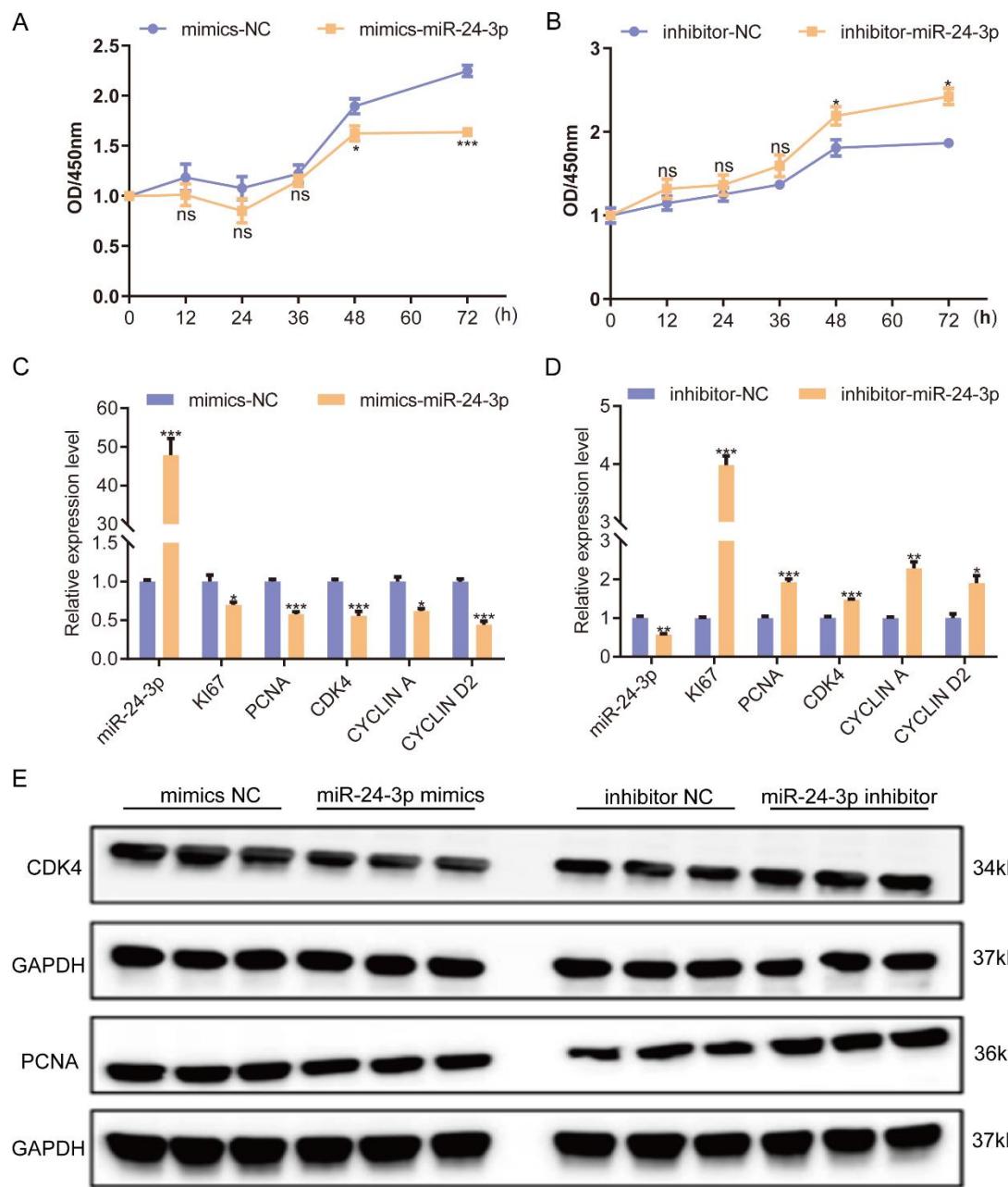


Figure S2 Effect of miR-24-3p on C2C12 myoblasts differentiation

(A-B) CCK-8 analyzed cell proliferation after miR-24-3p overexpression and knockdown in PSMCs. (C-D) qRT-PCR analyzed cell proliferation markers (KI67, PCNA, CDK4, CYCLINA and CYCLIND2) mRNA expression after miR-24-3p overexpression and knockdown in PSMCs. (E) Western blot analyzed proliferation markers (CDK4 and PCNA) protein expression after miR-24-3p overexpression and knockdown in PSMCs. Data are presented as mean \pm S.E.M and analyzed for statistical differences between groups using unpaired two-tailed t-tests. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, ns (not significant).

	seed sequence
Pig	ssc-miR-24-3p UGGCUCAGUUCAGCAGGAACAG
Mouse	mmu-miR-24-3p UGGCUCAGUUCAGCAGGAACAG
Rat	rno-miR-24-3p UGGCUCAGUUCAGCAGGAACAG
Human	hsa-miR-24-3p UGGCUCAGUUCAGCAGGAACAG
Rhesus	mml-miR-24-3p UGGCUCAGUUCAGCAGGAACAG
Cow	bta-miR-24-3p UGGCUCAGUUCAGCAGGAACAG
Chicken	gga-miR-24-3p UGGCUCAGUUCAGCAGGAACAG

Figure S3 conservation analysis of miR-24-3p sequence in different species

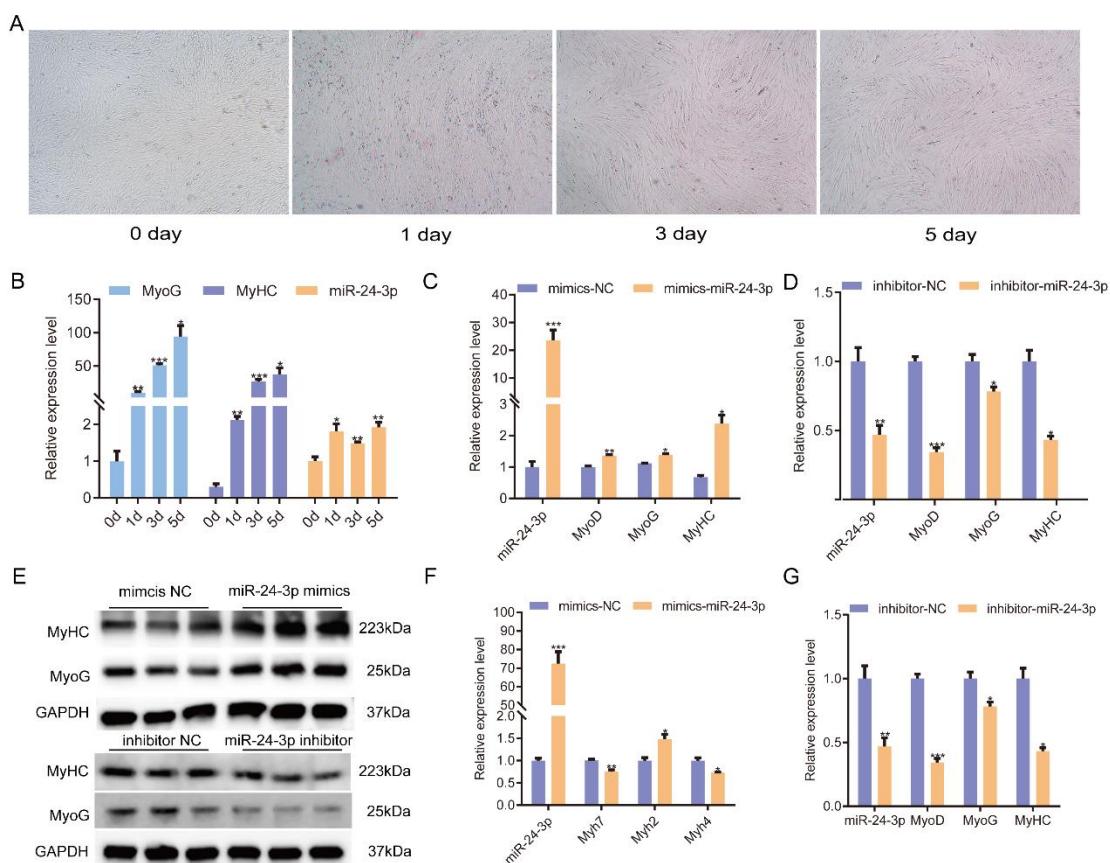


Figure S4 Effect of miR-24-3p on skeletal muscle fiber type transformation in pig

(A) PSMCs were induced to differentiate for different days (0d, 1d, 3d and 5d). Scale bar: 50 μ m. (B) qRT-PCR analyzed the expression pattern of MyoG, MyHC and miR-24-3p during PSMCs differentiation. (C-D) qRT-PCR analyzed the expression of miR-24-3p, MyoG, MyHC and MyoD after miR-24-3p overexpression and knockdown. (E) Western blot analyzed the protein expression of MyoG and MyHC after miR-24-3p overexpression and knockdown. (F-G) qRT-PCR analyzed the expression of differentiation and transformation markers expression after miR-24-3p overexpression and knockdown. Data are presented as mean \pm S.E.M and analyzed for statistical differences between groups using unpaired two-tailed t-tests. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

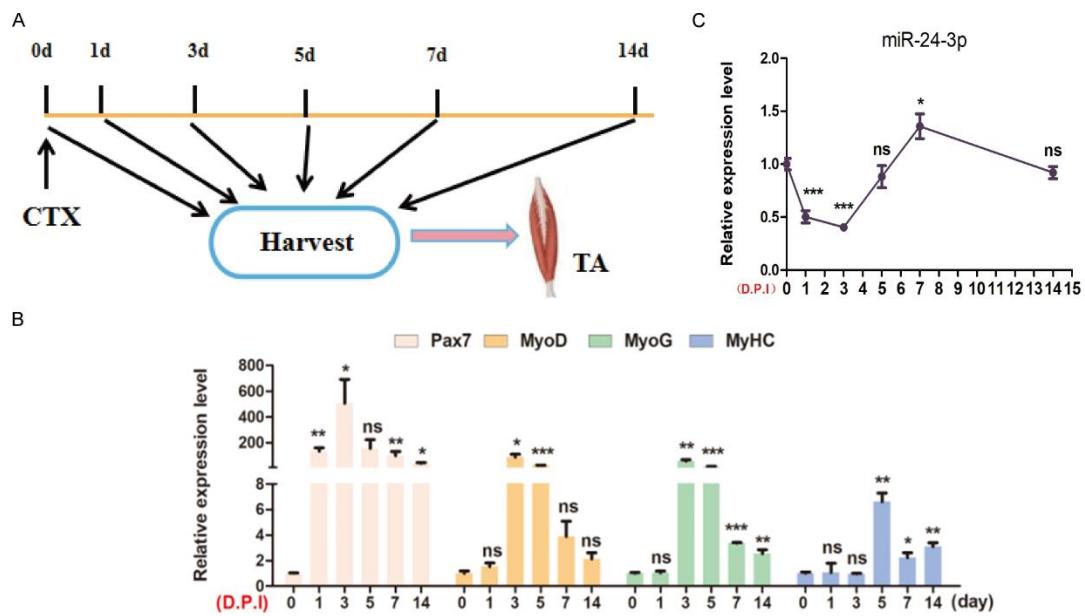


Figure S5 The miR-24-3p expression during skeletal muscle regeneration

(A) Schematic representation of the skeletal muscle regeneration. (B-C) qRT-PCR analyzed the expression pattern of Pax7, MyoD, MyoG, MyHC and miR-24-3p during skeletal muscle regeneration. Data are presented as mean \pm S.E.M and analyzed for statistical differences between groups using unpaired two-tailed t-tests. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, ns (not significant)

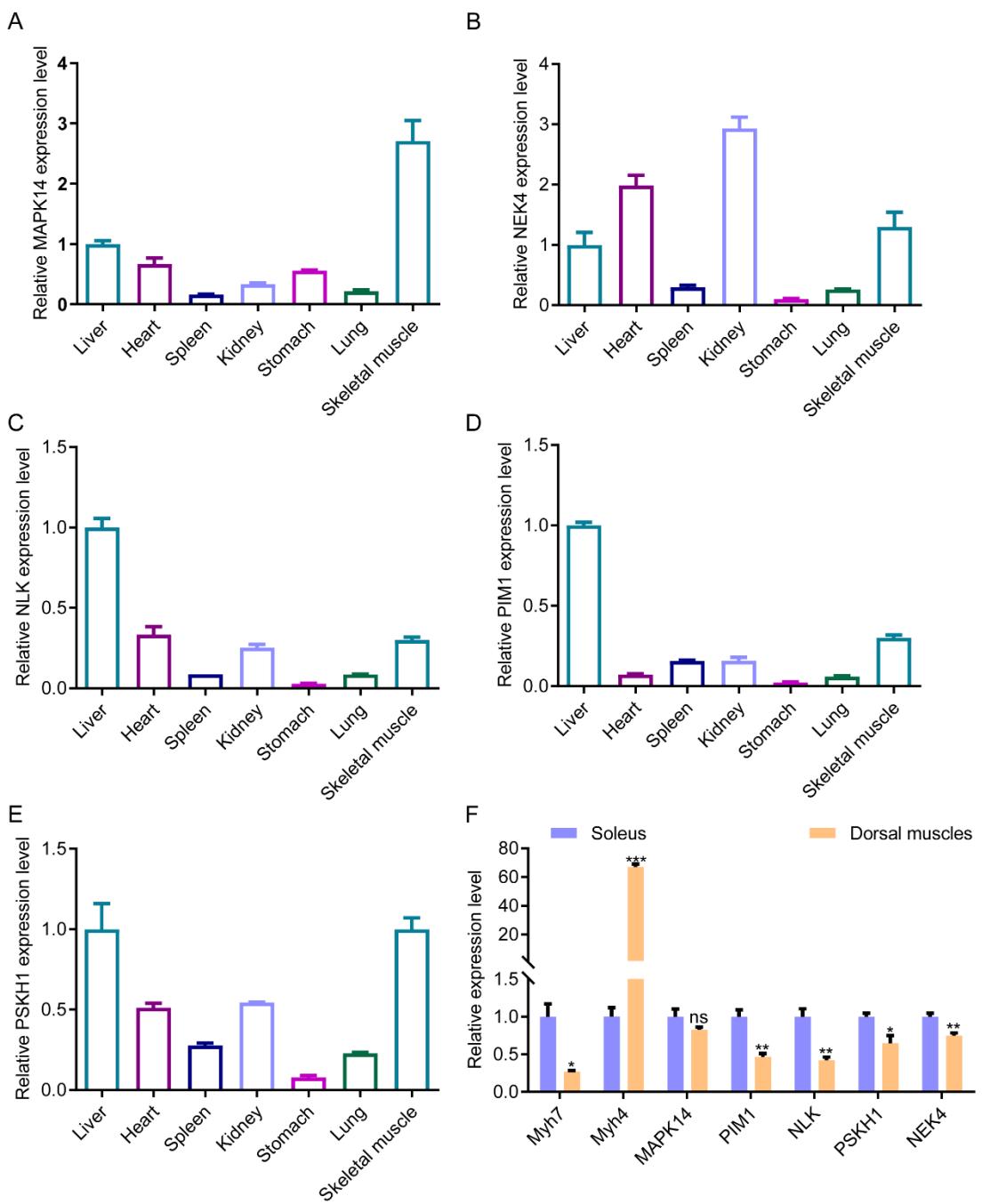


Figure S6 The effects of ssc-miR-24-3p on proliferation marker genes of porcine skeletal muscle primary cells

The expression levels of MAPK14 (A), NEK4 (B), PSKH1 (C), PIM1 (D) and NLK (E) in pig tissues. (F) Expression levels of potential target genes of ssc-miR-24-3p in pig fast and slow muscle. Data are presented as mean \pm S.E.M and analyzed for statistical differences between groups using unpaired two-tailed t-tests. * p < 0.05, ** p < 0.01, *** p < 0.001, ns (not significant).

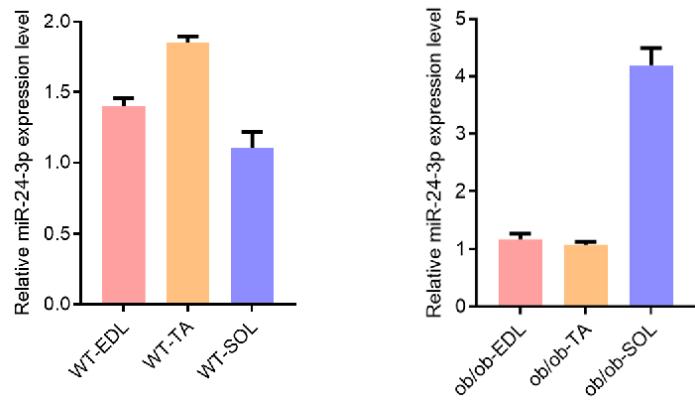


Figure S7: Fast and slow muscle expression in wild mice and ob/ob mice.