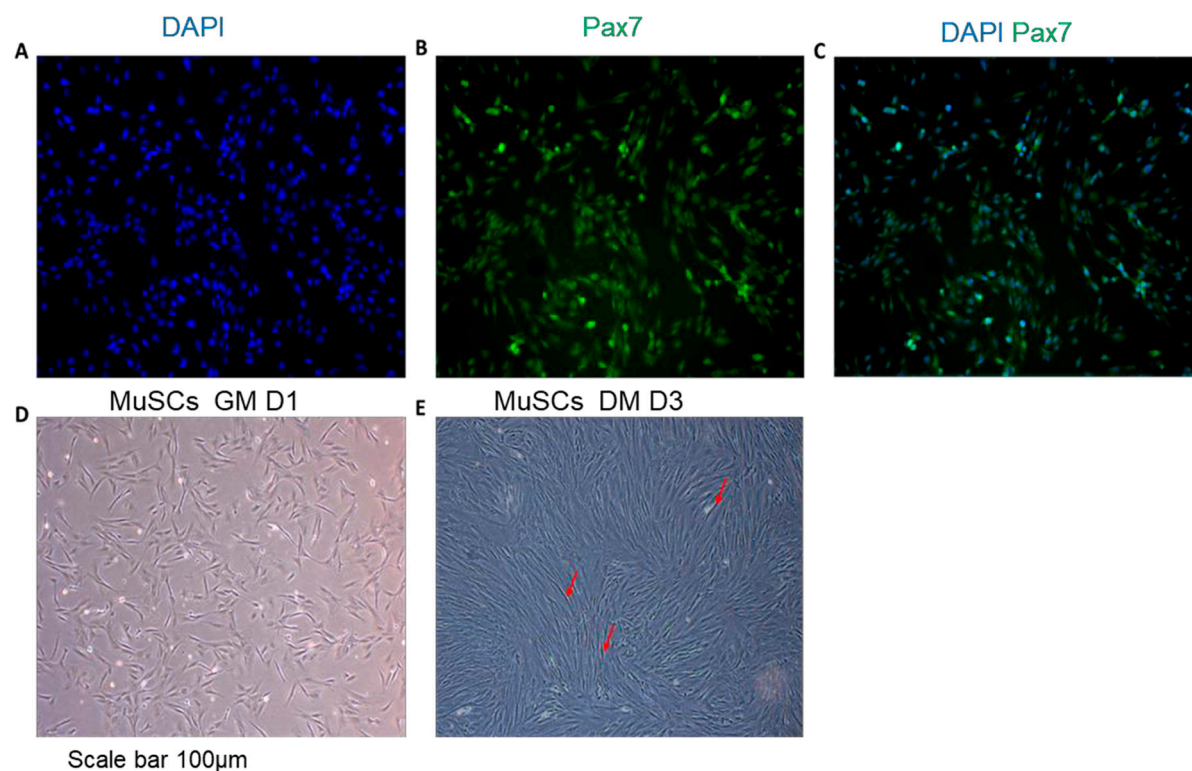
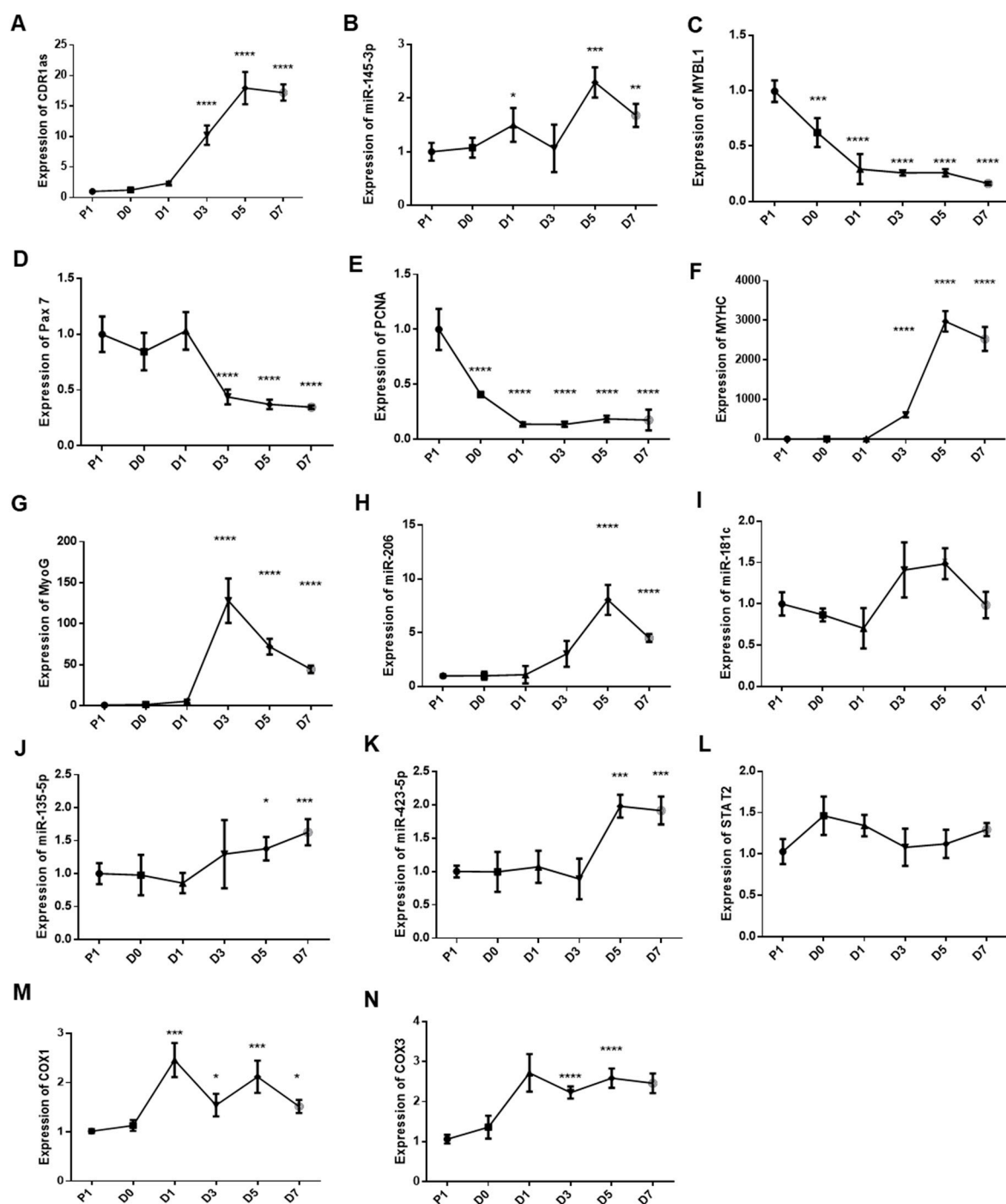


# 1. Supplementary data



**Supplementary Figure S1.** Identification of goat SMSCs. (A- C) Isolated SMSCs were stained for Pax7 immunofluorescence. The cell nucleus was stained with DAPI (blue) while Pax7 protein was stained green. (D) An image of proliferating SMSCs at day 1 and (E) differentiating SMSCs at day 3 with evidence of myotube formation pointed with red arrows. Scale bar 100µm.



**Supplementary Figure S2.** The expression profile of some genes and miRNAs during myogenic proliferation and differentiation of goat MUSCs. (A) CDR1as, (B) miR-145-3p, (C) MYBL1, (D) Pax7, (E) PCNA, (F) MyHC, (G) MyoG, (H) miR-206, (I) miR-181c, (J) miR-135-5p, (K) miR-423-5p, (L) STAT2, (M) COX1 and (N) COX3. All experiments were repeated three times and statistical differences ( $P < 0.05$ ) are differentiated by \*,  $P < 0.01$  by \*\* and  $P < 0.001$  by \*\*\*.

A

```

Version: RNAhybrid 2.2
Command line: /vol/bioapps/bin/RNAhybrid.bis
searching
dataset: 1
mfe of chi-miR-145-3p: -39.200001
Individual hits
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length: 2498
miRNA : chi-miR-145-3p
length: 21

mfe: -21.0 kcal/mol
p-value: undefined

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      CUUGUCAU GG UCCU
miRNA 3' UU AAA UA S'
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dataset: 1
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miRNA : chi-miR-145-3p
length: 21

mfe: -20.0 kcal/mol
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miRNA 3' CCUUA S'
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length: 2498
miRNA : chi-miR-145-3p
length: 21

mfe: -19.9 kcal/mol
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miRNA 3' UUCU AAG A S'

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B

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Version: RNAhybrid 2.2
Command line: /vol/bioapps/bin/RNAhybrid.bis
searching
dataset: 1
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Individual hits
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miRNA : chi-miR-145-3p
length: 21

mfe: -21.5 kcal/mol
p-value: undefined

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miRNA 3' U C A S'
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miRNA : chi-miR-145-3p
length: 21

mfe: -21.4 kcal/mol
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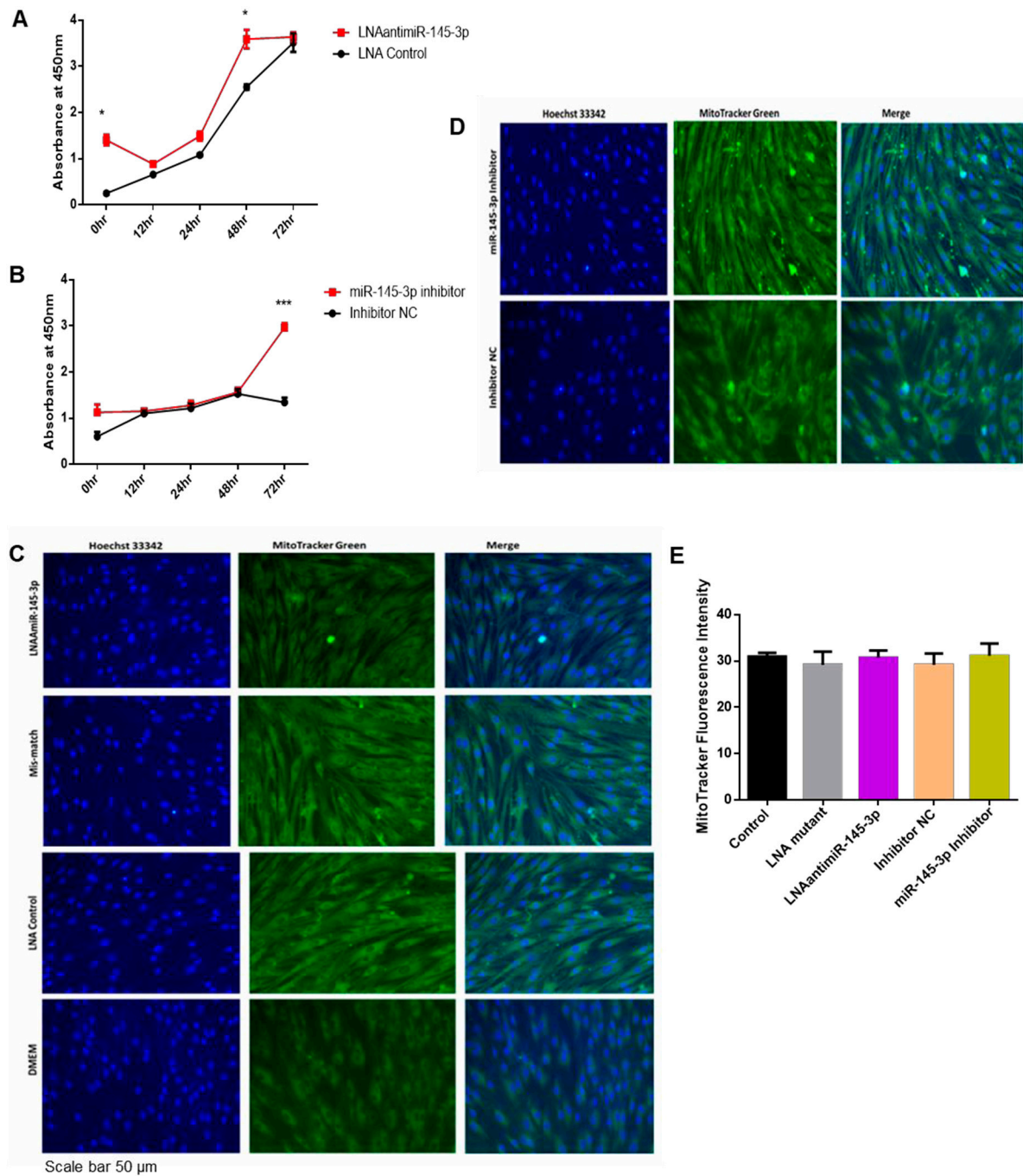
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target: goatcdrlas
length: 1481
miRNA : chi-miR-145-3p
length: 21

mfe: -21.0 kcal/mol
p-value: undefined

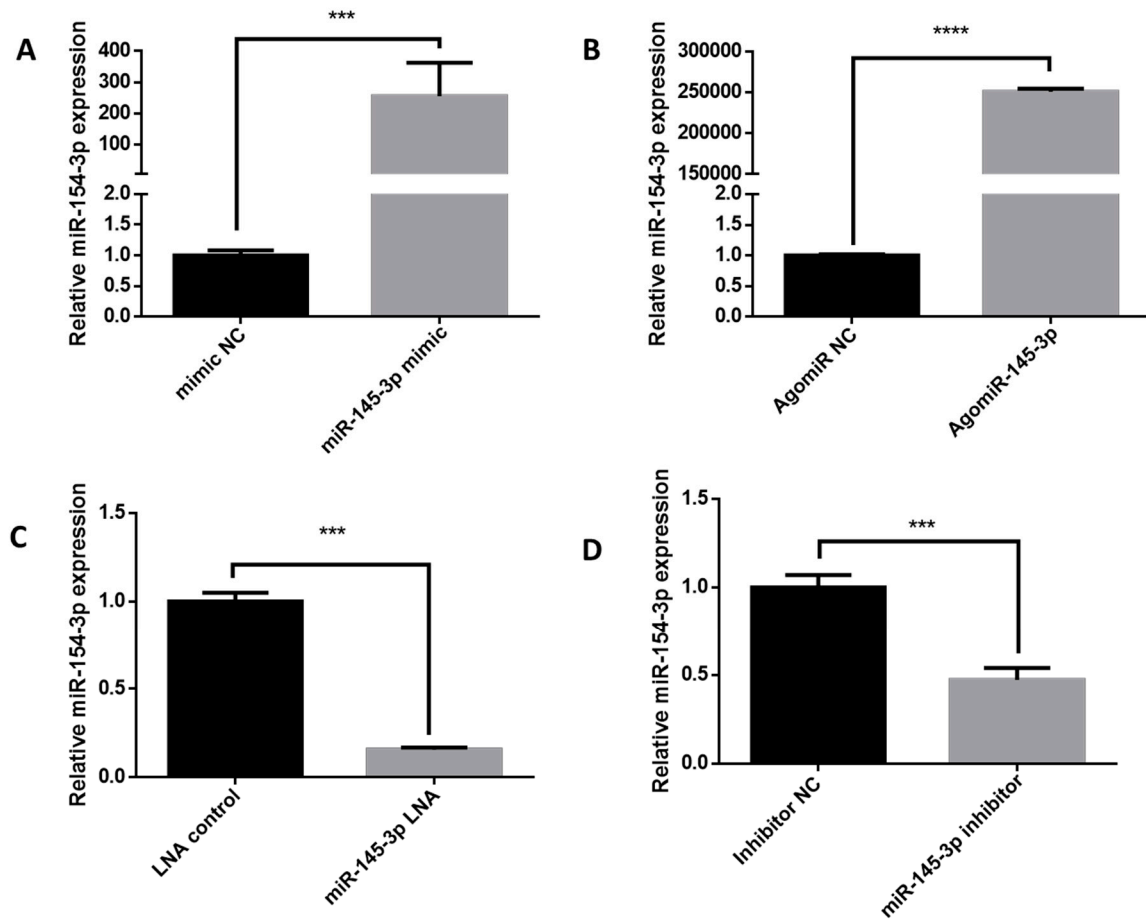
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target S' C A CCA C A 3'
      AGAA AG UGU UGCCAGGAA
      UCUU UC AUA AAGGUCCUU
miRNA 3' U G A S'

```

Supplementary Figure S3. (A,B) Binding sites of miR-145-3p to MYBL1 3'UTR and CDR1as.



**Supplementary Figure S4.** Knockdown of miR-145-3p had no significant effect on the number of viable cells and active mitochondria in proliferating MuSCs. (A-B) Knockdown of miRNA did not influence cell viability or (C- D) active mitochondria numbers. SMSCs were cultured and the nucleus was stained with Hoechst 33342 while the mitochondria were stained with MitoTracker green (E). Scale bar 50  $\mu$ m. All experiments were repeated three times and statistical differences ( $P < 0.05$ ) are differentiated by \*,  $P < 0.01$  by \*\* and  $P < 0.001$  by \*\*\*.



**Supplementary Figure S5.** The transfection efficiency of (A) AgomiR-145-3p, (B) miR-145-3p mimics, (C) miR-145-3p inhibitor and (D) miR-145-3p LNA in MuSCs. All experiments were repeated three times and statistical differences ( $P < 0.001$ ) are differentiated by \*\*\*,  $P < 0.0001$  by \*\*\*\*.

## Supplementary Table

**Table S1.** Primers used for the Dual-luciferase amplification.

Gene	Primer sequence	Product length/bp	Tm (°C)
circ-CDR1as	F CCGCTCGAGCAGAAAAGCCATGTCTTC R	456	63.8
	AAATATGCGGCCGCGATTTCCTGGAAGACATG T		
	F CCGCTCGAGAAAATGTTTTTTCCTTATT		
s1-MYBL1	R	126	58.8
	AAATATGCGGCCGCGATTTCCTTCCAATTAC		
	A		

ck-1-MutMYBL1	F TAACTCGTTGACGCCTTCTTT R TTTCTTTCCAATTTACAAAG	150	49.4
1-2MutMYBL1	F GCCTTCTTTATAAATCTCAGTGAGCTGAG R GTCAACGAGTTACCAATAAGGAAAAAACATT TTC	122	51.5
2-1mutMYBL1	F GCCGCGTTCAAACCTTGTAAATTGGAAAGAA ATC R GTCAACGAGTACAATACATTCAACAAAAC TC	150	60.3
chk2mutMYBL1	F ATGTTTTTTCCTTATTGGTAA R TTTGAACGCGGCGTCAACGAGTACA	200	53.5
1-1MutMYBL1	F TTTTCTTATTGGTAACTCGTTGACGCCTTCTT TAT R GCTCACTGAGATTTATAAAGAAGGCGTCAAC GAGTT	170	50.3
1,2chkmutMYBL1	F TTCCTTATTGGTAACTCGTTG R TTTACAAAGTTTGAACGCGG	500	59.0
3utr-MYBL1	F AAAGAGTCAGTATTTTCT R AATCCTTTTAGGTCTACT	1086	44.7

**Table S2.** Inserted sequence of dual-luciferase reporter vectors.

Name	Sequence
CDR1as wild	ccgctcgagCAGAAAAGCCATGTCTTCCAGGAAATCCATGTCTTCCATCAAATCCAT GGCTTCCAGAAAATCAATGTCTTCCAGGAAATCCATGTCTTCCAGCAAATATTT GTCTTCCAACAAAACGTGTCTTCCATCAAATTCATGTCTTCCAGCCTATCCATC TCTTCCAGAAAATCCTCGTCTTCCAATGAAGGTGCACCTTCCAGGAAATCCACG TCTTCCAGAAAATCCTCGTCTTCCGATGAAGGTGCGCCTTCCAGGAAATCCACG TCTTCCAGAAAATCCTAGTCTTCCAATGAAGGTGCGCCTTCCAGGAAATCCACG TCTTCCAGAAAATCCTCGTCTTCCAATGAAGGTGCACCTTCCAGGAAATCCATG TCTTCCAGAAAATCCCTGTCTTCCAATGAAGGTGCGCCTTCCAGGAAATCCTTG TCTTCCAACAAAGACATGTCTTCCAGGAAaAaatatgcggccgc
CDR1as mutant	ccgctcgagCAGAAAAGCCATGTGCGCATCTAGCATCCATGTCTTCCATCAAATCCAT GGCTTCCAGAAAATCAATGTGCGCATCTAGCATCCATGTCTTCCAGCAAATATTT GTCTTCCAACAAAACGTGTGCGCATTCAAATTCATGTCTTCCAGCCTATCCATCT CTTCCAGAAAATCCTCGTCTTCCAATGAAGGTGCACCGCATCTAGCATCCACGT CTTCCAGAAAATCCTCGTCTTCCGATGAAGGTGCGCCGCATCTAGCATCCACGT CTTCCAGAAAATCCTAGTCTTCCAATGAAGGTGCGCCGCATCTAGCATCCACGT CTTCCAGAAAATCCTCGTCTTCCAATGAAGGTGCACCGCATCTAGCATCCATGT CTTCCAGAAAATCCCTGTCTTCCAATGAAGGTGCGCCGCATCTAGCATCCTTGT CTTCCAACAAAGACATGTGCGCATCTAGCAaAaatatgcggccgc
MYBL1 3UTR wild	ccgctcgagAAAATGTTTTTTCCTTATTGGTAAAGAGTCAGTATTTTCTCCATAAATC TCAGTGAGCTGAGAGTTTTGTTGAATGTATTGTACAGTATGTAGGAGCAGGAA AACTTTGTAAATTGGAAAGAAATCTGTTTTTATAATTTATTTTCAATTTTAAAGC TTAAATGTAGATATTTAAACTTATACAGGGTGTCTAGAAGCCAATGTTGTTTCC



	<p>TGTTATTACAGATAACATAGTAAAGAACAATTTTGACTTTTAAGTATGAAACAG  TAGTAAGTTATAGCTGCAAAGAATTCAGTATCTATACTGTATGTCACATCTACC  TAAATATTGCACTATGTCCTTTAAATCATGTTGGTTATAAAGTAGTTCTAAAAAT  TACTAAATAATAATTTAATATTTTCTTTTAAATTATATGGGGGGTCATATAAA  TTAATCTGGTGATTTGTATATTTGTTTTAAATTTTGCATTTTGTTTTAAAAAATA  ATATGGTACTTTGGTCCCTAAAAACAGTCTGCACTTAGAAGTTTATTATATTTAC  TCAGTGTTTAAGAAGTAGAGAACAGTATCTTTTATTTATAAAAAATATTTGTCCTT  TTATAAATGTTTTGTGTTTCTCTACAGGTTACAACAGTTGCTTCAGTTGCCTGTTT  TAGGTGTTTGCCTTACTTTATTTCTTCTTGAAAGAATGCTTTTATTTGCTTTTGT  GTAGAGATTTTATGTAATTTTTTGAAACATATAATGGTATGCTGTCAACTTAAA  CACTGACAGGTAAATAGAATTGTACACTGTAGTTGTAATTATTTGTAATTGACA  CACTCTCTCCCTCTCCACTCCTGAAGTATGCTGCTATAGAAAATAGCAGAATCG  GCTTGCTGCTATGAGAGAAGGAAAGAGCGACCACCACTTGCCTGTGTGAAAA  CATAAAAAGTATGATGATGGCAAGTTCTCAAGTTAACTTAATGGAATCAACCA  TTACCAGGCAAATTCTTGCAAATACCAAAAATGCTCTGCCTTAAAACAAAAACA  GCTTAAGATTCTCTGTTGATGGAATGGAAATACGAAGTATTTTAATGCCTAGC  TTTTGAACAGTAGACCTAAAAGGATTaaatatgcggccgc  ccgctcgagAAAATGTTTTTTCCTTATTGGTAACTCGTTGACGCCTTCTTTATAAATCT  CAGTGAGCTGAGAGTTTTGTTGAATGTATTGTACTCGTTGACGCCGCGTTCAAA  CTTTGTAAATTGGAAAGAAATCaaatatgcggccgc  ccgctcgagAAAATGTTTTTTCCTTATTGGTAACTCGTTGACGCCTTCTTTATAAATCT  CAGTGAGCTGAGAGTTTTGTTGAATGTATTGTACTCGTTGACGCCGCGTTCAAA  CTTTGTAAATTGGAAAGAAATCaaatatgcggccgc  ccgctcgagAAAATGTTTTTTCCTTATTGGTAACTCGTTGACGCCTTCTTTATAAATCT  CAGTGAGCTGAGAGTTTTGTTGAATGTATTGTACTCGTTGACGCCGCGTTCAAA  CTTTGTAAATTGGAAAGAAATCaaatatgcggccgc</p>
MYBL1 3UTR mutant	
MYBL1 3UTR mutant (pt 616)	
MYBL1 3UTR mutant (pt 675)	

Capital letters represent the actual sequence and the smaller letters represent the recognition sites of the Enzyme Not1 and Xho1.

**Table S3.** Primers used for qRT-PCR amplification.

Gene	Primer sequence	Product length/bp	Tm (oC)
CDR1as (Divergent primer) (XM_013976302.1)	F AGCAGGCTCAATATCTACG R CTGGAAGACCTTGACACTG	118	53.9
COX-1	F CCTCCTTTCCTTCTGTATT R TGTGTTTAGGTTTCGGTCTGT	67	53.7
COX-2	F TAGAGGTAGATAACCGAGT R GAACGATTGGTATGAAAC F GAAGGAGACCGTAACCACATA	225	49.5
COX-3	R GGACAACGCAGAGAATCAAAC	175	55.6
CSNK1A1 (XM_005683156.3)	F TTATTCCTTATTGATTTTGGTCC R TTGCCTTGTCCTGTTGTCT	57	54.4
GAPDH (XM_005680968.3)	F GCAAGTTCCACGGCACAG R GGTTACGCCCATCACAA	249	59
MEF2C (NM_001314204.1)	F CCCCAGTGGTTTCCGTAGCA R GCTGTTGTTGCCAGCCAGTT	183	58.5

miR-1271-3p		AGTGCCTGCTATGTGCCAGG	20	59.5
miR-129-5p		CTTTTTCGGTCTGGGCTTGC	21	59.5
miR-135-5p		GGTCCTCAGTGTAGCCCAAG	20	59.5
mir-143-3p		TGAGATGAAGCACTGTAGCTCG	22	50
miR-145-3p		ATTCCTGGAAATACTGTTCTT	21	49.8
miR-16		TAGCAGCACGTAAATATTGGCG	22	50.8
miR-181c		CAAGGGTTTGGGGGAACATTCA	21	51.7
miR-218		TGTTTAATATTTTGCAATAATT	22	57.7
miR-379-5p		TGGTAGACTATGGAACGTAGG	21	55.6
miR-423-5p		TGAGGGGCAGAGAGCGAGACT	21	61.5
MYBL1		F CAGCAGAACTCACCGACAAAG	61	57.8
(XM_005689032.3)		R GTAGAGAGGACAACACAGCGT		
MyHC		F CGCCACCTGGAGCGGATGA	171	61.3
(XM_013972193.2)	R	CTTGCGGTCTCTCGGTCTGGT		
MyoD		F GTGCAAACGCAAGACGACTA	128	60.7
(XM_018058990.1)		R GCTGGTTTGGGTGCTAGAC		
MyoG		F GGACCCTACAGATGCCCACAA	101	60.7
(NM_001285733.1)		R TTGGTATGGTTTCATCTGGG		
Myomaker		F CCCTGGCTCTCATGTTGCGCTT	131	56.9
(XM_018056156.1)		R TGCACCTCCGGCCTTCTTGTG		
Myomerger		F GGGCTGTCTGTTGTTTCGTC	146	58.3
(NC_030823.1)		R AGCATTTTCAGGGGGCACAGC		
Pax7		F AGGACGAAGCGGACAAGAA	91	50.5
(XM_018054746.1)		R TCCAGACGGTTCCTTTGT		
PCNA		F TGAAGAAAGTGCTGGAGGCG	156	61.3
(XM_005688167.3)		R TTTGGACATGCTGGTGAGG		
PDE4B		F GACTTCATCGTCCATCCGCTG	128	59.5
(XM_018045239.1)		R TGGGAGGGGCTCTGGTGTAT		
SRSF11		F TGTCTCGTTCAAAATCCCCT	156	54.5
		R TTCATCGTAGTCCCGTGTAAG		
VCPIP1		F TGACCCTCTGTTTGTACCGC	84	60
		R CGATGAAGCACATTGGCGAG		
Vexin		F AGTCCAGCCAGAAGTAGAGT	79	55.6
	R	CTTGGTGAAGAGATGTTGAGAG		
U6		F CTCGCTTCGGCAGCACA	94	55.9
		R AACGCTTCACGAATTTGCGT		
GAPDH		F GCAAGTTCCACGGCACAG	249	59.0
(XM_005680968.3)		R GGTTACGCCCCATCACAA		