

Table S1. Information of Primers.

Primer name	Primer sequences (5' to 3')	Usage
qPCR-PPARGC1A	F: AAGCGAAGAGCATTTGTC	qPCR
	R: TCGTAGGTGGAGTTAGGC	
qPCR-COX2	F: GTAGATGCCCAAGAAGTT	qPCR
	R: GTTTGATTAGTCGTCCAG	
qPCR- β -globin	F: CAGCCAGGTGGAGGATTT	qPCR
	R: GAATAGGAGGACCCTCTGTTAG	
qPCR-ATGL	F: TGTCCAAAGAAGCACGAAA	qPCR
	R: GAGGTATCAGCCCACAGTAGA	
qPCR-CPT1	F: GCTTATTGTAGTTGTGGGTG	qPCR
	R: AAAGTTTGCCGTGTTTCAG	
qPCR-FASN	F: CGCAGGCATAGCAGGAAA	qPCR
	R: CCAAAGAAGGAGGCATCAA	
qPCR-GPI	F: ATTCACTTTGGGAGCAATC	qPCR
	R: ACTCCAACCTCTGGCTCAAT	
qPCR-HK1	F: CTGGATCTCGGTGGTTCTTAC	qPCR
	R: TTGTCGGCACGGGAAAGA	
qPCR-PGAM1	F: GCGAGGCTCAGGTGAAGAT	qPCR
	R: GTCCTCCGTCAGGTCAGC	
qPCR-PGK1	F: CCCTGGATAAGGTGGATG	qPCR
	R: TTGTCAGGCATGGGAACT	

qPCR-PYGL	F: ACATTTGCCTACACGAACC R: TGCCTCCCTCCTCTATCA	qPCR
qPCR-SOX6	F: TCAGGTTCAGGGTCACATGCC R: TTGCTGGAGCTGTAAAGGGC	qPCR
qPCR-TNNC1	F: GTTGAGCAGTTGACAGAAGA R: GAACCATCATAACAAGGAAC	qPCR
qPCR-TNNC2	F: GAGCAGCAAAGATGGCGTCA R: ATCACCGTGCCCAACTCCTT	qPCR
qPCR-TNNI1	F: GAGGAGTGGGAGCAGGAGAT R: TTCGTCCACAATCTCAACCT	qPCR
qPCR-TNNT1	F: GAGCCGCACGGAGAAGGAGC R: CCCGAAGTGGGGCATGTTGG	qPCR
qPCR-TNNT3	F: AGAGGGAAGAAGCAAACAGC R: GTCCCACAGTTCCTTAGCCT	qPCR
qPCR-ATROGIN1	F: TCAACGGGTCGGCAAGTCT R: TCCCTCCCATCGCTCAGTC	qPCR
qPCR-MURF1	F: GGACGAGCGGATCAACAT R: GGGAGATGATGGTCTGGATG	qPCR
qPCR-LC3B	F: GAGCAAAGAGTTGAAGATG R: GTCCTAGACGGAAGATTG	qPCR
qPCR-SQSTM1	F: AGCGACGAGGAGCTGGATC R: CCTTGTGGATGCCTTTACCC	qPCR

qPCR-ULK1	F: TCGTTGCCTTGTATGACTT	qPCR
	R: TTTATGCGAATGTTGTTGG	
qPCR-β-actin	F: GATATTGCTGCGCTCGTTG	qPCR
	R: TTCAGGGTCAGGATACCTCTTT	
pcDNA3.1- PPARGC1A	F: AAGCTT ATGGCGTGGGACATGTGC	Vector construction
	R: CTCGAGT TACCTGCGCAGGCTCCG	
pDC316-mCMV- ZsGreen-PPARGC1A	F: ACTAGT ATGGCGTGGGACATGTGCAACCA	Vector construction
	GGACTCTGT R: GCGGCCG CTTACCTGCGCAGGCTCCGCTG TGCCT F: GATCCG CAACCAAGATAATCCTTTCTTCAA	
pLVX-shRNA2-Puro- PPARGC1A	GAGAGAAAGGATTATCTTGTTGTTTTT G	Vector construction
	R: AATT CAAAAACAACCAAGATAATCCTTTCT CTCTTGAAGAAAGGATTATCTTGTTG CG	

Sequences in bold represent the enzyme cutting sites.

Table S2. Oligonucleotide sequences in this study.

Fragment name	Sequences, 5' to 3'
si-PPARGC1A	CAACCAAGATAATCCTTTC
miR-193b-3p mimic	AACUGGCCACAAAGUCCCGCUUU
miR-193b-3p inhibitor	AAAGCGGGACUUUGUGGGCCAGUU

Table S3. Comparative metabolome analysis of *PPARGC1A* knockdown versus control group gastrocnemius.

Separate Excel file.

Table S4. Differential expression analysis of miRNAs between pectoralis major and soleus in 7-week-old Xinghua chicken.

Separate Excel file.

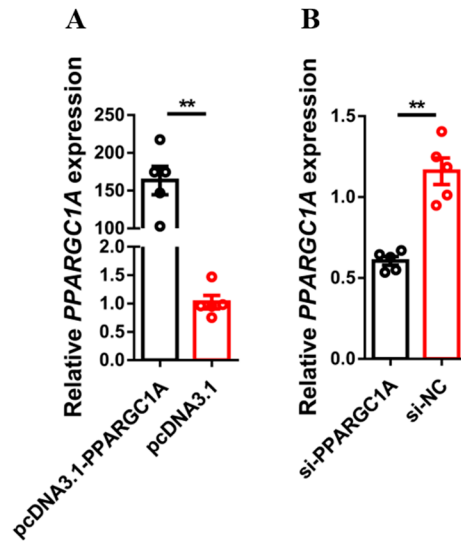


Figure S1. Analysis of overexpression and interference efficiency of *PPARGC1A*

***in vitro*.** (A) Relative *PPARGC1A* expression with *PPARGC1A* overexpression in CPMs. (B) Relative *PPARGC1A* expression with *PPARGC1A* interference in CPMs.

Results are presented as mean $\pm$ SEM. In all panels, statistical significance of differences between means was assessed using independent sample *t*-test. (** $P < 0.01$).

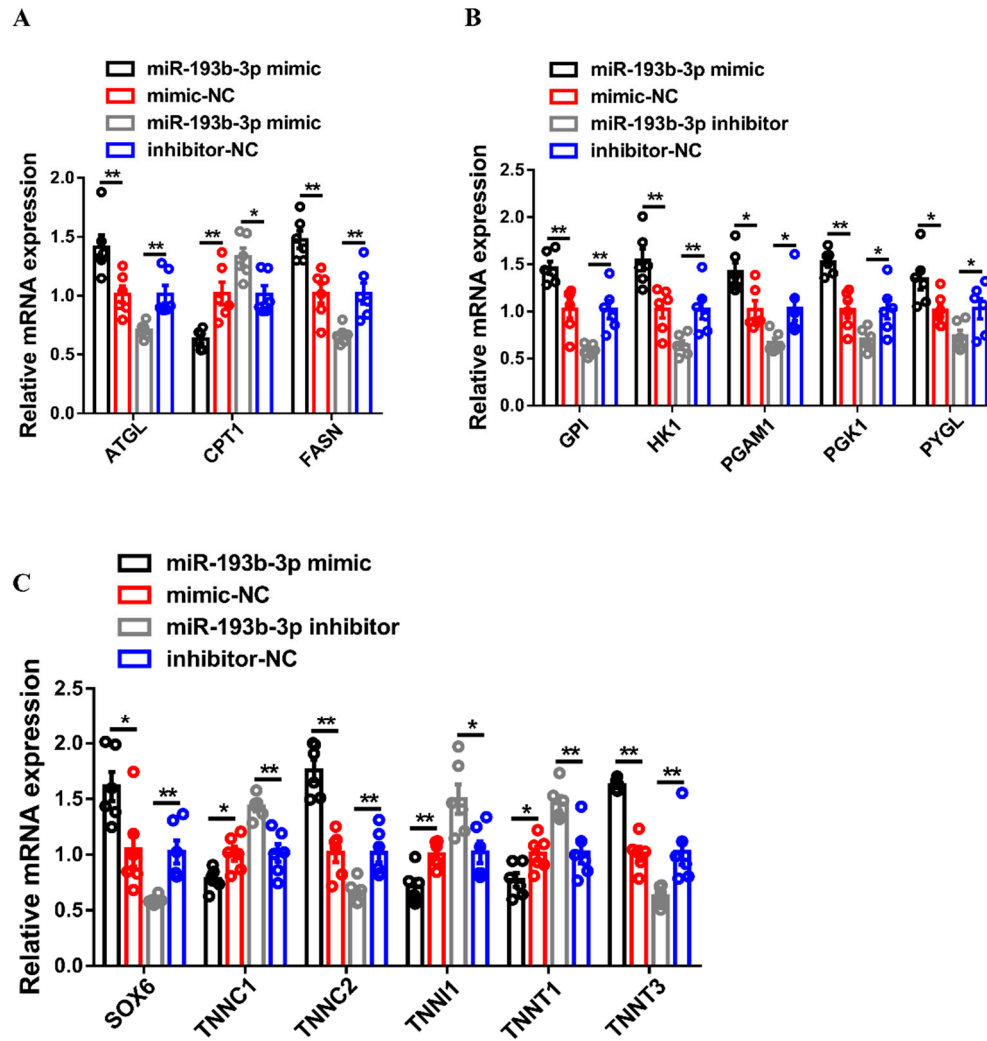


Figure S2. *miR-193b-3p* suppresses intramuscular fatty acid oxidation and induces fast-twitch muscle phenotype. (A to C) Relative mRNA expression levels of fatty acid oxidation or synthesis related-genes (A), relative mRNA expression levels of glycogenolytic and glycolytic genes (B), and relative mRNA expression levels of several fast-/slow-twitch myofiber genes (C) after *miR-193b-3p* overexpression or inhibition. In panels (A to C), results are shown as mean $\pm$ SEM, statistical significance of differences between means was assessed using paired *t*-tests. (* $P < 0.05$; ** $P < 0.01$).

A

gga-miR-193b-3p mature sequence 3' UUUCGCCCUGAAACAC**CCGGUCAA**
hsa-miR-193b-3p mature sequence 3' CGCCCUGAAACUC**CCGGUCAA**
mmu-miR-193b-3p mature sequence 3' UGACCCUGAAACA**UCCGGUCAA**

B Human

Conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	PCT	Predicted relative K _D
Position 1754-1760 of PPARGC1A 3' UTR	5' ... AAGACUACUUUGAA-GCCAGU... 	7mer-A1	-0.21	83	-0.21	4.356	0.48	-3.727
hsa-miR-193b-3p	3' UCGCCUGAAACUCCGGUCAA							
Position 1754-1760 of PPARGC1A 3' UTR	5' ... AAGACUACUUUGAA-GCCAGU... 	7mer-A1	-0.19	82	-0.19	4.356	0.48	-3.775
hsa-miR-193a-3p	3' UGACCCUGAAACAUCGGUCAA							

C Mouse

Conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	PCT	Predicted relative K _D
Position 1790-1796 of PPARGC1A 3' UTR	5' ... AAGACUACUUUGAA-GCCAGU... 	7mer-A1	-0.19	81	-0.19	4.356	0.48	N/A
mmu-miR-193b-3p	3' UCGCCUGAAACUCCGGUCAA							
Position 1790-1796 of PPARGC1A 3' UTR	5' ... AAGACUACUUUGAA-GCCAGU... 	7mer-A1	-0.19	81	-0.19	4.356	0.48	N/A
mmu-miR-193a-3p	3' UGACCCUGAAACAUCGGUCAA							

Figure S3. *miR-193b-3p* is likely to target to *PPARGC1A* in mammalian. (A)

Sequences of *gga*-, *has*-, and *mmu-miR-193b-3p*. **(B and C)** The interaction between *miR-193b-3p* and *PPARGC1A* in mammals analyzed by TargetScan.