Table S1. Primers used for real-time PCR.

Gene name	Primer sequences (5′ to 3′)	Annealing temperature (◦C)	Accession Number
lncRNA-Six1	F: CTCGTGAGAAGGGGGCAAAA R: GAAGGCGAAACCCAAAACCG	56	-
Six1	F: GTCAGCAACTGGTTCAAGA R: AGGAGGACCGAGTTCTGAT	59	NM_001044685.1
MYOD	F: GCTACTACACGGAATCACCAAAT R: CTGGGCTCCACTGTCACTCA	53	NM_204214.2
MYOG	F: CGGAGGCTGAAGAAGGTGAA R: CGGTCCTCTGCCTGGTCAT	53	NM_204184.1
MyHC	F: CTCCTCACGCTTTGGTAA R: TGATAGTCGTATGGGTTGGT	53	NM_001319304.1
Wnt4	F: GGAGGCAGCGTTCGTCTA R: GGCAATGTTATCGGAGCAG	56	NM_204783.1
Tnnc2	F: GAGCAGCAAAGATGGCGTCA R: ATCACCGTGCCCAACTCCTT	57	NM_205450.2
Tnnt3	F: AGAGGGAAGAAGCAAACAGC R: GTCCCACAGTTCCTTAGCCT	57	NM_204922.2
Srl	F: CCTCCTCGGGCTGGATGACA R: GTTCTTGCTGCTTGCGGTTT	56	NM_205329.1
Sox6	F: TCAGGTTCAGGGTCACATGCC R: TTGCTGGAGCTGTAAAGGGC	56	NM_001318451.1
Tnnc1	F: GTTGAGCAGTTGACAGAAGA R: GAACCATCATAACAAGGAAC	57	NM_205133.1
Tnni1	F: GAGGAGTGGGAGCAGGAGAT R: TTCGTCCACAATCTCAACCT	57	XM_004934839.2
Tnnt1	F: GAGCCGCACGGAGAAGGAGC R: CCCGAAGTGGGGCATGTTGG	57	NM_205114.1
β-actin	F:GATATTGCTGCGCTCGTTG R:TTCAGGGTCAGGATACCTCTTT	50-65	NM_205518.1

Table 2. Oligonucleotide sequences in this study.

Fragment name	Sequences (5′ to 3′)
miR-1611 mimic	GGAGGGCUUGCAGGCGGUGUGC
miR-1611 inhibitor	GCACACCGCCUGCAAGCCCUCC
si-lncRNA-Six1	GCTTATCTCAGCGCGTATA
ASO-lncRNA-Six1	TTAGCAGACACGCGGTCACG
si-*Six1*	GGGAGAACACGGAGAACAA

Table S3. Primers used for vector construction.

Primer name	Primer sequences (5′ to 3′)
pSDS-lncRNA-Six1	F: GGGG**GGTCTCTAGTG**GCCTGCTCCTGCAGCCCC
	R: GCCG**GGTCTCGTGGG**TTTTTTTCCTTTTTTCCTTTTT
pSDS-Six1	F: GGGG**GGTCTCTAGTG**ATGTCGATGCTGCCGTCGTTCG
	R: GCCG**GGTCTCGTGGG**CGTTCAGGATCACCGTCCGCTA
lncRNA-Six1 position 1	F: CCG**CTCGAG**CCTCGGGTCGTGGCAAAT
WT	R: ACGC**GTCGAC**CGGCCTTAGAAATAAGCCTACC
lncRNA-Six1 position 1	F: CAGCAAGTGGATGGGAAAGGCTAAAGATCCAACACAAACCTC
MT	R: GAGGTTTGTGTTGGATCTTTAGCCTTTCCCATCCACTTGCTG
lncRNA-Six1 position 2	F: CCG**CTCGAG**CAACATCACAAGCACTAAAA
WT	R: ACGC**GTCGAC**TGAGGGTGTCTTTATGGCA
lncRNA-Six1 position 2	F: CACCGCCGGCCACAGCTCGGCTAAAGACCCGGCCGGGCCGTG
MT	R: CACGGCCCGGCCGGGTCTTTAGCCGAGCTGTGGCCGGCGGTG
Six1 3′ UTR WT	F: CCG**CTCGAG**TGGACACGGACTCTCGGTT
	R: ACGC**GTCGAC**ATTTATGGGGCGCAATGG
Six1 3′ UTR MT	F: AAATGCAGAGAGCGGCAGAACTAAAGAGGCCTTTCGAGTTCA
	R: TGAACTCGAAAGGCCTCTTTAGTTCTGCCGCTCTCTGCATTT

Sequences in bold represent the enzyme cutting sites.

Figure S1. Identification of muscle fiber types between breast muscle and leg muscle. (**A**) H&E staining of transverse sections of breast muscles and leg muscles from 7-week-old XH chickens. (**B**) Muscle fiber area of breast muscles and leg muscles of 7-week-old XH chickens. (**C**) Muscle fiber diameter of breast muscles and leg muscles of 7-week-old XH chickens. (**D**) Immunofluorescence analysis of MYH1A/MYH7B-staining cells of breast muscles and leg muscles in 7-week-old XH chickens. (**E**) Relative MYH1A/MYH7B expression in breast muscles and leg muscles of 7-week-old XH chickens. (**F**) Relative protein expression of MYH1A and MYH7B in breast muscles and leg muscles of 7-week-old XH chickens. The numbers shown below the bands were fold-changes of band intensities relative to the control. Band intensities were quantified by ImageJ and normalized to GAPDH. Data are expressed as a fold change relative to the control. There was only one western blot performed per treatment, and therefore n = 1. In all panels, results are expressed as the mean ± S.E.M. of three replicates. Statistical significance of differences between means was assessed using an unpaired Student's *t*-test. (* $P < 0.05$; ** $P < 0.01$) vs. NC, negative control.