

Table S1. Primers used in the quantitative real-time PCR analyses

Type	Gene	Primer sequences (5'-3')	Ta (°C)	NCBI/Ensembl Transcript accession numbers
Reference genes	<i>efl1a</i>	F: CTGGAGGGCAGTGAAAAGAT R: CATCAAGAGCCTCCAGCAGT	58	XM_051391262.1
	<i>fau</i>	F: GACACCCAAGGTTGACAAGCAG R: GGCATTGAAGCACTTAGGAGTTG	58	XM_051408030.1
	<i>rpl17</i>	F: TTGAAGACAACGCAGGAGTCA R: CAGCGCATTCTTTTGCCACT	58	XM_051389216.1
Genes related to satellite cell activation and control of proliferation	<i>pax3b</i>	F: CTCTCTCCACAGGTGATGGG R: GAACACTGGTGAGACCCTCC	58	XM_051397277.1, XM_051397278.1, XM_051397279.1, XM_051397280.1, XM_051397281.1, XM_051397282.1
	<i>pax7</i>	F: GAGTGGTCTGTCCAGCAACG R: GGATGCTCATCACCTGTGGGG	58	XM_051426052.1, XM_051426053.1
	<i>c-met</i>	F: CCAAGTCAGACGTGTGGTCAT R: AGGGAAGGGTAAGGGCTCAT	58	XM_051382186.1, XM_051382187.1
	<i>pcna</i>	F: CTTCTTCACCAAAGCCACGC R: TTGTACTCCACCACGAGGG	58	XM_051423541.1
Myogenic regulatory factors	<i>myf5</i>	F: TGCTTTTGAGGCTTTGAGGC R: TCGCACAACTCTCGTTCTT	58	XM_051392417.1
	<i>myod1</i>	F: GACCGACCTGTCAGTCCAACCG R: GAGTCTCGGAGAAATAAGAGCTGTTGT	58	XM_051381070.1
	<i>myod2</i>	F: CTGCTGATGACCTCTACGATGAC R: GGCGTCCAGGTCGTCAAA	58	XM_051380371.1
	<i>myog</i>	F: TCACCTCACTCTGAAGCCCA R: TCGCTTGACGACGACACTCTG	58	XM_051413899.1
	<i>mrf4</i>	F: TGCTGAAGAGGAAGACCGTG R: GTATGGTTGACTGGTCACACTG	58	XM_051392418.1
Cell cycle and growth inhibitors	<i>cdkn1a</i>	F: AAGACCTGGAGGAGGCTTCA R: TCTCTGGCGAACATGGGATG	58	XM_051415913.1
	<i>cdkn1ba</i>	F: TTTTCTCAGACCGCCTCAC R: GGAGCAGGGACCTGAAGC	58	XM_051391902.1
	<i>cdkn1bb</i>	F: CCTGCATGTCACGAGCCC R: TCTTTCTGGGTGTGCGTTCT	58	XM_051382107.1

Regulators of muscle differentiation, fusion, and maturation	<i>cdkn1cb</i>	F: ACAACTCACACATCACAGACTTC R: GGAGAGATGGCAAGCGTTCA	58	XM_051381475.1
	<i>mstnb</i>	F: TTTTGAGCAAACCTGCGAATG R: CACGTCGTACTGGTCGAGAA	58	XM_051404813.1
	<i>mdfi</i>	F: AGCCATGCCCTAATGCAGATGT R: GGGGTGCCATTTACCCTCAA	58	XM_051413895.1, XM_051413896.1
	<i>dock5</i>	F: CGTCATAACCTTGCCCTGCT R: GTCCATCTGAGGATGCGGAG	58	XM_051422188.1, XM_051422190.1
	<i>cdh15</i>	F: TCTGACAGTGGTGAAGCCTTT R: GGGTCCTCCCTGAAATGTGG	58	XM_051379536.1
	<i>cav3</i>	F: AGTACCAGTACAACACCAACGA R: ATGACATCCTCAAACCTCCACCTTCA	58	XM_051415212.1
	<i>mymk</i>	F: GCGCTTCTACTTTGAGGAGTG R: TTAGCAGCATTTCTGTCCCGT	58	XM_051422197.1
	<i>mymx</i>	F: TGCTGCGGTCCCTGGTTATC R: ACTCCTGGGATCGAATGCGG	60	ENSDLAT00005060922.2
	<i>mef2aa</i>	F: CGCTTACTTCTTTGGTTGGTG R: ATGGGCTCGGACTTGATGTTT	58	XM_051382551.1, XM_051382552.1, XM_051382553.1, XM_051382554.1, XM_051382555.1, XM_051382556.1, XM_051382557.1, XM_051382558.1, XM_051382559.1, XM_051382560.1
	<i>mef2b</i>	F: TCTCCACACTCAGGTATCGG R: TGATTAGCAGCATCTCCCCG	58	XM_051376450.1
	<i>mef2ca</i>	F: CTCCGACATCGTGGATACGC R: GTTGTGGTTGTTGAGACCGC	58	XM_051412851.1, XM_051412852.1, XM_051412853.1, XM_051412854.1, XM_051412855.1, XM_051412858.1
	<i>mef2cb</i>	F: CAGGCACCAGTGCTGGAAATG R: AGATGGCAGATGGGTAACCG	58	XM_051423762.1, XM_051423763.1, XM_051423764.1, XM_051423765.1, XM_051423766.1, XM_051423767.1, XM_051423768.1

	F: GCCTACAACACCGAGTACCA <i>mef2d</i> R: GAGACGGGTTTCGGACTTGAT	58	XM_051405703.1, XM_051405704.1, XM_051405705.1, XM_051405706.1, XM_051405708.1, XM_051405709.1, XM_051405710.1, XM_051405711.1, XM_051405712.1, XM_051405713.1
	F: GCATGGATGATCTACACCTACTC <i>myhcb</i> R: ATCTTGCTAGAAACCTGTTCTT	58	XM_051414251.1
Genes of the Wnt signaling pathway	F: AATTGTCAATCGTGGTTGCCG <i>wnt1</i> R: ACAGTCATTCTGCCAGCCTC	58	XM_051425522.1
	F: GCCAGTGTTAGATAAAGCCACTC <i>wnt3a</i> R: ACTTCCATCCCTCACCAGGA	58	XM_051407837.1
	F: CGAGTAACTGGCTGTACCTGG <i>wnt4</i> R: GACGGTTGCGAAACTGGAAC	58	XM_051416222.1
	F: TACCAGTTCAGACATCGGCG <i>wnt5a</i> R: CGTTTCTCGGCTGCCTATTTG	58	XM_051426256.1
	F: GAAGCAGGAAGACAGGCAGT <i>wnt5b</i> R: CTTCAGGAACTCCCCGACAC	58	XM_051392233.1, XM_051392234.1, XM_051392235.1, XM_051392236.1, XM_051392237.1, XM_051392238.1, XM_051392240.1, XM_051392241.1
	F: GCCCCCAGACAACGGATTAT <i>wnt7a</i> R: AGCCTCTTTACTGCCCACTTT	58	XM_051425706.1
Genes of the Gh/Igf axis	F: GGTGGATGCTGAGGATGC <i>ghr-1</i> R: GGTGTCTGAGCCCTGGTT	58	XM_051422553.1
	F: TCCAGTCCAGAGCCCTAC <i>ghr-2</i> R: ACGACCTCACCTCACTCA	58	XM_051411650.1
	F: TACAGGCTATGGCCCCAAT <i>igf-1</i> R: TTGGCAGGTGCACAGTACAT	58	XM_051393202.1, XM_051393203.1, XM_051393204.1
	F: AATACGAGGTGTGGCAGAGG <i>igf-2</i> R: TTGATCTTCTCCGCCTGTCT	58	AY839105.1
	F: ACCAGTGCCAGAAAGTATGC <i>igf1ra</i> R: GTAGGTGTCTCGGGGACAGT	58	XM_051382543.1
	F: AAAGTGGCTTCTGAGACCGAG <i>igf-1rb</i> R: AACGCCTTGCTGAGTCTGAT	58	XM_051379301.1, XM_051379302.1, XM_051379303.1

	<i>igfbp-1a</i>	F: CTCAGGAGAGCATGAAAGCCA R: GTCCAGAGAGGATTTCGCACTGTT	58	XM_051377947.1
	<i>igfbp-3a</i>	F: GCGTGGCAACCGTGAAGG R: GCCTGGTGTCCACAGATCC	58	XM_051377946.1
	<i>igfbp-5b</i>	F: GTGCCACTCCTTCCCAAAGACAT R: CTGCTTGCCCAGCTTCCTCT	58	XM_051403863.1
	<i>igfbp-6b</i>	F: CCAGGGACCATAATGTTGCC R: TACACACCACAGGGCTCTC	58	XM_051424236.1
Genes related to anabolic signaling in the Akt/mTor pathway	<i>akt1</i>	F: CCCCAGGAGAGGGAAGAAT R: TTCATGGCGTAGTAGCGTCC	58	XM_051386473.1, XM_051386474.1, XM_051386480.1
	<i>akt2</i>	F: GCATCCCTTCCTAACGACAC R: TCCGTCTGTGATCCCCTCTT	58	XM_051397243.1, XM_051397244.1
	<i>mtor</i>	F: GGCACCTATGACCCCAACCA R: CTGTCGAACCACACCTCAGA	58	XM_051426465.1, XM_051426467.1
	<i>rptor</i>	F: CTACACCCAGTACATCCCGC R: GGTTGATAGCTGCCACCTCC	58	XM_051383911.1, XM_051383912.1, XM_051383913.1, XM_051383914.1
	<i>rps6kb1b</i>	F: GGAGTACCTGAGTGGAGGAGA R: TGCCGTCGTGAATTGACTCT	58	XM_051397158.1, XM_051397157.1
	<i>eif4ebp1</i>	F: CTGAAAGCAGCAACACTGGTGA R: CTGGAGACACTGAAGGCGAA	58	XM_051421432.1
Genes related to muscle protein degradation and autophagic lysosome system	<i>foxo1a</i>	F: GAGCAGCTAAGAAAAAGCTGTCC R: CCTCTGGCATGAAGGGTGAG	58	XM_051399747.1
	<i>murfl</i>	F: TGGTGCGTCCTGTCAAGT R: CGGCTTGGTGAACATCTCAA	58	XM_051428187.1
	<i>mafbx</i>	F: ACTGAGGACCGACTGCTGTGGAAGA R: TGTCTGTCTGTGAAGTGGTACTGGCAAAGT	58	XM_051407032.1
	<i>atgl2</i>	F: GACGACTCCACGACGAATGA R: CATCGCTGCCAAAACAATCAA	58	XM_051406206.1
	<i>map1lc3b</i>	F: TCATCAAGATTATCAGGAGGCG R: CGAGGCTAAAGGTGTGTGGT	58	XM_051383370.1
	<i>ctgba</i>	F: GGAGACTCTGCGGTACGATG R: TGTGGATACACACCGGTCG	58	XM_051378868.1
	<i>ctsd</i>	F: TGAAGAACTACCTTGACGCCCA R: CACCCACAGGTTGGAGGAAC	58	XM_051378447.1

<i>ctsla</i>	F: TCCTTACCTGGGAACAGATGAC R: TCAATGGCAACTGAGACGGG	58	XM_051423024.1
<i>ctsl.1</i>	F: GCCGTTACAACCCAGACACT R: TGGCTCATCATACACTCCTGA	58	XM_051385832.1
<i>capn1</i>	F: CTACAGAGGAAATCCGACTAAGC R: CGGTCCATTCCACTTCCC	58	XM_051428619.1
<i>capn2b</i>	F: AACGAACTGACATCCGAACTGA R: ATGCCGCTGTCATCCATCA	58	XM_051382680.1
<i>capn3b</i>	F: ATACCGACGGGACAGGGAAG R: GCTGCCACGCCTTGATCTT	58	XM_051407914.1, XM_051407913.1

ef1a (elongation factor 1-alpha), *fau* (40S ribosomal protein S30), *rpl17* (60s ribosomal protein 117), *pax3b* (paired box protein 3b), *pax7* (paired box protein 7), *c-met* (hepatocyte growth factor receptor), *pcna* (proliferating cell nuclear antigen), *myf5* (myogenic factor 5), *myod1* (myoblast determination protein 1), *myod2* (myoblast determination protein 2), *myog* (myogenin), *mrf4* (myogenic regulatory factor 4), *cdkn1a* (cyclin-dependent kinase inhibitor 1a), *cdkn1ba* (cyclin-dependent kinase inhibitor 1b paralog a), *cdkn1bb* (cyclin-dependent kinase inhibitor 1b paralog b), *cdkn1cb* (cyclin-dependent kinase inhibitor 1c), *mstnb* (myostatin b), *mdfi* (myod family inhibitor), *dock5* (dedicator of cytokinesis protein 5), *cdh15* (cadherin-15), *cav3* (caveolin-3), *mymk* (myomaker), *mymx* (myomixer), *mef2aa* (myocyte enhancer factor 2aa), *mef2b* (myocyte enhancer factor 2b), *mef2ca* (myocyte enhancer factor 2ca), *mef2cb* (myocyte enhancer factor 2cb), *mef2d* (myocyte enhancer factor 2d), *myhcb* (myosin heavy chain b), *wnt1* (wingless-type mmtv integration site family member 1), *wnt3a* (wingless-type mmtv integration site family member 3a), *wnt4* (wingless-type mmtv integration site family member 4), *wnt5a* (wingless-type mmtv integration site family member 5a), *wnt5b* (wingless-type mmtv integration site family member 5b), *wnt7a* (wingless-type mmtv integration site family member 7a), *ghr-1* (growth hormone receptor 1), *ghr-2* (growth hormone receptor 2), *igf-1* (insulin-like growth factor 1), *igf-2* (insulin-like growth factor 2), *igf1ra* (insulin-like growth factor 1 receptor a), *igf-1rb* (insulin-like growth factor 1 receptor b), *igfbp-1a* (insulin-like growth factor binding protein 1a), *igfbp-3a* (insulin-like growth factor binding protein 3a), *igfbp-5b* (insulin-like growth factor binding protein 5b), *igfbp-6b* (insulin-like growth factor binding protein 6b), *akt1* (protein kinase b alpha), *akt2* (protein kinase b beta), *mtor* (mechanistic target of rapamycin), *rptor* (regulatory-associated protein of mtor), *rps6kb1b* (ribosomal protein S6 kinase beta-1b), *ef4ebp1* (eukaryotic translation initiation factor 4e binding protein 1), *foxo1a* (forkhead box o1a), *murfl* (muscle ring finger 1), *mafbx* (muscle atrophy F-box), *atg12* (autophagy related 12), *map1lc3b* (microtubule-associated proteins 1a/1b light chain 3b), *ctspa* (cathepsin ba), *ctsd* (cathepsin d), *ctsla* (cathepsin la), *ctsl.1* (cathepsin 1l), *capn1* (calpain 1), *capn2b* (calpain 2b), *capn3b* (calpain 3b).

The PCR amplification efficiency of all primer pairs ranged between 90% and 110%.