

Supplementary Information

Supplementary Table S1. The primer sequences for SqRT-PCR and qRT-PCR

Species	Genes	Primer sequences (5' to 3')
Pig	<i>TRPC1</i>	F: CATCCAAAGGCAAGGTTA R: AAGTCCGAAAGCCAAGTA
	<i>β-actin</i>	F: GCCAACCGTGAGAAGATGACT R: GTGACCCCATCCCCAGAGT
Mouse	<i>Ki67</i>	F: ATCATTGACCGCTCCTTTAGGT R: GCTCGCCTTGATGGTTCCT
	<i>Cyclin B</i>	F: AATACCTACAGGGTCGTGAAGTGA R: GCTGTATCATCTTCTTGGGCAC
	<i>CDK4</i>	F: GCTGCTACTGGAAATGCTGACC R: AGCCTTGGGGGGAAACAGA
	<i>p27</i>	F: CAGGCAAACCTCTGAGGACCG R: TCGGGGAACCGTCTGAAAC
	<i>BAD</i>	F: GCTTAGCCCTTTTCGAGGAC R: GATCCCACCAGGACTGGAT
	<i>MyoD</i>	F: CGAGCACTACAGTTGGCGACTAAGAT R: GCTCCACTATGCTGGACAGGCAGT
	<i>MyoG</i>	F: CCATCCAGTACATTGAGCGCCTACA R: ACGATGGACGTAAGGGAGTGCAGAT
	<i>MyHC</i>	F: CAAGTCATCGGTGTTTGTGG R: TGTCGTACTTGGGCGGGTTC
	<i>Myomaker</i>	F: ATCGCTACCAAGAGGCGTT R: CACAGCACAGACAAACCAGG
	<i>β-1integrin</i>	F: TTACAAGAGTGCCGTGACAACTG R: GACTAAGATGCTGCTGCTGTGAG
	<i>Atrogin1</i>	F: GCAGCTGGATTGGAAGAAGA R: GAGCAGCTCTCTGGGTTGTT
	<i>Bmp4</i>	F: CCGGATTACATGAGGGATCT R: CCTGGGATGTTCTCCAGATG
	<i>Murf</i>	F: GCAAGGCTTTGAGAACATGG R: TCTTCCTCATCAGCCTCCTC
	<i>Foxo3</i>	F: ACAAACGGCTCACTTTGTCC R: CTGTGCAGGGACAGGTTGT
	<i>Fst</i>	F: TCTCTGCGATGAGCTGTGTC R: CCTCCTCTTCCCTCCGTTTCT

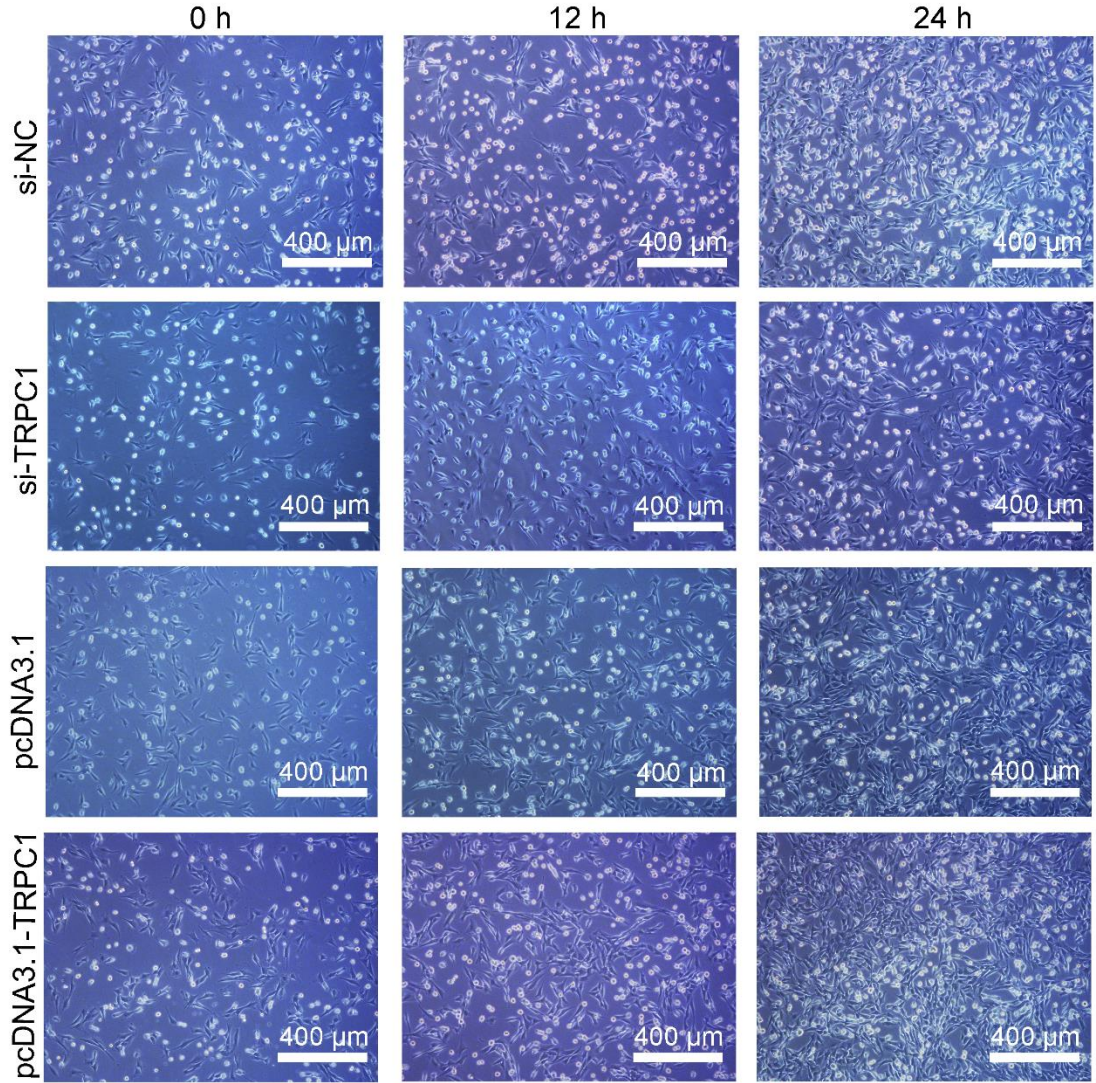
<i>Nog</i>	F: TGTGGTCACAGACCTTCTGC R: GTGAGGTGCACAGACTTGGA
<i>LRP6</i>	F: CGTATGAAGGGAGACGGGGA R: CTTTCTGTGGCAGGCGATGG
<i>LEF1</i>	F: ATGATTCTGGTCCCCCTG R: GCTCCTGCTCCTTTCTCTGTTC
<i>TCF1</i>	F: TGGACATTGACATTTCGCATT R: CACACGGTCAGTCCATGTTC
<i>CCND</i>	F: GCCCTCCGTATCTTACTTCAAG R: ACCTCCTCTTCGCACTTCTG
<i>Axin2</i>	F: GCTGACGGATGATTCCATGT R: ACTGCCCACACGATAAGGAG
<i>GSK3β</i>	F: TTTTTCGATGAATTGCGGG R: TTATTGGTCTGTCCACGGTCTC
<i>SPFR2</i>	F: ACCCTTTGTAAAAATGACTTCGCA R: GATTCTTCAGGTCCCTTTCGG
<i>SPFR4</i>	F: CAAGTCTTTGTACCTATCCCTCG R: GTGCGGCTGGCTATCTGCTT
<i>TRPC1</i>	F: GTGGTATGAAGGGTTGGAAGACT R: TCTGCTACAAGCGTGGGGTG
<i>β-actin</i>	F: ATCTGGCACCACCTTCTACA R: AAGGTCTCAAACATGATCTGGGT

Supplementary Table S2. Sequence, targets, and amplicon size of the primers used for SNP identification of the pig *TRPC1* gene

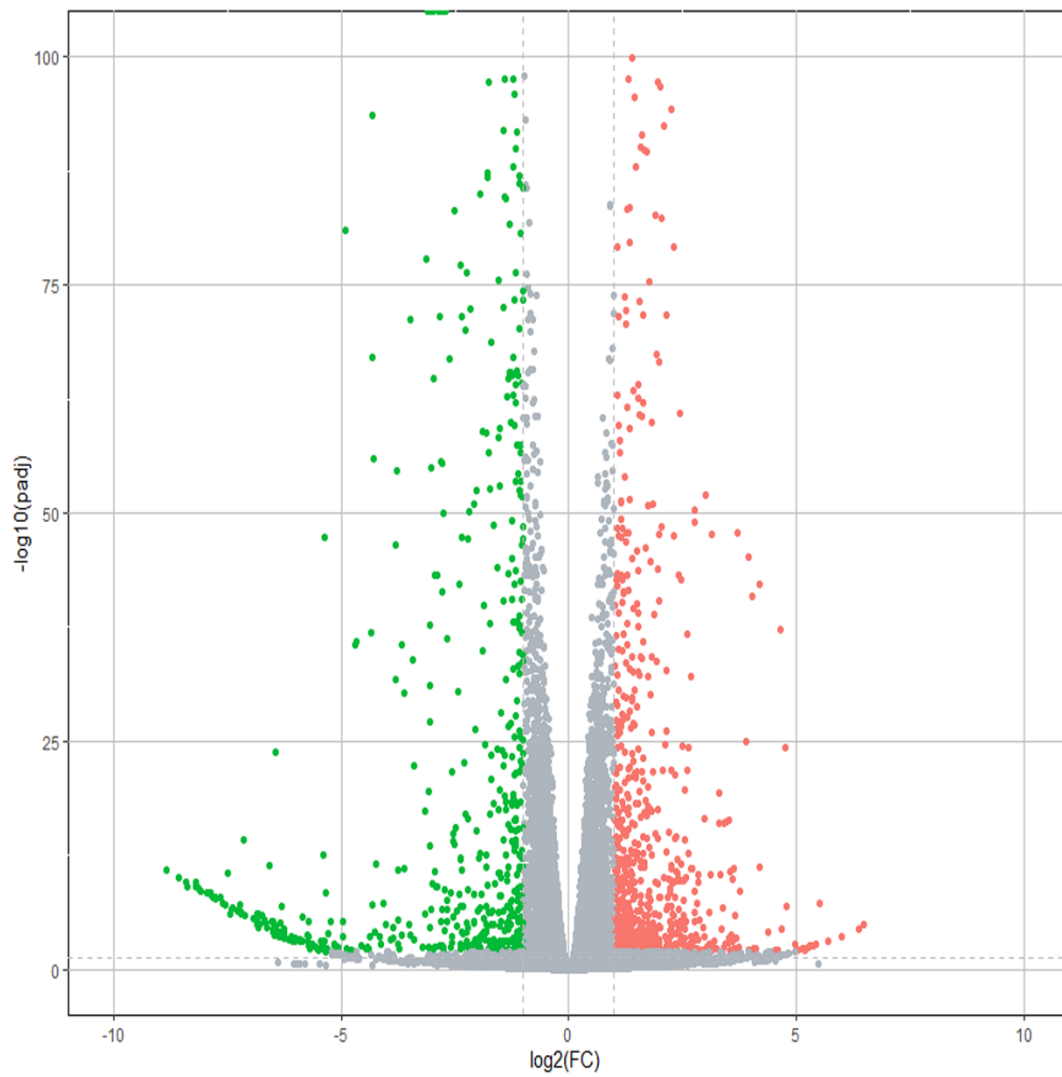
Primers	Target regions (bp)	Primer sequences (5' to 3')	Amplicon sizes (bp)
<i>TRPC1</i> -P1	-2142/-1548	F: CTAGAGTTGTGATGGGTCTTC R: GCTCATTGTAAATCTGTGGC	595
<i>TRPC1</i> -P2	-1702/-942	F: TTACCCCTAAACACTCTGG R: CATTGGGATCGGCTCTA	761
<i>TRPC1</i> -P3	-1121/-662	F: CAAGCACTAAGGGGACA R: GGTTGCAGGTTTGAGGTA	550
<i>TRPC1</i> -P4	-678/+121	F: ACCTCAAACCTGCAACC R: ACCTCCCGCACATCCTT	800

Supplementary Table S3. The sequences of *TRPC1* siRNA fragments

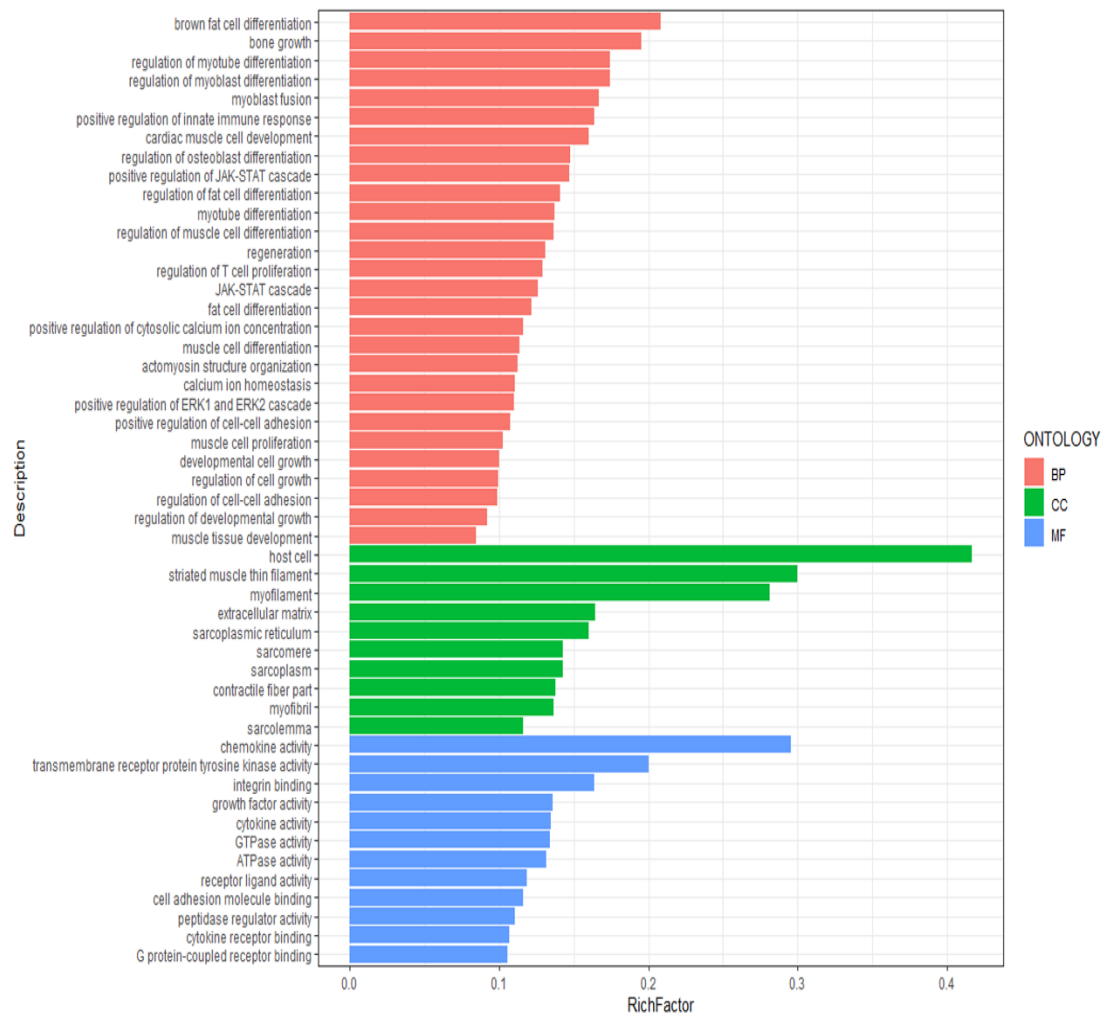
siRNA	Oligo sequences (5' to 3')
si-NC	GGGUCCAUUACAGAUUUCATT UGAAAUCUGUAAUGGACCCTT
si-682	CGACAAGGGUGACUAUUAUTT AUA AUAGUCACCCUUGUCGTT
si-886	GGGAGCUGUUGAUUAUACUATT UAGUAUAUCAACAGCUCCTT
si-1220	CUGAGAGCGUUUGAACUUATT UAAGUUCAAACGCUCUCAGTT



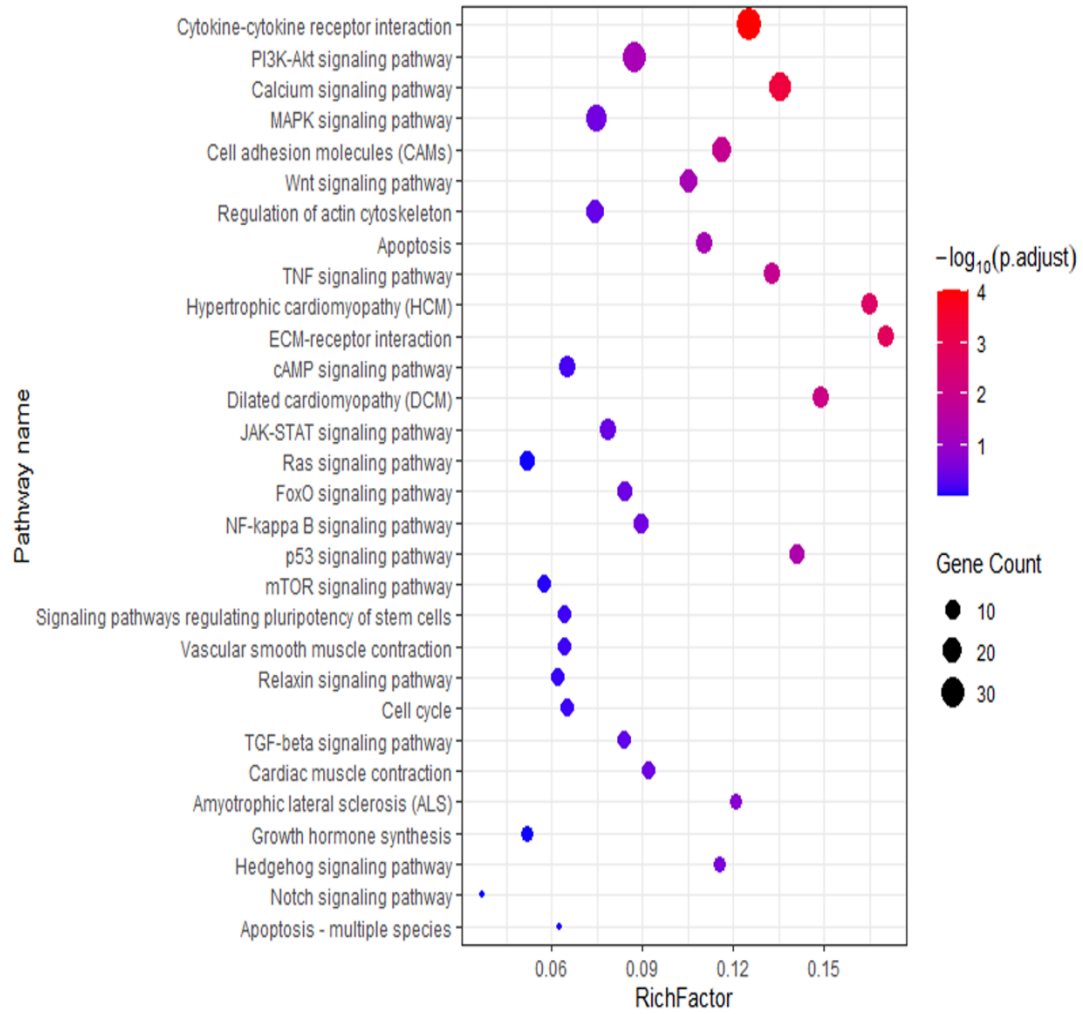
Supplementary Fig. S1 The microscopic images of proliferated cells. C2C12 with different treatments at 0 h, 12 h and 24 h, respectively, $n = 3$, scale bar = 400 µm.



Supplementary Fig. S2 Differentially expressed genes identification. Volcano plot displaying DEGs between *TRPC1*-overexpression group and control. Upregulated and downregulated genes are shown in red and green, respectively. Gray dots represent genes with similar expression levels.



Supplementary Fig. S3 Significantly enriched GO terms of differentially expressed genes. The green clusters represent the cellular component, the red clusters represent the biological process, and the blue clusters represent the molecular function of the GO terms.



Supplementary Fig. S4 KEGG-enriched scatter plot of DEGs between control and *TRPC1*-overexpressed C2C12. The rich factor is the ratio of DEG numbers annotated in this pathway term to the total gene numbers annotated in this pathway term. The smaller the P-value, higher the significance.