Electronic Supplementary Material (ESI) for Food & Function.

Supplements

Table S1. Primers sequences used in qRT-PCR analysis.

Gene name	Forward primer (5'–3')	Reverse primer (5'–3')
Ucp1	CCTGCCTCTCTCGGAAACAA	GTAGCGGGGTTTGATCCCAT
Sirt1	TTCCAGCCATCTCTGTGTCA	GATCCTTTGGATTCCTGCAA
Ppargc1a	CCGAGAATTCATGGAGCAAT	GTGTGAGGAGGGTCATCGTT
Lkb1	CGAGGGATGTTGGAGTATGAG	CTTAGTGTCTGGGCTTGGTG
Fgf21	CTGGGGGTCTACCAAGCATA	CACCCAGGATTTGAATGACC
Prdm16	GATGGGAGATGCTGACGGAT	TGATCTGACACATGGCGAGG
Ppara	TACTGCCGTTTTCACAAGTGC	AGGTCGTGTTCACAGGTAAGA
Cidea	CGGGAATAGCCAGAGTCACC	TGTGCATCGGATGTCGTAGG
Foxo1	CTACGCGTGGATGGTGAAGAG	TGTGAAGGGACAGATTGTGG
Camkk2	CCATCGAGCAAGTGTACCAG	ACTTCCATTACAGGCCCTTG
Foxo3	CGTTGTTGGTTTGAATGTGGG	GGTTTTCTCTGTAGGTCTTCCG
Ulk1	CTAAGCTGCCTGACTTCCTAC	CCAACAGGGTCAGCAAATTC
Cd137	GGTCTGTGCTTAAGACCGGG	TCTTAATAGCTGGTCCTCCCTC
Tbx1	AGCGAGGCGGAAGGGA	CCTGGTGACTGTGCTGAAGT
Tmem26	GAAACCAGTATTGCAGCACCC	CCAGACCGGTTCACATACCA
Cited1	GGGGTAAAAGATCGCAAGGC	TGGTAGAAGGGGTGGCAGTA
Shox2	CCTGCCCCATTGATGTGTTA	ACGCCGTAAGTTCTTCCATC
Zic1	GCCACAAATCCGGGAAGAAG	CTCACTTTCTCGCCGCTCAG
Lhx8	CATCGCTGTTCTGCCTGTTAG	CTCGGGATTCAGCAGTCCTTC
Eva1	AGTGCTGATAAAGCCGAGGG	AGCTTCTCGAAGTGTTAGTCTGT
Pdk4	AGTGACTCAAAGACGGGAAAC	GTGTGAGGTTTAATTCTGGCG
Cytb	ACCTCCTATCAGCCATCCCA	AGCGAAGAATCGGGTCAAGG
Rplp0	TGACATCGTCTTTAAACCCCG	TGTCTGCTCCCACAATGAAG
Nrf1	CGAAAGAGACAGCAGACACG	TTGAAGACAGGGTTGGGTT
Nrf2	AGAACAAGTGACAAGATGGGC	TCGGTCATGCTGAATTCCTTC

Nampt	GAATGTCTCCTTCGGTTCTGG	TCAGCAACTGGGTCCTTAAAC
Tfam	CACCCAGATGCAAAACTTTCAG	CTGCTCTTTATACTTGCTCACAG
Cd36	GCAACAAACCACACACTGGG	AGTCCTACACTGCAGTCCTCA
Fas	TGCTGTTGGAAGTCAGCTATGAA	GATGCCTCTGAACCACTCACAC
Fabp4	TGGGAACCTGGAAGCTTGTCTC	GAATTCCACGCCCAGTTTGA
Prkaa1	CCCTTCAGTAATCAGCCTTTTG	GGTTGAACTATAAGATGGGTCCTC
Prkaa2	CATCCCAGACTATCTCAACCG	GGGTCTTCAGGAAATAGGTAGC
β-actin	CATCCGTAAAGACCTCTATGCCAA C	ATGGAGCCACCGATCCACA

Fig S1

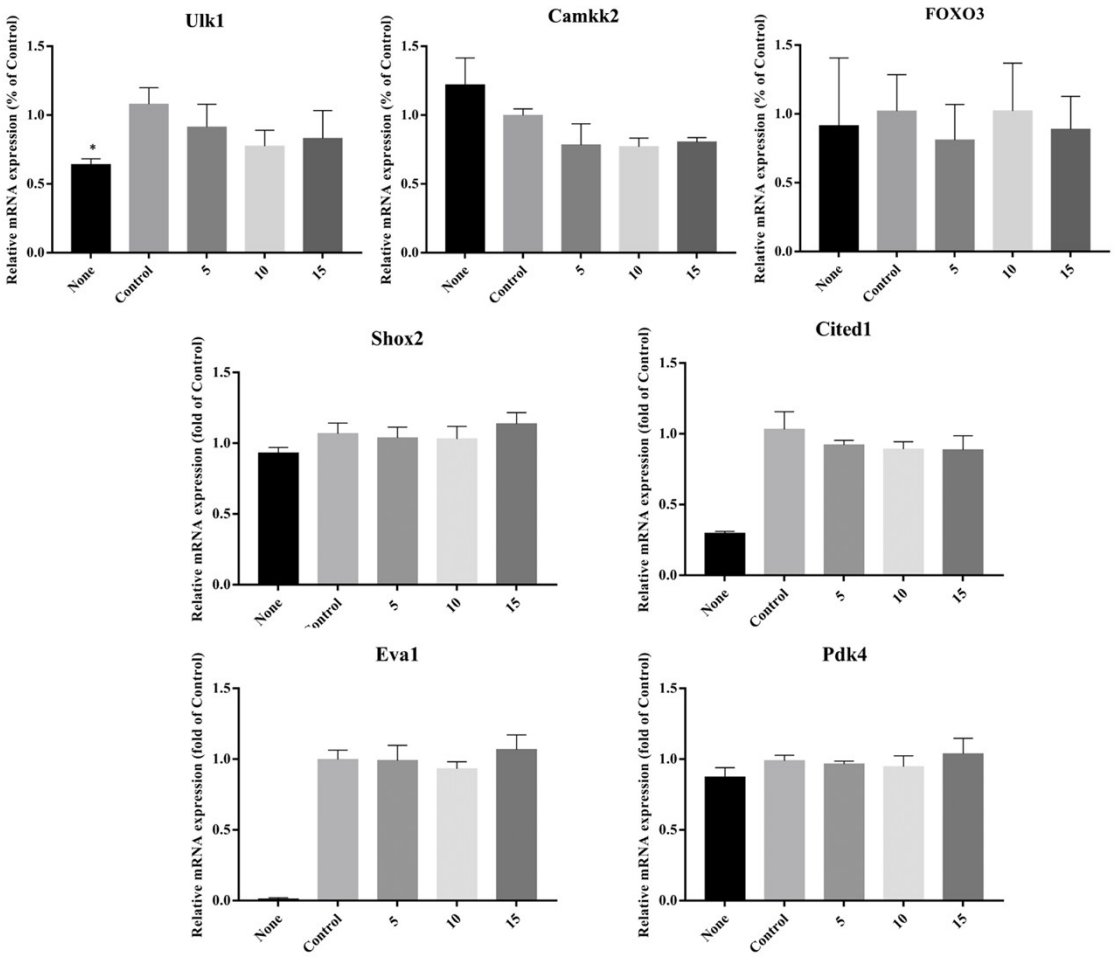
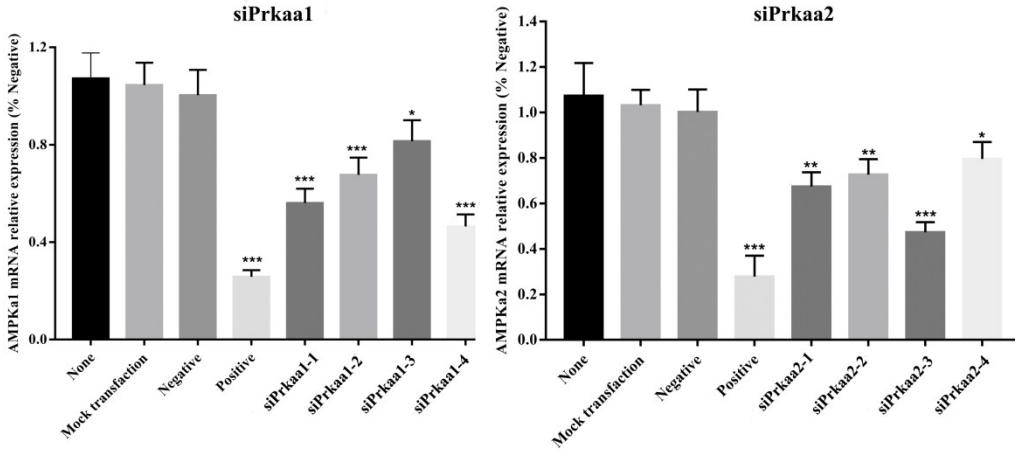


Fig S2



Selection of optimal target sequences for *AMPKα1* and *AMPKα2* gene. *AMPKα1* (*Prkaa1*, gene ID: 105787) and *AMPKα2* (*Prkaa2*, gene ID: 108079). None: Normal cultural cells without transfaction. Mock transfaction: Lipofectamine 3000 as a transfer control. Negative: universal negative control provided by company. Positive: GAPDH as positive control. Analysis was performed using the $2^{-\Delta\Delta Ct}$ method and normalized using *GAPDH* gene. The siAMPKα1-4 and

siAMPKα2-3 were selected for the further experments.