

Table S1. Primer sequences used for ground squirrel qRT-PCR

Gene symbol	Protein	Direction	Sequence	Source	Size (bp)
<i>ACAA1</i>	acetyl-Coenzyme A acyltransferase 1	Forward	CTGTGTGGAGAAGCTAGGAATCC	UP ^a	51
		Reverse	CCTCCCAGAGGGTTCACCTT		
<i>ACAA2</i>	acetyl-Coenzyme A acyltransferase 2	Forward	AGCCTTTGCTCCCAGTATT	IT ^a	180
		Reverse	GCTGATCCAACGGCATATTT		
<i>ACADM</i>	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	Forward	GGGAGCTTTTGATAGAACCA	UP ^b	91
		Reverse	CAGGGCATACTTGGTAGCTT		
<i>ACADVL</i>	acyl-Coenzyme A dehydrogenase, very long chain	Forward	GACATTCTTCGGCTCTTTGT	UP ^b	129
		Reverse	CTGTTTTCCCTGCCTCTCCTA		
<i>ACAT1</i>	acetyl-Coenzyme A acetyltransferase 1	Forward	ATTGATCCCCAAAAGTGAA	UP ^b	146
		Reverse	CCTCCTCCATTGCAGATACT		
<i>ACAT2</i>	acetyl-Coenzyme A acetyltransferase 2	Forward	GCCATGGGAGTAACCTTGAA	CL ^a	245
		Reverse	AGCTTGCTTTATGGCTGGAA		
<i>ACSL3</i>	acyl-CoA synthetase long-chain family member 3	Forward	TGAAGCAAAAACAAAAGCTG	UP ^b	94
		Reverse	ACAACCATCAGGGTCAAACCT		
<i>AGPAT3</i>	1-acylglycerol-3-phosphate O-acyltransferase 3	Forward	TGGTCATCATCCTCAATCAC	UP ^b	104
		Reverse	CTTCTTAGCGAGGACTTTGG		
<i>ARG1</i>	arginase, liver	Forward	GATGCTCACACGGATATCAA	UP ^b	114
		Reverse	TCCTGGTACATCAGGGATCT		
<i>BCKDHA</i>	E1-alpha subunit of the branched-chain alpha-keto acid dehydrogenase complex	Forward	GCCAGATGCCTGTCCACTAT	IT ^a	235
		Reverse	TTGTTCCGGCAGAAGAAGAT		
<i>BCKDHB</i>	branched chain keto acid dehydrogenase E1, beta polypeptide	Forward	GGCTTTGCGTCAGAGATCAG	IT ^a	160
		Reverse	TTTTCCGAAGGGCATCATAG		
<i>BDH2</i>	3-hydroxybutyrate dehydrogenase, type 2	Forward	TGTTGCTGGTTTTGTTTCATC	UP ^b	126
		Reverse	GCAAGCATTTTAGGAAGGAA		
<i>CACT</i>	carnitine/acylcarnitine translocase	Forward	GCTTCTTTGGGTTTGGTTTG	CL ^a	203
		Reverse	TGCACAGTCCAAGGTACCAG		
<i>CPT1A</i>	carnitine palmitoyltransferase 1A, liver	Forward	CATCGTCACCATGCGCTACT	UP ^a	51
		Reverse	CAGCCGTGGTAGGAGAGCAG		
<i>CPT1B</i>	carnitine palmitoyltransferase 1B, muscle	Forward	GCCACAATTCAGCGGTACTT	IT ^a	215
		Reverse	CTGTTACCATTGAGGGGACT		
<i>CRAT</i>	carnitine acetyltransferase	Forward	GGCCCATATCAACTTCTCTG	UP ^b	110
		Reverse	GAAGTAGGGTACGCATGTCC		
<i>CS</i>	citrate synthase	Forward	GGCCATAGTATCCCTGAATG	UP ^b	117
		Reverse	CTGTTCTCTGTTGGGATCT		
<i>ELOVL6</i>	ELOVL family member 6, elongation of long chain fatty acids	Forward	ACCTCAGCTACCTTGTGCTC	UP ^b	81
		Reverse	ATTCAGCCTTCGTTGTTTTT		
<i>Fabp1</i>	fatty acid binding protein 1, liver	Forward	CACTTCAAGCTCACCATCAC	UP ^b	115
		Reverse	TGTTGACCACTGTCTTGACC		
<i>FABP4</i>	fatty acid binding protein 4, adipocyte	Forward	GCCAGGAATTTGATGAAGTC	UP ^b	94
		Reverse	ATCCACTTCTGCACCTGAAC		
<i>G6PC</i>	glucose-6-phosphatase, catalytic subunit	Forward	GATGGAGGAAGGAATGAATG	UP ^b	118
		Reverse	GAGGTACGAATCACAGACA		
<i>GAPDH</i>	glyceraldehyde-3-phosphate dehydrogenase	Forward	AAGGTCATCCCTGAACTGAA	UP ^b	114
		Reverse	ATCGTATTTGGCAGCTTTCT		
<i>GLUD1</i>	Glutamate dehydrogenase 1	Forward	GTGCATTCTGGCTTAGCCTACA	UP ^a	51
		Reverse	CATAATTTGCCTGGCTGAACG		
<i>GOT1</i>	glutamic-oxaloacetic transaminase 1	Forward	CTGCTCAGGGAGCACGAATT	UP ^a	51
		Reverse	CACATTGCCTGTCCATTCTTTAAAG		
<i>GOT2</i>	glutamic-oxaloacetic transaminase 2	Forward	CGGTACTATGACCCCAAGAC	UP ^b	92
		Reverse	TGCAGGAGAAGAACAACCTCTG		
<i>Gpd1</i>	Glycerol -3-phosphate dehydrogenase 1	Forward	CTCTGAAGTGATTGGGGAAC	UP ^b	88
		Reverse	GAACTTCTCATCAGCCACCT		
<i>GSK3A</i>	glycogen synthase kinase 3 alpha	Forward	CTGACACTGCTGCCTCAAG	UP ^b	144
		Reverse	CGATGGACGAGGTATAATCA		
<i>GSY1</i>	glycogen synthase 1, muscle	Forward	ACCATCTTACCACCCATGC	CL ^a	51

<i>GSY2</i>	glycogen synthase 2	Reverse	ACCAGCACACAGGTAGCGC	UP ^a	51
		Forward	CATCACCACCAGCGACAGAA		
<i>HADHA</i>	hydroxyacyl-Coenzyme A dehydrogenase, alpha subunit	Reverse	GTAAGGAAAGGCCTGGGATA	UP ^b	116
		Forward	TGTCAGCAAAAGACCTGAGA		
<i>HADHSC</i>	short-chain L-3-hydroxyacyl-CoA dehydrogenase	Reverse	CAGAAGCAGTTGTGTCCTTG	UP ^b	76
		Forward	TCTTTGCAGATCACAAGCAT		
<i>HK1</i>	Hexokinase 1	Reverse	CTGGGTTGAAGAAATGAAGG	UP ^b	102
		Forward	CGTGGATGGGACACTCTACA		
<i>HMGCL</i>	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	Reverse	GACAGGAGGAAGGACACGTT	UP ^b	96
		Forward	GTACGTCTCCTGTGTGCTTG		
<i>HMGCS2</i>	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	Reverse	TAGCAGCCCATTGAGTACAA	UP ^b	138
		Forward	CCCTTTACCTTTCCACACAC		
<i>HPD</i>	4-hydroxyphenylpyruvate dioxygenase	Reverse	CTAAGCCAGAGCCATAGGAG	CL ^a	51
		Forward	CCTGAGAGAGGCCGATTCTCT		
<i>HPRT1</i>	hypoxanthine phosphoribosyltransferase 1	Reverse	GCCAACCCAGAAGGTCACAG	UP ^b	124
		Forward	CGACCTGACTTTGTTGGATT		
<i>HSL</i>	Hormone-Sensitive Lipase	Reverse	ATTTTGTCTTCCAGTTTCA	UP ^a	51
		Forward	TTGCGCGAGTATGTCACACTG		
<i>IDH2</i>	isocitrate dehydrogenase 2 (NADP+), mitochondrial	Reverse	CAAGCAGCGCCATAGAAAC	UP ^b	109
		Forward	GATGGTCTTCACTCCAAAGG		
<i>IDH3B</i>	isocitrate dehydrogenase 3 (NAD+) beta	Reverse	CGAGATGGACTCATCGGTAT	UP ^b	88
		Forward	GCCAAATGTAGTCCATGTGAA		
<i>LDHB</i>	lactate dehydrogenase B	Reverse	CTTCTGTCTGCTCACGAATG	UP ^b	78
		Forward	TCTCAATCTGGTGCAGAGAA		
<i>MDH2</i>	malate dehydrogenase 2, NAD, mitochondrial	Reverse	ATGCAATCGGGACTGTACTT	UP ^b	111
		Forward	ATCCCAATCACAGCAGAAGT		
<i>OTC</i>	ornithine carbamoyltransferase	Reverse	CAGCTCTGCAACAAAAGTGT	UP ^b	130
		Forward	CATCCTGGCTAGAGAAGCAT		
<i>OXCT1</i>	3-oxoacid CoA transferase 1	Reverse	GCTGAGGGTAAGACCTTTGA	UP ^b	83
		Forward	GGACAGTAAGAAAGGGCTGA		
<i>PAH</i>	Phenylalanine hydroxylase	Reverse	AATCACACCCAGTGCTCTTT	UP ^b	87
		Forward	GGACAGGAAACGAGCTACAT		
<i>PCK1</i>	Phosphoenolpyruvate carboxykinase 1	Reverse	TGCACCAACTTCTTCTTTGA	UP ^b	104
		Forward	ATCGACTACATCCCAAGAA		
<i>PCK2</i>	phosphoenolpyruvate carboxykinase 2, mitochondrial	Reverse	ACTTCCTCCTCCAGAACTC	UP ^a	51
		Forward	AGTGAAGGTCGACTCCGGG		
<i>PDHE1B</i>	pyruvate dehydrogenase E1 beta	Reverse	GCCACCCCAAAGAAACCATT	UP ^b	75
		Forward	GGATGTGGAAGTGGAAAGAG		
<i>PDK1</i>	pyruvate dehydrogenase kinase, isozyme 1	Reverse	TTGTATGCCCATCATACTG	CL ^a	164
		Forward	GGGATATGGGACAGATGCAG		
<i>PDK2</i>	pyruvate dehydrogenase kinase, isozyme 2	Reverse	GGAACGTGGTCATGTCTTT	UP ^b	93
		Forward	TCCAACCAGAACATCCAGTA		
<i>PDK4</i>	pyruvate dehydrogenase kinase, isozyme 4	Reverse	ATCAAAGATGAGGGTGTGCT	IT ^a	161
		Forward	GAGCTTTTCTCCCGCTACAG		
<i>PFKL</i>	phosphofructokinase, liver	Reverse	CGATCAGGGAGGACATCAAT	UP ^a	130
		Forward	GTGATCGCATCAAACAGTCG		
<i>PFKM</i>	phosphofructokinase, muscle	Reverse	AAGACGTAGGCAGCATCAGC	UP ^b	116
		Forward	GTGGTGAGCCTCTCTGGTAA		
<i>PKM2</i>	pyruvate kinase, muscle	Reverse	AGCTTCATGGCTTCATCAA	UP ^b	108
		Forward	GAACGTCGCTCGTCTAAACT		
<i>RPS3</i>	ribosomal protein S3	Reverse	TAGAGAATGGGGTCAGAAGC	UP ^b	149
		Forward	ACTCCGAGGACAGAGAGCTA		
<i>SC4MOL</i>	sterol-C4-methyl oxidase-like	Reverse	GCAGCATGATCTTCACTTTG	UP ^b	82
		Forward	GTTGGAAAACCAATGGAAAT		
<i>SCD</i>	stearoyl-CoA desaturase, delta-9-desaturase	Reverse	ATGGGTTCCACAAATCAAAG	CL ^a	51
		Forward	CCGACCCTCATAACTCTCGC		
<i>SUCLG1</i>	succinate-CoA ligase, alpha subunit	Reverse	GCCAACCCACGTGAGAGAAG	UP ^b	99
		Forward	TGGTGATGCAGAAGAAAATG		

<i>UGP2</i>	UDP-glucose pyrophosphorylase 2	Reverse	GGAGCAGTTAAACCAGCAAT	UP ^b	148
		Forward	AAGATGGTGCCTCTCAGTTC		
<i>YWHAZ</i>	protein kinase C inhibitor protein	Reverse	TGAAATAGCTTCCGAAATCC	UP ^b	147
		Forward	GGGCTAAGTTATACCCAAAGC		
		Reverse	AGAAAACATTGTCCTGCTC		

Source indicates species of EST sequence used to develop primers (CL, *Callospermophilus lateralis*; IT, *Ictidomys tridecemlineatus*; UP, *Urocitellus parryi*) and source of the EST sequence (^aYan et al., 2008; ^bpresent study).

Size indicates length of the amplicon.