

**Table S1.** Primer sequences for real-time PCR analysis

Gene name (Symbol)	Gene bank accession no.	Primer	Sequence (5'-3')	Length (bp)
Ribosomal protein S9 (RPS9)*	NM_001101152	Forward Reverse	CCTCGACCAAGAGCTGAAGCCTC CAGACCTCACGTTTGTTC	64
<i>Gluconeogenesis</i>				
Pyruvate carboxylase (PC)	NM_177946	Forward Reverse	TCCCCAACATCCCATTCCAG TGTCATGCCATTCTCCTTG	116
Phosphoenolpyruvatecarboxykinase, mitochondrial (PCK2)	NM_001205594	Forward Reverse	TGGATGAGGTTTGACAGTGATG TGGTGTTACTCTGGATTGTGG	127
Phosphoenolpyruvatecarboxykinase, cytosolic (PCK1)	AY145503	Forward Reverse	GGTGTGATCAAGAGGCTGAAG ATGGGCACCGTATCTCTTTG	125
Fructose-1,6-bisphosphatase 1 (FBP1)	NM_001034447.2	Forward Reverse	TCACCGAGTATGTCCAGAGGA GGGGCTTTTCTTGTTAGCTGG	146
Glucose 6-phosphatase (G6PC)	NM_001076124	Forward Reverse	AGCCAACCTACAGATTTTCG AGCAAGGTAGATTCGTGACAG	95
<i>Glucogenic substrate-lactate/pyruvate</i>				
Lactate dehydrogenase A (LDHA)	NM_174099	Forward Reverse	CGTGTTATTGGAAGTGGTTGC CACTCCATACAGGCACACTAG	139
Lactate dehydrogenase B (LDHB)	BT021009	Forward Reverse	CTTGCTCTTGTGGATGTTTTGG TGGAATTGGCAGTGACAGAG	127
Pyruvate dehydrogenase (lipoamide) alpha 1 (PDHA1)	NM_001101046.2	Forward Reverse	GTGGCATCTCGTCATTTTGC GTAAGCACTGTAGTGACAGG	98
Dihydrolipoamide S-acetyltransferase (DLAT)	NM_001205730.2	Forward Reverse	GACCATGGGCACAGTTCAGA TGCCAGGTAACCTTCTTCCTG	130
Dihydrolipoamide dehydrogenase (DLD)	NM_001206170.1	Forward Reverse	GACACAGATGGCATGGTGAA GCTATGTCTTCACAGGATGC	143
<i>Glucogenic substrate-propionate</i>				
Acyl-CoA synthetase short-chain family member 3 (ACSS3)	NM_001102137	Forward Reverse	GAGGCACTGAGAATAGGACAAC CATGTGACTGTGCTTTTGAGAG	133

Propionyl-CoA carboxylase alpha, mitochondrial ( <i>PCCA</i> )	NM_001083509	Forward	AAATGAACACGAGACTCCAG	135
		Reverse	AGCCGTTGATGGGAATATCG	
Propionyl-CoA carboxylase beta, mitochondrial ( <i>PCCB</i> )	NM_001038548	Forward	CACATGCCCAAAGATCTGC	115
		Reverse	GCCAAAGATTCCACTCCCTC	
Methylmalonyl-CoA mutase ( <i>MUT</i> )	NM_173939	Forward	GCTGATCTTGTTTTGATGTGG	138
		Reverse	CTCAGGAACTAGGGTCTTGTG	
Methylmalonyl-CoA epimerase ( <i>MCEE</i> )	NM_001045995.2	Forward	TGGAGGGATGCACCATGTCT	114
		Reverse	CCATGTGCTCCTATTTTGGC	
<i>Glucogenic substrate-glycerol</i>				
Glycerol kinase ( <i>GK</i> )	NM_001075236.1	Forward	GCTTCGTTGGCTCCTTGACA	131
		Reverse	TACAATGGACCCCTCCACTG	
Glycerol-3-phosphate dehydrogenase 1 ( <i>GPD1</i> )	NM_001035354.1	Forward	CACCCAATTTCCGCATCACG	126
		Reverse	CCTTGGTGTTGTGCGCAAAG	
Glycerol-3-phosphate dehydrogenase 2 ( <i>GPD2</i> )	NM_001100296.1	Forward	GACAGGGAAAGAGCGTGTGA	104
		Reverse	TGAAAGGTCCCGTGGCATTG	
<i>Glucose transporter</i>				
Solute carrier family 2 member 2 ( <i>SLC2A2</i> )	NM_001103222	Forward	TGCTGTCTCTGTGTTCCCTTG	127
		Reverse	CCAAGGGAATTTACTCAGGAGC	
<i>Glycolysis</i>				
Hexokinase 2 ( <i>HK2</i> )	XM_002691189	Forward	TTTCACTTTCTCCTTCCCCTG	82
		Reverse	AGACGCCTTGAAGCCTTTAG	
Phosphofructokinase-1 ( <i>PFKL</i> )	NM_001080244	Forward	TCAGAGCCGTGACTCGTATG	131
		Reverse	GATGTTGGAGACGCTCAG	
Pyruvate kinase ( <i>PKLR</i> )	NM_001076176.1	Forward	ATCGACTCTGAGCCTGTGGT	97
		Reverse	CCTCGATCATCTCCTTGAGAC	

\*RPS9= control gene