Supplementary Table 1a:

List of primers used in real-time polymerase chain reaction analysis in HepG2 cell line

Category	*Genes*	*Sense primer*	*Antisense primer*	*Product size bp*
NADH dehydrogenase (Complex I)	ND1	TCTAGCCACCTCTAGCCTAG	GTCATGATGGCGGAGTAAT	115
	ND2	CCTCAATTACCCACATAGGA	TTGAGTAGTAGGAATGCGGT	228
	ND3	CCCTCCTAGCCTTACTACTA	TTGTTTGTAGGGCTCATGGT	213
	ND4	CTGGGTCAATAGTACTTGCC	GAATGGCTGTTACTACGAGG	228
	ND4L	CACACCTCATATCCTCCCTA	GCACAATATTGGCTAAGAGG	108
	ND5	TGTGCCTAGACCAAGAAGTT	GTTGGAATAGGTTGTTAGCG	256
	ND6	ATCAACGCCCATAATCATAC	GTTGAGGTCTTGGTGAGTGT	197
Cytochrome b (Complex III)	cytB	TATACCCTAGCCAACCCCTT	GCTACTTGTCCAATGATGGT	296
Cytochrome c oxidase (Complex IV)	COXI	TGATCTGCTGCAGTGCTCTG	TATTAGGACTTTTCGCTTCG	519
	COX II	ACTAACATCTCAGACGCTCA	GATTGTCAACGTCAAGGAGT	265
	COX III	CAATGATGGCGCGATGTAAC	GGTGATTGATACTCCTGATG	270
ATP synthase (Complex V)	ATP6	AACAACCGACTAATCACCAC	GTAAATGAGTGAGGCAGGAG	164
	ATP8	ACTATTCCTCATCACCCAAC	GGCAATGAATGAAGCGAACA	138
Complex I	NDUFA6	GGTTGTGGAGTGGATGCTTT	TGGAATTGGTGCACAGTGTT	161
	NDUFB9	CAGCATCCACAGCCATACAT	GCAGCTGCTTAACCTCTCGT	199
Complex II	SDHA	ACCAACTACAAGGGGCAGGT	CGACCAAAGACAACCAGGTC	152
	SDHC	GAAGAGATGGAGCGGTTCTG	CCAGACACAGGGACTTCACA	220
Complex III	UQCRB	GCAAGTGGCTGGATGGTATT	GTGCCCTCTTAATGCGAAAC	168
	UQCRC1	TGTCTCGTGCAGACTTGACC	GAAGCGGCATGGAGTAAGAG	179
Complex IV	COX5B	ACTGGGTTGGAGAGGGAGAT	AGACGACGCTGGTATTGTCC	172
	COX7B	AGCCACCAGAAACGTACACC	TGGGGTAACTCTGCCAACA	150
Complex V	ATP5A1	CCAGGGCTATGAAGCAGGTA	TATCCCCTTACACCCGCATA	222
	ATP5O	CGTTTCTCTCTTCCCACTCG	GTGGCATAGCGACCTTCAAT	176
Mitochondrial biogenesis-related genes	PGC-1	TCAGTCCTCACTGGTGGACA	TGCTTCGTCGTCAAAAACAG	531
	TFAM	GGCACAGGAAACCAGTTAGG	CAGAACACCGTGGCTTCTAC	366
	NRF-1	CTACTCGTGTGGGACAGCAA	AATTCCGTCGATGGTGAGAG	212
	UCP2	GGATGTGGTAAAGGTCCGAT	AGCTGCTCATAGGTGACGAA	471
	CYCS	GGATGTGGTAAAGGTCCGAT	AGCTGCTCATAGGTGACGAA	184
	SOD2	AATCAGGATCCACTGCAAGG	CGTGGTTTACTTTTTGCAAGC	180
	SIRT1	ACATTAGTGCCTGCCTGGAT	TATAATCAGGGGCCTGTTGC	231
	SIRT3	TGACCCTCTTGAACTGAATC	ATAGCCCCACTAAAGGAGAC	204
	PCK2	GTGCACAAAATGTGACCTG	ATTATTGGACAGTCTTTGTGG	155
Control 18S rRNA	18S	GAGCGAAAGCATTTGCCAAG	GGCATCGTTTATGGTCGGAA	102

Primers were taken from Koo *et al*. 2012. Koo HJ, Piao Y, Pak YK. Endoplasmic reticulum stress impairs insulin signaling through mitochondrial damage in SH-SY5Y cells. Neurosignals 2012;20:265-80. ATP=Adenosine triphosphate, PGC-1=Proliferator-activated receptor gamma coactivator 1, TFAM=Mitochondrial transcription factor A, NRF-1=Nuclear respiratory factor 1, UCP2=Uncoupling protein 2, CYCS=Somatic cytochrome c, SOD=Superoxide dismutase, SIRT=Sirtuin, PCK2=Phosphoenolpyruvate carboxykinase 2

Supplementary Table 1b:

List of primers used in real-time polymerase chain reaction analysis in L6 cell line

Category	Genes	Sense primer	Antisense primer	Product size bp
NADH dehydrogenase (Complex I)	ND1	CCGTTTTCGATATGACCAACT	TGTGTAGGGTGGAATTCCTG	121
	ND2	CCTCACCATATTCCCAACCA	GAGGAAAGCGGTAGGGTAAG	123
	ND3	CCCATGAGCGATTCAAACAACC	TTCATTCGTAGCTTAGGCCAAGAG	95
	ND4	CAACGAGGAAAACTAACCAG	TGTGATGAGTTTAGGGTTGA	123
	ND4L	CAGCAGTAGGTTTAGCCTTAC	TTGAGGTTTTGTACGTAGTCTG	70
	ND5	CCCACCAATTATACACCGAA	TGGGATTGTCTTTTCTAGTCAG	103
	ND6	ACTATTAAGCACCCAATACATCCAC	GTTGGCGTTGAAGCCTTCAC	75
Cytochrome b (Complex III)	cytB	ACCTCCTAATCTTAACATGAATCGG	AAAAGTAGCTGATGGAGGCTAGT	87
Cytochrome c oxidase (Complex IV)	COXI	GCCTTCGCATCAAAACGAGA	AGGTTCTTCGAATGTGTGGTAG	102
	COX II	AGCTACAGTGACATCAAACC	CAATGGGTATGAAGCTGTGA	86
	COX III	GCTCAACTTTCCTAATTGTCTG	CAAACTACATCTACGAAGTGTC	115
ATP synthase (Complex V)	ATP6	CTTGAATTTGCCGTAGCCTT	GTTATCATGTAGGTACAGGCTTAC	72
	ATP8	TTCTTCCCAAACCTTTCCTG	GAGGCAAATAGGTTTTCGTTC	101
Complex I	NDUFA6	CGTACCGCACCAGTCTCTTC	ATATTCTGGGCTTCGTGCCAA	123
	NDUFB9	GCTTGATGAGAGCCCGGTTT	CTGAGGATGCTGGTTTTGCC	110
Complex II	SDHA	ATGGGCGAACCTACTTCAGC	AAGGTAAACCAGCCCGAGTG	84
	SDHC	GTCTGGAGTGACGGTCTTGG	GGGATCGGAAGCACATGACA	184
Complex III	UQCRB	AGTGGGCGAAGAAGTGATCG	GCAGCTCCTGTCATCTCCAG	276
	UQCRC1	GAGCAGTCCTCGCATCCTAC	GGGCGCCAATACTCTCTACC	172
Complex IV	COX5B	TCATCTGGTTCTGGCTGCAC	ATGTTAAACCAGGGGTGGGC	112
	COX7B	CATCCTTGTCTCCGCGATGT	TTTGGGGTGACTCTGCCAAC	240
Complex V	ATP5A1	AAGAAGCTGCAAGGATGCTG	GAATGGAGGACATCTCGGCA	177
	ATP5O	AGTGACCACAGCGTTTCCTT	TGGGTCAGTCTTGACCTCCA	112
Mitochondrial biogenesis-related genes	PGC-1	CCAGTCTACGGCTGTTTGGT	TGGAAGAACAGATGTGCCCC	153
	TFAM	GTGATCTCATCCGTCGCAGT	CAGATGCACGCACAGTCTTG	295
	NRF-1	GGGAAAGAAAGCTGCAAGCC	TGGTCCGTAATGCTTGGGTC	121
	UCP2	TCTCCCAATGTTGCCCGAAA	TCGTCTGTCATGAGGTTGGC	101
	CycS	CCATAAATATGAGGGTGTCGCC	CTGGTGTTTAGCATTGCCTGTC	180
	SOD2	GTGTCTGTGGGAGTCCAAGG	TGCTCCCACACATCAATCCC	149
	SIRT1	CCGGACAGCTTCAATAGTG	CCTGTGGCAGTAACAGTGAC	249
	SIRT3	TGTACTGCAAGCTTCAGCAGTG	TATTCCCAGGGAGACCTCATGT	207
	PCK2	CAAACTTCAGACAGTTCTCTCCTTC	ATGCCCGCAACAACTCCTAC	150
TSC2 housekeeping	TSC2	GACTCCGCCACATTAAGCGT	AGCTGGGACTTTGGTATGGG	107
	GADPH	GCAAGAGAGAGGCCCTCAG	TGTGAGGGAGATGCTCAGTG	78

ATP=Adenosine triphosphate, PGC-1=Proliferator-activated receptor gamma coactivator 1, TFAM=Mitochondrial transcription factor A, NRF-1=Nuclear respiratory factor 1, UCP2=Uncoupling protein 2, CYCS=Somatic cytochrome c, SOD=Superoxide dismutase, SIRT=Sirtuin, PCK2=Phosphoenolpyruvate carboxykinase 2