

Supplementary table 1: Mitochondrial genes assessed in the study (Mt – mitochondrial)

Mitochondrial gene	DNA location	Mt complex location	Mt location
<i>Citrate synthase (CS)</i>	Nuclear DNA	Krebs cycle	Matrix
<i>NADH dehydrogenase subunit (NDUFA12)</i>	Mt DNA	NADH-coenzymeQ ₁₀ reductase (Complex I)	Inner membrane
<i>Mitochondrially encoded NADH dehydrogenase 5 (MT-ND5)</i>	Mt DNA	NADH-coenzymeQ ₁₀ reductase (Complex I)	Inner membrane
<i>Succinate dehydrogenase complex flavoprotein subunit A (SDHA)</i>	Mt DNA	Succinate-ubiquinone oxidoreductase (complex II)	Inner membrane
<i>Cytochrome c oxidase subunit 4/I (COX4/I)</i>	Mt DNA	Cytochrome c oxidase (complex IV)	Inner membrane
<i>Cytochrom c 1 (CYC1)</i>	Mt DNA	Ubichinol cytochrome c reductase (complex III)	Inner membrane

Supplementary table 2: Endoplasmatic reticulum stress genes assessed in the study

ER gene	Location	Protein function
<i>ATF4 (Activating transcription factor 4)</i>	Target to the nucleus, chromosome 22:39.52 – 39.52 Mb	Stress-induced transcription factor, master regulator of the cellular stress response that promotes adaptation of cells to a limited availability of nutrients
<i>ATF6 (Activating transcription factor 6)</i>	ER membrane	Under stress conditions will get into the cell nucleus where it directly affects the expression of uncoupling protein response target genes
<i>HSPA5 (Heat Shock Protein Family A (Hsp70) Member 5)</i>	Lumen of the endoplasmic reticulum (ER)	Folding and assembly of proteins in the ER

<i>DDIT3 (DNA damage-inducible transcript 3)</i>	Member of the CCAAT/enhancer-binding protein – target to the nucleus, chromosome 12:57.52 – 57.52 Mb	Implicated in adipogenesis and erythropoiesis, is activated by endoplasmic reticulum stress, promotes apoptosis
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