

Supplementary Table 5. Genes and descriptions of enzymes in the three major metabolic pathways. Number (#) as in **Supplementary Table 6**, enzyme commission number (E.C.#), Swiss-Prot gene abbreviation and gene description.

#	E.C #	Swiss-Prot	Gene Name
<b>Glucose Metabolic Genes</b>			
1	1.1.1.27	LDHB	lactate dehydrogenase B (LDHB)
2	1.2.1.12	GAPD	glyceraldehyde 3 phosphate dehydrogenase (GAPDH)
3	1.2.1.3	ALDH9A1	aldehyde dehydrogenase 1 family member A1 1.2.1.3
4	2.4.1.1	PYGM	glycogene phosphorylase muscle
5	2.7.1.11	PFKM	6 phosphofructokinase
6	2.7.1.40	PKM2	pyruvate kinase (muscle isozyme)
7	2.7.2.3	PGK1	phosphoglycerate kinase 1 (PGK)
8	3.1.3.11	FBP1	Fructose biphosphatase
9	4.1.2.13	ALDOA	Aldolase 1 A. muscle
10	4.2.1.11	ENO1	enolase (alpha)
11	5.3.1.1	TPI1	triosephosphate isomerase chain B
12	5.3.1.9	GPI	phosphoglucose isomerase
13	5.3.1.9	GPI	glucose 6 phosphate isomerase
14	5.4.2.1	PGAM1	phosphoglycerate mutase (PGM) type B
15	5.4.2.2	PGM1	phosphoglucomutase
<b>TCA</b>			
1	1.1.1.41	IDH2	isocitrate dehydrogenase 2 (mitochondrial IDH2)
2	1.1.1.41	IDH3A	Isocitrate dehydrogenase isozyme 3
3	1.2.4.1	PDHA1	pyruvate dehydrogenase E1 beta subunit (lipoamide)
4	1.2.4.1	PDHB	pyruvate dehydrogenase E1 alpha subunit
5	1.2.4.2	OGDH	oxoglutarate (alpha ketoglutarate) dehydrogenase (lipoamide)
6	1.3.5.1?	SDHC	succinate dehydrogenase complex subunit C
7	1.8.1.4	DLD	dihydrolipoamide dehydrogenase E3 component of pyruvate dehydrogenase complex
8	2.3.1.12	DLST	dihydrolipoamide S acetyltransferase (E2 component of pyruvate dehydrogenase complex)
9	4.1.1.32	PCK2	PEP carboxykinase phosphoenolpyruvate carboxykinase
10	4.1.3.7	CS	citrate synthase
11	4.2.1.2	FH	fumarate hydratase
12	6.2.1.1	ACAS2	acetyl CoA synthetase
13	6.2.1.4	SUCLG1	succinate CoA ligase (GDP forming)
<b>Oxidative Phosphorylation</b>			
<b><u>1.10.2.2. = Complex III Cytochrome Reducase</u></b>			
1	1.10.2.2	UQCRC2	ubiquinol cytochrome c reductase core protein II
2	1.10.2.2	UQCR10	UBIQUINOL CYTOCHROME C REDUCTASE COMPLEX 7.2 KDA
3	1.10.2.2	UQCRC1	ubiquinol cytochrome c reductase core protein I
4	1.10.2.2	UQCRFS1	UBIQUINOL CYTOCHROME C REDUCTASE IRON SULFUR
<b><u>1.6.5.3 = Complex 1 NADH dehydrogenase</u></b>			
5	1.6.5.3	NDUFA4	NADH dehydrogenase (ubiquinone)
6	1.6.5.3	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha 1 (7.5kD MWFE)
7	1.6.5.3	NDUFA10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10 (42kD)
8	1.6.5.3	NDUFA9	NADH dehydrogenase (ubiquinone) 1 alpha 9 (39kD)
9	1.6.5.3	NDUFB6	NADH dehydrogenase (ubiquinone) 1 beta 6 (17kD B17)
10	1.6.5.3	MTND2	NADH dehydrogenase (ubiquinone) chain 2

11	1.6.5.3	NDUFAB1	NADH dehydrogenase (ubiquinone) acyl carrier chain (ACPM)
12	1.6.5.3	NDUFS4	NADH dehydrogenase (ubiquinone) Fe S protein 4 (18kD)
13	1.6.5.3	NUFS1	NADH dehydrogenase (ubiquinone) Fe S protein 1
14	1.6.5.3	NUOG	NADH dehydrogenase (ubiquinone) Fe S protein 1 NADH)
15	1.6.5.3	NDUFV2	NADH dehydrogenase (ubiquinone) flavoprotein 2
16	1.6.5.3	NDUFA4	NADH dehydrogenase (ubiquinone) MLRQ SUBUNIT
17	1.6.5.3	MTND5	NADH dehydrogenase subunit 5
18	1.6.5.3	NDUFS3	NADH dehydrogenase (ubiquinone) Fe S protein 3 (30kD)
19	1.6.5.3	NDUFA8	NADH UBIQUINONE OXIDOREDUCTASE 19 KD
20	1.6.5.3	NDUFB2	NADH UBIQUINONE OXIDOREDUCTASE AGGG SUBUNIT
21	1.6.5.3	NDUFB8	NADH UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT
22	1.6.5.3	NDUFB9	NADH UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT
23	1.6.5.3	NDUFB1	NADH UBIQUINONE OXIDOREDUCTASE MNLL SUBUNIT
24	1.6.5.3	NDUFB10	NADH UBIQUINONE OXIDOREDUCTASE PDSW SUBUNIT

### **1.9.3.1 = Complex IV, Cytochrome C oxidase**

25	1.9.3.1	COXII	cytochrome c oxidase subunit II
26	1.9.3.1	COX4I1	cytochrome c oxidase subunit IV isoform 1
27	1.9.3.1	COX4I2	cytochrome c oxidase subunit IV isoform 2
28	1.9.3.1	COX5A	CYTOCHROME C OXIDASE POLYPEPTIDE VA
29	1.9.3.1	COX6A1	CYTOCHROME C OXIDASE POLYPEPTIDE VIA PRECURSOR
30	1.9.3.1	COX6B	CYTOCHROME C OXIDASE POLYPEPTIDE VIB
31	1.9.3.1	COX7A2	CYTOCHROME C OXIDASE POLYPEPTIDE VIIA
32	1.9.3.1	COX8H	cytochrome c oxidase subunit VIIIb
33	1.9.3.1	COX7C	CYTOCHROME C OXIDASE POLYPEPTIDE VIIC
34	1.9.3.1	COX8L	cytochrome c oxidase subunit VIIIa

### **3.6.1.34 = ATP Synthetase**

35	3.6.1.34	ATP5B	ATP synthase beta subunit
36	3.6.1.34	MTATP6	ATP synthase F0 subunit 6 ATPase 6
37	3.6.1.34	ATP5H	ATP synthase H+ transporting mitochondrial F0 subunit d
38	3.6.1.34	ATP5A2	ATP synthase H+ transporting mitochondrial F1 alpha subunit isoform 1
39	3.6.1.34	ATP5D	ATP synthase H+ transporting mitochondrial F1 delta subunit
40	3.6.1.34	ATP5C1	ATP synthase H+ transporting mitochondrial F1 gamma polypeptide 1
41	3.6.1.34	ATP5F1	ATP synthase subunit B
42	3.6.1.34	ATP6V0C	ATPase H+ transporting lysosomal (vacuolar proton pump D) 42 kDa
43	3.6.1.34	ATP6V0D1	ATPase H+ transporting lysosomal (vacuolar proton pump) 16kD (Atp6I)
44	3.6.1.35	ATP6V1C1	VACUOLAR ATP SYNTHASE SUBUNIT C)