



mdh2	malate dehydrogenase 2, NAD (mitochondrial)	2.671	0.513	1.775	0.265	1.716	0.173	0.670	0.074	0.833	0.026	-0.363	0.030	-0.590	0.228
Glud1	glutamate dehydrogenase 1	2.362	0.897	1.534	0.152	1.850	0.115	0.917	0.186	0.950	0.019	N.S	0.214	-0.426	-0.095
got1	glutamic-oxaloacetic transaminase 1, soluble	0.664	0.223	0.310	0.022	0.342	0.037	0.170	0.023	0.215	0.029	-0.475	0.090	-0.454	0.164
got2	glutamic-oxaloacetic transaminase 2, mitochondrial	1.697	0.286	1.190	0.104	1.217	0.099	0.563	0.089	0.737	0.021	-0.291	0.037	-0.526	0.301
<b>Respiratory Complexes and Related Proteins</b>															
Ndurf1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	1.107	0.276	0.800	0.069	0.628	0.097	0.338	0.018	0.425	0.023	-0.240	-0.271	-0.566	0.725
Ndurfv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	0.888	0.194	0.690	0.052	0.585	0.091	0.325	0.024	0.341	0.032	-0.188	-0.209	-0.522	0.325
sdha	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	2.519	0.254	2.030	0.248	2.567	0.129	0.635	0.034	0.768	0.065	-0.235	0.343	-0.667	-0.102
sdhb	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	0.568	0.063	0.453	0.057	0.461	0.045	0.157	0.020	0.234	0.010	-0.242	0.061	-0.638	0.436
sdhc	succinate dehydrogenase complex, subunit C, integral membrane protein	0.220	0.019	0.201	0.026	0.265	0.033	0.100	0.002	0.099	0.006	-0.138	0.350	-0.466	-0.274
etfa	electron transferring flavoprotein, alpha polypeptide	1.260	0.276	0.797	0.115	1.110	0.112	0.243	0.024	0.387	0.054	-0.377	0.480	-0.672	0.069
etfb	electron transferring flavoprotein, beta polypeptide	2.549	0.572	1.863	0.225	2.177	0.230	0.628	0.086	0.708	0.076	-0.262	0.217	-0.647	-0.060
etfdh	electron transferring flavoprotein, dehydrogenase	0.835	0.197	0.531	0.064	0.645	0.057	0.216	0.018	0.251	0.010	-0.360	0.271	-0.568	-0.079
Coq6	coenzyme Q6 homolog (yeast)	0.040	0.009	0.025	0.003	0.031	0.003	0.017	0.002	0.015	0.001	-0.364	0.283	-0.302	-0.299
Uqcrc1	ubiquinol-cytochrome c reductase core protein 1	2.984	0.619	2.244	0.206	2.157	0.201	0.625	0.062	0.865	0.131	-0.234	-0.035	-0.715	0.423
Atp5a1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1	14.823	1.367	9.017	1.192	10.672	0.923	5.417	0.734	6.904	0.634	-0.427	0.243	-0.374	0.046
Atp5b	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	16.525	1.622	11.896	1.169	12.496	0.960	4.973	0.705	6.771	0.593	-0.298	0.072	-0.578	0.298
<b>Proteostasis Pathways</b>															
Cryab	crystallin, alpha B	0.142	0.020	0.044	0.007	0.064	0.003	0.044	0.010	0.056	0.012	-0.707	0.578	N.S	-0.171
hsp90b1	heat shock protein 90, beta (Grp94), member 1	1.056	0.142	1.293	0.097	1.112	0.090	1.236	0.251	1.243	0.120	0.157	N.S	N.S	N.S
hspa1a	heat shock protein 1A	1.974	0.110	1.568	0.137	1.491	0.119	1.451	0.224	1.497	0.295	N.S	N.S	-0.106	N.S
hspa5	heat shock protein 5	0.291	0.016	0.270	0.030	0.192	0.021	0.253	0.060	0.291	0.034	-0.139	-0.253	N.S	0.542
hspa9	heat shock protein 9	0.785	0.163	0.611	0.102	0.561	0.069	0.217	0.045	0.235	0.020	-0.160	N.S	-0.605	N.S
hspd1	heat shock protein 1 (chaperonin)	1.407	0.194	1.259	0.108	1.023	0.102	0.687	0.115	0.792	0.016	N.S	-0.214	-0.479	0.532
lonp1	lon peptidase 1, mitochondrial	0.205	0.046	0.176	0.015	0.204	0.011	0.095	0.006	0.117	0.007	N.S	0.168	-0.449	N.S
lonp2	lon peptidase 2, peroxisomal	0.023	0.003	0.021	0.004	0.024	0.002	0.008	0.003	0.012	0.004	-0.205	0.332	-0.625	0.175
<b>Peroxisomal Proteins</b>															
Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	0.465	0.058	0.544	0.071	0.645	0.090	0.217	0.022	0.200	0.015	N.S	0.262	-0.560	-0.262
Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	0.327	0.063	0.429	0.071	0.487	0.075	0.087	0.008	0.142	0.040	N.S	0.278	-0.752	0.187
Ech1	enoyl coenzyme A hydratase 1, peroxisomal	0.927	0.127	0.917	0.118	1.104	0.101	0.366	0.031	0.392	0.016	N.S	0.247	-0.580	-0.134
Ephx2	Epoxide Hydrolase 2	0.783	0.141	1.790	0.357	2.004	0.342	0.317	0.110	0.326	0.016	0.820	0.289	-0.809	N.S
mdh1	malate dehydrogenase 1, NAD (soluble)	8.040	0.796	6.655	0.859	7.770	0.741	2.961	0.234	3.708	0.597	-0.218	0.221	-0.525	N.S
Pecr	peroxisomal trans-2-enoyl-CoA reductase	2.617	0.911	3.403	0.702	3.605	0.611	0.254	0.086	0.394	0.128	0.269	0.276	-0.918	0.333
slc25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase) 20	0.485	0.090	0.330	0.027	0.274	0.025	0.195	0.018	0.220	0.020	-0.305	-0.170	-0.400	0.363
<b>Other Mitochondrial Proteins</b>															
Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0.139	0.010	0.138	0.009	0.159	0.035	0.117	0.003	0.179	0.018	N.S	0.046	-0.139	0.443
cd36	CD36 antigen	0.151	0.019	0.159	0.026	0.136	0.024	0.034	0.005	0.041	0.007	-0.071	-0.106	-0.761	0.345
Clpp	caseinolytic mitochondrial matrix peptidase proteolytic subunit	0.214	0.047	0.266	0.029	0.283	0.036	0.121	0.020	0.133	0.003	0.269	0.077	-0.537	0.059
Clpx	caseinolytic mitochondrial matrix peptidase chaperone subunit	0.105	0.013	0.121	0.011	0.122	0.008	0.127	0.005	0.146	0.007	0.137	0.035	0.089	0.109
ckmt1	creatine kinase, mitochondrial 2	1.898	1.389	0.473	0.079	0.568	0.091	0.314	0.148	0.245	0.068	-0.543	0.227	-0.460	-0.100
prkaca	protein kinase, cAMP dependent, catalytic, alpha	0.069	0.006	0.052	0.003	0.050	0.003	0.059	0.003	0.061	0.002	-0.239	-0.032	0.133	0.076
Rhot1	Ras Homolog Family Member T1	0.162	0.012	0.144	0.012	0.159	0.010	0.076	0.002	0.096	0.003	-0.129	0.127	-0.459	0.130
Sam50	sorting and assembly machinery component 50 homolog (S. cerevisiae)	0.395	0.039	0.275	0.016	0.248	0.036	0.167	0.018	0.209	0.011	-0.305	-0.149	-0.394	0.491
slc25a11	solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11	0.925	0.231	0.662	0.069	0.627	0.050	0.297	0.017	0.364	0.022	-0.266	N.S	-0.529	0.229
Slc25a4	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member	1.932	0.029	1.348	0.091	1.914	0.302	0.909	0.038	1.201	0.074	-0.313	0.348	-0.324	N.S
Slc25a4/5/31	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member	41.064	3.015	33.056	2.755	38.219	2.826	13.184	0.955	18.025	2.460	-0.211	0.171	-0.592	0.153
Tufm	Tu translation elongation factor, mitochondrial	0.412	0.079	0.357	0.031	0.360	0.024	0.132	0.010	0.192	0.019	-0.118	0.024	-0.622	0.416

\* The magnitude of effects are calculated only for those with significant changes; NS= not significant