Electronic supplementary material

ESM Table 4 Diet-dependent expression of genes for OXPHOS, TCA cycle and pyruvate metabolism in islets

Ensemble gene	Symbol	Description	Ratio (HF:CHF)	SE	*p* value
OXPHOS (KEGG)					
ENSMUSG00000016427	*Ndufa1*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	4.8	0.799	4.35482E-07
ENSMUSG00000025393	*Atp5b*	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	4.396	1.24	0.02
ENSMUSG00000026032	*Ndufb3*	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	3.577	0.61	0.012
ENSMUSG00000020089	*Ppa1*	Pyrophosphatase (inorganic) 1	3.538	0.963	0.004
ENSMUSG00000030647	*Ndufc2*	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	3.194	0.612	0.02
ENSMUSG00000000563	*Atp5f1*	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	3.04	0.637	0.007
ENSMUSG00000063882	*Uqcrh*	Ubiquinol-cytochrome c reductase hinge protein	2.978	0.781	0.018
ENSMUSG00000029632	*Ndufa4*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	2.795	0.484	0.014
ENSMUSG00000025204	*Ndufb8*	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	2.7	0.469	0.014
ENSMUSG00000036751	*Cox6b1*	Cytochrome c oxidase, subunit vib polypeptide 1	2.462	0.32	0.008
ENSMUSG00000002379	*Ndufa11*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	2.448	0.573	0.04
ENSMUSG00000038462	*Uqcrfs1*	Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	2.423	0.403	0.009
ENSMUSG00000028013	*Ppa2*	Pyrophosphatase (inorganic) 2	2.371	0.24	1.48026E-05
ENSMUSG00000022956	*Atp5o*	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	2.356	0.632	0.086
ENSMUSG00000030884	*Uqcrc2*	Ubiquinol cytochrome c reductase core protein 2	2.298	0.348	0.001
ENSMUSG00000018770	*Atp5g3*	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 3	2.253	0.348	0.001
ENSMUSG00000027673	*Ndufb5*	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	2.239	0.438	0.002
ENSMUSG00000022450	*Ndufa6*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	2.137	0.227	5.84305E-05
ENSMUSG00000041697	*Cox6a1*	Cytochrome c oxidase, subunit VI a, polypeptide 1	2.127	0.237	0.000211521
ENSMUSG00000000171	*Sdhd*	Succinate dehydrogenase complex, subunit D, integral membrane protein	2.122	0.346	0.005
ENSMUSG00000000399	*Ndufa9*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	2.104	0.311	0.000481295
ENSMUSG00000040048	*Ndufb10*	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	1.993	0.377	0.011
ENSMUSG00000031818	*Cox4i1*	Cytochrome c oxidase subunit IV isoform 1	1.97	0.431	0.034

Ensemble gene	Symbol	Description	Ratio (HF:CHF)	SE	*p* value
ENSMUSG00000031059	*Ndufb11*	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	1.967	0.239	0.012
ENSMUSG00000035674	*Ndufa3*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	1.953	0.223	0.009
ENSMUSG00000032330	*Cox7a2*	Cytochrome c oxidase, subunit viia 2	1.93	0.305	0.028
ENSMUSG00000024099	*Ndufv2*	NADH dehydrogenase (ubiquinone) flavoprotein 2	1.812	0.195	0.013
ENSMUSG00000021764	*Ndufs4*	NADH dehydrogenase (ubiquinone) Fe-S protein 4	1.8	0.187	0.004
ENSMUSG00000022354	*Ndufb9*	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	1.753	0.168	0.001
ENSMUSG00000059734	*Ndufs8*	NADH dehydrogenase (ubiquinone) Fe-S protein 8	1.701	0.288	0.068
ENSMUSG00000038690	*Atp5j2*	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	1.686	0.273	0.042
ENSMUSG00000000088	*Cox5a*	Cytochrome c oxidase, subunit Va	1.685	0.187	0.002
ENSMUSG00000024248	*Cox7a2l*	Cytochrome c oxidase subunit viia polypeptide 2-like	1.636	0.195	0.003
ENSMUSG00000002416	*Ndufb2*	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	1.636	0.262	0.082
ENSMUSG00000026895	*Ndufa8*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	1.584	0.162	0.002
ENSMUSG00000061518	*Cox5b*	Cytochrome c oxidase, subunit Vb	1.54	0.276	0.058
ENSMUSG00000025968	*Ndufs1*	NADH dehydrogenase (ubiquinone) Fe-S protein 1	1.534	0.155	0.01
ENSMUSG00000014313	*Cox6c*	Cytochrome c oxidase, subunit vic	1.482	0.137	0.019
ENSMUSG00000025428	*Atp5a1*	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	1.43	0.149	0.008
ENSMUSG00000026260	*Ndufa10*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	1.428	0.258	0.086
ENSMUSG00000021606	*Ndufs6*	NADH dehydrogenase (ubiquinone) Fe-S protein 6	1.418	0.185	0.023
ENSMUSG00000013593	*Ndufs2*	NADH dehydrogenase (ubiquinone) Fe-S protein 2	1.399	0.364	0.265
ENSMUSG00000036199	*Ndufa13*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	1.34	0.186	0.063
ENSMUSG00000021577	*Sdha*	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	1.329	0.148	0.032
ENSMUSG00000040018	*Cox15*	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	1.303	0.133	0.052
ENSMUSG00000022551	*Cyc1*	Cytochrome c-1	1.301	0.197	0.183
ENSMUSG00000041881	*Ndufa7*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	1.268	0.151	0.149
ENSMUSG00000037152	*Ndufc1*	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	1.244	0.106	0.084
ENSMUSG00000020544	*Cox11*	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	1.175	0.182	0.317
ENSMUSG00000035885	*Cox8a*	Cytochrome c oxidase, subunit viiia	1.171	0.153	0.293
ENSMUSG00000009863	*Sdhb*	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	1.133	0.057	0.039
ENSMUSG00000016252	*Atp5e*	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon	1.111	0.193	0.565

Ensemble gene	Symbol	Description	Ratio (HF:CHF)	SE	*p* value
		subunit			
ENSMUSG00000025651	*Uqcrc1*	Ubiquinol-cytochrome c reductase core protein 1	1.079	0.16	0.628
ENSMUSG00000014294	*Ndufa2*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	1.068	0.063	0.297
ENSMUSG00000050856	*Atp5k*	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e	1.041	0.217	0.851
ENSMUSG00000023089	*Ndufa5*	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	1.019	0.036	0.605
ENSMUSG00000020153	*Ndufs7*	NADH dehydrogenase (ubiquinone) Fe-S protein 7	0.99	0.083	0.91
ENSMUSG00000033938	*Ndufb7*	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	0.962	0.077	0.645
ENSMUSG00000037916	*Ndufv1*	NADH dehydrogenase (ubiquinone) flavoprotein 1	0.928	0.237	0.781
ENSMUSG00000009876	*Cox4i2*	Cytochrome c oxidase subunit IV isoform 2	0.833	0.089	0.138
ENSMUSG00000025488	*Cox8b*	Cytochrome c oxidase, subunit viiib	0.784	0.066	0.041
ENSMUSG00000042148	*Cox10*	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)	0.684	0.092	0.064
ENSMUSG00000030785	*Cox6a2*	Cytochrome c oxidase, subunit VI a, polypeptide 2	0.421	0.149	0.018
TCA Pathway (KEGG)					
ENSMUSG00000052738	*Suclg1*	Succinate-coa ligase, GDP-forming, alpha subunit	4.136	0.793	0.001
ENSMUSG00000026526	*Fh1*	Fumarate hydratase 1	3.324	0.317	0.005
ENSMUSG00000020664	*Dld*	Dihydrolipoamide dehydrogenase	2.573	0.652	0.038
ENSMUSG00000025950	*Idh1*	Isocitrate dehydrogenase 1 (NADP+), soluble	2.273	0.328	4.52E-04
ENSMUSG00000000171	*Sdhd*	Succinate dehydrogenase complex, subunit D, integral membrane protein	2.122	0.346	0.005
ENSMUSG00000022110	*Sucla2*	Succinate-Coenzyme A ligase, ADP-forming, beta subunit	1.996	0.236	0.001
ENSMUSG00000020321	*Mdh1*	Malate dehydrogenase 1, NAD (soluble)	1.948	0.185	6.92E-05
ENSMUSG00000019179	*Mdh2*	Malate dehydrogenase 2, NAD (mitochondrial)	1.506	0.205	0.02
ENSMUSG00000028405	*Aco1*	Aconitase 1	1.494	0.12	0.009
ENSMUSG00000021577	*Sdha*	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	1.329	0.148	0.032
ENSMUSG00000005683	*Cs*	Citrate synthase	1.275	0.066	0.003
ENSMUSG00000009863	*Sdhb*	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	1.133	0.057	0.039
ENSMUSG00000025545	*Clybl*	Citrate lyase beta like	1.114	0.075	0.153
ENSMUSG00000020917	*Acly*	ATP citrate lyase	1.106	0.056	0.089
ENSMUSG00000022477	*Aco2*	Aconitase 2, mitochondrial	1.096	0.118	0.449
ENSMUSG00000032279	*Idh3a*	Isocitrate dehydrogenase 3 (NAD+) alpha	1.06	0.03	0.074

Ensemble gene	Symbol	Description	Ratio (HF:CHF)	SE	*p* value
ENSMUSG00000061838	*Suclg2*	Succinate-Coenzyme A ligase, GDP-forming, beta subunit	1.047	0.12	0.696
ENSMUSG00000020456	*Ogdh*	Oxoglutarate dehydrogenase (lipoamide)	0.989	0.042	0.803
ENSMUSG00000004789	*Dlst*	Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	0.975	0.037	0.532
ENSMUSG00000027513	*Pck1*	Phosphoenolpyruvate carboxykinase 1, cytosolic	0.922	0.047	0.152
ENSMUSG00000002010	*Idh3g*	Isocitrate dehydrogenase 3 (NAD+), gamma	0.888	0.093	0.295
ENSMUSG00000040618	*Pck2*	Phosphoenolpyruvate carboxykinase 2 (mitochondrial)	0.88	0.074	0.188
ENSMUSG00000046934	*Csl*	Citrate synthase like	0.841	0.068	0.07
ENSMUSG00000030541	*Idh2*	Isocitrate dehydrogenase 2 (NADP+), mitochondrial	0.786	0.101	0.096
ENSMUSG00000024892	*Pcx*	Pyruvate carboxylase	0.703	0.069	0.019
Pyruvate metabolism (KEGG)					
ENSMUSG00000032418	*Mod1*	Malic enzyme, supernatant	2.616	0.453	0.018
ENSMUSG00000020664	*Dld*	Dihydrolipoamide dehydrogenase	2.573	0.652	0.038
ENSMUSG00000008822	*Acyp1*	Acylphosphatase 1, erythrocyte (common) type	2.097	0.354	0.008
ENSMUSG00000020321	*Mdh1*	Malate dehydrogenase 1, NAD (soluble)	1.948	0.185	6.92E-05
ENSMUSG00000060923	*Acyp2*	Acylphosphatase 2, muscle type	1.81	0.184	0.009
ENSMUSG00000024556	*Me2*	Malic enzyme 2, NAD(+)-dependent, mitochondrial	1.776	0.217	0.016
ENSMUSG00000000168	*Dlat*	Dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	1.767	0.183	4.38E-04
ENSMUSG00000024158	*Hagh*	Hydroxyacyl glutathione hydrolase	1.555	0.174	0.03
ENSMUSG00000019179	*Mdh2*	Malate dehydrogenase 2, NAD (mitochondrial)	1.506	0.205	0.02
ENSMUSG00000032047	*Acat1*	Acetyl-Coenzyme A acetyltransferase 1	1.463	0.155	0.016
ENSMUSG00000035637	*Grhpr*	Glyoxylate reductase/hydroxypyruvate reductase	1.348	0.167	0.038
ENSMUSG00000024026	*Glo1*	Glyoxalase 1	1.342	0.091	0.004
ENSMUSG00000026687	*Aldh9a1*	Aldehyde dehydrogenase 9, subfamily A1	1.205	0.112	0.079
ENSMUSG00000030621	*Me3*	Malic enzyme 3, NADP(+)-dependent, mitochondrial	1.204	0.102	0.066
ENSMUSG00000010025	*Aldh3a2*	Aldehyde dehydrogenase family 3, subfamily A2	1.137	0.113	0.234
ENSMUSG00000029762	*Akr1b8*	Aldo-keto reductase family 1, member B8	1.118	0.069	0.107
ENSMUSG00000053644	*Aldh7a1*	Aldehyde dehydrogenase family 7, member A1	1.106	0.079	0.207
ENSMUSG00000031299	*Pdha1*	Pyruvate dehydrogenase E1 alpha 1	1.106	0.098	0.288
ENSMUSG00000032294	*Pkm2*	Pyruvate kinase, muscle	1.077	0.228	0.743

Ensemble gene	Symbol	Description	Ratio (HF:CHF)	SE	*p* value
ENSMUSG00000047674	*Pdha2*	Pyruvate dehydrogenase E1 alpha 2	1.066	0.066	0.34
ENSMUSG00000021620	*Acot12*	Acyl-coa thioesterase 12	1.026	0.169	0.882
ENSMUSG00000035561	*Aldh1b1*	Aldehyde dehydrogenase 1 family, member B1	1.021	0.076	0.791
ENSMUSG00000061046	*Haghl*	Hydroxyacylglutathione hydrolase-like	1.016	0.053	0.775
ENSMUSG00000021748	*Pdhb*	Pyruvate dehydrogenase (lipoamide) beta	1.003	0.082	0.973
ENSMUSG00000027605	*Acss2 ; Myh7b*	Myosin, heavy chain 7B, cardiac muscle, beta	0.97	0.022	0.247
ENSMUSG00000027452	*Acss1*	Acyl-coa synthetase short-chain family member 1	0.929	0.164	0.687
ENSMUSG00000027513	*Pck1*	Phosphoenolpyruvate carboxykinase 1, cytosolic	0.922	0.047	0.152
ENSMUSG00000040618	*Pck2*	Phosphoenolpyruvate carboxykinase 2 (mitochondrial)	0.88	0.074	0.188
ENSMUSG00000020532	*Acaca*	Acetyl-Coenzyme A carboxylase alpha	0.783	0.082	0.063
ENSMUSG00000041237	*Pklr*	Pyruvate kinase liver and red blood cell	0.771	0.068	0.029
ENSMUSG00000029455	*Aldh2*	Aldehyde dehydrogenase 2, mitochondrial	0.747	0.073	0.024
ENSMUSG00000052131	*Akr1b7*	Aldo-keto reductase family 1, member B7	0.74	0.078	0.023
ENSMUSG00000030851	*Ldhc*	Lactate dehydrogenase C	0.74	0.1	0.105
ENSMUSG00000030246	*Ldhb*	Lactate dehydrogenase B	0.725	0.119	0.083
ENSMUSG00000024892	*Pcx*	Pyruvate carboxylase	0.703	0.069	0.019
ENSMUSG00000042010	*Acacb*	Acetyl-Coenzyme A carboxylase beta	0.674	0.079	0.042
ENSMUSG00000031958	*Ldhd*	Lactate dehydrogenase D	0.667	0.066	0.012

Data represent mean±SE from of five to six Affymetrix chips per condition