

Supplementary Table 2. Summary Table for All Genes. Summary statistics for all 119 genes: Gene, order for **figure 3**, e.c.# – Enzyme commission number; Pathway – metabolic pathway; F–within – F value for differences among individuals within populations from Nested–ANOVA; p–within = p–value for F–within; F–across = F–value for differences between populations from Nested–ANOVA; P–across – p value for F–across; Grand mean – mean for all 16 individuals, South mean – mean for 8 southern individuals; North mean – mean for 8 northern individuals; Correlations: correlations of gene expression with body weight, log₁₀ body mass, and three measures of metabolism (glucose, FA – fatty acid, and LKA – lactate–ketones–alcohol). Metabolic rates are residuals from log bodymass–log metabolism regression.

Correlations

Gene	Fig. 3	a.e.c.#	Pathway	F-within n	P_within	F-Acro ss	P-across	Grand mean	South Mean	North Mean	ratio max/m in	South ern ratio max/m in	Northern ratio max/m in	weight	Glucose Lg_bo e_RE SID	FA_R ESID	LKA_ RESID	
long-chain-acyl-CoA_dehydrogenase_1	1	13	1.3.99. Fatty acid metabolism	32.4	1.00E-17	10.9	5.27E-03	11.57	11.42	11.72	1.66	1.36	1.57	-0.133	-0.160	0.574	0.003	0.010
ATP_synthase_H+_transporting_mitochondrial_F1_complex_alpha_subunit_isoform_1	2	4	3.6.1.3 Oxidative Phosphorylation	5.9	1.73E-08	6.28	2.51E-02	11.59	11.56	11.63	1.23	1.18	1.20	-0.420	-0.519	0.281	-0.122	-0.039
triosephosphate_isomerase_chain_B	3	3	5.3.1.1 eogenesis	13.8	1.00E-17	1.24	2.84E-01	11.82	11.78	11.86	1.37	1.25	1.30	-0.427	-0.399	-0.054	0.209	-0.085
NADH-ubiquinone_oxidoreductase_MNLL	4	4	1.6.5.3 Oxidative Phosphorylation	97.7	1.00E-17	1.90	1.89E-01	13.97	13.88	14.06	2.50	2.32	2.25	-0.258	-0.255	0.228	0.299	0.350
NADH-ubiquinone_oxidoreductase_PDSW	5	5	1.6.5.3 Oxidative Phosphorylation	4.5	1.91E-06	1.84	1.96E-01	12.03	11.98	12.07	1.52	1.52	1.41	-0.150	-0.091	0.288	-0.037	-0.086
ATP_synthase_H+_transporting_mitochondrial_F0_complex_subunit_d;	6	4	3.6.1.3 Oxidative Phosphorylation	22.6	1.00E-17	26.7	1.43E-04	13.60	13.47	13.72	2.05	1.94	1.49	-0.605	-0.565	0.203	-0.076	-0.340
NADH_dehydrogenase_(ubiquinone)_1_beta_subcomplex_6_(17kD_B17)	7	7	1.6.5.3 Oxidative Phosphorylation	10.2	2.37E-14	12.3	3.49E-03	12.04	11.97	12.12	1.46	1.29	1.34	-0.482	-0.391	0.371	0.106	0.047
NADH_dehydrogenase_(ubiquinone)_1_alpha_subcomplex_10_(42kD)	8	8	1.6.5.3 Oxidative Phosphorylation	4.6	1.67E-06	5.11	4.02E-02	12.91	12.85	12.97	1.44	1.37	1.31	-0.110	-0.043	0.505	0.144	-0.070
cytochrome_C_oxidase_VA	9	9	1.9.3.1 Oxidative Phosphorylation	14.7	1.00E-17	0.14	7.18E-01	14.01	14.00	14.02	1.52	1.45	1.47	-0.254	-0.266	0.198	0.011	0.075
ATP_synthase_F0_subunit_6_ATPase_6	10	4	3.6.1.3 Oxidative Phosphorylation	46.9	1.00E-17	0.45	5.13E-01	11.20	11.16	11.24	3.86	3.86	1.96	-0.456	-0.411	-0.208	0.117	-0.179
cytochrome_c_oxidase_subunit_IV_isoform_1	11	11	1.9.3.1 Oxidative Phosphorylation	4.4	3.21E-06	0.01	9.34E-01	11.89	11.90	11.89	1.68	1.53	1.68	-0.413	-0.422	-0.112	-0.052	-0.048
NADH_dehydrogenase_(ubiquinone)_Fe-S_protein_4_(18kD)(NADH-coenzyme_Q_reductase)	12	12	1.6.5.3 Oxidative Phosphorylation	9.2	3.97E-13	0.09	7.63E-01	11.94	11.93	11.95	1.57	1.55	1.41	-0.439	-0.451	-0.053	-0.194	-0.460

succinyl_coA:3-oxoacid_coA-transferase	13	2.8.3.5	sythensis and degradation of ketone bodies	7.3	1.51E-10	0.61	4.47E-01	11.32	11.30	11.33	1.50	1.49	1.38	-0.279	-0.361	-0.048	-0.001	-0.382
ubiquinol-cytochrome_c_reductase_core_protein_II	14	2	1.10.2. Oxidative Phosphorylation	5.5	6.74E-08	0.13	7.26E-01	11.02	11.02	11.03	1.45	1.36	1.42	-0.255	-0.311	-0.113	-0.254	-0.646
phosphoglucomutase	15	5.4.2.2	2.4.1.4 eogenesis	6.7	8.93E-10	0.20	6.62E-01	10.76	10.77	10.74	1.67	1.56	1.57	-0.269	-0.307	-0.191	-0.094	-0.616
diacylglycerol_synthase	16	6	Lipid Metabolism	5.7	3.53E-08	0.26	6.18E-01	10.26	10.28	10.25	2.08	1.93	1.72	-0.343	-0.364	-0.171	0.050	-0.504
NADH_dehydrogenase_(ubiquinone)_acyl_carrier_chain_(ACPM)_alpha_beta_subcomplex_1_(8kD_SDAP)	17	1.6.5.3	Oxidative Phosphorylation	12.2	1.21E-16	0.58	4.61E-01	11.41	11.44	11.38	1.53	1.50	1.31	-0.394	-0.462	-0.215	-0.090	-0.368
aldolase_1_A_muscle_pyruvate_kinase_(muscle_isozyme)	18	3	4.1.2.1 Glycolysis/gluconeogenesis	7.5	7.24E-11	1.23	2.87E-01	12.52	12.55	12.50	1.47	1.44	1.32	-0.325	-0.330	-0.437	-0.367	-0.632
	19	0	2.7.1.4 Glycolysis/gluconeogenesis	21.7	1.00E-17	0.62	4.43E-01	12.47	12.49	12.45	1.79	1.70	1.50	0.557	0.522	0.076	0.024	0.402
Fructose-bisphosphatase	20	1	3.1.3.1 Glycolysis/gluconeogenesis	14.5	1.00E-17	14.3	2.05E-03	10.80	10.91	10.68	2.05	1.63	1.68	-0.331	-0.373	-0.484	-0.141	-0.123
phosphoinositide-3-kinase_regulatory_subunit_polypeptide_3_(p55_gamma)	21	37	Inositol phosphate metabolism	2.8	1.21E-03	3.76	7.28E-02	11.00	11.05	10.96	1.47	1.28	1.43	-0.222	-0.243	-0.474	0.036	-0.389
citrate_synthase	22	4.1.3.7	TCA	11.4	7.87E-16	0.88	3.63E-01	11.37	11.40	11.33	1.53	1.53	1.27	-0.021	-0.141	-0.092	-0.146	-0.252
enoyl_Coenzyme_A_hydratase_short_chain_1	23	4.2.1	Fatty acid biosynthesis (path 2)	4.0	1.41E-05	2.03	1.76E-01	11.28	11.25	11.30	1.22	1.22	1.11	-0.040	-0.029	0.341	0.109	-0.179
pyruvate_dehydrogenase_E1_alpha_subunit_NADH_dehydrogenase_subunit_5	24	1.2.4.1	TCA	5.5	7.38E-08	0.02	8.87E-01	11.13	11.13	11.12	1.25	1.25	1.20	0.116	0.080	-0.051	0.148	-0.188
	25	1.6.5.3	Oxidative Phosphorylation	62.7	1.00E-17	2.09	1.70E-01	13.47	13.40	13.53	1.81	1.66	1.78	-0.221	-0.169	0.134	0.398	0.277
fatty_acid_synthase	26	5	2.3.1.8 Fatty acid biosynthesis (path 1)	2.4	5.17E-03	2.49	1.37E-01	10.44	10.41	10.46	1.39	1.38	1.36	-0.011	-0.054	0.207	-0.141	-0.630
3-hydroxyacyl-CoA_dehydrogenase_enoyl-CoA_hydratase	27	5	1.1.1.3 fatty acid metabolism	3.2	2.74E-04	2.31	1.51E-01	10.87	10.83	10.91	1.55	1.55	1.36	-0.273	-0.230	0.009	0.013	-0.597
lactate_dehydrogenase_B	28	7	1.1.1.2 Glycolysis/gluconeogenesis	13.1	1.00E-17	0.22	6.48E-01	12.59	12.58	12.61	1.43	1.28	1.43	-0.051	-0.116	0.035	-0.495	-0.610
enolase_(alpha)	29	1	4.2.1.1 Glycolysis/gluconeogenesis	7.2	1.71E-10	4.15	6.09E-02	11.79	11.84	11.75	1.56	1.48	1.47	0.195	0.100	-0.193	-0.224	-0.574
phosphoglycerate_kinase_1_(PGK)	30	2.7.2.3	Glycolysis/gluconeogenesis	16.0	1.00E-17	0.07	8.01E-01	11.54	11.55	11.54	1.58	1.58	1.34	-0.278	-0.320	-0.057	-0.186	-0.392
glucose-6-phosphate_isomerase	31	5.3.1.9	Glycolysis/gluconeogenesis	6.6	1.30E-09	0.44	5.20E-01	11.39	11.38	11.40	1.22	1.22	1.14	0.028	-0.005	0.037	0.034	-0.222
cytochrome_C_oxidase_VIB	32	1.9.3.1	Oxidative Phosphorylation	40.5	1.00E-17	1.17	2.98E-01	13.24	13.28	13.20	1.59	1.59	1.24	0.204	0.183	-0.136	-0.104	-0.316
NADH_dehydrogenase_(ubiquinone)_Fe-S_protein_1	33	1.6.5.3	Oxidative Phosphorylation	5.1	2.22E-07	0.01	9.40E-01	11.31	11.31	11.31	1.57	1.57	1.50	-0.471	-0.495	-0.191	-0.099	-0.461

aldehyde_dehydrogenase_1 _family_member_A1_1.2.1. 3	34	1.2.1.3	Glycolysis/glucon eogenesis	5.7	2.84E-08	0.51	4.86E-01	10.70	10.69	10.72	1.80	1.80	1.64	-0.409	-0.418	-0.029	-0.094	-0.489
ubiquinol_cytochrome _C_reductase_FeS _mitochondrial	35	2	1.10.2. Oxidative Phosphorylation	10.9	3.34E-15	0.40	5.39E-01	10.75	10.74	10.76	1.92	1.92	1.54	-0.481	-0.493	-0.081	-0.085	-0.391
3-hydroxy-3-methylglutaryl- CoA_reductase	36	4	1.1.1.3 Sterol biosynthesis Fatty acid	4.6	1.46E-06	0.09	7.68E-01	10.42	10.41	10.42	1.87	1.70	1.87	-0.372	-0.360	-0.145	0.037	-0.450
acetyl- CoA_acetyltransferase_2	37	9	2.3.1.1 biosynthesis (path 1)	1.6	8.96E-02	1.07	3.18E-01	10.48	10.47	10.50	1.75	1.71	1.72	-0.433	-0.459	-0.130	-0.006	-0.499
acid_sphingomyelinase- like_phosphodiesterase	38	2	3.1.4.1 Sphingophosphol ipid biosynthesis	5.5	5.36E-08	0.01	9.32E-01	10.59	10.60	10.59	2.06	1.98	1.87	-0.395	-0.411	-0.199	0.066	-0.443
acetyl-CoA_synthetase_ Isocitrate_dehydrogenase_i sozyme_3	39	6.2.1.1	TCA	1.1	3.94E-01	0.00	9.75E-01	10.55	10.55	10.55	1.55	1.50	1.54	-0.457	-0.448	-0.245	-0.035	-0.537
fatty_acid_binding_protein_ 7_brain_(B-FABP)	40	1	1.1.1.4 TCA Fatty Acid binding	2.5	3.57E-03	0.36	5.57E-01	10.87	10.86	10.88	1.69	1.69	1.61	-0.371	-0.361	-0.209	0.035	-0.531
Vacuolar_ATP_synthase subunit_C	41	—	2.4	6.05E-03	0.04	8.47E-01	10.32	10.32	10.33	1.90	1.82	1.74	-0.231	-0.214	-0.050	-0.037	-0.603	
PEP_carboxykinase_phosp hoenolpyruvate_carboxykin ase	42	5	3.6.1.3 Oxidative Phosphorylation	1.6	1.03E-01	0.01	9.23E-01	10.52	10.51	10.52	1.78	1.77	1.74	-0.296	-0.262	-0.101	-0.063	-0.623
ATPase_Cu++_transporting _alpha_polypeptide_(Menke s_syndrome)	43	2	4.1.1.3 TCA	2.8	1.15E-03	0.43	5.23E-01	10.37	10.38	10.35	1.67	1.63	1.51	-0.323	-0.326	-0.169	-0.093	-0.631
triglyceride_lipase_triacylgly cerol	44	3.6.3.4	transport	6.6	1.65E-09	0.01	9.10E-01	10.53	10.54	10.53	2.02	1.96	1.85	-0.328	-0.326	-0.112	-0.059	-0.554
hypoxia_inducible_factor_3_ alpha	45	—	3.1.1.3 Lipid Metabolism transcription factor	4.8	8.58E-07	0.00	9.76E-01	10.64	10.64	10.64	1.82	1.82	1.70	-0.272	-0.229	-0.240	0.013	-0.628
heptocyte_nuclear_factor_ 4_alpha	46	—	1.8	4.19E-02	0.06	8.03E-01	10.34	10.35	10.34	1.76	1.68	1.68	-0.144	-0.096	-0.223	0.025	-0.665	
forkhead_box_P2;_ cytochrome_c_oxidase_sub unit_VIIIa	47	—	4.9	5.48E-07	0.00	9.61E-01	10.95	10.95	10.95	1.62	1.62	1.54	-0.306	-0.292	-0.161	0.011	-0.539	
NADH_dehydrogenase_(ubi quinone)_Fe- S_protein_1_75_KD_ dihydrolipoamide_S- acetyltransferase_(E2_com ponent_of_pyruvate_dehydr ogenase_complex)_	48	—	9.3	3.20E-13	0.43	5.21E-01	11.87	11.89	11.84	2.44	2.44	1.94	-0.304	-0.297	-0.262	-0.224	-0.629	
glycerol_kinase_ Inositol_Polyphosphate_1- Phosphatase_(1- Ptase)_(Inositol-14- Bisphosphate_1-	49	1.9.3.1	Phosphorylation	5.8	2.10E-08	0.03	8.72E-01	10.88	10.87	10.88	2.09	2.09	1.79	-0.314	-0.290	-0.150	-0.050	-0.480
	50	1.6.5.3	Oxidative Phosphorylation	21.0	1.00E-17	0.49	4.96E-01	14.03	13.99	14.06	2.56	2.56	2.01	-0.321	-0.334	0.002	-0.038	-0.431
	51	2	2.3.1.1 TCA	4.9	4.78E-07	0.35	5.64E-01	11.90	11.88	11.91	1.59	1.59	1.36	-0.407	-0.398	-0.093	0.050	-0.368
	52	0	2.7.1.3 Glycerolipid metabolism	2.4	4.85E-03	3.92	6.78E-02	11.12	11.08	11.16	1.25	1.14	1.25	-0.105	-0.054	0.120	0.231	-0.418
	53	7	3.1.3.5 Inositol phosphate metabolism	2.7	1.96E-03	1.10	3.13E-01	10.35	10.37	10.33	1.45	1.37	1.38	0.032	0.084	-0.182	-0.118	-0.598

Phosphatase)

ATPase_H+_transporting_ly sosomal_(vacuolar_proton_ pump_D_subunit)_42_kDa	54	3.6.1.3 4	Oxidative Phosphorylation	2.5	3.95E-03	0.45	5.12E-01	10.53	10.54	10.52	1.28	1.28	1.21	0.120	0.166	-0.245	-0.188	-0.715
delta- 6_fatty_acid_desaturase	55	1.14.9 9.25	Fatty acid metabolism	2.3	6.99E-03	0.02	8.86E-01	10.49	10.49	10.49	1.43	1.33	1.30	-0.109	-0.086	-0.001	0.082	-0.452
oxoglutarate_(alpha- ketoglutarate)_dehydrogena se_(lipoamide)_	56	1.2.4.2 1.1.1.2	TCA glucuronate	1.5	1.15E-01	2.54	1.33E-01	10.92	10.90	10.94	1.35	1.35	1.30	-0.116	-0.064	0.084	0.007	-0.564
cytochrome _C_oxidase_VIIC_	57	1.9.3.1 1.1.1.2	Phosphorylation interconversions	17.3	1.00E-17	0.02	8.85E-01	13.44	13.45	13.44	1.48	1.48	1.26	-0.560	-0.485	-0.268	0.036	-0.088
cytochrome_P450_2N2_(C YP2N2)	58	_	p450 Pentose and	77.9	1.00E-17	0.42	5.30E-01	12.30	12.26	12.34	2.68	2.05	1.84	-0.636	-0.628	-0.100	0.158	-0.017
aldose_reductase	59	1	transcription	15.4	1.00E-17	0.12	7.39E-01	10.64	10.66	10.61	1.70	1.70	1.54	-0.074	-0.047	-0.318	0.217	0.177
Musashi_homolog_1_ glycogene_phosphorylase_ muscle	60	_	factor	5.7	2.74E-08	0.11	7.49E-01	10.63	10.62	10.64	1.51	1.41	1.42	-0.134	-0.065	-0.192	0.419	0.177
dodecenoyl-CoA_Delta- isomerase_	61	2.4.1.1	eogenesis Fatty acid	5.5	7.01E-08	0.04	8.44E-01	10.93	10.93	10.94	1.31	1.14	1.31	0.159	0.152	-0.295	0.001	-0.331
dihydrolipoamide_dehydrog enase_E3_component_of_ pyruvate_dehydrogenase_c omplex	62	5.3.3.8	metabolism	6.2	4.79E-09	0.82	3.81E-01	10.61	10.58	10.64	1.46	1.46	1.21	0.407	0.364	0.086	0.312	-0.015
inositol_polyphosphate-4- phosphatase_type_I	63	1.8.1.4 3.1.3.6	TCA Inositol	1.7	6.67E-02	0.41	5.31E-01	10.86	10.84	10.87	1.26	1.22	1.26	0.313	0.373	-0.124	0.141	-0.333
cystathionine-beta-synthase	64	6	phosphate me Glycine serine	2.8	1.50E-03	1.84	1.96E-01	10.59	10.61	10.57	1.30	1.20	1.28	0.096	0.168	-0.416	0.012	-0.600
ATPase_H+_transporting_ly sosomal_(vacuolar_proton_ pump)_16kD_(Atp6I)	65	2	and threonine metabolism	6.0	1.26E-08	1.59	2.28E-01	11.00	10.97	11.03	1.26	1.24	1.20	-0.049	-0.091	-0.032	0.183	-0.365
cytochrome_P450_1B1_(CY P1B1)	66	3.6.1.3 1.14.1	Oxidative Phosphorylation	2.6	2.63E-03	3.94	6.71E-02	10.86	10.89	10.83	1.64	1.54	1.45	0.292	0.197	-0.116	-0.090	-0.327
acetyl- Coenzyme_A_carboxylase_ alpha	67	4.1	p450 Fatty acid	5.9	1.56E-08	0.01	9.12E-01	11.08	11.08	11.08	1.75	1.57	1.75	0.348	0.419	0.012	0.055	-0.322
glutaminase_kidney isoform	68	6.4.1.2	biosynthesis Glutamate	4.2	6.84E-06	12.7	3.05E-03	10.89	10.80	10.98	1.55	1.37	1.46	0.133	0.196	0.310	0.178	0.028
isocitrate_dehydrogenase_2 _(mitochondrial_IDH2)	69	3.5.1.2 1.1.1.4	metabolism	8.5	2.78E-12	2.76	1.19E-01	11.37	11.31	11.43	1.53	1.27	1.40	0.155	0.194	0.340	0.097	0.164
cytochrome_P450_3A30_(C YP3A30)	70	1	TCA	17.4	1.00E-17	3.01	1.05E-01	13.71	13.67	13.76	1.55	1.55	1.26	0.333	0.364	0.294	0.094	0.101
6- phosphogluconolactonase_ basic_transcription_factor_3	71	4.1	p450 Pentose	0.8	6.79E-01	0.37	5.54E-01	10.95	10.94	10.95	1.40	1.40	1.22	0.649	0.646	0.341	0.119	-0.020
	72	1.1.1.4	Phosphate pathway	4.1	1.04E-05	0.88	3.63E-01	10.76	10.77	10.74	1.46	1.46	1.21	0.714	0.622	0.305	0.068	-0.033
	73	_	transcription	5.8	1.83E-08	0.11	7.44E-01	11.75	11.74	11.76	1.44	1.23	1.44	0.313	0.276	0.115	0.153	0.241

				factor															
				Glycolysis/glucon															
phosphoglucose_isomerase	74	5.3.1.9	eogenesis		51.3	1.00E-17	0.05	8.35E-01	12.37	12.36	12.38	1.43	1.35	1.43	0.421	0.410	0.134	-0.054	-0.010
cytochrome_c_oxidase_sub				Oxidative															
unit_IV_isoform_2	75	1.9.3.1	Phosphorylation		22.5	1.00E-17	1.49	2.43E-01	12.26	12.31	12.21	1.98	1.86	1.67	0.334	0.277	-0.180	0.112	0.107
phosphoglycerate_mutase_(Glycolysis/glucon															
PGM)_type_B	76	5.4.2.1	eogenesis		19.6	1.00E-17	7.13	1.83E-02	13.36	13.44	13.28	1.57	1.57	1.37	0.344	0.313	-0.012	-0.199	0.328
glutathione_peroxidase_4_(1.11.1. Glutathione															
phospholipid_hydroperoxida	77	9	metabolism		52.3	1.00E-17	8.13	1.28E-02	11.43	11.57	11.30	5.15	4.86	1.94	0.709	0.581	0.217	-0.073	0.350
se)				Pentose															
				Phosphate															
Transaldolase	78	2.2.1.2	Pathway		13.9	1.00E-17	17.1	1.01E-03	11.27	11.40	11.14	2.02	1.82	1.27	0.566	0.429	-0.105	-0.193	0.235
				Pentose															
				Phosphate															
Transketolase_	79	2.2.1.1	Pathway		18.8	1.00E-17	26.8	1.38E-04	11.42	11.57	11.27	3.25	2.86	1.67	0.397	0.264	-0.011	-0.086	0.349
pyruvate_dehydrogenase_E																			
1_beta_subunit_(lipoamide)	80	1.2.4.1	TCA		12.0	2.32E-16	0.02	8.78E-01	11.03	11.02	11.03	1.52	1.52	1.39	-0.356	-0.429	-0.238	-0.359	-0.518
Cytochrome_P450_1A_(CY																			
P1A)	81	_	p450		11.9	2.32E-16	3.24	9.36E-02	11.96	12.01	11.91	1.88	1.88	1.18	0.631	0.519	0.200	0.015	0.405
GPX2:_glutathione_peroxid				1.11.1. Glutathione															
ase_2_(gastrointestinal)	82	9	metabolism		42.7	1.00E-17	27.2	1.30E-04	12.53	12.82	12.23	2.70	1.78	2.00	0.049	-0.059	-0.275	-0.307	0.249
fumarate_hydratase	83	4.2.1.2	TCA		24.0	1.00E-17	34.8	3.86E-05	11.90	12.24	11.56	3.03	1.93	1.85	0.518	0.443	-0.463	-0.344	-0.016
glutathione-S-				2.5.1.1 Glutathione															
transferase_mu_5	84	8	metabolism		34.0	1.00E-17	0.03	8.74E-01	12.24	12.25	12.23	1.99	1.99	1.62	0.309	0.266	0.077	-0.161	0.039
NADH_dehydrogenase_(ubi				Oxidative															
quinone)_flavoprotein_2	85	1.6.5.3	Phosphorylation		22.7	1.00E-17	0.25	6.25E-01	11.57	11.56	11.59	1.47	1.47	1.23	0.190	0.125	0.202	-0.189	0.055
ATP_synthase_H+_transport																			
ing_mitochondrial_F1_com				3.6.1.3 Oxidative															
plex_delta_subunit_	86	4	Phosphorylation		10.2	2.19E-14	1.43	2.52E-01	13.13	13.11	13.15	1.64	1.44	1.64	0.251	0.272	0.315	0.057	0.584
Aspartate_amino_transfeas																			
e_mito	87	2.6.1.1	Glutamate		17.7	1.00E-17	2.49	1.37E-01	12.49	12.44	12.54	1.96	1.96	1.79	0.439	0.408	0.352	0.288	0.523
NADH-				Oxidative															
ubiquinone_oxidoreductase	88	1.6.5.3	Phosphorylation		11.0	2.45E-15	4.88	4.44E-02	12.24	12.17	12.30	1.80	1.62	1.47	0.382	0.431	0.360	0.278	0.442
_19_KD																			
NADH-				Oxidative															
ubiquinone_oxidoreductase	89	1.6.5.3	Phosphorylation		33.0	1.00E-17	1.16	2.99E-01	12.35	12.32	12.39	1.73	1.71	1.66	0.298	0.302	0.350	-0.121	0.369
_B22																			
NADH-				Oxidative															
ubiquinone_oxidoreductase	90	1.6.5.3	Phosphorylation		12.3	1.21E-16	3.75	7.34E-02	12.50	12.45	12.54	1.82	1.55	1.69	0.324	0.383	0.308	-0.007	0.412
_ASHI																			
ubiquinol_cytochrome				1.10.2. Oxidative															
_C_reductase_7.2_KDA	91	2	Phosphorylation		18.1	1.00E-17	5.18	3.90E-02	12.46	12.40	12.51	1.90	1.90	1.54	0.343	0.367	0.284	0.109	0.521
cold_inducibile_RNA-				transcription															
binding_protein;	92	_	factor		31.2	1.00E-17	0.04	8.42E-01	13.12	13.12	13.13	3.00	3.00	2.45	0.471	0.445	0.201	0.141	0.543
NADH_dehydrogenase_(ubi																			
quinone)_Fe-				Oxidative															
S_protein_3_(30kD)_NADH	93	1.6.5.3	Phosphorylation		3.5	8.68E-05	2.11	1.68E-01	11.41	11.37	11.45	1.45	1.27	1.31	0.204	0.239	0.194	0.044	0.255

-coenzyme_Q_reductase)

ubiquinol-cytochrome_c_reductase_core_protein_I	94	2	1.10.2. Oxidative Phosphorylation	2.6	2.83E-03	6.61	2.22E-02	11.72	11.68	11.76	1.32	1.27	1.23	0.284	0.280	0.362	0.204	0.373
ATP_synthase_H+_transporting_mitochondrial_F1_complex_gamma_polypeptide_1	95	4	3.6.1.3 Oxidative Phosphorylation	39.4	1.00E-17	3.39	8.69E-02	12.39	12.31	12.47	2.40	1.80	2.04	0.093	0.129	0.146	0.009	0.427
glyceraldehyde-3-phosphate_dehydrogenase_NADH_dehydrogenase_(ubiquinone)_chain_2	96	2	1.2.1.1 Glycolysis/gluconeogenesis	42.8	1.00E-17	4.05	6.38E-02	13.43	13.52	13.34	2.97	2.54	2.97	0.259	0.242	-0.087	0.042	0.561
	97		1.6.5.3 Oxidative Phosphorylation	5.0	3.65E-07	0.01	9.34E-01	13.24	13.24	13.24	1.92	1.67	1.71	0.235	0.293	0.005	0.042	0.541
ATP_synthase_beta-subunit_cytochrome_c_oxidase_subunit_VIIIb	98	4	3.6.1.3 Oxidative Phosphorylation	3.5	1.11E-04	2.74	1.20E-01	13.86	13.81	13.90	2.07	1.88	1.85	0.226	0.261	0.132	0.006	0.481
	99		1.9.3.1 Oxidative Phosphorylation	27.2	1.00E-17	5.84	2.99E-02	13.97	14.04	13.90	1.76	1.57	1.66	0.290	0.364	-0.129	0.091	0.510
			Oxidative Phosphorylation															
cytochrome_C oxidase VIIA	100	1.9.3.1	Oxidative Phosphorylation	3.3	1.79E-04	3.03	1.04E-01	12.24	12.27	12.22	1.33	1.21	1.33	0.160	0.128	0.137	0.047	0.487
cytochrome_C oxidase_VIA_general_transcription_factor_IH_polypeptide_4	101	1.9.3.1	Oxidative Phosphorylation transcription factor	8.2	8.20E-12	9.11	9.21E-03	13.71	13.78	13.63	2.19	1.87	1.87	0.354	0.361	0.226	-0.038	0.415
	102		transcription factor	24.5	1.00E-17	0.11	7.41E-01	14.06	14.07	14.04	1.41	1.41	1.24	0.061	0.045	0.053	-0.095	0.441
			2.7.1.1 Glycolysis/gluconeogenesis															
6-phosphofructokinase	103	1	eogenesis	30.7	1.00E-17	4.60	5.01E-02	12.77	12.87	12.67	2.31	2.16	1.46	0.173	0.215	-0.331	-0.016	0.182
			3.4.24.															
matrix_metalloproteinase_2	104	24	Protease	55.0	1.00E-17	11.2	4.72E-03	11.37	11.57	11.17	9.22	7.77	2.98	-0.081	-0.029	-0.370	-0.049	0.018
Isopentenyl_diphosphate_delta_isomerase	105	5.3.3.2	Sterol biosynthesis	37.6	1.00E-17	0.12	7.29E-01	11.14	11.12	11.15	2.19	2.19	1.39	0.013	0.044	-0.139	-0.177	-0.164
methylmalonate-semialdehyde_dehydrogenase_(acylating)_NADH-ubiquinone_oxidoreductase_AGGG_NADH_dehydrogenase_(ubiquinone)_1_alpha_subcomplex_1_(7.5kD_MWFE)	106	7	1.2.1.2 Inositol metabolism	17.1	1.00E-17	12.0	3.80E-03	11.78	11.63	11.93	1.89	1.49	1.41	-0.250	-0.209	0.439	0.228	0.319
	107		Oxidative Phosphorylation	82.1	1.00E-17	2.22	1.58E-01	13.64	13.56	13.73	2.17	2.17	1.91	-0.158	-0.144	0.174	0.110	0.514
	108		Oxidative Phosphorylation	12.5	1.00E-17	10.1	6.68E-03	13.10	13.01	13.20	1.90	1.57	1.52	-0.041	0.032	0.515	0.340	0.385
	109		Oxidative Phosphorylation	14.0	1.00E-17	8.79	1.03E-02	12.23	12.15	12.30	1.63	1.39	1.42	-0.132	-0.068	0.515	0.300	0.331
	110		2.5.1.1 Glutathione metabolism	26.3	1.00E-17	0.95	3.46E-01	12.67	12.64	12.70	2.04	1.70	1.88	0.103	0.165	0.188	0.125	0.370
glutathione_S-transferease_A_hypoxia_inducible_factor_1_alpha	111		transcription factor	26.4	1.00E-17	1.38	2.59E-01	12.80	12.76	12.84	2.06	2.06	1.90	0.275	0.335	0.197	-0.015	0.378
	112		Oxidative Phosphorylation	20.1	1.00E-17	5.42	3.54E-02	13.39	13.45	13.33	2.07	2.07	1.51	0.173	0.188	-0.014	-0.170	0.457
NADH_dehydrogenase_(ubiquinone)_MLRQ_SUBUNIT	113	1.6.5.3	Oxidative Phosphorylation	3.7	3.84E-05	1.78	2.04E-01	12.93	12.96	12.89	1.70	1.56	1.56	0.056	0.053	0.082	-0.025	0.597

cytochrome_P450_2P1_(CY P2P1)	114	_	p450	4.7	9.55E-07	1.61	2.25E-01	12.94	12.97	12.91	2.09	2.09	1.76	0.241	0.248	0.206	-0.045	0.555
succinate_dehydrogenase_ complex_subunit_C_	115	?	TCA	4.8	7.43E-07	1.01	3.32E-01	12.45	12.43	12.47	1.71	1.64	1.51	0.308	0.325	0.363	0.030	0.586
succinate- CoA_ligase_(GDP- forming)_	116	6.2.1.4	TCA	5.7	3.22E-08	1.40	2.56E-01	14.10	14.12	14.08	1.53	1.38	1.53	0.134	0.180	0.134	-0.099	0.530
cytochrome_c_oxidase_sub unit_II_	117	1.9.3.1	Phosphorylation Oxidative	4.1	1.08E-05	0.22	6.44E-01	13.91	13.90	13.92	1.72	1.71	1.47	0.037	0.064	0.027	-0.116	0.474
ATP_synthase_subunit_B	118	4	Phosphorylation Tetrachloroethen	11.3	8.98E-16	0.00	9.52E-01	13.26	13.26	13.26	2.06	1.87	1.85	0.202	0.240	0.016	0.058	0.609
Epoxide hydrolase_1	119	3.3.2.3	e degradation	6.4	2.82E-09	0.74	4.03E-01	10.88	10.85	10.90	1.57	1.33	1.56	0.071	0.159	0.086	0.135	0.455