Supplementary Table 3. Summary of mitochondrial proteins and their fold change detected by MS with troglitazone administration

Individual protein fold change ratio relative to the control vehicle, as detected by 8-plex iTRAQ.
IPA-qualified functions associated with troglitazone-induced toxicity based on directional changes to protein expression are also included.

This table comprises of two tabs:

A) 14 days	Summary of protein fold change using iTRAQ channels 113 to 116 after 14 days of troglitazone administration
B) 28 days	Summary of protein fold change using iTRAQ channels 117, 118, 119 and 121 after 28 days of troglitazone administration

Column description (for tabs A and B)

UNUSED:	A measure of all the peptide evidence for a protein that is not better explained by a higher ranked protein. Considered as the true indicator of protein confidence
TOTAL:	A measure of all the peptide evidence for a protein
% COV:	Percentage of amino acids detected by MS
ACCESSION:	IPI protein identifier
NAME:	Protein name
AVG FOLD CHANGE:	Average fold change
LOG$_2$:	Log base 2 of average fold change
***P*-VALUE**	Quantification *P*-value * NA values for proteins identified by 2 peptides which is insufficient for *P*-value calculation

A) 14 days

NO.	UNUSED	TOTAL	% COV	ACCESSION	NAME	AVG FOLD CHANGE	Log_2	P-VALUE
1	183.93	183.93	64.4	IPI:IPI00111908.8	Gene_Symbol=Cps1 Carbamoyl-phosphate synthase [ammonia], mitochondrial	0.91955	-0.121	0.003625
2	53.16	53.17	43.5	IPI:IPI00114710.2	Gene_Symbol=Pcx Activated spleen cDNA, RIKEN full-length enriched library, clone:F830201B12 product:pyruvate carboxylase, full insert sequence	1.0633	0.088549	0.0147
3	50.83	50.83	51.6	IPI:IPI00114209.1	Gene_Symbol=Glud1 Glutamate dehydrogenase 1, mitochondrial	0.9862	-0.02005	0.1455
4	49.94	49.94	65.5	IPI:IPI00869393.1	Gene_Symbol=Cat catalase	1.672175	0.741726	0
5	48.03	48.03	56.8	IPI:IPI00461964.3	Gene_Symbol=Aldh6a1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	0.91505	-0.12808	0.1867
6	47.61	47.61	51.7	IPI:IPI00880839.1	Gene_Symbol=Hspa9 heat shock protein 9	0.9625	-0.05514	0.0555
7	46.26	46.26	49	IPI:IPI00554834.2	Gene_Symbol=Ehhadh Peroxisomal bifunctional enzyme	1.551525	0.633687	0.00005
8	46.18	46.18	45.9	IPI:IPI00111218.1	Gene_Symbol=Aldh2 Aldehyde dehydrogenase, mitochondrial	1.018825	0.026906	0.3416
9	45.37	45.37	47.3	IPI:IPI00223092.5	Gene_Symbol=Hadha Trifunctional enzyme subunit alpha, mitochondrial	1.048425	0.068224	0.2421
10	43.42	43.42	39	IPI:IPI00120123.1	Gene_Symbol=Dmgdh Dimethylglycine dehydrogenase, mitochondrial	0.852775	-0.22976	0.003

11	43.03	43.03	52.2	IPI:IPI00420718.4	Gene_Symbol=Hmgcs2 Hydroxymethylglutaryl-CoA synthase, mitochondrial	1.06925	0.096599	0.0455
12	41.56	41.56	64.1	IPI:IPI00468481.2	Gene_Symbol=Atp5b ATP synthase subunit beta, mitochondrial	0.9418	-0.08651	0.1163
13	40.72	40.72	56.7	IPI:IPI00117312.1	Gene_Symbol=Got2 Aspartate aminotransferase, mitochondrial	0.964	-0.05289	0.4159
14	39.24	39.24	63.3	IPI:IPI00129178.1	Gene_Symbol=Oat Ornithine aminotransferase, mitochondrial	1.14835	0.199562	0.06665
15	38.89	38.89	56	IPI:IPI00308885.6	Gene_Symbol=Hspd1 Isoform 1 of 60 kDa heat shock protein, mitochondrial	0.8668	-0.20623	0.0104
16	36.49	36.49	49.9	IPI:IPI00130280.1	Gene_Symbol=Atp5a1 ATP synthase subunit alpha, mitochondrial	0.9611	-0.05724	0.2422
17	35.03	35.03	61.5	IPI:IPI00653158.1	Gene_Symbol=Acaa2 Acetyl-Coenzyme A acyltransferase 2 (Mitochondrial 3-oxoacyl-Coenzyme A thiolase), isoform CRA_k	0.97285	-0.03971	0.3177
18	34.83	34.83	59.1	IPI:IPI00223367.5	Gene_Symbol=Uox Uricase	1.62545	0.700839	0
19	34.1	34.1	43.9	IPI:IPI00828479.1	Gene_Symbol=Acox1 Acyl-Coenzyme A oxidase 1, palmitoyl	2.051475	1.036662	0.000025
20	33	33	40.9	IPI:IPI00119203.4	Gene_Symbol=Acadvl Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	1.05895	0.082634	0.00565
21	32.28	32.28	40.8	IPI:IPI00875638.1	Gene_Symbol=Immt Isoform 3 of Mitochondrial inner membrane protein	0.840025	-0.2515	0.0653
22	31.96	31.97	50.1	IPI:IPI00459487.3	Gene_Symbol=Suclg2 Isoform 1 of Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	1.032925	0.046736	0.17775

23	31.15	31.16	56.8	IPI:IPI00154054.1	Gene_Symbol=Acat1 Acetyl-CoA acetyltransferase, mitochondrial	0.967075	-0.0483	0.17605
24	30.62	30.62	35.4	IPI:IPI00115607.3	Gene_Symbol=Hadhb Trifunctional enzyme subunit beta, mitochondrial	1.044575	0.062916	0.1358
25	29.71	29.71	40.3	IPI:IPI00121322.2	Gene_Symbol=Etfdh Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	1.02675	0.038085	0.2294
26	29.63	29.63	25.7	IPI:IPI00387491.1	Gene_Symbol=Aass Alpha-aminoadipic semialdehyde synthase, mitochondrial	0.980625	-0.02823	0.5859
27	29.36	29.36	33.9	IPI:IPI00261627.1	Gene_Symbol=Sucla2 Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	0.922775	-0.11595	0.04825
28	28.47	28.47	38.5	IPI:IPI00116074.1	Gene_Symbol=Aco2 Aconitate hydratase, mitochondrial	0.9813	-0.02723	0.3817
29	28.24	28.24	24.9	IPI:IPI00134131.2	Gene_Symbol=Scp2 Isoform SCPx of Non-specific lipid-transfer protein	1.403275	0.488798	0.002425
30	28.08	28.08	33.7	IPI:IPI00331628.5	Gene_Symbol=Hsd17b4 Peroxisomal multifunctional enzyme type 2	1.411575	0.497306	0.00045
31	27.76	27.76	33.9	IPI:IPI00136213.5	Gene_Symbol=Sardh Sarcosine dehydrogenase, mitochondrial	0.95265	-0.06998	0.0602
32	27.2	27.39	40.9	IPI:IPI00894588.1	Gene_Symbol=Acadl Long-chain specific acyl-CoA dehydrogenase, mitochondrial	1.06025	0.084404	0.149
33	26.25	26.25	33.3	IPI:IPI00122633.3	Gene_Symbol=Acsf2 Acyl-CoA synthetase family member 2, mitochondrial	1.0252	0.035905	0.2696
34	26.15	26.15	38.7	IPI:IPI00776257.1	Gene_Symbol=Otc Otc protein	0.9645	-0.05215	0.1359

35	25.34	25.36	48.2	IPI:IPI00323592.2	Gene_Symbol=Mdh2 Malate dehydrogenase, mitochondrial	0.971225	-0.04212	0.3869
36	25.18	25.18	46.6	IPI:IPI00119138.1	Gene_Symbol=Uqcrc2 Cytochrome b-c1 complex subunit 2, mitochondrial	0.9862	-0.02005	0.5257
37	24.48	24.48	29.2	IPI:IPI00857226.1	Gene_Symbol=Acsl1 78 kDa protein	1.2055	0.269632	0.00315
38	23.43	23.43	75.3	IPI:IPI00221769.5	Gene_Symbol=Ak3 GTP:AMP phosphotransferase mitochondrial	0.91055	-0.13519	0.0058
39	23.13	23.13	37.5	IPI:IPI00405699.2	Gene_Symbol=Aldh4a1 Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	0.983975	-0.02331	0.44755
40	22.18	22.18	43.4	IPI:IPI00331251.1	Gene_Symbol=Acads Acyl-Coenzyme A dehydrogenase, short chain, isoform CRA_a	0.965325	-0.05091	0.25335
41	20.92	21	26.3	IPI:IPI00553576.3	Gene_Symbol=Abcd3 ATP-binding cassette, sub-family D, member 3	1.72165	0.783792	0.00095
42	20.57	20.57	41.9	IPI:IPI00127841.3	Gene_Symbol=Slc25a5 ADP/ATP translocase 2	1.3849	0.469782	0.0173
43	20.5	20.5	50.8	IPI:IPI00223216.5	Gene_Symbol=Tst Thiosulfate sulfurtransferase	1.014475	0.020733	0.33105
44	20.33	20.33	30.1	IPI:IPI00133522.1	Gene_Symbol=P4hb Protein disulfide-isomerase	1.150175	0.201853	0.01485
45	20	20	23.9	IPI:IPI00129928.2	Gene_Symbol=Fh1 Isoform Mitochondrial of Fumarate hydratase, mitochondrial	0.970675	-0.04294	0.2004
46	19.9	19.91	47.9	IPI:IPI00454049.4	Gene_Symbol=Echs1 Enoyl-CoA hydratase, mitochondrial	0.922075	-0.11704	0.244
47	19.76	19.77	54.3	IPI:IPI00848492.1	Gene_Symbol=LOC100045699 similar to Electron transferring flavoprotein, beta polypeptide isoform 2	0.918025	-0.12339	0.027067

48	19.55	19.55	38	IPI:IPI00134961.1	Gene_Symbol=Acadm Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	0.965375	-0.05084	0.4371
49	19.08	19.1	54	IPI:IPI00648318.1	Gene_Symbol=Ak2 Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730019E03 product:ADENYLATE KINASE 2 homolog	0.876425	-0.1903	0.02365
50	19.08	19.08	45.2	IPI:IPI00154047.1	Gene_Symbol=Hibch 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	0.9482	-0.07674	0.0445
51	19.06	19.07	36	IPI:IPI00121105.2	Gene_Symbol=Hadh Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	0.9911	-0.0129	0.47315
52	18.6	18.6	53.8	IPI:IPI00116753.4	Gene_Symbol=Etfa Electron transfer flavoprotein subunit alpha, mitochondrial	0.9453	-0.08116	0.125
53	18.45	18.45	29.7	IPI:IPI00135651.1	Gene_Symbol=Slc25a13 Calcium-binding mitochondrial carrier protein Aralar2	1.225675	0.293576	0.032467
54	18.42	18.42	32.5	IPI:IPI00471246.2	Gene_Symbol=Ivd Isovaleryl-CoA dehydrogenase, mitochondrial	0.959925	-0.05901	0.183
55	18.29	18.29	28.5	IPI:IPI00881091.1	Gene_Symbol=Ctsd Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830005I10 product:cathepsin D, full insert sequence	1.463225	0.549152	0.000725
56	17.66	17.66	45.6	IPI:IPI00129056.2	Gene_Symbol=Glyat Isoform 1 of Glycine N-acyltransferase	1.08585	0.118825	0.0101
57	17.56	17.56	24.2	IPI:IPI00226140.5	Gene_Symbol=Maob Amine oxidase [flavin-containing] B	1.139125	0.187926	0.031567

58	17.35	17.36	22.1	IPI:IPI00308882.4	Gene_Symbol=Ndufs1 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	1.06415	0.089702	0.0722
59	17.09	17.1	31.2	IPI:IPI00230351.1	Gene_Symbol=Sdha Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	0.98835	-0.01691	0.4003
60	16.76	16.76	25.9	IPI:IPI00625588.1	Gene_Symbol=- hypothetical protein (Tu translation elongation factor, mitochondrial)	1.034675	0.049178	0.1525
61	16.62	16.62	36.7	IPI:IPI00130535.1	Gene_Symbol=Dbt Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	0.93305	-0.09997	0.50715
62	16.53	16.61	28.8	IPI:IPI00126625.1	Gene_Symbol=Acsm1 Isoform 1 of Acyl-coenzyme A synthetase ACSM1, mitochondrial	1.062425	0.087361	0.1822
63	16.23	16.23	47.4	IPI:IPI00133440.1	Gene_Symbol=Phb Prohibitin	0.964875	-0.05159	0.45405
64	16.12	16.14	33.8	IPI:IPI00468653.3	Gene_Symbol=Pccb Propionyl Coenzyme A carboxylase, beta polypeptide	0.9507	-0.07294	0.17235
65	16.11	16.11	24.9	IPI:IPI00330523.1	Gene_Symbol=Pcca Propionyl-CoA carboxylase alpha chain, mitochondrial	0.94055	-0.08842	0.0229
66	15.86	15.86	45.8	IPI:IPI00320462.4	Gene_Symbol=Bphl Putative uncharacterized protein	0.9445	-0.08238	0.1841
67	15.78	15.85	29.9	IPI:IPI00881401.1	Gene_Symbol=Cpt2 carnitine palmitoyltransferase 2	1.10465	0.143589	0.1562
68	15.7	15.71	17.9	IPI:IPI00850737.1	Gene_Symbol=Mut TIB-55 BB88 cDNA, RIKEN full-length enriched library, clone:I730049G19 product:methylmalonyl-Coenzyme A mutase, full insert sequence	1.236375	0.306116	0.13825

69	15.68	15.69	35.8	IPI:IPI00387379.1	Gene_Symbol=Decr1 2,4-dienoyl-CoA reductase, mitochondrial	1.00055	0.000793	0.0232
70	15.46	15.46	62.5	IPI:IPI00623553.1	Gene_Symbol=Atp5h (BLAST score: 326, P = 4e-88) LOC100044492;ENSMUSG00000068706 hypothetical protein	1.068125	0.09508	0.3109
71	15.22	15.22	24.6	IPI:IPI00113141.1	Gene_Symbol=Cs Citrate synthase, mitochondrial	0.95695	-0.06348	0.4751
72	15.08	15.08	30.9	IPI:IPI00322760.7	Gene_Symbol=Prodh proline dehydrogenase	1.009375	0.013462	0.465
73	14.93	14.93	44.1	IPI:IPI00321718.4	Gene_Symbol=Phb2 Prohibitin-2	1.010075	0.014462	0.63375
74	14.83	14.83	30.4	IPI:IPI00230540.1	Gene_Symbol=Vdac1 Isoform Mt-VDAC1 of Voltage-dependent anion-selective channel protein 1	1.067625	0.094405	0.2002
75	14.73	14.73	20.3	IPI:IPI00316314.1	Gene_Symbol=Hacl1 2-hydroxyacyl-CoA lyase 1	1.6912	0.758047	0.1458
76	14.68	14.68	32.8	IPI:IPI00341282.2	Gene_Symbol=Atp5f1 ATP synthase subunit b, mitochondrial	1.11995	0.163434	0.1057
77	14.57	14.57	52.7	IPI:IPI00117978.1	Gene_Symbol=Cox4i1 Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	0.992475	-0.0109	0.45525
78	14.55	14.56	40.5	IPI:IPI00331692.1	Gene_Symbol=Dci Putative uncharacterized protein	1.044025	0.062156	0.1146
79	14.55	14.55	51.6	IPI:IPI00118986.1	Gene_Symbol=Atp5o;LOC100047429 ATP synthase subunit O, mitochondrial	1.008325	0.011961	0.85075
80	14.49	14.53	76.2	IPI:IPI00222419.5	Gene_Symbol=ENSMUSG00000058927;Cycs Cytochrome c, somatic	0.904875	-0.14421	0.1161
81	14.36	14.36	86.3	IPI:IPI00263863.8	Gene_Symbol=Hspe1 10 kDa heat shock protein, mitochondrial	0.86505	-0.20914	0.0307

82	14.26	14.26	27	IPI:IPI00132042.1	Gene_Symbol=Pdhb Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	1.019725	0.02818	0.6924
83	14.13	14.13	17.7	IPI:IPI00330747.2	Gene_Symbol=Nphp3;Acad11 Acyl-CoA dehydrogenase family member 11	2.056875	1.040454	0.03195
84	14.01	14.01	24.1	IPI:IPI00116192.1	Gene_Symbol=Prdx3 Thioredoxin-dependent peroxide reductase, mitochondrial	1.0291	0.041383	0.2549
85	13.97	13.97	26.5	IPI:IPI00230084.5	Gene_Symbol=Aldh7a1 aldehyde dehydrogenase family 7, member A1 isoform a	1.044725	0.063123	0.4108
86	13.75	13.75	28.1	IPI:IPI00230108.6	Gene_Symbol=Pdia3 Protein disulfide-isomerase A3	1.1568	0.210139	0.04605
87	13.7	13.7	20.6	IPI:IPI00874456.1	Gene_Symbol=Dld Dihydrolipoyl dehydrogenase, mitochondrial	0.903525	-0.14636	0.0484
88	13.32	13.32	20.2	IPI:IPI00130804.1	Gene_Symbol=Ech1 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	0.9423	-0.08574	0.0997
89	13.12	13.47	28.8	IPI:IPI00788331.1	Gene_Symbol=Gcdh glutaryl-Coenzyme A dehydrogenase	1.104475	0.143361	0.04245
90	13.1	13.1	26.5	IPI:IPI00379694.4	Gene_Symbol=Hmgcl 3-hydroxy-3-methylglutaryl-Coenzyme A lyase	0.937325	-0.09338	0.2279
91	13.08	13.08	30.7	IPI:IPI00321617.1	Gene_Symbol=Ephx2 Isoform 1 of Epoxide hydrolase 2	1.588725	0.667869	0.002825
92	13.05	13.05	58.6	IPI:IPI00785410.1	Gene_Symbol=Cox5b Cytochrome c oxidase subunit 5B, mitochondrial	0.8478	-0.2382	0.017833
93	12.97	13.37	15.1	IPI:IPI00850133.1	Gene_Symbol=Kiaa0564 (BLAST score:3792, P = 0.0) 1300010F03Rik Isoform 1 of Uncharacterized protein KIAA0564 homolog	1.17035	0.22694	0.1358

94	12.9	12.9	28.6	IPI:IPI00454008.1	Gene_Symbol=Shmt2 Serine hydroxymethyltransferase	0.979175	-0.03036	0.1964
95	12.82	12.82	25.1	IPI:IPI00134809.2	Gene_Symbol=Dlst Isoform 1 of Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	0.907525	-0.13999	0.1808
96	12.52	12.52	21.4	IPI:IPI00776047.1	Gene_Symbol=Aifm1 Apoptosis-inducing factor, mitochondrion-associated 1	1.05125	0.072106	0.17465
97	12.51	12.66	25.3	IPI:IPI00119685.1	Gene_Symbol=Cyp27a1 Cytochrome P450 27, mitochondrial	1.05775	0.080999	0.0267
98	12.48	12.48	41.7	IPI:IPI00890322.1	Gene_Symbol=Bdh1 3-hydroxybutyrate dehydrogenase, type 1	1.0805	0.111699	0.0114
99	12.33	14.73	45.6	IPI:IPI00624210.3	Gene_Symbol=Glyal (BLAST score 619, P = 1e-176) EG240549 Glycine N-acyltransferase-like protein	1.0523	0.073546	0.0965
100	12.33	12.35	37.2	IPI:IPI00338536.1	Gene_Symbol=Sdhb Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	0.948025	-0.077	0.2533
101	12.21	12.21	41.6	IPI:IPI00121051.3	Gene_Symbol=Gstk1 Glutathione S-transferase kappa 1	1.047025	0.066296	0.0033
102	12.19	12.19	27.2	IPI:IPI00273146.1	Gene_Symbol=Chdh Choline dehydrogenase, mitochondrial	1.09475	0.130601	0.25325
103	12.02	12.02	36	IPI:IPI00875110.1	Gene_Symbol=Idh2 52 kDa protein	1.212625	0.278133	0.03605
104	12.02	12.02	36.4	IPI:IPI00776084.1	Gene_Symbol=Atp5c1 ATP synthase gamma chain	1.099525	0.13688	0.0347
105	11.74	11.75	43.2	IPI:IPI00109109.1	Gene_Symbol=Sod2 Superoxide dismutase [Mn], mitochondrial	0.95715	-0.06318	0.1666
106	11.46	11.46	35.6	IPI:IPI00115824.1	Gene_Symbol=Nipsnap1 Protein NipSnap homolog 1	1.062925	0.08804	0.42145

107	11.46	11.46	64.9	IPI:IPI00555000.2	Gene_Symbol=Uqcrb Cytochrome b-c1 complex subunit 7	0.9642	-0.0526	0.0631
108	11.22	11.22	22.4	IPI:IPI00122547.1	Gene_Symbol=Vdac2 Voltage-dependent anion-selective channel protein 2	1.1467	0.197488	0.0912
109	11.15	11.15	27.3	IPI:IPI00319992.1	Gene_Symbol=Hspa5 78 kDa glucose-regulated protein	1.045375	0.064021	0.1679
110	11.1	11.11	16.1	IPI:IPI00131695.3	Gene_Symbol=Alb Serum albumin	1.197275	0.259755	0.0488
111	11.02	11.11	18.3	IPI:IPI00123276.1	Gene_Symbol=Mosc2 MOSC domain-containing protein 2, mitochondrial	1.59825	0.676493	0.0095
112	10.98	10.98	54.6	IPI:IPI00125460.1	Gene_Symbol=Atp5j;LOC674583 ATP synthase-coupling factor 6, mitochondrial	0.7256	-0.46275	0.0254
113	10.88	10.88	23.8	IPI:IPI00653598.2	Gene_Symbol=Uqcrc1 ubiquinol-cytochrome c reductase core protein 1	1.03475	0.049282	0.0255
114	10.77	10.77	55.2	IPI:IPI00230113.5	Gene_Symbol=Cyb5 Cytochrome b5	1.0503	0.070801	0.3715
115	10.64	10.64	19.3	IPI:IPI00387289.3	Gene_Symbol=Ces3 Carboxylesterase 3	1.145675	0.196198	0.2859
116	10.19	10.19	27.1	IPI:IPI00113517.1	Gene_Symbol=Ctsb Cathepsin B	1.27465	0.350101	0.0238
117	10.17	10.17	27.6	IPI:IPI00153660.4	Gene_Symbol=Dlat Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	0.975325	-0.03605	0.15145
118	10.12	10.13	17.5	IPI:IPI00134870.3	Gene_Symbol=Acox2 Peroxisomal acyl-coenzyme A oxidase 2	1.854675	0.891166	0.1107
119	10.09	10.09	20.9	IPI:IPI00742309.1	Gene_Symbol=Kmo Isoform 2 of Kynurenine 3-monooxygenase	1.210525	0.275633	0.0227
120	10.01	12.03	21.9	IPI:IPI00874350.1	Gene_Symbol=Aldh3a2 Putative uncharacterized protein	1.37775	0.462314	0.03035

121	10	10	42.9	IPI:IPI00754739.1	Gene_Symbol=Chchd3 (BLAST score: 332, P= 5e-90) LOC100046321;Chchd3 Putative uncharacterized protein	0.839975	-0.25158	0.0391
122	10	10	24.9	IPI:IPI00169862.1	Gene_Symbol=Coq9 Ubiquinone biosynthesis protein COQ9, mitochondrial	0.8244	-0.27858	0.0479
123	9.9	9.9	23.3	IPI:IPI00318750.4	Gene_Symbol=Dhrs4 NADPH-dependent retinol dehydrogenase/reductase isoform 1	1.155675	0.208736	NA
124	9.7	9.7	19.3	IPI:IPI00314202.5	Gene_Symbol=Baat Bile acid-CoA:amino acid N-acyltransferase	1.68255	0.750649	NA
125	9.52	9.53	22.5	IPI:IPI00884472.1	Gene_Symbol=Ctsh cathepsin H preproprotein	1.260025	0.333452	0.0629
126	9.51	9.51	21.3	IPI:IPI00130460.1	Gene_Symbol=Ndufv1 NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	1.0448	0.063227	0.7192
127	9.4	9.41	60.5	IPI:IPI00131771.3	Gene_Symbol=Cox6c Cytochrome c oxidase polypeptide VIc	1.01925	0.027508	NA
128	9.34	9.34	37.2	IPI:IPI00785323.1	Gene_Symbol=Cyp2e1 Cytochrome P450 2E1	1.386075	0.471005	0.0643
129	9.32	9.32	23.3	IPI:IPI00331555.2	Gene_Symbol=Bckdha branched chain ketoacid dehydrogenase E1, alpha polypeptide	0.973375	-0.03893	0.0644
130	9.31	9.31	41.7	IPI:IPI00133034.3	Gene_Symbol=Hint2 Histidine triad nucleotide-binding protein 2	0.907975	-0.13928	0.24275
131	9.23	9.23	35.3	IPI:IPI00133006.1	Gene_Symbol=Ndufab1 Acyl carrier protein, mitochondrial	1.14715	0.198054	0.129
132	9.14	9.14	70.9	IPI:IPI00225390.5	Gene_Symbol=Cox6b1 Cytochrome c oxidase subunit VIb isoform 1	0.809025	-0.30574	NA
133	8.91	8.91	26.1	IPI:IPI00874482.1	Gene_Symbol=Actg1 Actin, cytoplasmic 2	1.3297	0.411101	0.00365

134	8.78	8.78	31.8	IPI:IPI00319652.2	Gene_Symbol=Gpx1 Glutathione peroxidase 1	0.851	-0.23277	0.0463
135	8.76	8.76	22.6	IPI:IPI00134691.3	Gene_Symbol=Ugt1a2;Ugt1a9;Ugt1a10;Ugt1a1;Ugt1a5;Ugt1a7c;LOC632297;Ugt1a6b UDP-glucuronosyltransferase 1-1	0.8771	-0.18919	NA
136	8.72	8.72	33.7	IPI:IPI00830581.1	Gene_Symbol=Hsd17b10 hydroxyacyl-Coenzyme A dehydrogenase type II	1.10775	0.147632	0.32685
137	8.62	9.06	16	IPI:IPI00128738.4	Gene_Symbol=Agxt2 Alanine--glyoxylate aminotransferase 2, mitochondrial	1.0282	0.040121	0.075
138	8.41	11.2	32.6	IPI:IPI00113073.3	Gene_Symbol=Aldh1b1 Aldehyde dehydrogenase X, mitochondrial	0.854725	-0.22647	NA
139	8.35	8.42	10.6	IPI:IPI00761408.2	Gene_Symbol=Lonp1 Lon protease homolog, mitochondrial	1.132775	0.179861	0.0161
140	8.29	8.29	29.5	IPI:IPI00117083.1	Gene_Symbol=Grpel1 GrpE protein homolog 1, mitochondrial	0.980775	-0.02801	NA
141	8.27	8.52	27.4	IPI:IPI00407499.1	Gene_Symbol=Abat Isoform 1 of 4-aminobutyrate aminotransferase, mitochondrial	1.170625	0.227279	0.32575
142	8.22	8.38	13.5	IPI:IPI00895390.1	Gene_Symbol=Scpep1 Serine carboxypeptidase 1	1.418	0.503858	0.0073
143	8.16	8.54	16.8	IPI:IPI00153144.3	Gene_Symbol=Suox Sulfite oxidase, mitochondrial	0.861525	-0.21504	NA
144	8.16	8.16	29.6	IPI:IPI00116222.1	Gene_Symbol=Hibadh 3-hydroxyisobutyrate dehydrogenase, mitochondrial	0.879	-0.18606	0.023167
145	8.06	8.08	13.3	IPI:IPI00759881.1	Gene_Symbol=Acad9 very-long-chain acyl-CoA dehydrogenase VLCAD homolog	1.01855	0.026517	0.8149

146	8.01	8.01	31.8	IPI:IPI00406442.2	Gene_Symbol=Suclg1 Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial	1.015875	0.022723	0.0195
147	8	8	34.8	IPI:IPI00896110.1	Gene_Symbol=Prdx5 Prdx5 protein	0.896475	-0.15766	0.17745
148	8	8	60.2	IPI:IPI00128346.1	Gene_Symbol=Cisd1 CDGSH iron sulfur domain-containing protein 1	1.226675	0.294753	0.0476
149	8	8	22.8	IPI:IPI00120212.1	Gene_Symbol=Ndufa9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	1.138125	0.186659	0.2204
150	8	8	17.9	IPI:IPI00125220.6	Gene_Symbol=Ctsz Cathepsin Z	1.124975	0.169893	0.16875
151	7.93	7.93	21.9	IPI:IPI00125853.1	Gene_Symbol=Slc25a15 Mitochondrial ornithine transporter 1	1.03145	0.044674	0.77735
152	7.87	8	13	IPI:IPI00420706.4	Gene_Symbol=Lrpprc Leucine-rich PPR motif-containing protein, mitochondrial	1.025875	0.036855	0.6179
153	7.7	7.7	46.3	IPI:IPI00125929.2	Gene_Symbol=Ndufa4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	0.870725	-0.19971	0.02825
154	7.68	7.7	21.8	IPI:IPI00132762.1	Gene_Symbol=Trap1 Heat shock protein 75 kDa, mitochondrial	1.0647	0.090447	0.3885
155	7.26	7.26	65.5	IPI:IPI00130322.5	Gene_Symbol=Ndufa7 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	0.969225	-0.0451	0.2927
156	7.19	7.21	22.8	IPI:IPI00877214.1	Gene_Symbol=Peci peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase isoform a	1.272075	0.347184	0.03125
157	7	7	13.8	IPI:IPI00130627.1	Gene_Symbol=Lgmn Legumain	1.045675	0.064435	0.32585

158	6.93	7.53	10.4	IPI:IPI00221556.2	Gene_Symbol=Acsm5 Isoform 1 of Acyl-coenzyme A synthetase ACSM5, mitochondrial	1.013925	0.019951	0.41985
159	6.77	6.82	23.8	IPI:IPI00895177.1	Gene_Symbol=Cyb5r3 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:2500002N19 product:NADH-CYTOCHROME B5 REDUCTASE homolog	1.050375	0.070904	0.0003
160	6.65	6.65	19.7	IPI:IPI00132728.2	Gene_Symbol=Cyc1 Isoform 1 of Cytochrome c1, heme protein, mitochondrial	1.18665	0.246894	0.09205
161	6.61	6.62	20.8	IPI:IPI00116748.1	Gene_Symbol=Ndufa10 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	1.16915	0.22546	0.0688
162	6.57	6.57	43.2	IPI:IPI00271986.6	Gene_Symbol=Atp5j2 ATP synthase subunit f, mitochondrial	0.9555	-0.06567	NA
163	6.55	6.55	9.5	IPI:IPI00110843.3	Gene_Symbol=Agmat Agmatinase, mitochondrial	0.76225	-0.39166	NA
164	6.52	6.52	15.1	IPI:IPI00850430.1	Gene_Symbol=Slc25a3 LOC100046151 similar to Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	1.083875	0.116198	NA
165	6.42	6.42	26.7	IPI:IPI00337893.2	Gene_Symbol=Pdha1 Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	0.968975	-0.04547	0.0284
166	6.28	6.28	17	IPI:IPI00276926.3	Gene_Symbol=Slc25a1 NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630026H16 product:solute carrier family 25 (mitochondrial carrier	1.176575	0.234593	0.0068

167	6.25	6.41	7.8	IPI:IPI00845652.1	Gene_Symbol=Ogdh Isoform 3 of 2-oxoglutarate dehydrogenase E1 component, mitochondrial	1.001025	0.001478	0.3259
168	6.25	6.25	28.1	IPI:IPI00125325.1	Gene_Symbol=Decr2 Peroxisomal 2,4-dienoyl-CoA reductase	1.644	0.71721	0.0932
169	6.24	6.24	48.7	IPI:IPI00135857.3	Gene_Symbol=Sod1 (BLAST score 313, P = 3e-84) EG667310;LOC545845 hypothetical protein isoform 4	0.9004	-0.15136	0.005767
170	6.18	6.18	21.8	IPI:IPI00753303.2	Gene_Symbol=Dapal (BLAST score: 644, P = 0.0) 0610010D20Rik Dihydrodipicolinate synthase-like, mitochondrial	0.842375	-0.24747	0.1678
171	6.13	6.13	17.8	IPI:IPI00553717.6	Gene_Symbol=Mccc2 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	0.809975	-0.30405	0.14655
172	6.07	6.07	13.2	IPI:IPI00136655.1	Gene_Symbol=Gcat 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	0.905925	-0.14254	0.1279
173	6.03	6.03	14.4	IPI:IPI00400301.2	Gene_Symbol=Cpox Coproporphyrinogen III oxidase, mitochondrial	0.84865	-0.23676	0.0031
174	6.02	6.02	13.1	IPI:IPI00330094.4	Gene_Symbol=Cpt1a Carnitine O-palmitoyltransferase I, liver isoform	1.289775	0.367119	0.0056
175	6.02	6.02	15.4	IPI:IPI00126635.1	Gene_Symbol=Idh3b Tumor-related protein	0.902225	-0.14844	0.0248
176	6.01	6.06	18.6	IPI:IPI00459725.2	Gene_Symbol=Idh3a Isoform 1 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	0.918	-0.12343	0.0866
177	6	6	12.3	IPI:IPI00131177.1	Gene_Symbol=Letm1 LETM1 and EF-hand domain-containing protein 1, mitochondrial	0.90555	-0.14313	0.1925

178	6	6	12.9	IPI:IPI00117214.3	Gene_Symbol=Hsdl2 Hydroxysteroid dehydrogenase-like protein 2	0.9598	-0.05919	0.534067
179	6	6	23.2	IPI:IPI00453777.2	Gene_Symbol=Atp5d ATP synthase subunit delta, mitochondrial	0.852	-0.23107	0.0673
180	6	6	6.5	IPI:IPI00321190.1	Gene_Symbol=Psap Sulfated glycoprotein 1	1.07115	0.099161	NA
181	6	6	13.1	IPI:IPI00170307.1	Gene_Symbol=Apoa1bp Apolipoprotein A-I-binding protein	1.01765	0.025241	0.7585
182	6	6	42.1	IPI:IPI00134484.1	Gene_Symbol=Timm10;Timm13 Mitochondrial import inner membrane translocase subunit Tim13	0.708925	-0.4963	0.0849
183	5.7	5.7	44.5	IPI:IPI00881750.1	Gene_Symbol=Ndufb5 14 kDa protein	1.11715	0.159823	0.3236
184	5.52	5.52	59.2	IPI:IPI00886222.1	Gene_Symbol=Ndufs6 11 kDa protein	0.979575	-0.02977	0.28
185	5.5	5.5	27.3	IPI:IPI00607025.2	Gene_Symbol=Amacr 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:2510003N10 product:alpha-methylacyl-CoA racemase, full insert sequence	1.11295	0.154389	NA
186	5.44	5.44	23.3	IPI:IPI00131584.1	Gene_Symbol=Slc25a20 Mitochondrial carnitine/acylcarnitine carrier protein	1.1764	0.234379	NA
187	5.4	5.4	38.6	IPI:IPI00120451.1	Gene_Symbol=Fabp1 Fatty acid-binding protein, liver	1.217875	0.284366	0.20105
188	5.34	5.45	48.6	IPI:IPI00120719.4	Gene_Symbol=Cox5a Cytochrome c oxidase subunit 5A, mitochondrial	0.931475	-0.10241	0.04415
189	5.26	5.35	25.4	IPI:IPI00169925.2	Gene_Symbol=Ndufv2 Isoform 1 of NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	1.068875	0.096093	0.22445

190	5.22	5.22	12.5	IPI:IPI00760085.1	Gene_Symbol=Agxt Isoform Peroxisomal of Serine--pyruvate aminotransferase, mitochondrial	0.961675	-0.05638	NA
191	5.01	5.01	11.2	IPI:IPI00461197.1	Gene_Symbol=Ldhd 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4733401P21 product:weakly similar to PUTATIVE D-LACTATE DEHYDROGENASE (CYTOCHROME) OXIDOREDUCTASE PROTEIN	1.039375	0.055716	NA
192	5	5	19.1	IPI:IPI00894832.1	Gene_Symbol=Ctsc Adult male kidney cDNA, RIKEN full-length enriched library, clone:0610010C21 product:cathepsin C, full insert sequence	1.132975	0.180116	NA
193	4.96	4.96	8.7	IPI:IPI00124372.3	Gene_Symbol=Aldh9a1 aldehyde dehydrogenase 9, subfamily A1	0.923	-0.1156	0.2909
194	4.92	4.92	29	IPI:IPI00387430.1	Gene_Symbol=Ndufb8 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	0.99785	-0.00311	NA
195	4.92	4.92	27.6	IPI:IPI00378120.2	Gene_Symbol=Glrx5 Glutaredoxin-related protein 5	0.97935	-0.0301	NA
196	4.9	4.93	24.9	IPI:IPI00895984.1	Gene_Symbol=Mup1 Major urinary protein 1	1.77775	0.830052	NA
197	4.58	4.58	10.8	IPI:IPI00658539.1	Gene_Symbol=Ctsa cathepsin A isoform a	1.4081	0.49375	NA
198	4.57	4.57	14.6	IPI:IPI00265352.1	Gene_Symbol=Gpt2 Alanine aminotransferase 2	0.82665	-0.27465	0.0612
199	4.55	4.55	36	IPI:IPI00120984.5	Gene_Symbol=Ndufa8 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	0.5566	-0.84529	#DIV/0!

200	4.55	4.55	54.9	IPI:IPI00224210.5	Gene_Symbol=Uqcrq Cytochrome b-c1 complex subunit 8	0.9077	-0.13971	NA
201	4.49	4.49	22.7	IPI:IPI00874574.1	Gene_Symbol=Clybl 36 kDa protein	0.7923	-0.33588	NA
202	4.36	4.36	17.3	IPI:IPI00648829.1	Gene_Symbol=Nipsnap3a Nipsnap homolog 3A	0.8607	-0.21642	NA
203	4.3	4.31	14.6	IPI:IPI00320850.3	Gene_Symbol=Mccc1 Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	0.9	-0.152	0.0449
204	4.25	4.69	8.3	IPI:IPI00751137.1	Gene_Symbol=Tomm70a Adult male thymus cDNA, RIKEN full-length enriched library, clone:5830412L10 product:Mitochondrial proteins import receptor (Translocase of outer membrane TOM70), full insert sequence	1.11425	0.156073	NA
205	4.23	4.23	19.1	IPI:IPI00133270.1	Gene_Symbol=Clpp Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	0.917625	-0.12402	0.4648
206	4.17	4.17	18.3	IPI:IPI00120232.1	Gene_Symbol=Ndufs7 NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	1.13375	0.181103	NA
207	4.16	4.2	7.4	IPI:IPI00621548.2	Gene_Symbol=Por NADPH--cytochrome P450 reductase	0.80895	-0.30588	NA
208	4.15	6.15	10.8	IPI:IPI00153143.1	Gene_Symbol=Ugt2b1 UDP glucuronosyltransferase 2 family, polypeptide B1	0.90955	-0.13678	0.0798
209	4.15	4.15	14.6	IPI:IPI00762346.1	Gene_Symbol=Aadat Kynurenine/alpha-aminoadipate aminotransferase mitochondrial	1.11405	0.155814	NA

210	4.11	4.13	20.1	IPI:IPI00133240.1	Gene_Symbol=Uqcrfs1 Cytochrome b-c1 complex subunit Rieske, mitochondrial	0.97105	-0.04238	NA
211	4.1	4.1	25.7	IPI:IPI00230715.5	Gene_Symbol=Ndufa13 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	1.20045	0.263575	NA
212	4.09	4.17	23.6	IPI:IPI00119945.1	Gene_Symbol=Nit2 Nitrilase homolog 2	0.984275	-0.02287	NA
213	4.07	4.07	17.9	IPI:IPI00170093.3	Gene_Symbol=Ndufs8 NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	0.94275	-0.08505	NA
214	4.03	4.03	43	IPI:IPI00880613.1	Gene_Symbol=Ndufb10 18 kDa protein	1.02315	0.033018	NA
215	4.03	4.03	33	IPI:IPI00132623.3	Gene_Symbol=Ndufb9 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	0.826975	-0.27408	0.0572
216	4.02	4.02	27.1	IPI:IPI00133284.1	Gene_Symbol= (BLAST score: 530, P = 1e-149) D10Jhu81e;LOC100046684 ES1 protein homolog, mitochondrial	0.9155	-0.12737	0.1868
217	4	4.01	8.2	IPI:IPI00128287.1	Gene_Symbol=Cyp1a2 Cytochrome P450 1A2	1.03955	0.055959	0.0452
218	4	4	7.1	IPI:IPI00127267.4	Gene_Symbol=Gldc Glycine dehydrogenase [decarboxylating], mitochondrial	0.939	-0.0908	0.1823
219	4	4	12.2	IPI:IPI00831119.1	Gene_Symbol=Lypla1 21 kDa protein	0.93055	-0.10384	NA
220	4	4	22.7	IPI:IPI00125776.1	Gene_Symbol=ENSMUSG00000045455;Timm8a1 Mitochondrial import inner membrane translocase subunit Tim8 A	0.654975	-0.61049	0.0963
221	3.99	3.99	18	IPI:IPI00129963.1	Gene_Symbol=Phyh Phytanoyl-CoA dioxygenase, peroxisomal	1.19925	0.262132	NA

222	3.95	3.95	10.3	IPI:IPI00828822.2	Gene_Symbol=Es31 Isoform 2 of Liver carboxylesterase 31	1.178475	0.236921	NA
223	3.86	3.86	25.8	IPI:IPI00230754.5	Gene_Symbol=Slc25a11 Mitochondrial 2-oxoglutarate/malate carrier protein	1.052325	0.07358	NA
224	3.81	3.86	15.1	IPI:IPI00273164.1	Gene_Symbol=Aldh5a1 Succinate-semialdehyde dehydrogenase, mitochondrial	0.8826	-0.18017	0.0182
225	3.7	3.7	29.1	IPI:IPI00875372.1	Gene_Symbol=Echdc2 Isoform 2 of Enoyl-CoA hydratase domain-containing protein 2, mitochondrial	0.946275	-0.07967	NA
226	3.7	3.7	24.9	IPI:IPI00125267.4	Gene_Symbol=Vapa Vesicle-associated membrane protein-associated protein A	1.221025	0.288093	NA
227	3.62	3.62	22.2	IPI:IPI00130640.5	Gene_Symbol=Hrsp12 Ribonuclease UK114	0.94755	-0.07773	NA
228	3.52	3.52	6.2	IPI:IPI00606097.1	Gene_Symbol=Tmprss13 transmembrane protease, serine 13	1.206375	0.270678	0.025
229	3.44	3.44	7.7	IPI:IPI00554830.2	Gene_Symbol=Gulo L-gulonolactone oxidase	1.3087	0.388134	0.0881
230	3.41	3.41	14.2	IPI:IPI00648852.2	Gene_Symbol=Ppt1 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920018O12 product:palmitoyl-protein thioesterase 1, full insert sequence	1.24245	0.313188	NA
231	3.38	3.38	9.2	IPI:IPI00126634.1	Gene_Symbol=Poldip2 Polymerase delta-interacting protein 2	0.9095	-0.13685	0.0139
232	3.34	3.34	28.8	IPI:IPI00855212.1	Gene_Symbol=1110020G09Rik Isoform 2 of UPF0465 protein C5orf33 homolog	0.88365	-0.17845	NA

233	3.3	4.2	5.8	IPI:IPI00222968.1	Gene_Symbol=Lamp2 Isoform LAMP-2C of Lysosome-associated membrane glycoprotein 2	1.361775	0.445488	NA
234	3.29	3.32	18	IPI:IPI00109275.1	Gene_Symbol=Slc25a22 Mitochondrial glutamate carrier 1	1.0522	0.073409	NA
235	3.25	3.26	10.6	IPI:IPI00788396.1	Gene_Symbol=Clpx caseinolytic protease X isoform 2	1.06815	0.095114	NA
236	3.22	6.44	19.4	IPI:IPI00876341.1	Gene_Symbol=Vdac3 Voltage-dependent anion-selective channel protein 3	1.4952	0.580338	NA
237	3.04	3.64	32.8	IPI:IPI00116896.1	Gene_Symbol=mt-Atp8 ATP synthase protein 8	1.0048	0.006908	NA
238	2.96	11.33	27.4	IPI:IPI00122139.3	Gene_Symbol=Acaa1b;Acaa1a 3-ketoacyl-CoA thiolase B, peroxisomal	1.878575	0.909639	NA
239	2.96	2.99	45.1	IPI:IPI00111770.7	Gene_Symbol=Atp5k ATP synthase subunit e, mitochondrial	0.804125	-0.31451	0.0103
240	2.92	2.92	17.3	IPI:IPI00133403.1	Gene_Symbol=Ndufb3 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	1.062925	0.08804	NA
241	2.89	2.89	32.8	IPI:IPI00133399.1	Gene_Symbol=Ndufa6 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	0.99485	-0.00745	NA
242	2.86	2.86	4.1	IPI:IPI00886014.1	Gene_Symbol=Acss3 Isoform 1 of Acyl-CoA synthetase short-chain family member 3, mitochondrial	0.965475	-0.05069	NA
243	2.8	2.8	6.2	IPI:IPI00889240.1	Gene_Symbol=Adhfe1 Isoform 2 of Hydroxyacid-oxoacid transhydrogenase, mitochondrial	1.0576	0.080794	NA
244	2.7	2.72	5.8	IPI:IPI00221608.3	Gene_Symbol=Samm50 Sorting and assembly machinery component 50 homolog	1.371975	0.456254	NA

245	2.62	2.62	12.9	IPI:IPI00125266.1	Gene_Symbol=Asah1 Acid ceramidase	1.067325	0.094	NA
246	2.5	2.5	10.7	IPI:IPI00137491.1	Gene_Symbol=Acp5 Tartrate-resistant acid phosphatase type 5	1.251875	0.324091	NA
247	2.42	2.42	9.2	IPI:IPI00274222.2	Gene_Symbol=Acad8 Isobutyryl-CoA dehydrogenase, mitochondrial	1.2061	0.27035	NA
248	2.37	2.37	3.9	IPI:IPI00111960.2	Gene_Symbol=Gaa Lysosomal alpha-glucosidase	1.05115	0.071969	NA
249	2.35	2.37	19.2	IPI:IPI00662861.1	Gene_Symbol=LOC635087 similar to NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	1.21915	0.285876	NA
250	2.33	2.33	7.9	IPI:IPI00874376.1	Gene_Symbol=Apool 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810024N24 product:hypothetical protein, full insert sequence	1.3363	0.418244	NA
251	2.25	2.25	9.4	IPI:IPI00170126.4	Gene_Symbol=Pitrm1 Isoform 1 of Presequence protease, mitochondrial	0.941825	-0.08647	NA
252	2.22	2.22	7.5	IPI:IPI00131176.1	Gene_Symbol=mt-Co2 Cytochrome c oxidase subunit 2	1.254975	0.327659	NA
253	2.21	2.21	24.4	IPI:IPI00222430.5	Gene_Symbol=Dbi diazepam binding inhibitor isoform 1	0.7018	-0.51087	NA
254	2.2	2.2	14.3	IPI:IPI00229008.2	Gene_Symbol=Ndufs4 NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	0.774075	-0.36945	NA
255	2.19	4.19	13.7	IPI:IPI00762185.2	Gene_Symbol=Mpst 3-mercaptopyruvate sulfurtransferase	0.9665	-0.04916	NA
256	2.17	2.17	7.8	IPI:IPI00855011.1	Gene_Symbol=LOC100046998 similar to optic atrophy 1	0.8715	-0.19843	NA

257	2.15	2.15	7.8	IPI:IPI00387282.4	Gene_Symbol=Aadac Arylacetamide deacetylase	1.47755	0.563207	NA
258	2.15	2.15	15	IPI:IPI00317074.3	Gene_Symbol=Slc25a10 Mitochondrial dicarboxylate carrier	1.244575	0.315653	NA
259	2.11	2.11	18.6	IPI:IPI00128023.3	Gene_Symbol=Ndufs2 NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	0.82805	-0.27221	NA
260	2.11	2.11	6.4	IPI:IPI00109169.1	Gene_Symbol=Idh3g Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	0.876825	-0.18964	NA
261	2.09	2.09	8.9	IPI:IPI00121218.5	Gene_Symbol=Fahd2a Fumarylacetoacetate hydrolase domain-containing protein 2A	1.01175	0.016853	NA
262	2.08	2.09	11.2	IPI:IPI00895479.1	Gene_Symbol=2810422J05Rik 27 kDa protein (Ubiquitin)	1.3855	0.470407	NA
263	2.08	2.08	18.1	IPI:IPI00133411.1	Gene_Symbol=Fam136a (BLAST score:280, P =2e-74) 2010309E21Rik Protein FAM136A	0.83045	-0.26803	NA
264	2.07	2.07	4.9	IPI:IPI00653566.1	Gene_Symbol=Acot2 Activated spleen cDNA, RIKEN full-length enriched library, clone:F830219O19 product:mitochondrial acyl-CoA thioesterase 1, full insert sequence	1.18165	0.240803	NA
265	2.05	2.05	7.1	IPI:IPI00122634.1	Gene_Symbol=Cyp2a12 Cytochrome P450, family 2, subfamily a, polypeptide 12	1.274275	0.349677	NA
266	2.05	2.05	12.1	IPI:IPI00132958.1	Gene_Symbol=Them2 Thioesterase superfamily member 2	1.020175	0.028817	NA
267	2.04	2.04	12.4	IPI:IPI00475322.1	Gene_Symbol=Msra Msra protein	1.10895	0.149194	NA
268	2.02	2.06	14.7	IPI:IPI00556699.1	Gene_Symbol=Gcsh Putative uncharacterized protein	0.94935	-0.07499	NA

269	2.02	2.03	5.6	IPI:IPI00845617.1	Gene_Symbol=Plbl1 (Putative phospholipase B-like 1, BLAST score: 1096, P =0.0) LOC100045163 similar to RIKEN cDNA 1100001H23 gene	1.22775	0.296017	NA
270	2.02	2.02	7.9	IPI:IPI00133877.1	Gene_Symbol=Cyp4a14 Cytochrome P450 4A14	1.1594	0.213378	NA
271	2.01	2.01	14.8	IPI:IPI00114866.1	Gene_Symbol=Mlycd Isoform Mitochondrial of Malonyl-CoA decarboxylase, mitochondrial	1.1877	0.24817	NA
272	2	4.25	17.8	IPI:IPI00135231.2	Gene_Symbol=Idh1 0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030024J03 product:isocitrate dehydrogenase 1 (NADP+), soluble, full insert sequence	1.074525	0.103699	NA
273	2	4	8.8	IPI:IPI00762478.1	Gene_Symbol=Acsm3 Isoform 1 of Acyl-coenzyme A synthetase ACSM3, mitochondrial	1.130275	0.176674	NA
274	2	2.33	4.9	XXXXXIPI:IPI00653	RANDOMIZED Gene_Symbol=Mfn1 Mitofusin-1	1.2749	0.350384	NA
275	2	2.02	6.7	IPI:IPI00274656.6	Gene_Symbol=Pmpcb Mitochondrial-processing peptidase subunit beta	0.88855	-0.17048	NA
276	2	2	14.4	IPI:IPI00118963.1	Gene_Symbol=Mrpl12 39S ribosomal protein L12, mitochondrial	0.896675	-0.15734	NA
277	2	2	21.9	IPI:IPI00114246.2	Gene_Symbol=Ndufb11 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	0.921925	-0.11728	NA
278	2	2	2.3	IPI:IPI00355248.5	Gene_Symbol=mt-Co1 cytochrome c oxidase subunit I	1.303575	0.382474	NA

279	2.68	2.68	17.3	IPI:IPI00608064.1	Gene_Symbol=Fech Fech protein (Fragment)	[redacted]
280	2.07	2.07	19.4	IPI:IPI00331322.3	Gene_Symbol=Mgst1 Microsomal glutathione S-transferase 1	[redacted]
281	2.13	2.13	15	IPI:IPI00115117.1	Gene_Symbol=Stoml2 Stomatin-like protein 2	[redacted]
282	2.04	3.35	16.9	IPI:IPI00319973.3	Gene_Symbol=Pgrmc1 Membrane-associated progesterone receptor component 1	[redacted]
283	7.65	7.65	21.2	IPI:IPI00331436.4	Gene_Symbol=Lap3 Isoform 1 of Cytosol aminopeptidase	[redacted]
284	2.36	2.36	11.1	IPI:IPI00877288.1	Gene_Symbol=Pgcp Isoform 2 of Plasma glutamate carboxypeptidase	[redacted]
285	2.09	2.09	11.7	IPI:IPI00457825.2	Gene_Symbol=- 47 kDa protein	[redacted]
286	2.27	2.27	22	IPI:IPI00127227.2	Gene_Symbol=Cbr4 Carbonyl reductase 4	[redacted]
287	14.61	14.61	32.5	IPI:IPI00903424.1	Gene_Symbol=Prss3 Adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010010O17 product:Trypsinogen 16 homolog	[redacted]
288	12.38	12.38	34	IPI:IPI00121833.3	Gene_Symbol=Acaa1b;Acaa1a 3-ketoacyl-CoA thiolase A, peroxisomal	[redacted]
289	7	7	31.3	IPI:IPI00831055.2	Gene_Symbol=- Beta-globin	[redacted]
290	6	6	26.2	IPI:IPI00132799.4	Gene_Symbol=C1qbp complement component 1, q subcomponent binding protein	[redacted]
291	5.32	5.32	13.9	IPI:IPI00123639.1	Gene_Symbol=Calr Calreticulin	[redacted]
292	4.8	4.8	4.7	IPI:IPI00271951.5	Gene_Symbol=Pdia4 protein disulfide isomerase associated 4	[redacted]

293	4.53	4.57	13	IPI:IPI00129526.1	Gene_Symbol=Hsp90b1 Endoplasmin	[redacted]
294	4.5	4.54	28.5	IPI:IPI00652845.3	Gene_Symbol=Pecr In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420405J16 product:peroxisomal trans-2-enoyl-CoA reductase, full insert sequence	[redacted]
295	4.36	7.88	16.7	IPI:IPI00875511.1	Gene_Symbol=Mosc1 MOCO sulphurase C-terminal domain containing 1	[redacted]
296	4	10.6	12.6	IPI:IPI00759953.1	Gene_Symbol=1810049H19Rik;Try4 Tesp4 protein	[redacted]
297	4	4	14.3	IPI:IPI00881534.1	Gene_Symbol=Ppa2 38 kDa protein	[redacted]
298	3.08	3.08	11.6	IPI:IPI00133108.1	Gene_Symbol=Klk5 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110030O19 product:similar to Kallikrein 5	[redacted]
299	2.89	8.89	21.1	IPI:IPI00403650.2	Gene_Symbol=Prss2 Anionic trypsin-2	[redacted]
300	2.89	2.89	11	IPI:IPI00222767.1	Gene_Symbol=Pdhx Pyruvate dehydrogenase protein X component, mitochondrial	[redacted]
301	2.67	2.7	14.7	IPI:IPI00409412.3	Gene_Symbol=Cyp2c67 Cytochrome P450, family 2, subfamily c, polypeptide 67	[redacted]
302	2.41	2.41	12.3	IPI:IPI00128154.1	Gene_Symbol=Ctsl Cathepsin L1	[redacted]
303	2.34	2.34	25.7	IPI:IPI00762203.2	Gene_Symbol=Ftl1 Ferritin light chain 1	[redacted]
304	2.34	2.34	4.7	IPI:IPI00761390.1	Gene_Symbol=Slc27a2 solute carrier family 27 (fatty acid transporter), member 2	[redacted]

305	2.3	2.35	5.9	IPI:IPI00309035.2	Gene_Symbol=Rpn1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	[redacted]
306	2.3	2.3	44.2	IPI:IPI00230241.6	Gene_Symbol=Atp5e ATP synthase subunit epsilon, mitochondrial	[redacted]
307	2.29	2.29	67.5	IPI:IPI00114377.1	Gene_Symbol=Cox7a2 Cytochrome c oxidase polypeptide 7A2, mitochondrial	[redacted]
308	2.23	2.25	3.1	IPI:IPI00848562.1	Gene_Symbol=Ubr4 retinoblastoma-associated factor 600 isoform 2	[redacted]
309	2.15	2.15	12.4	IPI:IPI00753211.1	Gene_Symbol=Echdc3 Enoyl Coenzyme A hydratase domain containing 3	[redacted]
310	2.13	3.84	6.1	IPI:IPI00756257.1	Gene_Symbol=Ttn Isoform 1 of Titin	[redacted]
311	2.12	2.12	2.6	XXXXXIPI:IPI00788	RANDOMIZED Gene_Symbol=Usp48 Isoform 1 of Ubiquitin carboxyl-terminal hydrolase 48	[redacted]
312	2.06	2.15	16.9	IPI:IPI00129516.1	Gene_Symbol=Uqcrh Cytochrome b-c1 complex subunit 6, mitochondrial	[redacted]
313	2.05	2.05	13	IPI:IPI00115454.3	Gene_Symbol=Sfxn1 Sideroflexin-1	[redacted]
314	2.04	2.05	9.3	IPI:IPI00134504.1	Gene_Symbol=Cyp3a11 Cytochrome P450 3A11	[redacted]

B) 28

NO.	UNUSED	TOTAL	% COV	ACCESSION	NAME	AVG FOLD CHANGE	LOG_2	P-VALUE
1	183.93	183.93	64.4	IPI:IPI00111908.8	Gene_Symbol=Cps1 Carbamoyl-phosphate synthase [ammonia], mitochondrial	1.226375	0.2944	0
2	53.16	53.17	43.5	IPI:IPI00114710.2	Gene_Symbol=Pcx Activated spleen cDNA, RIKEN full-length enriched library, clone:F830201B12 product:pyruvate carboxylase, full insert sequence	1.44945	0.535506	0
3	50.83	50.83	51.6	IPI:IPI00114209.1	Gene_Symbol=Glud1 Glutamate dehydrogenase 1, mitochondrial	1.2509	0.322966	0.00145
4	49.94	49.94	65.5	IPI:IPI00869393.1	Gene_Symbol=Cat catalase	0.4346	-1.20224	0
5	48.03	48.03	56.8	IPI:IPI00461964.3	Gene_Symbol=Aldh6a1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	1.071325	0.099396	0.0278
6	47.61	47.61	51.7	IPI:IPI00880839.1	Gene_Symbol=Hspa9 heat shock protein 9	1.1265	0.171847	0.002933333
7	46.26	46.26	49	IPI:IPI00554834.2	Gene_Symbol=Ehhadh Peroxisomal bifunctional enzyme	0.3947	-1.34117	0
8	46.18	46.18	45.9	IPI:IPI00111218.1	Gene_Symbol=Aldh2 Aldehyde dehydrogenase, mitochondrial	1.0302	0.042924	0.0592
9	45.37	45.37	47.3	IPI:IPI00223092.5	Gene_Symbol=Hadha Trifunctional enzyme subunit alpha, mitochondrial	0.9273	-0.10889	0.0255
10	43.42	43.42	39	IPI:IPI00120123.1	Gene_Symbol=Dmgdh Dimethylglycine dehydrogenase, mitochondrial	1.071725	0.099935	0.0224
11	43.03	43.03	52.2	IPI:IPI00420718.4	Gene_Symbol=Hmgcs2 Hydroxymethylglutaryl-CoA synthase, mitochondrial	0.99225	-0.01122	0.1694
12	41.56	41.56	64.1	IPI:IPI00468481.2	Gene_Symbol=Atp5b ATP synthase subunit beta, mitochondrial	1.06205	0.086852	0.0451
13	40.72	40.72	56.7	IPI:IPI00117312.1	Gene_Symbol=Got2 Aspartate aminotransferase, mitochondrial	1.1201	0.163628	0.002825
14	39.24	39.24	63.3	IPI:IPI00129178.1	Gene_Symbol=Oat Ornithine aminotransferase, mitochondrial	1.040925	0.057866	0.1265
15	38.89	38.89	56	IPI:IPI00308885.6	Gene_Symbol=Hspd1 Isoform 1 of 60 kDa heat shock protein, mitochondrial	1.138475	0.187103	0.001633333
16	36.49	36.49	49.9	IPI:IPI00130280.1	Gene_Symbol=Atp5a1 ATP synthase subunit alpha, mitochondrial	1.054125	0.076046	0.066533333

17	35.03	35.03	61.5	IPI:IPI00653158.1	Gene_Symbol=Acaa2 Acetyl-Coenzyme A acyltransferase 2 (Mitochondrial 3-oxoacyl-Coenzyme A thiolase), isoform CRA_k	1.009375	0.013462	0.7941
18	34.83	34.83	59.1	IPI:IPI00223367.5	Gene_Symbol=Uox Uricase	0.553375	-0.85367	0
19	34.1	34.1	43.9	IPI:IPI00828479.1	Gene_Symbol=Acox1 Acyl-Coenzyme A oxidase 1, palmitoyl	0.560325	-0.83566	0.00015
20	33	33	40.9	IPI:IPI00119203.4	Gene_Symbol=Acadvl Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	1.096625	0.13307	0.00685
21	32.28	32.28	40.8	IPI:IPI00875638.1	Gene_Symbol=Immt Isoform 3 of Mitochondrial inner membrane protein	1.037	0.052416	0.1641
22	31.96	31.97	50.1	IPI:IPI00459487.3	Gene_Symbol=Suclg2 Isoform 1 of Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	1.050225	0.070698	0.0701
23	31.15	31.16	56.8	IPI:IPI00154054.1	Gene_Symbol=Acat1 Acetyl-CoA acetyltransferase, mitochondrial	0.951075	-0.07237	0.073333333
24	30.62	30.62	35.4	IPI:IPI00115607.3	Gene_Symbol=Hadhb Trifunctional enzyme subunit beta, mitochondrial	0.99545	-0.00658	0.4414
25	29.71	29.71	40.3	IPI:IPI00121322.2	Gene_Symbol=Etfdh Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	1.01885	0.026942	0.3831
26	29.63	29.63	25.7	IPI:IPI00387491.1	Gene_Symbol=Aass Alpha-aminoadipic semialdehyde synthase, mitochondrial	1.32005	0.400593	0.001233333
27	29.36	29.36	33.9	IPI:IPI00261627.1	Gene_Symbol=Sucla2 Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	1.091375	0.126147	0.06155
28	28.47	28.47	38.5	IPI:IPI00116074.1	Gene_Symbol=Aco2 Aconitate hydratase, mitochondrial	1.08195	0.113634	0.06465
29	28.24	28.24	24.9	IPI:IPI00134131.2	Gene_Symbol=Scp2 Isoform SCPx of Non-specific lipid-transfer protein	0.5737	-0.80163	0
30	28.08	28.08	33.7	IPI:IPI00331628.5	Gene_Symbol=Hsd17b4 Peroxisomal multifunctional enzyme type 2	0.51495	-0.9575	0
31	27.76	27.76	33.9	IPI:IPI00136213.5	Gene_Symbol=Sardh Sarcosine dehydrogenase, mitochondrial	1.064825	0.090616	0.0201
32	27.2	27.39	40.9	IPI:IPI00894588.1	Gene_Symbol=Acadl Long-chain specific acyl-CoA dehydrogenase, mitochondrial	1.03285	0.046631	0.3924
33	26.25	26.25	33.3	IPI:IPI00122633.3	Gene_Symbol=Acsf2 Acyl-CoA synthetase family member 2, mitochondrial	1.017675	0.025277	0.2405
34	26.15	26.15	38.7	IPI:IPI00776257.1	Gene_Symbol=Otc Otc protein	1.0244	0.034779	0.0478
35	25.34	25.36	48.2	IPI:IPI00323592.2	Gene_Symbol=Mdh2 Malate dehydrogenase, mitochondrial	1.10195	0.140059	0.02095

36	25.18	25.18	46.6	IPI:IPI00119138.1	Gene_Symbol=Uqcrc2 Cytochrome b-c1 complex subunit 2, mitochondrial	1.03985	0.056375	0.0416
37	24.48	24.48	29.2	IPI:IPI00857226.1	Gene_Symbol=Acsl1 78 kDa protein	0.731225	-0.45161	0.000075
38	23.43	23.43	75.3	IPI:IPI00221769.5	Gene_Symbol=Ak3 GTP:AMP phosphotransferase mitochondrial	1.095575	0.131688	0.0242
39	23.13	23.13	37.5	IPI:IPI00405699.2	Gene_Symbol=Aldh4a1 Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	1.087	0.120352	0.0039
40	22.18	22.18	43.4	IPI:IPI00331251.1	Gene_Symbol=Acads Acyl-Coenzyme A dehydrogenase, short chain, isoform CRA_a	1.045975	0.064848	0.0478
41	20.92	21	26.3	IPI:IPI00553576.3	Gene_Symbol=Abcd3 ATP-binding cassette, sub-family D, member 3	0.55555	-0.84801	0.000275
42	20.57	20.57	41.9	IPI:IPI00127841.3	Gene_Symbol=Slc25a5 ADP/ATP translocase 2	1.1159	0.158208	0.02835
43	20.5	20.5	50.8	IPI:IPI00223216.5	Gene_Symbol=Tst Thiosulfate sulfurtransferase	1.09625	0.132577	0.03225
44	20.33	20.33	30.1	IPI:IPI00133522.1	Gene_Symbol=P4hb Protein disulfide-isomerase	0.64545	-0.63162	0.000075
45	20	20	23.9	IPI:IPI00129928.2	Gene_Symbol=Fh1 Isoform Mitochondrial of Fumarate hydratase, mitochondrial	1.142025	0.191594	0.0398
46	19.9	19.91	47.9	IPI:IPI00454049.4	Gene_Symbol=Echs1 Enoyl-CoA hydratase, mitochondrial	1.1311	0.177726	0.0293
47	19.76	19.77	54.3	IPI:IPI00848492.1	Gene_Symbol=LOC100045699 similar to Electron transferring flavoprotein, beta polypeptide isoform 2	1.0153	0.021906	0.0412
48	19.55	19.55	38	IPI:IPI00134961.1	Gene_Symbol=Acadm Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	0.9922	-0.0113	0.085
49	19.08	19.1	54	IPI:IPI00648318.1	Gene_Symbol=Ak2 Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730019E03 product:ADENYLATE KINASE 2 homolog	1.000925	0.001334	0.1762
50	19.08	19.08	45.2	IPI:IPI00154047.1	Gene_Symbol=Hibch 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	1.200925	0.264146	0.1157
51	19.06	19.07	36	IPI:IPI00121105.2	Gene_Symbol=Hadh Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	0.99355	-0.00934	0.0832
52	18.6	18.6	53.8	IPI:IPI00116753.4	Gene_Symbol=Etfa Electron transfer flavoprotein subunit alpha, mitochondrial	1.066325	0.092647	0.027
53	18.45	18.45	29.7	IPI:IPI00135651.1	Gene_Symbol=Slc25a13 Calcium-binding mitochondrial carrier protein Aralar2	1.07585	0.105477	0.0841
54	18.42	18.42	32.5	IPI:IPI00471246.2	Gene_Symbol=Ivd Isovaleryl-CoA dehydrogenase, mitochondrial	1.046025	0.064917	0.11625

55	18.29	18.29	28.5	IPI:IPI00881091.1	Gene_Symbol=Ctsd Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830005I10 product:cathepsin D, full insert sequence	0.830375	-0.26817	0.01455
56	17.66	17.66	45.6	IPI:IPI00129056.2	Gene_Symbol=Glyat Isoform 1 of Glycine N-acyltransferase	1.20295	0.266577	0.01005
57	17.56	17.56	24.2	IPI:IPI00226140.5	Gene_Symbol=Maob Amine oxidase [flavin-containing] B	1.0506	0.071213	0.0654
58	17.35	17.36	22.1	IPI:IPI00308882.4	Gene_Symbol=Ndufs1 NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	1.054175	0.076114	0.0583
59	17.09	17.1	31.2	IPI:IPI00230351.1	Gene_Symbol=Sdha Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	1.1603	0.214498	0.1472
60	16.76	16.76	25.9	IPI:IPI00625588.1	Gene_Symbol=- hypothetical protein	1.1344	0.181929	0.0722
61	16.62	16.62	36.7	IPI:IPI00130535.1	Gene_Symbol=Dbt Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	1.054425	0.076456	0.036
62	16.53	16.61	28.8	IPI:IPI00126625.1	Gene_Symbol=Acsm1 Isoform 1 of Acyl-coenzyme A synthetase ACSM1, mitochondrial	1.118875	0.162049	0.03645
63	16.23	16.23	47.4	IPI:IPI00133440.1	Gene_Symbol=Phb Prohibitin	1.082625	0.114534	0.0296
64	16.12	16.14	33.8	IPI:IPI00468653.3	Gene_Symbol=Pccb Propionyl Coenzyme A carboxylase, beta polypeptide	1.168175	0.224256	0.0211
65	16.11	16.11	24.9	IPI:IPI00330523.1	Gene_Symbol=Pcca Propionyl-CoA carboxylase alpha chain, mitochondrial	1.03835	0.054293	0.2283
66	15.86	15.86	45.8	IPI:IPI00320462.4	Gene_Symbol=Bphl Putative uncharacterized protein	1.034775	0.049317	0.38415
67	15.78	15.85	29.9	IPI:IPI00881401.1	Gene_Symbol=Cpt2 carnitine palmitoyltransferase 2	1.0996	0.136979	0.2824
68	15.7	15.71	17.9	IPI:IPI00850737.1	Gene_Symbol=Mut TIB-55 BB88 cDNA, RIKEN full-length enriched library, clone:I730049G19 product:methylmalonyl-Coenzyme A mutase, full insert sequence	1.132475	0.179479	0.0554
69	15.68	15.69	35.8	IPI:IPI00387379.1	Gene_Symbol=Decr1 2,4-dienoyl-CoA reductase, mitochondrial	0.9821	-0.02606	0.3025
70	15.46	15.46	62.5	IPI:IPI00623553.1	Gene_Symbol=Atp5h LOC100044492;ENSMUSG00000068706 hypothetical protein	0.969375	-0.04487	0.3089
71	15.22	15.22	24.6	IPI:IPI00113141.1	Gene_Symbol=Cs Citrate synthase, mitochondrial	1.016025	0.022936	0.18755
72	15.08	15.08	30.9	IPI:IPI00322760.7	Gene_Symbol=Prodh proline dehydrogenase	1.00915	0.013141	0.1901
73	14.93	14.93	44.1	IPI:IPI00321718.4	Gene_Symbol=Phb2 Prohibitin-2	1.05535	0.077722	0.24995

74	14.83	14.83	30.4	IPI:IPI00230540.1	Gene_Symbol=Vdac1 Isoform Mt-VDAC1 of Voltage-dependent anion-selective channel protein 1	1.081625	0.1132	0.045
75	14.73	14.73	20.3	IPI:IPI00316314.1	Gene_Symbol=Hacl1 2-hydroxyacyl-CoA lyase 1	0.59585	-0.74698	0.0288
76	14.68	14.68	32.8	IPI:IPI00341282.2	Gene_Symbol=Atp5f1 ATP synthase subunit b, mitochondrial	0.90935	-0.13709	0.07345
77	14.61	14.61	32.5	IPI:IPI00903424.1	Gene_Symbol=Prss3 Adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010010O17 product:Trypsinogen 16 homolog	[redacted]	[redacted]	
78	14.57	14.57	52.7	IPI:IPI00117978.1	Gene_Symbol=Cox4i1 Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	1.118625	0.161726	0.0431
79	14.55	14.56	40.5	IPI:IPI00331692.1	Gene_Symbol=Dci Putative uncharacterized protein	1.0077	0.011066	0.5725
80	14.55	14.55	51.6	IPI:IPI00118986.1	Gene_Symbol=Atp5o;LOC100047429 ATP synthase subunit O, mitochondrial	1.029625	0.042119	0.263
81	14.49	14.53	76.2	IPI:IPI00222419.5	Gene_Symbol=ENSMUSG00000058927;Cycs Cytochrome c, somatic	1.154675	0.207487	0.15395
82	14.36	14.36	86.3	IPI:IPI00263863.8	Gene_Symbol=Hspe1 10 kDa heat shock protein, mitochondrial	1.112375	0.153643	0.36535
83	14.26	14.26	27	IPI:IPI00132042.1	Gene_Symbol=Pdhb Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	1.0619	0.086648	0.2868
84	14.13	14.13	17.7	IPI:IPI00330747.2	Gene_Symbol=Nphp3;Acad11 Acyl-CoA dehydrogenase family member 11	0.46935	-1.09126	0.01775
85	14.01	14.01	24.1	IPI:IPI00116192.1	Gene_Symbol=Prdx3 Thioredoxin-dependent peroxide reductase, mitochondrial	1.29105	0.368545	0.065733333
86	13.97	13.97	26.5	IPI:IPI00230084.5	Gene_Symbol=Aldh7a1 aldehyde dehydrogenase family 7, member A1 isoform a	1.1818	0.240986	0.0133
87	13.75	13.75	28.1	IPI:IPI00230108.6	Gene_Symbol=Pdia3 Protein disulfide-isomerase A3	0.70755	-0.4991	0.003166667
88	13.7	13.7	20.6	IPI:IPI00874456.1	Gene_Symbol=Dld Dihydrolipoyl dehydrogenase, mitochondrial	1.084975	0.117662	0.323
89	13.32	13.32	20.2	IPI:IPI00130804.1	Gene_Symbol=Ech1 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	0.87595	-0.19108	0.00585
90	13.12	13.47	28.8	IPI:IPI00788331.1	Gene_Symbol=Gcdh glutaryl-Coenzyme A dehydrogenase	1.16455	0.219773	0.0444
91	13.1	13.1	26.5	IPI:IPI00379694.4	Gene_Symbol=Hmgcl 3-hydroxy-3-methylglutaryl-Coenzyme A lyase	1.01165	0.01671	0.4311
92	13.08	13.08	30.7	IPI:IPI00321617.1	Gene_Symbol=Ephx2 Isoform 1 of Epoxide hydrolase 2	0.55255	-0.85582	0.002325
93	13.05	13.05	58.6	IPI:IPI00785410.1	Gene_Symbol=Cox5b Cytochrome c oxidase subunit 5B, mitochondrial	1.027575	0.039244	0.2453

94	12.97	13.37	15.1	IPI:IPI00850133.1	Gene_Symbol=Kiaa0564 (BLAST score:3792, P = 0.0)1300010F03Rik Isoform 1 of Uncharacterized protein KIAA0564 homolog	0.91545	-0.12745	0.459
95	12.9	12.9	28.6	IPI:IPI00454008.1	Gene_Symbol=Shmt2 Serine hydroxymethyltransferase	1.165575	0.221042	0.0141
96	12.82	12.82	25.1	IPI:IPI00134809.2	Gene_Symbol=Dlst Isoform 1 of Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	1.096975	0.133531	0.0641
97	12.52	12.52	21.4	IPI:IPI00776047.1	Gene_Symbol=Aifm1 Apoptosis-inducing factor, mitochondrion-associated 1	1.103425	0.141989	0.115
98	12.51	12.66	25.3	IPI:IPI00119685.1	Gene_Symbol=Cyp27a1 Cytochrome P450 27, mitochondrial	1.04445	0.062743	0.2129
99	12.48	12.48	41.7	IPI:IPI00890322.1	Gene_Symbol=Bdh1 3-hydroxybutyrate dehydrogenase, type 1	0.859925	-0.21772	0.0016
100	12.38	12.38	34	IPI:IPI00121833.3	Gene_Symbol=Acaa1b;Acaa1a 3-ketoacyl-CoA thiolase A, peroxisomal	[redacted]	[redacted]	
101	12.33	14.73	45.6	IPI:IPI00624210.3	Gene_Symbol=Glyal (BLAST score 619, P = 1e-176) EG240549 Glycine N-acyltransferase-like protein	1.075975	0.105645	0.1511
102	12.33	12.35	37.2	IPI:IPI00338536.1	Gene_Symbol=Sdhb Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	1.1639	0.218967	0.0098
103	12.21	12.21	41.6	IPI:IPI00121051.3	Gene_Symbol=Gstk1 Glutathione S-transferase kappa 1	0.808775	-0.30619	0.0095
104	12.19	12.19	27.2	IPI:IPI00273146.1	Gene_Symbol=Chdh Choline dehydrogenase, mitochondrial	1.13735	0.185676	0.0628
105	12.02	12.02	36	IPI:IPI00875110.1	Gene_Symbol=Idh2 52 kDa protein	0.92855	-0.10695	0.4098
106	12.02	12.02	36.4	IPI:IPI00776084.1	Gene_Symbol=Atp5c1 ATP synthase gamma chain	1.03985	0.056375	0.3318
107	11.74	11.75	43.2	IPI:IPI00109109.1	Gene_Symbol=Sod2 Superoxide dismutase [Mn], mitochondrial	1.230175	0.298864	0.00595
108	11.46	11.46	35.6	IPI:IPI00115824.1	Gene_Symbol=Nipsnap1 Protein NipSnap homolog 1	1.138575	0.187229	0.23375
109	11.46	11.46	64.9	IPI:IPI00555000.2	Gene_Symbol=Uqcrb Cytochrome b-c1 complex subunit 7	1.171175	0.227957	0.01305
110	11.22	11.22	22.4	IPI:IPI00122547.1	Gene_Symbol=Vdac2 Voltage-dependent anion-selective channel protein 2	1.1011	0.138945	0.18995
111	11.15	11.15	27.3	IPI:IPI00319992.1	Gene_Symbol=Hspa5 78 kDa glucose-regulated protein	0.66245	-0.59412	0.017
112	11.1	11.11	16.1	IPI:IPI00131695.3	Gene_Symbol=Alb Serum albumin	0.6191	-0.69176	0.01265
113	11.02	11.11	18.3	IPI:IPI00123276.1	Gene_Symbol=Mosc2 MOSC domain-containing protein 2, mitochondrial	0.89825	-0.15481	0.1095

114	10.98	10.98	54.6	IPI:IPI00125460.1	Gene_Symbol=Atp5j;LOC674583 ATP synthase-coupling factor 6, mitochondrial	1.0838	0.116099	0.2739
115	10.88	10.88	23.8	IPI:IPI00653598.2	Gene_Symbol=Uqcrc1 ubiquinol-cytochrome c reductase core protein 1	1.118	0.16092	0.0111
116	10.77	10.77	55.2	IPI:IPI00230113.5	Gene_Symbol=Cyb5 Cytochrome b5	0.59435	-0.75062	0.0061
117	10.64	10.64	19.3	IPI:IPI00387289.3	Gene_Symbol=Ces3 Carboxylesterase 3	0.49915	-1.00245	0.0284
118	10.19	10.19	27.1	IPI:IPI00113517.1	Gene_Symbol=Ctsb Cathepsin B	0.7455	-0.42372	0.0281
119	10.17	10.17	27.6	IPI:IPI00153660.4	Gene_Symbol=Dlat Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	0.965325	-0.05091	0.2403
120	10.12	10.13	17.5	IPI:IPI00134870.3	Gene_Symbol=Acox2 Peroxisomal acyl-coenzyme A oxidase 2	0.5546	-0.85048	0.0518
121	10.09	10.09	20.9	IPI:IPI00742309.1	Gene_Symbol=Kmo Isoform 2 of Kynurenine 3-monooxygenase	1.106625	0.146166	0.4378
122	10.01	12.03	21.9	IPI:IPI00874350.1	Gene_Symbol=Aldh3a2 Putative uncharacterized protein	0.56135	-0.83303	0.003025
123	10	10	42.9	IPI:IPI00754739.1	Gene_Symbol=Chchd3 (BLAST score: 332, P= 5e-90)LOC100046321;Chchd3 Putative uncharacterized protein	0.999925	-0.00011	0.2147
124	10	10	24.9	IPI:IPI00169862.1	Gene_Symbol=Coq9 Ubiquinone biosynthesis protein COQ9, mitochondrial	1.10145	0.139404	0.29055
125	9.9	9.9	23.3	IPI:IPI00318750.4	Gene_Symbol=Dhrs4 NADPH-dependent retinol dehydrogenase/reductase isoform 1	0.6306	-0.6652	NA
126	9.7	9.7	19.3	IPI:IPI00314202.5	Gene_Symbol=Baat Bile acid-CoA:amino acid N-acyltransferase	0.61345	-0.70498	NA
127	9.52	9.53	22.5	IPI:IPI00884472.1	Gene_Symbol=Ctsh cathepsin H preproprotein	0.859225	-0.21889	0.03705
128	9.51	9.51	21.3	IPI:IPI00130460.1	Gene_Symbol=Ndufv1 NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	1.0734	0.102188	0.0523
129	9.4	9.41	60.5	IPI:IPI00131771.3	Gene_Symbol=Cox6c Cytochrome c oxidase polypeptide VIc	1.048025	0.067673	NA
130	9.34	9.34	37.2	IPI:IPI00785323.1	Gene_Symbol=Cyp2e1 Cytochrome P450 2E1	0.628475	-0.67007	0.0797
131	9.32	9.32	23.3	IPI:IPI00331555.2	Gene_Symbol=Bckdha branched chain ketoacid dehydrogenase E1, alpha polypeptide	1.160725	0.215026	0.006
132	9.31	9.31	41.7	IPI:IPI00133034.3	Gene_Symbol=Hint2 Histidine triad nucleotide-binding protein 2	1.0788	0.109427	0.0778
133	9.23	9.23	35.3	IPI:IPI00133006.1	Gene_Symbol=Ndufab1 Acyl carrier protein, mitochondrial	1.048975	0.06898	0.1125

134	9.14	9.14	70.9	IPI:IPI00225390.5	Gene_Symbol=Cox6b1 Cytochrome c oxidase subunit VIb isoform 1	1.13155	0.1783	NA
135	8.91	8.91	26.1	IPI:IPI00874482.1	Gene_Symbol=Actg1 Actin, cytoplasmic 2	0.814075	-0.29677	0.0008
136	8.78	8.78	31.8	IPI:IPI00319652.2	Gene_Symbol=Gpx1 Glutathione peroxidase 1	1.04715	0.066468	0.2622
137	8.76	8.76	22.6	IPI:IPI00134691.3	Gene_Symbol=Ugt1a2;Ugt1a9;Ugt1a10;Ugt1a1;Ugt1a5;Ugt1a7c;LOC632297;Ugt1a6b UDP-glucuronosyltransferase 1-1	0.8434	-0.24571	NA
138	8.72	8.72	33.7	IPI:IPI00830581.1	Gene_Symbol=Hsd17b10 hydroxyacyl-Coenzyme A dehydrogenase type II	1.210725	0.275871	0.10945
139	8.62	9.06	16	IPI:IPI00128738.4	Gene_Symbol=Agxt2 Alanine--glyoxylate aminotransferase 2, mitochondrial	1.052075	0.073238	0.28925
140	8.41	11.2	32.6	IPI:IPI00113073.3	Gene_Symbol=Aldh1b1 Aldehyde dehydrogenase X, mitochondrial	1.4719	0.55768	NA
141	8.35	8.42	10.6	IPI:IPI00761408.2	Gene_Symbol=Lonp1 Lon protease homolog, mitochondrial	1.095575	0.131688	0.0203
142	8.29	8.29	29.5	IPI:IPI00117083.1	Gene_Symbol=Grpel1 GrpE protein homolog 1, mitochondrial	1.301625	0.380314	NA
143	8.27	8.52	27.4	IPI:IPI00407499.1	Gene_Symbol=Abat Isoform 1 of 4-aminobutyrate aminotransferase, mitochondrial	1.016975	0.024284	0.6185
144	8.22	8.38	13.5	IPI:IPI00895390.1	Gene_Symbol=Scpep1 Serine carboxypeptidase 1	0.8961	-0.15827	0.0603
145	8.16	8.54	16.8	IPI:IPI00153144.3	Gene_Symbol=Suox Sulfite oxidase, mitochondrial	1.038425	0.054397	NA
146	8.16	8.16	29.6	IPI:IPI00116222.1	Gene_Symbol=Hibadh 3-hydroxyisobutyrate dehydrogenase, mitochondrial	0.909675	-0.13658	0.03495
147	8.06	8.08	13.3	IPI:IPI00759881.1	Gene_Symbol=Acad9 very-long-chain acyl-CoA dehydrogenase VLCAD homolog	1.0421	0.059494	0.01
148	8.01	8.01	31.8	IPI:IPI00406442.2	Gene_Symbol=Suclg1 Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial	1.0708	0.098689	0.1244
149	8	8	34.8	IPI:IPI00896110.1	Gene_Symbol=Prdx5 Prdx5 protein	1.0364	0.051581	0.2797
150	8	8	60.2	IPI:IPI00128346.1	Gene_Symbol=Cisd1 CDGSH iron sulfur domain-containing protein 1	0.8347	-0.26067	0.0346
151	8	8	22.8	IPI:IPI00120212.1	Gene_Symbol=Ndufa9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	0.955425	-0.06579	0.0469
152	8	8	17.9	IPI:IPI00125220.6	Gene_Symbol=Ctsz Cathepsin Z	1.15075	0.202574	0.0835
153	7.93	7.93	21.9	IPI:IPI00125853.1	Gene_Symbol=Slc25a15 Mitochondrial ornithine transporter 1	1.2672	0.341644	0.10435
154	7.87	8	13	IPI:IPI00420706.4	Gene_Symbol=Lrpprc Leucine-rich PPR motif-containing protein, mitochondrial	0.9884	-0.01683	0.9169

155	7.7	7.7	46.3	IPI:IPI00125929.2	Gene_Symbol=Ndufa4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	1.1336	0.180912	0.0184
156	7.68	7.7	21.8	IPI:IPI00132762.1	Gene_Symbol=Trap1 Heat shock protein 75 kDa, mitochondrial	1.0035	0.005041	0.0554
157	7.65	7.65	21.2	IPI:IPI00331436.4	Gene_Symbol=Lap3 Isoform 1 of Cytosol aminopeptidase	[redacted]	[redacted]	
158	7.26	7.26	65.5	IPI:IPI00130322.5	Gene_Symbol=Ndufa7 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	1.1324	0.179384	0.5075
159	7.19	7.21	22.8	IPI:IPI00877214.1	Gene_Symbol=Peci peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase isoform a	0.74095	-0.43255	0.0011
160	7	7	13.8	IPI:IPI00130627.1	Gene_Symbol=Lgmn Legumain	0.936025	-0.09538	0.4182
161	7	7	31.3	IPI:IPI00831055.2	Gene_Symbol=- Beta-globin	[redacted]	[redacted]	
162	6.93	7.53	10.4	IPI:IPI00221556.2	Gene_Symbol=Acsm5 Isoform 1 of Acyl-coenzyme A synthetase ACSM5, mitochondrial	1.029475	0.041909	0.2036
163	6.77	6.82	23.8	IPI:IPI00895177.1	Gene_Symbol=Cyb5r3 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:2500002N19 product:NADH-CYTOCHROME B5 REDUCTASE homolog	0.932	-0.1016	0.09785
164	6.65	6.65	19.7	IPI:IPI00132728.2	Gene_Symbol=Cyc1 Isoform 1 of Cytochrome c1, heme protein, mitochondrial	1.002925	0.004214	0.3792
165	6.61	6.62	20.8	IPI:IPI00116748.1	Gene_Symbol=Ndufa10 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	1.144425	0.194623	0.153
166	6.57	6.57	43.2	IPI:IPI00271986.6	Gene_Symbol=Atp5j2 ATP synthase subunit f, mitochondrial	1.136775	0.184947	NA
167	6.55	6.55	9.5	IPI:IPI00110843.3	Gene_Symbol=Agmat Agmatinase, mitochondrial	1.0844	0.116897	NA
168	6.52	6.52	15.1	IPI:IPI00850430.1	Gene_Symbol=Slc25a3 LOC100046151 similar to Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	1.05935	0.083179	NA
169	6.42	6.42	26.7	IPI:IPI00337893.2	Gene_Symbol=Pdha1 Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	0.9875	-0.01815	0.1327
170	6.28	6.28	17	IPI:IPI00276926.3	Gene_Symbol=Slc25a1 NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630026H16 product:solute carrier family 25 (mitochondrial carrier	1.157575	0.211106	0.0369
171	6.25	6.41	7.8	IPI:IPI00845652.1	Gene_Symbol=Ogdh Isoform 3 of 2-oxoglutarate dehydrogenase E1 component, mitochondrial	1.0916	0.126444	0.066

172	6.25	6.25	28.1	IPI:IPI00125325.1	Gene_Symbol=Decr2 Peroxisomal 2,4-dienoyl-CoA reductase	0.5281	-0.92112	0.023775
173	6.24	6.24	48.7	IPI:IPI00135857.3	Gene_Symbol=Sod1 (BLAST score 313, P = 3e-84) EG667310;LOC545845 hypothetical protein isoform 4	0.796675	-0.32794	0.003525
174	6.18	6.18	21.8	IPI:IPI00753303.2	Gene_Symbol=Dapal (BLAST score: 644, P = 0.0) 0610010D20Rik Dihydrodipicolinate synthase-like, mitochondrial	1.0744	0.103531	0.3263
175	6.13	6.13	17.8	IPI:IPI00553717.6	Gene_Symbol=Mccc2 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	1.130025	0.176355	0.1158
176	6.07	6.07	13.2	IPI:IPI00136655.1	Gene_Symbol=Gcat 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	1.08005	0.111098	0.303
177	6.03	6.03	14.4	IPI:IPI00400301.2	Gene_Symbol=Cpox Coproporphyrinogen III oxidase, mitochondrial	1.10195	0.140059	0.1316
178	6.02	6.02	13.1	IPI:IPI00330094.4	Gene_Symbol=Cpt1a Carnitine O-palmitoyltransferase I, liver isoform	0.996625	-0.00488	0.064
179	6.02	6.02	15.4	IPI:IPI00126635.1	Gene_Symbol=Idh3b Tumor-related protein	0.937575	-0.09299	0.28695
180	6.01	6.06	18.6	IPI:IPI00459725.2	Gene_Symbol=Idh3a Isoform 1 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	1.007225	0.010386	0.7508
181	6	6	12.3	IPI:IPI00131177.1	Gene_Symbol=Letm1 LETM1 and EF-hand domain-containing protein 1, mitochondrial	0.92685	-0.10959	0.04955
182	6	6	12.9	IPI:IPI00117214.3	Gene_Symbol=Hsdl2 Hydroxysteroid dehydrogenase-like protein 2	0.7485	-0.41793	0.0071
183	6	6	23.2	IPI:IPI00453777.2	Gene_Symbol=Atp5d ATP synthase subunit delta, mitochondrial	1.05485	0.077038	0.0439
184	6	6	6.5	IPI:IPI00321190.1	Gene_Symbol=Psap Sulfated glycoprotein 1	0.811425	-0.30147	NA
185	6	6	13.1	IPI:IPI00170307.1	Gene_Symbol=Apoa1bp Apolipoprotein A-I-binding protein	1.0437	0.061707	0.2709
186	6	6	26.2	IPI:IPI00132799.4	Gene_Symbol=C1qbp complement component 1, q subcomponent binding protein	[redacted]	[redacted]	
187	6	6	42.1	IPI:IPI00134484.1	Gene_Symbol=Timm10;Timm13 Mitochondrial import inner membrane translocase subunit Tim13	1.2218	0.289008	0.0531
188	5.7	5.7	44.5	IPI:IPI00881750.1	Gene_Symbol=Ndufb5 14 kDa protein	1.032325	0.045897	0.0507
189	5.52	5.52	59.2	IPI:IPI00886222.1	Gene_Symbol=Ndufs6 11 kDa protein	1.092375	0.127468	0.0637
190	5.5	5.5	27.3	IPI:IPI00607025.2	Gene_Symbol=Amacr 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:2510003N10 product:alpha-methylacyl-CoA racemase, full insert sequence	0.8017	-0.31887	NA

191	5.44	5.44	23.3	IPI:IPI00131584.1	Gene_Symbol=Slc25a20 Mitochondrial carnitine/acylcarnitine carrier protein	1.0216	0.03083	NA
192	5.4	5.4	38.6	IPI:IPI00120451.1	Gene_Symbol=Fabp1 Fatty acid-binding protein, liver	0.5406	-0.88737	0.0769
193	5.34	5.45	48.6	IPI:IPI00120719.4	Gene_Symbol=Cox5a Cytochrome c oxidase subunit 5A, mitochondrial	1.129225	0.175333	0.25645
194	5.32	5.32	13.9	IPI:IPI00123639.1	Gene_Symbol=Calr Calreticulin	[redacted]	[redacted]	
195	5.26	5.35	25.4	IPI:IPI00169925.2	Gene_Symbol=Ndufv2 Isoform 1 of NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	0.985975	-0.02038	0.0362
196	5.22	5.22	12.5	IPI:IPI00760085.1	Gene_Symbol=Agxt Isoform Peroxisomal of Serine--pyruvate aminotransferase, mitochondrial	0.79165	-0.33707	NA
197	5.01	5.01	11.2	IPI:IPI00461197.1	Gene_Symbol=Ldhd 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4733401P21 product:weakly similar to PUTATIVE D-LACTATE DEHYDROGENASE (CYTOCHROME) OXIDOREDUCTASE PROTEIN	1.5385	0.621524	NA
198	5	5	19.1	IPI:IPI00894832.1	Gene_Symbol=Ctsc Adult male kidney cDNA, RIKEN full-length enriched library, clone:0610010C21 product:cathepsin C, full insert sequence	0.984275	-0.02287	NA
199	4.96	4.96	8.7	IPI:IPI00124372.3	Gene_Symbol=Aldh9a1 aldehyde dehydrogenase 9, subfamily A1	0.9621	-0.05574	0.1781
200	4.92	4.92	29	IPI:IPI00387430.1	Gene_Symbol=Ndufb8 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	1.144825	0.195127	NA
201	4.92	4.92	27.6	IPI:IPI00378120.2	Gene_Symbol=Glrx5 Glutaredoxin-related protein 5	1.18285	0.242267	NA
202	4.9	4.93	24.9	IPI:IPI00895984.1	Gene_Symbol=Mup1 Major urinary protein 1	0.495375	-1.01341	NA
203	4.8	4.8	4.7	IPI:IPI00271951.5	Gene_Symbol=Pdia4 protein disulfide isomerase associated 4	[redacted]	[redacted]	
204	4.58	4.58	10.8	IPI:IPI00658539.1	Gene_Symbol=Ctsa cathepsin A isoform a	1.347875	0.430687	NA
205	4.57	4.57	14.6	IPI:IPI00265352.1	Gene_Symbol=Gpt2 Alanine aminotransferase 2	1.23005	0.298717	0.2485
206	4.55	4.55	36	IPI:IPI00120984.5	Gene_Symbol=Ndufa8 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	1.171725	0.228634	NA
207	4.55	4.55	54.9	IPI:IPI00224210.5	Gene_Symbol=Uqcrq Cytochrome b-c1 complex subunit 8	0.98595	-0.02041	NA
208	4.53	4.57	13	IPI:IPI00129526.1	Gene_Symbol=Hsp90b1 Endoplasmin	[redacted]	[redacted]	

209	4.5	4.54	28.5	IPI:IPI00652845.3	Gene_Symbol=Pecr In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420405J16 product:peroxisomal trans-2-enoyl-CoA reductase, full insert sequence	[redacted]	[redacted]	
210	4.49	4.49	22.7	IPI:IPI00874574.1	Gene_Symbol=Clybl 36 kDa protein	[redacted]	[redacted]	
211	4.36	7.88	16.7	IPI:IPI00875511.1	Gene_Symbol=Mosc1 MOCO sulphurase C-terminal domain containing 1	[redacted]	[redacted]	
212	4.36	4.36	17.3	IPI:IPI00648829.1	Gene_Symbol=Nipsnap3a Nipsnap homolog 3A	1.11605	0.158402	NA
213	4.3	4.31	14.6	IPI:IPI00320850.3	Gene_Symbol=Mccc1 Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	0.975875	-0.03523	0.5973
214	4.25	4.69	8.3	IPI:IPI00751137.1	Gene_Symbol=Tomm70a Adult male thymus cDNA, RIKEN full-length enriched library, clone:5830412L10 product:Mitochondrial proteins import receptor (Translocase of outer membrane TOM70), full insert sequence	0.8459	-0.24144	NA
215	4.23	4.23	19.1	IPI:IPI00133270.1	Gene_Symbol=Clpp Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	1.272225	0.347354	0.0201
216	4.17	4.17	18.3	IPI:IPI00120232.1	Gene_Symbol=Ndufs7 NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	0.982725	-0.02514	NA
217	4.16	4.2	7.4	IPI:IPI00621548.2	Gene_Symbol=Por NADPH--cytochrome P450 reductase	0.877625	-0.18832	NA
218	4.15	6.15	10.8	IPI:IPI00153143.1	Gene_Symbol=Ugt2b1 UDP glucuronosyltransferase 2 family, polypeptide B1	0.62895	-0.66898	0.0875
219	4.15	4.15	14.6	IPI:IPI00762346.1	Gene_Symbol=Aadat Kynurenine/alpha-aminoadipate aminotransferase mitochondrial	0.99825	-0.00253	NA
220	4.11	4.13	20.1	IPI:IPI00133240.1	Gene_Symbol=Uqcrfs1 Cytochrome b-c1 complex subunit Rieske, mitochondrial	0.98845	-0.01676	NA
221	4.1	4.1	25.7	IPI:IPI00230715.5	Gene_Symbol=Ndufa13 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	1.008525	0.012247	NA
222	4.09	4.17	23.6	IPI:IPI00119945.1	Gene_Symbol=Nit2 Nitrilase homolog 2	0.954675	-0.06692	NA
223	4.07	4.07	17.9	IPI:IPI00170093.3	Gene_Symbol=Ndufs8 NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	1.109475	0.149877	NA
224	4.03	4.03	43	IPI:IPI00880613.1	Gene_Symbol=Ndufb10 18 kDa protein	0.99735	-0.00383	NA
225	4.03	4.03	33	IPI:IPI00132623.3	Gene_Symbol=Ndufb9 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	1.1296	0.175812	0.2409
226	4.02	4.02	27.1	IPI:IPI00133284.1	Gene_Symbol=D10Jhu81e;LOC100046684 ES1 protein homolog, mitochondrial	1.146675	0.197457	0.0693
227	4	10.6	12.6	IPI:IPI00759953.1	Gene_Symbol=1810049H19Rik;Try4 Tesp4 protein	[redacted]	[redacted]	

228	4	4.01	8.2	IPI:IPI00128287.1	Gene_Symbol=Cyp1a2 Cytochrome P450 1A2	0.5516	-0.85831	0.0184
229	4	4	7.1	IPI:IPI00127267.4	Gene_Symbol=Gldc Glycine dehydrogenase [decarboxylating], mitochondrial	1.27705	0.352815	0.0261
230	4	4	14.3	IPI:IPI00881534.1	Gene_Symbol=Ppa2 38 kDa protein	[redacted]	[redacted]	
231	4	4	12.2	IPI:IPI00831119.1	Gene_Symbol=Lypla1 21 kDa protein	0.9175	-0.12422	NA
232	4	4	22.7	IPI:IPI00125776.1	Gene_Symbol=ENSMUSG00000045455;Timm8a1 Mitochondrial import inner membrane translocase subunit Tim8 A	1.070125	0.097779	0.0518
233	3.99	3.99	18	IPI:IPI00129963.1	Gene_Symbol=Phyh Phytanoyl-CoA dioxygenase, peroxisomal	0.56915	-0.81312	NA
234	3.95	3.95	10.3	IPI:IPI00828822.2	Gene_Symbol=Es31 Isoform 2 of Liver carboxylesterase 31	0.610425	-0.71211	NA
235	3.86	3.86	25.8	IPI:IPI00230754.5	Gene_Symbol=Slc25a11 Mitochondrial 2-oxoglutarate/malate carrier protein	1.08035	0.111499	NA
236	3.81	3.86	15.1	IPI:IPI00273164.1	Gene_Symbol=Aldh5a1 Succinate-semialdehyde dehydrogenase, mitochondrial	1.0085	0.012211	0.3859
237	3.7	3.7	29.1	IPI:IPI00875372.1	Gene_Symbol=Echdc2 Isoform 2 of Enoyl-CoA hydratase domain-containing protein 2, mitochondrial	1.290375	0.36779	NA
238	3.7	3.7	24.9	IPI:IPI00125267.4	Gene_Symbol=Vapa Vesicle-associated membrane protein-associated protein A	0.4726	-1.08131	NA
239	3.62	3.62	22.2	IPI:IPI00130640.5	Gene_Symbol=Hrsp12 Ribonuclease UK114	0.800925	-0.32026	NA
240	3.52	3.52	6.2	IPI:IPI00606097.1	Gene_Symbol=Tmprss13 transmembrane protease, serine 13	0.988775	-0.01629	0.142
241	3.44	3.44	7.7	IPI:IPI00554830.2	Gene_Symbol=Gulo L-gulonolactone oxidase	0.652075	-0.61689	0.06185
242	3.41	3.41	14.2	IPI:IPI00648852.2	Gene_Symbol=Ppt1 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:C920018O12 product:palmitoyl-protein thioesterase 1, full insert sequence	0.891325	-0.16598	NA
243	3.38	3.38	9.2	IPI:IPI00126634.1	Gene_Symbol=Poldip2 Polymerase delta-interacting protein 2	1.090575	0.125089	0.13245
244	3.34	3.34	28.8	IPI:IPI00855212.1	Gene_Symbol=1110020G09Rik Isoform 2 of UPF0465 protein C5orf33 homolog	1.014975	0.021444	NA
245	3.3	4.2	5.8	IPI:IPI00222968.1	Gene_Symbol=Lamp2 Isoform LAMP-2C of Lysosome-associated membrane glycoprotein 2	0.7605	-0.39498	NA
246	3.29	3.32	18	IPI:IPI00109275.1	Gene_Symbol=Slc25a22 Mitochondrial glutamate carrier 1	0.97195	-0.04105	NA
247	3.25	3.26	10.6	IPI:IPI00788396.1	Gene_Symbol=Clpx caseinolytic protease X isoform 2	1.02485	0.035413	NA

248	3.22	6.44	19.4	IPI:IPI00876341.1	Gene_Symbol=Vdac3 Voltage-dependent anion-selective channel protein 3	1.09615	0.132445	NA
249	3.08	3.08	11.6	IPI:IPI00133108.1	Gene_Symbol=Klk5 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110030O19 product:similar to Kallikrein 5	[redacted]	[redacted]	
250	3.04	3.64	32.8	IPI:IPI00116896.1	Gene_Symbol=mt-Atp8 ATP synthase protein 8	1.116325	0.158757	NA
251	2.96	11.33	27.4	IPI:IPI00122139.3	Gene_Symbol=Acaa1b;Acaa1a 3-ketoacyl-CoA thiolase B, peroxisomal	0.48545	-1.04261	NA
252	2.96	2.99	45.1	IPI:IPI00111770.7	Gene_Symbol=Atp5k ATP synthase subunit e, mitochondrial	0.98725	-0.01851	0.1059
253	2.92	2.92	17.3	IPI:IPI00133403.1	Gene_Symbol=Ndufb3 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	0.991025	-0.01301	NA
254	2.89	8.89	21.1	IPI:IPI00403650.2	Gene_Symbol=Prss2 Anionic trypsin-2	[redacted]	[redacted]	
255	2.89	2.89	11	IPI:IPI00222767.1	Gene_Symbol=Pdhx Pyruvate dehydrogenase protein X component, mitochondrial	[redacted]	[redacted]	
256	2.89	2.89	32.8	IPI:IPI00133399.1	Gene_Symbol=Ndufa6 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	1.12585	0.171015	NA
257	2.86	2.86	4.1	IPI:IPI00886014.1	Gene_Symbol=Acss3 Isoform 1 of Acyl-CoA synthetase short-chain family member 3, mitochondrial	1.017925	0.025631	NA
258	2.8	2.8	6.2	IPI:IPI00889240.1	Gene_Symbol=Adhfe1 Isoform 2 of Hydroxyacid-oxoacid transhydrogenase, mitochondrial	1.130525	0.176993	NA
259	2.7	2.72	5.8	IPI:IPI00221608.3	Gene_Symbol=Samm50 Sorting and assembly machinery component 50 homolog	1.006725	0.00967	NA
260	2.68	2.68	17.3	IPI:IPI00608064.1	Gene_Symbol=Fech Fech protein (Fragment)	[redacted]	[redacted]	
261	2.67	2.7	14.7	IPI:IPI00409412.3	Gene_Symbol=Cyp2c67 Cytochrome P450, family 2, subfamily c, polypeptide 67	[redacted]	[redacted]	
262	2.62	2.62	12.9	IPI:IPI00125266.1	Gene_Symbol=Asah1 Acid ceramidase	0.739	-0.43635	NA
263	2.5	2.5	10.7	IPI:IPI00137491.1	Gene_Symbol=Acp5 Tartrate-resistant acid phosphatase type 5	0.5586	-0.84011	NA
264	2.42	2.42	9.2	IPI:IPI00274222.2	Gene_Symbol=Acad8 Isobutyryl-CoA dehydrogenase, mitochondrial	1.123875	0.168482	NA
265	2.41	2.41	12.3	IPI:IPI00128154.1	Gene_Symbol=Ctsl Cathepsin L1	[redacted]	[redacted]	
266	2.37	2.37	3.9	IPI:IPI00111960.2	Gene_Symbol=Gaa Lysosomal alpha-glucosidase	0.93265	-0.10059	NA
267	2.36	2.36	11.1	IPI:IPI00877288.1	Gene_Symbol=Pgcp Isoform 2 of Plasma glutamate carboxypeptidase	[redacted]	[redacted]	

268	2.35	2.37	19.2	IPI:IPI00662861.1	Gene_Symbol=LOC635087 similar to NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	0.9756	-0.03564	NA
269	2.34	2.34	25.7	IPI:IPI00762203.2	Gene_Symbol=Ftl1 Ferritin light chain 1	[redacted]	[redacted]	
270	2.34	2.34	4.7	IPI:IPI00761390.1	Gene_Symbol=Slc27a2 solute carrier family 27 (fatty acid transporter), member 2	[redacted]	[redacted]	
271	2.33	2.33	7.9	IPI:IPI00874376.1	Gene_Symbol=Apool 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810024N24 product:hypothetical protein, full insert sequence	1.2031	0.266757	NA
272	2.3	2.35	5.9	IPI:IPI00309035.2	Gene_Symbol=Rpn1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	[redacted]	[redacted]	
273	2.3	2.3	44.2	IPI:IPI00230241.6	Gene_Symbol=Atp5e ATP synthase subunit epsilon, mitochondrial	[redacted]	[redacted]	
274	2.29	2.29	67.5	IPI:IPI00114377.1	Gene_Symbol=Cox7a2 Cytochrome c oxidase polypeptide 7A2, mitochondrial	[redacted]	[redacted]	
275	2.27	2.27	22	IPI:IPI00127227.2	Gene_Symbol=Cbr4 Carbonyl reductase 4	[redacted]	[redacted]	
276	2.25	2.25	9.4	IPI:IPI00170126.4	Gene_Symbol=Pitrm1 Isoform 1 of Presequence protease, mitochondrial	1.1092	0.14952	NA
277	2.23	2.25	3.1	IPI:IPI00848562.1	Gene_Symbol=Ubr4 retinoblastoma-associated factor 600 isoform 2	[redacted]	[redacted]	
278	2.22	2.22	7.5	IPI:IPI00131176.1	Gene_Symbol=mt-Co2 Cytochrome c oxidase subunit 2	1.030275	0.043029	NA
279	2.21	2.21	24.4	IPI:IPI00222430.5	Gene_Symbol=Dbi diazepam binding inhibitor isoform 1	1.1926	0.25411	NA
280	2.2	2.2	14.3	IPI:IPI00229008.2	Gene_Symbol=Ndufs4 NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	0.874875	-0.19285	NA
281	2.19	4.19	13.7	IPI:IPI00762185.2	Gene_Symbol=Mpst 3-mercaptopyruvate sulfurtransferase	0.8412	-0.24948	NA
282	2.17	2.17	7.8	IPI:IPI00855011.1	Gene_Symbol=LOC100046998 similar to optic atrophy 1	0.90025	-0.1516	NA
283	2.15	2.15	7.8	IPI:IPI00387282.4	Gene_Symbol=Aadac Arylacetamide deacetylase	0.488025	-1.03497	NA
284	2.15	2.15	15	IPI:IPI00317074.3	Gene_Symbol=Slc25a10 Mitochondrial dicarboxylate carrier	0.8863	-0.17413	NA
285	2.15	2.15	12.4	IPI:IPI00753211.1	Gene_Symbol=Echdc3 Enoyl Coenzyme A hydratase domain containing 3	[redacted]	[redacted]	
286	2.13	3.84	6.1	IPI:IPI00756257.1	Gene_Symbol=Ttn Isoform 1 of Titin	[redacted]	[redacted]	

287	2.13	2.13	15	IPI:IPI00115117.1	Gene_Symbol=Stoml2 Stomatin-like protein 2	[redacted]	[redacted]	
288	2.12	2.12	2.6	XXXXXIPI:IPI007884	RANDOMIZED Gene_Symbol=Usp48 Isoform 1 of Ubiquitin carboxyl-terminal hydrolase 48	[redacted]	[redacted]	
289	2.11	2.11	18.6	IPI:IPI00128023.3	Gene_Symbol=Ndufs2 NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	1.259425	0.332765	NA
290	2.11	2.11	6.4	IPI:IPI00109169.1	Gene_Symbol=Idh3g Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	1.01855	0.026517	NA
291	2.09	2.09	11.7	IPI:IPI00457825.2	Gene_Symbol=- 47 kDa protein	[redacted]	[redacted]	
292	2.09	2.09	8.9	IPI:IPI00121218.5	Gene_Symbol=Fahd2a Fumarylacetoacetate hydrolase domain-containing protein 2A	1.1611	0.215492	NA
293	2.08	2.09	11.2	IPI:IPI00895479.1	Gene_Symbol=2810422J05Rik 27 kDa protein	0.6956	-0.52367	NA
294	2.08	2.08	18.1	IPI:IPI00133411.1	Gene_Symbol=Fam136a (BLAST score:280, P =2e-74 2010309E21Rik Protein FAM136A	1.2381	0.308128	NA
295	2.07	2.07	19.4	IPI:IPI00331322.3	Gene_Symbol=Mgst1 Microsomal glutathione S-transferase 1	[redacted]	[redacted]	
296	2.07	2.07	4.9	IPI:IPI00653566.1	Gene_Symbol=Acot2 Activated spleen cDNA, RIKEN full-length enriched library, clone:F830219O19 product:mitochondrial acyl-CoA thioesterase 1, full insert sequence	0.612975	-0.7061	NA
297	2.06	2.15	16.9	IPI:IPI00129516.1	Gene_Symbol=Uqcrh Cytochrome b-c1 complex subunit 6, mitochondrial	[redacted]	[redacted]	
298	2.05	2.05	7.1	IPI:IPI00122634.1	Gene_Symbol=Cyp2a12 Cytochrome P450, family 2, subfamily a, polypeptide 12	0.560275	-0.83579	NA
299	2.05	2.05	13	IPI:IPI00115454.3	Gene_Symbol=Sfxn1 Sideroflexin-1	[redacted]	[redacted]	
300	2.05	2.05	12.1	IPI:IPI00132958.1	Gene_Symbol=Them2 Thioesterase superfamily member 2	0.90885	-0.13789	NA
301	2.04	3.35	16.9	IPI:IPI00319973.3	Gene_Symbol=Pgrmc1 Membrane-associated progesterone receptor component 1	[redacted]	[redacted]	
302	2.04	2.05	9.3	IPI:IPI00134504.1	Gene_Symbol=Cyp3a11 Cytochrome P450 3A11	[redacted]	[redacted]	
303	2.04	2.04	12.4	IPI:IPI00475322.1	Gene_Symbol=Msra Msra protein	1.1163	0.158725	NA
304	2.02	2.06	14.7	IPI:IPI00556699.1	Gene_Symbol=Gcsh Putative uncharacterized protein	1.25095	0.323024	NA
305	2.02	2.03	5.6	IPI:IPI00845617.1	Gene_Symbol=Plbl1 (Putative phospholipase B-like 1, BLAST score: 1096, P =0.0) LOC100045163 similar to RIKEN cDNA 1100001H23 gene	0.775475	-0.36685	NA
306	2.02	2.02	7.9	IPI:IPI00133877.1	Gene_Symbol=Cyp4a14 Cytochrome P450 4A14	0.4408	-1.1818	NA
307	2.01	2.01	14.8	IPI:IPI00114866.1	Gene_Symbol=Mlycd Isoform Mitochondrial of Malonyl-CoA decarboxylase, mitochondrial	0.996425	-0.00517	NA

308	2	4.25	17.8	IPI:IPI00135231.2	Gene_Symbol=Idh1 0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030024J03 product:isocitrate dehydrogenase 1 (NADP+), soluble, full insert sequence	0.532125	-0.91016	NA
309	2	4	8.8	IPI:IPI00762478.1	Gene_Symbol=Acsm3 Isoform 1 of Acyl-coenzyme A synthetase ACSM3, mitochondrial	1.0529	0.074368	NA
310	2	2.33	4.9	XXXXXIPI:IPI006530	RANDOMIZED Gene_Symbol=Mfn1 Mitofusin-1	1.31065	0.390282	NA
311	2	2.02	6.7	IPI:IPI00274656.6	Gene_Symbol=Pmpcb Mitochondrial-processing peptidase subunit beta	1.2861	0.363003	NA
312	2	2	14.4	IPI:IPI00118963.1	Gene_Symbol=Mrpl12 39S ribosomal protein L12, mitochondrial	1.0642	0.089769	NA
313	2	2	21.9	IPI:IPI00114246.2	Gene_Symbol=Ndufb11 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	1.08975	0.123997	NA
314	2	2	2.3	IPI:IPI00355248.5	Gene_Symbol=mt-Co1 cytochrome c oxidase subunit I	0.8147	-0.29566	NA