Supplementary Table 2. List of differentially expressed hepatic mitochondrial proteins detected by MS with the partial loss of *Sod2*

Protein fold change ratio relative to wildtype mice as detected by the 4-plex iTRAQ.

This table comprises of one tab:

WT versus HET	Summary of *Sod2* $^{+/-}$ protein fold change using 4-plex iTRAQ

Column description

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 of *Sod2* $^{+/-}$/*Sod2* $^{+/+}$
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

NO.	UNUSED	TOTAL	% Cov	ACCESSION	NAME	AVG FOLD CHANGE	LOG$_2$	AVG *P*-VALUE*
1	138.01	138.01	50.7	IPI:IPI00111908.8	Gene_Symbol=Cps1 Carbamoyl-phosphate synthase [ammonia], mitochondrial	1.3365	0.4184	0
2	75.53	75.53	75	IPI:IPI00869393.1	Gene_Symbol=Cat catalase	1.0964	0.1327	0.00567
3	73.64	73.64	66.1	IPI:IPI00828479.1	Gene_Symbol=Acox1 Acyl-Coenzyme A oxidase 1, palmitoyl	0.8368	-0.2571	0.00045
4	61.66	61.66	54.2	IPI:IPI00554834.2	Gene_Symbol=Ehhadh Peroxisomal bifunctional enzyme	1.0241	0.0343	0.2714
5	49.98	49.98	57	IPI:IPI00133522.1	Gene_Symbol=P4hb Protein disulfide-isomerase	0.7764	-0.3652	0.00258
6	48.65	48.65	66.7	IPI:IPI00223367.5	Gene_Symbol=Uox Uricase	1.1821	0.2413	#######
7	39.45	39.45	30.9	IPI:IPI00134131.2	Gene_Symbol=Scp2 Isoform SCPx of Non-specific lipid-transfer protein	1.0063	0.0090	0.1938
8	39.28	39.28	40	IPI:IPI00114209.1	Gene_Symbol=Glud1 Glutamate dehydrogenase 1, mitochondrial	1.2700	0.3448	0.0014
9	38.49	38.49	44.1	IPI:IPI00319992.1	Gene_Symbol=Hspa5 78 kDa glucose-regulated protein	0.9311	-0.1030	0.2786
10	38.39	40.39	49.7	IPI:IPI00230108.6	Gene_Symbol=Pdia3 Protein disulfide-isomerase A3	1.0625	0.0875	0.1803
11	37.08	37.08	52.7	IPI:IPI00468481.2	Gene_Symbol=Atp5b ATP synthase subunit beta, mitochondrial	1.1163	0.1587	0.0079
12	35.97	35.97	31.1	IPI:IPI00114710.2	Gene_Symbol=Pcx Activated spleen cDNA, RIKEN full-length enriched library, clone:F	0.9730	-0.0396	0.3475
13	33.23	33.23	32.8	IPI:IPI00331628.5	Gene_Symbol=Hsd17b4 Peroxisomal multifunctional enzyme type 2	1.0707	0.0986	0.0473
14	30.78	30.78	56.4	IPI:IPI00653158.1	Gene_Symbol=Acaa2 Putative uncharacterized protein	1.2022	0.2656	0.01283
15	28.26	28.26	48.6	IPI:IPI00130280.1	Gene_Symbol=Atp5a1 ATP synthase subunit alpha, mitochondrial	1.1714	0.2283	0.0357
16	27.18	27.18	38	IPI:IPI00420718.4	Gene_Symbol=Hmgcs2 Hydroxymethylglutaryl-CoA synthase, mitochondrial	1.2521	0.3244	0.00295
17	26.72	26.72	46.7	IPI:IPI00122139.3	Gene_Symbol=Acaa1b;Acaa1a 3-ketoacyl-CoA thiolase B, peroxisomal	0.9609	-0.0576	0.052
18	26.44	26.44	33.8	IPI:IPI00387289.3	Gene_Symbol=Ces3 Carboxylesterase 3	0.9145	-0.1289	0.1442
19	26.18	26.18	26	IPI:IPI00223092.5	Gene_Symbol=Hadha Trifunctional enzyme subunit alpha, mitochondrial	1.0859	0.1189	0.22255
20	26.02	26.02	39.5	IPI:IPI00117312.1	Gene_Symbol=Got2 Aspartate aminotransferase, mitochondrial	1.1223	0.1664	0.1024
21	25.52	25.52	41.6	IPI:IPI00111218.1	Gene_Symbol=Aldh2 Aldehyde dehydrogenase, mitochondrial	1.2663	0.3406	0.0094
22	25.02	25.02	24.4	IPI:IPI00316314.1	Gene_Symbol=Hacl1 2-hydroxyacyl-CoA lyase 1	1.0101	0.0145	0.46305
23	24.07	24.07	24.9	IPI:IPI00129526.1	Gene_Symbol=Hsp90b1 Endoplasmin	1.1891	0.2498	NA
24	23.82	23.82	36.5	IPI:IPI00123639.1	Gene_Symbol=Calr Calreticulin	1.2390	0.3092	0.1216
25	22.97	22.97	25.5	IPI:IPI00330747.2	Gene_Symbol=Nphp3;Acad11 Acyl-CoA dehydrogenase family member 11	1.0782	0.1086	0.2411
26	22.63	22.63	36.5	IPI:IPI00321617.1	Gene_Symbol=Ephx2 Isoform 1 of Epoxide hydrolase 2	1.1846	0.2443	0.08015
27	21.05	21.05	30.8	IPI:IPI00405699.2	Gene_Symbol=Aldh4a1 Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	1.2313	0.3002	0.01517
28	20.91	20.91	32.7	IPI:IPI00880839.1	Gene_Symbol=Hspa9 heat shock protein 9	1.1068	0.1464	0.16515
29	20.72	20.72	20.9	IPI:IPI00857226.1	Gene_Symbol=Acsl1 78 kDa protein	1.2222	0.2895	0.03793
30	19.31	19.31	33	IPI:IPI00154054.1	Gene_Symbol=Acat1 Acetyl-CoA acetyltransferase, mitochondrial	1.1826	0.2419	0.2654
31	19.27	19.27	40.3	IPI:IPI00129178.1	Gene_Symbol=Oat Ornithine aminotransferase, mitochondrial	1.9512	0.9643	0.01043
32	18.18	18.18	40.8	IPI:IPI00130950.1	Gene_Symbol=Bhmt Betaine--homocysteine S-methyltransferase 1	0.7033	-0.5077	0.01315
33	17.54	17.54	30.2	IPI:IPI00776257.1	Gene_Symbol=Otc Otc protein	1.3752	0.4597	0.00018
34	17.15	17.15	47.2	IPI:IPI00121788.1	Gene_Symbol=Prdx1 Peroxiredoxin-1	0.9771	-0.0334	0.32355
35	16.87	16.87	31.6	IPI:IPI00134746.5	Gene_Symbol=Ass1 Argininosuccinate synthase	0.6739	-0.5693	0.0256
36	16.84	16.84	32.9	IPI:IPI00461964.3	Gene_Symbol=Aldh6a1 Methylmalonate-semialdehyde dehydrogenase [acylating], mit	1.2957	0.3737	0.01275
37	15.92	15.92	25.1	IPI:IPI00308885.6	Gene_Symbol=Hspd1 Isoform 1 of 60 kDa heat shock protein, mitochondrial	0.9942	-0.0085	0.2862
38	15.7	15.7	49.2	IPI:IPI00895984.1	Gene_Symbol=Mup1 Major urinary protein 1	2.2244	1.1534	0.0025
39	15.63	17.65	17	IPI:IPI00271951.5	Gene_Symbol=Pdia4 protein disulfide isomerase associated 4	0.8400	-0.2516	0.2748

40	15.04	15.04	19.3	IPI:IPI00307837.6	Gene_Symbol=Eef1a1 Elongation factor 1-alpha 1	0.8866	-0.1737	0.0434
41	15.03	15.03	38	IPI:IPI00848492.1	Electron transferring flavoprotein, beta polypeptide isoform 2 (Score:508 Exp: 4e-144	1.2747	0.3502	0.0121
42	14.96	14.96	31.3	IPI:IPI00127206.6	Gene_Symbol=Aldob Fructose-bisphosphate aldolase B	0.8551	-0.2259	0.0348
43	14.59	14.59	32.2	IPI:IPI00125325.1	Gene_Symbol=Decr2 Peroxisomal 2,4-dienoyl-CoA reductase	0.9780	-0.0321	0.5579
44	14.16	14.16	38.5	IPI:IPI00121051.3	Gene_Symbol=Gstk1 Glutathione S-transferase kappa 1	1.7967	0.8454	NA
45	14.09	14.09	24.4	IPI:IPI00553576.3	Gene_Symbol=Abcd3 ATP-binding cassette, sub-family D, member 3	1.2306	0.2993	0.0075
46	13.92	13.92	19.7	IPI:IPI00309035.2	Gene_Symbol=Rpn1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase s	0.9294	-0.1056	0.3916
47	13.78	13.78	15.3	IPI:IPI00122633.3	Gene_Symbol=Acsf2 Acyl-CoA synthetase family member 2, mitochondrial	1.3406	0.4229	0.08045
48	13.68	13.68	24	IPI:IPI00136213.5	Gene_Symbol=Sardh Sarcosine dehydrogenase, mitochondrial	1.0657	0.0917	0.32605
49	13.65	13.65	23.6	IPI:IPI00115607.3	Gene_Symbol=Hadhb Trifunctional enzyme subunit beta, mitochondrial	1.1247	0.1695	0.08
50	13.31	13.32	24.7	IPI:IPI00875110.1	Gene_Symbol=Idh2 52 kDa protein	1.2787	0.3547	0.31345
51	13.23	13.23	20.5	IPI:IPI00314202.5	Gene_Symbol=Baat Bile acid-CoA:amino acid N-acyltransferase	0.9056	-0.1430	0.1275
52	13.1	13.1	57.1	IPI:IPI00831055.2	Gene_Symbol=- Beta-globin	0.3565	-1.4882	0.00308
53	12.9	12.9	30.4	IPI:IPI00113517.1	Gene_Symbol=Ctsb Cathepsin B	1.0735	0.1023	0.4338
54	12.89	12.89	35.6	IPI:IPI00890322.1	Gene_Symbol=Bdh1 3-hydroxybutyrate dehydrogenase, type 1	0.9697	-0.0445	0.4557
55	12.6	12.6	25.9	IPI:IPI00882287.1	Gene_Symbol=Etfdh Etfdh protein	1.1100	0.1506	0.1852
56	12.57	12.57	37.3	IPI:IPI00323592.2	Gene_Symbol=Mdh2 Malate dehydrogenase, mitochondrial	1.2183	0.2849	0.4488
57	12.37	12.37	26.7	IPI:IPI00134870.3	Gene_Symbol=Acox2 Peroxisomal acyl-coenzyme A oxidase 2	0.9183	-0.1229	0.0829
58	12.35	12.35	25.4	IPI:IPI00129963.1	Gene_Symbol=Phyh Phytanoyl-CoA dioxygenase, peroxisomal	1.0298	0.0424	0.4422
59	12.19	16.51	26.2	IPI:IPI00128399.3	Gene_Symbol=AU018778 Adult male colon cDNA, RIKEN full-length enriched library,	0.9231	-0.1155	0.274
60	12.19	12.19	36.7	IPI:IPI00117914.3	Gene_Symbol=Arg1 Arginase-1	0.9074	-0.1402	0.0427
61	12.12	12.12	48.1	IPI:IPI00223216.5	Gene_Symbol=Tst Thiosulfate sulfurtransferase	1.4592	0.5452	0.03945
62	12.1	12.1	28.5	IPI:IPI00110719.1	Gene_Symbol=Pipox Peroxisomal sarcosine oxidase	1.4121	0.4978	0.00185
63	11.77	11.77	16.5	IPI:IPI00123379.1	Gene_Symbol=Hdlbp Vigilin	0.8967	-0.1573	0.0508
64	11.71	11.71	18.6	IPI:IPI00134503.1	Gene_Symbol=Cyp2c29 Cytochrome P450 2C29	2.2443	1.1663	0.03623
65	11.39	11.39	17.2	IPI:IPI00381178.3	Gene_Symbol=Es31 Isoform 1 of Liver carboxylesterase 31	1.3862	0.4711	0.0457
66	11.15	11.15	30.1	IPI:IPI00135686.2	Gene_Symbol=Ppib peptidylprolyl isomerase B	1.2300	0.2987	0.2844
67	10.99	10.99	29.1	IPI:IPI00320462.4	Gene_Symbol=Bphl Putative uncharacterized protein	1.0932	0.1285	0.0081
68	10.93	10.93	21.3	IPI:IPI00119203.4	Gene_Symbol=Acadvl Very long-chain specific acyl-CoA dehydrogenase, mitochondri	1.1477	0.1987	0.1047
69	10.92	10.92	52.2	IPI:IPI00230113.5	Gene_Symbol=Cyb5 Cytochrome b5	1.0379	0.0537	0.0508
70	10.83	10.83	19.2	IPI:IPI00116074.1	Gene_Symbol=Aco2 Aconitate hydratase, mitochondrial	1.0444	0.0627	0.0968
71	10.74	10.74	29.2	IPI:IPI00760085.1	Gene_Symbol=Agxt Isoform Peroxisomal of Serine--pyruvate aminotransferase, mitoc	0.8776	-0.1884	0.21675
72	10.69	10.69	17.6	IPI:IPI00134961.1	Gene_Symbol=Acadm Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	1.2639	0.3378	0.13047
73	10.37	10.37	30.9	IPI:IPI00894588.1	Gene_Symbol=Acadl acyl-Coenzyme A dehydrogenase, long-chain	1.0032	0.0046	0.4222
74	10.34	10.34	23.4	IPI:IPI00321644.3	Gene_Symbol=Cyp2d26 Cytochrome P450 2D26	1.0759	0.1055	0.26127
75	10.03	10.03	44.4	IPI:IPI00845802.1	Gene_Symbol=Hba-a1;Hba-a2 hemoglobin alpha, adult chain 2	0.7561	-0.4034	0.2811
76	10	10	22.4	IPI:IPI00387379.1	Gene_Symbol=Decr1 2,4-dienoyl-CoA reductase, mitochondrial	1.0758	0.1054	0.4826
77	9.87	9.87	30.1	IPI:IPI00881253.1	Gene_Symbol=Rpl5 Blastocyst blastocyst cDNA, RIKEN full-length enriched library, cl	0.8408	-0.2501	0.42093
78	9.79	9.79	18.5	IPI:IPI00226140.5	Gene_Symbol=Maob Amine oxidase [flavin-containing] B	1.2530	0.3253	0.0178
79	9.6	9.6	29	IPI:IPI00331241.8	Gene_Symbol=Gsta3 Glutathione S-transferase A3	0.8658	-0.2080	0.0607
80	9.53	9.53	13.8	IPI:IPI00123924.1	Gene_Symbol=Serpina1d Alpha-1-antitrypsin 1-4	1.0017	0.0024	NA

81	9.52	9.52	16.9	IPI:IPI00125220.6	Gene_Symbol=Ctsz Cathepsin Z	1.5412	0.6240	0.15715
82	9.44	9.44	26.5	IPI:IPI00119755.1	Gene_Symbol=Nudt7 Isoform 2 of Peroxisomal coenzyme A diphosphatase NUDT7	0.9860	-0.0203	NA
83	9.4	9.4	10.3	IPI:IPI00130661.1	Gene_Symbol=Tpp1 Tripeptidyl-peptidase 1	1.1445	0.1947	0.018
84	9.39	9.39	27.6	IPI:IPI00454049.4	Gene_Symbol=Echs1 Enoyl-CoA hydratase, mitochondrial	1.2600	0.3335	0.0879
85	9.34	9.34	32.5	IPI:IPI00323571.1	Gene_Symbol=Apoe Apolipoprotein E	0.6721	-0.5732	0.0398
86	9.31	9.31	12.8	IPI:IPI00139788.2	Gene_Symbol=Trf Serotransferrin	1.0543	0.0763	0.2113
87	9.22	9.22	26.6	IPI:IPI00331092.7	Gene_Symbol=Rps4x 40S ribosomal protein S4, X isoform	0.8744	-0.1936	0.1761
88	9.1	9.1	17.3	IPI:IPI00465739.2	Gene_Symbol=Cyp2b10 Putative uncharacterized protein	1.9476	0.9617	0.0287
89	8.92	8.94	19.8	IPI:IPI00331596.6	Gene_Symbol=Pecr Peroxisomal trans-2-enoyl-CoA reductase	1.1176	0.1604	0.25973
90	8.83	8.83	17.9	IPI:IPI00128287.1	Gene_Symbol=Cyp1a2 Cytochrome P450 1A2	0.7860	-0.3474	0.22217
91	8.8	8.8	26.2	IPI:IPI00114331.4	Gene_Symbol=Amacr Alpha-methylacyl-CoA racemase	1.0016	0.0023	0.0843
92	8.69	8.69	17.4	IPI:IPI00153144.3	Gene_Symbol=Suox Sulfite oxidase, mitochondrial	1.2328	0.3019	0.0485
93	8.54	13.77	26.5	IPI:IPI00115867.4	Gene_Symbol=Ces1 Liver carboxylesterase 1	1.0332	0.0471	0.75
94	8.51	8.51	15.1	IPI:IPI00122362.1	Gene_Symbol=Pdia5 Protein disulfide-isomerase A5	0.7539	-0.4076	NA
95	8.35	8.35	10.6	IPI:IPI00120165.1	Gene_Symbol=Crot Peroxisomal carnitine O-octanoyltransferase	0.8881	-0.1712	0.0247
96	8.29	8.29	26.2	IPI:IPI00120123.1	Gene_Symbol=Dmgdh Dimethylglycine dehydrogenase, mitochondrial	0.9954	-0.0067	NA
97	8.29	8.29	35.1	IPI:IPI00785323.1	Gene_Symbol=Cyp2e1 Cytochrome P450 2E1	1.2721	0.3472	0.0213
98	8.12	8.12	13.6	IPI:IPI00123129.1	Gene_Symbol=Snd1 Staphylococcal nuclease domain-containing protein 1	0.8709	-0.1994	0.1166
99	8.11	8.11	22.6	IPI:IPI00116221.2	Gene_Symbol=Lactb2 Beta-lactamase-like protein 2	1.1568	0.2101	0.0493
100	8.07	8.07	23.1	IPI:IPI00331251.1	Gene_Symbol=Acads Putative uncharacterized protein	1.1007	0.1384	0.0783
101	7.96	7.96	15.8	IPI:IPI00653598.2	Gene_Symbol=Uqcrc1 ubiquinol-cytochrome c reductase core protein 1	0.9485	-0.0762	0.7187
102	7.82	7.82	26.3	IPI:IPI00626790.3	Gene_Symbol=Glul Glutamine synthetase	0.7169	-0.4803	0.03445
103	7.74	7.74	11.4	IPI:IPI00554830.2	Gene_Symbol=Gulo L-gulonolactone oxidase	0.9229	-0.1157	0.0116
104	7.7	7.7	13.7	IPI:IPI00471246.2	Gene_Symbol=Ivd Isovaleryl-CoA dehydrogenase, mitochondrial	1.1054	0.1445	0.3325
105	7.6	8.98	19.5	IPI:IPI00222489.1	Gene_Symbol=Ces5 Putative uncharacterized protein	0.9877	-0.0179	NA
106	7.59	7.63	15.5	IPI:IPI00621548.2	Gene_Symbol=Por NADPH--cytochrome P450 reductase	1.2271	0.2952	0.1698
107	7.29	7.29	14.8	IPI:IPI00127841.3	Gene_Symbol=Slc25a5 ADP/ATP translocase 2	1.2569	0.3299	0.2045
108	7.15	7.15	9.5	IPI:IPI00113141.1	Gene_Symbol=Cs Citrate synthase, mitochondrial	1.1854	0.2453	0.049
109	6.94	6.94	37.3	IPI:IPI00263863.8	Gene_Symbol=Hspe1 10 kDa heat shock protein, mitochondrial	1.3037	0.3826	NA
110	6.93	6.93	26.6	IPI:IPI00117978.1	Gene_Symbol=Cox4i1 Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	1.0480	0.0676	NA
111	6.92	6.92	7.3	IPI:IPI00658539.1	Gene_Symbol=Ctsa cathepsin A isoform a	0.8500	-0.2345	0.3115
112	6.9	6.9	23.6	IPI:IPI00222496.3	Gene_Symbol=Pdia6 Putative uncharacterized protein	1.2207	0.2877	0.38555
113	6.9	6.9	47.6	IPI:IPI00125929.2	Gene_Symbol=Ndufa4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subun	1.1127	0.1540	0.3455
114	6.74	6.74	26	IPI:IPI00624210.3	Gene_Symbol=EG240549 Glycine N-acyltransferase-like protein	1.1581	0.2118	0.1516
115	6.66	6.67	14.7	IPI:IPI00849363.1	Gene_Symbol=Cyp2c69 similar to RIKEN cDNA C730004C24 gene isoform 2	0.8440	-0.2447	NA
116	6.54	6.54	33.6	IPI:IPI00130804.1	Gene_Symbol=Ech1 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	1.4794	0.5650	0.0265
117	6.54	6.54	28.2	IPI:IPI00221769.5	Gene_Symbol=Ak3 GTP:AMP phosphotransferase mitochondrial	1.2375	0.3074	NA
118	6.52	6.52	23.4	IPI:IPI00173179.3	Gene_Symbol=Mettl7b Methyltransferase-like protein 7B	0.9726	-0.0401	NA
119	6.47	6.47	33.5	IPI:IPI00133440.1	Gene_Symbol=Phb Prohibitin	1.0249	0.0355	NA
120	6.41	6.41	13.9	IPI:IPI00122862.4	Gene_Symbol=Mthfd1 C-1-tetrahydrofolate synthase, cytoplasmic	1.0297	0.0422	0.2836
121	6.34	6.34	26.7	IPI:IPI00119138.1	Gene_Symbol=Uqcrc2 Cytochrome b-c1 complex subunit 2, mitochondrial	0.9011	-0.1502	0.2222

122	6.3	6.3	16.7	IPI:IPI00874456.1	Gene_Symbol=Dld Dihydrolipoyl dehydrogenase, mitochondrial	1.3090	0.3885	NA
123	6.3	6.3	23.4	IPI:IPI00759904.1	Gene_Symbol=Cyb5r3 Isoform 2 of NADH-cytochrome b5 reductase 3	0.8025	-0.3174	0.05595
124	6.26	6.26	16.8	IPI:IPI00406442.2	Gene_Symbol=Suclg1 Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondria	1.2143	0.2801	0.29875
125	6.24	6.24	16.8	IPI:IPI00130627.1	Gene_Symbol=Lgmn Legumain	1.2288	0.2973	NA
126	6.21	6.21	27.4	IPI:IPI00321718.4	Gene_Symbol=Phb2 Prohibitin-2	0.8284	-0.2717	NA
127	6.17	6.17	16.5	IPI:IPI00654116.2	Gene_Symbol=Acsm1 Isoform 2 of Acyl-coenzyme A synthetase ACSM1, mitochondria	1.5906	0.6695	0.13143
128	6.17	6.17	12.6	IPI:IPI00886297.1	Gene_Symbol=Hspa8 Hspa8 protein	0.7710	-0.3753	NA
129	6.16	6.16	13.9	IPI:IPI00230351.1	Gene_Symbol=Sdha Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mito	0.9737	-0.0385	0.835
130	6.05	8.05	22.7	IPI:IPI00874350.1	Gene_Symbol=Aldh3a2 Putative uncharacterized protein	1.0458	0.0645	NA
131	6.05	6.05	16.8	IPI:IPI00116753.4	Gene_Symbol=Etfa Electron transfer flavoprotein subunit alpha, mitochondrial	1.2546	0.3272	0.072
132	6.04	6.04	24.4	IPI:IPI00403233.1	Gene_Symbol=Chdh 2 days pregnant adult female oviduct cDNA, RIKEN full-length en	1.0946	0.1304	NA
133	6.04	6.04	21.3	IPI:IPI00338536.1	Gene_Symbol=Sdhb Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitoch	1.0642	0.0897	0.3673
134	6.04	6.04	40.6	IPI:IPI00623553.1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d (Score: 327 Exp: 9e-90)Gene_Symbol=LOC100044492;ENSMUSG00000068706 hypothetical protein	1.3363	0.4182	0.0327
135	6.04	6.04	10.9	IPI:IPI00116192.1	Gene_Symbol=Prdx3 Thioredoxin-dependent peroxide reductase, mitochondrial	1.0196	0.0279	0.7869
136	6.03	8.03	11	IPI:IPI00170363.1	Gene_Symbol=Acsl5 Long-chain-fatty-acid--CoA ligase 5	1.1243	0.1690	NA
137	6.03	6.03	11.4	IPI:IPI00466069.3	Gene_Symbol=Eef2 Elongation factor 2	0.9769	-0.0338	0.1389
138	6.03	6.03	21.6	IPI:IPI00407499.1	Gene_Symbol=Abat Isoform 1 of 4-aminobutyrate aminotransferase, mitochondrial	1.1504	0.2022	0.0231
139	6.02	6.02	25.2	IPI:IPI00379694.4	Gene_Symbol=Hmgcl 3-hydroxy-3-methylglutaryl-Coenzyme A lyase	1.4001	0.4855	0.035
140	6	6.36	16.6	IPI:IPI00129056.2	Gene_Symbol=Glyat Isoform 1 of Glycine N-acyltransferase	1.0322	0.0457	0.2346
141	6	6	15.7	IPI:IPI00404551.1	Gene_Symbol=Ctsd B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enri	0.7689	-0.3791	0.1282
142	6	6	24.3	IPI:IPI00132728.2	Gene_Symbol=Cyc1 Isoform 1 of Cytochrome c1, heme protein, mitochondrial	1.1772	0.2353	0.0196
143	6	6	43.4	IPI:IPI00116154.2	Gene_Symbol=OTTMUSG00000000426;Cox5b;LOC100046079 cytochrome c oxidase	1.0005	0.0007	0.0891
144	6	6	46.7	IPI:IPI00265239.1	cytochrome c, somatic (Score:210 Exp: 6e-55) Gene_Symbol=ENSMUSG00000062	1.2490	0.3207	0.0852
145	6	6	24.1	IPI:IPI00874521.1	Gene_Symbol=- 17 kDa protein	0.8601	-0.2174	0.0573
146	6	6	25.3	IPI:IPI00135857.3	Superoxide dismutase [Cu-Zn] (Score:304 Exp:5e-83) Gene_Symbol=EG667310;LOC545845 hypothetical protein isoform 4	0.5966	-0.7451	0.04303
147	6	6	35.2	IPI:IPI00128346.1	Gene_Symbol=Cisd1 CDGSH iron sulfur domain-containing protein 1	1.0375	0.0530	0.5291
148	6	6	22	IPI:IPI00120451.1	Gene_Symbol=Fabp1 Fatty acid-binding protein, liver	0.9046	-0.1447	NA
149	5.8	5.8	20.7	IPI:IPI00109109.1	Gene_Symbol=Sod2 Superoxide dismutase [Mn], mitochondrial	0.5273	-0.9234	0.0287
150	5.79	5.79	19.8	IPI:IPI00881401.1	Gene_Symbol=Cpt2 carnitine palmitoyltransferase 2	1.2442	0.3152	NA
151	5.78	5.78	16.1	IPI:IPI00875638.1	Gene_Symbol=Immt Isoform 3 of Mitochondrial inner membrane protein	0.8022	-0.3179	0.028
152	5.7	5.7	53.5	IPI:IPI00225390.5	Gene_Symbol=Cox6b1 Cytochrome c oxidase subunit VIb isoform 1	0.7770	-0.3640	NA
153	5.53	5.53	17.2	IPI:IPI00895479.1	Gene_Symbol=2810422J05Rik 27 kDa protein	0.8830	-0.1796	0.291
154	5.31	5.31	18.1	IPI:IPI00230185.5	Gene_Symbol=Gpd1 Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	1.1784	0.2368	NA
155	5.22	5.22	11.7	IPI:IPI00884472.1	Gene_Symbol=Ctsh cathepsin H preproprotein	1.1335	0.1808	NA
156	5.15	5.15	9.6	IPI:IPI00463764.3	Gene_Symbol=Ugt3a2 UDP-glucuronosyltransferase 3A2	1.3410	0.4233	0.0623
157	5.12	5.12	10.3	IPI:IPI00403058.1	Gene_Symbol=Ganab Isoform 1 of Neutral alpha-glucosidase AB	0.8631	-0.2125	0.0109
158	5.1	5.1	25.7	IPI:IPI00762203.2	Gene_Symbol=Ftl1 Ferritin light chain 1	0.8844	-0.1773	0.0715

159	4.96	4.96	12.1	IPI:IPI00331692.1	Gene_Symbol=Dci Putative uncharacterized protein	1.2078	0.2723	NA
160	4.93	4.93	44.3	IPI:IPI00880613.1	Gene_Symbol=Ndufb10 18 kDa protein	1.5621	0.6435	NA
161	4.85	4.85	22.4	IPI:IPI00788331.1	Gene_Symbol=Gcdh glutaryl-Coenzyme A dehydrogenase	1.0575	0.0807	0.2742
162	4.85	4.85	16.5	IPI:IPI00666161.1	Gene_Symbol=EG624124;LOC634044 similar to ribosomal protein S7 isoform 1	0.8959	-0.1586	0.13885
163	4.82	4.82	3.7	IPI:IPI00624663.3	Gene_Symbol=Pzp Alpha-2-macroglobulin	1.1870	0.2473	0.0099
164	4.82	4.82	39.3	IPI:IPI00129516.1	Gene_Symbol=Uqcrh Cytochrome b-c1 complex subunit 6, mitochondrial	1.0335	0.0475	0.0642
165	4.68	4.68	22.3	IPI:IPI00457852.3	Gene_Symbol=EG432502 similar to ribosomal protein L6	0.7815	-0.3557	NA
166	4.67	4.67	8.6	IPI:IPI00387491.1	Gene_Symbol=Aass Alpha-aminoadipic semialdehyde synthase, mitochondrial	1.2373	0.3072	0.43535
167	4.48	4.48	27.8	IPI:IPI00308769.2	Gene_Symbol=Acot4 Acyl-coenzyme A thioesterase 4	0.7412	-0.4321	NA
168	4.12	4.12	4	IPI:IPI00759878.2	Gene_Symbol=C3 complement component 3	0.7577	-0.4004	NA
169	4.08	4.08	12.4	IPI:IPI00331552.4	Gene_Symbol=Pabpc1 Bone marrow macrophage cDNA, RIKEN full-length enriched li	0.8693	-0.2020	NA
170	4.06	6.06	10.1	IPI:IPI00163011.2	Gene_Symbol=Txndc5 Thioredoxin domain-containing protein 5	0.8165	-0.2924	0.0021
171	4.06	4.06	9.3	IPI:IPI00221569.1	Gene_Symbol=Zadh2 Zinc-binding alcohol dehydrogenase domain-containing protein	0.9547	-0.0669	0.2949
172	4.03	4.03	10.7	IPI:IPI00309073.2	Gene_Symbol=Mttp Microsomal triglyceride transfer protein B	0.9193	-0.1214	NA
173	4.03	4.03	27.7	IPI:IPI00323819.3	Gene_Symbol=Rps20 40S ribosomal protein S20	0.8686	-0.2032	0.1738
174	4.03	4.03	26.7	IPI:IPI00130640.5	Gene_Symbol=Hrsp12 Ribonuclease UK114	1.2647	0.3388	0.0477
175	4.02	4.02	14.5	IPI:IPI00776047.1	Gene_Symbol=Aifm1 Apoptosis-inducing factor, mitochondrion-associated 1	1.0357	0.0506	NA
176	4.01	4.29	10.7	IPI:IPI00123342.4	Gene_Symbol=Hyou1 Hypoxia up-regulated protein 1	1.0932	0.1286	NA
177	4.01	4.01	7.4	IPI:IPI00761390.1	Gene_Symbol=Slc27a2 solute carrier family 27 (fatty acid transporter), member 2	1.0392	0.0554	0.42855
178	4.01	4.01	21.9	IPI:IPI00319652.2	Gene_Symbol=Gpx1 Glutathione peroxidase 1	1.1824	0.2417	0.0504
179	4	4	40.6	IPI:IPI00880850.1	Gene_Symbol=Mgst1 26 kDa protein	1.7882	0.8385	NA
180	4	4	8.6	IPI:IPI00754992.1	Gene_Symbol=Rpn2 Ribophorin II	0.7544	-0.4067	0.3704
181	4	4	22	IPI:IPI00453777.2	Gene_Symbol=Atp5d ATP synthase subunit delta, mitochondrial	0.9944	-0.0081	0.0302
182	4	4	12.3	IPI:IPI00336324.1	Gene_Symbol=Mdh1 Malate dehydrogenase, cytoplasmic	1.1020	0.1401	0.1557
183	4	4	6.9	IPI:IPI00894832.1	Gene_Symbol=Ctsc Adult male kidney cDNA, RIKEN full-length enriched library, clone	0.9768	-0.0339	0.7359
184	4	4	12.3	IPI:IPI00776275.1	Gene_Symbol=Atp5c1 ATP synthase, H+ transporting, mitochondrial F1 complex, gam	1.0295	0.0419	0.5418
185	4	4	10.3	IPI:IPI00308187.1	Gene_Symbol=Vapb vesicle-associated membrane protein, associated protein B and	0.8909	-0.1667	NA
186	3.7	3.7	40.7	IPI:IPI00889996.1	Gene_Symbol=- 10 kDa protein	1.0250	0.0356	NA
187	3.35	3.35	4.6	IPI:IPI00850133.1	Gene_Symbol=1300010F03Rik Isoform 1 of Uncharacterized protein KIAA0564 homol	0.8891	-0.1697	NA
188	3.3	3.31	8.6	IPI:IPI00341282.2	Gene_Symbol=Atp5f1 ATP synthase subunit b, mitochondrial	1.3778	0.4624	NA
189	3.3	3.3	11.3	IPI:IPI00462903.1	Gene_Symbol=Dhrs4 Adult male kidney cDNA, RIKEN full-length enriched library, clon	0.9383	-0.0918	NA
190	3.3	3.3	5.5	IPI:IPI00554860.3	Gene_Symbol=Lipa lysosomal acid lipase A	0.8901	-0.1680	NA
191	3.26	3.26	15.3	IPI:IPI00134058.3	Gene_Symbol=Txndc4 Thioredoxin domain-containing protein 4	0.8137	-0.2975	NA
192	3.23	3.23	9.9	IPI:IPI00134809.2	Gene_Symbol=Dlst Isoform 1 of Dihydrolipoyllysine-residue succinyltransferase compo	1.1520	0.2041	NA
193	3.1	3.1	21.2	IPI:IPI00876005.1	Gene_Symbol=- 11 kDa protein	0.8430	-0.2464	NA
194	3.05	3.05	13.7	IPI:IPI00278580.6	Gene_Symbol=EG244913 hypothetical protein	0.8801	-0.1843	NA
195	3	3	15	IPI:IPI00127560.1	Gene_Symbol=Ttr Transthyretin	0.8548	-0.2264	NA
196	2.89	2.89	13.5	IPI:IPI00322760.7	Gene_Symbol=Prodh proline dehydrogenase	1.1710	0.2277	NA
197	2.86	2.86	24.3	IPI:IPI00555000.2	Gene_Symbol=Uqcrb Cytochrome b-c1 complex subunit 7	0.7419	-0.4308	NA
198	2.86	2.86	6.3	IPI:IPI00387282.4	Gene_Symbol=Aadac Arylacetamide deacetylase	0.8349	-0.2603	NA
199	2.68	2.68	9.1	IPI:IPI00115866.2	Gene_Symbol=Hagh Hydroxyacylglutathione hydrolase	0.9905	-0.0138	NA

200	2.67	2.67	9.9	IPI:IPI00135651.1	Gene_Symbol=Slc25a13 Calcium-binding mitochondrial carrier protein Aralar2	1.3875	0.4724	NA
201	2.63	2.63	7.7	IPI:IPI00111960.2	Gene_Symbol=Gaa Lysosomal alpha-glucosidase	0.9764	-0.0345	NA
202	2.58	2.58	12.8	IPI:IPI00753303.2	Dihydrodipicolinate synthase-like, mitochondrial (Score: 661 Exp:0.0) Gene_Symbol=	1.2292	0.2977	NA
203	2.48	2.48	16	IPI:IPI00626504.2	Gene_Symbol=EG668300 similar to Acidic ribosomal phosphoprotein P0	1.1733	0.2305	0.0412
204	2.43	2.43	7.3	IPI:IPI00831534.1	Gene_Symbol=Ephx1 51 kDa protein	1.2664	0.3407	NA
205	2.39	2.39	8.3	IPI:IPI00755120.2	Gene_Symbol=Rrbp1 ribosome binding protein 1 isoform a	1.0746	0.1038	NA
206	2.39	2.39	16	IPI:IPI00137787.3	Gene_Symbol=Rpl8 60S ribosomal protein L8	1.0689	0.0961	NA
207	2.36	2.36	7	IPI:IPI00845652.1	Gene_Symbol=Ogdh Isoform 3 of 2-oxoglutarate dehydrogenase E1 component, mitoc	1.0583	0.0818	NA
208	2.35	2.35	8.4	IPI:IPI00112128.1	Gene_Symbol=Hdhd3 Haloacid dehalogenase-like hydrolase domain-containing protei	1.0954	0.1314	NA
209	2.26	3.41	9.7	IPI:IPI00762185.2	Gene_Symbol=Mpst 3-mercaptopyruvate sulfurtransferase	1.0445	0.0628	NA
210	2.25	2.25	5.5	IPI:IPI00112089.3	Gene_Symbol=Tmem135 Transmembrane protein 135	1.1089	0.1491	NA
211	2.24	2.24	7.1	IPI:IPI00313236.3	Gene_Symbol=Slc27a5 Bile acyl-CoA synthetase	0.9940	-0.0088	NA
212	2.23	2.23	14.1	IPI:IPI00230540.1	Gene_Symbol=Vdac1 Isoform Mt-VDAC1 of Voltage-dependent anion-selective chann	1.2970	0.3751	NA
213	2.11	2.12	14.4	IPI:IPI00831130.1	Gene_Symbol=Glod4 Isoform 2 of Glyoxalase domain-containing protein 4	1.1721	0.2291	NA
214	2.1	2.1	13.5	IPI:IPI00454008.1	Gene_Symbol=Shmt2 Serine hydroxymethyltransferase	1.0022	0.0031	NA
215	2.08	2.08	11.3	IPI:IPI00116748.1	Gene_Symbol=Ndufa10 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subu	0.8762	-0.1906	NA
216	2.06	2.06	4.1	IPI:IPI00322936.1	Gene_Symbol=Plg Plasminogen	1.0568	0.0797	NA
217	2.04	2.04	7.3	IPI:IPI00410819.3	Gene_Symbol=Ddost Bone marrow macrophage cDNA, RIKEN full-length enriched libr	0.8375	-0.2558	NA
218	2.03	2.03	5.2	IPI:IPI00855212.1	Gene_Symbol=1110020G09Rik Isoform 2 of UPF0465 protein C5orf33 homolog	1.0351	0.0497	NA
219	2.01	2.01	9.3	IPI:IPI00625328.2	Gene_Symbol=Rnaset2a;Rnaset2b Ribonuclease T2	0.7112	-0.4917	NA
220	2.01	2.01	4.1	IPI:IPI00554961.3	Gene_Symbol=Fmo5 Dimethylaniline monooxygenase [N-oxide-forming] 5	1.4455	0.5316	NA
221	2	9.52	10.9	IPI:IPI00129755.2	Gene_Symbol=Serpina1b Alpha-1-antitrypsin 1-2	2.1974	1.1358	NA
222	2	8.75	21.7	IPI:IPI00460335.1	Gene_Symbol=Aldh4a1 Aldh4a1 protein	0.8919	-0.1651	NA
223	2	2.04	7.9	IPI:IPI00113386.1	Gene_Symbol=Ethe1 Protein ETHE1, mitochondrial	1.0901	0.1245	NA
224	2	2	11.9	IPI:IPI00606097.1	Gene_Symbol=Tmprss13 transmembrane protease, serine 13	0.9916	-0.0121	0.0593
225	2	2	15.3	IPI:IPI00850377.1	Gene_Symbol=100039840 similar to Glyceraldehyde-3-phosphate dehydrogenase (GA	1.1554	0.2084	NA
226	2	2	42.4	IPI:IPI00322562.5	Gene_Symbol=Rps14 40S ribosomal protein S14	0.9547	-0.0669	NA
227	2	2	7.3	IPI:IPI00153660.4	Gene_Symbol=Dlat Dihydrolipoyllysine-residue acetyltransferase component of pyruva	0.7536	-0.4081	NA
228	2	2	13.8	IPI:IPI00137491.1	Gene_Symbol=Acp5 Tartrate-resistant acid phosphatase type 5	0.7357	-0.4429	NA
229	2	2	22.7	IPI:IPI00475031.1	Gene_Symbol=Prdx5 Adult male tongue cDNA, RIKEN full-length enriched library, clon	1.0653	0.0912	NA
230	2	2	3	IPI:IPI00330523.1	Gene_Symbol=Pcca Propionyl-CoA carboxylase alpha chain, mitochondrial	1.1234	0.1679	NA
231	2	2	13.9	IPI:IPI00153373.1	Gene_Symbol=Cmbl Carboxymethylenebutenolidase homolog	0.8931	-0.1632	NA
232	2	2	7.9	IPI:IPI00121550.3	Gene_Symbol=Atp1b1 Sodium/potassium-transporting ATPase subunit beta-1	0.8105	-0.3032	NA
233	2	2	9.8	IPI:IPI00903355.1	Gene_Symbol=Rap1a Bone marrow macrophage cDNA, RIKEN full-length enriched lib	0.7375	-0.4394	NA
234	2	2	23.5	IPI:IPI00886222.1	Gene_Symbol=Ndufs6 11 kDa protein	1.0714	0.0995	NA
235	2	2	17.5	IPI:IPI00885860.1	Gene_Symbol=Apoc3 15 kDa protein	0.9397	-0.0897	NA
236	2	2	7.5	IPI:IPI00875416.1	Gene_Symbol=Sord 40 kDa protein	0.9278	-0.1082	NA
237	2	2	19.3	IPI:IPI00850964.1	Gene_Symbol=LOC100046223 similar to insulinoma protein (rig) isoform 1	0.8622	-0.2140	NA
238	2	2	36.8	IPI:IPI00667117.2	Gene_Symbol=Dbi Acyl-CoA-binding protein	0.4849	-1.0444	NA
239	2	2	3.2	IPI:IPI00652358.5	Gene_Symbol=Arsb Isoform 1 of Arylsulfatase B	1.2365	0.3063	NA
240	2	2	16.8	IPI:IPI00344004.3	Gene_Symbol=Ndufa12 NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 12	0.8561	-0.2242	NA

241	2	2	16.4	IPI:IPI00315794.1	Gene_Symbol=Cyb5b Cytochrome b5 type B	1.1712	0.2280	NA
242	2	2	5.1	IPI:IPI00274222.2	Gene_Symbol=Acad8 Isobutyryl-CoA dehydrogenase, mitochondrial	0.8468	-0.2399	NA