Stab 1. Table of significantly changed proteins in four two-group comparisor

Functional Annotation	GO ID	GO Term	IPI	Gene Symbol	Name	Sham mCAT vs sham WT				TAC WT vs sham WT				TAC mCAT vs TAC WT				TAC mCAT vs sham mCAT			
						log2 Fold	S.E.	p.value	q.value	log2 Fold	S.E.	p.value	q.value	log2 Fold	S.E.	p.value	q.value	log2 Fold	S.E.	p.value	q.value
Fatty acid metabolism	GO:0006635	fatty acid beta-oxidation	IPI:IPI00119114,	Acadl	acyl-Coenzyme A dehydrogenase, long-chain	-0.353	0.117	0.003	0.093	-0.439	0.135	0.002	0.007								
			IPI:IPI00119203,	Acadvl	acyl-Coenzyme A dehydrogenase, very long chain													0.207	0.098	0.036	0.090
			IPI:IPI00116591,	Acads	acyl-Coenzyme A dehydrogenase, short chain					-1.962	0.751	0.011	0.025								
			IPI:IPI00121105	Hadh	hydroxyacyl-Coenzyme A dehydrogenase									0.364	0.146	0.018	0.125				
			IPI:IPI00331628	Hsd17b4	hydroxysteroid (17-beta) dehydrogenase 4					-8.791	3.409	0.030	0.050								
			IPI:IPI00226430,	Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxo					-1.892	0.503	0.000	0.002								
			IPI:IPI00387379	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial					-0.287	0.134	0.039	0.061								
			IPI:IPI00856855	Crat	carnitine acetyltransferase					-0.690	0.297	0.045	0.065								
	GO:0019395	fatty acid oxidation	IPI:IPI00120233,	Gcdh	glutaryl-Coenzyme A dehydrogenase					-0.434	0.115	0.020	0.037								
	GO:0046320	regulation of fatty acid oxidatio	IPI:IPI00131584	Slc25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitin	-0.913	0.257	0.024	0.243												
	GO:0009062	fatty acid catabolic process	IPI:IPI00330754	Bdh1	3-hydroxybutyrate dehydrogenase, type 1					0.481	0.135	0.002	0.007	-0.292	0.116	0.019	0.125				
			IPI:IPI00857778	Bdh1	3-hydroxybutyrate dehydrogenase, type 1					0.287	0.134	0.045	0.065	-0.304	0.124	0.024	0.147				
			IPI:IPI00890322	Bdh1	3-hydroxybutyrate dehydrogenase, type 1					0.464	0.133	0.002	0.008	-0.289	0.123	0.027	0.157				
	GO:0006631	fatty acid metabolic process	IPI:IPI00649159	Cpt2	carnitine palmitoyltransferase 2					0.300	0.129	0.035	0.057								
			IPI:IPI00895351	Ech1	enoyl coenzyme A hydratase 1, peroxisomal					-0.877	0.230	0.001	0.006								
	GO:0006637	acyl-CoA metabolic process	IPI:IPI00127625,	Hmgcl	3-hydroxy-3-methylglutaryl-Coenzyme A lyase									-1.215	0.390	0.036	0.186				
	GO:0006084	acetyl-CoA metabolic process	IPI:IPI00469942	Acss1	acyl-CoA synthetase short-chain family member 1	-0.248	0.089	0.008	0.137									0.183	0.082	0.032	0.084
Glucose metabolism	GO:0006096	glycolysis	IPI:IPI00283611,	Hk1	hexokinase 1					2.480	0.247	0.000	0.000	-0.924	0.179	0.000	0.001	1.560	0.228	0.000	0.000
			IPI:IPI00114342	Hk2	hexokinase 2									-0.793	0.253	0.005	0.045				
	GO:0006006	glucose metabolic process	IPI:IPI00337893	Pdha1	pyruvate dehydrogenase E1 alpha 1									-0.238	0.114	0.040	0.194				
			IPI:IPI00132042	Pdhb	pyruvate dehydrogenase (lipoamide) beta	-0.459	0.158	0.005	0.114	-0.556	0.195	0.006	0.019	-0.246	0.119	0.042	0.199				
			IPI:IPI00122251	Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2													0.505	0.203	0.034	0.086
	GO:0005996	onosaccharide metabolic proce	IPI:IPI00222767	Pdhx	pyruvate dehydrogenase complex, component X									-0.361	0.162	0.035	0.186				
			IPI:IPI00221407,	Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1					0.647	0.199	0.010	0.024					0.738	0.275	0.025	0.072
TCA cycle	GO:0006099	tricarboxylic acid cycle	IPI:IPI00109169	Idh3g	isocitrate dehydrogenase 3 (NAD+), gamma					0.556	0.100	0.000	0.000	-0.417	0.117	0.001	0.013				
			IPI:IPI00323592	Mdh2	malate dehydrogenase 2, NAD (mitochondrial)	-0.194	0.095	0.044	0.352	0.322	0.104	0.002	0.010								
			IPI:IPI00261627	Sucla2	succinate-Coenzyme A ligase, ADP-forming, beta subunit	-0.289	0.090	0.002	0.093									0.305	0.091	0.002	0.011
			IPI:IPI00845858,	Dlst	dihydrolipoamide S-succinyltransferase (E2 component of	-0.398	0.160	0.017	0.191	-0.523	0.183	0.007	0.021								
			IPI:IPI00318614,	Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	-0.233	0.073	0.002	0.073	-0.249	0.108	0.025	0.045					-0.287	0.088	0.002	0.011
Amino acid metabolism	GO:0009083	chain family amino acid catabol	IPI:IPI00115302,	Bckdhb	branched chain ketoacid dehydrogenase E1, beta polypep													0.635	0.183	0.007	0.028
			IPI:IPI00274222	Acad8	acyl-Coenzyme A dehydrogenase family, member 8	-0.409	0.125	0.006	0.115					-0.302	0.121	0.026	0.153				
			IPI:IPI00154047	Hibch	3-hydroxyisobutyryl-Coenzyme A hydrolase	-0.406	0.183	0.032	0.318									0.510	0.210	0.020	0.066
	GO:0006552 :	leucine catabolic process	IPI:IPI00471246	Ivd	isovaleryl coenzyme A dehydrogenase	-0.372	0.083	0.000	0.006												
	GO:0009098	leucine biosynthetic process	IPI:IPI00122442,	Bcat2	branched chain aminotransferase 2, mitochondrial	-0.414	0.148	0.011	0.156	-0.501	0.116	0.000	0.002								
Electron Transport Chain	GO:0006744	ubiquinone biosynthetic proces	IPI:IPI00467124	Coq3	coenzyme Q3 homolog, methyltransferase (yeast)													0.742	0.320	0.045	0.103
	GO:0022904	spiratory electron transport cha	IPI:IPI00117978	Cox4i1	cytochrome c oxidase subunit IV isoform 1					-0.425	0.197	0.041	0.062								
			IPI:IPI00116154	Cox5b	cytochrome c oxidase, subunit Vb													-3.424	1.404	0.021	0.067
			IPI:IPI00785410	Cox5b	cytochrome c oxidase, subunit Vb													-3.257	1.335	0.021	0.067
			IPI:IPI00320238	Cox6a2	cytochrome c oxidase, subunit VI a, polypeptide 2					-1.184	0.178	0.003	0.010								
			IPI:IPI00131771	Cox6c	cytochrome c oxidase, subunit VIc					0.469	0.104	0.000	0.003	-0.330	0.076	0.001	0.009				
			IPI:IPI00131176	COX2	cytochrome c oxidase subunit II													-1.899	0.604	0.005	0.023
			IPI:IPI00120136	Cox7a2l	cytochrome c oxidase subunit VIIa polypeptide 2-like					0.719	0.132	0.006	0.018	-0.845	0.030	0.000	0.001				
			IPI:IPI00224210	Uqcrq	ubiquinol-cytochrome c reductase, complex III subunit VII													0.413	0.141	0.017	0.057
			IPI:IPI00881846	Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5					0.358	0.117	0.014	0.029								
			IPI:IPI00882043,	Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5					0.268	0.116	0.037	0.059								
			IPI:IPI00132216	Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3					0.191	0.061	0.035	0.057								
			IPI:IPI00876321,	Uqcr10	ubiquinol-cytochrome c reductase, complex III subunit X	1.015	0.324	0.035	0.318	1.329	0.367	0.022	0.042								
			IPI:IPI00132728,	Cyc1	cytochrome c-1					0.434	0.112	0.000	0.003					0.366	0.126	0.007	0.027
			IPI:IPI00133403	Ndufb3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3					-2.074	0.365	0.005	0.016								
			IPI:IPI00882287	Etfdh	electron transferring flavoprotein, dehydrogenase													1.624	0.753	0.034	0.086
			IPI:IPI00119138	Uqcrc2	ubiquinol cytochrome c reductase core protein 2					0.310	0.105	0.004	0.015	-0.367	0.173	0.037	0.188				
			IPI:IPI00133399	Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6					4.123	1.560	0.014	0.029								
			IPI:IPI00116748	Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 1					0.512	0.091	0.000	0.000	-0.232	0.072	0.002	0.023				
			IPI:IPI00132347,	Uqcrb	ubiquinol-cytochrome c reductase binding protein					-1.724	0.596	0.044	0.065								
			IPI:IPI00400230	Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4					0.538	0.148	0.003	0.010					0.467	0.205	0.039	0.094
			IPI:IPI00121288	Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10					0.412	0.136	0.007	0.021								
			IPI:IPI00121309	Ndufs3	NADH dehydrogenase (ubiquinone) Fe-S protein 3					0.710	0.085	0.000	0.000					0.479	0.147	0.003	0.016
			IPI:IPI00225390	Cox6b1	cytochrome c oxidase, subunit VIb polypeptide 1									-0.265	0.126	0.050	0.219				
			IPI:IPI00121440	Etfb	electron transferring flavoprotein, beta polypeptide	-0.354	0.119	0.004	0.114	-0.370	0.127	0.005	0.017								
			IPI:IPI00308882	Ndufs1	NADH dehydrogenase (ubiquinone) Fe-S protein 1													-1.727	0.694	0.014	0.051
			IPI:IPI00128345	Ndufs6	NADH dehydrogenase (ubiquinone) Fe-S protein 6					0.636	0.185	0.004	0.014								
			IPI:IPI00886222	Ndufs6	NADH dehydrogenase (ubiquinone) Fe-S protein 6					0.898	0.228	0.003	0.013								
			IPI:IPI00757916	LOC10004569	similar to Electron transferring flavoprotein, beta polypeptid	-0.360	0.130	0.008	0.137	-0.372	0.139	0.010	0.024								
			IPI:IPI00848492	LOC10004569	similar to Electron transferring flavoprotein, beta polypeptid	-0.360	0.130	0.008	0.137	-0.372	0.139	0.010	0.024								
ATP synthesis	GO:0015866	ADP transport	IPI:IPI00115564	Slc25a4	solute carrier family 25 (mitochondrial carrier, adenine nucl					0.538	0.118	0.000	0.000	0.294	0.116	0.013	0.097	0.698	0.128	0.000	0.000
	GO:0015986	synthesis coupled proton trans	IPI:IPI00341282	Atp5f1	ATP synthase, H+ transporting, mitochondrial F0 complex,					0.314	0.151	0.044	0.065	-0.393	0.129	0.004	0.040				
			IPI:IPI00111770	Atp5k	ATP synthase, H+ transporting, mitochondrial F1F0 comple					0.398	0.178	0.038	0.060								
	GO:0055085	transmembrane transport	IPI:IPI00919068	Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex,					0.301	0.131	0.047	0.065	-0.404	0.086	0.001	0.013				
			IPI:IPI00271986,	Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 complex,					1.061	0.211	0.007	0.021								
			IPI:IPI00230507	Atp5h	ATP synthase, H+ transporting, mitochondrial F0 complex,					-0.443	0.211	0.044	0.065					-0.526	0.200	0.013	0.047
	GO:0045980	negative regulation of nucleoti	IPI:IPI00127598,	Atpif1	ATPase inhibitory factor 1					0.785	0.276	0.047	0.065								
	GO:0046939	nucleotide phosphorylation	IPI:IPI00221769,	Ak3	adenylate kinase 3					0.662	0.143	0.010	0.024								
Other metabolic process	GO:0008152	metabolic process	IPI:IPI00111218	Aldh2	aldehyde dehydrogenase 2, mitochondrial													0.300	0.119	0.015	0.051
			IPI:IPI00133553,	Mut	methylmalonyl-Coenzyme A mutase	-0.452	0.133	0.003	0.093									0.312	0.147	0.047	0.103
			IPI:IPI00320850	Mccc1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	-0.229	0.091	0.016	0.188												
			IPI:IPI00117214	Hsdl2	hydroxysteroid dehydrogenase like 2	-0.312	0.139	0.035	0.318	-0.566	0.144	0.001	0.003								
			IPI:IPI00649718	Hsdl2	hydroxysteroid dehydrogenase like 2					-1.128	0.342	0.030	0.050								
			IPI:IPI00649973	Hsdl2	hydroxysteroid dehydrogenase like 2					-0.752	0.248	0.014	0.029					-0.740	0.194	0.004	0.020
			IPI:IPI00113073	Aldh1b1	aldehyde dehydrogenase 1 family, member B1													2.406	0.698	0.026	0.075
			IPI:IPI00461964	Aldh6a1	aldehyde dehydrogenase family 6, subfamily A1	-0.240	0.082	0.005	0.114	-0.414	0.091	0.000	0.000								
			IPI:IPI00154054	Acat1	acetyl-Coenzyme A acetyltransferase 1									-1.356	0.647	0.039	0.192				
			IPI:IPI00320716,	Rtn4ip1	reticulon 4 interacting protein 1													-0.650	0.229	0.047	0.103

Apoptosis	GO:0006915	apoptosis	IPI:IPI00122547	Vdac2	voltage-dependent anion channel 2					0.509	0.087	0.000	0.000	-0.354	0.116	0.004	0.038				
			IPI:IPI00750490	Vdac2	voltage-dependent anion channel 2					0.537	0.134	0.001	0.003								
			IPI:IPI00122549,	Vdac1	voltage-dependent anion channel 1					0.202	0.084	0.020	0.037	-0.342	0.092	0.000	0.006				
			IPI:IPI00857067	Vdac1	voltage-dependent anion channel 1									-0.433	0.114	0.000	0.006				
			IPI:IPI00129577,	Aifm1	apoptosis-inducing factor, mitochondrion-associated 1					0.278	0.102	0.009	0.024	-0.331	0.081	0.000	0.003				
	GO:0006916	anti-apoptosis	IPI:IPI00133034	Hint2	histidine triad nucleotide binding protein 2													0.224	0.103	0.047	0.103
			IPI:IPI00308885	Hspd1	heat shock protein 1 (chaperonin)					0.328	0.083	0.000	0.001					0.313	0.124	0.014	0.051
			IPI:IPI00845678	Hspd1	heat shock protein 1 (chaperonin)					0.307	0.135	0.030	0.050								
	GO:0001836	release of cytochrome c from r	IPI:IPI00111045	Timm50	translocase of inner mitochondrial membrane 50 homolog					1.115	0.166	0.000	0.001					0.682	0.252	0.024	0.072
	GO:0042981	regulation of apoptosis	IPI:IPI00116228	Ppif	peptidylprolyl isomerase F (cyclophilin F)					0.430	0.161	0.013	0.029					0.493	0.170	0.008	0.031
	GO:0043066	negative regulation of apoptosis	IPI:IPI00133440	Phb	prohibitin					0.643	0.074	0.000	0.000	-0.293	0.072	0.000	0.004	0.355	0.088	0.000	0.003
			IPI:IPI00649084	Phb	prohibitin					0.649	0.086	0.000	0.000	-0.298	0.082	0.001	0.013	0.415	0.100	0.000	0.003
Proteolysis	GO:0000045	autophagic vacuole assembly,	IPI:IPI00111013,	Ctsd	cathepsin D													1.047	0.286	0.005	0.023
	GO:0006457	protein folding	IPI:IPI00133903	Hspa9	heat shock protein 9	-0.215	0.087	0.016	0.188	0.311	0.094	0.002	0.008					0.430	0.087	0.000	0.000
			IPI:IPI00880839	Hspa9	heat shock protein 9	-0.215	0.087	0.016	0.188	0.311	0.094	0.002	0.008					0.430	0.087	0.000	0.000
			IPI:IPI00263863	Hspe1	heat shock protein 1 (chaperonin 10)	-0.367	0.155	0.033	0.318												
			IPI:IPI00117083	Grpel1	GrpE-like 1, mitochondrial													0.374	0.137	0.023	0.071
	GO:0006508	proteolysis	IPI:IPI00331564	Dld	dihydrolipoamide dehydrogenase	-0.451	0.168	0.009	0.150	-1.790	0.796	0.028	0.049								
			IPI:IPI00874456	Dld	dihydrolipoamide dehydrogenase	-0.446	0.157	0.006	0.119	-1.583	0.707	0.029	0.049								
			IPI:IPI00331436,	Lap3	leucine aminopeptidase 3					0.871	0.227	0.002	0.008					1.184	0.296	0.001	0.011
			IPI:IPI00170357	Afg3l2	AFG3(ATPase family gene 3)-like 2 (yeast)					0.748	0.219	0.027	0.048								
			IPI:IPI00319518,	Lonp1	lon peptidase 1, mitochondrial	-0.300	0.125	0.023	0.238	0.405	0.145	0.009	0.024	-0.464	0.086	0.000	0.001				
Response to stimuli	GO:0000165	MAPKKK cascade part of GO	IPI:IPI00321190	Psap	prosaposin					1.445	0.377	0.019	0.037								
	GO:0042744	drogen peroxide catabolic proce	IPI:IPI00116192	Prdx3	peroxiredoxin 3	-0.223	0.088	0.016	0.188												
			IPI:IPI00312058	Cat	catalase	7.215	1.662	0.000	0.008					4.659	1.526	0.004	0.041				
			IPI:IPI00869393	Cat	catalase	7.024	1.590	0.000	0.008					4.563	1.463	0.004	0.038				
	GO:0000302	sponse to reactive oxygen spec	IPI:IPI00130589	Sod1	superoxide dismutase 1, soluble					-0.981	0.251	0.017	0.035					-0.716	0.212	0.028	0.076
			IPI:IPI00124699,	Txnrd2	thioredoxin reductase 2					0.591	0.198	0.040	0.061								
			IPI:IPI00125652	Txn2	thioredoxin 2									-0.292	0.091	0.033	0.183				
	GO:0071333	lular response to glucose stimu	IPI:IPI00132653,	Oxct1	3-oxoacid CoA transferase 1					0.255	0.125	0.047	0.065	-0.326	0.111	0.005	0.041				
			IPI:IPI00856651	Oxct1	3-oxoacid CoA transferase 1									-0.302	0.114	0.013	0.097				
ranscription and translatic	GO:0045449	regulation of transcription	IPI:IPI00420706,	Lrpprc	leucine-rich PPR-motif containing					0.464	0.098	0.000	0.001					0.659	0.150	0.000	0.002
			IPI:IPI00120414,	Dnaja3	DnaJ (Hsp40) homolog, subfamily A, member 3					0.846	0.177	0.009	0.024								
	GO:0070125	mitochondrial translational elor	IPI:IPI00230283,	Gfm1	G elongation factor, mitochondrial 1					0.795	0.228	0.004	0.013					0.939	0.271	0.004	0.019
	GO:0006412	translation	IPI:IPI00315808	Mrps36	mitochondrial ribosomal protein S36									-0.752	0.202	0.020	0.129				
			IPI:IPI00121359	Mrpl4	mitochondrial ribosomal protein L4													1.491	0.491	0.039	0.094
			IPI:IPI00274407	Tufm	Tu translation elongation factor, mitochondrial	-0.210	0.099	0.039	0.331	0.461	0.091	0.000	0.000	-0.447	0.095	0.000	0.001	0.225	0.095	0.021	0.067
			IPI:IPI00460132	Tufm	Tu translation elongation factor, mitochondrial	-0.216	0.105	0.044	0.352	0.454	0.097	0.000	0.000	-0.456	0.103	0.000	0.001	0.215	0.101	0.038	0.093
Transmembrane transpor	GO:0006820	anion transport	IPI:IPI00122548	Vdac3	voltage-dependent anion channel 3					-1.884	0.865	0.034	0.057								
			IPI:IPI00876341	Vdac3	voltage-dependent anion channel 3					-1.784	0.822	0.035	0.057								
	GO:0055085	transmembrane transport	IPI:IPI00127841	Slc25a5	solute carrier family 25 (mitochondrial carrier, adenine nucl					1.475	0.514	0.005	0.017					1.203	0.410	0.004	0.021
			IPI:IPI00124771	Slc25a3	solute carrier family 25 (mitochondrial carrier, phosphate ca					-2.621	1.280	0.047	0.065								
			IPI:IPI00135651	Slc25a13	solute carrier family 25 (mitochondrial carrier, adenine nucl	0.273	0.103	0.010	0.152	0.759	0.117	0.000	0.000					0.530	0.120	0.000	0.000
			IPI:IPI00648357	Slc25a11	solute carrier family 25 (mitochondrial carrier oxoglutarate									0.379	0.151	0.018	0.125				
			IPI:IPI00265371	Slc25a31	solute carrier family 25 (mitochondrial carrier; adenine nucl					0.623	0.191	0.006	0.018					0.566	0.229	0.027	0.076
			IPI:IPI00308162	Slc25a12	solute carrier family 25 (mitochondrial carrier, Aralar), mem	0.143	0.068	0.038	0.331	0.537	0.061	0.000	0.000					0.301	0.099	0.003	0.019
	GO:0045040 :	protein import into mitochondri	IPI:IPI00221608	Samm50	sorting and assembly machinery component 50 homolog (					0.592	0.164	0.001	0.004					0.572	0.183	0.003	0.019
Development	GO:0060562	epithelial tube morphogenesis	IPI:IPI00117657,	Opa1	optic atrophy 1 homolog (human)													0.516	0.167	0.004	0.019
			IPI:IPI00918980	Opa1	optic atrophy 1 homolog (human)					0.746	0.188	0.001	0.004					0.759	0.206	0.002	0.011
			IPI:IPI00919056	Opa1	optic atrophy 1 homolog (human)					0.752	0.248	0.014	0.029								
	GO:0042407	cristae formation	IPI:IPI00131177	letm1	leucine zipper-EF-hand containing transmembrane protein					0.871	0.164	0.000	0.001					0.569	0.163	0.004	0.019
Others			IPI:IPI00132799	C1qbp	complement component 1, q subcomponent binding protei	-0.508	0.173	0.017	0.188					-0.373	0.132	0.020	0.128	0.395	0.165	0.040	0.095
			IPI:IPI00115827,	Gbas	glioblastoma amplified sequence													-0.330	0.161	0.048	0.104
			IPI:IPI00845783,	Myl10	myosin, light chain 10, regulatory													-19.697	0.742	0.000	0.000
			IPI:IPI00113386	Ethe1	ethylmalonic encephalopathy 1	-0.408	0.107	0.001	0.049									0.278	0.106	0.015	0.053
			IPI:IPI00133562,	Chchd3	coiled-coil-helix-coiled-coil-helix domain containing 3					0.330	0.118	0.014	0.029								
			IPI:IPI00468653,	Pccb	propionyl Coenzyme A carboxylase, beta polypeptide	-0.448	0.091	0.000	0.001									0.363	0.076	0.000	0.000
			IPI:IPI00918838	Pccb	propionyl Coenzyme A carboxylase, beta polypeptide	-0.365	0.117	0.007	0.137									0.354	0.148	0.032	0.083
			IPI:IPI00122554,	Cabc1	aarF domain containing kinase 3													0.423	0.107	0.001	0.008
			IPI:IPI00113049,	Coq10b	coenzyme Q10 homolog B (S. cerevisiae)					-1.445	0.332	0.012	0.028								
			IPI:IPI00120671	Isca2	iron-sulfur cluster assembly 2 homolog (S. cerevisiae)					0.523	0.201	0.029	0.049					0.546	0.129	0.002	0.015
			IPI:IPI00555088	Immt	inner membrane protein, mitochondrial					0.610	0.217	0.048	0.066	-0.688	0.244	0.048	0.217				
			IPI:IPI00122740	Macrod1	MACRO domain containing 1	-0.289	0.111	0.015	0.188	-0.239	0.095	0.018	0.035								
			IPI:IPI00330523	Pcca	propionyl-Coenzyme A carboxylase, alpha polypeptide	-0.309	0.104	0.005	0.114	0.305	0.092	0.002	0.009	-0.249	0.104	0.022	0.133	0.365	0.123	0.005	0.023
			IPI:IPI00858124	Pcca	propionyl-Coenzyme A carboxylase, alpha polypeptide	-0.505	0.166	0.039	0.331					-0.534	0.139	0.019	0.125				
			IPI:IPI00462903	Dhrs4	dehydrogenase/reductase (SDR family) member 4									-0.203	0.095	0.044	0.204				
			IPI:IPI00170307	Apoa1bp	apolipoprotein A-I binding protein					0.592	0.198	0.041	0.061								
Not characterized			IPI:IPI00850133	1300010F03Ri	RIKEN cDNA 1300010F03 gene									0.190	0.087	0.038	0.189				
			IPI:IPI00126917	1700071K01Ri	RIKEN cDNA 1700071K01 gene					0.640	0.108	0.000	0.000	-0.324	0.109	0.008	0.064	0.374	0.131	0.010	0.037
			IPI:IPI00461249	Gm12141	predicted gene 12141					0.261	0.098	0.010	0.025								
			IPI:IPI00462250	Gm5529	predicted pseudogene 5529					0.778	0.151	0.000	0.000					0.778	0.179	0.000	0.001
			IPI:IPI00264082	Gm6293	predicted pseudogene 6293	1.015	0.324	0.035	0.318	1.329	0.367	0.022	0.042								
			IPI:IPI00475158	Gm12251	predicted gene 12251					0.664	0.096	0.000	0.000					0.474	0.196	0.023	0.071
			IPI:IPI00135857	Gm8566	predicted pseudogene 8566					-0.981	0.251	0.017	0.035					-0.716	0.212	0.028	0.076
			IPI:IPI00849166	Gm2893	predicted gene 2893					0.421	0.124	0.004	0.015								
			IPI:IPI00120715	Gm14494	predicted gene 14494					0.646	0.192	0.028	0.049								
			IPI:IPI00853920	LOC10004410	similar to thioredoxin reductase 2					0.591	0.198	0.040	0.061								
			IPI:IPI00850430	LOC10004615	phosphate carrier protein, mitochondrial-like					-2.496	1.228	0.049	0.066								
			IPI:IPI00850215	LOC10004888	similar to AFG3(ATPase family gene 3)-like 2 (yeast)					0.748	0.219	0.027	0.048								