

**Table S4**

Gene category 2 ENSEMBL_gene_id	Glomerulus cDNA clones ENSEMBL_gene_name	Clone id	log2(glo/rest_kidney)	Pvalue
1 ENSMUSG00000019278	Microsomal dipeptidase precursor (EC 3.4.13.19) (MDP) (Dehydropeptidase-I) (Renal dipeptidase) (RDP). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602476545	-2.86	0.00269
2 ENSMUSG00000028766	Alkaline phosphatase, tissue-nonspecific isozyme precursor (EC 3.1.3.1) (AP-TNAP) (TNSALP). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602475017	-2.77	0.00504
3 ENSMUSG00000033197	Fructose-1,6-bisphosphatase (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase). [Source:UniProt/SwissProt;Acc:Q9QZD8]	gbctl04_plate7_L17	-2.65	0.00312
4 ENSMUSG000000021490	Renal sodium-dependent phosphate transport protein 2 (Sodium/phosphate cotransporter 2) (Na(+)/Pi cotransporter 2) (SLC36A1). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602472912	-2.58	0.00239
5 ENSMUSG00000022821	Homogentisate 1,2-dioxygenase (EC 1.13.11.5) (Homogentisicase) (Homogentisate oxygenase) (Homogentisic acid dioxygenase). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602471885	-2.58	0.00307
6 ENSMUSG00000027227	Sorbitol dehydrogenase (EC 1.1.1.14) (L-iditol 2-dehydrogenase) (Fragment). [Source:UniProt/SwissProt;Acc:Q9QZD8]	gbctl04_plate14_J08	-2.57	0.00239
7 ENSMUSG00000028737	aldehyde dehydrogenase 4 family, member A1. [Source:RefSeq;Acc:NM_175438]	gbctl04_plate14_I09	-2.51	0.00300
8 ENSMUSG00000005269		MTG_602472323	-2.43	0.00239
9 ENSMUSG00000023013	Aquaporin-CD (AQP-CD) (Water channel protein for renal collecting duct) (ADH water channel) (Aquaporin 2) (Co aquaporin 2). [Source:UniProt/SwissProt;Acc:Q9QZD8]	gbctl04_plate11_J06	-2.39	0.00265
10 ENSMUSG00000025792	Mitochondrial dicarboxylate carrier. [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602473893	-2.39	0.00239
11 ENSMUSG00000020432	Transcobalamin II precursor (TCII) (TC II). [Source:UniProt/SwissProt;Acc:O88968]	gbctl04_plate8_O14	-2.38	0.00302
12 ENSMUSG000000028607	Carnitine O-palmitoyltransferase II, mitochondrial precursor (EC 2.3.1.21) (CPT II). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602472017	-2.37	0.00340
13 ENSMUSG00000036395		MTG_602472165	-2.3	0.00315
14 ENSMUSG00000002204	Kidney-derived aspartic protease-like protein precursor (EC 3.4.23.-) (KDAP-1) (KAP) (Napsin). [Source:UniProt/SwissProt;Acc:Q9QZD8]	gbctl04_plate9_O16	-2.26	0.00471
15 ENSMUSG00000026295	Secreted phosphoprotein 24 precursor (Spp-24) (Secreted phosphoprotein 2). [Source:UniProt/SwissProt;Acc:Q9QZD8]	gbctl04_plate3_O15	-2.26	0.00422
16 ENSMUSG00000038298	PDZ domain containing 1. [Source:RefSeq;Acc:NM_021517]	gbctl04_plate17_K20	-2.26	0.00272
17 ENSMUSG00000009772	SNF1/AMP-activated protein kinase. [Source:RefSeq;Acc:NM_028778]	MTG_602470810	-2.24	0.00276
18 ENSMUSG00000021335	Renal sodium-dependent phosphate transport protein 1 (Sodium/phosphate cotransporter 1) (Na(+)/Pi cotransporter 1) (SLC36A1). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602477591	-2.22	0.00272
19 ENSMUSG00000058620	Alpha-2B adrenergic receptor (Alpha-2B adrenoceptor) (Alpha-2B adrenoceptor). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602475509	-2.22	0.01048
20 ENSMUSG000000059666		gbctl04_plate6_E15	-2.19	0.01850
21 ENSMUSG00000018339		MTG_602475610	-2.16	0.00239
22 ENSMUSG00000030088	10-formyltetrahydrofolate dehydrogenase (EC 1.5.1.6) (10-FTHFDH). [Source:UniProt/SwissProt;Acc:Q8R0Y6]	MTG_602471275	-2.16	0.00272
23 ENSMUSG00000055312		MTG_602467761	-2.15	0.00975
24 ENSMUSG000000026726	Cubilin (Fragment). [Source:UniProt/SPTREMBL;Acc:Q9JLB4]	MTG_602472474	-2.12	0.01622
25 ENSMUSG00000027463		MTG_602470710	-2.1	0.00291
26 ENSMUSG000000000278	Retinoid-inducible serine carboxypeptidase precursor (EC 3.4.16.-). [Source:UniProt/SwissProt;Acc:Q920A5]	MTG_602296404	-2.06	0.00495
27 ENSMUSG000000028199	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinone reductase) (Zeta- crystallin). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602474534	-2.05	0.00246
28 ENSMUSG000000029090		MTG_602470853	-2.02	0.04447
29 ENSMUSG00000028307	Fructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase) (Aldolase 2). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602476083	-2.01	0.00260
30 ENSMUSG00000052520	Cytochrome P450 2J5 (EC 1.14.14.1) (CYP11J5) (Arachidonic acid epoxidase). [Source:UniProt/SwissProt;Acc:Q9QZD8]	gbctl04_plate13_I05	-2.01	0.00264
31 ENSMUSG00000024650	solute carrier family 22 member 6; organic cationic transporter-like 1. [Source:RefSeq;Acc:NM_008766]	MTG_602477071	-1.98	0.00512
32 ENSMUSG000000019810		gbctl04_plate7_A13	-1.94	0.00391
33 ENSMUSG00000031766	Solute carrier family 12 member 3 (Thiazide-sensitive sodium-chloride cotransporter) (Na-Cl symporter). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602470481	-1.92	0.00307
34 ENSMUSG00000036880	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase). [Source:RefSeq;Acc:NM_117000]	MTG_602468447	-1.92	0.00562
35 ENSMUSG00000001827	Folate receptor alpha precursor (FR-alpha) (Folate receptor 1) (Folate-binding protein 1). [Source:UniProt/SwissProt;Acc:Q9QZD8]	gbctl04_plate12_P06	-1.9	0.00900
36 ENSMUSG000000020456	2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor (EC 1.2.4.2) (Alpha-ketoglutarate dehydrogenase E1 component). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602472411	-1.88	0.02222
37 ENSMUSG00000022613	Inositol oxygenase (EC 1.13.99.1) (Myo-inositol oxygenase) (Aldehyde reductase-like 6) (Renal-specific oxidoreductase). [Source:UniProt/SwissProt;Acc:Q9QZD8]	gbctl04_plate16_D05	-1.88	0.00803
38 ENSMUSG00000033295	protein tyrosine phosphatase, receptor type, F; leukocyte antigen-related (LAR) PTP receptor. [Source:RefSeq;Acc:Q9QZD8]	gbctl04_plate12_P16	-1.84	0.01346
39 ENSMUSG00000000594	Ganglioside GM2 activator precursor (GM2-AP) (Cerebroside sulfate activator protein) (Shingolipid activator protein). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602472911	-1.83	0.00305
40 ENSMUSG000000054733	Peptide methionine sulfoxide reductase (EC 1.8.4.6) (Protein- methionine-S-oxide reductase) (PMSR) (Peptide methionine sulfoxide reductase). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602472804	-1.8	0.00333
41 ENSMUSG00000063903	Glandular kallikrein K3 precursor (EC 3.4.21.35) (Tissue kallikrein 3) (mGK-3) (7S nerve growth factor gamma chain). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602472966	-1.78	0.02265
42 ENSMUSG000000017760	Lysosomal protective protein precursor (EC 3.4.16.5) (Cathepsin A) (Carboxypeptidase C) (Protective protein for lysosomes). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602468067	-1.77	0.01341
43 ENSMUSG000000031161	Histone deacetylase 6 (HD6) (Histone deacetylase mHDA2). [Source:UniProt/SwissProt;Acc:Q9Z2V5]	MTG_602473484	-1.76	0.00331
44 ENSMUSG000000027070		MTG_602310631	-1.74	0.00380
45 ENSMUSG00000028173		gbctl04_plate8_P14	-1.74	0.00451
46 ENSMUSG000000061922		gbctl04_plate8_G20	-1.74	0.00620
47 ENSMUSG00000022037	Clusterin precursor (Sulfated glycoprotein 2) (SGP-2) (Clustrin) (Apolipoprotein J) (Apo-J). [Source:UniProt/SwissProt;Acc:Q9QZD8]	gbctl04_plate7_P19	-1.73	0.00423
48 ENSMUSG000000021822	Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA) (U-plasminogen activator). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602476446	-1.72	0.00940
49 ENSMUSG00000041488	Syntaxin 3. [Source:UniProt/SwissProt;Acc:Q64704]	MTG_602474906	-1.72	0.00658
50 ENSMUSG000000021133		MTG_602469422	-1.71	0.00265
51 ENSMUSG000000025716	Myosin IIIA (EC 2.7.1.37). [Source:UniProt/SwissProt;Acc:Q8K3H5]	gbctl04_plate10_I06	-1.71	0.01438
52 ENSMUSG000000029705	CCAAT displacement protein (CDP) (Cut-like 1) (Homeobox protein Cux) (Fragment). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602476536	-1.71	0.00690
53 ENSMUSG00000038991	Thioredoxin domain containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein E1). [Source:UniProt/SwissProt;Acc:Q9QZD8]	gbctl04_plate7_K23	-1.7	0.04529
54 ENSMUSG00000022105	Retinoblastoma-associated protein (PP105) (RB). [Source:UniProt/SwissProt;Acc:P13405]	MTG_602472704	-1.69	0.04441
55 ENSMUSG00000027984	Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial precursor (EC 1.1.1.35) (HCDH) (Medium and short chain acyl-CoA dehydrogenase). [Source:UniProt/SwissProt;Acc:Q9QZD8]	MTG_602310506	-1.69	0.00327
56 ENSMUSG000000032786		MTG_602476691	-1.68	0.00303
57 ENSMUSG00000018796	Long-chain-fatty-acid--CoA ligase 2 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 2) (LACS 2). [Source:UniProt/SwissProt;Acc:Q9QZD8]	gbctl04_plate9_E24	-1.67	0.00921
58 ENSMUSG00000028130	Selenium-binding protein 1 (56 kDa selenium-binding protein) (SP56). [Source:UniProt/SwissProt;Acc:P17563]	MTG_602474670	-1.67	0.00464
59 ENSMUSG00000024180	Transmembrane protein 8 precursor (M83 protein). [Source:UniProt/SwissProt;Acc:Q9ESN3]	gbctl04_plate4_L19	-1.65	0.02163

60	ENSMUSG00000030695	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Aldolase 1). [Source:Uniprot/SWISSPRC	gbctl04_plate15_P21	-1.65	0.00269
61	ENSMUSG00000013539	Ser/Thr-rich protein T10 in DGCR region. [Source:Uniprot/SWISSPROT;Acc:P54797]	MTG_602472153	-1.64	0.00387
62	ENSMUSG00000047728		MTG_602310514	-1.64	0.00272
63	ENSMUSG00000014303	GLIS family zinc finger 2; Kruppel-like factor 16 (neuronal); GLI-Kruppel family member GLI5. [Source:RefSeq;Acc	MTG_602471661	-1.62	0.00356
64	ENSMUSG00000032047	acetyl-Coenzyme A acetyltransferase 1 precursor. [Source:RefSeq;Acc:NM_144784	MTG_602474150	-1.62	0.00830
65	ENSMUSG00000036093	ADP-ribosylation factor-like protein 5. [Source:Uniprot/SWISSPROT;Acc:Q80ZU0]	gbctl04_plate14_B07	-1.62	0.02892
66	ENSMUSG00000038843	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N- acetylglucosaminyltransferase (EC 2.4.1.102) (Core 2 bra	MTG_602470561	-1.62	0.00342
67	ENSMUSG00000062054		MTG_602476657	-1.62	0.02675
68	ENSMUSG000000022175	Low-density lipoprotein receptor-related protein 10 precursor. [Source:Uniprot/SWISSPROT;Acc:Q7TQH7	MTG_602472264	-1.61	0.04419
69	ENSMUSG00000026687	aldehyde dehydrogenase 9, subfamily A1; aldehyde dehydrogenase 9A; EST AA139417. [Source:RefSeq;Acc:NM	MTG_602467725	-1.61	0.00695
70	ENSMUSG00000032359	Cathepsin H precursor (EC 3.4.22.16) (Cathepsin B3) (Cathepsin BA). [Source:Uniprot/SWISSPROT;Acc:P49935	MTG_602474123	-1.61	0.00317
71	ENSMUSG00000025742	Ribose-phosphate pyrophosphokinase II (EC 2.7.6.1) (Phosphoribosyl pyrophosphate synthetase II) (PRS-II). [So	MTG_602471640	-1.6	0.02494
72	ENSMUSG00000033161	Sodium/potassium-transporting ATPase alpha-1 chain precursor (EC 3.6.3.9) (Sodium pump 1) (Na+/K+ ATPase	gbctl04_plate6_C15	-1.6	0.01063
73	ENSMUSG00000064181	PAT-12 protein. [Source:Uniprot/SPTREMBL;Acc:Q64154]	gbctl04_plate4_H18	-1.6	0.01971
74	ENSMUSG00000022180	Large neutral amino acids transporter small subunit 2 (L-type amino acid transporter 2). [Source:Uniprot/SWISSPI	MTG_602472944	-1.59	0.00315
75	ENSMUSG00000031881	Cadherin-16 precursor (Kidney-specific cadherin) (Ksp-cadherin). [Source:Uniprot/SWISSPROT;Acc:O88338]	gbctl04_plate15_A15	-1.59	0.00313
76	ENSMUSG00000005682	ubiquitin specific protease 52. [Source:RefSeq;Acc:NM_133992	MTG_602475718	-1.58	0.00340
77	ENSMUSG00000030246	L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH heart subunit) (LDH-H). [Source:Uniprot/SWISSPR	gbctl04_plate14_J10	-1.56	0.00255
78	ENSMUSG00000019996	microtubule-associated protein 7. [Source:RefSeq;Acc:NM_008635]	MTG_602471212	-1.55	0.01581
79	ENSMUSG00000002032	transmembrane protein 25. [Source:RefSeq;Acc:NM_027865]	gbctl04_plate16_P17	-1.54	0.00272
80	ENSMUSG00000005362	cereblon; novel lethal gene; cDNA sequence AF229032. [Source:RefSeq;Acc:NM_175357	MTG_602475117	-1.54	0.00917
81	ENSMUSG00000029119	Epididymis-specific alpha-mannosidase precursor (EC 3.2.1.24) (Mannosidase alpha class 2B member 2). [Sourc	gbctl04_plate16_K19	-1.54	0.00871
82	ENSMUSG00000058735		gbctl04_plate13_B13	-1.54	0.04317
83	ENSMUSG00000021236	Ectonucleoside triphosphate diphosphohydrolase 5 precursor (EC 3.6.1.6) (NTPDase5) (Nucleoside diphosphatas	gbctl04_plate11_M23	-1.53	0.00313
84	ENSMUSG00000024782	GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3) (Adenylate kinase 3 alpha like 1). [Source:Unipr	MTG_602468016	-1.53	0.03235
85	ENSMUSG00000024866	Aspartoacylase 2 (EC 3.5.1.15) (Aminoacylase-3) (ACY-3) (Acylase III) (Hepatitis C virus core-binding protein 1) (	MTG_602471405	-1.52	0.00718
86	ENSMUSG00000039367		MTG_602475137	-1.52	0.03623
87	ENSMUSG00000063870	chromodomain helicase DNA binding protein 4; Mi-2 beta. [Source:RefSeq;Acc:NM_145979	gbctl04_plate4_I22	-1.52	0.03112
88	ENSMUSG00000013584	Aldehyde dehydrogenase 1A2 (EC 1.2.1.3) (Retinaldehyde-specific dehydrogenase type 2) (RALDH(II)) (RALDH-	gbctl04_plate13_J15	-1.51	0.01141
89	ENSMUSG00000026043		MTG_602472755	-1.51	0.02540
90	ENSMUSG00000027562	Carbonic anhydrase II (EC 4.2.1.1) (Carbonate dehydratase II) (CA-II). [Source:Uniprot/SWISSPROT;Acc:P00920	MTG_602472903	-1.51	0.00272
91	ENSMUSG00000028405	Iron-responsive element binding protein 1 (IRE-BP 1) (Iron regulatory protein 1) (IRP1) (Ferritin repressor protein)	MTG_602468537	-1.51	0.00475
92	ENSMUSG00000029545	Acyl-CoA dehydrogenase, short-chain specific, mitochondrial precursor (EC 1.3.99.2) (SCAD) (Butyryl-CoA dehydc	MTG_602477746	-1.51	0.00320
93	ENSMUSG00000049152		MTG_602476433	-1.51	0.01927
94	ENSMUSG00000003464	peroxisome biogenesis factor 19; peroxisomal farnesylated protein. [Source:RefSeq;Acc:NM_023041	MTG_602469571	-1.5	0.00272
95	ENSMUSG00000024758	Reticulon protein 3. [Source:Uniprot/SWISSPROT;Acc:Q9ES97]	gbctl04_plate9_B06	-1.5	0.02050
96	ENSMUSG000000025495	Phosphatidylserine synthase 2 (EC 2.7.8.-) (PtdSer synthase-2) (PSS-2) (Serine-exchange enzyme II). [Source:U	MTG_602475507	-1.5	0.00615
97	ENSMUSG00000027610	Glutathione synthetase (EC 6.3.2.3) (Glutathione synthase) (GSH synthetase) (GSH-S). [Source:Uniprot/SWISSP	MTG_602470595	-1.5	0.00325
98	ENSMUSG00000034285	NipSnap1 protein. [Source:Uniprot/SWISSPROT;Acc:O55125]	MTG_602472230	-1.5	0.00354
99	ENSMUSG00000022564	NMDA receptor glutamate-binding chain; Lag protein. [Source:RefSeq;Acc:NM_023168	MTG_602474321	-1.49	0.00307
100	ENSMUSG000000025651	Ubiquinol-cytochrome C reductase complex core protein I, mitochondrial precursor (EC 1.10.2.2). [Source:Uniprot	gbctl04_plate12_L09	-1.49	0.00658
101	ENSMUSG00000027006	ER-resident protein ERdj5. [Source:RefSeq;Acc:NM_024181]	MTG_602467634	-1.49	0.00272
102	ENSMUSG00000027315	Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor activator inhibitor type 1) (HAI-1). [Source:Un	MTG_602472423	-1.49	0.00831
103	ENSMUSG00000033416		MTG_602477479	-1.49	0.00474
104	ENSMUSG000000020777	Acyl-coenzyme A oxidase 1, peroxisomal (EC 1.3.3.6) (Palmitoyl-CoA oxidase) (AOX). [Source:Uniprot/SWISSPR	MTG_602473486	-1.48	0.00567
105	ENSMUSG00000026139		MTG_602469213	-1.48	0.00264
106	ENSMUSG000000041238	Similar to retinoblastoma binding protein 8. [Source:Uniprot/SPTREMBL;Acc:Q80YR6	gbctl04_plate6_H04	-1.48	0.02747
107	ENSMUSG00000062835	Friend virus susceptibility 4. [Source:RefSeq;Acc:NM_010245]	gbctl04_plate13_I20	-1.48	0.00706
108	ENSMUSG000000043323		MTG_602468463	-1.47	0.01315
109	ENSMUSG00000054735	Similar to CDNA FLJ32111 FIS (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BLZ5]	MTG_602467742	-1.47	0.00307
110	ENSMUSG00000022186	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial precursor (EC 2.8.3.5) (Somatic-type succinyl	gbctl04_plate4_H03	-1.46	0.02047
111	ENSMUSG00000055912	cDNA sequence BC014685; fasting-inducible integral membrane protein TM6P1. [Source:RefSeq;Acc:NM_14491	gbctl04_plate15_B21	-1.46	0.00378
112	ENSMUSG000000039168	death-associated protein. [Source:RefSeq;Acc:NM_146057]	MTG_602473447	-1.45	0.03727
113	ENSMUSG00000043587		MTG_602477701	-1.45	0.04915
114	ENSMUSG00000050447		MTG_602472584	-1.45	0.02086
115	ENSMUSG00000056608	Similar to DJ620E11.1.1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BYH8]	MTG_602468667	-1.45	0.00711
116	ENSMUSG00000023122	Sulfotransferase 1C1 (EC 2.8.2.-). [Source:Uniprot/SWISSPROT;Acc:Q9D939]	MTG_602471663	-1.44	0.00536
117	ENSMUSG00000027199	Glycine amidinotransferase, mitochondrial precursor (EC 2.1.4.1) (L- arginine:glycine amidinotransferase) (Transa	MTG_602471659	-1.44	0.00594
118	ENSMUSG00000028412		gbctl04_plate10_I12	-1.44	0.04675
119	ENSMUSG00000027875	Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor (EC 2.3.3.10) (HMG-CoA synthase) (3-hydroxy-3- $\pi$	MTG_602475166	-1.43	0.00888
120	ENSMUSG00000004668	ATP-binding cassette transporter. [Source:Uniprot/SPTREMBL;Acc:Q80T20]	MTG_602471535	-1.42	0.00638
121	ENSMUSG00000018677	similar to human CGI-69 protein. [Source:RefSeq;Acc:NM_026542]	MTG_602474063	-1.42	0.00302

122	ENSMUSG00000023960	ectonucleotide pyrophosphatase/phosphodiesterase 5. [Source:RefSeq;Acc:NM_032003	MTG_602468274	-1.42	0.00560
123	ENSMUSG00000031644	Serine/threonine-protein kinase Nek1 (EC 2.7.1.37) (NimA-related protein kinase 1). [Source:Uniprot/SWISSPROT;Acc:MTG_602468658	MTG_602468658	-1.42	0.02630
124	ENSMUSG00000053898	Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-). [Source:Uniprot/SWISSPROT;Acc:MTG_602470174	MTG_602470174	-1.42	0.01262
125	ENSMUSG00000005125	NDRG1 protein (N-myc downstream regulated gene 1 protein) (Protein Ndr1). [Source:Uniprot/SWISSPROT;Acc:gbctl04_plate3_A17	gbctl04_plate3_A17	-1.41	0.00340
126	ENSMUSG00000015090	Prostaglandin-H2 D-isomerase precursor (EC 5.3.99.2) (Lipocalin-type prostaglandin-D synthase) (Glutathione-inc	MTG_602476101	-1.41	0.01644
127	ENSMUSG00000022323	Ribonuclease UK114 (EC 3.1.-.-) (Heat-responsive protein 12). [Source:Uniprot/SWISSPROT;Acc:P52760	MTG_602476318	-1.41	0.00384
128	ENSMUSG00000022479	Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor). [Source:Uniprot/SWISSPROT;Acc:P48281	gbctl04_plate16_D20	-1.41	0.00316
129	ENSMUSG00000029103	Alpha-2-macroglobulin receptor-associated protein precursor (Alpha-2- MRAP) (Low density lipoprotein receptor-r	MTG_602474274	-1.41	0.00603
130	ENSMUSG00000034947		MTG_602472026	-1.41	0.00850
131	ENSMUSG00000058997		gbctl04_plate15_F18	-1.41	0.00415
132	ENSMUSG00000015970	Choline dehydrogenase, mitochondrial precursor (EC 1.1.99.1) (CHD) (CDH). [Source:Uniprot/SWISSPROT;Acc:MTG_602471695	MTG_602471695	-1.4	0.00363
133	ENSMUSG00000024072		gbctl04_plate16_A16	-1.4	0.02592
134	ENSMUSG000000027406	isocitrate dehydrogenase 3, beta subunit; isocitrate dehydrogenase 3 beta; N14A tumor-related protein. [Source:R	MTG_602470341	-1.4	0.00662
135	ENSMUSG00000056483		MTG_602467125	-1.4	0.00337
136	ENSMUSG00000063683	glycine-N-acyltransferase. [Source:RefSeq;Acc:NM_145935	gbctl04_plate17_G16	-1.4	0.00476
137	ENSMUSG00000025380	fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus). [Source:RefSeq;Acc:NM_17280; MTG_602476069	MTG_602476069	-1.39	0.00352
138	ENSMUSG00000033379	Vacuolar ATP synthase 21 kDa proteinolipid subunit (EC 3.6.3.14) (23-kDa subunit of V-ATPase). [Source:Uniprot/S	gbctl04_plate8_E09	-1.39	0.00902
139	ENSMUSG00000021646	Similar to methylcrotonoyl-coenzyme A carboxylase 2 (Beta). [Source:Uniprot/SPTREMBL;Acc:Q8K1L7	MTG_602469146	-1.38	0.00318
140	ENSMUSG00000029304	Osteopontin precursor (Bone sialoprotein 1) (Minopontin) (Early T lymphocyte activation 1 protein) (Secreted phos	gbctl04_plate7_118	-1.38	0.01251
141	ENSMUSG00000037523		MTG_602477084	-1.38	0.00382
142	ENSMUSG00000006717	Thioesterase superfamily member 2. [Source:Uniprot/SWISSPROT;Acc:Q9CQR4]	MTG_602473938	-1.37	0.00598
143	ENSMUSG00000021033	Maleylacetoacetate isomerase (EC 5.2.1.2) (MAAI) (Glutathione S- transferase zeta 1) (EC 2.5.1.18) (GSTZ1-1). [	MTG_602475818	-1.37	0.00302
144	ENSMUSG00000025871		MTG_602472626	-1.37	0.00305
145	ENSMUSG00000060625	Ferritin light chain 1 (Ferritin L subunit 1). [Source:Uniprot/SWISSPROT;Acc:P29391]	MTG_602475427	-1.37	0.02666
146	ENSMUSG00000015846	Retinoic acid receptor RXR-alpha. [Source:Uniprot/SWISSPROT;Acc:P28700]	MTG_602472096	-1.36	0.03235
147	ENSMUSG00000025428	ATP synthase alpha chain, mitochondrial precursor (EC 3.6.3.14). [Source:Uniprot/SWISSPROT;Acc:Q03265	MTG_602475884	-1.36	0.00302
148	ENSMUSG00000032577		MTG_602472330	-1.36	0.00302
149	ENSMUSG00000060750	Ferritin light chain 1 (Ferritin L subunit 1). [Source:Uniprot/SWISSPROT;Acc:P29391]	gbctl04_plate6_J10	-1.36	0.01554
150	ENSMUSG00000024359	Stress-70 protein, mitochondrial precursor (75 kDa glucose regulated protein) (GRP 75) (Peptide-binding protein 7	gbctl04_plate4_A09	-1.35	0.04232
151	ENSMUSG00000024644	Cytosolic nonspecific dipeptidase (Glutamate carboxypeptidase-like protein 1). [Source:Uniprot/SWISSPROT;Acc	MTG_602476864	-1.35	0.00436
152	ENSMUSG00000025980	60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60	gbctl04_plate12_F14	-1.35	0.01695
153	ENSMUSG00000042315	Beta-galactosidase precursor (EC 3.2.1.23) (Lactase) (Acid beta- galactosidase). [Source:Uniprot/SWISSPROT;A	MTG_602476674	-1.35	0.00610
154	ENSMUSG00000046873	membrane-bound transcription factor protease, site 2; RIKEmembrane-bound transcription factor protease, site 2.	MTG_602296353	-1.35	0.01692
155	ENSMUSG00000051397	tumor-associated calcium signal transducer 2; lymphocyte antigen 97; tumor-associated calcium signal transducer	MTG_602475188	-1.35	0.00333
156	ENSMUSG00000026820	prostaglandin E synthase 2. [Source:RefSeq;Acc:NM_133783	MTG_602475947	-1.34	0.00272
157	ENSMUSG00000001120	Poly(rC)-binding protein 3 (Alpha-CP3). [Source:Uniprot/SWISSPROT;Acc:P57722]	MTG_602471016	-1.32	0.00358
158	ENSMUSG00000014077	Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcineurin homologous protein) (Sid 470). [Source:l	MTG_602476369	-1.32	0.00884
159	ENSMUSG00000018900	Organic cation/carnitine transporter 2 (Solute carrier family 22, member 5) (High-affinity sodium-dependent carniti	MTG_602473895	-1.32	0.00420
160	ENSMUSG00000020665	Dystrobrevin beta (Beta-dystrobrevin) (DTN-B) (MDTN-B). [Source:Uniprot/SWISSPROT;Acc:O70585]	gbctl04_plate14_H17	-1.32	0.00415
161	ENSMUSG00000025060	serine/threonine kinase 2; Ste20-related kinase. [Source:RefSeq;Acc:NM_009289	gbctl04_plate5_B12	-1.32	0.00564
162	ENSMUSG00000031256	cleavage stimulation factor, 3' pre-RNA subunit 2; cleavage stimulation factor, 3' pre-RNA subunit 2, 64 kDa. [Sou	MTG_602474559	-1.32	0.03327
163	ENSMUSG00000031826	Ubiquitin carboxyl-terminal hydrolase 10 (EC 3.1.2.15) (Ubiquitin thiolesterase 10) (Ubiquitin-specific processing p	MTG_602476533	-1.31	0.00432
164	ENSMUSG00000002985	Apolipoprotein E precursor (Apo-E). [Source:Uniprot/SWISSPROT;Acc:P08226]	gbctl04_plate7_C12	-1.3	0.00466
165	ENSMUSG00000017144	Rho-related GTP-binding protein RhoE. [Source:Uniprot/SWISSPROT;Acc:P61588]	MTG_602470537	-1.3	0.00696
166	ENSMUSG00000029438	B-cell CLL/lymphoma 7A. [Source:RefSeq;Acc:NM_029850]	MTG_602472876	-1.3	0.00307
167	ENSMUSG00000030630	Fumarylacetoacetase (EC 3.7.1.2) (Fumarylacetoacetate hydrolase) (Beta-diketonase) (FAA). [Source:Uniprot/SV	MTG_602477122	-1.3	0.00557
168	ENSMUSG00000002957	Adapter-related protein complex 2 alpha 2 subunit (Alpha-adaptin C) (Adaptor protein complex AP-2 alpha-2 subu	MTG_602474083	-1.29	0.02036
169	ENSMUSG00000015095	F-box/WD-repeat protein 5 (F-box and WD-40 domain protein 5). [Source:Uniprot/SWISSPROT;Acc:Q9QXW2]	MTG_602476505	-1.29	0.00436
170	ENSMUSG00000015653	Weakly similar to tumor suppressor PHYDE. [Source:Uniprot/SPTREMBL;Acc:Q8BWB6]	MTG_602469385	-1.29	0.01664
171	ENSMUSG00000019590	Cytochrome b561 (Cytochrome b-561). [Source:Uniprot/SWISSPROT;Acc:Q60720	MTG_602473935	-1.29	0.00302
172	ENSMUSG00000021278	Amnionless protein precursor. [Source:Uniprot/SWISSPROT;Acc:Q99JB7]	gbctl04_plate16_O09	-1.29	0.02608
173	ENSMUSG00000033065	6-phosphofructokinase, muscle type (EC 2.7.1.11) (Phosphofructokinase 1) (Phosphohexokinase) (Phosphofruct	MTG_602471574	-1.29	0.00512
174	ENSMUSG00000041926	aminopeptidase B (EC 3.4.11.6) (Ap-B) (Arginyl aminopeptidase) (Arginine aminopeptidase) (Cytosol aminopeptic	MTG_602471554	-1.29	0.00307
175	ENSMUSG00000056516	NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3). [Source:Uniprot/SWISSPROT;Acc:P03903	MTG_602467008	-1.29	0.00272
176	ENSMUSG00000001119	Collagen alpha 1(VI) chain precursor. [Source:Uniprot/SWISSPROT;Acc:Q04857]	gbctl04_plate3_I09	-1.28	0.00339
177	ENSMUSG00000001211	1-acylglycerol-3-phosphate O-acyltransferase 3. [Source:RefSeq;Acc:NM_053014	MTG_602475328	-1.28	0.00471
178	ENSMUSG00000025176		gbctl04_plate10_H12	-1.28	0.00403
179	ENSMUSG00000028639	Nuclease sensitive element binding protein 1 (Y box binding protein-1) (Y-box transcription factor) (YB-1) (CCAAT	gbctl04_plate3_M01	-1.28	0.00612
180	ENSMUSG00000027774	Elongation factor G 1, mitochondrial precursor (mEF-G 1) (Elongation factor G1). [Source:Uniprot/SWISSPROT;A	MTG_602475423	-1.27	0.01832
181	ENSMUSG00000039953	Calsynenin-1 precursor. [Source:Uniprot/SWISSPROT;Acc:Q9EPL2]	MTG_602310575	-1.27	0.02070
182	ENSMUSG00000041625		MTG_602475310	-1.27	0.02108
183	ENSMUSG00000047250	Prostaglandin G/H synthase 1 precursor (EC 1.14.99.1) (Cyclooxygenase -1) (COX-1) (Prostaglandin-endoperoxid	MTG_602472169	-1.27	0.01300

184	ENSMUSG0000007891	Cathepsin D precursor (EC 3.4.23.5). [Source:Uniprot/SWISSPROT;Acc:P18242]	MTG_602468473	-1.26	0.00320
185	ENSMUSG00000020402	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (mVDAC1) (mVDAC5) (Outer mitochondrial mem	gbctI04_plate13_P05	-1.26	0.02101
186	ENSMUSG00000024378	StAR-related lipid transfer protein 4 (StARD4) (START domain- containing protein 4). [Source:Uniprot/SWISSPRC	MTG_602477738	-1.26	0.00456
187	ENSMUSG00000024962	Vascular endothelial growth factor B precursor (VEGF-B) (VEGF related factor) (VRF). [Source:Uniprot/SWISSPR	MTG_602470611	-1.26	0.00900
188	ENSMUSG00000055319		MTG_602310504	-1.26	0.03839
189	ENSMUSG00000001323	Serine racemase (EC 5.1.1.-). [Source:Uniprot/SWISSPROT;Acc:Q9QZX7]	MTG_602310559	-1.25	0.00466
190	ENSMUSG00000018171		MTG_602475157	-1.25	0.01270
191	ENSMUSG00000019558	solute carrier family 6 (neurotransmitter transporter, creatine), member 8; creatine transporter. [Source:RefSeq;Ac	gbctI04_plate13_E04	-1.25	0.02797
192	ENSMUSG00000019872	Acid sphingomyelinase-like phosphodiesterase 3a precursor (EC 3.1.4.-) (ASM-like phosphodiesterase 3a). [Sour	MTG_602469643	-1.25	0.01379
193	ENSMUSG00000028107		MTG_602467307	-1.25	0.00309
194	ENSMUSG00000002332	Dehydrogenase/reductase SDR family member 1 (EC 1.1.-.-). [Source:Uniprot/SWISSPROT;Acc:Q99L04	MTG_602474836	-1.24	0.00427
195	ENSMUSG00000026526	Fumarate hydratase, mitochondrial precursor (EC 4.2.1.2) (Fumarase) (EF-3). [Source:Uniprot/SWISSPROT;Acc:	MTG_602475932	-1.24	0.00411
196	ENSMUSG00000030541	Isocitrate dehydrogenase [NADP], mitochondrial precursor (EC 1.1.1.42) (Oxalosuccinate decarboxylase) (IDH) (I	gbctI04_plate8_A11	-1.24	0.00884
197	ENSMUSG00000033530		gbctI04_plate15_G03	-1.24	0.01347
198	ENSMUSG00000017929	Beta-1,4-galactosyltransferase 5 (EC 2.4.1.-) (Beta-1,4-GalTase 5) (Beta4Gal-T5) (b4Gal-T5) (UDP-galactose:bet	MTG_602310569	-1.23	0.00718
199	ENSMUSG00000021957	Transketolase (EC 2.2.1.1) (TK) (P68). [Source:Uniprot/SWISSPROT;Acc:P40142]	gbctI04_plate5_M12	-1.23	0.00927
200	ENSMUSG00000028603	Nonspecific lipid-transfer protein, mitochondrial precursor (NSL-TP) (Sterol carrier protein 2) (SCP-2) (Sterol carri	gbctI04_plate17_N17	-1.23	0.01026
201	ENSMUSG00000031310	zinc finger protein 261; DXHXS6673E. [Source:RefSeq;Acc:NM_019831	gbctI04_plate6_C01	-1.23	0.00963
202	ENSMUSG00000059456	Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase 2) (FADK 2) (Proline-rich tyrosine kinase 2)	MTG_602473227	-1.23	0.00436
203	ENSMUSG00000003420	IgG receptor FcRn large subunit p51 precursor (FcRn) (Neonatal Fc receptor) (IgG Fc fragment receptor transpor	MTG_602474622	-1.22	0.03845
204	ENSMUSG00000026791	Solute carrier family 2, facilitated glucose transporter, member 8 (Glucose transporter type 8) (Glucose transporte	MTG_602472123	-1.22	0.00358
205	ENSMUSG00000027367	StAR-related lipid transfer protein 7 (StARD7) (START domain- containing protein 7). [Source:Uniprot/SWISSPRC	MTG_602470612	-1.22	0.03582
206	ENSMUSG00000031065	Serine/threonine-protein kinase PCTAIRE-1 (EC 2.7.1.37) (PCTAIRE-motif protein kinase 1) (CRK5). [Source:Unij	gbctI04_plate6_L08	-1.22	0.00436
207	ENSMUSG00000034573	Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48) (Protein tyrosine phosphatase PTP-BL) (Protei	gbctI04_plate17_D01	-1.22	0.03489
208	ENSMUSG00000001665	glutathione S-transferase, theta 3. [Source:RefSeq;Acc:NM_133994	MTG_603994	-1.21	0.00520
209	ENSMUSG00000004069	DnaJ homolog subfamily A member 3, mitochondrial precursor (Tumorous imaginal discs protein Tid56 homolog)	MTG_602474729	-1.21	0.00803
210	ENSMUSG00000028571	cytochrome P450, family 2, subfamily j, polypeptide 13; cytochrome P450, 2j13. [Source:RefSeq;Acc:NM_145548	MTG_602474129	-1.21	0.00707
211	ENSMUSG00000035473	aldose 1-epimerase. [Source:RefSeq;Acc:NM_176963]	MTG_602475851	-1.21	0.00411
212	ENSMUSG00000054522	malonyl-CoA decarboxylase. [Source:RefSeq;Acc:NM_019966	MTG_602472542	-1.21	0.00647
213	ENSMUSG00000008540	Microsomal glutathione S-transferase 1 (EC 2.5.1.18) (Microsomal GST- 1) (Microsomal GST-l). [Source:Uniprot/S	gbctI04_plate6_A22	-1.2	0.00536
214	ENSMUSG00000021981	MO25-like protein. [Source:Uniprot/SWISSPROT;Acc:Q9DB16]	MTG_602138927	-1.2	0.00451
215	ENSMUSG00000028692	Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (Aldehyde reductase) (Aldo- keto reductase family 1 member A1). [	gbctI04_plate17_E21	-1.2	0.00512
216	ENSMUSG000000035637	Glyoxylate reductase/hydroxypyruvate reductase (EC 1.1.1.79). [Source:Uniprot/SWISSPROT;Acc:Q91Z53	MTG_602474459	-1.2	0.00665
217	ENSMUSG00000033386	stromal cell derived factor receptor 2. [Source:RefSeq;Acc:NM_009146]	MTG_602476253	-1.19	0.00415
218	ENSMUSG00000034850		MTG_602472477	-1.19	0.01625
219	ENSMUSG00000049755		MTG_602471626	-1.19	0.00842
220	ENSMUSG000000051483	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1). [Source:Uniprot/SWIS	MTG_602472054	-1.19	0.00772
221	ENSMUSG00000054226	MDRWS1 protein. [Source:Uniprot/SPTREMBL;Acc:Q8CHL1]	MTG_602476416	-1.19	0.00756
222	ENSMUSG00000020918	General control of amino acid synthesis protein 5-like 2 (EC 2.3.1.48) (Histone acetyltransferase GCN5) (mmGCN	gbctI04_plate4_C20	-1.18	0.01308
223	ENSMUSG00000022346	Myc proto-oncogene protein (c-myc). [Source:Uniprot/SWISSPROT;Acc:P01108	gbctI04_plate15_A06	-1.18	0.00781
224	ENSMUSG00000024843	Choline kinase alpha (EC 2.7.1.32) (CK) (CHETK-alpha). [Source:Uniprot/SWISSPROT;Acc:O54804]	MTG_602474696	-1.18	0.01145
225	ENSMUSG00000028403	Zinc finger DHHC domain containing protein 21. [Source:Uniprot/SWISSPROT;Acc:Q9D270]	MTG_602476526	-1.18	0.00342
226	ENSMUSG00000031247	transforming acidic coiled-coil containing protein 1 short isoform; transforming acidic coiled-coil containing protein	gbctI04_plate14_J06	-1.18	0.04197
227	ENSMUSG00000031977	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2; ppGaNtase-T2. [Source:	MTG_602475620	-1.18	0.04585
228	ENSMUSG00000001467	cytochrome P450, 51. [Source:RefSeq;Acc:NM_Q20010	MTG_602467247	-1.17	0.00415
229	ENSMUSG00000007656	cAMP-regulated phosphoprotein 19 (ARPP-19). [Source:Uniprot/SWISSPROT;Acc:P56212	MTG_602477288	-1.17	0.02277
230	ENSMUSG00000024661	Ferritin heavy chain (Ferritin H subunit). [Source:Uniprot/SWISSPROT;Acc:P09528	gbctI04_plate3_C17	-1.17	0.00385
231	ENSMUSG00000026853	Carnitine O-acetyltransferase (EC 2.3.1.7) (Carnitine acetylase) (CAT). [Source:Uniprot/SWISSPROT;Acc:P47934	MTG_602473466	-1.17	0.01342
232	ENSMUSG00000027947	Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1). [Source:Uniprot/SWISSPROT;Acc:P22272]	MTG_602470948	-1.17	0.04664
233	ENSMUSG00000032278		MTG_602476382	-1.17	0.01124
234	ENSMUSG00000042272		MTG_602476094	-1.17	0.03935
235	ENSMUSG00000049090		gbctI04_plate6_K19	-1.17	0.01414
236	ENSMUSG000000021238	aldehyde dehydrogenase family 6, subfamily A1. [Source:RefSeq;Acc:NM_134042	MTG_602471347	-1.16	0.00484
237	ENSMUSG00000023092	Skeletal muscle LIM-protein 1 (SLIM 1) (Four and a half LIM domains protein 1) (FHL-1) (KyoT) (RBP associated	MTG_602472327	-1.16	0.00931
238	ENSMUSG00000024213	nudix (nucleotide diphosphate linked moiety X)-type motif 3; diphosphoinositol polyphosphate phosphohydrolase.	MTG_602474525	-1.16	0.00446
239	ENSMUSG00000024781	Lysosomal acid lipase/cholesteryl ester hydrolase precursor (EC 3.1.1.13) (LAL) (Acid cholesteryl ester hydrolase	MTG_602471643	-1.16	0.03697
240	ENSMUSG000000039568		MTG_602476263	-1.16	0.00678
241	ENSMUSG00000040105		MTG_602469345	-1.16	0.03656
242	ENSMUSG000000051043	G protein-coupled receptor family C group 5 member C precursor (Retinoic acid induced gene 3 protein) (RAIG-3)	gbctI04_plate14_P24	-1.16	0.02022
243	ENSMUSG000000052459	Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (EC 3.6.3.14) (V-ATPase A subunit 1) (Vacuolar pr	MTG_602477178	-1.16	0.04384
244	ENSMUSG000000021577		gbctI04_plate4_A23	-1.15	0.02036
245	ENSMUSG00000031545	putative lysophosphatidic acid acyltransferase. [Source:RefSeq;Acc:NM_018743	MTG_602472154	-1.15	0.03499

246	ENSMUSG00000038014		MTG_602475260	-1.15	0.04470
247	ENSMUSG00000061410	BDG-29 protein. [Source:RefSeq;Acc:NM_080855]	gbctI04_plate6_L12	-1.15	0.01811
248	ENSMUSG00000027597	Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) (Liver copper binding)	gbctI04_plate7_C23	-1.14	0.00474
249	ENSMUSG000000031482	Mitochondrial ornithine transporter 1 (Solute carrier family 25, member 15). [Source:Uniprot/SWISSPROT;Acc:Q9	MTG_602467719	-1.14	0.01586
250	ENSMUSG000000032062		MTG_602475353	-1.14	0.00744
251	ENSMUSG00000003099	Serine/threonine protein phosphatase 5 (EC 3.1.3.16) (PP5) (Protein phosphatase T) (PPT). [Source:Uniprot/SWI	MTG_602470962	-1.13	0.00822
252	ENSMUSG00000009090	Adapter-related protein complex 1 beta 1 subunit (Beta-adaptin 1) (Adaptor protein complex AP-1 beta-1 subunit)	MTG_602477418	-1.13	0.01206
253	ENSMUSG000000028673	fucosidase, alpha-L-1, tissue; alpha-L-fucosidase. [Source:RefSeq;Acc:NM_024243	MTG_602471057	-1.13	0.01834
254	ENSMUSG000000036138	acetyl-Coenzyme A acyltransferase 1; 3-ketoacyl-CoA thiolase A; peroxisomal 3-oxoacyl-Coenzyme A thiolase; p	MTG_602473252	-1.13	0.00696
255	ENSMUSG000000038712	RIKEN cDNA 4930504E06; cDNA sequence, clone 2-4; NF-E2 inducible protein. [Source:RefSeq;Acc:NM_13385	MTG_602472305	-1.13	0.01205
256	ENSMUSG000000059400	Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH). [Source:Uniprot/SWISSPROT;Acc:P16858	gbctI04_plate16_K07	-1.13	0.02940
257	ENSMUSG000000025731		MTG_602474429	-1.12	0.02725
258	ENSMUSG0000000025781	ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14). [Source:Uniprot/SWISSPROT;Acc:Q91VR2	MTG_602467184	-1.12	0.00884
259	ENSMUSG000000025950	Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42) (Oxalosuccinate decarboxylase) (IDH) (NADP+-spec	gbctI04_plate10_A13	-1.12	0.02204
260	ENSMUSG000000032294	Pyruvate kinase, M2 isozyme (EC 2.7.1.40). [Source:Uniprot/SWISSPROT;Acc:P52480	MTG_602467405	-1.12	0.00767
261	ENSMUSG000000034424		MTG_602475019	-1.12	0.00474
262	ENSMUSG0000000037300		MTG_602474524	-1.12	0.01050
263	ENSMUSG000000055639	Dachshund homolog 1 (Dach1). [Source:Uniprot/SWISSPROT;Acc:Q9QYB2	gbctI04_plate10_L14	-1.12	0.00524
264	ENSMUSG000000003345	casein kinase 1, gamma 2. [Source:RefSeq;Acc:NM_134002	MTG_602475625	-1.11	0.03795
265	ENSMUSG000000019809	Peroxisomal assembly protein PEX3 (Peroxin-3). [Source:Uniprot/SWISSPROT;Acc:Q9QXY9	MTG_602470589	-1.11	0.00954
266	ENSMUSG0000000020941	Mitogen-activated protein kinase kinase kinase 14 (EC 2.7.1.37) (NF- kappa beta-inducing kinase) (Serine/threoni	MTG_602476535	-1.11	0.00628
267	ENSMUSG000000034903	cobl-related 1. [Source:RefSeq;Acc:NM_177025	MTG_602310687	-1.11	0.01359
268	ENSMUSG000000036427	Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomera	MTG_602469383	-1.11	0.00382
269	ENSMUSG000000048058		MTG_602474708	-1.11	0.03019
270	ENSMUSG0000000052369		MTG_602474145	-1.11	0.00944
271	ENSMUSG000000005069	Peroxisomal targeting signal 1 receptor (Peroxisome receptor 1) (Peroxisomal C-terminal targeting signal import	gbctI04_plate16_O15	-1.1	0.00824
272	ENSMUSG000000025209	twinkle; T7 gp4-like protein with intramitochondrial nucleoid localization. [Source:RefSeq;Acc:NM_153796	MTG_602471167	-1.1	0.02963
273	ENSMUSG000000026383	erythrocyte protein band 4.1-like 5. [Source:RefSeq;Acc:NM_145506	MTG_602474140	-1.1	0.04551
274	ENSMUSG0000000028691	Peroxiredoxin 1 (EC 1.11.1.-) (Thioredoxin peroxidase 2) (Thioredoxin- dependent peroxide reductase 2) (Osteobl	gbctI04_plate4_I06	-1.1	0.02475
275	ENSMUSG000000031299	Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial precursor (EC 1.2.4.1) (PDHE	MTG_602469742	-1.1	0.00528
276	ENSMUSG0000000035936		gbctI04_plate16_D22	-1.1	0.00756
277	ENSMUSG000000039105	Vacuolar ATP synthase subunit G 1 (EC 3.6.3.14) (V-ATPase G subunit 1) (Vacuolar proton pump G subunit 1) (v	gbctI04_plate14_N13	-1.1	0.02819
278	ENSMUSG0000000047843	Brain protein I3. [Source:Uniprot/SWISSPROT;Acc:P28662]	gbctI04_plate17_A15	-1.1	0.00818
279	ENSMUSG000000058488	klotho. [Source:RefSeq;Acc:NM_013823]	MTG_602477773	-1.1	0.01430
280	ENSMUSG000000004207	Sulfated glycoprotein 1 precursor (SGP-1) (Prosaposin). [Source:Uniprot/SWISSPROT;Acc:Q61207	MTG_602470084	-1.09	0.00899
281	ENSMUSG000000005982		MTG_602475618	-1.09	0.01788
282	ENSMUSG00000000021193	pitrilysin metalloprotease 1; nuclear transplantation upregulated protein 1. [Source:RefSeq;Acc:NM_145131	MTG_602472160	-1.09	0.03720
283	ENSMUSG000000028700	O-mannosyl N-acetylglucosaminyltransferase. [Source:RefSeq;Acc:NM_026651	MTG_602471965	-1.09	0.03169
284	ENSMUSG000000029455	Aldehyde dehydrogenase, mitochondrial precursor (EC 1.2.1.3) (ALDH class 2) (AHD-M1) (ALDH1) (ALDH-E2). [S	MTG_602470576	-1.09	0.00373
285	ENSMUSG000000030530	Furin precursor (EC 3.4.21.75) (Paired basic amino acid residue cleaving enzyme) (PACE) (Dibasic processing e	MTG_602475185	-1.09	0.02253
286	ENSMUSG0000000033307	Macrophage migration inhibitory factor (MIF) (Phenylpyruvate tautomerase) (EC 5.3.2.1) (Glycosylation-inhibiting	MTG_602477624	-1.09	0.02060
287	ENSMUSG000000037443		gbctI04_plate12_L17	-1.09	0.00813
288	ENSMUSG0000000013160	Vacuolar ATP synthase subunit d (EC 3.6.3.14) (V-ATPase d subunit) (Vacuolar proton pump d subunit) (V-ATPa	gbctI04_plate3_H01	-1.08	0.00982
289	ENSMUSG000000016319	ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2) (Adenine nucleotide translocator 2) (ANT 2).	MTG_602467047	-1.08	0.00379
290	ENSMUSG0000000020733	Ezrin-radixin-moesin binding phosphoprotein 50 (EBP50) (Na(+)/H(+) exchange regulatory cofactor NHE-RF) (NH	MTG_602477766	-1.08	0.00380
291	ENSMUSG000000022477	aconitase 2, mitochondrial. [Source:RefSeq;Acc:NM_080633	gbctI04_plate14_L23	-1.08	0.01618
292	ENSMUSG000000023010	testis enhanced gene transcript; Bax inhibitor-1. [Source:RefSeq;Acc:NM_026669	gbctI04_plate10_E02	-1.08	0.00899
293	ENSMUSG000000023175	Basigin precursor (Basic immunoglobulin superfamily) (Membrane glycoprotein GP42). [Source:Uniprot/SWISSPR	MTG_602469230	-1.08	0.00551
294	ENSMUSG000000027809	electron transferring flavoprotein, dehydrogenase. [Source:RefSeq;Acc:NM_025794	MTG_602472029	-1.08	0.00451
295	ENSMUSG000000031696	Vacuolar protein sorting 35 (Vesicle protein sorting 35) (Maternal- embryonic 3). [Source:Uniprot/SWISSPROT;Ac	MTG_602468875	-1.08	0.03841
296	ENSMUSG000000045934	cisplatin resistance associated. [Source:RefSeq;Acc:NM_181409	MTG_602471373	-1.08	0.00436
297	ENSMUSG000000047735		MTG_602473419	-1.08	0.03777
298	ENSMUSG0000000021414		MTG_602139088	-1.07	0.02494
299	ENSMUSG000000024253	dynein 2 light intermediate chain. [Source:RefSeq;Acc:NM_172256	MTG_602473673	-1.07	0.00921
300	ENSMUSG000000024354	Solute carrier family 23, member 1 (Sodium-dependent vitamin C transporter 1) (Na(+)/L-ascorbic acid transporter	gbctI04_plate5_G04	-1.07	0.01187
301	ENSMUSG000000024818		gbctI04_plate14_M18	-1.07	0.01359
302	ENSMUSG0000000032353	integral type I protein. [Source:RefSeq;Acc:NM_025360	MTG_602471971	-1.07	0.00899
303	ENSMUSG000000037669		gbctI04_plate7_D22	-1.07	0.00464
304	ENSMUSG000000050043		MTG_602476542	-1.07	0.01778
305	ENSMUSG0000000055720	Ubiquitin-like protein SB132. [Source:Uniprot/SWISSPROT;Acc:Q91W67]	MTG_602475784	-1.07	0.01899
306	ENSMUSG000000061838	Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, be	gbctI04_plate17_H03	-1.07	0.00446
307	ENSMUSG000000005683	citrate synthase. [Source:RefSeq;Acc:NM_026444	MTG_602477578	-1.06	0.00578

308	ENSMUSG0000009563	torsin family 2, member A. [Source:RefSeq;Acc:NM_152800]	MTG_602474383	-1.06	0.00656
309	ENSMUSG00000022199	solute carrier family 22 (organic cation transporter), member 17; organic cation transporter BOCT. [Source:RefSeq;Acc:NM_011573]	MTG_602474203	-1.06	0.00581
310	ENSMUSG00000024309	Prefoldin subunit 6 (Protein Ke2). [Source:Uniprot/SWISSPROT;Acc:Q03958]	gbctI04_plate7_P14	-1.06	0.00717
311	ENSMUSG00000025968	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I)	gbctI04_plate16_G05	-1.06	0.00561
312	ENSMUSG00000040813	testis expressed gene 264. [Source:RefSeq;Acc:NM_011573]	gbctI04_plate9_K12	-1.06	0.00536
313	ENSMUSG00000048763	Homeobox protein Hox-B3 (Hox-2.7) (MH-23). [Source:Uniprot/SWISSPROT;Acc:P09026]	gbctI04_plate13_G02	-1.06	0.04965
314	ENSMUSG00000002393	Orphan nuclear receptor EAR-2 (V-erbA related protein EAR-2). [Source:Uniprot/SWISSPROT;Acc:P43136]	MTG_602474704	-1.05	0.00436
315	ENSMUSG000000024187		MTG_602473232	-1.05	0.00528
316	ENSMUSG000000025453	NAD(P) transhydrogenase, mitochondrial precursor (EC 1.6.1.2) (Pyridine nucleotide transhydrogenase) (Nicotina	gbctI04_plate12_G01	-1.05	0.01884
317	ENSMUSG000000026832	pleckstrin homology, Sec7 and coiled-coil domains, binding protein; cytohesin binding protein; pleckstrin homology	MTG_602477258	-1.05	0.01132
318	ENSMUSG000000029247	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole- succinocarboxamide synthase (EC 6.3.2.1)	gbctI04_plate6_B05	-1.05	0.01335
319	ENSMUSG000000038879		MTG_602473359	-1.05	0.03873
320	ENSMUSG000000048833	CDNA FLJ11274 FIS. [Source:Uniprot/SPTREMBL;Acc:Q8BFU1]	gbctI04_plate5_D13	-1.05	0.01423
321	ENSMUSG000000054474		MTG_602477201	-1.05	0.02434
322	ENSMUSG000000005881	Serologically defined breast cancer antigen NY-BR-84 homolog. [Source:Uniprot/SWISSPROT;Acc:Q9CQE7]	MTG_602467769	-1.04	0.01660
323	ENSMUSG000000015027	galactosamine (N-acetyl)-6-sulfate sulfatase; N-acetylgalactosamine-6-sulfate sulfatase. [Source:RefSeq;Acc:NM_011573]	gbctI04_plate7_B06	-1.04	0.01741
324	ENSMUSG000000031447	Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (LGP-A) (LGP-120) (CD107A) (P2B). [Source:Uniprot/SWISSPROT;Acc:P26043]	gbctI04_plate6_D08	-1.04	0.02668
325	ENSMUSG000000032050	Radixin (ESP10). [Source:Uniprot/SWISSPROT;Acc:P26043]	gbctI04_plate16_B07	-1.04	0.03507
326	ENSMUSG000000036712	cyndromatosis (turban tumor syndrome). [Source:RefSeq;Acc:NM_173369]	MTG_602474533	-1.04	0.01093
327	ENSMUSG000000037049	Sphingomyelin phosphodiesterase precursor (EC 3.1.4.12) (Acid sphingomyelinase) (aSMase). [Source:Uniprot/SWISSPROT;Acc:P43136]	MTG_602477151	-1.04	0.00635
328	ENSMUSG000000041995		gbctI04_plate8_B05	-1.04	0.01734
329	ENSMUSG000000044443		MTG_602467955	-1.04	0.01990
330	ENSMUSG000000055553		MTG_602473619	-1.04	0.01046
331	ENSMUSG000000056124	Beta-1,4-galactosyltransferase 6 (EC 2.4.1.-) (Beta-1,4-GalTase 6) (Beta4Gal-T6) (b4Gal-T6) (UDP-galactose:bet	MTG_602470271	-1.04	0.02332
332	ENSMUSG000000060181	solute carrier family 35, member E3. [Source:RefSeq;Acc:NM_029875]	MTG_602475521	-1.04	0.02036
333	ENSMUSG000000000823		MTG_602476539	-1.03	0.01045
334	ENSMUSG000000015647	Laminin alpha-5 chain precursor. [Source:Uniprot/SWISSPROT;Acc:Q61001]	MTG_602475821	-1.03	0.01790
335	ENSMUSG000000024151	DNA mismatch repair protein Msh2. [Source:Uniprot/SWISSPROT;Acc:P43247]	MTG_602476651	-1.03	0.04834
336	ENSMUSG000000031708	Synaptic glycoprotein SC2. [Source:Uniprot/SWISSPROT;Acc:Q9CY27]	MTG_602474922	-1.03	0.03969
337	ENSMUSG000000032246	calmodulin-like 4. [Source:RefSeq;Acc:NM_138304]	gbctI04_plate5_D08	-1.03	0.03291
338	ENSMUSG000000033722		MTG_602472777	-1.03	0.00972
339	ENSMUSG000000038889		MTG_602476413	-1.03	0.00872
340	ENSMUSG000000040998	nephronectin. [Source:RefSeq;Acc:NM_033525]	MTG_602470182	-1.03	0.01003
341	ENSMUSG000000052151	Lipid phosphate phosphohydrolase 2 (EC 3.1.3.4) (Phosphatidic acid phosphatase 2c) (Phosphatidate phosphohy	MTG_602473038	-1.03	0.00866
342	ENSMUSG000000063931	Xaa-Pro dipeptidase (EC 3.4.13.9) (X-Pro dipeptidase) (Proline dipeptidase) (Prolidase) (Imidodipeptidase) (Pepti	gbctI04_plate14_C20	-1.03	0.01188
343	ENSMUSG000000002059	Ras-related protein Rab-34 (Rab-39) (Ras-related protein Rah) (Ras- related homolog). [Source:Uniprot/SWISSPROT;Acc:P43247]	MTG_602468730	-1.02	0.00807
344	ENSMUSG000000024527	Similar to AFG3 ATPase family gene 3-like 2 (Yeast) (RIKEN cDNA 2310036102 gene). [Source:Uniprot/SPTREMBL;Acc:Q8BFU1]	MTG_602470346	-1.02	0.01419
345	ENSMUSG000000025399	retinol dehydrogenase 6; retinol dehydrogenase type 6. [Source:RefSeq;Acc:NM_009040]	MTG_602475228	-1.02	0.03113
346	ENSMUSG000000025503	Transaldolase (EC 2.2.1.2). [Source:Uniprot/SWISSPROT;Acc:Q93092]	MTG_602477145	-1.02	0.02343
347	ENSMUSG000000029190		MTG_602468416	-1.02	0.03451
348	ENSMUSG000000032897	Nuclear transcription factor Y subunit gamma (NF-Y protein chain C) (Nuclear factor YC) (NF-YC) (CCAAT-binding	MTG_602471634	-1.02	0.01694
349	ENSMUSG000000052102	Glucosamine-6-phosphate isomerase (EC 3.5.99.6) (Glucosamine-6- phosphate deaminase) (GNPDA) (GlcN6P d	gbctI04_plate9_O02	-1.02	0.00871
350	ENSMUSG000000057562		gbctI04_plate13_F13	-1.02	0.00432
351	ENSMUSG000000001663	Glutathione S-transferase theta 1 (EC 2.5.1.18) (GST class-theta). [Source:Uniprot/SWISSPROT;Acc:Q64471]	MTG_602472489	-1.01	0.01100
352	ENSMUSG000000005514	NADPH--cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R). [Source:Uniprot/SWISSPROT;Acc:P37040]	MTG_602474665	-1.01	0.00708
353	ENSMUSG000000027634	NDRG3 protein (Ndr3 protein). [Source:Uniprot/SWISSPROT;Acc:Q9QYF9]	MTG_602476372	-1.01	0.01941
354	ENSMUSG000000039682	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase) (Proline aminope	MTG_602469881	-1.01	0.02163
1	EST		MTG_602469058	-2.12	0.04108
2	EST		gbctI04_plate6_I09	-1.87	0.00815
3	EST		gbctI04_plate7_A23	-1.84	0.02565
4	EST		gbctI04_plate4_A10	-1.74	0.04271
5	EST		gbctI04_plate14_L01	-1.72	0.02070
6	EST		gbctI04_plate6_G16	-1.7	0.00503
7	EST		gbctI04_plate6_O19	-1.69	0.03344
8	EST		MTG_602469860	-1.65	0.02394
9	EST		gbctI04_plate4_N01	-1.65	0.00312
10	EST		gbctI04_plate16_E20	-1.62	0.00596
11	EST		MTG_602468678	-1.61	0.03496
12	EST		MTG_602467489	-1.6	0.03387
13	EST		gbctI04_plate14_G11	-1.59	0.02933
14	EST		MTG_602467577	-1.59	0.02725
15	EST		MTG_602469355	-1.56	0.01920

16	EST	gbctI04_plate9_K21	-1.54	0.03235
17	EST	MTG_602468170	-1.53	0.03985
18	EST	gbctI04_plate15_P20	-1.53	0.00781
19	EST	MTG_602469792	-1.52	0.04332
20	EST	gbctI04_plate15_O20	-1.48	0.04620
21	EST	gbctI04_plate7_G16	-1.45	0.04471
22	EST	MTG_602468108	-1.45	0.03148
23	EST	MTG_602467460	-1.41	0.00374
24	EST	gbctI04_plate8_K13	-1.33	0.01053
25	EST	MTG_602476820	-1.3	0.04185
26	EST	MTG_602467106	-1.28	0.03656
27	EST	MTG_602471804	-1.27	0.03272
28	EST	MTG_602473555	-1.27	0.02355
29	EST	gbctI04_plate6_H11	-1.24	0.01206
30	EST	MTG_602477007	-1.18	0.01491
31	EST	gbctI04_plate5_O12	-1.16	0.00380
32	EST	gbctI04_plate6_D12	-1.12	0.03021
33	EST	MTG_602476883	-1.1	0.01889
34	EST	MTG_602476632	-1.02	0.03074

Table S4

*List of category 2 genes in Fig 1C.*