

Table S1. List of differentially expressed genes under selected functional categories

Probe name	Gene symbol	Name	Fold geomean		
			Group II	Group III	Group IV
Expression of oxidative stress and glutathione metabolism related genes					
GT_Mm_44k_51_P100 828	Prdx3	Peroxiredoxin 3	-0.497	-0.269	-0.984
GT_Mm_44k_51_P106 397	Prkd3	Protein kinase D3	-0.548	-0.685	-0.619
GT_Mm_44k_51_P353 183	Prdx1	Peroxiredoxin 1	-1.641	-0.405	-2.390
GT_Mm_44k_51_P386 880	Stip1	Stress-induced phosphoprotein 1	-0.640	-0.678	-0.533
GT_Mm_44k_51_P411 271	Nfe2l2	Nuclear factor, erythroid derived 2, like 2	-1.393	-0.607	-2.060
GT_Mm_44k_51_P437 336	Uaca	Uveal autoantigen with coiled-coil domains and ankyrin repeats	0.587	0.506	1.418
GT_Mm_44k_51_P483 280	Prnp	Prion protein	-0.740	-0.373	-1.998
GT_Mm_44k_52_P376 804	Hspa13	Heat shock protein 70 family, member 13	-1.796	-0.771	-1.582
GT_Mm_44k_52_P423 424	Ero1l	ERO1-like (S. cerevisiae)	-1.045	-0.432	-0.770
GT_Mm_44k_51_P231 184	Anpep	Alanyl (membrane) aminopeptidase	0.148	-0.387	-0.377
GT_Mm_44k_51_P260 169	Gstm5	Glutathione S-transferase, mu 5	-1.155	-0.307	-1.100
GT_Mm_44k_51_P287 810	Mgst1	Microsomal glutathione S-transferase 1	-1.133	-0.987	-1.582
GT_Mm_44k_51_P289 881	Txndc12	Thioredoxin domain containing 12	-0.436	-0.632	-0.845
GT_Mm_44k_51_P374 464	Gstp1	Glutathione S-transferase, pi 1	-1.513	-1.170	-1.670
GT_Mm_44k_52_P358 860	Gss	Glutathione synthetase	-0.856	-0.461	-1.391
GT_Mm_44k_52_P379 256	Lap3	Leucine aminopeptidase 3	-1.002	-0.697	-0.967
GT_Mm_44k_52_P415 215	Gstm1	Glutathione S-transferase, mu 1	-1.286	-0.868	-1.666
GT_Mm_44k_52_P432 124	Gsta3	Glutathione S-transferase, alpha 3	0.329	-0.406	-1.382
GT_Mm_44k_52_P641 758	Ggct	Gamma-glutamyl cyclotransferase	-0.516	0.848	0.657
Expression of defense and MAPK related genes					

GT_Mm_44k_00046	Defa-rs4	Defensin, alpha,, related sequence 4	1.262	1.845	1.173
GT_Mm_44k_01450	Mgmt	O-6-methylguanine-DNA methyltransferase	0.506	-0.826	-0.425
GT_Mm_44k_01532	Cd74	CD74 antigen	-1.725	0.747	0.604
GT_Mm_44k_02048	Ifna6	Interferon alpha 6	0.453	1.391	1.272
GT_Mm_44k_51_P117881	Leap2	Liver-expressed antimicrobial peptide 2	-0.137	-0.576	-0.662
GT_Mm_44k_51_P129012	B2m	Beta-2 microglobulin	-1.170	0.227	-1.353
GT_Mm_44k_51_P209527	Bcl10	B-cell leukemia/lymphoma 10	-1.547	-0.235	-2.186
GT_Mm_44k_51_P217218	Il6	Interleukin 6	-0.230	-0.231	0.501
GT_Mm_44k_51_P302576	Spn	Sialophorin	-	-	-9.855
GT_Mm_44k_51_P373619	Mbl1	Mannose-binding lectin (protein A) 1	-1.542	-0.727	-1.305
GT_Mm_44k_51_P385993	Rela	V-rel reticuloendotheliosis viral oncogene homolog A (avian)	-0.883	-0.532	-0.759
GT_Mm_44k_51_P402846	Stab2	Stabilin 2	-0.365	-0.682	-0.234
GT_Mm_44k_51_P405476	Fcer1g	Fc receptor, IgE, high affinity I, gamma polypeptide	-1.022	-0.077	-0.661
GT_Mm_44k_51_P432563	Tlr9	Toll-like receptor 9	-0.228	-0.486	-0.905
GT_Mm_44k_51_P454008	Lbp	Lipopolysaccharide binding protein	-1.750	0.227	-1.356
GT_Mm_44k_51_P500676	Dmbt1	Deleted in malignant brain tumors 1	-1.697	-3.165	-2.026
GT_Mm_44k_51_P506733	P2rx7	Purinergic receptor P2X, ligand-gated ion channel, 7	0.359	0.533	1.150
GT_Mm_44k_52_P21486	Hamp2	Hepcidin antimicrobial peptide 2	5.089	3.513	2.057
GT_Mm_44k_52_P321140	Defb1	Defensin beta 1	0.548	-1.418	-1.300
GT_Mm_44k_52_P435356	Cotl1	Coactosin-like 1 (Dictyostelium)	-0.798	-0.476	-0.434
GT_Mm_44k_52_P578732	Ccr5	Chemokine (C-C motif) receptor 5	0.502	0.670	1.258
GT_Mm_44k_52_P582059	Lyz1	Lysozyme 1	-1.130	0.413	-1.403

GT_Mm_44k_52_P590 625	Nlrp10	NLR family, pyrin domain containing 10	0.467	2.532	1.162
GT_Mm_44k_52_P621 991	Apaf1	Apoptotic peptidase activating factor 1	0.476	1.530	1.234
GT_Mm_44k_52_P669 922	Hamp	Hepcidin antimicrobial peptide	2.966	3.175	-2.870
GT_Mm_44k_01225	Ppm1b	Protein phosphatase 1B, magnesium dependent, beta isoform	0.504	0.240	0.632
GT_Mm_44k_01846	Arrb2	Arrestin, beta 2	0.474	-0.162	0.644
GT_Mm_44k_51_P104 418	Dusp10	Dual specificity phosphatase 10	0.533	0.350	-0.256
GT_Mm_44k_51_P117 952	Hspa1a	Heat shock protein 1A	-3.974	-4.569	-3.734
GT_Mm_44k_51_P170 371	Hspa8	Heat shock protein 8	-1.398	-0.302	-1.022
GT_Mm_44k_51_P170 807	Map3k6	Mitogen-activated protein kinase kinase kinase 6	-0.099	1.708	1.501
GT_Mm_44k_51_P184 385	Pla2g12 b	Phospholipase A2, group XIIB	-0.732	-0.246	-0.446
GT_Mm_44k_51_P274 223	Fgf17	Fibroblast growth factor 17	0.345	1.167	1.784
GT_Mm_44k_51_P305 003	Ntrk1	Neurotrophic tyrosine kinase, receptor, type 1	0.507	2.811	1.170
GT_Mm_44k_51_P315 904	Gadd45 g	Growth arrest and DNA-damage-inducible 45 gamma	-0.065	1.572	2.718
GT_Mm_44k_51_P318 488	Akt3	Thymoma viral proto-oncogene 3	0.358	-0.165	1.145
GT_Mm_44k_51_P345 393	Fas	Fas (TNF receptor superfamily member 6)	-1.263	-0.337	-1.117
GT_Mm_44k_51_P357 744	Jund	Jun proto-oncogene related gene d	0.347	0.086	1.160
GT_Mm_44k_51_P370 090	Pdgfa	Platelet derived growth factor, alpha	-0.074	-0.184	-0.172
GT_Mm_44k_51_P385 993	Rela	V-rel reticuloendotheliosis viral oncogene homolog A (avian)	-0.883	-0.532	-0.759
GT_Mm_44k_51_P396 273	Nras	Neuroblastoma ras oncogene	0.531	3.918	1.947
GT_Mm_44k_51_P461 748	Dusp3	Dual specificity phosphatase 3	0.675	0.205	1.080
GT_Mm_44k_51_P513	Rac1	RAS-related C3	-1.950	-0.878	-1.787

254		botulinum substrate 1			
GT_Mm_44k_52_P106	Egfr	Epidermal growth factor receptor	-0.143	-0.338	0.178
259					
GT_Mm_44k_52_P166	Taok3	TAO kinase 3	0.652	-0.186	0.944
755					
GT_Mm_44k_52_P168	Fgf14	Fibroblast growth factor 14	0.528	0.449	1.492
549					
GT_Mm_44k_52_P209	Cacnb2	Calcium channel, voltage-dependent, beta 2 subunit	0.498	2.137	1.171
514					
GT_Mm_44k_52_P235	Fgf21	Fibroblast growth factor 21	-0.719	0.440	-0.624
347					
GT_Mm_44k_52_P251	Tgfbr2	Transforming growth factor, beta receptor II	0.513	1.025	1.321
403					
GT_Mm_44k_52_P267	Fgf13	Fibroblast growth factor 13	1.338	0.488	1.789
243					
GT_Mm_44k_52_P297	Akt2	Thymoma viral proto-oncogene 2	-1.394	-0.974	-1.834
7					
GT_Mm_44k_52_P399	Dusp2	Dual specificity phosphatase 2	-0.637	0.317	-0.885
934					
GT_Mm_44k_52_P404	Hspb1	Heat shock protein 1	-1.509	-1.775	-1.141
533					
GT_Mm_44k_52_P423	Mos	Moloney sarcoma oncogene	0.391	1.301	1.225
32					
GT_Mm_44k_52_P611	Cacna1g	Calcium channel, voltage-dependent, T type, alpha 1G subunit	0.353	1.725	1.148
610					
GT_Mm_44k_52_P648	Dusp9	Dual specificity phosphatase 9	0.417	-0.151	2.419
601					
GT_Mm_44k_52_P771	Fasl	Fas ligand (TNF superfamily, member 6)	0.416	0.785	1.211
06					
Expression of ETS and glycolysis related genes					
GT_Mm_44k_00911	Cyp2d1	Cytochrome P450, family 2, subfamily d, polypeptide 22	-0.660	-1.147	-1.279
	0,1,2				
GT_Mm_44k_01406	Cyp4a1	Cytochrome P450, family 4, subfamily a, polypeptide 14	4.307	2.209	4.419
	4				
GT_Mm_44k_01473	Frrs1	Ferric-chelate reductase 1	0.793	0.303	1.262
GT_Mm_44k_01762	Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	0.385	-0.418	0.333
GT_Mm_44k_01942	Aifm3	Apoptosis-inducing factor, mitochondrion-associated 3	0.601	-0.809	-0.637
GT_Mm_44k_51_P100	Atp5j	ATP synthase, H+	-1.356	-0.125	-1.061

866		transporting, mitochondrial F0 complex, subunit F			
GT_Mm_44k_51_P120 295	Cyp2d2 6	Cytochrome P450, family 2, subfamily d, polypeptide 26	0.234	-0.419	0.446
GT_Mm_44k_51_P124 126	Cyp2d1 0 ,11,d22	Cytochrome P450, family 2, subfamily d, polypeptide 22	0.429	-0.409	0.300
GT_Mm_44k_51_P131 800	Cyba	Cytochrome b-245, alpha polypeptide	-1.616	-0.678	-1.112
GT_Mm_44k_51_P134 142	Cyp2c7 0	Cytochrome P450, family 2, subfamily c, polypeptide 70	-0.542	-1.009	-0.435
GT_Mm_44k_51_P138 152	Cisd1	CDGSH iron sulfur domain 1	0.466	-0.295	-0.828
GT_Mm_44k_51_P141 123	Cox5b	Cytochrome c oxidase, subunit Vb	0.324	-0.206	0.284
GT_Mm_44k_51_P160 744	Ndufb3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	0.384	-0.183	-0.430
GT_Mm_44k_51_P168 708	Atp5f1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	0.282	-0.469	-0.926
GT_Mm_44k_51_P177 552	Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	0.398	-0.330	0.413
GT_Mm_44k_51_P183 292	Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	-0.520	-0.421	-0.767
GT_Mm_44k_51_P184 284	Dld	Dihydrolipoamide dehydrogenase	-0.731	-0.804	-2.104
GT_Mm_44k_51_P263 756	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	-0.166	0.061	-0.605
GT_Mm_44k_51_P291 129	Fdx1	Ferredoxin 1	0.359	-0.700	-0.994
GT_Mm_44k_51_P295 610	Cyc1	Cytochrome c-1	-0.857	-0.529	-1.025
GT_Mm_44k_51_P301 289	Atp5k	ATP synthase, H+ transporting, mitochondrial F1F0	0.600	-0.399	0.219

		complex, subunit e			
GT_Mm_44k_51_P311 434	Cyb5	Cytochrome b-5	-0.509	-0.162	-1.565
GT_Mm_44k_51_P324 871	Cybasc3	Cytochrome b, ascorbate dependent 3	-0.275	-0.587	-0.731
GT_Mm_44k_51_P336 827	Cyb5b	Cytochrome b5 type B	-0.910	-0.484	-1.036
GT_Mm_44k_51_P338 728	Sdhaf1	Succinate dehydrogenase complex assembly factor 1	-0.153	-0.524	-0.248
GT_Mm_44k_51_P365 521	Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	0.106	-0.084	-0.097
GT_Mm_44k_51_P410 823	Sdha	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	-0.639	-0.851	-2.143
GT_Mm_44k_51_P472 671	Uqcrb	Ubiquinol-cytochrome c reductase binding protein	0.297	-0.117	-0.586
GT_Mm_44k_51_P478 303	Cyp2d9, 12	Cytochrome P450, family 2, subfamily d, polypeptide 9	-0.606	-0.947	-0.807
GT_Mm_44k_51_P482 051	Cyp3a4 1b, 16	Cytochrome P450, family 3, subfamily a, polypeptide 16	-0.488	-0.452	-0.942
GT_Mm_44k_51_P489 367	Cyp3a2 5	Cytochrome P450, family 3, subfamily a, polypeptide 25	-0.986	-1.262	-2.248
GT_Mm_44k_52_P136 153	Cox7c	Cytochrome c oxidase, subunit VIIc	0.123	-0.786	-0.804
GT_Mm_44k_52_P170 054	Ndufv3	NADH dehydrogenase (ubiquinone) flavoprotein 3	-0.633	-0.489	-0.731
GT_Mm_44k_52_P217 474	Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	-0.470	-0.513	-1.425
GT_Mm_44k_52_P380 314	Cyp3a2 5	Cytochrome P450, family 3, subfamily a, polypeptide 25	-0.540	-1.036	-1.462
GT_Mm_44k_52_P423 424	Ero1l	ERO1-like (<i>S. cerevisiae</i>)	-1.045	-0.432	-0.770
GT_Mm_44k_52_P444 628	Cybb	Cytochrome b-245, beta polypeptide	-2.624	0.021	-0.841
GT_Mm_44k_52_P449 14	Cyp4a1 2a	Cytochrome P450, family 4, subfamily a, polypeptide 12a	-2.327	-1.619	-1.530

GT_Mm_44k_52_P595 871	Cyp1a2	Cytochrome P450, family 1, subfamily a, polypeptide 2	-1.452	-1.410	-2.324
GT_Mm_44k_52_P681 787	Cyb561	Cytochrome b-561	-1.004	-0.584	-0.425
GT_Mm_44k_03237	Gm1029 1	Glyceraldehyde-3- phosphate dehydrogenase pseudogene	-1.704	-0.429	-1.079
GT_Mm_44k_51_P182 828	Pgk1	Phosphoglycerate kinase 1	-0.608	-0.164	-1.312
GT_Mm_44k_51_P189 442	Adh4 ; Adh6- ps1	Alcohol dehydrogenase 4 (class II), pi polypeptide	-0.809	-0.851	-1.289
GT_Mm_44k_51_P310 896	Pfkl	Phosphofructokinase, liver, B-type	-0.227	-0.625	-0.264
GT_Mm_44k_51_P312 755	Ins1	Insulin I	0.506	1.039	1.206
GT_Mm_44k_51_P327 295	Akr1a4	Aldo-keto reductase family 1, member A4 (aldehyde reductase)	-0.464	-0.413	-1.096
GT_Mm_44k_51_P364 146	Ldha	Lactate dehydrogenase A	-1.382	-0.866	-2.390
GT_Mm_44k_51_P404 275	Adh5	Alcohol dehydrogenase 5 (class III), chi polypeptide	-0.824	-0.275	-1.203
GT_Mm_44k_51_P426 886	Gpi1	Glucose phosphate isomerase 1	0.224	-0.356	0.641
GT_Mm_44k_51_P428 555	Adh1	Alcohol dehydrogenase 1 (class I)	0.286	-0.407	-0.650
GT_Mm_44k_51_P462 385	G6pc	Glucose-6-phosphatase, catalytic	0.765	-0.992	1.384
GT_Mm_44k_51_P510 418	Aldh1b1	Aldehyde dehydrogenase 1 family, member B1	-1.791	-0.650	-1.758
GT_Mm_44k_52_P259 537	Gck	Glucokinase	-1.039	-0.754	-1.248
GT_Mm_44k_52_P407 060	Ins2	Insulin II	0.472	2.214	1.194
GT_Mm_44k_52_P568 792	Pdhb	Pyruvate dehydrogenase (lipoamide) beta	-0.656	-0.537	-1.403
GT_Mm_44k_52_P748 882	Eno2	Enolase 2, gamma neuronal	0.406	-0.115	1.162
GT_Mm_44k_52_P983 87	Aldoa	Aldolase A, fructose- bisphosphate	-0.125	-0.361	-0.086
Expression of fatty acid, cholesterol, steroid and triglyceride metabolism related genes					
GT_Mm_44k_07860	Cyp4a2 9	Cytochrome P450, family 4, subfamily a,	0.453	0.818	1.476

GT_Mm_44k_51_P289 742	Slc27a5	polypeptide 29 Solute carrier family 27 (fatty acid transporter), member 5	-0.416	-0.486	-1.203
GT_Mm_44k_51_P324 633	Elovl3	Elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	-2.667	-2.918	-3.309
GT_Mm_44k_01454	Mut	Methylmalonyl- Coenzyme A mutase	0.893	0.136	-0.422
GT_Mm_44k_51_P153 170	Cyb5r3	Cytochrome b5 reductase 3	-0.979	-0.431	-1.647
GT_Mm_44k_51_P243 755	Slc10a2	Solute carrier family 10, member 2	-1.673	-1.427	0.248
GT_Mm_44k_51_P245 123	Baat	Bile acid-Coenzyme A: amino acid N- acyltransferase	0.291	0.072	0.395
GT_Mm_44k_51_P255 817	Scarb1	Scavenger receptor class B, member 1	-1.164	-0.885	-1.369
GT_Mm_44k_51_P278 334	Vldlr	Very low density lipoprotein receptor	1.328	1.674	0.759
GT_Mm_44k_51_P329 711	Idi1	Isopentenyl-diphosphate delta isomerase	0.212	0.433	-1.050
GT_Mm_44k_51_P336 060	Lcat	Lecithin cholesterol acyltransferase	-1.235	-0.713	-0.986
GT_Mm_44k_51_P355 943	Mvd	Mevalonate (diphospho) decarboxylase	-0.529	-0.660	-0.829
GT_Mm_44k_51_P380 881	Med15	Mediator complex subunit 15	-1.354	-0.346	-0.610
GT_Mm_44k_51_P385 598	Slc37a4	Solute carrier family 37 (glucose-6-phosphate transporter), member 4	1.101	-0.270	0.699
GT_Mm_44k_51_P461 429	Cyp7b1	Cytochrome P450, family 7, subfamily b, polypeptide 1	-1.130	-0.410	0.225
GT_Mm_44k_51_P514 449	Nr5a2	Nuclear receptor subfamily 5, group A, member 2	0.533	0.526	0.861
GT_Mm_44k_52_P150 236	Apom	Apolipoprotein M	-0.369	-0.383	-0.151
GT_Mm_44k_52_P244 193	Cd24a	CD24a antigen	-0.633	-0.727	-0.219
GT_Mm_44k_52_P251 403	Tgfbr2	Transforming growth factor, beta receptor II	0.513	1.025	1.321
GT_Mm_44k_52_P485 971	Scap	SREBF chaperone	0.379	-0.325	-0.503

GT_Mm_44k_52_P488 427	Sec14l2	SEC14-like 2 (<i>S. cerevisiae</i>)	-1.203	-0.656	-1.260
GT_Mm_44k_52_P636 752	Cyp51	Cytochrome P450, family 51	-1.426	0.852	-0.863
GT_Mm_44k_00911	Cyp2d1 0;11 ; 22	Cytochrome P450, family 2, subfamily d, polypeptide 22	-0.660	-1.147	-1.279
GT_Mm_44k_01406	Cyp4a1 4	Cytochrome P450, family 4, subfamily a, polypeptide 14	4.307	2.209	4.419
GT_Mm_44k_01692	Aste1	Asteroid homolog 1 (<i>Drosophila</i>)	0.926	0.055	0.450
GT_Mm_44k_51_P120 295	Cyp2d2 6	Cytochrome P450, family 2, subfamily d, polypeptide 26	0.234	-0.419	0.446
GT_Mm_44k_51_P122 170	Rdh7	Retinol dehydrogenase 7	-0.552	-0.638	-0.828
GT_Mm_44k_51_P134 142	Cyp2c7 0	Cytochrome P450, family 2, subfamily c, polypeptide 70	-0.542	-1.009	-0.435
GT_Mm_44k_51_P140 803	Slco1b2	Solute carrier organic anion transporter family, member 1b2	-0.432	-0.315	-0.645
GT_Mm_44k_51_P144 581	Pgrmc1	Progesterone receptor membrane component 1	-0.256	-0.116	-1.672
GT_Mm_44k_51_P153 170	Cyb5r3	Cytochrome b5 reductase 3	-0.979	-0.431	-1.647
GT_Mm_44k_51_P213 476	Pgr	Progesterone receptor	0.718	1.313	1.515
GT_Mm_44k_51_P278 550	Tecr	Trans-2,3-enoyl-CoA reductase	-0.455	-0.666	-1.096
GT_Mm_44k_51_P418 056	Sc5d	Sterol-C5-desaturase homolog (<i>S. cerevisiae</i>)	0.233	0.174	-0.998
GT_Mm_44k_51_P421 418	Hsd3b1	Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	-1.951	-1.899	-1.176
GT_Mm_44k_51_P430 973	Paqr7	Progesterin and adipoQ receptor family member VII	-0.698	-0.627	-1.802
GT_Mm_44k_51_P435 911	Hsd3b7	Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	-0.771	-0.791	-1.315
GT_Mm_44k_51_P445 662	Hsd17b 4	Hydroxysteroid (17-beta) dehydrogenase 4	-0.351	-0.175	-1.011

GT_Mm_44k_51_P478 303	Cyp2d9; d12	Cytochrome P450, family 2, subfamily d, polypeptide 9	-0.606	-0.947	-0.807
GT_Mm_44k_51_P482 051	Cyp3a4 1b ; a16	Cytochrome P450, family 3, subfamily a, polypeptide 16	-0.488	-0.452	-0.942
GT_Mm_44k_51_P489 367	Cyp3a2 5	Cytochrome P450, family 3, subfamily a, polypeptide 25	-0.986	-1.262	-2.248
GT_Mm_44k_51_P493 649	Sult1e1	Sulfotransferase family 1E, member 1	-1.252	0.405	2.340
GT_Mm_44k_51_P496 162	Hsd3b5	Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta- isomerase 5	-2.942	-2.279	-1.754
GT_Mm_44k_51_P510 418	Aldh1b1	Aldehyde dehydrogenase 1 family, member B1	-1.791	-0.650	-1.758
GT_Mm_44k_51_P521 128	Ncoa6	Nuclear receptor coactivator 6	0.306	0.136	-0.538
GT_Mm_44k_52_P132 165	Hsd17b 11	Hydroxysteroid (17-beta) dehydrogenase 11	-0.682	-0.503	-1.760
GT_Mm_44k_52_P189 567	Rnf4	Ring finger protein 4	0.617	-0.122	0.416
GT_Mm_44k_52_P283 258	Carm1	Coactivator-associated arginine methyltransferase 1	1.098	0.285	1.552
GT_Mm_44k_52_P449 14	Cyp4a1 2a	Cytochrome P450, family 4, subfamily a, polypeptide 12a	-2.327	-1.619	-1.530
GT_Mm_44k_52_P485 971	Scap	SREBF chaperone	0.379	-0.325	-0.503
GT_Mm_44k_52_P519 689	Rxrb	Retinoid X receptor beta	-0.511	-0.710	-1.144
GT_Mm_44k_52_P532 559	Thrb	Thyroid hormone receptor beta	-4.380	-0.746	-1.770
GT_Mm_44k_52_P595 871	Cyp1a2	Cytochrome P450, family 1, subfamily a, polypeptide 2	-1.452	-1.410	-2.324
GT_Mm_44k_52_P636 752	Cyp51	Cytochrome P450, family 51	-1.426	0.852	-0.863
GT_Mm_44k_01339	Mttp	Microsomal triglyceride transfer protein	0.077	0.155	0.066
GT_Mm_44k_51_P197 213	Pnpla2	Patatin-like phospholipase domain containing 2	0.627	0.404	0.959
GT_Mm_44k_51_P259	Lpl	Lipoprotein lipase	-0.938	-0.588	-1.496

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GT_Mm_44k_51_P290 207	Insig1	Insulin induced gene 1	-0.384	-0.237	-1.236	
GT_Mm_44k_52_P113 250	Insig2	Insulin induced gene 2	-0.227	-0.437	1.075	
GT_Mm_44k_52_P447 929	Tnxb	Tenascin XB	0.489	0.911	1.206	
GT_Mm_44k_52_P572 808	Agpat9	1-acylglycerol-3- phosphate O- acyltransferase 9	0.156	0.506	0.987	
GT_Mm_44k_52_P641 185	Ptpn11	Protein tyrosine phosphatase, non- receptor type 11	-0.454	0.124	-0.515	