Supplementary Table 2: Significant gene expression changes (313 probe sets) between treated and untreated mice as calculated by the SAM software, using 2 fold and 0% median FDR thresholds.

Affy ID	Gene Name	Symbol	Fold	GO Biological Process	GO Molecular Function	GO Cellular Component
1424352_at	cytochrome P450, family 4, subfamily a, polypeptide 12	Cyp4a12	192.53	fatty acid metabolic process /// oxidation reduction	monooxygenase activity /// monooxygenase activity /// monooxygenase activity /// iron ion binding /// electron carrier activity /// oxidoreductase activity /// heme binding /// metal ion binding /// unspecific monooxygenase activity	endoplasmic reticulum /// endoplasmic reticulum membrane /// microsome /// membrane
1438448_at	otopetrin 1	Otop1	100.60	ossification /// detection of gravity /// inner ear morphogenesis	---	extracellular region /// membrane /// membrane /// integral to membrane
1435275_at	cytochrome c oxidase subunit VIb polypeptide 2	Cox6b2	53.56	oxidation reduction	cytochrome-c oxidase activity	mitochondrion /// mitochondrial crista /// mitochondrial crista
1416023_at	fatty acid binding protein 3, muscle and heart	Fabp3	28.28	phosphatidylcholine biosynthetic process /// transport	transporter activity /// binding /// lipid binding	cytoplasm
1416930_at	lymphocyte antigen 6 complex, locus D	Ly6d	26.63	defense response	---	extracellular space /// plasma membrane /// membrane /// anchored to membrane
1433601_at	adrenergic receptor, alpha 2a	Adra2a	24.82	signal transduction /// G-protein coupled receptor protein signaling pathway /// G-protein coupled receptor protein signaling pathway /// fear response	rhodopsin-like receptor activity /// signal transducer activity /// receptor activity /// G-protein coupled receptor activity /// adrenoceptor activity /// adrenoceptor activity /// alpha2-adrenergic receptor activity /// alpha2-adrenergic receptor activity /// protein binding	plasma membrane /// membrane /// integral to membrane
1419504_at	monoacylglycerol O-acyltransferase 1	Mogat1	19.78	glycerol metabolic process /// lipid metabolic process /// diacylglycerol biosynthetic process /// lipid biosynthetic process /// cell redox homeostasis	2-acylglycerol O-acyltransferase activity /// 2-acylglycerol O-acyltransferase activity /// diacylglycerol O-acyltransferase activity /// acyltransferase activity /// transferase activity	membrane fraction /// endoplasmic reticulum /// endoplasmic reticulum /// endoplasmic reticulum membrane /// membrane /// integral to membrane
1415777_at	pancreatic lipase related protein 1	Pnliprp1	19.06	lipid metabolic process /// lipid metabolic process /// lipid catabolic process /// lipid catabolic process	catalytic activity /// catalytic activity /// triacylglycerol lipase activity /// triacylglycerol lipase activity /// hydrolase activity /// hydrolase activity	extracellular region /// extracellular space
1417867_at	complement factor D (adipsin)	Cfd	17.51	proteolysis /// immune response /// complement activation, alternative pathway /// innate immune response	complement factor D activity /// catalytic activity /// serine-type endopeptidase activity /// peptidase activity /// hydrolase activity	extracellular region /// extracellular space /// extracellular space
1429523_a_at	solute carrier family 39 (metal ion transporter), member 5	Slc39a5	15.67	transport /// ion transport /// zinc ion transport /// zinc ion transport /// cellular zinc ion homeostasis /// metal ion transport	zinc ion transmembrane transporter activity /// zinc ion binding /// metal ion transmembrane transporter activity	membrane /// integral to membrane /// basolateral plasma membrane /// basolateral plasma membrane
1440134_at	cytochrome P450, family 4, subfamily a, polypeptide 31	Cyp4a31	11.27	oxidation reduction	monooxygenase activity /// iron ion binding /// electron carrier activity /// oxidoreductase activity /// heme binding /// metal ion binding	---
1431056_a_at	lipoprotein lipase /// similar to Lipoprotein lipase precursor (LPL)	LOC669888 /// Lpl	9.93	lipid metabolic process /// lipid catabolic process /// triacylglycerol catabolic process	catalytic activity /// lipoprotein lipase activity /// lipoprotein lipase activity /// triacylglycerol lipase activity /// lipid transporter activity /// heparin binding /// hydrolase activity /// triglyceride binding	extracellular space /// extracellular space /// plasma membrane /// membrane /// anchored to membrane /// chylomicron

1443902_at	RIKEN cDNA 6430573F11 gene	6430573F11Rik	9.00	metabolic process	methyltransferase activity /// transferase activity	---
1417273_at	pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	8.87	carbohydrate metabolic process /// glucose metabolic process /// acetyl-CoA biosynthetic process from pyruvate /// signal transduction /// phosphorylation /// peptidyl-histidine phosphorylation	two-component sensor activity /// protein histidine kinase activity /// protein serine/threonine/tyrosine kinase activity /// pyruvate dehydrogenase (acetyl-transferring) kinase activity /// ATP binding /// kinase activity /// transferase activity /// transferase activity, transferring phosphorus-containing groups	mitochondrion /// mitochondrion /// mitochondrial inner membrane /// mitochondrial matrix
1434382_at	serine incorporator 2	Serinc2	8.87	phosphatidylserine metabolic process /// positive regulation of transferase activity	---	membrane /// integral to membrane /// integral to membrane
1415904_at	lipoprotein lipase	Lpl	8.85	lipid metabolic process /// lipid catabolic process /// triacylglycerol catabolic process	catalytic activity /// lipoprotein lipase activity /// lipoprotein lipase activity /// triacylglycerol lipase activity /// lipid transporter activity /// heparin binding /// hydrolase activity /// triglyceride binding	extracellular space /// extracellular space /// plasma membrane /// membrane /// anchored to membrane /// chylomicron
1422996_at	acyl-CoA thioesterase 2	Acot2	8.75	lipid metabolic process /// acyl-CoA metabolic process	carboxylesterase activity /// palmitoyl-CoA hydrolase activity /// acyl-CoA thioesterase activity /// hydrolase activity	mitochondrion /// mitochondrion /// mitochondrion /// mitochondrial matrix
1418989_at	cathepsin E	Ctse	8.65	proteolysis /// antigen processing and presentation of exogenous peptide antigen via MHC class II	aspartic-type endopeptidase activity /// cathepsin E activity /// cathepsin E activity /// pepsin A activity /// neutrophil collagenase activity /// peptidase activity /// hydrolase activity /// protein homodimerization activity	extracellular space /// endosome /// endosome /// viral envelope
1442508_at	RIKEN cDNA 4933404M19 gene	4933404M19Rik	8.46	---	---	---
1424716_at	retinol saturase (all trans retinol 13,14 reductase)	Retsat	7.67	carotenoid biosynthetic process /// retinol metabolic process /// oxidation reduction	electron carrier activity /// oxidoreductase activity /// oxidoreductase activity /// oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen /// FAD binding /// all-trans-retinol 13,14-reductase activity /// all-trans-retinol 13,14-reductase activity	nuclear outer membrane /// endoplasmic reticulum /// endoplasmic reticulum membrane /// endoplasmic reticulum membrane /// membrane /// nuclear membrane
1418213_at	keratin 23	Krt23	7.38	---	structural molecule activity	intermediate filament
1417963_at	phospholipid transfer protein	Pltp	6.98	transport /// lipid transport	lipid binding	extracellular region /// extracellular space
1456096_at	RIKEN cDNA 6430573F11 gene	6430573F11Rik	6.88	metabolic process	methyltransferase activity /// transferase activity	---
1422997_s_at	acyl-CoA thioesterase 1 /// acyl-CoA thioesterase 2	Acot1 /// Acot2	6.59	long-chain fatty acid metabolic process /// lipid metabolic process /// acyl-CoA metabolic process	carboxylesterase activity /// palmitoyl-CoA hydrolase activity /// acyl-CoA thioesterase activity /// acyl-CoA thioesterase activity /// hydrolase activity	cytoplasm /// cytoplasm /// mitochondrion /// mitochondrion /// mitochondrion /// mitochondrial matrix
1424943_at	cytochrome P450, family 4, subfamily a, polypeptide 31	Cyp4a31	6.58	oxidation reduction	monooxygenase activity /// iron ion binding /// electron carrier activity /// oxidoreductase activity /// heme binding /// metal ion binding	---
1422811_at	solute carrier family 27 (fatty acid transporter), member 1	Slc27a1	6.29	long-chain fatty acid metabolic process /// lipid metabolic process /// fatty acid metabolic process /// transport /// lipid transport /// metabolic process	nucleotide binding /// catalytic activity /// long-chain-fatty-acid-CoA ligase activity /// transporter activity /// binding /// ligase activity	cytoplasm /// plasma membrane /// plasma membrane /// endomembrane system /// membrane /// integral to membrane /// cytoplasmic vesicle
1441971_at	Transcribed locus	---	6.25	---	---	---
1419738_a_at	tropomyosin 2, beta	Tpm2	6.23	muscle contraction	actin binding /// structural constituent of cytoskeleton /// protein binding	cytoplasm /// cytoskeleton /// muscle thin filament tropomyosin

1435658_at	solute carrier family 27 (fatty acid transporter), member 1	Slc27a1	6.17	long-chain fatty acid metabolic process /// lipid metabolic process /// fatty acid metabolic process /// transport /// lipid transport /// metabolic process	nucleotide binding /// catalytic activity /// long-chain-fatty-acid-CoA ligase activity /// transporter activity /// binding /// ligase activity	cytoplasm /// plasma membrane /// plasma membrane /// endomembrane system /// membrane /// integral to membrane /// cytoplasmic vesicle
1425028_a_at	tropomyosin 2, beta	Tpm2	6.15	muscle contraction	actin binding /// structural constituent of cytoskeleton /// protein binding	cytoplasm /// cytoskeleton /// muscle thin filament tropomyosin
1428512_at	basic helix-loop-helix domain containing, class B9	Bhlhb9	6.03	---	binding	---
1443870_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	Abcc4	5.77	transport /// ion transport /// multidrug transport	nucleotide binding /// chloride channel activity /// ATP binding /// multidrug efflux pump activity /// ATPase activity /// nucleoside-triphosphatase activity /// ATPase activity, coupled to transmembrane movement of substances	membrane fraction /// plasma membrane /// membrane /// integral to membrane /// platelet dense granule membrane
1449065_at	acyl-CoA thioesterase 1	Acot1	5.69	long-chain fatty acid metabolic process /// lipid metabolic process /// acyl-CoA metabolic process	carboxylesterase activity /// palmitoyl-CoA hydrolase activity /// acyl-CoA thioesterase activity /// acyl-CoA thioesterase activity /// hydrolase activity	cytoplasm /// cytoplasm
1418328_at	carnitine palmitoyltransferase 1b, muscle	Cpt1b	5.67	lipid metabolic process /// fatty acid metabolic process /// fatty acid metabolic process /// transport /// transport /// long-chain fatty acid transport /// long-chain fatty acid transport	carnitine O-palmitoyltransferase activity /// carnitine O-palmitoyltransferase activity /// protein binding /// acyltransferase activity /// kinase activity /// transferase activity	mitochondrion /// mitochondrion /// mitochondrion /// mitochondrial outer membrane /// mitochondrial outer membrane /// microsome /// membrane /// integral to membrane /// integral to membrane /// outer membrane /// outer membrane
1417860_a_at	spondin 2, extracellular matrix protein	Spon2	5.65	immune response /// cell adhesion /// multicellular organismal development	protein binding	extracellular region /// proteinaceous extracellular matrix /// extracellular space
1421011_at	hydroxysteroid (17-beta) dehydrogenase 11	Hsd17b11	5.49	steroid biosynthetic process /// androgen catabolic process /// metabolic process /// metabolic process /// lipid biosynthetic process	catalytic activity /// estradiol 17-beta-dehydrogenase activity /// binding /// steroid dehydrogenase activity /// oxidoreductase activity	extracellular region /// cytoplasm
1417900_a_at	very low density lipoprotein receptor	Vldlr	5.30	lipid metabolic process /// transport /// lipid transport /// endocytosis /// steroid metabolic process /// cholesterol metabolic process /// positive regulation of protein kinase activity	receptor activity /// lipid transporter activity /// calcium ion binding /// protein binding	extracellular space /// extracellular space /// membrane fraction /// coated pit /// membrane /// integral to membrane /// integral to membrane
1423166_at	CD36 antigen	Cd36	5.25	transport /// cell adhesion /// cell adhesion /// cholesterol transport /// apoptotic cell clearance	receptor activity /// protein binding /// high-density lipoprotein binding	plasma membrane /// membrane /// integral to membrane /// integral to membrane
1450883_a_at	CD36 antigen	Cd36	5.24	transport /// cell adhesion /// cell adhesion /// cholesterol transport /// apoptotic cell clearance	receptor activity /// protein binding /// high-density lipoprotein binding	plasma membrane /// membrane /// integral to membrane /// integral to membrane
1426989_at	calsyntenin 3	Clstn3	4.76	cell adhesion /// homophilic cell adhesion	calcium ion binding /// protein binding	Golgi membrane /// endoplasmic reticulum /// endoplasmic reticulum membrane /// Golgi apparatus /// plasma membrane /// membrane /// integral to membrane /// integral to membrane /// postsynaptic membrane
1456424_s_at	phospholipid transfer protein	Pltp	4.73	transport /// lipid transport	lipid binding	extracellular region /// extracellular space
1433779_at	cancer susceptibility candidate 4	Casc4	4.72	---	---	membrane /// integral to membrane
1430780_a_at	phosphomannomutase 1	Pmm1	4.60	metabolic process /// mannose biosynthetic process	catalytic activity /// phosphomannomutase activity /// isomerase activity	cytoplasm

1421430_at	RAD51-like 1 (S. cerevisiae)	Rad51l1	4.49	DNA metabolic process /// DNA repair /// DNA recombination /// response to DNA damage stimulus	nucleotide binding /// DNA binding /// ATP binding /// DNA-dependent ATPase activity /// nucleoside-triphosphatase activity	nucleus
1450248_at	a disintegrin and metallopeptidase domain 11	Adam11	4.48	proteolysis /// integrin-mediated signaling pathway	metalloendopeptidase activity /// peptidase activity /// metallopeptidase activity /// zinc ion binding	membrane /// integral to membrane /// integral to membrane
1435893_at	very low density lipoprotein receptor	Vldlr	4.44	lipid metabolic process /// transport /// lipid transport /// endocytosis /// steroid metabolic process /// cholesterol metabolic process /// positive regulation of protein kinase activity	receptor activity /// lipid transporter activity /// calcium ion binding /// protein binding	extracellular space /// extracellular space /// membrane fraction /// coated pit /// membrane /// integral to membrane /// integral to membrane
1418123_at	unc-119 homolog (C. elegans)	Unc119	4.35	microtubule-based movement /// visual perception /// response to stimulus	structural molecule activity	microtubule
1455288_at	RIKEN cDNA 1110036O03 gene	1110036O03Rik	4.31	---	---	nucleus /// nucleus
1418949_at	growth differentiation factor 15	Gdf15	4.25	---	cytokine activity /// growth factor activity	extracellular region /// extracellular space /// extracellular space
1419349_a_at	cytochrome P450, family 2, subfamily d, polypeptide 9	Cyp2d9	4.25	oxidation reduction	monooxygenase activity /// iron ion binding /// electron carrier activity /// oxidoreductase activity /// oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen /// heme binding /// metal ion binding /// unspecific monooxygenase activity	endoplasmic reticulum /// endoplasmic reticulum membrane /// microsome /// microsome /// membrane
1449577_x_at	tropomyosin 2, beta	Tpm2	4.23	muscle contraction	actin binding /// structural constituent of cytoskeleton /// protein binding	cytoplasm /// cytoskeleton /// muscle thin filament tropomyosin
1438310_at	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930095L19 product:unclassifiable, full insert sequence	---	4.20	---	---	---
1419573_a_at	lectin, galactose binding, soluble 1	Lgals1	4.17	heterophilic cell adhesion /// positive regulation of I-kappaB kinase/NF-kappaB cascade /// myoblast differentiation	signal transducer activity /// protein binding /// sugar binding /// galactose binding	extracellular space /// intracellular
1438258_at	very low density lipoprotein receptor	Vldlr	4.17	lipid metabolic process /// transport /// lipid transport /// endocytosis /// steroid metabolic process /// cholesterol metabolic process /// positive regulation of protein kinase activity	receptor activity /// lipid transporter activity /// calcium ion binding /// protein binding	extracellular space /// extracellular space /// membrane fraction /// coated pit /// membrane /// integral to membrane /// integral to membrane
1454078_a_at	galactose-3-O-sulfotransferase 1	Gal3st1	4.14	galactosylceramide biosynthetic process /// spermatogenesis /// biosynthetic process /// glycolipid biosynthetic process /// myelination	galactosylceramide sulfotransferase activity /// galactosylceramide sulfotransferase activity /// transferase activity	Golgi membrane /// Golgi membrane /// extracellular space /// Golgi apparatus /// membrane /// integral to membrane /// integral to membrane
1453056_at	solute carrier family 16 (monocarboxylic acid transporters), member 13	Slc16a13	4.14	transport /// tetracycline transport /// response to antibiotic	transporter activity /// symporter activity /// tetracycline:hydrogen antiporter activity	plasma membrane /// membrane /// integral to membrane
1437580_s_at	NIMA (never in mitosis gene a)-related expressed kinase 2	Nek2	4.08	mitotic sister chromatid segregation /// protein amino acid phosphorylation /// cell cycle /// mitosis /// meiosis /// cell division	nucleotide binding /// magnesium ion binding /// protein kinase activity /// protein serine/threonine kinase activity /// protein binding /// ATP binding /// kinase activity /// transferase activity /// metal ion binding	chromosome, pericentric region /// condensed nuclear chromosome /// spindle pole /// nucleus /// midbody

1438676_at	macrophage activation 2 like /// macrophage activation 2 like LOC626578 /// similar to macrophage activation 2 like	LOC626578 /// LOC673101 /// Mpa2l	4.07	immune response	GTPase activity /// GTP binding	---
1447927_at	macrophage activation 2 like	Mpa2l	4.00	immune response	GTPase activity /// GTP binding	---
1455439_a_at	lectin, galactose binding, soluble 1	Lgals1	4.00	heterophilic cell adhesion /// positive regulation of I-kappaB kinase/NF-kappaB cascade /// myoblast differentiation	signal transducer activity /// protein binding /// sugar binding /// galactose binding	extracellular space /// intracellular
1434465_x_at	very low density lipoprotein receptor	Vldlr	3.99	lipid metabolic process /// transport /// lipid transport /// endocytosis /// steroid metabolic process /// cholesterol metabolic process /// positive regulation of protein kinase activity	receptor activity /// lipid transporter activity /// calcium ion binding /// protein binding	extracellular space /// extracellular space /// membrane fraction /// coated pit /// membrane /// integral to membrane /// integral to membrane
1448986_x_at	deoxyribonuclease II alpha	Dnase2a	3.94	DNA metabolic process /// DNA catabolic process /// apoptosis /// multicellular organismal development /// erythrocyte differentiation	nuclease activity /// endonuclease activity /// endodeoxyribonuclease activity /// deoxyribonuclease II activity /// deoxyribonuclease II activity /// protein binding /// hydrolase activity	extracellular space /// lysosome /// lysosome
1430700_a_at	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	Pla2g7	3.91	inflammatory response /// lipid catabolic process	catalytic activity /// 1-alkyl-2-acetylglycerophosphocholine esterase activity /// hydrolase activity	extracellular region /// extracellular space /// 2-acetyl-1-alkylglycerophosphocholine esterase complex
1447845_s_at	vanin 1	Vnn1	3.91	nitrogen compound metabolic process	hydrolase activity /// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds /// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides /// pantetheine hydrolase activity	extracellular space /// plasma membrane /// membrane /// anchored to membrane
1447774_x_at	RIKEN cDNA 5730469M10 gene	5730469M10Rik	3.86	---	---	extracellular region
1417409_at	Jun oncogene	Jun	3.81	transcription /// regulation of transcription, DNA-dependent /// regulation of transcription, DNA-dependent /// cellular process /// negative regulation of protein amino acid autophosphorylation /// leading edge cell differentiation /// response to drug /// regulation of transcription /// positive regulation of transcription from RNA polymerase II promoter /// regulation of cell cycle	DNA binding /// DNA binding /// transcription factor activity /// protein binding /// sequence-specific DNA binding /// protein dimerization activity	intracellular /// nucleus /// nucleus /// transcription factor complex
1434582_at	ELKS/RAB6-interacting/CAST family member 2	Erc2	3.78	---	protein binding	cytoplasm /// cytoskeleton /// synaptosome /// cell junction /// growth cone /// presynaptic membrane /// synapse
1439795_at	G protein-coupled receptor 64	Gpr64	3.78	signal transduction /// G-protein coupled receptor protein signaling pathway /// G-protein coupled receptor protein signaling pathway /// neuropeptide signaling pathway /// neuropeptide signaling pathway	signal transducer activity /// receptor activity /// G-protein coupled receptor activity /// G-protein coupled receptor activity	plasma membrane /// membrane /// membrane /// integral to membrane /// integral to membrane
1449773_s_at	growth arrest and DNA-damage-inducible 45 beta	Gadd45b	3.77	activation of MAPKK activity /// negative regulation of protein kinase activity /// apoptosis /// multicellular organismal development /// cell differentiation /// regulation of cell cycle	protein binding	nucleus

1419091_a_at	annexin A2	Anxa2	3.76	angiogenesis /// collagen fibril organization /// fibrinolysis	phospholipase inhibitor activity /// calcium ion binding /// protein binding /// protein binding /// calcium-dependent phospholipid binding /// phosphatidylinositol-4,5-bisphosphate binding /// cytoskeletal protein binding	stress fiber /// extracellular region /// proteinaceous extracellular matrix /// basement membrane /// membrane fraction /// cytoplasm /// early endosome /// cell junction /// sarcolemma /// melanosome /// protein complex /// perinuclear region of cytoplasm
1450971_at	growth arrest and DNA-damage-inducible 45 beta	Gadd45b	3.74	activation of MAPKK activity /// negative regulation of protein kinase activity /// apoptosis /// multicellular organismal development /// cell differentiation /// regulation of cell cycle	protein binding	nucleus
1429154_at	solute carrier family 35, member F2	Slc35f2	3.70	transport	---	membrane /// integral to membrane /// integral to membrane
1427981_a_at	cysteine sulfinic acid decarboxylase	Csad	3.68	L-cysteine catabolic process to taurine /// taurine metabolic process /// carboxylic acid metabolic process	nucleic acid binding /// catalytic activity /// sulfinoalanine decarboxylase activity /// sulfinoalanine decarboxylase activity /// lyase activity /// carboxy-lyase activity /// carboxy-lyase activity /// pyridoxal phosphate binding	---
1424167_a_at	phosphomannomutase 1	Pmm1	3.67	metabolic process /// mannose biosynthetic process	catalytic activity /// phosphomannomutase activity /// isomerase activity	cytoplasm
1419365_at	peroxisomal biogenesis factor 11a	Pex11a	3.66	peroxisome organization and biogenesis /// peroxisome organization and biogenesis /// signal transduction /// peroxisome fission	---	peroxisome /// peroxisome /// peroxisomal membrane /// integral to peroxisomal membrane /// membrane /// integral to membrane /// integral to membrane
1431278_s_at	phospholipase A2, group VI	Pla2g6	3.65	lipid metabolic process /// metabolic process /// lipid catabolic process	catalytic activity /// phospholipase A2 activity /// hydrolase activity /// nutrient reservoir activity /// calcium-independent phospholipase A2 activity	cytoplasm
1452716_at	RIKEN cDNA 5730469M10 gene	5730469M10Rik	3.61	---	---	extracellular region
1424118_a_at	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Spc25	3.58	cell cycle /// mitosis /// cell division	---	chromosome, pericentric region /// nucleus
1430307_a_at	malic enzyme, supernatant /// similar to NADP-dependent malic enzyme (NADP-ME) (Malic enzyme 1)	LOC624892 /// LOC677317 /// Mod1	3.58	malate metabolic process /// malate metabolic process /// metabolic process /// response to hormone stimulus	catalytic activity /// malic enzyme activity /// malic enzyme activity /// malate dehydrogenase (decarboxylating) activity /// malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity /// malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity /// binding /// oxidoreductase activity /// oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor /// manganese ion binding /// metal ion binding /// NAD binding	soluble fraction /// cytoplasm /// cytosol
1450884_at	CD36 antigen	Cd36	3.56	transport /// cell adhesion /// cell adhesion /// cholesterol transport /// apoptotic cell clearance	receptor activity /// protein binding /// high-density lipoprotein binding	plasma membrane /// membrane /// integral to membrane /// integral to membrane

1452864_at	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)-like	Med12l	3.56	transcription /// regulation of transcription, DNA-dependent	---	nucleus
1417008_at	carnitine acetyltransferase	Crat	3.52	lipid metabolic process /// fatty acid metabolic process /// transport	carnitine O-acetyltransferase activity /// acyltransferase activity /// transferase activity	mitochondrion /// mitochondrion /// mitochondrial inner membrane /// peroxisome /// endoplasmic reticulum /// membrane
1438659_x_at	coiled-coil-helix-coiled-coil-helix domain containing 6	Chchd6	3.52	---	---	---
1439478_at	acyl-CoA thioesterase 2	Acot2	3.51	lipid metabolic process /// acyl-CoA metabolic process	carboxylesterase activity /// palmitoyl-CoA hydrolase activity /// acyl-CoA thioesterase activity /// hydrolase activity	mitochondrion /// mitochondrion /// mitochondrion /// mitochondrial matrix
1448188_at	uncoupling protein 2 (mitochondrial, proton carrier)	Ucp2	3.49	response to superoxide /// transport /// mitochondrial transport	transporter activity /// binding	mitochondrion /// mitochondrion /// mitochondrion /// mitochondrial inner membrane /// membrane /// integral to membrane
1428083_at	RIKEN cDNA 2310043N10 gene	2310043N10Rik	3.47	---	---	---
1421425_a_at	regulator of calcineurin 2	Rcan2	3.46	calcium-mediated signaling	---	---
1451156_s_at	very low density lipoprotein receptor	Vldlr	3.40	lipid metabolic process /// transport /// lipid transport /// endocytosis /// steroid metabolic process /// cholesterol metabolic process /// positive regulation of protein kinase activity	receptor activity /// lipid transporter activity /// calcium ion binding /// protein binding	extracellular space /// extracellular space /// membrane fraction /// coated pit /// membrane /// integral to membrane /// integral to membrane
1419491_at	defensin beta 1	Defb1	3.39	defense response /// response to bacterium /// defense response to bacterium /// innate immune response	---	extracellular region /// extracellular space
1435549_at	transient receptor potential cation channel, subfamily M, member 4	Trpm4	3.32	transport /// ion transport /// cation transport /// calcium ion transport /// calcium ion transport /// immune response /// regulation of membrane potential	nucleotide binding /// ion channel activity /// calcium activated cation channel activity /// voltage-gated ion channel activity /// cation channel activity /// calcium channel activity /// calcium channel activity /// calcium ion binding /// calmodulin binding /// ATP binding	plasma membrane /// plasma membrane /// membrane /// membrane /// integral to membrane /// integral to membrane /// integral to membrane
1436890_at	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	Uap1l1	3.32	metabolic process	transferase activity /// nucleotidyltransferase activity	---
1451488_at	RIKEN cDNA 1110028A07 gene	1110028A07Rik	3.27	---	---	extracellular space /// membrane /// integral to membrane /// integral to membrane
1447186_at	solute carrier family 6, member 16 /// similar to Orphan sodium- and chloride-dependent neurotransmitter transporter NTT5 (Solute carrier family 6 member 16)	LOC672880 /// Slc6a16	3.27	---	---	---
1436314_at	SCY1-like 2 (S. cerevisiae)	Scyl2	3.21	protein amino acid phosphorylation	protein kinase activity /// binding /// ATP binding	cytoplasm /// endosome /// Golgi apparatus /// endosome membrane /// membrane /// cytoplasmic vesicle
1421422_at	RIKEN cDNA 5033411D12 gene	5033411D12Rik	3.19	metabolic process	catalytic activity /// transferase activity	---
1417336_a_at	synaptotagmin-like 4	Sytl4	3.19	intracellular protein transport /// exocytosis	protein binding /// protein binding /// phospholipid binding /// zinc ion binding /// zinc ion binding /// Rab GTPase binding /// neurexin binding /// metal ion binding	membrane /// extrinsic to plasma membrane /// secretory granule

1424245_at	carboxylesterase 2 /// similar to carboxylesterase 2	Ces2 /// LOC667754	3.19	---	catalytic activity /// carboxylesterase activity /// hydrolase activity	extracellular space
1429212_a_at	leucine rich repeat containing 51	Lrrc51	3.15	---	protein binding	---
1422906_at	ATP-binding cassette, sub-family G (WHITE), member 2	Abcg2	3.14	transport	nucleotide binding /// ATP binding /// ATPase activity /// nucleoside-triphosphatase activity	plasma membrane /// membrane /// integral to membrane /// integral to membrane
1448382_at	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	Ehhadh	3.14	lipid metabolic process /// fatty acid metabolic process /// fatty acid beta-oxidation /// fatty acid beta-oxidation /// acyl-CoA metabolic process /// metabolic process	catalytic activity /// 3-hydroxyacyl-CoA dehydrogenase activity /// 3-hydroxyacyl-CoA dehydrogenase activity /// dodecenoyl-CoA delta isomerase activity /// enoyl-CoA hydratase activity /// binding /// oxidoreductase activity /// lyase activity /// isomerase activity /// coenzyme binding	mitochondrion /// peroxisome /// peroxisome
1433924_at	paternally expressed 3	Peg3	3.13	apoptosis	nucleic acid binding zinc ion binding metal ion binding	intracellular nucleus cytoplasm
1425964_x_at	heat shock protein 1	Hspb1	3.12	response to stress	---	soluble fraction /// insoluble fraction /// nucleus /// cytoplasm /// plasma membrane /// Z disc /// contractile fiber
1427347_s_at	tubulin, beta 2a	Tubb2a	3.12	microtubule-based process /// microtubule-based movement /// protein polymerization	nucleotide binding /// GTPase activity /// structural molecule activity /// structural constituent of cytoskeleton /// protein binding /// GTP binding	cytoplasm /// microtubule /// protein complex
1455270_at	a disintegrin and metallopeptidase domain 11	Adam11	3.11	proteolysis /// integrin-mediated signaling pathway	metalloendopeptidase activity /// peptidase activity /// metallopeptidase activity /// zinc ion binding	membrane /// integral to membrane /// integral to membrane
1449079_s_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	St3gal6	3.10	protein amino acid glycosylation	sialyltransferase activity /// sialyltransferase activity /// transferase activity /// transferase activity, transferring glycosyl groups	Golgi membrane /// Golgi apparatus /// membrane /// integral to membrane /// integral to Golgi membrane
1436313_at	SCY1-like 2 (S. cerevisiae)	Scyl2	3.07	protein amino acid phosphorylation	protein kinase activity /// binding /// ATP binding	cytoplasm /// endosome /// Golgi apparatus /// endosome membrane /// membrane /// cytoplasmic vesicle
1418654_at	hydroxyacid oxidase (glycolate oxidase) 3	Hao3	3.07	fatty acid metabolic process /// metabolic process	catalytic activity /// (S)-2-hydroxy-acid oxidase activity /// (S)-2-hydroxy-acid oxidase activity /// electron carrier activity /// FMN binding /// oxidoreductase activity	peroxisome /// peroxisome
1416632_at	malic enzyme, supernatant /// similar to NADP-dependent malic enzyme (NADP-ME) (Malic enzyme 1)	LOC624892 /// LOC677317 /// Mod1	3.06	malate metabolic process /// malate metabolic process /// metabolic process /// response to hormone stimulus	catalytic activity /// malic enzyme activity /// malic enzyme activity /// malate dehydrogenase (decarboxylating) activity /// malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity /// malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity /// binding /// oxidoreductase activity /// oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor /// manganese ion binding /// metal ion binding /// NAD binding	soluble fraction /// cytoplasm /// cytosol
1422943_a_at	heat shock protein 1	Hspb1	3.04	response to stress	---	soluble fraction /// insoluble fraction /// nucleus /// cytoplasm /// plasma membrane /// Z disc /// contractile fiber

1448752_at	carbonic anhydrase 2	Car2	3.02	morphogenesis of an epithelium /// one-carbon compound metabolic process /// carbon dioxide transport /// secretion	carbonate dehydratase activity /// zinc ion binding /// lyase activity /// metal ion binding	cytoplasm
1419492_s_at	defensin beta 1	Defb1	2.99	defense response /// response to bacterium /// defense response to bacterium /// innate immune response	---	extracellular region /// extracellular space
1422262_a_at	LIM homeobox protein 6	Lhx6	2.93	transcription /// regulation of transcription, DNA-dependent /// regulation of transcription	DNA binding /// transcription factor activity /// zinc ion binding /// sequence-specific DNA binding /// metal ion binding	nucleus /// transcription factor complex
1459741_x_at	uncoupling protein 2 (mitochondrial, proton carrier)	Ucp2	2.92	response to superoxide /// transport /// mitochondrial transport	transporter activity /// binding	mitochondrion /// mitochondrion /// mitochondrion /// mitochondrial inner membrane /// membrane /// integral to membrane
1435963_at	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	Sema5b	2.88	multicellular organismal development /// nervous system development /// cell differentiation	receptor activity	extracellular space /// membrane /// integral to membrane /// integral to membrane
1459740_s_at	uncoupling protein 2 (mitochondrial, proton carrier)	Ucp2	2.85	response to superoxide /// transport /// mitochondrial transport	transporter activity /// binding	mitochondrion /// mitochondrion /// mitochondrion /// mitochondrial inner membrane /// membrane /// integral to membrane
1449619_s_at	Rho GTPase activating protein 9	Arhgap9	2.84	signal transduction	GTPase activator activity	intracellular
1428803_at	acyl-CoA thioesterase 6	Acot6	2.83	lipid metabolic process /// lipid metabolic process	carboxylesterase activity /// palmitoyl-CoA hydrolase activity /// hydrolase activity	peroxisome /// peroxisome /// cytosol
1446423_at	RAD51-like 1 (S. cerevisiae)	Rad51l1	2.83	DNA metabolic process DNA repair DNA recombination response to DNA damage stimulus	nucleotide binding DNA binding ATP binding DNA-dependent ATPase activity nucleoside-triphosphatase activity	nucleus
1424715_at	retinol saturase (all trans retinol 13,14 reductase)	Retsat	2.82	carotenoid biosynthetic process /// retinol metabolic process /// oxidation reduction	electron carrier activity /// oxidoreductase activity /// oxidoreductase activity /// oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen /// FAD binding /// all-trans-retinol 13,14-reductase activity /// all-trans-retinol 13,14-reductase activity	nuclear outer membrane /// endoplasmic reticulum /// endoplasmic reticulum membrane /// endoplasmic reticulum membrane /// membrane /// nuclear membrane
1423447_at	caseinolytic peptidase X (E.coli)	Clpx	2.81	protein transport	nucleotide binding /// protein binding /// ATP binding /// peptidase activity /// zinc ion binding /// ATPase activity /// nucleoside-triphosphatase activity /// metal ion binding	mitochondrion /// mitochondrion /// mitochondrial inner membrane
1418486_at	vanin 1	Vnn1	2.80	nitrogen compound metabolic process	hydrolase activity /// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds /// hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides /// pantetheine hydrolase activity	extracellular space /// plasma membrane /// membrane /// anchored to membrane
1427943_at	acylphosphatase 2, muscle type	Acyp2	2.79	---	acylphosphatase activity /// hydrolase activity	---

1449442_at	peroxisomal biogenesis factor 11a	Pex11a	2.76	peroxisome organization and biogenesis /// peroxisome organization and biogenesis /// signal transduction /// peroxisome fission	---	peroxisome /// peroxisome /// peroxisomal membrane /// integral to peroxisomal membrane /// membrane /// integral to membrane /// integral to membrane
1422147_a_at	phospholipase A2, group VI	Pla2g6	2.76	lipid metabolic process /// metabolic process /// lipid catabolic process	catalytic activity /// phospholipase A2 activity /// hydrolase activity /// nutrient reservoir activity /// calcium-independent phospholipase A2 activity	cytoplasm
1438740_at	N-myristoyltransferase 2	Nmt2	2.75	N-terminal protein myristoylation /// N-terminal protein myristoylation /// N-terminal peptidyl-glycine N-myristoylation	glycylpeptide N-tetradecanoyltransferase activity /// glycylpeptide N-tetradecanoyltransferase activity /// glycylpeptide N-tetradecanoyltransferase activity /// acyltransferase activity /// transferase activity	cytoplasm /// cytoplasm
1437724_x_at	phosphatidylinositol membrane-associated 1	Pitpnm1	2.74	transport /// protein transport	calcium ion binding /// phospholipid binding /// metal ion binding	intracellular /// cytoplasm /// endoplasmic reticulum /// endoplasmic reticulum membrane /// Golgi apparatus /// lipid particle /// monolayer-surrounded lipid storage body /// membrane
1434089_at	synaptopodin	Synpo	2.72	cortical cytoskeleton organization and biogenesis	actin binding /// actin binding	cytoplasm /// cytoskeleton /// tight junction /// actin cytoskeleton /// membrane /// cell junction /// axon /// dendrite /// cell projection /// dendritic spine /// perikaryon /// synapse /// postsynaptic membrane
1423669_at	procollagen, type I, alpha 1	Col1a1	2.69	phosphate transport /// cell adhesion	structural molecule activity /// extracellular matrix structural constituent /// extracellular matrix structural constituent conferring tensile strength	extracellular region /// proteinaceous extracellular matrix /// collagen /// extracellular space /// cytoplasm
1415965_at	stearoyl-Coenzyme A desaturase 1	Scd1	2.67	lipid metabolic process /// fatty acid biosynthetic process /// fatty acid biosynthetic process /// lipid biosynthetic process	stearoyl-CoA 9-desaturase activity /// iron ion binding /// oxidoreductase activity /// oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	endoplasmic reticulum /// endoplasmic reticulum membrane /// membrane /// integral to membrane
1433691_at	protein phosphatase 1, regulatory (inhibitor) subunit 3C	Ppp1r3c	2.67	carbohydrate metabolic process /// glycogen metabolic process /// glycogen metabolic process /// glycogen biosynthetic process /// protein targeting	protein binding /// protein phosphatase type 1 regulator activity	---
1427604_a_at	ATPase, class II, type 9A	Atp9a	2.66	transport /// cation transport /// metabolic process /// phospholipid transport	nucleotide binding /// magnesium ion binding /// catalytic activity /// phospholipid-translocating ATPase activity /// ATP binding /// ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism /// hydrolase activity /// metal ion binding	membrane /// integral to membrane /// integral to membrane

1416101_a_at	histone cluster 1, H1c	Hist1h1c	2.66	neurotransmitter uptake /// regulation of the force of heart contraction /// neurological control of breathing /// nucleosome assembly /// nucleosome assembly /// transport /// ion transport /// cation transport /// potassium ion transport /// regulation of muscle contraction /// regulation of smooth muscle contraction /// regulation of striated muscle contraction /// metabolic process /// regulation of blood pressure /// adult locomotory behavior /// visual learning /// monovalent inorganic cation transport /// nucleosome positioning /// regulation of vasoconstriction /// sperm motility /// regulation of cellular pH /// locomotion /// negative regulation of heart contraction /// negative regulation of striated muscle contraction /// chromosome organization and biogenesis /// reduction of cytosolic calcium ion concentration	nucleotide binding /// DNA binding /// DNA binding /// DNA binding /// catalytic activity /// protein binding /// ATP binding /// monovalent inorganic cation transmembrane transporter activity /// ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism /// hydrolase activity /// hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances /// potassium ion binding	nucleosome /// nucleosome /// nucleus /// nucleus /// chromosome /// chromosome /// microsome /// membrane /// integral to membrane /// sarcolemma
1416066_at	CD9 antigen	Cd9	2.64	cell motility /// cell adhesion /// cell adhesion /// single fertilization /// fusion of sperm to egg plasma membrane /// negative regulation of cell proliferation /// paranodal junction assembly	protein binding /// protein binding /// protein binding	plasma membrane /// membrane /// integral to membrane
1450243_a_at	regulator of calcineurin 2	Rcan2	2.63	calcium-mediated signaling	---	---
1419103_a_at	abhydrolase domain containing 6	Abhd6	2.63	---	catalytic activity /// hydrolase activity	membrane /// integral to membrane /// integral to membrane
1423017_a_at	interleukin 1 receptor antagonist	Il1rn	2.63	lipid metabolic process /// inflammatory response /// immune response /// cell surface receptor linked signal transduction /// insulin secretion	receptor activity /// interleukin-1 receptor binding /// interleukin-1 receptor antagonist activity	extracellular region /// cytoplasm /// integral to plasma membrane
1448694_at	Jun oncogene	Jun	2.62	transcription /// regulation of transcription, DNA-dependent /// regulation of transcription, DNA-dependent /// cellular process /// negative regulation of protein amino acid autophosphorylation /// leading edge cell differentiation /// response to drug /// regulation of transcription /// positive regulation of transcription from RNA polymerase II promoter /// regulation of cell cycle	DNA binding /// DNA binding /// transcription factor activity /// protein binding /// sequence-specific DNA binding /// protein dimerization activity	intracellular /// nucleus /// nucleus /// transcription factor complex
1416591_at	RAB34, member of RAS oncogene family	Rab34	2.60	transport /// endocytosis /// small GTPase mediated signal transduction /// protein transport	nucleotide binding /// GTPase activity /// GTP binding /// guanyl nucleotide binding	ruffle /// cytoplasm /// early endosome /// Golgi apparatus
1430388_a_at	sulfatase 2	Sulf2	2.60	sulfur metabolic process /// metabolic process /// metabolic process	catalytic activity /// arylsulfatase activity /// calcium ion binding /// N-acetylglucosamine-6-sulfatase activity /// sulfuric ester hydrolase activity /// sulfuric ester hydrolase activity /// hydrolase activity /// phosphoric monoester hydrolase activity /// metal ion binding	extracellular space /// endoplasmic reticulum /// Golgi apparatus /// cell surface /// cell surface

1416896_at	ribosomal protein S6 kinase polypeptide 1	Rps6ka1	2.59	protein amino acid phosphorylation /// protein kinase cascade /// ribosome biogenesis and assembly	nucleotide binding /// magnesium ion binding /// protein kinase activity /// protein serine/threonine kinase activity /// ATP binding /// kinase activity /// transferase activity	spindle /// ribosome
1455178_at	small G protein signaling modulator	Sgsm2	2.58	regulation of Rab GTPase activity	Rab GTPase activator activity	intracellular
1434897_a_at	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4	Slc25a4	2.57	transport /// mitochondrial transport /// ADP transport /// ATP transport /// glutamate uptake during transmission of nerve impulse	transporter activity /// ATP:ADP antiporter activity /// binding	mitochondrion /// mitochondrial inner membrane /// mitochondrial inner membrane /// membrane /// integral to membrane
1428176_at	endothelial differentiation, sphingolipid G-protein-coupled receptor, 5	Edg5	2.57	signal transduction /// G-protein coupled receptor protein signaling pathway /// behavior	rhodopsin-like receptor activity /// lysosphingolipid and lysophosphatidic acid receptor activity /// signal transducer activity /// receptor activity /// G-protein coupled receptor activity	plasma membrane /// integral to plasma membrane /// membrane /// integral to membrane
1422445_at	integrin alpha 6	Itga6	2.56	cell adhesion /// cell-matrix adhesion /// integrin-mediated signaling pathway /// positive regulation of cell-cell adhesion /// cell adhesion mediated by integrin /// odontogenesis of dentine containing teeth /// filopodium formation /// leukocyte migration /// leukocyte migration	receptor activity /// integrin binding /// calcium ion binding /// protein binding	plasma membrane /// integrin complex /// integrin complex /// external side of plasma membrane /// cell surface /// membrane /// integral to membrane /// integral to membrane /// basolateral plasma membrane
1422146_at	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	Sema5b	2.55	multicellular organismal development /// nervous system development /// cell differentiation	receptor activity	extracellular space /// membrane /// integral to membrane /// integral to membrane
1420722_at	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	Elovl3	2.53	fatty acid biosynthetic process /// lipid biosynthetic process	---	endoplasmic reticulum /// endoplasmic reticulum membrane /// membrane /// integral to membrane /// integral to membrane
1423266_at	RIKEN cDNA 2810405K02 gene	2810405K02Rik	2.52	---	---	---

1460251_at	Fas (TNF receptor superfamily member)	Fas	2.50	renal system process /// apoptosis /// apoptosis /// apoptosis /// apoptosis /// activated T cell apoptosis /// activated T cell apoptosis /// inflammatory cell apoptosis /// inflammatory cell apoptosis /// transformed cell apoptosis /// immune response /// signal transduction /// induction of apoptosis by extracellular signals /// induction of apoptosis via death domain receptors /// induction of apoptosis via death domain receptors /// induction of apoptosis via death domain receptors /// response to toxin /// gene expression /// T cell homeostasis /// positive regulation of apoptosis /// negative regulation of apoptosis /// negative thymic T cell selection /// regulation of lymphocyte differentiation /// regulation of myeloid cell differentiation /// spleen development /// negative regulation of B cell activation /// protein homooligomerization /// response to glucocorticoid stimulus /// response to protein stimulus	receptor activity /// transmembrane receptor activity /// protein binding /// protein binding	extracellular region /// external side of plasma membrane /// cell surface /// membrane /// integral to membrane /// integral to membrane
1441919_x_at	carnitine acetyltransferase	Crat	2.50	lipid metabolic process /// fatty acid metabolic process /// transport	carnitine O-acetyltransferase activity /// acyltransferase activity /// transferase activity	mitochondrion /// mitochondrion /// mitochondrial inner membrane /// peroxisome /// endoplasmic reticulum /// membrane
1417177_at	galactokinase 1	Galk1	2.49	carbohydrate metabolic process /// galactose metabolic process /// galactose metabolic process /// galactose metabolic process /// metabolic process /// phosphorylation /// galactitol metabolic process /// carbohydrate phosphorylation	nucleotide binding /// galactokinase activity /// galactokinase activity /// protein binding /// ATP binding /// kinase activity /// transferase activity /// phosphotransferase activity, alcohol group as acceptor	cytoplasm
1417883_at	glutathione S-transferase, theta 2	Gstt2	2.47	glutathione metabolic process /// glutathione metabolic process	glutathione transferase activity /// glutathione transferase activity /// transferase activity	nucleus /// cytoplasm
1434170_at	WD repeat domain 40B	Wdr40b	2.47	---	---	---
1437590_at	RIKEN cDNA 4833409A17 gene	4833409A17Rik	2.47	carotenoid biosynthetic process	electron carrier activity /// oxidoreductase activity /// oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen /// FAD binding	---
1434109_at	SH3 domain binding glutamic acid-rich protein like 2	Sh3bgrl2	2.46	---	---	nucleus

1436994_a_at	histone cluster 1, H1c	Hist1h1c	2.45	neurotransmitter uptake /// regulation of the force of heart contraction /// neurological control of breathing /// nucleosome assembly /// nucleosome assembly /// transport /// ion transport /// cation transport /// potassium ion transport /// regulation of muscle contraction /// regulation of smooth muscle contraction /// regulation of striated muscle contraction /// metabolic process /// regulation of blood pressure /// adult locomotory behavior /// visual learning /// monovalent inorganic cation transport /// nucleosome positioning /// regulation of vasoconstriction /// sperm motility /// regulation of cellular pH /// locomotion /// negative regulation of heart contraction /// negative regulation of striated muscle contraction /// chromosome organization and biogenesis /// reduction of cytosolic calcium ion concentration	nucleotide binding /// DNA binding /// DNA binding /// DNA binding /// catalytic activity /// protein binding /// ATP binding /// monovalent inorganic cation transmembrane transporter activity /// ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism /// hydrolase activity /// hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances /// potassium ion binding	nucleosome /// nucleosome /// nucleus /// nucleus /// chromosome /// chromosome /// microsome /// membrane /// integral to membrane /// sarcolemma
1435084_at	RIKEN cDNA C730049O14 gene	C730049O14Rik	2.45	---	---	---
1434642_at	hydroxysteroid (17-beta) dehydrogenase 11	Hsd17b11	2.44	steroid biosynthetic process /// androgen catabolic process /// metabolic process /// metabolic process /// lipid biosynthetic process	catalytic activity /// estradiol 17-beta-dehydrogenase activity /// binding /// steroid dehydrogenase activity /// oxidoreductase activity	extracellular region /// cytoplasm
1435902_at	nudix (nucleoside diphosphate linked moiety X)-type motif 18	Nudt18	2.42	---	magnesium ion binding /// hydrolase activity /// manganese ion binding /// metal ion binding	---
1415776_at	aldehyde dehydrogenase family 3, subfamily A2	Aldh3a2	2.42	aldehyde metabolic process /// metabolic process	aldehyde dehydrogenase (NAD) activity /// aldehyde dehydrogenase [NAD(P)+] activity /// oxidoreductase activity	mitochondrial inner membrane /// endoplasmic reticulum /// endoplasmic reticulum membrane /// membrane /// integral to membrane /// integral to membrane
1420603_s_at	retinoic acid early transcript 1, alpha /// retinoic acid early transcript beta /// retinoic acid early transcript gamma /// retinoic acid early transcript delta /// retinoic acid early transcript 1E	Raet1a /// Raet1b /// Raet1c /// Raet1d /// Raet1e	2.42	positive regulation of immune response to tumor cell /// immune response /// antigen processing and presentation /// positive regulation of interferon-gamma production /// positive regulation of natural killer cell activation /// susceptibility to natural killer cell mediated cytotoxicity /// positive regulation of macrophage activation /// positive regulation of nitric oxide biosynthetic process	natural killer cell lectin-like receptor binding	plasma membrane /// membrane /// anchored to membrane /// anchored to external side of plasma membrane /// anchored to plasma membrane /// anchored to plasma membrane
1424869_at	dehydrogenase/reductase (SDR family) member 7B	Dhrs7b	2.41	metabolic process	catalytic activity /// binding /// oxidoreductase activity	peroxisome /// peroxisomal membrane /// membrane /// integral to membrane
1426146_a_at	choline phosphotransferase 1	Chpt1	2.41	phosphatidylcholine biosynthetic process /// platelet activating factor biosynthetic process /// apoptosis /// phospholipid biosynthetic process /// regulation of apoptosis /// negative regulation of apoptosis /// negative regulation of caspase activity	magnesium ion binding /// diacylglycerol cholinephosphotransferase activity /// diacylglycerol cholinephosphotransferase activity /// transferase activity /// phosphotransferase activity, for other substituted phosphate groups /// manganese ion binding /// metal ion binding	Golgi membrane /// cytoplasm /// Golgi apparatus /// membrane /// integral to membrane /// integral to membrane
1429399_at	ring finger protein 125	Rnf125	2.41	ubiquitin cycle /// immune response	protein binding /// zinc ion binding /// ligase activity /// metal ion binding	intracellular

1424133_at	transmembrane protein 98	Tmem98	2.41	---	---	extracellular space /// endoplasmic reticulum /// membrane /// integral to membrane
1419104_at	abhydrolase domain containing 6	Abhd6	2.39	---	catalytic activity /// hydrolase activity	membrane /// integral to membrane /// integral to membrane
1422438_at	epoxide hydrolase 1, microsomal	Ephx1	2.39	xenobiotic metabolic process /// response to toxin /// aromatic compound catabolic process	catalytic activity /// epoxide hydrolase activity /// hydrolase activity /// cis-stilbene-oxide hydrolase activity	extracellular space /// endoplasmic reticulum /// microsome /// membrane /// integral to membrane
1451798_at	interleukin 1 receptor antagonist	Il1rn	2.39	lipid metabolic process /// inflammatory response /// immune response /// cell surface receptor linked signal transduction /// insulin secretion	receptor activity /// interleukin-1 receptor binding /// interleukin-1 receptor antagonist activity	extracellular region /// cytoplasm /// integral to plasma membrane
1433898_at	Expressed sequence AV025504	AV025504	2.39	---	---	---
1415932_x_at	ATPase, class II, type 9A	Atp9a	2.39	transport /// cation transport /// metabolic process /// phospholipid transport	nucleotide binding /// magnesium ion binding /// catalytic activity /// phospholipid-translocating ATPase activity /// ATP binding /// ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism /// hydrolase activity /// metal ion binding	membrane /// integral to membrane /// integral to membrane
1418321_at	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)	Dci	2.38	lipid metabolic process /// fatty acid metabolic process /// fatty acid beta-oxidation /// metabolic process	catalytic activity /// dodecenoyl-CoA delta-isomerase activity /// dodecenoyl-CoA delta-isomerase activity /// isomerase activity	mitochondrion /// mitochondrion /// mitochondrion /// mitochondrial inner membrane /// mitochondrial matrix
1455267_at	estrogen-related receptor gamma	Esrrg	2.36	transcription /// regulation of transcription, DNA-dependent /// regulation of transcription, DNA-dependent /// regulation of transcription, DNA-dependent /// multicellular organismal development /// positive regulation of transcription, DNA-dependent	DNA binding /// DNA binding /// DNA binding /// transcription factor activity /// transcription factor activity /// steroid hormone receptor activity /// receptor activity /// receptor activity /// ligand-dependent nuclear receptor activity /// ligand-dependent nuclear receptor activity /// steroid binding /// calmodulin binding /// zinc ion binding /// tRNA-pseudouridine synthase activity /// transcription activator activity /// sequence-specific DNA binding /// metal ion binding /// AF-2 domain binding	nucleus /// nucleus
1453836_a_at	monoglyceride lipase	Mgll	2.36	---	catalytic activity /// carboxylesterase activity /// hydrolase activity /// acylglycerol lipase activity	---
1418181_at	protein tyrosine phosphatase 4a3	Ptp4a3	2.36	protein amino acid dephosphorylation /// dephosphorylation	phosphoprotein phosphatase activity /// protein tyrosine phosphatase activity /// hydrolase activity /// phosphoric monoester hydrolase activity	endosome /// early endosome /// plasma membrane /// membrane
1420657_at	uncoupling protein 3 (mitochondrial, proton carrier)	Ucp3	2.35	response to superoxide /// response to hypoxia /// fatty acid metabolic process /// transport /// mitochondrial transport	transporter activity /// binding /// oxidative phosphorylation uncoupler activity	mitochondrion /// mitochondrion /// mitochondrion /// mitochondrial inner membrane /// membrane /// integral to membrane
1418210_at	profilin 2	Pfn2	2.35	cytoskeleton organization and biogenesis /// actin cytoskeleton organization and biogenesis	actin binding /// protein binding /// protein binding	cytoplasm /// cytoskeleton /// actin cytoskeleton
1428559_at	3-ketodihydrosphingosine reductase	Kdsr	2.34	metabolic process /// cellular process	catalytic activity /// binding /// oxidoreductase activity /// 3-dehydrosphinganine reductase activity	extracellular space /// endoplasmic reticulum /// endoplasmic reticulum membrane /// membrane /// integral to membrane

1415802_at	solute carrier family 16 (monocarboxylic acid transporters), member 1	Slc16a1	2.34	transport /// organic anion transport	transporter activity /// protein binding /// symporter activity /// secondary active monocarboxylate transmembrane transporter activity /// transmembrane transporter activity	plasma membrane /// integral to plasma membrane /// membrane /// integral to membrane /// integral to membrane
1425948_a_at	solute carrier family 25, member 30	Slc25a30	2.34	transport /// mitochondrial transport	transporter activity /// binding	mitochondrion /// mitochondrial inner membrane /// membrane /// integral to membrane
1426785_s_at	monoglyceride lipase	Mgll	2.33	---	catalytic activity /// carboxylesterase activity /// hydrolase activity /// acylglycerol lipase activity	---
1429947_a_at	Z-DNA binding protein 1	Zbp1	2.33	---	DNA binding /// left-handed Z-DNA binding /// RNA binding /// double-stranded RNA adenosine deaminase activity	---
1416488_at	cyclin G2	Ccng2	2.33	cell cycle /// mitosis /// cell division /// regulation of cell cycle	cyclin-dependent protein kinase regulator activity	nucleus /// cytoplasm
1418438_at	fatty acid binding protein 2,	Fabp2	2.32	transport	transporter activity /// binding /// lipid binding	cytoplasm
1427126_at	heat shock protein 1B	Hspa1b	2.32	telomere maintenance /// DNA repair /// anti-apoptosis /// response to stress /// response to heat /// negative regulation of caspase activity	nucleotide binding /// protein binding /// ATP binding	---
1418073_at	acyl-CoA thioesterase 9	Acot9	2.31	---	carboxylesterase activity /// palmitoyl-CoA hydrolase activity /// acyl-CoA thioesterase activity /// hydrolase activity	mitochondrion /// mitochondrion
1450391_a_at	monoglyceride lipase	Mgll	2.31	---	catalytic activity /// carboxylesterase activity /// hydrolase activity /// acylglycerol lipase activity	---
1417879_at	neuron derived neurotrophic factor	Nenf	2.31	positive regulation of MAPKKK cascade	growth factor activity /// heme binding /// transition metal ion binding	extracellular region /// extracellular space /// extracellular space
1425409_at	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)	Chrna2	2.30	transport /// transport /// ion transport /// ion transport /// signal transduction /// synaptic transmission /// synaptic transmission, cholinergic	receptor activity /// nicotinic acetylcholine-activated cation-selective channel activity /// GABA-A receptor activity /// ion channel activity /// ion channel activity /// extracellular ligand-gated ion channel activity /// extracellular ligand-gated ion channel activity /// acetylcholine receptor activity /// neurotransmitter receptor activity	extracellular space /// membrane fraction /// plasma membrane /// nicotinic acetylcholine-gated receptor-channel complex /// membrane /// membrane /// integral to membrane /// integral to membrane /// cell junction /// synapse /// postsynaptic membrane
1455025_at	progestin and adipoQ receptor family member IX	Paqr9	2.27	---	receptor activity	membrane /// integral to membrane
1437496_at	RIKEN cDNA 9330129D05 gene	9330129D05Rik	2.26	metabolic process /// oxidation reduction	acyl-CoA dehydrogenase activity /// acyl-CoA dehydrogenase activity /// electron carrier activity /// oxidoreductase activity /// oxidoreductase activity, acting on the CH-CH group of donors /// FAD binding	extracellular space
1435446_a_at	choline phosphotransferase 1	Chpt1	2.25	phosphatidylcholine biosynthetic process /// platelet activating factor biosynthetic process /// apoptosis /// phospholipid biosynthetic process /// regulation of apoptosis /// negative regulation of apoptosis /// negative regulation of caspase activity	magnesium ion binding /// diacylglycerol cholinephosphotransferase activity /// diacylglycerol cholinephosphotransferase activity /// transferase activity /// phosphotransferase activity, for other substituted phosphate groups /// manganese ion binding /// metal ion binding	Golgi membrane /// cytoplasm /// Golgi apparatus /// membrane /// integral to membrane /// integral to membrane

1428372_at	suppression of tumorigenicity 5	St5	2.25	---	hydrogen ion transmembrane transporter activity	proton-transporting two-sector ATPase complex
1450061_at	ectodermal-neural cortex 1	Enc1	2.24	ubiquitin cycle /// multicellular organismal development	actin binding /// protein binding	cytoplasm /// cytoskeleton
1459686_at	---	---	2.24	---	---	---
1457213_a_at	diacylglycerol kinase, eta	Dgkh	2.24	activation of protein kinase C activity /// intracellular signaling cascade /// diacylglycerol metabolic process	diacylglycerol kinase activity /// diacylglycerol kinase activity /// protein binding /// zinc ion binding /// protein homodimerization activity	cytoplasm /// endosome
1432562_at	RIKEN cDNA 1110006G14 gene	1110006G14Rik	2.23	---	---	---
1434671_at	RIKEN cDNA B230337E12 gene	B230337E12Rik	2.21	---	---	---
1424904_at	RIKEN cDNA 1300010F03 gene	1300010F03Rik	2.19	---	nucleotide binding /// nucleotide binding /// ATP binding /// hydrolase activity /// ATPase activity /// nucleoside-triphosphatase activity	extracellular space /// mitochondrion
1434599_a_at	tight junction protein 2	Tjp2	2.19	---	protein binding /// protein binding	nucleus /// plasma membrane /// plasma membrane /// tight junction /// tight junction /// membrane /// cell junction
1425120_x_at	RIKEN cDNA 1810023F06 gene	1810023F06Rik	2.19	---	---	extracellular space /// integral to membrane
1436038_a_at	phosphatidylinositol glycan anchor biosynthesis, class P	Pigp	2.18	GPI anchor biosynthetic process	transferase activity /// transferase activity, transferring glycosyl groups /// phosphatidylinositol N-acetylglucosaminyltransferase activity	membrane /// integral to membrane /// integral to membrane
1429570_at	mixed lineage kinase domain-like	Mlkl	2.15	protein amino acid phosphorylation	protein kinase activity /// ATP binding	---
1450018_s_at	solute carrier family 25, member 30	Slc25a30	2.15	transport /// mitochondrial transport	transporter activity /// binding	mitochondrion /// mitochondrial inner membrane /// membrane /// integral to membrane
1426857_a_at	hydroxysteroid dehydrogenase like 2	Hsdl2	2.15	metabolic process	catalytic activity /// binding /// sterol carrier activity /// sterol carrier activity /// oxidoreductase activity	mitochondrion
1437073_x_at	expressed sequence AV025504	AV025504	2.15	---	---	---
1425109_at	solute carrier family 44, member 3	Slc44a3	2.14	---	---	membrane /// integral to membrane
1448361_at	tetratricopeptide repeat domain 3	Ttc3	2.14	---	binding /// protein binding /// zinc ion binding /// metal ion binding	---
1455936_a_at	RNA binding protein gene with multiple splicing	Rbpms	2.13	---	nucleotide binding /// nucleic acid binding /// RNA binding	---
1451421_a_at	rogdi homolog (Drosophila)	Rogdi	2.12	positive regulation of cell proliferation /// hemopoiesis	---	---
1420541_at	retinol dehydrogenase 16	Rdh16	2.12	metabolic process /// metabolic process	catalytic activity /// retinol dehydrogenase activity /// binding /// oxidoreductase activity	extracellular space /// microsome
1419435_at	aldehyde oxidase 1	Aox1	2.12	oxidation reduction	catalytic activity /// aldehyde oxidase activity /// aldehyde oxidase activity /// iron ion binding /// electron carrier activity /// electron carrier activity /// oxidoreductase activity /// molybdenum ion binding /// metal ion binding /// FAD binding /// NAD binding /// iron-sulfur cluster binding /// 2 iron, 2 sulfur cluster binding	cytoplasm
1445597_s_at	HRAS like suppressor 3	Hrasls3	2.11	cell cycle /// negative regulation of cell cycle	---	membrane /// integral to membrane

1447602_x_at	sulfatase 2	Sulf2	2.11	sulfur metabolic process /// metabolic process /// metabolic process	catalytic activity /// arylsulfatase activity /// calcium ion binding /// N-acetylglucosamine-6-sulfatase activity /// sulfuric ester hydrolase activity /// sulfuric ester hydrolase activity /// hydrolase activity /// phosphoric monoester hydrolase activity /// metal ion binding	extracellular space /// endoplasmic reticulum /// Golgi apparatus /// cell surface /// cell surface
1421848_at	solute carrier family 22 (organic cation transporter), member 5	Slc22a5	2.11	transport /// ion transport /// sodium ion transport /// mitochondrion organization and biogenesis /// adult heart development /// locomotory behavior /// carnitine metabolic process /// quaternary ammonium group transport /// carnitine transport /// carnitine transport /// reproductive structure development	nucleotide binding /// transporter activity /// ATP binding /// ion transmembrane transporter activity /// carnitine transporter activity /// carnitine transporter activity /// symporter activity /// quaternary ammonium group transmembrane transporter activity /// transmembrane transporter activity /// sodium ion binding	membrane /// membrane /// integral to membrane /// integral to membrane /// apical plasma membrane
1429859_a_at	ADP-ribosylation factor-like 2 binding protein	Arl2bp	2.11	---	small GTPase regulator activity /// GTPase activator activity /// protein binding	soluble fraction /// cytoplasm /// mitochondrion /// mitochondrial intermembrane space /// centrosome
1460196_at	carbonyl reductase 1	Cbr1	2.11	metabolic process	catalytic activity /// carbonyl reductase (NADPH) activity /// carbonyl reductase (NADPH) activity /// binding /// oxidoreductase activity	cytoplasm
1426452_a_at	RAB30, member RAS oncogene family	Rab30	2.10	small GTPase mediated signal transduction /// protein transport	nucleotide binding /// GTP binding	plasma membrane /// membrane
1448700_at	G0/G1 switch gene 2	G0s2	2.10	cell cycle	---	integral to membrane
1450264_a_at	choline kinase alpha	Chka	2.09	phosphatidylcholine biosynthetic process	choline kinase activity /// choline kinase activity /// cholinesterase activity /// ethanolamine kinase activity /// kinase activity /// transferase activity /// protein homodimerization activity	cytoplasm
1421878_at	mitogen activated protein kinase 9	Mapk9	2.09	protein amino acid phosphorylation /// JNK cascade	nucleotide binding /// protein kinase activity /// protein serine/threonine kinase activity /// JUN kinase activity /// MAP kinase activity /// protein binding /// ATP binding /// kinase activity /// transferase activity	nucleus
1438001_x_at	receptor accessory protein 5	Reep5	2.09	phosphoenolpyruvate-dependent sugar phosphotransferase system	receptor activity /// sugar:hydrogen symporter activity /// protein binding	membrane /// integral to membrane
1420836_at	solute carrier family 25, member 30	Slc25a30	2.08	transport /// mitochondrial transport	transporter activity /// binding	mitochondrion /// mitochondrial inner membrane /// membrane /// integral to membrane

1422076_at	acyl-CoA thioesterase 4	Acot4	2.08	very-long-chain fatty acid metabolic process /// long-chain fatty acid metabolic process /// succinyl-CoA metabolic process /// succinyl-CoA metabolic process /// lipid metabolic process /// acyl-CoA metabolic process /// acyl-CoA metabolic process /// saturated monocarboxylic acid metabolic process /// unsaturated monocarboxylic acid metabolic process /// dicarboxylic acid metabolic process /// dicarboxylic acid metabolic process /// short-chain fatty acid metabolic process /// short-chain fatty acid metabolic process	carboxylesterase activity /// palmitoyl-CoA hydrolase activity /// acyl-CoA thioesterase activity /// acyl-CoA thioesterase activity /// hydrolase activity	peroxisome /// peroxisome /// peroxisome
1456769_at	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Dusp3	2.08	protein amino acid dephosphorylation /// dephosphorylation	phosphoprotein phosphatase activity /// protein tyrosine phosphatase activity /// protein tyrosine/serine/threonine phosphatase activity /// protein tyrosine/serine/threonine phosphatase activity /// hydrolase activity /// phosphoric monoester hydrolase activity	---
1427005_at	polo-like kinase 2 (Drosophila)	Plk2	2.07	mitotic cell cycle /// protein amino acid phosphorylation /// positive regulation of I-kappaB kinase/NF-kappaB cascade	nucleotide binding /// protein kinase activity /// protein serine/threonine kinase activity /// signal transducer activity /// protein binding /// ATP binding /// kinase activity /// transferase activity	---
1421116_a_at	reticulon 4	Rtn4	2.06	angiogenesis /// nervous system development /// negative regulation of anti-apoptosis /// regulation of cell migration /// negative regulation of axon extension	protein binding	nuclear envelope /// endoplasmic reticulum /// endoplasmic reticulum /// endoplasmic reticulum membrane /// membrane /// integral to membrane /// integral to endoplasmic reticulum membrane /// cell projection /// cell soma
1416590_a_at	RAB34, member of RAS oncogene family	Rab34	2.06	transport /// endocytosis /// small GTPase mediated signal transduction /// protein transport	nucleotide binding /// GTPase activity /// GTP binding /// guanyl nucleotide binding	ruffle /// cytoplasm /// early endosome /// Golgi apparatus
1435394_s_at	ras homolog gene family, member C	Rhoc	2.06	small GTPase mediated signal transduction /// negative regulation of neuron differentiation	nucleotide binding /// protein binding /// GTP binding	intracellular /// nucleus /// plasma membrane /// plasma membrane /// membrane
1417449_at	acyl-CoA thioesterase 8	Acot8	2.06	acyl-CoA metabolic process /// acyl-CoA metabolic process /// peroxisome organization and biogenesis	carboxylesterase activity /// palmitoyl-CoA hydrolase activity /// acyl-CoA thioesterase activity /// acyl-CoA thioesterase activity /// hydrolase activity /// choloyl-CoA hydrolase activity	mitochondrion /// peroxisome /// peroxisome
1436186_at	E2F transcription factor 8	E2f8	2.06	transcription /// regulation of transcription, DNA-dependent /// cell cycle /// cell proliferation	DNA binding /// DNA binding /// transcription factor activity /// identical protein binding /// protein homodimerization activity	nucleus /// nucleus /// transcription factor complex
1455520_at	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	Ppp2r5c	2.06	signal transduction	binding /// protein binding /// protein phosphatase type 2A regulator activity	protein phosphatase type 2A complex /// nucleus /// cytoplasm

1437455_a_at	B-cell translocation gene 1, anti-proliferative	Btg1	2.04	protein amino acid methylation /// spermatid development /// negative regulation of cell proliferation /// negative regulation of cell proliferation /// negative regulation of cell proliferation /// negative regulation of cell proliferation /// negative regulation of cell proliferation /// cellular process /// cell migration /// negative regulation of cell growth /// regulation of apoptosis /// regulation of apoptosis /// regulation of apoptosis /// positive regulation of catalytic activity /// regulation of transcription /// positive regulation of endothelial cell differentiation /// positive regulation of endothelial cell differentiation /// positive regulation of endothelial cell differentiation /// positive regulation of myoblast differentiation /// positive regulation of angiogenesis /// positive regulation of angiogenesis /// positive regulation of angiogenesis	transcription cofactor activity /// protein binding /// protein binding /// enzyme binding /// enzyme binding /// kinase binding	nucleus /// nucleus /// nucleus /// cytoplasm /// cytoplasm /// cytoplasm
1450395_at	solute carrier family 22 (organic cation transporter), member 5	Slc22a5	2.04	transport /// ion transport /// sodium ion transport /// mitochondrion organization and biogenesis /// adult heart development /// locomotory behavior /// carnitine metabolic process /// quaternary ammonium group transport /// carnitine transport /// carnitine transport /// reproductive structure development	nucleotide binding /// transporter activity /// ATP binding /// ion transmembrane transporter activity /// carnitine transporter activity /// carnitine transporter activity /// symporter activity /// quaternary ammonium group transmembrane transporter activity /// transmembrane transporter activity /// sodium ion binding	membrane /// membrane /// integral to membrane /// integral to membrane /// apical plasma membrane
1424790_at	solute carrier family 25, member 42	Slc25a42	2.04	transport	binding	mitochondrion /// mitochondrial inner membrane /// mitochondrial inner membrane /// membrane /// integral to membrane
1451290_at	microtubule-associated protein 1 light chain 3 alpha	Map1lc3a	2.04	autophagic vacuole formation /// autophagic vacuole formation /// ubiquitin cycle /// autophagy	protein binding /// microtubule binding	cytoplasm /// cytoplasm /// autophagic vacuole /// autophagic vacuole /// autophagic vacuole /// microtubule /// microtubule /// endomembrane system /// membrane /// organelle membrane /// organelle membrane /// cytoplasmic vesicle
1417268_at	CD14 antigen	Cd14	2.04	response to molecule of bacterial origin /// inflammatory response /// immune response	protein binding	extracellular space /// plasma membrane /// membrane /// anchored to membrane /// membrane raft /// lipopolysaccharide receptor complex
1429786_a_at	ZW10 interactor	Zwint	2.04	cell cycle /// mitosis /// cell division	---	chromosome, pericentric region /// nucleus
1424835_at	glutathione S-transferase, mu 4	Gstm4	2.03	metabolic process /// nitrobenzene metabolic process /// xenobiotic catabolic process	glutathione transferase activity /// glutathione transferase activity /// glutathione transferase activity /// transferase activity /// transferase activity	cytosol

1416308_at	UDP-glucose dehydrogenase	Ugdh	2.03	gastrulation with mouth forming second /// metabolic process /// oxidation reduction	catalytic activity /// UDP-glucose 6-dehydrogenase activity /// binding /// electron donor activity /// oxidoreductase activity /// oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor /// NAD binding	---
1456642_x_at	S100 calcium binding protein A10 (calpactin)	S100a10	2.02	---	calcium ion binding	---
1424282_at	PET112-like (yeast)	Pet112l	2.02	translation /// translation	translation factor activity, nucleic acid binding /// transferase activity /// ligase activity /// ligase activity /// carbon-nitrogen ligase activity, with glutamine as amido-N-donor /// glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity	mitochondrion /// mitochondrion /// mitochondrion
1423308_at	trans-golgi network protein	Tgoln1	2.02	---	protein binding	Golgi apparatus /// Golgi apparatus /// trans-Golgi network /// plasma membrane /// membrane /// integral to membrane /// trans-Golgi network transport vesicle
1447919_x_at	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	Ndufab1	2.01	fatty acid biosynthetic process /// transport /// lipid biosynthetic process /// oxidation reduction	acyl carrier activity /// phosphopantetheine binding /// cofactor binding	mitochondrion /// mitochondrion /// mitochondrial respiratory chain
1419382_a_at	dehydrogenase/reductase (SDR family) member 4	Dhrs4	2.01	metabolic process /// metabolic process /// retinal metabolic process	retinal dehydrogenase activity /// catalytic activity /// carbonyl reductase (NADPH) activity /// carbonyl reductase (NADPH) activity /// binding /// oxidoreductase activity /// oxidoreductase activity	mitochondrion /// peroxisome /// peroxisome
1418652_at	chemokine (C-X-C motif) ligand 9	Cxcl9	2.00	inflammatory response /// immune response	cytokine activity /// chemokine activity	extracellular region /// extracellular space /// extracellular space
1448927_at	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	Kcnn2	-2.01	transport /// ion transport /// potassium ion transport	ion channel activity /// calmodulin binding /// calcium-activated potassium channel activity /// small conductance calcium-activated potassium channel activity /// small conductance calcium-activated potassium channel activity	membrane /// integral to membrane /// integral to membrane
1442331_at	Aminolevulinic acid synthase 1	Alas1	-2.02	heme biosynthetic process metabolic process biosynthetic process tetrapyrrole biosynthetic process	catalytic activity 5-aminolevulinate synthase activity acyltransferase activity transferase activity transferase activity, transferring nitrogenous groups pyridoxal phosphate binding	mitochondrion mitochondrial matrix
1449945_at	peroxisome proliferative activated receptor, gamma, coactivator 1 beta	Ppargc1b	-2.03	transcription /// regulation of transcription, DNA-dependent /// estrogen receptor signaling pathway /// positive regulation of transcription from RNA polymerase II promoter	nucleotide binding /// nucleic acid binding /// RNA binding /// protein binding /// ligand-dependent nuclear receptor transcription coactivator activity /// AF-2 domain binding	nucleus /// nucleus

1452050_at	calcium/calmodulin-dependent protein kinase ID	Camk1d	-2.03	protein amino acid phosphorylation /// regulation of apoptosis	nucleotide binding /// catalytic activity /// protein kinase activity /// protein serine/threonine kinase activity /// calmodulin-dependent protein kinase activity /// calmodulin-dependent protein kinase activity /// calcium ion binding /// calmodulin binding /// ATP binding /// kinase activity /// transferase activity	nucleus /// cytoplasm /// cytoplasm
1423844_s_at	cystathionine beta-synthase	Cbs	-2.03	cysteine biosynthetic process from serine /// metabolic process /// amino acid biosynthetic process /// cysteine biosynthetic process via cystathionine /// cysteine biosynthetic process /// cysteine biosynthetic process /// regulation of JNK activity	catalytic activity /// cystathionine beta-synthase activity /// iron ion binding /// lyase activity /// pyridoxal phosphate binding /// metal ion binding	nucleus /// cytoplasm
1432543_a_at	Kruppel-like factor 13	Klf13	-2.04	transcription /// regulation of transcription, DNA-dependent /// transcription from RNA polymerase II promoter /// positive regulation of transcription from RNA polymerase II promoter	nucleic acid binding /// DNA binding /// DNA binding /// DNA binding /// RNA polymerase II transcription factor activity /// RNA polymerase II transcription factor activity /// zinc ion binding /// metal ion binding	intracellular /// nucleus
1419173_at	aminoacylase 1	Acy1	-2.05	proteolysis /// proteolysis /// amino acid metabolic process /// amino acid metabolic process	aminoacylase activity /// metallopeptidase activity /// metallopeptidase activity /// zinc ion binding /// hydrolase activity /// hydrolase activity /// metal ion binding /// protein dimerization activity	soluble fraction /// cytoplasm /// cytosol
1448989_a_at	myosin IB	Myo1b	-2.05	cytoskeleton organization and biogenesis	nucleotide binding /// motor activity /// actin binding /// calmodulin binding /// ATP binding	cytoskeleton /// myosin complex
1418050_at	glycosylphosphatidylinositol specific phospholipase D1	Gpld1	-2.05	GPI anchor release	glycosylphosphatidylinositol phospholipase D activity /// phospholipase D activity /// lipid transporter activity /// hydrolase activity	extracellular region /// proteinaceous extracellular matrix /// extracellular space
1458829_at	Fructose bisphosphatase 1	Fbp1	-2.08	carbohydrate metabolic process gluconeogenesis	catalytic activity zinc ion binding hydrolase activity fructose 1,6-bisphosphate 1-phosphatase activity phosphoric ester hydrolase activity identical protein binding	---
1420973_at	AT rich interactive domain 5B (Mrf1 like)	Arid5b	-2.08	transcription /// regulation of transcription, DNA-dependent	DNA binding /// DNA binding	intracellular /// intracellular /// nucleus
1427631_x_at	major urinary protein 3	Mup3	-2.08	transport	transporter activity /// binding /// pheromone binding	extracellular region
1424826_s_at	metastasis suppressor 1	Mtss1	-2.08	actin filament organization /// signal transduction /// nervous system development /// nervous system development /// muscle development /// actin filament polymerization /// filopodium formation	actin binding /// actin binding /// actin monomer binding /// receptor binding	cytoplasm /// cytoplasm /// cytoskeleton /// actin cytoskeleton
1418013_at	camello-like 1	Cml1	-2.08	gastrulation with mouth forming second /// negative regulation of cell adhesion /// multicellular organismal development /// gastrulation /// metabolic process	N-acetyltransferase activity /// N-acetyltransferase activity /// acyltransferase activity /// transferase activity	extracellular space /// mitochondrial inner membrane /// endoplasmic reticulum /// Golgi apparatus /// membrane /// integral to membrane /// integral to membrane

1443180_at	ERGIC and golgi 2	Ergic2	-2.11	transport ER to Golgi vesicle-mediated transport vesicle-mediated transport	protein binding	endoplasmic reticulum endoplasmic reticulum membrane ER-Golgi intermediate compartment Golgi apparatus membrane integral to membrane ER-Golgi intermediate compartment membrane
1443603_at	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	Pcmtd1	-2.12	protein modification process	protein-L-isoaspartate (D-aspartate) O-methyltransferase activity methyltransferase activity transferase activity	cytoplasm
1421214_at	cytidine monophospho-N-acetylneuraminic acid hydroxylase	Cmah	-2.13	transport /// CMP-N-acetylneuraminate metabolic process /// oxidation reduction	iron ion binding /// ubiquinol-cytochrome-c reductase activity /// electron carrier activity /// oxidoreductase activity /// CMP-N-acetylneuraminate monooxygenase activity /// CMP-N-acetylneuraminate monooxygenase activity /// metal ion binding /// iron-sulfur cluster binding /// 2 iron, 2 sulfur cluster binding	cytoplasm /// cytoplasm /// endoplasmic reticulum /// membrane
1450717_at	angiogenin, ribonuclease A family, member 1	Ang1	-2.13	angiogenesis /// angiogenesis /// angiogenesis /// response to hypoxia /// positive regulation of endothelial cell proliferation /// diacylglycerol biosynthetic process /// activation of phospholipase C activity /// multicellular organismal development /// central nervous system development /// rRNA transcription /// negative regulation of translation /// actin filament polymerization /// cell differentiation /// activation of phospholipase A2 /// negative regulation of smooth muscle cell proliferation /// positive regulation of protein secretion	nucleic acid binding /// RNA binding /// actin binding /// nuclease activity /// endonuclease activity /// pancreatic ribonuclease activity /// ribonuclease activity /// ribonuclease activity /// receptor binding /// copper ion binding /// protein binding /// heparin binding /// hydrolase activity	extracellular region /// basal lamina /// extracellular space /// extracellular space /// nucleus /// nucleolus /// growth cone /// angiogenin-PRI complex /// angiogenin-PRI complex /// cell soma
1435255_at	plexin B1	Plxnb1	-2.14	signal transduction /// multicellular organismal development /// positive regulation of axonogenesis	receptor activity /// protein binding	intracellular /// membrane /// integral to membrane
1424273_at	cytochrome P450, family 2, subfamily c, polypeptide 70	Cyp2c70	-2.16	oxidation reduction	monooxygenase activity /// iron ion binding /// electron carrier activity /// oxidoreductase activity /// oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen /// heme binding /// metal ion binding /// unspecific monooxygenase activity	endoplasmic reticulum /// endoplasmic reticulum membrane /// microsome /// membrane

1418833_at	alanine-glyoxylate aminotransferase	Agxt	-2.18	protein targeting to peroxisome /// metabolic process /// response to hormone stimulus /// glycine biosynthetic process, by transamination of glyoxylate /// pyruvate biosynthetic process /// glyoxylate metabolic process /// glyoxylate metabolic process /// oxalic acid secretion /// response to glucocorticoid stimulus /// response to cAMP	catalytic activity /// serine-pyruvate transaminase activity /// protein binding /// alanine-glyoxylate transaminase activity /// alanine-glyoxylate transaminase activity /// transaminase activity /// amino acid binding /// transferase activity /// pyridoxal phosphate binding /// protein homodimerization activity	mitochondrion /// mitochondrion /// mitochondrial matrix /// peroxisome /// peroxisome
1437040_at	ethanolamine kinase 2	Etnk2	-2.18	hydrogen transport /// ATP synthesis coupled proton transport	hydrogen-exporting ATPase activity, phosphorylative mechanism /// kinase activity /// hydrogen ion transporting ATP synthase activity, rotational mechanism /// hydrogen ion transporting ATPase activity, rotational mechanism	membrane /// membrane /// proton-transporting two-sector ATPase complex
1418653_at	cytochrome P450, family 2. subfamily c, polypeptide 37 /// cytochrome P450, family 2, subfamily c, polypeptide 50 /// cytochrome P450, family 2, subfamily c, polypeptide 54 /// similar to cytochrome P450	Cyp2c37 /// Cyp2c50 /// Cyp2c54 /// LOC639023	-2.18	oxidation reduction	monooxygenase activity /// iron ion binding /// electron carrier activity /// oxidoreductase activity /// heme binding /// metal ion binding /// unspecific monooxygenase activity	endoplasmic reticulum /// endoplasmic reticulum membrane /// microsome /// membrane
1434036_at	metastasis suppressor 1	Mtss1	-2.19	actin filament organization /// signal transduction /// nervous system development /// nervous system development /// muscle development /// actin filament polymerization /// filopodium formation	actin binding /// actin binding /// actin monomer binding /// receptor binding	cytoplasm /// cytoplasm /// cytoskeleton /// actin cytoskeleton
1449038_at	hydroxysteroid 11-beta dehydrogenase 1	Hsd11b1	-2.20	lipid metabolic process /// metabolic process /// steroid metabolic process /// lung development	catalytic activity /// 11-beta-hydroxysteroid dehydrogenase activity /// 11-beta-hydroxysteroid dehydrogenase activity /// binding /// oxidoreductase activity	endoplasmic reticulum /// endoplasmic reticulum membrane /// microsome /// membrane /// integral to membrane
1424401_at	aldehyde dehydrogenase 1 family, member L1	Aldh1l1	-2.22	one-carbon compound metabolic process /// metabolic process /// biosynthetic process /// 10-formyltetrahydrofolate catabolic process	catalytic activity /// methyltransferase activity /// formyltetrahydrofolate dehydrogenase activity /// oxidoreductase activity /// transferase activity /// hydroxymethyl-, formyl- and related transferase activity /// phosphopantetheine binding /// cofactor binding	cytoplasm
1417930_at	Ngfi-A binding protein 2	Nab2	-2.22	endochondral ossification /// transcription /// regulation of transcription, DNA-dependent /// Schwann cell differentiation /// negative regulation of transcription /// myelination /// regulation of transcription /// regulation of epidermis development	transcription repressor activity /// transcription regulator activity	nucleus
1441768_at	RIKEN cDNA 9430051O21 gene	9430051O21Rik	-2.23	---	---	---
1435666_at	microtubule associated serine/threonine kinase 3	Mast3	-2.23	protein amino acid phosphorylation	nucleotide binding /// magnesium ion binding /// protein kinase activity /// protein serine/threonine kinase activity /// protein binding /// ATP binding /// kinase activity /// transferase activity	---

1435254_at	plexin B1	Plxnb1	-2.26	signal transduction /// multicellular organismal development /// positive regulation of axonogenesis	receptor activity /// protein binding	intracellular /// membrane /// integral to membrane
1417785_at	phospholipase A1 member A	Pla1a	-2.33	lipid metabolic process /// lipid metabolic process /// lipid catabolic process	catalytic activity /// catalytic activity /// hydrolase activity	extracellular region /// extracellular space
1425623_a_at	cystathionine beta-synthase	Cbs	-2.33	cysteine biosynthetic process from serine /// metabolic process /// amino acid biosynthetic process /// cysteine biosynthetic process via cystathionine /// cysteine biosynthetic process /// cysteine biosynthetic process /// regulation of JNK activity	catalytic activity /// cystathionine beta-synthase activity /// iron ion binding /// lyase activity /// pyridoxal phosphate binding /// metal ion binding	nucleus /// cytoplasm
1440178_x_at	zeta-chain (TCR) associated protein kinase	Zap70	-2.34	protein amino acid phosphorylation /// protein amino acid phosphorylation /// signal transduction /// intracellular signaling cascade /// peptidyl-tyrosine phosphorylation /// peptidyl-tyrosine phosphorylation /// beta selection /// positive thymic T cell selection /// positive thymic T cell selection /// negative thymic T cell selection /// thymic T cell selection /// positive regulation of T cell differentiation /// positive regulation of T cell differentiation /// positive regulation of alpha-beta T cell differentiation /// positive regulation of alpha-beta T cell differentiation /// positive regulation of alpha-beta T cell proliferation /// protein amino acid autophosphorylation /// protein amino acid autophosphorylation /// positive regulation of calcium-mediated signaling /// T cell receptor signaling pathway	nucleotide binding /// phosphotyrosine binding /// protein kinase activity /// protein kinase activity /// protein tyrosine kinase activity /// protein tyrosine kinase activity /// protein tyrosine kinase activity /// non-membrane spanning protein tyrosine kinase activity /// protein binding /// protein binding /// ATP binding /// ATP binding /// kinase activity /// transferase activity	cytoplasm /// cytosol /// T cell receptor complex
1424934_at	UDP glucuronosyltransferase 2 family, polypeptide B1	Ugt2b1	-2.35	metabolic process /// metabolic process	glucuronosyltransferase activity /// glucuronosyltransferase activity /// transferase activity /// transferase activity /// transferase activity, transferring glycosyl groups /// transferase activity, transferring glycosyl groups /// transferase activity, transferring hexosyl groups /// transferase activity, transferring hexosyl groups	microsome /// integral to membrane
1423186_at	T-cell lymphoma invasion and metastasis 2	Tiam2	-2.37	transport /// signal transduction /// intracellular signaling cascade /// regulation of Rho protein signal transduction	receptor signaling protein activity /// guanyl-nucleotide exchange factor activity /// guanyl-nucleotide exchange factor activity /// Rho guanyl-nucleotide exchange factor activity /// GTPase activator activity /// transporter activity /// protein binding /// protein binding	intracellular /// membrane fraction /// cytoplasm /// cytoplasm /// membrane /// cell projection
1447458_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	St3gal4	-2.37	protein amino acid glycosylation	sialyltransferase activity transferase activity transferase activity, transferring glycosyl groups	Golgi apparatus membrane integral to membrane integral to Golgi membrane
1417629_at	proline dehydrogenase	Prodh	-2.40	glutamate biosynthetic process /// proline metabolic process /// proline catabolic process	proline dehydrogenase activity /// proline dehydrogenase activity /// oxidoreductase activity	mitochondrion /// mitochondrial inner membrane /// mitochondrial matrix

1426389_at	calcium/calmodulin-dependent protein kinase ID	Camk1d	-2.47	protein amino acid phosphorylation /// regulation of apoptosis	nucleotide binding /// catalytic activity /// protein kinase activity /// protein serine/threonine kinase activity /// calmodulin-dependent protein kinase activity /// calmodulin-dependent protein kinase activity /// calcium ion binding /// calmodulin binding /// ATP binding /// kinase activity /// transferase activity	nucleus /// cytoplasm /// cytoplasm
1418808_at	retinol dehydrogenase 5	Rdh5	-2.51	metabolic process /// metabolic process	catalytic activity /// retinol dehydrogenase activity /// retinol dehydrogenase activity /// binding /// oxidoreductase activity	integral to membrane
1451788_at	coagulation factor XI	F11	-2.57	proteolysis /// blood coagulation /// regulation of blood coagulation	coagulation factor XIa activity /// catalytic activity /// serine-type endopeptidase activity /// heparin binding /// peptidase activity /// hydrolase activity	extracellular region
1450970_at	glutamate oxaloacetate transaminase 1, soluble	Got1	-2.57	oxaloacetate metabolic process /// glycerol biosynthetic process /// amino acid metabolic process /// aspartate biosynthetic process /// biosynthetic process /// glutamate catabolic process to aspartate /// glutamate catabolic process to 2-oxoglutarate /// fatty acid homeostasis	catalytic activity /// aspartate transaminase activity /// aspartate transaminase activity /// phosphatidylserine decarboxylase activity /// transaminase activity /// transferase activity /// transferase activity, transferring nitrogenous groups /// pyridoxal phosphate binding	cytoplasm /// cytosol
1435245_at	glutaminase 2 (liver, mitochondrial)	Gls2	-2.59	glutamine metabolic process	glutaminase activity /// glutaminase activity /// protein binding /// protein binding /// hydrolase activity /// hydrolase activity	mitochondrion
1422701_at	zeta-chain (TCR) associated protein kinase	Zap70	-2.61	protein amino acid phosphorylation /// protein amino acid phosphorylation /// signal transduction /// intracellular signaling cascade /// peptidyl-tyrosine phosphorylation /// peptidyl-tyrosine phosphorylation /// beta selection /// positive thymic T cell selection /// positive thymic T cell selection /// negative thymic T cell selection /// thymic T cell selection /// positive regulation of T cell differentiation /// positive regulation of T cell differentiation /// positive regulation of alpha-beta T cell differentiation /// positive regulation of alpha-beta T cell differentiation /// positive regulation of alpha-beta T cell proliferation /// protein amino acid autophosphorylation /// protein amino acid autophosphorylation /// positive regulation of calcium-mediated signaling /// T cell receptor signaling pathway	nucleotide binding /// phosphotyrosine binding /// protein kinase activity /// protein kinase activity /// protein tyrosine kinase activity /// protein tyrosine kinase activity /// protein tyrosine kinase activity /// non-membrane spanning protein tyrosine kinase activity /// protein binding /// protein binding /// ATP binding /// ATP binding /// kinase activity /// transferase activity	cytoplasm /// cytosol /// T cell receptor complex
1459361_at	---	---	-2.70	---	---	---
1454880_s_at	Bcl2 modifying factor	Bmf	-2.72	apoptosis /// apoptosis /// regulation of apoptosis	protein binding	cytoplasm /// actin cytoskeleton /// myosin complex /// myosin complex
1446284_at	metastasis suppressor 1	Mtss1	-2.73	actin filament organization /// signal transduction /// nervous system development /// nervous system development /// muscle development /// actin filament polymerization /// filopodium formation	actin binding /// actin binding /// actin monomer binding /// receptor binding	cytoplasm /// cytoplasm /// cytoskeleton /// actin cytoskeleton

1424367_a_at	homer homolog 2 (Drosophila)	Homer2	-2.74	metabotropic glutamate receptor signaling pathway	actin binding /// protein binding /// GKAP/Homer scaffold activity	cytoplasm /// cytoplasm /// membrane /// cell junction /// synapse /// postsynaptic membrane
1439293_at	cDNA sequence BC031353	BC031353	-2.75	---	---	---
1458832_at	---	---	-2.81	---	---	---
1417017_at	cytochrome P450, family 17, subfamily a, polypeptide 1	Cyp17a1	-3.57	C21-steroid hormone biosynthetic process /// glucocorticoid biosynthetic process /// response to toxin /// oxidation reduction	monooxygenase activity /// steroid 17-alpha-monooxygenase activity /// steroid 17-alpha-monooxygenase activity /// steroid 17-alpha-monooxygenase activity /// iron ion binding /// electron carrier activity /// oxidoreductase activity /// lyase activity /// heme binding /// metal ion binding	mitochondrion /// endoplasmic reticulum /// membrane /// axon /// cell soma
1451681_at	cDNA sequence BC089597	BC089597	-3.65	metabolic process	catalytic activity /// binding /// oxidoreductase activity	---
1427472_a_at	complement component 8, beta subunit	C8b	-3.80	immune response /// complement activation /// complement activation, alternative pathway /// complement activation, alternative pathway /// complement activation, classical pathway /// complement activation, classical pathway /// cytolysis /// cytolysis /// innate immune response	---	extracellular region /// membrane attack complex /// membrane attack complex
1458701_at	preimplantation protein 4	Prei4	-4.18	carbohydrate metabolic process /// glycerol metabolic process	catalytic activity /// glycerophosphodiester phosphodiesterase activity /// hydrolase activity /// carbohydrate binding	---

1422815_at	complement component 9	C9	-4.19	induction of apoptosis /// caspase activation /// immune response /// complement activation /// complement activation, alternative pathway /// complement activation, classical pathway /// blood coagulation /// cytolysis /// innate immune response	---	extracellular region /// membrane attack complex /// extracellular space /// membrane /// integral to membrane
1452416_at	interleukin 6 receptor, alpha	Il6ra	-4.28	cell surface receptor linked signal transduction	receptor activity /// hematopoietin/interferon-class (D200-domain) cytokine receptor activity /// interleukin receptor activity	integral to plasma membrane /// membrane /// integral to membrane /// integral to membrane
1425751_at	cDNA sequence BC014805	BC014805	-4.48	transport	transporter activity	integral to membrane
1419857_at	Transcribed locus	---	-4.52	---	---	---
1425752_at	cDNA sequence BC014805	BC014805	-4.86	transport	transporter activity	integral to membrane
1455457_at	cytochrome P450, family 2, subfamily c, polypeptide 54	Cyp2c54	-5.63	oxidation reduction	monooxygenase activity /// iron ion binding /// electron carrier activity /// oxidoreductase activity /// heme binding /// metal ion binding /// unspecific monooxygenase activity	endoplasmic reticulum /// endoplasmic reticulum membrane /// microsome /// membrane
1455383_at	hypothetical protein C730043O17	C730043O17	-5.73	---	---	---
1428739_at	RIKEN cDNA 2310040A07 gene	2310040A07Rik	-5.76	---	---	membrane /// integral to membrane
1419559_at	cytochrome P450, family 4, subfamily f, polypeptide 14	Cyp4f14	-6.07	oxidation reduction	monooxygenase activity /// iron ion binding /// electron carrier activity /// oxidoreductase activity /// heme binding /// metal ion binding /// leukotriene-B4 20-monooxygenase activity	extracellular space /// endoplasmic reticulum /// endoplasmic reticulum /// endoplasmic reticulum membrane /// microsome /// microsome /// membrane /// membrane
1420405_at	solute carrier organic anion transporter family, member 1a4	Slco1a4	-6.09	transport /// ion transport /// anion transport	transporter activity /// organic anion transmembrane transporter activity	membrane fraction /// membrane /// integral to membrane
1451460_a_at	solute carrier family 22 (organic anion transporter), member 7	Slc22a7	-7.06	transport /// transport /// ion transport /// ion transport /// organic anion transport	transporter activity /// transporter activity /// organic anion transmembrane transporter activity /// organic anion transmembrane transporter activity /// ion transmembrane transporter activity /// ion transmembrane transporter activity	integral to plasma membrane /// membrane /// membrane /// integral to membrane /// integral to membrane /// basolateral plasma membrane
1436504_x_at	apolipoprotein A-IV	Apoa4	-7.13	innate immune response in mucosa /// transport /// lipid transport /// regulation of cholesterol absorption /// lipoprotein metabolic process	lipid transporter activity /// lipid binding	extracellular region /// extracellular space /// extracellular space /// chylomicron
1452893_s_at	RIKEN cDNA 1110065P19 gene /// RIKEN cDNA 2310040A07 gene	1110065P19Rik /// 2310040A07Rik	-7.56	---	---	membrane /// integral to membrane

1417761_at	apolipoprotein A-IV	Apoa4	-12.36	innate immune response in mucosa /// transport /// lipid transport /// regulation of cholesterol absorption /// lipoprotein metabolic process	lipid transporter activity /// lipid binding	extracellular region /// extracellular space /// extracellular space /// chylomicron
1435196_at	neurotrophic tyrosine kinase, receptor, type 2	Ntrk2	-15.19	vasculogenesis /// protein amino acid phosphorylation /// transmembrane receptor protein tyrosine kinase signaling pathway /// multicellular organismal development /// nervous system development /// feeding behavior /// glutamate secretion /// regulation of metabolic process /// cell differentiation /// mechanoreceptor differentiation /// retinal rod cell development	nucleotide binding /// protein kinase activity /// protein tyrosine kinase activity /// transmembrane receptor protein tyrosine kinase activity /// receptor activity /// protein binding /// ATP binding /// kinase activity /// transferase activity	cytosol /// plasma membrane /// membrane /// integral to membrane /// terminal button
1432517_a_at	nicotinamide N-methyltransferase	Nnmt	-26.83	---	nicotinamide N-methyltransferase activity /// methyltransferase activity /// transferase activity	cytoplasm