Supplementary Table 5: Significantly changed genes, as identified by SAM (≥2 fold and 0% FDR), with expression patterns highly similar to *Arid5b* (CC≥0.9400). The Gene Ontology (GO) biological process, molecular function and cellular localization is provided for each of these genes.

CC to Arid5b	Affy ID	Gene Name	Symbol	GO Biological Process	GO Molecular Function	GO Cellular Component
0.9899	1455383_at	hypothetical protein C730043O17	C730043O17	---	---	---
0.9882	1436504_x_at	apolipoprotein A-IV	Apoa4	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
0.9860	1451788_at	coagulation factor XI	F11	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
0.9825	1434036_at	metastasis suppressor 1	Mtss1	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
0.9799	1442331_at	---	---	---	---	---
0.9771	1449945_at	peroxisome proliferative activated receptor, gamma, coactivator 1 beta	Ppargc1b	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
0.9768	1424934_at	UDP glucuronosyltransferase 2 family, polypeptide B1	Ugt2b1	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
0.9730	1417761_at	apolipoprotein A-IV	Apoa4	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
0.9710	1419559_at	cytochrome P450, family 4, subfamily f, polypeptide 14	Cyp4f14	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
0.9679	1421214_at	cytidine monophospho-N-acetylneuraminic acid hydroxylase	Cmah	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
0.9640	1449038_at	hydroxysteroid 11-beta dehydrogenase 1	Hsd11b1	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
0.9635	1452893_s_at	RIKEN cDNA 1110065P19 gene /// RIKEN cDNA 2310040A07 gene	1110065P19Rik /// 2310040A07Rik	---	---	membrane /// integral to membrane

0.9614	1422701_at	zeta-chain (TCR) associated protein kinase	Zap70	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
0.9590	1443180_at	---	---	---	---	---
0.9565	1424367_a_at	homer homolog 2 (Drosophila)	Homer2	metabotropic glutamate receptor signaling pathway	actin binding /// protein binding /// GKAP/Homer scaffold activity	cytoplasm /// cytoplasm /// membrane /// cell junction /// synapse /// postsynaptic membrane
0.9559	1432543_a_at	Kruppel-like factor 13	Klf13	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
0.9552	1418808_at	retinol dehydrogenase 5	Rdh5	metabolic process /// metabolic process	catalytic activity /// retinol dehydrogenase activity /// retinol dehydrogenase activity /// binding /// oxidoreductase activity	integral to membrane
0.9463	1435255_at	plexin B1	Plxnb1	signal transduction /// multicellular organismal development /// positive regulation of axonogenesis	receptor activity /// protein binding	intracellular /// membrane /// integral to membrane
0.9441	1447458_at	---	---	---	---	---
0.9426	1454880_s_at	Bcl2 modifying factor	Bmf	apoptosis /// apoptosis /// regulation of apoptosis	protein binding	cytoplasm /// actin cytoskeleton /// myosin complex /// myosin complex
-0.9401	1416023_at	stearoyl-Coenzyme A desaturase 1	Fabp3	phosphatidylcholine biosynthetic process /// transport	transporter activity /// binding /// lipid binding	cytoplasm
-0.9408	1424118_a_at	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Spc25	cell cycle /// mitosis /// cell division	---	chromosome, pericentric region /// nucleus
-0.9410	1417449_at	acyl-CoA thioesterase 8	Acot8	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
-0.9423	1417900_a_at	very low density lipoprotein receptor	Vldlr	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
-0.9428	1438310_at	---	---	---	---	---
-0.9438	1450884_at	CD36 antigen	Cd36	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
-0.9444	1451290_at	microtubule-associated protein 1 light chain 3 alpha	Map1lc3a	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
-0.9444	1434671_at	RIKEN cDNA B230337E12 gene	B230337E12Rik	---	---	---

-0.9449	1419435_at	aldehyde oxidase 1	Aox1	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
-0.9450	1418486_at	vanin 1	Vnn1	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
-0.9451	1418321_at	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)	Dci	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
-0.9453	1451421_a_at	rogdi homolog (Drosophila)	Rogdi	positive regulation of cell proliferation /// hemopoiesis	---	---
-0.9453	1438448_at	otopetrin 1	Otop1	ossification /// detection of gravity /// inner ear morphogenesis	---	extracellular region /// membrane /// membrane /// integral to membrane
-0.9455	1456642_x_at	S100 calcium binding protein A10 (calpactin)	S100a10	---	calcium ion binding	---
-0.9458	1450391_a_at	monoglyceride lipase	Mgll	---	catalytic activity /// carboxylesterase activity /// hydrolase activity /// acylglycerol lipase activity	---
-0.9459	1422997_s_at	acyl-CoA thioesterase 1 /// acyl-CoA thioesterase 2 /// similar to acyl-CoA thioesterase	Acot1 /// Acot2 /// LOC100044830	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
-0.9460	1433779_at	cancer susceptibility candidate 4	Casc4	---	---	membrane /// integral to membrane
-0.9465	1450883_a_at	CD36 antigen	Cd36	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
-0.9474	1417273_at	pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	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
-0.9496	1424167_a_at	phosphomannomutase 1	Pmm1	metabolic process /// mannose biosynthetic process	catalytic activity /// phosphomannomutase activity /// isomerase activity	cytoplasm
-0.9497	1429523_a_at	solute carrier family 39 (metal ion transporter), member 5	Slc39a5	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
-0.9498	1419365_at	peroxisomal biogenesis factor 11a	Pex11a	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
-0.9515	1416591_at	RAB34, member of RAS oncogene family	Rab34	transport /// endocytosis /// small GTPase mediated signal transduction /// protein transport	nucleotide binding /// GTPase activity /// GTP binding /// guanyl nucleotide binding	ruffle /// cytoplasm /// early endosome /// Golgi apparatus
-0.9517	1438258_at	very low density lipoprotein receptor	Vldlr	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
-0.9519	1450061_at	ectodermal-neural cortex 1	Enc1	ubiquitin cycle /// multicellular organismal development	actin binding /// protein binding	cytoplasm /// cytoskeleton
-0.9522	1428083_at	RIKEN cDNA 2310043N10 gene	2310043N10Rik	---	---	---
-0.9528	1436313_at	SCY1-like 2 (S. cerevisiae)	Scyl2	protein amino acid phosphorylation	protein kinase activity /// binding /// ATP binding	cytoplasm /// endosome /// Golgi apparatus /// endosome membrane /// membrane /// cytoplasmic vesicle
-0.9529	1417963_at	phospholipid transfer protein	Pltp	transport /// lipid transport	lipid binding	extracellular region /// extracellular space

-0.9534	1424716_at	retinol saturase (all trans retinol 13,14 reductase)	Retsat	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
-0.9537	1449065_at	acyl-CoA thioesterase 1 /// similar to acyl-CoA thioesterase	Acot1 /// LOC100044830	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
-0.9540	1434382_at	serine incorporator 2 /// hypothetical protein LOC100044221	Serinc2 /// LOC100044221	phosphatidylserine metabolic process /// positive regulation of transferase activity	---	membrane /// integral to membrane /// integral to membrane
-0.9545	1419504_at	monoacylglycerol O-acyltransferase 1 /// similar to monoacylglycerol O-acyltransferase 1	Mogat1 /// LOC100047046	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
-0.9545	1421425_a_at	regulator of calcineurin 2	Rcan2	calcium-mediated signaling	---	---
-0.9548	1436314_at	SCY1-like 2 (S. cerevisiae)	Scyl2	protein amino acid phosphorylation	protein kinase activity /// binding /// ATP binding	cytoplasm /// endosome /// Golgi apparatus /// endosome membrane /// membrane /// cytoplasmic vesicle
-0.9552	1447845_s_at	vanin 1	Vnn1	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
-0.9554	1422811_at	solute carrier family 27 (fatty acid transporter), member 1	Slc27a1	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
-0.9554	1421878_at	mitogen-activated protein kinase 9	Mapk9	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
-0.9557	1426857_a_at	hydroxysteroid dehydrogenase like 2	Hsdl2	metabolic process	catalytic activity /// binding /// sterol carrier activity /// sterol carrier activity /// oxidoreductase activity	mitochondrion
-0.9563	1423166_at	CD36 antigen	Cd36	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
-0.9565	1435549_at	transient receptor potential cation channel, subfamily M, member 4	Trpm4	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
-0.9576	1440134_at	cytochrome P450, family 4, subfamily a, polypeptide 31	Cyp4a31	oxidation reduction	monooxygenase activity /// iron ion binding /// electron carrier activity /// oxidoreductase activity /// heme binding /// metal ion binding	---
-0.9580	1451488_at	RIKEN cDNA 1110028A07 gene	1110028A07Rik	---	---	extracellular space /// membrane /// integral to membrane /// integral to membrane
-0.9594	1418989_at	cathepsin E	Ctse	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
-0.9595	1421430_at	RAD51-like 1 (S. cerevisiae)	Rad51l1	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
-0.9599	1441971_at	---	---	---	---	---
-0.9608	1442508_at	RIKEN cDNA 4933404M19 gene	4933404M19Rik	---	---	---

-0.9628	1421011_at	hydroxysteroid (17-beta) dehydrogenase 11	Hsd17b11	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
-0.9631	1417177_at	galactokinase 1	Galk1	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
-0.9634	1415776_at	aldehyde dehydrogenase family 3, subfamily A2	Aldh3a2	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
-0.9634	1426146_a_at	choline phosphotransferase 1	Chpt1	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
-0.9646	1418438_at	fatty acid binding protein 2, intestinal	Fabp2	transport	transporter activity /// binding /// lipid binding	cytoplasm
-0.9653	1421422_at	RIKEN cDNA 5033411D12 gene	5033411D12Rik	metabolic process	catalytic activity /// transferase activity	---
-0.9656	1455267_at	estrogen-related receptor gamma	Esrrg	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
-0.9683	1430780_a_at	phosphomannomutase 1	Pmm1	metabolic process /// mannose biosynthetic process	catalytic activity /// phosphomannomutase activity /// isomerase activity	cytoplasm
-0.9691	1435446_a_at	choline phosphotransferase 1	Chpt1	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
-0.9696	1429786_a_at	ZW10 interactor	Zwint	cell cycle /// mitosis /// cell division	---	chromosome, pericentric region /// nucleus
-0.9702	1415932_x_at	ATPase, class II, type 9A	Atp9a	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
-0.9723	1422906_at	ATP-binding cassette, sub-family G (WHITE), member 2	Abcg2	transport	nucleotide binding /// ATP binding /// ATPase activity /// nucleoside-triphosphatase activity	plasma membrane /// membrane /// integral to membrane /// integral to membrane
-0.9799	1456769_at	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Dusp3	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	---